>contig13255 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61350.1|) 1e-109

MTKRRERNVHSPKSIITYWKRHYFVFLTSGDLLYFRDDTLSELQGRVDVRHAPTVRVTGE

QLIEEKKKDSGMFKFGKMPTLERETCLVWIATPPSKMFVLKLEDDHDDVSSGFTNGQKGG

LSSSGIGITSRKAELTASSKKWLHLLLQGHAETKYTQLEKCIATAEYRLTTEVISAVRAG

IP

>contig13369 Frame-1F|Blast-arginine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY67416.1|) 4e-27

MYAFEQASIIIEMAALDFMHPIHSIDTSNVIELKNSAANAVIVWVEYVLDVAGQYVVTTG

PAVRYAKQLIRFLPPVPSLACVTGSKRIVKATFCFDSLEGTIDMNFETENA

>contig15437 Frame-2F

MFTIVFLLAVAFAEVASSNSNADANPGPQAKELTPVLSSPTPWAMDNMHAFRGAYDNTPA

LEEREATIPRQGIEKTAKVVEESTSFLKVLKNILLWPFQKTRSTFKLWRFKRWMKNENEF

QADVIKATDTHTRYLACNIMPERWHQLMSEEKAIPQKNPFFHRGFTPESFYVYSKKLVGI

SVPSHHTVVRKSIDKTIRKMEPDLQNVVKERLERFESMFLDEHIPVAELVPFMTPVTVKY

VVEKTAEAQNFEEVLFAHDKSKWLEHRVLKRFLEFNKLYETRVESILYPLPK

>contig17909 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY53593.1|) 0.0

MADEWPTVASEYKIIEQIGQGAFAKVWKAYCLPKKIHVAIKIMDLEKITTSFEDIRAEVQ

TMKMTNHPNVLKCYCSFVHKDQLWLVTQLMNKGSCLHVMNLLKKKGLGEGLKEEFVAVIL

HETLKGLLYFHENGQIHRDIKAGNILLDSEGHVVIADFGVSGWMMEGGDRRKNRQTFVGT

PCWMAPEVMEQVRGYDYKADIWSLGITALELAKGYAPYARFQPMKVLLLTLQEDPPSLRT

YDDDGSGHPFGRHFKDVVKLCLQKDPSKRPGTSALLKHSFFKKAGDTTYLARSLLNSLED

IGESCMTAGIADALPGAGPLYAKGTKPPPGSEAEGSKYVPGTTWVFDDEEDDSSKMSIDD

FASQFDMVTGGEEYRSK

>contig19604 Frame-1F

MMSTFGDSTQSCLSAVEEVQTLVGDFMRKALSSLKPEVLTATSCLRALVDIFDKEALYYG

RWREFRGEVKYDENELEDVEEEELADELDLFAVSEADDVFNEAFLERIRFADERTKTMDW

SIYDSFARGRKLNFMKNKAHEFREWLDLENLSRASLEFLNFVAYHNIGRVVELAIKNRTG

NELKQLETPLLKKDITSVASAFCQARPLSKRTGRRPAAKSRRVGSNAANSKKVRVESEAV

ASEPADTKKFNTRSTFTGAKKSSSKSDPAKSIEPTVPRNIRATRLKKLR

>contig20006 Frame-0F

MRLTISRNTTKFWLILFILASDLPVDEFLQVN

>contig21584-1 Frame-2R1

MRSQSVSSSSLLCPSTTNINKPVTKNVIDVDA

>contig23519 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70513.1|) 9e-18

MDLRHYDSDSHHLGVSIEIN

>contig26170 Frame-0F|Blast-inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY64189.1|) 0.0

MYVEALRECHKVCIDRAEEGRHFKASTEKKSLVLRFLPINLHVQDMWVGPTADLRSQRSR

RTSPHVHVYSTVTVGAFAAHCYKFRHKGSILSLRANLQKRTLSRVQSDVSDRPTADVVDW

INADTRATDEMRWHLTTRFDMCFSQALTTLATSFCRQLENSLQHARNQTFLHTIEAIGFL

FQVESLLSTQGKEIGMLEDFSAAVNALQHVSFVLDTSPPAHLFSTILNLHMKNTTLPSVV

SVQLSKGSNKGSYICTIGVRCSEDLRSLIPSTLRSGELIRVVPVIFTQGINEMQTLANNA

STRKTTLQDIINRNSFLVLMRYIDKYRQLATERPDAVLMPISTIGPLLKSLEERIAAASK

RQVVKSKHPKIIQESSHLCRLLGAGRVTACKSAKDRTSMSVTLEQVRLLSSNHGLPEEFV

VRTVSTMRSNGVRLENVLKNTGKRQYAFNSLQRSLLPDEYKCPEGTYGRGNVS

>contig27061 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62486.1|) 2e-10 NOT\_ORF

MTTAQSIVSTLPERTCGPTYRQQNQDRSYIRSEHPRTSAQNRLAVN\*NSFDILKNLTIRF

AVFQSFVFGLYVCLVVLCTAKQMSGHVLLAIYSRLQTRD\*NYSTLGLPFAP

>contig28363 Frame-1F

MKSVSILRTFRLWRQQNWDDYFKVYDASWVLRREILYFATKGIQLGASNAKGTLENEHTN

PNVESIFSFTQRSGIFPWQLRLGAVSQSPNVLSFDLDGTTSGQKAIFRDFEPEIFHEIRR

MAGISRESYVQSFMGSTRERFSEGKSGSFLYYTGDQTFILKTCTPAEQKYLLYILPQYMA

HLRRNPNSYLCRYVGCHELVTDHHSVLFIVLTNILNNPSVNIDELYDLKGAWVGRHRGDS

PCGTQRVCKFCGHDFVVGMSEEACSQNPNVGFGHTEFVVGKDLNWSCRRLGLSTDVADQL

GSQLYADTEFLQRINSMDYSLVIGLSRQKLFSTSSGGETVLSRSGGPLVKSNFVVGGSSS

DEVGYMESISPYGASLLGIRPARGTTLTFSADACVVNMGIIDILTPWSIKKSFERWVRVR

LQCRDAKGISCMKPIPYADRFRRNVIDTVIFGRHLGSKRRQMNKQPGESIMVDFTSMSMD

VNFSMDLANLSVDTTSNISMEI

>contig28796 Frame-1R

MASVFVRNLPFGVTQEELEQVFSDIGPVKKIDVIKDKGKRRSELLTRGFAFVKFAVESDA

AMAVEKLNKKDFQGRKMLIDYAMEKGKRRPTTTTALVEKPKQEIQEHVEHEVAESEVTVK

EVKKERKAIKEERRAAKLVAKSVAEVSIKSHENTQSEEAKSKQIEEELEIETLRVPAAEK

AEKVASQQSERNARRRQHREFLRNVERRKEEEASVSQKSVLIFGFSADVTQKHVLKRVKK

IGLVDKVSLETEAHSGKTFALVQFKTTKDAALAVTKLDHHIFKGSTLQVKSAAKIVVASD

GKPGAVNVAPKAEGLRLIVRNLAFQSTEMDLEKLFGAHGPLFEARIVRMPVDKDTELSGD

KETSTDPVLGRSRGFGFVQYRDVADARAAVEKLNGTKLNGREMIVDFALSKTKYLEQQTQ

QEGDQIVAMKVEEEEENSGDEDEDQLVMATDDEDIEADSDDLGEEHPDIDETNAPAMKED

TEMQRERTLFIRNLSFQTSEDGLRRFFEAFGAIEYARVVYDKGSGLAKGVGFVRFKSADV

ALEVLKRGKQPHPDDNQKHKKNKKKPNVFTLSALASGGNDGLTLDGRQLILSRAVSKADA

EHLADANARERRHLDKRNLYLAHEGTLNVNKITDAELELPKMDIDKRRRAIREKKLKLQN

PMYFVSPLRLSVRNLSTALDDRQLKKLAHDAADAGLRANLVNSSEIKPELTSKGTPPIKV

RMAKIVRDMESAKDGKEP

>contig29126 Frame-1R

MISLKERVTVLLELRPTYISESYSICTFFLRP

>contig30906 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY62844.1|) 2e-99

MLERGDRTEIGERGINLSGGQKARIGIARAIYRAKTFDFVVLDDPLSALDVHVANAVFTE

GLQGLASKTTRLLVLNSHYHLLPDADRILVMAAGRIVGDGSLHELRDDFPFLHCSPQIRR

SLSNEIEEPLESELQVDTELHPTRKSIKTGHKPSSGKLIVPEDRQIGSVKLQSYVDYLAC

SGWNGHTLGILMGTLFAIAQFVLFGCDWFLSHWAKGSVALSPIDSLRVYVGIVALATLLS

FGRCLFFMAICMACS

>contig31040 Frame-2R

MSADASLEELEARLVTFTEQLQNIHELLQSEPDNAEYLGIAKDLVEVIQLTKETIDLKLH

AASFPKVVQEPQEPIPLELKYEPGSMVEALQQGVWYPAYIDSVTRNGSYNLKFLGFHTTA

ELNENALRAIEIDQVVELPVKEAITEGFHCQAKYYVDTVVYPCLITKVTELGFQVLFDTY

GNSEEVPYEYLRPAASSLDAEVGTGDPQASTTNADDGASATSSTEAAPKVAPAVLFKPIK

IPENLQILPSDTEAEKERKRKRLRAIKSLNRHKNIDNERNLKQHGWKSFQFKAKKKGLKQ

GVSGVLSKRGSSMFASPDTVQGRVGVVGSGQGMTSFQDTRSKKPKPS

>contig31149 Frame-0R

MTDIDPKVPHSERSYVVRRYDQKFLVFPLLLFKTTFLVNDLGYFWIVFEFVHVQ

>contig31264 Frame-0F

MVEWDGFDTMHYGPCEVWCDDVLAFSNWNCAVTFKERPARLPYDKSKCEGASVLASHWIA

LHTTPWQIYTACAPLKGASPKKAGKPTADTPETDDTLQINTSEAYTPDAETSEADEPPED

DTPEAESPEADIPAVETQETSTDASANTDAGKIDTSTYDTGGNSAADILDAPSLAPSTNK

CSVRRRHR

>contig31358 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY60261.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60174.1|) 4e-71

MYISVPKLDAEFMQNLSIDRVANYFSIPLEMDEEISPGIYMAKPGPLKPLAAMILKILNE

CGHKLLELKLADFGAFILANVTSQNLNNQEENATASGSAVHLVDQLVTTFPGFDDHYDLN

GEKVYFLKRAQLTVGCIHRRF

>contig31408 Frame-1F|Blast-HECT ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY61282.1|) 0.0

MSTLAYVGPERRKETVFMATNDFPSKYAHFVVITASLIVPAEVEFLKLSVHRDYMLEESM

DHMYCIQPKNLRSFMRINFLDESGVDAGGVHREWFMLVNELLASPTLRLFTCTNKADQCF

HFNPQSRIEVGDDHLSYYFATGRLIGRALLEGGVWGFHLALPLLKVILGVPVTFADMEFI

DPESYRNLRWLMDNDGVDDLELDFSLNEQINESEKVVVDLIPNGRNIAVTNLNKREYLDR

RFRHLLFESVADQMYAFLKGLYEVIPREMLMIFDPEEFDYLLCGSPEIDVSDWKAHTVMS

PNLVGADLTRWFWEIVHQMPNENRRRLLLFATGSACVPLSGFRGLTSYDGRLCPFNLKGV

SYKTTQYISSHA

>contig31493 Frame-0F

MEWAANAHLAAFYVFAKYLHVAKRIAGIHYIFVRKNRRPALNLSLLGYMLSLRLLAKAVS

EMKRFIWSYSKKNKTCEQKAMAKSGRYNPRSGRVPSALSCESEDTVNFYQQVKITDLANK

RQTQRKCALCLEKRVSSAATPCGHVFCWECIIGWCQKKAECPLCRQETYPQQIKRCYNYI

>contig32276 Frame-1R

MSQRERRLENLLNLTRAERFCVLPSVNYSTTTTCLAGTLLSALFDRLFCAPLKTSLAQGS

FLIGHFTSSFTSENHLFVRL

>contig32526 Frame-0R|Blast-pantoate beta-alanine ligase, putative [Phytophthora infestans T30-4](gb|EEY56971.1|) 1e-102

MNVDYVFHPSVNEMYSRHARCHVDPVGFDDLSEGHFRKGHFRGVATVVLKLLNIVQPTHA

FFGQKDAAQVVLIKRMVSDLNVPVQINVVPIVRDVDGLALSTRNQYLSQVERKGANVLYR

GLLQAQQVFENAKQQGKTTLEAAALSKVVCQVYERESLVTCIDYVSVGSKHTMEELSQVE

IATGAIISVAVKLGHCRLIDNIVL

>contig34102 Frame-1F

MLPYLDSSDGLPNFYYASVNPFKWLVRCGGVVGYGCPALRCLSSLLQK

>contig36553 Frame-2R|Blast-C2 domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY58870.1|) 1e-178

MGQGPSIARGNSNASRLLAPTLFPLPSDESYMPENTYLDVELEIVSAKNIIAGDYLGVTA

LLNGQLSSSDAYVVIEADGRRVAWTFPVFSTLEPVWNEKFFFRNVRLDSLCKLFLYDKDV

NADDELGVTQFTTINTDGAESTFELNISFHGRNAGTIVVRVKSFPVEPLSYIRLYEYGPV

RYSVHSSIAAGLMTMSTSNNAKIESLAYHIQLHNIPLFLAKNYEWNKDYPTIQRIFSSDY

PESFVLRQAIMTQHAVIYTHGPNKSKYGAISAPADFFELIHHGRRQGNPVLFTYVITQNG

WYFSETGATFFKDMLSKHMLHSGAAFSVLYAGEFRVDDHLFGEPKLVIDNDSGTYAPPKE

DLPRLVALMENNFPGMAVEAVDRENQESQRIRKEILEV

>contig38317 Frame-2F|Blast-fatty acid desaturase, putative [Phytophthora infestans T30-4](gb|EEY55958.1|) 0.0

MAILNPEAESAAKQASQSEAKQRELANAGYKHVSGAPAPLPLDVPNFSLRDLRAAIPKHC

FERSYVKSTYYLMKNLLVCAALFYGAAYIDQMGVMAYFLWPVYWFMQGSYLTGLWVLAHE

CGHQAFCPNEVVNNIIGLIVHSALLVPYHSWRISHRKHHSNTGSCENDEVFVPITRSGIA

SSWNETLENSPIYQLYRIVFMLVVGWMPGYLFFNATGPNKYWGKSRSHFNPHSAIYSDRE

RWMIVLSDAFLVLAIGAIAASVHHFSFFTVFQFYIVPYVIVNAYLVLITFLQHTDTFIPH

FREEEWNWLRGALCTVDRSFGAFLDSVVHHIVDTHVCHHMFSKMPFYHCVEATDAMKPLL

GKFYLQDHTPIPTALWRSFTHCKFIEDDGNVVFYKKKL

>contig39721 Frame-1F

MEPHSETWKDQKLQSRLRREALQQSHGSEKGEASGHEKVIEHQDARRGCYDAQTTSNQKA

YDSLNFPNMDNFCPYKMVKGMQREMPKDDEFVDAASFLKTNELGGDDSFSNDVGALADAQ

WAHVTSGRTSDFFESKSRSLDHVELSSPRNVDDSLLRGDDMLEIADIPELWTTKQQQILP

TDPGQVLESHNRFDRLSESGTSVMSGYDVHFDNATLMYTPNSLKHLQKKSRLKSAGERRV

EDGLSQDSIRDYAGEAETVTIKSPSLPELELSADPCPEYVAALQSGPEVIQASLREIDA

>contig40776 Frame-1F

MEIVENVMWRNLDSFIKFVIRQSQHEIMDDGRRIAINYLKNQYDTVTTPVAIIKTFQSSK

MGPKQIRGSFAELNCRCSTHGAVNDKAKWLIDKLTKSYDKELFIIMESYKFENLCRDVLS

ELSVRWKNDQAYSTSLVLEFIESFYGAG

>contig41685 Frame-2F|Blast-RAC family serine/threonine-protein kinase [Phytophthora infestans T30-4](gb|EEY53149.1|) 0.0

MRRLSSRVGGKNFSLKSEDDVEELMQTLVAQIHAKLKNELNLREIYIPNSKAEARCSIFV

SHNYAACSKLCIFMQPGEGMQPGMWSRTIHPKTGFQGSMIPYLKTAIQGGYGVVILNPST

NFSLVNGHRAKILHSNTPEAHVAYVWKNYVVPNAAQEISFIVHDTAGVLLKSFLTSISGP

EQQRVGGIAFIESAHQVLSNDSDALRALLRDKSVNFEASLEPMFTVIESSKARLGCTSLS

VGRTSSEATNREWTVHSVQTSAFVFLQSIASGIEESLHAIRATFPNKLIVTVNRARLTGQ

PYNNPFALVHCVGQKKETVGSHKHTMDPEWNQTFSFPVTSSEAKVVIVVKDRSFPMNTSL

GQVVVTMSEVGLNRADRRWFALRDEKVPTAYGNGEVELTLEWVHDTFVARSDSFIRGNRM

PTLEAQQHSRNNGSGSDNDNFCYLCKSTFVLHRRRYCRMCLRLVCTSCSDRLFLPGFSEP

KRVCSGCCDLQMMLHNKLPRMGGPGGQGTKVPSQDKLDEHAQRIEAMRKREEAERRPLSI

NDFDLLKVVGRGAFGKVLLVRKKDGKNSGQIYAMKILVKSHIIKNDQIENTKAEQHILKE

ISHPYVVRLRYAFQNADKLYLIMDYYPGGSMFYHLRKSKRFAEDRTRLYMAQLLTALMHL

HSKQIAYRDLKLENILMDPKGNIALTDFGLSKEGQLVDGAVRASQADMGMKTICGTAEYM

APELLRHQPYGKVVDWWSYGILLFEMLTGRTPFVDRNRRQMFKNIMQSEVIYPSHISPVA

RSLISKLLNRDPARRLGGGPNGGRDIMAHPFFEPIDWDMLMRKEIEPTFVPDVSSVDDIT

NVPEMFQNMAAVDSPVDKKNGEGHHFDDFTYQE

>contig42327 Frame-0F

MMQHQITDTSELEERLHTQFEVNSVIFSSRNAST

>contig42392 Frame-0R|Blast-alpha-actinin-1, putative [Phytophthora infestans T30-4](gb|EEY60523.1|) 1e-147

MTIDDLYEDLKDGIRLISLLQIICREKVCRKFNKKPRMRIQKMENLNFAFAFMQKKNVNV

TNIGSSDILDGNNKLVLGLMWTLIKAFQVAEIDVEGVSGKDGLLLWVNRSLADYPTIEVK

NFSGSWADGMAFCALIHRYAPTLIDFNSLDPKDAQTNVKLAFDIAREKLRIPQLLEVENV

AGQAKPDEKSITTYVSLLFKEFASGVQKKKAVTTISKALNIAQRHQELAIEFDKNASGLN

EWLQQQTERFQTLSQPRHIPD

>contig43553 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54392.1|) 1e-42

MRRVDEIQKARKRREAREAEREEMERLKSEEMRLKDVEQYEDWQLKEEQFHLKQA

>contig44035 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64619.1|) 4e-63

MREIDARVTGFDYSAYHAYTTEVEVDGRTWSLGIRYSTFFEFYTSLMALEKHFTVTFPPK

GGLFFSPPPEERQEQLNEFLMTTLAYFDMRGHPKRMEALLNELLQIPQHLGFKEDDEDRT

ASEGSSVAEELLLDTPMPTHHLDESFDEDKGVIETLNLEQFSPDKVDHELRSTATKTEAM

DTEFEEKPKI

>contig44040 Frame-1F

MKKKMLVISVVAALAIVVAVIVIAVTASRSHSSAKSEEPGDASNTNHKSRGPKPLRQIFR

ERASSGSLEEDEEKTDPLTETYTVSALAIGDWGRTIVKNGGSCCSRRKSFTVLDYNAMEY

VAILLGQAAAVAQPRPSVVIGHGDNFYWDGLHGATDQAYRFQQTFEEKYNAPSLAGIPWV

NVMGNHDYGGASFICTDGEQAIKCSSTSVLLEALDQKFRLQSQYVSPLDNRWIMPDHFFV

HSLADPASNVTIDIFNLDTNDADSHGAQQICCQCYGYSGKDDDSCENVKRGDSLCAGGDT

GLFDACMKKLKEWGDDSRSKLVEAAKASKATWKIVNTHYSPYNHYAPEPAEKWRELLEGL

GIQLFLYGHTHGEKHDYAAFKTHFIENGAGGGIQNESPSGIPPYAEEYVENIWAAGHYPY

GFFSLSVSPTWLQVKFNTFDDSWSMTADVDATKVGGIAINHCWYIPQHGGRGKSCKDAEA

QSDGSL

>contig44264 Frame-1R

MLRICLQIRMYNKFASMLYHAMYSRGQEAPCLYAKPFAQAMLTQVFNVGLLKPYRDFPTR

IWRFLNRERRVCRRSLHPHQDI

>contig44358 Frame-1R

MWHTWLMHGFRGFYSGLGSAVFQIAPYIGLSFGFYSILSERSINYDRDGEQSRKRHFTTA

LTYIGNGAVAGLVSKLAVYPLDTIKKRMQMRHVSRCATYGPTLMYSSSWSCFLDVLQREG

IRGLYKGTLPSLLKSAVASSSTFATYELTLEMLRYISSG

>contig44408 Frame-1F|Blast-predicted protein [Physcomitrella patens subsp. patens]gb|EDQ60125.1| predicted protein [Physcomitrella patens subsp. patens](ref|XP\_001775018.1|) 1e-08

MRKLQQVTTQQKRIRVVKWMIEDEVAYGKNGLFARAVHEFPSDFRGSVNANCTKASRWWN

NHNKICAVSKYGLC

>contig45906 Frame-0R|Blast-ribosomal protein S12 [Phytophthora infestans]gb|EEY57618.1| 40S ribosomal protein S12, putative [Phytophthora infestans T30-4](gb|AAY43416.1|) 2e-71

MSAEEVVATVEVTKELGEMDALKEVLKKALIHDGLKRGLHEAAKALDSRRARLCCLAQDC

DEPSYSKLVRALCEEHGVNLILVPSGKQLGEWCGLCKIDAMGEARKVVSTSCAVITDFGE

ETHALNVLLDYLKRQGEN

>contig47276 Frame-1R

MNQCEIYKYYAVCVSSSLVFMFLHCCRSALSSRPNE

>contig48167 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59635.1|) 5e-87

MAYEVTPTVGTSRASSLAAAAASGVVLWTFILYVVSTGFLGRNKTSHIITLNATHGVLST

LASTITLYFGLDTTLSVAISLSYFLVDLFVMVHSDGPRNILSLRQSRLMDYGHHILGLYW

GIVLFKNEATVCDASFGNAYVWMQTNEVSTGFYNWFRLTDSRVAGAMFAISFFFSRIVFN

TVYIIPRVATQCQPLYILGCSPYFVLQYVWFYMIARKLLSGGSQVHKIRG

>contig51217 Frame-0F

MSNPFGKGALINLLRQFAKLHQDKKQISVGFIGYPNVGKSSVINALRKKKVCKVAPIPGE

TKVWQYITLMRRIFLIDCPGIVYDTGDDEIETVLKGVVRAERLPQPTDFIATILQRVKKE

FIAKVYGIDEWNDEWDFLEKLANKCGKLLQKGEPDFNNVAVHMINDYQRGKLPWFIAPPM

RVEELAALERKGDDAPLNEAEADKDEPIELDEDDQIELEKEAEAPKDGPVALDDVNQLEL

ENAAEAPKNEPVELDEDNHTEAEKEAENKDN

>contig52021 Frame-1F|Blast-DNA repair protein, putative [Phytophthora infestans T30-4](gb|EEY61644.1|) 1e-26

MGVQNLWVLLAPVGRQIEIESLAGQVLAVDASIWLTQFVKAMRDDEGNMIRNAHLMGTLH

>contig52252 Frame-1F

MHRKFMLSSIVSSAKGCNWCIFSYNTRRRQDDISAAHYYPLLNADPSLDYVVYRFSCDWR

VACKARHERRAAIA

>contig52951 Frame-0R

MQPSLQNHPMQFADEVAINGNAQNSTKEISNTADAIATKTSFQHEEKLVATSFSPSVDAS

TVVARANEKGVTSTVPASLPDHTSPTMSSQDFDITTASIDAVDKSESVEGAQLQAASNFD

AASDGIIAA

>contig53259 Frame-0F

MLQEAILWSLTSFSVCVYVLLKKSGLRDEHKRSNRRQEIEKYMLHAGDDVASDAHACFFS

YRHYVRSNTKLYVCMRAQHREKVTSCSDGAMAPVAQQRGFIQVVG

>contig53989 Frame-1F|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY61424.1|) 5e-93

MESRERLQIDTEVPSNVFSLNLHKLSELAHIPEAELVRGMQSDDAVDMQGVVVNRGQEVP

FEAVGKSPEDEDNTFKPCNNGTPLSEKLTDVGVKQVLLTAASNTMCLDGSDTPKCLIQLG

EYTLMEHILAQLFVAGIERVVIIISYFGREIIDHVKSSFLYAKLQIDFLNLGEATSYGHA

RTVLSAREMFTQPFLIHTADHIFDHALISR

>contig54148 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54106.1|) 2e-10 NOT\_ORF

MVAGFSQCISDMCLYWMVDDGQMVVVGV

>contig54654 Frame-0F

MSVPRPAADHNGNSIRSGVPRDVVCDISIRRVHPVPECAHATSDRAILAGIEQARNKNDE

ASSVPMWNIPRPGDCPNGDMDGSG

>contig54922 Frame-2R

MRVNSCNAVLVYCGYGPFELKYVHSVVSTSCGQLIYARFFRAAG

>contig54997 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55062.1|) 8e-54

MDGGDDHAQCAMTIAMTVLPQLLVGMTRDEVQDLIRSSIRWNLAEVLDDPTFISKGDLQV

EGSYTKGLRFFSGQESTMRAFHAAAVEVYIISASPQLFAAEARNLIGLDNIVPSANVYGV

RFQFDAARRFTGKLIDKY

>contig55147 Frame-0R

MMTMMTASRCQNLMHRCAIVASKYSAVHFTARNHGPVSIEQLCKMQDKVRE

>contig55837 Frame-1F

MQDNNFELLSAQQKHDFFEQIETLLSPRRRRSKSILSVKSQTIKLSSETRRQATSIAIKT

EKMQEPMAEEAHDMLELGGLQHEKRPRKQRSFGGQASKKSKNASSFIDPGTLLLKDKKVA

LLPIGSDMGRKRLEILQGMIEKLGGKVVNLPVKIGPRTGVRSGSVIAIKWDEVSLIIASI

KVTPEKAAEFLRVDTFPPANIEVYTPEWLVYLLQEKMVPPAGNMLTWSEQHLVQREVTKY

DQHCKEVAKQLEQKGARVDKGDDSDSDEGSDLENTGTRQIMRVAPIQLNSQDCREQQVKL

DEKNRKLVEARTPIFYQNNPGFRPINETAVSGSKKVKGEGFICQRSSVVQQNL

>contig58009 Frame-1F

MRKVSNQEPIGSIVRIYTSGDITSRGDGNLH

>contig58218 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56954.1|) 4e-25

MNAAQAPSQRKRPPEKGSFPLDHYGECKPAMKSFLACLREHGNSHIDCKKLAASYLQCRM

>contig58650 Frame-0F|Blast-ADP-ribosylation factor GTPase-activating protein, putative [Phytophthora infestans T30-4](gb|EEY61406.1|) 4e-46

MSSAGTKAVFVPTEVRDAWFHKLRSSVANKGCFDCNKRHPTWATVTYGVFICLDCSGYHR

RLGVHISFVRSIDMDEWTEDQLKSMSEGGNAEARKFF

>contig59503 Frame-0R|Blast-NhaC Na:H antiporter (NhaC) family protein [Phytophthora infestans T30-4](gb|EEY66397.1|) 4e-07

MHPIIVAAVAIILCATNGAHTSSIRLQMPSVILQQVNFDASIELLELKNGSV

>contig00401 Frame-2F

MSDASDVEDLKTEVKGEASKVNSEEAKEKTNKDESVDASSSTIDNIVKGSKNGTDGALES

IKNVTDRAKSVADAALESSSVSASASCSGSESINDLTIEQQELSNEKLTLAEAANAAESS

QFIKVGAGVGAFVGMLAVAFAVIIRKVRSRISGDRFGRDEASVAMKSDLSADEEAFEDDS

VESNGLHKKGMAKEDDDVDADNEVEGTFVGPV

>contig00719 Frame-1R

MMRQVSSNSPSSTPSSISACFQRELTSPKLSEVDSSRLRSQTLLARLFRRKERSPLANRS

LYNEEEECKTRVESPMRALLRSLSLQRDRNKADEICASPSEPAHVLFEGELTLFDRRHCA

FLTRCYFVLDQAIENSTLLRFTMKQYQFNLERRRPGRVMAIFTLSHNDIVTNMRSHCQKF

FAFVLELASPDQRKKVAGEGVDDRQEESDVHILRLLAVNEQTHVMWMRTLKSCIAKLIAQ

ADTKNIFGIKSGWEGVSEPAKVVPMSEHVGRKASVLTIRGLERNGSAVSGASSEGSNNDS

EGDVSVNEIRAARQQFVEDNKKANGIIDDIQTSSRIAAADSNDESSVFGYNSPGGSNESS

NTQDPDTDNFAAEEKENNNQESEDDPIKDSFACGLASQDPVAFYKSAHLLNGDCTAYESE

GRKGEFTKTSSISSVAAGHGYPPRAALRASSSSYDIFPILRPQTHTFNVNGQLFTLDTRY

QLIKAIGNGAYGAVVAVSDVVNGGVNVAVKKITNIFEDLVDAKRILREVRILSHFCHRNI

PRLLDLSPPPSRKHFHDMYIITELMETDLHQVIYSMQRMSDDHVKYFLYQMLCALHHIHS

AGVLHRDMKPSNILLNANCDLKVCDFGLARGGIASCQNERPRIGELTEYVVTRWYRAPEI

MLNCLHYTTAIDVWAVGCIFAEMLLREPLFPGNDYLHQLKLIMKFLGTPKQEDIEFVKNS

KALRFLSRLAISKPEKWRNLFANSAAKKSVDAEAIDLLSKMLMFNPEKRISVDDALRHPY

LATFLDENDLVVSKPFDFSFDLPDEQLSKDALSNLLCEDIEKFHAPVPVAPMPPNSSVSR

FS

>contig05356 Frame-2F

MTNEDENERAQRKREFVRFTSESFSIKQDEARASTTELPHVGDEVRFRIAKHRKTGLRRA

VEMVIVVSAREKLEKEIELELATLSREMGVVSRMKNGGGFIKCCERPVDIYFPSHEIRES

DNEAMNAQGYSEESNVDEISRSIRRGKGLLLREGDEVSFYVYEVQEDDTSRSRSRLTALR

VLKLPVGTVSFEQLLRSNVEGMVVKAPKEPRNGPEIIGSIAIEPLSTEKEEERKQDAENE

IDESENKQLKKKKGMKTLQKVAFHLRDTEDMSYVPYIDDKVAFDEVLDKRTGTVKAVKVH

VVQLNQTNRECGVISAVKEDFGFIKCVERSSDAYFRFSDVMGASQNVSNGTEVAFDVFVD

KKSDNIRATRLQILPQGTVKWEVVVAEKLEGKIVAVPNSRGGRLSNRSGHEDKKKTMQKN

VHGKICFVTSKKQHYIDFIPNLKKKIDDVFLSSMDVSEQTFKPSAESEDNCKAELRVVYP

SALSKFERDALYEYSDWLGLQHESKGEGSHRQLEIFGHETITHTKVQEEIGSFCTRIDDS

IFGR

>contig05820 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67836.1|) 1e-42

MTIPFPGRMLNRGIVQLGDLVFNIRIGTLSIFSVITFVSFVVLLAQTYDLQKRYSASSDP

HIDLHYSADLQKKASRWRCERNWWISALTFTIY

>contig13672 Frame-1F

MTTMSMMKKKIVDEKEVGMDTIETDETITKSSKVLTTACIQSREEDVVVGDFRQEGLDTK

AKWRRKDYRLYAENQSSCLSVLKPRTRSTSRDTCQRQESYQQAVRNPMLSAPKQENHVSK

LDSLTCAKAAHVVAQARGKALEDCEFAGMPLLEIKDGTVQAKLMLIYAKACVAKQSFVEQ

SAKESQVPVNAATHFTSNRAQYLSYTILQNDPVHSKEFVSLTTDDEVSCENQNELVEYNC

PSILEGKSELMLEPTEGNGDESRQCLETVPKEEERRETRAISPVTSVPDFIPLHSFFIQE

NGKLTERVVVSNPSSANPLMNCESSEKEAKGQANDTNGGFMMNEDERN

>contig13971 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68201.1|) 1e-177

MPPKKKVGGPSKKSVEKQKEKAVEDKTFGLKNKAKSKNVQRYIQEVTKQVKGGNTRADRM

KEQEARKKKDAKAEQENLRSLFAAAIKQPKVPPGTDPKTLLCAFFKAGVCTKGNRCKFSH

DLMVGKKAAKIDLYTDNRAEKEADQMDTWDQKKLEEVVNEKHHEKNAKQTEIVCKYFLDA

IEKSLYGWFWACPNGGTSCKYRHALPPGYIYKSKKDRDLEKSNKVIEISIEEIIEQQRAK

LGPSGGTPVTEESLARWKAEKRARKNVEEAKKLKELAKRTGGRGIMSGRALFTYDPTLFR

DDADANDEAYSLHSEGEDDVEEHDLLPSIDAAAAVMDKSLYLQDVDDLESLKT

>contig19443 Frame-0R|Blast-vacuolar-sorting receptor, putative [Phytophthora infestans T30-4](gb|EEY57609.1|) 0.0

MKRGGYAHKEALFGYPAYSMGSLQTQLVYTNESGCEEINNSDWEPPFALMLDRGDCHFVE

KVRRAQHAGARAVLIADNKCLCTDVECLRETGDDFCETVLPFMADDESGGDISIPSMLIR

KSDGGAIRREIAQSKGVSNVMVKFDWGIPSPDGRVEWTLWQSAWDEQSTTTLAKLFDMVD

TLGDRAFFTPHFVSYNGTKVGCRGDGDSAASACGNMCLNNGRYCLLDPSPFHDRSTGASG

ADVVLENLRRKCIWKIESETDPGVGRKWWNYVKASGETCGQDENMFREQSCAEKVMKKLN

IDTKAVNECMQPYGVNVDKFNALLEEELKEQTALQLLRLPALYVDGVHARGRVDPTSILG

MVCAGYGVHNPPEVCSCATQSSVSLLDCVKVGSLANAAAITGSGGYSFTSLVAVLLIFVG

FVAAGGFVYWRRTQRHMRDQVRSILAEYMPLEDQAMEDDYDLEDERSQMLHPAERAAAKS

PRGYMPSRGFLEEDEDGM

>contig20007 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63078.1|) 2e-43

MAQQGEHACDMDVEDPTCWKITLTGKVLPVRDDRIIYAKKVLFSKHPQMQDWPKSHNFTP

YTLEIENIILLDFYGGAKRIPVKKYYQVKL

>contig21585 Frame-0F|Blast-putative membrane protein [Hyaloperonospora parasitica](gb|ABG23234.1|) 4e-06

MMDERDRKLAARAAAYKAKH

>contig23222 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69367.1|) 6e-07

MATPSPRRSSINSVPSSGRRQKEKSLHDIVATMEQNTIKSPPAGDNGVLTSSRQLDFGSV

NERDVNDAEDEDQVKIEPVESDEIEVDATRHSKR

>contig23518 Frame-1F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY70514.1|) 2e-55

MFREGYCDVLVATDVAGRGLDIPDVTHVVNFDLPSKIQNYSHRIGRTGRAGKDGVAISFL

TDNDEEVMYDLKQYLVS

>contig25417 Frame-0F

MSFFGYRTSSSRPSQQETHLSEVERLRGRQLASLVRAGGRAKNQEQTLFEVLIADTLRGP

FTLRLHLLTDFPVRVPRLKTSFPLQHRWLDVAGNVESHPDLNMWTAHSDLGRIVTEIVKE

LRIVASNLAENKLSTSPARHNLQASAALLESRASHASSSRQAHGQHLKPPQRPETSNIRR

TQIPVIPATFSELEEL

>contig26171 Frame-1F|Blast-inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY64189.1|) 0.0

MRVYSCANVTMSKNCGSSDSHQYGFIDVVALLDGREKLIRSNSHGPMSFVLSNSIVTGVY

TSSNTVALSVSLSYETISGVLKSAATSRRMQEVSVTTSGSIASSPTEDLGALTLATMTLP

SVQRGRLDSSLLWMDEDSEILVLSFSTSSIVGPDSSNPKVCANLRSPFCASKGRESTSTI

SFGLLSQASYVQGGNPFLNLYADPGGTNLRIESDNTTYFCVANLLPSGVKTNESWEVRTI

FTFQIQITRVVWSRNESQEVDEPSRLRLPSLSEVILLNGNDVLGSDCAQTLVRTQTHSKY

TLSVYSVMSVTLFAVALAGAILVTRMNGISFSRPTFYNDMTSLSVMMIFILCIVGNAIWI

SVSTKASSTSGTDIYYVLYAISLCFIWTMMTSVCFHWVTVLFHDVRPSRRLFVFGIYIVL

NVAFYSVQLFGVVSLTEFYKCTYDDYLRNPFYTRRLCLNDYCPDLQPSQWDYAVNTVCRD

VSYSKWFFPLQLSAELLLFLTSVGLLVLGTRVIQRGVRLIDQSGHIFDNHVVKVMKKSLI

TYLVVILSITIVLGTSSIMNLILHWKNWSMNSVVWYIFSIWLPTLVPPIGFLLLQWNPRL

HGMNWNPSLHVKDPQLLNRPVSNISEKVENGKVGISGNETGLSDGWAGILRFPDTEYNPS

AQENVDSSHNVLAVAVQLVSPIPLTHACFIELYVAENLAYEGGENEASGEDQYDDLPVLS

YHRSSISTLIESGIQQEGMLSRRSHPLSLVSSGALLTPRHMPNPATKWSRVSLTETVLPT

LVTNKSENGSGVTQIASFSSVLQIPLMPANPLLRFVVYELSETVTLSPSSDGDLRGSRHS

LRASSLQLDERARVARVSGMGMAPLSRPKVFCEFSCACDDMLAADEVELLARHGSTRHRS

PISTFLSDGVGTVSPSLSAATRAQTYEMDISMPRLRIKSMTVSPRHLKESSGFYSTKTFQ

FAKGDEMVIEDMIESPLTNEVPRQYLELLVADRTEDLARAQTEAVGFEARVKSGFVGILY

DNLIDQIRSENDQAVV

>contig26315 Frame-2F|Blast-Gpr7 transmembrane protein [Phytophthora infestans T30-4](gb|EEY70227.1|) 0.0

MSSRVLLLLLWSSWQSTARASIYPVESSYWIPPFQRAEKIFATNHGPILAREGNSSVTID

ISAVNVTQEMAGWRLVVFFYHVENYENFEAVSGKIQLLACSSEDEKKVDGMSDIERFVFP

VINNSAPILSANVSHLVSISGWTDTQIFVCSDDEGAPTEMLSFTGSMEVRNPYGYLPAVL

YGMLPFSGFLTVGYLMLDVFFVVLLIRHRLQLLSLHWCILLILIMGTTASAVSLYAFYRM

NTTGEPVCCPYPTTFLVSTILEHLFAL

>contig27060 Frame-1F|Blast-voltage-dependent anion-selective channel protein, putative [Phytophthora infestans T30-4](gb|EEY68596.1|) 1e-133

MVMLYKDIASKAENVLRDDYDFSRKLKIKTKAANGVSFTTEGDMSSNKSIVAKLSGSFAH

ASSGVVFKKLQVTTHGRLISEAEVPNIFIKGLKVTAKVEDGSVAKNSHAKRIGIFGWEYQ

HVRYSVDGAVDIGSKIISKSATYRFDNILLGAQTAFNYNKSAFVDHNAALSYRGNDYMAT

LQTKKKFNMLSGSFYHHLSHDTVYSAIFNYDLKSGQNTLSVGGRYNADKLTTYAGKIESD

GKVSLALVQKIRPFLALTTSAHVDVTNFDGDAHKFGIGLTLG

>contig28285 Frame-2R

MAKIVLNLEGIIRLTKLPPGLQVHYRPNFNSLNSNAPVQNENDFSIKIIFTFATFIEKEN

DQDLKAKLLLMPVPNPFKAEDCREKQFDEISRQTKPFLVPSGRILIQHSSGEKCPPDVLF

PFQQSDRHGFLFGSVYLTYELMHVGSSNEQIYVAKGFCLLSHLPLVSLLRKLAEEHIQSI

PKQSSFLAHEQLALLYHRKLSWKRPTITSHTSAYSETKSLNLRKFCSSLSLPSNAKKTDV

DVPLTVLFKHFGTAMALQILASAVLECSIVLVASQYSVLAMCAEAIRYLLRPFTWCHVYA

PVLPKSLLSYLQCPTPILVGVNSEFALRSDLPARGFYLVADVDRKVVEYVGNQRVAWRGL

GLQNNIDKDAIFLPRCFEAAKLKLDGLLYPEMMQYDSISKCGTTSIDTVSEHASSSNTEV

EQLSDVCVDLFLELLCGHANACLVVGDATESVVIFDETEFLSTRAEEDLSFYRALLRTQC

FSEIISAHRIDIDFKELDKADEDLQEGII

>contig28362 Frame-2R

MGGGGLRILPHKKWHVWLRDNIERVLRDERENEEKQQALEAKDRQLAQERRAQHLRADKS

ANSEQHINFFLTEELQETRKEGNVLSKKKLPAENDTLRRHGVVPWYAMTEDGAKKEPTLR

QERKRKRELEMADPLLDMRPKQHPLSDVRQFASYAAEGGPVDSDRRKYSSRYDRFSSGSG

NLYPSTDETQIRTYHSKESRKKHEHSRKKLQKLRRERDEREAKERLRVQRLFQR

>contig28528 Frame-2F

MAENVASTVRICVTRCPLQSAEENVHSLPCRIHFDGSAAIKSFFQPQTSDCKSNSTDLGG

LSSDEQDIDMDKNQESGNTSEKNKLIAEFRGIQLHGENLSLPHLGFTGLVLEDSGMRHPT

DEGRVWEVEDYFDQIMWWDVPNRTITEAQQLPQVLQQWRTLSSAVSRLTALH

>contig28797 Frame-0R

MALKKACKFRHDQFLKAVKEKTRLKEMLINAKAKSKERQTTENTRMVTSKSRKTNISTSE

SEFQCPHLDEQLVLESKRRKFDSSSQELPVSKRQRNDDCVEFEYLRSESVKFCEKAYSNV

VSRPPPISRQIFGRCNFNPNRSDAFNLTPSSETSIQIVGDWAAVNRRGYDETGKLTKYSK

EGDPRSETRKKLIPSMQHLLNAKQNNFVHGQRKTSSGQQEYALTNWLRNT

>contig29677 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57031.1|) 1e-11

MMHSNNELIIATRDGRVLFYRLNPNHTDRDEVHV

>contig31034 Frame-2R

MRTSFLIFVAGATLLIMTKATTTADPTKKTAVPAIEKPRHFKSISYNELKHGQSNPTVVR

RYVAA

>contig31148 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58046.1|) 8e-27

MAQQDVLHAPKSQRTVAFKWDKKFFSHSDDTLTRELRTYGSIESIRIKTSSAKVVFTEAL

AAANAVRIEGHKICWREV

>contig31409 Frame-0F

MFGLQTLTEDATRLRAPYLGDTYVDERLLAVPLEYPSYRDPLRSCTLKWRGLRRGAKVAS

GQFFSSRVTETVYIESSGVTVLSPGERIGYELLQSVDVPGFSGASKTEKPHAIISYCYVY

RQASSNVVEVFMLGSTSRDGVSIGGAIAKMHSLDQLERCAE

>contig34103 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59665.1|) 5e-36

MGNLLQVFVIDDDLFVIGGTKDGKYTTELHRIHL

>contig38316 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64226.1|) 2e-06

MDYYQTLEIDKTATENEIKRAYRKLAIRYHP

>contig40027 Frame-1F

MDNERSTEASMVYQGIGMLLLCTVFFVVWLMACRRNRHLLDMEVPLLSGESVDHRIDAAT

REAEAGYSACSSCEFENFKRFEHCVLCGDKLPSLSINTVDDDSDDEERQPQRHHKLQRVE

SNSSRGSSAYMVNAPRPSHILSPRPRKMSSLSRQQRRARNRREWSRKLDVEGNLFWYRSG

GNNVPVSSEVDSTMPGYTV

>contig40777 Frame-2F

MRLVDQVETVFLHGHALLGDVVHVCLGLLARPAADIAQCFAPTDTIPHPIETFHGTLCNL

LNAIEANKCVMELVADEQVVDMARMQRERFCQVSGLYFANETDRCGYWLKHFGFAPIKSE

PSGLNCEKDDLRHDSSRFVTHALTRWVEREATKLIPDRAAFRASRQSIYDQVHAEVIAKL

PFPCDLDVFGSSANEFGSEHSDMDMCLVVPKDASPSVDDKQRMLLEVVARLEARPDLFTS

IDTTRLTARIPIVMFVSRASGIECDLCVENRLAQRNTSLLRVYASADPRVRMLAYVLKRF

VKQRRMNCAAEGTLSSYGYLLLLIHFLQRQTPPVLPVLQALPLTWPENSHNSLPNVFCRG

PSDEQNASAVNPQGIETYFYDPFAFHDPKEKLTLLRDYCARNTQTVGELLMGFFRYYGLH

FDATRDVVSICRPDAGTVTKDEKRRTCQWRLTTRLSIEDPFERSYNVAHVLKGSRDKYIR

QQFARAYVLLMEGAIQSKEKPIYRTTTQSSASCQA

>contig42326 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53975.1|) 4e-84

MPFDIETSKGIDKENPLSSIRSQSLSTLHLFQRQVLTRVREKIKEWCSVEILSILKSAND

ITPAIGALVQRLFDELPENVLTEVTYPLEFVSCSQEASVNPHDLLKREFEKGHLLNVHQC

NGVYFVVENGTVGDDAQTHPDAGLAIPYWAYFELSVDHIVLRYQHFPRFSTASAEINRLK

VLTCLQLGVRAICRRVNQYLLLLQLHETRTCNGLLLPANGDLALSPRSPKQHFQSQT

>contig42393 Frame-1R

MLCGMGDFALGRCGLLLSFILNSGPVTIALVLTDQMGYCTPSADCCNFCVQRRLFLQFLD

WLGPLG

>contig43817 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61867.1|) 0.0

MSKPEHAFRTSSTDCHEPAERSLGDIVDEAKNRLQHLEISCRQILPPSGSVRARSIYEPP

STDLKLLQLEVAQLRAQLLNTMMLRENDDVIFGQAARFEAAKGTANGVLHALFDQASAGK

ALVLKTFLDTGSIPTRDGLKHWEMDLRTIRNEAGATLLHVAVGVSTARQNVKIKLVHLLV

DEVGFDPNVQDVFGRTPLHIAAMSGYPEVVQSLLDRRADPVAQDRSGLTALSLVRTLSRP

PQEVVQKLVIAESAAMRERTSRSKSIPLCKALTSGLFLQKLSRFALEQCSSALICQTSAL

VNALLKESNCSRVDFDRLLQEHVPILFNSVPAYHIVRLESVFAKTVYMDSNFINELRIEA

RGYDLSLISLEPSAEMPEGPTWIGVLSKLIQYLRLEMAEWAQNVIQTKDLGTPTDTSVFG

KHSTNSATITNPSTRRCLELSCPNLLSTKSHFAMHYADQITFVAQKRVVWFYAVLLKAST

IKVPGSIMLKPASNIAIASEDLSKYFPLQDYLLIGTAEYFAIEYDAETHCIRLGRVVHSK

SQGC

>contig44034 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68610.1|) 2e-64

MQRFLRLSATEAEAAMKPRLVDGKWKQPMISGRKIAMVKKHALRNGVVGTWEEGKGGWLE

TWNRPEKHHVMRPLKGHKNQRNEFERVQKLQAALAAMPSKIADHKKAVQQAKPLKGLDKW

LNEKDPY

>contig44409 Frame-2F|Blast-predicted protein [Physcomitrella patens subsp. patens]gb|EDQ60125.1| predicted protein [Physcomitrella patens subsp. patens](ref|XP\_001775018.1|) 9e-11

MIGDEAANGKKGLFAIAVQEFSSGFCGIVNTDCTKASRWWNDRDEFVQLIAIAKIWSLSI

IGNRGYARS

>contig46616 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63833.1|) 2e-13

MSKGEVDPAKDDEQNELQQHLQLEAYSGKYLTAQEIILLQLFQSASDATSSSSGVNVTCS

DLSISAP

>contig52020 Frame-1R

MAWQLRKQEDAHRLCLQLQQQQQEDEELKQLRVENCQHGGSCWKDVRTDVSFVERSRHRK

YGAMKSQERYLRRDVHCGVDSCSSCRKARALLPNKVLPRVDDGEYVVPDAFSLLQCMELL

EEESLFFRAVPHLLVLESVFNVALRLASSRDASRLRKFFKHDHRTGQNSIYLFPD

>contig52950 Frame-1R

MLVRVHQGISKISLRRARTLSSMRTVSLRGSDIALSSTSSRNLSLSNSLLSNSSSNKDCD

DTNLGDDNDTEDEDALWERLRLSGTTKSVVQCSMSGVPDSHRSWIWPILINQIPSPSDLS

QALIAV

>contig53881 Frame-2F|Blast-copia-type polyprotein, putative; 28768-32772 [Arabidopsis thaliana](gb|AAG51247.1|AC055769\_6) 3e-10

MNMARCMIFASGFPLNFWDDAVEYAPDILNWAP

>contig54431 Frame-2R

MGTLTKEHDQLLQSHMAESERDECIQSEGADERDLLINFEEDAVIAWNKANLPNKVVDK

>contig54655-0 Frame-2F0

MPPMFVMWLPLLMPLAILLSIFLTRYACTRSRNAASKNTIIGIFHPYANGGGGGERVLYC

TLLALVQHSRRVN

>contig54923 Frame-0R

MQQRQCTDKLCALRRIRKRIRFYALQKPKCFHERADVAAN

>contig56367 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63606.1|) 7e-13

MTYSLPPAGAVGKIFYMPPE

>contig57870 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64471.1|) 2e-30 NOT\_ORF

MERAYCTQWVIEAAENERAGRLIVLKQLLCENEK\*IQRRRQWAIATIEMEQAVRMREMFS

DNMEHTQWFQSTILR

>contig58008 Frame-0F|Blast-dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit, putative [Phytophthora infestans T30-4](gb|EEY60454.1|) 2e-13

MQINPDNNFGDRTEQRAFADYLFCNILLFLVVFN

>contig58174 Frame-1F|Blast-mitogen-activated protein kinase organizer, putative [Phytophthora infestans T30-4](gb|EEY69177.1|) 2e-21

MPIQILDDFRDSVTSMVVTDHEIVAGCVDGIVRTYDLRAGQLFREHIN

>contig58651 Frame-1F|Blast-cytochrome c peroxidase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57904.1|) 4e-73

MGTKEKTTQHVRDVFYRMGFNDREIVALCGAHAIGRCYPSRSGYSGPWTKAEWTFSNEYF

RELLETNWTIKKWKGPLQYEDPTGTLMMLPSDMVLIEDPLFRKHVEEYANDEALFFHDFS

NAFVKLTENGVKFPVTSGWRQFFGA

>contig58790-1 Frame-0R1

MMLWISRRIRLSTCQVELLFRTHCYGLRTLSR

>contig07209 Frame-2F

MITTKADQYDVKTKRSGSPIPSNLRPTAAAFIFNTAAPVFTPSKHTVVAPIGQKSQLKRS

AKPFVPSLSPPVVPTKNVPPPTTTDPETKPLLPTPVLPIAPVSTHKEPPNVTIETLETSS

TSTSSSNASEPETEDLGKESNAIFQSNSLNSITSPASIAAPTSHFEPPTSRLLYTIEQLV

HLQPAKEHCRIPESIANTIVAAENATKTLFNRTTSSSRPQEDRTPKTRSKRSFPLDTAPA

LEDCVPLSINDATRWKPSCRLATPVDSSSVESSLKQIKAILNKLSIEKFEILSNQLIHVA

VRNIDVLKGVIPLVIAKAQMEWHFATMYAELCAKLAHTAMPAMETTDHVRNTHQLFRKLL

LQHCQEEFEHKRPGGHEFLSLTNADHEKDILFKRASLGHIRFVGELFKQRMLSSRIMHQC

IGTLLGGNTTTETRDEDALECLCNLLRTIGAVLELQAHDHAEKVCIQGYYTRLKQYSRET

ETLSTRVRFLLQEVLELRKNRWIPRRKEIKAMTLAQVHAEIAREERAKERASRTTTRYQR

SHSMQETHDKRKVRGMASCDVVVKSCDADGWETVTSGSRSKGWKPRSVVDRMPTVLKVPR

VLVHSSTTLREEGHDELKRNERGRSKSASILDRKQFVTRDCCHYMLERK

>contig12517 Frame-1F

MKAIPPALLRPSRAHSDLSHLTSRFVMSNTKRQCPQQAEATATSTLASPRIHWSASRQPF

NCNYGSIRKSWRGYMDKLLPYPKVQQLALDAATFFTKPEDLDFHWPRTFHDKYTLGHKLG

AGTFGDVYCAVPKKRQGTHEVQLDLAVKIVPKSRVRCRNDYIALLQEAHMMDILSGTLQV

VHLFGTFEDQNTVFFVMEQCCSNDAWALKGEPLHEEQAKKNMREILHVVSHCHSLQILHR

DLKLENFLRADKKHNSPLKLTDFGSAVFLNKGEVLNDIRGTPVYTAPEVLCHNYSFPSDL

WSCGVILYRLLSGHFPFESGPLLNECIKHNTIDVTSSPWPGISNEAKTLLSQLLERDESK

RLSAEAALQHPWLSSSTVPLTPSMASKEIPEPALKVPWYSAY

>contig12588 Frame-1R|Blast-acyl-CoA desaturase 1 [Phytophthora infestans T30-4](gb|EEY60243.1|) 1e-29

MANIGQAYDLKRSRTAVKTRQRVAQQLHKDSLKLAQSPTISWWERQLNQVFFRQNRSPGF

PITHG

>contig12683 Frame-0R

MFIFQDSYFLRCLPGKHGKSWILWSKLSNYDYQVDSEGLSDILGREKLLHLWHQLTNFYR

Y

>contig13222 Frame-0R|Blast-GTP-binding protein, putative [Phytophthora infestans T30-4](gb|EEY59988.1|) 0.0

MNIQKRNNSFSDDLKLDGKLPEKNEEVKSSHELDIATSLKNEVERRETLRTLRLAFVGNV

DSGKSSLIGTLIKGDLDDGRGLSRQAIFRHKHEVESGRTSSVATAYLGFDEHGEQILSKR

SGKLIPWGELAKIAHKRIQLIDLAGHEKYLKTTVFGLTGMQPDVVVVVVGANMGVKRMTK

EHLAIAVALEIPIVVALTKIDIAPKNVAKETLATVRQILRRYGKMVMLVKTPEQAVTAAK

GIPSNRITPLLPISNVTGDGLENLRRILFETSPSALFKAGMSASTLATTKSINQEENISA

KTAEGESEFNKYALHVGDVVEMPIDETYQVPGVGFIMAGTLLTGSFKVNDALQIGPDYNG

HFHRITVRSMEAMYMPLKELVPGQTAALAVRSVNKKFVLNRSTFRKGMILLSPEIKTDDY

VSRVFEARVVILHHQTTVTVGYQPMLNCRTIRQTAEIISIESTHDVIRTGDKALVRFQFI

HSPEFLKKGMRFVFRDGQAKGIGKVVRIIHTAQSEAVVSG

>contig13671 Frame-0F|Blast-condensin complex subunit 3, putative [Phytophthora infestans T30-4](gb|EEY67563.1|) 2e-38

MNAEWTVTLQQVFQDVQLQAVEASGYLRNSSGLEYQRTLVPAVRRLHALYCNEVKDGERG

VVEEAFALFLDGLWTAVARVLVASKVSEVVLVAISSFIGEFFRRKTS

>contig13972 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63497.1|) 5e-33

MQSPLEVSHISLSQSTSSNYSQFTGLQGSRIFDVESPTTMSTNKDFLYQRPLAPNAVPLL

VRLQRLRILLTAVLGVALIGILMAFLQAGLVLESHIASKEGSVTLDVYNFILGLVTSVCV

KPLLAL

>contig13998 Frame-2F

MDKATALKIQEAIRKNSESDQLRIAEEVATKVKVDTKKYQQRIEAEVFEERREMSEKMAM

YVNENENLQSTLDAKEEMLAKSKEEITSLLEKVAELETKVGSLMATEKAMVDNEEKNKKL

EERLQILVTKETQLAECKKKIDELDKEIKKSNEENLEIVQLLAAAEEKVLVAENKASNAT

IAAAAAESNREADALKQQELQKAVTLLREELWTCRTQLASQEEQLNHQRPISILATTTTA

SPVPLSSMAVDSSASEEDKEVLRAQLVKALSLFAQVQALGLEGVTLLTNTKTVDLDEADC

PRTMSNLPLTSITNAPPQQATKSSIDPVNNFNPEAAIDYTTTESSQVKDASHDSAAEPKE

SPSILNGDKKPPLEQIAQFAITKEAIALSTLVALQSVDSSSKESPSNAGRLDSHGKSEGD

WEMLQ

>contig14344 Frame-1F

MKQLRAHKMEGFGGVSVKTAGPFLTAVDTTKYSDYLSIVSEPMDFAKIERKLKSDRYGSV

DEFSADVHLIFSNCHKYNSDPVEGADIRAMATILRNYFVELYNEKLGPLDGMANILIQSS

TNATQAAVVPTSLNSLQLKLPEEPSRSLVAKAHTKVGVLHKPVEKLPAPSPSKKQLSIPA

AANASSTIAREFLRAPEILKQVNTVAPAAIISTKPLDMVRTLITETSSSVASKELPSDSP

DLSNLTPEMSKRLRKELKEKRRKEKKIKKEKKKKDKEKKRDKKEKKERSKLTAPQELGLP

TEKNSTALALPPAIATVANPSAALAALPPTVHALGSAAVASKRGMVEPHVTTSSVSSKKS

KKHKKSNLKSWETACDRVLNRLGKIEQVAKLHFNHPLLEIFPHLATEYKTLVSNPMDLRT

LRELLHAHALTQADFLCKGRLIFQNAITFNCADDQASIQV

>contig16108 Frame-2F

MILCIPTFPTPFSLPIATGAMNVLICRNACYEHYRQLFSQTIIKTAKKLRDINFCYIELI

QP

>contig17648 Frame-2F

MELLPLALQREICSFTAATELIPQEIDAFLDNHRVRNFATHFTEPSASNLQRLARVCRNW

RDIVKTLCAEHEASRVLTIRFTTGHELQQQKQIIKRLATNEQGFAVLDLRIILTIEKRRL

WWDLDPETQNTNEEIVAGINHFQTIDWGLIFALCPNLQRLDLSGMPLHHLALRNVLDKSS

KTCKHLEALILPKRDKELENTRADINGRVFCALHMALHRWKIASEGKGLRQLTVPSWRQF

DLNHKSNEYLTMVRTTCPNLEYLDGWKRLYSEGTNFVTSEESLRVCLVVWQKFCASCLAL

REFSWIIVPFSDDFFLSFGHAVKPFLTRLQLAYNTRSPFHIRRNEYSTGALNIVLAGCPA

LKHLDIVLHRLQPCDTLLYPQIDEMIDPTVFNDDFCVALTDHCPQLRSLHIRMLGPLSNN

RNARVLSGKSITDRGLAALQRASRLSCIDIEEVRCSSNLILTFLKSDTDRVQAAVPRRIT

FRELGVCFGEVVQNALEELGSKAAPISTKRLVKMPLVLSLSSRRGYVFGRNWLVTMQQAF

QQTFPNGDLRFAAFCTSEKDTFRTSSCSSLELEKMVKTLTRAWVRGDVLRVKRLILYTNL

SALDKQERHVLERKIKFSSSWIVLTE

>contig18609 Frame-2F

MGGVKGCRHVGQAVRLVEARRELKKRSQLLCQACLLSPSSDPAATTLASWAKYTENPDLL

VCVSCGFVGCFSDGHFQLHFQVHPKHFVGLQLASKTFWCEPCRIEIPIDVRPKVERARQD

FCDVVEDIAAKKKRQIRNQMRVSVSSQTTLSPITTPKGSTRNSVNVDTRTDTPPLAEGSS

SSETNLHVDTTHTLLDTPLKTKAREDKMRRKLQKAALDRDLTPEPCVSPAFNHVNEVKTV

PLTVLGLTNLGNTCYFNASIQALLTAAHYFPEHMHMDELVQTKNTPITTTFTMLHETFLK

RALNAMTGNPLSERRKSRSSRARSSSSSVLTVAPLLKAIRQKFPQFRGHDQQDAHELFAS

FLWAIDEEMDPLLPPWTDFKEFSATTDGRRDSVSSIRSSPTPGSDKPDGVDESSRSAIGK

LHEDDSTDNEYTIDGDHEEDGSESDVEQEETNQMLIKSQTGEIIAMQVPKSATNKQLQQL

LAKRLNLHEAEILLNGLSIDSCASLSSRQSTVLHARSEKRQMCSQLNLTRTLFGGALTTA

VTCQACNNRTEIIEDAFHLSVSVPDTRHRTLTIRECLDTLVAETQLLVDANNGYECEKCS

RQVKVRSVAGRFMRKKRVGQTETKVVLRNAWMRLVVSCLPRVLVIHLKRLARSRKITQHV

AFDEILDMTPYVSESLRERDSEVTTHALCFELIAVIVHTGNKRSGHYSA

>contig19440 Frame-2F|Blast-threonine synthase [Phytophthora infestans T30-4](gb|EEY59976.1|) 0.0

MAFLSKYKSLLFFECSKAGSNFYLKIQLYWKDPPRKMVHFRSTRGGVRGLTFEQAVLTGL

AADRGLFVPEEGEFPTLPDDALDKWASLTYQELAVEVMCAFIDDKEISRAQLRSIVDKSY

NSSTFRAQEVAPVVKVTKQVLVLELFHGPTFAFKDIALQFLGNLFEFFLQRKNETLPPSA

LKYRITVVGATSGDTGSSAIYGLRGKENVDVFILFPEGRVSAIQQRQMTTVLDKNIHNVA

VKGTFDDCQAIVKDLFADAEFKAQYSLGAVNTINFARILAQIVYYVWAYFRCRERGFTGE

IAFSVPTGNFGDILAGFYANKLGVPIGKLIVATNENDILHRFFSTGKYHRHDIEHTISPS

MDICVSSNFERYLFALSGENHDILRGWMQGFEQTGKLTISGDLLAKAQDEMASYAVLQEE

VCSTIATYRKVHQYLIDPHSAIGAAAAMHFGREKLADKPDSTIVVVGTAHYGKFLPVVSM

ALGVAESEIQQHPILKNLESLPTQLSSADKSTAAIANYIRKMNAKKSNDTCSFGLMSSAI

SKGKLTTFAFAIAAVTVVLLLSRRSKYKQ

>contig20004 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54043.1|) 1e-138

MLENLVFDLVYGIEAEKAAAQKQWKQYRLENAITIATNDAKKADEERRIAQLIAEQQRLA

EERRQLQQREDSQFEADLELQKAQLMEVALGERNESDVSKLRATTTAIPIDQAVTAEMEA

AMMGFQPGGIGGPQPIPVPGGKRGPKFGVNESKKLRRQQQLAGGYDPDLSYHRNRAEAWC

GINFAPVDRKHANNGPTSMEIC

>contig21029 Frame-0F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY66312.1|) 1e-143

MILKRSLREKKEKYQTAKVRFQKSTAHLEKRVFNAEAVRRSLHNKVMELKGNIRVFCRVR

PILEHELTSSRGEKIFSFPDYRSERRQIELSANPTSHVGYGQHSSSNVIKKYSFDFDLVF

NSSCSQDDVFLEVSALIQSGLDGYNVCIFAYGQTGSGKTYTMQGSNNVANCKLRDLWPDL

GIVGRAFAQIFKGIEELRTGGWDFTASLELIEIYNETFRDLLAPIESHEKIELRQDSEGK

TVVVNSFSQKIGSDQEAWDLLRGAISKRSTNSTQLNDKSSRSHCVITLRLKGKNSLTNEM

RTGVINLVDLAGSEHVSKSGSDSSKKLLKEATSINKSLSALGNVMCSLAKK

>contig23759 Frame-2F|Blast-hypothetical protein PITG\_12042 [Phytophthora infestans T30-4](gb|EEY59000.1|) 3e-08

MRRSFTGVEAEIASSPSNISAAGLNVISEDDEEDED

>contig24725 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62448.1|) 1e-15

MLREEQTNEVVKELVSKGFSYNQVQSMGYMVSQPQSTLSAPAESAVQ

>contig24790 Frame-0R

MRTGQLADILMQQFQVNQKNELFRTWLIHLHGLIPPAPDGDWLEFRAAVVHLLPQFQHFF

VVPLSEAQAGKEKSKLERETKTIVHDFLQTRRRHLFGYHKLGNSIDDPSELISCTNLSRN

CLLLVLAGYLASFNPQETDVRFLSSSGGPRRKKRAKRNSEAETNVGTLTRKKKQQISQLL

IGPRIFKLQRLLAIYSNLRVEAEAGNTTADDDLRSFETREEVFTH

>contig25951 Frame-0F

MNSEKAAELTQVECEEIVQFDAIFFVSTLTTKLRRTDCEAVAKKSIENCNNAYDTKRGDY

VVVIGDHLAYRYEILSALGHGSFGQVVCCLDHCTRQLVAIKIIRNRPSSCGQALMEVNVL

TRLQRAEAGDAKFHVARMKRNFNFRGHLCIVFEVLGMNLYDYLQLRQFRGLPSHSIRTIA

KQLVQALVLLKQEQIIHCDLKPENILLDAKSVGQDDSNGDNVTLIDFGSCCYESAPMLTY

VQSRFYRSPEVLLGHKYSSAIDMWSFACILVELHTGHPIFAGENEWEQLACIMEVLDEPP

LDLVRNSKRRELYFDEVLDPADNEWVEYVPKPFENSRGRRRLPGSRNLVSAVQSTDLEFV

AFLAKCFVWNPTERLTPEQALQEPWLSRDSIECEF

>contig27063 Frame-2F

MMPTGRKSEWTRELHGTIHNSLESLRMKVLLYNIMFVNAVIMQTPNHYGESIISKHCE

>contig28286 Frame-0F

MDLLKTSDTAAIKAPIPERERPFQCPVPSCHGRFQRKFTLREHMKTHTGEKPYQCAIRSC

AKRFSTSGNLARHRRLHLLKKLECPVDGCTRIFTKSEKLARHLQNHLGSVAHICVVEGCG

KTFSTAGNLTRHLRTQHPPGAVAAARAAAPSYAQGLHARPSPLSVSDYTLWSLSSNGYSE

HHACVPNAANVSDHEILDVLQCLFVDECIPSSSSPGPRAQPQEQYRLQVDQPVLLYL

>contig28361 Frame-1R|Blast-60S ribosomal protein L8, putative [Phytophthora infestans T30-4](gb|EEY69751.1|) 1e-23

MNPVEHPHGGGNHQHIGHPSTVRRDAPAGKKVGLIAARRTGRLRGIKKIEKDT

>contig28729 Frame-2R|Blast-L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase, putative [Phytophthora infestans T30-4](gb|EEY55814.1|) 6e-72 NOT\_ORF

MWKPETSSIFPGNSLFIEHSSTDTKTSPVWQQWGIKDLLQSIK

>contig31042 Frame-1F

MATLARYIARVCINGRFFFSN

>contig31266 Frame-0F

MLHIIAARVSLSPRPIVLRARTIPARRTYLLVILNLSTWNHFTIEDVRASSQDLNSGSGR

APCVHECAQQHDHTARNLSRRLL

>contig32274 Frame-1R

MALYASIVPHFTRELVSPGVRVGYTDEGGVWQFVAPFITQRLPLRAIEWRNLVGVLKRID

YLPLTFVEIACGSRTLPMACMYLVQCEDLEHYKNVVRPSLRRWVDAMNTANVEWLVLYVP

LGTRAKAATNGPHLVYKKIVDRLRVDFASRKPSRLSSGVLGSPLTLLDRVCQLDTFIGTS

VLGQPQQYDAQYTDLLLCLKHCVMEAFQNKCIQYETQVKILQGKRHAVGWNFGTFFKTKE

TLALLYQQMNLQDDAIR

>contig32524 Frame-0R

MKLIICSAIVLAVSALSGQNERVCEPTPVYLDPYYVIDEKHTEKSMCTTTKFLTNSIAWN

TTFTVANDDLSVVKSYVRAQLVLKDLQIASIQSIPATISHAYTGESFVSTDVLDMYIGTK

SDTTTMSQVTSMTKETSMIHLPSPSIRILVVLATYGNGSLTWLVTKLLTVQIGNDKFDLY

EGYLDGFTVYTFVIYTGTKAFNGDLIEFIKRLPQGKTIDESQYLFSVQGGSQIFCGTNAM

YEATEFMVDYKVKTLAM

>contig32599 Frame-0R

MYFHISRAIQPLKRMAFVRRLGRSNRIVQAWRQPVNTLSYREHQENSQPSNLRTYHASTQ

RENTALIAGLGVAGAALSAKYALQVWAAYKSRPKIEKGNSWKYRNFYDGPFEERMTRREA

ALILGVRESASAERIRNAHRKLLILNHPDTGGSTFLATKINQAKEMLLSGGK

>contig34100 Frame-0R

MRVMAQIKPSNGGDNTVVASPVVTLSSTNEKPQNLCIRIQYVCQETILPSSKQLVLKRMM

VVLVNNVVLLKVPFDLQQVLKLHAITGNYFIGLGMSSLVLLTSWHLQKYPATTSWPTKKD

VDTIDKDSSVTTPRILWQSLTLHCTVHWPLQLLVTPELLRSYRHLFQFCFRLKRVAYALE

LAWKHLSLRAKSTVGFDALFAVGALRLRMSFVVRTLELYFHVFVIQGKFDQFVGQIQTAQ

DFDRVQRVHETFVASIVKSCFVYSKTVASALDELLSCCWNLVESILLYDRTTELSRDSIS

RLDQDFFHRFEAFYNVLQNSEARELLFLLDSNGFFATERERRKPQQLPLSHEYDYIFEKR

>contig34618 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60537.1|) 2e-18 NOT\_ORF

MSEIHRKYSADAWESAREAEACDFVVAMVALSLPQIEQFLVPGEYSCPYPFSMLITGKCA

ENELAAEAKELPKYILDQLRM\*I\*LHSRQCLNE\*SLLILYTCMYDRSDETSPILLAVGGK

>contig35024-0 Frame-1F0

MKENCRMLATLAMTSPFGLKLETLAMTFPTAVLLWLWWKQSETNLCNREKIM

>contig37390 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY67837.1|) 0.0

MDFSGADTARELLRVERLSYVNISFSSHEGEDKDVGGHHMQKMDNDGEGQPLRLGDVPNL

YHWRHIGLLVQYAAVGLLYGGLPRTVYPFLNNYLHLNGYQTLSARVLLSMPWSFKVIIGI

VTDCFPIFRSRRRAYMILGWLFCSSMLLVLIVVEQEPPYYTDSSLRGKDLSKLSAAELQG

RVNFDAPNSGSLYIVLMMLATLGYMIADVASDGLVVEFAQREPENIRGNIQSTVYLVRSI

FMIVAALVVGFGLNSDDYGGSFTWSLSMSQLMLIFSLLSLLAIPAAYWLIQEPALGDYSP

RFSEYMKKLWILVQNSAMVQILAYRFFSGIFDGFTVTAGDPIQRYWAGVQPLNESLFSVL

GLAVFSAALYVTKCIGLSWDWRRVISSTTVSVIVLDAIVGMLTIWGVVRSQWFWLGTPIL

EELPQAINFLVSTFVVVELAEPGNEAAVYGLMTTVSNLSSPFASCISKNVNAYFDVGVAD

IIRDSKHVRWHVTWTYLIAYTMKLLSLAWLPLLPRQKRETQALKRHSRPWFWGGVATILI

FSFALIWSVTTNLLAIFPKTACLVLAGGTGCK

>contig38315 Frame-2R

MHPFQGQDAEEIFRTFFGGQDPFSMFFQDSVRGGGGMQNVGNSRVHVSQFGPGFTFTSFG

GAPGVNLPGMRMNRVNQRQRAPNGQNFAGDHRPQRNGPLSQYRIGVGNLLLILFLLWIMG

MPFSYLWIALMLLSYLGLA

>contig40774 Frame-2R

MNFGSAFLALLARLLAVRLASATKFGSAAEEALIGVPALVAELAFSTRLLSAVDLDVPVR

IVLAREATSSASAVTARTTLFSAVTTFLIKGGFPIAAETKLDLCSRVSLPSSCTRPPRLL

GFCLLVGRNFGGGLSLCTGKLMSSSPFGSSAELALC

>contig41100 Frame-1R

MLNSALRVVNSVGASAVRRQTVINWLHKYAVASEQKTIPCSVCSSCRCTAAIHPQAERRD

NTMIHGG

>contig41687 Frame-1F

MVKYFGLGICSPTNMRSNLACTPEGENKPVNIIRPKDISCLTRLVESFAPIQRIVTPRDI

LGKR

>contig42325 Frame-0F

MKMATTPVAPSTALPHTSSATSCSKALLSTQQDQPQRQSADEYGSENMTTLWPDSRCYLR

NLVFGRECRSVFNLEPNTIFLNHNAYGVAPKPVMQAQAHFVNKMETNPDRFMRREVPVML

RQAASHLARFIHADAEDLVFVTNATTGMNAVLQSLDLQNDDEVLCLNLT

>contig43119 Frame-1F

MQSDEIQMMEPTEKLLAAGDVQEGTVLKEESIMTEPVVPSPRAGNGSAPAQAEPIEATIE

KKECDALGKSDITIATHESNGSVVESIIANTTLITEATNVSGETHTSPDTPTKRTLSHEN

DGPHDEKDSTLSTRAGMVTSVPHHDDEYDPVNPSRAFEKHRPAAEQEEYDPDHPSMTLSE

VAEADVVMKDTDALFRNRQNDLSTMKPAKRKESDKSHETTDNAANADSHSKRPRRDDDNK

RSVHRDDFHSGRPRRESGDSISPSKSRLRHQKEDHKGLSAAAWDRLMDFQTSGEFLVTQV

SRAAFASVGAMPEFAQIAIIARFVRTPMQDVRDKNGQLMRLFREYQKENPQIATLQPVEV

FLSDYKSDSSLFRFGYAPPQPTTGMSTVPVPYQRDQSKVETVTKHSPRQAKSLSSRSDSE

RHFHKDVDEFGRVVHPASGPFEANTRSASDHHLATPSRPESLTANKAMAVESHDQPPSHS

NIGAGRDPR

>contig43649 Frame-2R

MEEARKLKHEGNHRGSSESGTVGQLTQGIYYLRSGAKFFEYALKLQEVKLAYQEKNDAQH

AHSFGENCVTTLSQTTSLIESTIRVFQGAGSMRLAALGCKMASVVHLTVYRLQHRKLQSF

YTELFAPGRSPECRENGLTPPIDQNSNGTSKDAAIRKHLLKEMEHTLRGFELWRRYEACK

VDVMPRVTNPVILDLATFFEDLKTELDQV

>contig43814 Frame-2R

MEINGSLLANGGNACVDCYDSAGAGGSIILIAKNRIDGNATVQANGGRPSQFNRDELTGG

GGGGGGGRIVLDSMDAEESGPTQIEAYGGGFITNDDAPIKWCQLGGDGTILKRQHSTKDD

SGPYDESDLRRDDIEALVSTLLVSGGRLTQAEPVKRVQLYGCTPIFEQTSRGASFLPKSL

AHIFVSGGASVCAANIQLKHWKY

>contig44037 Frame-2F

MGCNQSKSADVAIPADNVTLKTAEPVAVAQKVSPRTEADEEQPQEEDDFVEEAPTVSKPI

ASVNGAPTIEKASTSPSVDVPDTVRANFSSFNISFIDPTLSAPTSVSTEPSIASSKAAVV

SQKEVLSVAESTAAAPFMEKSVHVKSAVELYQKLVADFATGVVLDNVEAEPIIERVNVME

P

>contig44266 Frame-0F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY59403.1|) 5e-24

MKDSTKASELRRLFATLEQQIQEDQLLEGEEWYLVSTVWWTRVVGTFVTDETDNEVDDSD

DALPQGHTDLQVHNAVLLDTNRSSRTRHVTVLKPMLLEGPDYR

>contig45254 Frame-0R

MDEGNNKFEKQDKVAEMTAAEFIDDDEMEDVEHALAAANEKQIMNQIQEEDESFEKEDEA

MNARNEVTAMEIDEEMIEKEESIQKEQQDKPKPLEKELQSDINAEQGTVENQMDQNLDDQ

VNTPKHSIQSREHELLDDEEKLLALPSKLRDVDLTNSMKDQDESGEAEAEPVKPLSPDEV

VAIRDELDLYIANWSSQSDQARGTDLWAKYTALTAGASQRLCEQLRLILEPMLRAKLEGD

FRTGKRINMRKVIPYIASQFRKDKIWLRRTRPSKRQYQVMLAIDDSESMADNCAGRLALE

ALATLCKGMTQLEVGELSVVKFGEDLELLHAFDMPFTDDAGSRVIGRFGFQQKKTNMVQT

LELILQLLESAKQSASTASSTVEFTQIVFLLSDGRFDSDGRVRIRKLIETALERQQLIVL

LIVDQGACESASQQQTSILDTQSVTFEKGKVRMTPYLENYPFPYYVLLPTSAMLPEILSD

SLRQWFEMLQG

>contig46989 Frame-2F

MTEFCENQVECRRTSLLEYFGEHFRSEQCHGTCDNCKNKRMGMTFEKSDVTDDCVVLATM

VQCLQESGDPTTLVQTSHIFLGLTVKGKEWKQTQYSQLEGFGKGKGRYSRSEVERILYHM

ILRQYLREVDQTNARGFTTTFISLGGNANRLFRGERVCIVCKTKYQSRASGIVEAPIEKS

VKKNESKKSAASKKTASVRQSVKTTKAKDVREEVSDTYDKDEVDGKIVAPPTSTKEYPLM

PERVSSRRIPKKHVEALAQILKDWR

>contig47274 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61758.1|) 5e-12 NOT\_ORF

MMKNLRHKVACSAVDLICILQRLYSDKDVPVSAAAATATVLVHYG\*ERKRSVQNKVHQAF

WAGAEVLRAMAQYHHKPLLFSTLT

>contig47524 Frame-0F

MGTVQPETSSSKRSAAYSENMDTSSVESNKVYTFEQEQTHQLAKAANAATNTHLIERTQP

IAYVHDTATHALSAEQVEEDNLDTSDGVQVVSTKSEMSQGGTDPVIIVLSSLGGAGVVAL

IAVVVMVKRKNIRDEKARDMEGPSMISVRSFDVGPTPSDRRQPLATML

>contig48165 Frame-1F

MAKSSSRLRSSLASLTPLPLILHHHDKPKTVSSALSNRWSRLMLYCGILYICGFVVVFWS

KHRALDTIQAISNFQSVASEAAQAEEHARSVKMLPEGPKRLREFRCVGWRATDSCSPYGS

RLPQLDKPCHMLV

>contig49764 Frame-2R

MTHTDDDWALRNSLQLCGSIIPPNYADLRTAAHLQTFDVFDGCAALWADSGKLFLVNILQ

SRVKPAKEQLLRHVTLEPSLQPREAAEVEQVKINAIGSQVLLVAKSWVKIFRLPSMKKLK

PPHLQRQTDRVATQRFLVRFEDCSEQEV

>contig50201 Frame-1F

MAVGGADTLPVYRLHCENTIEASLLRVGASLTEKVFGEMSPQELFAVPSEMTMRWTIEKP

SWWSSSATSGGGNGWMSDGTLQDLVRVAEQVERDVKYCGDVNELQAPLDVHTVDLDAADH

LLLANTDELTPVEWYAVNYVHGVTDKKLQESGDRLALATYADAAKDDGLVSCDESNGAVP

SEQRSFDKLALQEVNRQWQEGDAVSKLFYNFDVGTVGEASLEKLFMQLRMEGMETHFDVY

QPPQPPTSEARAISDNGLSSDCQMTFRVTYHVPPPPPPPLLSTKSKLDHSAGHHENSLHC

IKSIKKQKTNAL

>contig50739 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53629.1|) 1e-61

MKLVEVLAVDGTDSEKLEEQQRFVALQFPAQYGSSVIKHLSCHFQTLAALGFAHIKRLKK

LPEAPDTLMALVCPLVANNTVAAMSVTDLQQLEETFEAKLTTAEALKFPPRTRELFEKYT

QHWPLIFHSSVERTTAPLPIGEDESEVMKKHLAMALQIGGKHKRERQKILSCAWGCVVVD

PEIDEHAATSEINGNRWSQYAFEALYHPIMVAISRVGERDRRQNTEAEEKAVLKKHKHDG

EDAKHLKIEKDGNTSENKHNDSYLCTGYDVFLDQEPCSMCAMALVHSRVRRVVFDRSNPS

DGVLLSSYRLHTIKSLNHHYRVFQLALSSHESEV

>contig52023 Frame-1R|Blast-nuclear mitotic apparatus protein, putative [Phytophthora infestans T30-4](gb|EEY54191.1|) 4e-78

MTEMNKLRASEKLCKSGSDVESTESSAHLIVTGDSDDEYDQSNQISASCTIKKRLSMARK

EIQELRMEREQEREMITAIVKQRDMYRVLLAQSDNKFLEGGATSSGAESQQRTALVTSEK

HHASFDVSESRKLRELQKEFEDYKKEKRTNMRMLQEAMDQERSKS

>contig52250 Frame-1F|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY53844.1|) 1e-79

MQSATATRPKWSSVNETVNRMVIWLFLLLCFLCGIATTVQVLWLNDNVNESWYLIWMPSL

TSQWFVGFGYYFLLMYQMIPVSLYVTISMVMFFQAIFMAWDIDLYYEESDVRMIVRSMG

>contig52728 Frame-2R

MCGLSYVQIPCAVLLTMSTSLAGPNARVLLLNTSRLLPVCHWGSSAQPATCTLTVTGALY

AAYTVVVLCDQKRSKNFHCFL

>contig52953 Frame-1R

MDRLPTSTRSERSLQGHEIPSRSNKSTGNISSLRSSSAASSAETLVELPFVTPSCSLVLQ

FTRVRHVQHALIASKLATCQIKTFQQAVDAYAATNGNTILDKAQFIQLVRSVPDLQTDET

FKPMEETLARLFRSFHATNRTNLYQLLSGCLVLLPG

>contig53132 Frame-2R

MDIISAAWKRWQRFQRAHHGSVELDVKAKEAQYELVALGLTLHVNEVQDLFIEDARVLLS

LLTPLPTALTDLESVNRFHFTLVASTILLDEYLQSIVASETQKTRLLNSSVTTDVVLPLL

ALERHALLHQAALNFLRILLETQTDQEAIQKLFTEVYRLLREPRDYEITYNGLCRLLELL

QRRGLQAMD

>contig53868 Frame-1F

MTSSTEGVAAEGGHLVAMNASQIDANMDTEARVLMHDVRYSFRRISTIKYRVHLVLGTLL

HL

>contig54656 Frame-0R

MCKLVLSVCSLNCDLTGEVFSGTILVSIKINLV

>contig54995 Frame-2F|Blast-inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY65488.1|) 3e-38

MFTQGINEMQSVANHYLNSSLQDELNFESVQMLQRYFRVYQ

>contig55145 Frame-2F|Blast-predicted protein [Thalassiosira pseudonana CCMP1335]gb|EED91487.1| predicted protein [Thalassiosira pseudonana CCMP1335](ref|XP\_002291380.1|) 6e-06

MSDTKLKSPSKARRVLLQCSGFIASHCLSLCWGTYLLGLLWLLLHPAITITTGELKCRGT

YMSENAL

>contig56364 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53195.1|) 5e-13

MRDVQTLLELYMRRLTRQFGEFTIKPTLIKRRPSVTT

>contig57987 Frame-1R

MTAISGELVELLTSRSAELLNAGFQLILLLQNLTFAQMSSSFAASVASFHEQVLAFARSE

TSKTFVQSMAQYLPYICQHAIQLLHEVTR

>contig58652-2 Frame-1R2

MVAAGVGVAAWLMVSNRDTREPISPDRDPRAP

>contig58876 Frame-0F|Blast-conserved hypothetical protein [Talaromyces stipitatus ATCC 10500]gb|EED12566.1| conserved hypothetical protein [Talaromyces stipitatus ATCC 10500](ref|XP\_002488220.1|) 2e-19

MVSSSAKEIATRFSASRVFLIDAPNKTNRYILPLLHIVGITADNQSYTFAYYFMRNETGI

NYLWAMQNLRQVHEMFCIATPKILVVDREMALINALEGCFPFARTLFCRWHINKNIAAKM

RRHFDSAETFKQLQHMELP

>contig59039 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58032.1|) 4e-14

MTVDQVCDQILESYPKSELELGGKEHLRSFVS

>contig59084 Frame-2F

MPTNDVHEREPILSSLEMKTHLLPTEPCDVPEHILLSTNQAGPT

>contig02034 Frame-0R|Blast-eukaryotic initiation factor 4E, putative [Phytophthora infestans T30-4](gb|EEY53188.1|) 1e-95

MPKKIDVGTYQSNLQKIATFDTVEEFWRHYIHVKRPSQLSRDVNLYLFRDQPNCAPMWEA

FPQGGCWILKIKKKANVLGKMWQDLVFAAIGEAFGQLDVVGIAMAIRSKEDMLSVWNADN

TDDNTRFAIGEKLKEILMLDSNTLVEYKFHANSIRDMSTFRNAKPYVFAAA

>contig09664 Frame-1F

MALKQREEHARVLKEALAQCHPRLTTMKVSTTSASQGNSMTSRSLAKPLVATPLVAASIT

TKEVLSGSSRGIKKQKLEPTRSTEALKPKTEPSTSLTEIPTTVVPRTRSYLKLRRLIQQR

LCRHLKGQDVCVLSSFDQVNHAKWRASGRLEAGKVYSFHKKRQMTFAAYVQDELGRAVSA

CAHMFLIATRESIDAHLKVCDAFSDKDRESGPRLLNKTRQKRR

>contig11166 Frame-0F

MATAALRRFAKAQPRLYTASFIRMHFQRAPVLCAHGVRANPFAFNSCHKLGAFYSTDGKE

DGTDAEKPIDAKKDAESKSVEVVIENKLTPVGEGDNAPTYPHVLVMPALRRPFFPGIVLP

MTITNQEVTRALMALKESGQKYVGVFLKKTSKDPLNPAGGEDLITNLSEIHRVGSLARID

TMLPLDANSVQVLMVSQRRIAIDDVRDEGPPLRVNISNLDNPSFDPENKLIRAYSNEIVA

TLREIVKLNPLFKDHMQYFSQRVDIHNPYKLADFAASVTSAYGEELQQVMEEMSCEARLQ

NALELIMKELELSKVQQTIKEQVEEKVSKNQRTYLLMEQLKAIKKELGMEKDDKEAMILK

YRERLGQFAPDSIPASVNEVVEDELNKMSMLEKNSSEFNVTRNYLDWLTQLPWGKATEEN

VNLSKAKQILDEDHYGLKDIKERILEFIAVSKLKGDVQGKIICFVGPPGVGKTSVGKSIA

RSLNREFFRFSVGGLNDVAEIKGHRRTYVGAMPGKIIQCLKSTQSSNPLVLIDEIDKLGR

GYQGDPASALLELLDPSQNSGFVDHYMDVPVDLSRVLFICTANVTDTIPAPLLDRMEVLR

LSGYDSPEKLAIAKEYLVPKALEKTGLQKSETTPESLGLTDDAILTLVKQYCRESGVRNL

EKHVEKVFRKVALEVVEDIERAKDGKSQESGESTAAESVAGGTDNNNRFLITPEKLHKYV

GKPVFTSDRMFDKQFPGVVMGLAWTAMGGASLYIETTKVHTKGDRSGLITTGQMGSVMEE

STKIAYTYARSRMHAIDPETKFFEENEVHMHVPEGATPKDGPSAGCTMVTALLSLAMQKT

VKLDLAMTGELSLVGKVLPVGGIKEKIIAAKRSGVKTLILPIGNKRDFDELEEYLRNDLD

VHFADYYDDVFKIAFEQE

>contig11908 Frame-0F

MWFTVLEDFFNAELFLKETNAAKAITKESKGVRAITKKSKGAEVATEGSIYEIVVLELMK

LKKE

>contig12516 Frame-2F

MTPSSLLKNVLSKSRGALTHDGNNASIILDDKVLRDTPWTPKSLGRAKTAIVYKQTLNDT

LLILERNIFFIKGWVPYFVSLQDDSILMYSSRERWEQGLKPDKVIELHFMMLLGEMMVDV

NEGCTSLHGHTVNLRLFRRKLLGIDELDEWLNEEFRQSLVVSSGSKSNKLAVNNPNASSH

CVFEFASYNQRTFELWTKVIRRVLATKRKARKSRLRSNPSKNDTEFVCSYESSNLNTSWV

SPGQDSKVTLLQSEIWCSRVLSGEKEKAESELRRIVAMEKLVDQVTDARMALLVYEKVSR

VHELFSANGRREIESLDGRESAMPTDVINFFADHLKRKYSVFLILALVYGVNEEEIREAH

DRMCHENAAMNAGVGGGSGKLQRTVASYGFEDSESLELYEKYRDAASNYHKMNYGDFAAA

EEEDAIMHLPVMLQVAVIRGDCEEIIAMQSILDVVKERLTERC

>contig13973 Frame-2F

MYLVYIDKLLEAKISNQDPSGLKYFFDGRDKEVNEDTVAFFFVPQIERLIHSGDQTNKYV

GQRLLVGLIFRWLEKRVQSEKVSQYLNSMPRARHDELLHLYKNCI

>contig15434 Frame-0F

MLDKLPITRVFWVCVTIFRLWNALFVRTSFNPDEYWQSTEVAHRLVFGYGYLTWEWQEDA

QLRSFAHPALFVGLYKLLELLNLDSRWAVAYGPRLLQGIISAANDFFLYKLARTYFNDNA

AKWALLCQLFSWFTFYVMVRPFSNCIETMCTTAALAYWPWKFLEDRRDQKDKDISYKQNN

RAVALILAALGIIFRPTNAVIWLYLGIGHLWQTRDRAFLMFRLVVPIALVTLLTLLSIDR

LGYGQWTVVPINFFKFNVLDGKDKLYGKHPWSWYFLQGYPAIVGTALPLLIAGYFTVPPS

KKGLGRVSAWTLLVYSGAAHK

>contig16893 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66908.1|) 1e-90

MFKRFTVEEHVSTSSKVKSSQQRSIRAKIVEQYPELEPYAEMLMPKKAPMVVAKCQNHIQ

IVLHEGEPVFFNQRDGPFMPTLRLLHKVPHVMKQVRADKGAIPFVLSGANVMCPGLTSAG

GEMPESLEAGTPVAIMAEDKEHAMAIGILTLSTDDIRNVNKGVAIEMVHFLGDDLWTCEH

ID

>contig17177 Frame-0R

MARRTRAGLLGLAIVATLATVATRELHGSLDVFPSMKVRVTCKRPQQFFGKDNFVFFANP

VVSTNEAKVLYDGYATIENDGKIVTYIYVNGTGYVIRSDTDVQCLSSLPFYSIVSALNNA

TFISRAIIDGKLIVCTSGNLFKTVFAGAEVAI

>contig19063 Frame-0F

MQFITNMHVKKPILSYLKSRHCIVIKHLRFVSTATPLSRSGEANAVAKKLDYLKPTNPTN

EPAYKTHFKQTRFTTSETGEPIWENPTNHTVYDLNQITTIQETHHPITKMHERVAFLAVK

ALRTSFDVLSGYRGSGGAMSEKDWLNRCLFLESVAGVPGMVGGMLRHLRSLRLFKRDYGW

IHTLLEEAENERMHLLIFMNIKQPGYFFRWMVLGAQGIFFNGFFLTYLISPKTCHRFVGY

LEEEAVKTYTCLLKDIEDGHLDAWKTKKAPLIAQTYYKLPEDASVYDMIKCVRADECSHR

DVNHAFANLDQKKGVSPFVCNRIKDQEAAA

>contig25950 Frame-2F|Blast-coatomer subunit beta' [Phytophthora infestans T30-4](gb|EEY68492.1|) 0.0

MIWNYATQSLVKTLEVSPLPVRNAKFVARKQWIIASSDDMHVRVFNYNTMEKVTSFEAHS

DYIRHIEVHPTLPCFLTCADDMTVKLWDWDKSFICSQVFEGHGHYVMMVTFNPKDAHSFA

SACLDRTVRVWGLGSSHAHFALEGHDRGVNCVAYYPGGDKPYLLSGSDDRTVKVWDYQTK

AIVHTLDGHGNNLTAVLYHPRLPLIISACEDGAVRMWHSTTYRAETTLNYGMERSWSLAA

LPSANTLAIGYDEGTTVLRLGHDTPIVSMDAGGSGKLIWTSNNDVYTASLKGVVAEMGLQ

DGEKLPLISKDLGSCEVYPQKVQHNSNGRYVVVCGDGEYIIYTAQQLRNKAFGAALDFCW

SPMGTGDYVVRESVSKLTLFRNFKEVKSVKPRVISAEGMFGGAGAIGVKGNDAIAMFDWE

ELRLIRKIDVAVKNVFWSENGSLVVLACDSSFFVLRYNKEMVAQAFAAGTNSIEDGVDGA

FDLLHEISEKVGTGAWVGDCFLYTNAGGRLNYYVGGEVMTLAHLEQKLYLLGYLPRENLV

FLMDKMKNVVSYTVSLVMLEYQTAVVRRDFESANAILPKIGADQMDYVARFLESQGFKEE

ALELSTDPDQKFDLAVQLAKLDVAREIMLNEIDVGEKEKDMVDIETQHKWKQLGDLALND

CKLALAEDCALRADDFSLLLILYTSRGDKNGLVRLAELAREKMRYNIAFICYLLLGKSTK

CVEMLKETKRFPEAAFFARSYCPSKMQLVMDPWRQDLAAVSSRAAKALADPTRNVDLFEN

LELSIQAEAML

>contig26447 Frame-2F

MFKALSAAKMESWTHKAENLQAKADSRGVKEVANSIKAQTNSIQKLNEPLEKASENHFLL

IIEKARGMEDTKNAANAIEEELFSKWYTSKTHPQSLRHEWISTYQSLVNLPLETLLRYTV

YYARKSGTHIAIADMLFKDLPEHQLAAMLVPMVSNKAYKNNAKRLKVILFRKWYNEFKSV

AKDDPRFQVTTGDSENLAVLLDSYLMYCQEIKAIVQKVALDPTTNGYLSVPSLASMNNIA

NEYSDKFLKEPLNLYALLKSNFEDVVVTKIILADKVSDPMLFASMYSAQMTDWFSHQTPY

TLFSILKLNNADKMEPESLLQNPLFAHWNQFYEYYRQESESSKFFFELVDVLERHFDALY

LVRFFRYGLNKANDSSRISRIILELEEKLPQKLLTAQCQPDLVFMNLRFGTHETALFERV

ATVWIKYFKLLTGNGKIDVFPYSAITPLVEVYGEIPLINLIYPADKFSSEAFQQTLENGL

LCMWFNNNLPIREVQSWLQAATYLRPERAEAILLSYRRRLNNIAIVVQKLKGNQLSWADE

FAKIIAQTPNNVEPVATYALLRTF

>contig27062 Frame-2R

MVSMIKMDTSKLVIVGFEKIISVVIVSKMHNLRRSYQSRMRQVMLRRHHLLAGSRVIYLE

VFHHYLKLTAAGTPQETIAPIGS

>contig27941 Frame-1F

MARQFSNKASQVSQKLMESYGETSKIHAVAGKVKNTVKMAPDTDASRSDGVKGTKQNEAN

TEDSEQFKQSDDTIQDARAFVNNFISAIVAQKNKLFHFNNLPKVRDEWMEAVHELFGKRD

EKTVDEALASVRTPSMQKPNKKSGGDKEQYKGTSALVAVKGEESAWQRVSARFREAPIIQ

GILDAAKQAVKTEAGKKVWQTTKQVKDKISDAQEEVLEVWETSQNPWVYRLSSIYDGLFG

ETSMGVAIKEIRRAEPNFILEEWKESVEEVVLPGVLEAFLRGNSRDIKKWFGEAAYSRVN

IAIRERKSEGLVMDPHVLSIDNVEVIEATADDKQAPIILMRFRAQQINCIHNREGDVVEG

SEDEVLAYYYIFAFQRDYDEEQETLRWKIVDLHMQRGERYY

>contig28360 Frame-0R|Blast-60S ribosomal protein L8, putative [Phytophthora infestans T30-4](gb|EEY69751.1|) 4e-84

MGRVIRGQRKGAGSIFKSHTHLRKGPAAFRALDYIERTGYIKGVVREIVHDSGRGAPLAR

VTYRDPYRFQIKHELLIAAEGMYTGMFIYSGPKATLTVGNTLPLSALPEGTIVCNVEAKI

GDRGSFARASGDYAVIVTHDEDKGKTKLRLPSGSKKTVPSA

>contig28795 Frame-0F

MPTRLPKILKMGTQSLHQASTMIKVLFFSGEMVSDIINILCPPLAKKSDIPKSGMPIKFS

CRPWHRFKTRSAS

>contig31036 Frame-1F

MHTRYHFVSSLHLIIIADFPRSPATCSSRDDVPYI

>contig31043 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53818.1|) 0.0

MGKSPFTTNPYPHLVLTDADRDILLQLEKDLILEVFPKYEEFVVAEHRNVKRSQWKAIGE

DKNLHVYVERRGWNDNVLEEEEVVQESTDNWQKHMPIILAVGTFEGELNDLMFGTVNPTQ

EIMRVKASYVKDYSDGAVLANIVVPTAADPFRSVSIKWTQINLPLNQTGLVQNRDFVCLE

ATGILHFADGDRVGYQLLHSIDFPNTEPLPGVVRARHKIIGFYRQSSRNVIDTFAFDIVH

PGGKVFRSVALKASAEALLSTTNYVICGQAKKLTWKLQHRQAETRPFRHDSSPCSVSNGD

VACTACARNLTPGAFGLPRVAAFGKSVCKLCLNAVCYKCKRPKGITFLAPNGNLLRRKIT

FCVLCISEVSRMDAVPAAQDQANGYQAYSVMASLSGSDILSDDLNF

>contig31490 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61686.1|) 3e-53

MGRFLTDNAYDHVVIVLDKHTVLHVGIPSVKLLPLVRLLLPQRQPMVLRVPMSEPELQLF

LRSARQLIGCKYDIARASQLMLRLVLNRITGSKPLPRLHIDVKSNAWICSDSIF

>contig32275 Frame-2R

MKSFPQLLERAHDFIPSFLTDLRHLATTKTLEWHQPALWAVAACLEIASACERSYTGRDN

KEYTTTRISDISIEEMARALGTVVYLARCILKTYVRTPCPIPSDRTVTVPTSWYHHLDHM

FVHLSNHNTLPFEQCIVEISHLASMHFSHAKRYRFAMFLDHECAQYYLQYNTLSTASSLL

RSIAQQSHTEKWWRLYFTCMHQLCRTELARNQWQDAVVAWFQMIQVVSENHVETSHTDLF

DVIPTL

>contig32525 Frame-2R|Blast-RNA 3'-terminal phosphate cyclase, putative [Phytophthora infestans T30-4](gb|EEY69234.1|) 1e-139

MSPPQHSKVLRFQGCAHFRYRLICATLSSRPIIIENIRSEDENPGLAAFEASLLRLLDRV

TSGCLLEINETGTKLKYQPGFVVGGHVTHDCGTGRAVGYFLEFLAALAPFAKVPLHVTLD

GITNDHVDISVDAFRCTTLPLLRHFGLAEGLEILVKKRGGPPVGGGQVVFRCPLVRQLKA

IYLVDEGFIKRVRGVAYSTRVSPQTSNRIVETSRGLFNKLLPDVYIHSDHYKGAESGKSP

GFALSLVAETTTGVFLGAEAAAEPGDLPEDVATRASHTLCEEIQNGG

>contig33614 Frame-2F

MQLQIGTLFACDSMSETKVKEDPTRMNYQGESSTDMALLSGMVSKDFMLPDLLWNELTRG

ELRLALTTTTKGFAQFKANQAAPKLLLASRNKSNEPKWNHAQFLVIYQSIAQELKVDRFY

LRVISERIRDGSLQLGEVAKTARAIETGSHRGKFKNSSSLFFASMDIAKDPAKFFSEVYE

CWLQYLCLGNFPLLGAVDWSACKRNDFILNTGGEQDCQTMFIILIELANVFPDARLLTKR

RAGFITELLLNSNVAGEIHNIVELLAGLSQSKIAYTDMCTRRLIRVLLYMSLLSHRR

>contig34101 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59665.1|) 2e-48 NOT\_ORF

MRYWYSLTPLRGMSILYGGYGHPQRLSDTFALRFGSQMPLCLRRFGLIDINGL\*FVSRY\*

STNLDRTSDSRR\*SRAVINALGVRFQRPHVPFWRIRWQVSSWPAFYVRYWYVRQLVIMTD

LAVLVRRKGNEGSH\*LQMAKIKTQGHGPASRYTHSCSSIGPHLIVHGGNTGCLKGDTYVL

GFENDDDAPRWKLVKSDPPMMPRAWHRAVVYNNAMYMFGGCTAHGNDNKVIRVAFQDLLP

>contig34772 Frame-1F|Blast-2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [Phytophthora infestans T30-4](gb|EEY53799.1|) 1e-135

MTAKYQIVLIRHGESQWNVDNRFTGWHDVQLSAKGEQESHDAGKVLKAAGFKFDLAYTSV

LKRAIKTLWNILEETDLMWIPVIRSWCLNERHYGSLTGLNKQETVEQHGIEKVMIWRRSY

ATPPPSLDVSSEYYPGNDPKYAEVPKELLPFAESLATTGERVLPYWEQTIIPSIKAGKKI

VIAAHGNSLRALVKQLDNISEDTITGLNIPTGVPLVYDLDEHFQSVPHKDAIAPLTGHYI

GDQEEIKARIAGVANQTKAK

>contig36550 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68280.1|) 2e-55

MAGPIMDLLNNLQPMLEKARLRRSKLFIAMVIQSSKIMESVRLLHKSDLGDVPQVSNISH

RKCLRISEEIDQHKQKLVELNYYLSESLNQCQAISSSWESKVIQTTSAEIQMLEASIKEL

ERIREVEILRIVQYSKKVRDELKKEFQRTLNMRLQQTR

>contig36648 Frame-0R|Blast-Rab8 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY66102.1|) 1e-107

MARHENPFDMQIKLLMIGDSGVGKTCLLLRYANDSFSQTFITTIGIDFKIKNIELDNKKV

KLQIWDTAGQERFRTITTSYFRGAQGILLVYDVTDRASFQSIRNWVGQIQQHADVHVNKI

LIGNKCDMTDDKVVSTEEGQALANEYGVKFFETSAKNNINVEGGFIEIAREVKDRLTEEG

GPHKKENVNLNAKAAPAKKACC

>contig39551 Frame-2R

MFGPMRLAAQHLRRSSRVTSKSSTLIWHGQRFTTSKVNFFSSNSRILSDSVQKANVICAQ

PLIVKADPTSIVAGIAIVGALFGMGKMIWSASSSSAGEAKPFVCKDISQSEMALFFTELT

AATKDLFNQLPEIESAMRKYLKDNNQELNDAEFHQAKLSQLYQMMESIEHQIVASRQWSR

QCIQNALEKYAQDAEILKLQEDLNSLMLSVFPAPVEIPDELTADKTLDILKEIVASMEKA

MVDMLAHARAEGITDVEKAMKEFQSLYMEHVEHMTQAQMKACGISQQIFTAALQKYHAED

ELFRLKVQKIYAQQAKAFQKMGIPADH

>contig41619 Frame-2F

MSDGVELQSNFFKSKWRDVTQVMSTAANEFKVGQLAHEDDFNLFESMSALELMDPKMDSG

MLVNGAPMQSISARLENCSLQLEFSSARDVLATLDALFCCEMGWLDGLPLAQSLLTSVYT

HRDSLNALCAQLVTPLENLVKPDADIRLVLTKHVGKSAKDSLLLVMCAAILALLKTADLV

RDAALRADIYEEEDFSPGKGFDLGVLAPLSEQAIDTLLQVTLERLEGLLVQHKNLFSKKT

LKKKQTKKVNTASNSNSKSISASGYEMLHQNARIGAMLCEALIRRIQLRRELLTTYAGIG

LAEGALDLQHARNGFEAAIKLIQEIATERIELDPECLGGKPIGFDPGISRLLLSGSPPRD

VKVPSIDEALELMKKILSEMVVGCSPPNWRCIEDLRIFLTQFSRQLPTIVARSYVLLFLY

ADSKIYGKYNFMDWMTASMVMNGVPSVLLSTQEGVLYSSRCIETVYESLKVYLHNRSRQR

PRIECLLNEWSILQAEATAVDERFTTEMNIPRAAHPRYFTSWSLEEAVQLMLHYVVLGLE

LELYALSELGIIYWYLDYLEGTRLQNLDGTWALVEKMMEIMPAARLHEPLVIKQTHVSGK

ATKKSKAKSKKSYANHTPKALGPPRDLVDPIKARFLREIKYTELLRSLMRGYFQVFHALE

REGLVQVKVPIYSTLALRFQHRFAAFQKVHYPAALTFEDYSQNSNFSLYEIDLIYKSSEE

CFKSARVHAEALLNDEEGVNTIATTDGEWVVRGLELSSLLKVCISNCVRLAQRSGCMRKM

TTSENQMDFDFSIHPHFPILIFPSL

>contig41686 Frame-0R|Blast-RNA polymerase II subunit A C-terminal domain phosphatase, putative [Phytophthora infestans T30-4](gb|EEY68482.1|) 3e-43

MLERDMLTKDCPQRWQDLSVKELQSLDVVLCFDDRIFEIVLEDLQLRGVAQSCFRFSEVS

GNELITTWRPLHLLCLDTKDTPEHAKVGGSLALELCQA

>contig42391 Frame-2F

MPSTSQRSSSTDSSTSRPRGHLLRQESAVCDQLRRDKFNMALRINYLETQLQHLLEGKGY

TEAEVLAELAELRMTLTKRENELHEYALKSSLMTNEPDKNAKTTTENQDQTVADFVSYKS

MYTALQAELSATMQLKKQATDDADKLRRQVTNLSIDYKSQGIAMRKLQSDYKTAQDKIYQ

LETQGCCNNNVEALNDGLINKLGKNGQELIVTEV

>contig43550 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70543.1|) 2e-56

MTLLTEMETLKTTNEIKMATLLANKDEHACSIASQQIYDLEAQLATSEADKAVAQKDAER

LQKDLNALEGVLHRFQMNSKVQKERVAAMEAALERAKQELQSHQAILEPSEGIANDYQRV

LAKLAEKTRECEQLREALESSTMQYYSDREVLDKRLAAQLV

>contig44036 Frame-1R

MTLPLHRARQCNFTRVWAADATTAESVLNLQQQQLATWSATNASGVSITKGALELQNTTL

RITIPLNSTITLHRLAMRTHLPPNAQSKLEVQLNGRMLAIETPKGIARNEVVLTLQQTPF

VAIKLPCIQDTVDTFFDVELVWHNKWVRWYVDG

>contig46988 Frame-0F|Blast-replication factor C subunit 3 [Phytophthora infestans T30-4](gb|EEY69694.1|) 1e-175

MLWVDKHRPTTLSEMDYHSEVAKRLSNLSQSADLPHLLVYGPSGAGKKTRIMALLRALYG

DGALKVRLEHKSFKVPNRSTKVEITTVASNFHIEMNPSDVGSSDRLVVQEVLKEIAQYHM

ADANAQRPFKVVLLMEVDRLSKSAQHALRRTMEKYTATCRLILCCTNPSKVIDPLRSRCL

GVRVGAPTILDICKILEDVCCKEGLDYCAPLGKTIALRSERNLRRALLMLETCRVQCYPF

MPDQQIQLPAWEEYICSLAKVVLQEQSPAGFVVHLLSSWRFCQLFTFCFCCCSILKAREM

IYELIANCVPSEVILKVLCRELISRLDDDLKHEVVQWASYYEHRMQRGSKGIFHFEAFLA

KFMTLYSNNDVFDRSMPATCSSFLRRRRTARCVQATMLLTRCFKVNSILCRFHTSVGRRI

TQATNFQVWRIARAGGAFEECLNQRGVIKEQHRVVNISVIPCSLVLFII

>contig48164 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56197.1|) 1e-160

MDNEGPQIRVKFVTKDASIRVTETPFAVPTRLHRRGLSQVVNHLLAAADNSRPFDFLIDG

VFLRSSLEKYLQTHGVSEEALLTLEYVEALPEPQKHNQSEHPDWVSAVAAINDDLVVTGC

YDGVLRVYDTHGDCKASIKAHQGAIKAVSVALSHETGEFVISSSGKDQLAQLWKYTAESK

RLTPLAALAGHLNSVDAVQMDSSSKWVVTGSWDNTVRVWQTPHGLETPTEGSLVKKRKTT

ANGAKTVSFQQLQADIVLVGHTCSVTSVAFQPKASENDETVVVSAGSDRTVRLWDLLTQS

CSQSLVGNRAVSALSVNTGGLILTAHPDHCIRLWDPRAQQSGESIVQCTFRSHKQWVSSV

AW

>contig50200 Frame-2R|Blast-transcription elongation factor, putative [Phytophthora infestans T30-4](gb|EEY53186.1|) 1e-142

MEDAKHLHHRLLKFTRGDVADDSEALEMLRALENTEVTYAILKETKLGHTVGKLRKHENE

KIASLARLLVKSWKNMALSPRPAASKSQREASHNHSKSLENKMPMKAKEGSNGLKTAPRP

AAARANSAPFIPAGLDKVRATVRSKLKEILEASEGGDPSQVAAAIEVAMARTYQMGAPVE

QKKEYMAKYRQLSFNLKKNGELRQHMLDDSVSGDQLVKMSAEELATEEKRAQIEKLRDDA

FQEARLDWAEANHEKIQKQTGTEGTKGLFTCGRCKSSKTSNTQKQTRSADEPMTVFVMCH

NCG

>contig50785 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69992.1|) 6e-11

MLLHDICHFHAVVSISRTTRDGIRCTEVRRPFKASWTATQSRITTEVHARS

>contig52952 Frame-0R

MDRLTILDSEFIKMHWSGLYGCGKAEVVKADCRSNKTVITTESVDGYIVLAIVETLA

>contig54446 Frame-0F|Blast-phosphoserine aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY57574.1|) 2e-52

MLSRCFLDVCNRTLYLQRVTGDEEARALSLVLMELSRKLFGAQVAPSVANLLYLGLLQPS

ALSREQWLLETQSLPPLP

>contig54657 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64166.1|) 1e-66

MQTTEDINSATLVWTVSMRQRLQTCIAMELAKVRVAANAKTWPRWNPEQFIAPASFRYQY

SELADVLVLHDIYLANFVAARAEDLNIEVIDVAAFSEALLISVQSFENVLRILHERGLSD

SRQEAVLRLMRQALNKLVSKHPQHNLEVEFNCNDPLSRDSAFMSPAHSCDTL

>contig54921 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58623.1|) 4e-46

MPYLLMHVMYLPRISTDERSWFLRFIQFPRAMVRTDGSLCHEWSEDLVDH

>contig55742 Frame-0F

MVLLTSRQRNNLRFTIVVLFL

>contig57872 Frame-2F|Blast-mitochondrial folate transporter/carrier, putative [Phytophthora infestans T30-4](gb|EEY62449.1|) 5e-25

MTLNELLTQDQWRSVINTTAGLGAGAVSTVLLYPLDLVKVRYQVHEKSAHAYRSLGHAFR

SIV

>contig58280 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65987.1|) 2e-16

MDDLLLGFNGGLYLAQLVLYASLFLYDKNGIFDDEKQIHLSL

>contig59500-1 Frame-2R1

MHENGADGEIGLHLLNTVEISIQDGTRG

>contig00787 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56833.1|) 2e-84

MIATTLQVERENRSGGKSHGTSCTLMNYMEIARRHYEKALKYFGVMEIGKIFVLIHQELA

ELHLLSQRLEGIEHALLILLNTYEAFHFQLVNESRLEKEELGPLGHTIVAKVQTVLHDLI

RLCSIKQAQQGGSIVHAKSQKLERFKNMYKEVIYYDGSSLETVVSILG

>contig01766 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62841.1|) 9e-65

MLKGLRKDLTGRAKICTTATDFRQLQATWYLLPGETVMFAFISSKKEFAFTNEALIMIVG

ESATTTRKLVHRMSYQECPIYNVVFETTGRLDRDCAIQFRIGQTHVTIEIARKEEASVKR

FYKTLWLLGREQETRMRTWEQAQKGLDRAAKSLTIRKGHELVSQASHVAAWLENTFFQYN

SRCYRDIITAAMKSTAPSV

>contig02033 Frame-0F|Blast-eukaryotic initiation factor 4E, putative [Phytophthora infestans T30-4](gb|EEY66580.1|) 3e-07

MESEKTTKKEVAAKPAIVEKGDEEEHPLQTGWSLW

>contig03720 Frame-1R

MYTKNIHSKMTTTTRTATKNLATRIKATEPTQPEVLKKEMNNVKAATLKAVKLPINPIDL

KEPTMLKEGIVGSTTIAEDAFQSVVPSVKLSVPTDPVTPLLVAKEVETLSGETLELPVIP

ITVKEPRLSKEILVTVQEMSEDLIEPIENPAKGWRAERTAAPASEVLDVTPVTLERSDDF

GNTQTVVANEPTDNALIESLEQRALEHEFVQVELTQSMTLPQRDCELENTNVATVTTIAD

NKVLKVEPFDATEDLQMEPIVAIDAVASATGPYAHLSSWEAIGFSSDETFAIANETAPPA

SLDTSNESTEPLDSLVTDAVTENTVALDKDASSPVDRNDFLLGNRNRHRNRSKKSKNKKK

KTKKLLKQP

>contig04934 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69614.1|) 7e-50

MKELDDLLSQASRSQSMAAHQTLVDLIEAKAASQQLFHKIQAIREKAEQSEAMVQETCRD

IKQLDYAKRHLQTTLTALKRV

>contig09663 Frame-1F

MFQVRVVCVNQRGPPHFRLGVAMLKKKAIAIYQYHSTEKKYAFLREFSTQEIPEAMSWYR

NKVVVGFRKNYYLLNDKSGEAILINSPGIQDSSVYPIVKLLPKEEILIAVMDRVGVFVGF

TGDALPKNSFTWSQSPLHVEFSSPYLLALVPRVGVEIHRAIDGVLVQTMPLPRAVCMFGN

GMKWDMEPRQSGDTEDVILIGMRDSSGVSSVLKIEPMPLEQQVGELLDRGYIEEAQNLVR

KSIASLSSDKQRSKIKRFQRQATVALLRRMEFDQAADYMYRAAIEPCEFIAFFPDLQCAS

FAYEPAVLKPEVLPRGNTSAPNITSVVQELLSSPRAPLSSEIANTEASDLVNAAHKALLK

FLNQYKKHMRDKARARVPATSLRNRSTSNPKDTRRIEAIDTALFRLYVHFKRYKELLALI

QEPNPDVENHLLGSLGGCALELESCRAVLIQHKLFYEAGQLLTAHQKYDEALEIFALLHH

GEYKQRGGSSGMPKSPIEAAIDVLVSVPESDSTFIMKQSIWIIKATSAKQALRIFTERRS

PLPSNDVVAHLREHSNDPAIVQRYLETLVKTNGETGAALTSSNTIATGMDGRNGHEGSTR

GFGAFADPELGVNDSYSNFLAGEHDDDEEPPLRGFDERVDSIVIDPHHTRLAMEYLDETL

RLVAKGDVPSKSQPGKEPGKLGEARKRLLKFLKSSSSRFDVTPLVEKIKGKPLYNEFVIL

CGRGSLHEEAVTALVYELNDLRGAESYSVKYGARTTLERSSTNTTSKTGAVERNDALVEL

IKICFAPRDESKKSAFNDFGFQLLGRHGKRLDSAVVLEMVPPSTPLSKLGEFFAQALPHS

AHNVREMSITKSLSNVYNLQVQCDRVEHLTQSVQIDPNTLCPVCHKRIGDIVFAVYPNGK

VVHYNCTNSNLQLC

>contig13251 Frame-0F

MGQSYSKTKLLAAIPLLVAAALLIASMNVPLAFGSTERSVVSRRLAAPNVASTINHDEHL

LAKLAREISEKWNNLFFKKSDSIPSNPHDLLETIQVLERNTNTHLANQPIKNKGYPAIAK

ALLDKYDLIPLASKIAQFKEYGPEDLKPLFDGTLKVILSRMEAKKISVYDVAASIQAPIK

WWVFKNMPQGFFEGELLMVYAKTDLELAAAMATRFDSLFQTLYRYKQEILPQRIVDACTV

TLSKSVETLIRELGLHNAGNNLFRLPQMHALVILASTMNLPNYGFIHLWEELLKIYPNGK

LLKLARQKQNVQSVSPSVQSFVTFVLEREALFKSRAIPSNQMRVVRGRVRQGKRIAKTT

>contig13699 Frame-0F|Blast-protein phosphatase methylesterase, putative [Phytophthora infestans T30-4](gb|EEY62129.1|) 1e-75

MVIDVVEGTAMASLKHMGTILERRPSRFCSYKDAIHWALQSGTGRNSEAVEVSIPSQLEQ

LGDGSLVWKTDLASTSKYWHDWFIGLSKQFLSLKQAKVLVLA

>contig15433 Frame-0F|Blast-putative GPI mannosyltransferase [Phytophthora infestans T30-4](gb|EEY68034.1|) 2e-14

MKLHEKMRRKLFQLAIVFIVLPNVLCAFYFSRCH

>contig19600 Frame-1F

MFWSEAAEYAAYVINPIQPELVLIARRQPKCSPSGHLV

>contig21489 Frame-0R|Blast-lysocardiolipin acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58650.1|) 1e-104

MLSGYLELVGGVNLVVTGDEKLEFKSQECVLLICNHRSEVDWIFFWNLAIRLNVHDRVRV

MLKSVIRYAPGAGWAMLLLQYPYINRNWASDEKRLSEAIRSYKTAERGFWLAMFPEGTAL

CDTTLKKSHEFAEKQGEAAWNYVLQPRVKGFELCIDHMDPDYVVDLTVAYLELMNGIRPS

PVRFLRGQFPIEVHLHVKRYHRSRLMVHKGYMDL

>contig24796 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY62844.1|) 1e-90

MWSYPFERSKFSHNVASNGPSRVSKRFNEVSRRSSVSIEKSVVFGCKWRESGHLWTHWIR

KSSLMSVLFRVVEIPTSGRVWIDGVDIATITVRQLRAKLTIIPQDPMLFSGSLRLNMDPF

GEKSDADLWHVLRKVHLYETVSSWGNGLDYEVAEKGENLSIGQRQLLCIARALIRDSKVI

VMDEATANVDQESDKVIQQTMKESFGGIDCTVLCIAHRMETIMDSNKILVLDAGEVVEFD

TPAALLQVKNGVFRSLVVSGKSP

>contig25368 Frame-1F

MARGLSLSRVAGTSASTASNNSSSGPSRVWTPLRENHFEPPLLSARERAYLVRKSCEAAQ

SLVERARSVSGPVAWRYVEKANGVQIYTGSLRSTASGTALSTATMCGVTSVPGTVTEVAS

LFQLGSTRQMKEFARAHREWFYDGIVLHTLAARTKEKPFHQVTAKWMVMQMPPGVAHRDF

CYLECQDKFMDARGRKGWVLGQHSIKLPGCDDLKREFGLVRGSLYHSGFVVVESEERAGH

VDVIHVVQLNLKDHTAMTPALLQSRVMFVAQVRNMMRSKRLNEQRYLSDLELVPRKYRSR

CAVCQDSFSLLLLRKFNCRKCGEVVCAACSKEFPIEHRSFSATNGGDEVRKLRICMHCFQ

VITNASKPTSALVEPPHSSAMSASFLGYHDDDQRAVRVGGALGVGTEDAPQIFLQSMRRP

KPLQSQMSRTSPIPSFKMDYQPSNSRHRTREGLDGSLHQRSQSSERQSYEYGPYRDSQVL

RSSEFQFSQSLSLDDPIARGEGCFTLRMPGAAVPTSPASIFDRPVNGRSQHEAPSPQSRD

MSNFSRLQMLSSRERLEQLQRQDNLMSSSTNDQRMPDAYMSALEQASRDKLDFDMPSLMY

QGPSSDFSAFSATMDDHSGMPSDFGQTLDDPNGPPPLDMSALTSAASRIPIGFDNMSMDA

MLPTASKDGGSERKYYPLPEQYRESTSSSVASIDIDTYDDDLGPFVRIPPIVERLNQENG

HSVKQELFNMPPAVVSIENRMNAVRIRDTDDDSDTSMGASDDEEERRANAMLVSSPHEQI

DGATEETKVQDFSATLALPSFFSSGREARRSSPESPLPSKVLTDSQQETAFTSNAQGMKH

MHKGDDEDLNVYEQHLQHSKAGNLIDYQIHSNEQPAMRVEGEVSRDFNDHGQGLLEGKDD

KGLDEKSFDDLGCDLTFPDAHLRQSNYRDIGQSHDIGEQKFEGELPVDLSFPSARGSSIC

SMDLDSATPPVTSLPAVPSLKDAA

>contig25838 Frame-0R|Blast-trafficking protein particle complex subunit, putative [Phytophthora infestans T30-4](gb|EEY62375.1|) 1e-99

MESGRRSTGVSATNLHVLDRPLSRGKSELSLSAFSFLFSEMVQYFQGRVQNISDLENRLD

GAGFGVGVRVVELLCHREKSARRETRLLAMLQFIVSTCWKALFGKAADALERSTENEDEY

MIHELEPLTNKFVSVPPDLGQLDCAAYIAGIVRGILCSSGFGAEVTAHSVEVSSGQRAKT

VFLVKFDENVIRRERVMA

>contig26310 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65174.1|) 1e-155

MMELDQVLVARFVARKNAAPKVVALIPHAPSPGKGENFYAMWSQQLPYEEDLRNYEFPPL

KTRKFIPSDEQQLLADKLIDSLSIRDDKIDEVGKCFNPVIRRFFHAVSMRALDESAGIPP

LPAYIESNLKMDPIRQEKISDLIERFGDAFQLKEAVKKAKDRKKKSFWSDMP

>contig26440 Frame-1F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY65836.1|) 0.0

MHLRRSGKKLEERIAVARRLMPILYGHYDNVTGQYELHNGSCSGNVGYEDSNSETFDTVN

IAIIGASIGAGLVLITVCLTWKAFVECCTNSHRRSRHRAFVNRSNDGLKCEICLHINETP

QTECVFCGTAIEESNTSQSRREETHPLTTTASRIEDIASSPSKEATYLNMFSPPVSSIRR

FNTIISPDLNPRQLVARERHQWKRCITGQNVRWVSVPFQALQENKALCGTIISERDFQDW

KKVHPFSEPGTSRMSISSLNHSDSSKQQFTWLNSETAFVRDVKDPSSDTAVWCLAEEFSA

SSRQYSKTVLRTSALSFSAKAQWFYLYSLKLSSSIVDGFHTIRVHRERVLKQSMTLFMSA

PSGFLHRRLRVDFMGEAGIDGGGILREWLHLVCSQISTEALGLFALTSSSAHQGYWIKRT

STAKSAKHLEMYEFFGKVLGKALLEGLFFNMRLSIPLLKHILGVPLKLSDLYLLDETVYS

SMMWILENDNTNALGLNFTIEGIELIPSGTNVTLHDGNKQLYVAKVAQYYLFESVQTEVS

CIVEGLRSIISDSALHIFDFKELDLLLSGLPHIDLSDWRLHTDVQFCEQTAQEFQLVEWF

WEILEALSQDQLGRLLQYVTGSSCVPSEGFKGLTGMDGEIQPFTIQLGKDAITEYTILPH

ASTCLNRLDLPLYSSKEELERMLKMV

>contig27065 Frame-0F|Blast-hypothetical protein PITG\_05283 [Phytophthora infestans T30-4](gb|EEY69099.1|) 4e-11

MDLGTVNLILVLPRRWNVPARYGDVPNAYITAEKEEYLDIYFKVPNFFKRTVAQGFPSEN

PKLNGLLVEEVTSRPEAGWTT

>contig28280 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66642.1|) 9e-71

MVAPGSRKPLASRLDAASRERLNARYEALTHVEEKFRNFDIVWAKVQGFPWWPGVLFLSW

DVVRQAGIRTDPKIVASLKVPPPRKIPIIGAASGKEKVAFRVKRHCLIMFLDKFNFSLLE

LDPSNVASYTAHYHLYEQAVLNSKNSKYAKKKAEFRRALVKATQLLHMGNEYTTDV

>contig28389 Frame-2R

MIVFCDPFLYLDPTTLFFFSLSSMGNVFKCRNIKKTQQEPWTPVTNDEIHSVASYKPQVV

TPVNSMSKINCTPTADSNLPRRLPTPSTPLINASRGNKESHSVTT

>contig32522 Frame-2F

MSNVCWGDLERMQKLKLKLCEPVTILHNALEIPETHKNETDTSSGSQTSCSSHDIWDDDC

SDEGCSDDGFNTNSDIQSVLPFNNKAEPLQLVHETGQVHWSKTPPPLPSPSPLRHTLENQ

ESYVKTFPGLCRVMPIVIPLELTPPNEFDMRCTNGLMKCVNILAPLPTLEQLSAKHLAFN

DLQRIVDIWLRRALDKLDPNSKSKDTATLLLGGSWHLKVGVAESDLDVVALMPYVVTAEL

FFSSLCEHLNKEIAVSDLVARRKAAVPVLSFQLSAVRIDLLFARFAQSKAVPTHLPFLPE

DDLQVMQGMDVTSVRSLSVARVASFILDLVPNASVFRSCLRVIRLWARRRGLYSNKAGYL

GGISWALLVCFVCQMFPRASVATLVHRFFSVLASWRWPMPILVAHASPEGKTDQSVQWDP

HHNIHDRAHLMPIITPGFPAVNTAVNVNISTL

>contig32908 Frame-1F

MASSSSSSAVWDSATQTFHGGQDWKFLSIFKEDFSVTTNALGTPKKALEAATQAMKTIHH

YPPADFQPASSDLAEFLWPTTWEENLPLLLMGNGASELIDLVIRSVQPGGWRPGGTVTQY

KEYERSSTADGRKTLAWNDPTAALTCVVNPTNPTGDYMNVNDMKTYIETYCPDNHTIIID

ESMQPWIGPQWRHDSLIHQREWVQNLSETRHINVWVMTSWTKIWSCTGLRIGSVVAPTPQ

HAATIKRKQVPWSVNSMALAFVSAVVKDEAYLQETWNLTSKWRAHTVEHLTRQFPSWEFF

GKPFLSWIWVDTKSEAICEEACKLAKEHGVPVRSGKPGYHLATFLRIAVRSPELTDVLLQ

AWKLLQ

>contig36557 Frame-2F|Blast-serine hydrolase (FSH1), putative [Phytophthora infestans T30-4](gb|EEY58329.1|) 1e-31

MPSLHIIGETDRVVPKDSSLVLKDMFINPTVLMHPGGHYIPTNKERKDALRAFFEKRRTD

V

>contig39725 Frame-0F

MPPRRNSQQKESEQDTSRPRRGRGRGGGRGRGPAASASPAPAPGPPSAARTSAPPLTPAQ

PCVTSLASAFEEKVGLPDEPRLVQPVVRTHFPPRPGFGKAGKAVKLHVNHFKVNFRQAGD

VYHYDVMMAEDGRSFGNDGPPKALATKIMGALLNELKRQFPDVLLVSDARKNIYSPRRLP

FPSKVFGALKLGDDGGRDRDFSATVKEADPVAIRMQQLDELFAGRLNYTPYDALQALDVA

LRHSASQRFTVVGRNLFSATGSKSLGEGAELWFGYFQSLRATQNRLVVNLDLAATAFVEE

MDVLDFLVKSLNARDLPTTLAKYQHSAFSKAIRGVKVSITHRPGVKRSYRVNGLTKTSAQ

DTFFTDDDGKRVSIVQYFQQAYKLRLRYPKLPCLHVGAPQKKNYLP

>contig40772 Frame-2F

MGTARNGVLIMSWAIMIKEYLCDIKYGMGESMSPTIPDGSFVFSENMSRRWRNWKRGDIV

QLRSPTRYTGETITKRIIAV

>contig41106 Frame-0R|Blast-citrate synthase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY61713.1|) 0.0

MSTIIHSLRQTAASATRSIAAPVTARTLSTSASTLLDELKKQVPKRQEALKKLKAEHGHK

SLGEVTVDQTLGGARGIKSLLWETSLLDAEEGIRFRGHTIPNLQHCLPKIEKDGEPLPEG

LLWLLMTGEVPTADQAASVTAELHSRAKVPDHVRKLIHGLKHAHPMTQLSAAVTAMNTES

IFAKKYSEGIHKSTYWKYTYEDSMNLIACLPEVAALIYRNTYFSESNHAYDSSLDYSANF

NRMLGFDNAEFDELMRLYLVIHSDHEGGNASAHTTHLVGSTLSDPYLSLAGGLNALAGPL

HGLANQEVLGWILGLQAEFRTKGLDVNKETITQFAWDTLNAGKVIPGYGHAVLRKTDPRY

TCQREFGLKYMPNDELFRIVDTIYQVMPGVLTEHGKTKNPYPNVDSHSGVLLQYYGLTQK

NYYTVLFGVSRAIGVLSQLFWDRALSLPLERPKSVTSEWINDYFADKK

>contig41681 Frame-2R|Blast-RNA polymerase II subunit A C-terminal domain phosphatase, putative [Phytophthora infestans T30-4](gb|EEY68482.1|) 3e-32

MPRPMFAMLCANNVNRSTEAHDHLRSAGLRVCSFGAGNRVRFPGPSRDDPRIYEFFTPYE

TMYRELKAENADL

>contig43438 Frame-0R

MHSDIMGPMEKISQGVARYIVRFIDEFSRYTVAYFKSYKSEVVDRFTIYKALVEILMDFP

IKYIRTDNGSEYINKRFAEICRKLKLSTKQLCRSYRSKMDWQRKE

>contig43557 Frame-0R

MKVAMHLLASYALSAVRALEVHNDDALVKNLPGLLNDLSFKHYAGYMHLKTEEKLFYWYT

ESQTDPANDPIVLWLNGGPGCSSLGGFFTENGPFVAQDDRSVKVNRYSWNRKANVVWLES

PAGVGFSGSVQEPHYYNDDIVAAKTREFLELFFEKFSELQNRAFYITGESYAGMYIPYLI

DMLVTKPLRGVNVKGFAIGNPFTDNLIDGNAYIDY

>contig44031 Frame-2F

MGYSSEYDVSGIADPFLQVAILKLLRLLGKDNEEASEAMNDVLAQVATNTETAKTAGNAI

LYECVQTIMTIESDSGLRVLAINILGRFLLNRDNNIRYVALNTLSKVVTGDIAAVQRHTN

TIVDCLKDPDTSIRQRALELMYALVNSSNIQMLAREMLNYLVIASNDQKPELCSRVADAV

DRYAPSSRWHIDTLITMLSIAGATLPDERICSSLITLIQRNTDLHPYVVHKLFRALRDDV

SQLSLVHVGIWCVGEYSQFLLLDAPLSENTLSDKSHVDESSVVELFETILRHHASTDITR

AYALNAMVKLTTRFSSQSDIAKLNKMISTFNTSMVLELQQRASEYTMIGQPQWSTLRNDI

LATMPAIDASKVRNRNDNLVSSVMNPADLLGDEEMSVQKAEAPLKPVSTLQSSASASLLD

LDDIFGGGASTSSASVSTLAPAAPPAVDLLADIFSSNPVAPAGPAVSMFDSSSSSAAPSN

ANDLLSLMNFGTPALTANPALRAYEKNGLSVDLAITKPNSNDLSVTYITATTRNASVVPI

EKFVLLAAFPKYIKLKMEPPTGDAVPP

>contig44329 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53709.1|) 3e-91

MAVEGKCSVHSCDKFDASQGFCLAYGGGRDCLINDCSKRAIRYGLCSGHGGRARCKVEGC

EKYDRGQGKCKAHGGGYFCKVQGCSKKDKGGGLCVAHGGGKKCSFEGCATPCVGGGRCKL

HGGGKRCQAERCSNWAHNGGQCKQHGGTG

>contig45458 Frame-2F

MQQTHDVGAVAASERLKKKIKWFDILPVLLQNFKTQNQEQIRHLMLPRCELCERGKVDRK

AEVKCNQDGCKMKDQVMCLTCWRSSHSVECLRTHPQVLASVCRQCQVDRIAYWCAECDLQ

FCSKCFDLIHSVVMVKCHRKLATEDAPGPCVAKSHWSVNFQKVIRQMVAVQRHSHQATKG

FPGPGAGRKLKRSVEVIVIDDDEADDNDDLTCVQSNVSLSHENFGQQVGNEALKFYESKL

NLKVIRQDIKKHLLPLDRILLSLKVYNRLRIYYHTIQQLISQI

>contig46613 Frame-0R

METMTDAFMTAAVLAAVADGKTTITGIANQRVKECNRIEVMVTELRKIGVECGELSDGMW

IKGTAGKTNHLEKASIACHNDHRIAMSFAVLGSVVNNVIITDKECTDKTYPEFWDHVQRH

LGLQVVPVVDKVACRTETTVPGVFLIGMRGAGKSSLARAASVALKMDLLDTDEQLEKEFG

ESIADFIARHNHTWKAFRERQKELLLRLIANPPPATIISCGGGVVETVDIVDALEKYPYV

VHVHRDVKDVVAYLDSDEESHRPSLGDSHANVWTRREPLYQRSATFEFVVNASDVDFIRI

DRDFVRFLRVILPGLSTSFDYRSSCRSDTFFLSLTFPDVNDARPVIREISKTVDALELRV

DLLKYPDDMKFVAAQVALLRALSTLPIIFTVRSKGQGGAFPDGVEHESKMFELLHLGVRV

GCEFVDMETCWSRKACEQLLLHRHRSAIISSFHAVQKPISEAETKAIFHQCYAQGQVQVV

KVVVKAYSSDDVLMVDRVAKDVAKVWRQYMPIISLCTTSAGKLSRVLNRTLTPTTHPLMP

AAAAPGQLSVEEIMTLRKQLGLLPAREFFLFGSPIQQSPSPAMHMAGFESTSLSSFFTYG

LHDTTNVLDIVKRMEAPDTNFGGGSVTIPLKVDIMKHLNELSPAAQAIGAVNTILRQDRG

GSLYWLGENTDWLGILRPIQMRLAARNVPVHDLTALVIGAGGTSMAAMYAMRQMGIAKLF

IYNRTLDKSQAVAARFSATALSELTPETLGHVDVVVGTIPAQAGFQLPDYLVTQRADRSK

TVVLDAAYMPPITPMLAHAHAAGGALCIQGYEMLYEQGIEQFNRWHKATHAGTVNEEAIK

EACRRHVPVDQRLSQA

>contig47272 Frame-0R

MRKWKANSYVLSVCLLASEYVRQQQHSAQPRDDSIAPLADAAQPSEPAITTPSLNALACF

LSEEIQQPLQQNKTGSIRTGCTTLHNLLRRLEISLSNERDFQQLSWQVVSILTQIQSPDA

MCNVVERISECVAPLQSLSGVEQDVDSANSTLTRTS

>contig47522 Frame-1R

MRFQKLYRRRSLKCSTPHQLTHLCNNESLSCGLCATLSLLQSTKKWHPLTSA

>contig50207 Frame-2F

MLRERNTFVLKAICGNEERRHAITLHVNLRKQDLAHFNGTHDDTTSQDKLVQRLLDMLDG

DESFQT

>contig50508 Frame-1F

MKTIQAVQPFQSPVQQMQPLLHEQQGHTLQEMQRQHIQTMQLLMQPDQQPQDMTMASEFE

DHSIL

>contig51213 Frame-2F

MTKVVADDQSFQLMQDRADAECKIAKENELALAHTELEQEHERCEQACSRIDKSPITLPL

SSDKLCALQAELEQESDFHLRREAGTSQREGINQVCQEQSDAEFAFARSKQQLEDFRVDK

ECTNEELAECNDMLEVLTDDQALIKAENVMLKAQLKEIRLKFGVDDDASLHSLINNLLEE

KNHL

>contig52025 Frame-1F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY57593.1|) 2e-40

MSEEVMKRAEEQRKLEQLQMEREAVVKQMEALYTQRDKLEKEVKKSILSQSNIRDVLTSP

FLKNLHPTPNESGRQQELNSAEEQLLYDLEERIEACQAQLEYKEEKISEIAIDA

>contig52256 Frame-2F

MQTAPGVVIFMQYELLHFNINGCNYASHKFWNLARHNVNSLERHSHI

>contig53134 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55750.1|) 2e-24

MATKKRCGQRYDRIICLTLRSVQLAMCIVALAFVGASFQSHTLSFETDDGETHDVTVYYG

GPAVNLVMVVTFAACLYDLYFLLL

>contig53141 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70505.1|) 3e-08

MARQQRKKARVHGVAARSKSSVSHLNDPVQADALGAAAVAATFGNDAASTVDKEAENEPN

ALQNYSRGQRKRLKRRAAF

>contig54139 Frame-0R|Blast-pre-mRNA-splicing factor SYF1-like protein [Phytophthora infestans T30-4](gb|EEY57316.1|) 3e-70

MMAMLQPPSASEMTMTDSAIFEYEEATARQPFAIQTWTAYLRALADAPLTARCSIYERAL

QFLPRSYKLWKLYLDEFYDKQVRGQRVDAPSFGHLVALYDRALTQLSTMPKLWLNYLHVL

NEMRLVTGRRHVFDRALRALPITQHHRIWTPYLAFIKQIGVSRTAV

>contig54434 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59892.1|) 3e-08

MAAAYQLATERPHITLSSRRDVTGIDTLQTPITTFTELLNAAQTVETNTHKKNATAL

>contig54650 Frame-1F|Blast-CLPTM1-like membrane protein, putative [Phytophthora infestans T30-4](gb|EEY59215.1|) 7e-16

MTAAAVNDVAAPAQESLLDRLWPMLRMFLLYYAVTSAVNLFAPRPQHEPQNTNVVVKNAD

NSNSR

>contig55143 Frame-1F

MVLRWEPLRPAGPSVKNHTATAISAHELLLFGGYDGRRNHNALHLLDVSRRTWRELS

>contig55833 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53147.1|) 1e-21

MDSVAGVPNFFEKDAIFTYRRCSIFDNKAEDISGVLEGCIAFIGQAKYYG

>contig58287-0 Frame-1F0

MVKLVCALIGVKGVFSVIIDEKELVADLNKAIKTENSNIIKCDARELKLFLARKGDAWLS

G

>contig58287-1 Frame-2R1

MFEFSVLIALFKSATNSFSSMITENTPFTPIRAHTSFTICISSFSFEL

>contig58621 Frame-2F

MASPVSRQEFEFINVACRTFKSGHYQFFYAGRAWHHARTSLKGVTAKQTGLTTALIGHNM

PTPALKRIKSYKNICKNSF

>contig58654-1 Frame-0R1

MKSSLKKFRLEFFKYVFLQLNKNLSNGKSDGLANNLVKL

>contig58870 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69208.1|) 4e-17

MDLYADLPLAKGAKASSALDVDGKLKVSISSSSSVWASAPLMVPQAAKNKNKN

>contig59208-1 Frame-1R1

MGFPRLVLVNIRVYWTMNIIFKNGCRILFFVEIF

>contig00786 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56833.1|) 9e-16

MMKKLGNASNELGKYFLAAKQEYKEAFKWFERGCKIFSDI

>contig04427 Frame-2F

MVPCFSTVVLFIAMQLAAAAARTTTTSNVPQVAPPLGTRKVTTSRLKVNNATLINNEAEE

QERGFWGFWRPEETKLLRKFQTHQKKTITWNFALTKKFEKLGQLIHYRTKSEEAVATELI

KVIGEAELARFTDKQVSQLLFAPIYETIQSGLLKYWRSNERSVASIVQLFEIDPILLSQT

RLHEDVMLSAMIFIDQFPMNTVLKYLNPDNKHDHLKLIATLSERFNINAPEWIRIHYKNK

QTEVVKPLYAAAIAPVKEMVEVLGLKNAESISLSQIRMLLGFAQGSWRKKLNEVIEALPD

KCIYEAANELLNEPLNDFNRKFLGQVGAKFSKEFPNQPNPFLDPLAAQPHPNTP

>contig04492 Frame-0F

MYRPSSLRLVIFAAMTMTSGSQLVGTGTPEVHPPLKTQACTTSGCTDEDTSVVLDANWRW

LNKGGKNCYTGNKWDTTICTDPKTCASECALDGADYKGTYGIVTESDSLTLTLVTEGKYS

TNIGSRVYLMESDDKYKMFKLLNQEFTFDVDVSNVGCGLNGAIYFVDMEADGGMKRFPTN

KAGAKYGTGYCDAQCPQDIKFISGEANIIDWTPSKTDKNAGTGKYGSCCAEMDIWEANSI

SNAYTPHPCTSKIGGSHRCTTPKECGAGKNRYNGLCDKDGCDFNPFRMGNETFFGPGPKF

TIDTTKKITVVTQFLTSDKTAAGDLVEIKRFYSQNGVTHEIASSTFPALKGMNSITDPHC

SAAKKLFGDPDDHKIKGGLVQMGEAMKSGMVLTLSLWTDHAAQCLWLDSDYPVGADPSKP

GVSRGTCSKSSGVPDEVIAEHPDANIVVSNIRFGDIGTTVKGLPASKRTKKAAVAPPGEV

GNEAEVGNEAEVGNEAEVEAGGDAYSMPGTSCRRRS

>contig04935-0 Frame-2F0

MVRGDFKANDHSDDGTSAVGLQRKVKETLV

>contig12510 Frame-1F

MKTGYTTISPHEVRRWMAKPPQQLRTEFQGGLPYESISSITNEEDSEWFGDDPPKRLQRH

SEDMIQRTTKFTPNETLFLPTDYVEQQRRRCNTRIERSNSRQTLDPRFLVRQYSRATGNS

KLSSRALPIGCNPSMRSSRPEPLSIHEKQSINEPTDTGLVRVSCEKRYKSTTARSSFSKS

LMEQQMETLNQGHKVKGTPNLQSSCSSARL

>contig13225 Frame-2F

MAWVTDNIGYIAWLVPIIGICTMFGTEVLACLYHFTCSKNFPTLSYAATFKPEAYVFTSG

MSLTALCILVSVLLFFWYLQIHHNEHKSTPDNRVAAKVYLGFGVTSAFSLFGLAVMDMRY

HHVAHLWFTIVFFLSTWVMLLTAQLVRKRILQFDNCDNLALTRRPLTVLRQQSFWLVLCR

SRRLDNVTAYVLGHLFVCTGLASTLLFAIFFLCANDMWPNPLGLTALQEAFFEALAIVCQ

LFFMGTLSCELAQLHQREEFKNNAIKV

>contig13698 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58939.1|) 2e-61

MISSVNSLVASALAATCVSGHGYMYKPAAFFSPESGDKTQYIATIDSSGTDFLGVYNTAP

NANVEAYTKAFAASKYKSLKELIDDKAVITVTGATLTCGNADPAAVPQPLPAQVEWVHSS

GEGFTASHEGPCEVWCDNERAFQDDNCPAHFTTAPAQLPYDKTKCTGASFLTLYWMAMHG

PSWQIYVNCAP

>contig14736 Frame-0F

MSSPNACHFFQSPQGCFRGSSCTFLHNNDASTVNITLTATNPYIPTPNPLRTCHFFASES

GCRNGNNCPFVHTVVDINTLESFESVAYDEMVAPQLPPVAMSNGSAGVYNKSGLAITRPP

DYNESNKTLVVEKNNGNTKLQFQGNLQLQETISEILPVLTRDIEGPFFAIDVECVATGNG

TNDRDVARIAVVDVNENVVFDQYVKPGK

>contig15432 Frame-2F|Blast-putative GPI mannosyltransferase [Phytophthora infestans T30-4](gb|EEY68034.1|) 2e-18

MDFLADHIQGTHSICVYNFNLAGYIIYLVENSEVSIHFWTPCHATPYYSYLHQNVSMWFP

DCSPA

>contig15487 Frame-2F

MTESWQAACRDFHDNLQMHALTSSTCVKTPIIVASSRSSAIASNSASARQELSKDDYSPP

RSLLSFPLVAEFTNAVLSSLNELRQCAIVTLRTRMKKHYQSAIGTLLFTIAEFVTENGLN

RINCTSEENETNQSSKQTVLAESIHAMNL

>contig17805 Frame-1F

MPSIFAIFAATAALIFAKVDGHGKMTCPVIRSVTKLFRESCGALINIGDEQLTIAPLENL

AGFKQADFPPSPTFNLMNGCRGTVYEKGNNVTNLKAGKPFDFKYWIQAPHPGYMRLSVVK

PTTDSKGIINYKVYKEVMKLDSFATNGGDQSAPATMPADVTECAEPGECVLQMYWHSDRD

SQTYASCADITVTGGSGGKPSKPATPAKSVKQAKPAPSTPPSPTPAPAPAAVKANPSISV

TQSEVGADAEHTGK

>contig18479 Frame-1F

MNVRSFLASRCRSKQLLCTSFSCAEKSLCFRLQAITCK

>contig21949 Frame-2F

MSYLPNLLRTKRKMSGPVGTWGPLDDKSLVSWPEVIGVSLNVGGGRKTGSWYESVDNREV

ATFALFALYMVSDVGLGVMVWVTFFKFIIESDLNRSRATWGGIWLLFAGIFFYIRRLVRS

RVDIHLRSMMDHAEIFVAMSLVMVFSVNISFFLHVPAATPLKDLGFMLIPEQTLHSKWRP

VSDILTAGLPVIFLLQTIVMSRPSRCRIVSSFFRIATICYFLRMLTVSVTSLPGPAPHCR

AGNLDYFPPATWIDIVTRVGPIYGNYNSCGDLIFSGHMAYTNSAVLLYLRTL

>contig23226 Frame-2R

MGFSDMFSLPGVMCLDTTPLPTSRTEAAKVRLKSFFHSCLNVFRWRKHLGSELTQYYRPA

KPSEK

>contig24722 Frame-1F

MEPRGGVPKASLPGFVSTSILTSSDGLFGDNAEEKRVTEAPTSQLEATGVYKPLYEQLQE

RKETKDLEWKEKNNPFAPPKGLDEEEFEYFQDLESKKQDIKRKRQAQHEEDLAFFVAARG

TPKPASAVMFTAQHLQKYHDKGDVKTTIDSETPILVLKAKRKAENVTADSSTAESLTFIN

KKLKEVNSGKLLEKPKLSTAALGLGDYGSGSDSDDADEKQ

>contig24797 Frame-1F

MRRRLFFWHRTFICSSIYLSSSIVRKHYDHDSRQPKIILTKLLRAYAVQERKFIRQESCK

GRKSHSSLPGFLHRSRSFSVSTQSC

>contig25413 Frame-2F

MMRKCSLPRTRSESEVPRLQDLEHAVQAEIDDIRGHEELFLRSTSELTLMMKKLGRKQGR

AYFRYVLRDVFGEKSRLYETRGPPSTEQVCVYAKSVIQRLAKALHFAPLVLRACCHYMLT

EFRKAFPECKQDVRIVVGSLLFLRILCPALVKPELFEFPAHTSHSLLMGVQIAKLLQHTL

SGTPVGDSNLDDSNAFINAFQSDVATFLVRFPQIHNGFGRKELQNRPGMHSSPSSLTPSR

PADAATWAHVQSWDAHRSNRNLRALSMSFSDVIKNKTKFSLRFWSRGTR

>contig25956 Frame-1R

MFNSNPGDYAFGNMANVINQLMQNDPNR

>contig27064 Frame-1R

MPKAGQSEVQVHSSVRKRVAKARNPE

>contig27217 Frame-2R

MINSCLTSASSTSYYRTLSFHPPLIVHNLTAGSLDFCMATPCDWSPATNSESLSNVGKIG

WEVSEQRLRERGTINVADSLIWHLSGEETPLELSIRMKGYNWSEMLQLSKDTGELVQIKM

KDLVSDAHLYITAEIRISKGPCREIFLHVPYWIVNLTGLKLEFEFEKERMGREHSTSLLA

GQKRLDRDELLLQEGHGARSARRHRNPHLLYPISIDVNELTDESLNYAQPCVSPVPTVSF

DRRVSEHKRRHLQLLPSIPPLKGLLDLLPKRDNTDPRSLGQLEVLQVCHSNYNRKRGCIR

LRVSDDKDLAALDLRKKNEQRKWSDSFLLDQAGTIGEIEAVDFEANRKYCIGYSITPASG

QYSRTKVIMLTPRFILVNTMTYAVEVCHSSSKVMAPMKNDILHANSAMPDPRTMSSVNSV

VHLEAGGFADFHWTLQFSKTRTMRCRFTEIGWSWSGAVPLVDSGEYVVRLRHETTRESRL

VRVILKLDSPSVCVYFREERMAMPPYRVENYSLETLRTHQHRVRRSEVLLPHHSLDYAWD

EPTEEQLLVVDILPSAAGDNSRPLRIGSFNLDKIQRHPDALGGTLG

>contig28281 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62644.1|) 1e-36

MPYRRSPCPAINTLANHGYIPRNGQDINKYALGYALITVFNLGQDAAANFLTLVPDVFSL

DFLSTHNALSTMRR

>contig29123 Frame-0R

MKSDVCSLSVNVLEAHSLGNTMMFAVKVACKGTSTTVYKSKEDFKSVLNMFRLVGAMCRA

KNDRCEVCAECSAVCPVRVNDEESLDHFLNYVLSKLRKSDVAAIEKCSTHRGVVQILMDF

LNVRHGRYFCEHTSSSSPQDVLNNDVDHPLLRCSLNRKLSEQFAARDSVC

>contig30253 Frame-2R

MQASETLFVKSNANHYSKGLQLSFAIKNAFYGATLYVLDTLDASTFCWQKTARPLAEPLY

TGSLQLCRGDDTCSRDTLRASAAVSVYTLNGCPGQCYELFLITTLEGKSNQVYFILPLTP

GVNGGGEE

>contig31045 Frame-2R

MSERSTRKFKVVLLGEGRVGKTSILLRYIKGEYNDQQVSTLQASYLDKRLLVDNRRIALS

LWDTAGQERFHALGPIYYRDADGALLVYDITDAESFRKVRTWVRELRRIVGDDISICIAG

NKSDLHRNRKVPEDEAKRYADSVGAAHFDTSAKLNRGLEDVFVELTRRMLSRTGGKKKKG

SALIADDEDDEPSTRSSISRARPQPSSQPQ

>contig31496 Frame-0R

MKPLASKWKQRAEDNERSRENPKTLKIVDAPSTSYLLTQDAYFAGPEMGVALDQVVSRTI

DEMCSQSLRVVLCLSYLIETRPLFLTSATLSNIGRLHLPKAIIIYQRWRLSQWLTRQSIT

ESGKDSDACRTSSGTLMPTLLQSFFVTIYRKLYRSEHFKRALSVLQLASTRDSVRREAHD

VLVTFARELVQFVAQPNDALARFLRERHHVRVLRATLCCNLQALSLNCPKSGEDASLQQH

DHVHYYVRSIGECLALEGQNAAAIAHDDAHARWCFQQSIRCFSICLSNALLERHARVSRS

EKTLEPFIYDVVGFLKESIPRGYYDQLLGFLWTVVTQALSHLAHEDGGEETFAVQSFIWV

NVFKYSVEEQSYRDAHLALMHLVELTAALGGSDVAAEADETASECVNYLVKELYRCGHVD

LICELQWGSLESHVEKYLLWQAANATVFPSDGLDANAMRYYHLLYTFYMRKQQPANAASS

LYALALRLRLAAS

>contig32523 Frame-2F

MKLTKLRKNQQQQLALLLEAQNQNFQHAQLIEANQQDVENVLLVIRSALASGMNWNSLEE

LVRYEQKKGNPVASLIHKLDLEHNRVAILLCDEDDDGEGKDGGDGIGEEDKKAHVIWIDL

SLSALANARNIYTMKKKVGEKVLKATEATDKAIALAEKNTRKTLEKQQVKRNVIYQRRKI

FWFEKFHWFLTNEKYLVVAGKDAHQNELLVKRYLRKGDVYVHADLHGAATCVVRNRARIK

DPTTQALTPIPVATLEQAGCMSVCRSNAWTSQTISGAYWVHADQVSKSAPTGEYLTTGSF

MIRGKKNFIQPSRLEMGLAILYRIDESCIGNHTGLVEERELRGDIKEKGGSGEIKSQQEF

EVYTEETLAEEIEIKSPKLASENSIAGQHENINGDTNYPDDTAVPQQPQRDGKKRLSAKE

RRDMKKNTERHAVDGEQASPQRRQERNEASVAQPLQKKSVRGKKSKMKKMKKKYADQDHE

DRRLRMEALGHVIEKEPIVEQLTHGVDLMEQPTDAIEEDDESATNEEYIRQQRKKKEQFL

AEQEEEAEGADFFHAFTGEPMPHDIVLFAMPMCAPYASLTKFKYKVKLTPGSQKKGKAAR

QVMEFFFASNLKEEKDVNKAPGGVDDETQPDVNPTDVQRELMRCITDDELVSCMVGPVKI

SAPGMHGPNAGGKKGRSKRSSNKSKK

>contig33612 Frame-2F

MVIKSVVKVSYQGMPGAYSEKALRQLLGSSASIVSVGYSSFDETFLAVQNEDADFGVVPI

ENALGGSIHANYDLLLKFGLHIVGEYDLRVEHSLLALPGVKASDVTTVISHPQALAQCAH

TIASMGAKPRAEYDTAGSAKMVADNMWKDTAAVASDLAAEYYGLNVLQRNIEDDPGNFTR

FLLLSKSKDTGLDDSATTEFKTSLVFSFVDCNEKGQLYKALSAFSLREIDMSKIESRPWG

HTAERQYQASTDYSELVENGRQKYSYLFYVDLIGHQMDEKVGNALRHLREFCKFVRVLGS

YPTQGKLRNDVRQLLEAVGANPATSSPSSAIALHESKPVRLKIGIYGFGNFGQFLAKTMT

KSHDVRATSRTDYSSVAAQLGCQYFSSSTQLEQFFDQLHVLVVCVSILSFERVLSTIPRH

LLKNLVIVDVLSVKTHPKQVLLRDFPQSTSILCTHPMFGPESGKYSWRGLPMMFEKVRIC

SSEHNLVMDNFLRLFETEQCHMLEMSCEAHDEYAASSQFLTHLTGRILSVQGVKNTPIDT

RGFKNLVRLVEDTCKDSFELFQGLYTFNPNSEQQIQKFRESLDEVTHKLGRLPRCTSSDA

TMTEMYPQNPLLGTIASSKTVVIHGMAKQLEAEGKQVYSLCVGEPDFSPADRVLKAGMMA

LEQGNVKYTDVRGTMELRTLIAQYLKTCKGLTYDPLSEILVSNGAKQSVYQALLTITKPG

EQVLIPAPYWVSYPEMVKLTGGEPVILQMKQSDNYLIDPVKLESALMKNPRIKSLMLCNP

SNPAGTMHSPAQLESIAAILRKPQFRHILVIADEIYEQLVYQDEGEAKRIHQSFATLPGM

YERTLTVNGFSKSHAMPGLRIGYLAAPKYFVQVCTKLQGQLTSCANSVGQATAVEAMKFE

MECVSQNKERMTETLAIMDAKRKYVVKRLQGIPHLNFAYPTSAFYVFLDLTSYFEGKQGV

TADKSEVIKDADEYCEYLLRHYHVALVPGSAFGVMNGLRISYASSMETIMCAMDGLEQSL

GALTFE

>contig34680 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67602.1|) 1e-24

MRNEHMMDPTEILRFKNLQQARLESIARTVFYGLQIVYGMFWMVSAIVNSTKSRKKGKRA

>contig36556 Frame-2F|Blast-serine hydrolase (FSH1), putative [Phytophthora infestans T30-4](gb|EEY58329.1|) 3e-08

MTKLHILCLHGYRQNALKLRGRIAAFRRAFRSSVEF

>contig37322 Frame-0R|Blast-tRNA (cytosine-5-)-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY66741.1|) 1e-171

MSTKSKSSLGLYKQSFREYLRETNAVKDEIELDQLMKLLHEPLPVSFRLTLHRPDALGLS

ELLATKLQFPRDTCFYKDIPVNPPKPIAWYPMDKVAWQMDCGRVALSKSASKHEDIRIFH

SWLLTQTDRGYIDRQEAVSMLPVLYLDVQRGHRVLDMCASPGSKTTQILDILLSNMDDSS

REEQRGMVVANDADKKRAYMLVHRLTRNTLRRAVVTCGDGDTFPGLYDPETKTLRRTNVF

DRVLCDVPCSGDGTLRKSQTLWKEWHIGQGLTLHPIQLALALRGAALLRLGGIMVYSTCS

FNPIENEAIAAEVLRRAGGSLKLLDVSTKVPGLIARPGRTNWRVGWRSKSKSTHNGHVFK

HDNANDQSDEVKE

>contig39557 Frame-0R

MKGLQAVFGLDTAPLVSMHYRGQLFVLSAKDGNNEIIVLCVAVALQPDVDNWKWFLKNCQ

QAHVDFSTFVVIANRTDEFLAA

>contig40023 Frame-0F|Blast-polysialic acid capsule expression protein [Aquifex aeolicus VF5]sp|O67500.1|Y1546\_AQUAE RecName: Full=Uncharacterized phosphosugar isomerase aq\_1546gb|AAC07460.1| polysialic acid capsule expression protein [Aquifex aeolicus VF5](ref|NP\_214065.1|) 4e-17

MDNLERCTKYILQCHEKNCRVFVTGVGKSGFVARRLASTLSSISISSQWIHGGEWVHGEL

GCLKQEDVVILVSNSGHTLDLLSLPDKFRAAKCCVIGIVGDDCSPLSKYCDLSILAPADD

EVKCPVPSKSIIV

>contig40773 Frame-2F

MSNWGLRLNPFRKSYSQLEMDQMRFVHQAYCEAMEVTEEDLPTALKMDENFYPLHNPTLA

DFDENSYLRKMQDVVGLLRNPAEAIISSICAYQRERYDRAFTFSGYLNDPRTLLLEEFKD

WAMRTLGPATCTTESILNEVRCRHSYVLRLQHGQQGLFHSGSGERSLIGTLKDVRNVIET

RVLPTIETERAHSSAREQLHTLEARGTDGLMHGVQFLFYVLRNTPNTPADCTISNLQSQQ

HAGMKDALGSKSGQMLQVLLTTPSFKELFPQNQAAISPQDLLPSFLLTNEEEEEMIHTAV

FCDTDAKPQVPMVLARQLRRNSNSNEVAVSPSKYLQQSNSGVVALRREVQEETFGAFTKL

HGLLKLLADLLVSCRKARQLAGPGGDLLVYGPGGEEIRRLMQSLEAVQNEISKEVSQLTR

IGVRELDRLKPNQEKAWRWSFSKVLPLEGYLARDFGACVEPIQRMYASADPLHVQKMYKQ

FKQATGLWVEENSSICRYVTAALGGGFIEDDAYKQIGNAEKIEGNAKVGLLNDEDAPVMS

SALVVTGNNASHRNSSNHKVSPSNKEDRIVLLEDVSSENDRHAENQLVVATQAAIPAPKK

QSSSDGASFFSSLVSWGASAKTPPKLKQSESSPINSETDEDDDVEKGPSSSKMSREAADI

AAAQGGVLDTLLLVRQSIQRIGQLSWGVRTSYHTSSIDEGDFDAFIVLCSIYETAGVPCF

SDLLLRVRLHRTRLCQLLKKHIQSILSCVVVLQRRIVDEEKSIPGMTLVYRRLKVNLGDF

EHEMDNLLNKFKEMMLECSKMKAGILAMPLSQQRESNDVIGMGAYAYNSINALKSSIGAT

RVPSEAILSHGEYMTQMRSQLDLHWNSVSHLFQSLQGTVEAVATVDDRLKGYAKFPNITV

PPQQLDYIFEFNYDGFFRQTTRDLEILLTSFGTQQ

>contig42397 Frame-0R|Blast-geranylgeranyl pyrophosphate synthetase [Phytophthora infestans T30-4](gb|EEY59925.1|) 3e-75

MSSVLQNESKLLEPYVYISELPGKNVRGKMIRAFQSWLRAPDDAVLSIRSIIDQLHNASL

LIDDIEDDSEMRRGQPVAHHIFGIPATINCANYVYFLSLQKCQALGNPRALQVYTDEMLR

LHQGQGLDIFWRDHLQCPTIDEYLEMVQN

>contig44261 Frame-1F

MVKAGSFEVAVVCVAIVIVYMATKARSKQRKQNIKLLQQPIVSTKSELELVKDIVYINNL

TDPGSSFRLQHPSHLHSESRNKILVVGVCGGSGSGKTTLSRAIMSEFGADRVSYLSHDYY

YKDLTHLTVEQRAKHNFDHPDALETDLMVEHLTQLRNGETVDVPVYDFSFHSRCKTTTLM

KPNSVILVEGILIFAEQALADLMDIKIFVETSADIRLVRRLHRDMAERGRSAESVINQYM

KTVRPMHMMFVEQSKRVADIIIPHGVNSVALDMIISKLHSFVAVASSSRSGSECSGSIDV

EN

>contig44328 Frame-2F

MAFLNLFILLSLANYKNAGF

>contig46612 Frame-0R

MKDSADGFVLSDAWIDTFIRRHMLNCPYEESDVETTDCDERQEPVKVRHAAVSKSLKNGK

AGKTTRRLTKELVATRTPMAMHNDARIVGKRKRDHEQANQ

>contig46933 Frame-2R

MTYRSQELTRDPWNCFFEELILLAIKDLGQARKFLGMRIQYVEEKMG

>contig47909 Frame-1R

MRPLVTAWPIESAITQLRMGNAPTCTTLLSTSCIKNERTYPCLIPILYCFCYSKWMNFRS

NHCSFVKLYIHFLRSLTKRTRQFALPRTGYLLHKAKSEGSLVIFTP

>contig50509 Frame-2R

MPVFRSSSRAQPPLAKLSRHWQRLLLRSCMCSIKAVVIHTRVKMYVYTQ

>contig52024 Frame-1F

MLFTVLVAKVYFMFADSPIIYESLTGEMQLLKLVATTICVQSLYSGRKQQQYYRFHSA

>contig52257 Frame-0R

MGLVAFLTCGVCASRRKSGNGNFTETITIPTPAVQPHNAALAHHHAYDVDGSPAPAAHGH

INIVGDGHNGSKNEPRRDRRSSNPQQSISFSQNRVSSGQNRGSSGPNRISSGPNRPSTGR

SRTSSAQQRAHSGSRSQPQHSDPRSHPQ

>contig53140 Frame-2R

MNADKEEEAEVASSNNRANSVEHGNECHAAFLRSRTTKFHSTRLSIIDSKLKGEM

>contig54992 Frame-2R|Blast-aspartate carbamoyltransferase [Phytophthora infestans T30-4](gb|EEY53334.1|) 2e-37

MKRLGGLVLCVNESSSSSQKGEILHDTIRCLASYADVIVLRHPKKGSALIAAEATTKPVL

NAGDGVGEHPTQAMLDLYTIYSEFGDMATFTGN

>contig56363 Frame-0R|Blast-hydroxymethylglutaryl-CoA lyase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY58132.1|) 1e-11

MEADALAAAMPTVPTTALDT

>contig58268 Frame-0R|Blast-peptidyl-prolyl cis-trans isomerase 10 [Phytophthora infestans T30-4](gb|EEY58162.1|) 5e-22

MANSGPNSNKQQFFITYAKQPHLNNVYTVFGKVIDGIETLDAIEKA

>contig58620 Frame-1F|Blast-phosphoglycerate kinase [Phytophthora infestans](gb|AAN31474.1|) 3e-74

MVGVNLPIRAAGFLLDKELVYFAKALDAPQHPFVSILGGAKVADKIQLIMNMLDKVDEMV

IGGGMAYTFKKVINNMEIGDSLFDAEGAKIVPEIVEKAKKKGVTLHLPVDFVIADKFAAD

AATKNC

>contig58655-0 Frame-0F0

MDKFLFVGRKTYLKKSRQDFIE

>contig58655-1 Frame-0R1

MKSCLDFFKYVFLPTNKNLSIGKSDGLANNLVK

>contig58794 Frame-2F|Blast-short chain dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY53420.1|) 2e-11

MGDLKIFLLVYANSFLRLQNMATKTVLITGSNRGIGLAFAKYYKKEGWNVIGCARDVTNA

AE

>contig58871 Frame-0F

MLAAYTTSASVSKTMTRHISWDAGLRFAGCIQSRGNTPSTTAPMNILSVHVVTCFTQSIA

>contig59209 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54488.1|) 4e-26

MTDVRRTYGRVAPHKRATDYEDQDATEDLTTQLSEILHALAGRFPTVGYCQGMDYIAAHL

LNQV

>contig08280 Frame-2R

MCLYPRLVYEKKKNPPYFVTAPSFIVGLCHEICIEKSLIETTGICPVLFAIARLRNHPVL

GIVPSRSRLPPGAVSLYHPPTHTQSPTISSCRPPHARTTCRHLVFLVASFPQQLEFHLCC

DSMGSPV

>contig10278 Frame-2R

MADTTRKLKRQKIATSAYARTADGGLYLTRLQASPAAHN

>contig11116 Frame-1R|Blast-Sulfate Permease (SulP) Family [Phytophthora infestans T30-4](gb|EEY56793.1|) 6e-39

MRVIGVANLISGSLGCCGGCHYLSAMGIMKQFEAHEKVPALVSAFLVMLLWMVGIRLLQY

VPKFIFGGLLLSVGLHFLEAYL

>contig13253 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61350.1|) 7e-16

MSTPKGVISMTDATGICCFTPVLTAGKKLMK

>contig14735 Frame-0F

MRRSTWLGTVLAALLAAVPPLMVYARGVHVKLKASWPTSPFFPLMETSEFLADENPLYFW

QFLEQLEERTSYVELMSSDVDALAELAVVVAEFVAPGLQNVLELMLATRTYSVKVEMFRQ

LGLDSGVRPCGVYADTWAVFYREPHCVEAVACSVVDLDDSLRNMKQKISKKTCIAAGFND

IELRVDHKYPYVASTNEEITPMTAILYGLVGTTSFHAFHSTLVNEAKQSNIQYIVRHYPR

DSPLETLLQGYGVALDIKNMEYKTIDDSRMAGGDETAANGENEVDEDEDKDIDDEEVSGF

LFKPLLARHVAIAFKLKQFHDMLVKKSEQDQELRAWHLKDLGASAVRAIVDAKNSLKRLE

TLSQDFPIQAKRLAFSQKLISTELREEIASTRMQASMRGLTNKFIMNGIAIDPTERSFNV

FDFMKTLKTEWSVAKQLASLTLNQTELEDMLTHVRETNQEQPIVRIHVRGSMDGTTPLYL

NNIETDANSADWPSDINVLKRPAWSLIFLRKNMYECVLVMDPLTGTGRAALSHVEFLQAR

NAPIQWALLISSKELIASNTFDGRQALVEKYKTLKGTDKANPWHFTKLLMLAQAKEKCSK

VTIDGEKKQAKGGDDDTSNEKEKVDQVRSMKIVSGFLQRVGNDDSSIILIDRLVEAYAEA

AAEIGSPEENEDEAMACLSSDQFDDEVLSMTEFIILKHLPLNSFIFNGVIQKDLDIQGAI

MANFGRDQPLYINMAYRDMLNNEMDLIEQLLMEQNAYFAYLSIFESSRDRLGDKEVDLPN

HLVADDVDGRLKAAAQQAISYLHPRGSRNLPKKQTVIFPVYLNDPRDADHAYRVVKAVLE

DSDKSLRVGIVPQISSDVKSEGVGELLAAILAITGDSDNEVYLKFVLEALTCIVKKKSVE

ASRGKLKEIWKGTADSRDENDSIYIKVLTLLSQKPGKWLSTKQRGVLTRFNALLRSRFPS

TFTDESLSKSALPYIFVNGRQVDLPRHSLSDEDVATILSFDLKHRSQPVAKALIKRSATL

NAKEADKLSFSIMKTTGIVDKYVKIDRTSRMEVNENSLNTVRLDGDPSLQVTAYVDPLSE

AAQVMSSLLCMLHSQLNASIELVLIPANEYASFPLQRFYRYLFDKKLSLAETSVEFRKLP

VQPILTMKIDTPEAWNVQTFLAGDDLDNLRVDPESLAAVRSTTRAVFQLESLLVYGQCSD

ITFNMYSPPNGLQLVLEREVGAQLLHRDTLVMQNLGYFQLQATPGVWSLHLAEGRAAKLF

DIINSDTELRLEARPITVFDFGSHMHQFLVRKKAGMEHEVLLQSIEDAVSEDTTKTDSNT

LSSSHGEGALRSYWNSLLNVMGKNDDNLDTISQAAVKEVNETSAVHQNSTSLPQKRRTGE

TIHVFSVASGYLYERFVKIMMSSVLKRTNNPVTFWLLENFLSPDFKKSIPILREQLGMDI

RLVTYKWPNWLRQQTEKQRIIWGYKILFLDVLFPLGVQKIIYVDADQVVRADLKELWELD

LEGKPYGYTPFCNSRNIGFQFWRQGFWKDHLRGKPYHISALYVVDLSLFRQMAAGDMLRA

VYSQLSADPNSLANLDQDLPNYMQNQIPIFSLPQEWLWCESWCSDETKATAKTIDLCNNP

QHKEPKLDMAKRIINGELFDESWTELDQEIKDAEGKHA

>contig15431 Frame-1R|Blast-Poly(A) RNA polymerase, putative [Phytophthora infestans T30-4](gb|EEY68032.1|) 1e-151

MVHKVSGIHVDVSFNIAGGLATGDLVKHFMRVYPSFRPLTLVLKYFMAQRGLNETYTGGV

GSFLLQMMVVSFLQHHGRVLGSNHDDPKFNNLGYLLIGFLTLYGRDFNYSELAISVRNGG

SYFNKEGRHWYDDGKPFLIAMENPNEPSLDIGKNSYEMRIVKRSFDYARQVLQNEIYRHG

RFKSLPGSILGTIIQADSNLMQRDPPATFGYEILHHDPIKTAEIRNQYELRRDEEASKKR

SIAAAKSIEHESTNVPPYKRWRGRSNRAY

>contig16571-0 Frame-0F0

MKFGDDLVLQGYLHKQSKHLKIWRIRYFML

>contig17028 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54829.1|) 1e-110

MVFASEVPVISALNPYRKIEDVLLDVWRRTNPGQIAALQEELSLALPTVDEKMQAVVQDL

GATSAINELIQEASAAQTIRQVAKAQAKVVQSLPTTTPADIKADVVQFVTSTMHKSFGVK

KELAGIEHYQQQQKVVIQERNLVFSKKKIATLGDYKLLVGGKIDGRADGKVLEVKNRLKR

FMNPLPKYDLAQLQTYLFILDVQEGELVEHLHAKKAQTKVTKVKRDDEMWHNEIQPYLVR

FGSALTYLMRDETTQRDYLTAEAGQQREILRYLWSREVQQTD

>contig17374 Frame-2R|Blast-ribosomal protein L37e, putative [Phytophthora infestans T30-4](gb|EEY56064.1|) 8e-20

MRHNKTHTICRRCGRSSYHIQKSTCSSCGYPAAKMRK

>contig17778 Frame-2R

MLSIEGAIFPAFSLLLGKGTYSTFASF

>contig18245 Frame-1F

MGGTVADNSMKSSTLVNPPTIVQEVEMQEVETQEVET

>contig18515 Frame-1F|Blast-peroxisomal trans-2-enoyl-CoA reductase, putative [Phytophthora infestans T30-4](gb|EEY63788.1|) 3e-39

MDETMKKYKRIDFLINNVRELA

>contig19013 Frame-1F

MPLTQLPSLQHSQYGKLPSLRGSHPLNQLNQHFPLRLQTQQYLHQTQQALVQQTPVPVRK

EPTTVDLTLTGPLRRGKWTRAEEVYAAATISYFCDGLLAIQYGTTLRGYLAQQLHCDPMR

ISKKLLPGSVFAGIKINPKIGRRAYYPCAQDSPTAAHSKEAASHHLTRLRRAFIQSIEEE

EHVLEAAGIKNRIKTYSSPEPVAAIGRKRSFDDINSVVQPHHAAVELTEPQIFYRFPHSN

PLALLSSQYAPTSTTTTLCKLPKLVVPNDLSRRASYSTQHRSVSPVTIATSTTVLPPLRV

SLVRASMG

>contig19602 Frame-0R|Blast-unknown [Glycine max](gb|ACU16228.1|) 6e-50

MKISISLLLLLFCISTCFSSPVSVSDGVFSSDLALIGRNLLQAKKPCPVNFEFMNYTIIT

SRCKGPRYPADLCCQAFKDFACPYAEDLNDLENECSSTMFSYINLYGSYPPGLFASLCRD

DKVGLICPASAPGTARNGVGADTNNSHIIRNPSLLLSLTATFLILFFRWF

>contig20000 Frame-0R|Blast-phospholipid hydroperoxide glutathione peroxidase [Phytophthora sojae](gb|ABA29804.1|) 2e-71

MSFVKQYNVTFPFFEKHDVNGAAARPVFSYLKTKLPGSFGDFVKWNFTKFLVDRNGQPYK

RFAPKDQPMSMEEDIKTLLAQKSTDK

>contig21465 Frame-0F

MSSDLLTPTSQLKRFAANRTTASTVAQACRKAVADLENWSLWAYRDATGEEWDAQPACFI

TDYLLAVQCFAFAVYITLFAAADKGELSWYVMYFMALGISAALGGLLHHVAYEAMRDIAH

KQETHLVHTARVFGIKLSRANVDKMIEILWRFVLACSIFTNFALLSLAASRHLPETWAYL

IIGLAAVLYVVLAVWAV

>contig21582 Frame-2F|Blast-putative membrane protein [Hyaloperonospora parasitica](gb|ABG23234.1|) 1e-08

MPYQVLPGLVVISVAFSLMGVGFSVVNQWEARSKMQ

>contig22239 Frame-2F

MIEYLEVAMQRCYQDDDAFAPRKERFSAR

>contig23225 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64035.1|) 0.0

MEKAGMKLQLTDYNRFLNICYQQEYLDGAIQVLKQLRLLRSISVHTYMHWLLRASIVWRS

DAFFDLLMEMRLSQVEPEIMSLTSLESGRKDRALTVMEGVRAVGLDPCFAMASVFSSMQA

SVYQNGPSYQALTAQDLQHAREKFNGLTPIELEWPVSPTPQVLETQAAGLLLERETFRRL

KRQQVNHIDKLLEMLPITTNMTINLRKQLLRMSLLVNTHRVRRDRIQICKEYDSGRSLIE

LSTIHNYPPVSLMRVILRAKGKSQLEIK

>contig24479 Frame-2R

MHCDEALEPNELAISSNDLQVMRHSFDTMQQQLSRGLREIHEMRDLFTEALKKVDRRNVT

LTRC

>contig24794 Frame-0F|Blast-Ca2 :Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4](gb|EEY64015.1|) 0.0

MLCTAMIYLILQIPALFYTGTTAEDAHADNIVVARAEKPFAIAAFVISMLSFVLYLYWNV

RRASEVKEDVIDEVRVAAIRNGEISLSGILANEVAKLKREVVSHTTPLNATREQFDRVAD

IIRPFFHAYDKNRDHRMDADELQLFFKDLGESVSREEIAKWMIAADKDKSGFIEFNELVE

ATLRYMLARYEHEARGHSTMSMQRVVVEQQHSLALPPVDGDEDEEEEEEVPQDLAHLSIA

EQQKKIKTRSAYMMFLGTALVLLFSDPMVDVLSEIGARTGIPAFYVSFVVAPLASNASEL

IAAYNYAQKKTSKTISISISALLGAACMNNTFCLGIFAALMSFKSGGLVWEFSAETLSIL

FVELAIGYMAMKKTQRLIDGFLVLLLYPASIALVVVLENVLGLD

>contig25955 Frame-0F

MQSDLSLVNPSLRLPVTLITHTGVRYTSTLSDISHLVLSPLSPPLSLSLSLSLSLSL

>contig26176 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62326.1|) 9e-78 NOT\_ORF

MVSLEELVSGIADAHKRLDSLERSLDDLKRIKRVNLHLQHGKLSSAALKTVPSDYYSWSL

AQRASVLGCKMPHLCKTIIMENIACINSGNEDPLNSRYYCVVLQYNSKLDSEQLRRFVRD

SIPEADRPAKKKINFQHAPEKVRWLHSRICNC\*IIIV\*VSEELTGFQHNGVSFFGTKTRV

PVRGYVLNSG\*YLFNVLVQVIVSGAIADLRPSFIWLGGGAELIKLRISVQDLVQALKARV

AVGITALRTGLDLAY

>contig26312 Frame-1F|Blast-Chloride Channel (ClC) Family [Phytophthora infestans T30-4](gb|EEY55986.1|) 0.0

MQHDQEQTESAIRSLNIARWVMTFGVGLGTALVACFVEFWTSFLSTFRTATMESLVADER

EGIRRFGLGFVVYALVSVAFVAVASYCVAILCPVAGGSGISEIKATLNGIKIHRVVRLKT

LFCKAFGILFSVAGGLPVGKEGPMIHSGSVIGAGLSQGKSSSFGLDTSWTKFKGFRNDKE

KRDFISCGAAAGVAAAFGAPIGGVLFALEEGASFWHQNLTWRTFFCAMVSAFVLNFFMSF

MEVSEASGSTPGVGHVFIGGTLGTQTGTFTFGQFTGSKAYEVLDVPIFILMGMIGGLFGA

GFNGANTVLTQFRKRHVTHRYLRFGEALLIAFCMATASFWLSYFFGTCRDLAGDYSDSLS

QFYCPKGQYNDLASLLTVNYATSMKQLLHFTSTSSFTPFSLGMFFVVFYIFACWTYGIAV

PSGLFVPSLLAGAAYGRICVMIVHSIGFPVGAQDGMFALIGSACMLGGMARMTISLTVII

LECTGVIEWGLPIMVSLMAARWVGNGFNEGLYDIHIHLNHLPFLEFDPPYYARFLRAMNI

MSSPTTCVPQIAKVGEIYDVLKNCTHSGFPVILPRNQDAAGGGEKPNLRLMRKSPSFCGI

IYRHHLTVLLQRKDFFIEKPEPFVRTPAGDTTLLYNDQYALSYRDMEGSYPRYPSINDIQ

LDDDERDLWMDLTPYMNSTPHTVQEQTPVPRAFRLFRSLGLRHLIVLNRRNEVRGVITRK

DLTPPHLKFCLESLSENEKQRIQGYFHRDRAGSERFEDVEKKLLSINDNS

>contig27067 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62486.1|) 3e-10 NOT\_ORF

MIS\*LNKYPVVSFSPIRSPRILLKTPKSLIENELISTKKIS

>contig27214 Frame-1R|Blast-Chloride Channel (ClC) Family [Phytophthora infestans T30-4](gb|EEY64384.1|) 1e-58

MTIDTMLPAYARRTGRIGSLHEFQQRAARYSHHGLENGDKITIDKLLRDELTTDISEEYV

NVSSDRRDSDGSDLLESFRKYGGRKSVSGESLFGGERSRDPSERLYYRRQLKAVTFLILL

GVIGGPMTYGIRVLYTHLSDLRKYLVGEATTYVLKLAVWTAHTVFFSSLGIFFTQLSPVA

AG

>contig27548 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70395.1|) 2e-38

MPREDGPHALLNSVDFRYRQVDTVLALAYGGACFFSFWALAMHAQSPTRQTATLGFYLLM

GLASFTRMLWFATPLGVLSVLVAPPRIMRGDQNWVYFLVSEATEL

>contig27737 Frame-0F

MHVAMVISGGRLTGNAPNDVGNPESCKTVSLLSPKNNALTVALFYIDDNKEADSLGELVA

VEIPDSIKTKWNKNPPSGLFQRTIKDCSLVIGLHRGESKLTLCLFSIEGKTSSIKPYRKT

AVDVATSKILGIVSVPLLSIYQVIFATFDRDLQLTLWNVAYADELLIVKPAHHV

>contig28282-1 Frame-2R1

MLSISCFAASMAMILCTTSQIVSADELPVGAFYKPNPEEVS

>contig29069 Frame-0F

MGSLDDEHKKRSINEMFGDEDSDDSGDEHIPPTSVTTADASGLFGSDSESDDRESATKRQ

VAPPPNRIKSETERPADGDEYDSGGDAVATKEDDDFIDGDDDLADVLGEYDQDRQHFDDE

RPLEELAPPQEQKDDFFDRTLKSLKTGRARSKLNLSPQEMEQITQEVLYRMDKAYTDDLA

SIADRRPALEKIKFVDNALHILRKLQFQPMLLDFDLLTIVKKWIQPLENGALPNVGLRTK

MLEMVSKMPVFKEHLKRSGLGKVVMLLMKHPQETRENKELCRSLVERWSRAVFNKTLDFS

KLAELEAEKADNEIYRRRERARRTKEVRKSRHAPLSGAAMCSMGVALNLTSSRTFPSEQN

CPSSCILISCFVLSQRST

>contig32520 Frame-1R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY64164.1|) 1e-78

MHKSQEFSETDSLETDAAESNGPVEVQYRSWGAWVFGWTSKLATSVADEESRQRAHQIIP

EVELRELYKILEEPSRRSKKRVHKHHDLGGQDEFSDSFSSTELSQLYRVTVTLHRGSLAL

ASDPETNRMLIRDNRNYGQKYAPTDFLLGTFSQLQVAAV

>contig34683 Frame-2R|Blast-structural maintenance of chromosomes protein 6, putative [Phytophthora infestans T30-4](gb|EEY55333.1|) 1e-68

MVRKKHDAERIASEYEELKEAVDTIERTQKEKNDKLEEVNARMSDISHKKTAVKNRIREA

RRPLH

>contig36555 Frame-1F|Blast-DNA-directed RNA polymerase I, II, and III subunit RPABC1, putative [Phytophthora infestans T30-4](gb|EEY56906.1|) 1e-110

MSELTPEASRLYRVRKTTVKMLHNRGYIVSENELVMTPEAFQSQFGENPTREMMTILVEK

IDDPSDNLFVFFPEDTKVGVKPIRNYCNRMKDENVTKAILVVQEGITPFARQALNEMAPR

YKIEHFKETELLVDITEHTLVPVHRVLGRDEKAALLKRYRIRDSQLPRMQVTDPIARYYG

MNRGQVVKIIRPSETAGRYVTYRAVI

>contig39158 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60031.1|) 6e-20

MQPQTSLPLSITTLRPVFLQIQLTSIPFKRITPPLKDFQSCLSAAKSALLNEVSSYKFDS

FTMFFVAGLSVIIYFYLEIPLFAHFQSFIRGLCVCLVALCTANAKFGRVQRSVHSGVPTS

A

>contig40020 Frame-0F

MNMDTLSPSGEELQSPMGASSPVSQSSELNKRRERWTEDEHARFMEGLNRYGRKWKKIQT

FVKTKTAVQVRTHAYGYFAKLLRNMPEDDAIWELAEEMSSLPGAVLKGPGNNGKRRNEPK

TDEAGMEVLRRFVFSKKKIDDKKLVAVPMTTATDDRENVEMAEVTPLNANTQGLRDVWSA

TPQWRAEESDALLEIKRQRLK

>contig41104 Frame-2F

MPKRSRRNLSIMKKGSDRQAKVISSKATREKKTKAPKKNRIQEQVEAMPAVRDENQLLVN

QLVQLGDYEMKNGYTQRGLARLRAAKEIRNSQLVITSGAQAKKLDHVGPVMATKVDQLLN

EGLEAALSEYNTDTKVLPGSK

>contig42321 Frame-2F

MTTHCNTYCKPECQTRPCHKVHARACGTTWARTIAFSMSSSRACGTSAAVACLFQWATTP

CITTRIPALLVTHPRPQRSVFCANSSSYSSC

>contig43555 Frame-2R

MVSSVVIMESLTLINGFNSKINSYPSEKCLHDMFYEAAKRTPDAIAIYYEGKTLTFREVD

DQSERLADYLYNVGVRPNCISGIFMEHCVEFVIAYIAALKAGGAYMPLEIVYPPDLLERA

MQESKPIIVLTKKWYRSRLPAWQQVLELDDEWLNSIAKQKIPVMPAARTKTHPDDLAYVV

MSSGTTGVPKGICCPHRGAVHSYDWRLTQCPYSKDDRVACHVFFVWELLRPMLGNRPLYI

IPDNAIYDPTKLVEYLATHHITRILFTPSLLQLVLDTCSTDVLQQLTKLRLVWLCGEVVT

LELRNRFVRLFPDCELQNLYSVSECHDVSAVNLAALSESDISLSNKYASCGKVMPNVKAF

VLDDALKPVSLGVPGELYIGGPCLAIGYLNRPS

>contig43810 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58884.1|) 4e-82

MFEMNNVSMEIDHPFHALGEALSETSLEEKKEMPPVLARVKAALEKYAEEHKHYCCGEDA

HDHENENNECYTLGEDFVGVEGTALFSGICTMNHSCDPNCTVLYTKDGAAHVFAVQDISE

GEELCISYIDVDQNVNERQACLREYLFVCRCSRCEEERKA

>contig45250 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59883.1|) 3e-80

MGLVCAMATQALTTSQKTPSDSALVKQVADAFATAILCCVDPSSMLRARALSGFAAAAKK

CEPTQRAGGLSVELHNVANFVLVFLRTSRYLSNASFGDLSSCRPIFKASTPSVSSLPASF

VQQVYLLENIRQAYYRQINTSSMNINLVSCQQKPPIPSMPETTLMSTAREIQTKYTIPTD

VCNNSALVDVKFGFGPLGIVINYSH

>contig46611 Frame-2R|Blast-serine protease family S54, putative [Phytophthora infestans T30-4](gb|EEY63537.1|) 1e-29

MTSAQMLQLYTAMNLVGAAYQRYLRIDCVGHLGGQGTGLAFHKLE

>contig50689 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70090.1|) 1e-125

MANIVGLSSLNDRDGDGRRGNADQPNQYYAGGTTDRGGGSGLSVIGPGSEGDRVANIIGR

AQQDARAAATSGESTQPRHVITFYREGFTVNGGTYRARSDPANRPFLEALESGHVPQELE

GANRQEPVEISLVDKRQEDYVEPSPPAYTAFSGEGQTMGSATYATDAVIQGDAVPAERPV

IDDKKPTTTLQIRLHNGQRLREILNLDHTIRDLHAIIQLNDAGAQPYTLLAGFPPRPVSI

DLEQTIEHAGLKGAAVTQKLI

>contig50869 Frame-2R

MPTAAMTAGNPATIALSAPLRPRRASTRWGQPRVPPAPSALPP

>contig51211 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67796.1|) 2e-21

MDKGELLKELSLQEKLAFFYCSYVHEEKIELDTDRELVRLWEKIMTSRRKSRERVCILLN

QTENTSA

>contig52254 Frame-1R

MCASIDCAVCECPSHEIPAPWSQLDLQERLSREKMRQPCAEQTGESILSKVERKNAVAGE

SFEEWEEVSSANVWAV

>contig53136 Frame-2R

MRRLSSSASLKLRSCSENESYAQQMNGTQAVVGPSPWSPRRITESSRP

>contig53352 Frame-2F

MVSITISTLSTTVGLNTDATKNINKCRYKTGKCINARSSKRNGQPHQLCLYHRDKANMIQ

RKFDRQKRQAARSKKVCNPHGLVMSSPKAHHAVSPTSSTCSTSSSSTTSDATQLYSPDSP

DCELNESVWTHLPVVATTYFYEYVDMP

>contig53886 Frame-1F

MEYSEDVKLLTHVEQQLCAPFAGSNTRISNTDICELWKLVSDVVFSPLWLRIRAAGLLHA

CCNMEKPYLDGVIRTDAKGVQKLRAIVSSTCQAVEELDATNTKQAEQLFTWFGFLEIVMM

ATHSDVFAHVLRNSMYATC

>contig54436 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63199.1|) 1e-23

MVGPLTGTLDEVMFGLVSPTLESMRIKASYLHDFSAAAVLATIVAPTVDEPFRSVVVKWT

EIDIPG

>contig54991 Frame-0R

MIDYLYLSDSFSGARYCLFLKNAFTHLYELVATNSASARVAADSVLAWNAHIDPLKALLS

DNCTHFRNQVIEYVLRALGTEHRLSPVYAP

>contig55747 Frame-1F

MDASEMGCLDGCLNRAALVECIDGFCKCGDQCDNMRIQCGVMPSTQLIDCGRKGLGTKLL

EDIKAGSFVAEYMGEIVTEQEYHMRRVLYHNEKHRYMMVLSGGEVIDATRMGGWARFINH

SCEPNCVVEKWDVNSEERCAIFAMRDIFAGEELTFDYKFESFSKAEITECLCEAPNCRKV

IGMNNRVSKPSKKPKKAETAQPVRGPKLLDPVIGLKSRPVHGAKKADALMQRMARQRILS

SSETRILRRSHVLLERNLTWHMEDDFAHLALLPYFITKQSSM

>contig58623-1 Frame-1R1

MLHVLNHVLCDIFDSLVRTGRRIRNTLHGFANQSFVGLCVVPFTTTTSVQQASAAVKGAA

STIFFLLLRIIQTMTFIVFLDFRNLFRRLAFRGL

>contig58656 Frame-0R

MEEFFQYVGPNGGAESSTRVLLNRVFVYSSPRENRIDRVGKLRVGSYFACSSVLYYEDQV

WLKIRRGYF

>contig59080 Frame-2R|Blast-dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichyl-alpha-1, 6-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58713.1|) 4e-37

MQLVTRWVLGLMTFCGLLFFSDSVGLRFGRDVSRFFLLICACQFHLLFYMSRTLPNVYAL

V

>contig03316 Frame-1R|Blast-Gag-Pol [Ipomoea batatas](dbj|BAD34493.1|) 3e-17

MNNFCKEKFIKQEYTVPYNPEQNGMAERMNRTLVEMTRCMLKDSGLDKSYCCALCICVYK

G

>contig05826 Frame-2F

MSDDFEAPWVEKFRPRLLADVVGNRDTIASLQAMAIAGNMTNLILSGPPGTGKTTSILCL

ARELLGPNLKQAVLELNASDDRGIDTVRSKIKMFAQQKVTLPPGRHKIVILDEADSMTAA

AQQALRRTMEIFSATTRFALACNNSTKIIEPIQSRCAILRFTRLPDEMLLRRLLTVCQQE

NVAYHEDGLAALIFTAEGDMRNALNNLQATASGFNFVSDENVFKVCDQPHPAVVREILNC

CEKGEIDGAENRAIELWKSGYSSLDIIGTVFRVCKAMCIADGVSTLLQIHGLVARMCSAA

LAAKAEA

>contig12303 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57325.1|) 2e-63

MSSSSNISSIAVGTAGKVGDGVNSHHVYKISSADDVVVERRYSDFLWLHYELSKQCAGYV

IPPLPAKVLGLLQGSEFLEHRRAGLERFLRKVDQHDELRTSNLFHRFLKCSIVELSALKA

ASQGTDSLNATSMASVVQHTQQLHNWWGKTYQR

>contig13674 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55831.1|) 1e-140

MELASLDHHHDDIAAPFYSYSALIGPNDVQECDLQVLERQDPRLSPLNDRKGRPYPFTRS

KTRWRKRPGNELKYLRAQITALEDLLVTLSHSDSRARLLSGGKALHDHTNQLQLLEELVE

ESHVDRIETALAENRRLKARLSSQFQVAKALQAALDENMRFRARKVCWPSSAAASDELVF

ALLDEEKELQYAATDKVMDVSGLARIQHPHFSEPKLHRDASGVYIQHKEVRVLPFVVADV

VRALQLSLTHGSAIGPACHCREFFMQDMFSRAVTVDNVEVPGTVPAQIRGRHFLWSVVTP

KRTVINWSSFNEYDGAKHIQMVKKLWFIVEPIASGPQSSAQGCILRTIVRFTPVNAETNV

RDIEEMAGVVILGYKRDSIRVVMAVRAQLANLVAMRSKCGQ

>contig16570 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67619.1|) 1e-140

MTYSTKSGRKPRLLLTLGNIQVIDDQNLVCHPGNFVFVLQKPTRKLYLSATTEQERRRWV

AELRSMLQEAYFGLNRPSIDSDIARRSLISASKPTLSRWKRRLDCVSKKRRVERKRQQLT

KMKQTYAEIWQNVVSTLLSGRMRDDVSMLESLCFAGIPKEFRGRVWAWLLGNKLQVSEDL

FEICKSRAQAVQMEMSLKRHVDHSVIESLALSSGSFRGICELRTRSVSSASSASSISEPN

VEDDQSLVAAQCMALPLIAKNTIVETLSTGQLKAWSLDAFDTNNLRRARRSSAVLPTQNI

LQDAVSIAEMLVAHGERSIKLVNIDMPRTFGHHPLFQPGAEGTERTTEVLEAYICYRPDL

GYVQGMSYLAATLCFHMDSFTAFKALVALMSSILLFDMFRLGARRTFHYIGVYNEILRYE

LPVLAAHFHEAGIDPQMYAVDW

>contig17029 Frame-2F

MKLESLVIADQHAAVNMYPGPVHTARHTLGIGFARSIGPMITHDFCVPLVPQRLLVVLLA

HTTVGSSTGV

>contig19067 Frame-1F

MELRAHGEDVPELNISKGGRLSGKKRQQQQREQQMKQEQFHHQQIQQQIHAPHALTIQVP

PSQPLAPPVSQASNPFGLPLKINVPATMPKFSLRTPLGNSFPTPRSHEFSLLMGLPSPQI

DNSQLPSVLAMTNAGINATTSGLRTPGLDSFLCTGPPSVSRGSGNFLSLGLFPTPRLTDR

TSGGDESMMSDYMKLMGPDTPMPFHPNGHFGGATPLLENLGNVFEHAPLPQPQTSNLPRN

HMATSVHGHQRMKMDFLSPRGLAAHNFHSQGFPTSTSGDTLNLSSMSGSSDYSAQFFVDN

KVEKVRNHLKTSSVAAATTPTPKPTGVTAA

>contig21464 Frame-1F|Blast-S-adenosylmethionine decarboxylase proenzyme, putative [Phytophthora infestans T30-4](gb|EEY58397.1|) 0.0

MTQTFPEPIKLLDDETSSTQSETSDTVPNTFEGPEKNLEIDFKAGVGHVRGLREVPRHNL

DEMLEAGQCQILSRTSNEHIDAYVLSESSMFIYTHKIVLKTCGTTTLLKCLPFIKTFSEH

LGLSIEWVSYSRKNYTFPEEQKYPHTSFHTEVAFLSSFFPDGSAHVLGPLNHDHWYIYAW

DADIHEQPASRTQSPSYSSKESAANESTLQILMQDMHPKVAKQFFKSNDSSMTSRRMTIE

SGIRDLVPGAIIDDFSFDPCGYSMNGILFDAYYTIHITPESHCSYVSFETNARLRSYASL

LKNVLRCFRPAKYSVSVYTDRNALESSKGNNMFVEDLVKVDDDLLYKRKGGHTQATFEGD

YMCRMANFAQTDELPLRRSVLKIRSPSFA

>contig22238 Frame-0R

MSVPQQSMPPVSQYAPKTTVGESSNTTSIHTTTSVASSSHSSD

>contig26102 Frame-1R

MLPGLLTTKLCSLTSTEDHFAFSVLWELKLVGTKDVQIVDVQFCKSLIRSVASLSYQEAQ

EILDDPNAGRVYGQDVTEMKLKTGETMQAFERRQVLGSGIKTLNAIACRLRAKRIEAGAL

TLASPEVRFVLDTETQNPLDVQMYTLRDTNALVEEFMLLANITVAKKIVRHFPTFSMLRR

HPAPSKRQFDLLCSQAKAVGFELHVDTSRQLQDSLDGAEMIGPKDNEVTTLRKPSVKANP

YFNKLLRIMTTRCMMPASYFSSGEVAPSEFHHYGLAAPIYTHFTSPIRRYADVVVHRLLA

AAIGVAPLPHYLENKSHLHEISEQLNRRHHAAQLAGRASVTLHTVVYFQQYPTRTDAVIT

KVKNNGVGVLLPRFGIEGMIFLCKKGEQDNEEIIKFDGTHHMLTLVQQGNRTLQVFDRVR

VKVYVALTFGNRQELKMDLLDENDDEQGAMHRDEAQKEAEANLCNARKKRKVAA

>contig27945 Frame-0F

MTNTPAQEYDTPAIVMIDSSSDEDILPVRVKKKVDALEEMEEEDEQVVEQQSITVAQEKN

PRLKEVSTEESVVSKHQKSFKVRKCRLGEEDAAFLLFYG

>contig28364 Frame-0F|Blast-U3 small nucleolar RNA-interacting protein, putative [Phytophthora infestans T30-4](gb|EEY66316.1|) 0.0

MKRRNAMKRGAATQVLHKKRALGDNAFDWGDDDLDGVIASDSDASLEDGGANEDESEEEL

KESAQEKRLRLAKEYLGRIAAQEAGNTDGEDNGGDGVEERVGARLKQDALEAMGKLFKKV

AARYLTFEFDASSTKILKGHRLSVTSMCLMEDGKTAFSGAKDGSLLRWDLVQQKKTKLML

PKDDLAAKMATTDKDRCILALATSSDGKFLASGGRDKLVRVWNVEKGHLQESFSGHRDAV

SALAFRLRSHSLFSGSFDRSIKHWNLKEMAYIETLFGHQSEVNGLDSLYKERVVSCGRDR

SVRMWKIPEETQLVFYGNSGSMDCVKMVTDEYYITGGDDGSLSLWFNGRKKPVCVIANAH

DGKWISSLAVMPRTDLIASGSSDGHIRLWQADLQGRLLIPVATIPLQGFVNALCFYVKAR

FLLAGVGQEHRLGRWEKVKVTNGIAIVALPCVKGDKQEGDQDEKKTGNGDEF

>contig31032 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55660.1|) 0.0

MVQRIIAMTRSKRVETTACVDTRTPSLAKRIELSLYSRAASFHEYRDLNTLRRRLQSLVS

LSFHEAAVTRRRAAAMLSSNGPVTAVPQLGKRKHRMTTRFGVSKLTIKRPRAACIGSTSS

CTSLVRAQMKHEALFFLMDEAILGLVFAFLPGLETIRCMQLNRFARRVLPRCVVTLDVEL

RQLQHAYTLYAVATPTRPAATLLCQFPNLTGLTVYNSLKPLCDQHEAGPALHAWGCSELD

ISHDNVGEEVVQQLAEGIELGACRRLRRLRLVSVFTNTCRGNALHLLCAALVKGSCPVLE

DLLLGGNGFSDVGTVDVAWLLKVGSLPKLVRLDIRRNYIGESGLKRIMAALRGGRCQNLK

YLCMGGNIITDNCVKPVVELLSSAQCPQMRFLGLEDNFLSARGVQCIIQAAVAGGMMPKL

HHVSCDGTLGSEETSSVRVA

>contig31047-0 Frame-1F0

MSREQAWNKMDNPAIILESNVNYCRKSTKLQITSFRQLN

>contig31263 Frame-0F

MANSRVNISALAVAVFFYFTDAHNNMITPPGTYPKNFYNKNNPTGIIDPKVLPLPAGMTY

NAGADTNTDAYFKA

>contig31494 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68845.1|) 2e-16

MNNEAGIDFDSVDQTLAAVHKHLALFNQTTIEDFEASLSSLERAKVHVSLDLHYQCTAVR

VFKNARHLNTRCPTLSC

>contig33610 Frame-1F

MGFASLWRIKPMTVIQAEEMKEDIPRTINLFDLCCIGIGATIGSGIFSTAGSMISETAGP

AAVISWLIGGAICSLNALAYMELTTRIPSSGSTYAYAYHTIGELPAVVAAWLLTLEYGVS

GAGVARSWGDKVEEWLLLEYPDKSFHWLNLSSVNLSGGLIQFLSMVVLLMGVRFGKAFVN

TMTIIKVGVVAFIIIAGFAAMDPENLSPLIPPRAEIDGAMAYGSQGVITGASQAFFGYVG

FDEVCCLAGEAKNPKKNMPIAVMAVVIGTMIFSSLCSLVLAGMVPYLDASSFGDGFEGRG

WKWAGTIVRAGEIVTMPVVVLISFLAQPRLNYALACDGLLPPVFAEVDTKGNLFKNTLIS

GLIFTIIAIVAPFGVLWDIVNFGAMMSFVIANVALTLARMKPQSPRLAPILLAVLVVTAG

CSAFLYQDGYVNFSSTMSLILAIFFLIVTIGLSVTLFVMCPQTANSPGLFSAPLVPFIPM

LCILANWYMIAQMRPLALFLSFAWMAVGALSYFLFGYFHSESRNDWNRLMNNNFSHRNDN

FSISMLSAKYSVDTKSPAP

>contig34682 Frame-1F

MRTMIYCRDLARGLLMLAIVAGLHPSKGVIPIDFGPESTLAPRGEQYEPREVSYFVQRPH

QLLGIMVTALVVLISTGAKTGGGALLYSVNILVLKLPPDEAISLASVTIFGGAVCDFLLN

LWKKSMNTNSSLINWDFVLVMQPMLLMGAAFGASIISWFSAGLFSIALIVYLVYISLKTL

KKAQIVGYEEGWRCFRNQNSETISLLGTSSRNFESNDVSFQCKGGLPWRKLGINLGLLTA

TVFLTSLQGGKHFRSPLGIPQTSFFSFIVSMLPFIFLSVVSHYQMKGAVATYQRQQIPGF

ILLPNEVQWSPDSIKRLPLHLLGIGAISGAFGVSSEEATSVLLRQVNFAPVVVSAMSATT

VFFVSGMASFDFFLWGKLNLDLAKFLVPLGFLMTFLGRICLMKIACNAKSRTLLLFALTA

SMFISIVTFAFVELRSVFIF

>contig37395 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69806.1|) 5e-46

MNSGSGIDHYTSGCRLLGVALVVDDINKGCNLAFRYPAPSSEKASSFQTLPAPLLAKLFR

PKNALCNASFELVVDELRFVSHPVLVSPRLPSVAPSTDLLSSLVTPSTVVEQSIAGSQSS

TGNETTMFNIIFALDDRPLKRSQATTHTP

>contig39555 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY67488.1|) 1e-109

MNEIQLTASLNHPNIVRFIGVTWSSLENLAMVEEFLPRGDLQKYINRSGDLMTWAKDKID

MAIGIARAIYYLHTRQVIHRDIKAKNILLTKGLQPKLIDFGTSRVWEPNNMSAGIGTPYW

TAPEVLESSNYTEKADIYSFGVLLAELDTCQVPFYNTVGSNGEKMKPFHVLKEVVDGNLR

PSLTVGCPQRIRKAADDCFQRDPTLRPTAAELVRLLGG

>contig39726 Frame-1F

MHLYEILLFMLSQSQQPPAVTHLARPHMLRGLLEMLFLASPRSQRVNKLLLRKICCSGNV

KPSDVGAILGSESVFIDLLLDQVADSMTSVVAPVSPPALNALASSLPVATRRVTLMSSSE

SLSSQLGFQSGRISLVIASESVALLRRLLMEKQWKHHVAENLCNVISNISPFLAKKKDIS

PSLAMTDADPSDIR

>contig40021 Frame-1R|Blast-beclin-1-like protein [Phytophthora infestans T30-4](gb|EEY60515.1|) 1e-147

MDLEQLIHGTFAEGAFLQHLLGLSRDERQSVSVFAVHASDMLRRLQRYNVCNDVFHIWHD

GLFGTINGLRLGRLPSKPVEWVEINAALGQAVLLLATIADRANFEFSRNRLVPRGSFSRV

VNMYGKEYSLYSDGGMFRRRGFNQAMILFLECVEDAGRRAMKEEPSLKFPYKVERGKIGG

LPISLGNDEQWTRALKYMLTHLKWLLAWISKRY

>contig40771 Frame-2R|Blast-serine protease family S26A, putative [Phytophthora infestans T30-4](gb|EEY53723.1|) 7e-17

MERRGKITIPKGHVWVEGDNPTCSVDSRQFGAVPAALLTGKPFLIAREWKWVLL

>contig41682 Frame-1F|Blast-RNA polymerase II subunit A C-terminal domain phosphatase, putative [Phytophthora infestans T30-4](gb|EEY68482.1|) 2e-08

MDAIQNFENKKNVHLLYSLMHV

>contig42320 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY54022.1|) 8e-12 NOT\_ORF

MLFVGHNFQWLGLARTATFFA\*\*FHLSLFVQWQACFGQLFFCLMPTITRATIFGVLL\*MI

LFLLAEFNLRGSSIYIT

>contig43811 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69506.1|) 1e-63

MVSWSSPWPSLTLHERARVMLSALHAANIGRNPSNPSDPGRPIIFIAHSMGGLLTKEMLL

LDSNQHEHSGLADCTTGVVFLAVPHFGSDLANGVQYEAIRKLVQMHPALKDLGADPNGRL

KVLNDNFKQLG

>contig44047 Frame-0F|Blast-DNA replication licensing factor MCM8 [Phytophthora infestans T30-4](gb|EEY69900.1|) 1e-177

MKRLQETDTSDIGPGRMPRMIEVELSEDLVDTCIPGNVVTITGIVKSINSEIHEGKYGKR

AQTNSLYILYISANSVDNLAKVDKDKDKASDVDFTKEDLEQISSIINQGNVFDHLVHSLC

PGIYRNDVVKAGLMLALLGGTRRSDDKETACMRRPDSHVLIVGDPGLGKSQMLRAVSMVA

PRAVYVGGNTTTTTGLTVTMVKDGSGDYALEAGALVLADQGVCCIDEFDKMGADYHAINY

CGGES

>contig44263 Frame-0F|Blast-U2-associated splicing factor, putative [Phytophthora infestans T30-4](gb|EEY54549.1|) 2e-63

MKERGPAPVSMDTIALTKGSFDTGDPETTNLYVGNLAPTVTEEVLKAEFGRYGEVYSIKI

MWPRSEEERARKRNCGFVSFYKRRDADDARINLDDKQLEGQPMIVGWG

>contig44494 Frame-2R

MSTPAGKTTPESRHRHWKVPYSHRTRLRRRRCLPGLGNFRHYVTH

>contig46610 Frame-1F

MLSLARRTSFCRDIHRQSSHTDLFVFRGIKRRRHLVERIGHRCRSSPHDRVLTASLGLVS

GGILVSSVFTTCHHNGQLDSVHPYWSGDDVGLMYRDTRRQFNFPWYDDRNKRTIAALIAA

NTVVFGLWRVSFRNARLHQFMWRHFASSYDAVVYGKRLHTLLTSAFSHITFPHFGINMFM

LWEFGPHVLAPSNDFSGAWYKQAVANSRFVGYVKSTYSSLRRRQPELLSIEKFMALYLTS

AMTSSALSALVSRLRGNGR

>contig47468 Frame-0F

MYEILEKCRQLDEESWKASFAYRRLANALWIWTGKQFVYSYQIALEANASLEPLVYCCPS

EHIIPRSLLASFDLKLTFSTVDYLEAILRLPRNVILSEKQVAACLKIYQIFADDISSLES

ALESFATQELVLLDQFNHLVPAVQLTFDDMEWNESREARQGATFVCNKVPKTVAGLLGAA

SLHSKLAQTSMTSERVVCPSIRALQTILPPHSEWFHVLLQETIFAAEHFGGTQVDFFLDY

RHHPSQRVIQPSLQPLQYEALCIHIHDVVLSANDVNKLYQDESSRTGLLCGFVVSDCMQI

LSGEGFYVLDPTGAYLSQSTGTTAANTSALTSFGLRYNVHSHNFARYPDQLLPFTTLPSC

PSNVPSGLQSTLIRFPWRKSGSALSSYVLNTTKADKFIAIVKSQLYQTLIFTETVHRISL

WSVGKESEFALHCHGEASLDAPDQTLCKRRMTRQNQEWKKRFSLHSF

>contig47521 Frame-0R

MTGRIEPRDSPPLVPTTETISISMDLGTVHTSSIKLPRNHNLVKTLIRLMPPKSTPLQPL

QYACEPNMGAFAIPTLSAQPYQQNARYQTPLAAYLPQSPRYNSDNSTSNGTCVYPYTQQH

ASDSNGTVFKRRRRSANTPNYSKRCRVVHCEKISVSRGLCRGHGGGRRCQHFDCTKGAQS

RSDFCWAHGGGQRCEVKGCTRSRKSKSLCVAHLNLAITPLATDKHFLNHFELSVPAVVSP

ISLTIPTGSPRLPSLLEALRNTQQSSMIV

>contig50921 Frame-2F

MIFGSGTINRCVSSKSSITNRCW

>contig51210 Frame-2F|Blast-translation initiation factor eIF-2B subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY68074.1|) 1e-158

MPEPQVVTDFLRYLEDRDVAVAVAVIKALTGVIIRSGASTMMQMEVELQEAAQQLRTFQA

ADDIAQASRLHNSIATTAGCQLFLRYVTRCFLEFDDFDLCRSQLIDRGKVFAETSLSSRQ

RISDVGHNFIRDGMKVLTHGTSRVVIALLCEAARTRNFTVYVTEGRSNCFGMKTAEELAK

AGIPTTVILDSAVAYYMEQLDIVIVGAEGVVENGGIVNSIGTYSIAVIAQALKKQFYVAA

ESYKFARLYPLTQRDVPQKQMAAISGEIAGGEPTDETIKNVSFASPFFDYTPPRYIALMF

TDLGVLTPSAVSDELIKLYQ

>contig53142 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67179.1|) 6e-19

MIYAIFTMQFQLASVVLYAIPEHEYKLVDFISVSAVIYCVSGLALAITTMCSQSCL

>contig53353 Frame-2R

MVYAVGLCYRRRGYSAIDVDTRAIYCAALLCGLAAFFIFLVVTS

>contig54437 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54011.1|) 4e-43

MTLVVPFLANEICSTEVPLEESSCGKKIGITILLEIAMSSNPRDSELVRDALRVFCNCVS

PPHYEDCWQHPLKDIRQYTLTARSMRTNKDDLSQRLKSEEVDPEGLTA

>contig54653 Frame-1F|Blast-tRNA (cytosine-5-)-methyltransferase NSUN2-like protein [Phytophthora infestans T30-4](gb|EEY64040.1|) 8e-12

MGGRSRAALRREKKKKLKKELASAATDKVTATEATRRQVHYQSTSCDSDSESSNDMNRAA

TIPLLSLEHGNNVR

>contig54925 Frame-1R

MKKLVWRMRNLSRINSSLSLSNVRSSWTQQAPASVPKRCTLCSKSFGFLGAKPKRCKSCL

QQICSRCCSKRLVCVVAPDQRTVLEKKRSFCCSCLADSAHSDALEVARDELANSKAHYEA

CLAEAQAIARPSRASFMHSVVSRCSRVYS

>contig55140 Frame-0R

MQQWTGGSRLAQQGAADKGLSHRLCAAYHHATITRHGHDLALVLPQRAVHDSSTWSKEKI

S

>contig55830 Frame-2F

MMKRSRACNDLVALATEASAHRISTESSLRCAVDDWTPFVEGMHHRCKRSRAAVISGDED

SNEPALHEQHRLQCMVTINDVDLGSADAKLRSSSVTCLIDSLPLHRTLRENMLSRKKKQR

LEEGIRCWSDLAVTDSMAIDQTTLRAKPHLTSMAGTPESRILRGLRLHRESRCINQRNKR

QVQPFDMTSFIMLSISSKP

>contig55948-0 Frame-2F0

MNALYCAVWGFKAEEKHGLTMWTETSSMGGIALILNPYSTVPVFEPWREELWTEHWMTAR

IEHHGGDFVIANVYAPTDKHEREALF

>contig55948-1 Frame-2R1

MFVCWRIDVSDNKVATVVLNPCCHPVLRPELLSPRLKHGDGRVRIEDKSDPPHRTCFSPH

RQPVLLLSLETPYRAVQRVHLVLFPF

>contig56978 Frame-2R

MKIEEVKSTAKAQRIASHTHVKGLG

>contig58622 Frame-2R

MLSAGRFTEQLTLQCTCTDDTG

>contig58796 Frame-2F|Blast-AP-2 complex subunit sigma [Phytophthora infestans T30-4](gb|EEY61359.1|) 2e-31

MGGMVLETNINEVLTAVNEMNRMESVSSRRSLQSTIKK

>contig59081 Frame-0R

MHERIHVKQRQVASNCSLHCTCECV

>contig06583 Frame-0F

MAEYRGKECIMPLDHTALLAGHNYDTMTTPNHGDSAVAAIPPTEQREDEPAASPGESYDD

LMHGINSFWAIVSPVCVTMVVASLVVVNYRSTSIEASMSTYLVYGDSESESSGGSGIGES

LINAIVIIGGIAILTVGMALLYKFNCLKFLSGYIMFASTAILSFVGGQLVDEMVNVHLKL

AVDWLTFLFVMINFGLVGVIAIFYQKGMPKFIQNGYLVLVSVILAWQFSMWPEWTTITFC

VMFACYDLCAVLTPCGPLKYLIGLIQEKQAPLPGLLYEADVRDGVAHEEQRQQQQKQRRF

KESATNDEDGNQSSPSTSQSIRNESDASCAPTEPNEVPLAAPVDGTESTTDRTESSPIPL

MSSGRPRNVAESSFSTYDCETMEALVGLLSQFYEMFSPDDLWKAPEVAEKFFTTQDRLWL

LIFHKYTVCSCSIAMPCSVQARRDRRERQREEEEEDKTIKLGLGDFIFYSVLVGRAAITD

FSTFAVTFVCVVMGLGGTLFLLAVLHKALPALPISIFLATIFFFLTKYIFIDFCSFVMAF

PAAV

>contig07074 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60414.1|) 1e-69

MVDLNTKVYIACSSVLYAKFLLATLVQGGKKFRSGGRPPEDAVLGLNKTIGKGGKQTYGL

STTDDEKVLKAREVEHRWTRIVANDLEAIPFALLIFGGGVMAASNPVVHAGAMIAFTVAR

CLHTYVYAHCMQPHRGIFWGLGVFCTLVGIGNAIVAIL

>contig10276 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58073.1|) 9e-64

MVISKQLENMNEEIPDLVQHFACVPRMSTPNPADIPLLLRTREDPEMEEEDRLLMADKPR

SKNTEALQKLVMVHNEAVESFEETFNEMSDSLLKAIRVNKYVVKSKPQSTQTQQFNYIES

GTYK

>contig10760 Frame-0F

MEMPRTYVRTVKAQDLRFCQVDAVLHDIKTKNSPTWVVFTFAEQREKRNTLKVLASGHGN

ISDQSQWPSELFSPTSLCYGLTSIDCYDENSAPINVLSFCWKGRNLPIYLRTKYAEFNQV

IKKHMEAVAHVTLRNPEELMDGSVFLQTPRRRPRSSSRRFVTSDIQFTPEVTATVQDIRS

ELSPFNWAVCGYDHSDYESSIRRMIVVEKGMTGLYALKGIGGITSVLEDGSTMYIYLRVD

VPLHRGTERIVSKYVLVTWQSAENSFSGGTSDDEVDLWFGPGSNGERSPQRRDSFASSSK

LQRAVTAHVHSSEIYRVFPHHVHFFASTQSEISEEAIRERIRRAVDNDCLLLRVVCVQAS

GDTQAPVCLEIPFDATVGVLRQEIASNIGIPKDRQRIVWIRQTDDLAKDSQLSTALMLED

ENAGIRKDIGLAHGDKIHVDDKDNGKNSVLAKLFEQINSGAAAVSLSAERRHEVQRGVEA

REAELRKILTMTHYLIRRKAGEGLKPLKRMVDVVEEVVAKTKDHDSLSPTGNHKVVHRAD

SSASLTGSISEKLAKEDVSALQEHARVLESQNQYLEIPYESIHILSGKENELGCGKAATV

YRGLWMNRNNAAEVAVKSFRYARLTDKILGDYRQEVALLRKLKHPNIVLFIGACTDPKLM

ILTEYCSRKSLFEVIHSNNFKTIPWKFKLRMMLDAARGIQYLHSMRIIHRDIKSHNFLVD

DDWRVKVADFGISKVLDSDTAFTQCGTTGWVAPEVLLDEDLGYSFKADNW

>contig11594 Frame-2R

MTSTIIYLLWKLFRQVSSHKALDKPRIVRLKTNKQYGVNV

>contig11903 Frame-1F

MTAGDEADRKQKLSGVTAPTYEEKLYVSNSSKLQLKCKDGTTLDVTYEQAMMSSTLWVLL

QEKDPKIGLKQHIIPMFDVPTESVQCALDY

>contig17808 Frame-0F

MPSKCVGIAREVYNKWERRAPLTPSHVKELVSHGVQVLVQPSTTRVFSDEQYIRAGATLS

DDLGTANVIVGIKQVPVSAMLEDKAYLFFSHTIKAQPENMAMLDTVLQRRVSLIDYECIT

KENGTRLIAFGGNAGRAGMIAGFRGLGERLINMGISSPFVNVASAYMYADLAHAKDAVKS

AGTSISTDGLPNALAPMVFAFTGNGNASKGAQEIFKLMPHAMVHPSEISTLPKDKRLLYG

TVIDHPHFFVKSREEIDCKTMRDHYYQNPHQYDPIFHEKILPYTSMLVNCMYWDERFPRL

VTRQQIRELRKTGNHKLLGIADISCDIGGGIEFLERATEIERPFALYDVLEGKMREDGDS

RGLEGEDGIMMMGIDILPSELARESSQQFGDRLVGYVELLSTAASSSIPLHEREELPVEL

RNACIATKGALTPKYEYIHRMRAERDRSKHYKFLNAQDQVAGSTCILVEGHLFDTGLINQ

VLNLIEEHDGGFYLVDCQVRPNVGNEGVSNRSMSNVIVQISMKNREALDTIIAKIMALAA

LMSGANATVTELPDLCGTDYSKTRSAVVRKDAAAHTTVNVSVLSPKKRQIVCFGAGLVAS

PLVEYLSREQGNEINVVSGIDSEAKEMLRKIPRRNIRSQVLNVAVDAAGVNKLCAEADCV

VSLLPAAMHTTIALHCIQHATPLVTASYVSPEMMKLNDKAKDADIPILCEIGLDPGMDHM

SAMKVIDEVKAHSGKIVTFSSVCGGLPAPEAADNAIGYKFSWSPRGVLTAALNAARYRKD

GNVINVAGEDLLNSSECVTFLPAFNIEQIPNRDSLPYGDIYGISEAHSLYRGTLRYGGCC

QILYQLRKLGLFDTEFSESIPATWPDLLNRLGRQELSKDAHEFLLWLGVFDASTPVVKAS

SILDAFCALLQEKLAYQPGERDMAIMHHEFGIEYENGKKEKRTSTFVGYGSEKGDTIMAK

TVGLSAAIGVQLILQDAIQGRGVLTPTTPDIYVPALARLEVEGVRFIEKSFPQY

>contig18603 Frame-0R|Blast-phospho-2-dehydro-3-deoxyheptonate aldolase [Phytophthora infestans T30-4](gb|EEY69972.1|) 1e-25

MIQMSLVLVWGARMPTVRVARLAGQFAKPRSSDIDVVQGEQVP

>contig19068 Frame-1R

MAHIGWRTAVVVHLLDGYLLF

>contig19082 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59776.1|) 4e-23

MLGPTMRRAAPLTCSFYKRPVQCRFGGSLTKNRHIENWNNWRGDSEKRFQFNNNLFVSMA

AWGLIPFGLYYVIAADE

>contig19770 Frame-0F|Blast-elongation factor Tu GTP-binding domain-containing protein [Phytophthora infestans T30-4](gb|EEY68569.1|) 1e-122

MFCSFILDIVWKTYATVSKHIETDADMSHLTKLTRQLRIAKLVTARELKQSDRKHALQLI

MRKWLPLSPTVLKMVARVLPSPVTAQKKRVQKLCPLSSEQLSRSPQQALVVRSLELCHTH

ETAPLVVFICKVISVEANVLSNYQELGLDAFEEVYVGIGRVYSGVLKQGQALYVMDPKFQ

GVHQDVDENTMDFKTIPHVERIEKGLIRPYMMMGRDFFQLNHVPAGNIVGIVGLQEHVLK

TATLSSTLACPSLTRMPWQAKPIVRVAVEPKDPRHFGALEAGLQRLIDRIRP

>contig21023 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68436.1|) 2e-34

MEEKEKLLLTSAELIEKMRLSDALRQVDPDEPAVAFLNRSLKALIEKHTACVIRINGFLE

DLCAEIADLED

>contig21221 Frame-0F

MNEKDQKKAEVELKGDAGDNMATDELELLCIVRSSHRVKSFAFSPDEAKDGSTSLLLGLQ

NNSIETYSLSPSTLALEERYSKSHALTLSGHRSDVRQVAISSDDQLILSLSSTSVKVWNA

RSLQCIRTLSEGLSLALSTAFAPGNMHVVVGTKLGQLLLFDLNSGECIWKDEKAHNGSAV

WSIDVRPDGRGIVTGGADQHVNFWEFEMVRLDHAESNSTLRLGLSHVRMLKMSDDVLCVR

FSHTKDVKKLLVAVALLDCTVKVFYDDSLKFFVSLYGHKLPVMSMDISSDDAMLVTASAD

KNVKLWGLDFGDCHKSIFAHQDSIMSVRFVRKTHYFFTASKDKSIAYWDGDHFERILKID

RHHFGEVWGLAVSADGSFVVSCSQDRSLCKYIRTEDQVFTEEEKENEMEELFENDLVNTT

HRKTPALGNNKTQEMETSASATKRTIESVHAGESIMEAIDLAETELEAIADFKRIQIKKE

KEAKKKNDQKKDVETNAQSDTIEKEMASEDSSVLTRAPNMRLLGYAPLKYTLHTLRRIRP

HDMEEALLVL

>contig22237 Frame-2F|Blast-casein kinase II subunit beta [Phytophthora infestans T30-4](gb|EEY64204.1|) 4e-28

MSDYEEEDEKWVQWFCSLSGNEPFCEVAQNYIEDSFNLYGLRAMVPNYQDALNIILDMT

>contig22664 Frame-2R

MRLLIISTVDRFITKSTTIHSLATELFMSSLSIKNKFPHFFSPAYISNCNLSFI

>contig25364 Frame-0F|Blast-homocysteine S-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64674.1|) 2e-58

MALLVNSTRNTSMALSDLLQRLTDKSCIILLDGGFATELEKDPRVDLSSSSLWSAALLLD

KNQHLQDVVVHAHKTYFLAGSDVATTVSYQASVDGFTREGVSAIKDVEKLFAKSIDLAIH

ARDAVWKELQQSKRMKPLVGASIGCYGAALADGS

>contig25834 Frame-2F

MSTLVSMLIDFFIDVNPRTSVVGVLALTLLLKNGRTLDKHQMERIALDGAVSLVYWMEKG

TERQQENAVKILHDGVTDSAILLKFYEQIQDMSVQRESAFLLELGQQLLDVDLTTNPDGL

LKRCKLLEGLLHVTDLSALPIDCIEIIEEVTAYLLELVKDKEHEFENAIKNADEKKCWET

LLLAIVNFLDALAPSSTFHSTLVQQNTIEKLLSVLNGQKTATEPCAELIDRICRVLRKLC

MHEVPRLVACNGTEVLLETVMSHKVGERGVEHVAEMLETFNLIVDCGQSGKSALMETEGF

FESLVRGFKTVSGDFSEDQTGMNAIFFSTESDEPKANLEVACGLCALIFFLARGRTYRPQ

LYKNAYLVRHIVAVMAWFPSIFTRKETVTPELKEKFRLIIGSGLPFLEAAIVSAEELGLQ

LIDMNNLFKKAFSVYMKTIDTYADGHQCVDLFLAACDGLKSFLCSDRGLTMLNQQDKCEL

ELQVLHALKSSLNSIECRLALLEIAAIATQFAEPNDVESARSAWLVDRVLHALFQFESFA

DDLDVSILYTLLLQFSSSCRIRTLLFEHDEYDKLVRILVAIAIDGEWQRWRKKTVRVLQL

LGEDSALEQVHIDVERLPMLQASTMSLYRNRDSKQVT

>contig26192 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64060.1|) 1e-100

MVSSDAKKHELNEPWAIWEQREQGKNMSYGDKLYKLCTFSTVEEFWGYWNNIPSPSQVLF

DGFTRKKFADRTVEGFAVFKDGIVPEWEDPENKNGGEWSIRKEIGPQELDEFWEKLVLGA

IGEQIDPENEVTGVRVIHKNQKKDKKDAGHNYRYEIWLRGTERVKADEIRNRTLNVVNSS

SSAAPWVSNEFLHKIH

>contig26206 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY67807.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61136.1|) 2e-56

MDTLLPISIEKNGLAVVQDQKEITTEIVEAPPIKRIKNDIMSRSCQFCSSKKHVATGCCS

QACKKCCLKREGVCPAHPKEVKKMEPDPIQIKKPVLKNEFREPNFHYYGETLTIFCIRDF

FESKKLSQGVLKDQERAERVSGNVWGRRNKNSAADCKIKELIKSALGKRPAPDTITTLAT

VDASTK

>contig26291 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64143.1|) 3e-15

MRLYKPALYVQGVSGGSLLPTSLTESTATQHEFALSSMLILPDSFGCVYSLRKLYRNTRF

SIVT

>contig27069 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61399.1|) 1e-21

MAPAEDRIMPWQSSIFGRYSEVDTIEEIESKFMNLTVVDMRKTME

>contig27546 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60158.1|) 8e-41 NOT\_ORF

MTTFYSNEACVVSKNKKK\*SVFYALRTFAKVFGHCSMPAHYVIPSLFTWPKQCYGLPLGE

TIAMMEGSGKYFTEVGLNADQLRTFGFRYKLENGPY

>contig27652 Frame-1R|Blast-ribosomal RNA large subunit methyltransferase J, putative [Phytophthora infestans T30-4](gb|EEY55433.1|) 5e-94

MSSLYVRSRSALTCHCAPLRAIKSLRGKSNASARWVRRQWSDPAVKQAKREGLRSRAALK

LRELNDRFKLLRRGDVVLDLGAAPGGWTQVAVEATAFKLNNTEGPPRVVAVDLKSFDPVK

GAVIVIGDFRQSSIREKLSEALKGRKADVVLSDMAPSFSGTFLTDSQHQLRLCYNALKMA

ELYLRPGGNFATKILRCDGSEEFR

>contig28385 Frame-2F

MMSWMRFTALYTSLSVAQGVAHARGMGKLFVCNSRESMLFMIRKEVRKQPTCTHLKNRSL

FVSFVASEPCIRAKTVMLRSTVVDFIKRTIGRQEDTKRRVTN

>contig28723 Frame-0R

MSQVDGQLNSDGEGSDFISDDKAVNSGKKGSGVDSGNSEILSSASSSSTENDSANDIDSC

RSFSSRGSDAESGGTVAPTSPAAIRNDYLSQQSTDFPRIVTGKERRRPSIRVDSRNVGLP

SAVVELMRTDQAVEVNEEGSLDELNLLECGFRHPSHYARARVWLPEITDWCLDYADGDPT

LWVITPHAWYKIAGPLSGLLPHPSYRQTFKHVRYLFEASYLVAYVLKAWLPINKKVSYRA

TLQQIIELSLLGRYRV

>contig28914 Frame-1F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 1e-72

MGMVGIGQDITERIAQEQEYSRLIDTANAPIFGVDIDGSVNIWNRKAADIMQYSNEDVLG

KDLVAEFISTEYKVSVRSVLEKAFKGVETANFEFPLITKAGRRVEILLNATPRYNEHGEV

MGMVGIGQDITERIAQGA

>contig31400 Frame-1F

MMSKTAVSPRKRLPRFGDDELTFQYDERDVSLSVMPSSPSTTSTCSSADASFVNTKSKTV

LLPHDEHNSDTSDEKFDDTSRLQQLRNWLQRLQKTFGTSFLLLVSTVYVVQGFKSFSALA

INYFFKDNLQLQPTESQSLLTVMMAPWGIKPLYGIISDSLPLFGYHRKSYMMLCSAMGTI

ST

>contig31475 Frame-2R

MTTPGHHLPDLIVHSHQFWFRFSASEEIVEKGCYGYRFQVKPMANIRWFKESEVQANPSL

EWACWVLELLLNDANELLARGAVHNCKIYDALVRYLRSPGAPYKGRVVRLLQQLLHRPEC

FPTDEVPNLHALESIVRLALSRAELDRGSGKTFLSTHLLQLVELSVMISSTST

>contig31853 Frame-0R|Blast-DNA polymerase epsilon catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY63268.1|) 4e-53

MDAFCWVKRDSYLPQGSQGLKAVTKYKLGYDPVEVDAEHMLALARDEPMKMASYSVSDAV

ATFYLYDKYVHLFVFSLCTIIPLGSEDVLRKGSG

>contig32467 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66110.1|) 0.0

MDIGFGSRADVSVQTNLIDRKCVFVISTSQRMLMITAPSERMMTRWMARLQAAGAVPTQP

WDPLSETVKFCVRDTVSIHQWKRYDDPTSYIHMEGLLLKRGHVNKNWKNRFFRIEQGRLL

YYSENQREQKGNVPLKDTIVSPGMAQCPDGRKNYFVLTSKDGKFEMHLNAHNEQSMHLWI

EALQEAQMALGRLAGNKDTVTGLSLVVKRAEEIPLGKIGVRFQRSEDIDIELQKRTEALI

VVSSHRYHGIAVGSQLVSIEGRSILRESCAVARQILRASSFPLQLEFLLPPYKRGELIKK

SRSGFENWKRRMVVVTNGEIHYYKQVPPSTSGDKTASVQLEHRKHFSLYGCYLNLVHLPR

RDLCIVVARSPSDKLVLQMRTEIERMEWASVIYCSIRMVSQGITSGHIENLQLEQQYGHT

LRQSGKMV

>contig32904 Frame-2R

MPCIRVTGFKPLLYRPMPDKRVAGWWTEVLSSRHGERSRRREMTEVKKRGCRRTDEFYEK

RKDGTEERETQLACGARLRRVGSFEKTGCSVYDTCALDDRLG

>contig36434 Frame-1R|Blast-transcription elongation factor SPT4 [Phytophthora infestans T30-4](gb|EEY69459.1|) 4e-37

MADNRQRVAECTSAYFEGMIAMMQPKDSWVAKWQRIVRSIPGIYALSVSGELPDSIKRFL

EDRNIPYRVQN

>contig39729 Frame-1F

MSENYVESVDISSENAEVLMAVKSLRYGILTW

>contig40167 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53849.1|) 4e-13

MRFPLPADTFPTLVLSEEDRHELQTLSEGFVHSAIDEYTTFRFTHKCILDKEQWKVVKTR

DAMTSYRDLRGIGTERSQVFTHKRLGSSVMTSS

>contig44325 Frame-2R

MPHNLQISKIIGRWLSQTLGSSKVIQTSSYTGVLYVNIVIFRLKALVALLYPVR

>contig44350 Frame-1F

MEQLLLAASLEDCAKGFKEESDCWNRNKSNRKKKRTLAKFAKASKRLEAFKSKACGGATM

SNSDCMHQKLCGTQAKFSEESKHVIADTKISGDLLPNLSYADDDIVEVDEARPAEEGLYL

NVESRLNPDALEFQPQGHQPEVEEMTARDSFACEHNFGEYILCIPWDDVESGESTFIGTE

CSNGDQFNNARCLEKEGGQRHLWRNQRKSIEDFDLIWQLQQTYSFSSLLFGWDFTRQCVL

EDPGVVVP

>contig44475 Frame-0R

MPMYFHRYRNSSYRHDTKCSFRRLDFSNTGTSIYCAFQFIARYCLYADALLLFYRRIPRQ

TKLFSDYDP

>contig45807 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57599.1|) 2e-52

MSSRAKKTPALIRVKELSPLLNGKDVNVKVIVLECNAKDEGNISNNATLLVGDESGCVSV

VLPKTGAQHVRLGDILQMSASQVVLKNNRMYLWGGKLERVGEFMLLFNENNNVSNVTWIK

DPKNPDLLIPGRNTSKRPPSMPAK

>contig46983 Frame-0F

MFSLSCSGDPSAPNVDKLEVPPPLRQHLAYETFLEKQASVLEPQRPLTHVSEQKRLSRNF

DSLAVQVQPLHQANSLNKVPSKLMEIIRMPAPEEHKVRKNRSHA

>contig47467 Frame-0F

MTKGREIWSESIAYFLVTFAMSTVIYWPPCWCGIHYLNVLNWCRVSSQLQTFLTWLTNGT

VIVTVTLTITSFLALTDRELHRAPGNNCTILILDKGLHPRLGSWDKDGLTMVYLVQTFMG

ALYTQLASVTIDRQRSV

>contig49627 Frame-0R

MLIKCTKYLRPILSCANVSYALRSPGDMQKRNATLFTSLQQIDAGVDAKGDSLERSQGHV

D

>contig50290 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57264.1|) 0.0

MTLSTMTAVTCIPLEQKKMPTQELPEEVAKDYSMLIMRQKNIDISLLQKRIRDSGSELWN

PTQQTDNVPVRRAGHDSWGIGKVVFIYCDDYLQKVFTFPWFYSWQNELAPIIKQTRIPLN

RIVRCILASMPPGADIPVHHDTGSWVHFTHRMHLPVFTSPDIDFMVGLNDQNMQRYELRQ

GNLYELNNMSCHCVRNNWTQHRVHLIFDYADEGFPLKHLDLKQDTVVWQTRRSMDLATDY

GKRIPPSFVVIGAQKSGTTSLYDYILQHDLVWPAKRKETHYFDWRWNNDLSDPSTTKGAN

EHFRYYENTFLDRQVLYRYPTLMSGEATPSYMLGGNTVINRMKQVMPHCRKFIVIMRNPI

ERAYSHYSMTADTDGSKNQKRNRGHYFLKNRSFEQIVDEEIDELLKLGVHPEMSYEAFDE

KVLHHRLKFNHGAHSFVARGLYALQIAGWIKAYGESNVLLLTLDELKTIQSLHKTIDKVF

NFL

>contig52959 Frame-2F|Blast-midasin-like protein [Phytophthora infestans T30-4](gb|EEY58697.1|) 6e-14

MAHVDAQLLAGDFRANERSIDMNEEHLVSISRLFSGVQQMLAAVSGITMNAPQKHPAIQA

LMTSITSIEENDHHSLARLQLQALASCLVHT

>contig53251 Frame-1F

MTQHADFKIIFGSKSLHCGLVARQEHRLWVNIVNSNFQLVEWDDPPREIDQGVGAPVALA

SMSLDNPCNNLQELKMYWECRACTC

>contig53888 Frame-1F|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY67956.1|) 2e-60

MGIDNIHVVRNSLAGLAQALYVVEDSNFFGAVQKSRWLEHICNILQGASEVATHLERGDA

V

>contig54135 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63747.1|) 2e-57

MECDRLQHQLQDGVRENDFLKLELENRLQQLNLHKKEIAELCARIEHLMHGDHEQTRQLE

LLQAECLRLDEHNCTLQRLVEETRVEAEATMDKAHRVHDHSVEQHTIYENTVRSLVEEKE

AA

>contig54140 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66749.1|) 4e-36

MITNEHCISNVQDAINTKVEFLAQSSSCGGGETCATRGGCPGRVEVVGTTLVAVSEELDY

ALVRLGVGNSFID

>contig54438 Frame-0F

MTSADAGHRRMRTLSALLDDNWNEEDQLPEVCHDLFALVTAAPSTHPKDEQAAQREQTRR

NEYLCIECQAHDSALFCEQCHDYFCELCYSGQHRKGNRRTHTFQPRLPISTTKAEDLDTV

TRPNTT

>contig54751 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66234.1|) 3e-31

MDATIAILDHPFALGDLTRARNAVGYVLRYGLNACLIEQQQEVLLRAYLQKVKSEAKAAG

SNHHKIITILVELSYMFHSMGEASITQASVAI

>contig56977 Frame-2F

MKIEEVKSTAKAQRIASHTHVKGLG

>contig58210 Frame-0R

MPPTKNHHCILSRRQFAAADTCVILLLPAFFIN

>contig58584 Frame-1R

MSYGCSHHKDQVSASLTIWRIHNKYHLPSIAQLCCCCSSYCFDVSEFHYPSVTTSIISAT

GRLRRIYQH

>contig58799 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70395.1|) 6e-38

MPREDGLHALLNSVDFCYRQVDTVLALAYGGACFFSFWALAMHAQSPTRQTATLGFYLLM

GLASFTRVLWFATPLGVLSVLVAPPRIMRGDQNWVYFLVSEATEL

>contig59033-0 Frame-2F0

MDSILDAPNFAIWHEFLMWRNNLSLDETIKAEVSFIREKYSDDILVKKFGFIEMA

>contig59033-1 Frame-2R1

MNDTSALIVSSRDRLLRHIRNSCQMAKFGASRMESISLPIKKSYVLVFEYP

>contig03563 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57313.1|) 0.0

MVNAGHSVILFYKYVEIESPQELYQEQKQLCERLGLAGRILISAEGVNATLSSPSRVKID

EYVALLCSHKIFAMAAADFKHSYYACHRPPFAMLIVKHVKEIVSTGGVVSRPDMSASDKD

RGYLTPNQFHEAMREALEKKDETVVLDVRAHKEYLVGHFETAVDPKVKTFSEYYVFLKKR

VDEMKNKKVLMYCTGGIRCEKASNFLRSQGVYDVHHLKGGIHKYLETYEDGGFFRGKIFV

FDKRVLMGAQKSNEVVGKCIECQKPYDDFSGRKVCTVCRDLVLVCDNCFYARHGEIHCID

HQYLKRCYVTFLQYVPRPKLLEHQKSLENILSELLEDKSSSKNKRRSLRNQLNKIAARLE

AINLNQEAAAATLTIAPRPIHCRTCGSASCMGNCWGFWNDDVQSAQEE

>contig08005 Frame-0R

MTTLTDVGLAALCCQVHAEYVHGTSLPPSDRLPYEVEEGNVEYKLQLLTQDPDRLRQLTT

QMHWRLNEGRNTAFYEIGVKDNGEVLGLLEDAMVHSLGTLARLCRVVHAKMSLSRFRYGR

DRRHRAIRVKVARIVEPSSTKRLRVSVIGDFESGKSTLVGVVTRGCLDDGAGLARMHVCR

HRHELENGCTSSVSEHTIAVARDGHFRCIEEIQTCDFGEHDQDVRAQEERIITLNDLAGH

QKYLKSTASGLAGQFPDYAMLVIDAVRGVRDMTREHLQIATALNVAIFVVISKIDLATNA

RLQQSVTEVTDLMTTFCPRQQIVWPKSLPTVGEDHELIWPLTCGVTIPVFQISSVNGTGL

DILQKYLANLEPKRVWATTAQTPVEFQITQAYDIDQAGIIVTGLVQAGTLGLREPMLLGP

DMDGHFCEVVVKSIEVQHKAAQTLCAGETGAVRIRFVSTAQPASRIRKGTMLVHPSVCPI

ATRQFDAELHFLPDARAFRNNFQAVIHTGQVRQMAKIIRLEDPMSASVTKPVSTYSPATT

MCRLEFMYWPEYIRPDLPLVLREGRTQAVGRIVRTVPYLHQTTGVS

>contig11670 Frame-2R|Blast-60S ribosomal protein L14, putative [Phytophthora infestans T30-4]gb|EEY64494.1| 60S ribosomal protein L14, putative [Phytophthora infestans T30-4](gb|EEY55133.1|) 7e-62

MTFTRFVSIGRVVLINYGPDAGKIATIIDVVDENKCLIDGPFSVTGVNRHVINFKRVSLT

DLTVVIPRQAREKTLKKALAKSDTLAIWEATAWAKKLQNKKTRAQLNDFDRFKAMIARKQ

KNSLVKKAVAAARKAN

>contig11902 Frame-0F

MRLNVMALIYLVGIDFSLAFSLTISRSNESDITSRERPSESTDDIYVQTTPPQLSLHPVF

RTKIKSEEERNCFPFDFNWASWLTGKLASIWASFQLRPIITALEELPTVTNPNTALPLDL

DKWLANVEKLRAEKGFSLDAETLNVLLRKKYNEKDLMSVYVWLLKFQHYQSLAKKELVAA

ASDSTLRIAIYDAFSSFKFGPAYAFTFFDLSRLLHPKDGKYDLAIRDWFRFVNLCINVDA

SKKEAFSIKDLFYILTNALPESHRSENNDKLKSSKYNQLLKIIDYLKLEKLPRLASAMED

LMGLNKNQLDKIRKHNV

>contig12868 Frame-0F|Blast-beta-tubulin [Phytophthora infestans T30-4](gb|EEY57597.1|) 0.0

MRELVHIQGGQCGNQIGAKFWEVISDEHGVDPTGSYHGDSDLQLERINVYYNEATGGRYV

PRAILMDLEPGTMDSVRAGLYGQLFRPDNFVFGQTGAGNNWAKGHYTEGAELIDSVLDVV

RKEAESCDCLQGFQITHSLGGGTGSGMGTLLISKIREEYPDRIMCTYSVCPSPKVSDTVV

EPYNATLSVHQLVENADEVMCLDNEALYDICFRTLKLTTPTYGDLNHLVCAAMSGITTCL

RFPGQLNSDLRKLAVNLIPFPRLHFFMIGFAPLTSRGSQQYRALTVPELTQQQFDAKNMM

CAADPRHGRYLTAACMFRGRMSTKEVDEQMLNVQNKNSSYFVEWIPNNIKASVCDIPPKG

LKMSTTFIGNSTAIQEMFKRVSEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVS

EYQQYQDATAEEEGEFDEDEEMDEMM

>contig14145 Frame-2F|Blast-Sulfate Permease (SulP) Family [Phytophthora infestans T30-4](gb|EEY56793.1|) 1e-159

METDALPLERGGVEMTPLLQPVASAPVHATSHENFSLIHQNQQLMRRVRSVQDAAEERLL

FGFHSSTGSRLGPYGALDGRKYSTNIVLMQDNLYTRSEGDLASSALNTRQFQSILLDLVV

NVTSGVIAFLLSSTLAVSCASVVVGHGTPLASVIAHFIDINLLGTAILSVVLAWQSSAPW

TLGAIDVFVAPVMAEMAEKISTHLHGNLEKVVPTTVVMVALTSIILGLVLFLMGLFRATS

IANYMPYPVIAGFLSGIGAQLMKNGIHMASSKAVTMAFFTWKVQLLVLPAVAFASFARLG

QYLKFPVAFSFPCLLALSLLGFQLTSFLNQSSMESLSADGWVFAWDPVVVAQTPMWFPWV

EISFAHVQWHTLFHECTGFLVSLIILGALKYSVATTSLS

>contig21220 Frame-1F

MEGRNGKWVNVDYTNRIMEESGVLPPDGAFLASNVPNSGHENLTSFRPPSSRPLSSSTSA

SSNPPSSNIQVAVSEPVKQGEGMNSYISYKISTTTTRPQFVKSSFSVVRRYSDFVWIHGH

LNALFPGVVVPPLPEKLLVGRFSPEFIESRRRALQLFLHRCCLHPELQHSEHLTTFLEAS

EDQLQAFRKDPRHAAPNAQRGVLFQWIDETVNTISSTLIPPTTNLPKTPADLEIEDMMAY

IESLEPITMGLHKHAHGLTKRAREIADGLFELGVSFTLLGKSEDNVSLQEGLNQIGHCSD

TLSILAAEHAEREALHFEEPIFDYIRLVGAVKAALQKRNELRCAYGNAVTHFEAQKTMLT

KILQQNGHQGMLDEKDLVVEKDVQKAQEAMERAKLEDEIVTERVLREVERFKRAKLADFK

LIILDYIQIQIEYSKRVEDEWQKVIPKLARIQVENEKSESVTPGMEASTNGAFHQQGARV

GSCGPMIHEDYIPSNQQVTESFSDLTLMDHDRRGEDLYQRSPYGSRPLEDSNSDVAI

>contig22665 Frame-1R

MDFWQFRTRFQPRFRDTQPRPH

>contig23752 Frame-2F

MNTFSCDRMNVALPSIAQFGLVFPGRPVITDF

>contig24476 Frame-0R

MVLSLMTETPLSEWLFINSIADKTQRGFYELVLSGIAGYPFKEVLPADDFYSNMTEILNT

YAQSMNVGRYNVYGDVHVWLTKNEYQSVQDMDGRLLGDVLRKWLTPILHRPSDSFYLLPQ

V

>contig25835 Frame-0F

MLRCHAYFAVFIAAVQVVAVHSVTSICDKVEECSVNGSPSKVCNRTEKKCNKCLSEKDSN

SIWSTIGILTEYVCYAQDESGECPEGTVKCPSKLTKSIDNEQVSSIGSATGDGGSLAFDS

LANRTPLNTTLSFIRDTPKAIASSIVYTKKNSSTTTPSLTDSSSNTQDIPQSIKASTKKK

TNVVTDTSSSLSSSTLSDDLSRDSSGSDKSDALDTEDVKSPVQIDGVRPSLNDVFPEANS

VQATVSPSYSSTVDTSPTAVEPSTNQASAGNARSGGNDMSMIIGIVGGAVVLVAVAAFVT

WRKKKDEPDSDEDDSAFSPTKPAMNYKVAAQSSTATTAYSVPPTNYTNTYGNQYATQYNT

KYDANSYAYNYADQMAIPPGTGIVPPSYTSPGAIDNDDDYQPRRTDSILGGTGVMLSTTG

AEAPFEFSSGPSPSPRHSDIKDDKWKNMEDSFRKKRSASDVSVEF

>contig26290 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64143.1|) 2e-14

MSSANVASGPSSSTGSASPVPPASPVQPTLKVMRLYKPALYVQGVSGGSLLPTSLTESTA

TQHEFALSSMLILPDSF

>contig26531 Frame-2F

MLDLCLLTNVTIKVMIEESARVKVKSMESHMEGGDDDSATMEDPVSEEKLGPPISTILGI

FRGWQMDPITMSYKNMVYDDGDRCMDTHHYSVIVELIPSDSVESSPKLFGLIKTGMCSFK

ASLLMYVSEDDRFTKQGIHTPGVVDISDARASLPVICGEMNCQYGAITKRLRDLSD

>contig27068 Frame-0F

MESLGVSPELVAQISSGLPSHCEPNGNSPDQRQVFLVRAIEAFSGMESIVPCDLLNELMH

GVVILHHEAAQVLGTTQFSVETFFPLLAYTLVHCQLPTIHAQLHLLENFAITADNANGEE

SYYVYCVHAAVEYVCNTAGLGVPASLTQPVNMTSSAHLTPDLASATPMLSAIAPSNYQAC

SSELDSENAPMETSISMQPHFDNHSEAAVV

>contig28384 Frame-2F

MIPNGSKWVFPTYELVIDQEPDTREAANEFEAKLLAEFEKNNTQDTDEDDMDVSQRELNE

ALGHTTDQDPHYVRFLTRVAIAKKQVLRYSRWQNDAVLWVHSKGVLNHHDVPPCNHCGHE

RKFEFQVLPQLLTYLHVDHLTSLHNLTSRSCEWGTLAIYTCVESCSGASECVEEFLHYQP

AYLAD

>contig28722 Frame-1R|Blast-asparagine synthetase domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY63196.1|) 1e-172

MCGLGIVVTAHSNETPFLQSAVSSPCSSSETSFPCSPTPASEFDLELQRRLCQRGPDQYQ

KVIRHIFTRPNRQGTRRGYSIAMHSAVLHLRGEKVIPQPLIDLDDNILCWNGEVFGVNGP

EMDDPRILWQDSDTLLVSKKLQNAGKKLTELNTHRVSERDPVVDVLQSLHGPFAVAWLHE

KSKRLYFGHDRYGRRSLVYQACNDKSESVHLLAKLAGTTRTALLGSDLTSFVLSNVAINL

SRRDQTQYQEVPASGIYVLDMQTMEQNLPYRLEFYPYVPLVPKIPGKIRLVSETLVDSYG

VTFSFPFGAQSAEVSDKEDAAALLISARELFLTLSNAVGVRVRTIPLQDSAHGISPVARV

AVLFSGGLDSVVLAALCHFHACVNEPIDLLTVCFDGKSGFASPDRQAAKTAHAELCRLFP

QRQWNLVKINVPQTELTSVQGEILTLMAPCDTHMDFNIGAAFYFLSRGRGELQTSADNSL

PMTREEWNNNLDTEPAHLRLLTTKVAALGLFDLHSLPPDSLMCPVNHCGRKRKLGCVLGV

CKSCCVKLHRVVSKLFSSDDNRMNHHVDHREAQQCRNQINAMGLRCDSHLKELIKLLTLE

QPDIWCRVHQTRQIPTIQQTSPLEPNSKSGLMYESKARVVLVGIGADEQLAGYGRHRKTL

INRGEAALRAELQMDLDRIWIQNLGRDDRCIAVHGREARFPYLDDHVVSAIASFPVSSLC

HADLPRGVGEKRALRLVAEALGLSSCVRLAKRAIQFGTRIAKVSSNGSNRQILGTMKFRP

ECRNT

>contig29066 Frame-1F

MRYHGCHPEKLVPSWYEQVPRFFGSRFMFHQLCSLAGYQFDTLRRAKHSTMMMVHHYFNE

QIAQLNVFCCECSLLITRADFWSCRDCIRFALCDYCYQRNGHEHPHTLNFGPAPLTTPTQ

VQQIE

>contig29192 Frame-2F

MQSLHLKKLQPYLFFGLKWRFYVKSWLRLLQSIKVREPTEFMPLKCNKEKHVG

>contig31049 Frame-0F

MFKCISFAKDFHNLRIQCCRWAFPRM

>contig31401 Frame-1F

MKAKGGNRFPYHSNNNRASASLVPTPYSLATTAATPTLPSITMDARSLLRTPIRSTKSTK

RLSIYQLGNPSLGLNGISTGMIALPPPSPLPLPSPIKNDLDTHAFFS

>contig32466 Frame-0R

MNSNDEDSFPMGLVLNLNATVPIYVDDDVFPHNPIVSCATTEGFLIHYAFVDTTVSEVEF

VKRPSCFNENAKRTVTITNSCEVEKDESEFQNEIHKQEYGL

>contig32905 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62384.1|) 8e-90

MLLLRQVRARCGNLRNCISSAEFLRAFALLEACTNNTLIRRNTFATSLQRLEVDKLDLPP

LPTADEVDATIAAAEAHAQIQNMAKRVQHMPIRAVHVARKMDIASLFLKLFTDRFKVTHY

LHKDSIVLRLSGSKNNGHSGLVTGVAPPTAHNFSSSSNGDTVTTLSVGAGGKTVTSRRAI

DKWVVYFDYGAVVFFNCDQALVNTLIKHATRFCSDVFEMRGHEEEMLLVGDPAQQKWSTL

VENNVLVREIDHINVHVIAGV

>contig33982 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67626.1|) 3e-80

MDVKTRGLLSGVYATIGVTLAASAKLQWISKNAAASILSLVWLGFVLAISFTESWVKFRA

PFLPRHLAFDLGRTMFAALNSIEIGVCAGLWILHFFFVSTSGDAVWHLVVVTLLLTVQAA

WLYPKLQLAAEFTLYEALKDTGDSNLSFNQKMRFGEIRHAIQVNDRPNRIYHVLYVGGEL

VKILTLFGFALRYLKAIPA

>contig34613 Frame-0F

MNVLYFNTPTVGKYQSPLSNCS

>contig35092 Frame-1R

MLTKRRSMASKAHIFHLRSIDPVVQGIPRVRKYLDSRDTLKNAQSDKIGSR

>contig35166 Frame-0F|Blast-serine racemase, putative [Phytophthora infestans T30-4](gb|EEY54998.1|) 1e-111

MPENSPSVKQSAVRGYGADIILCEPTIEARSRTANDVVKATGAHFVHPSNDSDVMSGQGT

IALELLDQAKQEYGVELDAIVVPIGGAGLCSGIAMAAKSLQPSIKIFAVEPDGAADAYNS

FQKRELIGHTSPVKTVADGLRTVLGSNNWPIVRDFVDEIVLVSDDEIIMAMKLIWERMKL

>contig39728 Frame-0F

MGARCDTSVSLASIKARHRAWTIQWILPIELYCNAPLLRALSWGCNGLAITKSHQAYYPE

ELRKRVICRTLEQAELDTISCQVINAIHRISIDKFSDDFIPISHRRHDRKRRRLALYVSF

GIKFTCKSHVYDLSR

>contig40092 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63520.1|) 3e-11

MTFWKPPLGKDFAHELISQGYAKCIPENLKDYDNGSPAAMSYLAQRLKKLNAAQKRAQSM

QYGIWKDWQEAKLSDRLFSASKRATTKGFSRLFASFRH

>contig40166 Frame-2F|Blast-endonuclease III, HhH-GPD superfamily base excision DNA repair, putative [Phytophthora infestans T30-4](gb|EEY57249.1|) 2e-99

MKARESMETPIDKFGTHACVAPRVTSTKVKRFQLLVAALLSSQTQDAITYAAMYRLHHLG

DSVDGLTIAYVSKISEKKLSKALKPVGFYHRKAHQLKQVAAILLSQHHGDIPRSLDELQQ

LPGIGPKVGRVITLLAWNQVDGIVVDTHVHRLAQRFGWATATTPKNTKKELEDWVPQKYW

GKLSLAVVGFGQAICTAKLPLCSKCPLAEKCPSAFNADTRNRKII

>contig41613 Frame-0R|Blast-choline dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY64377.1|) 3e-85

MTGYICLLRGSKNGTLRLRSANSRDYPRIDPKYLAQEENRTSLRESVKLMREIFAQSAFE

DFRGKGISPKDTVQSDDQIDAWVRKYAGPAYHVACTARMGIDENSVVDPQTRVHGIEGLR

VVDASIMPNIVSGNTNAAVIMIAEKAA

>contig41778 Frame-2F|Blast-ras-like GTP-binding protein [Phytophthora infestans T30-4](gb|EEY64281.1|) 1e-101

MIFSNCGSIVYVIDAQDEPYAEALARLHDTVTRAHRYNPDILFEVFIHKVDGDLFLSDDH

KIDCQREIQQQIMDEINDGELDIHMSFYLTSIYDHSIFEAFSKVVQKLIPQLPTLENLLN

ILITSCNMEKSFLFDVVSKVYIATDSNPVDMQSYELCSDMIDVVIDVSCIY

>contig44324 Frame-0F

MVRIGTATRMLPFFWAMEAAALHTRDLEMLLDQNLLIESPSESVYVGHPSPCMLDLKMRK

RKLKEVSLRACLSLVGIPI

>contig44351 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY58105.1|) 8e-43

MISVEFNKQGHVIGGGFTTHYFEKSRIIDCRSRERNFHVLYQVLAGV

>contig44401 Frame-2R

MSVSDLSCYVKLPRNRLAELFHVVI

>contig45455 Frame-2R

MPTGADVNVIRALLFVFETHEDQLRKLFGLLMFREMVHTQNWNELFRANSATTALLREYT

CELGGDFITHALADVINELWENPNGYEVNPRHLQPQDDLHTNQQRLEALAERTLDRIFSA

ASLFPYQVAKIYRVLELEMMRLIERDRRSNVSLPRLSAVGMESTSVESTGLGGLPRLSSI

EEHLLEEMLSQSNSFSTTTSPISAAKEEFYMHLGGLVFLRFLCPALVVPHKMNL

>contig45806 Frame-2F

MTCFDIDDQDPAFEWIYMLFALHFRDGRVNDLYVAVSAHILSTLWSRVTPEQLILLRMFS

LWVTSTLKLNATTNMHDGDFWHPLRQNTYEFVKTTWLYIVSEGDEDRPNEADEMRKKVWI

KLEYEAKLMLLDVLGDLTVDRTIIDAKSGAELLQSLLLELERVWKLERQSPLIKNIRRDN

STLPMPLDQEPIGYRSGLIRVIGNFSFRHVCNQDLVREGGFLPLFLNHCNIDERNPMIRE

WSLVALRNLCEGNEANQQYIEVLRPQNMDTVLSSASQK

>contig47466 Frame-1F

MYHGAARDRGEKKRQRLTPPPNELWMEAVMNKIKKTDGCSLDPAAAVDEVAASSAAAWQE

RAMCGYSQMSMPLGPKYYASTSSYNVRPAECSLSFTEGPSDSSNAYQNRKSFANFSDKMI

DGVHRSQDRHINEFTGYQATVMPGSRGSQKDAVAMSSGLQRMKRKGLILYQGDAADEAAA

YQKRLIHEKFPIEGRIVDSSSERQLYQGDRSETSTLSEMGTTYKRDRKLPSRLEDMLREQ

VNLDESILLDAIAVAMEDLTPEKEANLVARGRCHLCGLSKTRLLPVVNFCPHADENHSLC

REHLRSVYRVRMEALFVGRNGSAPNRRLFRCLMCTRGCPCSGCTAEKAQDVQNYRRYLFD

TLRCNGHGLFNSAMSDQATDGAFGATSTSAMETSIVSTSESRLTYGIAPTINGRQYGQHS

PTSSPGDRR

>contig47592 Frame-2R

MVSLETLEEFKEVIRFERLRRSFCDQL

>contig50291 Frame-1F

MLLHDDEREALEAALSLVDDFPHVTPVYGDPQLANEALRGSPLPSCSLGVSTSTDTGGDG

KYGIV

>contig50686 Frame-1F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY70200.1|) 2e-73

MSARSDISASDNDHDDADLFDAALDDLHDQDSRDYFDSSAVTSPPSSSLPRRSASGRRSN

ASHMLEALEALSDNAEGEGVSYSIQELLEQLHSGESSVLDGMFPFSQLLQGPGGNSRFQR

IFEQIQSNQAEHTQTAALTELCETLSLSSEEALEGSGFRVDKFVPVVVELLRVPPSMEIL

ILSSRALSTILELFPGTAIPKAVAEHVLPSLCEKLLEIEYMDVAELALQMLDQIVCKAEQ

TLGFASTLTHNRKMCAQYRAEVINEN

>contig50732 Frame-0R

MAGWNPLKLGRDYAHAISERAAQWTWLLWRMHFLPFVRSSISMYGRIST

>contig50866 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54985.1|) 9e-76

MPRSDFATEFLLRELLSSLGQPLVKESEDSNSFSESLSEDTESQSAVKMSQSRVMLVRHT

NSLQQTATLVDRNFDIEAFIPTHVITALQQEYDYKTIGRLRGSVIRVIKYHFATSRRCLS

IDPQSATTSSSVSNESIQRARVYLWVEALAIVEENELAVEPKPSIYSHSLVAERLEMLNE

SELEKQLMNHQGLSLLSVHEIVSFNDDRPLLEEDCIIPEDQEQE

>contig52723 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69477.1|) 1e-38

MRFSIDAHTGLSLSRQDQRERQTRHIQSLQQIAFQSFKNSPAEELAIAPCSQIANAYNFS

ELLNAIASADRSQLNSLAIAVGVLSDQTEADSTSDADLIEYFKDEYSNQYMSDNDVFSSL

KPIFPT

>contig53917 Frame-0F

MLDGDESFQTLIHEMNDLRQLEQLVRAKAKERVHTLQCPDVTVQWQVADEPGLSSVLLRA

PNDDSRTSDSSVKSNTKLAGKYRPLPVRKLVVSVWIYPPHVEIPLTEDRIPTASDVTYPN

>contig54141 Frame-1F|Blast-mitochondrial import inner membrane translocase subunit TIM50, putative [Phytophthora infestans T30-4]gb|EEY70509.1| mitochondrial import inner membrane translocase subunit, putative [Phytophthora infestans T30-4](gb|EEY55063.1|) 1e-15

MLRLVLRNAQRGVGASAAMAASRQLVHLAEASVPSSVSKASSILSKVGRDIPLKVVPRAE

RRAARQAV

>contig54750 Frame-1F

MDADLTTKRLLLHVLVAICVVCGRVLGLKKQCDSSYS

>contig55946 Frame-0F|Blast-hydrolase, NUDIX family, putative [Alcanivorax sp. DG881]gb|EDX90966.1| hydrolase, NUDIX family, putative [Alcanivorax sp. DG881](ref|ZP\_05043545.1|) 3e-08

MSKERAFVVQSIGTSLVPLLKRNLARQQILPHDASFVHASVAAIFRWKEKEQKTLELLFI

RRSVNENDTWSGQIAFPGGRRQKKTTMDMHALDDISGEWSDWESLRETAQRETMEEIGLD

LKN

>contig56976 Frame-2R

MLSRRLFGLIVVGAFALSVHAVDRSKFRTCEKTQFCNKFRNLQRQELPTKFHVARASIQT

DSYANLVRFVVEDVAQRESVALSGSLAFVLNADKSKVPVVRVRLQEKFEDPKDLKTRWIS

DDILMLAADETRPIRQVSSQEAGFKTPFVEENVLLFAPEIQGAVHVVAALKFGKAPFGVD

LYLDGEKVVSSNDNGLFHYEIRHSSNAVVQSDEVADQLAVDAHQGKTIVDYGEDGLAIYD

>contig57878 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61382.1|) 9e-13

MTPRPSPDIQDFAPDNQDDAWNLKQFQQEEFTLGMVPTVPPPPELC

>contig59186 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56451.1|) 1e-07

MSAPATRLECLFLLVRDGSCAQIRENAAEKLGEV

>contig01768 Frame-0F

MHDGWLDGNKVRVLPEAPKTEPRRILRPSRSPRSRYRRTSRPRSSARGGRGRLRAASPFR

GRSRSSPRRTGRPRSPLFRRRASSPFYKTHRSPKGYRGNYRRSPSPFRRRRTSRSRSSRS

FSRSRSRSR

>contig04730 Frame-0F

MFAALAGQNADLENMFAFYLTSTVNESGSELHIGGYDLALVGPNASFHYTPVVKLPEYDS

FMYWTIQLNMFAILSKITEDSAVNTDISVNYCDHSCYAIVDTGTSLISIPVHYFDQVVRR

ITQGLHCKGISCDAVTATSFPVLRFGMEPDNVFLLQPTDYVLCSSWGQCKLQLQPSEKWW

ILGDVFIKTYYTLFDAERMRVGFACNGDVCQGGRGKVYGNTGENGAFHNWEHVFLVTSCV

AAAYMLVCVFNHHKKKKKTPLNHDTSSS

>contig10524 Frame-1R

MNHPKRHHFSHASSPDRKFQNAYHDIVTDAGIQNSAVMRGTLHFWKRSDCGAILRSRGNN

EMREMWCRWRRTRGKPTVTTLAVRQTSLDESWMAFVRP

>contig13363 Frame-0F

MLHVTPSHALRRASPASISSNRHRLFLARLFAVHSGDSCISEQDMLHALDKFQKESARKT

VPWFLANMPPSYFRSIHEADRLQHLNAITALVNAQQPEVMLRSSNHRVFSHFRSGKNFPG

RLANVLEQLPQSVNNATLARVKIFTAIDDSLGLDIFRFGQQAPFRNATPDEKLARDKIQA

FCAAIQANKYANDTSCPPPGSYLDANAVDRFLHQSNTMYVQYSNPRRLAWQMKLYAEVSG

TEGVAVDVEHQWETRSDENKLGGGSIPQTMLTIAASNVLPKSFMQKAATYLGLCNLNVVR

AHLDVVKDTSNRKGHVAMIRILVQPSADAITQEFQFEWSKISGNLKYLKWIDDRPVHLTL

QHPELGLSRAELIFAYGNMLHGVLAKKDPFAYSLTRIMETLEHAQNLPLASRIADFFLDK

FDPQRPSPMTEAQQNAMVEELQKEIRRNVEHEDAILLLNRMAEAVRGTLRTNKFVRDRYA

LALRMDPEVMGYGTVGKDTPFGVFFIYGRRFKGFHVRFRDIARGGLRMVYPSSTDAYALE

SARQYNEAYNLAFAQQLKNKDIPEGGSKAVVLCDPIVGPIGDVAPRDFILRKSVKAFSDA

LLDLNTMDEEVKSKIVDYYGKDELIYLGPDENIIPDDIVWMTKRAAYRGYPIPRAFISSK

PDAGFNHKVYGVTSEGVAVFADVALRSQHIDPKTQSFTVKITGGTDGDVAGNVIKILHRE

YGTNLRIVGICDGTGVLEDPQGLDIQELLRLVDESLPLSSFDDANVKASSVKYDINTQEG

IRARNSMHNRVQSDLFIPAGGRPNTINENNWRDFLDATGKPSSSLIVEGANLFITPEARQ

LLFDHAGVVIVKDSSANKCGVVCSSYEIVASMLLETDEFLAVKDELVIQVVDKLRALARV

EAQLLFREYKMDPTSALPPASERISRAITRVHDAVLAHFEDVCEADQQVLFTLIDEHLPP

KLRELALDRVQEKVPLAYIRSIVASSLASKIVYREGLQFTEALPDLNLGNMALQYLKQEK

KVQRLVQDVRSSQLLHKDDIADLLARGGVRAGMDTPH

>contig13697 Frame-2F|Blast-cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|EEY65526.1|) 0.0

MRFVSPFLFLSGLLLADARKTPLEYEREFSAWMEIHRIAFADALEFAKRLGNYIANDLYI

MEHNVENAWTGVTLGHNEFSHLSFDEFKHRMTGLVMPKGYYEQRLASRIDGLWSDVQVPE

SVDWEELGGVTPVKNQGMCGSCWAFSTTGSVEGAVFVSSGKLISLSEQELVDCDHNGDMG

CSGGLMDHAFAWIEDNGGICAEGDYEYKAKAQVCRSCNTTVKVTGFQDVNAQDEHALKVA

VAQQPVSVAIEADQKAFQFYKSGVFNLTCGSRLDHGVLAVGYGSDNGQKFWKVKNSWGAT

WGENGYIRLARDENGPAGQCGIASVPSYPFATLVPNTEQIRKTPMINEKSRAASLDEVVD

LLFDKHIDIDTHANTLADFFSAAKITQCGDAGTAIIHFSHLAVNPSSPQRGQPVSITCNG

KPKRDFNAASYKLEVKLAGMQVFGHSGALCGDTHIPIPLGLGHIDVHGFACPVTKGTTTD

LLVEVNLPIIAPAGIYEILLTSDDGSNSPLFCLNVELDLTASEQTAKKSHVYEPILFV

>contig17262 Frame-1R

MTAYRTRKHDSTRRFHRSRGSSDVTEAVVTSPQRPSFYSDIDDHTTNAVFSITDPSVNFY

QAKEHEEEEEDEVFEPNVLEQAKPGRIPMVFCTGIVPGTVEDAALGF

>contig17640 Frame-2R

MSTTMDVEMAEPEQQHPLQAQFEDAEDIMEALAPYASPDMAIQAFQSIISYADEDAALEQ

VQRVKEHSIYKLAQLYIQFGREKELASLLQALRPFFATLARAKTGKIVRTVIDMVAKVKV

FHAEKALQLQADLCLDSIEWCKQEKHSFLRQRIEARLASIYFQQQNFQPALDLITELLHE

IKKLDDKQLLVEIHLVESKLHHALRNVPKAKAALTAARSISNTIYVVPRTQAQIDQMSGI

LHAEERDYKTAYSYFFEAFEALATLDTVEGLKCLKYMLLAKIACGGASEVNILINSKQAM

KFIGIELEAMQAVAKAHEQRSLELFEAATTKYAPQLVEDALIKHHLGKLYEQLLESNLIK

IIQPFSCVEIAHVAKLIQLPLPQIELKLSQMILDHKFHGILDQGKGQLIVYDSPTEDKTY

TSGLGVIDNVGNIVDNLFRRAEKLQA

>contig17774 Frame-1F|Blast-sporangia induced phosphatidyl inositol kinase [Phytophthora infestans T30-4](gb|EEY54616.1|) 1e-142

MAGEGAVREEVAYLLDSLSNGFSGVPPTAVAQLRLPDAERAKRGAVQRFMSSSIGSMESF

GMPFHLEKACKFVPVEQVHRIALLDLRVFNTDRHPGNILLIGEMKPYSMVPIDHGCILPS

WFHLSEARFDWLEYPQSREPLSFEALQYIEALDAEQDSKILRNLSIREECVTTLKICTLF

LKLAAAQGKSLFWMGKFIARDGCFQHPSGMEVAIQKACKCVGIPYTFKSNQFDEQRGEIE

RGVLSRRPSRDFFLALEHLLRKAISNVER

>contig18249 Frame-2F|Blast-ubiquitin fusion degradation protein, putative [Phytophthora infestans T30-4](gb|EEY58728.1|) 9e-26

MFGGFGGEGNPFGVQFNFNNFPQRFDEHYRVYPMSFCDKAHLEDGDKILLPPSALETL

>contig18519 Frame-2F|Blast-peroxisomal trans-2-enoyl-CoA reductase, putative [Phytophthora infestans T30-4](gb|EEY63788.1|) 4e-25

MGDTMHLDGGWHQLGPLMDIPALLRTEQSNRKFSEVFTLKVT

>contig18582-0 Frame-1F0

MMCSATCDLPQVVNHSAIFLPNL

>contig18582-1 Frame-2R1

MALWFTTCGKSHVALHIICCELSVMKVCFD

>contig19080 Frame-0R

MKSFKRLTPLCDPQPVESKSH

>contig19134 Frame-2F

MKYLEEPQLSWLNSVLSSCEIGDRLITGKLELYSCKKAGSDKRLAKSLELYYQQEMEEVN

NPLSVSPLGPLAAPATRKVLINLISTMNASFPDYDFSAVRPQQFRKEVDFRRALQRINHD

LAEMFDGSGFMDKMWGAIAEVIKLDECDVYSYIPDMDADPFSDGNLWSFNHFFYNRMQKK

VLYFTCLCK

>contig19448 Frame-1F

MHRADPKLSISSISSVYGASLSMEQLATSTDSTMNQLATLSQSLSLNAVPSARGALYSRH

VRPEEALFAEMVADFYENLENVEISDLFCEKLLSGYIAVLQQQLEKLEESLASSSKLREA

PTKRLQSEIKELRDERNTWRLLFELRQVCHTTKDMADGEDSLMLVEGEIDELHFETLEDD

AGRLLETRNETFKIQKAVKTWLENMALESTIELNDKSGLKGSRTLRMIKKQKDLKRKVSM

DPDAIMRDGDANVLTDDLEDEAELMKALWLYLRAGRMDDAIDLCIRVGQSWRAASLSGGH

VVGASESNESTECALERWGNPFRALWKSMCWRLSEETAKGKLSKSSSLLAKSYEEMIYAA

LSGNIQVIIKSSLCESWEDHCWAYLHGSMEHQLDEILYKLLIVKTQTTQLIVGNNVHYRR

HYLSLLDKMKYLKRYQANLETIFDELRGSSSELVRLQAHEPHRQIQSKLVTANFQYIVSS

IFDTVLFTPNDDSYNWDLQLNSTGQSDVTSSLFLRFAAHFILFASFTGEHFDEQSGHMIL

KLYIRHLVKRRQLQFVPVYATRLPKFGATEIYVQMLSTVDDTFERELCSKRILEYAGIDV

LSIVLQSVVERLSNNYKEMAINQQEQKIQPLPSNVPTTDLDRRRIKTIEFLCFYSQHRAE

ALIRVNMLARQFIHEGKVAAVKELIEECLPEDSIGVLDMNRDGQLLRTNDEIERAMREFL

CWRVYIQACAQYDLWRNCINTRAMSFYSEEKEYLADIMVHVSRSTAAILEVLHFENGWLI

GCSNNATEDLALRKRCLPMLVFNLHFIQLESAKTIMRLTYFPTDAKTALAAPLLQKSIQV

ADVVADEHYGVYLALDQDQCRDLLHGFRESAISLIFVESLQLAPETVIT

>contig22235 Frame-0F|Blast-casein kinase II subunit beta [Phytophthora infestans T30-4](gb|EEY64204.1|) 1e-47

MMKKYREGDFGVCPRALCDGQPVVPAGLHDEWKKSEMKVYCPKCRDLYTPTSEYQTPP

>contig23229 Frame-0F

MSASNGSSPDGPTATAQPQGFVFFIPPPPTVWVQFNDGTQVAFTPSAPRYLHSLLSGAPL

FGNASADGNERDSFASALNELFQRAQAQHHGPPPTSKVFLDNLSVKTWTLDMQKTEKHTE

CVICLSDYMEKDGIISLPCGHTFHKECGLTWLVEHNVCPTCRYELPTQMKATPEASLQTI

VPVTTTAVVPTTRAIVSSSEREPVQQETTLSLTGVRRSRPAEPMPSRDVRQRLDGPLSSL

NEAVLDSLLEEEADQLIKEMENSRKLVCNDQSVEIDDRDVDEFMSESSC

>contig25959 Frame-1R

MAEVTPEFKNGAKTINFRRILLTKCYESLLEEPGSQSMDSNTLAHHSWRRHCMLQNVPFI

GELFRRQLLTENIMHVSVAMMLDDEVKPQAEIIMAACDLLSRVRKNLILKVSLFAHSCLM

SCRLETCSMALVQPLDEQWMNTLPFSFEFTSTATFQMT

>contig26532 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66206.1|) 1e-06

MITKGLLTERSASFNMTLEASKNTLGSTSRILERSLDLLHDVEDLQLTLIKRFSVKEDAA

KTRFAGQEAEQRNQKEDINLPDGLDRVEEQGRAVA

>contig26961 Frame-0F

MSDKAILVDEEDVSRANAGERELSQTMELSSSVATGAHESTSESIDAYDAQNNAEIEGDN

EEEEIVSFSENQQLPRSVHTKIRMPSKVPRSLSLGGFEVDDEDVVEMNAREQELLVNIQE

LQRQLSMVQIQTDKPQGETMPPIMDTRHRLIMVSNRLPISFQRNETTGDWSFTMSSGGLV

TALNGIRDQVPFLWIGWLGEEIPHEEQSKVREKLATEFNCVPVFLSKEIASMYYNDFSND

ILWPIFHYVPLPLFRPGSEKKFDLRQWDAYKVANKRFAQAVNQVYREGDFVWIHDYHLMT

LPSLLRARHPLCKIGWFLHTPFPTAEMYRMLPVGREILEGLLGADLLGFHTYDYARHFIA

ACGRVPGALTSPKGVEQGDHFSAIGVFPIGIDPEHFEENLNLKVTQERIQELAVKFAGCK

IIIGVDRMDYIKGIPHKLLAMERFLSLYPERCQDVVLIQIGVPSRTGVQEYQHLAACVNE

MVGRINGRFGTLTHSPVHYIHRPVTPSELVALYNLADVCLVTSLRDGMNLVSHEYVMCQN

QSCDPHREGPGVLILSEFAGSAQSLSGAIRINPWNTTDMANAIGYALKLPLVEREYRQTN

LYRYVKKHTASFWGRSFLTDLEDIVSRPKTVVKKLVRLPVNDVINAYARSSQRLLVLDYE

GTLFDSQTSGPSQPHGNVALPKTIIKRLIEALASDIRNTVVLVSANERDAIGKWLTDRRV

GIVAESGYFYRLPNDDEWQVMAEDTDPSWKKVVRPIMQYFTERTPGSRIDSRESSLTWHY

GETDPIFGPMQARDMQVNLEDVLCNLPLEVVQGANRVEVRLQGVTKTLLLDKVLKRFQSD

YQSNSPGSRGARREGLSPIQNRRKRSFAPQLDFVFYAGSGAEDDELFLYFKKHMALAKKE

EVSRPVSSRSTTLMTADREASVSPGVSLSALTKQANVFTCHVGSSKTEAMFYLERPSDLA

RLLRALAVDSRDGVTPSVLPDRSAVIEPPVVALTSAASMPSLLTTSN

>contig28369 Frame-2F

MLRNGALSITSYTIYWTIVFFWYALSFQTRDTYDKNGKFPPSHVFRAYSFTLSARGAVDY

LVWFTINRPSQIRPCWLQFTTDSADKEFSAQLNTALQEELIYFTIDGMTRAIQSAEDEFL

QASTRSRTQRLVSSDDERNDKFSHQDTTTRATVAKSTSSLFQTVQRNRMLSTITEAISAG

LYRPNSVDVDAKRATKEAEKSFQIPDNHSN

>contig29191 Frame-2R

MRLLDVLVAFVILAATSSAMNSAAQLTPSVDTQLADRKHSTEDVRRKLRGFNPITYLSLK

IKENVAKKVLSKVFS

>contig30805 Frame-1R

MSAVTKAWLKGELMSALGFAEVDDIVSYITNSFHSREEASSYLIELLGIPAERAGHISGR

LFLAESPAATFKTVDASPKQNNLDHHAAADMYLKSGKKSMNGASEMLNNAFIINCLRCGR

IEHKGSRFCDFCDSELHYEADLNRPNKLVQQHMNMPVALDDEEAQPPRMLDAEQVAKSKA

QRSSGESHIMAGFYFDKQQCVDDNITRNEQLPKDARQVVDCVLRKMCQNKRGSSGLKEHP

EVFNGIQNALVVVDDFYNLVFV

>contig31143 Frame-2R

MAHAVQKKGERIKKDPSVLKCPDKNAVRTGHVVCITNVPSALCVSERTVRDLFAEYGMLL

SVTIHHNLLDMKPDGFMYLEYAEKTEAEAAVTAVKDKRVGLAAQLDVTYKRAVASADITG

MNAVMAMSRGKPTCQVNESIRDILLGNLELNRFTQSQHEQTMNDDDLILQSLSQHSFTSS

QPKRKKKHRNSVDSMAKRPKSREI

>contig31327 Frame-2R

MGAFNPRGWGVAIMAHTRIHALTNSYIQAMFSLNTASYHRVGRLAFSQAAHCIFPQ

>contig31402 Frame-0F

MESLYARDTPTAQERKLKLAGRDCVIEDGQVMLKPQDPSHEGQNTSVHFDNAMDTSNHTI

ADADAKNTSNTTEYSAEETFEFNFSSLPREDLEDQWRQHRENLENSRELKKKTEERRLAE

LSGESILSVTKSKDSDNSLSISHETASAVSTILPNVAQHTRQSKVALNHRKQKPAITINT

STDLSNIGAKRPPPTPVSPPTFSWDDILRVQNLIERCLQQYWSKNDILVTLKEQADVDPA

FTNVVWQKLVEQNPTFFCAYRVQLQLKEQIIAFNYL

>contig31477 Frame-0R

MVGTMATTVGWGKTEKSGKLASRILRRLTLPIISNAECGKYPKYVGRITEGMLCAGTGRG

RDTCNGDSGGPLIVDGNILVGFVSWGSTCGEQPAVFTRITYVFDYIRDILRGGDGVDFFE

PTSESNSGSQEPFYALKFPKSLDKD

>contig31851 Frame-0F

MFASRLTEKARHQKTRFLRNMLSKSGCGLLVEYVDDVRALDCLYFDQID

>contig35165 Frame-1F|Blast-serine racemase, putative [Phytophthora infestans T30-4](gb|EEY54998.1|) 6e-06

MSSTTEYAISLASVLAAAEQINGLAHRTPVLTCHALDKIATGDSWPSKRLFF

>contig36111 Frame-0R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY69294.1|) 2e-17

MIQSIIKIYKEEGRRGLYLGMPAHLMRVAPNAAILFMVVEAIANKK

>contig36559 Frame-1R

MAISDNISNKSHEEYSKLQEMMKNGADEASSYLDSLKSKFSEYDTKNKSSTETATSYFQD

AMDRARASVDEFKKSGESVRKEGNNLSDSAMSAAKRSMEQTGSALDSLGKSAQDYDQKMR

DTINSKVDATKDDSASTMSDWKDSISSLISSTRDTTFHGFEALQNQFAATQKAIGEQASA

VADGISNKASEVSDKLTPADTTSKHEVLEGEPTLMGRATDAVSSGINYVTSTFQGAAGND

TSK

>contig37398 Frame-0F

MEFQASDFITVFDGLALARRSHVHGPLVSTTVAPTSVKLVASSLTVSKSAAPSMTESTTL

PVTKTSKVVEAAPIVSTRCTEEVNTVFPTTSTTATCATESESVLKASVSVQPSFIKPLSQ

LGATAEAVLSNNTGITLSTRAIVTPPVKTLEKETRVIEFASKGTKASPKLDTLTVQVDSV

VPVPQKSPPPASLSTSVVVKHTTPAPVTPVMTLTSKAPNVLVPKKKWDKNTQHRAEAAQP

LSNSSVIDIMPLANVNGIDAIEASGIARELLSVKPPELGFCCPAFLAFMRECGNEDGDDD

EDDPDEDSRSQLRLLDVVDLTSLSDSEDSDAFFTPRKEAFGQLDASAEDAVVCSIGFGAT

LPLDLERKR

>contig39020 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57621.1|) 1e-34

MDMPVNSDGTEPSRAHAAKDFTWMEAKSLEEKQSLWTRVKEDPLVPLGCALTATVLFGGL

VTFQRGQSKLGNKFMQARVIFQTATVVVLAVSASLASKDNHEREERKYEDRMKIELREH

>contig41610 Frame-1F|Blast-methylenetetrahydrofolate reductase, putative [Phytophthora infestans T30-4](gb|EEY60254.1|) 0.0

MIQWIADCKNAGIIIPILPGYLPIQNYSSFCKFTSWCKTRVPENVLTALNLVKNDDAAVR

RYGTQLAVETCQRLLAAGVHSLHFYTMNLAATVTQVLDDLQLLPTRNQRELPWYSTLQRS

NIEREMVRPIFWSNRQASYIARTAAWDEFPNGRWGDRTSPAYGELSEYYLAFKRPKVQRT

DLWGTPLTEEDVWNVFVRFIDGHVKQLPWCEQALSLESAAIRDKLQWLNSNGFLTINSQP

RVNGSPSSDPFVGWGADDGFVFQKAYVEFFVAPEKLQNLVTIMQRDYPHLSFHALNSRGD

EHRNTPQHCVTAVTWGVFPGVEIVQPTVVDSDSFAAWKDEAFELWQTQWATAYPEGSRSR

EIIQHIHDTYFLVSIVDNDYANDNSDFFRIFAHIITNTMDKEQLRARVLELDTKRDKMFG

TLASFQLLQEESKCELRAAHSVLACVRNENLLLNEKVRQLQAQLALASL

>contig43111 Frame-2R

MRLAVDTDMDGRKEVPTNGKLFSYCELIGTLMYLTTCTSPDLAFFVGQLSRYVQSPTQQH

IGPAKRVLRYLIGT

>contig43436 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68751.1|) 0.0

MSEPVPKQPEEKTNLYEVLGVEKSASELEIKTAYRKLALKYHPDRNAGSVDAADKFKQAS

AAYAVLSDPNKRRQYDVAGESGKDMEFESVDVESMGGFGRVVGALFTKIGMPIPTQISQT

VLSAARDLCDARNNSTQLPHVTQMVFGMERHAKVDKQDAHFYKLQVDKDRESIVFMCRSA

SKSKFKLVLFDQYGAVRMVQESVKKARFTAADMYLSSTVELMDLNPELWPGINSDTELPE

IFSKLSLFEVRRTLPLEKGEHLFCVYGDNWLSAVKYSIKCLKIDEQALALCSIQESEREL

TSIKHDLDALQKEYMTAKKAFEEVCARVEAKQIRTDELLQEREQSYESFLAGCDPNRTAG

PFDESRNSNTSQNGQKGSTNESASPAGGIRNIFGGFQNRFFAGKERASSMDATNNTFSSN

H

>contig43559 Frame-1R

MFSCIVDVHPKTAILGEMAAATTTRCPFICNVYTRRLRHLRLLSTIF

>contig44143 Frame-2F|Blast-deoxycytidylate deaminase [Phytophthora infestans T30-4](gb|EEY53332.1|) 4e-14

MAGVRYTQHMLRVSKVVIDFNATL

>contig44327 Frame-2F

MHRRSGAFRASVRNQRTINQLLPQEKKVPRAIIGVSSIPLSSRFTHLAVDTAPHHPRKQQ

HQVTAAKMLPKGKVHPVLRTIGGVKKGKAPVFVKNHVQLQKQKLQHVAQNHRNKRQQVVN

KHRKGLAPLETKPKGIQQKVLKNKDPSFQSNGSRGAERGGRGGRGGRGGRGGRSGRGGRG

SAKAKLPTGDDLDMEMAEYWHSAGKGPDPKAAQ

>contig44499 Frame-1R|Blast-syntaxin-like protein [Phytophthora infestans T30-4](gb|EEY61219.1|) 1e-120

MATRDLTRQFLRARVDIKATVLRRKNIVSQREAVSTIKNCAEQEGVSIAITPGWVDVVIS

TNQHVARIKEMTERLNKLHTSRLMVRFDGQDSKYEGEIEQLTQNVTDEFRSAEKGLRRMV

QSDWNREYSAANSKARQNVQRALATQLQLLSVSFRKSQKTYLSRVKDQKEGPVEFNFLEE

IENKQKRCGGADTWIFTNSIFRDRNCRRRYQRA

>contig46981 Frame-1F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY56413.1|) 1e-138

MCLAVRSSFHRSRLFPRLSALISLNSPRRYFAARSFLDLGVDARIVAGLEKMRITMPTDI

QSNTIQTVLAGHDVLCTAQTGTGKTLAYLIPVVEQILRRESAKISEQESENSALVVMGRP

SALVLLPSRELALQVASVAKQLSHLAKFASCSITSGERKSIQQRNTSRRLDLIIGTPGRL

AKCISKKDFFLSRIDTVVVDEADTLFDAKMGFRKEMDAILEPILASVAKRKQSLQIILAA

ATICSPIDQVLKKKFGNLRSVSDGKIHKTPTSIKEEFVRVSPGNKHSALRETLSLHMRHA

TKCIIFCRNALTVRSTEHMLREHGFQNMACLHGDMPPARRLEAIQAFKG

>contig47906 Frame-1F

MRVAKNSPRTKTFHDYEPHAFKKIRERFGVNNEAYLQALSATAKERLSEGASGAFMFFSA

DGSLIVKSTSKDECSFLRSIAHDYADYLCKNPRSLLLRFYGCHCLELYGKQFSFVVMANL

FDTDQVIHSRYDIKGSWVNRHGDLPKRGKKVTCRHCNRKYLYQNSAPENANCTVRLGGHE

PNVVLKDSDLTQKLNLDRDVAIELYQQLSADSHLLCSFGIMDYSLLMGINEVEYVVEEGS

GT

>contig49625 Frame-0R

MEADDNAFVAADVPASIPAAVPASIPAAAPSSSVSFRSSNSLSLPRDHEKLSNDAQVLNR

ALSACPEPMNLMPKPKLRAPPRRIRSGSGSSSNTSSIIINAACPMALAPLVTWVSSWVRF

DVEIAQSFALVHCQTRRQTMLFQCRLVPLQWQVRDASRSS

>contig50209 Frame-2R|Blast-tRNA-dihydrouridine synthase, putative [Phytophthora infestans T30-4](gb|EEY69480.1|) 1e-133

MLDPDRVRDICANMRRNIELARNEKPTFPAAEVSIKCRIGVDDNDSYEELHYFVATAASA

GVRHFIVHARKCLLKGLSTKENRTIPPLRYDVVYRLKQDFPDLSFTLNGGVQSIQHAREL

LNTTNADGIMIGRAAYNNPWNFRDADRLIFDADRNPNLSRREIIERYLNYAEELQEKWGS

NEPLSGSPYTMATSMLMKPLLSLFNG

>contig50506 Frame-1F

MAYTSIPKHLARSLRLKIARRDNSHRSLHTLIRLCKSSKRKRLPLRTKNS

>contig50685 Frame-2F

MKSSKSVMLSIVRAVLHCCPRSRWTRLTSRRIRCRNDALTIRMRCL

>contig50731 Frame-2F

MHSFLKGSSNRPNQIPMAAGNSTKS

>contig52258 Frame-1F|Blast-indigoidine synthase A family protein, putative [Phytophthora infestans T30-4](gb|EEY65631.1|) 2e-51

MWRRSGSALSQRLALSEEVSEALYGRVKRPLVALESTIISHGMPYPQNLHMAKRLEEIVR

SEGACPATICIGDGMLKVGLAEIDLIKLAELGPSAKKCSTRDMAAAVIDKNIVGATTVSS

T

>contig52720 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61883.1|) 7e-32

MTAISNKDLDARLRALQSKALIEEEDWIEQGRKLFELEDKFLRDTLLEGNILTGWGEPRT

APVRFRNAGVRKRKRER

>contig53253 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57815.1|) 9e-77

MTDDIPQQRVALVLAVCLSDLLLTGLVFGWAPLLLLLQEEGQYHELCADPSASTCVAQEN

RLNLIFAVASVVLNAGALPVGILLDMAGPRATIATAAIIEISGLTLLALADSQSFDVFVL

AYALIAFGGCITMMASYPASFLIMRYQTAILAAISCLFDGSSVMFLVLYAAHERF

>contig53437 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54074.1|) 8e-19

MTLSNGSCMLFMCFTAILMATTALADPHEIQTTDFTEEFGDDFEDVYAVSAIGELKMHLQ

FDLEHQLVAGAEFTPRGIVTIVTSASNP

>contig53442 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61913.1|) 1e-46

MAAMVWSWAEDEPSTTASNAMVFMDKNGRWVTSTTARPRYCACWSPVKLSFWFIVSFDEP

CPTGTS

>contig53983 Frame-2R

MCAVQQMQISTLPYTWYLVKEQFYSNLSRQVEEFVQYVDTTLAT

>contig54137 Frame-1F

MLRLHGLQTRRCVASANKYSILPQARLFSAASLEALAAQSMATTFRQFGHLQADLDPLKL

QPR

>contig54142 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69204.1|) 2e-56

MASTSADFELCELQQYYHLPLREAARRLGSCEAVIKRVCRKKQIQRWPYRQVSSKLIKIQ

HLCKYMAHVSDAEQKTRIQYKIKQLTQEYLELVGGQVPSELQLTPADVSTLPPPKYKG

>contig54753 Frame-1F|Blast-translation initiation factor IF-2, putative [Phytophthora infestans T30-4](gb|EEY60007.1|) 9e-56

MRSRGSELTDLLVLVVAADDGVRPQTIEVTRLALKNNVPLLVAITKMDMHEHDKKEVTDR

LGSELLKQGIVVESMGGDTPMVCVSGKTGEGLDQLKETIALHAEM

>contig57910 Frame-0R

MLKSSLGLFRKNPVLVGYIKRNQCDNPKLQK

>contig58212 Frame-0F

MLTRSLFRAASKVPSLAAATSQIGTAQAAW

>contig58586 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69518.1|) 1e-54

MFEAGLRHSRFIREARAIGFHYHCGSIWPRFFEARLIDGGLLILSRYPIVKRDQFVFSQG

SGSDGICAKGVLYARIQLSPAVSDFFHVFTTHTQAGDNRNEYTIRLTQLEEMHRFIATTI

QSDPQVL

>contig11423 Frame-0F

MDSMGATARTPRTRRRDLSSLLAPESPAIGRSYDGSSTLSMRGLPPLLGNSIKTPRHSYH

QIHTGPSATAMDDVHMSVAENALLLQYKDSPVLTPTQRKIKIGLYGVLNTVILVPLMISF

AQIIFRDPEFQPYMNDLVKLVLVSAAVHQLCFTCVSSLPFAMGQVQDAGLIFLSAMCSSI

IKSLHTIRGDAFSMDEVLATTLFTMAISTAGLGAALIITGKLRLASFVQYLPMPVVGGYL

AFIGFYALEAGLSMMTTESIKEPKDWIKLTEPTALILAVPGVVAGSAIFYINGRYNHMAV

LPCCLLAMLMTFYGLLLVTGMSLEDARAAGWVAEPPPSPRSLTQIYRFYAFYNINYSHLT

DQIPTWIAMYFVVAFSSSLDVAAVETALGRPLDHNHELQTVGLSNLLSGLSGGFTGSYLF

SQTIFTLRGQLESRLVGLLVFLLELLVVLCPFSIIAFVPKVFFGALQMLVCLDLMTEWLY

HARNKLLSREYAIVWITFLTMVFLNLELGIVLGIVIAGFNFIYSYIATASVHRVMKRSRV

ERNLRERVLLQNMRMAIVTLELQGYIFFGSSVKVMNEVRRHVLVTTTEKQDAQTLSGASP

MVLHRHAPSPYVARSLHDTFNEDLTTLDSVLEDHHIHGYSSTPRAANLHTSALHAARTRY

FILDFEKVSGVDATAVRSCFNATKELLAQHGIVLMFASVPTDAERLLRVHDVIEKEDGSG

TGSLVFNTLDQALEWCEDELLVSEGVVPLSESTPAIHSIDEGHHWQLLDQLLPRSNTLHQ

SHDIVRATKRSDEIQSVLTRELGEMYVSHSQKQDGNTLYRAGDLVNGVYFIGYGKVDVFM

PSKIHEGLGPGFRGRKRITRVCQGGLVGASELILHKRHQFTAQVQAPSSIFFLSKSHYAR

MQLAYPAVA

>contig11597 Frame-0F|Blast-general transcription factor IIH subunit, putative [Phytophthora infestans T30-4](gb|EEY63251.1|) 0.0 NOT\_ORF

MDAFDFLETLPTATLERLYQDPWACQAIFQALPPLAQQFVMRLLPTNVPVSRELLENWVM

PQPGESTQMPLQFQAALQKLEGLRVFVQKDEIFQPHPIFQKQLMHALSNLGGSPWERGRL

RLPKDPENMFAAVHLEQYARARWDSVLHYMVGSTAVQEPPQSVVDILLRTKLLQASESDS

RALHITDTGYEFMLKDIHVQMWIFMLEYIRTLDNTGTLKQEDILQFLFQISYCQTGGYYA

VADLTQTQRLLLGDFIDFGLLYRKHPNSDRFFTTSLAVNLIFGGSTGQKRSHVSLTSSFA

NVRAGKKSQVANSRQTTITTNGAQLLVVVETNFKIYAYTSSTLHVAMLSVFVDIVARLPN

LAIGFITRESLRSALIHGISAQQIYEFLTKHAHPKMRSNTPMIPENIADQIYLWERERNR

VQFMEGILFDGFNSKEDYESVYSYAKDLNVLTWSDSIHFRLSVASSGIESVRHFIQTQLS

S\*GCNTAALAFGHCTNCVKSKIVEIFIMSKS

>contig12435 Frame-0F|Blast-down syndrome critical region protein 3 [Phytophthora infestans T30-4](gb|EEY57169.1|) 1e-07

MGSTVDIKLNRIDRIFHPHEIVQGQVVISSPKGFSHQGVAMKVEGNARL

>contig15489 Frame-2R

MTSILREKLLQKLREDPQLALCVRIVSYLRRIDAFVEKDVGSVDYERKLKEEFLTCRNVW

LLSLCQGLSCSDPYQYIIQLIDIKRTSWFDMITQYSAIFGSENLEH

>contig17216 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55643.1|) 9e-41

MEVDPLVVLHAEKMLEELGFDENQTFRLLIASHFQQP

>contig18477 Frame-0R

MISKPKTVPLLYLYLLLSHAVVTSIQMTASSDGPHASKESLQNLRQVAHVTASSLSNESP

ENLRQVSNVTVPPPSHNFLENLQTHHPVVASPPMNVIPENQAQNSHGIEERSPSTHGILD

AVNALATSLKVDQFPRNGILKIVPKHFQKHRVQSLKDSKLISFITKFEGEILYDVAPNPH

NYNRLIEWIEGIKKEFRWRPRTAYSTIAVILSEELGTLKTCEVIAALKQHHSAETHLIKT

ALFQHWRNKDMDLVKLLEKDRWTSSEDVIKTLRNPGFDVINEFTSILEKEGKELRLDSFV

KKLHDSRLEDQVPKIIELGNAAYRDNIRVGNGFVTVENHLLNGWINKLRNEYSKSRIDEL

LRWVSVPPNSVDTITRTYKHLKLLFDAGYYKSLEDVVHDLSKSEEELKLFVVLHTMKSKT

NDHNVINGLLEQFRVKWQTSARTSNLEIDFFKLLHLDDVGSIRPKIYGIPSSPDLWKAFQ

DVLAGTKVSTESVLLSIPDQYKSNLANYEYIFKSGEFITK

>contig18518 Frame-0F

MRRRPGHPISTDTDAVQRAQYEDDPRLAITKALAVRAFKSPKVRIGLIVWAVGLFFMLLA

PGLRTTTTEMKTTYEGMVLEAANMPEYHQAYAKYTETQAYADEAKVWFWRFREPYKSMVS

ERQLVADKWAAEVARTEQEMENQMKKARAFVGLWSDFGMADVRSSFWSAFEQGKIFAQQQ

TFYHMLMRVLTAQDDDILSMVLNWVFVAVMNFTTGLLGALFFFFFSLVNMVFSYQPDPLS

ATAFVVLGFVGAASVVASYLFAIYGMVASGFYVVGKIVVRNALEQERRQQQLRGEQRSW

>contig18583 Frame-0F

MYCVRDRCIAAKIEKHLYFDCVLPADLWSVLFQG

>contig19845 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65329.1|) 2e-16

MLKQNRAIAGYVASRASSTHAHPNWLEKGCGNVPRHPQTLNAEVSEMVRGGHAIQVATAK

ILEAKVADFSVGKS

>contig21222 Frame-0F|Blast-WD repeat protein pop3 [Phytophthora infestans T30-4](gb|EEY60868.1|) 1e-65

MNGGIKRVTYWELVNTVASSVPLTNDFRVPSVMAGVVLATAGYDHTIRFWEAASGTCNRT

VKYPDSQVNCLQITPDKKYIAAAGNPHIRLFEINSNNPNHVTSYDGHASNVTSLGFQCHG

KWMYSCSDDGCVKIWDLRAPGCQRSYNAGVPLNSV

>contig21468 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62642.1|) 2e-14 NOT\_ORF

MGRKVTRAQSGPLAQVATVLGGVCRVAEGRSGQQICK\*CINCTAVVAAEASAVFLFSSAA

CSRVLGS

>contig22667 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61838.1|) 1e-80

MGGLVLAGAIASGKCSFGNSSSWIAMSAPMSGSMGTDYAVESCDGGHTTLMKVVGNVTGQ

CPVAASAKSLAYEGGKLASPSLNIAFEEAQVVYRTLTHAVICSDSYGGLFSTYQPKYWLL

GSALPHKSSKNDGLVEFQSCAGGRPLEDFGAHYSNLFYVTDLNHADTTFYYGDGLFGSNK

KPVKWFECVL

>contig23750 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54516.1|) 9e-61

MTIPTNLLDKWMERFEAKYRRDPNFMMKSQ

>contig24474 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65490.1|) 2e-37

MLAWMRVADDDFVYSDFATTLPTDVVTVKSIPIGPLRRLQNASCYSRVQRGTASAILTGI

TDPLMQRNVTRSHLEHQVAAAIVLKSSAEYRYWIQAYVKFLTHDADVSRLDDLCAEMMGP

FYA

>contig25837 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61701.1|) 1e-80

MRLESKIVAEYRDGHQYNASAKGKSTLSQKPVKESLDTAAKNGGDKVLDKELRTADNIHV

KTKAGLFTATEFEDQRKVAAKQKDFLQSVDASELGANAETVYRDKRGRKLDMLNELVRQQ

EVLDGKRKRAEREEYEWGTGEVQKQNRKTQQELLEQMKDTPFARHDDDEQLERKRRERIR

AFDPINNKLFQEDSLVESKMEKKMRKVDEKNKGLSKAKPKYAGPPAPPNRFGIQPGYRWD

GVVRGINWEEKIMTRQNVNAAVSEEAYKYAVADM

>contig25958 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59358.1|) 3e-07

MDVILKVFVGIPISCAQTLQETIGLLFDHAIAKPQSR

>contig26205 Frame-2R

MAIGGFLKQLLSTIGILVLSTLLYFSWSRALIKRVVRAPGQGPSEKVMQHGFFTAQVAGY

ADDGKLAVTAKILGDGDPGYRLTSRLIAECALSLAKHEMKTLPGGFYTPASAFGYKLIDR

LQTKKLLTFEYTNTASK

>contig26292 Frame-0F

MVVDYPLNQVGNHVLRVGVAYVDPVTGENKSLRKFYRFGVQNPLVISFKQSSSPQYEGET

IVEAHIRNVSKLPLFLDSITFWPLTPFISEELTVHEDEMKIENASIEELLSVVDGAQTLV

YPQEELQRVFRVWYDPESDTTLPTTEEGSQNLGRLHVGWKTSMGEAGSVESQLVMRNLLE

ETSEQPCDVTVAMKELPEKVIVGQPFLAAISVTNNTSRSMTLQLQFRKELMGGIMCSSAS

HQNLDIMEAKTIKDLWIEFFPIVAGLQTLASPVCVDTESGQEFIQKSILADILVASPLLP

DD

>contig26960 Frame-0R

MKSRRSCTTMPRRRLLLTAQRAQVGTVPSLRITTSSRMWSQFGATFTCMISLRMPNRMTS

VMSREKLRFHIFVDVSSVEVFVNDR

>contig27219 Frame-1R|Blast-dimethyladenosine transferase, putative [Phytophthora infestans T30-4](gb|EEY60865.1|) 1e-133

MTIMVLLKQLTGAVSSFGSVHARCAFSNSASLLRSTPHLKRKLGQHLLVSDDILGQIVAA

SKLSSTCCDIVRVLEIGPGTGNLTSKLLQLNPILIVHAIEFDLRMVEQLKLRFPAEINAG

RLILEHSDFEDFRFGEQTDSTQSEKRLISACVANIPYHLSSIVVSRLSNYMHRFSTTFKC

AVLLVQEEFALRLLAQPGDKIYSRLSANTALVADVTSIVKVPRKHFVPPPKVESRVIKLV

PRAATTPTLPSNEAYFFPKFDALLRLCFERKNKTLRALLLAKTARSQYLLNENAQIDTEN

EYQVITERVEAALLATNLTSNRAVKVSVSEFIHLMHELHKRGIDLRPSQTRHFRN

>contig27545 Frame-2R|Blast-DNA-directed RNA polymerases III 12.5 kDa polypeptide [Phytophthora infestans T30-4](gb|EEY65063.1|) 8e-59

MHFCPCCGNILLVEPDTDGMRFFCQTCPYLFQINDKVEKKVPLQRKQVDDVLGGDEAWEN

VDQTETRCPHCEFNKAYFMQIQIRSADEPSTTFYKCVQCKKQWND

>contig28368 Frame-0R

MKMRPTMAKVPITQFGVRIGCHALSFCCLNGV

>contig28522 Frame-2R

MIQVLLVGLSTTNSLARHYYLIHSESIMNNHFLFVVMLLLLLDASQAQEDKSTTKLSGQT

LDGSMPDNLKFNGTSDGVPIQEINHVKPERKAHVDIDLSSQSLSPTSDSSSRTKSTASLR

CLHKIAVHTQDVVAVGRHQRAPQAARDIILSTSPRSSFKRIPDFEAAIKTPVSLQPSLSL

SSRSDGSSIPLKAIGLSGSGSGSKYSPGTVTLKNEQPDLQSTALRLAAFSNQANAGVTPF

TTLKKTARVATDRAMSHDTITDNDKKHNNSGSGNSNGVSFIVCIVLGVACLISALHVKRN

RDASEIEASTHCSPLVLSARTSQVRVIIDGNNIALL

>contig29064 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62951.1|) 4e-65

MVSSSLPPSTLDALAPPFYPSMSWYPTITDDYYMERRHSPGELGFVIADHVDPVVEIPDE

ELFDSAYYPMTDAEIMELEQVDEVNEILAELELMECHQELHFKLSEKTRELRSSSDVDAE

IYSLMSKTSRSKSFSSKPKNFLPFRNNLHFKRNARSALHQPRSVK

>contig31142 Frame-1F

MEEVPTRDSRGGPSREWFQKEKQRIEDEIREGMQEAVSNMHIVHQNMEHLNDVGQEVVAI

SSVWVDFLRRMTAS

>contig31353 Frame-0F|Blast-condensin-2 complex subunit G2, putative [Phytophthora infestans T30-4](gb|EEY64046.1|) 1e-173

MKVLKDHRYSECKSFLREQINVESLEALLHAYSEDRLYDQEACSSIWRIIGCMGDMNKGV

LLQRLVQNFKTMNENSNKKLLESMVDCMVQWDQLPLLVNKLADHLDQWRMDKFRASIITS

KLKKSKTPYWNPVVVLGTIEYLIQLSNVKGLNTFLLPIIQVLNNCVDPILNFDADEAILA

YKANSFGFIRLLEVYAKAIVMAECANVNDETSLLAEMNLKRLQNISDLRDMQPSEFFNPP

KSLSSLFAWLARLMLDISKNLQAAAVPAQAKKRRRGKHANEDQLLPQKEMFRRWRNLFTL

VSLLSAECVAFALERKHWLQNGPVDDFIIAYSETLCGTLQKMEVFEPTVFYQAGQFAHLL

QSIRVKVLQTTTPQSASLASSLELWISMLQKALTSAHEKNKEECDSMWSAISALFNAHCA

IEPSAEKD

>contig31403 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58053.1|) 2e-47

MSTLEFAPGIGRITCVRWWRSLNGKNYCLVGGTESLISIVNVEENAEECRCELLNAGSIL

SIDLLQETFKKERRTSMLVKTKSEEWD

>contig31476 Frame-1F

MELKPFQPPDIISFGTEYMEKVAPSNRGFVEWPCHSNRNHLLRRWLLRSFGKTLGLQPIA

TRVIYAISFQKPRK

>contig31850 Frame-0F

MKITPLSALVLQSVTLLPRKMVGIPINCRLQKHIPDDKSEVTTNHSCFVIIQVINPTEIG

FRFRMRRRDDNSEERTCEADIECHCSRRFVIEVPRIHALVSDSGDHGTADVLNDLLAMEW

ETYFGSRGSLRINEFHLGFIAGMEQVKMELSCPPVNFYIQPFPEISASGLASGEQNGGTM

KLGFGKERDLSTEAPKFVQVTNTPFKSQTLHVEVFQYVPVAIVIQRADIASQQPISGVEV

EVIITDENEELCFEMNDYVMVVGLLRTLVQWTELMDISIKKHKIQCMFLSEGNFCVTVRG

RVLDGDGQRAGNEIRAYEPLHVHVRLKD

>contig32464 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54820.1|) 1e-94

MMDCVDTTLFSSAQLANWSQMKARLTVAAEHKTPVSFTTGDLAMVKAELARNEEFRPPLH

REASIQDVLACLLDQQPPSARLMSSQNAGGSFLVHSESMKQDMDSKPSLQKLLSSNNFSM

TEKKESLRHLLSFIDNSFASNTPEPLTQVYKDCEAGTLQRLSSLQLMRNFMTPVPPSSAG

TSTHGGMGMRTTSFEIIQAMLNATSNQAIQKPMTSQDSFRFQHLARTLESIETDVSAIDN

EDYGGDDVVQVDNLDHLLDYHGAHGSSSTHSVPSSTATTHGPSIGFKESQTLAHPTRSVF

HDVPSSNSMAGYPMYTSSSMETDEGYNPTVSTPGNLPTMANLNHPPPLSYQHHQQQVVQH

QLMRQEHKRQQQYSQLYQNAVMQQQPPNGLMLSTPGYASATQPMPHFPSMLMQPGAAMLS

QKQSHLRSGHFQQPMRLGTQNGKSIKT

>contig34611 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60537.1|) 6e-71

MGLGRFFLFGLALLVAMVALAWPQIEQFLISSGYSCPYPFSMLITGKGAENELAAEAKEL

PKYTLDQLRMYDGSDETLPILLAVGGKVLDVTSGAKFYGKGKSYSMFAGTACTRALALGS

LKPEDVNDDVSDFDEKKLKELSETKTFYYEKYPIVGELAFL

>contig35164 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54816.1|) 1e-140

MTKGEIRYLTDALNTNSTCGHDLQGLVHRTWASIQAFREKNPGSTENELRVAVQETAIVK

TDIAIVTSNCMELLLQQSDVVTAYRTRDTIRKTFRVIIDDLITKGKSNNGTSFQAQEDTY

RALNEGMSMWVCTGFDMTGISSMISDYFQSVCGPTQFIGEVDDGTHPDTLGLNMIQKAFK

NSTLSWTRQGDGNVIIRFKNNDVKDVAVNLKSGGDKIDEVYIAKGSHVVWKSTVKQLGGK

TLYMDRWRSGFLGLPSTKGGSLMLWVPHAAEGGHLDLDVKVNAS

>contig36558 Frame-0F|Blast-SCP-like extracellular protein [Phytophthora infestans T30-4](gb|EEY65662.1|) 1e-33

MHQKATFLLNGLVLALLCNTVVSRSSNCTGTPLNQTSGGRNLQLDTEFGVLLLAAVNKER

VSRGLSPLCMNMKLQSAAQKHSKDMASNNFMSHTGSNGSSMSKRVSAAGFKWTAVAENVA

AGQIDVMAVMKAWMNSAGHRKNILSRKFNMLGCGYAYKARTNLKHF

>contig36640 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64198.1|) 3e-25

MGWYDGGEMLLEEERQVRLGENAIVAGIAFALFWANFGLSWCISNRRVSEFSGFATAQKA

DWCS

>contig37074 Frame-0F|Blast-CRM1 C terminal Exportin 1-like protein [Phytophthora infestans T30-4](gb|EEY58164.1|) 0.0

MSEENEKRFLVTVIKDLLGLCEMKRGKDNKAVVASNIMYVVGQYPRFLRAHWKFLRTVVN

KLFEFMHELHPGVQDMACDTFLKISQKCRRKFVVLQNEEARPFVEELLEELPRIVSDLET

HQVHTFYEAVASMLAAENDAGRKEVLLGRLMSLPNEAWKSIMSQAAQDVLILYDSRGIKE

IVKIIRTNVKVCKAIGPNGFNSQMGYIFQDMLNVYVAYTQRIAVMVEQGGEIAVKTSEVR

SLRSAKKESLRLMDAFVEHAAGDDSSRQFVATHFLPKLLTTVLADYQNTIPSAKEAEVLS

LLATSINKLKHIIAPTVPMILEAVFECTLQMITKNFEDFPEHRVNFFRLLQAVNDFCFEA

LFSIPQEHQKLVVDSIIWAFKHTERNVADTGLATLFALLLNIQENPQIAAGFYRSFYLLL

LQDILAVLTDRLHKFGFKLHAAILRHMFSIVETNLVTVPLWESAPTTGVIPVGQTNSAFL

KDYVANLIGSSFPNLSRAQVVEFVVGCFDMSRDLASFKKHLRDFLVNIKEFAGEDNAELF

LEENLARTQLQEKQELAAKLAVPGLVNPNERPDDMADL

>contig39021 Frame-0F

MLSALQWERALIPITQNFTSRKLYKLYKLYPVDLDFVKKLST

>contig39155 Frame-0R

MIRGSKFPQLQALWGAGLSFSKCHAERRVPVDSHTLWMFDGEEFLRASRLWTNGYDFYSP

SELGSVIYHNYSKVPARFEYIKYNTKAKKREVEMAVNRYKHLIGQPVKGMVDMQELEKFG

FGSARSFDSYLEFSGVVLKKGSKDFGSCKQLHWVPYENATEIEELMGNKWKFEKNTKISW

PSADEENGANIGDDEQAEGSKPFLSLELLTRRSVNFSFSESLWL

>contig40090 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56554.1|) 3e-63

MDSNSQATNNTFLSGPSTQSMEMCRYCSRSFAEGRLAKHEAVCPRVFGNEGSWGRGVPSH

LASPLKPKNSRVGAVPSSVGSMTAKGQKLKDHTLQQSFKEHQATLVLCPCCHRKFAPSGA

QQHIAICKEVQNRPKNPIPLLRDYAIASK

>contig40164 Frame-1F

MRTPIFFKIGWGIVPPVVVILLSILLLSHTSTSFTMPVSLATNVNGTNGILMSATDYWAE

DHPYKNQSLWKRLPNGKVVANNDSGVRSFANFRDAVEAKTPWISRWVLSPEGRHTLKKDI

PRLLMYNLVSPMDYGKSIRSDNVRRRRNKAIGMFAADNLALPLIKSLGRVAWNLIQKHYV

GYFEDELFTQRLKLMNSSEIIKEFNLTLSDEAIANAQEQEDRPNTTCPFIYDGESQRSAH

YAQYTSAFVPYEGYS

>contig41611 Frame-1R|Blast-choline dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY64377.1|) 1e-151

MPAAVPLNLANDRYNWNYATEPQEFLNNRRMRYPGGRVLGGSSSLNAMIYCRGHAKDYDE

WQTKGAEGWSYADCLPYFKRSENHKLGADAYRGGNGPLHVVRNTQKDQPLFQAFLDAGVE

AGYPFTDDLNGYQQEGFGWHDLTIHNGQRWSTSAAYLHPVLHRANLTVMTETYVNKVLFS

GEKAIGVEIEDSRTKVVSNISTTNEVILSGGAINSPQLLMLSGIGDGDHLKQLQVPIVHH

LPAVGNHMEDHIGVHMQIACKQPLTLYRASKRYP

>contig43558 Frame-2F

MGLHVLRQARMWLNPVQVYDLSHQTPIEPLRRFVDLPRLRILICGGDGTVGWVLSALDEI

KASRQPPIAILPLGTGNDLARVLGWGAGFSAPIDVSEILSEVEVAHVSMLDRWLVEIGDS

KKRVVLNNYLGIGVDAQVALEFHEQRERSPGLFVSQFVNKLWYSQFGAKNFLVRACAGLS

HKIALVCDGKLIALPEGTEGVILLNINSYGGGSKLWFDDLESSDDDSDSASDGNEDRSRS

CSIDSFETSTNFGPSSRYDGLLDVVAVYGTLHLGQMQVGLSKAVRLCQAKTIKITLSDAL

PLQIDGEPWLQSPSEIDISFFQQAFMLSRTVEERDLVTNKVGEVLDWAELTHVISSRQRD

VLLVEIARRIEDSADSINATRSRACAHHRGHQRLSFKLADR

>contig44498 Frame-1F

MRECHQVYVALSRAKFALLSLYLARRWSSNYDMSSSNECSSQPPRVETTVRSGFHGHLVA

TCAVHCRSRVDRDAPVDVVLDLCLRYERLRSLLHRRHDFLQRVLQSPP

>contig46980 Frame-2F|Blast-alkaline phosphatase, putative [Phytophthora infestans T30-4](gb|EEY68014.1|) 2e-62

MSTEAMTEQLEAVFQGSDCVNGANDTCKIALLTLSTNLLTKYTNVTTSSHEEIVHLVTEI

ATAVDETRNLEKITIELGHVISLRASVDWTTVGHVGTDVNLYCKGPQIFERMCKGVHQNT

YLNKLMTMYLGLEHQLM

>contig50864 Frame-0F

MTQHPYAATRDAPDLHARPLYGINEEVWLAHHYGRGPTRRDGMPPRYYGMDRVEEKLEQQ

RERIQRRQRHYKLNRTAGYFLRRDARLRKLEEEQAEAGEDSDPPRSGCVII

>contig52259 Frame-0R

MSDYFVNGPLRAHCLVKRIDSSETSVELHQDMSASLHSDYQRSSSEKLPESSTPYFDAVE

MPNMKARKLNSETSSSPAYSRCIGGGGNHNIPSDAKNAPTNQDEN

>contig52655 Frame-0R|Blast-lipin-like protein [Phytophthora infestans T30-4](gb|EEY65912.1|) 1e-25

MDSTAAQPSPLAKFSSTSDLKEANEETSLSHPPKPIKSASMGVIDDHESYNLFGIDHAIP

VTTGVVKNLSPLASTAPVEDGGAGEIPVALTESTSPASYDLFPEMAITEKSEPVRKESEV

ISSFNRLNHSDSTSSASEGTRNVNGLLRGEYSQDSGNGLQIVNA

>contig53436-0 Frame-1F0

MDPESTVEGESQSHPSSLYKSSASSIEKSCVGLDLAAEFVLDEAASKIGSTVA

>contig53436-1 Frame-1R1

MDDAEDLYSDDGWDCDSPSTVLSGSMDDATASVTTGTPMAAAAAQVQKEEFSWGDDDDLF

ASPVATPMAPHAHLPLCTTSSSAGEVNDPNKLISPLHVRDVAESLSVASGNFEVEKESGK

AQVTSLPPAAVPSTPP

>contig53915 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60018.1|) 3e-15

MDPHTVNTMGMQGDMPMRMSMAMAGANGANHPAMNVGMNGAMGMNVYAVPPQQQHQQSSL

M

>contig53982 Frame-2F|Blast-exosome complex exonuclease RRP45-like protein [Phytophthora infestans T30-4](gb|EEY64757.1|) 3e-36

MCLPPVHSVIGNVHGEIVPPFPDRPTEGFLHFVVDLSPMASPSFEASSSAGRGSASSVAA

AELARLVERGVRESRALDTEALAVVAGEKVWA

>contig54143 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY64530.1|) 6e-75

MEFCPGGDLWSLLERKHQNRLPEKQACQLFHQCVRGVRFLHKHGIAHRDLSLENVFYSRG

LCKIGDFGLSTNMPLRGRGEAVGKAYYMAPELVNEDAYDAFAADMWSLGIMLFIMV

>contig54752 Frame-1F|Blast-calcium/calmodulin dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63540.1|) 2e-07

MRCFSCLFDCFGRSESPASPRNDVSTATAAINVEDRPIAALTPTGSQNSGKVTDLYTLG

>contig55889 Frame-0R

MLKQFQLLRLLIVSALHSKQYLETSTACSSNCSGKTVVASSYLTTTLTHGPYFVKKHAAR

SFIFETFKKLTFDDRKWVASINNPPICKLIFPCL

>contig55944 Frame-0R

MLVKIFYCQRPSQSAECMPTRVADVCCQQ

>contig58002 Frame-1F

MSQLYLTALRGRIVLLRVVDNTKHCRHTAFIKIGFMPTTKILC

>contig58213 Frame-2F

MLTRSLFRAASKVPSVAAATSQIGTAQAAWF

>contig58288-0 Frame-1F0

MVQRYVRAKRVTEAKPLLGCVHSEVVEGN

>contig07593 Frame-2F

MSSLNSCCGWVLLRDQKGEPHHQSRGSPLSKGLGEYSSCGLTPLQLARAMAMLVICCRLP

RVTRLKKLDWSNQYN

>contig10764 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61989.1|) 1e-168

MQLRVAVLALAHLIKLASTSSVRALDGFGNAVAWWSVLKLPTHVQFPNGTVLPTPCDCPV

PDCTNVPTAGWSALNSRATGLCYLYADSKMPQFQHFRDLGYECIGQGGNDPLSHTLKQNE

KSSYWALFNDQFNGIAANYDSNAFPNVRKSKHVCGGDDLFSAHAKGAVAFQNDGSGGYFL

QTSTPNYPDPTRNDSFVKLGCQTDNNVEFAQHMVAMSLQDKELFELGNKLQLARLCSSNY

YRDQSLRELLASTHLLKDGREQINTTATAFYHALLDPNLPIQHPSDPMKFEFRLKLTNEF

RKIKSFVFEPLGKFQKLLTCLSNEKEEEVRVLVKSPRAAVPPWALVAEMLDSDISVASWW

DGSYGIPTICAGDIYSDTPLKFCLNNSATGVELNGNGGAPYNIENLMQAT

>contig12432 Frame-1R|Blast-down syndrome critical region protein 3 [Phytophthora infestans T30-4](gb|EEY57169.1|) 2e-33

MKKTLHKTLEFVVEVPLIAPLSDSPRSILITPNSVEKMR

>contig13167 Frame-1F

MGGTRDFRLKKTGTKGFHQQMHRPPILCGRNVIICSALKKSTEWP

>contig13259 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67780.1|) 5e-82

MQDRRVEKDESHPGKVVDRHWYEKNKHIFPASRWEV

>contig17211 Frame-1F

MSTRKSTLRSSELGFLPCLSHESCDLITVAVLSTRDHI

>contig18193 Frame-2F

MAAKPLTKSLKRAVGTTGSWWKKRQKGYDVTWMNKQTEAFMKWMNYVLLKDRVGQESVGN

IQENGLRTEFTSLRVLVQKRMEEMWILAARALYRSEQLQDVLFALQDEIGNQRLVFRADR

PVYADVGLQEELLELLNRYHPVWLCLGLYAVLGTRVMQAEKCLLRTIFRTPYGTKAKKDD

KMPLVLRRVILKHLVKDENVAQNYRLVQNLKTPLDGSTADRMDGGNAFVNTKKHINGREY

FDSLTQSFMLKYLMLVLFLDRVMEHKTDTFEQLPCLFRKSSNVASQDSDKSCFDGKSG

>contig18470 Frame-1R|Blast-S-adenosylmethionine mitochondrial carrier protein, putative [Phytophthora infestans T30-4](gb|EEY69405.1|) 3e-07

MIGMVAPDYRYSPLVHVTAAAFGEM

>contig19086 Frame-0F|Blast-cGMP-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY54756.1|) 0.0

MHEASFDDSMSGTTSISVLFSGNEIHVSNVGDSRAIIAQENLKASTREGEGKLVAKPLSI

DQTPFRKDERVRVKKCGARVLTVDQVEGIEPLHENWGLSLGDEIDENGDPPRIWHPHGQY

PGTAFTRSIGDLVSEELGVTAEPEILCKGLNPHDKFIIIASDGVFEFLTSQNAVDIVSQF

DNPSEACHALVDEAYNRWLQFEVRTDDITAICIYLDGVTPAKERDGPRGSIYVGGEVLDL

QSMQRPVRGTTKNHARRNTIVGTDAIRLSLAEAFMDDKDEPGLLNLEENEGKTDKEEEWI

RKAVQGSFLFNHLSEKKIREVISVLKKLEFNAGEFVMRQGVPGNTFYLVESGEFEARHAT

VECADLSQKRNVLFEACGEVEQVYKPTKEYHPSFGELALIYPKPCANSVVTTKTGTLWAL

DRIAFRAILMRGRPLRDVVRRLRQISLLRPLTVAQTNLMAEEMRSKVFEPNQVVLHEGMT

EPGFFLITSGCIESTS

>contig19132 Frame-0F

MAHKLHPRTGPFFLIAIDLLQQNLSGSRTCAFSLLSSSSWLHLKGHPSLPQD

>contig19608 Frame-2F

MSNSLFGGASASTPASTGFSFGATASKPPASGGFSFGSNSGAGAFGSTPGSAFGAPAAPS

AFGTTPAQSMLGSTSQFGSIGGATAPSGSFGFGTTPSAAPGGTSNLFGAAKPASTSLFGS

TTGSATNGVFFGNTLGTGSSSLFGGANPSTGASGFGFNSGSSFGNTGASGFGGFGTLTTP

AAQTGVYQTTGNLFGQPQQQLQPVAAQPQNLVAAPDSNPYGAGLFGAGLVEQNVKAALDL

RSIKSDSSAFSRFTTLADDVGLSRGPFEPALVTRRQTLSNRHAIPVSFVRGSFKGSKNRL

STFASSALLSASSHRSLSGQDANGDKSSKENEFKFTSSLFRNSTTKKLVIDKSELSSIRD

NGTNSRVSIVPITENDLADVREIESCRTRLLKPGDDGKYSVTFCNQTNKKLFSLLLYPHQ

TVKQARACVKQLLRESSGLTTSSIADIELVFKGRIVHDTSTFEKLQLKEGDSIDVVVIED

CPIEKDRADQSAPSSFTTIDAQPCRQVASSKQFMTYDEYLAASSRDEDSKETQENVNNTL

VAPASSSCPALKNKDYYTRPSYESLQAMTDCELSEVEMFSVGCRGLGAVEWIGKTDVRNL

DLDELIHFEKKEVVVYQDDEKKHDVGNGLNKPAIVELLGIFPPRRSTSPEQYKERVKQRT

EDIGATFLDYSIEKGIWRFRVEHFSRYGFNDDDDDTDMGG

>contig19842 Frame-1F

MAGDDEVKYNDEASVDRASFATIKRLATMRSQMELGWRSAAQLWLVDAKQVIVSHLDALV

LVTIIIVALSTHVSFFQIGYLLLAVSLMVFYEQRRRFWRYLLLYALGACFAVFVHNIECT

ESVELELIGLQCYHYKLKTWGSLWPTLFSAQLLIIAQLVFQLVIYVANREEIQERLRTKD

HVGQNPVFFISRLAMEIDNCFRIGGAVLCYLAFIVVAIQFESGSTRLSTNLVGAVHLSLF

FIIFGNHLSGFHLAPRTSLRLKVLWSLALFIEGSILIARYVYQFDKVATYLDTHLFTLSF

ISAQDMGFEYHASTSSISNVFIYLLPTAILTGLCFWQLSSMMKDVKPYNFFLRGRSRTAD

RFRFVLESIQQVVISCSATALVLVTMVNALNPMSFVGFVYVVILIVGRALSDSWKQLWLP

LFWLASLSALMKYVIQLSAFNSEQIEVGSLSHSNEDSPWIGT

>contig21027 Frame-0F

MPVDTLVLDSVHKESLEEVHAVLKPFLVDLRGPLPSIPELACSLEFQIGRKNLLVKIDHV

RRRFERANEVSSAIFCSDLLRYLHSVVLRKTETDAEAQRGPAVVSSIMLVDSKSGFPAEE

LTRVPLKLLTYKNNLEALVSQYNFIARGPQAATVLAGFWNGPVRKQLQFLTQQEFDRFSS

ACKEKDRRIAELNVSLKEKECQVQEITKANTEWGRKEAEAIATIKQTYAEQVCSLQGAIS

STECQIESALAEQDTLYQKTMQATRRTIDTVDKVADQGRVFSGYLERYEKGHVFSTRWRQ

YFYVLKHATLTCYKSKSEYEEREPPFESEISIGGYRVVRSRTDELKIKLIPPEPNHKMFR

FRAPASVGRETWMKRFSEATQYTSR

>contig22660 Frame-0F

MDNERKAISLQQKAIDNEEKALDHEEEELWRLLNESQLQESVYREIRDAGTAQIDAMEHK

VKHLNILADMFVIGNDGEFGTINHFRMGQSASDTLEWNEINAAFGECALLLQTLANMVGL

EFT

>contig23515-2 Frame-0R2

MNCNRRCPIFPCRRSTLRLTSICARWSRMCRRLFL

>contig23757 Frame-2F

MSMCPVHFSRRAKMGACTSRHANRSLQRSNEWKVDDVDPAMANIAITSAQAGKLTAAATA

KNVKLSDLALNCVTYSSFLRNDCLTGWEDGTIQRLDWRLATTVALNVWKPHSRAVNCVVV

RDKLQMIYSCSRDTTVAITPVADKPASETATILRGHQSNVSTVAVDDAEQMLCSGGWDTQ

TIFWDLTTSHIAVKNTISLNVITCSTWLPGEKIVAQGSEDLSVKFWDPRTPLRVPVQSLR

GFVHFPLSIAADGEGTNTYLLTSSKGLNGVGCEARIWDRRTGKQVIEYHGHQQDTTACCF

LPQTVNSSGANIENRLIPVTASKDGTVKIWNDARLTPLAEAHAIGDKIMFTSMCRVNDST

ILTSTVGGQILAYSFDYNLRTLALLRRQENTT

>contig24473 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65490.1|) 8e-27

MECSVNESSYLLIILATGDLKIWNLAKRKLVLSTSIDPIT

>contig25733 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69478.1|) 1e-112

MWQAELGKTVDEFKENDTNTLESTTDTPRELAWYAKAHKYWDDEVNCPLTDNGVLGGFAF

VSGVDIRESKRFLKQVRETIKPDWVCHAAADCGAGIGRVSKLLLLPMFDHVDLVEQSPRL

LRGVPEYLGADENLQVRVRHLYCMGLQDFEPACASYDLIWMQWVVVHLNDLDLVHFLKRC

KKALTSNGFIVIKENIFHTAELYDLDRQDSSITRSGVYYRSIFQQAGLVVLLERRQRHFP

EELYPVKMFALA

>contig26109 Frame-1F|Blast-glycylpeptide N-tetradecanoyltransferase 2 [Phytophthora infestans T30-4](gb|EEY54243.1|) 0.0

MKSSPPPTSSKPGDFGVELVTVEEQEEFLEVIKQLNLATSQNTPPDRSVAAAQKEFKFWK

TQPVPALDEFPREHGAIDPSKNVSDVRQEPFVMPPGFTWCEVDLTKPDEVLEVYYLLTEN

YVEDDDNMFRFDYSIDFLMWALTPPDYHKDWHVGVRNQKTGKLMAFITGIPVKVRVYQQA

TTMAEINFLCVHKKLRTKRLAPVLIKEITRRVNLRNIWQAVYTAGVVLPMPLAQCRYYHR

SLNPKKLISIGFSRLPPRMTMTRTIKMYRLPETPSVSGFRIMQKKDVAEVTALLKTYLAK

FELIQNFDQNDVAHWMLPRKGVINSYVVENPDTHNITDFTSFYHLPSTIIGHDQHDKLNA

AYSFYNVATSVPLTELMHDTLVMAKQENFDVFNALTLMDNIQFFKELNFSPGDGDLMYYL

YNWRCPRMEGNKIGIVLC

>contig26202 Frame-0F|Blast-inositol oxygenase [Phytophthora infestans T30-4](gb|EEY67946.1|) 1e-160

MGELLAIAKPTLEVNASVSAGKAEDEFRNYKDSDRHALVSRHYALMRKNQTVAFQEKMQA

KYGNFANTKMTVWEAFTALKGYVDSSDPDSSLPNLEHMLQTAEGIRAAGHPDWFQLVGLL

HDMGKIQYLWGHAEDGQEGTADGDQWALGGDTWVVGCKIPDTVVFSEYNFTNSDMSDTRY

NTNYGMYEPHCGFKNLKFAWGHDEYLYQMLKFNGTTIPAEGLAMIRYHSCYPWHNKKEYK

HLMDEDDEDLLDWVLEFNKFDLYTKADVRPDVELLWPYYQAIIDKYLPGKLSW

>contig26448 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60421.1|) 3e-26

MYGSILLEETLSRLGTKRVEVLTDTGHWYQGLEHQYHFCGVALGAEASSFLTSFHQMEPD

APQGSIHIQATSDRLGQRVWRLEHLDLPAAIA

>contig26534 Frame-0R|Blast-hypothetical protein PITG\_03758 [Phytophthora infestans T30-4](gb|EEY66205.1|) 1e-86

MEDEGAPAIFKRVKIVTEVLAKANEPSLEDIAVINQTLDELQNLVAGCVKKRLRNISGTQ

LMNAGVKLYNSPRAFLKALEDITKQVDGKISSFPRYSLALTRFVAAKIMRLSLMSSCDYA

GEKLTDGKNVQLMDEYLDVLRSFGRIGMLMFESATVDCDRCEEYLSLAKDSYSSSMHLWY

CIGLSHLTKFKQGVELEDIIDDLWDICSGRVRVLQLLIKRSNNSSDEFRDVLSSLHELKM

LTPYKVTYAISLLDLIKWVSDEYRHSAHLELQKLFIEEALRIGDSIDDNIDGNFPHLLTQ

FKQHVLLNLLHSLCASGDLTRAETCYQLIPDNQKPKVLLLMNKLYVDNQQFEKAHRLLQL

LFRQNCFEDSISGARIFAQGFSFADKALDIYRELADNYGDKEFIINLDVACNLAFVEGKR

>contig27542 Frame-0R|Blast-cyclopropane-fatty-acyl-phospholipid synthase [Phytophthora infestans T30-4](gb|EEY63791.1|) 1e-110

MRGQFDRVVSIAMIEAVGYKNLSEYYDVIKRCLKDGGIALVHGIAANRSIEVPIQLWVLK

YIFPNGFLPSVAQMVTFSERKLIVEDVHNLGPDYDKTLMCWYERFQNHVKKGDINRPEVF

CRMWDFYLLYCAAGFRARTIQLVQVVFSKKRMERYDAVR

>contig28288 Frame-0F

MTMEDLKDLQQFTLEALKEPIYSRKQSRMGIVSTELFPMAPSAATMQDAFTRLQLVLRLF

GQITTMHHEKLLYRESLSRVNLFVNLLFGVYDGGTVRLRDNRDSTDHDAWLLVLYGATCT

ALYEKLDEIAQLDKVENVEKCDKI

>contig29197 Frame-2F

MDVSLFRRLAEAHPEATQQLSYQYRMNRDIMLLANRLVYGDKLKCGNDRVASNHLQLKWL

CQETVAQTSVWPMQVLTNDKGVVFLNTDAMGQATEESSSNAQNGMSGRRRMENVGEAQVI

AGLVASLVLGSISPEEIAVISPFRSQLAIIRQELAKIASVHQGGKADWIHAIEVSTIDKY

QGKDKDVILVSFVRCNKEKHVGELLLDWRRINVAITRAKQKLILIGSLRTLSGGSALFYV

LASVIEEHGWGYELPPDAVETLRHFAASVATPVEPDPEQGTTTPIPRSTEAVKISILRQD

AASSDIEALVSNEASLSFRPSPRHHLSQMKPISRNILGEM

>contig31268 Frame-2F|Blast-hypothetical protein PITG\_05283 [Phytophthora infestans T30-4](gb|EEY69099.1|) 2e-15

MRRSQRLVDCCYQGESHALDKNGVWAVVVPPKSSHVSHTKLMFKTKIDADSAIESFKPGS

>contig31354 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69239.1|) 1e-175

MSSPSQEKADQKLEEKPVFRTLTPNEHADLPQYRSMAVASAPPALSIMGPHTLHGQSGAA

FSGPTSFKMVSKKKKANLSDGSVGAPSFGTRVDRTKYVKVAPRDLPPAPFRLEMHTHFHV

KLESTQRVCGVVGVKLCELDTDFQFNADKCKWKVEYRRCGGAQRVSLNIIIFKTTKQEYV

IEVQRREGDITALMHLFHELKILFRRSQLLIERSPTVNGIKRAAPKPLPKLPLSPRSIKN

GVSALKGLLESKYADTQMQGVLGTISMSTVGEARLDMTSLVPQLVLLGQSKYANVSRLVS

AALARLCDHPQCRKIFIESDGWQYIVDLAAGGSDITPEVQRESLHVIETLCPLYYDDLAK

SVNAGRVLKLVQEWRNIEDPRLKKHACNAYRALEDAGVFA

>contig32597 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63779.1|) 8e-72

MLVNLQLNGDGVSVLRSYLATHLTARQLKEPAIRKLLEGDEKNVMATGHLRHVTTILSGL

RVLDASTPTLVSLLRQGQGTRARVVASYVYENEAAQVERAKYLAERRRKLLRLDEEIRYS

SMVRNVKPQSADKELAYHLISVRQHLSIGANMVMARITAFVAVYFVARNLTENETTRLMF

GLGGAIVMMMIEMVLFITRAAKFESIEIQRKKHKSIF

>contig34616 Frame-1F

MGKNRRGPRRAISQGDAIVVINASMLRRTTSSLMETPLNSTKKEQKKRKDQSIRTRWLKK

KQKPNHDANAVSSDYIDSSSLEVSPMNPRNENWTVLRVKRDADVLAGLYGVLLSRTTSRS

CVVVLPHRYETSPS

>contig36117 Frame-2R|Blast-ribose-phosphate pyrophosphokinase, putative [Phytophthora infestans T30-4](gb|EEY69327.1|) 0.0

MFALRSTATRLTPALAVFLGGATLGMTQSSFALAEEKRDLRDLEFGVPHDRKRVDPFSPF

FPSDKHPCTHAGMFIPGCHELKIFSGSSHFELADDIARRLGTRVGKIKLGRFADGEVQVQ

VGESVRGKDVYLVQSLASPVNDNIIELLLMVSTMRRASAKKVTVVLPYYAYKHHRRANPA

ATSLNSKFIQSPAADIAKMLEVMGVDRVIAVDMQMRVEGHEACFFSSDIPVETIETIMAG

VEYFATQVHLRRPLVVLAPNPECLRRARIFQKGLNKWLPDSPARFAVFFHGTGKKGSGEQ

STADIVGDVKGADVIVVDDLVDTSETLSKLTNLALSKGARKVYCFASHPLLNGNAERLID

ESNVSQVVVMDTIPADPKAFHTEKLKRLSVAPMLAELIQAEHFKAHSYIDKVNSREDFKY

VYHY

>contig36647 Frame-2R

MSRVSESNLATRILNSASQRQLIN

>contig40097 Frame-1F

MQHLDQNHDGVVDYQEFCSFFAEFSRTDYLQEIFEIDDTIAISLLNRCATLLQSPNKFMT

LRNAFDAFDHDKTGKLTVNDILKGTQELNMVPELDGKGAQLLYNSILLSYYGISQRHQWD

TRGLDWVVFEDTFSPDSTFQRRLWLTSLGTSNLNLAALDLRDSVSGDDDFNQHLSKNQAW

ADTFVDSVKHSLHEQRLYIKFLFRILDRKRHGYVTKSQFVATMQAINEEHGAPLKLSQLE

QLADAFAHRKTVRRMSNAGEEMEETLTYVSYPEFLRSLRIIDLGPSDGIPLTAGSQVVMD

ANNN

>contig43117 Frame-1F

MIKTIFSTEMNQLTIMPNKRFKD

>contig43430 Frame-1R

MGIFTPSPAINYSFVTGVYLFCTVLCAILSIMHHYTPQVEGFYIVLVPFVPCFFWSVVVR

HNWLKVKDCSVDGNEAKKTL

>contig44268 Frame-0R

MLWAQSSDAVLTLGSWLLLFVFSRFFFSWWLFRDYAVRSATTPLLFAASLTFSLSIFEMV

LFEVTDVMHVDSRQWVWRIDLIAMTVLVVLVIPLSLFYTLAREYGVARRQAAGTASALQI

LYLYSFWRLGGVLEQDLPRQSLDGTNLLVFCKVSKRLISIII

>contig44321 Frame-1F

MAETTCNSDSSRSHCVFTLHLYHQVSRSSLELRSKVSIIDLAGSERGSKTGATGLRMQEA

SKINGSLMNLMRCLETLRWNQQHPPSLQKMVPFRESKLTRLFQENLVGNDYGSLVMIVAV

NPSSHEFDETLRTLKYSAVARALVRTRTSIPRKAAPTASFYDLDGRLKKRRRQSTEASVS

SLFTIPVVDCKSSKTASSSRSRTKAEHQLSDCAYCRQCPYVDSSKMPRTAEVGTSPMESQ

RKVAEMNLHWAELELENEEYREQLAQIQAEKMEMEVRIRAEIGCEMREQLQQIRAQYQSM

QRLQCE

>contig44404 Frame-2R

MRLVMIVLKLHHPWKHLRGVMVNWLAGYPADLNTRNGSTISIEKQCGHHEHKN

>contig44471 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60870.1|) 0.0

MMRMMSPSISPDSYLNRKRNRSTDSDKAITAAIEASEKIHPVLSPIASPSAKPLVVAPVP

NDSELYRRARILQLAFTIVKRIHRFEEVAAKHKEPTPKVFRHSFEMITPMVATLSMLPPR

AKKYSLVTIPLSNPKLLSLCSNLVTVCVALVSSGLVEDMRQKMRDCAQAGRGVLAAYQHL

VDLLYNSVEAQVSRLPRRMHKSWGDPESADEGEWDLYEMLKSCEPWLIQEPWWVVLDDDD

QQQAEDKEEGALRPLPYMHVFSSYYRVIQDAVPSQQDVEVAASLRTAALTVATGLTGEWH

RQGEPDEHHLQQPQRVASVRLATAASSLSWLARCIHAHTTKSFHITETDTTMTLSLPNSL

VSADAVFLLQLDQQEPTVVLPQNYFPFGWSRKRSLMAYRAWRVRGIGDSNGSAVAVQFMR

WPDNNALEAVENDEEEEELDNDETEDSPEEPEEEPRSRLDRQPKRLRTRITIYFSVFSAT

TLQLRTIVEASLAPVVTLPSSSTAQPTETDMLKYFKSPSSWEMRSQISQQYTKNL

>contig47463 Frame-1F

MAARFSPQDVMETEVKRRLGPHVQRRGDGFTEAESMGLLQIVRSRWREGWDVVAQLHNAQ

FAKHNRSADSLKKKFSRLYRSNIPPRGAKNHQAITFAHIVHKEMNEGVASALAPVIDDET

PVESSEVSFQPARSEERIQDRSIESETNWVATPAEVPSVASPSSTAAVALPPAASIAVPR

PRRQMAEWQDSA

>contig50737 Frame-2F|Blast-Phosphatidylinositol kinase (PIK-L2) [Phytophthora infestans T30-4](gb|EEY59643.1|) 2e-76

MVGPLFQNDLDSSLVEALATIVKKITPMKPIIQQKLFERLSSILRTRHNEGTGSATTPTS

RRLKTTSISVTGGMLSNLFLSATGAKINAASENNALLTEVSSAIAMQALALETLANFDFQ

GNRLIPIMSFVHETVVKFLDHEVATIRKSAALTCCKLLLPP

>contig52652 Frame-1F

MDDDDNDVENQDEESEDDDDEAMAVPYMHVLPLYSLLPQDEQMKVFETPPTDHRLIVIAT

NVAETSLTIP

>contig53255 Frame-0R

MPFPVWAFRARSLPVNEMGLLFRGTCTTLTSASRLASRFGHERSVTMRFRSTQAARAIVL

PSDLTNAHSWPKLQHLQLNASILGQLQTQIQSIGSGPSSPRDAFYIVDTTAVEGRYKLWH

EYLPEVRPYYAVKCNPDPALIEGLSRLGVGFDCASQNEISSVLGSGVPASDIIYANPCKQ

GSL

>contig53358 Frame-0R

MSLISSTFIYLLRDTASYQRSHERLFTYARSELFSMAGWLKC

>contig53444 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61044.1|) 3e-15

MISSRSSDWRSAVERLALFMQRYAMPDERVAKQLGWSVEKLRTYLSPESRRLTTSSDIAD

I

>contig53866 Frame-1F|Blast-ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY54768.1|) 1e-89

MVYDHRSRRSQLLDCWASRAACDQRKGRAGRVQAGTCYRLFSRERFAVLEAQLSAEIHRV

SLEQVCLQVKTLNLGSIKGFLSKAIEPPCDDAIDAAIQALVDISAFQRMDMVDGNSSGSH

TEDLCTERVVLTPLGNHLAMLPLDARIGKFLVYGSILRCIEPVAIIAACISSRSPFVMSM

S

>contig54144 Frame-1R

MSARKELLTAARSAADFAGKLHRNALETLSTGRTCEIIKRRVLRWEGLTVSDPQNIKVRR

SARSLHLDRPIALEPAAAKAANPSGRS

>contig54449 Frame-2F

MQLGTHLFRRLKTFKQNLSGSCYNDVPRIKKSSEWLDHRRC

>contig54658 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63221.1|) 2e-13

MADAFLQALNADLKQTQRALSPRCLFCIPQNRALLLGEVITQDVVYTHFFTPADVDEQKR

PLGAYDT

>contig56223-0 Frame-0F0

MSSSLVIISGNSELQSRVILMSMAVVSNFIMLKP

>contig56223-1 Frame-1R1

MKLLTTAIDMRMTRDCSSEFPLMITKLLDMQIVSKI

>contig58179 Frame-2F|Blast-metalloprotease family M01, putative [Phytophthora infestans T30-4](gb|EEY56043.1|) 5e-08

MSNKSKVFQRLPTCVIPTKYRIDYELVDLL

>contig58261 Frame-2F

MRNYLFKAIALGSLAFVSAQEINIDEIEPLPGLEPNTTMNKIILQFQPQLHVSSGCQPYP

AVDSAGHTSSGLGLWKMGTKCNGSPLGSQVYARTDKFNGYTAIMYAWYFPRDYVVRPTGH

RHGWEHAIVWLGGYG

>contig10765 Frame-1R|Blast-U6 snRNA-associated Sm-like protein LSm6, putative [Phytophthora infestans T30-4](gb|EEY61990.1|) 5e-38

MAEHEQQASTKKTPSDFLKSVLGRPVDVKLNNGVEYKGVLACLDGFMNIAMEQTQEFQNG

QLKAQYGDCFIRGNNVLYISASK

>contig12275 Frame-2F

MVETTDQNATNTQDLPVLVVKESSPVPMSDLSDRLEKQSFLGHEDTAMAPEAAPANTAHT

KVLFLDGVRGLAAFLVFMQHTGEEPLRGLSLGSVAVDAFFVLSSFLLTWLFMKKSMTLLA

QKAGPRSWGIALIDYFQKRFFRVYPLFALMAFVLSIITFDMRKHYFFVGNIDNYELSKAL

LFYHGHRPHVFWTLPLEIGYYFIIPVFVMGLLSMRRYWWLGALVLLVWICYEGFTTIRWH

HMGLAPHLHTFLAGSLGAAAFVKSDMWIKRTGFAFRWWHIFILRIVEGLAIAMVLSVSFR

GLLFDWVFENPFTDLRGFGFVSVQMTTVILIEIIRPSCVAKMFEWNVLQYWGKISFSMYL

LHPFLVAYPPLYLQQNYFDRFVARFGLVLLFSTLSFYLIEYPSQLLAQKISRSLAARN

>contig16107 Frame-0F|Blast-PREDICTED: similar to mitochondrial GTP-binding protein 1 [Ornithorhynchus anatinus](ref|XP\_001518750.1|) 1e-102

MIDFGDDEDDVTFAAYEAAVKR

>contig17773 Frame-0F

MGEDVWMRKFADNRILHAATHAYTPVLTDKNDLLSKTGFKAVNSLNASRTKDSCILRGHK

KIAIATHTVKDDGNVAPIDLKNASKKTLLNTVKMKHFQKRSRSFENDKVFNSTDTSQSEM

SHAPSAKSQDHNTTEFQFNKITEDSTFEDKFLLDNQLIHVSTRKNKNTAGNIKSFQRSAN

QAPSYTPPLAGMLPREKTEFKQNLYQLSINKNARTGSHAKKTHAIASQINTQTFAEKSVP

AVFQQASAAVKRKNNGDSKMVNRVVSPLECLARLTKSTLRDEMKLRAIEAALKDRLSELS

KKSARVEKMRKKCVALHLQKKWPAFQDQPCIKNKLRESSSVRTLKSLSGDEKQRKSKHSV

LRENLSTTVKNIAPQLRAIATTNSEVPCGVRRLELLLDDIFCNKFDERIRIAATSFELDG

IKAKILNFPEVQAAIADLNDTKVCDSSGKVCCHTWKKRKACARGHASNIKLLECAWSP

>contig18471 Frame-2R|Blast-S-adenosylmethionine mitochondrial carrier protein, putative [Phytophthora infestans T30-4](gb|EEY69405.1|) 4e-80

MQTGVYKSLPNAFNTIRAAEGVAGLYRGYWSMIAREIPFSFIQFPLWEGLKHQWSKKQNG

HVSSLQGAVCGSIAGGLAASITTPLDVVKTRLMLGRDAKGVPYLGTLNTLSRVYTDEGLK

RLFSGVGPRTMWISIGGFVFFGMYEKATSKITEIIDFIG

>contig18606 Frame-2F

MKDAVKANIEVIDNKDGVLNCLDGNRTAIYPASVHYRGQSSLHFSKHQIAVNLDEAGELL

GFPTDQSFVLNGPTVDATLMRNHLAHWMFRGTERYSPRSRHIVVFVRDKLDVNDWSPRYR

GIYLALEKIAYTPNRVGLAQLNSACQSEEELSGGWAWQNNPLGYGDYSPNLILNEATGLF

GAGARPILTFPEPKVMTQTMREYFVTPTTGPLPRLYQFLHDNMTNPDSLEEHIDIGSFVD

YLLHSELSINSDAYRRSTYFFKDRSEPINAGPVWDFNLAYGRGGGKTTWMYTIHTFWKRL

VCNYKFASLVQQRWAFLRSTTWSNESIQSFIQTSTEPIQRQLSKCIAWKSDNLQCANVGA

NSKASYSEEINDLIQAVLGRAHWMDSNIGGFYKALDRDLCVAAGDLPAYNCAADGNDKRC

LTNPSSYINAVDFPKPRKPMPVTSCTNYSKKIEQPTIDPCWLSAGVYMTDGSITPFCSGY

GSCPEGPGAKCTCKMGHRLPTCARKDDPIIPHGGPIDDETVHESSMLAKNLSSSTNSYLF

FSLCALSVVALGVGLATHQRRRHQHYRPLVYAAATTNIEPSLHYGTS

>contig19133 Frame-0R|Blast-RNA polymerase III transcription repressor MAF1 [Phytophthora infestans T30-4]gb|EEY69641.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56820.1|) 3e-10

MDDETMDEPAAMDEDGEDGMEDYFGMTSD

>contig19700 Frame-1F

MGVVTTAESTWNSRLEQFRLHEKRNALAKTLSGGQKRKLSLVLALLDSSRVLLLDEPTAG

MDLKSRVDTWDALKKVVAHRAVILTTHSMHEAQVLCENIGIVADGKLKCCGSSLFLQKHF

GVGYKLTVVHTDGQLKDPRSSKQDASLLRILQTFVPDATIVSSNKWETR

>contig19775 Frame-0F

MCGHLTFHTLSSDKRQNGSYFNRQHRSYFVALEANSNSMLKAKSFFVIGKAILFLSRWDS

FENNQLFRGVF

>contig20652 Frame-1F

MPFYDVVVAGGGVMGFSTAYHLAAAAPNLNIAVVEKDPC

>contig21026 Frame-0F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY66312.1|) 3e-25

MICNLSPLGEHRCETLNSLRFAKMVNSCEIAFPSRVSRGL

>contig21589 Frame-0R

MLSLIEKASIDEAFMDVTEMAHKRLEQNVVFSSDFCQDPTNNDTKVFGIDLAGKNSLAFP

LTDNERLLCVGAVIAREVRDAIYQKLGYTCSTGIANNKLLAKLASPLNKPNGQVLVAPRF

VSELMKSLPMRKIRGLGGKLGKQLEDIYVSLCPGEVDVVSHRRISADETAKKLTANAFLQ

RCGLTELTKHVGKKLATHVHRICQGDDGDEPVQEKKVYVKTLGCVKQFDQRSGSALTRVE

QLQYWVHLLCEEIIIRCEDERIENKRFPSQLTIQFLCAKLGEKPRVLKLGIAQDTNVEDL

YKSAMNVTRFHLDSLFPLAAISMNAKTFHELESVDVVTISNFFSQKEEVGASVNLTAQLI

EKDAKQDAPKRNSNEISLQKRSRQKISEFFLASSSRCGHIKNRSTKADIDTDSENSAISL

VNNVNTKNVDAISTQAKVALTSTHYCEECRQDILEPRFEHEDFHFALKLSQTQHTDVMAN

AVATDKKKKKGPLDSFVISQK

>contig23514 Frame-1F|Blast-carnitine O-acetyltransferase [Sus scrofa]emb|CAP49176.1| carnitine acetyl transferase [Sus scrofa](ref|NP\_001106518.1|) 1e-15

MSRQVLTYELQSSLPHLPVPSLHTTLDKYLRSVEPYVSKEELEQTKKLVQEFQKPGGQGE

TLQAELLQRANEKENW

>contig23583 Frame-1F

MSASCSGSRSESDELLPSIARSDQANCLSQNDHEHEQMRDQVICMIFDLPETTQFYQDFS

CAIASTLAMHGRMYPTSSHVCFYSNVFGRERKILIPYESLCTIKKTTTLMFQHAIRLTTF

DQDEFTFTSFWGNNRDCCYDVICKTRKRMLSALHPTAVNFLSSSDSAPSSSRV

>contig26319 Frame-1F|Blast-mannose-1-phosphate guanyltransferase alpha, putative [Phytophthora infestans T30-4](gb|EEY57261.1|) 0.0

MSPGATSSGGANATPFPITKAVILIGGPNQQGNHFRPLSLDLPKPLFQLAGQEMIYFHVE

ACARVPNLQEILMIGSYDEGLFSRFFDSVWRRFNVQIRYLRETKALGTAGGIRFFRNEIM

KGDPASLFVLHCDICCSFPLNEMMHFHLKHSGSCTVLGKRVFHDEAKKYGCLVADPVTKE

ILHWAEKPETFVSNIINCGVYLFNVSLMDRIVSIGDKLSRQRLRSGSNSEANVQYDLKKL

FPDFNNLDNLRLEQDVLLPLADQHSLYLHELGDFWCQIKTPGMAITCSELYMQRFRFTNP

SALSSTGGKLSPTIEGNVVVDSSANVHPTAKLGPNVTIAAGVTIGPGVRIAHSIILEGVI

IKDHACVLFSVIGWNSIIGHWARIEGQPPNASQIQVHSAETALVRDVTIFGVSVVASPEV

IIRNCIVLPHKSLARSYHDEILL

>contig26540 Frame-1R

MLRQDYACTIELPGRMRTHPTFYVNRCHFYRFASLHGERIVMNTSPSGWR

>contig28726 Frame-0F

MEMEWREAEEMRKHAQWIDEESDVLSLLRAAGAYAFTGGRRDFCVKNHLHEKTMQQMLQL

RHQLTRIVNRLYKETKGFQTIDVQPKMPPPDVSTQGLLRQIVAAGFLDHVAKRVPAGTIT

EGTKLERNCAYLTATASVQEPVYIHPHSSVFTPIPNQLPSYVVYQHIMKTSRPYMKMVTA

IEPEWLASIGLKTPLCKYGAPLAEPLPFYDANTDQVQCYVKPQYGIHQWVLPAMCLAYPD

GPVDTKDGLRGKYRWFAKFLLDGQVIASFLPFSKALKEPSYTIIRKTFDKKIQFLVVKLQ

EHEVASRRALVMKWKRKPDG

>contig29062 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57629.1|) 2e-88

MLDYLQVEDPEAVFVAEPIANAARNSQQQSSLLLQPLQLPPFSRIGTIRNALKWAFDLTS

TPRPGFLRSLAAYALEKNDVAALMSPGIAAAIFETESQHQNLTVVDIFSHFSSIRLNFAD

FFQIVPRNATRYYSISSSRRLFPDTFSITLGLQKADTLPIPRCSSYLAMLKQGDVVRASF

RPSSFVYPVHDHRP

>contig30451 Frame-0R

MCKIHFVLEDFPQSVRGAISKDMDADVNGEAYRSFCDSLFLLQRYVFQQLLGIQPAHLFG

KVFTDPAHATGDTSEVCGDYHLVPRFIAVNEEPLLHVEDLHSPNRVGYAVGRLLSVQKIL

DYLDNSAKYTVRDFLVQFDHRELVDCIVSTRINGQPGVFRIDELVMKPLEIVNSELPSDE

RGVRTKDGRNFVRAIAHRSEGARNYDGAKSKKKIRKWQEQGNFLQLSPEVEILSQELKPT

SCHLTGLRTDLFEIGSAMPMVLKYVRHMSLLNSFAETMDLTFKDKTLLRQAFTHGSYIDV

GMQNVNTVEATRSRVRLGHVFENLDSLKRSRRMLLDDESSILSKAAGNDATQLRQVAETH

LSGDFKEEFHSRYLCPYERLEFLGDAVLSFLVASSSFLKLPDADEGFLHQTRVDIVNNGN

LGEMAKTANFGSLLLSAFDLNKLNEDIKAKITADCFEALLGALYKDQGIDSCRALLGTLL

NMHDPELRELCYLSSDELMTEAKNYVEKDRAEIKKWSKYTNTRLLHRRFVARSGVDITNT

HLWLQAFTHASFQRPHIGDDEFLGHDASYERIEFLGDAVLQLLSSEFLVDAFPYHQEHLL

TQVRSSLVKNKKLAIVARKAGYEEFLRISNHVKEHGNLYVDDVLADAFEATLGAIYLENV

GDLGKVRSILERLLFPRLTEAIRRRQWLSPRKVFMHYITQWSRSSMRRIPCRFKTIKLPR

ATTENNLLVPKNTENSTKNDKRSKARPCSQHAVALYVNNFQVARAVGRTILAAQDAACMK

ALTLYGVRLHDD

>contig31038 Frame-1F

MSNNVFVICTQGGQEKPDCTDVLMPVLAQNKEEVGRNIQRGRLYISIAYLHISITARSAR

PSFSDIGYGKDKNRANCLACTQGLDKERAIKKGYWWNSPIDVVGGVICLDLKGSMTL

>contig31470 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61440.1|) 1e-108

MPMVGEAAAKRQSFYVVYVPADETKELEEWTIKLPKDKEAQLGCLTERLRAHYKSRATAA

SKEQQDETFKQQLLAQMPKGATLTDTMLEMMQQMDSLVDSIPLVLNTAEVKHVGVNMYVD

DKGTAKALPTNVRASAIAQACGKRLEVKGDAFLARVFDNGNFEICEICEAFFVI

>contig31856 Frame-2R

MKLITFQFKEAANVARNMIDTGFYRYEHRRASHEFFSPGPLSTMRTTTAPSATFNLVSTI

IGGGVLSLPYAFDKCGLVVAFFLMVFAASASTFSLYVIVSCSRRGRAASYEEVVRKALGE

RAGHITVLLLVLLTFLTLVAYTILTKDLVSSLGAKFIFNRPISNAEQNILTISCVLLVSP

ALLARSMSALRFTSMFSLMSVLMLAITISIRALGVTLSHRDIQKEIHIKLTPDSLADAVY

AFPIISVAFLCHFNVLPVYRELHKPTRHRLKKIVASTMFSAWLFYMVVGAMGYLFAYRQQ

GGVQGDILKSFSDDDPLINFGRLGLLVTLQLGLSLIIQPCRANVFRLAKIATGYTRSKMY

STCDLSESENEEAADESTRLVTPNGGAIAGGHAQAGLTSNIVYVLLTVGIMTSVLSIAFL

LPTVAIVWNIMGSTVGLLVSYVLPCVSYVRIRREKPKTDRRIISAWLILVVSSLACAACT

TQAFLSVLSL

>contig32462 Frame-2R

MSGAQEVIELFSSSSDEASSIEEEKIQFQSHRRHFKRSNAGHDRNSGSSMSDSSQSSFTI

DKGTQSLLRLQRSRQFVAVKMAKVASMRRPRYDEGMQEITEGMNYQELQAQQKMLERLQT

QNRRKFYQNGKEKKLEKKEIFKEAKEMSLMKTRSHMHVIKGRL

>contig33986 Frame-1R

MDVPLDDTAVEQYTRYLDNLEKTDPEGYKHFIATMESQLQAAGLESGSTSVAPQHDANTA

LFDMLKTSTNASKGAAGTNTTDFRPRFPGDKVMETNGLRDTPEGMYVDVNPGFVIKTFDV

KSKKKVFVNVVFADQIQAFSEKIKLNEEGKEQDGIHIPLSLNAPHKVIDKKGVKSLTFDV

AVNTKVRDECQADKTDAFRNFVCELAIEYIDHKYQIKLDNRYELSRLTYCGKLPPPKHYI

RKEQIPIIQEMPATKATKKVGQEKSAQIATATYKIWEEHNGRRTICSRLPSVEKESLPLS

YEELEQVGDRLIVDIQFINKIDATSDIELALHAELLSVKAADHHNLEIFLPYPVMLFSAR

VSFYQEDNTMEMILLMDKSWSTIEPDCGSDPWRLARALDKNTGSGKGHNGDECASTASFV

EPKSLVEMFQLMNAAKSSDGRNGDKQTRDTCLLWDPVPKDDELPEDRLHRQDIMSMHLLE

QQRFERELMANEAEAKRNQKRTEGDSTQKKAIHTDKTWHDIDSSELISTRMDIEAIVQQE

KERLDRHHAKRQNKDFSIEKCVSTEEAMRAVMKWSESNTNSTLTLESALAFHLL

>contig34617 Frame-1F

MGKNRRGPRRAISQGDAFVVINASMLRRTTSSLMETPLNSTKKEQKKRKDQSIRTRRLSK

KQKPNHDANTVSSDFIDSSSLEVSLMNPKNEYWTVLCVKRDADVLAGLYGILLSRTTSRS

CVVVLPHRYETSPS

>contig36431 Frame-2F

MRVTSDSPTVPSFTPSIEPRRVQLSDYELLTRVQRVSVPDTTLDLDHLSSSRGWKRVRGC

TNGT

>contig37072 Frame-2F

MKYRDPFCNISQSIADKIGVNLHRQQNHPLHIIKTKIERYFDDQNRLHGCEVDEY

>contig40096 Frame-2F

MCWVLNSRAKEHSCSRAIQTNGGCQLDVGFIIVNFPACFSLGKSCNTYCGLHLTAAFPKI

MFKRRLHVTEEPPRKPKPRKKVLYVAAPQLIYICI

>contig41617 Frame-1F

MSNTFFGSLTQGVTFKNSKELQQVKQSIKASVSKAGIQRSSNVDALDFFGFDAVPKLTSN

QMQSRKITVDITPDCDPNIKPRKVKGSKLRRKRKLSEGALEKQRLKDKERQQASQLLAPP

KTKATKSKKTRKSCHLQTEPIGSEEASQQLDVDDEKASESEDGDENVTLFKPHGENMDDK

NTDAASLAKLKTKHSSKDCGASEKSVNSWESIQQLRRQLGIRVSGESAPAPITSFADMRL

NSSANSQLMKHVLLQNIERSEYKEPTPVQMQAIPCLLLQRDVLATAPTGSGKTAAFAIPI

LANLANGSATSTGIRSIVLAPTRDLAVQIRAEFVRLSVGKKQHITLLSKATAATIAFQTK

NKVATTHDVLIATPLRLVHLIKEAKVDLSTAEMVCLDEADRLLELGFVEQVDEIIAACTH

PKVQRAMFSATMLEGVEELA

>contig43431 Frame-2F

MANIEGLDGNPRTSASIALTKLRLNLHTLSADMLYKRYARLSQGIIYFRQSIQAIMPVEL

TPVRFAKISSDVLTYTKQQQLAFSCDGIEVNVKNMDKSVHVRVGSIIIVHNYSTLSGIAS

IQNMVVGHRTDELETSSASTEEVIFGANVEPSLWQLAIENYPEKMVSARWTCGGQSERTF

FLDVQSYQFHVSHHFIQSIAHFLQPQLYAPGFFAGKQILSKKSNPPIHRKAFVFTQRWSL

KILVAPSVISFWRQVADSKKKCGVWIKTGQLFASIGIGIDEASLHLRSSAINEINCFVAI

PTLKVMLSLDKVGLYTSDDMPTVEVRFQKSTVGSILTPTWSTYPQYLKYISNAPASQRLV

QDCSFQVTGNQDQMVEQVVA

>contig43646 Frame-0R|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY67956.1|) 2e-88

MEAMLPVCRVRVMQLWVGQYQKAIGHMRLQQREFEMLQLIRQQEADLTRLYAALT

>contig44038 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68163.1|) 1e-150

MHTADYVAHLRSILVFRGGDGREYLNDLHALQIDTMTWTKIRTRGQAPAPRANHSSALVG

NNLLIFGGWDGQKRLNDIHVLDTKSMTWSGVADEYKVDTRRYVAPPLPRAGMTMARHRDR

LFIFGGSGPSAKCYDDLHVYDPHRHHWVETISILTTESQGKQRQRRTKSCQLIRSHTNAR

FRSNIYEDDDQQIDSWLGNDAGESINDSDSDEEFKDAHSDREAMMVAQRLATNSCDLANP

NETCDFTFKETINRKEPVVILGRGPGRRAGHTCTVVDRKLVIFGGSCGADYLNDCFTLDT

DPPPRASVSLLSPAKMLSHALVQYVDGEEFSDISFLVEGRVIYAHKLILSALSARFRGMF

SSGFREAREAQIVVPDVRYEVFLRLLKYLYTGNIKTHDDTFAIFSGLQEDDNSLQFASNS

IAACPQSADGLDEIEESRRRIEEQPESCSLELKRELETLLELLVAADQFMLDHLKQRCER

TLQYAVHIGSVEAITEAANRANALQLQAVCRHFRRNHLAIAQPLSDELERNENVEAGRCF

SVKPNSKVK

>contig44144 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61154.1|) 8e-91

MRSTSQPKPSPMPLALITKRSSRLPSLSARAQFANCASMTRNFLTKSFPTPKRKLWGSQK

SPTGVDDPMEVNMASDEQDNEGARGDIGEMIVVAIQKVTVSGSDEGRASQFGSRIVPKSS

IWGATKWSQGQSRLPQRIQCTVRSGTTNKVSAQSERSANEYTFDEKFVFERRDHDVQYNN

VIIEVSCTASNLKGKHILGQVAADLDIEFAAQAPDPIYKHTALTRVDGVDMALEIHYVLH

RLVVPDATAAAASRVLTRSSTSLNDDDDMNAYGQIFPDLWYLC

>contig49622 Frame-2F

MLDSSCAGLQEYSLQMMESCIEETINFYQSSRQNYIFLVEAMKTTLSQDFIRQSVLHELK

LTANSLPHDEKLNASSSDIVAFLNQFYNRVAPLLKAYSAHHIVRVFVALSRIEFIREACT

SPNMNKCMLAITQQMEEELEQSTVSMNALVAPVLRSVTTTRVITEIIIEADIVAGCQMLA

VGLVMQRKIRVLLMQCQELIDDALAIVFLSLFNVFEPADAFAHQFLGLCLARFGQLLPIY

SIFPHYLQVTLAAYPSLACSHDLTKVCGTIFGSLFYSKALMLPSEQDYTSVETAERMTLW

AIQKCCQRCIEILAEEIKLVKTSVATDILEIDGLPANSIKPANANETNGMYLAGLVFELL

KMAPMTILKATAVEVEQLIAQFGSNPVVLRQLKNALYERISQDCEAEKRAWLAIWCVELD

RQ

>contig50682 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59543.1|) 1e-67

MREVVTLLVRPEWASFLPSLVRFCSCLLAVSFRERTQAALASNLIASSVDSLIALIEFGT

SVQAEALILLLTIVSQPKKLLLLSKAKAGQLTRSVLCWSVAEVIAVRFLELAKRNVSALA

SSSHLFLDHLHGIASTTNESEIDEKYPSYILELLCSTMALLT

>contig50862 Frame-1F

MKISVQCALADVSTRLDRLNFGSNTTEMCWLDAIFMPESTLRRLDLNGVSRPILQSGDSI

ETMKVDWQTSEQWDLQHLERLKWSSGNIELSEKLFGALSSEFQSGFIQMKHLDIAFMQDA

DSHMEKKFADAILGIADFAELRSCRIRYSTRAAISQEFSASVANLFQNGLQECIDLELYV

PQLHLTKQAIFELLSNACFPKMHKMNIAVGVATDDSLMQPIFTGCFLQMQKAQELKLDFH

VA

>contig53254 Frame-1R

MRPVATLSTDIAVPVLNELCQLLKLLLNGDACPHSMSIFMESASGVTHGRKPGASGFPSY

PTMATMLFYMISFYTNDKMRQAQQGVRNVTLQMVQFLHLNDVYGFIHFFRDTVLLLEDCF

LLEENKNAIDVSPGGASISCYLDTAIHVYQDADGPLGSKNNVTLCGCMAIADVSQLYERR

DQLKRMLPS

>contig53359 Frame-1R

MAPKFERFEHRKEHRRMKQFARVGIGIIYPSA

>contig53913 Frame-0F|Blast-negative elongation factor, putative [Phytophthora infestans T30-4](gb|EEY61455.1|) 3e-37

MQKDADTTSAEYVHIRMVRSKLNRV

>contig54145 Frame-2F

MYPAMAEKYAQTKRPARRSNVAVEPCASTSTSRSASRSLSFEDTQRSKTRHKRASWSGHS

RVSNTSTASRRECKSARK

>contig54659 Frame-1F

MERDLQSISELLRSISIMQTYNENVVEFISGHGEIWSAKILAAVLSQTMETQGKKERYCF

VDARDFLIVEPDNEHGPVVQYDLSEQKLQSILQSKGDALTHVVITGYICSTIDGVMTTLK

RDGS

>contig56972 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56147.1|) 9e-16

MEIECKTLWMGDIQMHWDEAYIVSLFASASEQPVVKLIRDKVTG

>contig59201-1 Frame-2F1

MKQRGVGCITLVNYIKFHASVISSSGFKTFAAHLML

>contig07205 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61900.1|) 5e-90

MSSSYKQKKMKTLATRKKTRKRRIDDGMALDDIPVHLLQQPSTRDPLWKKPLLDAVVSSA

IKSKRQKKAAKKRRKLARHQNEGDNDQTDVVQQEASRCDEELMEVLDENLTSDVSSELSK

TPSLELCSSLDDVVNQAALKHAEIRLRDGRQKARVLLLVDTRSIFKVMKKKLNIRSEMVK

AKSKRGVGSGKKPEMAFKNIGLVKTPLDRYKGVNKSVLAGYKSGKLSTILAQDLSFYPYI

EFKVQHVIFVAKEAASAINLDPKLLHNVQLHRYVINDSNSLKLT

>contig10766 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61989.1|) 3e-20

MEGFPCSKQCNGSQAGRGGTFFSFLQPKLHKSLAEAVISKACSCSAELLRKSKRMMNETL

QDPRL

>contig11592 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63250.1|) 1e-156

MPSIVESRPEARTDHIMVLHLSSIYIFGGYNGSSRFNDLCGYDINAQRWSREQAQGAIPS

RRFGHSGVVHTETNRLIVFGGWDGRDTLNDLHEYSFTSKVWRKMETRGNSPPHRYRHTAV

IFGDTMFVFGGVDKTHCRFNDLQRLDLVTNTWSEVCTTGSIPSSRTFHRAVVVESTMYLL

GGYDGTDRLQDLYSIDIGALSPPSLLDICADFVRTNLDCVLETTTFKDFPREIVDQVIFK

RDLEGRLRGTCKLCRPGRCCVYRMQKNDCCPRDIQNSPSTCHSICICGHSTFHHNVVDES

>contig12203 Frame-1R|Blast-metalloprotease family M01, putative [Phytophthora infestans T30-4](gb|EEY61331.1|) 0.0

MDAKAYYTTTIVASTRYTNIITNGDLAPGYTSNTGVPIFHPVSTILGRTDLSRHGLKYYN

HTVNMAPYLFFLGVGTYETYRRTLEFPDGDTTMLEILAFPGYFEPSEAQAAVQMLYDSIL

WVFLSLGPEACEHSTERQRMYELLIEREALKAQEGLLCRGPQDEEVKYPLSTTKATRLGA

VRTELKALLQKWHKTGYKYTGAVYREIAMENSYYGGMENVGNTTIVSSCLCPSCRMDDNS

YEYMEHVKVHEYYHNINGSQVTGQSPFEIWLNEAVTVHMERKRGAAIFGDDYARLNEVLY

MFTPAIGPLAQDKSATSLSIEPQGFNQTQELVSVVTYSKAPEFVRMVELLLGHDAFHKAL

DDYHTKYAFKNATSMDWIQCMEERSSLKLQNLAKTWLNRPGHPDVTYEAKYDAKLKEFVV

EMTQTGFENMPAENNGPWEIPIDWSLVKDGHSIRNDVFLFKTENAKLVISDVFEEPDFLS

FARGWSFFGTSKQKNSSIPQLRKQALSDPDAVNKYRAYRSIADLEKAKVIEGLLTGNTHV

KISKEFVDLHGLILFSEKLTPCARALTLGEPKTIPSRDDLSHHYVAIKDATTALLQAVWA

TYSTQIEAAYKKLCDLARPGPHVEQFQERALKRHLLLLIAAGGKAPILDTTARVAPTIKP

VELALNLLKSSTFVTDQATGFRLVLEDDTFADRAKIQNEIFHEWSKTPDMLTKYISIVSS

LNAKDVGQQILTLLAHSSFNPSQSSHGRTLTRGLSQIRDFSLATEEGLNVMFQVFEKIGK

INQMSAYPLLQCFDHIDRFDDNWKAKLFATLQRMQDAIDKKKEESLYNQLCLILENK

>contig12430 Frame-2F

MVMQDVLTQRVLHTTIAHVAKPSGSGAHTYTQYLVRVSDDRSPALNWTVYRRFSEFRNFK

LALDEAVKHGDMCAHCAIMSKRTSFVLFPRRRLFGNLKTKTLEMRRKGLNIFLDAVAKHA

RTCRESMTCQTRPLMDKFLMVNDMRYTYLNVDMSEARGAEQSSKTCSSERDIHAKRDTLH

RSLSMVSRTDRLSGYSDCEDIVRSCTEEWAYSEKDEFTKSLADPKVDQSRDELITTKYST

QEDNQLHLHESRLAAKRNTMPDLLTYINNRHLCRNDNTSCRPSLTTEGECAAYNQLPSST

STSRHSDPGLSRNELLKFCRGSSTGGGRIHNGENRLRSRKVHLSSAAKRVKRLEEAEARF

SMQSQSRKPKCLPRLETIPE

>contig13165 Frame-1F

MRINFVPLIVTALIVAGADSALVPPATASNLRNALDAHSNVQSPAAPCADNRVRNEADER

MENMISPLKKIFQPSQSKLKKLLAKVVEADNFWAEPIFVDELNQLVQEHKMGSRSLRNDL

FASWEKSGLSFEDMQHELQHTKPMLSIKDLTILHDYFRHVYTKRNPILDASKGNKIHKYI

ILLVDAQRKSDTKNVATANLNDLLATLKFHRVTVSEAFKLLYYGQSASDVIQSQYLTVLE

QYITLLNKPTTLLKTLASHFGEASVAEALEMVSRTRVDLKDFVTKLQSEQFATWDKLCNP

GGGRYSKAIRDVVSGFDDLLNLKSALLENPRFLALWKYIKRARVSGNSLSLMETVTTGMD

EKIIYLSILADAAEHLSSRKLAIELQNEGIADLVNKYDDPVKFFRQLQLGTKPVETLQSK

NLWMFQRYLEAKNVQDPHMTILEALVGCYREIPVAKALGTASKDMQKLIRLLRAKLFSWW

FQTRHYSPSIVVRMFDLEKNGINEASYTILKGYTSYFNAKQKVEDNFIATLENGMGGKKK

LARVLNSQSNGDRSSKALLKMLFEGLATSHANVIKDLQIGSTVENIVLSDDFWMLEEYVA

ALKRSRDVDTTPVALLIKFFDNSIVAEGLAHLSKMEIKKERVHQLQRDQFAMWLKDLSWV

KAQFTTTRMTMRFRLLSIDFCNSLTEFLKSCDNGSKFDTIMMALTENLDMYLTFVAEAIK

ADKVLLAKQLKKMLILYWMKQKMNFESVKELLTSVDEGVKNSFLEKYRLALRR

>contig17020 Frame-1F|Blast-sugar phosphate exchanger, putative [Phytophthora infestans T30-4](gb|EEY69680.1|) 1e-110 NOT\_ORF

MEASAVSRGWKEVAANKRGVFLLTFYSYVLIHASRKSFSAIKGEMGDEQWIHSDIYSRDQ

QVEMYGLMDTLFMGFYALGLYISGMLGDNYNLRHMIAGGMWATAALVLLFGIGAFINIHA

FSFYAVLWGLNGLVQSSGWPANVAVMGKWFDQSERGAVLGIWSGNACLGNIVGTALVAVL

FAYFDKTIAWKIALILAGTLVAFHGLLIYVFLYPDPRDVSYRHQTIEKAQPDVAIHQDDF

NRNANTKKDENAKGIGFFHAWAIPGVLCITPFAS\*KVSYANVYTCIQVFPYAMAYACLKS

VNYALFFWLPFYLTVSLHLDNSHAG

>contig17213 Frame-2R

MFKDFPKDSIKSTSLLEALAIIKCGNIMF

>contig17907 Frame-1F

MKKLHKVILKELTANDGKISHLKTFATLAISITICIGFLFVLGLITTSMIKMKQNYSSTD

>contig18472 Frame-0R|Blast-GTPase, putative [Phytophthora infestans T30-4](gb|EEY69406.1|) 8e-14

MLLIIVFFSSGAKTKRWDCKAVMGIIDRIKEIEDEMKRTQINKATEGHLGRLKAKLAKLR

TE

>contig19703 Frame-2F

MVFQLSVSSHSTNARSPVDYLDLDVKLKANKASRKFHLIWQRRLREYGHLLS

>contig19840 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65329.1|) 1e-15

MLKQNRAIAGHVASRAFSTHAHPNWLEKGCGNVPRHPQTLNAEVSEMVRGGHAIQVATAK

ILEAKVADFPVGKP

>contig21227 Frame-2F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY70221.1|) 2e-36

MVASALHDQEGMIHELFNQCLFARP

>contig22662 Frame-2F

MPGYIGHRQHDHELPRSRLERVYDAAVIDHQAVLPVHHHHMNDAGGPAQHIEQVVRYPDA

NKKLAIRMFDGAELYEGLGSGFLEWGRRFERQVNLTQPACGFLWPEDVKVDLPGHYLRCV

AERYYHKRLETWWNQMPPLNTQWRKCLRHLKHNSLRHNR

>contig22815 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63189.1|) 2e-08

MEKQRLYGSRAHDVHEQMTSPPGSHGGQAMRLRPQTIAPPTFGAKDIQQQSSTTANLANG

PVVEL

>contig25418 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53552.1|) 6e-22

MTSLVDFTHLRDEVLHSNRVTANTTIGYEIELRELQKVVEARRLKLQAAQQALVVKQARQ

RRIVA

>contig26543 Frame-2R

MRCRCTERKRFPSLRRRWFGVSEETNGVGLLLSWKSKASTWYIVDYHLGSQRRTREDFF

>contig26965 Frame-1F|Blast-T-complex protein 1 subunit beta [Phytophthora infestans T30-4](gb|EEY68636.1|) 0.0

MQHAVLDPDSQVEKGENARMSSFVGAIAIADMVKTTLGPKGMDKILQSMGGPDKGISVTN

DGATILRSVYVDNAAAKVLVDIAKTQDEEVGDGTTSVAVLCGELLREAEKLIDQRIHPQT

IIDGWRIALTTANDALVNSAKDNSQDVDKFREDLMNIARTTLSSKLLTYEKDHFAKLAVD

AVLRLQGSSNLDYIQIIKKAGGSLRDSYLDEGFILDKKIGVGQPKRVENAKILVANTSMD

TDKIKIYGARVKVDSMDKVSAIEDAEKAKMKSKVEKIAGFGINCFVNRQLIYNYPEQIFT

EKGIMAIEHADFDGIEHLAAVTGGEIASTFDHPDAVQLGECKLIEEIIIGEDRMLRFSGV

KTGSACSVVLRGASTHLLDEAERSLHDALAVLTQTVKYSQTVMGGGCTEILMAQAIDMKA

PSVPGKKALAMEAFARALRQLPSIIADNGGFDSSELVTQLRSAHHHGETTAGLDMRNGCV

GDMEILGIREALKSKTQ

>contig28383 Frame-1R

MAVSSASICSSDAFQALTGTRLGDSPIFMRALVEGDQVCIEYQLDASVASAAAWFGVGPS

RGSSMVSSPAANVMMFFKDAGVPTSYLLGGYTNSDVSEESAQSSFVAGPASSATMSFSFQ

RTLAAASSSDIAISATEATSFIWAYGTSWPISTHQSDTNGAATFNIAAAATAGAAASSSI

TSSANTGWCADKNCPAIVGGVAFGIMALCGLLLTAMLKSSPVGKLLLHRTVSRPPVKLTT

NAAVALPHTTFLQLLADLHLGEVLVMLLFMAAVIGLIILLDDADNYVVSGQVSLLILMFL

ILPVARLPLWSVLFGSSFERIVKFHRWLGVAMNVAVIVHLIQASDVVDVTLSDQYGAVTP

VHGFIAFLAFAAMLVLSQEFIRRRCFEVFYYTHRILSIVGFVFSILHAPRFIGRALIVPL

ALYALGVCYRWYSALTGSYKVSATVHAGSNSTTLVLQETHETGKLAMKVNPGSYYFVRLP

AISLIEWHPFSSIVTPDGKTIGFTIKAMGNGSFTRTLMEKAGTQYELAANLCGPFGKIAL

DLDHYDTVVLVAGGVGITPMLSLINQTRLFPKATSATSKAFKSSDWYVLWSVREPEDILM

MEQFLPTHAQMDYAAGIQDPNTAILGQNAPAPFHVHWLFHVSNAPSDGVVTRANGETVSY

RGGKPILDELINTSRFHARNVTVVACGPPTMTVEAQSLARNCGFDFHKEVFKW

>contig28725 Frame-0F

MNERRKKMSKKKARLAVSHRPSNNAKVVEKKTLVAVPPSLLPLRLPPPPPPALSTFSSSC

NSFSDSSSSSSSLMSDTEKSFTPPPPPPPPADKIDYKAAGVGATEAKPPKQKVTSADGAS

SSLKVTLKLPPGFVANNDCAVGSRPTADISQSLHLQAEDSNATTENGPRIAINLSRLSKP

VTNSRSAKKSMFETRGPCAHASGSAASAPQMNGSRFPGLSKPISADFTLLAGEIRGAKEL

SFVDPAIAGNHPDETIEANISQHFNDSFAHDGEILRLLDMFYFCDENGKAISLEILDCPK

EQRLKIMGFGTVVEHLPLAERPLPIKPILASPAFPSRSKKRPRADSSSFTPAKSSSKARA

RP

>contig28912 Frame-2R

MLSDINLCHASTASTFYSLSNLNFEAASSQSRPQKNKLQSIQRYQRQSSLKGASTSFCSN

ASQTEHAPNSPSDQSRYCSAWR

>contig29678 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57031.1|) 7e-34

MVKGLTALVSINGLVSLFSSSGQKQWDFQVPEAIVNAGKLEMTARGGGRQDA

>contig30801 Frame-0F|Blast-thioredoxin H-type [Phytophthora infestans T30-4](gb|EEY55747.1|) 8e-93

MPTFQFFRCGVKCDEMRGADKNALEKLIVKHYKEVELSEAETLLANKDDEIGANLCEGLR

QRKPSVKNVATEEEWAQLMQENQEIGTVLVVDFWATWCKPCVEIAPFFEELSIQFPMAVF

VRVDVDELE

>contig31356 Frame-2R

MPFPSSRIPCPSGRPSSKPSFLVPPTVGPGERNTSAASRIQSPVPQRLTKRLQLPLQQPS

NRKNETSVSVMKPQSFLAVPSVDPSSNADAQSNNIRVMLRIRPSSGKDGKKAVEVAPDQR

GVTLAPLSQQEKRFGFDWVFAESCEQDDIFQNAGRVAVENTIKGYNGSIFAYGQTGSGKT

FTMLGASTADVQELRLSPLRGLTPRILEHLFVRLAALAEEHNASFCNEHESEQVFVYTLA

CSYLEIYNEKVFDLLEPRGSMAAQQPKSLREDRNKEVYVD

>contig32902 Frame-2F|Blast-Folate-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4](gb|EEY60273.1|) 0.0

MADFPQDRQLPAAAGIRGRNKKNDEAYSIENSGAEIIDVAKTEAKPSTTIAEDVNSMTST

TEKKKKASLSNGSISSVKAILQWWISMRVQFGNALLFQIFFVYFTQGIRSTLCSLGTSYY

LNETLMLSPAQSESLRATAAIPWIIKPLYGILSDSVPIWGTRRKSYLLIFSAISALAYLV

LSIPGLITTYALASIVLVVASLGIAFCDVVIDGKVVEAARGEREDMTGNLQTLSWISLSV

GSVLGSMVAGAALNTFGPLGVFFLSAMGPLSIVLLSIVIPEQTYVPQHDTGFVQTVQIQC

RALASVLVHPMCWRPVLWIFLSNALPFSVNEAMFSFKTIELGFSKSFLGFISTVGSVTLL

GTTALYNAYFRDMPFRRLFFRIQLASACVSIIEFVLVSRLNLAVGISDEFFIFGDEILSD

VVGRLKHMPSLVLCAKICPPGIEGTMFALLMSLYNFSWSIASYGGSWLCSYLQISKTNFT

GLATAVTLRSVAKLLPLCLLFLVPATTSISSSNAMKAYSNDTNNCSRDRKRNDAA

>contig34614 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53302.1|) 1e-116

MLTMRLSAGWEDAQEELVMLEREKEDILNNLFQTVDMPAALDLHARIASFSSEIKAVASV

KKQADRVEELYRKALHLLRVALAAVVSPDYSGSIREFAMNSYPLAVEAGQLIEQACRVIQ

PEARRKYEAFALQLTHVRPPKFPQPVTDFARRSRTHYDPHSALSIEGMRNLHAAENVLIL

MQRLVIQKIEGIEKWQRKLMKDQEAAESAYAQMETKLQEQVTVVARSV

>contig35028 Frame-2F

MDVFQSGVQVFIPAALNRPTHTLYSICMLVQPTNQEWTVNRRYSQFLQLRKDIQHKLAAR

SVSCTNCASFNRAISSFRFPSKSLMRTNSVVRYRVASLQDFLKLLVERVYNDLPKCSICD

EGVKGMMRPFLIRGAQPLNGSILSKISKSLSLESYAVADNPVRPVPEPASLISPSLIGRE

LFSASKSSRKPIFTHSQTKSIFSNSKGMSTSSTRSDDASTQPNESEDPIMGYSDSDEDGY

DKRFDDQRCYDEGVSLEEAMKQVVVPKGVNLTCEEVVVRLTSMWASYDLNEALSSLPPDR

LSQRANFPIDDNEYAF

>contig35161 Frame-2F

MQRNSAYRDSGNPNHGGRFGGRGRVGRAGRGQRSYVPAHISSRGTLNPQSSSEPAINLEE

SFTMEIHEAFQAL

>contig36115 Frame-2R|Blast-phospholipase A2, putative [Phytophthora infestans T30-4](gb|EEY63036.1|) 2e-82

MSVATAQEYQECCDWHDACYSTCGMPKANCEKRLHKCFKAKCSALQDATKQEECTTTAKI

FYISANMMGCQAYQDAQKEACECVPTDKAATATRERLEYFLEQNNAPEEELQDDALDALL

AKYKGQEPTLFLRLLKKYPHALKHDASKTNYMDTIVNDVDTSVKKKMKKQRAKKKEVPVD

EHEDL

>contig38319 Frame-1F|Blast-nucleoredoxin, putative [Phytophthora infestans T30-4](gb|EEY57926.1|) 1e-53

MIVQHPEFELVFMSSDREPAAFAQYYGEMSFLALPYEERSTLQAISSKHSVKGIPMLIFL

DEEGSLLTSDGRSLVADSSGDVNKLWDELTK

>contig39150 Frame-0F

MATDLSASAIGGVSAGAVDAATGASGRPENAYEKLSREVHQMQITGAIHTDWLENPKGFL

LKPDFKRKAQHVGAGGKKLNSSRVLRLHLPGNSYRVRWFVLDGMILRYFKTSTEEQELGA

IHLTSVNAVLPSSVADAPEHALDLVCADRIYTVAGNDREDMVRWATVLTLVLRGEYKPKL

MQRPESAIIRGSSVIPRSSTVARKTAALTQASRFTDANKMRMTGTLMNDSEAKTQGDNYV

KEKIITVTFDHPGPLHLILRGTVDEEVMVCGFQYTIGPSGEVGPAEASGVIRVGDLLCSI

NSHYFTNIEFEHAVELIQGAGRPLTLRFSRIDCYATPLIDTTRVAEGWVLSKEPSAHRYR

IRMLQLQDDKVKLYKPSMQGGRVDEPCFILRMDQVTDIRPTNDTREVVTACTQCHPKQWG

VTLEGSQSIFTFYTRNRDDMMQWVDLLKNSPLFSSKATRLSIPVHPVALVEFDPAHEPKV

MLQDDVGKLGDLLPTFSCYHFLLLEDGKMMYYVSIESAATRNRPIGTIRCDNIVSIVPSQ

VTEDTLQQKDSVASAISSNGEHLMPWRLELGILVQGSTQKYRRPFIMCFSTQEKMMKWGI

GIGKEAKRSTGQEYDLSSISRRASRSSSQSYGPRHSETP

>contig40095 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61910.1|) 3e-82

MQPPSTESSYTTGMNPSLASKNEYIQVPDDVKDLLVQQIIGAVEDVLDSMMHEETRDKHW

RSKMCKDDVVYYEDRTSVSKGQSRFCCISATSASVEDVIKLFLVSDTDTLLQRCRVMYDN

IMDAKILSVLEHPSEDNPMRSSYIRYTAFKTPTLLRNHRDMCVVVATDVIYCPDGSTVGY

CVWDSLSLPKGSAFDVP

>contig41614 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68372.1|) 1e-105

MKNVTLGDTIDSLNSSEITSLQSALESESNCGYDMKRLLDRAWVTVAEMRRNDPSISEDD

IRIAIGKSNLVLYDIPAATNNCMPELIAESNLVKAYAARDTLRKGFSSIVNDLIKSGTSS

NGTLLAANEYAYVIANKAASFYGVWDRTNIGGAISEFFQTICGPTEYVGEIDDGTAEEAL

GLKTVQDAFKSSSGHWSKNGDGSVVIHFKSVDVKDVAVNINSNGNQVDQVYVLAGQNVTW

KSNVTFLGG

>contig42071 Frame-1F|Blast-sterol O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY59689.1|) 0.0

MGPRVEPSSNMRSSTASNGGIKKFRDVVSPLDPADARSGVHSSEFRGLYNLTMLAGVLYV

VTTLITNLLMRNEPADLKLLLSVFYSTHLLEVLATFVCQALYAYTALIPVYMAGTKGLSN

RLIINIVHHTLQSLLFFFTIVFIVWRDWNLIHAISAFIEGLVLLMKMHSYIRTKLEIART

ANKPPSLDVKDFTMYLLIPTLVYEPNFPRTNRIRWGYIAEKIFSVIMGISMLYIIVTTHV

IPRLEDSGTVSPVLSIVSLLLPFLGCYLLTWFVIFECICNGCAEVTYLADREFYTDWWNS

TTFDEFARKWNKPVHEFLLRHIYLETLDTYKISKVNATVVTFFMSAALHECVFILMFRSV

KMYFFTLQMVQLVIIVYGRGLRGTRLGNMTFWLGMIFGLPLQAVIYSREYHGGEPIFMVI

MMPAMTFGFGAVLVASLLHLSRSTKKEVLKN

>contig42329 Frame-0F

MFRTLFCSLSLVTSTTCCRHTTGTSVPHLLGNSVATSCKHSKSTRRYVSSRDWCVYDCSR

SFAVSMAPRRDKHESNGCDSRR

>contig43432 Frame-0F

MVPVMIQTRGRPTGSLRRDPSQFERVGNQLEALRRRCRNCNRKGHNARTCIKGRARPASP

QNTPST

>contig43818 Frame-0F|Blast-asparaginase, putative [Phytophthora infestans T30-4](gb|EEY56768.1|) 2e-86

MAYTASALSFMLEYLGKPVVVSGAMIPLHFPHSDARRNLIMSVMCATSLAIPEVCIYSNN

KLLRGNRTTKVANMSVDAFHSPNFPSLAVTGVEAIVDQPLILPYPRSRFQVFTNLSTNIC

VFHLVPGFDDECIEAYIERHKASKD

>contig44406 Frame-2F

MMEVDAMAGQDIVIDTQVIAQEAQENAARMDVDTNDTIVRPEFPALSVQQSGGKNDFRRV

RVPAHRYTPLKKDWPNIMKPIVEHLKLQIRMNTKTRCIELKNSLHTADAGALQKAADFVQ

AYMMGFEVQDAVALLRLEDLFIDTFEVNDVKMLKGDHLSRAIGRVAGQDGKTKYAVENAT

RTRIVLADQKVHILGSFANIKLARDAICSLIMGAPPGKVYNKMRNVASRMNERF

>contig44855 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64902.1|) 4e-39

MVVRLALQLISWLALQSLRLALYLAPAAAALTAVVGIVLVSSMMAQALEYGVLTAVYRSK

WHKNSQYDDLRSYFYRAYWLATLLYALSSSFWIHYTERADFRQAFGFIFFALWWALQLVL

VLALTPFGKILPRMKAAIK

>contig45258 Frame-2R

METLCDIMLPLVEPDPENDLCNVNLLEEHRRKKRVFKQPTKSLIKPGLVSSVGAFSNNET

CGCSDEKLVTPKLSDATSLSSVGSNKAERQRRFRKSKYFPITSLSTEEIVVHPPRDHTRI

SHPWGSVANSTPVDPATSQINPVTSPRANCQSATRSSVEAFP

>contig45452 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64089.1|) 1e-102

MEKMCGDATIMAATEAHKAGVERFVFVSNSRVRSGYPSWLPLYGYYHGKERAEAAIREKF

PITGVMLRPGFIYGWRRTKQGQGIPLQLLGAPISMLARDLGAISSAISYMPFFGGEMQAA

ISVEAVAKAAVLSAIGPVPGQTLDTTRMLELAASFHTEDNV

>contig45801 Frame-2R|Blast-phosphatidyl inositol kinase (PIK-A) [Phytophthora infestans T30-4](gb|EEY59733.1|) 1e-106

MASRLKEYRYYLSSGVSTCISVKISLIELAPALGCSVSGDTPKRAINETPCVGLEQLAGT

SSEVRNSPVSEIFLTAQLFSDGLPLHPMVISSTSPTKCSNSTIYWNEWISFPVRYRDLSR

NSLLAITIWGVGWVPIGGSTISFFTKQGVLRDGVQCLRIWEGREADSSPTTTTPSEIDEE

WVRQECFRLDKLREKYERKEIA

>contig46938 Frame-0R

MKRLPIMPSHCIDDVSFAAYDVDTEDYYAYLPSDGSISDDEDAFASSVASKTHDPVNELT

SVIAASSCIGSASAAHMVMKPIGNISGSKHTLQDALKTQKPSPSLTEGVFSIGGGKVRKV

SRYTLEQHHIRKVQLQEAMAAATLNEDTMTDQSFQEAPFRFVAPLKPKETASNEADCSSA

SPGPVIERMEGHAPEKQQMGKRTSSATQEGDEKESDPLYDEQLDDVDEQWVQTNWRT

>contig46985 Frame-2R|Blast-protein MYG1 [Phytophthora infestans T30-4](gb|EEY64505.1|) 1e-177

MASATKAATFVASSPCFAALRNVQVTSSLVEGSAKKYIGTHNGTFHCDEALAVSMLKLLP

KFASHDILRTRDEAKLAQCEIIVDVGSNYDPSTLRFDHHQRSFTGTFDGRNTKLSSAGLV

YKHFGREIIQHIAAPTTLDDSTLDILHVKAYKNFIEHIDGIDNGVEVATAPEGAMLTYNY

QVSTSLSSRVSYLNPRWNEDQSEQCVNEQFLQAMYMTITEFTDAIHDLVHSWLPAHEIVE

KAVANRFQTHASGEIVFFPEYCPWKSHLHDLEEKLLIVGQIKFVLYNDATGNMTRVQAIN

VEPGSFSLRKGLLPAWRSLRDDELSRVAGIEGCTFVHNAGFIGGNRTYSGALEMAVKSLN

NTLK

>contig47278 Frame-1F

MKDLLRGLHRASSGAETSHAHRCASSRFGRVVQRDFVSALKPISELPESFAQNRKRDRLK

KYLNRQPRSRTKPNMMSFPLPAIQSTEKGMAETLYVTYGDDADVIKVPSESDSEGKYVIP

PVEIPDMYNRKDRHGGITVAGARVVFTYAGFKRQQMILVKLQSVPELADQFAVPLGGTSC

GCVVVNT

>contig47528 Frame-0R

MDKSGHRKRALDVDEGKDSARESKESERKTSYHLDVDIAGIGPDCGRAIGAVKSRRISLD

SSESTFKLSLKSAAPPALHLMANSDCHMPRVSEPLETIGIGGHCRPYLNFKTTQNEDNKL

DSAPLGTSRLVAEDINRSPAHIRRSDRAVSFQKARPGVSRVDSLDSNNPVVNVMVHEAFL

IIIRLQKTLTIVFSLHNCGR

>contig47595 Frame-2F

MSQSKARMLLNTVSRKMAEVEDKMLKDTTLLHQLAVARCSDAENDEFLDEIKHAVCAFVQ

NRVLVLLEDHVHEALYTVTDWYDEKALKAKIKVLQTKPQSHFGVPPHIIAGSGQDWENAR

RELRRVNEFALPLDKLKCLARAAGAIFQTCGASRSSVSLDTRNSVLSIEEWNVALLPSIT

TDEFLAVFSFALVMSNMAQLLITREFLRIMCDPQDITGELGYYLTTFEIAVDLLVNHEDP

QQAMLPY

>contig47902 Frame-1F

MIVGAAFSEKNLLPLLTLSQSGQGILPPRILFL

>contig48169 Frame-0F|Blast-predicted protein [Physcomitrella patens subsp. patens]gb|EDQ80476.1| predicted protein [Physcomitrella patens subsp. patens](ref|XP\_001754506.1|) 2e-15

MDTEKTLGFRGDNDVKYSDVVSGGMDMTMVVRLTGGPGATICSHL

>contig50502 Frame-2F

MAPMSTSSALVASSSRASPPIEEDSELPMDLSQLPSIPVAKSLLLINNFVANTTRFLNHF

AYECEDRIMRVSTNVTRVEVLLAILEAKLNSIPDLNVTDSTTYGNDNRDTKHLDLGISDQ

DLPSMEVNEMPLPPPPPPITEESLMIEGIPLPPPPTSIDGLEGALVVPPSLSLDSMPPPP

PSLMGDFDDNHDDELNGNNGPILLKLKDDPVYAKYFAMRRLGIPDQVIEHKLMMDGINTN

ILNMDPEGPSPSGKLASTIPAEPTGPMLPIMAPPPPSDLESDFSDDEIMELPPPPLSLLE

PNKIERRSSENIGLPFPPPPPLLSPTSSIGGPASLFGDGPPPLPSFISKSALSGSDMGSS

SDDDIEEFDADELPAAGVMKLKDDPAFEKYFKMRKLGMPDSVIQHKLNMDGVTLDILSMD

PDGISPNATSKAGTAQPPLPPGLPPPPAKKYEDSDSDFDSD

>contig50735 Frame-1R|Blast-Chloride Channel (ClC) Family [Phytophthora infestans T30-4](gb|EEY66699.1|) 5e-09

MSSRTSSTPSDSPAIDEPSTNASHTPPPESLKSIIKSVASGATANANATSWAINQAKIVI

EHSKASQIKAHKRYRPLQLLDDEDSDDEWDGEAQGVPSFIHRASDTTITLAR

>contig51219 Frame-1F

MLLEKPEDVKHDNLSGTVCAIYGVDAHPKLQIFATAGGDNAVKIWSLQAPLDGSISTFEL

LATLSNHQQAVNCVRWASHGRYLASGSDDQLVLLYELQVGAPAAVPFGSNARPNKQKWVR

CSTLERHTMDVADVAWSPDDRMLATCSIDNTILIWDVGIGVISEVMTQPLQTLTGHNGWV

KGVAWDPVGKYLSSAGEDKTVRMWKVADWQQSSVLCATHAFSSKKNIASL

>contig52724 Frame-2F

MLRADLTVRFKAEQIWIPGYQNHPIDAMLMPPLQSDR

>contig53257 Frame-1R|Blast-mitochondrial folate transporter/carrier, putative [Phytophthora infestans T30-4](gb|EEY62449.1|) 1e-106

MSPALYGATLSWGIYMLVYQNAKERYARMTAEGWIQGSWQHFFSGIEAGVVCVPLTNPIW

LIKIRMQVQIIKQLKASTTGKDLASKLVDTTPYRSVSDAFRRIVAAEGVSALYRGMIPAL

FLTTNGAIKFVVYERLKNTYQAHWSSEMDLIPTLLMGAIAQSVASTATYPYQVIKARLQQ

GGPSANKYAGTWDCTIKTIR

>contig53446 Frame-0R

MLEPMDGALMSEVETQRSDWWRLELLSFVLLYNSSF

>contig53864 Frame-2F

MVLQKKTDWCIFAYDGSQIYCGSQADHELLESRELLQDQGMRITEPMQMKMDNQAAIKQL

ERQKIWQVPSMWILLATTLAPKLLDHMWRDGSRFANVGSICAKMCRTA

>contig53910 Frame-2F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY53550.1|) 2e-28

MQEKSKIAYGVSIVELKKLLTEPESSRLNVTLQTLTHTLAMTDASED

>contig54133 Frame-2F|Blast-tetratricopeptide repeat protein, putative [Phytophthora infestans T30-4](gb|EEY57886.1|) 8e-70

MQDSAADGSLGAVLELLEQQLLPVERAVLESDYKFIINEQQALKDMDEIGPLLAMAKLIC

EGEYASVFRLPQAHKLLQFVVQMRREGHSIEDEDMHICNSIASTLQNYLLDQCDTVENRL

VAFYEILFVGIAFFNMYVQANYTGPAFETETLCNILELCTRLVTFSTERDDLKSHSEALV

ALQVDGESPFSICQYPQFLLVGRCFLSFVGNFDYD

>contig54146 Frame-1R

MGIFAFLLCAFLMPAVTLPVGPAIFFTPAFLLLLTAVIITSSSESLIATTASVATREVEQ

SLLAYCSAKC

>contig54757 Frame-2R|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY57226.1|) 5e-66

MKHHAESIDQSTGVRQVDGMVAYSTTRGAYQAFTTPGDSADSLWEIKESQPVPDDFY

>contig55149 Frame-1R

MLHRLLKPSLTVSPRVSSHLVRLSTTALPTTLERLFDNNKKWREGKKLLDPDYFGKTSRG

QHPQYLWIGCSDSRVPAEELTGLSPGEMFVHRNIANLVVSNDISSLSVVQYAVEHLRVKD

IIVCGHYGCGGVNAAVDNKSLGMLDNWLCNIRDVVRLHHDELQAIDDHDQRMRRTVELNT

IEQCINVFKIGLVQRHQVKYGFPRIHGLVYDLKNGKLNEMDIDFHSYVRQYQSIYQLHPF

PKGEAPMLRSQLQGNMIRLLVEGHVEEPNWIRVEFVKDSMSKEPLLFSESEINSAIVRAQ

DGEADKKMVDVERLIQCFDH

>contig55941 Frame-0F

MSRFNIQQSCAKKRYVASSR

>contig56971 Frame-1F|Blast-SEC1 family transporter SLY1 [Phytophthora infestans T30-4](gb|EEY53279.1|) 1e-105

MIQPTTLSLQEKQRENLLRMLDFNSESANGFTDASPSSVECWGDQWKVLIYDRFCRDIIS

PILKLHELRKKGVTLHMLLDTERDAIPDVPAIYFVEPTKKNLERIVSDCSKELYSSVHLN

FAYPLNREMLDFLAHASVNAGCTSMISKVYDQFTNFVSLEPSLFSLNLPASYQAYNDPNV

ADVQIEQSMNAIATGLLSMLVTMGSVPVIRSPSTDGPSRMVAERLSSTIRE

>contig58216 Frame-0R|Blast-CRN-like CRN4 [Phytophthora infestans]gb|EEY61565.1| Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|AAY43398.1|) 7e-18

MVLDVAFPKSFVVASHLFRRSNEYVAGTFLKISDIDDARNGIVLF

>contig58582 Frame-1F

MIPIFYVQLKASLFIAKNVINKMHPSSWNLDMGEFEV

>contig04065 Frame-1R

MKKVGDGLVGLLVLGVFFHAVYVLSIFDIYFTSPVVPHIENVDYTDSPPAKRVVVFVADG

CRADKFFETNESTSDLRVSFLRNIMLTQGSWGVSHTRVPTESRPGHVALFAGMYEDVSAV

TKGWADNPVDFDSIFNQSTSAFLFGSPDIVPMFARHVSHAFEEHYSHEEEDFAKRDASEL

DIWVFERLQKLLRTASTDTKLFSQLHQDGVVIFCHYLGIDSNGHAHRPNSPNYLNNIALV

DELVEKSARMIDEFYNDDQRTAYVFTADHGMGSKGAHGDGDPANTRTPLVVWGAGVQKPT

IVPFQEHFQVSLPTHSRGQIQAQLRAQLQQEQAAITQWGALRTRLRKDVMQADIAPLISA

LLGRPYPRNSVGVLPFSYLTPGAYRANAVHSNAHQLFLHAKRKEIEKKAHTLFYFQPYQV

FQERVPKLRQELRDANAPSRTQDDYKRYIQVETLSQELVEICLDTLAYFQRYDWFFLLST

VVLGYVGWILVVLLAYWHPHVFHLVWFLGPRGHYLDIKLSIIIFAAFLYLALEKAPLTYY

LYLVFPLVFWNCLLNHRDLIAHTWDSKIRKTPCSTEYWKQPLAEGFLIVVSLELVVYGYE

RRELFSLLFSGLAFWTYVSKSPSRHDARARFLWPSSCWTGSCLLLSVFPLLPCEYGEHTA

LVLIGGLLLILATGGVQCQFASFPPLSSKRAFFLLQAMPVIISLITLQMTMQYLDGERSK

PPFGLTLTNWLVASMPIAALFSSFHCNRHDAIAQGVHQAPTHEEFALSRSLQRLVAIMLA

FGPSYILLSIAYEVLFYVVLCSVLVSWLLLEAHTASSINIQMA

>contig04111 Frame-1F

MLLNDTITMQCNKNRDAFTFYNTIQYNIYIYIYICIYIETNHSIKSASSRSNTQTKGRLS

AISVP

>contig07187 Frame-2F

MIRQLEVLLLNVAFFFFRHTLGFNYQPSRCAKTKTDDRSPSQLVIACDFFFIILMQGFGL

>contig10712 Frame-2F|Blast-mitochondrial inner membrane protease ATP23 [Phytophthora infestans T30-4](gb|EEY67990.1|) 2e-81

MELTRKTFRSATLNASEEEKRRQKCEFMRENALTKCSRVKFLVDVMEKTGCSLKPGFFSS

VYCTEKINGGFHLDDKGEAGVLLCQNHIPDQEWMNRTIAHELIHAFDQCRNNVDWNKCEH

HACSEIRAAALSGDCDWKNELFRKNFNVSKQHQLCTRRRAKLSIEQNEACKGRVCACVHA

L

>contig11904 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63800.1|) 1e-122

MLDWENEFISLDSKELCDLAKVASNLDIQPLVDLTCRSITQIMSATTEADELRKKFGLQE

PSDVENSCELRSDMAGFDFDMFNTLDHDLSTEEYGLVEIDQPSVDELVTFINGSGSHPNA

TPSQLQQHQAVTLKNTCQLHGENGSDSGNLTNGSKGASKKKRRKHKKKKVSQRTDQVDTK

SSIVINKCVKRHVASDHESSSSDEKEELNSTLSSSSRCQFGNPNRPWTLEEKVQLARQNP

SAVFEESQFEDDDDEDMAKMIKMFELNLESAYQDCDRKEKPRLEFAPREVFRSSLGQSSQ

FEFVQRRISATMT

>contig14349 Frame-2F

MKGMLQTVKRKLGNNGEHFGVNSPDRMDVGPHGVGSPLGDVARSDVALPKRERRRSFMAR

NQKIQALKDLPHLKDTSLQRREALFQQKLELCSVIFNFDDPTSDKRGKDLKRQTLLELVD

YVNNPAGQKIFTETLMPDLMAMVSMNICRALPPQTDDFDPEEDEPVLEASWPHLQVVYEF

FLRFIVSGEVSAKVAKKYVDQKFCLAVIDLFDSEDPRERDYLKTILHRIYGKFMSHRSYI

RKAISNVFYRFVYETERHNGIGELLEILGSIINGFAMPLKGEHLQFLIRALVPLHKPKCV

SMYHQQLSYCITQYVEKDPNTAVPIIQGILKFWPWSCSSKQVIFLNELEEILELMGSEQL

QQVHKALFQGLAKWLGSQHFQVSERSLFLWNNEHLVNNGCLSKQHAHLILPVIYGPLHRN

SLGHWNTTVEGLAQNVLKLYMDYDMALYDQCAKDFSLKEQAMVDRKSNEEEKWRQIESMA

ATKISLSTA

>contig14899 Frame-1F|Blast-transcription factor BTF3-like protein [Phytophthora infestans T30-4]gb|EEY55669.1| transcription factor BTF3-like protein [Phytophthora infestans T30-4](gb|EEY55587.1|) 4e-79

MADAITLARERLAAKFGDVRTGGKGTVRRKHKAAHKTATADDKKLGATLKKLGVTPIPGV

EEVNLFKADGQVIHFQGPKVQASIASNTFAVSGFNQTKSLQELLPGIINQLGPDNLANLK

QIAESYTAAQKAAKAASATTIAEDDDEVPDLVDNFEDVSQQD

>contig17212 Frame-2R

MPIYDYEPSLSLDHEDPASSTGDGVGSSFPDTPQSNGNTFKDVEHEVVVKEASVCSDIEE

TKEPADSDDQELNTESSDTHALLPCPQSR

>contig17645 Frame-0R

MCITFVVFKKRQRLQAFYMSRLSPAESECSRKSKPSGPLIAPRQQQNRTSMRRTEQETIG

DFSRTLRLPNKDDSPINEPAPIMEETLPRSRRNTAPSHLRLQGSHVAIEFNAPPFHRGSV

PVVSALSREAPSRSTSRAT

>contig17771 Frame-2F

MKDEHVKREAAMFARRREEMDALKLERKERLKTSVTASFSGKQKKEQLRARKQRLASRRN

EMEALDLEKVQYEDFYADKSSLIEENGVGANAEAFSAEASNFTRNNDLENNFNSRLKLTV

ALGKNNIDAVGKELSSFFVKESKEQIQLRIMEGQRPLDLAKRETPLLASICDKDPILDHP

KRPKWTYKMSKGKVDNNESIMFDEWLTKIHDKYNNEHLNHFEHNLEVWRQLWRVTERATH

IVVVADVRNPLLHIPASVYDLVTNELNKPIVVVLNKIDLIPTAVVELWQQFLVTQFPKAV

FVCFSSRCNAVHGNSDVSTRRRVLSKKLEVGNAMTMKGAVDILVACDIDATEAQQLVEEL

NDSSIEQESLYPEMTQNEKNTNGRRRSRRKRNNQCVVARRDESLITIKVCQHCGCNDAVV

ACMSCASMSCASGSRISSADANVANEAEAIARGYLLCTRCDEEEHAEMRGHFQVRLQSAL

AAELKESSTFGSVGATGQTRAPKVTIGLIGHPNVGKSSVLNALAGKKIVSVSHTPGHTKH

LQTIMISPEICLCDCPGLVFPFAGVPKHLQELSGLYPYSQIREPYSAVRFLAEHVMLEKI

LNLKPRTQLFDNLHEEL

>contig18190 Frame-0R

MLRVWGVYFTDKSSTYILMLVLFARDVQALLPFLFGSILGFLFSSTRLGRLRVPSFMCSI

FSLLHPLFDVVPPSVLAFQRQRRALEARRRVNARLNPGGLAVPADAGQGFRDQLLPGAAG

GALVADGAFMLPPHMAAAPPSEDAIQQLTALGFERHQALRALQSTDNNVEAAANRLLNGS

>contig18473 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59575.1|) 1e-45

MQMGSTEITLNPWMASLEDQQKFGMTRSIQFRVPIEAPIGPKSSQVDVLQCLKENVKGVR

AVESSTRLVDIPYGDYFSVEDRWTIVPLSSDLNACQIFIEIKVVFGKSTFWKNKIEARAI

KDNRAKWERWIESAKKFLDSRGLITGAQCVIARPHTSGTSSEIFAPAEIKTDDEYTKCRK

SGLHKQTSSDAICSGARTARVKVFTWVILIVLLLIVLHLLQTTLSSIERIVLINFELIKD

LKKQMSDIQAQGCPAIV

>contig19131 Frame-2F

MHRTRHSSLDCLSGGAYPQDEWSEFLSTSMMALSTADSEA

>contig20650 Frame-0F

MSQYGTQFLRNIKSNLTVVGHDAPDVQFVEGGYMFLASERGLDVLYQNYATQRAAGADVQ

MLDPVALKKRFPWINTDGVSQAVLGVKDQGWFDPWAFLTALKQKSLALGVDVLEGEVDGF

DLGEKNQIEVVHINVNKSLDYSDFKSVRGGVVVNAAGCWSSKLLEACGSFDYPVKPRKRS

MFAFHCDAEEIWKGDAATPLVVDVNGVYFRREGAGGRFVCGWSPEPDNDYDGQSTDELDI

PDHIQFEEQIWPTVAHRVKKFEAIKVLSAWAGYYDYNTLDQNAIIDLHPDVPNMYLVNGF

SGHGLQQSPAAGRAISELILYGTFKTIDCSCFNFNRVRTNEPFVEQGIV

>contig21024 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68436.1|) 1e-10

MEFQKCLTLLASRPANAHEKCEKQFAAQGECMSKTFIESAEPTDFKELEDMPLSGSRELV

QRFLRLQETRVQIYAVFK

>contig21482 Frame-1R

MDVAPMHKVAPSVTTKTESQFRTPLQIAEAREQQLLSCVGVELISPLQVKRRLRAYARLK

ALKSRREGLVAMKKNPRKKILAEGVAAPEKKSRGVVKVEPMEAISRQLRKNIEFKEYGPG

SPTVVAIHSKFIAIGTSKGLVIIFDHFQNIRQVLGNTNDTDGDGPVTAVDVSPGSDFLVC

GYQSGRIVLWDMIKGTSLKAVSDAHENPVVSLRFLKDQKPMLVSVDTNGLVNKLNFSKMM

GMVYVVDVDPLYDGSAGRIMSISVLPQSAGNAKISYLTDQYCLAALSTETVTFIVAIEPE

VRVIYRWARPDDIAPDDPVLPSLAFAWISFPGSSRALAPVLARGWGNRVQFLEVVFPGGK

NYSLARHGFPTFDEHDQIESSSAVMATQWLGDQVVVYLNSHDEICVYDVMSRQELEIVDV

SSLELVFASYRGKNARSFSNSFRGCYNILYLLGLKELQTARVLPWTQRIDLLVDDGEWLE

ALALALDHYEGLKMAAADRAARDRFPPVFFRDKQNDQCLVDILHMCQTNQRTGEKEDVFR

HEESAEEVRWVCGEAPYPPDIAKKLEETLQKARSGERTKNFVPISVAERVADLLIEYVRL

AIANAPGSTAAAGGELSLNKIGMKLDLAKSHYQMLAGVCIEYCALIGRTDLLFGEIYTRF

KDANKLSVLVELLEPYILSEKLRSLSPAAMEEFVRHFSAQGKIAQVEQCLLHLNVAELDL

DTILKLCHDHELSFALIYIYNEGMDDFTTPIDVLLEACLDAMASKSKPAINSITRAASGN

RVSNIASAFGAAARATSSTSTIAKPVALSAREKAEETALSGPRRRRLFGYKLLLYISYAL

SGRTFPKHEQISSLKLGKVRSQVCYHLFEKTVSGSSNPRPYPRLETLIGLDARALFNIMG

RMFDTPSVEFEGEGKDCSERPTSRYDSARNAEMTKCPSRLSIVLSLAEVIFDPNSPFSSV

EHAHFFMFEARLLSGGSIEPQEYADARAAAIGEAGSADGASMMDSLMNFLALGPASLLSD

GSSAVSAETSQEEGFDKAGREVMLVRLLTKLNKATYNHEALLASVIREKMNRAAVLLYKD

KGDFTEAIASYLADEDHEYQMNAFSYIRMETDKAVDGEDMEPRDSNGTEPIRRRRKVIEE

AVLNHASALMKTNGYAFVTLILGQFPNLNNKIFKSSCPWVKEVLSLNFCT

>contig22663 Frame-1F

MIDSFTMSLAKGNSRVQQMIMGAGKTTVVGPLLSYILADKEHLVMHVMPTALLEQSRQVL

RNRFSNSIFLKRIFTFEFDRAVSDDPIFASQVFKKLDRARRHGDVVCASPESIKSMMLKL

VELLHSIEGSTDIIMLPIASASQNTRRLRRVLEDRSAMADELYKTLRLWQNGILIMDEVD

VLLHPLRSELNFPIGTKIPIDLAANRWELPIYLIDAILTMPHSSNDQFDLISRLHAVLDN

GYSAHTLQRFPHLVLLDMEFYELRMLPLLSELAMEWLLKLIRVGKLEIPVDRLKFYIECS

PSDLHSNSSIRYDIENALSEASIKLLNLARDWLHTMLPHILSKINRVSYGLLRGSYQAAA

NFGNSVGKTHSRMMLAVPFIGKDVPSRSSEFAHPDVLIGLTILAYRHEGIRASDLVRIVS

QLKQDFGRQLGPRDQRPACLRLCEWVQMGLGELSPEKHHDFGGVLPLPLFQLHDSAQVSR

LHLLIAKLASLVHYYVRQHIFPSCMNFQKLKITACGHELGSNSLFAKRIGFSGTPSNLLP

LDLGECHYEPRSDGSIFGALTNKRIVTIERKVEWTARKLLLDIAHANPPVHALIDTGALI

TGFDNQEVASFLLKELPNDMEGVVYLDENDRQFILLRDHNAPMPLVQCGLSPSKRFTFYD

QVHTVGMDIKQCVNARAILTLGKDMTFRDYAQGAYRMRGITTGQSICLYLIPEVENRIRH

EMRLACVEMNSQGTAQDRLQEFLVFVPAWLLINSMRTESMQLVQLSLQELNNTWRTSALR

YLLDEIETASINKSSLSSRLRRFIDYRSDSSKAWLRKCIAIFRVEISYTVDAVVPLRKQL

LDIIEELIRNHDEFVKTEEESFRVAAVKQRLAHSSGIEPQQGDLRLTAEVVHENEAEAEE

EAEEEAEQEEQKMSAFTRDDEHPIPWSASILGQPPKVAEALTTESDEVTISSLILDEASV

FYPFAQFQAHSDCPKLAFPAELLMSGNFYRRRWIGLGERRLKNIGFILEWSPQLYQESMK

ALVQQLFRAFLASDGSKCNANDIAVKAIQAAAVIASTSPESVSDALKNAVAVATSKMPVY

MATLSLAEAETIRRMIHTKHPVFQISQVKLRTSEGEVVDSSSIFSSWSRKADSAVLIELK

HRDRTIAVGVECLRFFNNEMYFSPRKLGLLLEGLAAVPINSRLEFFECLLRLRLRERHLW

GDTPLAKVFTAPNEWHLLTARARLQQFQQSLGRKQLQHQKKRVKARDSKPSTAALHLAVA

LRQFDEDEDDQLSFEQVHKCFESFHLGFSSKELHEIIDLIANARSKTDKKD

>contig23516 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY70514.1|) 1e-179

MASREAKIMGTHWSEKSLDEMKERDWRIFREDFDITLKGGRAPHPLRKWSEANKMLPDAV

FKAIQEMGFERPSPIQMQAIPVGLQKRDIIGIAETGSGKTAAFVIPIIAYIYSLPATMVA

RTGEQGPLALVMAPTRELALQIEQEAIKLCKYTSVGPSEAMSPIKTLSVVGGQSIEDQGF

RLREGVEMIIGTPGRLMDCLESHYLVLNQCNYVVLDEADRMIDMGFEPQVVAVLENMGSL

LKSENEEEMEQQLMLANGSQPGQELLHRLRVTTMFSATMPVEVERLAKTFLRHPSIVKIG

DEDSGKNKRIDQRVMFMNPGKKRSKLVEVLRGFKCPEWLNATITKRKSSGWRENHCVCKH

>contig23754 Frame-0F

MCCLATTVTAISHKTESPSDLYIALVSIPVLDKVLPLMHLAEALLSRGVRVGFALPENCR

PWVRDLKGLEFISLNDIVGKGRAVEQSLKAFESLGVYESYANSLRYYASFQRPMYRALLA

TFAVDQPDLVIVDRYTFAGFDICHRLQLPYVINNPHLLLDMDAPPASISAPFSNYVMHTT

SVLERCLNSIYRLRFRLEIVRIYHEIHAVRHEVGLERSNYNYQLPGHVLVLVNSVFGLDE

ARPLVPQFLMVGLLQSESLQREHLLATSTTVGHSKLPVALSAWLHTSEDLDKPLVFISSP

FNEFLTPIFITYGACS

>contig24470 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61068.1|) 9e-34 NOT\_ORF

MISTKEKESKVFFYRLRDDTSRVTKMNGSFGHGL\*GDWRLELFKICLAKIEGKLKTKRRK

FRLKTKNEINTLKRRIFFISSELEREQMTNEDALSSIDASRA

>contig25419 Frame-0F

MARNEQHPTDADTGYSCDFFGAGRANVSLVTCVDIVNK

>contig25730 Frame-0R

MQRHLKQLIEQTATYAAALATSFQDFHEKQETSDFLRQTKPLVNTNATSDDSSDDGVYEV

TDEDEDDETTIEEEEEEYGVVSKSAAEAEVASLQADNELSIDALRAKYAFTEDHEDEDEV

VEHVKTSRRSRGTNRRLHERTNRYKRPYLLTSRLELREYQEAGVTWLLSMWERRINGILA

DEMGLGKTIQTICLLAHLACVKGLWGPHLIVVPTSCLVNWEMEFKRWCPAFKVLTYFGSA

KRRKELRHGWSRQNAFQVCITSYQLVVQDAHCFKRKKWYYLILDEAHNIKNWKSLRWQTL

LTFSSQRRLLLTGTPLQNHVLELWALMHFLMPHVFASRKEFSYWFQNPLALVV

>contig25833 Frame-0R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY69921.1|) 0.0

MSLKVFQTTFQQLNATYDTVWTNCQDRRKRAPGASNKTHVANLYAKWKTVSAKLLYINKS

RLVKNLKAEEDMNSIVFMQSFVLARTQRRKFMTFKHAQVVISRRYRGFQTRKQLSSVMWR

SCKIALLGVRTEFERYLGKKKRRRDSLDRHYQGDYIGVNKYPAYASILQAYSQGRGQKPS

SGRGLKEKLLFLDTVEKVNERWAHQTRVLMISQNRIFNLKADKIPQPKERRVFELKHLTG

VSMSTLPDNYLIFRVKGEIDMMVQVAQKTEVVQALRARVEKGYGRELTVEFSDELDYNAA

KGKQLKVKFVFDRSMKDSEWHKVDRHTMLVKVGIV

>contig26201 Frame-0R

MRLRGSLVALVATIALFSHGEASADSQAAPANFKHVRSPIQTPPNIEMESVPSLQMTRSL

RVDENRSGVPNPGAVEKTVANFVQVRNKSLGKLAMEIKNNPRYPPKSITKK

>contig26964 Frame-1R

MTGLHDILVECFDISARNQASTLAIGADDANISPHRCLVFAHLHKTLDLTEKMLEDALPG

VRFCRIDGKTTHAKRLHIVQKFNTDPSIDILLLTTSVGGLGLTLTGADTVIFIEHSWNPF

VDLQAMDRAHRIGQTRTVRVFRLIMENSLEEHIVHLQDYKEQVASTVVQKSDVKNSTNIN

TKEVLNLLRASSSIVAAKGSRKSAQKYRKTGKHLKAVLPKVAKNILDQIGELWDESQYKC

LAFPESNHI

>contig28526 Frame-1F|Blast-Phosphatidylinositol kinase (PIK-L2) [Phytophthora infestans T30-4](gb|EEY59643.1|) 4e-69

MAIEAKPLENLTTNALNFGQSVANGSVVGIRIGNGNGGSGALDGSGEEEAQRLGRSLHLT

PARKVAESDKQTSGKLTNIILEVPPD

>contig28799 Frame-2R

MNCKALTSLASKFKDSRIEWVMMRLEETMNVSRCFDLDVRWLACSGIAADEFVSTLRRRA

KQAGLDLRRVPEYSRVSRIQFHPLVGSVFLPLPSQIYEYLIIAMTQSLGFVLDDEQIADG

VRKKYGIGIDQKASNSKSTIIMGHRCLPPTDARTLLQRWQQRGYKQFIHRRIHVFVRLFN

DGLIWIPGYGNDCKGDEASCVAAIDNLFLKVCQTIELQLGDFRS

>contig29060 Frame-2F

MKASMPLLRNRCFCCDFRSNVARRYLRLMHIVAKYARQYPRRSTCRVDMWLAILGRIGIN

YYFQCLREAPA

>contig29129 Frame-2F|Blast-isoprenylcysteine carboxyl methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62713.1|) 1e-34

MYASEAFQSDRGLGKVALAAFGIGVFVALHASLLIYAHFVALTDLSRDITSTLRWRCLEQ

WSLYALALGFFHLMEFMLTAAYRPANVSYE

>contig31146 Frame-2R

MSLVNDTSKPERKGEENEDEDAVTVLQNSMRHMKLVGTLASVNCGLYLKLDTTFKEENLN

VFFAKASRYAVIMAFVAMAEIYFLLRQLQVSSTQATAAKVSLLTIGQQGIVDSYLCLGHL

TVGIVAQNVFAAFASVAFVKLIIFSVFEMRYLLIIWKARRPQGFSEGWLTFRRELTTLYT

RFYLSLCAGIGIFYHASNHLPILIFICYSFWVPQIIHNVHREVRNPFDPGYLYGISALRL

FLPLYFYGCPDNFLLAFPMYESKIDPHFCYVLVTWVGLQVGILVLQLRYGPRFFVPARYL

PVKYNYERRIDLPQLTLLKDSDNLIDCVICMVELEIEARDYMIAPCDHIFHRDCLLGWMQ

VKMECPTCRHVLPEP

>contig31472 Frame-2F

MDCSSWELLALRMESKKETALSTLLTPLVSHIVTNKRIYRASAVSVVSTVQPEGGTFKTN

GVAPFSVFLPYEIVRSPTL

>contig31854 Frame-2R

MGSKQKSLIQPGARTCSPIAIALKTLITNKL

>contig32594 Frame-2R

MRGKSQWDFLLEEMKWMAVDFAQERNWKRVLQHHLAVNAIAAQNADNIRLEQESRQIARG

IALQISAFWRSMERIAARSRVRFEAAGSEILDHGEQNKLLPCNNVEDRGKQGNGKRFDSA

GTGDCALTLKFCTAYSLRNNGLGSNRDVKGEIKPEAVASAKSHMTYIVSAGKRARSAMTS

SSASSADANKSSIWCQREAAFRDLQVRCSTLQANGGPPIILAAFQLLALRWMLDLYSSGL

NFFLNDQLGMGKAATLVAFLSLIEIVSSQKQHVQRREGDVVSASPPQDSIVDEPIGPHLI

IVSGEELHKWRYYLRIWHPHQRIQLYDGAGSTHAHKAQLQRDWKIKSRLYAHKHDDIFFI

NSPFGSDDDDDGFDDECVKPIYCVLCPVRAFTEDKEAFVAFTNWQMVIVENEHDGQFNDS

VCVSGLQQLRQQQRRVLCNGQSIENWKSAALRLQYADYLVQGAPRLMENNATEGDSHRVA

LQELLVEWSSVAEVLQQYGKSSSVRASLRQAGSQDDSPQYISASLLALSCLSLRRVRSEV

EPELGKIEEISLSCQLSPSQKTQYQNVLSGFAATLDTSSGREERLSVWLQLILHLRAICN

CVDIVNDMDKLGHADLRLLTSCSAKLEILEPLVRRLTLQEGKKVVIYSQFNAMLPILEMF

LYLLGISYVHVTGTIIMQRRALCHFADRPVIRVALVSTRLSKADGRRAVSVYGGEAIIVV

DG

>contig32903 Frame-1R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY60180.1|) 1e-137

MVTSSLDKNTSTGGVVAARLLGSTCSGMCELLIFHPVDTIAKRLMTNKESIQGLVAMNQV

IFRDAYEQPVLARYRSLFPGLGFAAGYKISQRIYKFGGQPVVKDYMLKDHAAYFEHQFGE

RNAKTMMHATAGSLIGIGEIALLPLDVLKIRAQTNPAAIASKGVVHIIQTEKFALYRGAS

WTAARNAPGSFALFGGSAFTKEYLFQLDDYNKATFFQNFVASILGASSSILSVATAGCDQ

DTHSIASI

>contig33618 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66333.1|) 1e-83

MAPKKTNREFGGLTENEVRALLLGNDGNLTRDFEAVLTRLYISFLEKPTDKSLTLEKLRD

FSKICNNGKQFSDAEILEIQTYFQCDEKKGLTLKGFKDMYHTQSSAEPLETWRDMKKLGF

DKELLEKREAAVRCRACKSPSVLVCSRCKKVRYCGSECQKQDWKASHKLKCKPPAV

>contig34615 Frame-0R

MASKQKKEAFQRFQASVDAAMSTHAMILVTTDHMCASVRANAMVVLVGAVNNTAMTHATT

FLQVYYVTTTDFKAVHTFQLELSTPCLQQLQARFNIAQQIVAITQHVAKMEGRNEQTAKW

VHKITNGADF

>contig35029 Frame-1F

MVISTYVNLTLFKVDQPPSIDAWDQAPLESWVRQRRQCEPKIHN

>contig36114 Frame-0F

MAFESVAIAPAKKSSSSAVTFKTLKRVSSTSAVQAPAVTSVRVPSSNFTYRAFIGGAVGG

MAAAFVTSPLEVVKTRLQICSGSGVFGSQTTFGMMRYIGKTESVYGLWRGIMPTLCGVIP

ARAIYFGSYSTLKEHFTSQGLTGRTFNFLSATGAGSLSATLCCPIWVVKTRLQLLPVHAV

TGAMNRQNVLSVGFAELNSRPATTSRPQCLNFCQVAVNMYRNEGPKSFFRGLSASYWGIS

ESAIQFVLYEECKNHIEEPSNLKLFLAAGACKLFASVCTYPHEV

>contig36819 Frame-0F

MPLSNLPFRDAGLVSASSHLPYVWASALSFHLSVSDQFRVAAAKSLCFWLALQICPKEFL

DYLTTSLFACKCLHFRQYELSLTFFFVLRSEGASLATLWDGVHRREDTGCVRIVIVPQAQ

LHPRSSSSSLSF

>contig37070 Frame-0F

MLVPQDHVSRKVTDTYYVDKYRVLRAHTSAHEVTTMKKGYTSFLISGDVYRRDEIDANHY

PVFHQMEGVRIFTELDVFIPRKEKVVYVQQELKNTLEGIAIELFGDVEMRWVEAYFPFTE

PSLELEILFNGEWLEVLGCGVLQQEIVRNAGLGENVGWAFGLGLERLAMILFGIPDIRLF

WSGDERFTSQFRDGQITRFKPYSKYPACFKDVSFWHDDNFHENNLCEVVRDIAGDMVEQV

>contig38318 Frame-1F|Blast-nucleoredoxin, putative [Phytophthora infestans T30-4](gb|EEY57926.1|) 1e-53

MIVQHPEFELVFMSSDREPAAFAQYYGEMSFLALPYEERSTLQAISSKHSVKGIPMLIFL

DEEGSLLTSDGRSLVADSSGDVNKLWDELTK

>contig39025 Frame-1F

MSLSRITMRRVLSSLGPAITTPFALARFSSPAANRRAQRSRKDKVIANTTALFDPSIVAD

IDELSRNGLAQRVEMPTELLSRITSILRSRTHSQLELLREKHVGDRRNTRQIPLNMTNTP

LGWTMDRGQQIPPFAYGPDETLSFLSHEMEDSYAGTYAVFAELLKRLPGFNPNSMLDFGA

GPGTASWVAKYFYEQSLKKYRVVEPSQSMVDAAEVLLEDFPGLSMRRSVADLSRDINAGN

KYDLIAVTYVLSDITNDFERIATTSALWELLSDNGCLVLVDRGSPWGSHQVRSARQFVLD

SVHRSKNEMEGIHVVAPCPHQFECPAARNTWCHFVQRSPVVNRPLEATAKRWHGQKGSKF

SYVILQKTCIESVVDAAVENRGSYARMIRGPLLATRHVHLNLCTPEGTLERRSVTKGKAI

REVYRASRKALWGALWPANELSYLKNK

>contig40029 Frame-0F|Blast-ER degradation-enhancing alpha-mannosidase-like protein [Phytophthora infestans T30-4](gb|EEY63780.1|) 1e-43

MRGKSCLRHHVGGAWWHYEWCFDSHVRQFHPVAKGLNTPERNITLGVFDAHKAQSLRILA

VDNLDKLADPSRMGYMVQQLYGSGDFCETQQAPRSVNLHVKCCVLHDNETYVE

>contig41615 Frame-2F

MSMRKALGLNLQTSVVQDNVPIEVAAGLFVGSIHASFNLEALKASRISHVLNLAGSTVAF

PNDFTYLSLSIRDKEYANLLSCLPIAAVFINAGLNDGGVLIHCSGGRSRSPAVAMAFLMM

KQQLSYSFILAHLKSLRPIISLNAGFDAQLKCLETACGNVFVANQHVLKARLAHLSHQFE

NGELKSVVVKTRHLSRPTDNVASSVLISKNGRLLSGCDKRGMIGERVPSGFYLSMRPGSD

PINDRAKKTSSLSFIPALRSMGTIFGCQCCGEALFCAGAIISPHNIAKLTYQTDTCQDNL

RFLEALQGQQGNTRNVLIAEKHHGAGKGTTKPFLSKLRLKPHSPSLTEKENVRACSYPIS

TTQQDAPLTEPDSSHFDNQFELKSLQQASDKGNSSNLLTLSPTELREELEKKSGGALWRS

FSSFKSPKRTCYAAIESKKFNTQLNCTQLSKPSILTASDRQSYTEMESSAYAVFLKQNAI

EWNRNMRQLLDVSNMKTSSKRSQSTFDQLKALLDEDLTVWLSLNDCHEWHVEPQVWAIGQ

ASGHSEGDIQCPREACRAIVGEWRWNGSSNDCGDSVASAFVMKKSAVCVLGNMNSNPF

>contig42328 Frame-1R

MKRKKTSLIWGTTTIVHLRIGLCHLSRERNVPHVLLREMYGTGRY

>contig43644 Frame-1R|Blast-nucleolar GTP-binding protein 1 [Phytophthora infestans T30-4](gb|EEY57350.1|) 1e-131

MLGNDDWTQDAIPEIWNGKNVADFVDPEILKRLEALEREEDEAMANNAPMDIDEDMSDLD

DEQKDKLLRIREKKAIIVAEHRQNKNKNHSTVARKVRAKLRTLTQTKKELEALGVDTSHM

KHAEAVVAKRKAGDESRGRKRQREDMDVDMEDATESSDLRVRARAKSVIRSKSKNRSQSL

VTPRDQAGFGNEADMALVKRATRLTQRKAAKMGRAGEADRKSVPKLAKWQNSGKRGQGNT

YSR

>contig43819 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69343.1|) 2e-57

MGDRAGSLGTVDMSLLSNSTGYVDDSGAGHVRASGSMKNWSNILPNDTAVRIIYEGSGSA

EEIVIIPTEDSASRSMESLSNGSFSIGSLGGEDNTVVLPQSSSSREGSSENEKEVVKTGS

NPTTLLVVTTILSAITIATIFAVVRYSRRNRRQAYSENSGEAFIVGSLPHQAAPQHNILG

AEIRPDLWVEGQYRYSPTMSGLENSLSGTAILSDNKTISAHNRLTVDAYPFGTSTRRGSR

NNGPLNSIQRRHHENVFLDDISGRSRYRRGPSPVVLYEQESYEERKTNTSRRNYQQRRSS

QRQRR

>contig44407 Frame-0F|Blast-dual specificity tyrosine-phosphorylation-regulated kinase, putative [Phytophthora infestans T30-4](gb|EEY63005.1|) 2e-07

MESTCASRCLLPALIPMPPTSESASAAPHKVEQLQQLVDSQSLLANKKPTSLVQIFFNRR

PLD

>contig45259 Frame-1R

MSLCGGWKSVVTTASRSSRLQHDYLNRSKSKRLLFTEADVFEKPRPRRKCVAYRLGRVDY

ETAWNWQKQLVQERVVAMRARRTVKNDVVLIVEHPSVYTLGRSGSMENVKFDPKKEHVKL

VRVDRGGEVTYHGPGQIVVYPILDLTQHRKDLHWYLRQVEEVVIRTLARFDILGERVDGL

TGVWVEQEKKTSACQAGNNEREMRKICAVGTHASRWITMHGFALNVTTDLREFDRIIPCG

IENRAVTSIERICSDATIQDVQSAAIEAIREVFHFEMEEIEATAPV

>contig47594 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65663.1|) 4e-28

MHQNGTTYATHEDLGLALGTSEG

>contig47903 Frame-2F

MPFAKDAFASISLASSAPSTISTNRQNNCRREARPMTLFESARIYNESGQMLNHDNFDHL

GSSPDVTSENNSNPKRKLKRRVGRHRHEMKRSNAADTLKPDEVVIELMCVLFPGVEVTHE

INLLLLGGAQHDDVFRFDEDDVDGIPTSKPKTGVLDIDLLKFQAALTTMLFHSNSSIQKL

PSRGALAEALLKLCFTPRWISCEMLAMIELDVLAQYDRFAVMVAIFRMIPTLRPSILTAA

RMASLAIFQHQSLVE

>contig50734 Frame-0F

MQILLIDQVVRVLGMELQRLKKMLEKEALVKTVAIEAHVDESEQTRGAAVEELTPLQKTE

QELKCLHSKGLEWFHLLTNLDTKLLRSVPSVREALWRSIKQLGRSFVCIDERETCTLLQL

MLQDPSRIHLLSDCFCPSAAPSRFVEMFAMLMSPSNSFKLSSEQKLTLLYRFDFQTWLQS

KTSQTQFKFDRDTILCIILKDVRVQFPADRNLVETAQKAKDTIVLDHLNQVLRVYAKILL

VICSAHLADHVETMIRAVV

>contig50929 Frame-0F

MSRHFRMLGGQNSSTTAVAEQQQDPTNVDSDFVVILAALLCALICVLGLVAVARCTWIRR

ISGIVIIGRTDHSPPAAANKGLKKK

>contig52651 Frame-0R

MATAPSTKLTDEELHIDDVSSATRKTKKVIAGACSGMISALAFQPLDVLRTHQQGAFAMH

GEQKTFTGLSNLFLPATIKTSRPDHDFIARLRSMWRGTSPTLMRVAGGAGLYFVTLDHCL

NMFPSSAINTFLAGAFARTFAGSIMSPLTIVKSWLEYLPPGTFDSNLRVVRHVLHHEGVR

GLYRGMVPTLIRDVPFSGLYVLVYTQLRDSWTIRYPYLPNYSVHFSSGLVAGVLATSIVH

PADVVKTRMQLAINNGKIPSSLILNSFTMRQTVSKIYRYEGLWGFAKGIIPRVAKRTLST

AVTWT

>contig53256 Frame-2R

MTEALDSSRLKKLSGMIGMKNNIPKRLVRMRACWSQLSQVMLCEASGVRISPLHNELVTC

VGRTYSSITSNMEALVGFTNLILL

>contig53865 Frame-1F

MQLGTRISGGHPSAPCSTNPISIAVLEEQRSAHGATKRSASSVQSAGPKVKQRSRIPDEI

TETISTLTNTDS

>contig54756 Frame-2F|Blast-histone acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY55004.1|) 6e-46

MPAHISYLSRGLYLFQKHEGMEVCLFTIYAQEFGDECELEANKRAVYIAYIDSVRYLKPT

SARTAAYHLILLAYFDYLRRHGFSRVHIW

>contig54998 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69628.1|) 2e-27

MYHSSCFRRQFPKLAMGINNRQWYCLD

>contig55940 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53613.1|) 2e-07

MLRRLLTQEKVDERRLAMFCSSGLTSYRQLLQRSTWDNANAADLSICAI

>contig56220 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55002.1|) 2e-08

MANVMLTSEAAKDPNKPFALRVEDVCTKFD

>contig56369-1 Frame-0R1

MQKTRNAVLITGASQGYGRCLALDFVRLLQDEGLDL

>contig56970 Frame-1F|Blast-tRNA pseudouridine synthase D (TruD), putative [Phytophthora infestans T30-4](gb|EEY58382.1|) 1e-11

MAIRELLKQSSNLHVQLQLKQKFEEEKST

>contig57568 Frame-2R

MMARTSTTSKRDGDLSETTSTCASNTSTSAAMTPRPPPNMQDFAPDNQDDAWNLKQFEQE

EFTLGMVPTVPPPPELC

>contig58091 Frame-1R|Blast-predicted protein [Trichoplax adhaerens]gb|EDV19242.1| predicted protein [Trichoplax adhaerens](ref|XP\_002118239.1|) 2e-17 NOT\_ORF

MLMYSNEQTPALNTLIFSQ\*TM\*VHQSTNLMAERQSHKKCFEYP\*VHTPKGSGPDIQSRN

PTTSFLTATTLIYAIGAGITAAAGTRLALQLILVKGFKLYSFQLPDSKSQSIVIYCHYLP

VSGLGNL

>contig58217 Frame-2F|Blast-CRN-like CRN4 [Phytophthora infestans]gb|EEY61565.1| Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|AAY43398.1|) 9e-26

MERPSARQIHVLVVLPEQENDLVKTAFMDLVQVMVPHMLIMAPTTRTTRNNFFKHKLCKF

YKNYQRNGTWVRCMLLDVAFPKSLVIASHLFRRSNKYVADKLLKISNINDTRNGIVLF

>contig59034 Frame-1F

MNFYMRILVLTFVILFVSSSSSSPAITLS

>contig59180 Frame-0R|Blast-catalase [Phytophthora infestans T30-4](gb|EEY62821.1|) 7e-26

MAGRERLTDNIASSLVNASEPVQARAIENFTKCDPHYGRRVQEKIQEMTVQKENDKP

>contig59203-0 Frame-1F0

MASSQTSNTMTSATPSAVEDVFKNLKTTKTPSDSYHMPAVRAVHARVQS

>contig59203-1 Frame-1R1

MWYESLGVFVVLRFLNTSSTADGVADVIVLLVCEDAILFDVDEVELLL

>contig05599 Frame-1F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65627.1|) 5e-71

MFPNGISVRQGFEKAGGNDSFTYFNGMFINGSVSDKDLETAVKHASAHEFTVVVIGETHY

TEKPGDIDDLALPAGQVRYVEALAATGTKVITVYFGGRPRLLGSIVENSVAVINGMLPCE

LGGQALVEILYGDVNPSGKLPITYPK

>contig05670 Frame-1F|Blast-memo-like protein [Phytophthora infestans T30-4](gb|EEY63140.1|) 1e-71

MSMDVDEDEHSIEMHLPFIF

>contig06631 Frame-0R

MLSRRMGGEDLEVLTTGEVACELNDVEALLYSHTETEYNAGAGTFWGDQFIYGSLVHEVQ

FPDESPNFDPNWAEKGASRQIVRLTAEDQMAVRTASFAHSRTFARNEEWCFLDHFRPHLV

FPSPLSNSLVDASEESSGFSIVMTSLPESELLAGKMKKECVVQLHGIVAAYVVQRLPPTV

GCRDPRVRVSFHATFTASNNLPEGYADSSIVSSRLLSLAKSLHRLPTLVQQRKRSYSQST

IQCSYSSRSGQEQWETQVASSSRCVACTKRLRMKHLIAPTRRSKRCQICMYRACASCWSN

ESVETFGGHTTRMVVCRRCHENFGTREYAHIYVTLLRT

>contig08567 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62186.1|) 1e-102

MSVYTKFAIIGAGGVGSVVVDELLKKGGAVSVAILTRDESKSELQAFKARGATLHQVAYD

DVSAVTKALSGNEVVISTVAAYNIDVQKLIIPAAKAAGIHLFVPAEYGVTVTEGPNVVKK

EVQDLLTQHEIPFTIFYTGLFSEYVPAFFGLNVEEGVMTVVGKGENPFSITPRTDVGRFV

AHVVSTALKTELCGAKIPFEAGRLSPMQIRDLVEKKYKKTIEVRHIDFEENKKKMATDFG

AFLTTIFEEGRGVAGTEEEVKESVAKFFPDWHPTTFESSLA

>contig10153 Frame-1F|Blast-uroporphyrinogen decarboxylase, putative [Phytophthora infestans T30-4](gb|EEY57967.1|) 1e-29

MGEVTTTSLAIAVSAAAAAAFILHRQNEAKKHSIKQKLPFPMTRTPLVRVPLDDLPKLKN

DLLLRALRGDRTERVPVWCMRQAGR

>contig15789 Frame-2F

MSRHRNVRNRAYSYEDEDYDEYSDDVTSTSPTSNEFMYRRNSPSRQQSVFSFVHQEEIQE

HSDHQNPHDTALLDTLVPKIQEIVGSSFVISQIIHELRNTNYDVDKTVVALLENGATTSA

FDSSVRLEEVALGIENNETVTKKSMMPAPAKGKTMAIGQAMASFPKKSANVIKPLGSVTA

DTITGMPVVSRTRMQCTLAEKKAFERAELKTQNEATRVEEAARSEGKTKISMVVIGHVDA

GKSTITGHLLYQLGYVSQRLMHKYEKESREAGKSSFAYAWVMDADDEERARGVTMDVGTS

FFETSSKHVTLLDAPGHRDFIPKMIAGAAQADVAMLVVPAVTGEFEAAFEHSGQTKEHTL

LVRSLGVSQIIVAVNKMD

>contig16735 Frame-2R

METWPWWPALVTVRAPGSAQGSLNLRLEKRLLVDFLDTEEFTERCRCWVEKSKIAPLRQE

RKKVSGSIKNRKNIDKKFNSLELSTKLLASCDAGEDFPKFAEGTLPVQFNTNFTRQTAKL

RKEMG

>contig16740 Frame-2R

MGVHSVLPSHRLSCKSAVFLALSHLPKLIKSKRFVFGSFHCCKMNPISNCLVSLSFQSSP

>contig21144 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY66001.1|) 3e-65 NOT\_ORF

MCYVSPVPTLQKWFPDYRGTAAGFAVAGSGAGAVVWSKVYLPTIAAVGLSWMFVLLGEVM

STAMFLCVLVLRVPPSDFTVHGVDIHGQSVNRNNDIEDNPSTTYKICTTPTTAIHAATSS

SSTPPMYPFTLKQALWTPDFLFMYLMFFANQLFGVIVLSRLYSMCTD

>contig21614 Frame-1F

MRMLLTLEFAFLDKRIFHPTFSRTMINLLQLARSLTITRRDEADQN

>contig24190 Frame-1F

MASMRSPGQGGTISKRFNKARRRGNSQGEVISSGNTAFGGMSPGGSFDSNGRNTISFGKP

VLPSSPATTPGHHMNALKEDASGFVSSKTGFLTKRAMSSMDAFANWKERFFVLAEGHLSY

YKQGGGFFNTGKEDIVHLKGELELTVDTIVRKSTIDDKANCFEVVTPTKKMFCQASTAKE

MEDWVKSVRAHITALKKSQMRGSFHDAPPVNLAASNGPGGTAGTGAGLPSSILDTDYSRR

SMLEDHEIVRGADKSSDPKDVLIKQLLEENRTLREQLTMKDHVIHELETTGGRSIDVQSG

GAGKVRSTAPQMILDLRDVKKKQFQLFDAAEVGNWHLIATLLRDNVV

>contig24532 Frame-2R

MKAKGVTLSVMPSSRKRPRALDEVESEVENFRNVLKDFFIPPTTTNPS

>contig25041 Frame-0F

MIARLEIAGLRMCVKTLLRSRGAYPTVSHQYWVPRHATLTTMCCAIFILKEGWEQYTSSS

WNQEGRQTPNSWKMAPTVSCVSIQKRK

>contig25294 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68246.1|) 2e-93

MPSTAIALGVAQAVLQWFDTSFQCQKKIPLAEWTVLAGIVVSSPPTTTCSGDTFRVLAAA

TGNKCLGRCDLNAEGLVVNDCHAEVLARRAFLRYLYVEALIWQQNGQRSSEHSFFALHPI

SRRLVLKPHYSLHLFISEAPCGDAAIYELRESVVNEMVQQREAREIGQLDQRYRNKFRLT

GAKAQKNRLKEAQFQADIDTLLDSKSAQAVGRARIKSGRSDLPLEKQTLSMSCSDKVAKW

NALGLQGSLLLQWFEPVFLTSVVIIEDDRAMSIERQNMALYRAVCSRLIERSALVEGTQL

ICETSVVSVNPQFSRRRNFYFDRPSSCLAINWTTQEPHWTQAGEIRSPTDALKVACRAMD

AARFLHIFFNDFDLEFLMAASGFKQGAKKTSKMDIIAMEKVASRLAKRNLLRAFYHVQCQ

NFNLNSTFCLKYLRLKQMKKASVSPAKLSTSTAFTSDIARRKQFFGAFNDWVGVPATFKQ

FTL

>contig26703 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56097.1|) 2e-20

MCTLLEWSVSGSILAIVQANSSSLVLWEPTKIEQHQLVELPCKDISYLKWSTSPNSLM

>contig27465 Frame-2R

MIMKAVGRDSFCATLFRPRFLYRGRLYNFVARPFLERARQIHFPCAQRSRLLHSRKPYDT

RFVNVCLGTIRYLFF

>contig30007 Frame-1F|Blast-phosphatidyl inositol kinase (PIK-A) [Phytophthora infestans T30-4](gb|EEY59733.1|) 0.0

MANYFYWYLKVEAGDQTNDSDIFRTVLNKMLTEMKRDEEKKPIYDMLIAQRDFMSHILTI

HNKAREEKGRKDQKEEKLRQFLKQFPWPRGAVISLPLDPTVYLSGVVPSSAKMFKSAMYP

AVIQFQTVIPPTDQLHHTINGEGDSNHPTNLSQSIFGGSDMNIMRESLPTRMISYLHREK

EGPMYKFMVKNGDDLRQDQLIMQMFILMDRLLKKVNLDLKLTPYRILATGANDGLMEFVQ

DSYPVSYVVSHFESPQIIGFLRKHNPDITAEFGIAPEALSTYVKSVAGYCVLTYLLGIGD

RHLDNLMMKAEGHMFHIDFGFVFGADPKPYPPPFKLTKEMVEGMGGPTSEHYQRFTTYCC

QAYNWLRKSADLILNLLSLMADSGIEELSANPATTLLKVEEKFRLDLTDEQAEQFFLGLI

NDSVSALFPLLVDWIHKVATKLK

>contig31624 Frame-1F

MASSVVNALFGSYDLRNAKQWRNEDMIFREQEIQWLNDDIVRAHQWRLADTERFLRREKT

QSEHLVCEARAEQLSTVTEQATLLCGFIISAMCNVGVPDNVHAHVLFLYTVSGTAVCVAM

LICAVMCTNLLLAVTRYAAHTLEDSVRAMDLSQLEWKSPFSSWWLTRCEKEQMTAYKFML

FGVAAFFFYLGAVSWIQFYMSTGTSISITSLSFVGFLIWQLRIASKWRYLLTPPTFGMVR

GLEALDPNADVSPSYVSTPMTPDSSTRRKAMLDPTADASVNTTASILSRDTLKAVQGPRM

>contig32085 Frame-2F

MRNLYRNDFIHGSVVHVLPSTNGHKQTNPIELVPRHDTQVAVKTSVFLHSKRFALNEQWC

FLERAHVTTSDPTKQRHQSRSFTLTCSSMDDTELQGGKVKAYARVKLLHHLTIGFHFHEQ

RDPKCIRVTFFAQFHPQDVPNKTRFAQASQMRARVMRLAKGVTHLQESIRRRRFQAQPLA

TPNTFLAMNTHCTCCIKSLRVLTRKHQCHV

>contig33226 Frame-1R

MESDLHLLESAASASANFDAFAWIELALVSSPENFSALLPLVSQLDLRLQTLSQTMHASL

QHVSLSDQMLQMQIQEIQQAAVPLSRGINLMHEACTSDSASSATFAASRQDMHHLVLLHE

AKHRIQSCSQLLVETARWDRNVRACFSAVEDPTILSYFFKGNGAELKTRAIAFNGAKNLA

HRVREMQKSLDILEDLPGALDRRKTMERLCAQIEAAVIPRISTTLREDALDDKLPLQWCI

DVLDSVDRSHLVRAEFCRARPAYVHRIWYACSDKMQTEVDDELEKEHAFSNWLDTFYSKV

LHMLQQESCNIRELFGSDIQESVLAELLHNTLEPLTESFRDHLGLREPSGLSFGRLMHCF

QVTRAFGGQVVQLFRSVKNDCGNNRANTGDTAGRAESIIRDIFEPYRIYFKEYTHFTSEA

LVNTLLRLVPVFDVTNESHTQEGYDEEERNRAARPLKDFCQCLEEASRAACAMIEATLQQ

CCEFTGGAAFPEAVEAIGTAVQQFSMALRAKIPAIRKFCKAETALQEADSNSASEAFPLD

WSQFHASLAILKACGSLERQICALDGQVCVRMREQLAQNLGDVSKTLSPRDHRQQKNYSA

ANITLADLVDPTNLVAIVSKTWLYDEDPIRLERFYQFQMILLDYDSGSLASSTLYPSATL

LVEAQRAVHLWTKDVQLLTYDTVSLPIARILAKLPDNKNWRKVPDAALGDLPTFSLMPQD

YITLVADLLLSLLPQLEPLAESNGLKNIFVGSCGAQEICVQSDWTRLGQLLRLTPLELAA

CQHFFESAERSDISESVVTAAEFVDLWTAALASGALATLLRAICSIPMLSDAGAQHLAVD

LGYFHNVLSALGCDDNIIVDELRHALGMNLQTQIQHLNDLRAKRDSPANQALAKLNDCIA

AMRQRALEQSC

>contig33381 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69477.1|) 0.0

MFVRMGEIVEIADSTGNAIDDETSVAKGNKRSLTLKLDGKQYKSDLEAGHLGAYEQVNVL

IRLKPHKNNFKIVLDTIASVLRDANREELLPEWLHDLFLGYGDPAAAAYKSIYKSRAEKN

VAIPLGELLQDGDHALEAGGVEKLVNINDDTHELCSKDAMAPFTYVEDLRTGLSCIRAYD

RKSLLSSFQHFSPPLRYTKSQVAAVRTAQCEGLTLIVGPPGTGKTDVAVQLVLNLYRTTP

FREKILVVTSSEQALNDFFARILSYNVINEAEIVRMKQELPITAKTIDGHEKSDLNFAKL

TCEGRVAFLMERRAVLLAEVEQMAQWLLKRDATRYAGLAGGSASYSCENALIFYQFHMKP

ILDIATKATELTSKSDSVTAFLEFFTMRKRAVPDKIDALRQFVMDIESYFAELRRLQPIE

LLQKSRQRGEMYLVHHARIIAMTCTDAASNHCKIRKLGLAFGSLIIEEAAQVSELNSLVP

LLMACSSKVEPKANKAYESTRLKRVVLLGDPKQLPPVVRTMALKMYAHFDQSLFT

>contig33442 Frame-0F

MSLITSRVTPRQRNRRRGRSRSVMTLEKDKCLVTLRLLPDGTLRGTSREVVQPQACPLSG

SWQANRLAYVLEYRVREAVGHFRYTGAVIIESSDGNEAPSSTIDKQKNAQRRERLCGSWY

NVDDGHAVGYEGGRGKFELELVRVEFTPITVKIEQIEHALVDHGQSRPELDDDDDDVMNA

FTTGKYELSGCATDVDGYEYAFTLQLQLLPGGKLVGHCRERVFDQTSPVLGSWNPRRLTY

GQRYVVKHEVGRYTYTAEMSSHGAEIRGSWRNTEEEFAFAPSEHGTFALIILDSTRQWST

YSHAHYPPSFRRGVLMTLMASARTNALPVSLWISVFAFCSESWFHRQEMNI

>contig34083 Frame-0F

MAPSVGMEPHSAVSMAELEKPVNSVQDKWKLLPYFLQLRGLVKQHIDSFDYFTSVDIRNI

VRAQANNVVRSDADPKFFLQYTDIQLGAPSIDEEAFVSASVTPHQCRLRDRTYAAPVYVS

VRYRRGNKIVTNNKVLIGRIPIMLRSSRCVLAGKSEAALAKLKECPYDPGGYFIVRGVEK

VVLIHEQLSKNRVIIEEDSKHNVCASITSSTHERKSRTNIFLNKGRVYLKSNSFGSDIPI

VIVFRGMGMESDQEIVSLVGSESDICDAMSASFEEASDLKIFTQQQALELIGSKMNANIK

VGVASGRHRGGVSRPQNDRSLVDAARSALANLVLNHVPCENYNFRLKSIYVAHIVRRILF

TDKDRTRMDDKDYYGNKRLELAGQLLSLLFEDLFKRFNSDLKRQADMVLSKPNRASVFDI

LKCVRTDTITQGFYYALSTGNWTLKRFRMDRAGVTHVLSRLSYMSALGMMTRISSQFEKT

RKVSGPRSLQPSQWGMLCPADTPEGEACGLVKNLALLCHVTSDEEPAPIKRLCFDLGVTD

VSLSSGEEINHASNYLVMLNGVIIGTHVNPRAFVTRLRRIRRAGLIGEFVSVMIHDVQHV

VYIASDGGRVCRPLLLIDPLTHQTRLTQRHMDELRAGVRDLSSLIVEGCVEYVDVNEENN

CLVALHESEIGDRTTHLEIDPVTILGVVSGLIPYPHHNQSPRNTYQCAMGKQAIGTIAMN

QYERIDTLLYTMVYPQMPMVKTRVLDLVNFDCVPAGQNAIVAVMSYSGYDIEDAIVLNKA

SLDRGFGRCMVFKKYQTMIKKYANGSYDRIVGPPDFDSVATSSGTGMGFRTAKYSSLDAD

GISRVGGIVQNGAIMVNKEQPTQFNDSVDGRDPLDVTFSPSPTTYKGPIPAYVDKVLLTS

SEANHFLVKVLIRQTRRPEIGDKFSSRHGQKGVCGTIRNQEDMPFNDQGVCPDLIMNPHG

FPSRMTVGKMIELIAGKAGVLTGRRAYGTAFGEKYGSADNVLDCSRELVRNGFNYAGKDY

ITSGITGEPIECYIFMGPIYYQKLKHMVMDKMHARARGPRAVLTRQPTEGRSRDGGLRLG

EMERDCLIGYGASMLLMERLMLSSDAFSADVCQGCRMLGYEGWCQHCKSEEKVVSIRIPY

ACKLLFQELQAMNIVPRLTLKEY

>contig34209 Frame-0F

MISKVKPIPLFYLVLLLSYRAVTSFKMAASIKATPLSKDSLDNLRQGSHDVAPPLRNNFL

YSFGQDFLVVATASGKSSVDNLRQDSRVIEERNDEFMKLEDIVKTVAKTFKSKGTNG

>contig34450 Frame-0R|Blast-ribosomal protein L18 [Phytophthora infestans]gb|EEY64878.1| 60S ribosomal protein L18a [Phytophthora infestans T30-4](gb|AAY43426.1|) 5e-56

MYKEYRDLTLCKAVEQMYSELAGRHRARPRSIQIMRTAIVAAKDTQKQNVQQFHDSKISF

PLPHCLPRAAEKHHKTVFKASRPCTFRG

>contig34968 Frame-0R

MPITKVSPVSPPGMSASTKLNDPPIPPSASIPVVEPIKPPVSTIGANHDKPPVS

>contig35585 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60019.1|) 1e-137

MFASRTTYCLLDYECILVNDWDEDADQTPMYVRTMQSCYSPQCQSWLEEVGSKPTDLQPA

GFMVRQARDHEGYVEIQLVASILEKAQLPMASRRAKLRALCAKIARLEEVLTSRRLSQSL

LVNAPHWVHNRERLGCRICDARFGISRRRHHCRLCGEICCSDCCPKMDVALPDVGSTSVR

VCIGCVQKRRKSCESAASSSIASTRVSFLSPKKEATSISPPIPSHPALRSASSSSSDYYS

SSSSILSSATSSFTSASSLGERKPSLASSISRR

>contig35967 Frame-1R

MMKGATNVLFGGEGVFVTTLTGPGKIYLQSLPFDRVVGEMAARIPRGGTGGMMFPFMMGN

NGSDKDASASGSGDQAAAETIDVDSEGAAEAVGDEIYNGSSSKTDLSSWSESAAVDSGEA

EGSSDGNFMSIFKRFFGDSDE

>contig37187 Frame-2R

MVHWGTVFVTVTASSFLLGRRELPKIGRFVGLYVGRSVGAILRAKKEFFDATSDNNLVKL

QREFQRGIEELNEIRSELTSVGSMRRPFKPQSGVTTTTTEPLSTVTVSERQQIPLPAGGR

SSVSLASTAEYAMQDGLQNGDEVGLAMAELKLVEQGKFVSRVENQEGGADYVSASILDSL

LLNQRKKTDATS

>contig37877 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63751.1|) 6e-27

MGRGILKDAHSLGSAVPSFDTHPTPINVSVLHKSQQVMREPTREPVTATTVESVGCGCFI

C

>contig38278 Frame-1F|Blast-GPI-anchored leucine-rich lipoprotein [Phytophthora infestans T30-4](gb|EEY62321.1|) 3e-22

MYDRDQRFYYQLQQDGITGHPFTNLVSGEDFYSKMMAMIDVYKNVSKDISTFYVNNSQHV

F

>contig38560 Frame-2F|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY57167.1|) 2e-25

MVYIHKSHSTNKKPIYTMQARMKAPYSYYELEKGQGTPFTKYKVRKDHVAVSVRDNKAIR

IGLSLCIWYFFSTSATFTNRIIDQGAPCVC

>contig39220 Frame-2R

MHFMHELRLGDDMIALPATFRSNYFVLNLQSFSPVCVRWFLFRILHGSRIGAHRLENRCC

GTFTSWLKSL

>contig39255 Frame-0F

MAPVVPAMRELVDQPLKELSKLYENSLKAMLVCGLEFYLSASMVASFFQCPDENMDADQE

LQTLYTLAWVPMVLSITLVYGPKTSLSFFPSPEHFERNMLRCKIFTWMYAFVLLIWDPDM

VFKTGPSLGVSILFCITDLGRFIMDMKHLTSVEYDENGNSFIIKDKTTEQGQGLRNIQQH

FQQPQQKQNQSYTTHSIEISA

>contig41209 Frame-0F

MHNLVLLQRRIWALEASSASFDQCVASASISGDDHVFFLRCSGCIESLHLDEEDVHCQSK

DLAFKLDLRQCIELNDTVGPSWKWMNYVAELGALVCASTRGALVSVDLDTMEGEEVGCVD

SGLRAVAWSDNQEVVALITGAGSLLVMGNDWKILYEVEINAFLPSGSELWICEPYDNKWL

CELCWRDDSAFVALNIATNIQGEDRMEQKLMTFTAQLEFHALGRHEDGRALSTLGKALDW

SQRLALIASSEVRKGRWHVVFFEANGLRHGEFSTPASYCSPEYEVGVVRWNLSSDILAVS

LHGSENGDDSSRLSKIQLWSRNNYHWFLKQELTLKSNDGLVSLAWDEEKSGRLNIVACSF

RTQALTLYEYEFAWDCCCLEAERLQSSALRDGEALSHSSVAVTAVIDGAQLLLTPLHQAI

VPPPFALHETTFDAAINSVAFDAQGSVLLVLLATGDVILVNQYLVSDASASFAGLPPAIK

TSAHTRHVDALMQKVPVKLLGNMTEDPFCTLSSILWIHFDAVSGRLDFAGKTGRRDHLVL

CTSRGSTTITDDEIVVSVRLIELFGVRRACEVLWIHDEAGETIADKTFTKVAIQTHSGAM

YTLNVFTDDEVVPIREGLKLPTFSHMTVLASLSTTSSTDGSILVIGHEGSSARLYVNNQV

LASACTSFKYSLPSSVLLFTTQGRESRLCIASLSSIQRFVSSPMAMIKFESRSIERGALL

VAIVNCRASVIVEMPRGNLECMSPRVLVLALVIQHIQAREYVMALEICRRHRLDLNLLVD

FNPQGFLEMVSQRLVHSLLVTRPATVTSDRLCLFITSLHVVDVWTTKYAATMDSFAVKQS

PTTENKLKSAIGDAKVNTVCQEVMRVIHDVTRDGNDPEAALLLPYITSAVKQSPPRFDEA

LGPIQLLLSQA

>contig41425 Frame-2F

MRSDNLVFRKGVSWGGAGYFLLTN

>contig41591 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64094.1|) 9e-37

MTEEELQEVADGFFLAAEYGRSDVIKALVDHARGQLSLSNVIDPVTGRSPVHVAVASGKK

DALRVLLAAGFPPDHQSNQLDENDHTNRSAYILAQKLNAHALLQVF

>contig41872 Frame-2F|Blast-alkylated DNA repair protein alkB 8 [Phytophthora infestans T30-4](gb|EEY61697.1|) 0.0

MSTCQDFQLTDFVADDQPSRFLKLTMSRRIHEVAIAKSRLVPFLLQLLQSASVSILNTSE

PGSIIRRVLYGTGSRRVVLLCMTDVSNAQRLRFLLHQKPCELLNQRPMYVDFAIPRKEQE

ARDRLLKVQDVRRNAGPSALRVPGLCIVENFITEAQADACLALFERENGIHWANSIRARQ

VQHFGYVFNYDTRRCDPNEPINEPIPEVLLPILEKIAEYGIMDGERPDQITVNEYLPGQG

IAFHVDTHSAFTTTVASLSLCSEVVMDFRHSDGVRSEGILLPVRSLAVMSGPSRYMWEHA

IVPRTFDVIDGEQVPRQRRVSITFRKIRSGPCECSFPNQCDTPDCREQASIKNGEENSII

LESTSRAPTEMEQQYVHDFYETVAAHFSSTRHSPWPKVVQFVKALPKGSFIADIGCGNGK

YLTCIDPTHSFGVGGDRSSRLVSICGGRGLEAMVADALAVPLRSQSCDAVLSIAVLHHLS

TLGHRQAAINELLRILRIGGRGIIYAWAHEQMKGSRRRFKEGQQDFMVPWNLDKRFAFPT

EDGFVDAKKYQKCSSETKNTSFIDKSGSKTTAKLEKRLVVQRYCHMFKQGELETLVKCAK

NAMVEATYYDDSNWAIIFRRVS

>contig42187 Frame-0F

MDAFHNLLREATHPRNAGSTGSSSMPTSVSLTQALQNAGGGHGMGMTLPLSMPGLQAGGA

NGLAPIHSGRMNSLMTVNTGLIPSLGGTGTPTSIMATSGAPAASNTPVTAAPMPEKKKTI

TKKRKTPSSNADAESGEEGRKQPEEYEDPKAKRRAQIAKAARKHRQRQKDELIALRAKVK

DLKEQIEVLQSSEPSEHNTELGWKQEAEQHAEIRARVDQENDFLRKTLMEQMKFIQRLQD

YFTKQPLLNMPSLDMILNSSSSGATSPTALSNTISSVSPVLQLQAGSFRDRLIDMATEAM

TNSDKQLTACETAFRNPKTSTMTYFGLQVQYEMGKNEMGIFFRHHLYGCNSIAVMNDLWS

VLGDYTFEKGFAFTDVAEILEEVDFNTRYIRRVINLTMSNDAAFGGGMMKEESLTINRQC

NHPDGSATLVSRSVLDDPSHPKSVDYIRRNATTTASLKNFSDSTGQGCLLLWSVKVELDK

KPDECAKSFNNTDIILKNLFEVAPVFVKGIVDRARGSIPQR

>contig42590 Frame-2F

MPIPNSSKAIQALQLMHPSWPRTALLCQLVLKVFGLPPSNLALIDGSPWLCCHIYKLALS

DHRTHKQYRLSGRVQGG

>contig42716 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61820.1|) 2e-77

MVTGERLAKMLKSIPSEILWKSFKSIPSLHKTKNNDKLNPRVQNAILKRAVEENDIFLAE

RIVDEGTHQMKILPNSMTYALMLRLYSSQEDQVNFYAWWCRMEQANVKPTLYVFRALMRH

LSYLSIIRDSVTSLNTFAVFLEQRQCRNEIEGAKNNESTKDFAARLGQGVLDKMSSRRMR

PDAICLQNYLLLSQESDHVARALDNVEDAISARLENGIQSVEDCVDLTPRLLHTLFTALA

GFPDG

>contig43337 Frame-2R

MCFSVPKSVPKSEIPGYLRGLSQGPVSSRDPGEDRRRYNIARQAVRNCQWGTFNFKTLET

ATVPIWKKDEIAYMNTRS

>contig43382 Frame-1F|Blast-cellulose synthase 2 [Plasmopara viticola](gb|ADD84671.1|) 0.0

MYDRVCDPSEEMEVYAWRKLHSSANLPSPSRVKVVNRADCAVGSFRDDYRYPGLPHVTFI

GRVKPETHYSKAGNINNCLYNEGANGRYLIILDTDMQPHPKFILATLPFFFDDEDRQDKA

KYICCGIGCNSVAKLCCASCQIAGVPEEQISYCSKDCFENAMHVQSAVHRRQVNGTMSNT

QASKIDMRCMNCDTKLPKSGVCRKCGNKGNGDGEDVSSLNAYSDDVRDNAVAFVQTPQYF

RDCIQLQIGDPMGHRNATFYDAIQTGQDGYDCASFAGTNAIFRREALDSIGGIQYGSLTE

DCYTGQVLCTMGWKAQYFRKDFEGEPSERIRLAEGLIPDSVAGSLAQRKRWAKGNFQIAL

MNKKTQYFDPEWKLPEVQTPTCHKPNGLMRRVFYFNSTLYPLGSITAILFYYITIYFLFS

GYAPIYMAGVRLVYALVPKLLVQGVLSALSNRTVENSDVIRSQEVWFAYAFTNCSAVLEA

FWWKITGKEPKWFNTGGASRGSIAELPNVIIFFGTVVGVLWSVVRFLAGFNSIQTSHGAS

LLFASLMMGLFLAVKLAPSVRMSIQEYFGWSYESLTDQGNVLGSISIAFGLVFITLWVWI

EQPTSNPF

>contig43764 Frame-1F

MMQCSQAGTVELQPPKIAYIFKLWNKLSLSTVNQKVTTATGPEAAMWQVKFHCAEYNYGA

FEHPSA

>contig44624 Frame-0R

MMNVSKAFLARVLQMEEIFTNVSGTFANESYKTRLPGLIHDCVAHNRRRFSEDECKRLLQ

LASDMAADAVILLPSQYPEQIAKSPLSDQWENLLKGKGYTWQNSPWFLSEQYMFHLILLL

AEYYTTGIDPFHSIKIAELKDNTPWRLLQTAVDLDVAKRSDDHLKRLMK

>contig45007 Frame-0F

MTPPVRKKPRFIAKRTSNYYTPSSTV

>contig45757 Frame-2F

MIDDVAVFEKVAKKSWQSFSTMRRFVDEAVRLENASWRLWFIKGTHVASSTDSSDEFVSE

DDGASAKELRPVCVYCELHRASLRCNGCCHDAYCVSCFKFIHKKGNLATHTAERIQFNER

LEVIHNCVPSIVDEGDLSTKSHRKSSEGDTETSSGGSSTPQNAKESLLNKPWELQMDMLL

QRLMSNSLYSNKNISVHNIDNRVSLLHLDTLDSNVATFEIEKQ

>contig46226 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54340.1|) 1e-123

MDRVQPYLQCLVSLLKKNEKHESDESTMERDRRWMSFEDYTQATSYTCDDVLIDSVEVEE

PKVCISTLESSLHVESTLISEYLLRDFRPVAAPKPVDYVIICPHSPSQWLASLALSYFTC

FRSMYGQCHMGDLAPINLSNVEKNHYANVDVANGLLLVNCAKSMVDPFANFRAAGKVLSP

VMSSGAIKKKQAFSRSAVANVVFIVAPFRRSDVKHRMWVLGAFSSGLFGSESTFEASEWR

QSVTIEMVYLEDLYEVDVNPSPFVLMPSCFGLYNRVCENIRL

>contig46381 Frame-0R|Blast-imidazoleglycerol-phosphate dehydratase [Phytophthora infestans T30-4](gb|EEY58663.1|) 1e-87

MGFPVQAILLDMDGVLAEVSQSYRQAIIATAHHFGVSVTHEDIDRHKLLGDANNDWLLTH

RLVLDGLRATSATPTLEAITTQFEALYQGVDSTPGLCELETLLISKGLLAELDRRLPKGM

AVVTGRPRKDCEKFLKTYQIDHLFPVQICMEDCPPKPSPKPLLLALKALGVEAHHAVMIG

DTVDDIVAACKAGTIAYGVLTPQ

>contig48268 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54440.1|) 2e-30

MVQETDVLIDDLPGLDKTEAEQMEELRRLQIQSEEEAQTLRQVAEEAERWIGRARDSLRV

ISETCLRR

>contig48909 Frame-1F

MLAKHQKVHTGSCVHTCSIDGCGKTFSTAGNLTRHVKTQHRAVLLLANSRQRLQPKPSEM

EASIRMNQLLYEEFPVLDYSAMMFLSPIEEPMQQASFLDTPTILSDQDVKDLLECLF

>contig51042 Frame-1R

MYRDARGGKKGGTWIVWNPHAMLPLYRVELTKTNREKVMLCLPKSSQLSVQPRQVFFKKP

SGVSKEDHEILATKAATVISDADIHKLRDLVATVSPYFEKLNVWHTWEGQTLSTGAVEAI

PQRTEKTLASKLCFVPMSLANSAQQRAKEPFGGYKYVQLLQSQGKLKEDGDLFIALELLT

VRKQDVSESRSKLESYVTRVCGQEGGYAHPLVIVAIARLAARLSKTPASEIQRQLLEIFS

K

>contig51781 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53609.1|) 4e-50

MQRFCWRDRSEKLNWSLLRDLDVIDVMQQGNPAILEPYALHITFARLPSTSRNPKTRDAW

FLVHILQLAMEYLLSARAGDSDMLKSLHQELRLLEQERNKIILSLQKWKVRALSCDKQVE

KLRQVLKNIAKLLQIHG

>contig52520 Frame-2F

MGNTLEEFHRTRPMNVFSWPELARQVCQMAMEFKHPSADDHLLKSIKGLKSYRDDAVTHL

LRKKLHRRGIKLLEGVAYDEENEDATANDSHRLSSYSLASEGSILPSDHYGAVLVGGVLR

NFTVVEKHHHLVVSEIVAPHDISLAVTEDLSQCVTSEAKDENADRIKVGDYLIFMNGKDV

RKVSLDDFKVLASELPTPHGLL

>contig52836 Frame-2R

MPVLNSTSDQRSSAIIVCCIYRIWYRSLDISCCIEKDS

>contig53633 Frame-1F

MLFFCPMYLEPADAAAADCCESLHSVPYPAASSEYFDPTRLAMHIHSTVTNGLSATKNSY

SSSAVDAT

>contig54333 Frame-2F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY64164.1|) 9e-42

MLIPYVHKNYRQKHGAGFNGSSKFSASLPAYIADVYNEEQEYELVERFNINVIIRMSTLS

LDATLTRFYIHADLPALTFNLSHEKYRQLVALADRFSLANANALKYSRKSENGDNYPAEV

AFADVDCVL

>contig55059 Frame-2R

MSSQDLAQTVLLMLLESQHQRDLERDQEREERRLERQRWHDEMHEQRCRYEQERIEDRRR

NDQFMQVMTTLVGQIAAGQQRSGLN

>contig55330 Frame-2F|Blast-diphthamide biosynthesis protein, putative [Phytophthora infestans T30-4](gb|EEY63922.1|) 6e-23

MTVALAFESDDGSRAIAAQVHVEDSDGVRQDQCDISIYYDIARTVDQIRWGGYTKIALQF

PDSLLPDA

>contig55406 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63802.1|) 7e-15

MASLFGSLPSAAVRNHGRSTALLSATDNCSDRTLRWIDDEETSNCMHCNTSFTI

>contig56595 Frame-0R

MPEQEGTNSTRIPFNNPRNPPSAPGRTYSNGSDYSSQQSWQAPSNVPPASASAEYQSTDP

HTAAPLINSATALPFSHPLYAMDDDGMIHLKATGKGLDDSDLAVHQDEIINTVVKYVHDS

MKKELGFQEVYLPASSTIETSVKANLFVSPNYASCKKLLVFVAVSRGLYPGLWSRGLVLH

AGIKSGSMLEYFRKAMKEEYGIIVANPNKNVIVVRDGKQRVPIPGSSSPEEHMDSLWDTY

ITRSSARRVYFLGYSYGGVLIKYLLQSRGDQLMRRNGAIALIESSHRIEDGDSQSVKSIL

AHRTMYWESNDGLFQTKLNGDAPHRTGCTCLSAGRPPRMHANHYYVTAFCINQIQDALFR

FLETRDATTYVVEEIPRIDTPVAIPGSTTNGSTSTLPTNMPVFQRQDSSRREATNSKMTL

SEKHCNLCLFHFTLFDRRHHCRMCHRAVCNACSRDRLFLPGSSTAQRVCTECATEGPRVT

APVPPHSTYPRLQRTASDAVNMTNNSSNMSQARTRSDTQMSNQGRSESNAHSSQNSKLSV

EDFDLLKVIGKGAFGKVMLVRKKVPDSSCHVNAIYAMKVLKKASVFAKNQVEHTKSERRI

LRDIDHPFVVRLRYAFQNDDKLYLVMDYYNGGSLFFHLRKSRKFSEKRARFYAAQLLLSM

SHLHELNIAYRDLKLENILMDEHGFIALTDFGLSKENVDVPDGAKTFCGTAEYIAPELLK

GLPYGKAVDWWGFGTLLYEMMTGQTPFFDRNRKRMFHNILHRDVVFTQAFSEDAKELLTG

LLRRDPAKRLGSGPSGVQEIMDHPFFASIDFDKLLKREMEPPFKPVVNSEADTGNVANIF

TREMARDSPVTQELGATHRAQAHFDGFTYMPGNEHLN

>contig56601 Frame-0R

MFKLNPLSNSLRDADIPRCLEQIFRDLKLDEFKDDLFALPEYAFFARLTRSLEQRGVSYL

FIRDKLVKQFSREKYDQLVFNALTNPLDHPTFRRAAELEFESWHWQRIQPSETELLKKLS

TSEELLE

>contig57066 Frame-1R|Blast-transcription initiation factor TFIID subunit, putative [Phytophthora infestans T30-4](gb|EEY53960.1|) 3e-31

MQYQRIRSQATSSTSTIASLAAPSSTQSPDGDASRGSRPVLTMEDLAASLKEYGVNICRP

QYISDVAIDPMD

>contig57668 Frame-1F|Blast-predicted protein [Phaeodactylum tricornutum CCAP 1055/1]gb|ACI65571.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1](ref|XP\_002186101.1|) 3e-11

MNVIDAEYQFDRHKLTFFFEAD

>contig09473 Frame-1R

MASSLCMILVVRIIPMSSKKKLRSGQTNASQI

>contig12042 Frame-2F|Blast-actin-related protein 2/3 complex subunit, putative [Phytophthora infestans T30-4](gb|EEY61531.1|) 1e-131

MLFLESENKIIKEVLTGRLGEKAPRPVQPLEIRLCDFDDVQYDMSIADNILTISMAYPPY

TTLEGLGAKQMFAVTYPEFQIVAPKTGFDLSLQVNVDVITPTNAVSFIERLSVIKRNILA

APFEQCFAALQSGNASTLGAVQIPFRRNETVYVLPQADRIVIVCSVCFDDKTDQAIARVF

LQEFVDTRRTVNNAPPVAFGRDPPLELRGAPGLCQSPDLVGYLSLAIFPTHVDTAEKRIK

AATLVQGLRNYLHYHIKASKTYLHIRMRKRVDLLLQ

>contig12789 Frame-1F

MLTRLHLPSDRVSLQFRGRRCKVSQAVRFFSTANLRGINSKKSGDDELTNSKLWEKVLSN

HPEHVEEKGGDLLYEYPRKSYFGYMSAGSLAHIAFWSWLKGYEQSLVE

>contig15788 Frame-1R|Blast-glutaredoxin, putative [Phytophthora infestans T30-4](gb|EEY55395.1|) 1e-133 NOT\_ORF

MTAVTGSVVSVQSVAQFDEATARESTLSVSFFWADFHEACRPNGQLDVVVRQLATLHPRL

HFLKVAAEELPELSERFQIAVVPTFVILQGHTVLEKLEGANVAELAKRVDVLSKNVAKQN

AFSTSTDDTISKPTDEARQYRLNRLINASPVMLFMKGTPTEPKCGFSRQIVALLDDEKIQ

YGTFDILTDEDVRQGLKDLSQWATFPQLYIHGSFVGGLDILQERKSKGLLIEQLGLLQTV

EEATATVEANLRDLVASAPVLLFMKGSPSNPKCGFSKSTVKLLRDHQIAFSSFDILSDEQ

VRQG\*KSFSSGQRIPNCTLMAN

>contig16741 Frame-1F

MGVHLMLQSHRPLCKFAVFLALSHLPKLIKSKRFILGSFHCCKMNPISNCLVSLS

>contig17452 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66164.1|) 5e-67

MNATAPALIPPFRFSTMQQGLYRGAYPTLKNFRFLRRLGLNTVVSVIPEPPTSDLADFCA

NEKITLIHFYAEKFTSDNVTVLPATAAQILNLLIQKKNLPLYIHCLDGANVTGTIVMILR

KLQNWTKLATVSEFCR

>contig19911 Frame-1F

MHVVTSDFRTLSHRASSDHVYGIGEAFLATFSLGFTEGCLHIQRRPIPLRFALWYAAANV

LPSVVWRSVPVHHVAAATGIPVSSLVNEIALASSRSVAVGHQLVLCQSIRAMRLAAGSYG

LAWGLWHYWHEHATNKIREDTIFSTFREKVVRVASVDSPLSRVSKQNHGNHIFTMSAKHR

DAAVDWETFGLLVRNAELNKRVKVVEVELSALENGLSDAEVVKDMVSMVKGEEICSVAVL

PGGGPIVPLSVVESFDVCFNPLSAVLKFIASICNERKIFHIILVSSRMEKFPFSTSQVAI

GLLHRHGITTSQWTLEDIKDDESFICEEVASQSAKHVFYFSSSSKNGHLMAQKMQELGHL

RPENEYFIVEERFNDEIALSHL

>contig20520 Frame-0F

MPCVELPPPSAYLQSPTKSVVVAVPLRSTIDVTTPTPSMTSNLTSPTSSSSNEPSPQAAD

VNFKSLKDAELAPDQDPAQQQENDSVSDDDDVEELKEALLRRSTGSIAIMSRQQEALDYR

RHTFTTMSADSRASMRRRSYDFTAQFGNTFPPLTPPRPLLPSLKAHQHFRLYGKTTGPVK

IISECHEQGSPMVAFVSPNPTSVWTRGKPVVIQWNKLDIKIETLCIELLEDGLNATTLIA

KEAPNTGSYTYPKVPWGMESGSKYFLRIAATEDKERYCTSSFFQISSAP

>contig20753 Frame-1R|Blast-26S proteasome non-ATPase regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY58751.1|) 1e-162

MPLESTMICLDNSEWMRNGDYIPSRLEAQHDAANLLCGTKTQANPESTVGVLAMAGKSVQ

VLASPTDNMGSLLSAIHRIKIGGSTQLSNSIQVAQLALKHRRNKTGGQRVVVFIGSPIGE

DEKQLTKIGKLLKKNNIALDVVSMGDLDANSAKLQAFVDAASSNNNSHLVTVPAGVLPSD

VLVSSPVLHGDDGAADAVASSGGGGNESFAEYGGVDPSMDPELALALRVSMEEERARQEA

AQKRAAEAEAASATASTTSLAPEQSMGLAKLTTEIPANHMQFTQNPVPAVAAASLSPSSS

SPPPARDSTLPFMDPKFVNSLLSGLPGVDPNDPKILAAMAQMTKKDEKKDEGEEKKEDQ

>contig21145 Frame-2F

MISSSHLGSAIGETSASLCRALCVRSGNVVALGMQKAAVLNCAGMTLFRVFQGNVEVLGF

RPPMGVYFSLQSPKWNNLLVIEGRSGSEETQAPFGPSNATLLQIMEPNLPAEYANEDEEM

AADTLAMQLVNNFPIVIILRSIPVTYGNVSCFYENARPHKSMAVLPGFKLIVLKANQHLL

SDLTSGANPASVAPLGTDPSHHDWKSPERVLAELLVVDAFKTL

>contig23925 Frame-1F

MTFQPPKLVGCLILWTRDNGCLEPFQYIRMNLPLTRRIRLESFKTIGAGIILSK

>contig24894 Frame-2F|Blast-ubiquinone biosynthesis protein COQ9 [Phytophthora infestans T30-4](gb|EEY57962.1|) 2e-08

MASKVFIKRSARLATTVSCKRNIKSFTSLLGSDPLSKKVPNASQIRLQTTHTTGDKGEAP

HQASPGDPEQRILAKAMDNVLVH

>contig25040 Frame-1F

MWLHDEAGHGKEVERKKAGWKIDAAVQSRLHCVVECPYPALMHYQTAKKLIVMAILEMDQ

APLCPISPFPKCFRLRWDGTQWQRR

>contig26805 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61492.1|) 5e-94

MNHFRGINMHTFGPLVTRRVQATSESLAVARDSCNELMAEITQVEAEKHPIEHHGLIWIA

TVLSLTSSCWALAFCGFDNYTSSRLVAVCFGPFGALIRWCLSLQNRKPMYTRFPLFTFLP

NVVASCLSCVMAIIGSIVLQDGDAAYRAFIMWGQGGVMVGFLGSLSTVSTWVYELEDLSS

KRLYWAYRYGVVSVVVSQLASVFILGLYVTYGSHPLRI

>contig27378 Frame-0R|Blast-hydroxyacylglutathione hydrolase [Phytophthora infestans T30-4](gb|EEY59814.1|) 1e-101

MILTTHSHWDHAGGNKNLVDLIAKNEHRSIKVVGGPIQAVEAQTQTVTDGDVLKVGNLDV

QVYYTPCHTRDHVLYHCQDALFTGDTLFIAGCGRFFSGSPKEMHHALNKVVAKLPNATKI

YCGHEYTASNLRFAVHVEPTNKAAKEKLVWAIEKTRGGEPTVPSTIKEELATNPFMRVTE

RTVQTFAKGENDPVKVMEFLRAAKDKFKIGK

>contig27842 Frame-0R

MIGTSFYLVAEVPWAIVLYAYIVMLYTWAFSLLDSARDAPFARRIGRSETSLALRLGFQW

TFQCFLLLVVSFYGVVLVAGIVMGHLGNILLVATVVKVKTISEDFRLERLNHLPGQFAKL

GVVLGFGFITSILTG

>contig28645 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56830.1|) 1e-76

MEDTLQNHVMWRHVGDATMAKARDGIEKYVMDKVSDIALNQLEECQQWRKEDEKLLRRMQ

ILSFVTPAMLDIKPCLRNEVVWSMAEDELRRINSFRSPGDKINCIVRCCNVIFSGLNLAR

GDSMSRPGADDFLPLFIYIVLHSRINRLHANCEYISAYRNQADLMSKAGYCFVNLKSAIE

FIMMMDGSMLTISHDEFQRLYTEQEKLLFSS

>contig29303 Frame-2R|Blast-hypothetical protein PITG\_06381 [Phytophthora infestans T30-4](gb|EEY69865.1|) 2e-42

MAGRVIQSAAQRWLGDKGTWPVLVTCVAAAGLCTAQCVRYLAGHPDVNWNKQNRQDIFRY

KEEKGADWQSHRRKIATLHKNAINEAKGLNK

>contig29484 Frame-0R

MTIMGRLGKMAFILTNLREAPWRKKYFFITSSYASWIATL

>contig29570 Frame-2F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 0.0

MAQEKETNRLIHAANAPIFGVDRDGLVNIWNLKAADITQYSAEEVMGEDLINRFVAEERR

ATVKLELQRAFEGEQTNNFDIPLITKTGRRVEILLNATPRYDELGHIFGVVGIGQDITER

IAQEQELIRLIDTANAPIFGVDSEGRVDIWNKKAAEIMQYPTDAVMGEHLVEKFITNDYQ

EAVSYVLSEALNGVETANFEFPLITKTGRRVEILLNATPRYNEHGAVIGMVGIGQDITDR

IAQEQEYMRLIDTANAPIFGVDSDGHVNIWNRKAADITQYTNEDVLGKDLVAEFISKEYK

IPVRCVLEKAFEGVETANFEFPLITKSGRRVEILLNATPRYNEQGEVMGMVGIGQDITDR

IAQEKEYMRLIDTANAPIFGVDSSGLVNIWNRKAADIMQYTTEDVLGKDLVAEFISEEYK

VPVRSVLEKAFKSVETANFEFPLITKAGRRVEILLNATPRFNEQGEVMGMVGIGQDITDR

IAQEQEYSRLIDTANAPIFGVDANMCVNILNNKAAQITNYSFEEVIGEKYVETFIAPEYQ

AIVYGIMSKALHGDETASFEVPVITKNGRKLNILLNATARFDQHGHIVGVVGIGQDITDR

IAQEEEYARLIDTANAPIFGVDANGLVNIWNKKAAEITQYTPNDVMGENLVEEFITEDYR

EAVGLVLSKALEGVETANFEFPLMTKSGWRVEILLNATPRNNEHGEVIGMVGIGQDITDR

IAQEKEYMRLIDTANAPIFGVDSNGLVNIWNRKAADITQYTTENVLGKDLVAKFISEEYR

VAVRCVLEKAFEGIETANFEFPLITKAGRRVEILLNATPRYNEQGEVMGMVGIGQDITDR

IAQEQEYSRLIDTANAPIFGIDANMCVNILNNKAAQITNYAEEEVLGEKYVETFIAPEYQ

AIVYEIMSNALQGNETASFEVPVITKTGRKLNILLNATARFDQHGEIVGVVGIGQDITDR

IAQEQEYARLIDSANAPIFGVDSNGLVNIWNKKAAEITQHTPADVMGENLVEKFITEDYR

DAVSLVLSKALGGVETANFEFPLMTKAERRVEILLNATSRFNEHGEVIGMVGIGQDITDR

IAQEQEYSRLIDTANAPIFGVDSNGRVNIWNRKAADIMQYANGDVLGKDLVAEFISEEYK

VPVRSVLEKAFEGVETANFEFPLITKAGRRVEILLNATPRYNEHGEVKGMVGIGQDITER

IAQEQEYSRLIDTANAPIFGVDVNLCVNIWNRKAAHITNYAIDEVMGENLVETFISPEFR

PVVAEVLSQALRGVETANFEFPLITRPGTRIEILLNATPRYDTNGNIVGVVGIGQDITDR

IAQEHEYFRLIDTANAPIFGIDTNGCINEWNQKIEEITGYHKSSVLGLSLVHTFIIPESR

QQVRQLLNQALIGIDVGEMELPMTTKRGAFLLLLVNASSKKDMHGNIRGVIGVGQDYTAR

KHMEAAKVNFLASFSHELRTPLNGVLGMLELLKEQSLDKAPERYVHMAYVSGSLLLNLIN

DILDLSKIEAGHLELSAAPFQMHELLDYSIEIFKFKARERGLKLELKCDDNVPKVAIGDV

VRLRQVLLNLLSNAIKFTNEGSITVTCSVVYTPELPKAFKKLLFQVIDTGIGMD

>contig30006 Frame-0F

MENPYDSAENLDQYASAAGLMQLRSAVAVANAANCEASDSISNDICSYSNSCDSSTVFSS

SDRTLPPDWHRIIHDSGLPCYVHEKLRIVCWTRPYPLNLSGHVTLSQKDLDRFVKQHVPP

VSIFTSESDVADRKRNYYPGANDIVLKKSLPPFQEARCLKKRKLDVATNVKKKIDKQQAL

TLEEFKTLDIGDPRVLQACMELSVKTPAQVLQEYQNRNRGVSINYNTISVDGEGVKLFKT

IVTAGSTVAEGVASTKKIAKQLGAQQLLAALHERTANKYHEVADMYNSSLKGQSVISEEY

VNRTAIPLVISGRSGRTGNVDPRLQRGGGVLYRGRRARRSPPFQESGAYRGYTADRRSNA

SPHWEVYNHEKSQYIPQPPGTWTVGSQQSDSGVGNVGPERVVVYSQAAARNAESYGGGRH

YNSGGKVWGSYPDVNHPMPDSDSNLSVIHPHLLNNGALDGNQLPPERGSFNYGSMHERSL

DRPTTSTPKRYD

>contig30697 Frame-1R

MPNIAYNSELKPLEVRLSLLGSTEQAWEVTIAPTVLPQPTLDVTEDLFFQENVTFRSAVE

EVSWGKEFDSSDDCSDHNMKSPLWWSQRSDFSSICTDDLSEMDSLSQ

>contig32703 Frame-0F

MHLMNLLREARSIGARSRFASTFGVAFDVDGVLLRGKTPIPGAREVLLELQATNTPFAIM

TNGGGYPEAIKARQIEHILGGNVSIPTDRLCMSHTPMRELARKHGNELVLAVGKDGTELH

QVLANYGFKHVVTVDQLHQHFPSMYPDVRVHEPLEHNGRFNLQPFGAILVLIDPIYWGRE

LQVIMDVLCSP

>contig33380 Frame-2R|Blast-CorA Metal Ion Transporter (MIT) Family [Phytophthora infestans T30-4](gb|EEY58668.1|) 0.0

MVSYDGFRCGLEAMGIACGNDEQFQTFIQNIDDDQSGGITYHEFLFAIQEIKLAQLFNEN

FLRKMLPEYTQKNGNKTNKNARLGSIEYSPDHIRSVYPIEQVQRFIYSTKPGWATMRWIN

VEGIDPLLMRRLSVRYRLHPLAIEDTLDADVERPKYEEYDEHTSLILQTIHARDFALVKK

YQSMYRASLYVHDHDVSPFDTMTKQEILERLNQLHIGSVMTKPQQLSLYIMEDVLISVQE

NSSQPLWSILKQRLDRSYSKVRKHGTAFLVYTIVDVCVDELAPITHTFGAKLMMLERLLK

LEPRSFDINLVGSSFKQIKGLQVLCKPLSEVIIQLSESEAFESETLRYFRDVLDHITTIE

EDCDRHLDRCRSLIDDFHNMRAAQQNEVSYILALVAAI

>contig33443 Frame-1F

MARRKKIVAPLKTSTPKSNDKRKENKKAADCAVIKHKKNPLKAVKQIVSDEDNDDEHSET

EESDDADEEGDDGFEDQGSSSDEDSGEEEDGDAELSELEKKTRRFTVDREKEMQKMREDG

SLSLASQLHVDDLSSDDEENVNTIGNVPLRWYEDYDHIGYNVEGTKIMRSNNGDGIDNAI

AAKDDPNYDRTVYDAYNDRKIVISDRDMEIIRRMQAGAFAHPEFEAYPDYVDIFSSNKMI

HSMGNDLEPKSRFLPSKWERMKVIKIMKGIKEGRIKLDHGPEKKQDVYQMWFDDDQAQTR

KGPAHVQAPKMPLPGHIESYNPPEEYLFTKEERRAWEEADPEDREHNFMPKKFKSLREVC

GYGGFVRERFERCLDLYLAPRVNKRKLNIDPESLLPELPKPQDLRPFPNTLELVFEGHTG

RIRSLAVDPYGQ

>contig34082 Frame-2F

MYRSFVKKPKAVAMPSTNEATSATAGGKKRHSLVPLLLVFLCLVVSLSLIVQFVDLGTAT

IDKTVSTVVMQHERPYNYSDVKTRSLCYAQRDVGILAAVNKSARTFCGDGGWDSVHQAPM

SAKKATKITMYEAKGGIKTATYQNLMLDLYGIQIHKPIKSVAQDGGDHNPLFRYNPIIVN

CACDELANYFLSITNLKKRWAKQIWQLHLEALPKRGNATETFCLPSRAAKGRRSLWDFVK

DPLQPPDPNKLIVFEDPVVLITRRDDHNPFFQISVAFNSWIMLQVLGWDVTKTRVIHFDG

GFPSPIDALHQQLLAPNFPIIKGTSLMGKRVHFRGSVVIAPYESRGPLMEHLNNDEPCHD

SALIKSFRAQSLVALNVTPEMERKLADTSRRPMIVTVITRRPIRGRTLQRMWVNEDEILA

LMRIQYKSLNVLIQSIEYANLTLYDQITTTIESDMIVGMHGAGLVNVLWTRPGTTVVEIF

PKLKFRWGYRNLCQFLGCDWHEFRGGEDLGPDPAPETKNKRIIYDEWMTFFHPLFNEMYT

AYLRRRASD

>contig34451 Frame-0F

MSAASCAGFSESSLPSASSASFKYLIFASIYACGVLFLVPGIIAGRRIARNWSQDHTAVR

LYGLLVLGSTLRAVAFVLVALWMLSRFCSHDFGRLDRKVAYLHLSYAQLVFIWQVLATSA

SLVLGGVFLLVFNTWATMVDEVQINGHAISSKIHRVGDRASESLLQSLHTPNAGEMREVG

VISAIPDSSLKFSPPPRALFTRLVVTVYLLRMGTILFAKQKPGSKMRQSLLLVAIILLVC

CWAACVILLPAYGKQMCVLLDKVAEDVTSRKRNIRRIAVISAVFCFMHLMSSFLLAASQT

AKFSGEASSSIRKKSSQPSDFPLFLQNIVEAYPGFFFPSGTEMDMTANTNDRLLSWILLL

ESLKFPTEWAMLMALLCVLPARSALPAFKGYQPIPDRSKWPL

>contig35584 Frame-0F

MRKTPQPIVTKNQWSDAKEDKLIEEFFDCASEYEIIDLEAMAEEEFFDCLDLMNEVSVQF

CNGSFEEEKSTVKETIAHTAKLPIRNQIDFPPGSIVNTPFGLATVQDWRGCESYAIVHFV

CCKFMVGYIKKNHIVRGVSKAKIEMNENLESKRAKLAECVVARYSLEADEAASTVRGLVA

ASRDGALDSGIRAAGGVALASGMLRSSPGLGGAVAAPLTIASIIVDIGKEYFQYRKQHAC

RKSLGGLSSTTEQLMMREFRLKVGEVIACRTAAAAGVGIGAYSAASILGMCSTAGLAGPV

GIVAATSAAFVGGMLGYFAGSKAYSASTVAYFNSQQNAKEHIDHLELGARILFNEFDSGA

TGTISTEDCITLIEHLYNALSSVSRTRFEKTKAVIKSDTFKGPVTWNMFWEWVSFEAAQT

LCALELIEESKRSSKSLAGDYWWKPSYFSKEATPLLAEPHAVMYPSVLAVLGMVSTDFSA

PESNHALSQANKPEEDTLVLNAQIECLANNGHLTGEDAFQLQEHLASDNHLLNESARKTV

VAINESLAHYGQQQNFVCDGFGNTNGDMTELPAIETDLKPFASRTKNADSEEVTDVKKKL

LSNCDRQFDVMCSLLSQEGLQNFLQQQDILGADLDYARHEDSQCLALAAAPKI

>contig36765 Frame-2F

MSRRARRGDVAVVFGLFWAVSCIFLVWIRIKPRTIKVADTSSASKPRVFQPTWPSDSDSN

SLFTNNATISLVETLPLGDLNLSSSNLQTFEALTCHVRNAKHSIDLSAMYWDLLGEEDRK

SYSEAEMTQFGADRGKNLLLALKDAALRGVALRVLTSKPTDQMSCSPLPHEVEILVNAAK

GNIQVRCWSGPEWYGSGILHQKIWIFDNRHAYVGSANMDWKSLAQVMEVGVIMENLLPSS

SVIQDVSKLFETWWLFASPELVPVETDSYYSEKYQHTLQVPKWSLYLAKESRSEDPFVVA

GFSALGNISHQLQTSFLTLSNRDSKSVSKACEMFISAAPLEATAGHSRAFDEHALVYTIR

SAKAFVSLSVMDFEPFSMYTPGPLYWPALTDALLAGVYSKPGLRVRLLISQWQHSSPQML

NALATLEQQAEYCQHTHARCSGRLEIKLFRVPGWQNTTSRSGPKASWPSYTRVNHAKYIV

TDTRANVGTSNMEWGYFYTTAGASVNTNHEPTRKALEDIFMRNWNSSYAKSLRNVMLESL

>contig37663 Frame-0F|Blast-soluble calcium-activated nucleotidase, putative [Phytophthora infestans T30-4](gb|EEY56716.1|) 1e-127

MHYEGVSKMKPLQAIPEHIIMEGDGINGKGQKHEWATVKDGELYMGSVGKEFTDNDGNVL

GDGNLWIAVMDLVGDVRHEDWTANYAAVRKALGCEWPGYVVHEAIEWSPFHRQWFILPRR

VSTKPYNDMEDEKRGSNKIVIASEDFSRIQVREVGKITPLRGFSSFKFIPRSDDSVIVAI

KSEEVEDQQLQTSFITVFDVDGNVLLEETEIPGAKKYEGVAFAHDWSF

>contig37876 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63751.1|) 2e-10

MEHELRLKFLFANKDGVQMEMTFPKKATVAEVTAQLMHSWP

>contig38143 Frame-0R

MRVCHFALLAAAISITITLASTADELTTHNEGTNFVTRLRVPSDKVIAHDDEERVLSRVK

GFLQKMGLAKKPSHSLKNANVALSNQNDFVATKTFRNWVDSNSAYILPTTPSLMGELKLS

DIGMAKAL

>contig38279 Frame-0F

MCEKDVKAKEVAALGLPSIQRGRLVRQHCSRIRVESKAQEEDVVVALTMRLNAKNEELQR

VCDENARLRDEVAALQKSSRDLQSVVADYENNRSIDKTLMHSLDTPCLELENRRGEYSAA

CNFFANSGSSRR

>contig38514 Frame-2R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY64164.1|) 1e-29

MYPSGDGDDVNVSKLSGAVFLMSFEINPANYSAGASLFVYMEPLEIIWSPTARCWDRLGI

FMDTPANLGLWEELEVASF

>contig38680 Frame-1R

MEDASPAVEARPEDTEAGESEPSTHSPPPPNADADVMSQLRAWKERGARIEHLLAKKNAK

IQEMEETENKLKRLLAMAKRSIDNSKQELVEKDNTVQKLRLELSTNQQDRHSWVVNAFTR

DPRRVLYKVAHLDLLWCMIEYAHENEGNESKEYAWHCFHSEAEIQAYANRASGEPLTLPD

FSLTPNEVDRVKKSLKEEIDRVQEEFRRYRVRSEITRKQKDAEIRKMSANVVARQTEMIS

ETDLMGELQSSKAQIRRLANAQAEAEERESDWRRKFEILQKDYEKLSGTMGETALAMEWR

ERYEQSAREKQQLEQKMEELKLMPSGAIGGSSDKSNAGFQSLRQDFANYRKQALNVVEQK

EKELSDIQAQYHDTGKGIGGHKSSFREGIARRMSGESNSSLSGFEMPNATKTNEYLKNIV

YKYMASDQD

>contig38727 Frame-1R

MGVLSIKDLGEVSKFLGMRVVLNDSTYVLDQQATSKEFCSGMDLSTRTAYIRPFATTATP

QTKTLCSYRRTGEWRKRVSFRDFQSRVGSFLWLFRCTRPNLSLAVHKATRRTHQPTVRDW

KPAKRIMRYVKHQSNSS

>contig39254 Frame-1F

MSLGFLTESALVPSKAKEIKIDAKSLVDLKAVVFQKDQERRKRLQDALNVEDDDETTTSH

TALRLGKYAHLRCGNKRQKRSGDKFMDKRHYNRGVKIRNQRDEELAASEAPSENDDEAWI

KRSAEMLRKKAKLYEEIANGEGSAHINDTCLVDFQAKKIMKKPTEFEEKPMVDITDEFGR

TKKVGADSSELAATLSTLHQQRVEELAERHSNEADRVVGGDGGSFVVSQWDKRLKSTEKH

HLMEVHKRATFAQSLAHPFSSAGKKKTRKQLRLERLLKEREEFNLSECIAPTDSATEIIA

SQKATEFLAELM

>contig39368 Frame-1F|Blast-Rab7 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY65636.1|) 4e-45

MSHRKKALLKLIILGDSGVGKTSLMNQYVTQKFSNQYKATIGADFLTKEIMLDDKLVTMQ

IWDTAGQERFQSLGVAFYRGADACVLVYDITNP

>contig39971 Frame-2F|Blast-phosphatidylinositol kinase [Phytophthora infestans T30-4](gb|EEY59985.1|) 4e-41

MVLSRLDESSDYHLSEAEETPSTSRADDILGEVATALSSMKLSNAQGQRLMKLAGASWIL

KVLMQLKETCALSIGTFTPALIAPPKFGFVVAITNACCSLLAFVSTPKGSMKRLRANELL

TSFHDRIGKEGIWKSFIGLNDVFNEVGLFAVALQEEFVSNLYGRKIGISTHSVTHIKEIL

KNFDGREDSESYFPMSTSNDTNDLNLLIETELTDLPGVCKFLAAGFAFIAKISRLVSMLH

QMAMMTGDEAKCM

>contig40470 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64683.1|) 8e-67

MSESPVTLLAVSDLTTSSNHSVNVATTALHLERYATELLQWLQCSNAVALADEALYYFET

RHPELLNDIPLLFAWLSLFLAQHEDMSSGKTADVAARTIEQLDIIDVMPDTASKFVLKSK

LTLLYWKHESDRQQLSDQRTDDSETGETTSSRPRATFHDEKGLLQWMFTHKDAPLTRQDI

IDHVFEKYPGFAAAKTTAALKVWLSRFLRKHIRPNSLSASEPIVEPAAQMTIHVNMETPV

ITTEMHENVVMPISLAETHEDLTMPLSDVMTASVLPLLLPPSKPVSEESEIMRAQYAADS

ASLIQYSGKRRSCSGRYMLFSNEFKLRAVTMLDEGKSVAQVTAELGLKNSNGLHYWKSIR

DKLVTSERKRFRLAGGGRRSSCSFEDELLTWVSKRHQQGQGTDVKAVLDYIKQSHSSFTE

GKKEATLRKWILRFFKRCWRAPSSSVDSQDAEKSYIFV

>contig41424 Frame-2F

MRKVNSTICIRNLKSSILSIIKP

>contig41451 Frame-1R|Blast-nucleolar complex protein 3 [Phytophthora infestans T30-4](gb|EEY59642.1|) 1e-69

MAVILPNEHARALMDEYDPYTNASFTFKPKVPVPPCNPLHKKISSEKSKSDSRKRSRQRR

VRQFFVRDPLNCLDEQYRKQNASIFFQNCIELDNQCGDNKALKFRK

>contig41873-0 Frame-1F0

MAWHAKCEALQNEQRDSLKEIDQQRDELENTVKELNVALNASKQQCVEQEQEVNESLVLV

VKEKNELMTHFKNAREEVNVVAKEVDNVESNSAR

>contig42591 Frame-1R|Blast-phosphatidylinositide phosphatase SAC1-like protein [Phytophthora infestans T30-4](gb|EEY54523.1|) 2e-28

MAFECASECVGTFVMVFLGTASIATATFTDANSYTMAVGNVAAGWGFAAMLATFLASPGS

GAHLNPAVTLAIAMSPYTKNAFPKRKLPVYILSQFLGATLAGFAVYLMFGSGIKRYENRL

HLIRGTPQSSL

>contig42663 Frame-0F

MSEYRQATAHVEALEAHLSSIRTGLTDDMINSDLSKNLGFLLAAIDGEIDATMNKLRARC

TMVDPVTKNPRFGPTMLAKVQNLLHRYDIVKLAVEANAPLRIHIEAKLSQLIEQEKALKE

EA

>contig43383 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54720.1|) 2e-37

MMHRMRIQPMHQLNHPDHNYLVRGIKGTTSKSSKLHAMRVPKFLRSLYDILQYEDQSILT

WSKDGSYFRIFDTRRLEISVLPKYFKHGKFASFQRQLNNFGFRKWTKTQASVCTFSH

>contig45697 Frame-1R

MYTIAAHIEKNTSLLVLDWHPRHLAVDALLREGFTNVHILTVFHKKCHQRTTTLQLKLNK

CVVGTASGPIGTSWKLETCGHFILHSACEVPSIFNHDQETITVTFKNEGLSASIACILDM

NFISRGFRRRTKTTSSFFPPIISHDRPARICV

>contig46227 Frame-2F

MVDIMRSSYDCLVIICLAPAPHNRLRFPEYLFDHRRSSVFRVIWKKRTLLYSLFWTCRRD

MVIYTQKPAAVLQLLVSISTCQ

>contig46779 Frame-2F|Blast-proteasome subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY57121.1|) 8e-71

MFRNQYDTDVTVWSPQGHLHQIDYAMEAVKQGSACLGLTSSKFVVLCGIKRQSLELAEHQ

NKVFKIDEHMGIVMSGLTADARTLARFMRTESLNHKFVYGSSITVGRLVSDVADKKQECT

QSYIRRPYGVGLLVAGVD

>contig47084 Frame-0F

MPRSEPDEGEAVVDNQKEENDNRDTASEKARKLSASWVTSMQNKCNKENQSASNHEDELH

RLPLDTLQSRECDHQSNVIKSHPVNIWKNAENGLDDDYVSNKSPIASPTENCFSLSSEFV

VKPIREGLDSDDRKAAETRITPGMSLIDRIQEDFPRTPSPEYAEELLTGRTGFDGRDQQS

QSTFDIDEGIEKLGIGNYYSAPSYDSVGRFGGQGAMSPTNQHVFGLRHEGLGGHGHLIGR

SMSARFGVPYSGAMPHTFSSPYSCGAQGIPIMMAGQLRWAFSENAYSFASSPHGRAPSDF

PDMNLGPESALPEYSIDYVGANCGLKPPEKIFKTRSMYHAAEHSMYDRHTLGDYSPHPQM

LQRPKSGGLRRHASEYIHPIAHSYSSNTLLEEFILAPKSEKWGLAAIKGHLFIFAKDQTG

SRFIQQKLEKADDRLKADAFNEIFPNSLVLMQDVFGNYVIQKFLEYGSLEQQQLLVELMT

RNVLNLALQVYGCRVIQRALEVTQLEEQLALIRQLKGNVMKCAVDQNGNHVLQKCIEAAS

WKKATAINELMPQRCVTGKDIQFIVDSFVGQAALLSEHSYGCRVIQRVLEHCLPVQIRPL

LDEIILKCRDLVKDQYGNYVVQHVISHGEPDQRDIVMQAVLPEIARWSQHKYASNVVESC

LEHARKEEISQIVDYILQCDESGATCALLPMMKHMYGNYVVQKLLERADEKDRRRIVCII

RHNEDYLKRFTFGKHVLSRLERKEQVNCYY

>contig47170 Frame-0R

MSRRVKEASDKAIHLQALLDSKVDLQLQHSSSETAKLMEENRRLQHDLKKFPVKVKELDS

ELIHLQNEREERVITEMQQKIAVYVEDSQAQVSATDDSHNHLTAVIERYKQDILAQLDEK

EKEVIELQGEVAEMQSKLEQ

>contig48269 Frame-1F

MEVANIPSDQADQGKDVNMVDADSTDGMITLDKVSLLQESVDKTALSMFNALRLLPASNG

DDTKKEENKDA

>contig48373 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54011.1|) 5e-67

MGSVGEDGVIVMPSPEHHEEGLKHLVMLELLYTLDCLGSMGEYLELLAPALKEDIVGTIV

TFLHSKNHAVISHTMTLTSHFLAHKKFCFSLIETGGAELLFAILKGQQAAGQVGLFDRSL

SMCLHGFASSSAVVERLVSMNPDSMLTAAFHLLASP

>contig48801 Frame-1F

MTQPQDAQTSFSCSSPTKGSNSAFIAAKRAVMPQPAPVMHLSPAIEVAIRLLPGNDRCVD

CKAVCPQWAGVSFGVLLCLVCAGKHRSLGVHTSFVKSLVMDSWSMNEVRLLKAGGNAKWL

AVCAGIRSGNICMEEKYSSSVARAYSSQVSLAALKATDSVFTATSFLSTLKDTVLLREDM

SAFKEVNEPLSTPMMKTHASSDIDSVKCTTCSSMVSLSQLDSHSQICTISSWNAMTWRK

>contig49194 Frame-2F

MAEPTVYVNVSGYGFCVFPLEQLRQLKQQLLTIAACFKDDQLRGTILLSTEGVNIRLSGT

SEAVEAMKG

>contig51461 Frame-0F|Blast-acetolactate synthase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY64201.1|) 1e-69

MGITRPCTKWNVQVRDVRDLARNIREAFHIATTGRPGPVLVDLPKDITAGLCKSSVITEP

QLLGYYGEKKIMENRVNQDANLAAAIKMINNAKRPLIFAGAGVQHASEELRALARQANIP

VTTSLQGMGAFDERDPLSLH

>contig51627 Frame-2F

MRRTSKHFYLDLKSGCFKISLRSALDTQRQLDSRMLSPSMTVIC

>contig51780 Frame-0R

MYPPLHYIVLLALVTTSISKFFHMKLMPPAHRTTHHRAEILATAHVTIGHEVDVSVRLLP

KVRVHLTSS

>contig51887 Frame-1F

MLYPHRVNAVVFPCIAHLLKRAISSSRRTFSHVSVSRHLLHPATDTRGLYTTRGIATVPP

SDNDKKKVAQDQFSCPQCGTA

>contig52172 Frame-0F

MRSMASVLATDVVEHALVKTQVDETIEDEPQEAVERKTRRMMSSGVLLSLLEDLDEDVAM

EASRTIARLS

>contig52468 Frame-1R

MSLQTIATQWSAYARKNTCAQAKKLSWKVRKDCGWTCQSSRPYSFVNEFDSFVARTRRLR

PAISSEPTCCVVCHKTSSFIMSIRRTCTSCKLPVCSKCVVKKTVVALAPDKHSVLEKRRV

FCVSCITAVESCDVMPIAREELVDVRKAKDDVDVYWNRLSSVTVNSSCYSSVLSQRSSLS

SLSSSFNRRTLVDRDGSDFIRMDSV

>contig52521 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68591.1|) 2e-11

MVKAPKAKKAALHYQPYQANISSESDEPSMDLGMTDIPLQLDPVLS

>contig54862 Frame-2F

MHCDPTANWPTAAAEILTTAFPDLIAEVNNNGLTARQTFEQDIDAEDPVEEAPVKSFAKI

NRRSKDKSECIHGNTLAARAAAIAHSRKKVVPISKQGTSMAPYVWAALIFAVVAVLSALL

ST

>contig56600 Frame-0F

MFKLNPLSNPLRDADIPRCLIFRDLKLDEFKDDLFALPEYAFFARLTRSLEQRGVSYLFI

RDKLVKQFSREKYDQLVFNALTNPTDQPTFRRAAELEFESWHWQRIQPSETELLKKLSTS

EELVK

>contig56886 Frame-0F

MLDLSSQLSASRDIANVPVLDEGAFRLGKYHDGSVLKFRGVIRDVQDPEFVVLDDTAVAL

TDDEAMRKQLVERVPLLVTLFPHASDWTHIAYRAHKPTQSDGNQCEENACFATSKRSKRS

MEDQLNCDLQQEKNDVHGKRSKAENTLKREQNQAFFPPEAVHIYVYDGQHKNISLDAFKV

NEAFEFVGILDLMIPGPH

>contig57067 Frame-1F

MPQHSNIRSSYGRAYGVGSQSMGMQDGRFNNQQHPQPIKNKSVKSMPHVVPTGAPLGSRD

PFAGLGLP

>contig57669 Frame-0F

MRQPLRRYPKSLQFVTFAQTLIVLRNGQPGGMQNVRSKASF

>contig58435 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY67897.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY52978.1|) 1e-136

MLTSGTLTIKIQSIEAKFGEAHFNDKNLAVRIAVGTAEHTTKFQKHNVRIDESATLRVHD

AKADATLTIELLQEKGKKPIVSARKKLAAFQSHQPHRQLTFTFGAKQTPSMAQLVYSTDW

QSSETKLTTFETHRPWFMRVGYYYDTTKNVYRYTTSFRVVAPFARFGENTANTVVEKVSG

KSLHEIDEAWVGPGINALDDKVDATLTSVVETLYSGQQYALQKKNEAVDVASNVVKKTGE

KVSGAVGATVDTATNVKDYTTEKVVLATSTVYGTVASVADYTKTQVVHASSSTYGTIKGV

TVTALSYVPVIGHKVAV

>contig03061 Frame-2F|Blast-pyruvate kinase [Phytophthora infestans T30-4](gb|EEY55428.1|) 0.0

MSGAIGLSRKGVELESIMRSDKAGERKTRIFCTIGPSCWTAKGLGELIDTGMNVARLNFS

HGDHISHAEILNSLRAALATRPYKNIAVMLDTKGPEIRTGFLANKDKVTIKKDATLELTS

DYDFLGNETKIACSYAELCQSVKVDGTILVADGSLVLTVLEIKEDSVVCRANNTAILGER

KNMNLPGSKLLLPTLTAKDEDDLVNFGLVHGVDYVAASFVRTGQDIDNVRHILGPRGRTI

KVIAKIESQEGLENFDDILTKADGIMVARGDLGMEIPPEKVFLAQKMIIRKANIAGKPVV

TATQMLESMIKAPRPTRAECTDVANAVLDGTDAVMLSGETAKGEYPTEAVAMMAKICLQA

EGAIHYNDLYQALHNSVLDTYGHMDTQEAITSSAVKTAIDIDAKMIVLLTESGNTARLVS

KFRPSMPVLVLTALGTTARQAEGFYKGVTARCMGSMIGTESILYRATDLGKQFGWVKPGD

NVVALHGMVEARSGSTNMLKVLTVE

>contig06633 Frame-0R

MPKQPHWSFLSCRRNSSSNGERHDEVGNDPWRSNYLSRSKRTVLSDKWSPASPSYLHLDA

QEHLPL

>contig20444 Frame-0R

MSFRSLGSIYSIMGEKAPLLYPKRGRSLAKEIEVNVAEEFYSLTWMALQVSLSTFARIAL

ISVDSAFLGHLGTSSLAAASLASTWTNVPLAGVWSGATALITLCGQAWGAKNGELTGIWL

QLGLVVVTVLSIPVIIWYLNIRAMLQMSTSDAEVVHLGVRFARILSLSVWPSLVYACVRL

YFQSMGIMFPVTVVGTLSIAVACVANYALIFGAFGYTGLGFNGSPMATVIAAWFQPIALI

SYCFGYKKMHRSTWKGWNWSHFTRDRLKLFLHIAGPVAANSMVSNLANSALTFSSRKAWI

RCNCSKCR

>contig20523 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69882.1|) 1e-118

MEREILFRSSEIDHFATSSMAMHGKGLMKSPKSMVICKVGGCQRRVRSKGFCKTHGGGRK

CSIDGCKKSSQNGDFCIGHGGGKKCKEANCAKAAQSHGLCKAHGGGARCKFLNCNKSSQG

GGLCRAHGGGKRCQAIGCPKGAQRGNFCATHGGFRNCKIEGCIRTDRGGGYCEVHRRGRL

CKVDGCKKLSRNQGMCTMHIREDKQMYDQPESPVTSVEL

>contig22543 Frame-1F

MHIQDRFASLIINSTIHSQNHSKIMLILALGVVLLPVAQVVGTASQLDYPACAINFSPQY

YCCNLGTPIGSDESNSLVYVRYQKPQGDSFTHYFNEGWLKSRQINYDPDGSVSLYAPNTP

RYVYGDATKTCRLRDIAINGTIVSSLQCTFAADNNAIYTQNTSLAVDAMDTSIYWSSTSN

PRNNNASLPIGATCRSIMLDDGSVNTTAQSLCTSASGFPFYRFNSFTELPIVILYIIYAI

GFISLACWAQLRTMSKVHESSNAVVSLTSIAEGNKKLLDHREGLDTPCCRNTLESRSSQE

SFEKPWSKEVVQTGYSDSVVGYVMLGYFVLMIVLLNVLLLLTIQDNQGKLATDAYAAWFN

PTTVVIKVFISLWVIATVWFSLVVVYRHQIVNFFRYPMGLDKCTHVLMYKTEITETMLVD

HSGVSQMVFKIESFLFPRSRQGIQETVTVQMTVEGARYLEFQHVRYTFDEVKRTFIPGSI

TLPDTYDKILSDSQGLTRDEYAFRLNIIGRNAIEVKMPSWLTSVVDEFFSFFYIYQLMCY

YVWYFTDYVWVSVLNFVVIMLAAAFNIYAKRNILASVVQMTHYVAEVAVKRDGVWITIES

PNLVPGDLVRVAENWELPCDLLIIKGSTVCDESMLTGESMPVQKVPVPGDSHDVYIAEGN

GKKHTLFSGTKTLSSGREEEILAIVQATGAGTCRGQLVQAILHPAPVRFKYDEHLKAVYM

VLFVIGLIASYFAMKFLIENAGLSNTLFAFVYGMFMFSAVLNPLLPVVMTVGQVNAAKRL

QKSNIFCLNPHRITLCGKVRVFCFDKTGTITKEGL

>contig24192 Frame-0R

MSPEEAAQSFYGLASYPWNVAADRIVYIKSRLSWIAETYLDGGLVASGRINKFTTGRTYH

YLLELDTDGNIVGGEWVYNSTKHHIDFIWIPKAKPHISTITSIGLSYANVSMLLRKSAAC

SNEDPGPEPEVSGSTHASADESTEDTSDLTENAPDLTEDAPSLTEDAPDLTESIPGLTED

TPDLDENVSVTTAPFNDSLLLDH

>contig24530 Frame-0R

MRTLAREASTCESWSIAIEEQRKALRSGKGNKRENLSSSAPVPEALPSPSLLARNHKIYS

HLVASPPRVAMVSVVHLNERDGRPAEKVIKRRTEWGERLDLGVIPQGGACVLLLQNGGLG

RIGTQALMSSWDSGCVCWIEMNDVEFPTEIEVSVTCKVLSQETRSKSPKTPRTPVGLPKW

VEWVDEGTSIGFLLMCLFVHLLYGVDGFHWSHKCCLTVGAALAISTILNGSSTCKIPPSP

VSNTRHASPTSLLPKLQFTLTVHRCRIKMEGTDYIYPLITDPIQ

>contig24585 Frame-1F

MCVPNAAIKSPLVANQTTTPPRVSVPVLSFTPFHHWNCPNGFIYFHSRGSLRVCELPSSK

TSTILPSSGGFVLQKAEFGATLHHMLYLGNHGPGGVAEALVAPTYAVVCSLRMKPADAEN

ATEVETVDDELETETLDANGNVLLGSNVMAPTTEMFSDLELSAFPHTEEDVYELRLVQTN

EFREWDFRGVFRVHFERFEVVLCIRLMYLFDSSLLHDEVASTSVEWHRKKRPYLVIGTGW

VGPHGEDESGRGRLLLYELDYAQYVNEEGGATSGKLPKLRLVFMKEHRQGAISAVAQLGP

YVLAAVGSKLIVYEFKSEQLIGCAFYDAQMFIVTLNVVKDFILYGDVYKSVHFLQWRELQ

RQLLLLAKDYEPLTVSATEFSVFETKVALLAVDMDENLHVLQYLPQDIESRGGQRLLRVS

DFHLGVQVASMFRKRVEMAGAGAYTRKAAVLSCYVNVLGTSEGGIMALVPVSERVFRRLY

TLQNVMINTLQQNCALNPREFRMLKTNGQQRCGRGDAWSKKKWKKSFLDAMVLFQFLTLD

YVAQKELARCIGTTSEVVIHNLLEVQHATSAFL

>contig25043 Frame-1R|Blast-polysaccharide lyase, putative [Phytophthora infestans T30-4](gb|EEY62246.1|) 2e-17 NOT\_ORF

MPQAFKFIIILVVAISVKVSFTELFLIKAGKVYDNKMKTFDRSNIKSNG\*DDGGATTSVF

IFEAGATITNVSIGVDQAEGMHCFS

>contig25159 Frame-0F

MNDSAPLVLVPPTALLLQPSLTSITMSDSQRSKQLPGESSDRLRSPTESRLAAGRRHLTP

SHGTMASASAPSYQPLDAIESVRTANANPNGGGHEVILSGTLFKRGQIFKTWLPRYLVLS

RDALHVYRKNPYMQQQEKDVAQWEKKLLKMEVVQADGIRVEATDAFKNHPFCFVLIARKR

SRHLGPFQSSGSDGCAKKSRFFSRAGCRGFQHRNLSNIDSSDGPVVLYYFEASKDTERQR

WIRALQRWMEDTSPTKLGRGILNYIVNNDYSNHRYGKKVVESSSKKSVGLVGDSGLVLSP

ASHAGRSVEQEFPVLANLIRDLHDCKKEDEMIYILDQVFGEVQDGANSSYIKKLISTAGE

AKLEESAHIWTTHVKTAYATIMKALQSTPSEQEPSSQAPTLRAPNYAMRQHSGVSIESSG

SNQSLRTLDVVSFHRFYKLGRKLGSGAFSVVHIATHRETRKQVAVKCIAKVSLGSQDVRS

LKQEVEVMSSLNHPNLVPLLDYFEEDRYYYIVTPLCTGGELFDDLVKRKSYTEEDARVLM

RKLASAIDYLHSRGIVHRDLKPENILLKTSAPGAEIMIADFGFARSMNGSRRGTACGTPG

YVAPEVVRGEPYGAEVDCWSLGVILYILLCGYPPFPGANHATVLDKVVKAEYTFEVPYWD

GVSDEAKDLVMELLTVDRTKRLNASGILAHPWMDEVRASAMGMTDDTESRKRFTRKCSDL

LPALHQMRKHSLTHGSPKIRPSDMNVDDIE

>contig29300 Frame-1R

MKEPVAKDVVVHLVNCGHLLLHQRFRAAYVERLVSAKAIDLSETDESGVLSISLRALQSS

MDLVHLLSYKREFVFHQNECAVAKLYTEHTVQSMGVTAGADLRVIQRQVAANLSPMRLEV

ASKFFEEFADHLRTLGFRSLKIITTDSSHLQACSVDPKLASGDSKALDGETFYEYFSIPE

KAVAEPGSWTMGADDSAHDSVSIVVLEVKCDNRGLLLSAVLVSSQDLMQQDLRCQQNLAA

KSGFKIIGASGARVQGVASWLRAQLQTQALVYNFTVRYFQQHLLQWFEASHDNIDQQKGQ

SHTVGKLLGDNDALVLSPLLSWKKVSTYQNIVNGLRCFLHAFPDPPEDHDKATRASTFSP

TGISLSKQCKATIKSKDKFIIADSKAFEARAGDVNRPTSRALTRFARRITLKKAQQKPPH

NQLELDSDPAPLSLILRSCVIRVATMTLQPALLQTDCSDLIVEQILLRYIACHCSRYEVL

DLLQFGTPDTIVCHSFSGSFFHRPSKINSTICNRDGKPFIGYSLLITTQPSVFQPLELNS

VQLLLLKSTASTKGVGSEVLPVERALQEAKLFTKELFHVAAQHYERDLLWSRLLYDNSHG

PACYVARTLAHPDHLFRVEVGPQQLEECLRLSICTPLEVLDPRLHELLRVTGVCWQELAL

RLKDIYANQLREFQFQEEDESSSHLLLLCPDAFDLIIHLTFITHKSPVLPPKEDEEEVAS

ISDGESINCLSQSGDSYVTSLNEQCSEKDIRVEICRREEPTNKQFTFAQRRSITEFVNSI

VHWQWRSLIYD

>contig30755 Frame-0R

MPASRFSRQVLTLCVSLWLLAAISASSSVHNDATSRQLGSEHDKNKAVPFYSWSNTIETL

KNGLSFVMVLVAAHPLGLLFPKLFRLPLITGYLVIGIMAGPFVTGLISQEIITMLAGYVS

ALALSFISFQAGQEIYLPDLRPHLKAIMTLLIVLYITSMTILSGAILLTEEAFFYQGLSV

NCQVGIALMFGSISVLGSPATVMAIKIELNSVGPFTSLMLGATMTAEFIVLVSFSISRIG

SSI

>contig32018 Frame-2R

MSGSSDFVQMSTGSYSTRTGLSKVWRTVKTHAGVYTGGKVDFFNGHLDANTETRAFIACI

LHDDVAIIDAITGELQCTLQQGSKDNDTKESIVVFAVRLGKYNQIVTASRNLLLRVWDLE

TLKCVRVIKAHDSPVLAMDIDPSGTLLATGGSDRTVRVFDIDKGFCTHNFRGHAGIVTLV

QFHPDAAQLSLVSASDDLTVRIWDLYTQKQVACIQDHMSLVTSVAFSEDGSTMLSAGRDK

VVNFWDLKDRKLIKTVLVHEAVEGLVVVPSSFKCATTKKFKDAKEIYFLTAGEKSVLRLW

RSSGSSCEVLYTEKSDTSSALTYLNLKLGKVRREIIVVTSEQNLLVFNENLTRRTQIIGY

NDDILNLKYIPKADASGAPSEVLAVATNSQSIRLLNRTTLSCELLSGHTDIVMAMAVSPD

GRWLVSASKDRTARLWDLRPTGGKKMKMTLPRCVATCAGHTETLGAVAISQRVSSFSAGA

AFFVTGSSDKTLKLWSLKPLASA

>contig32087 Frame-0F

MKTHRWTTPLNCETITRTWHDAVYLASKNLVLVFGGERSAAIDSELDILSDIMVLDTECF

LWYPPAIHGTPPSARSGHTCTAVGNEVVVFGGTRGRSRQSSVHILDTNYWHWKAVKVDGN

PPSARTYHSAVALGEDRIVYFGGNDSSKSFHAVHVLQKVPKKKNGAVWTWVYPNVTGVPP

QERTGHSATLLKDGNLFVFGGWDPQRGDVNAPTSVFDDAFILDTKTWEWQPVPFNDGRIT

SRGRVGHGAVLDCNEKLYLFGGQNGQEERLQDVCTLTLLKQDSMVE

>contig32173 Frame-2F|Blast-tubulin-specific chaperone C, putative [Phytophthora infestans T30-4](gb|EEY62994.1|) 5e-24

MNTPVTIGMRCELLSPNLKGGLRASLKRYGEIAYIGKVSGLPGDNWIGVRLDKPLGKGDG

SVQGKRYFDCK

>contig32700 Frame-0R

MEYIGGVTADVDASYEQVTDRITKELQNEETRRLYSRGFVSRDEFETQMTQVEEYYIHEE

ARLQQLERLRTLEAKQAAEAKKTQLTQRMDEQELASNDSNSIPVIVPVISEEKSGTRFNA

IHEHKAITSNTSKTIVPVTTISEHATVTSSSPVPAPLLSVCSLPTTTPVSISTTSIPRSA

PQL

>contig33088 Frame-2R

MHFNGQPPGQRFCHVGAIYNSNLIVFGGYDGSSRLNDFKQFQFKDHELQLDIPDST

>contig33299 Frame-1R

MIKDSSIFSKLIFIIRVYSTSCILLKVFFICTGGYLLYRLGYMAINNFKL

>contig34377 Frame-2F

MKSTSIPSLLFRKSTTTRWTYRLMATLWELAVQRTRKQHKQSQAPSKQFDVLRCHDASKV

GYKLATTKLNETSIMHEAALSVLACGVVSLADLEAVTGYSPVMRTNASSKATIETTSKNA

SIAGSDVCEKRVVYEATASSSAENQCAWTPLCQNKLTNSTSEPAKWVCVGYGRYSKVP

>contig34427 Frame-2F

MAFSADRAKVTEIILPATKPTARSRYPSTSSTASLQQVREQSVLSSASSVASMANHGGDA

SMFDSPRSRSFPNGRSNSVDSSLLVKKSSFQNRMFKDSGNLEGFGRTSFTSVSQLSELAA

IPVEDPYDRRGSLSSSSESGSTDQLSSKLSNLSDADLMKRSLSRKKDFLMVTSEVFRDEG

GDYQTRKILFQARDDDFSVASRVPTHSNSGRELFPPGRAASTSSASSTQKPRRLGSGNKF

GSSSRLDSACSGSAVSGTMGSAMGSAMGSAVGSALGGKKRSHQSIQGSGSSVSSSSRSVV

TDDGHLEEFDMDGIDCVQVTEIDDEDDEDLFNVGNRKNSGTSSRHFHHHTSDSSRANSSH

ERSHTSGMSDADSDSDDSDYSDVECDVDVDATFSELITAPNQLDLISQDDEEVAPIVTHK

MSYTSVTDLLSSNNSGNSLTLGTLASMTSASSATSLVPLLDIVQVYVSSKIRENLTLSIR

SGYAEAKGARSYMEDRSAGQTCCDLSRYPSTLADFYASVAFFGVYDGHNGTETAVKLQKD

LHHRIFAEAAGLIKSPVSCISSVCEAIDNEILEKQNRSVLPKRKRTMAAEELRRHLQSDD

SENRLTEGECCEIDGEIVCGEETKALLQPISFSGAAGVFAVLAKGKSRLPNNLNHTTTDE

ATARADAVSDEAETDQPVRLYVANVGDCRAVLCTAEAIAVDLTTDHKASLPAEKARIEAS

GGFVHNGRLDGILQISRGFGDLAHKQDGHLVVTPDVVERIVDPSDQFLLLASDGIFDVLT

SQQAVNFVLRKLQTHGDVQLAAQELLLKAQAYFAHDNVSVIIVALNQKGEV

>contig34593 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64665.1|) 7e-98

MDITVRVEVQYVAPENALIRDVLQMFRTPAWVRFMVRYISPHLKNAAPADKSVMDSLASW

TVGSDVTSKAGTKRPISSVASSSVCAQDCVICLSELQSSDDQFVSLPCGHKFHLTCIRSW

LKLRSTCPSCRFQFRKAFFGSYAVRTLNSALLLKQEHRPLPKEEILNTCVSRETIRAVVN

VTLSQIAAHAKQSQYPCV

>contig35473 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66099.1|) 1e-123

MDTILLKTARAHVGERVHFIAAVQQIAMGKRTLVARQRIQPCHVLLVGDATRQFFKVTCW

GEAQPTLVHRSTSEDISDRVQVKSADAELQVGDIIKFSFCCIKLYRGNVEAQFFLRDEES

AISSTAQLLYRKDRYFSTQGTSIKDLYPMIEWYKHNCRETGMIEGKTPKKINNRVMIKDL

HENTVASVVCKLQLLNEKARAYIGKEEAKAYELHGVLLCKLVMFDSVQDSMTVNLWDQHA

DKALLLVY

>contig35587 Frame-2F

MWLVGWPLGLLLSAISSIFGIAGKLLLKLAHLERDKDELAVAQFNLHGSPNSPRMGCTYF

YCGLFCMMVLNPALGALAYCFATQSLLAPMAGLTICWNTLFGPILLPHERLTTSDFVGAI

LIFTGCVLVGISGTHESPPLPVELLKARFQSFSFIVYSILLATLLCFLIHHAKHALHYTT

TTRRAGVTSSPVSKSCPASSTCPRVIKYLCWRHEWAALFSRRDYAYSSR

>contig37185 Frame-2R

MDDHLRVAVIGSQTRNPGTSRAYTVYRTSVNYNGLCYHRLIRFRHFFHFSKNLKLAPEAP

PIDVKMPHKIWWSRKASMQPETIEARQVMLNEYIQQVCARPLTPRSRERLLKLLQLEDYA

PKEEEDRVIDSRLGSRRSNTSFTEPASEIGGLYSIQSSIEEQESKEDLLALQSGKKERQP

QDSLTDEKENATTEQIGLDTTVQRQNSDASSDPAKDSSPRVRAPSAPPLLSRQVTTRPFS

MSLNSQNMKRVMFDPSLDSDRLFLKKEDRDSIGSALEYVSTPEHHYVGQIKQCIASIEEI

VDSSRYFAAQMREKQEANRLTSVAK

>contig37875-1 Frame-1R1

MDNLVIYAIISWSTNKCFPFSERPDGIVLSGNNSHLSNCWLRGGVTLVLKQYKRKVPRYT

ARMNI

>contig37949 Frame-2F|Blast-choline dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY64381.1|) 1e-119

MAAIGLKWIFQKTGMGASSHLESGGFIRSAPGKRHPDLQYHFLPGSLTGQLTPGAYHAMQ

AHCSPMRAQSRGWLKLRSNNPHEHPTIEPNYLDVEQDLVDMRNGLKLTREILEQQTLDEY

RGDPISPSDDVQTDAQIDKWIREHTESAYHPSCTNRMGVSDNTVVDPQTRVHGIENLRVV

DASIMPNIVSGNLNAPTIMIAEKAADIILNRKPLQKSTVPV

>contig38588 Frame-1F

MRQQAFDQLEKRRECVVRESALKLQSLWRCRQQRCRFVRWLELCRRIQMRWKAIFEKKRR

IAQRNNAAQVVQVFMHSWVQSIKCRRLQSAVIIQRLFRRWLRSRFASSVATRVSSRTLRH

DDKFEDRVGYSGRESELTIETVGEEDVFSTATASVGTSAYSDDLEHSPLDALRFRRRMRD

LDERRDDENAMLQKALHEVERFRRRAEAAE

>contig38683 Frame-1R

MATRKLKFEEAVAVLPTLRYGILIFGVEFGPSLITIDLELVWWQLVLASTFAGLPTSRCR

RLV

>contig38724 Frame-1R|Blast-5-methylthioadenosine/S-adenosylhomocysteine deaminase, putative [Phytophthora infestans T30-4](gb|EEY54489.1|) 4e-60

MSLLRGLSDDKPLCNWLTEDIWPTEGKFVGPEFVKVGVTLAVAEMLRSGTTCCNEMYYFP

DEMCEVLETTGFRGAVGLVVLDFPSPYGSGP

>contig38863 Frame-1F

MFRSGYFVQNLGKAGSETKVAYLVGLEAGGAAPRLAARYVMPRFGAVLNRVIAHVTRKQF

DPEMFAPRSEWADIRTAEFCQCCSEHFGAIKLLDTRRYNCVICGNAICHACHHVEKVAVP

DACSNATVAVCVGCKMTTRTKSQSKSRRESSSALTEVSEL

>contig38984 Frame-0F|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY66973.1|) 0.0

MVAAVGNIATFNIQHGYVEGLVRGFRSGFLDDVDYHHLTQCESLEDVKLNLQETDYDQFL

ADESLGSISPGLIQAGTTNKLVEEFNFLRAQAMEPLGRFLDFITFEYMIDNVILLLKGTL

NGRDVNELIIQLHPLGKFDESILRSICTFESNAKGYSDLYETVLIDTPIGTYFSQFLEES

AGGDRMEGTSDVRNVLEEVQMELIKNSMLKLWLDDFYNFCQEIGGDTGVIMGEILKARAD

RIAINITLNSFGTPLNEPAMRISDRKPLYPSIGALYPEATALLAEAGDESALGAVLDSFP

VYREIWEVHQSESVGSKSIDDAFYERDVQMAELAFQGQMHFACFYAYVKLKEQEVRNLVW

VSECIVQNQRDAINNFIPIFSDNAPWRSKSSNNK

>contig39907 Frame-0F

MQSLLLRLFAHDNPAVKRLFMSNFMKTCLECWDKTTTSSTSIDATLSFTCLPNFQLFVFQ

DLLRACNDPVLYKNAHRARFQVVVSRFLATFLAFQIVVKKKKHVLDDFVFAVNEAIFGKN

VTSHSPEALLSLLQVFQSLYLMHKAIFASCEIQLSTRAVDQLYILLDVHAMQSFSQAMRS

KMLCALTHALTGGFVNASALSLSALARIFHIYPFRILLTDDGAT

>contig39972 Frame-2R

MGMIDIAKMYVQSDDLDGVLTLEFVENLIESCRNGRKIPRNVLVRVLTETTTLLRKSPNL

VEFRIAPANHVTIIGDLHGQLDDLLLILRENGLPSETNPYLFNGDFVDRGDRGVEIAIII

YLFKLLYPNHVFMNRGNHEENSITQVFGFMKECEMKYDRYVFDLFCESFRHLPLATLIDN

RV

>contig39998 Frame-1F

MTDHVVACFITELALASLSHLSTCMMHLFSLSLAFMATVATVSAGSPYQENPLKPILFAA

TYTRDEGWINGTGKGIYTYQFDTTTGSLTPWGVTPVGINPIFVLSTTKVFSTGQRVIYAI

NAVNENSAKLPGTQTGYVSALTLQHDGTLKLLNTLETLGGSPTHISLSPKQDHIIVSCYG

GSLTMFPLKHD

>contig40309 Frame-1F

MKSLYVWGSGQSSYIERHRSLLKESIP

>contig40587 Frame-0F

MADLLAAVNSTPHAEEGERSGAILGLSESQVQVMKEQAIAYAATHGLLVGCRNTNSPNES

ARAFTHIPLSLLPVQFSKAQFEHGVKLSPIYGRLVDRVSRDVEWLHRCVESVVAEDAFTA

RLLELSKLVQKEGVQQKTYLGIHRSDYMLHETLTDSPRLLQVELNTISSSFASISSLVSG

MHRFLLSRLGKEVPALEKHYGIAWTEYCNRLPINNAITELPKALAAAHNHYGVKGAIIMF

VVQPNELNTIDQRWIEYNLWELYGISVLRRTLAEVNACGKLVERDGKHTLVIDEREVSVA

YYRAAYTPNDYPREHEWAARMLIERSFAIKCPSIAYHLAGTKKVQQVLAQPAVLRRFMSE

IEAIELETSFAGLYGLERDSLMIEKVKKMAMDNPRSYVLKPQREGGGNNLYGDEVAVALQ

TMSSAELESYILMERIFPKENAAVLLRNNLTSSGPTISELGMFITSLFDSEGQEILNKHA

GHLLRTKVSGTDEGGVATGFSVVSSPFLI

>contig41081 Frame-1F

MFLKNEEVDIETLKDFPRALLRRYVRRQGVTSFPTAKLVISAVLLEHFGAKLDTIDKRKI

AYSGINDIKNKPIIYIAEELDVDIKDFNEMPKGPKARAFLLFMGLKRGGADSLGWIGNVG

QIVDDTRAKFTPFGRYMWLN

>contig41427 Frame-1R

MPISTEAVLLPFDNGPFAAKWPDQMATEEIDGCGPSTDVQAACSGYIKLVAADNSPMKGQ

NASKIQQKPTIKVEANGLN

>contig41870 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61676.1|) 6e-58

MIAYRRAVTLVTSSFRVPKNALVISRNKYAYFFVQRPPSVRSPPSLIPPTICRTSSSASK

SSHDHVASDAAELTHVGRLKDLWRKYGVVAIGTYMTMYGAVLGSIYLAIDQGWLRTTKGS

HLEMERRSDENFNLVTSTNKLVKIAEDWGIAQYLEIERVNSKTGTLLLAWIVTKFTEPLR

LGVTIAVTPRIARFLGRAPKLPPKMNGQTKMMIDNQTLAKKKQKT

>contig42592 Frame-2F

MDLHGRLEKRGISVATSWGHQSVSSLFLLVTAHRGFVDHAFKDVSWEHSHTLTTLSFAIK

LDAKSSGLVVCTRDHITISSELLLLTIIHVASV

>contig44626 Frame-2F|Blast-periodic tryptophan protein 2 [Phytophthora infestans T30-4](gb|EEY57501.1|) 0.0

MDPFNVYVWSLQTGRLTDVLSGHTGPVTSLSFSPSSSAEPILASASWDHTIRLWNLFASK

KSFIEPLAHPTDVLAVAFRPDGKQLASTTLNGVINIWDVKEGEQIGSIDGKRDIAGGRKD

TDLITAASNQLTKHFTSVCYSADGSLLLAGGRSKFVCIYAVQPQILLKKFQISHNLSLDG

ILEELNSKNLTDSGLSKRELDAHLDDSEKSRMNGGDDLVGAKRAVDPGSRRKNIEVLSKA

VVFSPTGRAWAAATTEGLLIYSLDETLAFDPFELDEEITPDSITQALEHRAYSRALIMAL

HLNEEPLIARCVEGVPVESIPLVAQTLRGELYLQRLLQLLAKRMERSPHLEFYLQWSLAV

LNSHGQTLRDDPASSATCLPTLRSLQKSIARHLQDLATICDDNQYTLSYLKNLSKMQMPK

IH

>contig45629 Frame-0R

MSNMSTSRNVEAGPSLSLIPTRDAKKREALLLLLRTVGHINVSCTALACTFSIPSKVMHV

CDVLIAHSSVNDFSRAVSGRGPVLVSRIYLGLADTVRKIYFSITSLFYTLS

>contig45694 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63449.1|) 2e-78

MAWGTKGGVDDLLQKLTNPKTARCLCVMSTRSISDDEMAKLAAAIANNTLLEELYLSGHQ

LGPLGLQAFADCLAANSTLKHLSLGSNELGDKAVQTLCAGLTGNAQSGLQCWDLELKSLG

EDGAAAVGELLMTNQTLTTVLLSRNIIGDQGIKELVKGLRENTQTGIKELHLTEVGISGL

GLDHLATLVESESCS

>contig45755 Frame-1R

MVLFGALLLARSLCAAEPRLHGYTICEAQ

>contig46224 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67786.1|) 1e-25

MPATGVKRYSLLQRSVRLVQTSLRRLDRWASVRVPGLPNPPEIEDRLRKPRFVDLWELSF

ADHRRIFHEVW

>contig46440 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69516.1|) 1e-150

MLTTNQEMAKQISHLAITQEKALALVKQEQEHKRRNPVLKVNPLSQDQCAEIARSSYLYI

KSFRESDTCFSTGTSVLGWRDRHVLHQNKLMFSLEKTFHGRATDMMAKNLWEILSLPEPI

VIMRPRDADAHFHVVQRLNEDAVVYYYTLEREDTDVQIRAFILAMRVDLGANGCMVILRS

LDPKSYLSHDGDCTAPVRRGRRKVEQQKEYFWLDVFVWSIYEYAGESLEDCRQTFGGEIE

GTALASTGWWSIEILEMALRMECRGLASRGLLAF

>contig47018 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66605.1|) 4e-62

MGGLMMAAAVASGKCSFAPSVTWVSTGSPMRGSMASNYLLDACHGGTNLLVKDFANITGR

CPATAAIQSLAYENSTYASPELNQAYKDAQEVYRTHVKAAMCSFEYTGLISKYQWQFLVL

GKVMPHYSGANDGVVEFQSCTGGIPASMFGRTYRDQFYMTKLNHFDVTFR

>contig48370 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57346.1|) 1e-159

MLHDNADRASSEFELLFAVLLKHLDPSGVDIEARYAATSCVSNICTQAGKTPEIYHFFSS

LLRMVVENFRQQVLSLLKGHNDRILVKACTSSMKCIFTIINSNFDRLNDRIVATLPGLLN

SMRQVVGYGLVLKGRQNDVVVLFQEELHPNDSDTSVCGSDSSAGGRHIGDGLLARLRVTV

LYTLEAIAQHFPSAVTSSMELYLPEQTTPFMTLFNNTPSVLTLLMMDPSEKARIVAAKFL

DAFWEQIPLKQYFRRGSGAGVSSAIFTSSMSFALMPKRISLMLYQVHVTLVYCIQHEKES

APLV

>contig48464 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68253.1|) 2e-65

MATTLATFDTVETADCVESCPVSGFESSMVVATYQLHEAVQNGEFPNRRSGTLQHYQLGC

NDATTTDGAVVSVRKMKETTTSSGIFDIKWNTEAMNGKAMLGAATASGLLELYELVLENN

LQTLRHSGLTADAEAESMCLSLDWNNRVLSNAQPSICVSHSNG

>contig48648 Frame-2R

MDYDEEAVMEDLSSQSKFLPPLEVQSQLQLMWKNEDGLMELLYGDRNIANGRILDLKPDG

WCKFFLNVIPVAPSRFRPPVFMGDKQFEHAQNSHLSKIMSFCDSIV

>contig48802 Frame-1R

MMTVPSLMHIRHELVDLDNETDHQKIKLMTSSNVDEIVELCLSSSDDEVQESTSLQSRTA

QRPIAKYRRSRRTQTRISSLATNSLITQEKMVESERLAKLEKRRKRRKQFRQSADNSEYL

DNSYLPAVALRMKTLASKTHPCGSCCWIGANPNESFSCQQVDTILVRKIASAH

>contig49197 Frame-0R

MHFLNFFIVLPRSTLCKISSSLHPLENVFFQHLSLRCKSRFFIQLCFVSDTQKRLSDYVL

KYDPHCSSAQMIL

>contig51174 Frame-2R

MQRSRATRSKDASAFRECFSAAPVRAATSRIYAATANAEAQRRETLVSVRSQFAGRTVQS

NARAADAGRSGLPLNQPKCVYDVRQAIIYARSVQALRDGTGVTATSGQRGGGQSVGPRAI

DIVKFAVLVVPL

>contig51417 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66506.1|) 2e-26

MLTTSHNTVLTLTAHINQCPQYVIDQSRVTIHFVANKQDWYYCATRLPEALMLGFDTETR

PIRKKIPATQSMRFVADCNARCQSERGSLHPRSAAPIPL

>contig51462 Frame-1R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY64287.1|) 2e-57

MMQQQVALARKPHIVVATPGRLVDHLENTKGFSLRTMKYLVLDEADRMLSMDFEEEINQI

V

>contig51699 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62822.1|) 3e-11

MPESVYRRIVSELDMNSMRRISEALLLAQNRARRATDRANQAEHVLSLVLSQTMASHLHG

DSSTD

>contig51839 Frame-2R|Blast-cysteinyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY55299.1|) 1e-44

MLRLRCQYSLAFQSHSARRWQSTSSSLSSCRDLKVYNSLTGQCEPFPRENCEMPNVLKWY

ACGPTVYDRAHLGHARAYVSHDILRRVAERTGGYKVQLVMGVTDVDDKIIMRAKEQNVPF

YEFARDQEDQFFTDMAQLYVKSPTAITRV

>contig51884 Frame-0R|Blast-tRNA wybutosine-synthesizing protein, putative [Phytophthora infestans T30-4](gb|EEY66227.1|) 9e-63

MFAQLKRESLRKLHAMEDKSPKGCIDKPIASMINTINAHPDYVTSSSCSGRIAVFCGETA

TLNGNEARTDLITKGGKWLIAEHATITFEQLATGLRLAGADSSTSRMLIFKHEPFIMHVV

CRNLDSAKALLQWGLASGFRESGVVLG

>contig51963 Frame-0R

MAPHGVLETRLTSKQDALLHSLERRVQLKIQAEAHAPLYSERHPNAPETLRDFIARRPSS

IPSASFKFDPSFIHVSSKIDQCMSQWNAVYAHAHASQALVAEMEASHAQVVTKTQALYQS

FEEILQQVDALDTRVASIAAPMPYFTAIDTVAHTLGFGVKYAAPSSESKQHVLMKNTS

>contig52522 Frame-1F

MSRNLWEDWNEGDASFDVKFNMLTDKVDTASSSEIMTDLHSSIGSGYEQQQSVSNSTMHL

NFSPNSESSAFSTTDVAGKPRLNIQRSLSEEIVNMLDENNEAALSKQLDGNQRGIAPSQS

LMFNADRMTAQHQKLQSQYQPHSNTQYWQQYQQQ

>contig52834 Frame-0F

MREKALASNDKVPQTASDYERLLAVSPQSSFLWIQYMAFHVSLTEVDLARDVALRATS

>contig52889-0 Frame-2F0

MASFVSSPKSSLPKAWYDQLAQQAESSDRYSEPHMSSILEMAPVNLKFQEPG

>contig53631 Frame-1F

MHETKERDVDNTLEGLRERDRRAFRRKMDKEKEMIMNGDSVPNESEDEDM

>contig54331 Frame-1F

MSLKMESMVEALYARVIQRVCQSYREASHECSKADINELQKKWQEKLQLYTGKISSATIE

ENATNSSA

>contig54861 Frame-2F|Blast-tRNA-dihydrouridine synthase, putative [Phytophthora infestans T30-4](gb|EEY69480.1|) 2e-25

MSRPIMAACAPVSRLSIAPMMDWTDRHYRFMMRMITKETMLFTEMVVDQTLLHQKKNLDY

FLGHDPVE

>contig55332 Frame-1F

MTDGSSAPAVSCKAIRRQYQQQPIAQLEHHYHHQHQWPTITQHEMPYDSNSN

>contig55347 Frame-1F

MEEFDRAQSQAMELLIQQCIRDENECPSALPADPGPAAANATILDLLAQTCADANAAAQE

L

>contig55404-0 Frame-2F0

MPLLRKLLEDLGDAPANMTAEQLFASSIDAQEMRTQRKLAAALCSASLMSMSTRAQKQRS

>contig55404-1 Frame-1R1

MDISEALQRAAANFRCVRISCASMLDAKSCSAVIFAGASPRSSSSFLSRGIEGIR

>contig56049 Frame-0R

MLFHSKATTFSHKGAISNDSPRFKDLPCLPARAQAFPYHYSLSARP

>contig56719 Frame-2F

MSFDTMKFTIPSPMNRHQTTLVSDNARALECQPQQATNLKNAPSLLCTTAAETSKEHTGM

HLTTLLTSTTSLLSHRPLATTTRDKKIGSYTPTERKRRLEKFHEKRKNRTWKKSIKYDCR

KKLADDRPRIKGRFVRVQENATMCEQGHAMAAGYASPTSLIDSKLSPLMAPVVKTQVPRT

ASLTLGTTVKPVALSISVPPLSSSNTTSTLACARMIASV

>contig57064 Frame-1R

MDQNRPGPVTIAFPLKSNILGVALP

>contig57248 Frame-2F

MSPIAIQFRHGALLVRRHLASRKASTGFSYPGPRSLEQIVKLELLESEQAAKIRSIWEEF

HADKDDAIATTLRGSEFEALVTRAKSAPYSILPVYRQDGFFNMLCQFQQSCFLVTYLESF

KENPGTAPPCVAITLYDDLLLKKEITLVRADVINMLDKSESQQLVQQIFTSYQDDKLYDH

VDKFNNKPDLFDFEAYRLMLKERNTI

>contig57770 Frame-0F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 3e-35

MAFAKCVLEMCHGWHLLVSKESSTTSSRSFSYGMALGARILWNGGFAGLFGLMIYVPLNE

AR

>contig00137 Frame-0R|Blast-guanylate kinase [Phytophthora infestans T30-4](gb|EEY57193.1|) 1e-120

MRVALEASKTLVSLAVQESSHLNERKEALKKENAAYVEAHPEIKTLLSDFMSALLLDKPQ

DVVAYAAEHFSAFKSPPTALQPIVIAGPSGVGKGTLINLLLEKYPNTFGFSVSNTTRDAR

KGEVDGEAYHFTARDKMLKEIESGLFLEHAEVHGNLYGTSKRAVQDVQRKGRICILDIDV

QGAQQVKKSGISAKYLFIAPPSLEALEHRLRGRGTETEDKIQLRIKNAEGELAYGQQPGF

FDAVLVNNSVNDSFRELVDMLKQWYPTVELK

>contig05035 Frame-0F

MKASQFILFMSGAIFHLGGIHTSFVGKLASLHEQRFHLNTALKTACQYPAFIFLRFSRSH

AQVFARMTAKSAKLNATNKK

>contig09853 Frame-0F

MDGDCMISRSGRRMYERDYRAVTKHVSPLCEGTPLNVMLVAITRADVDTLMVNLAESPEV

LESEIESFSYLNESAITGMNIDEKPPVTAPFGLYPKPYIYDDDLVEASLFTKTEWKDSMI

VENVTDEVDVRTWFRFLGCFVGQAILDERLLNLPFARPFLRALRGEKMVGDGVSIDRSLS

YVDELNPTVANSLRYLHNLAVKYAAIKGSDKCEMSSVAPWMREVDAMCLSFTMIGADDIP

LVAQGGDISVTLPLLHKYVKLSLEFLLDRSIKCQVQAFLQGFEQIYGGNAEYRMCRFFES

FNVRELEELLCDRGTGSTMWDRDGLDLREHMVCDHGYTAESLTIANLVSILCELSIDEQR

LFVRFVTGANRLPLGGLRNLEPKLTVVRKLPETTDATSIEENDAVLPSASTCTNYLKLPD

YSTR

>contig12710 Frame-1F

MLRSSLRKMPRPQPLRCNATRTHLHAQATCHLAPFVRFQSDFSSYRNRHQPSIFLAQPLA

PYPRVFRHAHFREFATLPTKSPLTGPAIPSSSTDVAAHKKKVAAARRRRSKIRVLEEKLE

SALEKGGERRLLRVTEKELPKVPERAVSLLKRTPQLAIQGIQAVAHAFQVLCTDPASVKA

WLLTLKGKVKHEVDHYWLGTKLLYADVSTSTRILRRLLKGNALSRRERKQLQRTVADLLR

LVPFAFFVVVPFMELLLPVALKMFPNMLPSTYKDSYQREEDMKRQLQLRVALAGFLQDTV

KEIMQDTHDTEGVSEERKATASEVMNFIERAQCGEPLTADETLQVAQLFNDELMLDNISR

PQLVGMCRFMGVQHYGNDNLLRFQLRNRIRQLKKDDQAILWEGLDSLNKEELQFACVERG

MRATGLTKAGYVRQMRQWLDLSINKNVPASLLIMSRALNITATDNLEQALATSMSSMDEE

VVTEVALAAKASMVSE

>contig17450 Frame-2F

MSANLNDRSTSVPPRRDPFHILNVDDVDASSRTGPLMSAASISSVASVGSSFNFTTSRQD

DVAIASLLPKDQRPAQPAEQREYFERMWAENFKNSEAQIKSSSGYLPVGAAGRLNRIKGF

SFARDQVSHKLYAVFRLEIECIVSEKQWTIYRRFHDFKQLAHQLKSESVRISAVPTRTLM

RSLDPTFLRKRQLELDRWLRGVLMLISLENCKVDTDRCTECCGNRGFHSSVRLIRHFLTH

EANAPPVFEGLSSNTDGASYNGLLSSYNGFSFLNSGRPLSSSTFEQKTDSESMSHETEEG

CNSTRGCRSRGCSADKGSTSSRSGLKRVGSKEFSVYKNLTARRASDDQSLRSRGYKNRTN

SLDNGLSMESSRVEPFNVPPLLEQRRSIILQDVEDEASYDDGKSSDQLRHKVTLKQFDVL

RMIGKGSFGKVLLVRKKHSSQLFAVKILSKPAIVKKQQVEHTRTERRVLASISHPFVVCL

HYAFQTTNRLYFVLDYCPGGDLFFHLSRCGCFPEAMAKFYAAEIVLALIHLHEQGIVYRD

LKPENIMLDVDGHVKLADFGLAKEGITSELNGTYTMCGTPEYLPPEILNRVGHGTAVDWW

NLGMVLFEMLTGRPPWYTQDRQELFNRLRNAELAFPQGLTPEAMNLIEGLLVRDPAKRLG

AIDVREITYHPFFADIDWNLLYNRQVHPLYRPCQYTDPIDAANFEEEFTKLPLAQIDSAG

LSIATDELQKKSGSGGAAGRDPAHNVVAAAEAAGVGAGLYNGMFGSTETGSERNSTLRNL

SYTFAGFTYDGSNSSLAN

>contig20751 Frame-2R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY57494.1|) 0.0

MKYLATISQHRNATADSNVMKQILSSNPILESFGNARTIRNDNSSRFGKFIKMEFSPEGS

LIGASIQTYLLEKVRLAYQAESERNYHVFYEMIAGATDDEKKRWNLTTPTHFHYLNQSSC

IKRKDGVKDADQFQVLKKAMQTMGFNEDDMENIFVTIAALLHIGNLEFDATHHTSGTVGS

KISTMCDNSLTVVMEFLEVDKTGLEDAICNRTIRTKNEEYSIGLLPDAAENARDALARYL

YGKLFEWLVSRINEIVENEDCNVPFIGLLDIFGFEDLENNSFEQLCINFANETLQQHFNR

TVLRMEQEMYEKEEIQWSFINFPDNGPCIELIQGKPFGILPALDEECIVPQGNDQNFSRK

LYRQHHANPHFCASKTDIANHLFVIHHYAGAVTYDTFGFCEKNKDLLYSTMTAIIKRSSK

PFVRGLLQVTPEKKTLSKRNKGVASSIASRVSLGQQFRIQLKTLLETINVTDCHYVRCLK

PNDEAKANVLVAKRVCLQLKAGGVLEAVRVNRAGYPVRISHQQFIHRYRPLVNGH

>contig20904 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56815.1|) 8e-09 NOT\_ORF

MCICGDASLYRRAQRTGIRVVMAKVR\*ALGRRKCRKRFLKWEMCV

>contig24896-0 Frame-1F0

MCRDAGHNMRSCPLRTVPTATASEVD

>contig24896-1 Frame-2R1

MLWPASLHMPHLLCNGVLGSFRSKALALATNSNSDGFL

>contig25297 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59180.1|) 0.0

MSTPSDANMLEKLQQQLESMVTAKADNAVAGKQLDEKLRVAFKHPPRRPNMSAERLKEEM

ERKEWHRNTTSMVSSDERVLLRELQQLKEKMVQQAACDEFQTMIDRTRKERQERFEQHKA

FDASIQQLQLEIRKLTLAAHLKTAVAEFVTIDVTIPANKMGAVIGKQFSHVHQMEKECFA

ILEVDNKQNVVKITSAPEQAQAAKEAIEDITLATTQSMGLHPDTVKVLMFQQAKHLHELQ

TSLKLKIDINKMDGILTVDASPDKLKQLEQSINDLTAGKVDILLPSEIVPKLIGIKGESI

NQLMEDTGALVDIDKVTNNVRLVGTKESVNSAEKFIRELIEEQSQREKNFTPDDHDIFEG

SEFTKYKFEFFAEFLMFDKAKQLRLLRTDALNVRVKVYKKERRIHVMGNKKQIGAMDDAL

RERLKDFEQHHWVTKVADNHLLSLIIGKKGSKIKDIENEGKESNIRIDIQGNYVCVFGDN

DAAINDAKKNILKIVDTNQRAFFGTSRYLIAVLMASKREKLSEIEISSGCNVHLPRPPHE

GATRSSESESEQIKISLTGTVEAIQKAKEQLGALEELYGVRYLPLDDDEIPIVIGKKGET

ISDLESKSGAKVRVLRGTNGQPSELEMVGTEEQLKLAQEAVDGLLQTQNRQILQLDAFAT

SCLIGKNGERIKALRLANPGATLDAFINRGQVRVKAVNSEALEACVNNVLKTLQETYLTE

SVHMPQQAQPDNTNLSRGCTGSVLPNFKTLLEKHESISMRLQELEAEGGEGMKVSLQDDG

NVAKIRGPAMGIGKIKRFLEMLVTPDSPFVETITLPSISFASALEVSGQVAKLNENALRI

CKKTGCELRVKRVPSNMSSIEVVNIRIEGNNASKVYEAKTEVENVLQFYYTDCFQTLDDL

SPAIVTRVFELLPTLRAKFNVVLSLPAKTSLKIFTDSKAQTQEITQLLKNKIKVWKKQQM

EMPIAGWLVPILLGRNGETIRKLSLDCNARLDLNTPMTSGSRHEDRVLTISSRDDEAIKH

AAEKLEEVLTNHKKRSSIVDVSKAKLDVALSVRKDAAKGIHFHVIDSGTKEDLQVVIYGE

DYHERERIVEKMEHLLETTVIKNLGSSHVCVSCHYEFDTWIFDWQERCQNSLNAKAVFEC

DDRYSS

>contig26807 Frame-2F

MAKKVQIKFYMKGYRLKNIEKVMYVYKSATIREALEVACEEFAKESDITVPSKGNVRLRG

YNDYNSLLSDTYNCKEDMTLSSLGIYSGQQMFLEVKAFDEEWEEYDPRKLQLFIRRFCNL

EANSPQKSILVLRDQYMARCVQVDEELNLGSLCELIAKKFAVPADRMIRVIKKSATTYSM

SAAKVLNANDDESTRQLSLKLDLHIINGTELYFEETHDLQLPSLAEAFFEREANMITVNF

KYLSRSPESIQIDRRETIRTLKELISAKINLPSDRFKLLRGINSAGVEIKAIDSTLIKLS

IGSNHTVFALEGTPLNTGEYNFRLMFYTSCPSNEHQSVITPNDGHDLFDIDEVFVATGKD

ESLLVYVNQVVISEEMMVDDIREKAWKELVAKNLIPTDRQLSSSYIRLRDLRQSTFTSVL

VNGQKLVEASKLAVYEGRSIVAELLSEPETLDITHRIVEFAYVDRAKWRFGKNARKEVII

PAYEEEQRPDTYLADAASAVLSIPADRLAFARIPYHCNTISILDVLSYDFCPPSAYAHAE

SEYQELYLVIDTDVRITTMSNYERQSIQSFLLKKTEEKDQAQACQILVTQ

>contig27466 Frame-2F

MKSLLASMTLVFFSAMRLNLETSSAHRALDTSASRRLSTESALSSVFIPINVDDDSSDGA

EPLPTHQLAALPLPNRRPSLFNPAFGTFVSSISTKRRNSMIPGTTNGDSTQKHDAILQNS

SNTSTREQDEETTKPPLNFFYNHEVQSTPSKLRRENTSHCVHDYSSPAVEKLHEVISATR

SSICGQKFDRCELEFSNDYVKLAIWEERETRWKGSIKYAHMVRFCFAPVGRPPYILLLQL

DSIRGRSDFASFYDPIFAKVWEDNEARKQISSKLYGVVFYFEEELDYIRCQSMSDKYPKL

AHLFHESLSESEVRECVRLDASSRLRPRVDYKSSTFKTTGGRNLALLVGNQARSAIDSVA

SFFRPTSRPSVLENENFSVISDSGNSTRGKALDFTQKHHEESATDMAETKITLLNDHESS

NGKKSLGSIANAASELLKSYTQQDVTHERGLTMTAPFSIPQDENTSATIESSIRPATSRR

EADEMKRRQFESRRNEVLLTYPYDGSDASGRISVTLGDVDRLAPGEFLNDNIIDFYLRFL

WRHLSMWQQLHTCFFTSHFFTQLHGTNGAFELNQAGPDERFARVARWTQKETNLFEKRFL

FIPINDSF

>contig29419 Frame-0F

MALEVVAPIQCDHVQNVKNSVSEAVGLKILSSHTLGRLSRLLSSQRSSRSASPTSNESDE

SCSINTSSSTSVSTSPPINEDTEALCPPNALVKAKTKANLSILEKRMRIGKTKRGHTRCK

YIDRSFKPPEGNVINLQHEQYALTYGMMCGIRDSAGLQKPFKQRLTMDDFMSIDIKTFPQ

NSQLQHPFKFKDYSPDVFRQVRRRFGIDLADYMLTLSGDFNFIEFMSNSKSGQFFFYSHD

GRFMIKTQTKDESKFLRRILPHYFKFVMENPNTMITRFYGMHRVKMHHLRRKMHFVIMAS

VFDTPLDIHARFDLKGSRVGRQASPKELMRGSSGVLKDNDLLAKGFHLQMGVARRTFFLV

QLRRDVEFLKRMKIMDYSLLIGVHDAGCEPQSNLYSRSKSSGIVVSHQGDYATSDPTSPT

RSKLGLSMEVTRWRPFRSSSAPDNAIALQRPLSGASASIQTHLTLSPPSLPSYGSSSLGL

DRGSETSSDGGNGISFENAVDDFSSPANRSSSGSSLTPRSFGSPTEPLSPRLLDTAAYGE

CPESVFCKDEGGIYGRDRHGRKNGFVYFLGIIDILQQYNTRKIAETFLKGLRHNRRQISS

VNPDFYGDRFIEFVEKHVVQDDTLISSRPLLSPTYATSIVGTSPFKQKNSC

>contig29486 Frame-0F

MLPMIKLGGLVARTLTKPMARVVKSRSKVHPLLRVICEKLGQQQHRLSIKLHMGFRGIAN

YNIKPLSSDQAVEQGADLMGELLIFSVALGVASFEYSRSAANARNKEATHKELQLQEERE

METRFARLESQVVKLEKRLTELARIKDSEMGTRLELVVAETERQNKIKTIAHHTSSGASN

IKRGAQQSDQNVHVGIDIDENLAAKITSSAAKLWTSTSNALARLF

>contig30387 Frame-0F|Blast-trafficking protein particle complex subunit 2-like protein [Phytophthora infestans T30-4](gb|EEY68291.1|) 2e-39

MGFHYIAHMSLDVIEEKLRGAGSSSSKDDMYLGFLGPIEDYRVYGYVTNTSIKFVVVLQD

APVRESELRP

>contig30628 Frame-2F|Blast-WD40 repeat-containing protein [Polysphondylium pallidum PN500](gb|EFA77608.1|) 1e-77

MLKEFATLKGHAREVTSIAWHPWYERLFISGSYDGSLMYWEVGKENALASIPQAHDTAVW

DIQWHPVGHVVATGSNDHSTKFWCRNRPGV

>contig32086 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59419.1|) 3e-55

MSMGLMAAVPLAFVLSPSPLAFPVDLALGVIVPMHAHIGINSVISDYVPLKMRTFARLGW

LGATSLMFLGLLRVNLEGPGITEVAKTIWRESPNKKVVKA

>contig33016 Frame-1R

MDDSGTAGKNWASFLDEHIPTEDHLVQSTSFNKQYSNDRLTSSDRITSIDRLTSSGHFAP

LARGSNKKIRDLISKSDLVSENTASKWLDVLRYDELQASIEAKEIFTGFEEPAIRFLPSF

PRQVGVAAKFSMVGERSCQKFFCDLDDEMLVVDSPPAYKDRILAHSLSDTKSRIKNIGYW

SCEKIVTSTHKPVCSIYELEIDRFFSYNMDEAA

>contig33063 Frame-0R

MLGDRARTLTPTLLQGASSWWEGEDWVLSFHHTFPGLSVPADPQQEALSRFWGTLGWSTN

PWIQDVKGLPMRASAYDRIATCTILT

>contig33225 Frame-0R

MWINSRDLTGDDDVGGSQGSVWGFASSSRSPVHKSIGAAGSRVLWNRMEPAEEEREEEAL

PSYLSYLQPSLQSASASLNPHAPPTRQSLYGTTPGLLASPPSKPMVPSSAIEQVTRKSAE

LAQALEQVVRGAMHGNCSIPSRKCQCNCDHIISQLQEMGTQVQALQNHVFELTKPSFSTS

LNVGNALKNGMWTAHAPPFVPKSSKHLPSPPLASIDNGIATVLSDRISTLEGRQSAFQSQ

LAQIVKVLGIPTGKANKHGPVKPLLQTLREEVDCKVEQATAKLTAQWEKKFVETTKVVET

NDFQHQMSSNVVLAALAKEHETSLARLSDSFEALVADETRQRVALEARVCLQLNQHEEWL

QQLEGVFGSPHAVKPEFEPRCKNVCAKVTELEQKWNDCWDRCQRFEQVFSNVARSRALKP

LCSANEDNCSG

>contig34303 Frame-0F|Blast-Amino Acid-Polyamine-Organocation (APC) Family [Phytophthora infestans T30-4](gb|EEY66603.1|) 1e-175

MPRKRTTSWTNICFCFGMVFVGILANAFSDVKALAFFCLYFAVFFVVIFYMLTRVNLLKG

LLYISREFLLYFRCKHGNFASYRQNSGEAHSFVGCIMVAKTIESIKNTPIVFFCKVANLP

MINEAVRYIMQNEDTYCLRLVHVCDLDAPLPLEFDDVVNLFDHIYPSLKIDFIAVTGTFD

PA

>contig34453 Frame-1F

MGSSNSKKQLTSGAALATTGNGVRAQITSKDKAILDLKNARDRLKKHQARLDIEASQLHD

SAKRLLQAGKRDRAKLALKLKKYKEQQMHQADEHLIQVLSLLDTVEWETQQLKVFEGLKA

GNLILNAIHK

>contig34871 Frame-0R

MIHRTHVLLFMFFQCKIGRVSHDMKSLVFPRILFG

>contig35201 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60459.1|) 1e-53

MAISLSPTILLYVRLALRGLQFVCSLLAMALAAAGFYGGGATHSSTFVLLMGYTGMLYGL

WYVVVVEVFHLANRPTLRMEQAVDALLVVMMLIAGITLAASDFTRNCGFGWRCNNLRAAT

AFDFIAMIFFFVSLCLTFVNVTE

>contig35964 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61660.1|) 7e-29

MNMTSSSHVLRLYHEMLRNAAKIETYNFRAYAVRRVKEDFRKHKTLEIGSPEQNKMLEFG

REQADVLYRQMVISKLYPPPIHSVMETLGK

>contig37184 Frame-0F

MLRDTPLNVPHPPPRSSVAAFIHWCGTRRHSRGYKHTGQFKCSALSFKPPPPSTAWETHD

VCARP

>contig37661 Frame-1R

MCLKRLRLDEAVRTVSAINMIQSPLFCIIINKSRLLPFELDL

>contig37874 Frame-2F

MSVIGVDFGNVDCVIAQAKRGGIDIILNENSNRKNPNMVCVQGKQRFIGEAAISMARAHY

KNTATDIKRLIGRKFKHQEVQNEIAHLAYTCVELASGDVGIVLNYNDEPVTFSCEQIVAM

ILNKMQSIAAAANEGVNPAYCVLSCPGFYTDIQRRALLNATKIAGLNCLRLINEHTAIAL

AYGIYKSARNLFHESEPQYVMFIDLGHASYTVSIVAFVQGRLTVKSATYDSFLGGRDFDM

VIAKDVAAKFAEKYKTNPLENPKSRIKLLSACEKAKKNLSPYGVTATQLNIECLADDRDY

NSQLTLEDFEGLIAPLLTRLDAPIERALIDAGIDKAQITNVEIVGGGTRVTSVKRHLAFV

LGLDLEQQNFGLSSTLNADESVARGCALNCAILSPLFKVKEFSVTDCVHLPVRLLWDGSA

STGTDAAADDEEDVNMEASTSDDSSLVIFNRKDEYPKTKRITFRRDKPFSIDAVYDEAAK

AYLSSDYDMSIGKYTISGMPGQEAGTEAPKIRVNVQQDMNGLFSVASSQLMQEIKEEKRA

EANTPVKEGDEKKDEILPEPKKKRFRKIELTIQAQVGGLSANDVDTAAEQELKMAHQDRV

IEETFDKRNELESFVYEMRNQITDKLAGFITGEEKGNLESKLVETEDWLYTDEGFDSTKS

VYQQKLDNMRNLSSPVEFRLTESTERGYAQAELTAVLEEYKRMVNSGDDAYAHWTDEEKT

KLRQTCLDAESWLFDGLTKQADLKPTDTPVITSASIRSKVVAVRAVALPITTKPKPLSKV

ETHDSSESAEATQAEDKNEANNMDLD

>contig37948 Frame-0R

MSSRNRARYCVFYLFVFYKQKKLKTIEYYIIRFSQVIPVYYYINMDSFNCTP

>contig38563 Frame-0F

MKIKTVEMDFQEKQEHRYPLAGAHGRSYALRYTNQSDESFNNDSDDTDDSEGTEDADEGE

HVQFVARHPVPLDESARLRWLAMHPNMISHVMDLPDLALLCTIAHEELQCDAAVVTLFGA

TACSIIASSDPALRGFEIPRDQAICGHTVMTNEPLLIRHLEADVRFAAMDQVRCQGLRFY

FGFPIKLACPRQNDTVVVGTFCCVQGG

>contig38725 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67918.1|) 5e-10

MDDDLDSGDLYSGLTLPKKTKRERLEEDKSKEKVGATAIENVMVKRQRMAEEPLDLRATV

AKLERY

>contig38798 Frame-0F

MRELEKIKQEREAERLQKEEADRKVVEQQSRDEILQGNPLTQQGVGSAKMKRRWNDDVVF

KNQSRNEPDVKKRFINDTIRNDFHRRFLSKYIQ

>contig39256 Frame-2R

MRNFKHVHGCGNSMESKPPATRLAHFTKRILVTGGAGFIGSHVVIHLVKHYPQYYIVNLD

SLDYCSCVGNVHSAISSSSCHSHQLQSANERSTEHEINHMKTSIVNEKQLRQRLHASFCK

PRDEYRSDDEFLPSNYKFIRGDVTGSDLINYILDSEAIDTIMHFAAQSHVDNS

>contig40308 Frame-0F

MATEKISELEWEQRHTQALRETAESLQAGRATAQLLSMQAEQLGRSERIVDETHATVALA

SRVLRGMTWSGWIYNKVLAAPQLSTCKELD

>contig40519 Frame-0R

MCLAQNDMTDIAPRLTFRRFTEQMYRRKGTSTKPFMRRLLRHRHCFMLSTAKLWRVDSTA

ARRSSVALFNDYLRQAKLRLTQLPLPSQVHLFLGNEAADADSIVSSLCYAFLHCQHDSDR

LHVPILPICRMDLALRCDVTLLFQELGVDTDALVFVDEFPWKIKSIVEVTLMDHNAVTNK

NIPHGYDLQVVEIVDHHSDLGQHLNAQKREIAFADGKALVASTCTLVAEKLFEFDSHDVH

KLLATMLLGVIALDSINFDPTAKKVTPRDAKAAKLLEEMAFARKEDLYDWLQNAKFNPGR

WQAFSLEETLRVDHKEFTFVAVDGSAKKIGISSVLIDLKAFMLKAEDASALCRGLSSFCN

QNELALSLVMTMYMMPDKQCQRQLLFFEEDGIYSKHCVDFITKIGFLEVVPLVLPAVYRD

ERIVAFDQLNASASRKQVAPIILSALTKVPRRA

>contig40964 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57288.1|) 0.0

MQSMDASEERENDYLRFLRGMRPEDASIQASMPDLSTSQASELDFRTTFVETDGLTEIDH

DGAEFARLLLAQAEQEQKETDLETDEVVVAVQTEVEEAHYAVDSVLHLSDLPSHNRAQSK

PLASTSTDAFVLTKKSCRFYNRERERCKRAATGLDGRCAIHKISQFCKHPKCNKYNQGNG

FCIKHGGGKKCKHDGCEKQVQGYGYCSGHGGKPLCPVEGCENKRMEGGFCKAHGGGRFCQ

HEGCKRRDIGGGLCISHGGGKKCNVKDCTKVDRGGGFCKAHGGGKKCESDNCRNWALGGG

ICPEHKGPGKRCKMLGCTKYDLGGGFCIAHGGGRKCVVEGCDKIRQVNKRCRGHGGKVLC

CVPNCDRAAQNRKLCKAHGGTKLCQYEGCTNKQKGKGMCIRHGGGTRCKVEGCNAIQRGG

GYCKGHGGGKKCSYTFCKKWVVGGGYCDDHLDLELSRQSEEISRIAASTYLASESV

>contig41303 Frame-2R|Blast-40S ribosomal protein S15a [Phytophthora infestans T30-4](gb|EEY65467.1|) 2e-33

MDHHEARRKHTGGKIIGFFY

>contig41426 Frame-1R

MSSASALGLTLIVSGVSALVLICVVILCARYCRNSDESVTIEFVDVRNLQLREDLVDTVL

DPGRIEWQCLVCAHMNHPNHELCLLCGTSIEFSTMEETIEDPQTRKRTRRVARTTFLGSD

HTMLLSSTLLESMASTSDTTNALQDSLAPATLQKAQTLPILRHYSSENDA

>contig41453 Frame-2F

MKKVFLRKQPCKIGGLTQLLEPLSFGPLVSNSFSFFSLSNHVQRIKSFLDVLATVALPTT

GLGISVSVESDGIAIDDQPRRFLLSGRSEGVAFMI

>contig42593 Frame-0R

MLFMAFRAFIYLPRETALALRERQDYRGGWYYLLCWYVTKMAAELPALVAYSIALFAPVF

VLVKIDEGFLIYVSMQIVVILAGWVAVALAFFVLSALRDATRALMVYVVIVTTFIVMGGF

FLNVTNIPDWLLWLHYLSPITFAYEAMMKIFWQQVKTIACGNTCVAHTGEQVLELYRLNS

SRSALSDSLLLFAIGIVLYLATLCNLLLLATKKRHSTLQWRYDWKYTTLVHRKKRPKTTL

THVT

>contig42661 Frame-2R

MASAQDKQKEYADRNGRKNNERFRVGEKVVLSTATLPKNAISVLPGGTTKLLSRFIGPFT

V

>contig42715 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61820.1|) 1e-147

MQPSLSIYENAIESCHKAKKWIKAKHLLEEMRTYGLIASIKLYKASIRLCIVSEEVTATQ

VLFDALCCAHEEELERETKKEIMTDLFNAAVDVQSLPQSLFFREKLLADKFCLSKKDYTH

LVRLCAVKRQWHMARVLLQQSVDMNAPPPVAAASSRYTDEIIPLLNEMKENDMEKPLIVY

NAALRNFGQLSLLKNAMAVYSDMQKENIVPDATSFAALLCSCGSNVEQSEAYFREFQLQN

CDPSLDVMHAYLLVPSRAKQWNEVLRRYDMIQHDACLQNNLTLNSDVRIQSLLAVAYGRV

DRSKDMLRIFTSMKVKGMEPNLHVYGEAMFAYIRQDQWRHALMLFDHLFQQQTPEMQENR

RLDSFPMIWDAAVLACVHGGE

>contig43381 Frame-2R

MMSSLSSQVRLKWDPVDLTLRGLSISSVKVVCCVSSIRAASHTLSSVGSETHTCAPTSIT

AYN

>contig44627 Frame-1R

MSLGRSTRRRHHHSIISPLQNQDTAMILRSCHSRIYCPLWHCMPDD

>contig45387-0 Frame-1F0

MFLKRNDESLQPKGDEDSIQLRQMLTSCMINRQIL

>contig45387-2 Frame-1R2

MQDVSICRSWIESSSPFGCRLSSLRLRNMFVRIGILKFVGKIK

>contig45552 Frame-2F

MLPPNSPTRSAIALSELRSSIVATHKVGGHTDYAIRVQADRFDDLVYRRFSAFLQLQQLT

RRHFQDHVVCCDGNKSCLLAPFLERVFVDTEFPVMQGCFLGKNSKTVVRERVLFLNAFLL

ELEESLCKCPPLVMTRCEKQNCKITKLLKSFYGCLDVSGNNSD

>contig45628 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55642.1|) 7e-79

MVTEMLEQIRNQQEYVDSVYEDRTQRTEEKSFVNKLYQMEIDRLRYMVTSYLRTRLHKIE

EFAFYILKDSAQTQRLSAKERNFAQQYVMLYETHMCDVALGKFGDENRTLTAEGMVATPD

LDTFVFCQGKEAGGVQCDDKGGDFVQVTSADRYVLRYRSVQNHVQAGKIDLI

>contig45695 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53532.1|) 3e-44

MQERLFGRYPDLVYDDFSVLSDHREVRKLVHD

>contig45754 Frame-2F

MRVLALKVAGLATHHNIHPAPAPPP

>contig46063 Frame-0R|Blast-ATP-binding Cassette (ABC) superfamily [Phytophthora infestans T30-4](gb|EEY70549.1|) 5e-12 NOT\_ORF

MHTLLKAQHRWLFDDQERKLLIMEPLSLSTPNGTASCD

>contig46089 Frame-2F|Blast-DNA repair protein, putative [Phytophthora infestans T30-4](gb|EEY57036.1|) 7e-65

MPKISGIVVAQIHEATLRDAHAVQQQHTIDKAIDWNQKLVLRRWAKLVKRLLLRQRLDED

YGAV

>contig46225 Frame-2R

MEVMNAYERESENDTDRDSSQNTIHRSSELLIDETTSPVEHFISRSSSDTLESDHDKEDD

EDDQDNDNHTIPTYVCEIHDPKPILIAEHIPCHRVDILPCDSTNGYTETILFRYTISIGR

VQQTFECLPSKALD

>contig46575 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62203.1|) 1e-34

MCRNCRRLFFRPLAIAADTSAFCSRDCQSTFEYRRYLQNTAKKCEP

>contig47019 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67598.1|) 4e-50

MSPAAVGKVDTRSIFRIAMELEHAKKLRLLQLPLPARNVSTKFRALRCIVAPGYEHNDVF

IQGFVKNYCRDERLRRIYRNADQNEVVCFHKSENEKDYDIRHWSSRKIVRTSLSATEAKA

GVLKEVILKSSDGREGQAAKSEVISQ

>contig47608 Frame-1R

MKSMKIQELGQFEQRMKNQLGILVNVIYQVMLVRWMNRKMRFPESWRVLDCVEEARSEDV

KGTGLSAMGGTSESGYDGTDVESIEHHDARLLTSRQKANSSFRRPCVVSLREVHSKAISL

KQSVGKNDGSETSREAMSMVTKRLYGQTTVTGLLEQLQWSTFASKSLKETDSMSEDWRVT

CATCQVCSVTEKALRLMETNASHDGDSATEKRLSSFSSETKVASIKKGS

>contig48371 Frame-2F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY54394.1|) 6e-80

MQAANAGVKPRAPPTDQERKLMDVLLQASESRFVPLLACIKGWSLEAQADLANWRPVLVK

LHNLLLGALQMCPHLLFVKTEVKTTDQPIAMQTEQELIELVCEVLKFSGFLLENSSNKAV

YPSAEPVMALLAARNERIICEATKVAAMLATPPQIHRHTTDPTSFVDPAAGKNTLLRRRL

LTIAQGRGAPKNSLEVVDYLHAAGADAPKDIDFQFYSS

>contig48465 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68253.1|) 4e-76

MTRPLVVYEAGGGIWRLKWHPEVARKELLLAACMDNGFQVLELAASDAQVNKVASYTNHK

SLAYGVDWWLHPASLQASAPVVGSVSFYDHAFHIWRSSIAARTDC

>contig48803 Frame-2F

MLLQMKILWMTAFTFQTQRPQMTLQTPMAALGLPQSRDRGRTVALSPIKEINRDRRRGAI

MVVVATALCACVIMTWRIIMQLPSSIAFVAIAPPHRSQHETLLRDAKQNFFSNKQQQMAV

EHQYNNQNQTRGFHDEKQIVMVLTHFRDSDTCAQLIINARDTASLAIRIHFRIFEELYLT

QEYTCVQRFCELEAEECKRMLRSRQLQTQRRDASGALGETVARYLAEGMVERKFQNDFYL

SVDSAIVVFTENWDLKLLKQWYSVGNVMAILSVAPKAIELRGLSNSTMLVHCSARIHSKS

LDAVVEFNAPEPMPRQGTALLSPILQTQYSELFHFGPTRALFDVRSDPHTPLISIGHEYA

RATRFWTRGYDFYAPNDDVLFARYLWKEPPLPMSSQSMNDDTVKWRQRRVDEANRRIRRL

LGLPVSILDGQLEQFETYALGSIRSMEAWQQFSGVNPRKAYNESTTNQFSRCS

>contig49196 Frame-0R

MVIYIVSSYRYKQVKSAIASDDADFAGRTCDIKASALMYYFRHCMRWSCRNCFLHETCSR

LFFLQRTDNLARSVVSCYKHTCECI

>contig49202 Frame-1R|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY63580.1|) 1e-68

MYELQLKRWPEPSLSGVIGQTTAVQTHFVSDERLRDLNNASFPILIVSAMRDDVIPPTES

IILKEHLSGDHVHTLFFDAGGHGAICQYADEIADEVVETMRRASPCDNL

>contig49574 Frame-1R

MSVLFGKRRRKLTCDESIPKDSSESEASSDSEAYSNNDKVLVENAPNVLTSFLNLGVDPW

LVKRCELMGIRQPTPVQSHCIPPILSGRDVIGCAQTGSGKTAAFALPILHTLSKDPYGPY

ALVLTPTRELAFQISEQFNAFGSSMAIRCAVIVGGVDMLKQSLTLQQRPHIIVATPGRLR

DHLLRVEPPNISLIKYVVLDEADRLLDISFAKDLSFILARLPAKRQTLLFSATMTANLDR

LEQTALSKGAFRFDASPSVKTVATLKQFYLFIPA

>contig49893 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70220.1|) 6e-17

MHYGFVDGLEVTYGNALAAGNGFHRVTTADGVAAEVAPHTYLWYKLSTETIPFTSCET

>contig51489 Frame-1R|Blast-transcriptional regulator ATRX [Phytophthora infestans T30-4](gb|EEY59457.1|) 4e-40

MSLVETLKWLKLSKLPGGCRIAR

>contig51782 Frame-1F

MNFAGHEACVCKFCGIYFSSAEYLETHIVRRHGRKSVELETLATVKIQRRFADADLKEN

>contig51838 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53711.1|) 7e-76

MASCTWRNVPLLDACSSLTSDGVQLLEHIENEERLVIITLMGTSSTRTRRCELMAKLLGQ

TEAAIPSSHDESLVLLASVINLDDEFQMLVFDINTTETGTSAEPLSPKQLVGVFCALSSL

VISCFEDNGSPSSLAPYLPQFQSLFQALTKEFALMEVFDMLPQMLSIDWSTDRSLGDMLA

DFENENSVCIANTLARLVKYMNLGICYPPGAVQMTFDDFTGVQATVKRLFGLEMTGEMFS

ALLQNVLVQLLKQEPLDFGSAWDDHVEDKCR

>contig51962 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64236.1|) 4e-28

MKDGGMTTSLYKSMDGDTAEELISIFQQLENLVLLNPQVEHKSKLVVYNATCVHQLVALL

HTGDNDTIRDTALRVLQSLLSSDCALYVVPSKQ

>contig52170 Frame-2F

MRPAEDLPPFGVDTDVLCTSLLIVHAVVVRVIHSTLLPQLVQSTTLPSLKWRPEKIGSLN

LCLPLRARHIFCGRLWQVEMAGAGFSPKLSFAR

>contig52835 Frame-1F

MNKSDADDTLAWMLDDICKENARLLIQGKARLLKRIERLHRELKDFHSEHLALAGSHSVS

KSDDGKAVLLRLLDAFEF

>contig53630 Frame-0F

MVCPTRSSRLGITAVHLFIILITTICSIYCHQKAVTSAYHASCDVCAKVIKLHYFVELCN

KIVSNNGRCCIF

>contig55333 Frame-2R

MNTSFSDLTTDTTMSMHLCPCQQITSITNPLLYFANLNAAASFSFNTRSSTELLHITQSW

RSVATFNGFKLDNLALLCCCARVDMDISEALQRAAANFRCVRISCASMLDAKSCSAVIFA

GASPRSSSSFLSRGIEGIRMMVGCH

>contig55405 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66327.1|) 2e-12 NOT\_ORF

MYTRMATMVSEQGEIISRIDDDMNLAYVQHRYRDVCVVCNT\*QMLIFRQTNVESAHNELL

KLFTMVH

>contig56596 Frame-1R

MDSMLDRKSLQSILPMGKCPTASYETAKATQAMQKVFRCMFPGCGREFHLKGNLKRHGHI

HNGDKKFSCKFCGKKFLRKADMEVHYRVHTGEKPYRCHFKECTKAFARRSDLLSHERTHT

GKKPFACTFPGCTRHFARRFDLHKHQRLHNNQRQASKLPTKKRKRL

>contig56718 Frame-1R

MKTSSNPVDEIKPLICLSRQDKLKSVTTQRTKRPHFTTVVPNGSDVKKARRDEKLPIESE

LDRDGWTSEEYLRAMDFDDRLSQDIEWVDDMDLALTIEDHAPTDDVNDFSFQSSFLRGSV

AYDELAEMTSIVVEPVYTPSDRS

>contig57065 Frame-1F|Blast-T-complex protein 1 subunit delta [Phytophthora infestans T30-4](gb|EEY58178.1|) 9e-19

MQVYHPTAKMLVDLSKSQDIEAGDGTTSVCII

>contig57771 Frame-0F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 1e-34

MAFAKCVLEMCHGWHLLVSKESSTTSSRSFSYGMALGARILWNGGFAGLFGLMIYVPLNE

AR

>contig05601 Frame-2F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65627.1|) 2e-62

MLFLIQPIQEISVPNVKMLKKFKKIELSAGESMDVAFTLSEEDWGVYKPQIGKGLLRIVE

DTNYVVAIKPDTECNVYNGPLTNPLCAQFTINLSGTPVSSDALYSPVLINGGDSSQSTGA

PVNGVDYFQSTGAPVNGVDYYKSTGAPVEMVTVHDLTLNSLDNSGAGNNGDVVQLQTSTG

VVNTVQPQVGSD

>contig09995 Frame-0R

MCVQPVAIYAVKTCRERLLEHFGHQLGNKLQYVDFSSKASPFSIRGYIALIPEEPKALGP

GIKQAKSYYQFVFLANESIKECHRVCSRVITEAAVKILSAIPIFVLKIEALRDTYDDFGV

GVTDGVLFKKPKEITEFLFEFIKSLIKTDPILSKSEFQVLSKPCENVSPDQTMAPDSEED

SLKTFNCFQDSNCATQYWRNAIRPTIPRYCSQVNDIDLDYFNEDDGCPPSIQGHCELAAP

CQLQRNLIETPSICHGCGRAADVSESNTVLGTDNKRNKLRGHSRGGHKYEGFERSRAVHS

YEEICFPSKALSPLLKPSPPADV

>contig10157 Frame-2R|Blast-glucokinase, putative [Phytophthora infestans T30-4](gb|EEY70573.1|) 1e-175

MSGDLIISGDCGGTNTRLSLWLIPKGSVAFKGSVAPGEITFAKKYHNENYSCFSEVCHLF

MKEARLQERLPVACVLACAGPILNNTVEFTNIKDGWKIDGPGLEKELGIATVKLINDFAA

MGYGLLTLKPHEYIILNDAKKEEGMPIATIGAGTGLGECYLTAGSDGHYSCFACEGGHTD

FAPADEIEIELYNSIKEELGCSRRFSVERIVSGPGLATIYKFLAKKYPEKVDKKVHDAFM

AAKSLQGKIVGDNAKTNELCNQAMELFVDAYGREAGCAMLKYLPRGGFYITGGLAPKNLD

YFTKKDIFLNACFNKGRVSPALQAIPIYLVLTEDLGERGAHYFAYQLLESYNTSLLGNTI

ARERAQAKYATPGHLALYSAIASASVAAGVVVGNLLRK

>contig12717 Frame-2R

MKISYTTFAATILLTNLSTISGAEITNFGPTDTEGHLPMSESSRSPTPLVQEETPTMTVF

MSNSTGEGTGEPVVNEINGMQPLPASESMTGLSDLLNVNAVEEPLGVEEPKVGEEPNVEE

EPKVEEDPKVEEEFLSSEELTAGEEPKVEEEPNVEEEPLSSEELTAGEEPSNVEEVKVEE

EPSSIEEVKVEEEPLAVEELKVDEESKGEEELKGDENHEGDEEPKGEEEPKGDEEEDSSD

DSSQERKNVNEEDPMKSEE

>contig13000 Frame-1F

MGDRNENGRVVMIVHANSPRHVDGLSVSPGGNPSDPLAHNLSVMEVDWRQQQFQRQRMQL

LSMAIFLCFLVLFFDNRAGDARHSRAVTDSLGHNRYSLPQNAFNDSDRVQKVHELETLLQ

RQSGYRHHEVPLNVTGIYSGTWLSLHVEDYNAKKTVYEDIIPYLKVDREIQLQQYSQPVE

KGHTWLFLKMKAPVSKELTKEVAYVTGQLVIYEEHASLAATILPVQGVFFRKLAKLTLFG

NSPDSSVQILYRKDVYGGKIQPMG

>contig17457 Frame-0F|Blast-phosphoribosylaminoimidazole carboxylase [Phytophthora infestans T30-4](gb|EEY55751.1|) 0.0

MPVLTTDIHGAPPPVVGVLGGGQLGRMMANAAHRLGLQVLVLDPLGAASPAGQTGLHAIP

GSFTKEDDIAKLAQKCDVLTVEIEHVNSAFLQQLQDNKAANLQGVHPAPATIALIQDKYQ

QKQFFNQVHGVDVGPYDIVTSLQAACQVGNHFGYPYMLKSRRYAYDGKGNVVIRSEQDLV

SAFEKLGAKELVTHGGSVDATQLTKDEGKLYAEKWVPFVKELAVMVVKGANGDVRAYPVV

ETTQRDSICDTVLAPAQISADVATRAATMAQMAVAELKGRGIYGVELFLTATGDVLLNEI

APRPHNSGHYTIEACETDQFEQHLRAITGLPLGSCAMRVPTALMVNVLGDATASEDVTFA

LLRQSLHVPGAVAHFYGKEGVRAGRKVGHVTITASTRDELRTRAFALSPEIVKRSSLKSL

KTTPVVGIVMGSDSDLSTMAAAADILEHFHVPYTLTIVSAHRTPARMYEYARTAVDQGLK

VIIAGAGGAAHLPGMLAALTPLPVIGVPVVTSTLNGQDSLLSIVQMPRGVPVATVAIGNA

TNAGLLAVRILGAGNSSLVEAMATYLDTQKRDVEDKIEEMATLGWKTYLASKSTQ

>contig17538 Frame-0R

MADDTKTTIVETNVAIDGDSTEITRTMNTTTRFNFPFTKAASLLAAYEAWVGTHANLARN

VETSLYVAPQLVPKQVMEPEMATQFGYSMVGLLHWYHDYILWKKSNHDTDPPTNWLTFYR

LVRVPLSFISHTQVLAEVVARRVSGDVGKWRFILWFEVLKAVLRLVLMTQHRQAMLLRGG

KYQGVESMPQPSVFTRFQKVKQPGARTGKIFGKLMSKVPEPLEEKSAEETIQLVFEDAIE

VVENSRENFLVAGELCHILRPVVYAVLRRRRAPTSWTPVLVSMFIELSGLALSVSAVKPV

KSINIDKARNELATR

>contig18023 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY59777.1|) 5e-69

MSLQCVSKKLASHAVAPTLARAVTTNTYSAKQASLGRPISPHVEIYKFPVTAISSIANRF

SAMGISAAFVGGSALALLGADVPALIYSAQNNIPLFAPISKALVAFPVSYHMLSGVRQSL

WDYKPELINNVDGPTSSYALFVASGIITVGAAAYTIKAPEDKETDQ

>contig19547 Frame-0F

MFSPWDLVRPTLWHPMSMLELSMMEPSRLLQPPVSVTLIPGISSDEEFFKDLPTSVQQQE

KDESVEAENQKTFSSYSISSSTILDENGQKVMSTRRRYEDSSGRLKAEHEREVSNKRVKT

VWNRMNAKDDGEHHTICSQVTPDEFEKLWSQTSFGKAQEKKHQELKESEEGVTSGQEQQM

EVESAPVTNAP

>contig19961 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56544.1|) 6e-74

MSPEKLLPNKVLRTSVNEFLRRARTEQQEREQLVKEAEEKALAKQKAAEAAASSASRRSG

DSADATLDIKKSKKGDGGDEEDDEFGGDIFGDGDDLEGANSPLKSLTPAFPSPPQPPEQP

PLPKDQAKALKGGDTSSPTQKPGDESSTVGGQA

>contig20756 Frame-2R|Blast-GJ10066 [Drosophila virilis]sp|B4M5A7.1|IF3D2\_DROVI RecName: Full=Eukaryotic translation initiation factor 3 subunit D-2; Short=eIF3d-2; AltName: Full=Eukaryotic translation initiation factor 3 subunit 7-2gb|EDW59818.1| GJ10066 [Drosophila virilis](ref|XP\_002056706.1|) 5e-38

MKLGYVSRLNFKDPYSHVVLGMQSYNPKTFATQIALNQNNTWGIVKMLSELLLEQPEGKY

VIMKDPNKPIVRLFSVPLGTFDEESEDDDNDEDYEQ

>contig20903 Frame-1F|Blast-RNA exonuclease 4 [Phytophthora infestans T30-4](gb|EEY56804.1|) 6e-87

MGGKRKRSEGLMPVRQVNKTAGKATQYATRKKKSSTSIKASGLTMPKLQKKTEFMTVANS

NWRALKSKIQQKDQLYKRGKTIALKQDLNVVAQKQLLRQEKLAKRMKERTAEWVDNSIIV

AMDCEMVGVGLSGKTSVLARCSLVNYHGAVLYDQYVRPVEKVTDFRTHVSGIKSSSLRHA

IPFKECIKDVGKLLENKIVIGHALQNDFQALMFTPPKQLIRDTAFYRPYMRRKMKGT

>contig23050 Frame-0R

MDDMVSSKKLVEASASHSASTSSICACLRLRCRRIFFYS

>contig24583 Frame-2F|Blast-alcohol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY57441.1|) 1e-155

MLMPQSHYEIPTTQTAVVYEANNAPLQVRDDWPVVQPKDLKTGQVLVRMAYTGVCHSDLL

VWAGQGPPLLKPFPMIGGHEGAGYVAAIGANTTTQLNVGDAVGLKWIAHSCLNCEDCRKG

YEPLCFKAGIHGLSCRGTFQQWCVSFADHVTPIPFKLDLASAAPILCAGVTVYKALKQIN

MSPGEYVVIPGAGGGLGHLACQYARAMGYKVVAIDTGIEKRELIESYGITDFIDFKSGNV

VEQVHAATGGRGAHAALIVAGSQDAYKDALTFLRPRGTLVAVGVPKDAAIVAPVVPLVSN

ELRIMGAYVGNRQEAIEAINMAADGRVKSTYVIESLTNLPDVFMRVRQGKVQGRIVLSCE

>contig25045 Frame-0R

MAEDNDECDSLEMAEIGQEGKSDAVFTGSKSNLSFSPYQGEVNVGTVSPPP

>contig26707 Frame-2R|Blast-UDP-galactose transporter [Phytophthora infestans T30-4](gb|EEY68799.1|) 1e-141

MKIKEPLRGKRKAESFHIITNPGELLRISVPAVLYVVQNNLQYVAVSNLDAPTFQVMYQL

KILTTAIFSVIMLKKSVLITQWGAIVTLMMGVALVQMDDNTSSSTSLKHDDYQSTIRGLS

AVIAACVCSGFAGVYFEKILKGVNSKATLWERNVQLCILGLALSGGGLVYNDFNSITIRG

FFYGYRPVVWAAIATSAFGGLLTAVVVKYADNILKAFATSIAVILSVIFSALVFEKIPTS

QFIVGAVLVNGSVYVYGKAPEWGKDRSKPGPAPTRDNVLKEIKHIA

>contig27159 Frame-1R

MSQSWGRNRSQNRSGEIRMKCIPTETMLESLAEYQENTQSDELNPLLSLKSYTMTSTSET

RKVYFALLHIHPMDFDITFRSDVFQTSTTLSLHEANTFKKSDEEMKRSNSAPTTFSKSNG

DEISSVSWAIPSLTMHVPDLDNAPVRLNALMIEHAFGTSSDLTRRVSKYYTRQLWKQLHK

ILGSFDFLGNPVGFLDHIGTGVRDFVYEPLEGLKIGGKGFSKGLAKGTASLMSNTVDGTF

DAASKISGTFGQGFANLSLDDHYQQNRARARRRHVRGLREGLIQGSRELSLG

>contig27414 Frame-0F

MGERRTLSTRCNGSFLVLFMPNCTFMVNTSNMSKVSKLISFKLINYGPHFENSASLSYTK

RGR

>contig28640 Frame-0F|Blast-methionyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY54201.1|) 0.0 NOT\_ORF

MSTTADLAKRMDQLEVVQQGHDVRLNQLREKVEAKYTVNKTFYLTTAIHYTNGQPHMGHA

YENVCSDVICRYHRVFGRDVHFLTGTDEHGQKIAQTAEAAGVTPQELVDKYAGIFKQLTK

DLNMSNDDFIRTTSDVHKKFAQWLFQSALDTGDVYLGTYEGWYNVREETFVTESEAQMTD

YKDPTTGTPFKKMQEQSYFFKMSKYHDRLVKHIEENPDFLQPEVRRQELLRRLKEPLQDL

SASRNTFTHGVPLLNDSKHVLYVWFDALSNYLSAIGYPDGPRARY\*PANVHIIGKDITWF

HCVIWPCILMSTGIPLPKRVFAHGFVNAKDGSKMSKSIGNVIDPYEMINKYGLESFRYFI

VRSAKFGQDMPFSEDDLINIHNSELADTLGNLVHRTVNICKKYSEGYVPSAKADKPFDVY

ALLKYSEDSYKEFSLQGACIAIVNALKDTNKYLTEKEPWHMKENELRLVVVRTCLEAIYV

LAHYLSPIIPETARRIFEKLGTTSTTLTALSPDYDNLKPGTKVSIDDILFIKILTEEEKQ

KQVAASAAKALPAKAKPTNVAKPLFSSLDIRVGVISKVWKHPESEKLFCEEIDVGEDEPK

QIASGLQAFYSLEEMQNRKVLVLLNLKPAKLGGFKSNGMVLCGSDEKHENVQFVEPPPNA

KVGERVTIASESGEPLSASQIKKQKVLEKILPYLLTNKDCVATYKGEQIMTSAGPCTTKS

LKEVCIN

>contig30555 Frame-1R

MYRTLFAIVLQSRSHVGPDAIGGVAWYAQSAPHGSVFVPFSCTQDSVPQSYLLGRQSQFH

PQSAWWAFNFVNNWSLLRYNAMSIDIHEKIRALQKSAFLLRNKIETEGQNVHNETQLVAS

IEKQSNDFAEHVITQWWQLAWTLVSKYSDGYMTTGEAPDQQASIGYPTWWLQASEFASWP

GDSFLPDMRIREKLVIDSETAQGFLRRTATFDKVIVGIQSYPLAIAWVILGTALIVTVVV

YAKREKSRTGYHILE

>contig30753 Frame-1F

MSVGSVVVSRPENSLDDIVECKYINYSASGPKNILEGACAGVGAFAHVFASGLKDVVVKP

AEGYSEEGAKGAIIGLAKGLSGLLISPFKGTVMFADNLASGVNNNIREGEEMKKSATITD

KANIFNVINAKVDGYSDGNALPSTQVTIQLTLEEKSKLIERFTALMDKQTVQDDDEHKLS

KDAPSNAVCMENTEEAAHFVASSKKAANNESVTFNIPSASAEKVADLLLNDNARKVKDEI

CFKKKGKYNDRLVRKVRPRMNIVMMTTGTWEECVQQYVAIGLRLKADGHRVRIATSGGFR

ERILGAGLEFYPLGGNAKTTESFMQYLHQQNQQQPQHKSHLINYAHSALNHWRESPIPMD

DLRDLVFSLWPACVDDDPLEAKSPFRADAIIAHPTLFGQTIVAERLGIPLHCFSCNPHSR

TQAFPHQISPNMKLYRPHRYV

>contig31758 Frame-1R

MIFFALLAALATLIKAVAAKDGSCVLIDFTAADAEFAELNAALVSPSVKKQLGSMMKRID

PIEKENVTLDDASFGALGLGLTLSTTIESLSVSGLSTIALLNVDVKDSNSVSIKAGSPGK

VNFTSKMTIHIKELHATIEAQVRFVLVKPKFKIGIEADMFACAPKVPESQCSNLTVAGLQ

SDFVSLSSKSHHHASILKKLLMKFKKASATSFSLKFESVTGLTTKFDSPNALVKTLIRVL

PEYSEATISPTKSLYQKLGPNLNEHVPLMLNTMIASKLEPFFGATCLSEEQSQAF

>contig32175 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66154.1|) 1e-23

MHLAAFVSLVEAAISGQDGTLMAKMLKLNGKCTEVDLKALTVQQVRQVSHNRLARLDGYV

EVVASIMQARKHLDLRSFLDAYNAQIGAV

>contig33011 Frame-0R|Blast-delta-6 desaturase [Phytophthora citrophthora](gb|ABH10627.1|) 1e-150

MVDGLKSKRKITWQEVRQHSTHANAWIVIHLKVYDISKWDSHPGGMVMLSQAGEDATDIF

AVYHPTSSWKLLDQFYIGDVDESTEPRPVDLTDEQKAKKAKTEEFITAYRRLRMKVKGMG

FYDASLAYYTWKMLSTLSIWMASVAICWHFDSWPMYVLAACVMGLFWQQSGWLAHDVLHH

QVWDNHTIGNIVGVVIGDIWMGFSVQWWKNKHNFHHAVPNLVGNANTKYLGDPDIDTMPL

LAWSKHMASRAYDSSWGPFFVRHQAVMYFPLLLFARFSWLL

>contig33385 Frame-2R

MASVSPLDGNQSTNSSEHESHIDTRFPSSASFDDSVSTAINAPYRVGNVDADTCSYHALL

PGASCRKPRMCYECLNSDVASLATGCLLAPSGFCEDMSSFALSLDFRRNTTNDELREYNY

FPSTNTTYCEPIDEACLLCRQLAKTDATRQQDTINATNELERRFCVGQNNCVCLMVCESA

HWEANMPLECNSSDNLSK

>contig33572 Frame-2R

MNRSNHECPLVMRGIALELLEFIVGAGHFRHGEVPSWLQDFLQEWKGGDHKIDS

>contig34069 Frame-2F|Blast-S-adenosyl-L-methionine-dependent methyltransferase mraW-like protein [Phytophthora infestans T30-4](gb|EEY60150.1|) 2e-88

MLQEVITAMSRNITDVSKPRYFVDGTAGFGGHSTAILQHFSGSKLLCIDRDPEVLRIAQT

NLIDFQDRVSFQTGSYANMAQHLKASSFPNQVDGIVLDLGANSYHFDAAKRGFSVLNDGP

LDMRFDQQDASLSTAADAVNTLSEVQLTRIFKDYGEERLAKEFAKAIVREREERGKVFQT

TKDLRECIERIANMWKSAEKQKRMGKRANKMKNIHPATRCFQALRLYVNDELYHVTTGVK

QLVNHLAFNGRLG

>contig34304 Frame-1F|Blast-histone-arginine methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64570.1|) 1e-170 NOT\_ORF

MSEQKLQQTAAKKAISPKLQAYDVSNVTITKNKSEEDDDVNPFSQYYGMLLHQQNMLQDH

VRTGTYERAMLCNPTDFRDKVVLDVGTGSGILAFFAIKAGARKVYAVELSSMADCARDLV

AANGLSDRIIVIKGKMEEVQLPEKVDIVVSEPMGFFLVHERMLETFVTAGKTWRRQAPGF

KMFPSIGTMFMSPFTDETIYREQMAKVAFWQQQDFYGINLSTLRTRALANHFSQPVVGYF

SPDQLLSSKYAAHVLDFAEISNEQLDTFEFPFHFVVERTAIMHGLGCWFTVDFIGSDARI

MLSTSPHDVGTHWYQCRLLLATPIAVNASQSVSGNLHFVANTKFSYDIDMEVRLDGTSIV

SQNHIRLHDQMYHYLYPPNTASVAASSDGLQPPS\*SHFCQQIKSLNNELKGTLTIE

>contig35475 Frame-0R

MLMFKILCVLRVSQALYTESKTWKCLTFLKSIRFFHVFDSSKSSLKLSIMHLCNCKTTIL

QFTVEQRDYWPVTILAPDVKSLRNKNLYVKLL

>contig35581 Frame-0F

MTSAELQFLVHFNQTLCVSLSPNIATVSSILVLIQQFEGVPHSLLDLYVNGRKLDVFSHV

PSFPTIIRARLRGGLRGGKGGFGAMLRSMGKASGGRTTTNFGACRDLHGRRLRHVNQEVA

MLKWHQEAEDRKKNDNNAFEDREVLDEETPSGIPGWYLATPSWAEGIKKSYMKRRRNMVL

CRSWLKAREGGCIPPSGAPRWWGCPRGRDCDFAHGEEELRGGSLTELKRAKSETDQQAKQ

NQLQEYVDFEQEMPEDVMDAIMNGLRRRKKKTEVPRIQQEFHASVLIPDASSYICVRSVR

HSVPVVKKWLKLVGSEEGDGSVTTTFQHGLCELRGRGNFGTAAMRHCCALTQGKWYYEVR

LVTAGVVQLGWADSTLEANSATGDGVGDHERSWAYDGARRVKWNGGKDEEYGSDDSWSKN

DVIGCLLDLNEGTVAFTRNGVDLGVAFRNVKHMSSDRGLFPAISVEQTEIMLINIGSQPF

VYEARGFDPVIEALDAEELGGFDNDASVKSYGSYISNDEVSCTVGLDTTKKQIEASVLES

VKTDTPKGPQTEATTTTPIDLLKFKTIASLEALGLEKLKVELSRRGLKCGGNLTERAARL

LTVRGKAWDEIDAKIKAKKRLWM

>contig35963 Frame-1F

MLVEKEFILRLSDPEWEVRQLVVREVCDLSANCLNVVSGECLRAVGERMKDKKVALRKET

MTGLSQVYNKHISSYWEEQVDTKDWTLSLSHHTIPSDHIKKLGWIPDYVLKSYAYPQQEL

KLRVIQLLDDFLLPKALPAHIRTNGLVFLYHSLDPTSKEALRRVFHERATCQHVVAQFVA

FKAQNRSQKRVDESTLERAIHELYQGLCPLFNDIANLKKLIEKLATWKDHSVFKHMKTLC

DETQSLQQTRAARDELVRSVGSKTQLGDFLKKLCRKLSFLTMNQASIACLLDYLLAKKGR

QTKENRSVVDLLVMATKELPKLVGPFIRDKVAALLTKCTNDADSDNEDEPSQQDSNVILG

AFNILAIYAQYFAGTREFDHSSMNHDESNCPSKELIDLLEKLCRGHCSVKRMNFSAVKEN

RAAELAALSIAHFYPRTKRTTILIKQLCTKERISLCSESDALPTLQSLHVFSKHCSHQFV

ENSVLFARLWSL

>contig36333-0 Frame-0F0

MWLISNSQSRTRPIFTLWRY

>contig36386 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56866.1|) 6e-74

MKLVHSDAEQLRNLVAFWVLGFINNIGYVIMIAGAQEIAAGGVGLVYFFDIVPALLVKLS

GPYWFHLVSYRHRTLVGALWMLLSFLVVANGNDSLWLQLVGVAFSGLQSGMMEASFLALS

SLYARPVHCLTCWSSGTGLAGVGGYAWIAVFHLWGNLSFQTTIELASIFPILYVFVFLVV

LDTSKLPPRTYSYMPLPNGCSQNLAPIKYIVPPPKEKQMEKENVPKESACDASTLQLKDK

LAFLKMLGPYMIPLTTVYFAEYTMQTGVWSAIGFPVQSKAARARFYSSAGLTYQAGVFLS

RSSGVLYQATRPILYVMPVLQVLLLVLFTFVAITHWWYNWSLLIGCFIVGLLGGGVYVNA

FTLLSKEISATRVEFALAAASVSDTVGIMLADCVGLFLQGCLYSINSLPGAAINVTC

>contig37594 Frame-2F

MVSPLFRYQGQFSYHSRHVFSSNTSRVHLLHIVIGSALCKSISCCNSF

>contig37666 Frame-0F|Blast-Rab3 GTPase-activating protein catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY64864.1|) 2e-96

MLSERMRFGPGHEHIWQQMWESSAPVPACRQKRLFDPVQESEKVYHYMETLSPHELFHQM

LAGAISSSVFALETALPVRVSSETLPCVHVALQTLRLRANRAIALLDDALVESQAAFSSA

SRSKQQLDEGHQQSALHDQQLQVAFEMALDACWKLVRSLDTVEALVTKTLALLHYFPVTI

GDQSSLELVNLLLLPILTHSQQVQMSKLLERERLREQVAALVFTNPTSLAENDFSAYSHS

A

>contig37712 Frame-1R

MAKLLVWGDALFLVRCEFGELEVQRILVCADKKSTLRRCSVKIDKATVLPPDARLVATKE

VVDTQLAIRYPVLVIRASGEGAKEFLADPSPVFCKSQRPSEGKNTDTTLVDKS

>contig38072 Frame-2R

MPKPRYYARLSKFYAVKCRVVDVKYVFPTAGEHARCNTIKCELLIAVLAVPTTAVRQIVR

DSEEKEQEGETKENTSFDTANLFTPESSPFANFTSVDEHLLPSAREPTARFHFKLLYHSN

DVANFLVLDHVYESGVCGNWCVGDRVQMPFVQLNQHGLEIEAKLSYGTIENIIQKPLATS

SFKENSPWECVIVNWDDPEDDTCSVCPWEIESASADKRREKRILSLRRRSTRLYISRNIV

GEKCEALLQDMDQILTLSISRDFMYPVDEETFLDYPISIANPIDLTKIQQRLRLGYYRQV

EAFLGDARLLSTNCEAYNIPSSPISQNSRNLVAAILTQTQRHFPHLTRYATLRETATERA

SAIFSYPPSDFLTYFSEDPEEEQLALLDVGLLTQTSLSSTISNDATLENTPLDVPAAVAS

PAITAEHISSPRRTLRLRTHSREEITDEEVEKKVDCIAEQELSVSAETSQAQSTGSNRMD

ESTAAASGPRRLRNREVAELPLVLTRTRRSPRATIMTAS

>contig38209 Frame-1R

MPMSFKLWKPPMQIIPRTIGKAVVGASFPLNVIFKREDIVVDSHAGKDYDFITCFSVSKW

IHLFHGDDGIKKVFGKIYNLLTPGGRLILEPQPWKSYHKRKFTSEITAANYSKIQLRPKD

FPKYLIESVGFRSCDFLEICQTSSKGFRRPVYLAQK

>contig38511 Frame-2R

MFVFEAVHCGALALADVTTKTNLPFDELTVVAGRIQNSCQLTCLGGRLKRDGKRRLLVIP

LRQAHGSSTPSAQVLNVGKVAVNFLHGVRDCFPSLVKKDIKTDESDSDSDEEEGYKKKKY

DNNAKSPADAMAIEVQRLEAEAVEYMNLIEVKILASLDDLFNAFQISDPIYIKTLLRHDP

SVPSECQLLCIDCPPLGLSKPGVQQAVSHVFSTSKFPPEPYNCGVMFSEMALTNEITQFL

HIPIPRSPIKPALKGQGKVHIQESFQDATVLTFGTKREVTVYNGGKTCEEMVENIRMRHA

SGTFCTLVLPTKTWQQLVDEYKLIVPQASELRGKLRLRRLTGNAPCGASTELLLESL

>contig38982 Frame-1R

MKRQTIIDPSISQPDVTITK

>contig39224 Frame-0R

MTNTVSAASLNKTFVTLSLGMLDKLCLAPLKFVASLPLPINQLPTIVFIYLALTKNEEGA

VWYT

>contig39251 Frame-2F|Blast-AP-4 complex subunit mu-1, putative [Phytophthora infestans T30-4](gb|EEY56356.1|) 0.0

MSSSISQFYILSTRGDTIIFSDFRGDVESNSAEIFFRKVKFWEKGDAPPTFHVDGVNYLF

VKKNGLYFVATTLYNVSPSYILELLTRLCRVFKDYCGVLSEETLRKNFILCYELLDETLD

YGLAQDTSTEGLKVHVHNEAILVGDAVLSKPKASSKFMNRSSNIKAASAVKKPVATAGQS

SKKQDENELFCDILERLNVVFSSGGQMLNASIEGRIQLKSYLSGNPELRLALNEDLVIGS

TGARQYGQVVLDDCNFHDCVQLDEFERDRVLIFQPPDGEFTVINYRITGDFRAPFRIFPF

VEELSPTKIEMVLKIRADMPENNYGANVIIRFPVPQSTVAVSCDIGKNSAGQLAEYRENE

NQVRWAIKRFTGGTELTLRAKITLGQPSPHVRREIGPVSMNFEIPMYNTSSLQVRYLRIP

EHARHPNYTYKRWVRYVTQSSSYVCRI

>contig39677 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54965.1|) 3e-47

MALVYALGIKGMYIEIRGGLCLFLAFQLAYTGKLSRRCPVKTRGE

>contig39901 Frame-0F

MATSRRKVNRNSDLFDLVDDSDANSPSEQANLSKDVLIRSTRTKTAKTRNALGFDKEDFS

DALAEDDGDEDFKLQDDSDDEEQSTPTSKVKPRKKLSTPLKKATKAASNRKRLRSASDYQ

HNEVSVGVPTWIEASRTSQGSIAFDLCSESEHEESAPTKRAKQTMTKSSQPH

>contig39974 Frame-0F

MIAKHKRSASLCCLFLLSCYHIVTCVQNVAVVEAPDVDNSRQLRSSVELDERSIQVPEGL

ANSMKTLPERVGSSLRSRSARMKNKAATWRWIRRHFPQSSVRLAKDKVEAARKAFPRTMT

NISPNFLQSDAFNNWVKLIRRSVKGTREEVDEILIAALERKFG

>contig40206 Frame-2R|Blast-UDP-N-acetylglucosamine transferase subunit, putative [Phytophthora infestans T30-4](gb|EEY61108.1|) 1e-67

MHAFVTVGTTKFDALIAALDTDACLSALVVRGYTSLRMQIGHGKYLPRATFPGLVLSFYR

HDPLYKRDVAEADLIISHAGAGSIMDSLALNKNLVVVVNTMLMDNHQTELAEAMADLKYC

IQTNVQGLQKVLETGDWNDLKQYPQPDKQAFPNLVDKVMGIAKEE

>contig40475 Frame-1F

MLGARHYLPIVAKYAQQLDIFLCTSFDGVFKVRLNVVECTLMSASAKVWKHKGLI

>contig40963 Frame-0R|Blast-WD domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY64535.1|) 1e-172

MSSPVEFSSSPAALRQIPIVCPGHSRPLTELYYSRSNLLVSACHDKLPMLRHGDSGDWIG

TFEGHKGAVWSAKLDNEAEFCATGSADFSVKIWDALTGDVVTTLEHKHVVKSVAFTTDGA

RLLTAGHEKQLRVFDVLCVKEQLHAYKAEGRTGIVVLPPSPLVEMQTAQQIRKVVVLNDL

LAATGEVDGTVTIWDLDTFTQTRQFKVDADVMDMEASRNGQVLTIAAGKQVYFFDVQNEF

TLLHAFPMPISFAEEGGASLHPTESKFVAGGSDTWVRVFDYKTGEILELHKGHHGPVRCL

RYSPNGDSFATGSEDGTIRIWQNDSTSAAATSVADMATSSS

>contig41069 Frame-0F|Blast-proton myo-inositol cotransporter, putative [Phytophthora infestans T30-4](gb|EEY58761.1|) 0.0

MTFMHDGALNCQETTPLVANAHPNTTTLYLLTLCSTLGGFLFGYDTGVISGVLVLLKDPK

VFQLTNFQSESVVSAAVFGAITGSALSSCGNYALGRRPVILLSSAMFAVGSCLMALARSF

AELLLGRLVVGIAIGFASMTVPLYIAEVSPPHLRGRLVSLNTALVTGGQFFAGVLDALLA

NVDDGWKYMLGLAAIPASVQFFGFLLLPESPQYLISKGKMEEACEALKRIRGTLDIQTEA

FRIKDEVLHAAEQKVSIWDAIRSRAVLKALGLGCFIQALQQLCGINTVMYYGATIIQLAG

FTDSTTAIWLSALVSFSNFIFTFVGIYLVDRRGRRMLTLGSLCGIFLSLTALGASFYAAE

LQSTKTMGIGKCSQFSTCLDCIASINCGFCLEGQTFETSATTMNLCLPGVPASTIQGSCA

HSNWAFASCPSRTRTAGWIVLATLFMYLACFASGMGCMPWTINAEIYPLHVRSFALSIAT

SVNWICNLIVSFTFLTVVDVLEPYGAFWLYASFALFGLAYLYKELPETKGLALEEIQKIF

EAHDISN

>contig41087 Frame-1F

MEGLAASDGKAGGRPNTGGPVYKDRGPLSHGGRSTNGGHYGRENPRRGSSNGSGRGRPRS

QSRGNSRERRNCVGNRTPLGVSGSPALRLRERKNLLLMHRTGARRKGLSPTDAATRVIGM

DLKYMKDPEHPHLTDKLAMFPNVFPTNAEFPEEQFRVHALRNAAYVSPLPRGFNQQWHQQ

YSAFIDKKLALFDDLTRAKRAIQQLCEEMDSKATDRCDSSAVADERAFTSYLIRHVRRLD

ERTSHTWMKELASGAQSAA

>contig41421 Frame-0F|Blast-pre-mRNA-splicing factor CWC25-like protein [Phytophthora infestans T30-4](gb|EEY57940.1|) 5e-50

MERVDWMYEGPSASGEKIAEEYLLGKEYTSEGNKTIQEDVDLSTTSNYGSLALNKTTLPA

NDAFQRLHEDPMML

>contig41788 Frame-2F|Blast-peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase, putative [Phytophthora infestans T30-4](gb|EEY63832.1|) 1e-81

MNENLTDAQSILAADRQQRDAKFLDAHHRQHQPSMRQRLQYGLQRAQSYEKKHMQEEALK

RIPVENLRERARANAAPMPLFEHEVLKQLLHWFKHEFFTWMNQPRCSSCNHEHTRSVRVE

KPSTLEEVAGQASRVEVYECPVCETYTRFPRYNDPLKLLDTRTGRCGEWANCFTLCCRA

>contig41919 Frame-0F

MSKGGGGKSSQLHWINVFLLAIHHCCIELLLCLLTDCATCGISLC

>contig42594 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY61608.1|) 1e-145

MMSTTIINTIEAEKDFETLLDYRQLCKGDVQIILRLLTCKNEVVAFCHSKALKWIGSMMD

RSHHLTTLLEVVHQSGIIRVLCNLLHASEGSYSPEVQLSNNGQNVELYATYALALFVHPD

AKGWNSLPPFPVLVLVRDDAVSMKNARMQDIRPLNILRVTIHSEVASQLLCTGVDRLIAL

LGDKMMERGKLYQSGNAETDGEFSVGEEDNDQSTICCILKILLHACRSSAPLSKKLTTIT

TTFQNRPDADVFAILRLGFASKRLHRIEQYFATELLSVILRREILSQRLIWNCAQTLFSV

FLETSDTALLSALSKFFAELIETCHIDESVLESGLRPDDLNSLYQELWSLLVHGALSSRC

SDAIARLFSTATERKHSIASEAHMLTSFGVRAQGLLDS

>contig42873 Frame-0R

MSMKSLGTTAEWARERRSPSLPTTQFELVVPKLDQFSEKRLPICTWPLKVGHSQMVAAQG

NEDLTRLRPLQEPPFVRPRSILQRVLATPSNSGPSTPLHSPRRRSSVATSCIGCSQRVSD

KFDKRDFLAPHHCTVPDFSAYESSSNCSSRCNSPLPPSHFRDGPIPSDDEDEGDKEVLVS

VLRRQVALLLKSLEEEKKRRASEQQLMQTKIIELQTLIRRNSDDVTSDDVDNIRNASPSR

LQGVILTQETEWLKNLQNQSWSASLEEKEEQKVPSSCSSKQDNWVGDKTVKLQLARLRAQ

MHAIVIDTQRETQTLRAQLEGAKRSNS

>contig43333-0 Frame-2F0

MVESLIIGLEVVLSYSSDAGRIMRGSCLLVVFKVSSLSTASFIDAFIMFRFCVMR

>contig43333-1 Frame-2R1

MKLAVDKLETLNTTRRQLPRMIRPASLEYDKTTSKPIISDSTIQYL

>contig43386 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55558.1|) 6e-17

MLTVAVADPQVKIQELLSQIKAKQQGLCIQGYLNYGGVPLRASRSLKDYGIQN

>contig44620 Frame-0R

MARKTAKNVGNRAATLGVKCEAKHKEENELLAPTATIGWVLRLFVVVAVVVASYFLRKYH

DASTTHYIARTDVTKHLRLNVTCAPPEQSTPIVPGCHPENKTMCGRAVIDNYLSPDKVLQ

MRDIAETGMQNRSRLGGPTIMDINTGFVRDSDGLVNIYQPEKRIPNTDKPGVKRFSQKQF

SLYRSIVQKIRRTVMKEFGLKKLYFSAPTFITRMIGNASWNPREIHDEYWHPHVDKENTN

YYDYSGLLYLSDYNEEFTGGLFSFIDDTFETIIEPARGRLVIFTAGSENLHVVRKVETGT

RYALSLWFSCDERKEFQNFLDGTMHKHFRRP

>contig45003 Frame-0R

MSKAAYISERDSSLSFGSNTAERFPGCSRTNLRWKSKYGLLVGVNSSKSAILKNTVIYVD

KI

>contig45692 Frame-1R

MRKRRMQAEASVSSARETACVDGPLNEWFLQIDGSTNGVKRMENIQRFSSNSSPVKLLLV

STRAGAEGINLHAANRLVLFDVSWNPSNDHQVYILFCSTVTLLTHSL

>contig46011 Frame-0R

MRHHNSSLLAAAIVTLMAFGSAITGPVKDFETKALRLVSDTRDAANAVRLLKIADNEEKR

YSLNDDDGNQDNSSKISDDSSDDASVSSSELPQWSYDDALYKRQMAMERHNDTGTLLRKG

KEANNFSF

>contig46709 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63504.1|) 2e-36

MEASAHDDEMLALSLHDVVDSERRMSSKPRTATAASFETLSHENPRSSEPHLSMPLTLPT

SPSLLPLGSSLSTTSCLHRHQQLSVQQYFQTENSTTGDFHTEMQKSNDEYRYLTDAINLN

VPTGTSSTRGRLVHEGPG

>contig47081 Frame-2R

MSSISATGVIATMIVVLHALSLLSNSYIVTESNTMQFLSATIGFFLLVCAQRTTPTRRAA

TGAAVAFISATRLSSALDPPNIIKASATLERTFAPLLAIATLAIGFSVHLTRSTGYKLSF

VDRLIIASSTINYCICAIFWAASPIAVSFWRQWLPRFVYLIFVGTLVCTLMSCARQAKQK

RHHDLAEQRTIQHVFLLWQYIPAFMLVLGPTSPLSVLCQLVQYTSFLYVFTSCQSSSPSY

EDITPWVVLWASCSYQTYFTSGHANTFTSLQNAAGFVGFDTFNFYIAGALLGLNTFGCFA

IPILALPCFLIKQHQLQSGKATALLAFSTYFSVNALVSTVFVALQRRHLMVWAIFAPKFI

FDGIVLLATEILLLVLLPMI

>contig48462 Frame-0F

MDATVVVCLSMGVISVVLALESAACVGGLERACILSQSATIMTLILSSVTLVPVVACLVT

AWLDTRAKLYREHEPLLQSNVTTSIPTRRVITYLYASHLLSASGDRLWAFAVPIVFMDIF

VDTLLPSAAFSLATYIVCIAIIPMIGHHLDTWNRWTSMKYAILLENVVVVVNAILLGLIV

FVTNADGVHKPEWTWQLVLMFVGTLVCGSVGQVLNDAQTLGIERDWVVVIAGPDNSNNLA

KLNRMMRRIDLSCNILGPMAFGLIVDCVSGDATSRAMVGVAVVGLWNLISTPLEYCMTYD

IYHLVPELSIRTYVKDNNTVKTLKQKQTATNEGPTIARYATMWSNYVKHPVFLVSFSFSA

LYMTILSGGALNIAYLRWRGVSNSILGLSRGAGAVAGLMGTLIFPLLHQWLKRIESVAIL

SVWLFWLCLFPILLVFLVVGESNVSDAAMILCVVISRSWLWCTDLAETQIMQEWIAPNQR

GVINSMQTATYQFFFILIHLTGVIFHDPHQFEALVFFSLAAVLASAIGFTYWGTNTVATS

T

>contig48871 Frame-1F|Blast-WD repeat protein pop3 [Phytophthora infestans T30-4](gb|EEY60868.1|) 1e-107

MVMAASASGNVIEPEATGNGSISSQRQLSSSSMSASMGPIAPPVPSSAGLIHTLQGHQRW

VWDCAFSAVSSYLVTCSSDQSARLWDLSQGEAIRQYSGHHKAVICVALNDATADY

>contig49205 Frame-1F

MQASNSDIRRHFKQFDDELQDSDQTFSQSVQYSRPRHRPSSIKDASNNSVKPLRCRFPTS

AFFSDSTDDDVSRPIATSPSRSQLSRSACNRSKYTKHYNVPLHMSVGPREGQIGKTHMPR

LHVHPIQFPITRSVLWDRRPLSAGP

>contig49894 Frame-2F

MAVCTEWWACEWNKVQSKAWTQCVQTLKTRHAGRLRYAAWLADSKPPEDEATDFSRTQLL

AFLSSQVPRLNALMADQAALKEKVSELVKQMEYLASNISDTSAVADADLHACIQNVYSKV

TGLFEYAQTLSDLVQGVSVIETSNGDIQLEVDVVGHSLFQSASSAIKELNLRNEALKEAV

ICTQKFQVNLEQKQKMCDAVLLRKNAVENAFHLECLGYKDMVLEVANVLRMEIKKTGIIF

NQFDTLNPVSEHPYSNSVKTDHQRQEQTEVHDSLSEDCLAEFSLMENDRLAQLLLRSIRS

VDNLLPLEKVLEDHGEVCTSLRATLSQLDKVLSNFTTQADQLLDTDAAGHQSRLCMLLLL

DLIKALRVVKTEDSSQAKTSLTNLNDNASMPPLVVARDLLRECVKLFFKATEMADRLTYS

KENELREVAFMPDELDTVEAESNEDVATLEPDKSDTGISCDTTATAYQHPEKNQYGLHVL

KRIEEKISGVVAEKADTQVILTVEQQASWLIDEATKPDNLCVMYEGWTPWI

>contig51411 Frame-0R

MSTTSAVSPVILTDLCLSSYSAFMGRTICTLRLQLHLKGQVQLTYCR

>contig51464 Frame-1F

MPQARKRILVIGSVNADIIVEIDRMPARGETVSTPRDDTGRFSPGGKGNNQAAAVGKIIG

TNHPSLCAIFAGQFGNDTHGKVLESALQRCGVETTLAGHPICPSGQAFVFVYPDGDNSIV

IVGGANRTWPEQLPTALTDAIKSAAIVLLQCEIPSRVNSIIAKIAAEANVPIMWDTGGDD

VSIPSDILPLLTYVCPNETELSRLTKREINNMDDAIAAAQYLQELGAKNVIVTLGSEGSV

FVPVDNPNIVRQKCFKIEKVVDTTGAGDCYRGAFAVALAEGRQVQECLIRASAASALCVQ

RVGALPSMPTGDEVLAFLRLLGLES

>contig51622 Frame-0F|Blast-brefeldin A-inhibited guanine nucleotide-exchange protein, putative [Phytophthora infestans T30-4](gb|EEY53921.1|) 5e-24

MSWLYPLLTDLVSVLNAEVRIALSSVFGKAVRKLLPSL

>contig51785 Frame-0R|Blast-beta-secretase, putative [Phytophthora infestans T30-4](gb|EEY53259.1|) 1e-40

MIADTGSSNDAVLGTGCCGSDAKTTYSCDASSTCTDGGGEQVLLAFAGAKIQGQFMTDTW

SSTQIGSIPKTFLVIERQDTFYRTTYDGITG

>contig52199 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53392.1|) 2e-64

MYFVLYVFNNTMRQNYVLGKTSADRAQLCNRIRQIGIECKASARCGCLQRIMKTSPSTIT

RRAWSHTIQYDQCRAFQTFINDMALNFVDQSIQCEAMQRTRNLLKEFLEIADQRITVTNL

DLIHVSSAALPGAASVDLLSFDRDSDGTSDDSFECSICCGNLSDDPTQRLPCGHNYHAGC

VRVWLNLQRT

>contig52551 Frame-1F

MQDICLHWKCDGSDLVIVGVYVDDLLAIGTNATAVDRFLESLRRLFYRGSRH

>contig53637 Frame-0F

MFKKLSTALVLSAFELSITTVNAGLLAYGICQTGCNAVVVACYAAAGNCVCRGWHSVRHF

WL

>contig53718 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY60675.1|) 1e-30

MLPVLRSAAAKRFGVAVINPSTK

>contig54218 Frame-0F

MASTASKRKRLKNLNPMATSTAFPSIEDKFQTLEMWYRALNVDMSELRRECARVRLELEK

VD

>contig54337 Frame-0R

MGQRLSISRGGDVSAANNSPSSTPPSPHTAPQSSPFTEATDLSPNQRPAIEDFILKQSES

NETVLLVESIVDEGSSSSQKHQSDGKLAVDDLRLSETDSFPSALPNPKTDDSHPLTRRSS

MLRAPVPPKLSRFRMSMDMEKFPPPASSSSSDAHSLDSSSSSSDNELLGSGEELVSDWLD

EPEDAILSPQSHPKRTRQASACSSVSS

>contig54548 Frame-0R

MEQSAQTKWLSLTYEISSDVFR

>contig55402 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54757.1|) 1e-43

MLHSCSTFASCSIAEEVYRDWEGL

>contig56605 Frame-0F

MTQAKVKKYEGFRDCLLKSVHEEGLGVVWRGALCRIVSIMPTTGICFGVYETIKHSFFQG

DLEAFDIE

>contig57776 Frame-2F|Blast-cyclophilin B [Phytophthora nicotianae](gb|ACR82294.1|) 6e-46

MASSSKFLLILFLTALMLALKADTSLKTTNQVYFDVSIDGKHVGRIVMGLHGETVPKTVE

NFRALCTGEKGVGKSGNPLYYKRSIFHRVIPDFMVQGGDFTNFDGTGGESIYGAKFPDEN

FKL

>contig57888 Frame-0F

MPAPQPKQIHVLVVLPNEVPLTISPNSGEARFVE

>contig05033 Frame-0F

MTGQSSAGGLGLFSPVKNSTFYIADRKNIIHTHYT

>contig05600 Frame-0F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65627.1|) 2e-68

MLSYLAAVASAAALFSGVVVGDPFEARARAMVDTFTPAQLLGQMCQLTLGTVMNSTTREL

NETLVRQYAKQYVGSYFNTYWDQGINGRYGYNASEFRALINRIQEITLEETNGHPIIFGI

DSVHGAIYVEGAVMMPQQINYGASFNPDLVYKIGQITARDTEAAGISLIFGPILDISHSK

LWARTYETFGEDPRLASVLGAAIVRGIQSYNQS

>contig06634 Frame-1F|Blast-nuclease C1 [Phytophthora infestans T30-4](gb|EEY65585.1|) 3e-59

MEYLTQDALRIKHETNRANSKFAVDCDIPEQFRVNPKLYHNSGYDKGHLVPARDMSHSQK

AMDESFFMTNMSPQIGLGFNRDYWARLEGFVRHLTSQYDAVYVITGPLFLPKKNKKRGGY

MVSYSVLGDPPDAVAIPTHFFKVILCKKEHGNGFATAGFILPNKIISENKSLRDFQVPLN

VIEKQAGLLFFNK

>contig07422 Frame-0F

MYEVLHDVMRRADTGINVGYAIIYECVQTVTTIYPNSTLLDAAAASISRFISSDNHNLKY

LGVTGLAAIVKDHPRYAAAHQMAVIDCLEDPDETLKRKTLDLLYRMTNPVNVEFITDKLT

QFLREASDVFLRTELVSRITQCAERYAPSNAWYIQTMTNVFELGGDLVRPEVAHNLLRLI

AEGSGEDEDQDMELRRDAVDTYLELLERPVLPDILVCTMAWVLGEYGYLSDAMEQDEICE

RLVELVDRPFDQEDTTRGYVLSAVTKITAQMGHSIDVADAMMDKYRSSRSTDLQQRCFEY

LALTKNFSFMNEVFPEDASCEDIDVDVNLSFLTSFVEKAAAQGALLYDPPEDSDEEDESY

GHRRKESNRLNFEAYKKPEIPYPTKLPTTDQQGAFGMNKWGNTGQLSNMPGLGNSSGPDP

SGGFGAGKRGVVKNVWGPSGLNAHDHVATGPPAPSNYPPENQGRMGGMGGQGGYGGHGGY

GAQPPAYGGQGGYSTQPPQQPVQQPVPQLPPQDYGTPYSYDNGDPTSDEEANGNVDERQI

LASAIFGGIPGAPAPMSGVRRGSSARATGNASRRPTRPTVRRSSSRNEQQQQQQPPQTFQ

NVAPLEQTLPPQQLQPKVEMDLLDISFGAPAPPPNGGMFHQLPSQPQQQPILNRDPFGIG

SPLAPKPAPEATPQAAPASLDPFDMSGLGSSMNAAVELGKSPASNLNVLSGSSGNTSVFQ

FNGRQLEPWKIATQDFGGRWGTCLCEKKTRVNPSGIRTLEDFMGRMHQFNVHTVEAIPT

>contig09477 Frame-2F|Blast-Der1-like family, putative [Phytophthora infestans T30-4](gb|EEY61542.1|) 7e-37

MYFVVRYCRLLEEGSFRGRTADFVYMLLLGAIFMI

>contig09994 Frame-0F

MALNFLDWETCELMKVSYALPDLETAIKQVIYNSIDAHANAIQLLVDVATASFTAVDDGD

GVEPDDLSRYIGECYASSRVHPMKNFLKKKGQLKNYGCRGAFLRELVVLSEEFEIESRVK

EHWTSYRKVF

>contig10831 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70657.1|) 4e-62

MLTDLQLIAVLVTGVTAVLLIMATRVLLPQKSDESDESLQAMINGFDFALPDEVELYRKG

KEEHPDDTDKCFQLLFRRAMADIPLIRKIQSESSGIQRLKKNDILKDGSFLSYKFAEELI

NDEINEVRKEAEELKP

>contig11371 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55002.1|) 2e-17

MEKSPKNVDLHRQIQTAGNLAQVMGDFRYFLETGTDVSHQTNQHKL

>contig12679 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66986.1|) 5e-93

MSSFVRRHSTFSSQYRTTGMLFTLSSAIASVPLLFVIRSLCIDAHSWIDCIDTDRSKIYD

QSVNYIFGGASGNGYCGGYGAGFPGRGENGIGPGYTYKMLRNEVEAGVPVCQIVDPNTYS

DWRKRISLTSGQKAFFAYLPNGHIVKDKKAVGTQHGIYWTGKPNTALLTTHDMKPEHLIN

GHTMNYDDGNCGETFDRNNQPSGRAGDGKPCIGSFDIPAGTTPGIYKMVWYWTFWLDDVN

SYVDQSEGKGYFGAAYSTCFEVEVLPGGDSVEQIDVPGALAPLPNVSQNDSFRLKEIIKQ

PDLTLNLTMNKDLDETLDQIPTDVLQGEDNEVDAEESNSFHGSEEEEEESRKADPDKLHL

GFNDVEDGNSTATVSRDAIEDIEQDDVSSMMSENESGSLSDGIKTISLENVAISVKYNER

LALLGFVVLLGTLL

>contig14512 Frame-2F

MHPRHLWEPSTPLSTCLTASVLSPAHPYPHPRSFVHAGGDTATLESSESWDHHSVAKTYM

VPCRSGYRKAGDATATTSSSAELTVEKTVTPRAQRRWRLLRAHVRVPRRRLHNHAFKHAR

QFTVAKKTLLEACVEIFSTTNDPLDLIQALWTQLVVLFETEWCRLHFKLAPAMVMVYEGQ

EFRPSTDLDENEMAFARQQARGALHLSTFYTTAKACTEARIIPPNGCIPLQSYLCLPLVD

CHDHVQAVVEVFNSRHKACEIQTWLTECESASVLPIRPLREFCGFLGALLRAASLIEALE

HPPSRISSSSSRTGNDTSEGMLVLFGILQ

>contig16378 Frame-1F

MGGGSWVVQEGFLLCQRDEAVSLSRIKESKPSQTKATIGNVQSLHELYVVLTMNRKLEFF

DNSDAETRNKIDGGYLLGFGGWDGNGLLKVDSYGLELKVERNVKPRMHLAALNRVDLEKW

CRGFMAVLDPHSTAGEEVRRERRRVKKEEKRLQKDREEQIRKWKEKKARMIQEEQDRLLA

REEEINNMTPLERINDIGSLDDNTARMLEKRKQRLQRRHAPTMERVNKAAYRRRLDEAAG

GKTENMQPLHTRTVEQKAKIRIELPPPGQFFEVGGVVHRDVPIRLGSSGSDVSDTSSISS

RLSSVSSVTGYRHETSSLPPPPPTPPRWTGSSSRTSSSRTTMGFPPPPPPTAPFDHVNDR

ASRISRSSSSLRSASFDSLAFGQDEDSIAHRSSFSQTSQRALKASRGHQSIQDNLAAIIG

RERSSRTSRTTHRRDSFGAVRSSITSVSYGAPERKIKETMKRAIEQESALTSEPMMANAF

AASLAAIRRNRADTFEEVDITSFASSPVNVHGKMRNRDSQLSAEGKEIFKKAMAQEKSLE

VKLKTTCGRKGLFDDSSEDDDGSDTGLFGTGTRDSKAGNRTSRVSSSFRSSDLSTEARPP

REKKATNVPSVRSDDSSSDSDSDNAPLTFTQPHAKSVPTNNIAAGGAGPSVVVLITSSAL

RTEGKKKLGVFTFTLQYGNLEHTFSLTYSEFEEIHLHLMSAIPELTMLKFPSKHRLRNNS

KPENMEKRAQELRLYLQQLVAVPGILLNEHFLSSYRIDDVFARSLVSGENEKNFNGVQLN

GRPPRSPVARHLRKDQTNLPIPSRSEKKLSLGIAKPKVSKDLFGLEDSMSDPESDSDTSV

DTPQPIIQQQRLESTSSAQRRKARTSDLSSSNISMSQNGNHWDKKSRSRSRLSSRASFRA

SFASSQITAESPVSFQPPGRPNPFAGGRGDLLAAIRQGAPLKNIDVAKSTSSGGPLASKT

KASSPLALTQPSSVNEAISNAMAMRRIHVEYEETKSDCESDSDDDWD

>contig16428 Frame-1R

MSCRFGTPANSTRLSNKKFIQVQQALQNRSETLSSEVLSKMASCENVVSKIIKEEWVPME

EIKPNLQNSVKSKAKVESEISQGIRMQATATFGAATETKQPSDSSNGAKVMKDLKSFKKL

PCRRLVNDIDAQLCNAYSIMAPTRRYSAKNQLTVLVKEEA

>contig17539 Frame-2R

MGNHLTTSRKHPRSLSSRFKRRPQSPVPYHVMSPTSPVVAGAIASKPKRCSPSEGVTSEC

GTTVSMTDSHWPRMSK

>contig19216 Frame-2F

MGTMVSNYNLTAEIGGHSPNQLETTEHLGTPYLTSKTSSVSGMRRSGSLRTCVQCQGRGN

GDEKL

>contig19960 Frame-1F|Blast-strumpellin, putative [Phytophthora infestans T30-4](gb|EEY66160.1|) 2e-50

MEFLAEDNDCGQTLLHLVSRGSAIIAELLRLSNNIPGVFMGASHVEDPEQLKYLDILFDF

TYLKNPEDFETMVNSSTELLDVDDEFMDNHEDILDRFYQLFDGIY

>contig20443 Frame-0F

MRGEMEEEMMPILLNLTTIPFKKAPRSHYYVLLVVAGIAVTPVLIIIMKLCLGDSTSVSF

NSVQSHQSTTNINVLPSHLQSECKENYFTQTLDHFDVGAPTYQQRYFVCDRHFQSNGVLF

FYVGNEADVELYLNHTGLMWENAKEFSAMLVFAEHRYFGKSVPFGDEMIKHMKYLSTEQA

LADYAVLILHLKNIWMYDIPVIGFGGSYGGMLGSWLRMKYPHVVDGVIASSAPILSFLGD

VGTLDKGSFARLVTFDASKRAGSAPLCAANIRRTWSVMKTLARSEKGRNQLKEALSLCEV

VKVESTKDIARVMIWAKSAFDYMAMGNYPYPSSYIMNGVSVLPPYPVRVACSYVADDFAA

DDEIGLLSAFSKSLGVYYNSTKDQKCFELTASSNASAQNSNFWDYLFCSEMYQPQNVDGV

TDMFWPIPWNFTADKELCRSKWRVDIRPLWATIQYGGRKALKVASNIVFSNGNYDPWSGT

GVLQNYSNSVVALSVEGGAHHLDLMFSNKLDTPSVLAVRKVEKQYMHNWVREFYERKAVL

ASE

>contig20524 Frame-0F

MDSTPFIRGTWNVTKHAVAWASSSLLLLWLLHSRSMSTTSDNSFLAQQLLLQFVLHVSIT

RRFKFDLQPALLYAMHQTANICLIVLALRHFGLLFAFLLQHVEMLLMQVKQWLDTKERIG

ALLLLLGHVLVAGINANEYGALMYSLLLLGAALGLQLAAQSPMLRAGGKVSPPSIAGIMV

VAVVLVLLMPKISISFQYTPFQQTVQDGGIKGTSVWYICLIAIALSHFGVVCLEKKKKFL

SSRGQAKNQLIYSFTGMTLANFFIILEFGWFRGLMNALACTPILYFFVNQWQRITTSFRG

KDRVYQCGYENETENSGLGKLAAKVLAVLWRRRASRQMLMFLSINIAFMFVELGVGLYTN

SLGLLGDAGHMLFDNGALFIGLVASYIGQLPPNANFTYGYGRVEVLSGFLNSLLLLVVSF

RLIIEAASRFSDPPEVTKDHLLLTSIVGLLVNLVGLFFFHDHVHGHSHGHDSTYG

>contig20902 Frame-2F

MLEPLCLANSIHRSGMTSETKKLKTLDENAMKGLTARELRRRNRNSLSYGSGLTLKSGIW

SCGTCGCSNPRSSLNCSDCRVERTVTKSPREESMALSTSLKSSEIKVSVSLPVDASSGST

LLTEMMTPTKKASTVAAQDTVKSITSPAVLAATRHSLSRPTVSSAAKIRGSHSTTSKSIQ

PVLKSRTRCSENRSKSPVPCSVVSTQPIRNSLASASVLLDTTNAPKGSMSLSSVSKPIPS

RRKKRAFSLVDKHLTTPDVKVMRRDQKDVKMDTTFIATPGSVSGFMRKHREVDSTPIPMA

MPFSSASSRKTPQKSPRNVFGITGVTAETRGVLQCAIHAIDANMANDLGHRKARVVKSVD

YAAGVTHLIVGRDTKRTIKVLFAIARGAWIVTEDWAFSSLEQERWLPEEQFELTIFANKF

SRQHPESRHIFKGIQFFVGPNVEPSRDVLQSLIQVA

>contig24267 Frame-2F

MASFVNEFVVTYVRENPDVMIQTDCASQVMEKVFVTSAVFENYAVDARKLQTVQTEMEFG

LAWLLRSSCHDFIHANKFTNVANAAITALLKRFAHSPVKAPNGLDLVERLRFAFVETRYY

GDAEDKFIQYLQRCWVNYNPKNIEAPYATVVQSSGFGKSRMLYEVARKAQVGWKESDQSL

DLKVIYTCMRDRESPGYPAATPCLRKWLLPTKSTAKIIASRLLSLYRYAEQHWENVQDEW

IDLFIDEKADDMVEQKLKQAQSYDVGTKALISSDIQRTLAGKVILLVVDEARHLLDDECT

SIMYDGIVNDLSLLRRALVLVNNQINADGGIFGVLIDTSLKIADFTPSIAHGLSTRNNSK

PSKFSFPPFVLTHTMDAHWKLCIKTFASNSKTYCPIAEAKEGVDDDTEGEKLQYTIAAYK

AAVLSYEKNAFLTLLRMGRPLWWSTYMSESFMPPMEDVEYFAASKLLLGSLKCSIRRACM

VLRRCSVD

>contig25044 Frame-1R

MPRRCNHQIFSTARVCRCAGNCCEFKALYRMLQSYAFPSHRLLRSRLIGLDNAAINERLG

ALAAFVAQLYDFFYTFASAQVCDRVQDGTCIVLKTYLNFLGASEHFFTDSSAVLHRPLAL

ISWRQLCAEQMLAQDDEKRTNTTVVESNHDESQCHVKGKSMTWLRIENDEAQLLAPLPSL

QIKTVCAHTMHSFLEEFCEQVLSRFATDIEELNAPGLTQARRWEICLYVACRIGHAYAVR

LILFNHADINTVMADGSSCLHIAARMGRTDIVEILLDEGADANKANNTGVTPLIAACRNG

CFEVVKLLIESGAFVSVCSKRGTYPLHAAIVSQNFKIVSMLVERGANVNAMTATGITPLH

FAAKLGSLSISEYLLRHDADPEKRTKNDSDAMMIAEANGHATVCDLFQQFSGCITKNHVA

SNYLLPNSISDAGQSSFVPMHISHCLSYKH

>contig26009 Frame-2F

MSMHSRRSSTKTICYVASVYSPLKSPIRPNEGITKRSSKLPRVLHPRTNICQRRNCSNFA

HRAP

>contig26706 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56097.1|) 4e-21

MCTLLEWSVSGSILAIVQANSSSLVLWEPTKIEQHQLVELPCKDISYLKWSTSPNSLMVN

L

>contig26801 Frame-1R

MLERPRQTPNVHDAIIAGMCLPSMCSRKDPNHM

>contig27415 Frame-0F

MSRPGASRPPDDQTKLKKQLTELTKLDENKFCADCGSRGPRWASINLGVFICIACSGIHR

SLGVHVTFVRSVNLDSWTFEQVQQMQRWGNARAKAYFEANVPKDYRLPTEHSSVRDKEIW

IRDKYERKSFVGDQLREMEGRKERRKKHDSSDDEEPRRRKDKDRSSSHVASEVASNETVA

SSPVVTKEILSFDVFSAPAVAPKVVEVPIAAPKQDDWASFTVSTTPPLKVPDAFAPQPPA

PVDQHVNKMANIMASFGPSSQPQPQPNTFPLQQGMMPVPMMNGMNGMNGMNVMNGMNVMN

GMNGMNGMNGMGLMAPRPMGMNVPMNMSMGGMGIMNSMMQPSMMGYPPMSNQMLQNGMM

>contig27460 Frame-0F

MSAVDDVAARIRRLDEMRAAKSAQLRQLRNELRYNIVAGVDERLDNGRSVARLDVKVEAG

RQMLYNAGFLSGQRTYVRVTVEVLINNQGDKQFQRCTVTEQKLTAKIPVGSTPRWNETLL

FEGLPAAVGSVKVDVMQEEKIGSDEVVGTVTLPLTRLQDQRFNEKWHVLKKHDKVMINEI

LLGCRFYRSPISALELELELLQNQANELYLFVGRHQNLVELPRDTTMPQSKPLHGKEVIS

DETPEQTASTRFSAVASFPCGIRKRESMENVSMDTEVFETPRPKRQRRGVDLENQKSSFS

DRIANWLLPTISTSTTPIAKAASGDNSTMPSSHFFPFKQTHTAPPSRRPRRSGRLFSTTS

QKSPSALQAIEKWLFTDKDGNPRDRPFGRQASPF

>contig29480 Frame-0F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY69525.1|) 7e-24

MKTFVHVKDPDTFCLCLRWKYNNNAQLVSSFFEMTPAID

>contig29862 Frame-0F

MEYRVRKRDIHGADRLPRSLEEALPDAVVRRFLLRAGFCSSSDRAVTKVRRHVSDFFRRI

VSCMVVMMQHDGRRSFRLIDVKRACEHFGIRMYGYDDMCLLAAGRLCGPEAFHVTELVEC

NSLFGRPNGMSNEPDTEPGAFYKRTDFVANYMSWKRELGETDDQVSESSDWAFSDSDTES

QGDQDVDMDTSQPWQPDEDKFVASLQDAQELVDERLLHPAEDEEAEGETGQGYFSDFDSS

NEPSYVTTQKVFDADEDAQWKKVGNLHTLQNDEDCYPAKLQGFGGSLNVYVIPRQEFSRI

FGALLHLTLNIGELQITSVALSALHNATEQCLHRSLTEGSLHYQLTAILENQNYTDKTNW

LESELQMHRD

>contig32080 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67250.1|) 8e-35

MSSSCTLVADRTDDAVQMLLGFLALSSLYAKWHYEHPRRPAKVWFMDAMKQGTSAAMIHV

LNIFYAIGLVTYSDTPSDQ

>contig32174 Frame-2R

MSLSTSRAIILHPLVAPMDNILSLEARIVAKWSRSLSPCDDVPDAEPLRLVDFACDENLY

AVLSFLDGPSLCSARSVCRAWKRLSNDDELWRNLCLQEFHVSPEQLTSHPDSYQKLYQFA

CRSLKTLLRDYLHEQCLTNLQNSLRIPREAAMTLIASRSFP

>contig33065 Frame-1F

MTDIYLRDTSVEMLQTVEDSKKASCAFLLKYKVISRPKHPPTRGMGLLRITRSMRQMDVP

AAEDEPKGPADQCFATPYILGTILVFCGEVPALTRMACVNKVCRDFIASERKLVKFCVRY

GHLSPRIRFAYWEKVANVAKIRDASELDYDTYLQMALSKGD

>contig33573 Frame-2F|Blast-nardilysin, putative [Phytophthora infestans T30-4](gb|EEY61296.1|) 0.0 NOT\_ORF

MIPPVFGQHHQKPSDLIASLLGHESQGSVLSHLKKRGWISAITAGVTDTDGYDCGTYAAK

FDVTMKLTLDGLSHWEEIVYVLFEYLHILRVNGCPEWVFDELAALADISYRFQEESSAVE

RCEELGAIMQSMFKVPAEDILRYDLFQGSFKKELVEKLLSSLTAETVCLSIVSQTFVQST

EFVSKAVTEEWFGVRYSRENILDTTMQYWKSAGLNSKLHLPRPNQFIPRDFSIVDAKSVK

DLVCETTAFGKLWYKPDRVFATPRAHVALMLHLPSVVVSVECWSHTRLYVKIVRDALNEY

AYHANVAELMYSLQVKDTGLELIFGGFNDKLHLLVDVVVAALFDTEISEARFEVLQEELL

RESKNSITKVAQKSKYMRLQLLEKRSFPLKECLKSIESATVDSLKKYVSSQLWKGKAWLD

SFVHGNISQAGATALIANVEKQLQRVCAPLQFCDFPRRPINIVPRTPVGLLLTERSENET

ETNTQVEFYYQIGPLTLRSLAYADLLHQIMGEPLFDTLRTKQELGYDVSCTVRVTNGVLG

FSVMVQSSLFAAQYISRCINRFMIDFEEAIEMMADKHFQDHVQAQILLKLEPDHNLLETT

QHYWYEITTRRLTFDINAQLAMKMETLTKSEMAQCYRKWILERSKKLIVHVIGRSNAAEN

LARQQGKVACNSEFAGLHASNQATQISDLYQFRSELPSYPDLIERNSADDAR\*EDKLIEL

>contig34455 Frame-1R|Blast-adenosine deaminase-like protein, putative [Phytophthora infestans T30-4](gb|EEY66073.1|) 6e-26 NOT\_ORF

MSVTSNVYTMARNRRDEECKYLFDNKSKTLKLCACGFTSHPHGRLLANMRCQEQQLDIYP

MRLCTDDCGVFDTTLSIE\*MRAAQAFALDEARLLAIARAPLYIFFIKTKSLD

>contig34594 Frame-1F

MRNNLSGMSTLIAGRAGGEREFSFVLIKVVMCEHCERVGVRLKFISLITLKRCLFEPIGL

LFD

>contig35962 Frame-1F

MTVEDNMHECLDLGESDFSEIGELVEGGELADECDLTEEADMESLAEVTSHLVEEGLTVL

LNSEVNLADDIVKDDILDDAEVGTVNEEIESDENNAWDLEEGSDHDHDKKGYYERGNAAP

HKINSPSGQRRSSVDGAVQAEASKVDFADTHESTDDFASDRDIANDDDIVDDILMQQTSK

DKVEANQPKSAKSSLHANLAKYKKKGKTGRGVNKLPALMEEAALTVPLIAPNAVNSTVQV

RGRPKPKSTMADTPDSTTYLIKWKENRSIGLQLKEVRLAKGTYPLVTDVCQEPCCELLRH

ICVGDVIIEINGRNTSTMGVKKTVSFLKACTKTTLMKIRHGPGFVIERVSATV

>contig36332 Frame-0F

MQLSMKKQQLDQENKDLKLMRAMFTKFQLKTEHLLEITPQVTLEPPLIA

>contig36387 Frame-1R|Blast-elicitin-like protein [Phytophthora infestans T30-4](gb|EEY70305.1|) 8e-53

MKTAIVSAAALIVGASYSLASDCDVAKIESQLFPNATKGLANCGNATGINIFAVSQFPTL

DQVTLLSENVDCANYLNQINQVANVEIQCNVTIDGVPINFGKLIASFLTGKTGNETDTDP

SPTEVPSSSASKLMDSDSSPLPTSPRPNVSANAPSPVPAESSGASRNIAVSFISCGLVTM

VIALS

>contig36761 Frame-1R

MLLGRSSTNPRRKVIRSKAFSKTEPTHFHKCWLARFLRRICVAVDQSTTPDSTSSWHTPS

QIEAANIGAVDSEIAFHQHNPPTFAVSTRSGARAYNEDRFRAIDNLDLYGRGLLEVVPSS

LPPFLVDLLKSRVLEKFVVDGCAPGLSAHKLLKYERASEDTQFFGVYDGHGGAKASSLLA

LLFPVYILAAPEYTTDLAAACHSASMAMNEEILNREKEGQCEGGATAVTLLIRGNTIMLS

NTGDCRAILVTTRDKVAQATQLTTDHKASNDQEKQRIEEHGGMVLYIKGVARVNGHLAVA

RAFGDAELCQLVIADPEVTAHELHREDEYIVLASDGLWDVLTNDQVASCISNNPWLGVQG

IANMLADHAIELGATDNVTVLVVDVRGRIP

>contig37182 Frame-1R

MIEWWTKTHELMIGYGISKDTVKKAVDESGITLREGFMEMFDLLARENVPTLIFSAGLYD

VIHAVLDKEYAATSSKTLPKNVHVISNMMRFDERDKVVGFDGT

>contig37713 Frame-1R|Blast-hypothetical protein PITG\_12147 [Phytophthora infestans T30-4](gb|EEY59574.1|) 2e-33

MTSALFELVACVYVSKVYCSNPHLLIHARQISCLLTADSHSHIWSILELDSGPKDTLRCD

YLTTEGIDIDRVTCCCFISNLKKCQFSACNDLINWNVRTTTRLCSRKLMVSALVVAGTTN

NTVLVHANGRVLVSYVLPARPADIWLLDENCENQNYVFCVRCDDVKRSFFVLEFCSNVQN

DSMDLLLSFNNVGHGYAGYFTNYSLSDSRQVLLLNSIPGLVHTDDNAIVNNKLSIDTYVD

YGQLIKRSVLITQKTSAAKTKLTCHRLRLHTEEKSKRAIHYLKRSRNEKNGNLINSVVKE

VG

>contig38147 Frame-0F|Blast-Ufm1-conjugating enzyme 1 [Phytophthora infestans T30-4](gb|EEY53159.1|) 4e-76

MDAPIDENTKHTVQNIPLLATRAGPRDGEAWTQRLKEEYLALIHYVKVNKEAGNDWFTIE

SNKSGTRWTGKCWSFHNGLRYEFDLEFEIPATYPVANPELCIPELEGKTSKMYRGGKICL

TIHFAPLWQKNVPRFGVAHALALG

>contig38208 Frame-0F

MPMSFKLWKPPIQRIPRTIGKAVVGASFPLNVIFKREDIVADSHAGNDYDFITCFSVSKW

I

>contig38723 Frame-2R|Blast-5-methylthioadenosine/S-adenosylhomocysteine deaminase, putative [Phytophthora infestans T30-4](gb|EEY54489.1|) 1e-07

MPPTPQAPIDIDASSFKQKVDLIIYAAHVIPVVPRGVVLSNHAV

>contig38983 Frame-1R

MEVTVKGADARTITPRHYLILNNVQKIKNVKNMLMSASAFGVKEVFVVGQKKFDLQEQAS

FLNSLSCSTTRVATLKDCRALCNERRIQIIGVEIMHDAKSIVEEPFNGDTAFIMGNEGAG

MNSAQMAICDQFVYIPQYGGGTASLNVTVAASIVLQRFALWAKLPIAETLHTVTTTE

>contig39676 Frame-0R

MGLVVELGLLDLSLCVIYLISVMIVGLYFTRKEQRNKLLQSKRMYHQACDAKDRNETNNV

FRGLL

>contig39975 Frame-0F

MRRSQELVRVFAAVYLISSVSAKLDERNRKMQRDRSKVVGNERAKGSFRVDNVVEEDTSN

QERISEGYFAALAE

>contig41068 Frame-2F

MESGATAHSLLGHQDEIWTLDWSPTSEFIVTTGARDGELRLWDIRRSGATACLLCLNQEG

KAEVPRRSNLYTNVIRNSMPMSMTARKRRRRDG

>contig41305 Frame-0F|Blast-nucleolar protein 6, putative [Phytophthora infestans T30-4](gb|EEY54789.1|) 1e-170

MHAKTGFYVQIGHELHSRYQMRCEVATDCVDVLIHGYVFRIVIRCEKELSVVTGATGRKK

LALVHSWEYVKLKRETEYLSKHASLIHALHTKNSSYGSTVRLVQKWLAAKVLSNVLSIEA

VELIVADVFSTSSSMRPPQSIFSGFIRFLKRVASFKWQHAPLIVDLNASLTDTTCREILK

RFEASQTSGSTHPGMFIAAEYEDMDCLSSWTRFGVDQVLVQRFRNVAQASYNELITWLSS

GASLSGWKRAFRTSNTKEFDAMLMLAVENLPSKQMCVPGDTKHPFVASVYKNMDLTAIPV

MIGFDPVQELLRDLHCAFGHVAYFFINAVDTTEIRITWKPQAFLPIKFRAITAKYQMPLR

SSNTEEDCKDSCVSVPNIFEILSDMQRMSHGIVLNVVVQPFENA

>contig41370 Frame-2R

MKFKLQKSENLLYQIKEHQPSIEEEGFIDCCLRDPSTLGPGLEALIAERPWDLSSASGLY

VESVGDTITARDNQLMKSRMFSVV

>contig41455 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64788.1|) 1e-163

MLTLMPELPTVPIPEVVAKTDQSITLRMQRLSYVHDDARYKLQASHSEHGYVYYSWNDSA

FFSTRMFAVNGLKPNTTYVFRVRVVHESKRQCGEWSLLTPYVRTFTEDEDAKRSGTVFEH

ALKLERQHKSVLQGQISKLTGMLNERKSSREVEQKVQVHEDMLASRRIIDSRLTKLQREL

SMQTAALQSVKSQRAADENMISELLNEQEKLRAAQNEQQGQVKYDLEVQTLREQLESNAE

ALRKHQEQVNASYEQIERYEASLEAKKSEIIEKEEEVERIMADCNRIVQEQADVAHVKQL

EVEDALLEAKTSLEQQLDINTYLREEVSRLREENHHLKNHIEEVDSEVVPRLVRLEDENE

QLRARLSAR

>contig41918 Frame-0F

MEELLELDKSDTSGAHELVKDNEIVVESLAAQGLLRDTSNVVGLERIKGDDLPVLTPNEA

NVSVCRLLHYMSQDTLLTLSERRTGRTNLLLLQRLLLKARERERERDTTTDFTV

>contig42667 Frame-0F

MTSATSTRVNVAILQLAFSSGSMVSNKAFEMEGILNTQSSLSRVFHKPQTRSKSSFRNHN

EDEEENSRKYSTGSSSFALDSPFDNEADDVEQVLRDIASNMIGRNVPFHSPFGTKAQVYA

DYTASGKSLECIEKFIHDHVMPTYGNTHTTTSVTGLQTTSFREEARQVIARATNAHTTKD

VVIFAGQGCTSAINKLVTALGINKGC

>contig43332 Frame-0F

MASKLDAFLAVMPANACVRSPPKSAPAMLTFQSLESMVAPDVGSFTDKTPQPPMAYHSCL

QLCKYNSILNLALDDKSSSQIRPHDDRNISGPSPLTLFINAHAGAAMAKSYTKKHEIQVL

HFARHGGGTNLNAKSEADPMHMASVQGLHKRRVSTDTTLLDRCFSQLDIRLDSVQYFATV

PVITATSGVTEALQSELNIDNNADEEHTSADLHGLNPEKLIAIFRAGDTISVSSAIEIVR

RATTLMSLEQNVISLRAPYTLVGDLHGQFQDLLGLFRVHGFP

>contig45002 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64786.1|) 1e-41

MRVFKATASSYRPQSTQPMRLPTDRTSAVTSSGFGGNDEKEIRGRLTSRDLRTVLRLHHE

NPQGWNDEVLADKYGLDINTMRSILSSVGPPNVVAPKGLNDYPVGVWFKDVSSPC

>contig45381 Frame-1R

MSLQQHKCAEALVQLKQAEKLLAKRSFFRGSPDYLSAAPLLDKAGELYRLGGDFEASKLA

FKRCAEAQQNNQSPFRAAQAYENVAKTALQQLKAERTGSRNLQQVTAEARKAYESASMLY

VDMGEFGKAADALVKGAQACENNGVGADNVLPLYWQACDLLEAQDKPHFAVDTFRKTLSF

LVKYGKHSEAVKLLDRMNALYEAMDQQHNIHKMQLCQIILMLAVGDVSAADALYSRSLQD

DSFLSSDDCALAEDLVRAYKMGNEELLQATIRKPGFLALDNQIGRICRKLSVYSTGNTPP

PPHQHRPDPSSGRSLPRQKQQPQKQRNPFAPSAHSSSTQNTSAPSARTPAVGNEYDFPVP

ERSNSPSSEVRDSDYEAMLADALGEVDVSEGKKKKSFAYTQKKRAQEFASPSLRDKSTSL

SPTRMPSPQLGTLRASARMDDELDGLEFAMPDPKVRQNSSLYELEDSTNAIANAPSTKSS

VKTAYDEFDLT

>contig45554 Frame-2R

MGNFLVSSVCHAHGRSEAVYAIMKDNVLALRDSQSRYSPLRRQCAVHQAALLRVISAKLA

LYIVTIERWAATASRRAMATLKKPFVLFAQQLVVGTIPQLPLPQAEYDDVFCEFDAVFET

TPHSSKTLRELQQSSKLMTTGSGKDPLQRQAEVEQSETLKDGEHSSSDDTDDEKQASDLD

NADDTKQASNLDDEYVVLPALENNREFYIELLDTQAGSEGISDSSIHFEKFIICGKHDKF

EKISKDVDVYASKASNSAKRSIVRVLLAYCAHKNDSKYTSDMVLTAENCLKVWHGDEDRA

FKSLVAL

>contig45693 Frame-1F

MEAISGNKKSSLTSEFDDLAFSDFPERGDPRFCV

>contig45752 Frame-2R|Blast-bifunctional folD protein [Phytophthora infestans T30-4](gb|EEY66137.1|) 7e-13

MVGDRQDSALYVRNKNMACRRSGIRSDNFFFDESVS

>contig46065 Frame-0F|Blast-unnamed protein product [Candida glabrata]emb|CAG59469.1| unnamed protein product [Candida glabrata](ref|XP\_446542.1|) 2e-16

MKVITSLVLLAAISVKTSAESFSDYSLDDILDSTTILSHSSSSTAPTSTSSPQTRTASSD

STSSESTTTRKPSELSHTPSTKSLSFENSSTKPPSALFNSTTKVPVKFSNSSSKSKTTST

NISNVKSLSTSTERVSSSLTDATSKSSTSTPAAEKSTSSKAVRSSSGSANDFMASLSS

>contig46223 Frame-0R

MPQQIDSVAYDTSEAAIHHTSRQAGSSS

>contig46384 Frame-2F

MQFDNLVRTANGDTIDFRIDSGLISVECKDHKRPLSLKTLKEILLHVP

>contig46573 Frame-0F

MQQQFRSAVEMAAALKRKDVHGTAVAIRKIIITNNTREEEMILTTLHQATQILLESQNSS

AADATPVLAVTVKKEDQAVIAAPEVIADGLKVAQDSGLHEAEAAQALTGLRSTTSTSSAR

PPAGPKPSVSAPQASFPSFVPGPPLTITAPMPQHASLHFQPPELFTTGTVRSPPTPSSLP

SLFARRLLAPLTSPSSVTDPDERLVRGMSDKEYQNPMIIMEQRVSKGSCAVRPDTSPASL

TPVYYSSFPALPSNKAVNADAPLTKRTTSASPVKRKSITSKQL

>contig47080 Frame-2F

MWTCEAVTEAVENGQYLDCLVEGLPFNEQCREIAIKHALKLGKMDLAKQMLLPGGCLLDY

GAGCPQV

>contig47707 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65182.1|) 4e-10

MLSVMEEHKEEILGIVLGGLLSVMLKMLQDHLRRSR

>contig48377 Frame-0R

MQEASRFAPFPCPLERLIKLLAAVAYPKWVTKVLLQTSAMRTFAFASVALNLIFMALTLA

LTAPVKVYRKVLVRRVCVVEPSVLHTNAFQSVNTL

>contig48463 Frame-0R

MRAMCLSFFYEIIVLRAACFLVAYVFEHLFSWWLITAESWSFVDS

>contig48870 Frame-0R

MQTGGYYAKESFVSSRVTAFLTRG

>contig49190 Frame-2R

MAVAATRYELKIVSQLWVNACYVGKKRMDERPFFPIAQQNLLDCGSQSVTLPPKRRQSLG

AEALQLSTTTLLTTVADKAIKEVSTASKLPLKALKGLHRGRRKR

>contig49204 Frame-2F

MGQSRQNGQMSVPDMSTKRQQTTTALNAMRILERRYGVQDSEYFQHGEFQSMDYKRFIAS

TARVGEQNDEFYLSLSQPDADNKVAFAKNDGIFVSKLGQDHTLKVTLSKKRKNRRWSTTA

LTLIFGCIAIPVAEGIAVFQVFPMSSAASSINIAFFKVNELL

>contig50062 Frame-2F

MLVFGRLLPHPFVECIFSCPLQLYSLGGSTRTLPISCSRTRRNQL

>contig51308 Frame-1R

MKVDLPPSSRVNVSSPTHVAHVLPLMRSCSMGRWLPRVLLLSSLLYALVILAWSLHIHSY

SRASIAAFGKQKSEAKTASVILRTSYTTGIIAQQREQEAKVRATSGNVPNALQVETDLSM

VQKGLRIPQEAAVATIQIEDVHDTASKSQSLIRNNLYKKK

>contig52176 Frame-1F

MTMLRLQTEEDCERMTAKSAKRKPWDIFASGDHKDDLQSPFRHAQALKASAEADSPLVSS

SSSAASALLDVKSCVSFDTLKSSLLATLGNESNDKTRSSDLYWIEIEPPRASAALRNDFV

KNHEVWMAEQQSYCEQVDMFLQQVCEDVLPKGILVLALPQGDLSLLRYLKALRMRTKWRD

ANMSTDNMAIEELHAAVNDAFQGAMD

>contig52525 Frame-2F

MSKRRGSDASPDARMCSSIDAADWSRNTYRKTVCRPHWLGEEVAMHNIVALGRSTATHKN

VGPCCRNQNHANQTREKAITRNGEGSPTR

>contig52550-1 Frame-2R1

MISYHVYLYSLSVYPLQTKVHHKRVMAQRLRINSDISGLSCGRA

>contig53636 Frame-1F

MMSTMDVGTTDWTGQQQAQELIDGGVGVYGDDAENLGYRHATRYYSSSSGTAGGNDGLLS

GVHDMESSIHSGSDYLTACFLNADYHVPVNISEHLLSMPTNTAAGLQPSPRLGIRSHATE

RLKRVEQAAPALNLDLSISVTVLDLSKLCGVSSILTYQSEVVPRGIALAALLPPISMTSK

RKKSQVGAPNRPIISWMLRAAERIPGKHGASSKNHLTRVLEGLISEGDAAAKTQLSDGNV

YIDNSCNALAAKCAQNAVTAMLAGRRDLQRIW

>contig54219 Frame-1F

MALMDALHLIFAFLNLFTKLMYMSTKLFAFFSMLSLALLTR

>contig54336 Frame-0F|Blast-Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4]gb|EEY68576.1| Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4](gb|EEY61751.1|) 4e-18

MVIEDARSLDLYTTFGINALAALTTILGGCIVFSNKLLQLASPKCMAVLLSVSGGITLFQ

ALL

>contig54549 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69208.1|) 2e-21

MTLSLSVGRGRGMTMPAWMRKKMFAIICLMVTIEWSGANCFAVTVKKM

>contig54866 Frame-2F

MKQDKAAGIPQIFCASCVTCTQCESLRGSKKQ

>contig54888 Frame-0R

MSWHHARGRIASMYVCDLLGIKNVTVNFQQAVSSYFDFAATIALEIGNMVRSVCISTWRV

KVTMNQDVLCFEKMQGLIPSEDNAQTQRISGFCFAPLSTRVIPGLTTHNAPSLVQTVLSS

VFETETLLSLMWIIG

>contig55335 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54784.1|) 3e-11

MYSAWDTFDVEKELALVDQQEQSEAREKQQCKLLQAKESVETLATRKAQQSADILAAQA

>contig55340 Frame-2R

MIARAALESANAHMIILFTDMPSQSQCKSNY

>contig56604 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY60503.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54783.1|) 3e-96

MEKVQVYMDKWAKDLEKFPVLQQAQDATGVEKLYLVASGAAVLLLLLLVGFGAGLICNVV

GFVYPAYCSFKAVESDDKKDDVQWLTYWVVYACFILVEIFVDFLLYWIPFYYAFKLGFLL

WLFMPSTLGASFLFMHFLAPFLKSQESRIDRAMLEAVSNSSSVISDISGVARDIGRDVSK

VVASQLIDNTTQ

>contig57063 Frame-2F

MKTEVEFTVWLLDDTSEHVVYILGDAPNLGAWDIDKA

>contig57618 Frame-1R

MRSFKSRAAFLSVVISFQVN

>contig05603 Frame-0F|Blast-cellulose synthase 3 [Plasmopara viticola](gb|ADD84672.1|) 0.0

MGLTGAGVIASVIGVVGGLSLSCGGWSSLSLGARSLFVTTQFVSAFAMGFVVAFTAIVSL

SETNEWVAIAAGGGAGFAIALVVGFMTIVGPYVLILLTGGIIAMYLLLIDAYNGINVFPD

DNQLARQEFVIAFMIIFELVCCSSSKTSDMENHRFKYILFSAITGGWMTADGISRLLDSS

AVLSTVGFHSIQDGGKAAMTGIDAGGQTVMFMIWAAIFVIGGLNQLSMRWGLVCYNRVGT

HAQMGPVDEQLPELPTGATLPAQTMTERVRLVCENCFATVPAGTAFCTECGEAMPSEDAN

PDVSISQAQMPSVSMNNKGQVPDRWQQVPHRTFMSTTSFVDPKLAKEGGVSMKDNSRSIR

FMDSGVQGPDGKMGQYNDSIAGVRNYYEPSFRSFAMSTYSIANRAAEPVETPNIRKYKMS

GSGMFHVFYFSTAATGIFWLYYLTTMYPQQYFCDHARPTLPCNELPTSETTGCYSSTVNF

DSGSGDGYCIKDVPFMSWMMYAMMIFSEFLNFFLGLLFNFSMWRPIRRGARYMNDFKPPI

PKEQWPTVDIFLCHYMEPVTDSMQTLKNCLAMQYPPELLHIFVLDDGYTKSVWDANNHFK

VTVNTKVIEIAGDLRGDLARLMHERVVGPVQDDQSLKSWRRQHSSVRELRKEGGKGVQRR

DCAVGSLSDDYDYRDRGIPRVTFIGRMKPETHHSKAGNINNALFNEGADGKYLLILDNDM

KPHPKFLLAVLPFFFSEGEAVDGGGRQYSDDISWNQVSYVQTPQYFEDTPQLTIMGDPCG

HKNTIFFDAVQCGRDGFDSAAFAGTNAVFRRQAFDSIGGICYGTQTEDAYTGNVLHTSGW

DSVYFRKDFEGDAKDRIRLCEGAVPETVAAAMGQKKRWAKGAVQILLMKSESEVDPDWRP

PRVPAPDPKPSLAFPRKMFFYDSVLYPFGSIPALCYVAIAVYYLCTGDAPIYARGTKFIY

SFLPVTFCRWVLNLLANRAVDNNDVWRAQQTWFSFSFITMMAIVEAIQARATGKDKSWAN

TGAGQKTSWTEIPNVLFFFTLMFSQVVALIRFFEYENATNPWNYVSAMFFGFFVMSQFYP

MVKMSITEYCGWDHTAATFTANVFGSLLVVYVVVFVQLWQVYYEGNLLVAQGADGGGGAE

TATAV

>contig08983 Frame-1R

MLRVVLFLVAACAKTSYSHTVALSTRNSQYIASKANEHATIPEDINLNRRLRKAAVITEV

AETLESIIEAFNPLRTLRSDVRSEMSSKTKLEQDAMLKEPSFYFRMLKPFSEFRIRACFE

VYEIDTLILFGTSPHLLKQYIQNGIPRGILPESVTVLATTGEKLKRFQRQFDIFFNPPTG

SKPSKPSRAWPYARGPQVQANFKKIYSSDHIKFLAYAFHHLDDVNILAKLSSSIIYRFVL

DNFKECRATIRYGTVEDWYKHPMLNKLLRVH

>contig09728 Frame-2F

MYVIKRDGRREAVKFDKITARITKLCYGLNPDYVDAVKISQKVVAGVYPGVTTSELDELA

AETAAYQSTQHPDFSKLAARIAVSNLHKNTTKVFSDNIEVFHKHIHLKTGAPAPLIADDV

YEIVMQHKDELNSAILHDRDFEYDYFGFKTLERGYLFRVNGHVVERPQQMILRVAVGIHK

HDIAAVLETYELMSLKFFTHATPTLFNAGTPRPQLSSCFLLTMQDDSIEGIYDTLKQCAC

ISKWAGGIGISMHNIRATNSYIRGTNGFSNGLVPMLRVFNDTARYVDQGGGKRKGSFAVY

LEPWHADVLEFLELRKNHGSELHRARDLFYALWIPDLFMKRVEANQKWSLFCPNEAPGLY

ECYGTAFETLYEQYEAENRARKTLPAQQLWFAILEAQMETGVPYMLYKDAANRKSNQQNI

GTIRSSNLCCEVMEYSSRDEVAVCNLASVALPKFVTHGVFEYTKLYDVVKVMTRNLNKVI

DVNYYPIPEARTSNLRHRPIGIGVQGLADAFLLMGFAFESPEARTLNKHIFETLYFAAME

TSMELAKELGPYETFQGSPASQGIFQFDLWGVTPSSNLWDWGTLKRQVIKYGLRNSLLIA

PMPTASTAQILGNNESIEPFTSNMYNRRVLAGEFTIVNKYLMQELIELGQWNADVRNQIL

HDGGSVQLIPGLSVAMKEKYKTVWEIKQKAVLDLSADRGAFICQSQSLNIHIADPTISKL

TSMHFYAWKKGLKTGMYYMRGRPKADAIQFTVDKQGLDRQRAKEEAVNDAARIVEFPPRA

GEDDDDECLVCGA

>contig09997 Frame-0F|Blast-T-complex protein 1 subunit zeta [Phytophthora infestans T30-4](gb|EEY63990.1|) 0.0

MAYRGMNSNAEIVSKSQALMVNVSASKGLQGVLKSNLGPRGTLKMLVGGAGQIKLTKDGN

VLLHEMQIQHPTAALIARAATAQDDVTGDGTTSTVLFIGELLKQSERFLADGLHPRILSE

GFELAKDEALRVLESLKTTNVDILKDRELLCSVARTSLRTKLDQKLADQLTDIITDAVRT

IAVPNRPIDLHMIEIMHMLHQSSSDSRLVKGLVLDHGSRHPDMPSSLEKCYIMTCNVSLE

YEKSEVNSGFFYNSADQREKMVEAERKFTDDKVRQIIELKRDVCTEANGKTFVIINQKGI

DPLSLDMLAKEGILALRRAKRRNMERITLACGGMPINSTDDMEESMLGYAGKVYEQTLGE

ERYTFIEDVQHPKSCTILIKGPNEHTIAQIKDAIRDGVRAVNNAIEDKGVVPGAAAFELA

AHEALNQFKSTVKGRAKLGVQAFADALLVIPKVLAENSGLDVQDTLIAVQEEHQNSGRPV

GIDLFTGEPMLPDQEGIWDNYRVKRQFIHLATTLASQLLLVDEVMRAGKKMGGGGTGE

>contig11729 Frame-1R|Blast-formate-tetrahydrofolate ligase [Phytophthora infestans T30-4](gb|EEY57946.1|) 1e-117

MTFTNDEIRSFVRLDIDPDTITWQRVLDTCDRFLRHVMINYESAEKGLSRLTGFDITVAS

EIMAILALTTSLADMRERLGRIVIGMNRSGEPVTADDLGVGGALAVLMKDAIFPTLMQTV

EATPVFVHAGPFANIAHGNSSIIADQIALKLANVDGYVVTECGFGADIGMEKFCNIKCRT

SGLIPHCVVLVATIRALKMHGGGPDVVAGKP

>contig13002 Frame-2R|Blast-SUMO-conjugating enzyme (SCE), putative [Phytophthora infestans T30-4](gb|EEY55734.1|) 4e-86

MSDDSIAVQRLRQERRNWRRDHPAGFWARPIANEDGSLNLMTWHAGIPGKVGTNWEGGVF

KMSLVFSEDYPSKPPLVKFTPPLYHPNVYPSGTVCLSILNEDKDWKPSVTIKQILKGVQD

LLDQPNMADPAQREPYMDLKNDPELYKRKVRQLALKNRES

>contig14942 Frame-1F

MGTLEMGNEDKNDSTGTINNIEKNFSDIDDEKNYDSDDPLGVKTSVTLEKESNGFDSEKL

RKYELQKLRYYYAVVSCDSVKTASAIFDQCDQLEYETSSNVLDLRYVPDDTTFTNASKES

CDSLPDHYKPALFATLALQQTDVKLTWEEEDDQRLELLTRPADWKDAHDDDFKAYLASEG

SDGSESDTDCDGSNDEGGSKSKVDTAEFHGKKKSKKKAKIKKLRNRYRSMLLSSDAEDEV

EDTLSEGGLKASSEEEGNDLADGDMEMSFTPGAGDILKAKRQKELEATETPFERYTRERK

QEKNRKLHEKRERQKQLEREQREILQKKGRGAKETNFLREAINGGGADSEAEGSDNDHEK

RNFDMNKIAKQEKFKSLKGKRRVNEMKKLATQKVSGGLQESFKFDAADPRFQGLYAKSSR

FQLDPTDSKFKKTEATQAILKERRQRFSQNAASMGTGVATESNSSANESKHTLNIMVESL

KRKSQQHSEKMSKKSKTLVVQKS

>contig15350 Frame-0R

MSKLFVDDHLTEAAKDSWNAIEASDFDSRMTEFIKMTQMEQTKSLRTMVLRT

>contig18379 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67980.1|) 0.0

MIRYHQMLRSETEGALEEVVRAAHTYLKANETQISWILLLTEALSRLRRHTEAVAWYKKG

LKLDPDNLELQNGLKKSRVAVLNDLLESSEEEDDNVLNSFKIVDPILKIVSTKDSAESSC

EMRLSEEGGMPRSLQTAQMQSHTTSEVSGNRREGTAEQDGKLITRAVIQGKFERMLEHFD

MRKLARIVAVSIFLELFDVRNVAIGTGFLFLGLLAQAIIHRQKIMVITMLIICFYRSQLK

MQAQSFLQKWGQTSQDKLGVFMLAPQIVFVIPILMKVFGQLKFMLFLQQDVCLAASVVFV

AGTLVANALRVNAGQYAREWGEGRRLKFAAYFTALVYWVIWRGQWASTTRLLGPALIDAG

GIVLGSVSSSELQDVCRRAFMRLYNYVVNDMQAHVDLDAWFILGLSNWIVEYWQQPTDIS

PEMLLRMLAEYFDSLEKAAVRTFSVELRHLRYQVNNRQITSELQLLIEYLKQSLNAVPPS

WTFGMAVLFAKSCPSFVLFGLLVICSGVFSVPLLPFVVSEFQSARTLYGLNRTGILQEMD

GFEVMLMDSPLKYVWKNLKSCVYCLEGGVTFTKAVTTGKHIVVAAANISWLVGFVSEVKQ

NGIFANIHEIPECIASVFTITKESSLIEDGVRFLRESTHFREFQASVINWWSKET

>contig19215 Frame-1R

MGRTRSRSEGRKAQLRATKCEQIQKRTSRRN

>contig19916 Frame-2F|Blast-histone acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY57625.1|) 1e-43

MSSLPEGFVRDKNAFVSALRKTLADYTGPPGKCVETYKFISPAIDGKHSTTRSFQINECK

LEDNEHAQKLLANLQTLSLWFI

>contig20358 Frame-1F

MKLKRLVANRDALSFALDRPRDWSQMTQLQYQASVLDRSQNESVERALEKSYHQITELGV

ERFIHGQSLNLQGKLKLLNELIRLQKASAHDFSTVLEACGRQGQVDDALSVLNKMKSYAK

MCPPCAPTTWSYNALLNAFAVRGEVHKMESILNEMIMNDLHFDQVTVNTVLKAQTNLLKE

CVDDTPKTRLSTMIQALSIYEQCVEYQNFNSDVSTYFSLFRLFATYLNTCNNEAVTNAYK

DGVSLHDSAEHNEIDSIESQEKEVIAYIKNKITATCRDAPAEKLDIGVFNNAFDCYYRLG

DVAQSFKLFEFMKRLGFQPTDTTFGLIFATCATQQQFEVGLNFLDHLMTNDGYKPSLKVL

IGAMQLCAKSNNPEGAIQLFRAIEASNAFTLTVEAYEPVAFAYARVGNVNSAWEIVNEME

EKLGSVFFGSYNWILQACAVAALPGRALEVLDVMRREKGVAPDVISYNTCLDAFVRAGQR

AAWWKKNRVNKLIGDREKDLDEVEEAAEKDTKDLKGSVEGSPSIKRVIDAKNVEVTAALN

MQRTKAAWARASVIDILEKMQLQRLKPDMTTYERAIGACSVNEDNEGVIAIFDKLITRTR

SRFAFNLKSNLVSESSFSAYLVASTALQDKNRVLEAPTLLRQWHLATRQAPSEFVVAQLL

ESLELLGEWRCAVQMLPEWKSLFGVRPSVVVFNKVMEMCNRANEHELVAPIFATMQDATA

NHICPNPDSYIERIYAEEQLENWGIATNLFVEMRKKFTSEEISHRQLQKLSLGRYSLRHN

EYKC

>contig20527 Frame-0F

MSLDPIYGMISSNRAKSFYIFMNHFVNPSKIESWKLGQALLAKASDPRSLTRLTK

>contig22792 Frame-0F

MYGGGGDRYGDSSSRRDYNGGGGGGYSSGSRGGGGGYSGGGYSGGGGGGGYGGGRGGGGY

GGGGGGGDLGSNLDTRIQWDLSKLPVFEKNFYYEHPDVTKRSVEEYEKWKRENQIIVTGK

GVPKCVLSFEEASFPEYVLEEVVRLGFDSPTPIQCQGWPMALSGRDMVGISATGSGKTLA

FLLPAIVHINA

>contig23922 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61487.1|) 2e-57

MTSEVRTDVQFQLWEKLKYEGFFHVEWLLVKDVPNFVFTGIKMSNTPTKKSITSCRDCEE

VLFDEASEFLSLFVEFKSWSSAWDDYKHYDQLQKSIEQKRKLKLPIGVDKTDLELFLKPL

CSNESAIVG

>contig24196 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65597.1|) 2e-31

MFYLDTQDKVEQSIYREEIMGGTIEIESKAVGKDTPSKESLPRRRCKKKKICDTK

>contig24893 Frame-0R

MDNVLVHGYDIISSLTIACGSSKVLVPCK

>contig26705 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56097.1|) 1e-19

MLITFSVDARHHGVGPVRYAWDPRDSYVASTGASRVVHIFSRRGKLVDQIVPPSP

>contig27416 Frame-1F

MQEENDKMYVEDNNVELKATARLKRGADTVEEDKKDDANSLKKRKLIAETAFGSPQPSKD

DEKLATLADAVNSEILD

>contig28219 Frame-2R

MVFQLGISQIQSSYIKLKGLTSVGVMSRLESCSA

>contig29861 Frame-2R|Blast-serine protease family S09X, putative [Phytophthora infestans T30-4](gb|EEY53579.1|) 1e-78

MFRVVFNFRYTFPGDLFCNIDIIDKVRSPVTIIHGTRDEVVPFWHGEGLFEMCSQEWRCK

PLWVTDAGHNNIEAYLSTIGDDFFQHLKEFVNVCHVTATIRAAEAKAGNTG

>contig30001 Frame-2F

MKTLPVFAHRDEILKNVKANQLTIIQGETGCGKSTSVPQFLYDSWARSNATSERPVNIYV

TQPRRIAAIELANTVAKMREGNEFKEDGIVGKVIGYRIGQKQMISSETKITYVTTGYMVE

RIIHDPEALMKITHLVLDEVHERSMDVDLLLLLLKLQLKDHSHLRLVIMSATMDAQVLIK

YLQKALSTNLVSKKPLFVGSKRYPVENVYLDTLSDWFPGLWRRRQKELVLMKDQFHVLSQ

SRLKASSQMAKKAIVKIHEKQMTLIQEMVLLLIEGQSYQAGPQSQCILIFLPGIGSINAL

YDSLSPLAARGQNVQVMVLHSGIELEHQQEAFKLLSGKSTKIILATNIAESSVTIPDVTH

VINCAIEKQIEMPNAGCSHAEVLVDTWCSRASALQRAGRAGRVMPGMAFHLFTEAFRDLC

MADYNTPELLRKPLDRIVLQLKGQLKDFGVPSILLQQALDAPDLSHIDGAYKLLAAFNAI

DSTEEEHSRLTKFGSFVCHLPLSLELCRLLMTGTYLVQDVTSTNGSWPLLFNIVILVAIL

SVPDLFVMPSFYHVQSVQLYVNEMKKNLQAKLELDGGMWSEPLSIWLFYMKTMSEQRVDV

KRSLNSTFRKMCISARRFQTLNFLISDLCARLVALSKSKTGDFKQLLDTKAIIMLSKLDA

YASSQRMDKELLAYAQDAVAHKQNEVCILRFLIIQNYGEHLIGSTREKPSKFADDDLEGN

DRVDLTINKDDAANFNILSNRDKATLFNQLAGSADPMDELAALAHDKNIVSIYSYATPRH

QTEDKKECFSEFTKDTVERMSFPVSLVYYIRGEKFPINLSIRHSPHEREQGFKFRVAGSN

SCNLSWKQQRDNVKASTGSRSLFSLPIRSLTTQMKKGSPEPKLLAVYADRLFTGDETRMW

CTNCTLLPPTSMCYYAIMLLVTARTHTNIQLLVDATAGGILHVKVGAQDAIFPRKMALKV

TVLLTINAVRTALSDALNASVGAKRVCVTDLLALSDDNIFMMESKANAQQCKWQRLAITE

TDKVFRGQGETPACFPELFLI

>contig30751 Frame-1R

MSSSSIQSESVPLPTPIRVCAFVTLGKLCLRDKELAKTCMTMFIRELRTCEEHEIRSNIV

LILGDLCIRYTSLVDAYLPTMALSLLDASRLVRRNTLLLLSQLILQDYIKWRDSLLRYFL

RAVVDEDDELAHLARHVLCGPLMQKCPHLFTQKFIEMIFVFNGVVSDKISCRNAYEEEGT

RQLALQGKRLYARRARLYRFLLHHMSDEQKLQICMKLCSEVLEEVLEGTLPLCANPSEIT

DHGTEAVLKDTFAILCCPEIKLTSVKDDDDDELDQEDIGLEEHALVATQLAVAKGKLLSK

LSKKTFLENVVPVLIGLKHTLEAKHSPLVRSLLYYIQQLFQVYRHEVKDIFTSTDPQMAM

EVEYDLRQLHLHQEQSRRRENAQEEGLLGVFSKQGMTPRRNEKE

>contig31622 Frame-2R|Blast-AP-3 complex subunit delta, putative [Phytophthora infestans T30-4](gb|EEY62953.1|) 1e-172

MVNPDNAALIIRELMRQTLSADGAYRHELITHILHVCSVNKYANIHDFDWYVHVLVQLAR

VPGNTAVSVDASLSSLLFSSGSALDLSSEDSKSKGMKNELAKRSHGVEVARQLIDISVRV

KSVRSVTVDNMMELLMEKEALGGPGASTLEEVYYAAAWITGEYVMEFLEDVDDDDEEEED

DEDERETEEEKLQRLEDLVDKMLEPCSTRLPGLVQTVFIQALLKILTATAERADDDTVER

IATTIMERLPAFVRSEYIEVQERAVCLQQILLALGIGLGALTAQERTERAFNGTTYLDPA

KRVDILNSYFTERLAPVGNRAQRKVPLPGDLNLDEPISSAEAKFLESDGGVSAFAGENEL

EVSFVSQVYAGVGGG

>contig32083 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67250.1|) 5e-74 NOT\_ORF

MNVVIDTTLGVYIAYLLLQASTVLAVRQHWISLRYHGYYGSPPSWQIWGFQLLQWCTILI

SMKVFVGVILFTLSTPLGWMGSLLFYPVHQHPKIELLIVMIGCPLVMNMVQFWIQDSFLM

NHDVRRSEDVPLLSPLVDRRTPLQKPRGLSSSSNAADMYEVL\*LRSARL\*YKRLRLALIN

DRCVPLCRRTHPRETVVRIN

>contig32177 Frame-0F

MNPFGAPPPGKPQMCRDMPSNTGIVATSRGQLSHQERLLVNGSSLKQSHAMVQRPGKRPP

LPPGPPPSKTIQVPSQPPLPRGSFPDRPPPPPSSAPPFPSLPLPPSTVQANRGVLDAYST

TAACPLTDESCDVRVVAPTKGEKLDIMAARREVVVHAKIRSLVPVALRVQRQVHAASNSN

FTTSSASRTPDSRCPVPAPLPTASHPSIALAFPSNRAKSKPEPFDAFIEEVEELL

>contig33444 Frame-1R

MTDCQAAWCASYLANPSKLTGVAKGYLSEGLRISGLLQILRALCFYEYGAHEISHSKVGD

VATILLL

>contig33570 Frame-0R

MKYLPKTVKLEMQDNDFWDSEEITTPGLTLDTPAPRRYFYITSVTIPNDKPLKNDTAYSL

FSNTAFASKLEDVTTSGFIDIWGGSYTKTIKPDTTAWKHDNNLLLIRWDMRSTAANVSFA

DSSVTTTRENFYKFVKVYKDSGGLPGGFLTYIDDLLSIVEVAYYMFFGNFKRLQAIKTKY

DPNMLFNSDPQAIPALSVS

>contig35204 Frame-0F|Blast-V-type proton ATPase subunit H, putative [Phytophthora infestans T30-4](gb|EEY58149.1|) 1e-22

MERYEKELRTGTLNWGLLHTDKFWKDNFMTFENK

>contig35477 Frame-2F

MINSSSMTLSALIERNCLSCRNPNAKNRCGGCRRAYFCNRDCQRQSWKSHRPSCLPSPVK

SLNDLVHVSTNDIIDAPVTASPFKCVDLATGPVHVTDISVEPSAATPKSKKKSAKNKKKR

IARSNSMHLASTSTPRQERKNRSASLGGKKHVLWGDVQAREFARFPGGGSAVPYDGTWAL

GLGNKVADIDLGTVLEVEKVREMELQERANNLSKSKRRNVSVGETRQFDYRRGVDNPLFS

RLSEDERKKVFTQDRIAQEDLAIEAQLSSSSDLEKPRRKYSTRSASIFDNFDGFQGYIES

SLTSLDFGCVSIEQLDEFARIRDSRDGACGCSCGDLVKKVAKMNVKKLRAFLHDYNIPIL

DTGTGKTELMTAAKKVARAHKNCSTADADCECARNGVPCHSDVCEGCSDDCHNPFQRYEY

KESEVKQYRKVQLDKWRNLQQSIKATSSCKILREDNYPTIFPPKAHAQSIK

>contig35583 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66286.1|) 5e-08

MSTVEQVYGKAAAMRLRTEKTVLEHYM

>contig37710 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68198.1|) 1e-27

MDEASVSASAAFNLYQAGLAPEQILQLCFLRRRASRKLRLERIKIEDEFVLPRPELKIAN

VLPPTNISFKQLLTSSSVLRKPCDNEIVAQNTSERARDSARQHFLQPQQAAAEEVRQWSA

LAKSDWLEIFNSSQGGQNYGMMRSNADAVV

>contig37871 Frame-2F|Blast-xaa-Pro aminopeptidase, putative [Phytophthora infestans T30-4](gb|EEY68419.1|) 0.0

MAAEKLFELRSLMSRSSVRLLRLRHLLGKTEKQIKDQFANRPLQAFLVDTTDAHQSEYVG

DAHKRREFLTGFSGSSGTALVTPSQALLWTDGRYFLQAEQELSDEWTLMKAHDPDVPSIE

LWTKKNLLDGSFLAIDPYLISVFAARNFVKSLKGTKIELVALYDTENLVDLIWKDRPMVR

PSQVTFLSDEYIGRSVLQKLKSLREAIKEKDADAIVLTALDDIAWLFNIRGNDVECNPVV

TSYAIVTSDAATVFLDAANQDDVMRQFSLSNVACKPYQSFLNDLVALTHTNEDIKILVDP

SQCNVAVFMAIPAVNRKEDTSIVMAQKAIKNAVEIEGMRQAHLRDGAALVRFFSWLQKEM

DSGHEDEWDEVLVADMQEKYRRQGKNYVSLSFETISSIGANGSIIHYAPKRGKCAKMSTF

DMYLNDSGAQYLDGTTDVTRTLHFGQPSAYEKACFTYVLKGHIALASTVFPEKTEGVRLD

AITRAPLWKAGLDYRHGTGHGVGAFLNVHEKGVLLSFHLNPDGLKIRNGMILSNEPGYYE

NGKFGIRIESVMLVK

>contig38144 Frame-2F

MILVREDEDGKGLENALLEMMQKMLHFYALFGEKSVFVITRLSGLAGVSSLNVKELSAWE

QLRSSRMENLIPMTYEPHLSCILLVQLTAASYDEVQLRDNPSSTVLYFSDNLGLAIMSPR

NDTAARDSSRALYNKGNNAWKITTMNECMLAENREERVLKVTLMLVLQSSKDGPVIELIS

SSMMNTILRDFQALSYLTMHPITMERQSPLPYHLAAISRMSCEL

>contig39226 Frame-2R

MNYLEKPTSCALSGPFIKRYLKHCLLENIKPIVADIRSIT

>contig39253 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58290.1|) 3e-42

MESIRLGKTKMKLEEWHKIADQRDRDTHHLKEVLGILQDLRKTYRDTQMHGMTHDLLVEL

QDDIAFFRNLKERTKERMRQTLQEARERIHELNGTT

>contig39675 Frame-1R

MLLGVLRSQMGALTLSAGAGSAFLNNVARATLSTSSIANETAAGDEMAAFLSSTTPVEPR

TVKSMKRAIRASPRKLAYLAQQIRGLSANEAILQMKFSPKRKAEIFQKTVQNAINLADIK

YQLEPENLMVAECFVNKGTYLKRLRIMGRGRSGVMHHPHMHLTVVLREFDPTKKPLNHYM

TKKLAREKAKKETTTA

>contig39976 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61699.1|) 0.0 NOT\_ORF

MMSLLLRLVDTEDEEENDNESMPEYEGELSQPNIEEEDGTPIISSEERAKLDKVFGGDMY

NPQAFRRSELENKQRDQLPFERIAHQLREYNVSSISTPLSRKRLMFRTLCHREQVGASSK

AQLIKLQETFMPFQENKMCRVVDSVRDRLYCGGFNSSGSRFMTAGQRGEIVLYDTIHWAR

AAFLPVRDVSWTVTDAKFTPDDNNVVYSSINSNVRMVSTNFDEDGKEHVFALARSTQGRG

AGQSMRMSRLGRFGVWCIDINASGTEFVAGTSQSSVVLVDMETSVPMSHVVGHHDEVNAI

AFVDGPLHTNVFVSGSDDSLIKLWDRRVLSESNPKPQGVFPGHTDGITHVSSRDDGYYFI

SNSKDQTTKLWDIRKCFSSDDFNGLPHFCKPYAWDYRYQAYPGRNIKPVEHPNDRSIMTY

RGHVVIETLIRCYFSPLHSTAQKYIYTGSADGRVYVYDSISGDLVEIFAMKPNGLTRDVR

WHPFEPMIVSPDFYGKLCVWQRQDEEESKIFNEQSARRNYHRAA\*LHCYALLH

>contig40477 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67569.1|) 3e-21

MHKKEFKFSMALPRTDSGGPLVSARDASYWLTVASTPSSSRSGDYSSASASFSSRSLDAN

SFLLNLRNNNSSFLDGSNPSFVDTHVPTSPSQHDNLDTSTSFSSLYASAIHASQTTGYNT

PPNFYVGCRSESKRPLIVAEEVYEHQRYHLLLGWGSKGHLLPLDPDKYMRVVRHSKLRRK

RHPQSTEATQDDAEMLLEWSPSSTFPDIALPEPLAIDRVTVNTR

>contig40583 Frame-0F

MNAVTSCRLPVTKVLKRQFGCQLLNSSVFQPMNYRPFTVVCMS

>contig41298 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61264.1|) 1e-28

MPMTEPLPFRTYKATESELQSELKLVYEIMQSSNDEELRSLLWSKAILVRCMLVRKNEAM

SADSSMTTIRVPSKIGFWLFMT

>contig41423 Frame-2R

MEVQLEIAEEAVKVFVAALQCLAQVGKEFSIECEPTARRLTLRALNDSRSASGQFVLDKT

FFSESQGCSVTLEGVNITSKEILKARFNGRTPFLKCKVFAKSCCNVFRSLKHVQSVQLVL

LVDQEELEHADASQENASQSEIFEVDLDCIELRWQLRCDFDITKTHHMKVQSCQILRAVF

DKNACPNRWRTRCHHLSSLLAHIHHSNEVSVTCSATHVKFESYFPSITDGKPQLQTETAV

ESTDFSEYILQPMSTSIDSQLIFCIKEIRALLAFCKSSDVLEVSFFYSASGSPVLWMAES

TSMARFSIELTLSTIAAFLPASQALCEEEVRLDSTK

>contig41874 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60893.1|) 1e-18

MIVMLGRAAPHLFLSLRQRFDRVSHSAIRCASTLPDNENPPHFENGLQFIAGVLRRSLPW

LRNLSKYQVHRVFTESLSTAAQCWLLMQLYMPQRTSIDLLEFIKGAKTATEANLRAMNCV

DFSKSLADNKHDSHVVAVLKQYNTPAYYNKLALQVKKNYLHHSFYKECT

>contig42134 Frame-0F

MAARKFTLLLLALCTLALISAQTRNSGINDDPSPFETDLVTTPTDMSSAGTPSTSDTLTT

PLETSTSTTTTPTLTTTTALTNSTTPTLVTPTTRTTTRDTPITAAESTPTPPTPPPTPPP

TPPPPADSAIETPTAPLESVSSDLQDPTASAAVDSTLTPPAPDTAKPINPSGSANAGTSS

SSSSSSSWIVPVVVAAVVILALLVITFYVRTRTHDDPEEFDRPSDVFFEAPRSNTSNYAN

TNGNNGAGGSATAEERAQKAASMAIRKESAISAAPAVIPSASSKMRSDSVTGGPPQLRNR

QDSVPLLAEPRFTLQQQVEMEQTHNPPSSRAANGPGGKTGMSAPGVTL

>contig42268 Frame-2F

MVASLLFILALLTAFVQPSPIYQTAGTVRNIADEKFRPASQFDNKVWDIERDDASIFVPS

IDKVHVAAELGSVTLIAMPPLLNDGEDLVIQWSGVERPHQADFLGLSCGPKAHDKDFLVT

VDITAATEHELDGSKLSNSVRFSSLYMMRCNYTVEYFNFQPKGNFFALLAQTEVGMVDAF

TAPKHGHIALTENTDEMSVMFNSASREKPAVRYGLDPATLNKHAEGTFQTYTAAQMCHRP

ANLTSQQWFRDPGIMHTVILKGLKLGTRYYYKFGSDKDGYSSVYSFVSRPDVSVKSAKFI

AYADMGVNSAPAATSTAVRSFQEVMDGYDSFLLHFGDISYARGHAHIWDDFFHLIEPYAT

RVPYMIGIGNHEYDYVTGGNNDPSGAAGDDGRMDFHPSWANYGEDSSGECSVPMYYRWGA

PLNGNAIYWYSFDYGGVHVVQISSEHDWRRGSKQYKWLEQDLKNVDRKNTPWVVLTSHRM

MYTTQIGDKADRQVAQHFRDEVENLLWRYKVNLILVGHQHSYERSCAVRNGKCTKDNKGP

VHIIIGSAGADLEKQGFSSELGEWSVAHVGEWGYLRFNSTEESMNIQFVLNRNGVVYDQV

VLTRWE

>contig42664 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70351.1|) 6e-50

MERLDDVNVEDPHFDASAFFGIEWCRVGKSSR

>contig42710 Frame-2F|Blast-metalloprotease family M12A, putative [Phytophthora infestans T30-4](gb|EEY56337.1|) 1e-156

MTVWARSYMFMMLVVSVTAKQEATMLSTTFDILNEEASSTAPSRARGKNCESNGVVLRHR

TLKYYGENSYVACSNGVVGCYLIERVHDKATEVACPTTDLQQRIDRETNYRELEKRFKKE

AQRDDDNDSNRKLSLVVVSTTRIWDGGVVCYQLSKEFPFNKTHEDYIYKAMNRYEESTNV

RFVNTAKCKKEKLSHCDSCVNYVDFKHPTVGRDCNSSIGITDDGPQIMNLADRCFEVDDD

LKTVYGSAMHEIGHSLGLYHEHQHPKRSIGVLWDSIEQSLWSEMSIRELSVGGPYDVESV

MHYPRSYGFCQPNICSKSVEKNCVKEGTIFCNLNDDDNCIEITEAMCNETATNAIGQRKY

LSKGDLAAINELYHSAAWPLSKSKIRD

>contig42871 Frame-2R

MTPSMRRQLQTSGSEASSSTTLANTDTPTTMAPTTTSPPTTDSPTVTTAPTTTAPTPPTD

APSTSAPPVTATPTTTAPTPTMAPTPTTAPTTSDPPTTEAPTPSPAPPNEPIQTPSTTTA

PPASTIAAPTDTNSSPEITATAPTTGTQETTTAPPTAAPSISFNPPMSAPSDGTTASNSG

ADTN

>contig45001 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66398.1|) 8e-17

MGAGNGYWARLLQLRDVDIIAYDHRVAGDEEEKEEKSISGEESDGVAHEASVSSDEEVIE

DTENVNEEVVDVEEIIWTDVRKGTP

>contig45557 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55728.1|) 5e-42

MASTKRSSINGKGSLDGAYKLFMKSAPVYVTTVLIATLIAEGVYGSATNYIWEASNRGRL

YHHIDWSKFAAHDDEEEEEEEDNEENDQDEEKEEVEEEVEDAQEEHAREYHEDDDE

>contig45690 Frame-0R

MAASSQIEAIKLLMGRREQELQQAAEYGLGLLEANEELQMEAAALKIRLETETHEISVER

DTWQRRTAHAQQESAQWERKFLRVKEEMAGLAEEFEQFIDRCQCRRGESKATSNDRRHLH

QLDTIAQLEAELQELHAAERLNEAELAFLRQFKKQAEQQQQEALECEALVAQSEESYRKQ

VEAERRKMQQLLAKDKSEVKLWRKTAYLYEAEAKELRKQLILAEEARDDAEVRSNGLSEL

LLSSKSRCNRLERELELLEHVSYFTQASVDRDDEESDSDDESIKIKEFETDMEHNKPQVT

SVHSTVTKCAAVATPSPLRMKRRRSFFAETQVSSSSMAVVVQDGSKAPVSESEMNTHKKL

YHYFYLTAISIINENNLHDRCFSSSSRVTIEMWYREILAKDVPFLLWHSWLINRISQVAA

SVHEDDNLQHPSPNSSFVGSALSDAFHAFLLRKNSHNESKQLSPKTSSPATSPAVRVPLT

MARAFFRLLRKNTHAEAGSVPDS

>contig46066 Frame-2F|Blast-conserved oligomeric Golgi complex subunit 6, putative [Phytophthora infestans T30-4](gb|EEY58675.1|) 0.0

MHAHDPVRYCGDMLAWVHQAIATESEFFCVLFGGDVDLCPPTASTNEALDGNPGLLAARN

GNSTRKVDNIVCTSMVGCAFDGVAKMLQVRVKQTISSSHGIVIAYKLKHLLAFYHRKLDK

LITYSEVAQVLCYCREAANEAFNCQFEQLMDSFAASAQDYAASLAATHSSLDVSHRLLTL

LDVFQTSLVPEEDKEAELAPLFDSCVQALELMCQRSVASLENVDALVFRINNFSCFQDPL

GRIPEVSKWHLNICSDLDRWLQELSEVHAKHVLDRCRATALLDHIQEFQQNHACAMELSP

ADTPGLDGETITQVMD

>contig46220 Frame-2F

MSSEERDSAYCDWFSRRIIELDTHFGQLFFAYELSKLALQCSSGWSSQRAQNSLVKLVRD

VERLYKCVYSFHLSASRFL

>contig47704 Frame-2F

MYENRIFQFWVNLACVRNQEAEAVQILVELATRGYLRYMYPILAVNSIRLELLDTNKPKN

IMRNVAA

>contig48374 Frame-0R|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY70283.1|) 0.0

MVLFTYEDMKISFNLLCCVCGIGTLGLPGNFARAGPLFASLAMSFMAFANIYASIAMSKV

MLLAPSTVVTFGDLGEWAMGKIGRWLCTGSQIISCVLIPCVFLVLGGGLLDGLFPGAFSP

TVWIILMAAMVLPLCLIPTLKEGSGVAFAGCVGTLVADAISVAVVVRGMRGHTSIPETNI

NFSEVAGTFGNLALSYGAGIIIPDLQRQHSEPHRMPRVITFTMGLISILFVVISVIPYTS

AGCQISGNILYTIYPDASTGLTSLGFEPNWGAVVLAYLAMQLHITSAFSVILNPAFYMAE

FVFLGMHKQDKSSDVENGLQYVISTNPNDELAKQTNDSTHRKCECNCHDRIDEEAAEYRG

ANAIRYVILRICITGVLIVLSILFKDHFSDFANFVGSSSLTMNCILLPVAFYLIKSWNDI

RMVEKIAAIAVFVVCLILGCYSTYTAGNHLFAPSDSVALFPYCEPKFQNTVFYNSTASI

>contig48460 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66430.1|) 3e-74

MVNERISSVELVQRKEEYYELLATSDRSLQDVLNQRGGLVLARVGRYQPWPARFSEPGEF

AKMAKYRAKKGQACVYFFGSRNYGWVSKASIQPFPEDLTMLTASNKYNQQHIQEALDEAK

LVMDVTDETGKRFFDRIMERKEEAVDL

>contig48778 Frame-0R

MDILVTDTIVIAILCFVIPVIACLIWSRRSNQAPEEVNHDRVPVHGPLLSLVGWKTYCAK

VVSQQRTLENVLVTSKRQEREDTADVAAPVGLSTLQVVTLSMEFEDPQHPLTAVTSTGRR

RSSINNTNVVR

>contig48806 Frame-2R|Blast-PREDICTED: similar to retrotransposon protein, putative, unclassified [Nasonia vitripennis](ref|XP\_001599390.1|) 9e-08

MLADLMTKALDSTKLVALRKMMHIG

>contig49207 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64250.1|) 4e-57

MNTQLDSVSVSSSNADTEDSSSSCSHSTLADSDEEGKPQSQPYASLGEHLKRILEFFGII

FDYRKNGLSVRDGGYIYRLAAFPPSYVGKPALVIEDPIHPDRNVSASSYAFSMSWRCSKT

RTMPSSIFARPSSLRQPSAAC

>contig51044 Frame-0F|Blast-gamma-tubulin complex component 4, putative [Phytophthora infestans T30-4](gb|EEY58027.1|) 3e-24

MHHELFVALLGHTGDVIERRDDGFFVRKDATFLSSSQRTVLDRLLCLGFAFTTLDEFVSR

ASKYPSVYLRAL

>contig51620 Frame-2R

MRHQQTRMKNIVFNRDSNPRQVQCTVNKISSISRTLKRSSPGSPGASRQQHVVAFSISIY

LNTPHFTPFISTRVSPRQVRDRTNGVRRFKKFRVRPFYYNELATLLLGTL

>contig52175 Frame-2F

MAAITISRLPKTHMIPSRERFQSLNIKAHTYGPQNEPMRLKPAG

>contig52830 Frame-0F|Blast-pre-mRNA-splicing factor ISY1 [Phytophthora infestans T30-4](gb|EEY70156.1|) 1e-62

MYKHIEPDYYGFRDDEDEQQLQDEKEAENRLRQRAIDEWEAADAKRQAQMAELVQGTVSQ

>contig53635 Frame-2F|Blast-cleavage-associated kinase [Phytophthora infestans](gb|AAM21157.1|) 2e-38

MSGDCTSACDMWALGCVLYITLSGSHPFDLDGMATDSVVEHRVKTEAISFDFSAWHDVSV

>contig55336 Frame-0R

MTALQQSSDFLLHEAMTQHAAARDLESSGSAFSDTVARYIAAADTYMLALNALPPSENMA

RATLKEQIEYVIDYISLLKAKNQMNQQNDSSRDDVDVAVLQWPDPPIGQPDVVLANASGP

TPLADSTKE

>contig57378 Frame-1R

MIKNIYFYSGGSMRAFLSDQTGAKDLVDDTIRKVGPNIAGFLITQHGSTSDKQIDHIRMT

GIQANDHRDLNKYTSSSHWVSEVTSEYALRKLGKIVKPTYYEEMWF

>contig58432 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70439.1|) 9e-34

MPVAPKKLDVFLTTSDYSKTYVFHEEDHTLGNALRYILMRNPDVDFCGYTIPHPSEPMMH

IRLQTRQGAPADEAMRAG

>contig09475 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69869.1|) 2e-40

MRVGVGAGVVAAAAMTAATFWQSSQDSPFEKYATARKADRN

>contig09996 Frame-0F

MLQVIRQVDRKFILVQADTTRGKLVLCIDQHAADERIRLEKLEDDIFGPDGTFRRVQIQV

HDPPIVLQMYLRERETLQHNKDLVESWGFSYEPVAPRPGLFFNIGEKTCPDETITILLHT

TPMVEMKAANADDFREYIQLLHSAGESYQISHIRPPVITRLLNSRACRGAVMFGDYLSLG

QCRDLIEDLKTCQLPFQCAHGRPSVVPIAKIHNIGF

>contig10154 Frame-1F|Blast-uroporphyrinogen decarboxylase, putative [Phytophthora infestans T30-4](gb|EEY57967.1|) 1e-159

MGYDFFTMCGVPEIAVEVSLQPLKRYHPDAVIIFSDILIIPQAMGMNVTIKPKEGPLIHD

PIRTPQDIDKLNLTPNIDDTLGYMLDALNLARQKINGEVPLIGFVGAPLTLMCYMIEGGG

SRTKALLKTFLYQHPKDAHRLLQGITDVCVNFLVAQERAGAQALQVFETVGAEALTQDHF

YEFVLPYLAQIATRVKTASPRTPLVCFSKGTPYAYEKLVMTKFDCIGLDWQSDPVTVRQL

ARGRVSLQGNLDSSVMYASTDVIYDEVKKMLQRFGTQKYVANFGHGCFPDMSPTHVDAFI

KAVQQLSLEMN

>contig11373 Frame-0F

MSAITATTRPYGDLKDAISSKDCYCLNEDPNKSFRNIFMGDETLVLQSDADEQLLLYIEF

QDAVKVFSLNIVAPPGEEAPRIIKLFVNRPNLGFSDAGDVEATQTIELTEEDFKPENDVE

LRFVKFQRVKSITVFVEENGGAETTVISSLRFFGEPLAGTNMNELKKISDE

>contig15687 Frame-2R

MLLKQLLQDPEIHAHVTLLFASTLQQEVVKQSVKTTLSEAIHEVLSQNDVQNHAKEFVSN

VVQDQTVQAQSGDAIWSTFMYALTPAWLSWVWQRSLDTTPVEALVVAAAAEDHIKKTKPV

KEPTQKNAH

>contig16394 Frame-1F

MMPVPSELVITQHRRILLLFLALLAGVTIVMAATTAPNAVAGVFRRRLREVPNALVDGQN

DERNSSPSIAVRQIAEKSLASAKTKGILPKNFEEFAENFSKNNYSGNDDLDHRMYAFLNA

LTKNKREALEYVFSPNWLQKPHALRFYNFLVNRWSKQKLGQNLHLDGISRE

>contig16732 Frame-1R

MATMRRICFLFVFNLAVATSTQGISDEISPDIPETSQAVIDGHRLKGSSKVSKATTGSEE

RFIRSQLQFLINKIFGARGVAKVLVEEGPKSGVFNKLKEILVKISKFEMKGDMLYMVYIY

TILFLSIPIILGVAMYINHHVESSYIH

>contig19544 Frame-1F

MGLESPYKPSNRGSFLSSPMPTNNPAFEAPACSPPSHHASVDDCGSSDSSDTTNEFPQAE

QLLVSHLRFAHALRKNDAAMILQYLAKDVILVSIDGSIHEGQSAVLASLVGARMTKLSAN

LHIKGCPTRSGCCQSTFIYEHGIVFKDPLFMEVLDWKLSSATITRITHFALPNAKSGKTP

NDFSKSAPLRLSFGARWSDEEDPSGCINDSDSSEMWDAETSNQAAFQPVQTRSRRLKSTS

SADYSSTSAVMNISSASLKRTGSSSSNQSGGYEASIQPLTPRTSVIPSARSSAPLFTLAE

ISCRGLKPIRKRKDCEPICNSSVPRDGICLEKSN

>contig20755 Frame-1F|Blast-eukaryotic translation initiation factor 3, putative [Phytophthora infestans T30-4](gb|EEY60161.1|) 0.0

MASYETPRVDVNVNGWGPTVLPEQFLNVPYAPFSKGDKLGKAADFVSNYAPRGSRYVRDP

SGVNAEFQYKHDTKDDATFQLVDTSKGTRPKTEDRLRPTWNQQRFGGRGGRGGQGGRGAY

TTDKPDPNGPTTSSAQLRMKGMQKQNKRWDRLSNARRAFTFRRRDEVRADRVASVLVQPT

WNLLDEFELQQLTKLQANIPPTNDVKWCGELREFDAAFDRITSRTNTRVHRFDDRDFYYV

TTTDDPVIEELAQQGQARVFATDAILSHLMTCTRSVYPWDIVAQRVNNMVFFDKRDASNF

DLLSVNENASDPPTQDDVEHMNHPDRLSLEATMINQNLSQQVLKSGNGAFFKQFDAPNPF

ASDDGKPASCAYRYRKFDLGGGLNLVARCEVQSVAVKKGTQHYVSTFALNEYDPKFPGSI

EWRKKIDS

>contig22340 Frame-2R

MRFAFVWLVVMIVASVAGSDTTNSTRKALATKETVTSVVVTPSVPQRRRLGWSSKISEWS

TKFGQNSFIQKLKAFFQKHWFFKPAKIVKTQPVDNPSFPR

>contig22793 Frame-0R|Blast-putative RNA helicase [Phytophthora infestans](gb|ABW71831.1|) 3e-73

MIAPTRELAVQIQAECNKFGASSKIKNTCVYGGVPKGGQIADLRRGVEICICTPGRMIDM

LSMGKTNLRRVTYLVLDEADRMLDMGFEPQLRKIMSQIRPDRQTLMWSATWPKEIVTLAN

DFLT

>contig24265 Frame-1R

MLFLIGFVLMSEFSLTYPIKRIETWCGMNIQAASVKKLMTEAVSLMTVFLWKYFFLNSDW

RWCVFSCFIILTMTPQLVYYIMATLEPSARNSYVYAVVSGLTGFIRTGIVILQLAITAEI

APVGGESAFLGMVVSMASSIQLLTHTVSHAIGFLFDVKVVGSSHDDIDRMQVAFALVLSY

IIQVMALVALVFLPKQKRELQRLHRFGYKDDKCTTWWIIGCLVVSFIESTVLNKK

>contig24669 Frame-0F

MSGREKRIYDAVNHLQSHYSTALIEKAASLLYQIVSNIITHPTDEKFRSIRKANRLFDGQ

VAKFPECLEFLLALGFEDQLDKFVLVREDPALLWIGRSTLESLLSAEA

>contig24892 Frame-0R|Blast-ubiquinone biosynthesis protein COQ9 [Phytophthora infestans T30-4](gb|EEY57962.1|) 1e-95

MFSRGAVELVDYFMDSCLTTLRKTLISNTDTLQAMSVAERLKFGVRTRLAMLEPVVATWP

QGMAIGALPQNAPNTAKKLANLSDEIWYFAGDKSTDFSWYTKRAILAGIYASTELFMLID

KSLDFHDTWEFLDRRVDETIQLGELPQNMNDVVGMASIGLQSVFSAVTSLAGPLAGQLIA

KSPISS

>contig26704 Frame-0F

MEVEVGARVAFGAGKTGIVRFIGETDFASGEWVGIELERPEGKNNGELNGRVYFTCAPNH

GVFVKKSMVRAVLSASASTTKMPLARGPLDVDSGTVRHLSSVGTASLPTSELAAISGARL

AAPRSRASIGSISSKASMFIPSVARSRLSLRGSTSRSSVASDDQLLEARTRISKLEEELE

L

>contig27417 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57345.1|) 6e-41

MDAIKTHCYVTYPTLEIAKQTSKALDGKVWPPENGRSLHVTFAAQSAMEVSQIGELEPPI

PSERKDIDVAQATQREMVTIDEFFQKTETKPVLYFLPLTDEEVQEKKQRQSQQLEGQSRK

RRHRGG

>contig30000 Frame-2F|Blast-arginine n-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY66512.1|) 2e-57

MKAIKSKISISDAIVEDVQLEDIISSRELLYEIKVEHVKYDDLDFHASFTLSITRDATMH

GFVSSFDVAFERGCYCPESFTTGVEGTPTHWHQVSFHVPKPFKVQKGDTVDGKWWLRRNA

ENPRFLDVEVQWKEPR

>contig30556 Frame-1F|Blast-phenylalanyl-tRNA synthetase beta chain [Phytophthora infestans T30-4](gb|EEY57734.1|) 0.0

MPTVGVKRDELFAAMGQTYTEEEFDALCFEFGIELDDVTSEKQLKQRETKGQSKDHSAHS

DAVIYKIDVPANRYDLLCIEGIARALRIFQEKERPPVYTLTPRPEGALLITVKRSTKLVR

PYIVSAVLREVQFTQERYDSFIDLQDKLHQNICRRRTLVAIGTHDLDTLSGPFTYNALPP

NEIEFIPLSQDKAYEAKELLDFYRTNPEVKHIKPYTDIIYDSPVYPVITDKNGVVLSLPP

IINGEHSKISLHTKNVFIECTATDITKAKIVLNTMLAMFSEYCAQPFTIEPVQISYEDEA

ANENELTPDLSKRLVEVPTKDIYSMLFGKGHSINLDVERICKLCDKMQLDAKPVGNGTTI

LAEVPITRSDILHPVDVIEDVGIAYGFNNIPLTIPQTQTIGMAQPLNKLGDLLRDEISRA

GFIELLTHGLCSHKENFEYLNRKDDGHSAVVLSNPATIEFEVVRTSMLPGVLKTIQNNKA

MSIKEGLKLFEVSDVVVIDNSSDIGAKNVRRICAAYTGPTDGFEIIHGLVDRIMQLLGIP

SKLEIPAGAKEFYTVDPAEELTYFPGRCAYLTLQKENVKPLRLGTFGVLNPEVLKNFDLH

NPTSVLEMDLEPLL

>contig30691 Frame-1F

MANQHLLSGIQSFSSADRPSESPANTLTHSHCWMALQTATMDDANDAIRTGERLQHCCGC

SVGDSCYWSSSVSTNPNANEFIEYTFQHPCVVSAVQIVPYRVFWHPQSPTYAPKRVHFAF

YDEKSIRPQDVLKWRLEPFFATGEFVVENEMKLQEFSLGQKVAIGRNTIMRVTLMGRQQA

QTFVLPQTFPNENEHPKYYCCLSYVNVCGVRWKDKKTANVALATSSAMTSNLRVAALTGL

AVYFTACYKGLIGQSQRWE

>contig31623 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY63216.1|) 2e-69

MTQRDPQLLPLLNPLHVASPCVITSKSSSTTDPRNDTDSSLARNRISIRPFPAATELESG

SDRTDGQWQVLHTYNGLLCIKLHYVLEFVQLKRVNFGFRWRATNLEGNTDVLPPSCMIGP

HWHIMLITWSIFFITAFCINALTFRKASGIELAAGLVVSGLCLVCYALVACSNPGIVQSI

QIPPDDTYTYCDHCESYRPE

>contig32176 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66154.1|) 1e-107

MVANDRAPLEHNKKMGALFIVNQLFKIYFKLNMIHLCRNLIRAVEGPAFPKFELFKKSEK

VTYQYYVGRISMFEDQYHKAEMCLDYAWKHCHSGKVRNKRMILQFLVPVKLLLGIMPSPQ

LLAEFSLEEYTGLTDAIRDGNLHLFTEYLAQYQESFIQQGVYLLIEKLRLLVLRNLFKKV

>contig33067 Frame-0F

MCEDLDALKVDGVWEVVIHPMFCTTSGCLSQRQMQRKIQCSTRRILSKHFSVCCSHKTK

>contig33139 Frame-0R|Blast-quinolinate synthetase A protein, putative [Phytophthora infestans T30-4](gb|EEY53156.1|) 0.0

MRTAQHIFRRVRLPVGRLMPKHFVTAAPASLSASWDRPFPSILISADGVSAQGSFAEAQA

NYFQPDMQIVKDLDALLNEKKMGIVAHFYMDPELQGILASLSWPHIIVADSLAMGEAAAK

MAQSGIRSVAVLGVDFMSESVRANLDSNGFQHIPVYRLAEQKIGCSLAESAEKKAYLAFL

QKAAKTPNSLHIVYINTSLRSKAFAHDLVPTITCTSSNVVQTVLQAFAQVPDITIWYGPD

TYMGENLQQMFEHFAVLPDEKIRQIHPQHNRKTIAELLSRFHFFKEGNCIVHHMFGDKVT

KRVRDEYSHAYQTAHFEVPGEMFTLAMEAQNEGRGVVGSTSNILNFIKAKTAEAVKKQVG

EKLSFVLGTEAGMITAIVRGVQETLNAQKTCVKPEVEIIFPVSADAVATEGEELVPGVAG

GEGCSTAGGCATCPFMKMNDIDALFRVAEGVTATSDGVDPLANLYPQKYSELIHGRTVTD

VGVQPIMHMKALMEGRKLSDVLVRDIKTRNRSLDYPSA

>contig34084 Frame-2F

MVGVVWQCLVNGWQSGQLLTSRTGTEYVPVVIAHHGSTDHEVLTTHEEAKVYYFKGQLLF

SSVASFREYFDVIHDPNVVVLDMCDCTFADFSAVEALREAAVRYRDAGKTLVARNLDKKS

LDMLNHDFGWTFIDHIKMFTPGTVFDDDKESKEKMDKERSSHASLVSLHQLHGLSPEASK

STFL

>contig34457 Frame-0R

MPIILDQIQPPRYSKQIKIMAIKAHEESNIFEPSEAPLPPPPPPPSPPQDDINTKKPRTS

HVDLTMHKNKKQDFRDILALFYDVQMNAAESKRQWNELWQTVLMDSQEEHRRRRQKERHG

LKRKTSGEHDHGPVSVGTGSGPLSRHSTNMHDNFKKARQGSTASTDSSESGKGIRLGGRF

LKNVAKGSKLMQKFGARP

>contig34875 Frame-0F

MKERDRYGRDRSRTREEDYNRRKRSRSQGRDRRSRDRRDQDMYRSSRSRRKYNQKDDVSS

REIELYGIYNGRVSKVMDFGIFVELDGFSNDQKKEGLVHVSNVSIHRVSNVKDVAKRGDR

VKVKLISISGMKLSLSMRDVDQQSGDDLMPQRSSTGIERARQENKALDARSWINTSAPGM

QRSQFEEDETKPQRAVKRMSSPERWEVQQLINSGVLSVEDYPTFDDEHGLLNTETTEEDF

EVELNEDEPV

>contig35582 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66286.1|) 6e-10

MSSASLPLIRAPPDALRFGFYNASEDVRSVHEVQRLQTS

>contig35960 Frame-1F

MKQGDQTQQQRLQQSQQQQREQLFLREQQREQQREQQEREQQQQHLEQQQLLREKQEQQL

LREKQEQHLLSEKQEQQLREQQLRDQRLREQEQREQKHNERLVREQREREEQKRRHEHSS

RNITQSVSAGSNFLSSESATQEMLHRNQLPSPTIKRASTTPPCPTSPQVLGFSNSNTGLG

RANAQVPTSKSPIMSQIKRVAQKISASNHEVSPKAYNLIKVQSLHEFATSPSSRGSCGAS

PSMGSSPKVSSSPLASPVSSLAASGIENGKSYLNLANNDYSSLGEKDGNGLISKESGHSS

YE

>contig36330 Frame-2F

MEHNSYLTTGLELFGWREQRREAPDHVKFTLKKRFIGYSPLEMSLRAWRVVSSPRGLAGL

YSSTMRLSLKVLQVVDDYNVVMHRVMTSAGTMRTVESLFLISRFQIDTGYAILFRSIDRN

RLRKRCEDEMVEIRGEGRQDKWLDMFA

>contig37665 Frame-2R

MTTSTRDLRKIPSPSFVSPPPASKPLKALTLGSQPTRKLKSTKPMTHEQTQKLHHKAKLS

SRSTRILEDISNTSHCANFFRSDPTRKLDFCTPSKSKTKRVNDPIETSSSSSCNSSSDDD

SNYSSDDTQAILNATSSGTRRMHQKPSPLVATNALAPGLEYNFAVSSTVSSVAIAPNGKF

LVVGFYNGMISLYPLNHDAVTFRQGVLVDQIMPRGMYTQIMVTVAIPQDGKFIFAGVYRG

STDIRAFEVDSIELPTSNDMLSYRSDDDNISTFGIPTATVISHTFSDAKLKGFAAVTSVT

VNRLSHYHTEYRLLCGLGIKNIHLWRFYQQSTAPFKWTWECIFDKQTNGISLEFMTFHPT

LENQILSKSEHQNVRIWYLKEEYKALENTVTVSKTSHMDVKQTTDILAIYGNYAYGGTES

LVVVDLLSASRMELDLPLTSSELRAQEEALFASRREKSLRAWHPRMNRRRGIEDMNGPRH

MRTVSKLASHDMAPFTVGRCSDGSVFYHQIKPETGLATPLEHIEGYEQFFEDPSLDFQAQ

YSDLTRVNTNGLLAVLPLPETDKEKWMIVAANQNKLVVRSLNAFLHCKETKKEVLRSDLK

YVVRNDLKREESAFVGSSDVQACGATHCTHQYSKKADKLSIKRRRYERASTINDTRCTRQ

SSRFVAMVESSHESRNASFKQVKKVHVIEEKMAAVTTPKRTMLSTSAASPVVSISSSSSS

SNPSTPVEQRKHATKDFTALQELSWTLSPQKHNMVTDRVTLSDTQASPQAQLVDKLEKRL

DCSQYALKKHDVFKKESKNTAQSIALVDDANLPKQLESAIESVSLFQSDKGSLLTAVMYQ

YGTRASSSTEAEVPESDGLEMDIVAMEQSHLLLQFAHENERLKRNFSNDRARLYKQVDCT

CALHPKKTTTHAMNWRRGVAHQYHKRQHLARRHQKQLAAKFHELRASYAIQIQELLALQQ

MQAKALWARQQFNHLYRRLSRAQTPLGSASPLFLSTLPNHFVEATTLSSSTLFAEIFSPN

>contig38721 Frame-2F|Blast-5-methylthioadenosine/S-adenosylhomocysteine deaminase, putative [Phytophthora infestans T30-4](gb|EEY54489.1|) 3e-07

MPPTPQAPIDIDASSLKQKVDLIIYASYVIPVVPRGVVLSNHAV

>contig39902 Frame-0F

MDGLLLFWDFFRGRVKYSIDLNADVDELCSTSQQIFNPPLVHSLAFAPNGRSFVAGLGDA

SVAVVNFSSRQIVRRLKRHAAMVSQVHFPAFCPEDRLVSTANDAKVCIWNYQAAFSAPEV

DNINYENDLASNSMILLEFSVKASPNAITTTSKQNMIVVADSSKEISAYFVR

>contig40582 Frame-0R

MMPFFTSTIIIAIAAAAVSSAHRIHHTRVMRGLQTDTSINHSSMDMITSEMSNSTMDMQS

SAINNNLSDDDYRCPVCGMSTMNMGYNNLNHVGFVNGQIIYTCGMAARSFGDYGFDLTDT

AYLAANIAEFIVNPSDATNYAECRSSCDECTNGIKDPLTGDNVNTSNYQYVCLSNGQKIY

FASAANRVKYLNNVKLEPRYLVNNIICQNTTCADGESITALSAAAQAFVPETTSTNSSDS

LGETGGTNAVIAVKAPMHTVFALTCVLTAISCMT

>contig42597 Frame-2R

MYCRWPSKVLSDLVEKCAKMSRPILSFQTR

>contig42711 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61504.1|) 4e-66

MIRIVLCDSSSSKLTGSVIPVPSKGKEIKSQLSYESTRTLLFCMIGKPSNPMIPGMNIDG

TPVQEIVIGTNAGTESATVSSPSRTKSLPESDLDGSGSVVENVPEADLPDLVQLLIELSV

ES

>contig42870 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64311.1|) 0.0

MFSGTVSEGERMHSTVRLNHFTLQFEDASLEKIYQAGLHPRKKALWLRSLLPAAASQILF

ALADGLDHPVENLLVSVPMRVLIAMLQVAMWMLVRWDLVQAKEQTMLLVSVISGIPTLLL

YTLQRSSLCHWDALFVTFGLSFYTIPKVTPLGYVSSFYGSWATAAMYTAIALVVRPPPRR

TEIVLGTFFLVPMVWVFNTIAYYSEYNARERFALRRRLRRESITLAVACTSAGGEALLQG

GEDDGWLLLHTLSVRGFMAANNNSNTTSFVLAVILWGAFTLGGWTSLPNALKFVDEATGW

AWFSHCAGVTVFLVVVTRRLRWLLVVPVVGAFVLWVMSLAMPASWIIVSAHSVGYGLLLA

SVVIAMGVFGWFVCAWKELVGFLTRSCFLYPQLQAGMEREYPLLVRIVSEYTAGFD

>contig43763-0 Frame-1F0

MNGDFLHAINGDWDSLLTVVRENRK

>contig45000 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68255.1|) 2e-96

MLKSRSFCRSLVLAPTYRRLLSFLKGAAPTPQLLWQHASNLDATHCHDLLVSESDLRMEL

DVITEDEERVLSDECTSIFKRRRFEENHWDNIIIKYKEMERSRWSCESQQILQKIRKTTI

LPENLTYFSAVHVIELAEDGYIKPHVDSIKFSGRVVAGLSLLSPSIMRFKEEHGDSIIDA

YLQHRSMYMVTGRIRYHYTHEILPGNQVFKENILVKRTRRISIMLRDDFREEHVAKYHTP

>contig46139 Frame-0F

MCRDDRASKAKNSKVSSIDSLWMLHVDDILAFYERFCDRSRR

>contig46221 Frame-0R

MRFLRARSQFCIEIGLNFLYLSFWWISFRIGPVAYKLELPQVNLLMLHFKLLRIAYNTSS

LSVLVVIDD

>contig46571 Frame-2F

MHESYFHMPRRRHSTFTMNQRISSSSICGPMNRRHSLVEGYKLHLLATMIDKVPVPSRSK

SEDGQQCTKLVTEMMAQRLRSSIQTSQGVQFEDKHYKHQLKLYSLIALAADPYTSTINAR

IAQKALKYRNKSYCKKGWK

>contig47082 Frame-0F|Blast-DNA-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY69219.1|) 4e-75

MWRHTSPLASSSRLQLLQALSSMVQIDELFHRFGRDTFEMRKTELQDFVGFVKLWERFSP

SMSEDGIEFWSQHTMVQNTIVDFLLKTASDQGMLSDEIQLSLRRGMSNTILQYASAAIIC

NIPALASKMLKSYRELCNTHQLPKLSVQMIEVFVAHMLKLVDRQGY

>contig48029 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56717.1|) 1e-06

MTSSKHEEVAALEALRDSSAELVRYLENIDRMLLHMNQQNE

>contig48375 Frame-1F

MGFKEFSGHVLLDNVSLVSVDTNGINKNGHRLIENIIMNLSLSYVHKTKLRDSHHLATLA

FHQDACFQHKLFFNDYSATTSASVWRCSHRLAF

>contig48461 Frame-0F

MLVGSGRSHCAGASSLILLRGASCHCEVENDFSALLNLMYHSNGLLGADQSGSTYVRLCA

RSFVGANYQLGRVRFPTFPAMPILEN

>contig48999 Frame-2F

MAMQKIMTVAQRSMLAAAIVVRKILYLARHCWPSIGLVLVFSVPSTTLFGTLSLHPPASS

VRR

>contig49192 Frame-2F

MAQFCEVCTTADAKYKCPTCRVPYCSIVCYKKHKDMLCKPKPLLEQQQMPLQATPAPAIA

MGVDEEDLEKIKDEEMDVLKTSDRIKEMLLLPAITQMLKQ

>contig49570 Frame-0R

MVSLATETRGNVPKVRLNLGIKRLDFDSMERCLVLDLYSRYDLILDVALLERYEPLIDGG

LRP

>contig49897 Frame-2R|Blast-pre-mRNA-splicing helicase BRR2, putative [Phytophthora infestans T30-4](gb|EEY64887.1|) 0.0

MAVSEAKARIKISTLPKWAQSAFAGMESLNRVQSKMYPAAFETSENLLLCAPTGAGKTNV

AMLTILHEVMKARDPETGDIDLNSFKIVYVAPMKALVQEVVLNLSARLSSAYNIQVRELS

GDQNLSREQLSDTQIIVTTPEKWDIITRKSGDDRAYTQLVRLVIIDEIHLLHDTRGPVLE

ALVARTIRNVEVTQQMVRLVGLSATLPNYEDVAAFLRVDPARGLFYFDASYRPVPLQQQY

IGIMEKKAVKRFALMNAICYEKVVEQAELDNQVLIFVHSRKETASTAQALRDLFVENDTL

ARLIKPNSASSEVLLQEAEKIMRNDDLKDLLPYGFGIHHAGMKRQDRTLVENAFADGHLK

VLVSTSTLAWGVNLPAHTVIIKGTQIYNAEKGNWCELSPLDILQMLGRAGRVQFDTQGEG

IIITQHSQLTYYLSLMNQQLPVESQLMSKLADNLNAEIVVGSVQNVLQAATWLGYTYLFI

RMLRNPTLYGISIAARKADPTLLQYRTDLIHSAAMLLAKHNLIKYERRSGVFQVTALGRV

ASHYYIAHDSIKTFNEYLKPRMSDIEILRLFSLSNEFKYVIVRSEEKLELVKLLERVPVP

VKESLVSTALGGVVAGSGSAKVNVLLQAYISRLKLDGFALLADMAHIHQSAARIFRALFE

ICLTRSWASLAERMLSFCKMVDKRMWLSHSPLRQFAPGISETILKRIEKKDISWEKYNDL

EPADLGQLINNPQYGKQLYKMIHQFPKLELSAHVQPITRSMLKVDLVVTPDFEFTRDVHG

NAEGFWVFVEDVDGETILHHEWLLIKRRFASRETYLSFTMPLLEPLAPLYYIKVISDKWI

HCESSLPVSFSKLILPQKNAPSTELLDL

>contig51539 Frame-0F

MDTYKRLTPSQGQNNAAKENSKKVKLSHDSTLSGTSGEAAEKQLQTAALEGRENLVTDDD

SSVESGQSGAVLSDLEDLDESNDEGAPSSI

>contig51621 Frame-0F

MTDEGLVAIAQRATTQLQAMSKRPVIIGQWKRLARSKPECQVYESLSKAKDQFSVMVSMN

LPCSLQEILTVFSTANEAEFHRSMEAVFGDQYVYGINVRSVDCAAYDEDALGVGRRASED

SLND

>contig51881 Frame-1R

MRHRRRSAKVASIHVLDTEPAHYNTHRSQLQIVRSTRPRRIKHTRDELAQSVCPTNNCNV

RCYKCYHGKLDGGTSKETICTMAMDTELTALAAKVALSQQEKLLRTKAFEDVRELVTSAF

QSATVQLFGSFSTGVDTFRSDLDVTVGISMSLSRPMPSEVMVDREYCSDEQRGRCPESGS

ASVHDTVQKSEDKCSFSLNLALPLGVI

>contig51966 Frame-1F|Blast-elongator complex protein, putative [Phytophthora infestans T30-4](gb|EEY66437.1|) 7e-75

MHQEMVLANEPIAIDLTSVKTSTDVGAIAAYDHLYLAIENVVLKHEQNRVDQVLRIGILG

LGSPEMGSTDAAHMRALFIFFKRFRTLLCQSTNAVSLILVASDTLGAFPATFINELRHVS

DSVLTLNSFAGSRDLLTEELQAFQGSLMLRKLPRLHSLTCHAPSNARFGIKRDPRKLRIE

KFHLPPEGSRTNDKSKGCNSITPG

>contig52174 Frame-2F

MSPSVEPKVSPPKPRQTFHIPLDSSSPVEISFKQLLTERTRQLACQNPTSTSPFNVAASI

VKTMENSVPASRP

>contig52527 Frame-0F|Blast-Rab3 GTPase-activating protein catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY64864.1|) 1e-24

MFLLDVDAMQLPAPDFHQCLLHQKLQLLNCCILRQAQDLKSKLKANNDGKTEEQSSRKLA

PPDSDVENSSLSDDEFFDSIELGDIPQSSPCQTMRAPEGIRNEASVIVCLHTNEPLLEPV

TQS

>contig52552 Frame-0R|Blast-type I inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY60218.1|) 3e-59

MVLFALTRAASFVDQSVARNLLNRASLCLFFSLVLFQTVLWIDIANPKISTRSRRIWIGF

LVANGLFYATILGLSVLHEVRVAQAKYTMTRIDQSTLWTGVLPVLLIAAGSLINSLGLVY

STCKMRNRV

>contig53634 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54402.1|) 8e-06

MNDIKNQRLRAKAIQSLGTPQERVVSLNNVLEVPFRADTSADWNVLTRWMLYELDKVGPR

AAVEELTT

>contig54864 Frame-2F

MSSNHASDSNFRCCSGLFYHHRPGVNRAEINNQSQPSNSV

>contig55401 Frame-2F

MSLKKDTNPVVSIEQSIVSMESLPVRASNDEVTPSGLNENAT

>contig56606-0 Frame-2F0

MNYGGGYEAYGNDDYSGNGGGFMSSQPSGSQQTPTKRSSGAQSIFPVTI

>contig56880 Frame-2R

MCAVLNAHERPTRVCVFLSLSRWL

>contig57379 Frame-2F

MAKDGASPNRHRRRSRSHSRRRTARSSRRRLPSNARHKRPRSRSLTSRSSSSGGSRSCEA

RLSSKVV

>contig05245 Frame-0F

MICQSSAGALGFPHLLGTVHLTSPNENTVYDAFHYSHVDS

>contig11727 Frame-1R|Blast-C-1-tetrahydrofolate synthase, putative [Phytophthora infestans T30-4](gb|EEY64549.1|) 5e-41

MQHHLRNDLKFGVAVVVAINVFVSDSFREVDLVKQKALEAGATAAVASNHWAKGGKGAMH

LGNAVISSCYTMRDQKSMFKFLYPLKLSIFEKFQIIC

>contig12674 Frame-0F

MAEISPCSVAAAAPAPVKLSKNAMKKALRTEKSGGVKKEKDPNRWAPKSDKKKKKEEKVT

SKPPAFVNRTPKGEKKDMTEPMLDAYNPNAVESAWQDWWEASGFFSCSDDKIASAKPNER

FVMVIPPPNVTGSLHLGHALTVAIQDALTRWHRMLGHATLWVPGTDHAGIATQSVVEKRL

LKEEGKSRHDLGRDDFLKRVWDWKTQYESRIHHQFRSVGCSVDWDRQYFSMDDNCSRAVR

HAFCQLWEEGLIYRATRMINWSCKLKTALSEIEVDYIDIETPTKLAVPGHDSKLKYEFGV

LTSFGYVVEGTTTEQVIVATTRLETMLGDTGVAVHPEDERYKHLHGKYVVHPFNGRRIPI

VLDPVLVDMAFGTGAVKITPAHDPNDYECGKRHNLEYINVLTDDGAINENGGDFAGMMRY

DARVAVEKALEAKGLYHGKQDNKMRLGICSRSGDIIEPLVKPQWFVNCDQMAKDAIAAVA

NKELTILPEGHEKTWFRWLENIRDWCISRQLWWGHRIPAYFARIKDEAFVDKNAENASDR

WFAGLSEEDAREKAAKKLGVPLEVVDLEQDEDVLDTWVSAGLFPFAVFGWPNDTSDFKSF

YPTELMETGYDILFFWVARMVFLGQKLTGKLPFKRIYLHSMVRDKYGRKMSKSLGNVVDP

LEIIAGCTLDDLLKKLESGNLPAKEVAKAKSSQIADFPEGIPECGADALRFGLLAYTQQG

RDINLDIGRLVGYRNFCNKLWNAVRFAMSNLEGGFTAAENLADTILSNAVVNHRDRYILS

RLNHAIQVCNDSFAAYEFGELTMALYNFWLYDLCDVYLELTKPVMNGACTDAKLTAQQTL

YVCLEFGLRLLHPSMPFVTEELWQRLPGKRSTASITIAPYPLLMEKWTNAEAEANMELLR

EVIHAARSVRAEYGLANNVRPTFFIKCSDTIVKNIIEAQLEDFCTLAKAGDSKCIVDEEP

PQGCAMHSVNDKAQIFVLLSGLVDFANEIAKLEKKLRKIAPSLVSLDKKMSRDDYKTKVP

ENVRDADAAKKVALQTEETGIKHAIAEFQRLL

>contig12894 Frame-2R|Blast-lectin, putative [Phytophthora infestans T30-4](gb|EEY59218.1|) 2e-23

MLHSAVTVISLIVLAFIASISGEPLPSLTFTPPFEHVNSAGRRQISESFTYGGATDVKKN

FIRLTPDRQSKRGFIWSQQLIDRNELTTILTFRI

>contig16450 Frame-1F|Blast-pyruvate kinase [Phytophthora infestans T30-4](gb|EEY64214.1|) 1e-110

MELSPERVFLAQKMIIGKANRAGKPVVTSTQMLQSMTTKIIPSNAECTDVANAVLDGTDA

MMLSAETAKGMYPKEAVVTMAKICIEAEQALDYAELYRFHRVANRNRVSMCESVASSAVE

IALDMGVRLIISITESGISTMLLAKYRPKANILAITSSELTARQLSGVSRGVTAMLVEYV

TQLENLTSEGIAFAKARGLVECGERVILLHGLDDAQSKSTKVIKVIEVSDEGYLSPRNNW

VDAHMT

>contig16641 Frame-1R

MRPIRKRRRQSKRLRILCVLACLNFLRLSNLLSEHTSDKKVIQRKNYARRPTNTERLGTC

ACLRSWWVQKQGHKDTPNVNKDCNGVYRY

>contig18377 Frame-1F

MIDHGSDFKTHRSPVGSDLIVATAPHNLSADTDDLENSVVEFGACQSLYNGEIYGSLRKG

GAVAFFSQNCLGLVAATFAFTFSTECLNSIVQPMLRDHYGFKPATLAASERLTTLPFAFC

FFVGLLSDCYPIFGFRRKGYLIIGLTMTAVSFFLLAVVDRYIDTLEKGAPGAAFCTVIIA

LSTLASTGIVATHVCVQTRVLELSQREPLSTRGAITGTFLIFKCIVFIMTDVIVFYFSST

STNRFVSLTVFGLVVTLSIPV

>contig19374 Frame-2R|Blast-hypothetical protein [Monosiga brevicollis MX1]gb|EDQ89917.1| predicted protein [Monosiga brevicollis MX1](ref|XP\_001745339.1|) 2e-08

MALIQKGVHPEALAAVVKDLRKQAAEKAYEPRARTFTGGKQPLSTQELQVSQVCQRSKSA

LSWNRNHSRFLLL

>contig19918 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64072.1|) 2e-42

MDASIIDGFRKNVVQKPEVFFTPSEEVANEIKMFAKHAYDRTSKYPSKSGGADPLEELYI

DGFDADQVWEQLRLLNGPLVTELTQRIRTFCKNPDNI

>contig20529 Frame-1R

MDVVDSTSLSYEEFCSRYMECNRPLLLRNVTNLWFPNTRKWHDGHKINFKYLREYYGSAQ

VPVTSGNEADLENRSTMKF

>contig22453 Frame-2F

MDEQALLGYAAAIVAVFFFGTCYVPAKAYVTYDGIIFQWFMCSGILMVGIVWGLLSNNWS

HFSQSGMYTFPEGLLGGALFAIANLLIPTVVNTLGLGVGFMLWNATNITLGYCVSRLGLF

GVVPTVPSMPWISLLGIVFMLASIAVYGAIKPTLKAPKARQSTFKLSQHRLHDKSGQNDS

NSSLASEDSPLLPQFAELHNITSKRRESLPQSLVHPELPNFGPYMMPNELGEHVELIDAD

AEKTRKVFGMCVALLVGAFLSCCLVPFVNWKQRCSPADPIVEMCNPLNFVFSQCLGIYLT

STIVFLLYSLFHRFVLKRSMPRSVMRPAYICGMLWGVGLCGQLYAIGKLGFDQIFPICSI

GPAMVSMLWSAAYFKEIQGSKNLRTLALGTVLVLMGTGLRVVSM

>contig23407 Frame-1F|Blast-GTP-binding nuclear protein spi1 [Phytophthora infestans T30-4](gb|EEY68817.1|) 1e-122

MAQNVPEFKLILVGDGGVGKTTFVKRHLTGEFEKKYVATLGVEVHPLTFHTNFGPIRFNC

WDTAGQEKFGGLRDGYYIQGQCAIIMFDVTSRITYKNVPNWHRDLFRVCENIPIVLCGNK

VEVKDRKVKAKQITFHRKKNLQYFDISAKSNYQFEKPFLWLARKLVGDNNLTFVEAPALR

PPEVTITQEQIAQIEADASSAAAAVPLPDEDEDL

>contig24198 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54250.1|) 2e-56

MCNSQLASLVIQRWKTLRGSNYAKANDLAFGVWADENIMTFLNASAASLFRQLAQCRNGD

WRSNTIQCAFVDTQTCNGTYAEQVNDLRDSVLNRAHWMDERIEQLYKPLSAKICSGVGDL

PKFNCGLDGNDSGC

>contig25153 Frame-2F|Blast-60S ribosomal protein L32-1 [Phytophthora infestans T30-4](gb|EEY58734.1|) 8e-71

MVQVTPVIRPKIVKKKVTKFKRHQSNRFKRVPESWRRPKGIDGRVRRKFKGAIKMPNIGY

GSNKKTRHLLPNGFLKFVVNNVAELEVLLMHNRKYCAEIAHDVSGRKRRDIIERAEQLNV

RVTNPNARVRAEENE

>contig27371 Frame-1R

MKNNLKRIGSKISTRKQSFIIKTRQLINMVFLWKPLLLLFCTSHTLTAKEANGANHTYIR

PSGPDVSGFPPPNSASNHRSPCPALNSLANHAYLPRDGKSLTPQLIRDAVINVFNIDPAL

AKRLTKALPPQLTLADLSVHGLTEHDASLVHDDAWCQHDPAQINSTLVDFLISTSKNGEL

SKRSLAMARRERETQCKKENPTYTLPLKTQVVAYGEAALLLIAMGNYESETITVEAMKSF

LLQEKIPNTFKKSNKPLTTAKVVFLSAQIRLLAMFGAELETRNARASERD

>contig27418 Frame-1F

MGKDLPLDIGLRVDVLDDEGIWNTGVIVDVGKEGDEEKVKVEVKYDGWEDEYNQWIDIAT

QRLAPLHTYTIVKKCWAKLAKWPWWPAFVVLRAPTSALAAHGLEAETKLYVEFYDSFQED

KRSRCWMQKKNVVAFRDGFEERASKSIGKSFSTFVEGMQRAKAGTSPLLFSGPGTLPIEY

SSKMAEPLEEKKKECSTEQWFHLYRDFSNRYQDLYGYSMAPSKALPSSGNSGKRGPGRPQ

KHVEPVLSKDKIEDEEDGIGGEAAPHTGDEDDEAVPSGRPMNPRSKRTAAPASPSNRSTR

PRRAKG

>contig29412 Frame-2F

MSPVAPDAAMLISRMALSLTGVNEASSVSGTNDVAALQVSPAPTQSNETELNPDETPSLV

KTSEMQLQVSKMEARKNDSNSLKRKREKSDSALIQTATSIKSKEILTRHPKLINERRTDV

AKKIHLLPDLPFRLQFSVKINTSAQCGAADSSIDYRAENWISQAVVEVNVHNLMNSNPGE

IVELGPVYSTVKYSEGSEIKWI

>contig32179 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68473.1|) 2e-30

MAKSVNPMEAYRREQKKKDLKKHRMERQKEKMAKLSAMKPIEIQEQIKYLERQVAAKPAD

GPAFKRKQELEDTLQVAIKKQKLLDDEKKSKKKNAIKMPL

>contig33068 Frame-0F

MRLLQKSFADSDKIIHKPESRKTGDLID

>contig33705 Frame-2F

MESVVAPHVEPSCARVDHLAAVKSPLMHSKVEAETETSLVAEPLKLQQPHEDGGESDKAR

TDSDDDDDESSLKPLQDEVMSGNDETVTVPGNEVLIEGDHVTTSREGVEAGTSLRFDAVE

DPL

>contig33846 Frame-1F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY54394.1|) 1e-65

MPWILSESGEGAEKVLSSLPDFNLADLLCNHNRSCSSNPIAEKVITVGKYLRVLAVLEWL

TSVLISTLEVAHTHMQSRRWFADFTASPTQQILTRLFCVDRSVQFERASLAAL

>contig34201 Frame-2F|Blast-peptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-4](gb|EEY53376.1|) 1e-113

MSAFNRSKLVRGAGDAMSRGGARGWGWYHRSLKKMNAPEAEIVAYDSVVPTPDQPRPRAF

MDVSIGGATAERIVVELAKDIVPQTATNFMKMCTDGFQSKALGAGSYKNSKFHNVTKGVY

IVGGDVLEGDGTGGHAALEENQRFFDDENYALQFSEVGVLGMANAGLHKNASQFFISLKP

LPHLNGRNVAFGKVVDGKNVLKNMQGVYCVKHKPLTDIEIISCGIL

>contig34296 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57696.1|) 4e-75

MQDSGMFMMSPMDSAGEMRLAKARACIRKTFGPSGSGRRTKRALEMADETPMPSKTPRTK

IRQRIAKASLLSTEKLFFQQFGSSEELMSEAFDLARPAGRHTVHRKRAKTSQQHVAHILP

STLTHAVPKPIVVAPTSYFSFASKAASNSTFLSSLPPPSTATVSHLTRPMHIHTPRKASS

KRDRAGESSAEKELVLQKPRLSGVRGKNMDLSDFDAKASNSRQLVQAPSSSYNARKSFAF

VTNRVDSHQPIATTSFFSRASPSKIQFSSSATRLFSQRQVPRR

>contig34308 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54711.1|) 0.0

MVSLRCLKTLRRAGNFAGKLPVNNVPPLQLVLQSHLFSQGHTPSRIVDPGDIMRPEVPKD

AKPQLSLKQELPNLPKLKPASQLKAPLTETSVLPSGLRVISQETYGQAATLGIFIDAGSR

FEDDDSVGVSHFLEHLGFKSTTSRSHAQLVREVEDIGALTTSSIGREQIIYTIDLLRDNV

EKGLMLLADTILNVDLIPEEFECIKAIMRIQTEDLLENPPAMLQEFIHAAAYGADTSLGR

PLQCPLDKIDALAAENIRKFRAKHFVAQKMVLAGSGVDHARLVKYAEKFFASVTVAPAGT

KLSSSSSTDTLEPVIYTGGLHSLPKSEAEFSYAALAFPTGGWHHEDLVPICVLHTLLGGG

DSFSAGGPGKGMYSRLYTSVLNRFYWVESAFAFSSIHADVGLLGIYGACLPSHTSNLVAL

LCNQMLSVANRLVDSIELARAKNQLKSSVLMNLESRMILYEDIGRQLLTYGKRETPESVC

AKIDQVTAADIQRVVKQAMQCPPSVVYSGDISLFPQYQQVVAGIEEGLVK

>contig34458 Frame-0F|Blast-alkaline phytoceramidase (aPHC), putative [Phytophthora infestans T30-4](gb|EEY56592.1|) 1e-127

MTSSSLRSPASVGFWGPPTSTIDWCENNYEHSYYVAEFWNTISNLLFVVLGLFGLYRSIK

MGFEPRFHLQFVGIMVTGFGSAMFHGTLQHVFQQCDETPMVWSILAWIFIVYNNEIEQIP

IKNASKYVVALLTTIGAIFTFVHAIYRFTTVFQVFFGVLAVLGAGRLCAHYAEIKDPKAC

AVARSYVASSLIGFAFWLMDYHYCHVFRGLPVNPQGHAWWHVFMGISTYHGPIFMQYVRM

EQLKKKVCIHDTSLGIQTIVVERHGLQKPKQF

>contig37943 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64640.1|) 2e-24

MQHHFECPVCKAGVSEQNVVPVYARGAEAADPRIHYQASDSGIPRRPQGQRPDAERLRRR

GPFNFGIFDRYRQGNAVSMW

>contig38205 Frame-0F|Blast-dual specificity tyrosine-phosphorylation-regulated kinase, putative [Phytophthora infestans T30-4](gb|EEY57617.1|) 1e-171

MENTCGSSATRRLLRDAPRHQLSRGLLRTLNVINVNYYRKHNPKHSGMPTKKRRKMPANY

VFSENGEETFNNGRYLVRRCKLGAGSFGQVVEARDLVTNQLVAIKVVQKKQQYTNQAQTE

INILQMLHLPRQHDATNYIVKMTDAFMHKGHQCLVFERLGPNLFDVLRGTNFHGISLKLL

RKFTRQILKALEYMQHPNVNVIHCDLKPENILLVSHGHSSIKVIDFGSSCVSRNQIHRYT

QSRFYRAPEVLLGMRYTAAIDMWSLGCILVEMHTGKPLFCGYDSADQLHRIVNILGMPPR

DLIARANSTYRREYFDEILTTEDDIKRVEYRLKVHKVVPPKGVDV

>contig38582 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65544.1|) 4e-44

MHQQEELLVSSEEFEYFQDIEDFVKGLSFCLREKIRVIEVKKEEIMNEREQQVRKIRQEE

KLAIEAEVKFYVNSGVLQPGAIFGQFRDNYEDAKVEPHT

>contig38689 Frame-1F

MPSFCPRCGDFLDVEACVKCGEKAVTAKENPWKAGSVPGGDPSSVPAVPTAFTAAARIKL

MGVQPLPEPTRKEQAVARFHFVPQDASTQLALSKGDEVDIVRKDDDGWWFVIKDGEKGLV

PG

>contig39228 Frame-2F|Blast-phosphatidylinositol 4-phosphate 5-kinase (PIPK-D3/GPCR-PIPK) [Phytophthora infestans T30-4](gb|EEY69389.1|) 1e-100

MDYSLLLSVHNTKYVVEHSGIDSSKPSPTRRKINYPVCHPEGDDSFLSLFTDGSDQTEVS

INEDLDEVESGNRRNFYRNCRFSIVGQYDGNSIIIQDNTPLLNRTVLRYDSVSYGPVEAS

SHNNDKSKWIGTRTLAKRGYQACVVVGPDFYTLGVVDMLQTWTWSKRLERLWKTIVLRRD

GLGISAAPPKLYADRFQRKMRDILMVSSASVGFDSK

>contig41010 Frame-2F|Blast-Rab1 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY58069.1|) 5e-18

MSRDYDHLFKLVLIGDSGVGKSCLLLRFADDAFTESYITTIGVDF

>contig41065 Frame-2F|Blast-phosphatidylinositol kinase (PIK-L3) [Phytophthora infestans T30-4](gb|EEY66032.1|) 1e-163

MMQMYLLLNRLLLRHKETKKRNTVFHVPKVIPLTPRVRLLEDNRDFVTLGEVYELDCQIE

NKDPDFPVELYRKRMSEAYAEAGTEDDSKMQEEEQVALAKAHAFHEICNEHVPETLLAKY

INGISAHSDAYYQFRSEFTKHLALSSFLSYALFIGDRAPHRVLFSRRTGRVVSTELRPGY

ASSGILEATTTMPFRLTRNLHSFLTRSGVQGPFSIAMTAAAEALTSEEDILSNQLCLFFR

DDLLSWHASKARINALESQASGRTSSPGESVGPTSPAQRRVESQVQQRVEANVSLVLERI

RGVSLNKENAKISRGKSVQELVAIATSAEHQQEMYPTWHPWL

>contig41458 Frame-0R

MTSKAPLVLSLATSGAFLFAASKISETVAHTPFITIAFIALIPTLVSIDIVTDGRGCFIL

AYLWKTIAVTNRSNQGLKVAAIENLAAARIELIRTFGERWPQHTRASLKRPLGLSSHGYD

VLPLATSGGSLYDQVRGRLTDHAISYSKDDAPVYLMDSETGYFLRATQHRKIVLTSKPNA

SCLFHVERGKTHHWGFRAAATQRYMGQNIVQKLVATSKKLHAWEAFRILQRPGEKEVGGC

SPQVYLILCSARFGKGMWLANKPGLTIAAPAGNSAKDILGNDQILVSQQNHTFQQRKCDI

FLSKQIDYAIGLMYSSDLSALLAAAGSQNRNLSRLRALERAHTAPHSSVDMRQRDSTSQP

TSMQGNDKLQQLSSQGNCTMQQASRQNYGDCFLKNCEPRLNSSIERTSSFFEKRKDDTPE

LMKSTVPSSSKTESSV

>contig41599 Frame-0F|Blast-L-aspartate oxidase, putative [Phytophthora infestans T30-4](gb|EEY65025.1|) 1e-169

MAARIGAKLKNMQYVQFHPTTLYIPNERRFLLTEALRGEGAILRTKNGRAFAKEYHPDGE

LAPRDVVARLILAEMEKQDEVCMFLDITHKDGEWIQRRFPTIYQHCRDRGIDITKEPMPV

VPAAHYHCGGVEVDLQGRTSVAGLYAAGEVSCTGLHGANRLASTSLLEGLVWGCSSADDY

MKRISLFDSKNLMHACDPFASLSGGRDSYANEIEAVMLATQRIMWESVGPIRTAAGMESA

VEKLALLEVKADKLHQECRVTRETAGLRNAVRAAKEIALAALKSPVSVGTHYVVQDLVAL

V

>contig41784 Frame-0R|Blast-heme/steroid binding domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY67727.1|) 1e-103

MSFEKEDLDSDDLSDLSFMDKETLNDWVTKFSVYNSYPNVGRVLRRRDLTLHELRQFNGV

DNPRHIVYVALKGNIYDVTLDGLNHYGPEGGYKQFAGRDCSRSLACMSFVDEYLDNPTLD

NLTEQQQETLDKWEEKFKEKYPAVGKVVI

>contig41915 Frame-2F

MSFRDVTDFTIDRRVATAPRDLRVTRHPIRNSWYDPIDQAMVSSHHARA

>contig42572 Frame-0R

MDEAKLEFSIAIGEQSYLLKADDKNDAERWVKGLQARQHRPEGTPSDVFSLRSERMDAES

DASTSEYGGRRSRNTSSDPDNRRLAQSYTDVQNPVVPNAAAIARLSQSHADAPYFMNARA

SSSVTDTHDPFSAHVASTGPKFPMLTPNQQITQSTAPRTKKAEEKSTINAQCCVPCAPM

>contig42598 Frame-0F

MKVSPSDFEAGTKVSLAHFLANVAPGNTVLFQTGVYELNEVVEITHSVRFLAVPDAHVEF

QMHSSRAHLRWSARGGVVRGFYFTRTKSVLDRTAWEIEPSSKATTATLRQRKRVLRKHDK

KLGNWQHLLSVVGDGQLRVECCEFDGNGLGNACVCVWGRGDMKKKRKRRKSRQRLTSKSR

SQVIDGLAASIPRVSSSSHALSLAVPVVSTSPTVSTLINTSTSTVAPTADALDLSSMRPM

LSVPVSTITRLSVVSTPVQSVPRTTLSMSKALALPRETSASLPRPQETMIPAADTLLTLV

NCRIRGAGSSGVLLVRGSLVMAYNTVEKNHHSGVTILGGHALLRRNKIQRNGRFGLRFLY

>contig44754 Frame-0R

MDERMKSMELSQSRIAEDKRMRGTVDSGVFSSNFGTGFVGKLHVNALDWPDFRNHQALRP

AVDRL

>contig45559 Frame-2F

MNESTPLKPSSAPTAPSAAISTVPSRIVAHSRPPKHVRLSSTTSRILGTVTTAALIVVVA

VYTINGSTEAVGGQGLKVVTDSTMNAATTTLRSVDSVEVLDSQTEDMHNDDVLFLPGFGA

PLEK

>contig45623 Frame-1R|Blast-ribosomal RNA methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY53213.1|) 1e-124

MTKSTEANRDIYYRKAKEVGFRARSAFKLLQLDEQFDFLRHVQRAVDLCAAPGSWSQVLS

RKMYDASNGCTAGNGDVRIVSVDLQEMAPIAGVQLLQGDITSKRTAEQIVSYFHGSKAQL

VVSDGAPDVTGVHDIDEYVQAELLVAALNITTHVLEENGTFVAKIFRCEQYDLLAMQLSV

FFESVSCSKPISSRAQSNEAFVVCTGFQLPENYTPVMTSHLLPRYGLKENEPHDSILVPF

LASGDLSGYDSDEQFY

>contig46082 Frame-0F

MRMRLPFSATLEPIVAMTIATSGINVAVATAHRVLGIDARGGPRVVAEWGADPAGLASLL

PHLSLTAITSFLDTVAYLVLGTSTGYIVLLDSRTGRYVIKWQALEAGARIVHVVQISKSQ

LLVLGAEKEARVWRVELQTAGPPQLRMTITGVPEGVCAAQVTVQSGADTSVLYVAFGARV

YCALLPMEPRAVVLIQPPVMKRMEVWQLSEPGGASRSSRSRVVAQSVAVLPLRQLLLLGT

DDGCLKCV

>contig46136 Frame-1F

MGLYASVCANAPGQALQRRLLDRNWRLPALFEAELDTRLPETYVQLLRWFADSPDVECRY

SIHHMVKLGMQYDKLPGEWYGPTTAAQVLRDLVNVHRRDFGGEIAMYVPQEGVVYSDDVA

RLCVSHLDEESREKETGNDLVEFFDPLLHPPASDIKRKWSTALLILIPLRLGLDQLNERY

VPAIQQTFTFPQSVGIIGGKKGHSVYFVGTQQDQLHLLDPHDVHSAPELSAAFPTATHLR

TVHSSRPLVMNVNTIDPSLALGFLCENIADYEDFQQRVERLHEEVKADGGMCPFSVAEHR

PDYAEGGDLLMADCLLSDEMNEDELTNAGPKENDEEDYVLL

>contig46293 Frame-0R

MARQHQKPSPRRSMPRLIPTLSMSLRSRRVEHPALTLELPQLDRYHDRAERALSKTVTAY

GAPPQDVNQ

>contig46705 Frame-1F

MGLRDTTRKLLRKLDVRDKKRREAEQLQPVALAGASKLSTTRSELCSSFAATVVSHEELE

GRQKALSESSAEYDRCGMCARNFVAGNHYAGYCSLDCKSAALYSQSARLFSGRYR

>contig48808 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69980.1|) 4e-16

MLPKLASVDLMNLTRAWVAVASNPSMEHCNNLFWEQVASTYAASVPPTDKQRTTEELESQ

WKSLRPAMVAFVTLFSQKYKKANHSNDAIRQAFEWAIKTFHATTKRPF

>contig49102 Frame-1R|Blast-DNA replication licensing factor mcm4, putative [Phytophthora infestans T30-4](gb|EEY68142.1|) 1e-145

MELFRGFLHQYRPRNSDANDTPYYIKALRTLALTQSLVFDLDTQNLRQFHSVRKLYNQLI

LFPQVLIRILDMVVTEEYHALLASPGAGLERLDNLANVALQVRPYNLREVSPMRHLNPAD

IDQLVCLKGMVTRCSGVLPDLKEAFFRCAICHATTQVALDRGRIEEPTSCTRCQSRMCME

MIHNRCAFTDKQMIKMQETPDAIPEGETPYTVLLFAFDDLVDGVRPGDKVEVTGIYRAVP

MRSNSRQRVVKSVFKTYVDVVHFRRVDELTRREEGENG

>contig49209 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55787.1|) 1e-75

MVNYMIVLNSRSAVKVFTRNGQIQLGSELDIAVGPIGRAASASLNVGPGGLAPNYSYSHS

MGLYGGIGVSGAVICTRKSLNAKCYGPNVTARQLLGGEVACPLAEPLWRALDEALGMQRE

YVNGFPVLAPTYTGMACDACGHV

>contig49872 Frame-2R

MLKAAKNLPLGIACICRFNVFSTRIVASRTIRLCRSFLHIWFKSKLVGQASKYAAWDHLV

PDIFKILRKRS

>contig49898 Frame-2R

MLTRAIGGQRVLSKPTKCMLPKRFHHFKSRNQSTKKEGLHRSYKFVLAGVVLVNLVQLIL

VYSVSSWAFSMVAWRPLHSENDALDSAVAISASTISNDTVLKEKLPYQVPDHVRTGLYLC

STLSRRLVQSDRDVMATQHALRACDLAVKFAPQGSQEAIEALVVRGDLRSLLSLFDNAME

DYNAAVTLVQKAQELDNKRSFALGLLQQLELKRVANRWTQLYLKREFKDLRREVKTGISN

SNTDVKELAHDWLNAFKRKKPVLDALIRQRGWTLRRLKYESLEDNVVDIN

>contig50373 Frame-1F|Blast-CRN domain-containing protein-containing protein [Phytophthora infestans T30-4](gb|EEY64621.1|) 3e-14

MSREVWFQLVNREGNTVGTVDCVDLAEDAKVFRLRDAVQMKYSNSHLEGIATSDLIVYAN

GTAYDTKQALEEDSPIGPLGGSK

>contig51370 Frame-1R

MRNDGYIPQTVTYSHALSSALKSNQHELVLEIFDDMIKNRLELNIIIYNNILNSCARAGD

VNSALGVLQAIRQRCLDMTQSTYHSLAICAGKTGRWELALDALESMQQKGYKPTSIIFNS

VFSACAKGKQWETIIDVYDVMSDELRDSLNGLYLGAVIMAHAKAKCEKLRLHGLDIFHKY

KARQSEEELNLFAYNAALIAMLETNQLEKVHPLANEMKSYGMKWDTVTYQTIILSYIRAG

AVETAVQMLQSNAKRMGKTTMCYREAIEFYDEKRKNPREAVRLTMQMMQLNKRLSRLDWH

NALRIALQLPERAPYWNFRKWMDIRAKGIVQDVPSHLMLPKHADQHRLLSQEGAFCGEAP

TMSFQQDDYHT

>contig51536 Frame-2F

MVMGDKRYLARQLCQLTVHQWQLHQLDAKHRKSQFTSLSYLSNQTRDIPSSRLQGFLDMK

TIVKTSNTARSAAMNQDSNILSKGLSAQIMLQQFRVLSYAPSSSLLHVEVVLRNQSGSSF

NDAFVVLTAPEGSAAQGWTCSS

>contig51693 Frame-2F

MVKVIWGPVILMCGLALHACKETAQAREEPAPRAVNASATGEQLLSNFEERAGNDMYLLK

PFSKITHAIAQDIFDTVNTVQKNLMGEEVESFTFAHLSKWINDIKKDYNAMSQKDRDAYK

AMYDALAAYYSVVDRARIIATCQLAPKLQRHMENMRSFVLNDLVAQEKSPEQMYNMLGFD

AKDPYFLKDPLLELFLTYLDRNHSKNYKIVRDKLMEAYVGDKQKLMDLLKENGQIAKKLK

YIVP

>contig51969 Frame-2F

MASTSTSSASQSTSARNVPMQPQEPGATALDASQAFSYDPASYQQYAQENTMHGQPGHNS

VPVMSGSASAMKSQKEHAITSSLRAKIDTFSANTSPTSVAKVQIQASSASSSIVTPSSSA

AKTSSALARNDALKSNRL

>contig52195 Frame-1F

MWRIAAAYEFPLKRMRSPPLRGTLCNYQANSGLLSYPMPNVL

>contig52331 Frame-2F

MARYFHMSQREAAQQLGVATVTIKRNCRRLGIVWPYRLMKSKKHAINWAAISREDAERIR

QERALERAKAGRSPSSRKYCQPSNSSDDEVAANVMAMLSHTKNSRFELTEAGRAFARLPI

DSQVGFH

>contig52461 Frame-1F|Blast-exosome complex exonuclease RRP41-like protein [Phytophthora infestans T30-4](gb|EEY64817.1|) 1e-130

MAAKAGNATVLGANAGGDVISIAGLRIDGRRSDEVRRIRTRFGLFSRVDGSSYYEQGNTK

VVAVVYGPRELANAAAASFNSGAAAVGTGSGNASTNTQPRATINCDFTQAAFATSERKPP

RSGDRKKLEMSLAVKQIFEACIQRHLYPRSQIDIFVQVLHADGGELPASINAITLALIDA

GIALDDFVVASSAGYLQQSMLCDLNFAEEVARAPQMVIALNPRTQKLNLLQMECKLPLEL

FESLMEVASEGCNQIYDILQNAVRENTWKHLRLHNMGAA

>contig52528 Frame-2R

MSATTTTTIPLCNLVTLSPLLNDQNLNKCAEESSFNFADATLPTQDEINRMCTMQSCLDL

LSAALALDPTECILPVGDNIRLREDLLEGIPARCPVSNTRNTPAKSVAANDATTQSEEDD

ATDDPTTAPSSDSDPNEEQSAAMGHYATAVSPVKRFLSVMSLGALAFMTYYL

>contig52883 Frame-0F|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY66120.1|) 2e-47

MVEGYHAHIEVEDPNLTSVAAWANTTLFGDDGDAQSKRWLHVVRLIGLKADTRYTYEVGN

AQYASWSIPYVTKTPPAPLANRRKPTPTRFLITGDIGYQNAATLP

>contig53714 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59889.1|) 6e-27

MPTLNTRRKANRARCGIFECTKFAQTQGLCKAHGGGSRCRETGCQKLAQSKGLCIAHGGG

RRCAFDGCQK

>contig54544 Frame-2F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60560.1|) 2e-59

MAFGLHAVSMMDEITTGLDSSSAYDIVNAQRRLARQQRQTVVISLQQPTPEIWALFDNVL

LLAEGEVLYHGPRDHVQAYFEALGFVCPPKRDLADFLCDLASPQQIQYE

>contig55338 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63485.1|) 2e-20

MNSVYKRTAESRTSMADCSCSQLLNEESSQALGVTMHDVLIETNLKLEAELRGLRAGIKA

THLSENDTNKVLGPALKRAS

>contig57615 Frame-0R

MVFKPFRALSSDFFTKKIDNVVTNARWRKFITILCVAFYKVRQIKTKIFYQL

>contig58764 Frame-1R

MIEQVLILLAVLLALRVWLVIIPRRIKAPISSYLDPLFHQLHVDNRKKRRQVRVMAVLGS

GGHTTELLKLMKNLKRDVYTPITFVVAKTDNTSQAKTELDWKP

>contig02850 Frame-0R|Blast-serine protease family S08A, putative [Phytophthora infestans T30-4](gb|EEY68685.1|) 0.0

MHENNITGSSIVVGVTDTGLYIDHDQFDQESRDMYDQEDLQARKVVYYQTFANNVDEAAE

ITCGHGTHVSGIVAGSSYSKKYPDLGIASSARIAFMDIGKQASHCVGTSGCDVSLETPGE

VANLMKAQVAAGAKIFSFSWGTGANDYNTQTQQVDEYLYDHPEILIIVAAGNSGDKGEFT

ISSPSGAKNVISVGASLNAGPSFVSTPCESVLNELTVASFSSIGPTLDGRQKPDLVAPGM

SITSAQSEKPGETTKSSAMCSLQGTSQATPVIAGMAVLIYEWLRDGWWKHGVADPRYGME

VIPASLLKALLLHSGEAMSRRLVEPSTGVTSCVALEATAKTLTSYPDVNQGYGKPTLLNL

VSFAGDKGQTSELANRNTNTIYFFPNSSSGSEPSVKEGAETSFHFMLTEGVNLRVTIAWT

DPPGSVGSKTTLQNDLDLTLKIANTSAIYYPLSGNGSRDSVNNVEMVEVSYDTVFEAITK

AGITVTDGYIKVQAIVRGHSVKAGESATTIGQKFAIVASSTPMTTSASSRDTLDAAFWQP

WMTIGAIVVGTLVLLFVIALIWRVRAKAPRDNLKAVPAEYTKRVMEERGSIVSQAHSN

>contig06032 Frame-0R

MTVISDYDIGMKEEEEGYVLFGERTFDQVGD

>contig08878 Frame-0F

MIPIYATDSWLSLRFKDAALYLDLMRDSYEGYVIYLFLALMIAYLGQGSNERVIAAMTSL

PPLHHPWPFNNYFQPIHLGATFLRDCKKATMQFVVVKPLMALVAIVLRLYGMYEQGNFSV

EQGYLYTSLVVNASITYAFYYLVLFYMALKTQLAPYNPVPKFLCIKAVLFLSFWQSVVLA

FLSRFEIIHELGSWSVENVTTGIQNLLICFEMFFVALAHHRAFPYTPYMHGNLALRTGIL

ADHLALEDAMRDFNEVMPVVLPTPFKPGAATVKTKKKLHVASSNAFATSETMKLLSQEEA

VSDTESKAATNSHIKPASRGWQL

>contig09077 Frame-0F

MDGEGQRERDAIHLSIDTLEHTLLPSLNPLSIKNQSKANAVVRL

>contig09143 Frame-1F|Blast-peroxisomal targeting signal 2 receptor, putative [Phytophthora infestans T30-4](gb|EEY62520.1|) 9e-19

MLPDGGLIPIRAFDTPQGIY

>contig12675 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53927.1|) 9e-21

MEKITHFTAKFNPTDKQKVHACGEHYASHIDFEAILAN

>contig13805 Frame-2R

MLVRENMGMDTGPARSDSEDEVMERSARKVKTDDDESGLMSRELSYRMFGDSSEEEDLAP

QRANNYLGNDEYESDDIDEFIVDDDEEGREGPRRRRKQEPIPVSMQGPSVYQMGEAEELF

GDMDGFLDASSEKILGKTPAKPKKATLLEKFEPSVLKEHMMTADVIAVRENDLPERSQYL

YKSRDFPDAEDRAEESEWISDFIIKNLERRNQRSSAASRGEIVSAIDTVLRFYHDEKLEP

AFVQRYCKEYWKVVGLHTENLYEILDLDVKWDKLERKRRSFQSGIQRVIDSSNAKESAFI

RKCYEQLFGTPDEKIYKDLSEFFALDAQESNGDDKESSDHKYRRPVRRTFYQICTKAGLR

LVSLAFTMNSSVLGGIVAGVDHEDSLRDVPTPEESPGVLALKYTTKEFPTVDDVMKGARH

IAASKVAAEPNVRKCIRDLYRQHAVMNTEATAKGREEIDEFHYCHGLQYIEKMPVLEVFE

AGDLWLRIARAEKEGLLTITIINEKAQDLMDPLEPIYLSNSNASDEEWQSQRHLILQEAI

NNFLVLSFENELKRDLTVASRDMVVKMCGNALRKKLSVRPYEPADGVDPFIVSIWIESTM

DSIAHIVALDVNGEMVDKTESYCKRDVTSVDKLTAALVKFLTEHSQTHVVVINVSAGMKC

MDMGGVVDEVRRLLGRDDASRFGNGDGHDFLDIVFLNDDVANMFSRSKRADQEFPEESEF

VRAAVSLGRYLQNPASELCAMWENIALDDPNRGRELLFLNVHIMQHSLVKDVLLREYDRV

FVQMVNKYGVDINLLANHKHTSYQLQFICGLGPVKAASILNKVRAKNYVERRQELLSKGF

VGKIVYRNCAGFIRIRERDALREAPLNPLDDTRIHPESYYMAVKICGDANNNSTIDMYDP

NHYSYAVEDTMYHSASAIRSRNAPQNTRLGDAEIQDVLSELDLSAYAGRLELQKKGPKLL

TLEYIKRELRYPYFDKRAKYQVPKDQELFFLLNGETRETLRVGMIVPATLLHMSGDDYVR

VRLQSGMRSSLHREYLPDYLKDVRPQSFPKGITVNAKIVEFKVDREGRYELQLGCDRRSI

ISMSMCFYPERFPRYTNEKLVESDSMERIDRLINEPPIDEDKTTFTQASHASRAHSSRRK

KRQIAHPLFRNITCQTAMQYLREQPIGEVVIRPGTQGSDHLTLTWKMLDGVYRHFDIQEK

DKPSEARIGQMLIIKEEKYENIDELIARFVDPMNSLVDDVVHYKHYKNALTESVEEDLIK

QKKEHPSRIPYALHVYSKFPGCFSITYIARETPRSCHMEVKPGGYRFFGRIESSILPTLS

QALQFFKLKALVGPTSNASRPDSYHRNDRSSGPFAQRSSAPYFGSGGRPRQSSRWSDRRG

GDVIARQW

>contig15780 Frame-2R|Blast-fat-free family protein [Phytophthora infestans T30-4](gb|EEY57907.1|) 1e-13

MNDHGMNRMQELLSSYYGLEDQESQQEQQRNIDSPGFDSNVYV

>contig18376 Frame-1F|Blast-Solute:Sodium Symporter (SSS) Family [Phytophthora infestans T30-4](gb|EEY62785.1|) 1e-151

MSGVVGMLVLALVGPYMRSALGENNTMTDVVSTRFGYTMQLYVCGISMFYQFICLASEYT

CIAQLTTMLSPNAHPIVTILIVAFLTNLYLTIGGLQASLATDVWQGIGVVGLVTVVCVAM

FLHVSIPAGAWAATNVAAFTTAGFETLVTLNIAVTAASLFFTGFWQRVYAAYDDNALRNA

ASLASIIIALFTVALAIAGMVSYLAYPDGVLFFAILIDMGRGWQVLIVVVIAMLSSGVSD

SIQMGLVAELTTCFPKLSLLNARVICVLLNAPAIAIGYQQYDILTLYLIADLLCTAAVGP

MLLCTWKRATRTGAMAGSGAGLVTIFVCGVIMQGKFVGGFNWFILPEGLYSQNSMITFIV

TLIIPPIVTVGVSLMTQSAKSEDAKVDSYALEVSPVLETTTKTF

>contig18826 Frame-0F

MEGYLIRVPVEACIPDPRPVWRQRADASGPVHSRVLYYIIEDGYLRGYESTPGHLDEPVE

SFQLTSFRIEVNVMRSLNLIEINTKAVQLPPSHQCIDGTTTLNSSEDLAKPQIADLSPGS

GNSHAIYFAPSTELAQLWAVKILNWSRFVFGNPSIPDDVKLVQSKAKIIDAMQVVSAANG

FLKPIVLHPIDTTSDEAVIVPLSADDSCHIPAPVTSPSKVNYIANSLTPTESIKSSVQMA

EDERVSEQNLWWHISLGRSKRISAYSFRH

>contig19281 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56921.1|) 2e-11

MLRSLLAVALYLTTVNALFADQAGEFDWKFENIGRVQFVAFEDSVNREPNSVVPKN

>contig19919 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63959.1|) 2e-58

MNFIKCADRPFVFEDLHRDDSRGKWMLTFGGGELKMPFLPETLRISVSTGRLYHDVQTKF

VAPGTSEGVALIRSQLAVELGKHIDVNSLSEVVGSGQDIKTLEIGGFMWCDQRYAIYAIE

>contig22548 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64066.1|) 0.0

MKLAKEREHWTSSRANMKREDEMCRDEDARYTQEHDYVRLEAEARQKKVKTIEADLLALK

TEINARTRSIAQRRSRHEGLDEEYEKEWRVLQTKRFSTTKARLSEHDARITRGKKRTDVF

SDQLDRQTKSQRMLLFKRAALTDERKADCTLFDEHCEDCKNTLDEARNALVITPEYVARL

EADMKVRASELQAVKESNKRIPQEGSDTEVDERDEFMNEVRRRRAQFQKELDDQAVQLET

ENKLCTSLLERMNQHIKNLEEEVKNAAQEESMIDEFHKLIKTETKLLADEETMREEKKRL

ITELMNSAGNWVLDSLHDHSNRKKVEANRLVNQAVRAADLQKLVQHFTHRVIDQEERIMR

QKQRILNGEHKVEMLKSSENWYQYVTGHAADLGKKDLKILEAGRNERAEDLKESSRLQKD

DELDIKGVVKELSLSRKCAKEKVEKREVWAKVEDVYSVSKQQEKDEDMMMTSQIRSLLLQ

LAEAFEMLTNRLLEEDESLQHASTQLEGEIESIHAFMERMESEESALCATEKTSLAKESQ

VRRSEADLIEQRARALIDNYKQMQAEHMKYPAELSKIKDRRSDRAKPIQPREAELEAAKK

LIKNRNYYDRKACGEFAKRFKVDHEMKEVRDVFDWLKLVIERDIKHMEKWLDLSRKERKE

IENLKVKGMEINWDEDTLERIPALKEIQRKIARPSGTSSNHRGGNSDAKMVDGVHPSEQW

IVELLKFKKKIAQIDTRLLSDIRGTMDSAVTEEDMVNANLKKMKIDKEYVLNSIRFIDQE

EAKAIRSTGKGGVPGRHSPSSESGSFISVDEQATPKARTQSPHMTRTMSPSPARTSSPAP

GRTASSHVARTMPPSPARTMSPSPARPNTVASPLSPSRSAFSKSTTAPLQPRAIEKPRSE

EF

>contig23356 Frame-2F

MSGNQDVMATMGFTSFGQARRYTKQPKAKSTNLLPQLIHGTELITQRAAFSVNSVETGSH

GVLYLLCASKDIDALKNALDGEKNSKKIITRQSMMPSALRLLQKLQQEKEKFSTMENSQF

LIARAATNEFETLGKHRFLNRSAMKLVSLDYIFKWTYDQTVCGNVFSFADICGGPGGFSE

YLLWRTGQRTTSGQRAHGYGITLKNASNSCDWRLPPEYRNSMTICYGEDETGNLYSIANI

YTFRDVVRRRHPCGVKLVTADGGFLDARSQFNQEFMMNRLILAEVLAMYAVLQVNGDFVC

KTFELVTPGMLELCWILHKSFERFAIVKPITSRPASSERYIVARGLRAGYPTSTLVACLE

NQLVQ

>contig23406 Frame-1F

MQPISAPLSTTLNLFLRAKKTAQFYGKSHKNATICRRGSRKHFGDKK

>contig24199 Frame-2R

MISPIRNIKFPLKLMIRSHRIYRYLQLQLMQVGVLLTLFTSLQAIHAQQQARSSNECYEL

PVVIVSALNQSFPDLNCNHLRYPAEFCLKVPIQTRVEVIDNGDGDLNCINGARTAVYEQS

KANYRGQTSLFFKKHQFNLQFPKQMPFLGMVENKAFVMNGPFIDCSLLRNHLAHWLYRAT

GRYSVNTRHTIVYMRTNPGQEELTYVGIYLLLEKPTYDKDHENLASLNAVCAALDPKVMT

GGWAWSNDPPNYGSYSPNMVVDRYQNEFGMGERPMLAYPHGSLLSQQMRDYFVNTETGFL

PQLYRVLWNNMTTPLELQKHLDRRSTFYFKDRNQTINAG

>contig29202 Frame-1R|Blast-Poly(A) polymerase, putative [Phytophthora infestans T30-4](gb|EEY66225.1|) 4e-87

MPILTPAYPSMNSSFNVSTHSLAVMKVEFKRGLVIVQDVLNKGGSEWGPLFEPSDFFAVH

KHYLAVEVYTVKQEEEQAWCSFCESRMRKLVEALAYNPALCSLRVYTKKYPLGHVTDGDA

GFSGQSKCQSVTQSPAKVQKFGVCFYVGFDVDRRHLRSREVNIDSSVDYFKSNDLYRWNK

RTPSMDVRVTP

>contig32178 Frame-0F|Blast-signal recognition particle, putative [Phytophthora infestans T30-4](gb|EEY62414.1|) 0.0

MTKGVVKAKEVSTAKVEVLTAHILETVKAAQLQNGLRHRDFQRYRQYCTRRLRRIRKSAK

FTHGKGKQFIGKKVDIETATENRLLYIPLYNAERAWSYAMQLKEDDNLDRSEHGENANSR

IKFHLNGRLRKAVEWSQRLATICAARADIRTSLEAEAFAAYMAGNLAFHREEHVAALDKF

GTAHRIYADLSQVGTSSQKELFARSADELQPFIRFCEHRLALQGHPTSSPDTSPLELQSS

GDGVNNALLQSKIDLVLLEARKQKVADLGFVEWKQQQLTVPTQELGMAMLRTTEISAKLD

AAQDDKTREGRFLELLSAYDALLQALKTAITKLEQQAKSGSVLVHKDLEILAALEEYVRF

QKLSKQVERQAFVYQTLKNSSSSQHTGELTHILDMLVQTVSEILSIPGIRELEDRRAAQY

SAYYAVFRACRASTVAQTYLLEKKFAEVMALYQYAQGFLAEAEKIVAAQPAVKDKVLQQL

NRVMHDELAGAASRTTAQHFLESSTRADVMRLKLEQLTLSSGQEGGKKNRKRKKRQGRAL

VDRQGDFEPGSIEGHHELVNLMPRFQAVPCKPLLFDKAFDELAFPDLTNRAKTDAEKAAD

AGAAGNETSSGLFGWFRK

>contig33771 Frame-2R|Blast-glutaredoxin [Phytophthora infestans T30-4](gb|EEY68449.1|) 2e-42

MVSAKESVEAKISSTPVVVYSKSYCPYCTKTKVLLEKLGAKFEIVELDQISDGNEQQDAL

EQITGQRTVPNTFLGGKSIGGNSNIQELHEAGDLEPLLKQNGAL

>contig33847 Frame-1F

MLSFNPECRISVCSAILCKWHMFLTTYKLN

>contig34309 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57462.1|) 6e-50

MSTTDSPILPAPRRMRAPPPPVPTSAPEPTPEIASDSGKQQPAIAAMVPTAGVKPASKPK

HRGLVRAIGGFFRRSCGGSTCAMVPEESESSQRRTSRLSRWSHSQRHSLPEAPFEVVAMV

SPERAPIQENLAAAEAEFEVSPFEKNGLTVTSPACLKEPPTKKVKAVMSKITMKANPLLS

KAKQSPTDPSELLTTSFSDKVRLEPEHVSFLFFGGSDADTTFKPELRPSELDDLHENEIR

PSLKAKMPLFFSSAQVENIRRSSILSDPKEYEL

>contig34459 Frame-1F

MVTLKLPQLPPSLLLRESSI

>contig34914 Frame-0F

MKVPTSFIVAVLTTLSVCTASESSELSPEQMPLVPPTSTDTAEEMPLVSPTSAETTEQTP

LESSSSTEEMSDTALTDWKESLTTDLNNPSSDATQP

>contig34961 Frame-2F

MLGTRLGKSNRPILRAPILSDSSAVDIDRRIASPIRPPKRKTTFKTKRIGQTILEKKGPN

GVSHQDSAAHAAAS

>contig35478 Frame-1F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY56412.1|) 1e-118

MQITVPSEDVNLDDDRILSPRTKVDTPFGTGEVVGLDPHVGCYAINTEVNATDDDQFLAF

VQIKDVTVHVEEEEERAIVEDASLP

>contig35513 Frame-1R

MEIGHANIHSCTRATVCDIFRTGANRKIVDQETSNFTSSGTASFRQKIVYHSAGERNIFA

HIILPAKNFTKESYHFVTFITTNVLANASTEDKKASSGLSIGVTVGLVIGAVVFVTLVIL

AVVFWRRKRRPGQDMDHSNNSGFGLPASYVANKSKSHLNWNAEPETRLTSHDSGFKDNYG

GRSRGPGLNASALMFNERLSRQNKTVSSSGSLHSSRGQNENYSGYDTPMQRS

>contig37942 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64640.1|) 1e-15

MQQTFLSRFLLIVGSLVILCLITF

>contig38569 Frame-0R

MEKKKLDLVKVASEYKEIKRRQFYQELVVYFVFLTLLFSLLSWLPVQDSFYQNDVVGALT

CREEGECGIKTFDDIYELAGKLRDTVCERQGVTAQWVRVGGVGFRQVRVKQQRCRLYDGW

EAPCYPFYSSEVEDKAPLLGHNGSGHVYKWRDGLGELSPEIYRSFVDWLFFAPSMSYGSG

GYAVDLCDLENVNELQQDKYLSEHTRATAFKFILLNPITRVFTIGMHVITVDPSGHIDHY

AHSSHVRVIGHEKRDQFTIHSHNQEVSSVFWQLRKVLNAITSLISLVREAFDVRVLLWVA

IVLFFVTYCIGEMTEMTSMGMSTYLGSDIWNLFELTHLVVLAALLNIMVQYYLASSSFAL

HLAELREGRGVEELSHLQSQGLLTKFQQLSDLASLGSAISLLKVFKFLRMNATLNLLWRV

LGMAMSDLMGFLVIFNLIFLGYSAMGSYAFGFALEEYSTISKSYGTCFQMLAGEMDYGRL

KQANPRVAPLFIGTFVVLVFQILVNMFVAILSEYYEVAKNDETASGEDVEYDVLARIRSF

VSACSPTVVVPKDHSVIRLIPWQQVRLISTNLVDQEETRQRVRKLFRGAVWRVVALLRFG

MKFDRRINFGDRKAHDGSNGYGGNGIGSSNGKDGRELVSHIRLSENFDHKTIKEMIPVGI

TVRLQGDSLFGDGLALKVVHHSKLSVECIVIGPNEAEVAKFGANASGNLNAFAPPRSISS

LGSFEDDSDFDDQAPQERILELLGGEKLRIPRSRLAVHLCRIVFREFKISLLRATKLWNY

SKNHMVDDYHLGLLFDSVRADGRTSLRFDEISRMLDLYLRKDKRRVMCSQAEVRREALQV

MHRFRKSLIDMPSREKEGHNYRPKPVDTSAIELGHLEHLGDVLARNCHDMWALERLKQGW

>contig39229 Frame-1F

MRQHNRKNGDESWNDNGKTHQHDKGHDIWGAYGNTHQHEHHKNMYK

>contig39694 Frame-0R

MTVVTEFLLQEYFAISREKSNSGSISVFMLNLIVTATWFLTRIIYRVTVSWVFLLLQRCG

NF

>contig40302 Frame-1R|Blast-proteasome subunit beta, putative [Phytophthora infestans T30-4](gb|EEY55735.1|) 1e-124

MARNMPEAVAWTTSGDATLCLRDSVSSEKVQEQTRASWEPYDFNGGTVLAIAGEDFVVVA

GDTRLSTGYSILSRDESKLHALTPTTVLGCPGSHNDIIQLRGVLSIRAQMYRHDNETAMS

SKAMAQLLMNTLYSRRFFPYYAFCILCGIDENGKGVVYTYDAIGSYDCVTRAAQGSGGHL

MIPLLDNLVEHDTRMDPKKTLTLQETKNIIKDAFITAGERDIYTGDNVEILTIKATGIER

EMFALKKD

>contig41011 Frame-1F

MWSYSGAFLAIVVLIGFLSMSITTLVMIFGPGIDRHNPRRGAPHSASHQEFLLTHVRVGN

EETGLLERPRYNGETIRLFYRFWLPRHLDSAKDSKAIVVVLHGVNSHSARSNKFMVEVLQ

HGFLVAGVDHEGMGRSDGRHGYFSSVEKLVDDAIAFVELVKAKYPDKKVFLLGASLGGLI

ILHALSKCGSEFVQGAVILCPPTEIHEASRPSLVVERIGRLLQEFMPKLPLVKANNGKNS

SPEVAAIVDADKYADPLYYPGKMRIGTGLALLEGITSIQDKLQLIKTPYLLQHGTADRVC

SVKGSAALHIKTQSTDKTFKIYEGGHHDLASEPPRIRDAVVQDLVAWLEDHL

>contig41297 Frame-2F

MEWKPSIYDFLNAFRAYGFQDSKRSMSVKSKISETPPSTIRSRVLPFPTVNMHYVLMYMV

LCLRTKTLILNGYDAFSFTMFFLRMQFESNIHASIIDLTTICIEELLDAFPRTEWRREWA

PQLVLRIAGLNEGLFDYAAGWLAVARSLPRTMRGTQLTTGLAIYVLQHRIDKVPQKGALS

EKPLKFPIQSGLVVDIVAGIVEDLTQKYVEIRKRSKEAKAKPPFDLLCKKIALMDLALQT

FLNVFTPAEMKIMLDKLDRLADAHKSTMSAKWHELKTLISLMHRKYSLENLSVGRSQRAS

>contig41961 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62019.1|) 2e-13

MNYVVAALLLLMKDSQDAMALYLEKFSMQEAAFWLTLALIRHRGMAELWKPKMP

>contig46137 Frame-1R|Blast-superoxide dismutase 2 [Phytophthora infestans T30-4](gb|EEY64834.1|) 1e-73

MAKAVCTLYGDDATVYGSLLITQAHEDAECVITGELKGLTPGKHALHVNIFADVSQPAGA

LLGGVFNPFGKNHGAPEDAERRVGSLGNVEVGGDGSVRVQIEDKLVKLIGPHSIIGRSIV

VHEGEDDLGKGGHELSLQNGNAGAIKAYGVVGISS

>contig46847 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57898.1|) 8e-39

MNTPMIDEELEFHDVVVIGAGVAGLRCASQLVHTKNVPDVLVLEASDRIGGRVMSNTNFI

EGISIEMGAEFMHGANTTLTRLAEDTNIGLREIFTWAQVRKIIRYT

>contig47602 Frame-2R|Blast-pyridoxal biosynthesis lyase pdxS [Phytophthora infestans T30-4](gb|EEY57884.1|) 1e-156

MVSEVTCSTSAAPTEGTFLVKSGLAKMLKGGVIMDVINVEQARIAEEAGAVAVMALERIP

ADIRVDGGVARMSDPQMIEAIKKAVTIPVMAKVRIGHFVEAQILEATEIDYIDESEVLTM

ADEENHINKHKFKVPFVCGCRNLGEALRRIAEGAAMLRTKGEAGTGNVVEAVRHARAVQR

ELRRLASMDEDELFVAAKEMQAPYELVKQVARTGKLPVVNFAAGGVATPADAALMMQLGM

DGVFVGSGIFKSGDPVKRARAMVQAVTHYNDSKILKEISTDLGEAMVGIQDLKASAVNFR

DREGGLHGAW

>contig48261 Frame-1F

MDPVAVFKLVSIVCIWVVGLVGGLIPACLAARHEKSMTLSYLSAFSGGVFLAGGFFHLLH

AAIENPALRKWSTENDGRYEFPYAEMFCTLGFLGLLLLEQSAQAMLDANIGAPHYMPAKS

DDDGKLHGASESDVTYREDLDEEPGIDSNLIRSPGHSHFGVSSKETKASSMAVAMVLFIA

LSFHSVLEGLGIGAQTETAWGVFCAIIMHKGLAAFALGSGLVQSAMPVMHAMMYMVVFSL

MSIIGIILGWIIAADSSEKSAAAGICVALASGTFIYVAVMEVIPQEFPRSRHKGRGSHGS

NHNSSRVTLQKSIALVAGYAIFGLLAKWS

>contig48643 Frame-2F

MCFMRLVLCVLQLLWKLVGVPLRWYYALKVKYNNNRNVVLLKKKMAIVRFCHLHFLLVIE

KLKREMKDRTREEMQQMVVALGALQQKKGTRVTLPAILATLRKIQAIEGRLKSEKFEEYL

TDINQGGRYEDDIDSGLPAAWTRLQDVYASFVRIQATIIRQQTPKKTWQLQQENVDGRHV

RQLSSSKDSTKEVLLELQELTRQLPQGFTADMFKSLGNAMHGSSGAVERGAELELKTHSL

ITLPSIPVAYENSYTPQKRHNIPRR

>contig48900 Frame-1R|Blast-multiple inositol polyphosphate phosphatase 1, putative [Phytophthora infestans T30-4](gb|EEY64239.1|) 1e-177

MSTKTRYAPPVMSELDTMNSTCNPVQLNFVIRHGTRNPTMKDISRINNTHSRLLAARNEK

SPTWIESWNNPYPAETEAWLADSGIRELIEMGHRLRARLSPVPLNYASSNFVFDHTYKIR

TKQSAEAFAFGFFDGLQPVYYQSSPIGQDEILRFYDNCPLFKTQIDSNKSSTIEHSKYRN

SEQMYKNLVKFQILANFLNATQNDMEAAYAGCAFDVAVQAVFDQWCSLFDSKMLLSMDYF

QDLKHFYRKSHGHALSYEIATPLLQDIFRTMKTRVDKTSSVDGYFRFAHAETILPLASLL

NVSYFDRHASDREGHFRADTPLDLAQKRKFQSSKLTPFSANIGFVLYECDAQKDESQATS

SFKVKTLLNEREVIFRECNG

>contig49873 Frame-1R

MVLVDELQDAEATLGSMMHERSFFHCLSWFHMWRVSRNLHFCRNVAPSNIECLCVDSDMM

CLSGRPDDVTGFDSSRFGSRYSRWTRPRSGVDAP

>contig50372 Frame-0F|Blast-acetyl-coenzyme A synthetase [Phytophthora infestans T30-4](gb|EEY58107.1|) 8e-19

MDQAYAVPDGFSEAAHVQSMEQYESMYKRSFEDPGGFWGDLGRENLEWFRPFDHAMAGSV

HKG

>contig51304 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66475.1|) 2e-08

MRPSAASYRDAESEMLHGKMLYTDRDCKKSNATDSERDYLDMEEQLTAFVEFVGYLH

>contig51692 Frame-2R

MVSYSMLIRSFTGSHGAFTTPLRTNTFSSISRNYR

>contig51788 Frame-0F

MTRGSENNPSQAISRHLLYTGSFDALLQGHDDWVTSVQWIEHGSALLTSSMDNTLILWKR

APDTTELWSPSIRVGELGGNGLLSAGLLSSLKSRLDLISLGFGGQLERWEQQPAPSNSFL

PSISVNGHGAEVSDLSWSPRGDYLASVSFDQTARILAPFNHARNSFQEWYEISRAQVHGY

EINCACFVLREREAISQFVSGADEKILRVFEAPDMVRSFIHFAQNDKTAIAEVPYKTDLQ

ARKVPHAYQPELSLTNKPP

>contig52194 Frame-2F

MWRIVAACEFPLKRMRSPPLRGTLCNYQANSGLLSYPRPNGLR

>contig52529 Frame-2F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY57664.1|) 2e-42

MHNTHFIGLDGFSANVDAQHGLVEAHRSQYTDAITEDEIQKHAQRDELTGSINKLDVSMN

QQLQKFVTTLKIQTTA

>contig52882 Frame-1F|Blast-monooxygenase, putative [Phytophthora infestans T30-4](gb|EEY58018.1|) 8e-46

MIKPVRVLSERIMSRGFEPTVTRLMENVQKVVRAQPGLMSLETLSDMNDHHKYVVLSEWR

SLKDYHAWTSSEAYKLCTDQVNEVLDVPGKRTTIYKQPKEDIFLL

>contig53045 Frame-0R|Blast-unknown [Phytophthora sojae](gb|AAP86963.1|) 1e-125

MPSVAERSLNGLMRLVRSSNDQVVAESVVVIRQLLHRQTIEMDRLLIVRSLAAMMVSGRI

SSPSARASILWMLGEFNDNGNGTTCAAESLRMLVKDFSNEATQVRLQLLNLSVKLGLREP

QARTIQLLLQYVIELCKFDIDYDVRDRARLIRAALSGDANLVNPHKLFASKKLAPLIGYD

DDAKTRFMLGSLSNVVHHSVPGYLPLPEWRSTKPD

>contig53715 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56920.1|) 7e-23

MRKDREEEVEQLACETQHELLSLEISPESFLDQHRQDLISFCERLLSVVRHARSATFSQE

VTTKEKKMIKTAMQVELRSTGHWYRCENGHPYAIGECG

>contig54215 Frame-0R

MGHAVIQHILVFSLDPRRFLKLDQPSDKKWSLSASGCLHRVKRKTRLSVTSVSI

>contig55050 Frame-2F

MAKPKEMVVKLIRSCLDRVQESQLPSLQVLLKLMEGESELFRGSVNADLQAAAHHIAAQV

PAPRPLHVWSRLEEAMQSVASIATP

>contig56042 Frame-2F|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY54291.1|) 1e-130

MKELAYVALLADFMCILGLLVVLTIDLSYMNFDHDQIESIGVASAIPFFFGVASYCFEGV

GMVLPLENSMRNKHNFQPILVCTVVIITTLYATFGICGYLAFGDETDAVITFNLKGSGSL

VTLVKIFLCLGLFFTYPVMLFPVFEVLQPLLLCGNKLEETQITQKKRILLRAGIVLITAV

IAAGIPDFGRFISFIGSTCCMLLAFILPAFFYMRLHRDEPRSCRKWLHQLFRCAIIFLGF

VMLGMGIVEPLANVW

>contig56608 Frame-2F|Blast-replication protein A 32 kDa subunit, putative [Phytophthora infestans T30-4](gb|EEY53901.1|) 5e-06

MQLQSLHASDDDTLRLDGQELSHR

>contig57243 Frame-2R

MGRRPALKHDFSTSLPVRGQRYDPHLPSHTNCCGVSCGE

>contig57427-1 Frame-2R1

MHVSQKDFRLVKQALKFTLVPPPLATSCTKISPNLAS

>contig57661 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64213.1|) 4e-18

MSVALRRRGLPPGPKYRTLKLGGSVELPNGEILEASEVVGPEAGGRKVAILGDSADSSRM

FDIAQNCDVLVHEATLSHEMIKQ

>contig58336 Frame-2R

MMSMPATCSCVYLCVLKDTIIVSMIFFLIDTRNATHT

>contig02853 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57692.1|) 1e-118

MPLGRHITISALISTSANLTVAVVYSCALAQVRVHGTPVRCQIYREQVATVLNAMDHTHT

NETVTELTESINKRNVFPEDSRDMGYVVREPIINATFGDIRFRRGKARRVSVRSLGWDMK

VFIDGIYSVPLDYGVQAVMKVADEPKYVLRTVDFSSLPSSAPRK

>contig05247 Frame-1F

MNLDYFTYTNFCGSAYLPFKLANLSDLVFVPTICASKPQFP

>contig06750 Frame-2F

MYHRQGQFGNDKGEVTRHGLTKQ

>contig09074 Frame-2R

MMPTTYRQEMYPPPLAREETWSKNCHALHDYYPTIVDQPLPSYQPYQSSTLYNYTTVQPP

IATGPWNPMVINHPYPPNGAMYDGGNYLYVTPRSNPMGYVSHQPVPMGLRSSTTRLHHHG

RHVYTRMPPPLPGMSPLHSPRKGFTIGTKQCKFYLQGHCRMGHKCKFGHSGSPSTIERNY

SMVTRERSPGMYQQPLVSSTPGMPLLPNEENPYTPATGRQQPRYNLVNTTLSNLPSTPDV

LSLNTALSVADIETRVFVMSKDQNGCRLLQEQLEYTDRKDLCDVIYHESLDHLPEMMVDP

FGNYLFQKLLERVRPRQRLVMIRRVSSNLVAAALNLHGTRSVQKVVEVCATSMDVLEDTR

VGNHDNCDEFPYLQETETNAVERGELTRLSDLIVHALKDDAVRLCIDSNGNHVIQRTLQF

MKAEYNQFVFDAVCLECTTVGTHRHGCCVLQRCLDAANTTQKTDVIAQVERQAMKLMQDP

YGNYVVQYVLDSCTSEEAYGVIRTPLGHIYDLSIQKFSSNVIEKCLEKAPECVRHDYVAE

MIACPKMNKMLQDQFANYVVQRALCVCAEEQCRLLVKAIRPHLAAMKNTSGGRRITARIL

KRFPTMDLSLDGGFVSSSSDLLFDGMDETPRRMHSLVALTRNEDYLHPPPMMASSFMYGM

QGFQFQEGHDEMNLMRREDDTTS

>contig09724 Frame-0F

MSYSGGSGGYGDQRGYSSRSGETGRSYDDPNRPSNGGNEGYSGSYGQGYDQRGYDQRGQQ

SYDQRGGYGSRSGDYSRSSSGYDDYQRGGGGYSSGARGYESTQGDYSASRYDDRSRGGSY

ASGGGGYGGSGYDDRGGYGGSSSHGQSSAGYENRSGYDHNRGGGSYGGTSSGYDDRSRGY

SSSNYDDRSRYSGTRDDRGYSGGRDDRGYGVSTSFSGDRGYGASTSASNDRGYGGSSSIS

GGGDRSFKGREDRGYNGTSTRDDRSYGGSGDRG

>contig16926 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63133.1|) 6e-35

MRQRGAMEAKNIDKTSLGPNKKHLAKAREVKRLDEADCRRKLGKTFRRGFCEITDEEMKK

RAEQMVEDAKQREEYIVKRGRVKKDELDTRESEVTKSNPEFLRKLHSEAYLDNERNMSDR

IRRNVHYIQKKADAAKFLSK

>contig19282 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56921.1|) 6e-12

MLRSLLAVALYLTTVNALFADQAGEFDWKFENIGRVQFVAFEDSVSREPNSVVTKN

>contig19549 Frame-1F

MATGMLICSAVAVSARCSPLETRNQYDEDYQGYPRSSKDTRASSVDFTFERAHERNPPLP

PPQEPLQRSRARSFSYSQAYGPDGYNPFNGNKPFAPVPHHRVPPQQATGPEISQAHRTLY

PGSNMMQPPHTGVRLPRVSIPTDSPMHQFQYGPPMPYRRYSDAFAVPPYQDFYPDDQQEN

QSHQNNTGRGMRSYSIEYGNYTMTRQMRSQSMEGLQIFASAPPLEYPSLNRSNSAGGGFD

WLRKQIDLSPPLPPDMRGCSVNGTSHFPPPPPEAYYDVEFKRGRQEIFAGRASFKPGEYV

KVEADRGEDIGRIVQRTADPSKIGSGEFGSPGEEFIGRCKRHDLLTKKIICVANQRECDM

LN

>contig23405 Frame-1F|Blast-threonyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY59771.1|) 0.0

MSSEPARVQTRLTKGSGPKVTGEASKTKIGGTFTLTPNPPFVAARVAVYDRIMAEQKRQQ

EALAAEQISIKITLPDGAVKEGLAWQTTPLDVALGISQGLADQVVVARVTYRGKPLDPFS

VTAADVDGNEAIDNAGDACCGAVTDSSELWDVFRPLIGDCRLELLKFDDADGRMVFWHSS

AHILGESLETLKGAHLTIGPPIEGGFYYDSYMGTETVLESDLSVIEKACLKVVKDKQKFE

RIVLTKDEALELFADNVFKTQIIATKIPDGSKTTAYRCGPLIDLCRGPHLPHTGKIKALA

VTRTSSSHWLGKTTNDTLQRVYGTSFPDKNQMKEWKHFQAEAAKRDHRRLGVSEELFFFH

QLSPGSGFWLPHGSVIYFKLLKFIREQYRNRGYTEIITPNIFNMELWNISGHAQHYKENM

FVFDVEGQEYALKPMNCPAASLMFDFRQRSYRELPIRLADCGVLHRNELSGSLTGLTRVR

RFQQDDAHIFCRDDQIKKEVLDFLTFMKYVYDVFGIKFNLELSTRPEKAMGELEQWERAE

KQLAEALNEFVGAGKWVTNPGDGAFYGPKIDIMITDALKRQHQCATVQLDFQLPIRFNLK

YRTDDADNFKRPVIIHRAIYGSLERFVAVLVEHYAGKFPFWLSPRQMLVVTVGAAFIEYG

YEVKDALFRAGFDVEIDDSGKTLNKKIREGQMAHYNFILVVGAHEKETRSVNIRTRDNKV

RGTKTLDEAITMFKDLETNKSADE

>contig23856 Frame-0F

MIARAEKSNDKTVKDFAEGMRDELKKR

>contig24268 Frame-2F

MVAIIKEDNTVKPKRSSFALGGFLSKVPTYRKEKSPHEGLLEHAAEEEPVHNGQSRELPD

FSSERRSLECVPPASSAASMAAAAIRRRGMSIEQTASTLYRLMNARQSSAPEPSETSKIS

PTGSDGTAPLPQSDAELTMRRGMCVATKYGTGTVLDIRVDDGFFVVQLGPKSIAYVREDT

IIREIKSVVGERVKTRWGMATVEQYYVEEDMYSIALDWRWDDEHVWRMKATTKKFEKIAP

RGTLIQNTKNLLFEGYSSLRESVGSKLNNTNKSIAVNMKHDAVEKPDLGTAQTPFGICTV

LEVRQDECFVVMTSFGATAFLTPDSVRMLGRRTHFMKGDRVNTPYGPGHIVHFRDDDETY

AVELELPLLDGPSPILFLSDERAATDLTLAPAAANTRLSSLLNITRTSMINAGERMRSAS

VAAGGLTTLPTNLPTLPGGLPTLSSVKARVSTMATIKMAPKTKFHKDERVLTTFGSGFVT

EVRPYDKIYQVYLRRLKCSGYFYETSIGPFPYERVTHFVVDGRTIPAPPIPKNASDYKRR

AVISKAIKSARAGTYLTLTTRANPEEQTKSEEPAIAMDATSVVSVPALVSVAE

>contig24664 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62772.1|) 1e-134

MKIGVIYVDKKQHTQQEILHNDNGSRAYELFLLQLGWHVDMETHRGFVGGLDTNPKSLSN

GKTTLYYASSHSEVIYHVVTMMPTKASDLQQIDKKRHVGNDYVHIVWSDNVTQNYDPSTI

TSHFNDVQIVIYPLRKAQRGLFLIKIHMKDKVPPFGPLQSGMVVHQIDLARLVRQTAMNA

NRVCRSQTMLYVRPYPTRKKLVDEIVERYAVEYKESQLLTMLFGNSAGSPSSS

>contig26709 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56147.1|) 1e-160

MNWGAGGRRIETSDDHSIFVGDLSPDVSDDLLLSTFSARFSTVRGAKVVMDPITRMSKGF

GFVRFGSKEEADQALQTMNGVYCSSRPMRVSVATERNKARQQAVFSMGEEDGANTTVFVG

GLDPSTTEEELRARFGALGEIVSVKVPPGRGCGFVQYTTKEAAEIAILQMNGSVVSGVKV

RCAWGRSAAARAVNQGSYYPPQYGQYPAGYQNYYGYTAAYGYPQYQQGAYGYGAYGQYAQ

QGTQAQGEYQQQQLQTIGMQQPQHGNYGHQQRHLQDQQPDFTLADDIEAMNLRFASQRAY

QTMPPASNSSYTPMGADVASGTAMASSM

>contig27373 Frame-0R|Blast-reverse transcriptase [Phytophthora ramorum](gb|ABG66535.1|) 1e-15

MTVRLATGASITVMKRVVKFHYTLRDLQYDDDFIVLDLDDKF

>contig27849 Frame-2R

MALKRKPNDSLLGGPTTRGLPTRKEIC

>contig29308 Frame-2R

MKHLTATFQNDDVKLSKSIILTETKPSAKSLPAIEMRNMLRRWRDASPIVSPEMSFSILV

ESVHKNDPNLIECPGFAWWVHYNVKHMPDSIIDFWGQDKVLERLIFLQDDEGKTILDGNQ

FAEALKSFFELDEVDSLVDALQLGYLNGIPVNQFQSDSRLEILVRLLDLKQSSPSVYFSQ

LQKSLGEVRLQLMLTNEAVWFKCKSLSPRLRTNLHNCFVESWTNKLVSLVLRQDSDFIAK

NFPERQSLVDSLRYKGGAMKNNVDFQLLLNSIIKVERLFNQAADDLHSPI

>contig30621 Frame-2R|Blast-flavin-binding monooxygenase-like protein [Phytophthora infestans T30-4](gb|EEY69261.1|) 1e-66

MHAVTAKCLREVGHDVIVFEKADYVGGVWKYDAAAHASSSVLYESLHTNLPTAIMQLQDF

PFQKGVSSFPSHVDVLTYLQSYSNHYGVDSCVRLNSVVTSVLKASKKWKICVSSTDRGDY

AEEFDRVVVCNGHFSKPSYASIKGIERYKGEVTHSRSYRTPDAYKDK

>contig32601 Frame-0F

MQMLVYDNYSTFINATDTIHKVKNNVASMEDDVGRVVKSMETITAKSESINVALVPHRSK

VEKLLGVQRLLKKFEFVFDLPERLTTAVKQKEYANATNYYLLACRILERYEHISFFKTLR

FEAEKGIQQLERILKEQLLDMTLTSEELCETIVLLHQLNACSDENRIQFLEWHQVYFKQK

VATFKTQETPVSVFDFLQQFHADILSAMSRVFAVYTTHFKPEIVAREMNDAVQDTEFFKF

VNDLFALYATECTVQFRRPFSDFGAINDNFSIFSETDVSPDILESEFFVLMCVMKDFVSH

VYALDKSMPMCGLAARATNIVKHCIHFQIQGVFHHLQRNVIELLVTSYNNVTILRQNTRD

QGLSIRPLAYDSTRTFIDNVQQVLERLKPMMEAGFTMLPAISPLFTDL

>contig33707-0 Frame-1R0

MHGTGDMFFASGNSSSESSEP

>contig33707-1 Frame-2R1

MARATCSLRVAILHPSLQSQ

>contig33844 Frame-2R

MEDRSYDKFTCLQDALYVWHNEALLYSTKDNFVDPKRKEETSLYRNDDTCTPSYSGIAKE

INCLPMTKEEELTALLRLTPPNMRNDIRNRLKTRDETEKCIMTALMVEKARCQLEESVAI

MRDVLKELGRAGPWRKHVKNSQTLQREQAVQAAIQEKLLMHQWARYYTKYEDDALVQLQA

HNSSIPSEGMASGDNQSQAECASACVGNAPPITTDTSSTLDPADSPDVIEMKRLRQEIIL

AKENLLRDISGC

>contig34878 Frame-0R

MAPISLTSTSEHNLHSNDAFLIQATAVKSHVVQKYNPVPNKEDILSQLSLTLCSRSPNDY

DKDQEKLEKMAGAVITLLECIGEDPTREGLVKTPMRMAKALLYNTKGYGQTLADVLNEAV

FEEDHDEMVIVRDIDLYSMCEHHMVPFTGKVHIGYIPNGKVLGLSKLARVSEVFSRRLQV

QERLTKQIANAIMGVIEPKGVAVVIEATHMCMVMRGVEKSGASTVTSSVLGVFKSDPRTR

SEFMSLIHRK

>contig35208 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY70558.1|) 1e-34

MFMLCEGFMVPFDDMPDYWKWGYYIAFHTYSFESFMYEHFSGVNTEEAWAVLRRFGMEDV

NVMENMIIL

>contig36245 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66217.1|) 2e-50

MLCHYEVLAVARDASAIEIKKAFRLQALRWHPDKHKQNGTSSEEATKQFQVIQSAYEVLS

NPHEKKWYDEHREQILRDKDSKNNEGEDDELNLLRFFNTSVYSGYGSDAKSFYSVYGDLF

LKIDQLDLECGQGKRSAAAPAFGNDEASINAVNDFYNHWKSYTTQRTFAWMDDYQTTHAS

TRLVRR

>contig37264 Frame-0F

MEMATQSALHAAEVPAIRGKLVQSGVFQALIPLALIHGTHSHVRKKHSLQESRLKFSKGA

GQAMAKILISTNPNLLSSSSLFSSIKPLIELCKGEDELMHFEALMALTNIASVSMETKAR

IVNEPHGLSTLQYLQFSDHELVRRAATEAICNLLPNELVINQVFCNDEKIRLWIAFASLE

DETTDFEIARAATGALAMVSQVPQVCWVILRQNGFQAFGAILENRLNVEILHRALVAMQH

FLETICSAMKDAEKAEERMKVLAEITLRYATMKQKLSGHCQVAEIKEAAQACMKALDDVI

RYIPKRHDQEN

>contig37668 Frame-1F|Blast-CorA Metal Ion Transporter (MIT) Family [Phytophthora infestans T30-4](gb|EEY67748.1|) 1e-105

MNEFESQVDGVRRVLMELLDNEEDLRLLYLSKLHEEPDLLTDLYSFDSEEAEVLIENYLQ

DIFSTRTKADLMQHRITNTESLVMLKLDSMRNYLLRVDLVFSLVAISLSVGTLLAGVFGM

NLLSGVEDAWGWFWGVAITCVVVFVLITAAGILFFRQKGVLQI

>contig38207 Frame-0R|Blast-eukaryotic translation initiation factor 3 subunit E-interacting protein, putative [Phytophthora infestans T30-4](gb|EEY66690.1|) 0.0

MGDRRDEKPADFLLPETVKGWFSLMYTHLISGNVTEMARLYDREFHNLTNNYFKQTSWPE

PSAVESLVDSDPTFLILYKQIYFRHLFSRLQPGMDMKVASWETYVAIFDGVLDGTLDLEV

LPSQWVFDIVNEFVYQYQSYCQYRAKVATKSEQEITAYKESLFIWDSSKVFGYLHSLIRF

SKIEAILQEEKGAQAPTEFIKELGYFSLITLARAHVLLGDYYTSLKLLEPIDLFNKSSRG

ETKTTAQIHEKSPGCHVSVFYHMGFAQLMLEDFTAAIRSFSTIILQVNRNRSYYSRFADF

EQLHKLMEKAMALLAIALFLCPGQRVNDQIHSLIREKYGDKQSKLQKGDISALTELFGFS

CPKFILPTVAVENEVPINRSTEASQRQQNAFSDMVVRQQHVPAVRSYIKLYRSIDLEKLA

AFRGVDVELARAELMALKVSGSRLKSDVHFFLNNNLVLVDEEASNQRTGEFFVNHIHKFA

RIVDECAVAP

>contig38434 Frame-1F

MRRLNYSLVHSKWTQHLILDIHPLLAANCSHLNTLSCTIQI

>contig39363 Frame-1F

MGSNYKSSGNGDLQKATLNRIQPVVHMYKVPVSTTTPVPSTSTSSGKRYVAVLFFDTSWP

MGFSILLAN

>contig39697 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63803.1|) 0.0

MLLQRFVVTLYVLWTRVQHIKHKKWILLVLFSFYMGLWFSQKSRVVENSNDIFINEQSTN

FKEKVDSMAPTQLLAPWTNDSFECVGWKRLYSCEDKMLKDDEVSTTEPEKEIYGCSEEIG

PLMAGYCIVRNRTSGDLYKLMVSGCNSLPAGHFTCNMARDFSEFGYHSIDYEHAPVAPAL

ALPYVASTKRKRTNGIAMIVYERVLPSAYATIRMLRLRGCTLPVELWYRPDEMSIDNPIM

QKLLSDFNVRVRPIFDLRAVGFHVKPYAVYYSNFDNVLLLDTDNLPAKDPTYLFEEPEFL

RTGALFWPDYWQPSNSLFQLLNTSFLWQLTGIRFVDMFEQESGQVLIDRLRSKRALDKLM

YYSTHQPRLLEQLNLIWGDKDLFRLAWLNTSQPFHFIKYPPAVGGQDSRKEKGVFCGLAM

IQHDVQGNLVFFHRNSVKLDGTLDQPRIMSHIQEYSLEGNSRDYRIFQAVDADKKCCYFI

GTATLPDGRPAAQITPIGETIYAPIEELAIQLSVEARQLLLSDAIANDRGFRNMRVQSMV

ALLLLLCVAIIITFVWCKGRPARERLPSRFKSMEFKEI

>contig39990 Frame-1F

MQRIRAIIQHENLSIERSVIVFWATGMRQRRAIGKWELGRADTHLKGARLGGGRFYSSHA

LMCAYLQSQ

>contig40510 Frame-2R

MTTVVISPPIRPASSPPTVPTGTKTVVRSVAVETPSANDTKEASQATLNTSKSTIIDFVQ

NCQEHDVKSMEASVEKQDSEKSIENKDDGAVVVEQRLPQKRRKVLFECADIVEFEPTVYT

TSITSGGIPIGLSLDERSRSRRRLDSFEMERVQERVGRQNYMEKGYLDPQEREVILTNAG

CQAPVMASVEAEVNAIIYNRLESNVIDHDFLYGTTDLSVEDANIDEEDDGHSISWRQQED

GAESNDSEQEQSDNTRSSLK

>contig41012 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59154.1|) 0.0

MLIGKTISPVIKNLIDGVDTSPVQRMDESVIINQILSIFCDTFQEQVAHRVFFYKSSRLL

ARGLVKLHRGRWHSTAGDLVDQRVELDRRVLDWVVGLDTEMNELVEGSDLYTPIVQLDQV

VLPEEHKSTILETVESYESFRRYRKKSGLEQAGMAYGNGLVLLLCGASGTGKTMTVNAVA

HHMKKRVLLVDFPSLQGKRQEGMESDADLRGLFREADMSNAVLFFDECENIFRQRDGGGD

RLLNALLTEIERYEGIVFLATNRPYDLDEAMHRRITAVFEFKAPDHIQRRKIWDVLLLRG

SLKTEEGIAWDAIALKYELSGGFIKNAILSALLKAIARHSESPVISEADIVAGCALQMRG

SLHMKTFDHRVVPTTGLDELIVEDSVKVKLRRIVQFEKARSVIYGQWGFDFGQSNKQQKG

ISVLICGPPGIGKLNAAKAIGFEIGRPLKVVNFGQVAADSTAETRKALRAVFDDARLMDA

VLVLTGFETFGSHIEGGMIPMTSLESSPRFRMEVMRLVECMDTFPSTTILLANVERTAAA

SLVQSEFCGRLKFVIEMRNPNAKLREKLWKACFPPTAPLDTKKPIDFQRLAERYDLSSTG

IGDAVFRAAASAALRDETKRVITMKDLNDAAEIERQKARGSAAAMDNLFV

>contig41878 Frame-1R

MVDYGVALSYCKLCEEEKSVRLPTKGSRHGSKREPESSKGMEAQGRGLKNESRRRALIDK

QERQLPWLLHEELNGKRIHCL

>contig41917 Frame-0R

MISRQWSMLSNAAIARAIQRFQFVSPLTRIVFELVAMIWYFSSPMPFTKSLKDASGIYFM

R

>contig41962 Frame-1R

MYHKKTIMQRCSPSKGRNFPVTGPPASLQSPQKSSDSKIAAEVCSSSLLMMNESTFVQYD

EPIQGLNQPSIPPHTDEQTNNVAPLGLHQRHNTSKPSALYQKGEPSNVTLESMLRDLYRK

HQPDKLKNAITVAKQYVGKERELVKLLKGKYGALSVKRLEENLELLERVHDANRRRKHVG

KNRIFFVLTISLGFWLLSLSVMIVNFVVLDAWECHRVGRDMQPAKECALFNKELEAFTYD

RVADYMSQTYPNACFCSEWNARKSGLHSNFSRYELVNMAKLVPFSPNSFKVPWIASVKGL

AISQVFNASAKSVVDQLLSAGLFLWSTVLDFADFSKTKAYPVEDNIAHTLLLEEERNR

>contig42138 Frame-1R

MSESNEVTAGVGTYLYASPEQVAGKKYNAKTDIYSLGMILFELCHERFGTTMERYITLRD

ARDSKFSSGLRAAKRCPEILDMLRMLLSHDPTARPSADEVVQWGQMMYETSIAQKALEVV

RSPRNLGVVRAPPFLPGIDHLMAGSSLEAVVASTFSLKVEAAIEHRIGEDGGERRLPNHN

LLKQVCDVIAGVSNGKVEIKKCGLHMESEGATILEFELDPQAALADAPDFDVEGTVIVAI

EALTGVHLVHRVK

>contig42668 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53515.1|) 1e-46

MDHEHAASLTARAVKKVLPESAILTKDARQTLNSATSVFTLYLASLAHETAVVNKRSTIT

LKDVLQTLRDVDFEHFIEPIESCLQGRFGWIDSRAINQKLTLLLLQKQKSQQIEAKPRKP

MLRKMKVARLRTKS

>contig43388 Frame-2R

MDLADLQMKILHHLVSGSTCKFVHYSREIGKRATALGYHGYIALCIFVRATAVTSGRFKM

TAKQNSNKNAQEVFRGKSLLVFGRASNKGAVGMSFRYDDTSFAFVTCHLASDSKSLKRIK

RKKSSGAMNLRGGDNSIDYSYNGSIARSSIGDSGVSKMSITDDMMMETHQPPSRVERRNH

DAMEILQQLYLDDEDYGFGFPHLHHHTFILGDLNYRMTRKRATPMDMLELLMNARAGVCQ

TVIDTITSSSPSSPAMLQMSMNELSPRFNEEGFRQCMTPKVQSPKPIFATDRDHTYASCS

ANTSKNNCSGSSVPFLVEEHDELYHLCRSQQVFHGFQENKITFFPTFRRIRGQALREPLD

ATSFQQNYSLVAVHGGYRVPSYTDRVFFSSLVGVRNLLQCLSYDSCEDVTSSDHKPVSAC

FEVKLLAAPFKLPQTSFSAEDVLWNANSTPTDPMILRTESTLSGARMKDVPGACEFRLRI

EFRSIHWIDAIESALFDRAEHVEFGFLFPLPCEDVFAHQRKLHEVAEHLTFGGSDNGNSG

GLGFESSISPTSNFHTVKWHDFVNGGLRYHTIAGAIGQKHVAIVLRSLGRGRSMSKTSSA

SRLLGGSCSPSPHTSATSVVSTCSTTPHNSIASSSSSLSSDKLFGHGAFCTEGMIKKREV

CVPLTLGGRLLGRLYLRVSLQIRPRN

>contig44756 Frame-1F

MNSDVALWLQVSKTFSIPPGGIGTITLDVEILDHPSLYRIVYEKYEPTPIQAPPAVAESS

LCVKNLDTGKTVSVGSVNNLVLNEIKSSRSQNKSSKLSSSARPAPKSDKASSVMRRRSTT

RARELIGEATAEEDDEGERTEFSVDETITAQAVVEHPTVTSITGVYKIVAMGVVSVSMLK

TAKANEYEITIHRKGSLGLQLAPKIESLKRSPRLIVHRSKGQSAAVNPGDCLVAISNANI

EHAGLKHALWALNDAKRPLVLRFRRGNAKEKSSLFKTGLSKLTGPRRQSLVAV

>contig46291 Frame-0F

MLVPERTDDAEFTLLITNQITVGYSSRNQRMQQPSSLNHSCFYLKTFRLPYSCAAHRWRR

RVWQRRPILQQNRGVKASIVSKKPGVERQSRTNAQDGAQLGSKHDVCLSAAAAFLRRRGS

VCGLHTKSQSNPSEHEAGVPTRSADRKGTETARDRRFWLSLQCVSGPSQEFAETSCAGRH

GI

>contig46448 Frame-0F

MSFCQHICGRTPKITKRSASTTSLVSSHAMALKAAKCGPSSVSAFVTAPASSRSAGTAAT

NATRVSQMPTLPTSPRPDCHPSPLVHCTHRYYAVMAAVSTRCSQQIPTIVCSFRRTTTPL

TTHTVSAAASPAV

>contig46707 Frame-0F|Blast-CRN-like CRN4 [Phytophthora infestans]gb|EEY61565.1| Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|AAY43398.1|) 8e-28

MVIDHSRNKKVLDETQVTELHESISLTQEPCEFNVNTTFGDLDGSALAFIGVERPYNRCL

YLQASVARVLAL

>contig47010 Frame-2R

MMDVRATKSRRAGFTIDELQEALMQSLQKSVADTVADVCQNSQLSGAVCTREGGDYDEYY

NSCRRLVDYIQQHMETSSDFEEQMDRIILACHSGATGRVLNSVVTKKMWFHRRTATSPDT

CSSSVERATTKRKIKRGSASARMETAEDLATSAKSVSGRKRVTKAHVQHAKRPRRATRNV

VNENSEGDVYGKAVKKKAKSASKTNTRQERGKEDDDDSLLSFSDAIGELCYPDRRTDSDT

KVFKERLQKSIQFVDALLCNPPPGKVCGRTCHKIRAQMCSSST

>contig48024 Frame-0R

MVYDPQSSGASSNLYRSKTNHGNGNSAMHAQQRNRRFKATPILEDELSGHTIQLETSGDD

LGDSIQSTDDNSSQVSEYKASERNKAKNKDASRSFKSFKGSQSSSSQGSQNSDTSQKTVS

IQILAKARSARYGIKSDFPLKVPPPPPSPLQERSVSGRRLHRNKNDSHSSKGRNSKGIAT

RKVLSSSPTRGSRSSHRAPNVPHYVALPAAVAKRDSFASHSSSRDSTRSSDRMSASREQV

R

>contig48262 Frame-2R

MAVGEREGRVTIWDNTTIRVITRELDPTLIAVDSSIPVNSEDSFRA

>contig48903 Frame-1R

MFFPALAALALGVAGATSMSNALQTMSFNGTSVASRRLDETSAAFKKVAEALDGDKLRNI

FGHDMLNNVPHEVAYTQIQNHLKHLEHLRAELKDQAVLALMEKHYGVPAVSRYVEKTFSD

PNSMKGKVFNVA

>contig49311 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64256.1|) 1e-126

MYENLRQMKELNALTPVALATLERMLWPLPYLKAHEKVVLEWTERVQKCIASKHAQVDQL

QALLDSGSGLLLEQGAFKIVIDEARKARVWLLKLKKRLRALMTKGCGRMSMNTARSLVEE

GEDIAIDMPVFDYLKEHTEIANDWENRVLASGIETGQARVATLLALLNEYECVHLVIDLD

MHRDVLKSATERYCICRQPFDGLMIGCDYCDDWYHDSCIGMSKEKVEKA

>contig49441 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62336.1|) 1e-170

MPSSLSKAVIPAVAADNFITPKFMHALMNALRFEDFRVASARLEILRAIRKTFSTKRLHL

SRALADAIALRLEYVQSIETRAQTLGVEISSNKVIADHLHDHGHGFVEFLRYSIEHIEEN

LVDTPPLEGSDAARELEEQRQELVRNCLASLVSLWRAHWIDPAGSDEDELISCAGQFVAY

MPSVTGPLLKRLLNFWPTRFPKQEVCATRMVARVIMSGLPLHQVDSSLALQRRVFKQLAR

ILKSPHVDAAKEALAFTGCQFVLVHFLKQDKVIYEVITAALHVNIESHWHSGVRNTSA

>contig51048 Frame-2F

MDGKLRLWNATSGEHQFMNYEGVHRTQPRAARNVQMAVVQESGAYESTFVFLPNGSDGAL

SSYRVFGDSGAQVKSATAHYQQINACLYRKATRELYSAGEDGLIMKWKSLPTNLYPSMST

DIDSETPNCVSKAEIDALDDRDAWSDDDTDFGTGGHEFIPPILRDEY

>contig51691 Frame-2R

MSPSLLSLRWRCSLPLLGVFVSLLQVLARYNCGGHHVPLIRTHFGIHAYHGDFKHSSRTN

RHIQRFIFVTSAYGHRLRLTRMPTRSPLLRHPNVITRLGSRGPLRLSDNRIPKYS

>contig51831 Frame-1R

MIAFASLRIACCLSIGVLILIFIVNCSLVHLLLQ

>contig52179 Frame-0F

MTQQVLEGISIMTLLETNQQRLIKAGVVWQLLELFSRYDVELDDADVQTRLQQYSDSEEE

EYATISLECQNALAITAVRALCSLEGLYLDDRKLVSFSNRLVRQVVDALMTPNLSSLLVL

SSHHEFLKIYHGDCESYTLFWNEEMRQEQKKFLSPIARIEPSTMMKQHYNDAVKFRFMYL

ADLFYIGGLYIKMLMGSLLAIKESPDPAPINELGQLFFEELFS

>contig52197 Frame-0R

MQAPLARDLCSVDVTSSTFVNDVPCADDGYDNELTLTYSKLDDLSLNALQELRRRLCLDI

QAESAQYVLSYSELNNATNTDSLNAEQAKNRLSTLRQKLNAVDASFKRKKT

>contig52333 Frame-1F|Blast-twinkle protein, putative [Phytophthora infestans T30-4](gb|EEY59593.1|) 1e-41

MRAIARLGAARRVMRRLQVLGSNSFIRHPLSTESFVSRHYQFQGSQDIAEFLHRKSLTVR

ETDSHFVLRDCPFCHATRNKADNFFKLYVHKTQGMYKCHRCGVAGSWFDFKRKMQDNVGV

TSPGGALQGNNNARAPTNSMIVKVIQALDNEKAMSIQNNLL

>contig52463 Frame-0R

MYSESITALFEELAKHGCKSAYCTESGSA

>contig52881 Frame-2F

MHKDNASRVPDASTDLIERLEGLLAGMAHQQAQFMANQQDQLNRRAVNVPAKPS

>contig53639 Frame-1F

MQRRLLKWSGALNNRRNAGNLMRSIFASPALFSTAKAERKVMPRKRSQSPLKTSPTRARG

RNSLNQVVINVEALVQESKRDGKSFQPCMDYLRRVSSVLQLCKTREQCTAAIPLCHIVQR

AQFIHGMAEMECLRIYQKAGRNKEVITLAEILMNRDVFLLNSALSSVIQACAALEDIDKG

FQIFDAAVRRGSIPNARVFSALLAVAGASKDPQRVQNVLTKMQDVGIEMNDITYHNLMSA

YARGGHVTEALALFDKMQKQGIAAD

>contig54339 Frame-1F

MFSPVQESSASTSIDAYDLAQEYGTDAAAKLSRVLKALENAGFYKAHVNSYSAFERVLSG

IVWLFQ

>contig54546 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70513.1|) 1e-16

MAGRRATVGLSSSLYADFLAENIRLNERLEPSPRSRHSLAINAVTPSGTAIGLQSCV

>contig55053 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64653.1|) 3e-23

MANVLTELDAYRETGEWRQALKLLDRVDKDKALPALDSVMYERAIAACARMGKVEVLPGL

>contig56838 Frame-0R

MTKLVTTDLNKETDSFYVEPKRRVSRTKNKDF

>contig57240 Frame-1F

MLKLPRRRSSLRNDVVSGCFLFAEALPASCSAIQRIGNRTPTTYSASNSATSAAMTICRQ

MALNFQLC

>contig57374 Frame-2F

MGGGPASSDVVRSSCFVTFPEHTRAEPVPVDAWYLFAAGLTFLRRLARDRVGDDMRMALL

LQTLGDEEGERRYVSVNNNTVLQHALQETFDCPDKALVLHVIDVGKVQGQKRIHVRPEVN

PNVSPEPVERLGLVFPMLSVNGLVTPTAVEVPSARIMHESLYEQMSRSMFNYRKDDSVRV

SGALEKPSASLRHSAFIVEERDYTETLMRGRKEEEPEISGAVNAGGGLMLSSEQADWELS

SKKEELVDESDIPMATVVETEAMLIPSDYVMLELQTGAGLPEVPGITRSTYFISSRWAEQ

ADEMSASMRLDRPSMPGARVTQARVADRIPTAINTTLDDSFVILERHEL

>contig59471 Frame-0R

MSLSPRHLRGMNKSSHSRKQSAQSSKAILTPHR

>contig02629 Frame-1R

MPRRRLLQLLPLHRRLFCILPSLQSPPVPITRFTATRYYRVSSSNESTKNRRDSSSASWN

QLVLALRTFHSLERHFAVPFSFVIPTCSLWPKELHQLPLGVKVHRFLQSVSKSTVKKPPP

QTPKHIAQLQELDDMGFPLYEWHDYQFQEVCLPALQTYQELYGDLFVPQKFTVPDNSKAT

DGNLWPRATRGFKLGLAVAKLRKQMQQQKQRAQQPQRQDSKTSMRAVLPPLAPRHVEALN

ALGFVWRVRDTKWYDFFLPGLRKYKEIEGTADVPLAFTVPLHSLDPRWPKALEGYLLGRH

VYMVRAGKYATQVRECLNELQDLGFSFRLMDKVWTESIYPALHVFATQYGHCDVWQDFVV

PYDDLWPMKSWGLKLGDTVKNIRRGAYNTQVKTVRSELNAIGFV

>contig05246 Frame-2R

MNLFYFNSTNFSCKQTGRGWLYQKGCVLIPVP

>contig09075 Frame-2F

MTMKFVLPARTPATRSSYSEMRPESKNLHLESSNVFRFENSREEFRGMPYTDTNETTKAA

APDHLPPDPSRLDGVLLSNQTTHERHESTPSPATTSTVPHFPGPNRRKNSIEMFLSQSPS

QALGGDFLKLSLEDRHLSLESINRKHANAKVVVNDRTRTTRPETNVYASG

>contig09516 Frame-0F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY65941.1|) 1e-80

MLRSGNTNGNGSEREGSSGSLMTEALELQRQMCDEAMSLVNAGVAMQNASPPNAIEAERK

LTRAVDIMEQALSVRYRSVEEKDAADRLNNKMIRYVKMIKSQRAKNLVGSGLKGRNLIKH

NILELERPPEVYTPVLELLNHSAQLGDICDTLKHVFGFQESSVLNQKEHLVLLLTNFKEQ

>contig09725 Frame-2R

MNKIWLDISIIPTGPKSGPEYCPTLLACKDLTGGVGFNKPMQITPSQVDGHRCVELTCLD

DGCMDAYHFPKDDNKTHTCPLSTNFDLTFCPGGSGDAKTAPPSYVAPPPAPTSSPSQAPT

EAPTQAPTSPPTDAPTSPPTTQAPAPVKDESPAQEQPPPNIFVPTTEEPQSPEQVQLPSP

ETQTTQLDPEPFKTSLGSKDEPSNPPTPGSLDGNVPQSRKVGFMQPVYRSSNEQQSLTKS

GLSQQIGGTPASDSNNVQQINTQSEQSNSGSTTIVVASLGGMAGMVAAAAIFAVRKKKKA

LDALESKTPVTGVPDCVLTGMRTPRDNISVL

>contig11724 Frame-2F|Blast-enoyl-CoA hydratase/isomerase family, putative [Phytophthora infestans T30-4](gb|EEY69912.1|) 1e-93

MSTQHKSVVRCHVHAGSIYVAELCRPSTRNAFNDAMYEQLTAALKKFEADDSLDAFVLTG

HGDYFTSGADMNELAFLLSDNSLRPFSQSPVFTFLHTMLKCKKLLVAAVNGPAVGIGVTM

LMHFDLVYAATSATFWTPFLRAGIMPEFASSYTFPHFLGPTVAANLLIRSKVYNAQDALL

VKLVGSVIPTHGFLNTVLQELTVLVTNCSNKKLLPLNKSLLRHQSAPQIQEALDREFKQL

DHLVASGDLLTTIKECQKQLTKKSSKL

>contig12897 Frame-1R

MGTLAANGGKRQFTSYPGHKWVLKIKEYVVLEYVVTKNTGEMQKVTVPLMDEHGATGFKD

AKSEATVNEEL

>contig16927 Frame-1F|Blast-6-phosphofructo-2-kinase/fructose-2,6-biphosphatase, putative [Phytophthora infestans T30-4](gb|EEY56397.1|) 2e-06

MSPVNVLEEEDHLFPAVIKWSHPCESVGVTGTFN

>contig18099 Frame-1F

MLRYWRMEPDGSYFICFQSTTHPTCPRTSDAVRANVMGMGFIISPRVQEDSVHHFQECWV

TLSIQMNPKGYLDSKLARLWYYVHAYGVYFLEIITAITAWKGQDTCRPTTALDCSRLSSE

TKGALEAIKFATLERYRTNIRVLHGLPTKFWSEPSAETFLVRGPQYVPCKTKVPSARQAF

RLVNVALYKSKDMIQHVGVSSIHTNDVDSMDMKTRDSVFFLIINFMVPGFLHHSLVLYFT

P

>contig19377 Frame-0F

MLSAVLFLVAACAKTSFGHSVVVSTRDLKIYASNSNEYSTIPEDFDSKRRLRGAVNNINR

IKERDAAILSEILGWNINSKLSKNFQRWKKMNPRVMENDLFKIPETYKRLLEFTKSLSKK

AATKPVSFETLHLLGVRPQQLKERIPSRTAVIRKGKVDRYKKYLNNAFYNPVRRKKPFDT

SRLDDGKVEQAFRKLYNDNVLELLKTAFFNIVDVEKLAALASGPVYRQALEADPKYKEMM

SSIPLERWPENSILKKLIAIHEFFLKTDD

>contig22450 Frame-2F

MTDHPPVGGLRSTSKDMPLMESIVSVVGLPVETSSCGGKWKRLTRDFRFVEFAISVVMYG

LALFFAKVQVAQREIPNIEVQLDPTTSVWARDPTINYMEKAQQVTMASLIGVGVGAPVLI

NLLINYALPKFHGVRIITHDTRDFLLTLVQSTSMATLLTQFTKNMTGRFRPCFYDMCKWD

YEVVWDGVTNLCQSKSGEKEGRKSFPSGHASFAFATMLVLTLYLLGRSSLNCENRSETVM

RGGRKMLKLFLCFIPTFLASWVAV

>contig23354 Frame-0R|Blast-phosphoribosylaminoimidazole-succinocarboxamide synthase [Phytophthora infestans T30-4](gb|EEY55596.1|) 1e-163

MTSVVSEAEKRTQTYVDKITTGQTLTSTSLDAIRTELPVFEQIKGKVRDVYVFADRVLLV

STDRQSAFDRALASVPFKSRVLTLTSVWWFNQTKHIVANHLLGMPHPSVMLCKKCTVFPV

EFVVRGYITGSTSTSMWANYKNGIRDYCGHQLEEGYKQHQKLPRNLVTPTTKDKDHDELI

SGQEIVRTCLMTQEQWDFCEQKALQLFAFGQQQASQRGLILVDTKYEFGVDETTGDILLI

DEMHTPDSSRYWLADSYEQRMANNESPENIDKEFLRLWFREHCNPYDDAILPEAPQELVT

ELSRRYILLFELITGLKFEFPSPNSKPEDELIEGIRKTMLYG

>contig23404 Frame-0F

MASEDSSVLTRAPNMRLLGYAPLKYTLHTLRRIRPHYMEEALLVL

>contig23857 Frame-0F

MVRVYVAALAAIFALSASATLHLTLANASSVTTEEGDGRPQGKLRVNAATNVESDERFLD

GLKALVRGFYDLTPFAPRFQKDTYSNLLLKLNLSFEQFSGKDTLQLRRFYDAARRHNKVN

PTNPVSVYTGLVEKYGEFEIVNMVYSLKHAQSSKSRDVLKRLGKEEKWYWKDKKDAGKMY

AEALDLGNEFTVKNMVSKLSKLEQFLNRIDQKASEEQLKALVVADIERVKTKKESVSPSD

VEM

>contig24171 Frame-1F

MLGITFDVKLLKGVGKFHAGFHPNEPQSLRLQPLSREKTLSIQ

>contig26708 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56147.1|) 4e-15

MEIECKTLWMGDIQMHWDEAYIVSLFASASEQPVVKLIRDKVTG

>contig28214 Frame-1F

MKDTYLQRRMTVPTRVRQSARRRPHRPKSKVDSNTESIASVSTDVPPQLKSKAQVPLRAG

CRRSTPKTKLVRKQAAGATRFDSLVIQYQDAQEDNVLLQEQSPVIIEEVPATAATKEGLL

>contig29200 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57238.1|) 2e-28

MPSARSTRAIYRCLLRDARKLQQTPHFFIRRDLQLEQWGHGRFVDSLPLSDGQTKRVIGS

EVLSSLEDFRKLRDNAFQMGSPRLDPIKIIQLSFRQNVKLSDRK

>contig29309 Frame-2R

MDEDYKLAKEAFVAGLHGTSGLEVFLVFAIAPGCLWLYSEHMLVLEVLGVRQIGSNHLNL

VETILIEFIVTVMPTMIGLSFTQYTIPILAVVYTLSAILCALSRYHAKDFVRKHCRKEKR

NQLLDKELSFLTNFRAQIMISTCFAILAVDFSVFPRRFAKTETYGFSVMDIGVGAFIVSS

AIVSAPARKVRQIADKPRLNSDGIIKKGYNFLRPIALVLIFGVARFVTVKGVNYQEHVTE

YGVHWNFYFTLAGVYLVYSLLRACGKWAVSPIVALLIAFGYQLYLSQFGGEYYILESPRD

SLLSQNREGILSLAGYTSLYLVSIYTGQCIFGAIEPNTFKSHRNMRWLVISLFCISGLLW

AATFLSIRLIAQPSRR

>contig30620 Frame-0F

MHCTGYLYSVSEFFPSKLLFPGACVQPDDLNEAEIAVFHCLTNGTAVAPIYKQLFAIEDP

TAAFVGLPFSNLPFVCFQLQARWIARVFGGTAFLPSKSDMYADFYAYVGFLDGDLTKLHQ

LGPLQKYYFKYVVLVTLTPKILLKSGVDSYSELAALSNFQLGQEIHDIYEDVRFLRQMFP

YKYRSADYRRDEATGRWVRRIEASNSLSELVREFQ

>contig31757 Frame-2R

MSGLTPLNSPRDAKDSVNFQSKFEGNALSMASPMESIACNKPESERFLKDEALVREATMA

MHIGDRRAEGASGAHVASKSIEMGRHEVFSQENQLRFVSPPIIGGSRDNFPTSSRRNSPP

ELFSRGFGYRHVWDLTQGDVDSDCYAKDGNFSSGHTPPPCSQSGDSPDNNWSDSSNSLES

LSFTIELDLETQNKVSQANRKVDRQPINSTSPPLYTDVVARSTRFLTALPARLALAQIEL

ALKLTPCPFPYDYSKATQKVAIDWSKYQLEVRYAGLLTCTVQVFLFQRGVYLVEFRRSHI

DFFQFQRFYKQICAQILESLEPRPSSGFRKRNKSLSN

>contig32600 Frame-2F

MCQELARYGIANCLHDCMKWLPPLVSSIHNSIDNPPMHQLNAKHVIQLTRDASNALIQHV

ARYYGHEMCEICFNSIAAISWPHPPSEPQHVQEMLGIVETTMRFGTEIANILGDTQSVSR

FNNIRSNDWDVRGRTSVLHSWNAKVTASSGMNVDRIFARRIQIVPSELALSTDAIVLTIL

KIGLKGFIENLRLVELSMFGLQQMQLNAAFLCRLLLPMVTPGDAEEELKSLLSALLLTAR

TRAFEDVLMDESTVVAIVNATSIQLRSRLESC

>contig33081 Frame-0R|Blast-inorganic pyrophosphatase, putative [Phytophthora infestans T30-4](gb|EEY64780.1|) 0.0

MSSTIASFANFLKQSKTHAVDNREVLIAGVLYKKPERNSLLWKKRYCVIYAGELQIVYFL

SLDDFEKRAIRGKIPFSSVHPWDGKPNGFQFYTPADNCFRVYTDSAEDQQQWVAIMQQCL

DNAPDKKDGEKVEYTRPVASSPITSPKGAAFRSKRSDSWREEDPDVLSMAVELEDLRSEV

TTLKAELASYEQAEKRYGTEVVVAKTRRGSVLDDGTELNMEPREMERMRAIFNLFDVQGN

GFISEDDLLDLHAKLGEPISNEDAREAISYMHSKSANGQIDFNSFMKWWNDDHAADNQTE

AMRRYQAKFKFLKARIANPEVGNIETEAVGAFPSFEFRVNFYHASPTGVRQQISPWHDIP

LYNPDGTVNFICEIPKWTRKKMEIATGEPFNPIKQDTKNGKLREYGWGEMMFNYGAMPQT

WEDPSHVTEGTGCVGDNDPIDVVEIGTKQWRTGSIVQVKILGVLALIDDNETDWKVICIN

VEDHYAPLIHDVADIEAHMPGCITAIHDWLRDYKLPQVNKYGYEDKCMGRDFAEATVAET

HEFWKLLIEQRGGQATV

>contig33449 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55645.1|) 1e-13

MKGTSKLDTMAAEDTYEVHILPGFVPFFWCFVGVGILLFCYSLKYAKIYSTTAAFILT

>contig33706 Frame-0F

MAPKKGRKSANKSATVAADNIDDLLNEINFSETATTQQKQFDQVTSKVEESHEKRSGVDA

AAAAYLATLGVAPSPGGEKKDDKKKKKKGKKKPSADAKRDDDKKPTSAAAKAVMERQAVM

KAEQERLERERIEQERIDQEEEAKRLAEIEREEEIRRKKKEARAAKIERQKKEGTYMTKA

QKQKAAKAQAALETMQQVGLVPEAGDKKKVLYSNNNKKSSNKNKKEFKEEEVEDKEQSVL

TEEKEEVLVENAAETLEEVVAPDAWDDEDWETSKVVASLEDKLQVYKDETAAAACDSEGD

EDLLV

>contig34013 Frame-2R

MVAYAFSDDSGSHQPMFDLVALEKIEQEERNERETQMRKEAPVQAEATGEKIAKLDSLLE

KASLYSSFLFSNMESAATVGDGVKIEEEKELGRKGKRTRGKVASQKVYKKPKQGVEKLRE

VQGDTSLDTRQQPTKVKLDQPAFLTGGTLRDYQLEGIQWLCNLFENGLNGILADEMGLGK

TIQVIGLLTHLKALGVRGPHLIVAPLSTLMNWATEFHKWSPHTPVIIYHGTKNERKEMRR

NALHPQKKSDMDFPVVISSYEVMLSDAKTFAASGFVWKYMVIDEGHRLKNMECKLVRELK

RGRSENRLLLTGTPLQNNLTELWSLLNFILPDVFDDLELFESWFTFTPDAAATAAATGES

VAEQDVLQGEKKVEVIAKLHEILRPFLLRRLKRDVVDEMVSKTEIFVYCPMTTRQREYYG

MIRDGTLAKAMQEKYGKFKAQQAFKTTTLRNKMIQMRKCCLHPYLFDEPLTASGDVITDE

KIVEASGKLKILDQMLCQLKRKGHKVLIFSQMTRMLDILEDYLCMRKYSYCRLDGSTKLV

DRVDQMEKFNKVSAGVTSANDENNVFVFMLSTRAGGLGINLIAADTVIFYDSDWNPQQDN

QAMDRCHRIGQKNEIIVYRLVTENSFEDRMTQRAFEKRKLERVVIQRGGFKERTTPAESA

KMTHSELEDLLKDDIEIRQGIESGGITDEELNHILDRKLVVKSFVKSKHDNV

>contig34066 Frame-1F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY69845.1|) 1e-106

MRVRSEAPPGAAESVNYITHTALARVHGKFFRNYVAWCKFLRASPRCSLSEKGNLLRMEK

EVALFLLLWGEAGNLRFMPECICFLYHNMAAKLELLDTLPTVYEGYYLTEIVRPMYLVIA

QMRVATAPKGQRPFDHQDTTNYDDVNEFFWTTHCFECDERTVAQVVAVQDPKTFKEKRSV

FNPLLAFFR

>contig34295 Frame-0F|Blast-zinc transporter, putative [Phytophthora infestans T30-4](gb|EEY60501.1|) 9e-66

MMAVLYEDMAACTGVLMAGCGIGASHITENPLWDSIASISIGLLLGGVAVSLIRLNQKFL

LGQSVEPDIENGIRELLLARPSIDNVYAVQSQWVGPSTFSYK

>contig34916 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58966.1|) 1e-83

MVLFVLYVKAELENVETVVAPPLHQWCLDVKEPRGDEKREAVFVSDEEEVDVAGGRSEVH

FTLKWPGANKPSQMTVVRDVKKLTRAITGADSGEYVPFVGFECRGLEPFAWHPESGYRVV

SKGRHAAFDDVNLSEDWADYDEEGEQAVGIYNVEWKFMVHK

>contig34963 Frame-1R|Blast-sphingosine-1-phosphate lyase, putative [Phytophthora infestans T30-4](gb|EEY57798.1|) 0.0

MTASLLNGGHPEVCGTLTSGGTESIFLAAKAHRAYYRQKHGITTPEIIACVTAHAAIDKA

CEILGIRLIKVPMDSQSLKMDLHAVRWNISANTILLYSSAPNFPHGIIDDIAALSQLAVQ

NDVGLHVDCCLGGFVLPFARQLRTTIPVFDFALPGVTSISCDTHKYGYGSKGTSVVLYKT

SELRRFQYFSYPDWTGGLYVTPTLAGSRSGALSAAAWASMVRLGREGFLEKTKGILDTVD

EIKTGIQRIDGIHLLGDPLVMVVCFAGDKGINALRVGNAMAKRGWSLNSLQHPTSVHLCV

TVCHIGKSQKFVSALEEAVNEVKQDPNASLEGGSAIYGMASSLPAGPVDDILRIYTDISL

NV

>contig35511 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57870.1|) 7e-21

MGNKQAKQTPPPRSAPTNAAVSTIPTPIAPSKTPTTSSPPPLATPSHLELKLADVSVSSV

FTHHEMLSIRKHLAAVLNQHENDAVVIHKDEFFRFLAGGDGSTSSLYVNRLYAIFDMNKK

GHV

>contig37669 Frame-2F|Blast-acyl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY53109.1|) 0.0

MVQVVRLTRALERRIATRGRRFGTLFAPLTQLSEEEMMFKSTVHRFAADVVAPHVRAMDL

AGEMNHSITRGLFENGLLSVEIPADYGGSEASFMSLCLTIEELSKVDPVVGLLVDLQNTV

VNNVFLVHGTEEQKEKYLPRLCTDMIGSFCLSEAGSGSDAFALKTKAEASSDGSYYSITG

HKMWISNAEYSGVYIVFASVDLSKGYKGITCFIVDREMEGLEIGKAEEKLGIRASSTCPV

SLTNVRVPKENILGELGKGYKIAISTLNEGRIGIASQMLGLAQGVYDQTLPYLFERQQFG

TPIGEFQAMQHQYAEAALEIETTRLLVYNAARLKDAGQPFVKQAAMAKLHASRVAEKTAS

KCIELLGGIGFTRSLLTEKFFRDAKIGAIYEGTSNMQLTTIAKLVAEEYRK

>contig38206 Frame-0R|Blast-dual specificity tyrosine-phosphorylation-regulated kinase, putative [Phytophthora infestans T30-4](gb|EEY57617.1|) 1e-41

MRMLSFDPDSRIAPTEAMQHPFLLSLRQLQPDDTTEKLVAQGKYKHMRASTMRDVHGRSN

KNQIPPLDRAKQQRLNDKSSHER

>contig38930 Frame-1R

MRLPTSWLITKTHLDKIATAETDLISIFTPTVRLRNVNSVKRATESFKPYVKERLLNHSP

NYDAF

>contig39991 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64310.1|) 1e-150

MLKEIFSAYLKREWLSLQPHDSRVEDLAEEGIGRPTSQLGSHKYPKTSRPWNGVTFAGTL

SRWKNYNGFILSEERRGNSIRAANARSRNKANKITGTSVSAIRTDEEIFIKHNPTLFQWT

TFSPYLATYPDADIVRMTEVPRNFWLHRLKYDGEFFSNFMGFVCLHAANTALDADVVWTS

LPGYTLLIRVSLLLIKEACWAKWLYVHDMSGPLPSSSMEIEPKSQDEDCIPFELESIRAI

QTVLDNVVQLLRNNQLLESCVLAMYECTNVLHARSVEVCLTRFEEWFSATAMLTDFGGLD

QRRGNGMMVYRLPPEFRGQTFAMGMRFMLSSE

>contig40300 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54836.1|) 6e-82

MGFICPECKIKFLSADQLEAHYTKTHSSFASIKRESDRLVAQQSRSSQETQQSTTHTRDI

HATFLSDLAPQLAELKDQSLALSDALDLHHMGLDRLDTKVGQVHHDMKQVERQAHKIMGR

TIPAVFRFRCAIQEAKMDKFLCTKNGDAVLSADVVVDGCTFRAYTLGDDSDVWGFQCEKT

SRFVGINRYGNLKVQGVEFHSYEQFLVEAKSTTTIFCLSSYFGLGGWIAMKDLGTTSKLT

IIRGTPENKAFAAQFRIVPV

>contig41066 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60984.1|) 3e-12

MEQAKLRAAELQQKLEVGKRLLLDALQEEKEILINGGLFWIGRADKCVL

>contig41088 Frame-2F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY53550.1|) 3e-71

MLFLFDSHSQLVTVFVREKIYTELLNGILQILQSSSEALRTNTLKLVAMFTRIVCRRHAP

GSACCTPDSSSDHTLSFKTTTSLTRKRQPMNSLPDPYVLPTLLLDFIRVDSIAAVDIILK

DGADLNFPNMCDLKGNEIDKPLNVAVEFASLRMIRLLLKRGADIHQVGIGGTALHVAARL

GRCDVAAILLQCGARVLAKDRQKKTV

>contig41963 Frame-2R|Blast-peptidase, putative [Phytophthora infestans T30-4](gb|EEY53249.1|) 1e-135

MLRPMLENMNTQMHAAPEDQLFSIPFNDASRATLDVPATVASTPIKASVNLVSHRFKVSG

SPTLFLERTVQRIKTLNSTQLLIEAEISALNSLLVHVKEDKKQVNMALNIKLWKIIAKLL

AQGSESDFFFPGLCVFRVLLLQPPQELDAVSDTQACFDIIVNVTAMDSSVLSSAQKTVLL

TVLLNAFANSGFRDMALSNSPRYLPFIFATITDSTCHEESRVLGAHIISNCCLAIKAEKN

PMVTTIVCGAIETLDQISRLQSNTTMLQQIIEGIIIGLGRLLHNFEAARSLSIELGLGEI

IQRLNVSPGLHAIELLVSEVVQWL

>contig42669 Frame-1R|Blast-histone-lysine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY67226.1|) 2e-73

MLHVLYRLGIEDKLDLFKEPVTEAIAPTYFDIIKTPMDLSTIRQNILNNAYTSVNFIAFR

DDFELMCLNAVTFNTKERDFLIWREAWRFYGQGQRILRQTAPKARMKQRGGRFYDALKVA

AKRQLPNKSGLVG

>contig43244 Frame-2R

MDEESLSSVDQFLRDNGFRISNSMSRPASLSGDEQLINELLLIDADIRRTPDPPRFVLLE

DEDLLLARGCTRRSGDTTNERGEEMEATGSHYHQNDSLDRSMLYGGSESSRVSDTSPISD

IRPLSAASSSSMINLQFSDNSRTSLFESRYQMTSPEQIKPADLVSAASSTSLPPSLVHSG

SYRLSSSCLDDELSIALGVQTSCIGSDKLSMSTPETHEPNLVEEIKVDHHSWSLSSPRIL

LHDKLSRNHDDVSVDRKSCDMSTDLSQSKE

>contig44757 Frame-0F

MRVRFTTLSTIQKIALNGRTPLEALLAIR

>contig45620 Frame-2R

MAIWSSAIYLGVFGDPYLRSTPYEAGGDPQALVEMLSDFAQLLQPQQQADSALDTALSVQ

QERVLQSKLLPQLISCGQWAEKGSRVENAMQFQAFLAEWKAVLHKLQVGQFMLVPGGYVG

TLSSHSIIYIVKKTSD

>contig46081 Frame-0F

MDLPETECLDHAGSSTQLPAVNKFPNRRKPNLTDTQRLIMAEFLLNHNQGKTHLPRAVIS

AAADRFEVHRNTVSRIWNLMKTALDGGASADVVMKQVLSKKRGNSGRKRKDYSAALEQLK

QLPLSQRGSIRALSTAVGVPRTTLFRLLRYEKSDGSAVDTTDDQHDSSSEAKPRMVNVIK

PALSARNKHGRLKFCSRKIQPNGVFHDMFNVVHINTKWCALRDSEKTKAMFLIAVGRPQ

>contig46290 Frame-1R

MKGIAYDGSTRSDVACQNRSMSLSKQKHVRMGRSTQNASTWGLFVDEFVGKDEFIIEYIG

EMVTQEEADRRGAVYDEVDRSYLFNLDTKTVIDSTRKGNKTRFINHSSELPNCACKIMNV

RSDFRIGLFAIHDLQPHTEVRDEMV

>contig46845 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57897.1|) 1e-165

MLMYDDDDEEFIKLNNAVSALSDLNDIDQIPHDRSMRSYFDEIGLSSSMMKLCESGYANT

AGGPLEQISMRMTCRYEKQWIELEDEGDYRAVPSLMRFVDHFAAGVTTCLNWPVASVSYS

QSDRILVTSTTGKQLLCRALVVTVSTAVFSKIAYTPALPQQKLNAVASFDMRRAGKVLLH

MKGRFWPENTHGVICSDCFLPEFWINSTEGIGHLKANGDKLCVKNEIKNPDDGEAQYLIT

GFAGALYADKFVGMEHKLIIEGFLDQLDMIYGTLDEPSPAHKYFVKGTYKDWGDEPWIRG

GYAYPRVGQSDTASKDFAAPVNNRLFFAGEATAYEQPGMSVHAAVDTGTRAAI

>contig47011 Frame-2F

MPSKKTENDALIADRLAKSSADSAARPSLPGPIDSKVISSENEEMKLRRLPKGTFFGEIE

LVRPDGRFLPRIATYRCAEESDRPCKVLQFVADDYLNLKGTYESINHRLEKTA

>contig47600 Frame-2F|Blast-DNA polymerase epsilon catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY63268.1|) 3e-91

MIIAARPYGEKVTERAIPTAIFATEDAVMKHFLKKWLRDPHLQDFDIRSILDWDYYRTRF

ASTVQKIISLPAAFQNVRNPVPRIALPDWMRKQVREKNAKHQQGHMKQFLLGCCKRV

>contig47709 Frame-1F

MAITRPSDRLPLFVCVRHIDLTCCYPINFIARLLGEGVPHSACTTISFYLRLE

>contig48216 Frame-2R|Blast-tRNA wybutosine-synthesizing protein, putative [Phytophthora infestans T30-4](gb|EEY66227.1|) 0.0

MYVYGGRDAEQVFGDLHALDLRPHHPEWRRIENLPGISNRFDHVGAVVGSTKLVFWGGMH

SLEDVDCSIERDSGACVIFDTVSNTWTTKRLANIKNGSQPSALFSASASVISGHQVIVVG

GISSALLAKRVQAVQKIYLLDVGKLQWSELGEVKHKNAAFVGHSTTWLSTNNSLYILGGG

YQCFGFGQIYSSTYQCCLSVARPNEVATIVARSQLANTPALDRSTSLNVEPLGVRVDKEH

VKQVKSLLEKAHAYDKSRRIHVAEGILTNEKSESTKMFLIPVASNFREVIASTNDVELQK

LEIVIDNDVYLNKFGKMSGLNRNDVIRSAIEGFASKHYLSPEVIKAIPNKYEFIGDVLLV

PRDSFLDEEWTLFADKMWAFVCHSSSPTFTRVARKAFIDASEKRQSHVKLLYIDKKALVS

KCHTKAPGWVEIRENGIIYGWDLTRVMFSSGNVTEKARMAKIGCCGETIVDLFCGIGYYV

LPFLVHGGAAFVHACEWNPDSVA

>contig50370 Frame-2F

MRHRDYGGSSSRYARAGAFSIPDSDFQRGNTTLKRQRHLSPPRGARHTSRRSVPFKGMRA

RSKSHTRPLARKAPNQEFIPLGSNRLPDISTHDSNKASFHHREPSVALTRTTARARSRSS

GGVRQTLWTDTSQWVATGRHHTASIATRTRSKSATRG

>contig51049 Frame-2R|Blast-RNA-binding protein NOB1 [Phytophthora infestans T30-4](gb|EEY60575.1|) 4e-26

MQSAFGENVAHDLGVKAEKQTTIRVGYGRMNPNAQKGRERRGKKKRN

>contig51306 Frame-1F

MNSDAAQFVASCDRLIALLSENGFQASAEKCAEAIVEADAGEQRLKLLEAVTNKSLRCAE

LIAKSLETSATLSQLQNSLKNTYDQVLNGGSKEDEEMEDVPEDVPEDETTTLLLQDLVAA

GDEVEDATKTYARLGIVRKVADASRTL

>contig51535 Frame-2R

MQQKPLEFLSSSKQLGCSQMWLRYLQNGEEQRSSREGKRQRRTARKIVFKLLLKMNDLLP

TPVKKN

>contig52178 Frame-0F|Blast-SCP-like extracellular protein, putative [Phytophthora infestans T30-4](gb|EEY64510.1|) 9e-62

MKNLSLFAAAAVAVRGESYDELDQAIWLDRHNYFRTTGLPWSASNMRRIGWDAGLASKAA

STATTCSATTDKGVNVYLASSNDATSAIDDAIEDWVVETAFSTLNVMPQPGFSGLDVGVG

YYNSYSQVVWAETTSVGCASATCSDVILVVCEYSPAGL

>contig52196 Frame-1F

MSTAPGTDFKRQKCQKGLESNEQALSSKDNLTHDMNITRSL

>contig53047-0 Frame-0F0

MREFKDRPRCRHLGTFFGIMLEVRSDTPLHEICFRRNDD

>contig53047-1 Frame-0R1

MMPKNVPRWRHLGRSLNSRILLWSQTAITTFLRDRRQYEGKVAEQCRATVEVEALCCEAY

DEHSSHWY

>contig53717 Frame-0F|Blast-serine protease, putative [Phytophthora infestans T30-4](gb|EEY67871.1|) 3e-31

MLPTVEDDDTVQEEKAERKPRLIKLVSGQEEDHDRACIVSIRTITGYEQESEMPLLTRRG

DRLGANTVVLIHAHEVLANQLRALECVDVVVDL

>contig54217 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69102.1|) 8e-12

MPCWLSQSGERNATTYYSQGMGLWLNYTEHVGDPR

>contig55052 Frame-0R

MTALLPEQHVPNDLLDFENGKEVRTSEARTLAKQLLRTHELEVAVTQIKQLVKLMPLEQE

MDDNEIKWWTKYAVKVVAHAYALKKRNAKADKSLQRLDKQG

>contig57241 Frame-2F

MASNQSISKKKPTMPNKECPACKLGDDTHHPSAVKTTGCEESYLRVDG

>contig57425 Frame-2R

MLCWILASNGLQESIRLHPFTMVYERNYLLELSESATTNTGDAVK

>contig57616 Frame-1R

MLCWIIATDGLHEGIRLRPFTMLYERNYLLSLSYLAITHTGDAVD

>contig05595 Frame-2F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65627.1|) 2e-62

MQWDFGAGLSYTQWNYSAVTLDRTIVSGADDTVTATVTVTNVGDRTGKETVMLFLIQPIR

KISVPNVKMLKKFEKIELNAGESMDVTFTLSEEYWGVYKPQIGKGLHRIVEDTNYVVAIK

PDTECNVYGGPLINPLCAQFRINLSGLPAVSGPQSAKSPAPIDITGLNGPAPLVFTNGPV

PSHGEDSSSITEERIDTSSVTTEAPEPRNESAISDDVDLDHLPIPNGEVETLEYDTDYLK

>contig09146-0 Frame-1F0

MNVCSCVGVCQYFRDVHVAMCNGHMERIEE

>contig09146-2 Frame-2R2

MWPLHMATCTSRKYWHTPTQLHTFIKLDS

>contig09722 Frame-0R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY63309.1|) 6e-31

MTNELTGIILSFDAPGYPAIPVYGEVYLRTLGMEYTHRYYDIAALALGAIVLQVLAYGFL

SLLVPTHRVMDEHSKKTT

>contig11723 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69913.1|) 8e-90

MTDVHGELLKCVLQLAACSDKLRMTDAMLGNYLTRMQRDLPASGLPHLTSKLAVVPANPV

RPAQTLEEKFEEAFDQGMEATERLEVTKSRLEKELKRRSQNFRDLVKSRNTDIQEEYARM

LKELDDQVESLDHDIAKEREINADRVKRKRTVDCEKKAIKKRQLEGESTILKEQLDGVTS

EIQHLQRVFAMLEKEDESQESENETINAQTGKERQRLEDERAENEIIELQQEIVLLKEAQ

EAIADKINKQSLKAQYEEEKQDVVEEIAH

>contig12784 Frame-0F

MSDHDSDLDAPSIKGPRPPPPPTPPSLVTKPKYSGKARIIQSSVFSSRDSGRSKGRSQVS

RKTTGLPQPSTASNQDGAGSDPDPLHARPAHMLSVVELCTNNEEDDGGSSITPVFDTPM

>contig15712 Frame-2R|Blast-biotin-protein ligase, putative [Phytophthora infestans T30-4](gb|EEY59618.1|) 4e-39

MERIFLMHGFEPFVADYLARWLHTDQVVQVASGNDASGKMTSAVIKGLTSTGCLKARGDD

GSCLELYPDGNSFDFMTGLLKRKV

>contig18373 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59476.1|) 1e-14 NOT\_ORF

MRLIVYKEQHELWCALNDRFHAFRVIVRRLVVRYDARHVLPQNRLNVVRHITFDHLVSLS

HAIQAVEVKLQLATSRSF\*CSSRLEGLDKVFTP

>contig19284 Frame-0F

MGQDFQDIANALLFQIIGTARNSNTAVRQLGSKLLSKLSEVARYDLSLMRRVFAEMTHEK

ARVLILEQIRIILVYWSDEDVLVWEKDMLEMIRSGLEDQNESVRKTARETLARFSSRSSE

DLDRLVDMLSYHSKLGLLREHRESLLAEAVSQKHPELIAKVESKYRNKQDTFQPRGGIRM

SRQEKRKQTINIDAPVAVPLKQHESIAAYNHDSVSAKVTTLASDAAVMNVTLQGPNSKGV

NDEDDVMKDLRGSQMRNGNSQQLEIKSLQPLAPESRAISRSSSSASSEGQRSSISSIEKS

ALHLLGDQTVQELNVKTSTDRSIGSPINKLEETQESSGLWLSSPACSKETPRGDYDHNLP

VQLAKFDEEEINSKPLNTRDDFIRMPLTSSTVASTLPSTNNITLRPQREFSIGQDQDLLV

QSEDLNKSSPAMTTPAPSQKKIGMSS

>contig20352 Frame-1F|Blast-cyclin-C, putative [Phytophthora infestans T30-4](gb|EEY69286.1|) 2e-10

MKDVTKGDLRKRNPQDRRHLSDDEIDSIHLANIS

>contig21618 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65350.1|) 1e-162

MPSGRHVMALLAPLLMASMAQAKNYFNQSAGYVVEIATEDWSNYASNGGCVTCPYTCIAP

TEGYDGTRINASNITMSASLPSVYTQVRSNGCCYSATSVTQPSCSNEASPASAENCGFLF

GPTLEWRINNALRPLTDSLTAILFASTDCENFWAVGKQDIRYTSNTRSIKGSKMIQNGCY

GDPSGTPMVLSGCLTSQLVYSKTKSYTWKNLAEKCEGLAGRCVITNAVWEQHLKCCTSRT

GMASDWDTTYETYTKTPTSTTKLSGPAITAIVIGGVALLMCLIHFGAKVRERARQTALMR

EQEATDDYEEIMTPLTAG

>contig23928 Frame-1F|Blast-Argonaute1 (AGO1) [Phytophthora infestans T30-4](gb|EEY67432.1|) 0.0

MIKFTCTPPDQRKRSVEQKFLEAGFSRDPTLKAFGLDVEPRMVETTGRQLPPPTIEYSGG

ARENPRDGAWNMRGKKFNKPAQLTSWAVISMADARYCNQASIEQFFKAVMAQMGQLGMRC

PPKVPPVLLKQRREDSVRGMFQAAVKAATQTFKTTPQIIWMINPRMDAQTYGELKLMSDS

EAGMGILSQCMLSKHIPKCSPQYIANILMKVNTKLGGMNGIISGPLPIVSQSRTIIFGAD

VTHPSPMDKTRPSVAAVTASMDANFIRHASSIRAQGHRVEQITNLKEMVIELMGQFYRQT

RGKPERIVFYRDGVSEGQFHMVLNYEVTAIREACQALEVGYLPPITFVIVQKRHHTRLFP

DNSKDADRSGNVKAGTVVDTGICHPIENDFYLMSHAGLQGTSRPTHYHVLLNEIGFSADE

LQMLTYKLCYTFARCTRSVSMVPSAYYSHLVAFRARFFLVDGSDTASTVSGSTDTTLETD

CRMYNLHETMKGAMYFV

>contig24176 Frame-0F|Blast-phenol acid carboxylase, putative [Phytophthora infestans T30-4](gb|EEY63169.1|) 1e-97

MPCKSSFVNSCHLSQSFSCLSKFKAMPLQIPGYHSNTPLHPSFNDDIRDLHLLYDYDAEG

PDGEPEKWRYEMWFFSENRIVYSIHGGPMAGRLNYQTVAFQCIRPGELWQCNWLEETGTI

VSLVYDIKEQKITTMIGFSKGHWEHPKEAHGDKRNPEDYARWRKLAEHGTNRDRLILCEQ

ATILETFKGAGNLVPIAPDAETL

>contig24899 Frame-0R

MNDFDQHWWLHRPEPTVNEAPSPVTMADALKRISVEFEGESFLHRKRYLLEGALALPSSA

ALVRDPVHMQGRERPLGSTQKNQLKFEFVARTLD

>contig25157 Frame-1R

MHGYYKEKVIRCAWWVAGALKLMLSAAFKATFCFLNCELAKNMKFNSTAELAMVYVPVSV

ALLTACIQLLLVSRNGVKIYEFYLIVL

>contig27469 Frame-2R

MHAMSHKLENCRLAKTSTHSYNLFEDVAYINQLRTANGSALRQVYPFNYGPLQAILAWHY

FLLLWWWRYIEILMSKCCFG

>contig28213 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63793.1|) 1e-07 NOT\_ORF

MCCGLHGCGGEDWASFTTTKIIGDLPWIGRDACVQEIIRQVVAKTKDTNLPIIPDGDA\*F

LVYI\*PDIVKS\*KKRYPNPECSECYVMCFREISIHFAS

>contig29416 Frame-1R|Blast-20S proteasome subunit [Phytophthora infestans]gb|EEY54387.1| proteasome subunit beta type-2, putative [Phytophthora infestans T30-4](gb|AAY43418.1|) 1e-100

MDSIFGIVGKDFVLLAADCKVVRSILVYKDDEDKSINLDDHKVMVTSGPQSDRLAFGEYI

QKNMKLYELRNGVTLDGPATANYVRGELARFLRRAPYQVNLLIGAVDTTIENQSVPSLHW

IDYFGAMVNVNFGAHGYGAHFCLSIFDREWKPDMTLDEAKDVLKKCRLELDMRFLVRNGH

WAYTLIDASGISEVKVE

>contig32089-1 Frame-2R1

MHRSVMQSGIALRERVLLGVRHFCK

>contig33842 Frame-0R

MYRYRESIRNLRIPSRRCLIATEASGQSSI

>contig34061 Frame-2F

MQLQVNYFSVLLDGAPTEILKYHVDVARSPDTAMDMKYGPSAKENDATMAESTDDGHASV

HKVEKQDKDVEMSDAVAPLKRETRPERPLPRSLVRNVINAALRQYESDFNGIRVVHDGMA

AMYAPAMLPWDGQAKTFIDVNPDGISPTPPPPAAGDAPRRPFRGPRTFVVKIKLAEAIST

STLKDYYSNPDVNVMPVLQALDVAARHLGAQRLISVGRNFFSMKKTHPLKGGKELCWGYH

QAIRVADRKLLMNVDQAATVFYAPKELMELVLPALNARSANDIRTLSDRDGKNLARVLRK

IEVVPTHRKDRKRAIFGISSQPANQTMVDIKGEHLSVADYFSKRYNMTLRYPNLPLVNVG

SKRPGKENWLPIELCEVAPGQRCANINDLDTAEIIRQTSQPPRARQETILDQIRQAGFEN

DPYLAAFGMKVEQRLESTEARVMDPPDVQYANVSERPSGGQWNLRDKRFVEGATMRNWGV

VVSANVSERDVQSFIRSLLDMAGKSGLVIEDSNPHMVHGDQYRGAQVEELMKMCFKELEA

RNRGPPQLILVIKQDKSVGSYSDIKRMSDTILGIPSQCIVSQNVRNAKPQYCANVCLKIN

MKLSGKNSILREPLPLVSTAPTIIIGADVEHPRSGMGSRPSIASVVASLDRYSAKYVARV

AAQKASSDIQLLPHMLRDLFLAYYQSTNRKPEHVLYYRDGVSEGQHRDILLTEMRALRKA

FKMISDGYNPPVTFIIVNKRHHMRAFPTNSRDADRKGNVVPGTVIDTGIVDSHRFDFFLY

GHSGIQGTSVPCHYTVLHDENKLSADDVQRLTYHLGYTFARCTRSVSFATPAYYAHLAAA

RARFFLNEGSDGVSTVNSFNSNSSHFDFAELHNELKNCMFFI

>contig34429 Frame-2R

MFHLQHSSSTRSFQYWSWPREIETSLSKLSWSGNQRAVTWFQYTPAELPCS

>contig34780 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59734.1|) 1e-169

MDTPSEDVFDIICDLASNALKSPIAAVSLLDEDREWFKASVGLAQNEVPRSVSFCAHAIM

SKEPMVVMDTLLDKRFAKNPLVTGAAKIRFYAGAPICTPSGHLLGTVFVFDTQPRNTCDI

ATLEKLSNVAMKNLEDRKNAVAAPLDNGDAVEIIETNDQQAEGFKRPADSLRRSGIGIAN

QVVAHPAASASQDLVATNAGDGQVSAGPKMETMLMDLLCRTTETQQQLATQQGAMFHTLG

QHTADIDKLANAMARMEAKLDAMVE

>contig34964 Frame-0F

MYNAIASAMNTWNKTFRPGYICQGKVLGCTRFARLCSS

>contig37576 Frame-2R

MPLLLRSTAPSPSIDELVFTSSAAPLSSQSSQRFSSSAMPTLPRCPTHGRLSLSLRRRRS

TVGTETEFSTCLDDAGNVLKDLPIQRSSHQGKLRDCASGVPGTKDTEDFRDSKLSHCTQL

DEDHASSDGSYLTEAERASNFLSCSCSCIDIDANDFAVTSSSVIIEDR

>contig37947 Frame-0F

MEGSQAKDREFAVSLRSVKSALSN

>contig38201 Frame-2R|Blast-alpha-tubulin, putative [Phytophthora infestans T30-4](gb|EEY54333.1|) 1e-105

MVFNAVGGGTGSGLGSLLLERLSVDYGRKSKLGFTIYPSPLVSSAVVEPYNSVLSTHALL

EHTDVAVMLDNEAIYDICRRSLDIERPTYSNLNRLIAQVISSL

>contig38274 Frame-0F

MKKMSRKPFRSGPLFSSKASSSTASSNSSPSMNNSGSGSLMRRATWADKIREKLPPLGEN

EYEVLWERGVLGVIFLEREKDGIPYVSKATESCISPAVSQGDILTYVNVVRSKDHSFSDF

FKILATMKKPVLLRFERLSASTPPSDEDDTSELFNMQHSSLSNTSNIAGQFARQNMPNLD

EGDPTGKHWRADSAPQKDQKPPKATRGAFWRAPSAKDADKSAQVAVSNAGHERSQIRRHV

PSSKDQQASPEGVAANRSETQTSHPPL

>contig38432 Frame-2F

MKSNLPATPTPIGSRDMHLNYQSPTADKAQQSLRLQVAAHNIKKRAACDSPVASDDTVSS

MPVTTCSFPALSRHFHLPLKMAAEKFGVRATAFKKRCRAIGIRHWPYRKVRSLKRSLQEL

EQCQQQAQDGSGPPLSEKQLRQFSSYQSQLKRLLSPETYGIDPFRQMLPGHFFHGDGFDG

GHTLDDNDSDEDSCRSQSPRPRVELIACINKARKHLFTDSPSSTSSPYRDNIVIGSPIAT

SATSEYNRLYSNFSRTGFVPPQVGFAFDSMYDPFGELGTSSMDPYGQYDHPSSGYSLDTA

SYDFFSLQPSPTMAMREFNTTARHLSLSSRPDEQCALNGLDGMDDDIFRHISPEYGCLV

>contig38519 Frame-0F

MTLRLLCLCAGLGAYLCSSGLLRLNEVFFQSATADSLNKSNAQFDRPQKLDAAYDRLVIV

LIDALRADMVLGSAAMRKDDDITHVFSKKELNIDMPFTSSLVTSGRALGYVAHANVPTVT

MPRLKALVTGKAPAFIDILKNFNSVAIDENANLLSMLTAKGKRIVFYGDDTWLKLFPNTF

LRSDGTSGFYTRDTKEVDDNVTRHLREELDPAIHNHKSQDWDVLVLHYLGLDHVGHLRGP

RSLLMEKKLQEMDKIVQLVLESLQAQDALRMQKDKSARASLILLCSDHGMSEVGNHGGAT

VEESSALLMFMRGDGKPLHPLRDNNYRQKRNQVDLVPTISSLYGLPIPPYSTGLLLEDVV

RASFEANALSNSSYWHALYRNFQQLHALATIKFHATALKKFDDEFHVPLDLLRKSLRDDS

DMDLFDQHAAKEVERACEIMQAIVTQSDGSEYNVTVFLLGLAFLVVSLTAALEMLARALQ

KKSEPFLRNIHVVVLGVNSILQIASLSSSSSIENEHATTFFMATSLLIAIGIALIQIQKS

YEALYSVGLVIVLLVFTRTLRARNQIINFWRLNGLKLDTNVPGSEFATDDSV

>contig39365 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65150.1|) 2e-09 NOT\_ORF

MSLPRGRRRHQDKWDRVWCIGSSICPIHIWMTRNA\*VYRGRG\*PNRDTAQTIWKAALRQL

RAIAKRDHSRPARKTKGARLHACL

>contig39435 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68130.1|) 5e-18

MLSSKFSRTRLRCQSQRQFWGHPSNFLAWVGFNNRTNSCPSLVPSSSSKDELPAITPSLP

QALPLTNHFAAKCNVRPSLPADVAVPKLQKLVDDCKRKSAAQALDRLLHKIRHVPTLTQL

LDAWLVVSQCRPFVVETDMSFRVRLATVEDVTTEKP

>contig39996 Frame-1F|Blast-histone acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY54596.1|) 1e-175

MMISRDDMAKVEEDSGRLRFIVITNDETDEHMIQLTTLKNIFAKQLPKMPKEYIVRLVFD

KNHQSMLLLKNNIHVIGGICYRPFTANHFAEIAFCAINASDQVKGYGTRLMNHLKEYVKT

KGITHFLTYADNYAIGYFKKQGFTKSVSMDRPNWYGYIKDYDGGTLMECTIHTQINYLQI

TSMIQQQRKVIQDKINQRSRASTVYPGLTTFADDRVMDIYMVSGVKEAGWSQATIRNNRI

GTRDQGSLKSQLLQLLKAVSNHRSAWPFHEPVDTSVVVDYLDHIKEPVDLQLVSKRIDSG

AYLSKAALKADLEKMCDNCTLYNTPDTNYYK

>contig40589 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61852.1|) 6e-38

MGTVTALNVWEAGIRPGDVLETVAGKKVHAMDTEAAIVLVKMSNSPSIIRFRSSNCGNRI

RFDVVLARQKLGVVFMGDGIRDVPVVTRVVGQGTHNVNGDFSSPSRVRVGDVLVAVNSKD

AIAAGLDMTTKYLETCPRPARLTFER

>contig41061 Frame-2F

MGRIGSLVDRTEWSMSSADVNAYYEATANKIVFPAGILQPPFFGQNRHPARNFGSIGSII

GHELTHGFDDSGRHYGGDGNLVDWWSHATATEFQERTSCLVAQYNRYQVNSSTEVDKLLG

HVNGNYTLGENIADNGGVKLAFMAYHAFLAKKTRQLHTSVIDNTKEATRSSEKHKLPPVV

ADRLFYISFAQTFCSKKSDASAIRSLASDPHAPERWRINGVASNSPDFTQAFSCPAVSTM

NSKTKCQVW

>contig41292 Frame-1R|Blast-enoyl-CoA hydratase/isomerase family, putative [Phytophthora infestans T30-4](gb|EEY64059.1|) 1e-118

MSLINLMLASSSSARTVPRCFARFLATQAKATQFKVEALHGKDTGIVVFNMDRPNARNAL

GSQFMAEFRQALDQVRFDPTVRVIVVRSIVDNVFCAGADLKERIGMTPSEAAASSRSYRM

GFLDLEQLPMPTIAAIEGAALGGGLEMALACDLRIAGAKAILGFPETSLAILPGAGGTQR

ASRLIGISKAKELIFTSRRLNSESAEKIGLVDYAVSEGKAFDKALEIAREILPNGPVGVR

MAKEAIMKGAEVDISSGMAIENACYAQVIPTKDRIEGPG

>contig41964 Frame-2F|Blast-peptidase, putative [Phytophthora infestans T30-4](gb|EEY53249.1|) 4e-29

MPLVTLNVYDLSHGMALQLSPALLGKTIEGVWHSGILVYGKEYFFGGGGIQVMAPELVVQ

RYGMQPVRSFTLGETDRT

>contig42262 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63806.1|) 3e-78

MIAYPKVVAGLYAIIRTLRYLGCALPVEVWIDPTEMRPKHSVLLELVKYYNVVVNVIDDP

NASKFLAKPYAIYHSQFESLLWLDSDNIPIRDPTYLFETPEFVMHGAMFWPDFWRPSIGT

PFNVHHQSALWTLLDMPFIDMF

>contig43243 Frame-2R

MYHEGGVLRHNFDCVDEIFQLCLLGERPSTLWSDTWPPQRIDPLKCAPRRRHTVVVSTYI

CAKTCIENGLIFSFFFCVRLVVISNGQR

>contig45627 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55641.1|) 3e-42

MSDHTLAREYDPLFSRSYAASSATSTSTAPRCYGGFEQQKRVWESTARRSQRIRLIAGLQ

LLLGLLISGNYLWLSNIFMFIVGVVGLLAVRSDRMSWTIV

>contig46019 Frame-0F

MGEEANLVNAGAIKWHRNLSAFVWAQAPAMNQCACVVRTGATTPRQDQSQVCDPPQQFEN

FMFDLLLSQK

>contig46086 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53886.1|) 2e-35

MENSRNSGAVKEKAHEKALAKKQNMFYRMATMKSTPWDSEPKEREAKCEDLCMLNSFWEF

QQGRNCYNNPSELCPVYKAGLASMDVVLTVTECTCNDSPNTSSTNSDD

>contig46132 Frame-2R

MVLVGNSAEDIIKWREERRKNWFAMSQQPKPMPTPSAMVAAKRKLSVSSDEDLEEGEIEE

DEEAKAQVALKSVAKIDTGVPSIATHESPVDTHEPPVKKLRKTMLCKWFSRGQCRFGETN

CKYSHDRSSFACRAMMFKSSCSKGICCPFSHDTAVLVGSRERSLKVSKERDAEQQWRGER

KSLLRKLLAKDVRVEQHKMLQIVRYLVANDYLHGEEAEPVLSIKLLGKKEMSLIEASEPI

EVVSDESTVMDEASIDAKEGPNGRSEPLVTIVTSNLLLPKVEASPCESQVDSTISDSDKM

SNTVKGKEERVKDVASSADAEPVDPEKDRKALPMEEIVDNALDCNQLSDTVY

>contig46297 Frame-1F

MSQSSAPPSAPDHYAPDDTKSTQASHGSASLLWELPTNRCPIACEAPIILDPNDSWIAVN

GSQSAVLVQDRMQVTWTDLHSTKGTGDTSLRKVEALVTVQAMALSACGAFLALVNAEGML

SVYNLHAKRVLKHAFDIEHSDRIVSMQFATFDEQKSSSVALELVIVTKLGFLFWLSDLNL

PQLEKSHNALHEIAQDICVKQLRVGCLQDHAKSRMLVHQVSSEKCLFLGNHDAFVSMWQL

QKTSRHFE

>contig46842 Frame-1F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY70363.1|) 4e-06

MDAPASDATVSLTPVAVNDSIQHPVDVPTSFHAMRSPYRHRRRARQASITREGTERQSPP

PPLRHDLLLVNSTETPSYRLRDVSVNLKGRTHSSQVSEPSSERTNQWPQPL

>contig47016 Frame-2F

MQLNSRRPVLLQKPFFGIGKMLIETPSFTQQRHRSSFAFAQKTSPPVKFISLFYIPNATT

C

>contig47089 Frame-1F

MISTSAPATTAPSPVCHHDGHELWEAVTNNSSSAGSQEARIRVSDLNSIASTLKDVEGVT

NAMQSLRVMKLPPTADDGGNYEQQPFTSSAPVGTATASAHGPLDPVLVAGLENARERMTL

LQFEDQIVRFLRNTKEPHLNFPPL

>contig47607 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63149.1|) 1e-24

MARSFRFARLRGALGTAVACGLFESDTMTHANSCMLRLRELEIGVTVQADENEGSVAEKF

VKQAIDLLRRVSLDMATCVE

>contig48264 Frame-0R

MHELVSQRTPWAYDYFDEEEVPSDEESEFDPHEKVNTLEKDGLCHKEQDDIDGDATCIGA

FKEKCTSEAATTSKGKRSEEFIVNEEVV

>contig48772 Frame-2R

MAAMQVRSAMHRAVKFLQNKLATTTQTPALIFVPLALNGASLPFPSNLLSDAIWLAAPKS

KVTPSRKKIRNNDLSKRLKNIVHFQDCTMCGEKKLRHRLCMSCYKKGKYFV

>contig48879 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67126.1|) 1e-124

MTGIVDDEQSMERNEKNQDRIDCVAQLASQAAAIALNGAEKFKGRAMKGLDRTSPQILQA

ASFDRQYIEAIKQAKEEQHLLLFKRRGREAELLQQVVAAPKDDEESVKRRDTIDSWTSLH

GILTEKDFQVQTLIQENKILSETIKESKARAAALVKAYSACKLELANVEAQTPQDEKAQM

QLVQLRELVIKSEGLKQERHDYRTMCRVELEDLKKRVEKLRIQFAEKATTQDTKALRLKK

FEQVHTQMAKKHKEMTIAAAKQTRALQLKMKQIDEFPTPMELVQYEKRFLELYDEVALTL

DETRKYYCVHNTLKTTHDFLAKEVSLINSIAENFDVAMGSKTSTQAFFKQIESIIQNLQE

TLVKQQSVRNEHQLCVEALECTYHVLLEQERKYVNAVREFQKECEKNEKLVARLKGP

>contig48905 Frame-2F

MPLFSLSPSFRPIPISVYRLELADRLISSPIGDPLKEVLCVVLQCKHVSTHSSE

>contig48992 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58068.1|) 5e-43

MSLPHLNKSPEFLQLDRPNVRRVVYEVKPESMADASGYQEFVNYLIQGRNGHARAGGAGE

MDPQGFKVFILPPGQASRQLGYEGDHMIVVLRSR

>contig49199 Frame-2R|Blast-phosphatidylinositol kinase (PIK-L3) [Phytophthora infestans T30-4](gb|EEY66032.1|) 3e-20

MAETDANDSSVSQVEPLQKVMSQDAVKATQSQLLQVF

>contig49317 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59883.1|) 3e-34

MLIDPEQNKYCCLRDALRADTYQVGGMISREDMYYLAILRRIVAEAKLPLVDGPITVLAL

GNIIPDEHYHTSKELFSIGFETLVKVYISKPVIIAFQLRCST

>contig49876 Frame-2R

MHATTYLPLLSNGNVNSLDPPSILQWLQYCNIYLPSLSSSKCGLEVEANVFTKVETVLNE

IGSNVPAKL

>contig51301 Frame-2R|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY62213.1|) 9e-53

MGGNCGDRVILQNGFYIHPSGFHYTFKCMQVGVGVVSSLLWLNHPIHSGEDSRYG

>contig51486 Frame-2F

MAAMNKPTYMAIQAHSIDKPVVIFVSSKAQTKLTALDLIQFCVASNERDESKRFLRMDEA

VMSTLIQSSQIKDETLKHTLAFGIGLFHAGLTRREREVVEKLYTDQLIQVIIATSSTAWG

WTLPTHLVVIKGTEYFDNGQYRSYPLSDLLHMIGRAGQYNVDDTCVACVFVEEGTKNRMQ

RFLEEPYAVESCLASQELTNHVNAEIAAERIGSMKECVEYLTWTLFFQRVMSNPRVYDTE

EGSPRTLNRCKDDVRGTFLYRLIQSTMDALVSHQCVVLKSSQCFEPTFAGKVAATLYVDV

RTVSKLLTAFQTCTST

>contig51837 Frame-2F

MPRELMIIEQYSPFQQDFVLASLFFSKGGGDILSACVGRSHFISSSAIYYDRRRNYTALE

SGPTDNITVQ

>contig52191 Frame-2F

MWKWQSRNRTLEHATRLTELMHDSVAMLETDEVVYLSKPQRGHPL

>contig52887 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60433.1|) 2e-25

MTSIGSEKEERTASGGICECCHHGAPWHRLGGGTVSENTQSGYLLSQKGSKGAIRKNSSF

LRHSIESLGSDYYDEYDPEYESDESDEDDAIANEVARPYLMMMRTPTPSLTQLFTRSEGM

APRRESLVSSKERFGLPPRL

>contig53710 Frame-2R|Blast-oligopeptidase A, putative [Phytophthora infestans T30-4](gb|EEY64174.1|) 6e-29

MSMSSKMAPSIGAIDTMHCDLREKCIAIARDEVATVAEYAKQHGQTARLAPWDLSFWYSL

CHLCFVLLQIDTFFLIAIGRTN

>contig54881 Frame-1R

MIESQTRARRKANLSKFCKRLHRLNTTNSQICVHKHRLALDCSLTFRYS

>contig56599 Frame-0F|Blast-luminal-binding protein 3 precursor [Phytophthora infestans T30-4](gb|EEY57932.1|) 1e-116

MVLTKMKQISEGYIGREVFDAVVTVPAYFNDAQRQATKDAGTIAGLTVQRIINEPTAAAI

AYGIDKKTQGEKNVLVFDLGGGTFDVTLLAIDGGVFEVLATNGDTHLGGEDFDQRIMQYF

IKKWKKDKNIDISK

>contig57246 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53367.1|) 1e-156

MAMMKRRREQENGAHADAIDKAKKQKMVQAGGKKYMNKQRVLVFCSRGITTRYRHLMDDF

LKLLPHHKREVKLDAKDTLHVVNDIAEIKGCNTTIFLEARKRQDLYMWISRIGTGPSVKF

LVQNVHTMDELKMTGNALSGSRPLLTFDKAFDDVPHLQLIQKLFTQVWGTPKAHPKSKPF

IDRVMSFYYADGKIWARNYQLADDAETKKAEMAAFHRGEDLVQLIEIGPRFVITPIRIFD

GSFGGQTLYQNERYISPNENRRDAKADKRDRYVSRKTAEVGRKEREPERLLPEDQFADVF

AGTG

>contig57880 Frame-0F

MLRRRALSVFSRSTLLSPRSRALHLQATKASIE

>contig58760 Frame-1R

MEFVNGGRAVNGYVKRAYPLQSVGSVSAVECSTSTIHGD

>contig05240 Frame-0F|Blast-60S ribosomal protein L17-2 [Phytophthora infestans T30-4](gb|EEY65827.1|) 1e-102

MPSYSQEPEDAQRAAKARGSHLRVHFKHCREVCHAIKGMPLNKAKLFLQAVLEYKQAVPF

TKFTGGCGRHAQGKLRGAAGDKCKWPQKATKIILDLVKNAEANAEVKGLDTDLLYISHTQ

ANAAIKQRRRTYRAHGRIGPYMSNPAHIELILTEKRANVAKAVEESKPIKVSRKRQAQLR

LKSGGGVPAN

>contig05594 Frame-1F

MTAVLQSLDGKVPAQVDEETASMIKEKCDEKSISSEPDPDAELLNTQVFMQENHDTTFNE

SLIKAHVKSYSTHNQSTSTQEHAPFQAHASPTFKSIPSPTNVVKPFKTTENTSDPLDEFR

AKGPEGKFTRVFPSVSKLVESDGWQIAHGLNTLFCAMPGVQFFNFKPNINVFDSKRKACW

KFIQLVGATTGDDHDDNGLWDLLWPIAENEFKWFTMTCGTETWYVKPQTKFEDFIPNETV

FQSKKKAVLQCLAEEVGDIPLGESVEGFQVLSFAPLPKVESTVTKAKTSLFKTPSPAVKQ

IKGVQDTTAKSASFVTPAKHTQVASTTSSTKRKLASSGKRSSGSLKGKPSKVVLKHTNLR

KQETNEPSVSENTTSLDEFHFLAPEFRCSFGIVYKKLQAEGWHCKSGTFEYDYFAPTYTK

ATKALNVNYFHSQADFEDFLKVSGTWKRIENELRNEHDVAVEQERELALERHHQRLEQQA

ARKRSVALYGLSSLPKSKKVKKASKKATRGDVARSPLITQAKVLKVPSMKFGTVLKKLLA

RGWYYRPGRFEYDYFKPSANPKTAISGEDRFESASALEIYLKTTGLWEQLADEVAQDEWD

ITETVEHAKQTKVTSPLMAAAVVSKKSPSHVVEKDVVKALTNDIWANSHEFDFNE

>contig06757 Frame-2R

MKTRHPSQIVGLRSFSLAVASSLSSRTARADLLTLRRSKKCYQTWKKIYKNTSFAIFEKW

MRLVYSIEWFRTKQLRARKLKGQRKTK

>contig09147 Frame-2F

MGISLRQSRQQFAYMPLELKQLLRHKMHEMASEFGLDDLFYGSFQRQFAFQYQLCAADAV

YGLQALLEAPERYIASVFETETRAREKALVTLFAQDTSMSSSLWETQDPDGNTDSFRQHN

FMLAHTALACHSVTSSKLMESGIQVAMALKQAIVRVGLSIMQRKLLVRVKHFRYVCLHVP

ENEQELFANANVLTQLALFLLNVHRASGKWGGPPTRGRQKVVNEENEDEEDRDEDVHETT

SAIVPLVLITRNPQENCFLVIGLTCPSTPGEIHRNTLGTAFKLAAGETGANFRQDGFTSA

VMEIQIARSKTLSSNFTMCSMPNFISRKNYLIQLPKRHFRQLFPLLAEKGMATQLYIPII

PLQQYNIFFCNTQCIIATTTLPLSTELPFSHKWHVAHAKQSPLGKHISLPRNLHKHLSSS

RLIQWQHKSATLGQLVQKCLRWTFCGSTNVDKMKWRFIGQSVPAIVAPHRHNSAF

>contig09828 Frame-1F

MNLRVLVLAVFLAATTRGDLATDDVNSTSLRLPSIEKRADGYGNAFNEEKVLNLRQITDP

SNFPNAHKKHLVAAVSKFWVKPRIPQEDLAQQTFKVFHVERVKSNLFTSKRWIKWVERVK

VAIPDRTKRDEELTRIMVEEFGLPLFFQKLHEASKNPETSETAKYFERLEYDRLLKNKVF

PEEFREQLGLQHLESDIELTRYYLKFRSRFLMLATPVEELKVPKLLKEVMDEPTKRTIEL

FGEFGKEEPDMVAKMFELKFNNEREVEHPLFNIWIDFMMAYLDEKFVASATFLQTFRLLE

SSAAAGNKRSLQIKETFSRRWISSDRSLKDVAKMLQLGKNQADSSWINRLELQLYMSYMR

KYILTHRKADPMLSWVLSKLVGLKHERSRKYQTRFVNFFRDNFQPSEVLTILRLDNEGGQ

IKNRPLVEFGLQYVASFLLKNPKAEPSILKTLKLLCHQGNSDDMFAFAKLWVSLETTPET

FLKILGIKKIDASILNHDLRDLWLAFLAHYGARLPSQALPHEMLQTINHLTTSAMMDNRT

SREALAKIFHFWSRKDLTQDDMFKMLRLHTFRPHYFINPLLSTWDMYQLTFVTMHPTEPQ

QQLSDMIFRCFNVNDVEKLTAGAKHIPDMLHSKVKTVVKELQDKVDHFFGRT

>contig11379 Frame-1F

MPNCRKVLGGTTASRLMTMSIIEEEPCHMRESRLDELEKHPDHIMPSNDGFEQAMENLSL

HSRTKSSPNAVDSRPPSASLSYTSAKKKMNMPADNDKEPNARDSRAVSVPHRSSRLDFRH

DVSEKRHSRHYASPSRQDQFSRNEEHYSNDMSMNQEDATHTRTWTPSSSEEDEHNRKHRS

LQNRLKKSPKNTHAIATSIPLPSSKQKLVPRQTAKSPLRSLDRKLRKNKLIKIDSMHSSN

SRNDNQSLGSRPSSKRDSVMLIKTRAKSSPMLPPFREPYAERQLVLSNAPQSNTTNLVRE

RMPRKTPRYNSPSRTSNSHKPKAFPPQSSQPCLTDIDMYEDLRAQEIKEATSSRRKRLES

KPRARLPTYTDDSRQVSSCRESKTYVIVSPKKLNSANAAEAQQFVSRNPFLSSHRTRSSS

LIPNKSPKSFPKNTTVPRSASASNLSSHGSMPSSPRPSTPHTPLRLRHYEGRFSNRRLQT

LFYFSLFPAEKAPLRGIVLCLHGIGDHCRRNVNLFERLCREGFGVITYDLLNHGVSDLDQ

HKTRAHIGNFRHLVDDTNDFITFAKRFIYVDALRYWRTHYCVDNQKTFSDQTLQPELPLI

IAGTSFGSLIGIHTILAGEHTFHAAVWGSPTIGVTWTPLLWAESKLSKPLAAILPTAKVV

PAVQHDRLCRDPKFLRRFKADPLTSMDMITTRTGYESLQAMALLQDDKRVTDPGSAFCAV

STIFLAGSADGISDQQAALKFFGLMGNFDKEFKLFDGLFHLVYEEPEKEDVFRYLARWLH

RRFPVATQVSDM

>contig13562 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56981.1|) 4e-41

MNPTRHLHAVFDPDGHKLVELPNGGRVAIPYDPLDEAERFAAEAARHIAPPDELRCRYKS

TRCINLRAKKRRGELHNLCQLHRERANQNQRNSEQRKRHCRQPIQGIIQRKSECKQHHVN

DHNSSKRTICSQMYIPEPFRTADGSSFEPTFEELTETALLLSFSDL

>contig13801 Frame-2R

MPQITQAALSNVVIKKALMTTTYKSNKI

>contig14466 Frame-1F

MASDASTFKGALGWDDWIWYSAFGGVALLIFLLLLGCCVCVQRAKRKGRQEALATLQTNV

SRPNPARGPSRPQRVHSTVQRYQPPVYDNAAPSPSRGTRGPSGVSETTRALFSRQNSESK

PYPSDKLQHTNQMRDHRRQQASPNAYMARYGYEAAESLDPLSHTDSLRDMDPYSSRVIGP

DNLPYPVVTSPTQYKDYRYSDQNVATSVIKRPAVVPSKALSSLDPRTSTSSKASSGTLQA

RIDALRAAEPRSSGPNDLNRPSPGYSRAMSTQDSYASTLARRSGLQMGSVLSPHAYVATR

SLQSGQSDDSYGSDRSMPNELVHSMNSDISERENRRPTTPKRATHGRGSIEF

>contig15713 Frame-1R

MFSYQNRRNNDALCHRAGISLRAQNILKADRRRPIRDINPNSC

>contig16455 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64213.1|) 2e-51

MSRATRRLAPLTQISERQALLKTVPMRSCNTMFVPPPQLPFTGFELMFLGTGAGSPSVRR

NPTSVCLRLARSNWMFDCAEGSLRQLIKSVMRVPLTTKFFVSHLHGDHLYGLPGILCTLD

NHNAEYKDPQSKESAPRQIDIYGPLGLFTYLNTAFFTSSARLVNLNITVHELVCPFTLSK

MSRHEKYTRNAPKHP

>contig16738-0 Frame-2F0

MRRMWGRRKHNGIEQAHANTTLQQLKATESAGLNTKAMLVFANLPDEKDERGWRDFFDSC

IYQIEGKDSAATLVSSMDSRRDIAFHVSHTRIDM

>contig16738-1 Frame-1R1

MRHMECDISSRIHARNECCRTVLAFNLINARVKKVPPATFILFIGKVCKDKHSFCIQPCA

FSGFQLLQCGIRMCLFNAIVLPTSPHSSHWIACSQVRQYRVHEQC

>contig19285 Frame-2F

MGSIATFAATETPKHEDGINRLNASFHQVLANSEQPGSTEKLANGKMVSLTELLSYADNT

DKILMALGTIGALAAGVSQPIQIVFFGDVVNTFNPSSPGADIENDIQSVALNFVYVGIAV

FVAGTFQVACWTITASRQAKRIRSEYVSAILTKEIGWFDVNEPMQLGSRVAEASVTIQEG

MGRKIGDGLNFFSMAVSGIVIGLVKGWELALILLAFTPFIAFTAFFSMKVLSSATQEGLD

SYGKAGAIAQEALSNVRTVHMFNSIDHFIAKYQNALGQSTVAGVKKGFAVGWGTGLMFGT

IFLTYAGGMFFGALMVANDNLDGNVCTGSGCYDGGRVLTVFFAVIMGAMALGQAAPSVEA

ITSARAAAFPVFQTIKRPSLIDPLDDEGKTLEKVRGRIEINNVTFAYPSRPEIQVCRNYS

LTIEPGETVALVGPSGSGKSTMVSLLERFYDPLSGSVTIDGVDVRLLNVKWLRSQVGLVG

QEPSLFATSIMENIRYGCPTATDDEVIEAAKMANAYTFIQEFPQGFQTEVGERGAQLSGG

QKQRIAIARAIIKNPPILLLDEATSALDTESERVVQASLDQLLANSHRTTIIVAHRLSTI

RNANRIAVHSGGAIIEIGSHDELMKRENGHYRLLVEAQNRVASAEIEEVAPKALNEEKTR

ADSLVRSGRSSGRSMSRHSTSEMERSLEDSQSDDVSLPPVSMARVWKMSFPEWKYMVAGS

LGAIANASVFPVWGVLLVKVTVLFFKTDITKSEMMTDARWWSLGFFGLGVLFAGSITLQH

YGFAVVSQNLVTRVRLMTFSAMLHQEIGWFDLEENSSGALISRLATDSAVLQAMTSETLN

RGLVNFTTIAIAFAIAFYYSWQMTLILLAAFPVLAASSYVQAQQMTGTSGNKKNNDADTA

AGSLLSEAIGSVRTVASFSMEAALNALYTGYLNVSKEADVRIGIVGGLAFGITQGATFFV

LAVLFYVSGRWISREIITFEDFFMVLMVIMLSTFAIGMAAQGATDGAKAKRSARRVFGVI

DRKPLIDSTASTGRTLDHVDGDIEFRNLMFMYPARPDAIIYKNYSLKVARGQTVALVGAS

GSGKSTAISMLERFYDPAAGVVTLDGNNLKELNLQWLRENVSLVSQEPVLFAGTIAENIE

LGKPGSTREDIIQAAKKANAFDFIQQFPNGFDTDVGDRGAQVSGGQKQRIAIARAILRDP

AVLLLDEATSALDNESERVVQASLDRLLALKQRTTIIVAHRLSTIRNANLIAVTSDGAIV

EQGTHDQLMQLPDGIYKRLVARQMNAH

>contig21149 Frame-1R

MLTLELPHRQHHIYTSIREQLNTNKLIQDPPTIREEAGHQVSAIIQRKETFQFLSTSMQK

IKLGYPIHKLEYLIHKPVTFPGAVFFKQQDIMPGVAGCVLHRFPPSINQVIYLLISMIFK

KKHFAISPFAFSF

>contig22799 Frame-1F

MENDKFPLRYYSYLPLIWTRLLVLERRSSWRRF

>contig24807 Frame-1R|Blast-calcium/calmodulin-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY69769.1|) 7e-73

MAAFIQANGMLKGRCGTPGFVAPEILCAGKGEAYPSGVDMFSAGVVAYTMLCGYEPFFGV

NDSDLIQMNKLVEYEFEEPEWASISEEAKDMITRMMEKDPYKRITPKEVLQHPFLREATV

ALEDLFIRL

>contig27125 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY61222.1|) 0.0

MSTPPPIARQASKSVADVEVLPVELGHVIWVPGTDRVWDKATVMTIGGLKVTVRTQAGKI

QQVDRGLAVPQNPREADDMTSLYYIHEAGVLHNLEERCKLDGGDGRGQKPYTFMANVLIA

VNPLRDLPNPRISGVVNSAGSSPHPYSIAEMAYQQMVYNSGTDQPTNQSVVISGESGAGK

TESSKIVLRHLTTRGLYGKKARGEEIESMSKTRQEHGTSLDHRLIEQNPILEAFGNAKTL

RNYNSSRFGKFMKLQFTADGEFKLAGAFVETYLLEKSRLVYQVDGERNFHIFYQLLAGAS

SAARQEFELLTAEEFCYLNQSGCYIAEETDDHACFDAVVRGLSCVGIDEQVQHVIFSVIA

GLLHLGNIEFVEEDTSEGEAAVIDKDSAKHAIATAARLLGVKEEELWKVIMTRDIVTREE

TYTVRRNEQAAVYARDAIAKALYSRMFDWVIKQVNSSLGHDPDPLPYIGVLDIFGFESFQ

RNDFEQLLINYTNEVLQATFNNQVFIAEMELYKREGITVGKIKWPDNRECVDLIASKPNG

ILCVLDAEAMNPKPSDVKFLRTLHFKHSKHPYFPRPHPKDMEHMFIVRHFAGAVSYTIGA

FIDKNNDSIPADMSNLFSGSSNKLVPAFFKQEPDNSRPGKRKLPKSVAAKFSNQMQELVD

TLDATRCNFIRCIKPNAMMRVGMFDPRYVVGQLRCQGIMQTAQVLKVGLPTRVSYSELVG

AYKKFMPSDAQRLFANQSDPTLITAILWAFQVPMDAYKLGITKLFFKAGKIAVLDAILKI

NWATEGPHIVSRMKLWLARRRWRVGLAKVMAQNIFSKLLRRIHFRRNSVVRIQRWWRALS

VRRDFKKKRSAVVVVQALFRGMTARRLFKSKKQEMLALAAARAAEAKRQATEAKRREEEA

RMAADIARRESVARAAAEGDRLRMEVEARRAEEEAIQLAKEAAAAVAEAEAAAAEATAAV

EHERQAELRAIAEAKELEERMDRERQEAEHRKAQALLEAASISASLLSGLAQVNSVQTAS

GQVHVVEIPDNISQENREQLQQLNDLLLSGAISQSEYDELVPFLLEKPDLAPSGAALTAE

QEESLSRLYTAGVYGIQIRCPACGATNNTANGNHCDDCGSLLTTSDDSAAANANSGYSGY

GDQSRRQRSVSTLTAPLGSFTTENGRIVIHDGFFEAQMHRTQILQDDNYTEYTVYVLRCQ

WQPKESSEATTWLVSHRFSVFEKLHKDLKRKIPAAVASIPLFPRKHVLGGVFKGKTGNSS

SIVEERKQGLERYVAQILDLCARLPENLNVPELDRFLNVSRQVEQHRRQLASGSGDESGA

AGVSSRALNVSAGGAEGMAAREQARLPTELPTPLDEEELSHTEQAVALLNASIRSARGDL

RRDSQVQHHLKVCVQLLPRLQISANLDNPFANVDLIPRAMQCQEDLEMTMGLYNDSLLAV

TETYALSAQESGGVQAPPPYVPGQQNSYQPSYGV

>contig27150 Frame-0R

MGLFNPELLVGILLVFVQLRLRSYFSIATWLVNNLTFFLPPEDELIATLNGQPVSKGSKT

AVAQPLSAAEKMEIFYIRVAKTEHGVFNQTLFYELYEMFVVLVSSATIGSFIGSILTFVT

PWVTPEATDHADVITYGLVSALLVALYFPLQLNFAQGWAGYEARLGLAIGFLGFILSGFL

LFAPKGLFDFNVEAVAPVPSNRVILLLRAVGFTDADLVRLAPFIEVPKVSLYVSLTCLAA

VFTCTTFLPSFRFARMYSAMIQDKQVSVLQKAFLHLNSVLPMLLCVLWIPCLSSHFLVPF

ELVKCSPRALTRDCLESDVLGLTRAMSRDIWSWYSLTESQFQSLRIDVVLFACLVRLLCF

RLYIQTFLLEPRAFMTSLVCRPGLVNGAVLQNKVRLQFNYVPIIALQYLAPVGVLLTSA

>contig27374 Frame-2F|Blast-pyridine nucleotide-disulphide oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY68267.1|) 3e-38

MNIPLGPYGGVSQLPFSGGIVVADWFTWLLKSSDYFAGRIWASIGALVPT

>contig28119 Frame-2F

MHYIYKASLLAAHEQRGADLLEHVLNHDEKESRRDVASPKAQDDEGPSIFPDEECKETDV

KVPVSCAGLTSSSDGEGWIELDERKESPASLKEPISALTDLKVVERDEAVDEVSLDWGDD

VDLIVPEIQTNVLWEEHSNEITTATHEDSSKRGEDWGEWD

>contig29417 Frame-0F|Blast-Monovalent Cation:Proton Antiporter-1 (CPA1) Family [Phytophthora infestans T30-4](gb|EEY53561.1|) 0.0

MESLNNGMDPEILFYALLPPIILEAGFNMKKKGFFSNFNAIMLLSIVGTLVATFVTGGIL

LWIGNMGLITKLTAAEAYLYGALISAVDPVATLSVFKKNGVPPLLFNLVFGESMLNDGVA

IVSFTLFQGLVRDGIADVTLNDAGLIIVKVFGIGFGSVGLAAVVCFTSAFILKKADPALQ

RYPSYEISIVLLSAYLSYVIADLVGMSGIVALFFSGVLMSHYHLYNIAEESATALRHLLT

TSSFMAENFVYIYMGMSVVAYSGYFTWDWGFILVNMIACLLGRMLNTFPMCMLANLGRSE

DNKIPLSYMVVIWFAGLRGAIAFALALNVYSPNRIHASVIQSTTLFTVMFTTVFFGVGTS

PVLRYFGLTARQKQEQEFDDVAAQERLLNEEHDHDADTSFRPIDRFVPSRNISGIHGVWE

IIDEKYLKPLFGGFTRDQQHELEQSAAARKRATMGHVVDNSMPLSRNKEQDQEQGLTKVS

SPDSSTPHLSLVEIAKNHDVVDKEV

>contig32606 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54792.1|) 1e-09

MDDIATPLTAVNAVQSTYRNWVGPWSQSA

>contig33700 Frame-1F

MLFYVLHEFLKSFEGDRLQHVQREWFQTIDEVLHACAREIRYGEKRNKEENRKRVFKTLA

RWEELKLFPNKIKTWKLLVLGEGKPRRAPIPLPRSESERQTEAPDQLQSFDLPPPSLSHL

HLDRSNCPLVFERTDFQLKVDEKQHWRYTAIAFINLLTQCLGLNSDIALTACVYFHRVFD

RGIYAQERYKFAAACVFLSAKASSKRMKLFRMVRTMYDILEKPLLAGDEELLEIERLQLL

YYEMEVLQGIDFELTIDMPFYYLRRVLNNMPEKFRDSISEETQSVLEELFYLPVCVHKSP

QVLGEAAAFIASWNQGKDFKFQWCSSSQRGGVLNERTAKDALLRYQVLQKWKKRQQLEFE

TFVKSASALEGDETDRLKLVFKSQLGGLRLDPSMIRNEAEFTKKTEDESKEWVQSRIKNE

QSRHDTRLKYSSTRYRDDKETRIKVENRAESRNLSRYGLSHERERTRCRQRSQSRSISKT

RYDKRSGSSMKYVSRYDYDDYDDDDRHRDYRREEDKYYARDRGSAVYRDIEYYDSSYLNH

RRRKSDRNGGLSGAHERDSSSHSRSRSWSRSPRDYSRRRSKRRRIYSSYGRSDSRSRSFS

RSYSRDRSSYNRVEKTSVLSTFEGNRKNKISATRSTYRHSERSHIKQERSAA

>contig34060 Frame-2F

MNFKVTYANGTSTKLIGLPEDTTLDGLRGHLYEKTSILPQDQYVMTGYPPKAIEGPGESS

LSSLGVRTGSVLFLKGVPQTGDTQVKSKSVFLRRVMPADNSCLFHSIAYALSKNKMISGP

MMRKLIKETILADPNKYSEVFLGRPVYEYCGWIMDDKSWGGEIELSILSTYYKVEMVVFD

VTSMTRLCYGEDQGFTQRLFLLYDGIHYDLVVEAASVTASASQDATLFAINDFSKVERAS

EVAVEAHQKHEYTDVSRFSIMCLVCRSSFVGQVCKVVLLFEHFN

>contig34293 Frame-2R|Blast-zinc transporter, putative [Phytophthora infestans T30-4](gb|EEY60501.1|) 2e-30

MRAVLSMQTKSSRTSEREAMSRALALLARTFVRKTELDRN

>contig34781 Frame-2R

MVGASWEARVFDIPYRELGFMRRPIIEMVLLQPSVYYLVKLERIQEWLYDIDICFTTGTA

NLNWKRIMSTIKSDYRFYLDTDGYGVLEPARWEFVKI

>contig34965 Frame-0R

MKFILLISPLLSLVRSFSFERADESQALVDTNTKAEKYGYVAAIHFEGPESKAYCAGTLI

APRFVLTSSLCLLTSMHDVYVSLGSTLRPRGDTHEFESIRVVRSFVHPLMTLEEGDLTPE

HDVGIFMLATSSKNQPANLPAAKGSVGKPGAMATTFDWNYQDGKQDFHSLNAETTKVIRN

DKCSQIYDDVNQTTVEHYVICTGIASCKGHMGSPLVVNGTIAGVMTTGLGIEKCGKVPPL

FARVSIELEFIDEVLNGGDPGEMTSLLTDGTGFPLEDLFQI

>contig35306 Frame-0F

MHVWNQQSRAKGLRSKLRVKALHESVKRKREQIMCVSATTEIWCQFLFRGWLLGSTAIND

FFLIIKSDLLAKTVQDLEEFAPN

>contig35588 Frame-2F

MLHLQMYDSALLWGRCALELQVDAWFLFGSKQSVKKNSNGAFLRPMPALRRIVGILLTLG

GYVHNSNCP

>contig36769 Frame-0R

MSLISSNSPPFRSQELSDPFMSMFMTRNIGGYCILDKSSMEELVSFLSHSRPELRKSASS

LIIKLTASDKSMFQLLQLKDLDVVQSLCRAVSDMRPIAEDAIKALINLTAANPTACERAL

KNDLLNRIMTQVEVDDWRLTDYSMMLLANVTTTPEGATALLGYDGEVTDATIVLREKKIR

MLTNSFLKGEPEPDGVDDNTGEPRWDDEYQYVANILANISQLEQGRNFLLKIRQSTSVAG

ALLPQLKSPNVVRRRGVSATFKNLCFDSDNHFYLYDQLDIPTHMMILLSGPEKLDADDKV

NMNPAVYCQGDKKKREYDRLVRLAAVESLLLLCTTHNGRKDLRRKKVYPIIRNAHLIEVD

EEISDQIYKLVDFLIRDEEGEEPDWNEIRNKLRTAEQETGGSGVIVSPSTPEAQHKIIKT

LTDTELAVNLKIKSTPLKKPVANTSSNLVSSGEDEQVPDDVADGFYNEILALDVTSDEEK

EENLGMD

>contig37263 Frame-1F|Blast-cation-transporting ATPase, putative [Phytophthora infestans T30-4](gb|EEY69151.1|) 0.0

MVKSIDTNVELAVTGQAFYFLVQMKDMETILLQIRIFSRMTPQGKVDCVKLHMKTGAVTA

MCGDGGNDCGALRIAHVGVALSDAEASVVSPFTSKSRTLQSTVDLVLEGRGALATSFASV

KYLILYGLIGIGCRSVMYYNGVFISQFGFMFMDGAILVGISYGLTRARPLNKMGSQRPTS

SLVGPTTVSSLVGAAVIHWLFLFAAIRHLTSQPWYCPFQPSNVNLVQWWLLQDSTLGSSL

WFIISFQQMSTGITMGLGSRFRRPIWHNVFLLSWYALLFVVLVVLFVGPPSRFTDQFRVA

SSTNVIGLPDIPLPIDFRWELLGWGLADTAAVLIFEHFFVLSHVRDYLRTKYHQDALPMK

L

>contig38275 Frame-1F

MVQFELNLTAMHTFDLAAATTTAPLTVQAVFDQV

>contig38518 Frame-2F

MRARHTGEFELAHPQEMLSYDPTSTRAMGASILDGSPTKLSFTEKSRGILVYLPHNRFAC

VTVEVCSSNLMSEVFDRVCIKCGFTGVLDIKDFQFYELALPRFVSLRSAGRPESERWYGL

PISITSKVESKGRRHGFHLCHRMTMTTIRLYDEASTASSHHMTPRSLVSSSKRSNPAQIR

PMSWGAVLPYSSGGKHW

>contig40306 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69681.1|) 1e-46

MMHMREIKERRPRWQHPESIDDEMEKTETDPMVPEVTTPQRPQMKSWVRFVFDKVWSFAL

LVVAALGLYEANFVSDILHTPAANRIFVHLGILFGTLLGMFACYIEVYRSMILGEHVRYE

SARTATHGMLASMLASGF

>contig41204 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64838.1|) 4e-24

MLGNVFTIYELYAGEETLGSSIHGMEPWLLREALQALEREGKAALIAGETCEEDGVKFLA

AE

>contig41293 Frame-1F

MDELSTTTTPPVSLSGSVPSSSGFVAAMRADKFDRGGSSSANLMPNGMLSGYAAAVRFGS

LKSPNAMLSSTGVSSPRPRSCHGDLHTRNGIALDTCAISGVADALSSLVLGDGLSNCGID

ALCGGTVATSPPLSAGSSRGSSDQLMEAVTRNGHMSPLDVAYHPLHNDPVIEQWKLSPSL

GPQLSPRAPLGSPSKSGFLPHGIVDTTTEHTSSLSWQATPWQHQSWGSSPLSRGPQQPQQ

PPLPPAPAPLFSIFSNQCSGGTSLDGSSPWPTNSDATYSSNKDNAVNDGFGHGMMGIGLS

IDTGFGRTDNGRSAFGISSENDNVASYSSLSSYLKSEYRPADQERHHQDPGSAKELLESV

SFGDMMTSDVASDADELRKEAIFLDYDVPSSAAEYRRQYR

>contig41378 Frame-0F|Blast-cyclopropane-fatty-acyl-phospholipid synthase [Phytophthora infestans T30-4](gb|EEY63791.1|) 4e-94

MPDKQKSALIAAMALTGVTAGSYLLRVVMRPVLRAQAAAFFKCMLADADIIIDRDIRVYD

EDIFLDWVHRGMLAIGESYMAKKWDAIIPLDEVLTRLLSLPADKRRKILKAWNAKFIALG

GKIFNYQSPSRAGIVGAHHYDLGNDFFKLWLDPYMQYSCAYWKGVEEKHDLDAAQQNKLH

>contig41910 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66538.1|) 2e-21 NOT\_ORF

MNFNRIFTCFALDELFSVFNKLIAA\*LSIHIGIG\*KKTIFMFSLPNSFFNPNSSWPAWDA

AMNSASIVLSDTPICFLHAHDTTAPFIVKTYPVTDFRSDLSAAKSASLQLSILIGSSITC

EMLMHDFNLFVSFRYLATC

>contig42577 Frame-2R|Blast-deoxyhypusine synthase, putative [Phytophthora infestans T30-4](gb|EEY58052.1|) 1e-167

MRRWRLSDDPISVDEYDEKRMNMEFRKTIKTKIFLGYTSNLISSGLREPLRFLAQHKMID

VIVSSAGGIEEDIIKCLGATYIGDFNLNGETLRRRGINRIGNLLVPNDNYCKFEDWMDPI

LDKMLEEQKTQGTIWSPSTMIHRLGKEINNEDSVYYWCYKNNIPVFCPSLTDGSIGDMIY

FHSYRNEGLVVDIASDIRRMNDHAIRAPGKTGVLILGGGMVKHHILNANLMRNGADYAVF

VNTGQEFDGSDAGARPDEAVSWGKLRLGSKPVKLYADATLVFPLIVAETFAKDFNNDKTE

EAAA

>contig43769 Frame-0F

MSVSVPMAVESLLLHADTSTSHVRYDSHPEANH

>contig44751 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61288.1|) 1e-50

MDIDAGADDFFAALNNGATVDVFAGFVAAVEINAAAKANGRPSLDDEPLVMNDKKKKAEA

AKQAAKKEAAARAAAAARAARQADGPALPMEDRIVNLLVPELKVNDVMLLIRKMRQAGKS

DADEFSELDAEQK

>contig45626 Frame-2F

MARSKIIFSLLGLQELFKNSMIGKEVKQMIAAVDTKGDGYVDYAAFQGLTAAPHR

>contig46296 Frame-1R

MMNIFANSQFLILLMIAGRGSIHARPCTSTDLGVFNDVSNQVSQCRQDSQLNFLIPPHMS

LTKTEQSALCKSKACQGMIGSMDDLDIPMCEATFDLKNMTLQMSLDKFVAACDTSTPAPS

PMKRRKSLESSSFNDSDSKTRRYENVATAI

>contig46843 Frame-0F

MTCFGGPLHVLQTGLSFLDHPNNSFVREFLFFLPWLESLSQRWQFFLLKPIAYRLLLPSN

>contig47088 Frame-1F

MISPKVMSELLQAKHVPTQFTVPKPGEHAWSLAEQRRFWEALQHFPQGPWTAIANHVGSK

STRQAMTHAQKLRQKLSRWKRRVRSESIGSVSPDFSAPILTTTPGRRPINRIESQWLPRS

TRKRGKIAEFCIVNRNEEEDMRMSICDSTNSKANNERKLQHLDNHTQVLHAPDDRYLEHL

LIDIEPVLEHVAYFTKDSQSAGTVSQPLATTG

>contig48210 Frame-2R

MEKKVFRTVSVDFTVCHSAHTKDNIYWLLQQVSLLSTIGKTLKSSHVHCHFLQSRTCWYY

KNPWNVHACVVTGC

>contig48904 Frame-0F|Blast-tRNA pseudouridine synthase [Phytophthora infestans T30-4](gb|EEY54710.1|) 1e-166

MQMNEGVKTVEAELERALFEAGGIADSNFGFLRKIGWSRAARTDKGVHAAGQMVTAKLHV

GDDIAAFVAKVNIALPEDIRVLQIVTVTKNFNAKMSCDQRTYEYLAPTFIFGKRCINAPN

VSKGDEENLPVKALSDLRGSEAGFDENVVIDDTTLETHKAFRMSQNTLDCLNATLKQYVG

THNFHNFTSKMEPTNPRSNRYIISFVAEHPFLQNDMEWVRLRVIGQSFMLHQIRKMVGLA

VEIVSGVAEPLTIQNALQLKKMDLPKAPSVGLYLAQAHFEVYSSKIAESIQTSHPPLDLK

DPAVAATVEQFKRDIIFDHIIKHEICTRTYAKWLRTMELLPFSYAAMPYLAWKKGKEEEA

ILTDRAGRRELAKATRAEIASGTCDAKTLLADETAEHMKLPTDS

>contig49107 Frame-2R

MGETYDDGNGYTLEQEQCIRELLVANGLEIANSTRTPIGDEQDDGGEGNYLSKSNSGSNK

QPAFAIFQSLIGSLLWIARFIKPDISLRYIERDDNSCTTRVRLAMGYRIVNYLNGTMKLS

Y

>contig49316 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68433.1|) 2e-56

MLVRGFATRIRAAASTKIEDTKIDLKTNRKRAAIVIATTSTIYSPFKFWSELCAVAYSAF

QQETKKIEYLPVIVTLYHALFRVLYECDVYRVTEDTEEREQFQTMEKVLSSFVAILNAEF

YDGVTSNTDQIKKECDIV

>contig49877 Frame-0F|Blast-threonine dehydratase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57603.1|) 1e-154

MVLSVRVCTSVRRISMQSPPNYRRMILESRVYDVADQTRLQEAPALSRALQNRVLLKRED

LQPVFSFKIRGAYNKMANMSKEEKAIGCVCCSAGNHAQGVAISASKLGIYAKIVMPLSTP

DIKVDAVRHHGGKFVDIVLHGKSFDDAAAEARRLVEQEKLTSVLPFDDPYVIAGQGTIGM

EILQQTSGFGDNLDAIFVCTGGGGMLAGIAAWVKQIRPSVKVIGVEAADAAGMTASLQAG

KVVELDHIGLFADGAAVKKVGTETFRVCSEYVDEMVTVSTDEICAAIKAGFNDTRAILEP

AGVLSIAGMTQYAKTRGISG

>contig51375 Frame-1F|Blast-chromosome segregation protein, putative [Phytophthora infestans T30-4](gb|EEY67985.1|) 1e-102

MAYDVRRGLQAVREMQGRIRGIYGPLIDLVRPVDERYCIAADEAAGGALFHVVVDTDDTA

AALMRELEKKNLGRLTFLPLNRLKLKECFEYPRNEDVVALVEKLEYPTEVRKGVMAVFGK

KLVCRDLDTCVRYAEQTNMDCLTLDGDMVHRRGALNGGFKDPRRSRTRAMMEVKQAQLEL

EMMTGRA

>contig51487 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67872.1|) 3e-44 NOT\_ORF

MQSYPEAFTELQKLSNQMGRGITLRAIAEFGVAGFATKVYAIYHSVFESVLFLDADNVPV

RDPTFLFESPEFKETGAVFWPDFWHPTSTIFNIQPHSLVWELLDLPFINMF

>contig51533 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70260.1|) 2e-68

MPLVVFQCSTCRSIFGDSYAFLCSTEQLWLITLSHVINVTLAPEVQTANKGFDAGSSYYE

LLCRNCQAILGRQYLTTPVALDGIRDLFSFSTEAITSYTLGDPMQKGEGEEDEHMKQAAA

LCHTTMQKLAA

>contig51696 Frame-1F|Blast-aspartate carbamoyltransferase [Phytophthora infestans T30-4](gb|EEY53334.1|) 9e-24

MEPSTRTSSSFQAAMKRLGGLVL

>contig51836 Frame-2R

MQRPRLDYDELIASNKTKARIASQITKVKECINSSANKAVNPACQALRRLSTKCWFLQDS

MNLKTLSLPMKLQPPVSVFESNYGQSPEALGLRDRTTFDEIAEWYRDLFCRRCFIYDCIE

HG

>contig52464 Frame-1F|Blast-T-complex protein 1 subunit epsilon [Phytophthora infestans T30-4](gb|EEY69814.1|) 2e-43

MSMVFDEYGRPFIIVRDQQQKERIKGVDAIKSNILAARTVSSLLRTSLGPRGMDKMMVSQ

DGDVTISNDGATILEQMHVEHRVAHLLVELSKSQD

>contig52886 Frame-2F

MLCSLMNKIKPGMISRIQTAPMPFKQMENISAFVRACRTIGVAEFELFETVDLYNQTNLG

QVVQCIHALGRTIQKTMPNYDGPLLGVKESSINPRQFTEAQLYEAAAAVPILATASQSVM

ERLPCDHSTSVTFRYDTAINAAATADVANSETKLPQPLPENASKEVSAV

>contig53041 Frame-1R

MPTIERILHALGVRQRRVRSFFVHDHAATERLHRRQLYQSHRMAFNTRHFQRLHVRGQVP

STRQHSCALLCQRVHIRARRVNALTTPIRKTMRQREPRAVVLHS

>contig53711 Frame-2F

MGPSIDRRDRTRRRSPSRSPRHNRHKSSIKSANSPSHQRYHRHGPHVVDDSPNPQNK

>contig54541 Frame-1F

MATTSRSTRTMNYMTRPPRQSMTAVPGLSRKKGGRLLSRGTWIRADRRCHL

>contig55054 Frame-2R

MRSNADAVVPSISDICWVMEQCPSEAFIGFVWEHLLALLLQQRKDLMNFQRFMSRLVAHD

SISLLSPKDFRAKVRARNLREVDDTLGAQAELALISVYRLQRESRF

>contig57373 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69889.1|) 1e-173

MKTSLVEEGEVAGDYEAHWYTTFDFAFLIGMAVYAGVMVILTFIYEPQWLHETKFWIMQF

PKLVIMMVVSLAGGLICRCFCDVDEKGYIITNKSSTFKVNYTRKLQHFAAYMVPLVIKSE

YPGPIALAWGDFFTMMGFLVLIKPIREHSKFFMLQFNSLDRPEDRPHTLKWIILGNIAPG

MLILMFFKWLFAAQGALTFILVFITGIGDGLAEPVGIMWGRHKYKTHSCFSTNKYTRSWE

GSACVFLSGLVFPALQYTAFDNFWQVLLSMVILAPTMAYAEATAPHTMDTPVLMIGCGVI

LYAIVNLV

>contig05236 Frame-2R|Blast-sugar phosphate exchanger, putative [Phytophthora infestans T30-4](gb|EEY69680.1|) 3e-59

MDGASYNMTAILLLLSGFMLGGPANLISTAISADLGTHESIQGNAEALATVTGIIDGTGS

VGAALIQYLVGYLANCQYVPKGCDFKSPHCVQVCSWGPVFVLLEVGTLLSCVCLAQLLHH

ELHLLRNQHIQK

>contig05597 Frame-0R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY67459.1|) 2e-33

MLLSDFMEVYNLFEYHRVVESREEASAVSLLHTSLDMNMVPLDTDFIQHGLKMLETYPEK

EARLRESVVRIVTLKLKTGLYENPLPGADYVSLVGNEKDREIALELA

>contig09144 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY62521.1|) 6e-15

MYVTKVLAYTNTNTHDHQALIR

>contig11721 Frame-1F

MQESELCMQRLNPETLTLEALIQIRRAWDFYIVPPYTPGASTIPP

>contig12391 Frame-0F

MEIAKIKIKINASGNNSNGNDNLEMDEATRREMEMLQAEDAEFLKGLDELPTDESESESE

DLTQFYSEDEDSDDNDVAQANALRNQQLSAVEIDEIGESRLDLETKSKSKLEEGDVNGSD

VKSAIEESTAVDESLRIEEDIYGRPVIRTRDGTKPPSTYLPPHLRRKAQSEADTITVTDK

VKPLHMDEQAMRELTRRINGQLNRISESNMESIALEMERIYRDNGRSLVNGILFDKLLQT

TCHPRQVMASLIKVCSALVAALYHSVGSEVGGFFVEKLTRKLVESVAEEIKLIELNQSKL

EDNTEDESSRTSKVPVNLMLFVMMLYNFGVVHCSLVYDLFRSFVQSFSTTDIELIHQLLK

IGGAQLRADDPDALRQMVAAVQQKVGEVHHTIDKTQPPERIGFILDLIYDLNKSSKQAKR

RTESASGGVLDLAPLKKWLGRVKTRCGNANNPLRVSLQELLHADEDGRWWIVGGTWVGFQ

QKLASHDVNDDENAVETNRLLQLAEKQRMNTDVRKKIFVALMGANDCFDAYERLMQLHLK

EKQEREIVRVLLRCGGQENRFNKFYLALAEKLCEMDSRYKFTFQLAFWDIFKQMETLKPR

TLFNQAQILAGLVLRGHLSLSCLKVLDFTQLEEKSILFLRVIMEEILKVESEFEMAQVFH

RLLQTKKAQLTIDGLAVFFHQHLTSFCNEPDQKVQTLLKRRVKSVKSLLDQLAKSAALAD

REAKY

>contig12786 Frame-0F

MGQKTFAAENSKKSLLGVFHAAIKAEPEGSYTILKSIMKQLKSRDDFEINDLLALGQIAS

HIDPSRQDIFTLIMDELCEILLETGCFPAKTPVGVILQNAAQLAFSNSRHQQEVEFGVHA

TSSFTEKFLTYTNALLLRPARSDPLEIQVAFGPSTVFEWFFRMSFDIAKGTEDSRYFVVA

ANIAERSDEIFGENSPLMHRSQQCLLAAVSSDMKKIETLDQSQLLGVLEVINRIGCFQDK

VASVAATIMCYLAKAMIAIKLRLRDANTSEIFELCKATHHSVPDLLEIGGTS

>contig12892 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59219.1|) 8e-28

MPSDLPMKYRHPFEFTRTNEAIGTKLFESNSWELNMVRECSTKLASYPLKGSAVLFYSQK

PNGEVDPMSLHGGCPV

>contig12926 Frame-2F

MGPQVIEKDRNVVPEMKFVEMKVPRRPQWDKSTTAEELNRMERESFLAWRRDIATLEASS

EHLEVTPFEKNLEVWRQLWHVRERSDIMVQIVDARNPLFYRYYQFWSLYVNLNFLTFILF

DMRSTDLEAYAKESETVKRTLMIVNKSDFLDERQRIEWKSYFHKEHIEFAFFSAKDAQHE

VDEKAKQMRLELKVDGSHENEVIEAETTHQDLNMEALVPVKNDPYRVLSRDELLNWMTKI

AAEVLDEVGLRVKDKGLIKFGMVGFPNVGKSSVINALLGASTNLHKTQRVAVGATPGKTK

HFQTMILSEKIMLCDCPGLVFPSFVNSKAEMYCCGVLPISQLRDHISPCQLLCHRISKRV

FEQTYGIKIFGSKTAKDTDPVEIYALLETYARNRGYTTTGKGGPDTSRAARDILRHYVAG

RLLYCHPPPEVSDPTIFDIHEIAKARFPLASPCAQ

>contig15134 Frame-1F|Blast-PpiC-type peptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-4](gb|EEY58608.1|) 1e-103

MRHKTLTIVATLQLWCLVLATEKAPASVPIQAHASHILVDTEAQADELNAQLSATANLSV

MFAKLAKEHSKCPSGRKGGDLGVFGRGQMVPEFDKVAFGGEIGVVHKVKTQFGWHLVLVT

RRIDGVEEPSMLYDIKQALYKSMPFLGPLLLVLFVAYGIRKSQSGPRARAYHILVKSEAE

ADALYTEIAASMDPKLKLAEMAATHSTCPSGKKGGDLGMFGRGDMVPQFDKIVFESDVGK

VAKVQTQFGWHVLLCTERVGDAKKLK

>contig15808 Frame-1F|Blast-Annexin (Annexin) Family [Phytophthora infestans T30-4](gb|EEY59583.1|) 1e-120

MTIELYPASVHNLFFGREFKYPRQVVEAAQQIHNASKGHGTDEQTLFAVLSSKSPEKRNL

ILLQYKELYHHSLTSLLKKSEALDNFKQLLRMISTPLAETEAQILRDAIKEMGSSVSQII

HVLAGRTTEEMTILKRAYFELVDEDLAVNLSSKLSGDFRKVVMAVLQSSQVPYNSAVHNA

AKAEEKATVLYKAGQGRLGTDEETFIDILVKASPEFLTMIDAVYVARYKINITKAIDKEF

SGDAKKSLNFLVRSTLDPYFTIAELFEKTFKGFETDESGLSTTLVRYQSLLPNVKAAYKR

LYQNDLRDRITRKINGKYKNLFLQVFDAPQDPPRIKLAGLTAPHLPSPTEKNPPLNSSTP

TKQQPHCQASQVTPVQTSYVLTSFLTQTLNSGGCLTTTPISKPAIIRSERKLDVIPSTFQ

VQETENNTALSYSSVQHQLASSGHQPLSLQHQQVSSFGQDSTNQPYQQLVPEQQQQQQPL

PQQILNDENQGQTFQQYPELQHQPYSQSFQQYPAFGIQAPCQPYQENFAPGRQHLSNLPY

PHDSLAQQQAPYPTSSYQQCSTMLGRQQQASYQQYQHYASPGQQPLGQTYQNLTGNEPQQ

YAVAQPPSYHP

>contig16456 Frame-0F

MLEPKDEVRIKTSGNSSDSSSDSPRTHPDPTTSAVGSVASITSSQISKLEIADVEINESE

CALETHDGEMTIMNDDDAELSELEEVQENAIDFSVNRATVTRAGVIPCCVFVGRVRWEST

DWEIYFGQKQLLRLHFNLYIHCLFNKHKIMRGVSLPWTIWREKRAEKRVADVYVVQDYIR

KLLKDKELRNSEPLLSFLEVSPSRAMLRLGPSLKEGYVHMRINGPFQLPLYTCFNRTIEN

LYRHLYRAWMRIAFVSSIVGFIFPICLVIITSLPTFFSPQKELVHSESGTKEMSTKLNTA

GVFMGLVVLAGIIFFAGFVYKFFQHRLGVIRRWVVLKPSCFAAYRNRNDLEPSEVFLFDK

NFTARKGSYRQGVSWMPSGLVVGSKAGDIEIDTGHYYTRLTAFVALMGVCYGIMRLSNSI

YDFEYLTLDKNLGMPITDAPGYENWTESHDTRYCGYYFTVPDGVTVYAESTNEFSVISQL

QMPSSNSMTANLGYFWQSDSMGYSLNVITNAVGGGTMISVVKPINAASDRFFESGTNFSL

PSMGILTLEGVNTDIDVQSFNNAASLCAISVRIAPLTWRSYVYYVLFLFAGGIIAPIVGF

LANYLVTYLGVWHPHVRRDHWYRCVHRLQKLKRQETTTRFHSFAPQHISSVDDDQSVAIK

AKAARLPADAQSDGSAINQVVDSVVKLEAETNARMG

>contig16922 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57469.1|) 1e-148

MANAACCSSLEARECMAQLQLKTATKHVIAAGRVGRSSYCDHSGWGLKQGSIIKSWKRRY

FVLKGRELMYFEERSPSGKGIDEKGRLRISGVEFTSEFSNTLLVRGELKNQAVKIQVDSN

DECKLWYDKMMNALEAALSDVMSHNNLKGDARSRVVAMKGWLLKEGQNFKTWKRRYMTLT

GRLIQYRMQPSEKPLGETRVNAVNINLSRPFALDIYSDNNRILRIAADSFRDIEAWDQAF

AKATGKRPCFKGPYAGQDAPFLGETFEESVQCEGWLYKRGQRSREWQRRYFKLMGFKLLY

QDGPGESVPKGAGTVVGLELGEEG

>contig19372 Frame-2R

MKTTAAGLCPQRPRHVFRSLALTLLLSCCSAQSLTVNPLPIQHMTAESVVEPGEGAFATI

MYDFGEDSEALLLATRVLMRSIKESHTKYRRMVIVPQDGLSENSERMLKGDDADLEIVRT

AIPNVFAHMPLTDHRTQLLHMRNKLVVWDDSQISSLKRVVYLDPENLVLRNLDEIFACHQ

FCAVDNGQSVVYSNGLLVISPESIAARNLYSDAIDSFMITGREYNYIGIIQGFMPGLFEA

FEESPLFFLKREGDDDGEKNDYVDDGEDGAIDTSVVHRLPFYYSINHMVFYERMNWDLYK

CKDKDLASGKIPGPLLSFKYSGATVKPWFWLPYIYFQVFWYWQDVRAQLGEDHFSYFLGK

VVSFLVIFVFIWSAYISLCLKLFTEPNGRPRRLSGWKLPTSGNAKPLSIDVFDSRVMRRA

CQFSCNALYAVASMPLVSSVAIVVVLTYCSVHMIPILMQPTYAGFLWVIVHNLMLMTLLL

IFAVAHTLRTARWKKDEVPATSDMLLEGIWWCVKKLPLLVLAHLQFLYLLGRIDWFLNPV

LRPVVTFFVFAFAAFLECRILFIEMRRITRN

>contig20350 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59823.1|) 2e-98

MTLTLYANLISQPSRSVAWVLKVKNVKHEFVRIIPTDDFFQSEEFRSMNPNVLVPVIKDD

GFVLYEGMAILQYLGDKCEWTGPKDLYPKELKVRAKINEFLHWHHTNTRLFTLNILRPEI

AKKSKTDTPKDREFIAAKDALIEKEFSMLELFLTNDFIANTDYPTIADYAAYCEIDQLEL

MGYDFSKYSKVSAWISRMKAQPFNDEIHEPLRGFLKHVDLLA

>contig22455 Frame-2F

MFLEQKLRKICDAFHARLYSLPSIDNRAAIAHLIQSNAAELHQSSHILRRNRESCVLLCR

DVAETLEGWKWSVLQEKATYHALNMFRADVSGMLRAEGWVIQDALSSVRGAVTRAHFAAE

DKSMPSLVDTVSKPWPVPPTYFETNKFTDAYQAFVETYGCPRYREINPSVFTAVTFPFLF

GVMYGDIGHGFCVLLFGLYLILTERKLEQPGGMGEMMASIYGGRYMLLMMGAFAMYAGVI

YNDFFSLPLNLFGSKFAYPDCLESHDRETKCVAQYWIDGTMSYVNATDVSTGENVYSLGL

DPIWKTSSNELLFFTRLR

>contig24589 Frame-1F

MCTELLGRAHICKTIAYHRNLLGKHLLRMYGKAMMSCRIGTHVTDDAVNN

>contig24660 Frame-2R|Blast-pectinesterase, putative [Phytophthora infestans T30-4](gb|EEY58368.1|) 2e-26

MRFLSYSLAACATFVVTTYGDDCNGSPNARTTPPPGAVVVDSTGKYAGSVTTINLGVAQL

QASSSPQSLFIFPGTFNEQIFIGKDVKSLIIQGYTCDTTDYTQNQVTITHSKSQNDLPSS

VTS

>contig24804 Frame-0F

MKSWPLNCRMHQVDRPALYGMNVIAEDNSMTSEDLAPRLKELTATNAGNTRPNWHADSWF

LPCLAMDLPFDVFLQLRDVKSATFASILSGPPSSRMAFSGWVYMKIPGSHWAKRFLSIDR

NNLWEYLDANETSRPVGHANVYEGTVHQQSLTELVLKYDWGSSTASERRELWLQFESHKE

TTQWKAIVMHAVHLQIEDLFDLTPDSPTGIPLPNLELGKGRFSVVRRAREKEDVNDPIRS

RDCALKIIDKHLFWDLVARETERHDTVVREILTQTLLTIRSGSSYCPVIRLLSLFETRDY

LVLELELMKDGDL

>contig26796 Frame-1F

MEIARQKQEEVHLSSDMSQKPLSEQEEDVDSLVFEELDTFRVADVEMPINTAEDKRASEV

LNSKQDVVKSWIELPDGTHIPLAEYLRIGPDNEAFFKSKATGGVEEMRQDNLLKPLSHGQ

AERQRKIGLYALRTIGIVISPIRALIEFVLLCPRIIWDVLSSPEIFGSVVDKLPKFPYPS

RFIWFRQFGGGSLYDTYSSVVWAARVVWDAPVYAYYYLFPQLNDALKLPVAESLRKVLSE

IDAAIELLEQEHKDNLETGNIDYGPDRAYFALKDKCIEKRIEKYVYKFCAFGEIKQDTTR

LGKWAGWETADTENLSLSRGTATFNYTKMQFLNGHRCYNGPDRSVLVHLQCGKDDEILSV

DEPSTCVYEMVIRSPLACSPEVVAKALRDVAFWAQTH

>contig27377 Frame-0F

MRLEELETLCSAKTLEQNHMNTLRKQCEEELGRSRFDRTQEMQECTRLQTTLEAVTRKLD

EMNVLKEEVWKVMALLSSYDDDEVTVVDTLTTTVWECKEIATICEKLGIILNEFNSTRTQ

WRTTQADLCALCHERDSQMNDFQSMDWRVFANDGEDEASVRNKFKTTLNYREVVAVAMVN

SVRWLEELEEVRLNTMRERETLTSLENANEWLQNQLKASNAVLQKFEQKNESLHEQVVLL

QQKNEAWNDSRSLEKRKEQETHQQNVLQLEQQLEQERHAFEKYRKRSH

>contig29414 Frame-0R

MIEQAEADFGLIYDAFLSVEQFGIVILISYPMVNILRKLSHMCAEHSITKLFQYAEGILK

>contig29869 Frame-1R

MLVFESKTIPSKCIRKKCQALYAALKVNFTVHRSCQTFLERAENRLVRVTVADFIPLSFV

SPHC

>contig30759 Frame-0R

MVPEQLSVRIANLEQKVSPTSKTCVQQVACIYGLKMVSCDDEAIFCSLSGFADTKQQVAV

ACLLHWQLQQINERGAAVMLSVSTVHTFLTLAELFHCEKALLESDKVKVLGAQMFVQQLL

EIRELKECMVQIVDCREQNQYLGLVSDEQVSGHFDGARNVPFASIFTAVKKEEVAKRDAA

QPTIDRSGKKVSFLPLDEMRHVFDVNGVDLDRPISLVASIPAEAAAVATALLLAGQTTDI

RLCIEPLTDTFIASFPNVYTTNIFREGQLLYKDDKGEFDLSPESREILKSSVEVETIKNL

EKAFNDMLMETARSKNREDHFVENKMVGDEVVWIKGGRRFFDMPSPVSKNDFLDASRTIF

CVVSFVLAPFGFPASLRKKRSLQEVKALCGSLFQDVLEVCSDLVYQEKE

>contig32014 Frame-2F

MQQGFVAPLGSGVFNGKDCEHSVNLMPNVSGMAPEPPRLPDQKEYSYASGSNAHVQEPRY

QFAAFPAISQANSGLEAENFGVYEQSSVSIEKQFLAEEKDKKVVGELDEINEQVTLILDS

VERKQTTIEMISESFRELDELRHELVTLVVKRDRLRSALASSSLASDNSTDAKVIRAVEL

TLQNLVDNQKKLVQQLQRDISRHEGELEESILSAKLQQKMSLDPQPSLIATGATQNDFDA

PKSKDNCPPPAPPLHDIANLLPSPVVTTSAPFISAFTSNATSTSDLDAFNNLGSFTRSNA

NTRLILTTRKSSNSLISPTPSSSQHAIATDTLDAFDFSQTKSTPSLLAEFEESPTKSLFS

VQPPTAKHDTPFDAFADTVVPSADLKTETSTYSIVTPSPAAINDLDLNDIAELHAAESAA

KSICTESCASLDPVTKTEAFKILPFLPPPASKATNFDAFAAPPLSINTMETSTKSVANEI

LIFSPVKANSKECNAFDNFGAATVNASENEVSFNEVSFTATSTVGIESSSKVLEPFGNSL

GPTSMPTENLPSSQFASDKNDFDDFGDFSSASVESIVSSSASQLLVDDSEACTQDDFGAA

LDNVASTYEPLYVSGNLAAKTPSSGFDAFNDSHATTEEMPNSTVFSHFNSKANDFDSFND

GDSTSTLAKCATTILTSSKQVESDRDAPFVEVNSLDSCTEFSRSSLDAAGDTESIKFGFF

DAASGIAGRDFESLPENFSSAAFLAPAVDEEKNSPVTRFISDASDLESLGNFESTLASAE

SAILSNSSDKLAESTRNPKLIEPASPVEFSGTFLNAMDDTESNTFGNFTTAASEAGIASD

RLNSTSSPAESTNYRFEASSYSSASIEKVSENLPLSASGKNNFDDFSSALAASDRATSSF

TS

>contig32605 Frame-0R

MTWSSLTCFLLALIYTTATIKALDWNILNHDDDSTLTLNPNYSDEILSPETLNEMMGSDY

LDRVKEMIYSRKNKIPDSSSEI

>contig33228 Frame-1F

MTLPMCVECEDTAAAVSCDDCDDLYCALCFEAQHRSGSRLHHTKMDLIGSCSDVLNVNAL

PPRLSVMPLEEKASNDTQSIPPLSTLNLSLATETPLNTEVVVNNTIPKEAEGAEVVQEIK

EETVTALLKDASYIPLRLNEHERALFNLLDAALNVSEYTDKVDVLSNRSPLKRVIQELNE

AFSVLSGLMVANDFRQGRRLVQGKDFNENHEFFCQVFEIGRRYKIMNPERMRNNYGKMVY

LLQDANLRDLKEYLGFSCVRPIKTVASLLQEREALGMLLDSRCEVATSVAATFELLVDSV

ALQRFASTKKQAIEELVRDYSSALLSEEEIRLCLASISDSQSYLTSNLSPITRMISYLET

YFTPEKAEPGLSLEIRAGKNGARLSHSHHSQYEYVLQSLLLWKNMTSSMLRLWWAVEKDM

LGGSMYRLRDTGQGLNRMQHAPETSRLMHSILQHTKKLRPRWVGSSMVHLGDHNVPNALL

FIDKYTQISRILSPIVNTVHDIPALAAEPNTRAYIEDSFGGAESLQKRILCDFFKHGFDG

SGADNFFDAGSCIDGRLTSAWNWCSRIEKKPFFHIFLMAGFVGFDGHFEK

>contig33703 Frame-1F

MKPFTIFCRRSLDIERPTYSNLNRLIAQVISSLTTSLRFDGSLNVDITEFQTNLVPYPRI

HFMLSSYAPVISAEKAYHEQLSVAEITNSAFEPTSMMAKCDPRHGKYMATCLMYRGDVVP

KDVNAAVATIKTKRTIQFVDWCPTGFKCGINYQPPSVVPGGDLARVQRAVCMISNTSAIA

EVFSRIDHKFDLMYAKRAFVHWFVGEGMEEGEFSEAREDLAALEKDYEEVSAETAEGEGE

DEEFAEEY

>contig33776 Frame-2F

MLALQVRTQKRLLLNATTASVALHKRFASAPVITEDHEENEEALSVGEPSGFERDTLDTY

LNSLQKYNPPIKTGLKGLNIIHDPLYNKGTGFPHVERDRLGLRGLVPPRRLSVEAQLSKL

YDTFSQERDPLGKSRFLTDLHDRNETLFFRLLIKHMKEMAPIVYTPTVGVVCQKFGHLYR

RPRGMFFSTRDRSQFGAMVYNWPCDDVEVIVVTDGSRILGLGDLGANGMGIPIGKLALYT

AAGGIDPRKVLPVMLDTGTNNQTLLNDPYYLGVQQPRLTGEAFWSMVDEFMRAVRHRWPK

VLVQFEDFSSEHAADVLNAYRLKQLCFNDDIQGTGATVLAGALSACERVKIPLKEQRIVI

LGAGSAGLGVASTLLQGMLREGMTIPEARERFYILDQYGLLGEARDSLNSGQQFFSRSDL

ADKTNLVEVIKQAKPTMLMGLSAAAGAFTQEAVEEMAKHAEQPIVFPLSNPTSVAECTAE

QAYEWTTGKCVFASGSPFEPVTYNGTQYNISQCNNMFIFPGVGLASSVIQATRVTDGMLY

SAAKALSQCMTSDEIANGQVFPSVENIRDVSLKVATAVCETALDEDVAGVRPKIRRGGTL

EDFVASKMYFPAYHALVE

>contig34207 Frame-0R

MSFCSGQSNRIPLPRRLSPDRAKRKTPPPRALIVLLFTMLVSRQFLLRVSKSVNHPSVLS

SHVVIRNPYLRPLPSTGLKRSLFIITHRGKLKQLKNLEQTANANPEDPYAQVRFLQELNR

HNYPAIVVRRIEENRFALDESVQKEYIKALVKTGRLDTVDLSQLTQPMMTPQFGAVTASS

PAVSHSFQGLSAQDPMYVSMVEGSFKSNMWKTLRTLGVAFLVVSALGAMLDEKVGKIGSS

SKVLGPTGSDKRFSDVKGANEAKQELEEIVQFLRDPARFTRLGGNLPKGVLLTGPPGTGK

TLLARAIAGEANVPFFYSSGSEFEEMYVGVGARRVRDLFESAKRKAPCIVFIDEIDAIGG

TRKLKEQQAMKMTLNQLLVEMDGFDQNKGIIVIGATNFPDVLDNALIRPGRFDRHVTVDL

PDVAGRKEILEYYASKLPLKDDVDLDVLARATPGMSGAELSNVVNEAALRASMKSADCVD

MNAFEYAKDKILMGAERKSAVITPESAKLTAYHEGGHALVAINTPGAHPVYKATIMPRGQ

ALGMVSQLPEGDQTSISRKQLLARLDVCMGGRVAEELTFGENEITGGASSDIQQATNVAR

TMVTKYGMSSDVGLVFHDLRGNDTSATTRKIIDDEVKKLCDASYERAKDILVSKHADLEK

LAKALLEYETLSGAEIDKIIKDEPLDRKPME

>contig34290 Frame-2F|Blast-alanyl-tRNA synthetase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY59826.1|) 0.0

MFRILKSSQVMSGLESKVASLEKAITTSEARVEALESKVASLSPFSAESWPAARIRKTFV

DFFQSHIDLPHTFYKSCPVVPLDDPTLLFINAGMNQYKPIFLGQVDPSHPMAKLVRACNS

QKCIRAGGKHNDLDDVGKDVYHHTFFEMLGNWSFGNYFKNEAVHLSFTLLTQVYGIDPNR

LYATYFGGDSTQGLLPDDETRQIWLRYLPTERVLPFGCKDNFWEMGDIGPCGPCTEIHYD

RIGNRDASKLVNADLPDVIEIWNNVFIQFNRKQDGQLVSLPHKHVDTGMGFERLASILQG

KDSNYDTDVFTPLFAAIQKSTNAPPYTGKLGSEDLDKKDMAYRVVADHIRTLTFAITDGA

VPSNDGRGYVLRRILRRAVRYGQQFLNAPSGFLTELVPVVVTMLGEAFPELLQKQAEVEE

IILDEEHSFGRTLNKGIERFKKIASGIKEANAGSNEALIVPGEDAFFLYDSMGFPIDLTE

IMAEEEGMRVDIQGYEECMRLQSERSKMDRKKGGSNGARPLVLEARETSALAEKQVKVTH

DMAKYEWDTTISAKVAAIFTSTKSASEFVNEVKAGEYERVGLILDKTSFYAQAGGQIYDT

GVLSATNFKLDVDSVESYAGYVMHMGPIASGSIRIGDIVECNVDYTRRAKIAPNHTMTHA

LNFALRKVLGSAVDQRGSLVDESRLRFDFTTNKALKPSQLAEVEAICDDMIKQQLEVYMQ

ESTQAKATRIQGLRAVFGETYPDLVRVVSIGQPIDAMLENPENSKWSEFSVEFCGGTHSK

NTKEAKKFVLYEEGAIAKGIRRVSAYTCDLAIKAEMCGAKLQAELDAIEKLDGNEFVESV

SAFKPVLDQALISLPLKDALRKQVDGLVNRVKKIKRDAAMSRAANGVRDAIVEAKKAKEA

GQEIVVVKLQAGTDSKLGREMLEAMSARIPSGSFMIFSIDLDAKKTAAFTQVSQQHLESK

QLDARTWVNHAMTVMNGKGGGKDALNATGQAKTVDNVDEAMALAKAFVSR

>contig34913 Frame-2F

MALNALTSRPRLQSRGIETMNSTTATDASQASVDVCFDLENADTTTETTQLLDEDDTNHS

STQVKSNLEPFDDQKLREKGSSSTKAIVIVFWLSMWFGQNIAMTFLNKQALSVLSLPVTL

TFVHMTCNTFGAVLYIHVYRGIERQQLKPGQKQLMIYFSLIFVSNIITGNWSLGLVSISL

NQVMRALVPAIVMVLSMLILGKLYSLKRKLSLLPVACGVYLACTGDNSCTLLGFIITLVA

ILLAAFKAVLSNKFLNGDLKLHPVDLILHQAPLSAIWCLVTMFLSGEVETLLQNREVMPL

ASFWFLVTGMISFMLNVTSFMANKVTSAVTLTVCGNVKQVVVIVMSILIITT

>contig35305 Frame-0F

MRADTFSPASQQKSSTLTYLSRNSSQVPRTDTKQVNDSGSSLLLLLSILSRHGDYYILNR

IGDIMMIMHKLNDSLIAKRIGKWQALSLQILIQLAALSARHRKVCHCDLNEHWTNIWQNL

LRPELPYIQITEGIGLMRGETGDAVLTLLNCCISFQLVSINAIESHSKTLWNLPAFGPPS

GDGSAFRGDRIKSCARTSVASICIMLALLHHLQIPPAGTNLPAVTSEGPNLFSLGENSFT

NHDLKLIQSLFDHLQAQVFQTNASMAGNLGNSYTKVDWQTEVSSFIYASVIDSFFGLKSP

FFESKDVILTPDLIRKLSTRTVSKCEGSHSGEEFNGFGIAFCMLDTGLEYLSVDFTDTTT

GVKPDSFPLPFQALTGKYSGASDVNWCHGVESCADDTEDQFERLAVPKFFKKLIVSQDNE

RILSYRCFPKEIYTQSISIERSRTLQTKVNKLFTG

>contig35969 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57596.1|) 1e-39

MLCLSVLRFMPNVVEFSKLVGVKQARALCSTIPDGWEAITRANGEVVYYNKNLRKSFRHL

PGDEIKATTSAKGKTPKNESEEVNAQPKYENELFVPINFDAAVSIDGHDSQVVNIELKPK

QCLRAETGAMIYMTEGVEMETTTAGGFGEGMKRIMTGENFFVSRFTYNGNEKGRVALGTS

FPSKIVHIRLRDFLG

>contig36339 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54182.1|) 1e-44

MIAMYNDRIRNGQSLHMRPLPSVQSLTDSNPECYKNSPTCASAPFGCKRSMLSQICSVCL

IAEPECKTPPAYFAFPNLSQI

>contig37189 Frame-1F

MDNLKKDKKFEDCEDSVTDKTKRDVTSSMRRAKTASKGRFDVDDILSEIDKLPTPIDKNG

SSNGRKLTPAISTELPNSIPSHAKEIVCTLFDTQTNRSGPSSIETNTNTVFDDGDEEDEV

V

>contig37945 Frame-1F|Blast-rnf5, putative [Ricinus communis]gb|EEF34780.1| rnf5, putative [Ricinus communis](ref|XP\_002527599.1|) 2e-09

MEPRNTVEDATKANEDRKPLFECNICLDTVCIPVVTLCGHLYCWPCLY

>contig38203 Frame-0F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72305.1|) 5e-30

MIPQLEGIWSARRLVRLFRVISTGLACIRRYVLGADLEICQRVKPSSSSQAPLRPLLTTS

EAWRSISMKYIFGFTPDNKGRTGILVSVGPYNESSHSCYGAYHYS

>contig38276 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62595.1|) 4e-39

MSASSATGKPQRLTLEEKVWYDRRRSEIEYCAGVGGALGAAVLAGVTALGPFPRRVQFFA

IAGGVLIGGGVGFLYADTKALERVQDLSASSNLRKQYQQMCVVYLTGKQGFI

>contig38430 Frame-1F

MFALQVPALFVLQPAPISNGRKEEKLLTESNLKLPPPNRAV

>contig38795 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66263.1|) 9e-93

MAGSRSRKRDAPDFQCVNSAADSKRQWKYAKVSNSQLYAPEDTVLVLGDGDFSFSRGLVK

HRGTGRGVLATSFDSESSVKRKYSNALECIAAVRSSHGLVIHDVDATKLHDLPEQVKTGA

CIRAIPDYFQYIVFNFPHSGQQRVHINRALLFQFFESARNRLAVHGEAHITLKTRPPYSN

WLIEDQAKAAGFVMKERRKFNMKLFLGYYHRTTDPQAKKFEPHRCVTYVFVVNRSKFPFQ

SSQTALIPASSEIAAARQHNLAAAIYKIMQVNFAAGTKNWNQRDCIPHQIQEKVARKKSV

SCVAIAESICMRKLWKPLHHQSFV

>contig39693 Frame-0F

MPLMSSQASTRAYGVLPRTPVSEICTRKWTKQPKNIGHLTILKWIPDQEFPTEALQKGNL

KKSKGRKRGAGEVGRMTRSVRQHMAAPLELLSEYPVRVLSSRQSSPSRNAVDLNPSERTH

LSTPYSDATIAASKQSRSNPHASTYIKKTAKQEHTAGMSIDPMSSLPTRNYALDAGAAKT

ARAAPDSTLQVVQMIQPVSTHMMNVVPSDEQLEMALDDLPMLDADDSFNLDALDPAFLPT

PLATAAPPPKVQPYNNTYLRQHSVDNSSVSVSEDEGSANSGSPMPSASPHSSPEMMSRST

SP

>contig40305 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69681.1|) 3e-23

MWPVWQWLTFPYLLMWSWGVVVQLLVILPPILQRMVLLGAYLWFMHSYLSTYLTGMQ

>contig40514 Frame-1F

MLLSRAISVLALLACIRCGVHAQNTEQNLKTQLTTDSAMITSQRLLRTSVDFKDSEERWP

TESSRIRSAIKDYFREFPEKVSIAMAIRQIDAHGVRHVEKVLSQYKFPAADQGNIRLAII

HHKAPK

>contig41063 Frame-1F

MCLFGVVLSESIVAEGGKTDSGRPSGYGDGNQVCVLVRARQQDRNIAENFDVLTELCLAN

RRTPSWQWSLQQVFNLTTSAREYQAIKAISFFPNDLKQVLLRGQLAPKTAEKSAALSSML

SPPLLKYLHKHYNDSQLQAILGCLGEDRWIIIQGPPGTGKTKTILGLLSALLDGAGLSSR

SKAQGSSRIRIGASFHSAPTLSVTSIRIMVAAPSNAAVDELVLRVLSEGLYDGKTGETYR

PRIVRVGRSESQQLSGFNASREASESRKNRNKIRKYASEVEEVLLESLVSKHRKTFSTGK

QTRQAILKNAQIVFCTLSGAGSAAMCDFAQEFDALIIDEAAQAVEASTLIPFKFRPQRMI

LFGDHRQLPATVLSKKLVLMGYDQSLQQRLVESGSSVLLLTQQYRMHPEIAAFPSTYFYS

GRLVQDDNMRDWTGQDYHNDRNFKPLLFLDVQGAQSQVNGSTSLRNMSEVDAVIQILRGL

ITKYPSHEWMKRIGVIAPYKQQIYEMRGAIQKLETVVDCRLGIEVNTVDGFQGREKEIII

YSCVRTSNGGRKWRSYKSDQQEKTLDAFWADERRMNVAITRAKSSLWIVGNSVLLKQSTA

WRALIQHIKDHDRYISGDHYEVFHE

>contig41782 Frame-1F

MGLRRSGKSSIQRVVFHKMSPHETLFLEGTNSLDIKYIANNSLVQFQIWDFPGDY

>contig41966 Frame-2R|Blast-peptidase, putative [Phytophthora infestans T30-4](gb|EEY53249.1|) 1e-104

MLRPMLENMNTQMHAAPEDQLFSIPFNDASRATLDVPATVASTPIQASVNLVSHRFKVSG

SPTLFLERTVQRIKTLNSTQLLIEAEISALNSLLVHVKEDRNQVNMALNIKLWKIIAKLL

AQGSKSDFFFPGLCVFRVLLLQPPQELDAVSDTQACFDIIVNVTAMDASVLSSAQKTVLL

TVLLNAYANSGFRDMALSNSTRYLPFIFATITDSTCHEESRVLGAHIISNCCLAIKAEKN

SMVTTIVCG

>contig42718 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58303.1|) 1e-111

MPNYYPYRDLFPQLDLLKHNYHVILEEMEAVQQMTTWPFWPEKHYTDGNNEWRVFPFCYT

FPASDASKITWVPRTCSMCPRTTELLKKVPHIRTALFSKLGPDTTLSAHRGWADLANYVL

RVHFPLVVPTLSNGDPCCAMVVSGETTYHQERKFIVFDDSKLHYAFNHHPDATRLVLIID

LYRPDHLPRGRARGGHSDELDAFIESFGKQTLLKSNEER

>contig42879 Frame-2R|Blast-tRNA pseudouridine synthase, putative [Phytophthora infestans T30-4](gb|EEY57959.1|) 3e-20

MRKRNLLTDKGGMVTWKDVSPLLLLSKKRKVKPLATRDTGYSVDERKVIDQDRKRRRDKE

VQEGAPQVAIED

>contig42945 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54275.1|) 1e-131

MISVSTENNALRNVVAASLAQELYDVLGKMMTGDVLAVALAPVFVKFLEASADIERTVMC

SVIRVMYSVMHNSAHFRDFFQVALSPSGDSSSFVATNQQTPNSIEHPRIALSGLRYTSLN

DYLSSRLNPDSKERNKLLLSLPAKTASEQRPICRKLMKALCRVINTNLKEMDVVKYGLCV

LDFWADLGLTHSQAPTLEFKPLLTSNVIPSILAAPTSSFMLKTQAVGLLNKLLRMPEVLC

EMQSEFKKSLLFHRCAKLLAHDGEQPSVEDAKNLRILKSQIVKLMLFIITNLPSEGIRFV

LESTHGFPDEADGYRSIIFFLAQLLHFETFHARSTRDRKELLMDQNRMELIQDSFALLGL

LSRYVDMRKQLGG

>contig43241 Frame-0F|Blast-phosphatidylinositol kinase (PIK-I) [Phytophthora infestans T30-4](gb|EEY57127.1|) 1e-128

MTEGYYKRGHGIVIMLFFVTNVNFGESRSVLPQLLFPHAPPHQRESLAKLFDQLYEYVRQ

TYAASQRESPFFEWLLARSKEEIVASTRNIQKQFRVGDGFLDPFPLDYFEEAQLMILENR

RSHIQQFVETKQRMWNRPALHSFGDEFRLVRFLVDLCTYSKGKHIRTFEA

>contig43339 Frame-0F

MQQFIIGLEVMVESPNKEQSSLAVLSSTSIDDRLNQLEPRLSWFYVRLLLLTGGSWAIQA

AELVLLIFTRGLVAHDIGMGTPLLQLLGVSLFIGSIVGGPFFGHVADRFGRRMALIVSMI

FSLGGLTMTARADNKPMLLIARAVIGFGFGGQLTSTFLLVYELSPRSMSGRMVSLLDAFT

GIGGLIGMMLAFALALQSGWRATYLMTSGLVM

>contig44752 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61288.1|) 4e-66

MAGNLRRAAEFVEMNLSQMGKDERRTRIGYKDQ

>contig45698 Frame-1F

MTSIRHVSRWQLCYPPQASPDIQTNKTLSKPPVSLRYLNEFIGKLNCAPELLQHGLYPDA

KEITESMALFNAVRRYIEPKSSNNNSSESSSDKDDGIVVVGDGNTPRTAALFAFRMRGWK

CFSVDPAMDKGPN

>contig45759 Frame-2F

MPQPQALKRVVPRGNSAMAQFKPSRWQVENRCGICNVEFSLMTARHHCRYCGLSVCGKHS

RNKVIVPTSLAKVPQRVCDKCYPTCRNIISGVVPPPRRDVPDDKVRRPALETTSERDYGK

RMRIPGDREERRDMKTWNGKEGRDDPRRMGQRNEEPHTVNPA

>contig46084 Frame-2F

MVEPKKESKQATIFRFFSPSKSSTESDIIMEESDFKSVGAKRPRSIEDDVTSTIITNDPQ

KALKPATKARIQPARTTNSIVKSTPMVQAKTRRKKGPDRFRSPHAAANSDEDNDSDDAFQ

TPEAKRAREELGICTVI

>contig46228 Frame-2F

MDIGTVSSKLHLGVYKNMSEFIAGMKLVFDNCISYWQSDPQGQTYCESAETLLRLLRSQS

TIFINLSGSNAASKDKQRPHVPALFKAKSASDTSSSLSSSVSTAEIEHEISKKQPSSKPY

PSMSSKLSKSSKYLKSSKSSKSSKLSRSRV

>contig46295 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59108.1|) 9e-43

MSTLPPFDDITALRRFLQTQSVDIICHDIIPKLLSGLRRHPGLVDMHEPTSVPLAKVGDF

LDAILLAHADRSLNQDNDFLLNDGPFSFVAKDAFLAQFCTHSSTEALCGYLFQRNDIVFN

CKTCQSDETCVLCLKCFQNGNHEGHDVFFHRTNPGGVM

>contig46840 Frame-2F

MADVTGSESEDDLNDVNTKGSSAGIHSEDESAARTPQLEQSSDSDSSDDEASSPIKNFSS

ESEDESQDEALAKKTGQKSAKSCSVMKDGLDNRSSFKPVLKQSKKSTKTASASKKQVFSS

SSSSSSSDASESSNHEAPAFAKRTRTTHPAPGRNYKAGGISDGNSHTIVKKIEAFNDSSS

SDELHLNASLNGFERLLAHDCAERLGLGHESVGDGLDRHIIISRSNAKRADSSQIRKAKK

SKRSKP

>contig47014 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62191.1|) 0.0

MAFARLTFLCVDVVVREVPQVEALYHVIAILKAFLDVSKVLSVAIAAQNQPLNSQSLMLL

EHAAVREKKKLFYWSSELKRHYRQYQFETALNHAAARGFYAGVTWLRTKYYPKGKFHGAE

RAALYSGNLKMLHYLHDNFGNKMVDDVAVDSQDAIAHAAANGRLDLVKWYCEMKGPYAFG

WNVMDAAIAHNHMVVVQYLNQVLGNRCTRRGLERAALNGHLRAVKWLNDSRYYEIRTFKS

LENAIIGGHLDIVQYVMQTVEVAYTSWNQAALAAAVTYGQRHILEWLHVRASKAEVAHNR

YFRFEVFTNQLYGVAKSGYLEVLQWLHENHYPVHCRRAHAVRGAVAGGHKNIVEWLEKTF

KGLIRQRHRIRIDKAGGFGDLEFVQWLYYQGYRLTAHTMDNAAADGFLSIVRWMHESVEN

SKCTVAAMDRAAANNFLDVVKYLHQNRAEGCTTAAMDDAARHGHYEVVKFLYLHRSEYCT

ALAGETRSVAVLEFLKEHKRLRTRLPKTVEASNRGDLALLQWLYSHDRRHFGFEAVGDEA

REHNHFHVLRWLETLPEAGRLV

>contig48266 Frame-0R

MYQLRPEYWFAAHMHVKFAAIVVHPDQPSGLKHLANRKAAEVDNMQEIKENEAAKKTRRQ

PAITKFLALDKCQPRSDFMQVLDLSTASCATTDPDALVCGTIQKTKTDSLKIMFDLEWLA

VLRATHHLASSNRVPPRVPQQEMKIESSDIAWVKKRLQDFIAEKKLDKVEGEWITDFVKT

APSHEDKEDPVLVTGNPQTDLLLELLKLPHVVTAPFVGESGVEDPNEIDLIEDGDDDI

>contig48644 Frame-0F

MQPCRRERSSSVVLLGKLSAIVRRGSLFQEDSEDAHSSSNDKYVRDKESENGRSSQKGRR

QHTRRRSVGATPSIQSNLIVGNSSQDKRLQFYPAWPLVAAKVSKPLGE

>contig48770 Frame-1R

MTSTLISDTEPKKLEFVCTRKSTPHSRSKQSETAEKKMPTPRRRASPRNQNGPEVDNQQR

DEQEQVDLSPAIEASNEDQQQEQEESNKTFEVKMEEERQPGTANDDTPELPPAQDTQLRR

NYLQRIYRQLQSTHPNKDDAVIRQTATNLEMEI

>contig48990 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69506.1|) 2e-33

MIDWILSRGQALVAVSSFSRRLASCNKSKCHHLFVRKNFSVPSALSVTFGVGASVLLLAT

SSVETRRLRQVAHSGALILQYTGIVTAWKDALDLAMQFTKILSHGGINRMQDELVRLLLT

FILHVQDDEQGQRKLLCLINNGVMPLLVQYAAFDNPVEPIRLQQLVGSMTKLLKFSAQNR

EVNLRLSVTALGQALAQIMKQQDDLV

>contig49104 Frame-0F|Blast-structural maintenance of chromosomes protein 6, putative [Phytophthora infestans T30-4](gb|EEY55333.1|) 0.0

MRARIESKRVELQSAESELKEAQNQAQTRPQELDEVETRHDNCVRHLREAETETSSTQYR

INQLKGQKRDSLAIYGSRIPQLQQLIAHNLSRFALPPIGPLGLYVKLPERYMHFAVAIEV

ALKGTLGSYLVVNGRDKALLDELKRQIHCPQNQANIIISLRNGRRYDSLRLAEGNLAAHA

ICNILEVNNDEVFNALVDVCSAESKLLFDDRQLAETSVLSGSSGTFRMARYVSEVYFPTG

DKFVVRSGNLAFIANKGNRRSSIICQDLEGEIRELEKKIHYLQGNAEILRRDEARLRQER

EDSRQQMKQQNDRIDYLSRRLNQKRAELRSLEEELSDDMQQHTLDTSVLEDEVRSVENEL

KDYDRRGEELNELLSKSNPDLEGQLHELEELDVLEKEIAADMNLFQEDADTIYKHLSEMK

VKEMTCQKEVAVLRDMVERWEDELAALEEECVEQRQKAQQHCERVVVRHSHEYYGKRLTD

IKHQIDHER

>contig49315 Frame-1R|Blast-putative fatty-acid-CoA ligase, putative [Phytophthora infestans T30-4](gb|EEY58460.1|) 5e-58

MLSFVDDKGVVVSSLTCMELNKRMQNLAGLLVASPQQHSKGVGLKPGDRVLLVYPPGLDF

IVAFLACLKAGVVAVPVYPPDPRRMKKDISMFVAVTQNSQATTALTCSMYYNAKKISSMK

EKFSFSGSASWPEHLHWVVTDDLMHSKGIDPETLWLFQ

>contig49874 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69296.1|) 4e-44

MSAGVRIYVKEMKIIKDLYRSLTILLNSTEDAELIIFSMAILARLVLTESLGNKIFSDKN

VGQALNLLFSVLDGSWYDSTEKRYLDSNTILNRRSLLQVVSVDLLCTLCGR

>contig51835 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58467.1|) 1e-104

MTFPNRVNYRQQSRETSQQAAALTAGDSPVASFATFNNAESDGFLIMEEKPETSLTLCVT

DHALWPLTHKFMTLIAQPAKLLAALLVNCDTQTSKETFWAKATAYQHSELQGMATSWCRI

LEDVEMYELSVTDTMMLKATLFYWRMWQSVCIACVDTVASIEESAISVPLKLEAKLWTSV

LQKRTAASISPPLENKCIDALSQGMILSGGSGMSKRSRINRKSNEFLIAWFLAHKDNPYP

SPDERLEIADKTGLAEQQVRNWFANMRKRHWKPNRANVKKPRCLVDYMLRQTDA

>contig52193 Frame-1R

MKAQVLSLSLNEFTSFLQAREMWLKNVDERARLQLVEMSEGSFAMVLDDMEPTQTRDRDI

VLTVVKRHNSCSIVSSAAAIARVKALLDELNAADEGGEDGYDSLEFEGE

>contig52337 Frame-1F

MSRTLFEQLDGEMLSMLLSNRDFDSNNFVHLVQIETLNENRSCCAKLSLCGAFEFNNVAA

SQNSS

>contig52467 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57264.1|) 5e-16 NOT\_ORF

MTADTDG\*KKRKRNRGHYFLKNRSFKQIVDKEIDRLLKFGRY

>contig53712 Frame-0R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY64164.1|) 2e-17

MLNMQIWIVSTDRKADMCGCMLSADLVAKYNSTLDEAKSSTFVNRSDSVTASVELSKVKV

MVASSDTSNIDQQILFRSMQTLVEDF

>contig54212 Frame-0R

MSKRSTTKKVLRRCLGVVPKLQLDFDCIYHMSSYFDHSVTFVNGRTTTTLCGVISNSCTG

TSYLVCRCGGSARYTAKHYRSWTGSMHQNCCEICREPAASALSVTGHLLLVLFSTS

>contig54542 Frame-1R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY64041.1|) 8e-30

MVSLLRVLLVHPSLHCAGIVRLVHMTFNGLKLTKRWDALNAVSTQILDAIYAKIIPKDTK

S

>contig54883 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60187.1|) 5e-30

MAAVGAVVDAVFGSYDIKNAKHWRDEDLLHREQEMQWREDSIRREYEWRRADLQRERRVV

KLENEKRI

>contig55057 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69102.1|) 5e-11

MLYSLLAVLVVLHVSYKFQRFQQALRQHYQMIAVLNLPTPLVIMKSEYTQDEKSDQGG

>contig56889 Frame-0F|Blast-oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY53324.1|) 4e-32

MLARQSGHIVNISSDAGRKVFPGLGVYSASKMFIEGISQALRLENVGSGLRVTCIQ

>contig57613 Frame-0F|Blast-bifunctional folD protein [Phytophthora infestans T30-4](gb|EEY66137.1|) 2e-19

MVAKAVSPVPGNVGPMTIAMLLQNVVEAFKRHVALTC

>contig01116 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54868.1|) 4e-63

MTFLPYTKQYLKSNMLRLEARDVARMEKEKLDRALEPLMERITTYALRATTEPFDTIKTD

IAKDKELGTLLHMLLEHQDAWVLKENDY

>contig05237 Frame-2F|Blast-sugar phosphate exchanger, putative [Phytophthora infestans T30-4](gb|EEY69680.1|) 9e-10

MLYDAGQIVGGFIGGIASDRMGVRSPVVVTMLLLS

>contig06034 Frame-0F

MQWKDHTVELTGNYLTCQVSKRTPSGTLRTRPCNPTKRVMVLTSVQRVPELTFDRQDCFL

VTTTTSHSWRFQAHSKHDCHAWIQAIQQALAIAHGVLPKHLVLPQTLTSNFCHSTSQWQQ

TTCSPTHFPPQPVCVPAKNIPTPSCLSNHDVLTLLPHFQRNGRMKEALQLMHQHTTLRQD

YWPLIFHYALTYDPNNTT

>contig06755 Frame-1R

MVSIRVGMLMNNAFVALFVFVLAIHYQLFNRFEHT

>contig08915 Frame-2R|Blast-cyclophilin A [Phytophthora nicotianae](gb|ACR82293.1|) 4e-89

MPNPQVFFDMTVGGEPVGRIIFELFADKVPRTAENFRALCTGEKGKGPSGKPLHYKGSAF

HRVIPNFMCQGGDFTRGNGTGGESIYGEKFADENFLLKHKGEGILSMANAGPNTNGSQFF

ICTVETSWLDGKHVVFGRVVKGMDVVKKIESVGSQTGQTAKPVVVADCGQL

>contig09721 Frame-0F

MWSLGVFLAFGFAYSFVHSSSSASTDGGVCDPDYEQLDDLGESCECLDGFSGLGCRMCTA

STDFDVCSTAFGADYACVTGFSFDATSTGKTYTCSLSSDLQALFPNGSIDVTCDRNEQGT

GSCLAAVYNAKDTVNGEHVIDCNMTECSFPTGSVNAKCGAINCHCGPQCSSMSKSIIEST

FSGQPVEIQVMEATQVLTLVIENSPLPLSATCTASACERGGQRDRTISKAQSTPASTSER

VHGVALAMMACIILALLFLVACFSFCCVFLDKRRNVDEADLETELLKVSSRVTNKLEFIK

ISCYGQKSPPNQDERMILNSISGSVVRGQVMGILGPSGSGKTTLLNAIAAMENGTSTITG

ELLLDGQNVTKDYRRLAAYVEQDDTLFPALTVRECITYSAQLRLPLEMTAAAKTAMVTRV

LAELNLTPIMNSRIGAVGGSTSMRGISGGERRRVSIGMELVTSPQILLLDEPTSGLDSSS

AYAVLQVIQALARHDRMVILSIHQPSGRSFLLLDQILLLRKGQLVYRGSPMESKPYFLDQ

GFACNEEDTAADFILDVASNAENVPMFQQCPENLKRVHENASLAKSSGLIPTELFSPKTP

IGSPLYETSLRIADTSEGTSWGVLFQTIMLEIRVLSTRTALNLFRHRSLFIQHVTLSFVL

ALVTGLLFQNVSDNLAGFQNRMGAFFFILTFFGFASLSSMDLFISERPIFLR

>contig12952 Frame-1F|Blast-regulatory-associated protein of mTOR [Phytophthora infestans T30-4](gb|EEY69298.1|) 0.0

MSAASEQNTSTKQRDAHVQPSAPISKGLRSALSVGNFQQYQNKFQQGADATLGPDDGQAV

PFPAVSIGSSLCRGQYRGQLLSPTSGGSRAPKIGTSNNENKACDSLAQETSSLFSYSRHT

LFPLPLVSTFYERQKAHFNDPFLDPVLEDEDPLSEKGAERWECNSRYNRIRVAAMKLAPG

FALPRSATLDPAAPNTTEDLRYLSSHDPASYLPIEYDVARRVSTLGYHEEVKEFTLNLRQ

RAVLNNDAEMTSLLLFHPYETMLLVADEKDQISLYSFEETESKVLSFANKNPPGSRLTSL

NWINKNEKSLLTCGSDDGVIKIYYGLHSPHPTNHNPALLSAFVAVPDLVPGTRGSGLVMN

WQQDAGAMYAGGNSSMLRGWDLRQEKCTVALSTQTDSCITSMASDKCFPEILVAGFGDGT

LRVFDSRNKQDYAVKITMKEHSSWVVQTHMYAGRNELLTGSVTGELKFWDMRFPKNSIKT

LEAHRSPMTALAVHDYAPIFASGSHNQFIKVFRSDGEQLALIRYHEGFLGERIGPVTCLA

FHPHRLFLAAGATDSVVAVYSSDK

>contig13560 Frame-1R

MFCCFSFLVCSLLNFDQCISTKLFHFLLLPLLPLDALFLFF

>contig15359 Frame-0F

MDVGAEVDVQVGPQNWRRAQIIDRYARSIEASGAVVVVKFEDGSIAERAVPSDVNQDAPD

VRLLSPGQGQRFDVDDLTQLIELDESSILSALETRFAENKIYTNTGAILLAVNPFQKFPN

MYNKETMIKYLLTFESKSSSTRNKRNESMPPHIYQVAGEAYKAMMLGMNGIMSDQSILVS

GESGSGKTESTKFLMEYLAQAGVNNVAANAVSKSPEGIAAKVLQTNILLESFGNARTLRN

DNSSRFGKFIKLHFTSGGQLRGASIQTYLLEKVRLVSQSKGERNYHIFYEMASGAEPAAR

KRWLLDPPQGHAKSAGDHSNFSDASRQFSHYRYLSQSECFQRNDGVRDLEMFRRVMDAMD

IVGFTSVERAGIFDIIAALMHIGNLSFEHDENSDKAGQSTDSGAQESDLAPSCIWSRDAA

AMLMAVDASELERALSVRRIRAGTDFVRMKLSAAQANNARDALAKALYGRLFDWMVKKIN

HFLRMDDSEKAKGGLHFIGILDIFGFEVFPKNSFEQLCINFANETLQQQFNDYVFKAEQR

EYESQGVDWKYIEFCDNQDCVNLISQRPTGILSLIDEECVMPKGSDTTLASKLYRACGSH

PRFEASRIQRARGLFTVVHYAGHVEYSSDGFLEKNKDVLHQEAVDMLAYSTRKDSFARTL

CEGIGGSQDRLKSSPRQRAQTSKNRGASVGLQFKEQLTTLLETLQRTNPHYVRCLKPNEL

CKAGKFESERVLSQLRCNGVMEAVRVARAGYPIRLPLDVFVARYYSLKTKKTLVNKKHKM

SKGLPDPDAGVDMAVVSNEAKELLDDLLKIIPKENDANPQGACERPEQGHFVSKCFAVGI

QMGSSKIFLKKTTYDILEETRTQQLHRHMVKIFYAVLALTARSRYLRYLRAIQILQLRFQ

YKKLRKVYRRHQVLMIRRKNAGTVKNFIRSVVQRKKYVCFLAVVRMLQCRFRHRRRMLAK

RRMAAQAKKLADSKRQQQLAQTANQYTESSTVSSDSSSPQSLTSLFNDIESSGISNVSSK

DADEMFAYNENFPKHNLNTVDEQSSHLDPRASQRVSLRKTQSTNSIPQIGGLQVSQIHDS

NSSQGLLVHTPGSRSSRKSSFRNTRSSRAVALPRLDVIQHTSWVNDEDRFSCHICNKRFS

IFKRKHHCRACGEVICNSCSLYHRIQSRSMRVCVSCVAFHSLDSPTSAGSTGLLRTGGVS

PFSSNSSRKTSNGSAPDRNRSSTLSSGVWLNPWPEPPYPLDEDERLIVLHELNIRELGLS

GKFNMYCEVAAKTMKCPIAYVSIIEDEEQLLVANIGMAHTTLPRELSFCAHTICQPSVLV

VLDTKNDERFRENPMVKGEKGAVKIRYYAGATIFSRDGHALGTVAVLDTKPRREADQEHI

GMLQHLSFLASEKMTQSTIQEDSESDFL

>contig15665 Frame-2F

MIGSLRINAAFVPLDPGFPCERLRYMVQDSNLHVIITQRKFTDLALYVSSSSMDHDKIQS

PFVLYYEDMNLIPAMAPQTMKRLQRNSKSVTAYILYTSGSTGHPKGVMVSHAAILTTLWW

TVRKYSVSPSDVFLQSTSATLDGSLSQLLTPLLVGGSVRITRQNGLHDLHYMQTTLLGVP

SITWCVFVPSYFALLIDMLNDQGKSFPNSIKYVILAGEAFPMELARQFYLKHPSTTTCLV

NEYGPTEASITSTAFLMPREFVTSKSTYFLETLNSVPIGKPIDHHPVLVLDSQRRLVPIN

VPGELYIGGLGIARGYWNRPELTRQSFILHDELTDGVNLVEYRGQRWYKTGDLVKWVPSG

DLVFLGRTDAQVKHHGMRIELEEIRNVLLRHSNVKAAEVLSIPELGPALAAFVMPIHSIM

QEESTMLDRSDNVLRKFLQTHLPIHMVPQYIHFVSKWPRTPNGKIDLRVLASMANSLKNE

TCASKPKELQTNEPTITVQFAIDILRQVWVQALKLEPLHEDMVSNQFEANFMSKSFFELG

GDSLAAIRAIALAQSRGVLLSLEQFFGTSSLIEMAQQAATAMVDLRNVTSQTLVPLNYET

KATRVLFLFHDADGTVWKLYELARQLPFQVIGVQAAQLHVSSLEELAAIYWKEINAYQLE

GPYALGGFSFGCRVAHEVARCIVRDGHQVLPLILLDGLPFEILDTTETEREMAQLQVEQY

AREAFQ

>contig15711 Frame-1F|Blast-biotin-protein ligase, putative [Phytophthora infestans T30-4](gb|EEY59618.1|) 9e-81

MFGKQMTDELRYYARSERYLQTLQFWLEKSKPLYPVSVASGLSDPFISKFFSLLKTQELG

SIVLYSLTLGSTQTLLRETLKPPAPAGVLCYTNLQSSGKGRGSNAWSSPEGCLTFSFQSV

FTDGSTLPFVQYLVSLAVIKAVESIHVVVSSGSNPVKIKWPNDIYANQVKIGGILCHSDY

SNGKFNVTT

>contig18370 Frame-0R

MFLLKPPSSSPSVPDLSHRRLCVDLVASEWKYVAEGGANVLFRHRPAADATTSAVALEFK

GKLLRVKKCDVAIDSSRHECARDGAKPYVPHYPHPRQVLEYATHEIMPYMQQQLHRRDGI

RAANHRENTYLQVAELVDVAQAFLEGLNDHLLALESRPAHRRQSQIDVSLQCVMVLPDVT

LPPPDEVYLPQFFHSSQRVQEAAIETENNENYDAEACQDDCILNDEKPCWNESTNEEIIP

KRVPRTRRGTGNVFDCCFRNICVELKPKIGFKPHGPFVSRLKTQACRFCMHQHYKKRTGK

VEEISQYCPLDLFAHDVARNRRALRALQRTPQNNYKVFVRSAQDES

>contig20351 Frame-1F

MTDKVVKTKAVVFISDASDDHDASIPCTQVASSPSSSIVSDSDSDVKLEEMLNYLSSNTK

IKSIRKSAKLKSPPRTKKKVRSCSITTTSSLEKTPEPALKRRASEKSVSSPKTPPASRSS

KQKPITPSSTQ

>contig20449 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65879.1|) 2e-12

MKKHRQSPLQLTASALELHNETHKAQMQPQKVCPYGDGGGRRPHIEEKSIHEAKR

>contig20908 Frame-0R|Blast-nuclease, putative [Phytophthora infestans T30-4](gb|EEY58702.1|) 8e-07 NOT\_ORF

MCAAVFDDGNGFDWSRA\*EEHVSSDGSARV

>contig24588 Frame-0R

MFIWRWATKGLAANVRQEMYRTRSHCSASNFRQPPLILKHKLQRQILLLKLKPSRLAT

>contig25154 Frame-0F|Blast-serine palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56490.1|) 0.0

MGSRPELKEVAVKALTKYGCGSCGPRGFYGTIDVHEILEKDIAQMMGTTDSITFSDTEAT

SSSVLPAFAKRGDLIVMDDGCNDSILVGANLARCTVLYYKHNDVEDLERVLKSVREEDKR

KKRGSDCQRRYVVTEALFRNHGDMVYLPQLVELCNKYFFRLFLDESFSFGVLGKSGRGLT

EHYNMDVSEVAIICSSLAGSTASVGGFSTGSQEVVDYQRINSAGYVFSAAAPPFTSACCS

EAIRIMKNEPELFTKLRDNAKHAHDALSAGIEGYYRISSAVISPILHLRLLPSVVACAGT

EENQRVLQRKICDTVMQKCLAKGVAVCSPRYKTDQKLEPLPSLRVSVTATHSPQDLDAAC

NVIVTEAVATAKEILATFPVAAAPASGLRQRK

>contig26380 Frame-0F

MPNGLAASTAPVEMDDHTIDMWRDLADNGVECELCNEQYDDDDGDDGHIPRLLTCGHTYC

QSCLNDWATAGMSHMGTQSGELECPTCRRVTRLDGVEGARTLPKNYELLRARQEMETQTQ

THLRKLQAMWTTQVKEKEQLAKEAEEHARTAQRESVQASQKAIFLAKQVEINEQEKKRAQ

ELAEDARHRALVASQQAEALQIETENLKRQLQKDAAQLARVQLDASSAAAVAKELHTKAE

SLQQQIDCVRAQLSLHSGRHDPGKLVVLVCEPTTVGSWLLPYTRYAVISIASDTAKGAHA

IDPYQAAKTWTQLRQVEEPCSSVKVYRRYSDFVWLHLELQRQYPFELIPCVPGKQLFFNK

EKEFVGERMRLLQAFLRGVLRQPLLAVTEEVRAFLLSTTEELESLRRATAIYYSSIEDDD

LLAMNEDVTIDSCESRKVSPNSSPPTSMIVSKRGSKWSAWSAVSAITSSAAKLVSTTGTA

LTGIGSRTRTVGYPEVPEVELSSSFLAVENADATTRMVLEHRRKYIDVARSYQSVAQKGC

QLSRASRFQSHHLHRLCELLYDMNKLDQDHARRRRQRLAASVDVKAHQEDEDDDMETQAF

DERASDVFSAISLNTKNDADSMEYALLEVVRMQTLELGGIEDAFARVRCREEGLQAPQEA

SKCAGSEGEPLFPALALKCEELEAHRRELNAKITKLDPGRSQFVLSVLCKNTSEMHKLAK

TKRKLFQASQQQLVNVQR

>contig26797 Frame-1R

MFLMVPEEVPKRFNHLKYNNAESELPCLTPRVGRLASCT

>contig29204 Frame-2F|Blast-Poly(A) polymerase, putative [Phytophthora infestans T30-4](gb|EEY66225.1|) 1e-166

MQSSTFTVAPYVLEQAYKAIRTTPPEPKDLEQSAKLQSFMDEHFPTESDLNITRRSIILA

ELRTIFRSWVKKVCMEKGVPEEMAADAGGQILVSGSYRLGVNEPGADIDTICVAPRHVSR

EDFFSSLKEIFLKHPKVSQLVAIEGAIVPLITFDYEEINIDLQIAILPRNSIPENLNILD

DHVLVGVDPATEKSLNGPRVTELMIKLTPNRESFICVLRIVRRWAKRRGLYSNKMGYLGG

VNWCILVCFINQLYPTAAPSTLLLRFFMVLNNWKWPLAIQLCKSHDTKLGLEIWNANAGH

NR

>contig29415 Frame-2R

MSRSRQRFDPSQDYLLAVQVNTDLPFCAPYGGLMARWEKIALTLNDSKAFKMHHLKGPIA

KNRFERLVSRYRNWVKSGSHPTNASSQDAAFQSVMEEVIPKLDVAEKELLSQTLGKRGRP

RKFQSESNEAPENKKPLSKLSHVALAPSPLQPQPSLPVDSDNQLQPAGAKASRQRFTPKD

DLLLATFVKETLPFRAKFGAISMAWEDVATKLGKSSEFSKENIKGPIVRYRFENLVSKYR

ERIKRNEGRVVGPKGVPAGELEELMTELVALLDGGDAATAAVLARNVVTGIGAVDSAAPR

ASTTQDEDSNSCTQSESSPPPRSSPELASVLNQSSPTEQKRSESIQLAGKSAELLNEQFL

ASSNKTNLTDVAELKRMLNKMMEHQIQFTENMMLLQREERLNEAERQKAEQVRQREEREK

DRQALTATVTSILMTALNSYSAARIENESSTL

>contig29868 Frame-1F

MGFTNDVAFAAGPVALEEFGDEPHQELQQAGSLRLPSYTSSVGGGYTLEGDLHGINEQLQ

RVLAFCENQRESPQRLQAKIRDLQEELRQAIAEKNYWIKRCKDLTSHYPRSTETTEVDLQ

CAKSLSHKRTNSELIVIADTWEQPGRDGIVSVENSTVVGSDASTSNEADSLVNYSTVPRA

IFRLMQCSDEQCEVFIPTNRRIHTRHRSRNNVQLMWDEPPKTVLVIKKPNEPETTEMLIM

LTSWLLKEKKMDVFLEPSVFEELALANTKTWGHKPEDWVDCQNKIDFVVSLGGDGTVLWV

SSLFSKSVPPVFSLAMGSLGFLTPFDADNAVEHLTGVINGGFYMSLRSRLSCTIFRGSTE

RHIAGNLHALNEVVIDRGPSGALVELNCYCDGLEITKIAADGIIIATPTGSTAYSLSAGG

SMAHPSVPSMLFTPICPHTLSFRPLIFHDSATLKIEFPSTSRASACYVSFDGKDRVRLER

GDSIVVRVSSYPLPS

>contig30624 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY62320.1|) 1e-115

MFAPMPQSNGLQQPSTSIDIQYGHPATPLSSNRHHKKKSKRAGSDVFRSCSVFPEYFTRV

LDYRQMDLDATFYQMVTLCVQPSKVYKSAYYRKQTKNRWARDDPAFIVIQFVFLLVATVA

WAIAFHVDSVAKFISLLFHAVVVEWLGFGLLISTFCWWYANHHLRQRNIVGAGGSLYVEQ

QVEWQFAFDIHCNSFFILFLFQYVQQFVLAPILMSDSFLMLLLGNLLYSFGWGLYTYITF

LGYLALPFLHRTEQLL

>contig32604 Frame-1F|Blast-riboflavin kinase [Phytophthora infestans T30-4](gb|EEY53210.1|) 4e-35

MPITGLMTVLRLQATVVEGFGRGGKQLGCPTANLSSKDLGDQLELLPTGIYCGWATVDGI

GPYKAVASIGWNPYFKNK

>contig33131 Frame-0F|Blast-ATP-binding Cassette (ABC) superfamily [Phytophthora infestans T30-4](gb|EEY69033.1|) 5e-24

MRTSFEKESNVTKSFTVFDTLAFSRPERRVFVMGLVAAALVGGALPTSAVLISELVATMT

RSYTLLKESNVQSARDDLKQDVTVYGLCYV

>contig33294 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53037.1|) 3e-77

MADRVSIAFRGNEWTEPKLLVTAGWIEGKLDDVMYGVSSPDAQSMLLKATVVKNTLINGG

VLACIDAPCDADPFRFLGIKWFVKGPPNG

>contig33777 Frame-0F

MLLHGGGFEHYDTGRVTHVIATHLPASKLLQLQKAKKPLPVVHPDWILQSIEQNKLLPLQ

RFLYTGLSDPTQSSILNLSNSEVSVEKTDDDICLDAAVEASERNDNDDNDEDQFQMVESP

SIVRNRNSTPKLRTNSTKDGPDFVRHYFAKSRLHHIGTWRATFQQKAAEFQAAYKGPAVT

KASVLSNNRVILHVDMDCFFVAVAVRGKPELKNVPVAIAHSDKAGSSEVSSCNYLARAKG

VSAGMYMQLAKEKCPELVVLPYQFDAIQRVSFQIYKVFFSHTPYVQAISCDEAFLEFGHG

TNGMVKAETIRQEIHEQTGCIASVGVSFNMLLAKLSSTKAKPDGIFQLATLTQAEEFLLS

RTVRDLPGAGHVTVAKLEAIGIQTVQQLMQLTKNELIQSVGKAFGEMLYNYARGIDTRAL

SMELNMMRKSVSAVVNFGIRFEKWDDATVFLMALGEELGLRLRNLKVRAQCLTLLIKKRA

EGARIEPSKFMGHGICDNFSKSHVLPQATDDDVVIGKTCIELLRQFDFPSHELRGVGVQA

TKLISDVSIGNQRRGQLFTAWLENSAQNSKDAAGSKSTSAKTIASGAGSNTDTNTNEFEA

TTFSQINMEVLEELPKHIQREVLASYKHDVPRPTNIQLKHNG

>contig33841 Frame-1F

MVKRAPTCPPIDRGTVGTLHEPINRYVGIG

>contig34291 Frame-2F|Blast-40S ribosomal protein S9-1 [Phytophthora infestans T30-4](gb|EEY55616.1|) 1e-103

MPKISRHRNYRKTYRTPSRAFEKERLDQELKLLGEYGLRCKREIWRVQYALSKLRKAARE

LLTLDPKDPKRLFEGSALLRRLKRFGMLAEDENELDFVLRLNVQKLLERRLQTKVFKQNL

AKSIHHARVLIKQRHIRVGKQLVDVPSFLVRMDSEKHIDFAVTSPYGQGRPGRVARRRAA

QRAAAGGEEDEE

>contig34912 Frame-2R|Blast-serine protease family S28, putative [Phytophthora infestans T30-4](gb|EEY54987.1|) 3e-28

MGKSIPNNNLSTENYQFLTVQQALADLKHFKDTYQSLLGTEDADQWIAIGGSYPGALSAW

FRVAI

>contig35968 Frame-2F|Blast-ribosomal protein S10 [Phytophthora infestans]gb|EEY57701.1| 40S ribosomal protein S10 [Phytophthora infestans T30-4](gb|AAY43413.1|) 2e-76

MLVSKANRIAVYSYLFKEGVMVAKKDFSLPKHEAVDVPNLQVIKLMQSLKSRGYVKETFN

WQWFYWYLTNEGIEYLRSYLHLPAEIVPATLKKQAARPTRPQAPSAGGFGRGRFDKDKGV

GPSGDFNPEFRRGGQDGYRREGAE

>contig37261 Frame-2F

MVKRIPAASAEFLQASSTVSTTSSACAGNVPPLANGPASVSAVWSFFEKDQSGNSICKFC

ERVIKGHHSSNLLSHLRTAGRTDPTHQHANNVCEEHRETKRYHKRQKMGLQAVAGGQSGV

DFVAAAMYPPPGNSQTLAAAVAAAGSSPGIFTAPIKRDPASNFYAYPPPALNFSGLAITK

EQRLALGSAYGAQPVQINADQFTQDLAFMALMDNLPLNFATKSGMEYLMSQVLGDKKLPL

PNEETIGKCILFLQESMLLTAKMVLTRAKSVAVSLELWQHPSPALLRPTQYLAVKIHFSV

NF

>contig38202 Frame-1F|Blast-cryptochrome, putative [Phytophthora infestans T30-4](gb|EEY64676.1|) 0.0

MEDTWEEITHEIEEIAGPELQFTLPEVVDFGYVVPDRHPFIYGGEQIALSILHDYCRNEG

RVVKFEKPKTSPAQMTPSASTTSLSPYLYFGCISPRTFLHHVRGIQEHYAKALSATPVSL

DGQLLWREFFHCHGRANPYFDKMEESPTCLQIDWRWHTIPEKEEDLTDDDKLARSHFKSW

TEGQTGFPWIDAIMTQLKVEGWMHHLARHSVACFLTRGDLYISWVRGLEVFQERLIDHDW

SINAGNWLWLSSSYFFAAYFRVYSPSTFGKKWDPEGLFIRKYVPALSNMPNKYIYEPWKA

PMTVQYAAGCLVGKDYPFPIVDHKIAMRRCMAGMKKSYGINKFGTPPVPRVLSSPRTKRL

REGSFS

>contig38277 Frame-1F

MSRLTFISSLALLVTSCKAQIRANDEICVMGDFNYCPVDDLTPSALDRSIVIFPGGATRC

AFDDFSVPGANYTTNSTYFFQVFPAPSKTKLMLYFQGGGACVDEATCSFGVQCMFQTFNA

NAKPLSNGVLDRSNVENVFNDYNIVHLPYCTGDLHVGSTMKSDFGSTLNSSLNRPECLGH

NMSLHMVGYNNTMAVLEWAVTNYPNPEEIIISGYSAGAIGAQMVSGLVADIWHVKEKNIR

YSVLSDSYVGVMHNEEAAGKILSTYGMCDLDLKLTNSLQDACKQTTVSFTGIISHLITAT

TDVQWLFIQSMYDRDQRFYYQLQQDGVTGHPFTSLVSGEDFYSKMMAMIDVYKNVSNDIS

TFYVNNSQHVFL

>contig38431 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59383.1|) 8e-20

MWFNRYESRVVDLNSLSVKLHYRGWTSKLDEWISKKSNRIAPLHTKITNWRAFTVGDGVM

VGREWRTKRF

>contig38729 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53577.1|) 1e-118

MKMGAFEYTPPRDKSSGLGGEEKEIDGTNSSIDSFVVPEFSTVRLSTSTREKCAINADDE

QGSSDTSKSVSNRKRKRSIAGEIRQTPVFPKTLHHTKSSSPFRSPSLRRKYSSRSNVSSP

SHHRAHLSVASTPTRQQNDARFDVDTPRTPDFNLASPLLRTQLKAMTPNTPLSNRLVGAS

LDVGSVSQEARLLDYDDSFSAGEPTPKFELSLLPVVFQRGVGAVQVSTLYSKFQGAEGDK

PAISVDQLSEMLPDYGKEKIEILLDTLV

>contig38989 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69630.1|) 4e-76

MNVSDAGNLLTATGFSLCTVDTDFIQVKYPNAFLLMEHLRGMGENHAVDSRGAPATRESL

LAAASIYQSMFGNPDGTVLATFQVLYLIGWSPEKSQPQPLRRGTAQHSLKELGRD

>contig41206-0 Frame-0F0

MPQGGRMAVVENLISCGHGRWEDESKTRCRIMWKKPVEWAAEIYDF

>contig41206-1 Frame-0R1

MAAADKVFHYGHASTLRHVPRNFYVLEQSRGKRLEKRQFMRAMVLENKLLPQYKLLFARV

TYGLQREKRRKVVVL

>contig41783 Frame-1F|Blast-pre-rRNA-processing protein TSR1 [Phytophthora infestans T30-4](gb|EEY65644.1|) 1e-118

MAVPVTALQARLEAGPLVMGALLKHENRLSVLNFSVQRASSFAGETLKSKDEVSFHCGFR

RFQGRPVFSDQSLKSDQHLFQRFLPHTGWSVATVYGPVTFQPASLLLFKSDGQLVASGTL

KNVNPNRVVLKRVILTGTPVKVKKRNAVVRYMFHSAEDIRWFKPVELSTKHGLSGHIKES

LGTHGDFKAVFNKPIKQHDNVCLHLYKRVYPKFP

>contig41912 Frame-0R|Blast-mitochondrial carnitine/acylcarnitine carrier protein, putative [Phytophthora infestans T30-4](gb|EEY64441.1|) 2e-91

MAGSSAGLVQVIFAAPSEHVKIQLQTGAMGAEHSSLTVGRMIVRRYGVSTLYRGWQMCLL

RDVPAFGAYFCGYEATKQWLTKGNSENETDLKLMMAGGIAGMFSWMSSLPQDVLKSCIQS

QSLEGTQLSIPQIARTRLATEGPGFFFKGFGATMLRAFPVSAVTFLVYEKVLQYMS

>contig41967 Frame-0F

MLSIITVCTLGCQDKSNTMVLSPQTSKGLAHDMDIRLWRVEVALAMRKLLSLGRTFEVKY

ALPRGPVANLQLATHFGISVSSLMNSHVFQVQKVEVSPYSMEFVEKIAGRTLASIYTIET

DDYFVGINAHDFLLCPRKLKQLHKDVAALGEEVTIKQENCGNKTLVLRFIRMGKSVQPDL

RMGRTPGRMLQLLDELTIHHQQLVRRYDAII

>contig42188 Frame-0F|Blast-chaperone clpB [Phytophthora infestans T30-4](gb|EEY63422.1|) 1e-168

MLANRYLTERKMPDKAIDLMDEAASRLRLQQESKPEPIEKLDREIMLRRIEIEALRKETD

SASKKRMAALEEEVKKASEELRVLLDEWNAEKLKLEEMQRAKRELDEARRDLIAAHNAGN

YARAGELMHSVIPKLEVQVAHEEEEVEERRLGGKTSRTSLGDAVTADHVAEVVAQTTGIP

ASTLMEGEKQRLLKMEDHLNQHVIGQEEAVKAVSNCVRLARAGLHAHNRPIGVFMFLGPT

GVGKTELTKSLSEFLFQSPQALTRIDMSEYMEKYNVSRLVGAAPGYIGFEEGGQLTEAVR

RRPYQVILFDEFEKAHHDVSNLLLQVLDEGRLTDSHGRLVDFRNTVIILTSNLGSDILAK

LPEGAPSVMAEADVMNVVRSQYAPEFLNRIDELVLFNRLKREDIYRIADLQLRQVDQLLE

EKELTMKIDLKAKEWLATTGYSPLYGARPLKRLIQQYVLNPMAVKLLDGTAGPGQVLHVQ

A

>contig42944 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY69399.1|) 2e-61

MLQQQFNQHVFVYEQEVYVEEGIDFSRLEFKDNGPCLDLIDKKPLGILPLLDEQGMLGRR

ASDEIFIQKLHQTHLQKGKVREGSVIYYSKPRF

>contig43338 Frame-0R|Blast-inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY65488.1|) 2e-28

MESIDKFAAMSRKSAPFLGNSSEKILTLNEAVALHKNKPLAAKLTPQIQVPSSPRQTLSH

SLPVTQSSRQRKSESAAIKSSSSKSDKVKVGHGKIVKDAAPTIPALSKDDGLIQLSDASR

LTEQTQRMKPKLKVSESGRFEDQYYHAHDGSNAMARLRKRAYQKNRTVHMTGNDVEQFSD

ADIITSGYLSQRGFVLEVVATPLFLS

>contig44753 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65867.1|) 2e-57

MQSNTQLTRLMKAALLQTLLHAIRTGSVEGVKVAIERGVQVHYLDSRHRNLVMLAIKCDT

DSRLRIVIILLDAGCDMNHKDQLGWSCLHYA

>contig45624 Frame-2F

MVDDVEIKSSPTPTKEKNDIISDDGDNERCNSCVGLQDAWSDSKSRNEAAKGAQGRSK

>contig46131 Frame-0F|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY67420.1|) 1e-116

MAHGHRFAVLGPRSSGKTRIALEMMAYQVAQAKANGEQPPQFVFVCIGKSLSRIHQIIDA

LKQSEALPYTTIIASSDRDSPVLQYLAPFTGCAVAEFLMHNGKSDQSVIVYDDLASHTMV

VEGLIQSLKLPRAAHASLSAHTVLMERSAQFKGSTQKEGGPSLTSFVLGDAPDSSEIATE

FMERIVSIVDDYVSLEYSLAQSRVFPPINVLAPGASVRGPPFQSATRWKFVSRLRARINA

AAQVKQNIETARKLG

>contig46229 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70496.1|) 8e-38

MVLQLLQHQPRVDDILGRILAMQKREQTARLQQRRDEELMRRLFSDEQRKLFDAASRRNE

ALDEKLACLAADCNSLHEKLKARETEVYFQKHSLEEAIEPLNKRVEAIEASHAQQLSILR

QIESKISVCNGFIDDGTSLRQLPG

>contig46294 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57513.1|) 8e-55

MELETDTKLWPPDVQNSKLPLYQRDEDTLVLMKRALVFLQELLRCSTSFESHHLISEREI

QQVLLPILHFSRRAIGIQAHEVGRHTGVSEDGVRLPLSVVYAMLPRVHVQGLDLLSILME

SAGLCALRHASKITRVLLVALESSKNDDDLQALAHTIAVCVRSLGPVQWKNLVCLCYTR

>contig46702 Frame-2F|Blast-kinesin heavy chain, putative [Phytophthora infestans T30-4](gb|EEY57642.1|) 2e-68

MVTAAEIRAGIRVCARFRPQNKLEQKHQAVDCVYLEDSIAAHVRCEARGVLDAHSFTFDQ

VFGTKSTQLDVYKATAKPLVKSALRGYNCTCFVYGQTGSGKTFSMEGVPGDKDYEGIIPR

VMADIFDGIQKMQAELEFIVRVSYIEIYME

>contig49105 Frame-1F

MVISCCMPPFLSIVSSTLPHHAFIVEFHLCKAWN

>contig49578 Frame-0R

MSMKPEKWSAVSAIIKLSVQTDVVIPQDRTNEEAIRIISWNHEHYLLFSLWLL

>contig50068 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53794.1|) 5e-14 NOT\_ORF

MQRLLHTFATKITPALSMKLSAAPRSASSTWTEHYMYPVASEACGGADNLAQDNTLSYAD

TS

>contig51179 Frame-2F

MAPLGPFVESEKAQMELYNTPAETNSEEILEEELLVAGQTLNRFEVSKRKKRQRRRSYIS

PSLHAPSLAGGAQRVQIPTQLYKHESDDFHIESDDTILRIKPEIDMGSRRVSVLALQSKS

EEFEESTSLQLIEEPVFSKKTVSLDSISTTFRVPHLISRQIKSEPTMKQRKAFPLREKEE

IHQECYADMNFFHDG

>contig51302 Frame-2R|Blast-phosphatidylinositol kinase (PIK-L3) [Phytophthora infestans T30-4](gb|EEY66032.1|) 1e-53

MSCVAFQDTEVFQLLVVEYLSSKSPTRKYAKKCIDTIASLQDLSASALLYP

>contig51485 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68496.1|) 2e-35

MSVFSRGFADFKGKMQDHQA

>contig51531 Frame-2R

MNSVVQRKLNHRALNSTASASPHTRCANDAIYRRRFKCLLEHPILVVLCPHRNSSVGYIQ

QSIK

>contig51629 Frame-0F|Blast-peroxisome assembly protein, putative [Phytophthora infestans T30-4](gb|EEY68846.1|) 2e-31

MALSRAFPAAGACAELLLSEGKDNVYEKELKNLLREVLERGCGAHLMSQLLPELAALSSL

LYYTLSIGMLQPSQTLGEEFCDIVRVTK

>contig51694 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58265.1|) 1e-94

MELQRVLEAYRAMAPVRHLIELIKAQFDADCQWASLEVQAQVMQVVIHDKVCEDFAPLKK

YTYNFLKTYVEAIEAEHASLDDGLVESLMEYVQSPQWNEDTLNAEAMHYVSYTIPSIDKS

VVVTCRVASVINEVGLKVWEASSLLAEYIIAYQREFRDKKVLELGAGVGLTGIVLACVCH

SRSLVLTDYAPNVMQNLRYNVEINSSHFCCPVQVQALDWETWEPHDDKSERPDVLIAGDC

AYDVA

>contig51834 Frame-0F

MNIFTNIPSPSALQARHLWHSCLPSIVFLHSCLLKFLAFPVGHYSHSEALYVLLA

>contig51889 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55608.1|) 3e-11

MVNPLFKSKASSYLPTLAEMLEGVQWIRDNPVIAAGVVVGITSYSVIKYCERYADHGAEE

DDLIKKQSIAAR

>contig52839 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70526.1|) 4e-09

MLRLFRIASKVSAPRTRPLHNSAPSSFLLRSLEDVRQSGRVITSIDDALET

>contig53713 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68151.1|) 2e-30

MFPTAEDCWNCHHATDCCSFFCTACKAIQPIDTGCHCDYFEIFKV

>contig54213 Frame-1F

MPAKHSRDELSGSSDDEGPMPMPMPLPPVKKRTKTLPFESMYLNNLPSAAMYERSFMHRT

TVSHVLVAPETQFIITASVDGHVKFWKKMGKGIEFVKHYKAHLSEICGLAVSADGLRLCS

TSADRSIKFYDVLAFDMVNMLSVTYTPAECCWISAKGAIDPKVVVADKASSVLRIYTAES

SSNEPVHVISKLHAASVTALCYNAMANCVISADHNGLLEYWDADTYVFPRKEPRAIQFKF

KSETDLFELAKCKTFATAIDVSLNGQSFVVSAKDNQIRVFRFATGKLRRKYDESLTVFED

AQADEALHLDALDFGRRAAVERELANSDVVSNCVFDESGFFILYATLVGIKVVNIETNTV

ARVLGKVENSDRFLRLNLFQGKPKVSTQFEKHLKATSGLKYEAQVMTDAINERDLIDPTL

FCTSFKRNRFFLFSSREPEDDEQQATGTGRDVLNEKPTLEEAQVATESSSVISGHTAVMH

TTMGDITLKLFGKECPRTVENFCTHARNGYYDNLIFHRVIKNFMVQTGDPQGDGTGGESI

WGGEFEDEFHRNLRHDRPFTLSMANAGPSTNGSQFFITTVPTPWLDNKHTV

>contig57245 Frame-1R|Blast-ATP-dependent RNA helicase DBP2, putative [Phytophthora infestans T30-4](gb|EEY64135.1|) 9e-85

MDDHQKYSTLQDHLRDIYEGGRIIIFCETKRGADELSRNLRNSRYMCKAIHGNKSQEERD

YVLREFKEGKTQILVATDVASRGLDIKDIRYVVNFDMPKNIEDYIHRIGRTARAGTKGTS

ISFFTASNNGRLAGP

>contig59474 Frame-1F

MCKIGLLPILPASMSASSTLSPHLQAMKPLASTATTSAVPMPTAMVGALNKRPSTSVSPT

PRSPLKKPRTIPPNRGKATAAEVAALSAAASEMVSQELAQASVADIRKEADVLTHTSIEL

GTERRIMTEGRVRMVEQLRCQKEAWVEKDLFNSEKLRMQIRDVSRRAGVELGSQSSDVMA

YALHVYLKQVIEEMVEISKQRSDVQAQSLEALQKAQQMGTLMMSGRSGPMELTATDILRV

SCEDSYTKLRQEDLMLRSQLLEDAKREEQIERERAKKRKKVDRSKLTQDERDEADMDIEE

LARKDLRERLLQQDKSGLLKVGGRVNESIATKYIQRPIDNQVTMEDASYWLMSQKPYIRP

KLFVRAEAARIVTKSLL

>contig06510 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61223.1|) 5e-06 NOT\_ORF

MGWLLFL\*FASQLAKKAELRAERFGLNGETKKRLDRAKRFGMENSKFVRSLLVGSLSYSA

F

>contig07162 Frame-2R

MVPKQKLSILTAMPFPFRRVTSKIKQEALQHFMSTEDQVEVQNTAVRWQQALHYFTFPAD

PLPTFILLNRASTGSTSDLFCGGMQRECQREENDFFTARWNLWQEAFRDVYINFRYQFSR

QMNAGGKEISFYLCSSDFIVTILYEAEEQDASKLDMSIIDLCHQYDAKNESMQVANKKSS

QTCRIRAVMSRSSARIRKSLHQLNVAYTMPYIEANQARREVGEFHLLEEELKASHQQNKN

RHSGTGIAPLTPTTATPEAMHGADSLLLFHGHESVHGLYEYLINRTPMSNQDVPKLYALH

PFANASIQSLRVATFGQVDTITTRSVSVEPISRSVSLFRLEILGFCFPSSITKLLAVLAD

EWQANYSSSH

>contig07687 Frame-1F

METVTNVSEYEAKRLLRIEENRKKLLSLDLPTLPTLSPLKTHSQKRKWDADEKPPEPSRK

SLRQHQTRLLKSEQRKLENKPFQPQFQLFPKELQQCNPSQDMLEKHQLKRHKELLNESFC

RSKRELKEKTYWEEEAVIRATQPQSEQHLKVSDWKLRRKLEAQPERRQSLLNVREDQKAQ

RIQDTAERIKQRVIAQEQKRRTKEQQRLEKFVLKELEKEQRYEEHQCMRQEDALARQWAK

EHTKEARKQRRIEKEVANQTKRLMRIVAKNLQAETTRDKEVYSIRKIHIPFVSISIATAK

YKHKLPSDLKVDTHVFHDFALGKQFLPPGKMAVIQSLCPGGYTASVCQDVNIYVWKNALT

LFINGANAMYYHHFFQETTHCGRNYVFFRYLRCEDFTPLILERLCRVEKGKEWLRFATNY

YDIPESRNLEPLLLFIQYP

>contig10508 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70527.1|) 1e-153

MEIEKDLPRTFPVALCPSMRQSQEFSQECDSFGELRRVLQAYSLRNPAVGYCQSMNFLAA

VLLQNMGEEEAFWVLAAIVEELTPQYHTRTMTGSRADQRVFSDLVTQKLPILANHLQELG

VDFEPFTLKWFLCLFLNTLPFEPVMRIWDVFFCEGSHVLLRVGLVLLKLNQPRILACNDA

LDVYEMFKLSHDTLQALTAPYRSGLLNRDECVCDTLLRLAMDKSFLGTISFDTLHELRQY

YRCEIEAEVEEDEARRLVRQHRAYAQAIKREATSSTFRSVCEDRALMMEYDFVDDYACST

QSETSPVWHIRFMDLYDSDDSSADYFVDVMYDFSLQQCR

>contig11653 Frame-0F

MKSKQPKWKNFHCPPLSGSRKEQIIREANHACNELLRFSASDTFRSTDSSLDSDEDNLQW

EYTEQLESIRIEKLKITSGTKKSVYYFRGITDAEASIEEIMELYNVDMAHPHIQLDKKLS

PDILHSVVLYEIKPYRVDESTVFIGIRWLALRSPYVLVRNRDFCYLEIQRRFCLPDGRRG

FVRCLHSVKIKSCPDMEKSHGFVRGSIYRSGLVCIESKRDRKTLDIIQAFYTDLKGNVPQ

WVAIKGLRQRLLSLEHLKKYVNMKRVANQTFVRRSELMAPGKVKTCFVCVDDIGTFSRRY

NCQKCGEV

>contig12292 Frame-2F

MLGKMEMSAHSYRHLYVLFATFQCFLGAGIIFGWTSLLPTLEKEKIYFELCTAGENTCKA

QSDHLQSAFTMAVSTSMWSNLPLGLLFDKFGPRVTISIALMLLIAGALLMGQAHYRAHAQ

EHDLLLYGMVLVGFSGPGIQLCGIHMSNLFPESTALVACFIVGGLQLSFLIFTLFDLAYV

HLGMSMATIFELYAAILLLTLVGTLLTEPDKPFEAKLKTEHELLSPMRLPSGLKDETPLL

LTTPELNMYRRNQRFAADEGLFCSDLRNHSFKTQVLSKPFLLIIFYFSILSLWCNFFVGS

ITGLLRWKGFTESEVASLLAKLAFVLPGSVVFIPLTGYLLEKCGYTNSSLLCTLVALCST

VMLSSKSPGWIVAGFVTYAFFRTLMFPLLFAYLGHRFGFQHYGALSGIAFCIGGIVGLLQ

TPIASIGDFQTIGYVQFGSLLLTFIMPYYERQRRN

>contig12483 Frame-2F|Blast-ATP synthase subunit gamma, putative [Phytophthora infestans T30-4](gb|EEY62471.1|) 1e-118

MIENSTSEESSRMAAMENATTNAEDLIGSLTLVYNKARQARITTELIEIISGAASLDG

>contig13413 Frame-1F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 9e-07 NOT\_ORF

MTYDLLDGNVGDVMVTHRSERYC\*VNSIITTWEDTGAS

>contig14315 Frame-2R

MCILFYILYICKTICVTILF

>contig16854 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54480.1|) 1e-35

MRFTLKLSMGTSHEEYQNLAKKNQMDDLHLSIVKLRDRVSAIQRNQDYA

>contig17758 Frame-0F

MTINVVATISEDLLPGKDLDNIKATAPRVPNNVLLLFVICFSSFQRCNERRAGSPHGFER

RNTRLILKESTELRYTGR

>contig18416 Frame-0R|Blast-urease accessory protein ureG, putative [Phytophthora infestans T30-4](gb|EEY67689.1|) 1e-121

MKHSQSPDHRHSHDHGHSHDHIFSHDSNLSAGHNFLQSHDHESTHLVDGDDAVRRFSKSH

GRAPTLDEENQTRQHGHTHEHMEHAGIFCERDVAKSGRNWSHRAFTVGIGGPVGSGKTAL

MLELCRGLKDTFSLAAVTNDIFTREDGDFLVRHKALPEERIRAIETGGCPHAAIREDISA

NLQACEDLTDEFNPQLLLVESGGDNLAANFSRELADYIIYVIDVAGGDKIPRKGGPGITQ

ADLLVINKIDLAPHVGADLGVMDRDAKLMRGEGPTIFAQINQGKGMQDIIDHMVKALKAV

A

>contig19792 Frame-1F

MRPFTTCKNSFSQFETEGCLALTSTKSNDVNTALRGRQLTTVFILHVNSAKVYQFIPIEG

AQLIRFQNFPRTPGHSLHGQICSATVQYMYDMQYPATNARDTHTPSLLCRWHRSAIQRHG

CIIR

>contig20899 Frame-2F

MPAEKHSLEQLKDDVTQVLGKVKDIEATLEKVPTTAGMTYLQVKNHALLSYTKMELFFAL

LKVEKPEKVKDHPVFKELVRYRTLLERMRPLDRKMKYQVDKMLKVALSGGKGLDEALNYA

PKPDQLAAEDEPIDDEDDDGGDRSKDGVYRAPRLAAVPYEEEERAQVKQAKKDERNRKRM

QKSTILAELREEFSERPTEILASGTSGVDREIAREEAEKKEFEESRFVRVVTSRKDKIRK

RKREMESNRADNVSSIDNFAAVQDILALDKTKHRIPTPRESKTVGGATGGIFSHLDRPKE

KTRQGTRNAGEKRATRNAEALPANQLSTSKGVGKKTKVVFTNVFS

>contig21203 Frame-0F|Blast-heat shock protein 90 [Phytophthora infestans T30-4](gb|EEY69894.1|) 0.0

MSAPEAETFAFSADINQLLSLIINTFYSNKDIFLRELISNASDALDKIRYSSLTDADVLD

TDKNLEIKVIPDKANGTLTIQDSGIGMTKADLINNLGTIAKSGTKAFMEALAAGADISMI

GQFGVGFYSAYLVADQVVVHSKHNDDEQYVWESAAGGSFTVTPDTSEPILRGTRIVLKLK

EDMLEYLEERKLKDLVKKHSEFIGFPIKLYVEKTEEKEVTDDEEDEDEKEGDDDKPKVEE

VEEEEGEKKKKTKKVKEVTHEWDHLNSQKPIWMRKPEDVTHEEYASFYKSLTNDWEEHAA

VKHFSVEGQLEFKACLFTPKRAPFDMFEGGAKKKLNNIKLYVRRVFIMDNCEDLMPEYLS

FVKGVVDSEDLPLNISRETLQQNKILRVIKKNLVKKCLDMFAELAEDNEKYNKFYESFSK

NLKLGIHEDSTNRTKIAKLLRYHSTKSGEEVTSLDDYISRMPENQPGIYYVTGESKKAVE

NSPFIEKLKKKGYEVLFMVEAIDEYAVQQLKEYEGKKLICATKEGLKMEESEDEKKAYEE

AKAATEGLCKLMKEVLDDKVEKVEISNRIVESPCVLVTGEYGWSANMERIMKAQALRDSS

TSSYMSSKKTMEINPLHPIIKSLREKADADKSDKTVKDLIWLLYDTSLLTSGFSLDDPTT

FANRIHRLIKLGLSIDDDDEISDETMEDLPPLEGEDEEESTMEEVD

>contig22259 Frame-0F

MKSKVPTFPHFLVLVNALSLLASLDAAPLRDAAASHAISVPSKTEDPSSRIEERMINVPY

FIQKMSKVPEKAVEDVSEAAVKVGENEIEHDKSIKELYNFLVDVEHRKPTFEEAALTKPL

EEEYTRLKFVTEATDISNTKDSTEKNHKHQSDVPETLSANEASTIAKLILNNPNNLNLPS

LKSFLDSYPGLYYQVLSVELEKTFSHDIESLSNLLKQGGDIGMILQVHRLNNWRKEIDSS

SFSPLFEVPEFEGCLEYLTSKDFENWIDLITRINVDAAPYKILLRELKNRLSFDQLAQLL

LGASTEREFVQLVGKNLERELFKSWLDHCTQEQVRELLKIEKLNTNELFKSPVTRFICCT

SLKVRLLCRQNVWSG

>contig23252 Frame-2F

MSSAYGSRSAKAKNSAKNKKVGLNEEQQQEIREAFDLFDTDGNGTIDAKELKVAMRALGC

EPKKEEITQMVSDANKDGTGTIDFPEFLELMTSKMSEQDSREEILNAFRLFDDDQTGKIS

FGNLKRVAKELGENLTDEELQEMIDEADRDGDGEISADEFLRIMTRTSLY

>contig24419 Frame-1R

MFLMLTILVAFHLVRAATPLMARQDVLPRANVSARNDKVTRMNTTPIALIKSGDEERLFG

LFKSKEEIAQASKSKIERKIVKLVERFDKKLEPTELPKLKYVMKKLKSVSSSTSKTSHED

LVSHLAGKLKAKLGLKKLYLYIQGGKGSTAARELEQGLYQSFGKLFVESSANAFSLGNKE

TTTLKELFENPLLEAFISYSRATIGKEFDLYVALSLILEYEDELAKMVNEIMVMKSSVYQ

PTAKILNDGLNYPIAEMFHFLHLDKAVENPFDDALLPSAIFYAEQYSKRHPNEQTFIQQM

AIIYGKEKLHQNIQAALKKGPPTNGVVTKIQAMQSLQKTSTKAAKPIRNTNSMSPQSFEK

PVDGASTNDHVASTTLKTADDHIVSTRPKTASPLHTFFAKIRGWFSRIWAKLRGMLRTKT

ADNVVSDDHKLRRH

>contig25430 Frame-2F

MYAIYVGSVVLPACVGMYRVADDSFCDPKQKEKKSLMISAFWHALTPRGKIIKGRVGNAH

QACQSKLITRLADERNKKNNGMEKNVGNLLESKEESAILLTDERPSVHFSSRVFENHFEI

AEEDSFSSPLIADDEREIDENDQDVLKWQQHLRWRWRLRRRVLAVFTSDKPLLIKLLCFP

QAVLVFARDITVPLFDDGSWSRSKACLSPVTVPLLLAMTSGYANIDMSGGRCAHRIQLWQ

ALTVIGGCTCAIISYSTHRSHAPQSLKSSGLLLSLAFTACVCWIYTVANELMALLVAVGY

ITHVSNSLLGLTVLAWGNSVGDLITDVSVARAGFPRMAIAGCFGGPVLNLLLGLGLPMAF

AFVSGSSAKLSLDVHAWISLSFLSVSLVSSLLVFRHYTYRCPSWFGKVLMGFYVIYSIVN

VMIAIFKGQRSDPL

>contig25856 Frame-2R|Blast-U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein, putative [Phytophthora infestans T30-4](gb|EEY59391.1|) 1e-23

MKLLLGINGFDSTKGKEVDENTKSAAVGTARRESKREYRQYMNRRGGFNRLLDK

>contig25922 Frame-2R

MHFAAEYGHLSTLKLLCDHFTVWTDVDKFGRNALHSAALGGNKECAYWLIRKAQDSSEFL

SLTLTNKSPSRCAFEAGHSSLANYLQAWEEGNDEYSTNDEKSTLLLDTTVGEGEDSFASR

SRNIETVYNWLKFFKMEEYAQYFEKDGFDTLRGVATIDEDDLIDMKVKKGHRRVVLSHIE

ELRNQLTLLDESAEATGTEPLSSPTLSMLPAITKQSSISSIVSTEGISYRHERRGSVTAP

LLQSDV

>contig26985 Frame-0F

MFETNCREALIPRGNNCIRLRSDPHIALGKKNDFSGTPQKFLPSRRDDGRSQGQVQRPTS

ICEVCATAKQTREVFTTSKAAQTVIGGALSYAVLCSVLGPVNPAFKSGFKYVVTSIMMRS

RCVNVYPLRCGVARILLKAQSWKQVEVAIVGRIVYIFDLFSLNYVL

>contig27568 Frame-2R|Blast-tryptophan synthase [Phytophthora infestans T30-4](gb|EEY70396.1|) 6e-91

MFHPFINDTNVAIYGVEAGGDGVETLRHSSTLLGGRPGVLHGTKTYIMQDAAGQVAETHS

VSAGLDYAGVGPEHAFLKDSGRATYVSVTDKEALEAFQLVSLQEGIIPALESAHAIHFGV

ALASSLPSDHVVVINVSGRGDKDMLQVAKELGVNLNEDLTDT

>contig28842 Frame-2R

MQWSTKETRFFLLRPNPELLVIHTFALRSAPNIMGTAVTGDYQAVKFLRVIKAGRYIRTG

HGVRVLDAIRIFPTLCICVRDDTTEG

>contig29175 Frame-0F|Blast-copper-transporting ATPase, putative [Phytophthora infestans T30-4](gb|EEY69314.1|) 0.0

MSCASDCARKVEKALSAISSVESATVNFLLKRATIQLEAGSNLTNSDLIKVIRDASKTCD

AAVYVPSLRPRAVMLEIEGMRCAKSCARKVQQALSEIEGVVSAFVDFKANTATVEVDPDG

QFSDNDLLQAVRDTGLNFRARLVKPTLQGLLDMVEKAESSALEQQKVSDKALADAEENIS

ISVDPDKTEAGQVTLLIGGMTCTSCSNSVENVLKQTEGVISAVVSFAAEKATICYDKNVT

GIRTLVNAIEAIGYDASYVAKKEVQKALGDQRAKEVRRHRVDLLVAMGCAFPILIMMMVL

KKITFINRELFSDVISGISWQTLIVAILATPVQIYAARRFHIDAWKGVRNRVLGMSFLVS

MGANASYFYGLLSLFRAISLNNSSVANPEMFMTSSMLISFVILGKFLELVAKGKTSEALS

KLMDLQVKSATLLIYSADGTSVQGEQVVPIELIQQGDILKVMRGSSIPADGVIICGEGRI

DESMLTGESKNIKKVAGDRVLGATVNADGLFHMKVTGVDNNTALSQIIRLVEDAQTSKAP

IQAYADYIASVFVPSVIGFSLLTFLVWYALCIFDVVPSSSIPSTDSTFVFAFNFSIATLV

VACPCALGLATPTAVMVGTGVGAEHGVLIKGGEPLQAAHNVNTILFDKTGTLTVGKPVVT

DVVVLTKKLSTEELIILAGSAELGSEHPLSRAIIEYAKFISSNLDQPTGFQGVSGRGISC

TIGAHKVIIGNREWMIDNGMKRMKSIVLQQATVTFQNAGKTSIYMGVDNELSALFAVADA

PRSESIRTLKKLKQMGLEVWMLTGDNARTALTIADQLGISRRNVMAEVVPSQKSSKIKQL

QSTGRIVAMVGDGINDSPALAQANLGISIAGGTEIAVETAGMVLMKANLYDVITALDLSR

TIFNRIRLNYVWALGYNCLLIPLAAGVLFPYGVSIPPMFAGGAMAISSVSVVMSSLLLRY

YSPPAPPEDFCVDDTKSLLFKKPTVTTPLLASSTLV

>contig30205 Frame-0F

MLLGSHTGRPISFIYFRNFSSSLSTCNAEINYASMMDRDTPIYCFADFCTITPFVVNTPS

NRLSIRLVCREVCITPACKLDFIILCATTHGKLRVFCCLQISGNAIATSSP

>contig30436 Frame-0R|Blast-hypothetical protein PITG\_08294 [Phytophthora infestans T30-4](gb|EEY54747.1|) 2e-79

MPMPPHLHAKCARLHTELTRHALAWPFQEPVDPVALNVPTYFDVISQPMDLSTMGAKLNA

GEYSDPTEYRADVLLMFANAIEFNKDDQRVESVANIARQFQGVAMALWDQIFSEAASADW

AVEALHQTQQRFIQRAKEARVISRWKKDSFVARLNRDKLDERTRLASTGE

>contig30955 Frame-0F

MDVEYDGQTAFDAAANGDFPLVVLLWGMSMAVHPQPVDLLAVKDSGGNTLVHYAAASCED

TCDTLHFLMQQMHVSGREEALMDARNDAGETPLTRAAHAGNLLLAGALLHSGFVDILAQD

ARGNTPAHHAAAEGHLWMLHFLLEAEQRHNMVSTNGEKAKKSTTLGGYSLKRQNVLFYAC

MSESKPIVQYALNRGFDANEMDAEGKKCLDIAKQRNLLWLEDLLSDKAKTADPPTHLRQT

RRIVAVVQGVLLLFVLATAYWLVWWLALPFIVIVLSILLLAFRQHGQDRSLSGHSHEAAS

SALGNVHPSKKNAVVAKNVSLEQVEVGLLKDVSARSKKSSVKLRVGIRTFVSAQPESMMG

IWIAWLGVFILMYVMLWVDPCYKDFRNSYAFFLAITGGIKAVFVIVWARLAFICPIDPGT

LKTYDRDVKAMLEKASRCEVPDMTKFCRTCLIMKPIRSKHCAQCNICVARHDHHCAWINR

CVGFGNHRFFFAFLILHCIVLGLYAVLCTLVLHDATHNLHAKRVDTDGSGDRENLSTFDV

WIEIPSLLKNHLLVIIVLLWDVMAFFALALMVTQHLNNIEHNLTINERMNWRRYSYLNPE

LENNKKSSPEAISNPFDHGMKNNVAEFFIRSGRFAVNYRNLFTIPN

>contig31084 Frame-2F

MAQKYGLFSKSSGKKGAGRFIHVAKVKKNSSMEKVSLRLPSVHLDAAKIDWFPPIVKTYM

AKYPSPISDEVADPYCAKDLTPLASAPLKGSGRNGKPLFKPLLSHFKETKIKIQKTLRTE

AMKLPVHGYRNEILRLVENNQLVVVSGDTGCGKSTQIPQFLLDDALARGRGEETRILCTQ

PRRISAISLAERVSRERSGTDSKEVGHAIRFDSNYDAKRTKLIFCTTGTLLKWLQNDPLA

QGFSHIILDEVHERDQFTDFLLILIKTAILKMRPKLKVILMSATIQVEKFSQYFQPDFQA

PILQMVGGTNFPVTTLFLEDVLALLEKDRRSVVPMMDFSSLGSIESTVHGQVTASVSENL

DLECPLCGSARLKDVEAFGIHVASCFGDHLIDYDAPAATELIPVSVPVSSMGDFLQAVLS

GITDEAKDALLSSYMKQLDALRQDNAVDYDLLLQLLSLVDRTFPIDEKENGAILVFLPGW

EEISFMERAVLNSPATSHKYEIALLHSRLSNEEQRRAFLTPPHGKRKLVLATNIAETSLT

IEDVVFVI

>contig32250 Frame-2F|Blast-putative chitin synthase (Chitin-UDP-GlcNac-transferase) [Phytophthora infestans T30-4](gb|EEY61714.1|) 0.0

MYLAEDRILSFEVVARKDCKWTMHYVKDAVARTDVPHNLVGLISQRKRWLNGAFFATLFS

IWFWGRIYSESHHSFKRKLAFLVFHVYHLLYTLFSFFLPANLYLALYFIVFQGFQQNRLK

FIDTSEYSQTVLDGAVYMYNLAYLFGLLMLIIISLGNNPKHMKLTYYFVGAGFGCMMMLS

SLVGLGIFFSTPATINSIVISSLIIGVFFIGSALHGELHHIFMTFTHFTALIPSFVNIFT

IYSFCNLQDLSWGTKGLHDDPLLAASFDETEKGDFNDVIAKRRAIEERRREEKERTENRK

KIFEAFRTNVLLTWSFSNLIYALFIVYFSKSSTYMPLLYTFVAGINACRLLGCIGHWIYI

HTAGMRNSVLDKSECGNGTGRYPQTSYMQLE

>contig32500 Frame-0F|Blast-mediator of RNA polymerase II transcription subunit, putative [Phytophthora infestans T30-4](gb|EEY63002.1|) 2e-48

MEKQRENSARVDSILIQLMKKHAPEIAEKLENNNAAAAAAASQGLEEIPSMEQENASDAE

ITKRRKVT

>contig32575 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57190.1|) 2e-36

MPRIRNNVAVELRSRLTKGDWIDVLDCDGVWNVARVLSVPSSEEVEITYDGWTKEYDEIV

KVESDRVAPYHTFTWTVKCWVKYLNWPLWPSLV

>contig33965 Frame-2R

MTDSIQNSCYVALVSLMLASNFFIIPVPVQLITSASSIVYIGSTMSLKLKHAREASGEQN

VEVMKAEDAYMFPLLGSGVLLGLYLLFKIFDKDLVNLLLTSYFALIGAYSLTEAFSPPVS

TVVFKGNPKVFTRNLTVPYYGAYKLELSTAWMLTFVFAAIFATAWFQTKHFLLNNIFGVS

LSIKGIESLSLGNFKVGAILLCGLFFYDIFWVFGTDVMVTVAMSFDAPIKLIFPREFATE

TEKQKNSILGLGDIVIPGIFVALLLRYDAHRANAKSSNDKFPKPFFHVNLLFYTLGLVTT

VVIMFIFEAAQPALLYLVPACLGSALVTALHRGELKELFEYSEESEESDSQDDKKDVDDQ

KDVNDQKDVDDQKDVDGNKVDTEDKKSK

>contig36597 Frame-1R

MCRPEDIRKEFERYGEVRDVYIPKNFHTKEPKGFAFVEFCSEHEAEDARGSLDGVCIDGR

NIRVVFAQERRKSTDQMRERERTERRGGGHRSRSRSPRRRAPRSRSRSRDRRASTRRSSH

SRSHAKVRSRSRSGTRGRISILSRSPAPRAPPSPRRSGTPRRSISPAARSRSPSPQRSKD

RSYSLSPRHADGRRSPFDPPRRTSGH

>contig36830 Frame-2F

MHAHASPASSDVPKNKRPCHVRVSSSSRASVRVFDVETLLERLLVMLDLPSVVNLIEILA

SNVSWQSVLLQHEFWDNMLVTHFGGDLPRVFKHRFESDFIGSEDEESEEEDEKKSEEEEP

SATTQMATTSVAETTQMATLKSENGGPNLLVCLKLTNFVRSAEQLKQFDTLVQIVQGDIE

RLKTIGEQRVDGLVIPTESRFRESKTDSAASAIFRRAGSKLRDHVAKLNPWGLVDNAIVT

AGFDAGVDKLILYEFPSRDTYVPHPMRYLILTYTSVLKRIQQETLHCVAVLSISTRYMGL

PVDRAAWIALCTIQQYIRSVSWTATIVIVCRSADTFSAYTKSKAKVMNQFNAAAVGAYT

>contig37019 Frame-1R

MHNSLDREQLDTGPRPGSAVRGSEVHCQRRLKRKHYLMSNQDEDSLAMLTSLRSEQQQLL

CKYKSGKCSNARATKRNGKLHTLCHFHRDRQNEHQRKSDRKQRLVSVTRRSKLGSIDVAG

DSARQQDLYSVTSIKASFPRGSSISPLKHHDQNASHLYIAQNTADGTISGTGRLPSPAAG

TTRLPPISFLMRRKLDGYRVTSNIIP

>contig39178 Frame-1F

MYEHYGTFLVCIRICTHHARKKSPFSSSSASCYFRSFETFYIEKRLLSRREKLYLRWITQ

SPQYKN

>contig40000 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68230.1|) 9e-61

MAAAGMRFCRECNNMLYPSQDREIRRLVFRCRNCGQSEDVEESCIYVNELVKDTRVQLDV

LPGDVIDDPTLQRDHDVACPNCGHNGAVFIRSQDGVKQATLALIWVCLNRDCQVDEEGNR

LPSYRWMGI

>contig40075 Frame-2F

MGPNIFCKHHGFLLIKRKDGLQFILLLSESSYN

>contig40725 Frame-1F|Blast-O-sialoglycoprotein endopeptidase, putative [Phytophthora infestans T30-4](gb|EEY69366.1|) 1e-177

MTQPMLAMGIEGSANKLGVGIIRYLADGSTEILSNPRKTYITPPGQGFLPRETAWHHQNH

IVGIVRTALIDAAISPNQLDCICYTKGPGMGGPLCSAAVCARMLSLLWDKPLVGVNHCVG

HIEMGRSVTKAADPVVLYVSGGNTQVIAYSMQCYRIFGETIDIAVGNCLDRFARVLELSN

DPSPGYNIEVLAREGKKYIELPYIVKGMDVSFSGISTFIEKEANNKIESGECTKADLCFS

LQETVFAMLVEITERAMAHCGQSEVLIVGGVGCNLRLQEMMEIMAKERNGRVCAMDQRYC

VDNGAMIAQAGVLEFQYGQTTPLEEATCTQRYRTDEVSVIWRTD

>contig43089 Frame-0F|Blast-alkaline phytoceramidase (aPHC), putative [Phytophthora infestans T30-4](gb|EEY56592.1|) 1e-118

MASTKHPTVRAADTFAPVGFWGPPTSTIDWCELNYQHNYYIAEFWNTISSSIFVFLGLYG

LGRSFNMGLEPRFHLQFVGVMATGFGSAMFHGTLQHVYQQCDEMPMVWTILVCNYAVFHK

EIQKIPFKYAESFVATTLALIGVAFTGLSAVYRFTIVFQVFFSILAISTCLRLCAYYVEV

KDYRARAVAQSYLTLMLSGVGFWLMDYHYCHMLRNFPVNPQGHAWWHVFMGISSYHGVIF

MQYVRLEQLDKKARIQETFIGIPTIVIDPVSPV

>contig43456 Frame-1R

MQKRTGRPVHPLWAHFHRGEKRNRYHYHAYCSYCVIRYGMDRVPPTRGVSSDLLRHLESC

PNCPRSVVESVRELCEGRIRASNAKKNCAVALNQVKSTGSTNTVTAKASGALKRTASEVL

EVEMLYNTDFSEHSDTSVALKRKTTTLVKCLNVNPSRNETPEDVLMEWKRSLLQVAITAG

VSPLARL

>contig44084 Frame-0F

MRIDYISLLVIATVVTNANSASLRRSPIDTSKHSYDNTHDFSTQETDVWHKEDERMLNLL

KSYIKSPVEAASLTKPLLLSSKRIYEPNSFEGLAEVNNLARYIDALQLKDRQTNDFVDAK

LNFLVYYFGYSAVARELMKVEQSLGADYIWKLLFRNKESLPGNSKEYLDVIDFGILYQFI

KVAQRHDEMKELPQLVKRYFVVKQKQMSPKHSGYDFSADVEVNAFKLMFTDVPTSSVITA

MRNKYVELEFPDENSVLQMLAKIYSTFHNEDKQQMLDYFFLSYLFVHNNENSRNFIRKIR

SDLKSVSAKTDIMP

>contig44307 Frame-2F

MTSNSKISLSVSQTASSTSRSRIRLLSVFPTAIVWFTFKPSKSISCGIFEKCRSSYNVAL

TLSSEAVLKRFNVAVSSRPCKQAFVVRIITYFNTFFMRCLVAFRVDQNKFRLGNDAIANA

NRKK

>contig45199 Frame-2F|Blast-tryptophan synthase, putative [Phytophthora infestans T30-4](gb|EEY57659.1|) 1e-131

MATVSEARLKGLTLPVVLMGYYNNILQYGESKICPDAQKAGVDGFIIVDLPPEEAKSLSD

DAAEHGLAYVPLVSPTTSEDRMKLIDSVAHGFVYCVSLTGVTGARSELPPNLDAFVAKIR

DNVKKPLALGFGLSTRQHFVQASAVADGVVIGSKIVKIIEDAPDTAARAAAVEAFARGIV

NP

>contig45205 Frame-0R

MTFAGVCVVRSPPAAVAVVATVVETIDHLRASASFTCSPFPSIKARHVAAAATTNQSCDY

D

>contig45920 Frame-1F

MVHIMSVREGCTNAGPQYRDCISRACLGSRAGGIDVACTSRWSSFYDIKSFYKTTSRVNF

QTRQYPSRRAIARPPLKPLYF

>contig46671 Frame-0R

METSTGNSIRVFDGTTDFRVWRARVENELMRYHLLGYVMVRGYDGSQTFTYNGEVVPPRM

PAILEEDGQQQQSSLKEEARTCHSGGNPQGRLGRWAVLGESAEAKGILQRYLHPDVESVI

LNKNVYDSWTMLCTLYGNRDSPGAHDVYEMHRVLHNVRLGDKKGEPVKEFLTRWEMVLQQ

YARAIGIELTEAFRSVSLTQTLPSAWKPMVASWRGTRPFVPFTELVKKVTLTRKQAQMPL

ETASGPSSVVVEAHSPLLDSP

>contig47225 Frame-0R

MLDTACDVGRVPTELAQHFVAQQDIDFSKLNSTWWLNDGAGGPSNASRATIVAPKTPNEV

LPLRESQEDLDARIRDFVTKLEERPEQHIAVVGHSSYFKRMLGMNRKLHNCELYEVSFAQ

IRLRCA

>contig47250 Frame-2R

MSSISRCASAPLRLSSRYSSVLESALISLGREDAVVNSTRKIRRKRHYEASHSPFRKLAQ

SFSAPAQRSQTPIDDDEDPFASMKLIKSIKKKKRKRKDKDREQRASSPAVTRSASKLNKL

RKRCYAGVLEMAGHTPVTRSMARMKEKKRSSLEMIEDVEIEPEDEDH

>contig47500 Frame-1F

MNVAFKLLGWCIAKDKVYVVCMKVFISLLIRLTCPSFVPSALHITLETSRR

>contig47575 Frame-2R|Blast-COP9 signalosome complex subunit 5, putative [Phytophthora infestans T30-4](gb|EEY66023.1|) 2e-83

MSSLGSQVVSILSEEFLWMRTLSSNSMQERENRDRFSERIQLLANKLDGCEAHLMPRTGR

GASRIGEYYVPEKQQPHKESEESALDKISQAAKELAIENSLGQGLQVTKKALFND

>contig47966 Frame-0F|Blast-hypothetical protein PITG\_02020 [Phytophthora infestans T30-4](gb|EEY61682.1|) 2e-56

MLLTEAVVATLSFPLRGLEFSCFAFIRHDVDSVNDTQLQIHTRRMKAFIYQENTLKLLAG

SASIFDGGISLSVLIFDEKAAATWLPYFFEHIYKTDFCGGAQCVDQLLTMLEELMRQNDV

GQLREAYWFAALLNTALIACSSRCAGADVDVNIHERLRLITSKVLQTLSIVSLPALTQES

DTFSQLNKEALGLMHSTQCARLSIDEHRASWTCIRQMSEKSSSAVQLCVSDIWNARIKKL

ELAGNRPSLQLFLPFTLWLSGALIYSQSFLEEPSTDMRRWEHAFTSYVTDVYLHIEFEGV

TCNLLQSWLITWITCNISRGQNELLMLALLPSQVTLFRRLGLTSSRSSQQDQASTSLWLL

IFKAIDLALNGDTANNSTFFEQATELVLSTLITLELAELSAISDFSHFENVQDVEPLFKE

LESIFSR

>contig49649 Frame-0R

MKRVPSAAPGIFSALLTSLRHNLQIVNGRAISRERSRTLRRNNDGVLVVQFFAAGRVITQ

RELNIPLAESRHLWLSPRQQMHKRKLYDAQLVPMQLSLNERIEVQMFWGSE

>contig50272 Frame-1F|Blast-hypothetical protein PITG\_00684 [Phytophthora infestans T30-4](gb|EEY58072.1|) 2e-16

MAMLDRNPRAEKHVLVIPLEHIPFVDDLLPMHLSLCTSRAISPVDIESI

>contig51271 Frame-2R

MKSHILACGLFRIAMSLQKARILNHTSV

>contig52281 Frame-2R

MPNPVAVVRGVEILLSIFPKWERETLQVILEANEFIMDDTIAAVLKMEQAEHMTPTDETS

SLYVVNRKNWPVKNPLPFDFLRLPDDNGSEIEALKHAPSDEGIAEDDDEECDESEKEGIE

ETQEVAVRNDAEKNRKERSSSTLATDDGTLYGKGFDHVSASTDEVVTPMLNQAVMLAKQK

IVADSMNQKFLPKELRNESSSIFDIAHIDVIKKSKLNLSEAEKRIRHREPHLMFELL

>contig52678 Frame-1F|Blast-Poly(A) polymerase, putative [Phytophthora infestans T30-4](gb|EEY62302.1|) 2e-70

MDLRAVQSFGAYINTISPMDLPEARVRKLHVLKQLSDLLTKWVKMVGRERELSEAHIALT

KGSLFLAGSYRLGLDDPNSDIDIVCVTPWHVTHDDFFGSFCQLLQHTPGVSQLAPVPHA

>contig53417 Frame-2R

MRFLTRSHCVPRRLLLHSSNACSYGAVLHADVLSRCKAAFCMSRSRSLTQISTLAHPQCQ

SSISNLSLRSRSVSHISSSRPAVPNDEYEELKDFLAKPVNVGPSMERAKEIVTGWMNQHV

DPSMPGQDATVMVMVASAMEDPYFVMQV

>contig53844 Frame-2R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY53382.1|) 7e-75

MARTLYASIFLFLVSKVNSMSSMIQQPIASSTRTNNKNTPPCIAVLDIFGFEEFDINQFE

QFCINYANEKLQYQFLQDILLTEQQAHIEEG

>contig53938 Frame-0F

MEISCAHEMKLNSPANNKHG

>contig55121 Frame-0F

MRASCVVIERVWLQYLSRGGARLVRQQMLADWHAAVNRIQVCWRQSYARQAARMKRQQLW

QQRSQAVRT

>contig55929 Frame-1R

MRWFPSTTENIRIRISWLLPSQFLPLHCQNICCVTICQAVKLRY

>contig56340 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53637.1|) 1e-10

MIREVWRIELGLGVGPFRLGASIAEVLHVLKSRLP

>contig57934 Frame-2R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY67459.1|) 9e-45

MGDFELLNRFVPSFKAAIDAGALSVMESYSSINGEPVISSTKILTDLLRNDLGFKGMVVS

DYNEVYNLFDYHRVVPSREKASEASLLHTSLDMNMVPLDTDFIQHGLKMLETYP

>contig58023 Frame-0R

MHYLVYRGPYDAKERRRWAQDWRKNWCPNFTYWILLDRSCYSVDPLAIASR

>contig59572 Frame-2F

MKGCCAGKALSHQFNAVNRLCHKASCSNAQN

>contig05460 Frame-2F

MEENIQMGEVFAMSNTQIGAIFEVAKEVFLDAATFDYVDRTVLSSRGVDDHVAFALEKMW

KYRDLSLRKQIALAHKVKFPVLMLRKSDWRLHLEMGSSNCKGLSQTKAIFQLDLVDTRTD

EAEKLDIELSHAELRSLFTQLNAIQQEELDVALISSRADN

>contig06511 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61223.1|) 7e-31

MTIAASMIPKKMKVSELRAALESRGMSSNGLKTELIQRLELALDEEEFGSEAQEMEELKM

KSPKMSKKTELKRRDGLTAATALSKSPKSTKPDITSPVKSRYPSVEKISNKVEEEPVFVA

AEQVSTTTEEDKASNARNIESAKIKATSIRMAEKEKRVIRAAKFGITLSLDDK

>contig10509 Frame-1R

MCKPIHTSLSKPSYKNKRPLQWVIRRRRSLVLAAGA

>contig10783 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY69419.1|) 6e-49

MWEMIAGGLQNPFIGMAPIKFYNKTINAGIRPPIPKGMDSGYINLIIECWKSDAADRPSF

DVIVSRLEQMLLDLGASIDLPPTFQGGYHQAKIAPNS

>contig11652 Frame-0F

MPQPRAFLVMNVIRERATIDCKRAQTTDRELHFSHNRNIRINC

>contig12419 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69247.1|) 1e-155

MADVSVRYACKCGHLAPVSLLFYSETRQKLVCRLPQCSVEEFESFYCGNLLVNMPSKEAS

MYQNRSSRCFSCPTCQTILSTAFHESCQGYFLLCAHCRWDSYELEWVDDDPDALIMAAIT

RERQAVHEDVFQALQSYYITPSVSLASGGNAATMTSSFKNAFGRGSSLQALADSMKELQR

ENHIKKFKYKRLVAMGGWKYDQALNKLQEKEMRLIQNRLEHQWPELKKQLAVLQNEGASW

KEDTPEMTRKMLKVLSQKCEMGEVSTLHQRLQNPLNQSRDVKLLTPYRPLLRAKRAWRCA

ESIKHGTAGILVKPQISPMSGDSSLPVSASWFKKANLAAYHVPIVTFQRLPYRVEGTGNL

ECVLFVENPLDDAIRITFRSASANLGAGGDIRENGQV

>contig13603 Frame-1R

MDATIRITQVDTFDTVLEAKVPSASPFIRLRRLHEEAMHAKSTDERHAYDTRPNTGWEML

PHVPSPLVHVVLDAETRAGVYTTWIHVLAGTRLLVIPVHLTVLDPGLYPIPATMDFGILL

NLDDDAYRKITIDLINTNVYAVEVLDVVLAENNLIQSTQFEGHSVVVPPQTRINHALVFQ

IQLDQDMTGRGAAS

>contig16125 Frame-0F

MLKKKMAITQQTAILRGPLLKEYAALQDQKASRKAQCRQYIHEIHAFRNEMLDMTETIHQ

KMETMQGLEKKQQLAVERSKKKDVMTRTMYLSRIMEIIQQVYKQKHEISKILNDVKNLQR

ELKECRKSSNDPKLWRMRNCTVLLPRVNVRTILRPKLILNVIVSLLTFANCLKSSFWSLG

MLEKRKMPRVIYERGFRNWKRVRAVAKCQIYLLIYRVCVLRMTRVKLNCVD

>contig17009 Frame-0F

MVVITYVSYMAEGNEEGGLGFFFRIFQARQNKIRAHAFYTIFLSVSGLLAMKAVMQIWLH

GVRLYKNFWMALGVYCRLFWHFLFFALFLAVAFSPDEGALFGNWSSLLPGGGTAGSYLSM

GLLYTAIYCIPVLFVACLRAFVPRALWGFRLLSALDGTSRQYVGRNTRQPWANYVQYASS

WSGIFFGKFLFTMQLMIRPLMAPSIEIYGIEVDDDGVLQSRRNILFILALWAPILVVFMY

DTQIWFILYQSIVGLIMGKRMHLGHYMGLAQLKLGMAAAPKLFDDRVVSLRTKTPTLIPL

SSAQLPPDSNELRHFDVVTLRFAIIWNQIVDNFRLNDLLDDRETVILQYRILNKGEHVED

PIFLLAGKLARAVEIASRAKTHKWNTMTLVKHIATADALEGMKNGMDLIRSIFSLLLKED

EEQDAWSIIEYIYSSPDVATLLDLSYLPQLADNIVELLAVILDMPEDIASIEDFHAIPED

LRLELHVQVAQVIERLRVIALTVELMLHDDAVAQKLHRCRFLQTTTDLKFQIEQLVFLYK

ADALSETGLIAVHPRDDSSIPLPRFAPEEFISSCTRLFFLLRLDVANSLPRCEDAKRRMG

FFLHSLAMDMPRVKSLEAMPSFSVMTPYYSETVLFTLEELNNPVHSNPLFAELEKKQKAK

GWTELTIMKYLITFHAEEWSNFLERMGAGSLEEALEINAQEVRLWASMRGQTLARTVHGM

MLYEDAIRLLRWLEVYSLQDMSLDEKLEEMNRISALKFSYITGCQIYSKQVANNDPRAAD

IDYLMKKFPSWRVSFVDSITEQVDGEEVNRFDCVLVKAEHGEIVEVYRYELPGNPILGEG

KPENQNVALPFTRGEYLQTIDMNQEHYLEECLKMPNFLATATSTGEDVTVLGMKEHVFTG

RASSLARFMTLQELVFVTLTQRVLAKPLRSRMHYGHPDVFEKSFVVTCGGVSKASKGINL

SEDVFSGYNVTLRGGLVTHVEFMQCGKGRDVTLSQINAFEAKLSNGCAESCLSREGHRLT

NSLDFARLNSMFYGHFGFYICNALTVFCVYVYAYCKLYVATHSEVEMAAIMTTDSLNSLA

SVMTTQYLLQFGMLTTLPLFATLFVEFGFQQACFKVVELVTTLGIVFYVFLTGTKAHFYD

VALIRGGSKYRGTGRGFSITRDPMVNFFKEYAVSHFRKAVELIGIMVLYGIYGSFDIGSG

ALEAYCATADFDCDLTPDQIPANITSLAAYSEKSQSYGIASFAVLFLGACWLMAPFVFNT

DGLVLQKSKLDIAHWFAWMMRSRSCDEHEEKEVGTAPVQSKDTWDEWWQSDVDLMLPLGG

MGRLTYCLRELRHPLAMYYVFKTEFSLAWFALLFAAIGSTWCVLWLGNRMNQCSLQQWKR

KSLSFQGLVYMVAVIGGILLVPLVIGVIGSWSVHKCFTFSVSMFLGFNAIVQYALAFHGV

FGFQVAMWSPVITLGFLMDMIVGLFLIVPLFLLSLLPFMRILQTRAMYNGGFSRALSSGS

EVAASLVLLLGVLGGFVHGFTTSFVYTLGYINSTSDNFINRSFYYFITTNLPNKGSEMLK

YMENGYLSMTCASMSIVAVFLSLGIGRVLGRRGNMVLGSSLIIISVGLNFIARTSIIILA

CGLAAMGAAIMAMNYLLWSFEICTKGWRGKSVTIFLMGSMVGWMIHSLLMANTNATTMTE

NWANAPTNMWRLQPLFVQPALIVAFFGIVWFVPESPVWLLAHKREDAARSVLTRLRRRVN

VTPEMELIKAELAQKTRENHLLFRFSLVIALQSLFGLLMSQTIIVRRPLQMNANDSQSAN

NYWQVYFALCIATGLAFGSFLVDNVRRKTILKEFLPFVALMAFTCGVIGAVSRADGSLLQ

TMLCLLYISAGLSLVSVTWLAALEMFPASRRPFYWTISLSVYYLIQLGVYYIKPSFALAN

FLLSGGCILLTIILFLYCASTKLGAIQTKAEKKYQRSIRESEPEVREAMDTFIVDEGRKQ

QTRIAQTSAMNRSAGVGASQINFGHSGASYSTISGPPSGGAASQARANASQFGFSGVMGK

DRSRSGLGDSKTDPFSFRRLDSEEDRNHSREVRYGTSTGLSANESFEAAAPVDLSIDRRR

LTSRMSSTFDFEAEFEAEHLEDLRQGQISYPQGQPRSVSFLQSQQYPDADLLAETQSVRL

>contig17092 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66184.1|) 0.0

MFFKQLHRLHENYTLREKRHQKEMAQREARRAKRENERLEKKQRVENERQRLKDEREEER

KQKEEEQKYPVDDLQLLERDAINSNIFPLDCSTLKGVQGPLLGELVMAWQTICTFKDFVG

LESISLEALAECITARCDKGTHIGLTRIFLAFLRVILSEKSFMSQLDDLVVEGNIKVSDL

FLNSERTYGICERAHSDMLNAVTWQEILRQLMSKDLGIDTSIGQVDSLVGCEIVRQTLYM

QNNSAPFNFPVDTSSKGLEDYTQLVKNPMDLGTIKQKIVLGDYEVPGGWELFAKDVRLVW

DNALLYNGEDSEVGRAALALSDVFEQDYDRFVVGRIRANESRIEACRKVKETLQNLSVYD

VQSFQYSDVVYGLYCSEFFELPTAYKIGALSWICSEFLTLSSIRTYMASQVDQEMLILKN

YRMLAADLDSRRKHSDRMRRERDNAFRMDCANQGIHPNSHNVFSEGIKRRHEFIAKFFED

LQAEKMEDEKRLEQEKKKQAQEMASKLKSLVIRVSPLGKDRFHNSYYMFKHDAKPRLFIE

RRDCGNVIICSTKAHIVAILEWLNPKGIRELDLLTKLNAVKDVLLSGSEDEESQASDTLA

GIAWTNKANIELQTFPLPGGAIASEIMTITDADRVIESHSIARDMLLCLKKHLENTNTLS

ASWEGAQTWNTRVQEATLFKEQLDLFAELENAAVSTSKLGMETIRPSWRRKRHEWRLALK

GSCTYAQLVFLLHLLLEELINVEAFMDLHICLDRQEWLKLRPKETHNFIPEVGKTVLYFG

NGHAAALKEDEKSKRRRFTQKSDLPARNATLICTVKKISYHHGGGDPYALAVLKPISNMA

QHECIRESGTLFCPLPSREQRLARVFLRILAKLKMLTDAGPFLEPVSDREFPQYKEIVLH

PMDLGTITAKASNLVYKNSVEFMADLRLMRDNCQLFCEGRFPTLPPLAHNLLYVADGHMK

KWSREIHACEDASSESSSIDTDKFSLDTESGFKLDESDHEASISSELPTRIIETVLRLEN

RLPEYVVDISRYSWAVNRRWRCGENFRMLFRNAQGQPGDYYNGVTAGSLPFNCHGLLPWE

SLRITWDEDDGSDDNCINPWEAEFSPKI

>contig18417 Frame-1F

MSEITTYLGSAHEETDYRSRDVTSPEFLVCWVRSLARPPQLPHCTQEKQVQTASSLC

>contig19726 Frame-0R|Blast-2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative [Phytophthora infestans T30-4](gb|EEY66237.1|) 4e-08

MDPVEPGYACGSDTAHMSILG

>contig20168 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66087.1|) 4e-07

MSKKIVLDEDEYVEALSSIIVRDFFPDLPKLQQHSK

>contig20638 Frame-1F|Blast-gamma-glutamyl hydrolase, putative [Phytophthora infestans T30-4](gb|EEY53659.1|) 1e-141

MKLKALMIYAAIGLPITTASDRGPIIGVFAHPSSYHGDYIAASYVKWVESAGGRVVPIPY

SAPKPYLEQLLPQLNGLLFPGGAAAVNDRAEWLYHQALGLNDQGVHFPVWATCLGFEWLI

QLTTNDTDSLTKSLDSMNITLPLNFTESARTSRLFSQASLEPFSWLGEKAITMNNHELGI

TPERFDQYSSLAKFFNVLSTNVDRKGIEFISAIEAKRYPVYAVQFHPEKNSFEYGEYEDG

IPYEVINHSREGVAAGNFFATFFINEARKNKLRFKDPKVERKALIYNYPTSTITYPGFVE

SYIFKHTYQMGFWSVM

>contig21299 Frame-1F|Blast-DnaJ subfamily C member 2 protein [Phytophthora infestans T30-4](gb|EEY54567.1|) 1e-175

MPSLILSLPTPPSGAKDSNVVLKLGGYFTQKRVEPVGRAYSKRARNMARGRSVSCDDVDD

AAKARDALRKHEDLVLRKYRRSIRGKNFLDLTMYQQLGVADMGFDVTDDQVKKAYHRVLI

EHHPDKTGKTENDPNYLAVQKAFATLMDPQKKRAYDSQCDFNEWIPTGNEKIKENDPNAE

GKSFYDLYGPIFLANARFSENKPVPVLGKDDKPIDEVYAFYDFWNKFDSWRDFTHDSEHD

VDSAEHRDHKRWMAKKNESAAKKKKKKEYARLASLVDRALANDPRIRRVKQEEKDRKARA

KLEKEEAAQRLIDEENRKKDEVERAAKEAEEKDKEASQGCQDGQGQAEKVVQEG

>contig21413 Frame-0R

MLIFPSRSAALSDAEWSLVLLTGRPTRAMLKYLPRGGSYITGGLAPRNLDYFT

>contig21927 Frame-2F

MLKMDDLEQSSCPTKGASTERIGNIQVCIVSETAFQSVYFPSRDGWKTEDNVLYLSAIVS

VFMSLWFVTLVLLHFVKNNRQQATTDKLQRDTVELSLPSRQWSQSKEEEFPNDIRFDPEF

ESCRIDSADIMQVRTLAHGNFAMTSLVHLGEKQSVMKKFSAHFQGRDRDQMIAFMDEIRV

IAKLRHPNVVGFLGFTWSSILDLSVLVDFIPNGSLAAYLKEMATSQSTLTWMQSHAESPS

KLSLSLQLSKALVYLQSFAPPVIHGHLKAASVLLDSALEVKLNRIGYGTNIESRSIKDQT

WIAPEVLVSREFDGKSDIYSFGVVMLELDRCKHLKIAPCQGVDGTRLEPKFREDCPPQIM

EIAISCLSDDPSDRPTVNELCNSLKQLYHRCE

>contig22144 Frame-1R|Blast-cell division protein kinase, putative [Phytophthora infestans T30-4](gb|EEY68005.1|) 7e-33

MESMLRYDPSTRISAKEALRHPYFDDVDAEFM

>contig25758 Frame-0F

MLDPASQVDPSSADFISSVREFTHLKGYAVSTLRSDKAKMILKCCRGGSYKDLVNHAPKR

KNATRLTGRDETLGVKSWRRGGIMMAR

>contig25857 Frame-2F|Blast-U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein, putative [Phytophthora infestans T30-4](gb|EEY59391.1|) 3e-17

MRRSRSSSLDSLGRRRRRKASPARRPRRSSSSSSRSRSRSSSHRHRSSRRSRSRSYGRKR

SRRSRSRSHGRNRDRRRRNYSHSRSMSDSPVRRPRSPS

>contig25996 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69867.1|) 3e-12

MPFFELSEKSSAGLKMSDRDEKVSLRVFTDWFKDVGYQTHPWLKLVVLHHWPAAVNVCGS

TGLPY

>contig26229 Frame-2F

MLASASSDGSVVLWDITIQTQAYSQTTKLKADVNNVQNCHEGPVNCLAWSLNSRFLLSSG

SHSNIIQLWDRT

>contig28087 Frame-2R

MEESPSRVEERMDYTNVIKDVEDLAERAVKAVSKVVIDLDNYDEAVNEASVINLSRIPKK

RPYWSENNEHGEAALSKSGINHANANKKTRTIAEAIDVPDKEVMTVSTHNDLLHRQNKRF

TDAVPKLAEFDLKDPNLLQDPLLKRFLDDNPSINYPMLSVELEKTYSHETEKLSELLKNG

DYIGMRLLVERLNNWHKEFDIDPSDLTDNKSRSEYLEKYGFKNVENTIINDYEDVASYQI

LLRELKYKLGFDQLAKLLLAAS

>contig28313 Frame-2F

MHIDLLDIFGFESFEHNSFEQFCINFANEKLQQKFTLDVFKTVQEEYEQEGVAWEFVKYQ

DNQNMLDLLENSMGIMALLNEECVRPMGSDLSFVSKLVSLRESHPRFERARLNQMHFLLH

HYAGSVLYDAEGFVEKNKDSLQTDLLELLGSSSNGLMSIVFGNDSKTAFMTDADLSVRLA

TMMESGRRSVVSRKTSSFMQETVSYKFKAQLSLLMSDISRTDVHYVRCIKPNSQKSPNIY

EIDAVVNQLRCAGVVEAIRITRSAFPNKMAHEKFLRRFVMLKSKQSTKMTNKSTTVADAC

EQLGQELLSTSAFDRTQQGSEHSTTPNFVVGKSLVYFGKGVLEFFELRRTTFVHDRAMVI

QQAVRRWVARRRIKRIRVLIAKLQALQRCRTQRRFYLDQRKKCVVVQSVWRGVRSRQRVY

LLMKEKCAIKVQTAYRKHLFERKYASFRNAVIKLQSRLKMKKQVGKFHRLLRERKEQDAM

ETEVELLKHRLEDEKRARVEIEAENSSLQKELNEVRLSSVPSAGNSIVEDEAPFQHPNSM

QASRYERESMDDGKLLDDSERMIDYLQKEVTKGREFIQMLSQDNENLKAENKKIKDAYTA

AGASFAALNQHNKQQSKANLRLMSTHATLIKSQEEKMKKYKKQVADLKDDLRMLRSVYSA

ELKARVKQQDFIVEIANLAEVEGASMDLLERIRTMAVDLKSTSDNERRGSEYYNHHLSSA

SKVSRDNEFRESRSLTATSVDSPPVAVSIGSEPSHTERRATLDTIAHNSMHHGDSPQQAD

SLGSPDQSALNRSTSYAEDSHRKSRIGGMFKKMFKKEE

>contig28843 Frame-0R|Blast-peptidase, putative [Phytophthora infestans T30-4](gb|EEY53248.1|) 1e-145

MTTHTNDCLSCDFRIVKVPAQTFKNGAPHNVVLAAFDYPRYVGNARGNDYVPENLDTHFF

NWTTTRPIGTIPESLQTFAYIEGAYGIINEHQVAIGESTCPAKFWTKPVTQGGHALFDIS

ELSRIALQRTRTARDAIQLMGDLAEKHGYYGAVWEGEDVYEEAGEALTVTDAKEAWMFHI

LPDDTGKSAIWAAQRVLDDHISAVANQFVIRELHLNDPLNYLASKNVHEVAIRTKLWTPD

LKTPFDFTQAYAQPRIATHRYYSSRRIWRLFTLANTDLELSPITDVLATDYPFSVRPTSP

LSPRDLLRFQRDHYENTP

>contig28977 Frame-0F

MHLLRFIHKAICQLPQANRQTMGNALSCYKTTKKNTSTTSDANELRDDFDLRTEPYIATP

THAAQVKEKNAFPENVQKDVK

>contig29624 Frame-1R

MSGTKDNKSSLSHRAQQKFNAGKYEEAVDALEKLVEEIGPRQDFKVRHNAALTRFVAGLD

NPVKLQEALRQNLRTQLQEHEKNKTFTSSNDGETQEAESALSINRETTYLRYNYAASLFM

TKQYAQACAVLEAMMRGVDPIDENVAMHTSFLYLDVILHSSRGCVSTERERAATRNKAQS

ILTFLEQPHCFNTVQEVADHLTQRDATGNVLETDVQRRSRWDVTEFRFRMHLYRAKFMLL

QSNLKTAKKEVKSALEIFQKEIKIYDRSESNTFASSSSLSLESDKTSSAIGHPCLVVQNT

TALFLKANLEYLKKNYKKCIKLLASCTQEAVSESVLLNNMGCIHFQMGQRKAAQSYFARA

LQATTKATKLDAVVLASAFHHEILYNNGLHFLLQGEYSLAFRCIYGSSKMFYNRPKLWLR

LGECCTAAFAKEQKLAAVAGNKSGLIKDIVGSGSHRRVLLPSSLPSAASQDFKLPLKIGT

SNGACSASTDATDEDESPTMSLSFGAKCFKNVVLLCNQLLESGSTNGNTNLNAGESTNLE

ALDASALDNLRQKALVNLTYVYLSIFEPLLAIATAKELLALPSCSKATSFLARSYAAEAL

CTLSRASEATEILQAERDLAVMAEEYASEAKIQLSQARAGVHVNNATSLLLQGRTSEAEE

SVTRAVRENPNCRESLELLVYVLLKKGDTKKALRVLKEAQVVQ

>contig29651 Frame-2R

MAATEGYHSSVFLYGQTGTGKTYTMQGGRGDPGIIQLSVQDIFDHIARQPSMEFLLRVSY

LEIYNERIYDLLAAGAKSDIKIYDVQPPNSTMGRHSLGPKDVVIRGLREEIVLSMEHVLS

LVEVGNLHRHMATTESNDQSSRSHVVFRMVIESQAKRKSRDSDEIVPVRSATLNIIDLAG

SESVRLANTSGQALEEGKYINRSLLTLGHIIWTLSRAQSSKSARLSGPLHLPYRNSKLTR

ILQPSLGGKAQIAIVCTASPSVECLSETHSTLKFATRARRVRNRVVVNDGVGESALLRK

>contig30437 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68158.1|) 1e-111

MSAASSELLKGVLMDNSNDDGYVQKMLPSTLASMASSKSCAVASTGTSNDGNIRAFGEIV

EEKLEALCARGTRVTGNTQMHKVDDAVVAFVLERVKILYEDVEFIDEMDQSMHDRLQLLT

TMIEMQLKQVLAVQKNAIDARTSMENLKKKTERALAVQQNLSKRAAAVLQAVKENQPHLS

RAEREFKSELELMALEVRRMKPRIAEMTVEGQRAVRLLESAVRSASSPHHCWASCSSSGS

LSVLSNEKKKMCFDVLRAETQLIDNTKVLLDDLSSNVQQLKE

>contig30868 Frame-1F

MAERASAEGCKVLLGAAMGKGMKPYFVDERIELVGDLTGPMHEDVHLVLEYAEGDTFRGY

TSPRANRYYLNHDVQNAHLSVLEDFEHSLIAFQPDLVVFGGLQLMEVQTDAHLRSKRLAA

LSQVLQNLYVARTPTHYEFAAVSDFSHFNDTVRLVLPWVHSIGLNEQELFILHHYLVTGN

EGVATTSRPTVADITAQLHDLIQLASKARANVHNVALAQLSRIHFHTLQFHIVCQHQSSK

WADPTTALIQSALMSSKVACGKSFNASSISEKPTLMRTSADMEVDPERIEILLAREQVLS

ARQALKLTLDPLSPVYTWQEADFQCHLVPMLACKKPDHTAGLGDNISGTGIAYHRIHKTT

NEPKL

>contig31306 Frame-1R

MLGTSCPVNNCCTPLMRNKQGKMFCARCNQFVITEEESIKQALQNAADKAAAKKEDISEA

CNENERRRLIEQQFRLEAHARQVQEMPGEDQIKIQQAHGA

>contig32251 Frame-2F|Blast-40S ribosomal protein S15a [Phytophthora infestans T30-4](gb|EEY65467.1|) 2e-15

MVRMSVLADCLKTMYNAEKRGKRQVLIRPSSKVIVKFLQVMQKT

>contig32501 Frame-0F|Blast-mediator of RNA polymerase II transcription subunit, putative [Phytophthora infestans T30-4](gb|EEY63002.1|) 9e-61

MEVVAHVDDYNASFRDTVWLQSFPLNAQTVLHYFALSSFYDRSCNNERLKMQRLGLEQLK

NLRGVEYELLPNAAKQLPQQLYIIRKQRRNGRTQVEPLAVYYVLDGTVYQAPNIHAMLTS

RL

>contig36181 Frame-2F

MQRKSLETLLPFLLAYENGFLSVVDLVVFAPEWDWVCLGNGNDDQHIIYIL

>contig36457 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70204.1|) 8e-09

MQEAAKAFVVENVGRKSRTSLRQTMLAMLGSKYIMNPCFGVTPFFPCAALVAEAYDAMDL

ANKYDFTNTQPPLSADTVTPRELAENKIKLHETRHAAFDRLLPIKLE

>contig36523 Frame-2R|Blast-lipin-like protein [Phytophthora infestans T30-4](gb|EEY65912.1|) 1e-121

MELQERGRCMFITGGLIIPPEDLCFADLSEVHPNLVRFEHYQKYTNTVRYVDAKLHLWGP

NESVVVVDLDGTLTISDVEGHIRTLRLGQYDFLHAGSCDFFTKLHELGLRIVYLTARPLD

WASASRIHLENAVQHSISLPPGVLITNSTGLTGALFTEVVNKTPHLFKIQVLNELQLTLI

HAGRVTEHPVFVAGFGNRPTDVVAYQEVGMDPSL

>contig36596 Frame-2F|Blast-aspartate aminotransferase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63770.1|) 0.0

MKAKQHVPFFDCAYQGFASGDASHDAAAIRLFVKEGHNVFLSQSYAKNFGLYGERVGAMS

VVTNSKDEAERVLSQLKIIIRPMYSNPPIHGSRIVSTILSDTQLKQQWYRECKGMADRII

TMRTALRAAIEKVEKDSGLESNWNHITEQIGMFCYTSLTEAQVTRMIEKHHIYLTKDGRV

SMAGVTSKNVEYIAHAITEVVQNA

>contig36844 Frame-1R

MRDKRPPQIPQEVQNTTAPSIPVRPRSNTTSRTTRRARRDTVAATSFVTVATTASLSRAS

ALRTVEILWEGRTALGFTLKRKRTGTILVSTLTREALDSTSLKIGSELRLVGGFPVSSLT

LEDVKKVILRAPKPVSLVFLNAENVILGPVHPINDFNDFSSIQFLPSTSLRRSTSMCTRV

YPSDESDSDKSTALAPLFCHSPSKRHESKKRKVSKLQAALSRLNQLLHRPVRQAGLHFSA

NTSIVV

>contig38370 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69944.1|) 1e-101

MGISRATSTGNRLQPALPSQVAEPQHTTRPLIILDWDDTLLPNTHLSKLGFFSEDVVFKL

PEECVPVLEELATEVENFLRACLKIGPCCIVTNAESGWVERSSQRFLPNIVPLLEQMTII

SARSSFESVYPGRPIEWKIAVYRDLLVKRGLGQAAVVENHGIYVHQQKRETQQLIAFGDA

QVDRYAIQYVARRTPNTQLKSIKLLENPSMTQLQKQLRLLGGFLVQLSCHDETLDLELSN

EMLQ

>contig39179 Frame-0R

MAAPLAATCIPVWAIHRICVNNFDMNCKNIKNSRKRFFVTIFLSGVDCLKNAKCRCR

>contig40001 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61425.1|) 3e-26

MSKLWFLLLKISARQVSVVTKECFKSWYEYASTHGFIATGFEMASTGCSIGYFGLSYLYQ

AALNVSKQVWQ

>contig40074 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53260.1|) 7e-37

MVCGKARRMTSMITPVKQALTKATFAK

>contig40108 Frame-1R

MLGSYPLRFRQNGSVQSLFKTKT

>contig41635 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70671.1|) 1e-75

MLLEQVDYHWGSITFPSGLMFFGLVCACVAMYIVGRHHVEKLMASKGGAVPVPLTRTEDG

WITSHAVVEQWVLFGEIFLTSQGLHVRNQKTRSNSGVDTEIAGRRILQQVKRLLIRATSE

ENIGNDDPERRIRNILRRKTSGSYSDIVLEVVDTPRSPNNAKR

>contig42018 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64533.1|) 4e-26

MMRLVKKVQAFEKMIMSGTDELCAGLETTVESNSNHENDTDASDKESSSRISTLYNGLTA

MDASTNVRVDESGEKHQSLHDSFRSTWNLPGLSRDLNLIQDYTSETKCKLLRFLAGERQY

FYLEPLESSSS

>contig42340 Frame-1F|Blast-hypothetical protein PITG\_03354 [Phytophthora infestans T30-4](gb|EEY65828.1|) 4e-19 NOT\_ORF

MSCLPPRRDRPAEMIKFVSMPSSSFSFACFFLAALMSRLDG\*DP\*KVIPASCNRSRKISS

ASFVDSARFRSL\*T\*GFKTPAARPNSFNDPSPGGSNCVTAFIFFADGNLSLLFRFFGRFI

SGLLSTRAVASGDLSPLGPASSSSSTLLPSSISSSSLASTTAIRFFR

>contig43181 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61202.1|) 5e-41

MELPNTCPRLRTSWSRCDQAVARAAPIATTTCQVCSKCVAKGEWQLGLMFIHIEGFMLME

WYHLQCSLSLQGSGLDNVLEAVQSEMSPAQKEEFQLAYQNLP

>contig43596 Frame-2F|Blast-60S ribosomal protein L13, putative [Phytophthora infestans T30-4](gb|EEY61519.1|) 1e-17

MVFEKPIVVDCRGHLVGRLASLIAKELLQGQHVVAVRCEQLEISGS

>contig43831 Frame-2R

MGEEVKEMDIQWRVPLGDNSYENLKDARHATSSVKSNLRRDRQLAQRSRLGAASTRFKRK

KFSKQLQLLCLQRYAQYAKDYGRISDKFETQQILHQSYVQFLKGGGEPEEPRLSYTEFLK

IVRNRRSEINARAHRTKHDEDEIKQVVVLSPAKMRKQVERDKIRELIETIDRTREQIGRK

PSLQYRD

>contig44456 Frame-0F

MFIRKKRLVHVSFNCMQGAATSLIPMKMLMKKIEQMEIDEEAAKEDETMLQDLSLANKEL

SIAPDALLWLDKYKPQSFLELLSDERINREVLSWMKSWDRFVFPHKRRTNGSHPHSPGKF

GISGKSQWNLESSKKDQNGNAVEDDEDKRPISKIIMICGPPGAGKTTLANIVARHAGYNP

IEVNASDDRTAPVLRNKIVSAMEMQSICGKGKGKPNCIILDEIDGAVNGSDGKSAIDVIL

EIANAPWRTNKARSKTAGKNCHPLTRPLICICNNLYASVLRPLRQMSTNFTLSAPHSRRL

ISRLKFICRSESVKVSTNVLAVLCSSAGNDIRYCLNMLQLQTTQLRVPRSSKSAVITLDS

GLVAQKDHVHGMFEALDLVFYEARAKMSKRETPVADNIIQAVASLGNFSLLISGLDENVP

KMIFNDPTMRKVCEIYQWLGLADECEHRACNEQQFAFQAYIPFAAIATHASCCTCSRRRV

EYPRVHFKAQKRRDRSERILVALKEGAQLQPILRKSTSILVLDVVPWLVASLAPNIRRSN

PSLHTQEEKVTIQRLIELMASLGLSFRHNYFPDRGEDYVLEPPLNELVKFRSSEGVAEDH

IILPLTMRKMIAREVELEKLRRNENSTLLVQKKESKGL

>contig45204 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56106.1|) 4e-62

MPTQELYHERQTLYRCGLHALNNALQGPVFSKDDLERACVELVALIDPNAESSGMAWAWN

PYRAPLGLGNYDVNALTYALQQKGYTMKWLDKRLPMDDNFVKFDEVEGILCNIEMSTMLS

SVWTQRHWFAIRKIHGVCYNLDSKLEAPVPFPLESECYKFLQELVNTGECELFAIKNSET

>contig45437 Frame-0R|Blast-glutamate-cysteine ligase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY54367.1|) 5e-59

MGLLVEGSSLDWPEALEWLQHVRAQGIDQFLHTYNRVKDIEGDELKWGDELEYGVFQMDK

ETKHARLALRGAEILRQLQAKEKNSEENGVDHKYIKTIAMPSVDGCNWVPEYGAWMIEGT

PSAPYGGFTS

>contig45868 Frame-1F

MKLATGLILAAISVHGACGGSPLYLRSSDVDTSASTGNANIANEK

>contig47224 Frame-0R|Blast-phosphoglycerate mutase family protein [Phytophthora infestans T30-4](gb|EEY59690.1|) 1e-33 NOT\_ORF

MTDISATKTLYCIRHGESTYNEWRLRSLWSFSWMWVRDPMIVDAPLSTMGHKQVAKLHEL

IQSTHLDKKIQVV\*T\*KLKVFD\*ALTLKLQIITSPLTRAIETAIGVFPATNVPII

>contig47408 Frame-0F

MKFDVMLIIILTRYPSPDALHQFSMCLKLILA

>contig47574 Frame-1F

MPTTSTVPLLSLDSRKSLQRSAAKRRCIKHSETDVQYVIKRLKRRRSNHGLPVDSSDDLI

QKLQEMDKAFQVAKNMRSLCRCWSCQHLRRWSSSFQPYQCNFKWCMIAFESFIDMYEHQL

TVHGRLNPKTGLVVCDTYRQQRGTLAYPPATVYAAQQHMCPSCPPVPWKSIDELDGEAQV

VRDKLSKYNSYCFETL

>contig47967 Frame-2F|Blast-ADP-ribosylation factor-related protein, putative [Phytophthora infestans T30-4](gb|EEY55576.1|) 2e-25

MLTNSELSEVPLLILANKMDLEDAQTINQIAGILAVERRQGAIASYPICATKREGIEEAM

NWLVDAVKASDRYIEKAATGST

>contig48100 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70274.1|) 4e-94

MEGHVRGVTRLKTFAVAGASILASASVDSTIRLWDLATYQCFKVLSAEENGHVDAVMDLE

FWVNGNESFLMSGGLDCEIIVWSLTPPFQQLFKETQDSQVTALCGTQDAAQAPILLIGMA

DGTISIKELPSFAYKTTLSANLNRGHQDAIRRISTGPINTFFSTGNDRKMIAWQIIGDAA

AIQPK

>contig49734 Frame-0F|Blast-sterol 3-beta-glucosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY55441.1|) 7e-48

MFPQPWVPTVAFPHPLSNILYTGKAKTVNYLSYKMVDLLMWQGTQKMVNAFR

>contig50273 Frame-1R|Blast-hypothetical protein PITG\_00684 [Phytophthora infestans T30-4](gb|EEY58072.1|) 1e-31

MHLSLLKHMLMIGKHILITDGFVDKESCRFGFHRSPFASVSHLHLHCLGLPFRPWWNQLR

FIESVLPSYVNAESVVATLRNKQDPLNNS

>contig50567 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65505.1|) 2e-43

MRYADAYNMRHSNVFDRSSPGYKEYWGTLRDVYTTTGTTSGGSGLENATSFRKSRHPPTQ

VESKETEADSTTPCDSGSSEDAFKPAVAIHDALLASAIERLTDATSSHIATLHQKGVSDT

TKTLVELTTVMTDLRVQHSSAFERIIQLQEKQLEVMEGLLKIKLRKEAVRNNSDSLNSSN

SGGGSTSSLSETITVSAQTA

>contig50808 Frame-1F

MDTNCISFCSRFAMDERRTIKFERSMPATILKRATLLHYYEPFNHLDLPYTAACRSEFVK

>contig50974 Frame-1F

MPYTPIFGQTQRDLVWEHVRELASESKHWATEAQARPTTNCATKRSAREDFNYMPSERS

>contig53845 Frame-1R|Blast-exosome complex exonuclease RRP45-like protein [Phytophthora infestans T30-4](gb|EEY64757.1|) 5e-34

MTDYSTMHAPIALREDPSIEKTTQQNSSMADLMESLESAANYRESEASALVPGGLVMTEA

ARNSFQQLAKSDVVSGLMRGSLSETSANKVTTA

>contig54116 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67585.1|) 6e-17

MSKRAHSTITSGGLLDSTLNSLSRTNESALTAKKAEAQVAKLTAGRGQTISVDDAS

>contig55120 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69767.1|) 1e-14

MTAVMSLANAPTLRYRQLHQDLLAFAGRSMIDDDTPLFIASLEAAAPELLQVLTLPPPNA

>contig55850 Frame-0F

MPAPQLRQIHVLVVAPIVAVPRIVPEKILTISPNSNKAETVERYETLSKTLAKQEQVESL

SNAICAILEGNFEITPFVVLESSSGMGKTQMAFNLNATGKFDVFYLWVDNVDDKGQDISA

AYTSRTDVFSICLNNDFELRKNLGDGMGSIRSLQGTKYLWLYRFIHAALLGKNEVDDAAR

SREDVEKALKDRATSGKKPFIFFLDEFPREIDRKATSSNPEAYDQKRRLRLMLNVFRSFG

LVVIVSSTSGTGRNLVSVSSGTRSNLDYLWCIVHPLLPRTVIGNDIRILPTVLQDIIANS

RPLFAWKA

>contig56248 Frame-1R|Blast-presenilin-like protein [Phytophthora infestans T30-4](gb|EEY57615.1|) 3e-59

MLIGYMMFSSAMLLGMLGGNMLVIVVAKLKIPLDKLTMLFAMYNFSIVGVLSVFYQKGLP

MWLTQAYLVVTSVIVAWQLGQFPEWTTWALVVLLAFYDLCAVLTPCGPLKWLVTLVQQEG

RPLPG

>contig58022 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55822.1|) 5e-25

MKTEVAKKAAEGKARDDVRGQKIIPDYAFVHKPITDEAIILDANRSVDDIKERVAVLLAQ

KKL

>contig59267 Frame-1R

MPANPTKLPTAVTSGLQLLSPTLHHAIQHSTQEAHEGTKAHA

>contig06512 Frame-2F

MSQFSSEFELSSPIVWRHCCSWLAVMSSVCHLNRHHLPCRPVLLLQEGNAH

>contig07278 Frame-0R|Blast-ribosomal protein S19 [Phytophthora infestans]gb|EEY55509.1| 40S ribosomal protein S19-3 [Phytophthora infestans T30-4](gb|AAY43414.1|) 2e-80

MADYDEEETAIGVTVRDVKPADFIKAYAEHLKRSGKIELPAWWDVVKTASFKEYSPADQD

WYYIRAASIARKVYLRQYTGVGALKKVYGGAARKGVHRQHFQKASGGLIRHILQQLEEMK

VVEKCPEGVNKGGRKISSHGQQDLDRIAGQVVRA

>contig07630 Frame-2F

MARGKLESGSESSDSDSEDSDIEETQTEEEEAEDIPLGTETRRFAVLHCDWTRIRAVDLF

ALCQSFAPATGTVQNVTIYPSDFGLQKMVHPNV

>contig08248 Frame-0R

MFQRFSLRLAGVFLLIGCGSTLEAIDTNSDTFGTRHSTDMNQPSAAISSNTRSLRLLKAN

AMGLNGLEGISHSILPNKNFFQNFNLEKLGLQRSALIKRNAVDNALKYRGGRIRPGLEKN

GFPNSVRTKRYSENNGYRNSVRTRVN

>contig10735 Frame-2F|Blast-glucokinase, putative [Phytophthora infestans T30-4](gb|EEY70574.1|) 1e-147

MSYAMLPVVSSDLTSDTSSVYRHDLVISGDCGGTNTRLSLWRIPAGGVAYQDSVTAGNIT

FARKYHNENYACFSDVCHLFLKEANIKNSLPVICVLACAGPILNNTVEFTNIIDGWKIDG

PGLEMELGIPTVKLINDFVAMGYGLLTLMPQEYITLNDAKREEGMPIATIGAGTGLGECY

LTAGNDGHYSCYASEGGHVDFSPADALEIELYNSLKNELGCDRRFSVERVVSGPGLANIY

RFLAKKYPEKVEKTVHQAFLSAKSLQGKIVGTNAKTNELCNQAMEILVDVYGREAGSAML

KYLPRGGFYITGGLAPKNLDYFTKTDIFLKACFDKGRMGPVLKAIPIYLVLTEDLGERGA

HYYARQLLESKNCRVLSTKTSNEFVQEKTTVQNTVKQ

>contig11008 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59538.1|) 1e-14 NOT\_ORF

M\*PSIALVQVANYPFTTRGISVGHIFVEGVSYQVMAICFDKFSSRININLNHEDRRHSWL

NLSPRRKSKHHRAASDCYYGEDACRKPRE

>contig13411 Frame-1F|Blast-ribosomal RNA assembly protein mis3 [Phytophthora infestans T30-4](gb|EEY63939.1|) 1e-79

MIKRELAKDPKLKDENWERFLPSFKKQNVQTKKPKNVREKKVYTPFPPAPTASKVDQEIE

SGEYFMKEHERKALKKAKKQEEKAQVLQKRKAEKMAELVAPSDKDAIKKRKKQKAQAQDN

HKRATSVEALKQKFLTQKVRVTCVSKMK

>contig13600 Frame-2R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY53336.1|) 9e-82

MAADDLLTKSKNKNAKHGINTGTTHGKSNGKGAGVGGFQHLGLSPLVFRGVMAMGYKVPT

PIQRKSLPIVLSGKDCVAMARTGSGKTAAFLIPMVEKLKEHSNKIGVRAVVLSPTRELAV

QTLRFTKLVSKFTTLKMALIVGGEGMDQQFEAIAANPDILIATPGRLMHHLHEIPG

>contig14124 Frame-0F

MLAWILALLLVLAGAGYLHLQQQVRAKQEACKLQKEKEELAREHLHAFPNKKAKHKLPKV

DVTAELKKKKEQASAAERSDTEHSSILHVLKGHKYIVTAAAYSPNNRFIATASLDRSIRI

YFRDTLKAKKPKVHQINLEYDHVTAMCFSPDGRNLVIATVNGHVKVYQKLRIKPDIFADF

PISHSSDVHSVHMNDIGNWATIITCASESDTEVKFWNLRGELLQIVNTNQVANYHCVGSK

DNRYVAVAAYTPEVKIYEITREKAGNFKKANKIMTLQGHRAGVMDLAFNGSDTLAVDRVV

TIYKDASIRVWNIN

>contig14674 Frame-2F|Blast-60S ribosomal protein L10a-1 [Phytophthora infestans T30-4](gb|EEY54168.1|) 4e-97

MSKLNSDLLSQAVDNILAFSAGETVTINGNEHKGKKRNFNETIELQIALKNYDPQKDKRF

SGTFKLPTVPRPGMKICVLGNAVHCEMAEKEGFEYMTVDDLKKFNKNKKVIKKFAKKYDA

FLASDTLIKQIPRLLGPGLNKAGKFPTLVTSSDSLTEKAEAVRATIKFQMKKVMCLNVAI

GHVGLDKQHIVVNTQLAANFLASLLKKNWQNIKVLYLKSTMGPAVQIFF

>contig15453 Frame-0F

MGNVCYRRPTITHLRFRLAGRPSFGWLLVCLLAYLRRCAIVPTYFQFQYLTTRPIENKRR

HAGASGQLFTCSITKYCITISNDVLMS

>contig16126 Frame-0R

MNNPPYQTYGGPPQQNTQQSQTPHTAAFRPFNPAQVNAPLSGSGGITPVRSGSSHILSAG

PLHQMGSGPSSFVPKNSNFSSGPASQPSAATSQQFGRNPASMSGSRSYGPSIGEPSSLNQ

PQMMRGPPPSGMVPPMRQGIPGPPPPGAEAAIHGPPTGLTHQFASMGLNSTGPSGPGMAG

LPRGPVPMGGMMAPPGAPSMAQQSSQQPLMYHQPSVLNQQQGPTTSQQPVAYSNLPSGNY

KQP

>contig16856 Frame-0R|Blast-3-phosphoinositide-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66101.1|) 2e-17

MVKDGHVCLMISGSSSINNVTSVMIKTSEDEADEYKCDIVLCKAPWGGASNVIHCSEVTR

EEVRTTAFDVAHPSTSDTSKLSLPSFELEVEDDVVAADIVSLT

>contig17091 Frame-0R

MQVLYLLHNAIYSLNGKQISKGQTVYRYPRVLPLHTYLSVTMLLGCGLKVRNHARCSSIA

HIRCLLSTKIDTLSLSADKFAEMLRNCGVSKNRLHHDLYPLQQGINAPKDEFPMAVALSG

GADSMALMLLLREYLQYNRIETPLLAVTVDHQLRLGSSKEALEVANICAQRGGIRHITKV

CEWHSESKKQKIDEKQQYNMSRPVKPRSSKMEEQARQYRYSLLRQVCQTYRVRCLFVAHT

RGDQLETTLFRLGRASGINGLAGIAKVHPFFSFDSMPVHSINTSNAQSMATLIRPLLSVT

KKELMATCARFHQTWIQDPSNDDLVFDRVRIRQALKRVENEHGPEILDLIARFQLSAEKA

KHEFERIERAMLSKYIIIWELNRVVLRIAVIHDPGMFLELLYRIVSIIVVHVGSKVTPPR

LASIQRLARDLECLAKGKQLTLGGC

>contig17666 Frame-0F

MNISATIIAAATIVAGVTGNTVHTSRQLILGGHTAESSQQYVVGLCDSPSQNSFCSGVLI

TKSHVLTTSTCVDQVWDGISMYAAIGARFNTGLNFSNGMQNGEHIKVETIQIHPEFNNDT

TSYDFALLTLRKASQFTPIQQPTADAKPGMYLKAFGSGSPTYPDTLLQVVKLEVWSNDRC

DDTYEIDDSMICAGGENGKSTCIGDIGGPLVHETKSGDVLIGLVSMAECGNEGTPDVFSR

VWSARDWLIECIESDMLL

>contig19493 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68483.1|) 2e-76 NOT\_ORF

MRQAYERTENLCNSHFLKLPHDEEEVGDGMANTELTLDKYLELAAPPGN

>contig19725 Frame-1R|Blast-2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative [Phytophthora infestans T30-4](gb|EEY66237.1|) 2e-08

MEKRYVVFVLIDGLADVSLEELSQQTPLEIAQTPAMDAIA

>contig21058 Frame-1F|Blast-serine protease family S09X, putative [Phytophthora infestans T30-4](gb|EEY69004.1|) 0.0

MGSSESREASPSSSSSSRSIRRSLPPQSSIEVGDAENQGIRAGRRSASMPNEREVVATER

RHVLLPRPFRRHRSSSSSSSSNDRIPRERGGIERGQEATEETSSQLSYWYLLKHGYTELV

NLIIRPPRTDYDMNDIGPMKFFYAGRTFVREDFTVLNDRKQKLVCSLWRPATLSSTELMP

CVVYLHGNSSCRLEALGVLRTCLAAGLSVAAFDTAGCGKSDGEYISLGYYERDDLRDVVT

YLRAEKKVGAVALWGRSMGAATALLHADRDPSIAGIVVDSAFASLEQLVEEVVERGRQEG

LTLPGFLVKIVLKFIRSSVKKRAHFNLRRLAPIDHAPVSFVPALIVAAVDDTFIAPHHSD

QIFAAYGGDKNLVKVDGDHNSSRPQFLLDSAAIFLQMALQVNETESGVRSRFFGDTLMDG

GGRAPWEGAIGHTSSLSMCLSSPASSFQTTMEARNASKALDGHSDEAMVLCVVYI

>contig21924 Frame-1R|Blast-DNA-directed RNA polymerase III subunit RPC5-like protein [Phytophthora infestans T30-4](gb|EEY55502.1|) 1e-161

MPEPPRRARVKPKNQLMQLDFPVDQRSEHFDQDAEDYIKQKTLRLQSSCVPALSNYAVGV

FRQGQLHLTPLSSIMQMRPSLSYIDDAINEEEIDIDMEEKVEPPPAEMKEVQFQFKKKQS

ERALSAIQNSYAFKKQQIDAENWIELQVHELSTAGADDEFENLFSEKEEEIVLDMTPAQY

IRALQYRALATADKSAALANPAQVDAEDNTEMDDTMEPIKGHLLDGVNAKYSDVLRILAT

DQIMHFNTLALLLPTHKEEDLIDALEHVAIHVLGRLLPASALIFRGETTIRARNEIIKAL

AKSPTGVSRTELVKQTLLEASIAKNILSEFAILDPATRKWSFRLGPDNLFAKRFPTLANS

IKL

>contig21999 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53323.1|) 4e-14

MPMVQQLRIRFLIGMNIYVRGLPIACLCAFEQGDEEEKSSCNDKSNQLRKSFDDATVLSK

ATEKMEDELETLLFGLKL

>contig22882 Frame-0R

MAAALIHAEFGYDCDLYGVLCVKRTATSKEIKRAYHKLALKYHPDKQHGNEATRTKATAK

FQALCAIHSILSDKCSRAAYDDSGIIDSNDLDYKSTSYQMWTQYFACVFPKVSKEKILKF

ENEYRFSSEEKCDVLAAYTKYEGEFKHVMHSIMLSTEDDEERFAEMIHVAIKENKVKKFP

KWREYVEKQTKMKNRKTTSVIKRHGIKRRKKEACEAEELYNAIRGNQQQRDEDSVLCFER

KHDFESLLGSLEAKYATKKKKAKGL

>contig23250 Frame-0F

MSLLLESSMEYLHQILQLIDTRIGGGLVSTNNSIISIPDSVKEVLIVLEVCCLPYQGQDW

DYLQRTKLMPLLMELISWRGWQRFIQYEESNSIDADTESVETYVILPASIGLRDLSIKCS

QNLTFGTDLGKVKVAHYDYDATQSLHSRSGNGGLVVLDRCFYRGRWYWEVSIHT

>contig23531 Frame-1F

MMAARKVLIVIGVLVVVAVAIGIIVGVTSNGSDENANTSSSDKTSIGSGLGSKTVFDSTS

AVSEADLLTDMTNSSSSAENNEPDSDPEEAKAALTMLAIGDWGATTDKPGSCCNKYRKVA

NDSLDMKIDYWAQINVAEILAQAAGDIKPLRIIGHGDNIYWNGAGPDDIDYRMETTFESV

YDQPALEGIPWINVVGNHDLGGSEYICGDKDYNFRECESTEEMLQYLNLKFSLQQEYKSA

QSDRWKLSDHYYKESVEENGVSVDIFNVDTNFADSHGVMQICCQCYGYVKKKNLSAADAK

KLGTTCNDRIPGDELCAGGSTEMYHACSDTIKMWWDDSLEQVKKDLAASTATWKVINSHY

SPHFHMSDDKMKEWFMITKEGGAHVWFNGHTHGFNHDISKWGTHFFENGGGGGIQSETSG

MPPEVAEKYVNHAWIAAGNPYGFFMLHFSKDWLKTEFVTFDDSWVFSVEKDEIVKGGYQK

GHCWHVPVTIGVGKECGTSES

>contig25432 Frame-0F

MLRMSRAVETYLRNYEGDEAHHQDILEITLCYGVQCLVRTFSLKGISCNELRAITNYDTA

KTRDYHVRHAFSRKNSNTIVPQRTPLEVHSKPSHLWRDGEADALDILKPTDAGPLKIKPA

SKIDEAALFSLPPTCKQFDFYAKVLAKQLLDLVWKTLVGRDKVQICTRQGLDDMFLRISQ

MKAPASMPIVSFPVISLADFLGAYVTECVRHSHETG

>contig25995 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65152.1|) 1e-107

MSLQFLGQKSWHPASKANQKRVWVAEQQAKELEDRELRNAKEVRKAADLLQAQQAAAAAG

DTAAARLVNTAQVNFLYAIPPGFSEAMKKESSINKLQEDEDVLEFRRKTERRGDTQRSKL

ERYVGRRAQETLTLKDQVERFPILKDAPVEGKYTETIKVNFNPLGLRLRNVRCIRCGVWG

HQSGDRECKLQDQNPNDATRQKWEDPVTEIQKRKSEKHKLVLKRGALPLELQEKAGEEFE

ILQSDE

>contig26679 Frame-1F

MARRSLYGPNRVTPPVNCPSWVCCLLPCLMRTASMQAYHEALPREATVRRRVAAAQGQVS

FRCMRMDVMSLVYGDVVELKAGDVAGADCRVVECSDDCIVDQTILMGDDGEDEEAGIARC

EKHVTTVTPPLHLQQKPLQCNNIVPMTARVVKGAAVAVVLSTGDFTLWGRMLACHEWPRA

PGTVIRKGDLEEQSGLIV

>contig27676 Frame-2R

MLLSWVPWALMQALLPTSAIEVLQDDTERQHLRDELMQTIQVYSKVMLHWVLRTAQIFTA

ISFLFVTASLFYALLYYLVIPSRFHEQDVIFHYGRRHMKICEQGGHPLSLPHSSLDLQNP

EHQWQTLLPKQMEKVRPVLVSGVKYDVIVELTVPESRNNAEVGVFMVSTTLYSEQEKGLA

TSARPAALHDMPAPVRWLKLMFWLAPYTLGFSEPTQTLRVTAINGYPETTEYPLTRVDIE

LNTPELHVYSAKLIVIAQLTGLRYFMYHWSVPTALLFILNFVFVEALVLSILYAVYVLPQ

LDEEAATNAAVLEAAAVYASDKATEVLATESALDPDDKECKKSEASIDKISFKLIGIEEV

SSGFEEAIDNIYEENTDVKLEPVVNCPQ

>contig27993 Frame-0F|Blast-cytochrome c1, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY69490.1|) 1e-130

MFERPGKLSDPLPRPYQNDEAAAAANNGAIPPDLSLIVKSRHAGADYLFALLTGYVNPPE

GMELLPGLYYNPYFGGGAIAMERQLQDGQIEYEDGTPCTTSQMAKDVSVFLAWAAEPEHD

VRKKMGMQTTAALLVLAALTGYYKRLKWAPLKTRKITYTT

>contig28084 Frame-2F|Blast-geranylgeranyl transferase type-2 subunit alpha, putative [Phytophthora infestans T30-4]gb|EEY67249.1| geranylgeranyl transferase type-2 subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY67248.1|) 8e-75

MQKIEQNFSNYSALHDRSILLPRPFTADGLFEEIRLIQQAVFTEPDDQSAWFYYRWLVTS

MVELVASCPEDTAGFLKSQIVWLQELLEMENEAKWVVVTLANLHYRLSTIVTVSGWEEAK

TQCAKLYDRASIVDPDHRHYYDDMKKKCS

>contig28501 Frame-0F

MGMGRMTQAFRDVQFVLQHVPTNKAAAALARTIQEHVRQDIHGVQKALDSIVMGVHGEDG

NIRLQEILHTQDTTIEALQYLEMKSATEIATLPEEISKRKGLSVLWNAVQQLLPLSTKPA

PLNKSILTILSHVVSLLSLLASTSMEFTQKTFETNNGVLWNLLEFSQHHIALEYTENKAK

KDISQPLRGQKALIRLAACLFKYLFLQVKTIDTTSLRRVLNGVLDGLRSQERVLQVAAID

GMLHVLSAFSTPTASPRSSDNTLKPHGNRQFTILAQEVGLYSLLHTTITSVLPGFVKAAS

KESIDSTLTSVILTRVPLVFTQCLAQVEGDDMKLQKLVHDWCISPVLAARPSQRKTLAQA

SASCLLLSSLFLSNAKLGIHAVQATSNDGTAFLSRLHEFLAASRTFDDCKAHTRQLQEIW

VDCVASICGVDQGPACVPRALRMEIYRLLQASLDEADDLILRASALSIQVKLGIVEKTLV

FPSTEGDYLVESVLKVLARAETIETKHLEGDQTNDKTQTSCTKKDVNIPFYQSTVSPKER

GIEALSYLITYTSVKDAFVKSPMAVASVFHVEFPTDINTTSCQVFRSNVYYGIGYILHHV

WTSEAAIKRTQMEGMDMTADQYEELQKALKQQSVLE

>contig28758 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54204.1|) 7e-69

MNESFIQTTLQNTDAWSLHAYESSVITKQRKVYIEWLKISDVQVTITARVSIPVLNSFDC

TPLHFGSTKMREVFSFPDQLYKDVAANYVVDTIVCSPMLLMSLNI

>contig28840 Frame-1F

MPKKRVCSQQSSTPSKSEMNPLLWATSLTKVKKRSLGVVANTSSSEKSASLSIDRNLQRC

NNTFGKALSSPSVKSSLPLVSVSLRGNVNAPKRMNLPPQRRSRNPGNLSLDLSQVDIATA

TPRTSAFNNVKRRNDEAAECSRLLDFLYIGGATVAKNKSMLTQHGITHIINCAASVTP

>contig29652 Frame-2F

MPLYAKGGRESETKASKIVPSGSRRRRERTPPQCGSSATVPSSHPRRDPSWCLLHKHKRD

GYGKAQFQVAKLRQKRFLHWRAVATMYWQGNDGTKVRHTQKTWSCVLL

>contig30207 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70649.1|) 1e-122 NOT\_ORF

MKKFQSRCGTKLSDKDMEHHREYMKKFKMQSSDADQKKMLYKDHYEVLGINRDASHTEIR

RAYRKLALKCHPDRRPSPNALERWEGVPVAYAVLSNPNDRTDYDATLPTRDALIEFYRAY

NPSKLDNTTIETIIDGWAGREVELFEMLNQKYEVLPHKGIAKAVHGAAVMSISRERSHKV

ALDTQMDTSKDAATVEITWKNTIVSAFCCKNALIRCFNSFNTTYYVVDTTSPGSLATRGS

SDTPGQAMPGNRRSPAPPSKLSKPLSPDFDLPFDAENSSTATTTDGSPPSGDECYARSRN

EFIVS\*SAP\*ANLNFVAAVTSKANSD

>contig31086 Frame-0R|Blast-pre-mRNA-splicing factor SF2 [Phytophthora infestans T30-4](gb|EEY65533.1|) 2e-89

MSGTRVYVGNLPMDIRTREVEDIFYKYGRIRDIDVKFPSRPPAFAFVDFEDSRDAENAIR

GRDGYEYDGARLRVEFANGGRRDSVRESTRESSRGSNRYPRNIRGTGDFTVEVSNLPPRV

SWQDLKDFMRKAGDVVFTEVDGHGGGIVEFSNKRDMKYAVEKLDDSEFRGRSENSFVRVQ

EAGKRDR

>contig31529 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56936.1|) 0.0

MFDREKEAIASSNDVIASLSRMETNLRIFRTAQAQFSQCFETAMTPCRPPSKLRQRWLQV

TTVAICLTAGGVWVLNNQSAFYAGIAAARAAFREFLSEHMLEPLQAIFEEVVLNQKPEIQ

DALALMDTKESLRRMLADFVKDTNPKVSPMEMNRIMNDMDMSVVSLQYEKQLASAVKNLM

TGDIVRMLLIQVQFIKKELMVAMGAIDELMHANQLNMQIMATIPTFLVFGGLYKFVTSAF

HMIYKRLSDRLFYDSNEIAGFLRNNLRDIERLLNKQNRGSNGTEDAVLGVRDLGFLILLL

HQLRDLFEAYRALFQEEEQERFEEDLDDLIGEGLLVSQQLAVIQRMYHSHPFLYSTKPQK

ARWILD

>contig31594 Frame-2F

MGTRSRTLKYLPGHELRFAIAPVSRNSATGNVDEAVCLFCKHFGREQRVGKKRKCASTVK

YFRDSFRPDQYTQHHQLQHPTQWQLYKDLNDDEKLAFFPLTDKMTTASTDRGGTNNVIAE

VLVPELHERGRCFDIKAAIVEIVAVIAVGMGPVEHTVQTRDRLMYEYMTHHHYEREPPSN

CPRWDPPPNTFKKCYVVRNEPPMYRVVLYTKAQLDFVMELAAQGLSGTQIAASVKVLRRH

HSVVCNDLSKPISKSSEKHATATEWQTSRVTNNMHPEFGEVQTSEIVRLGVALSLNIIST

FLEESWAFSLEFCTVVHAQSFSYLDLRVRFYNQIGGLRSAHLLAIPNSNNTCDLMMRNTL

DRVLTVVLSDWKSKLLGISTTGSIPFSAHINKVIAHFQNVATRSVLYRTSNCVCQVQHIM

RCFFSSIDDGQFLKTLKSMSAYVRQEPCVLSEIKTLPGFWDQLNIDAYGDSSPSVAIGRE

VDMLVAHAS

>contig32227 Frame-2F|Blast-hypothetical protein CC1G\_11409 [Coprinopsis cinerea okayama7#130](ref|XP\_001829673.1|) 3e-29

MDNQAAMKQIENKASSASGKHVDVKLKFLRDYATKGVIKPSCVKSHDMLADLLTKALPAP

RVLELRLKVGLK

>contig33912 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60964.1|) 6e-28

MVAFSVYKSSKYLFDCVSTTDVAPSQPYSMAKQDAFEALQLDSVDVVKRIDNAELKTLIA

CCEEPPLEAIVTPVTHGDIVPFQTFAKYLNNRQ

>contig34636 Frame-0R

MVVTTQDQAVRIVDPRIGQCSAPDIQAAHNGKRHLSVVWCGRTHHFVTCGSGLTQEREVK

LWDPRHLATCVHRERLDAGGVGHLIPLYDSDLDLLYILGKGNSSARLFEVDLTRTPHVHA

VNHTALGTMTLAATLLPKTTCDTNVCEVARILNLSASGSSVGGSCEVVSYRVPRKDATHT

FQSDLYPDTLAGEATMTSLEWQQGRNAEPMKRAVVPSVKAMEDTSTSVFGRPTSGHHGPS

SWALPGGGVGASTKRRQYSSWGQALPSAASSNTPSETVLITKTGWGSGSRKWNESEPIAQ

SSHPGFIQWNSNESAATAPVPSSLPNFIAETRENNDEALAPAAMSMELPFKTESSSIADV

VELSDKAQRLGAKYGHKLKYLHGQEASRNDVFYFGDMSVANTTQASPIVAANATYWAVPI

TGAGGPVLVEKVGAVGKAQHGSASVINGQKAEVSALAFNPFHDHMLATGSADSTIQLWSL

DMHTRSESGQLIQALSGHTKGIRSLQYNPTAANVLCSSSQDLSLRFWDLEAGQQKLCLEG

KLDDITWNIAFSQDGALLATASRAKIVRVFDPRQSEQALVAMGCGHESNKPQFVTWADSM

RLLTVGVNSRNETQVSFWDSRNLLEPLQIPIGLNPTASSASTTTPIPLYDASSHLLFLVG

AGSRHIWSYEVDSTAATVQANLPFIMAGTSTIGGVALLPQRTCNIREIEVARMLVAASNV

MECVSFSIPRAQKLKEFFQDEIFGPVPKQEPSLTAAQWFLGESGSPIYESLCPVGMTPLS

KRPIEIAPARPKTLDFQARKREEEEKERRKAAQFARLSSLAAQPSLHQSQVNTSISPSVA

EDSDDDWNE

>contig35077 Frame-1F

MAAEQAKSRGNRAFAAGLFSDAVACFSEALAVAPSDSNAHVFYSNRSAAQLKLNKANEAL

NDADQCIALQPTWTKGYSRRGAALYALGRYTDAYRAYKDGLSQDASNTGLLEGLRAVEAK

LVTPGATTSSSSTSTPHATTTLTTFLFGSKHNMFQLYQFLLRSLLLLCFGNFWVPTLLSS

SVAYANFFKLSLVNHASFLAFTHGIPKWSASYAQRLLLDPAAQLFFFCLVFWVSEPHGLA

MMPVFLLEIVHYFAYLNSLMQVLGLSDSSVVKIVTSKALVPLTALVISDPSFPALSTRAK

WAKLYTRVPQIAANIDVAIGFALLFEMLTPSRNFLLLVLYWQVLRVRYMISPHLQEAFRS

LHATILTFVNSPRCPAVIGIVYG

>contig36638-0 Frame-0F0

MIRGGCTFAQKILRAQAAGAVGVLIVQTADVWPYTMTDSSGEIVKIPAFMMSAKVGERFV

AFLRTKYQEGITATFIVRKDARECAICQVDMLMGARVTKMPC

>contig36847 Frame-1F|Blast-fatty acid synthase subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY57114.1|) 1e-58

MVAGMTPTTSLEGIDLVAAIQNAGFHGELAAGGLSRPNLFEHAVKKLVSK

>contig39583 Frame-1F

MLRVMVRRSYIQRSVHLVALASLALLASTLLFTVAPWLNDDLCHSQRKSLGIQFDSLAVD

HAVVFITILPPLLWLLLSQIAYSHTTSWLDIALLVVRVTICVTATFALTVLLTEFFSRRA

TVALGILAYASIGLLYSWSVPIWKWYQEEVRHRGLVRILPKSMQELLLETSLLEWLTDTT

LSDKVAPFLPFLLPLTKMEQIRLMEQMAPEAQVMLTKPGLLPLLPYSIQKVLLPAADYDS

EQDKNCRSTLT

>contig40727 Frame-1F

MESKSESDFFDSSDSARPNKTSANSDLNANGVEANQSFSRDNDRVPHLQSPSSQSIAILA

VLAVLEQSQTTMLSSMTLKNKNDGLGLFPSCQEALNYIRIHEFVLETIVKNRELVCENRK

VPLKILHIIELSLRIGKASGMVQKGYKPELSLIADTTSYIYEHSVTSALTSRAWVDGVKD

ASQDSATKTKLSATLLKLDVFLLQVPSTVQMWLKEDTVCDEAKERLKALVAVVRKKLSPA

DEKSFQRGKGKSRQRLLGVVPLIKKRRKRLRSRHPIIDAFLNEEDGADAFADLEDFIE

>contig43168 Frame-1F|Blast-DNA topoisomerase 2 DNA gyrase B [Phytophthora infestans T30-4](gb|EEY61057.1|) 4e-31

MLQELHFTPAYALQNDNIIHDGNLGRIAGGRDQEVAGDLHSNCDDYDYLLQTSLLSFTQE

FTERLQKEHDTKQEKLKQLQETTPAQLWQQELEQLRAMLVQDPDFQVGHH

>contig43520 Frame-2R

MLSIPNPMLSAPTSPFMVAPELTFINLADDPQARDSNDNMMAWQWALIGLAIACTMGLLL

FFLNWFKHRPQSGDNRQEVVQSLEQSRLPITESVDVAPIALSANQARFESSKYANLAPKT

MHSFNTILSQVSSSTDGSYRTNIGKKMSSTLTDTEIVAQHQERMFSPLSDSTCSRSSDYL

QSTEANKVNNDARVRDSSSDLDVRSSSSSYSAASDMISELKSGDFDLGIRKFARILHKKS

TEF

>contig43595 Frame-2F|Blast-60S ribosomal protein L13, putative [Phytophthora infestans T30-4](gb|EEY61519.1|) 2e-76

MLWRTIRGMLPHKTARGAAALQRLKVFDGIPSPYDKQKRMVIPAALRVLRLKASRRYTVL

GNLASEVGWRHAELVKRLEAKRVLKSDAFYKKKVAQKKRLVEAEAKVYADNSELKPLLSK

YGQAL

>contig43832 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54198.1|) 1e-101

MASSAIAKLGLCPKYINEEPDIPDNVQGELKKLEESAVQLLETALTHGRVIIVTAAETGW

VELSASLFMPRLVPYLNTRIKVISARSTYEYLYPDCPHQWKIEAFNKEVFPVWEVYGEEN

LAGVPRHIISLGDGPTEREALINVKMQAIDVCHGKSMKFIAYPKISELQLEVELILANME

HLCTHEGDLDLQITWEMLNVAT

>contig43847 Frame-0R

MSNPNAHRKMTPKGQMSSSGMGPAIMHLPTHLKILFEPNPPLDHLSRLVKRKMPPYTGLA

DFADTFETEKPPMRNVQETPKERRERRRLEKMAAHDAKTEKDRAKWDPNAEDSRKTQDAY

KTLFVGRISYETTEQQLRHELEQYGPVKRVRLVEDPEGKSRGYGFVEYEKEADMKAAYKY

ADGKKIDGRRVVVDVERGRTVRDWLPKKFGGGIGETRKGGADVNVKYSGREAIGHFQVGA

VRDEGASRGAREPPRDRSRSRGRVAIGENRERRRSRSRSRDRRRDRGHDHSRDQDRGRDY

DRSRDRRSRRDSRDYSRRY

>contig44086 Frame-1R

MTTATIISFKGEERLVGESAVLASSTNPCNTIGFLSVLLGKNLTDVQRQLERLPGCQPTF

EVNEADHVVALVTYGKNGTITKLTVEQLTGMLLADLASQMKKRFVDEPLHALHVTLAVPS

VWVDKEKRALRMAAKIAGIPSLAIISRDAALARCFHCKHPLKASAPTDDGDVCMETARHI

AIVDMGHTSTSVTIAKLTPAGETLVATEADVELGAETFDRRLFEHFQNEVQEKHQLSVVL

HSKEGKRLYHACEKLKRLLSTIGEASVTVENLAPEKDINISISRDKFQALCTAERKNVTE

MVQKALETAQDIVASADIAAVEIVGGGTRIPFVQEAIIAAFPAQQHRSSTLIGRMLDSTT

SIALGAAYFSEAATTAVTNAVESVENTAELARCVALEQEFQARDAQLMAIADERNAIEAF

VYEIRSKSSGKFGNMLDASKLNPLLEAAEDWIYSEEAEFATLDAISAKRKAIETEIRAVC

EDYFSAMEADERALEKQLEQESQKAEAERQADGGDEDHDIRKLKKPERMRMVVKNKEEGN

ELFRDGNYKHAAARYVKALTHASKFFDLSEADKEEVNSIKLSLYLNLAQCYLKMEINSKV

VANCNEALILDPKNVKALYRRAVAYEKENKVEQAADDVKAALRIAPQDRTVIKLDERLKL

CLRRQLEKEKKMWSKAFA

>contig44305 Frame-1F

MVRTSNCDIIVQKEFSSLILVLDQASDDVVQCLKKLKKKLAEYDFRHNNSFLSSAKSYMH

SDIRFAKDISSELKSVAHQISKSDIYSKFEVELARNSMNATANAMEVLTTKSRIYDETDG

RATGVKGIIQNIMGGAHKKDDKSEDNLMLDNQVGISPDTVETLVESTLLNGFDLKGLIEQ

INAAERTLVPSVIERANEAMDDVREAFKADEPSLTPEMMFSAFS

>contig44455 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53304.1|) 0.0

MVTMQNVHNASQLEKIFLGNEKEYVQAGKQVKAMGAQFEQGQYLKESFGFDEETFRFLAK

HYLLFPEDRTGKNKRASTTSGGGNSHDRATAAGVCFAEMCAHNALAAFVTGNSHLCQMWR

ILEVLYTNEYIDTALVKHDNYQSTNDQDSRSSADGLVTDRGLLDEVDRMYSPHIRHHDDQ

GNEYEQREERQDINDLGHTNHRNVNLNHGSNASETTMLLEQLDHVNPQAMEGFDPYPYDP

SGKYTNENGRDSGNRNGSSGIANVRDNSSMIMNGSAVMGDLGHLRDDVLKEVLEYYTEIG

DLQSSVAITVVVGKVTSIEKIMGKVWLQHIYMHYIDLLHQLQIYTTANELIANCMDQSIR

QMNMKSTSVYFNCSRCSKPLESSGSSELGGPLSLCKNCNNAATLCSICQLPVRGLYVWCP

VCAHGGHLDHLTEWFALKRFALLVARTIAH

>contig45207 Frame-0R|Blast-peptide chain release factor, putative [Phytophthora infestans T30-4](gb|EEY61793.1|) 3e-80

MTADSQPNDEIELLIKDLRIDTYRSSGPGGQHVNCTDSAVRITHMPSGIVVQNQSDRSQH

RNKAEAMAVLRAKLYKRKLEKEAEVRQEHTKGLGENAWGNQIRSYVLHPYQLVKDHRTNY

SESNTTNVLDGH

>contig45298 Frame-0F

MTCSMVLPLSLDSCKSICINCIL

>contig45922 Frame-2R|Blast-succinyl-CoA ligase subunit alpha, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY61690.1|) 1e-170

MFATTPVKKSSAVALVTRRMSASAKVWINKDTKVICQGFTGKQGTFHSQQAIDYGTNMVG

GVTPKKGGSTHLGLPVFNTVAEAKNETGADASIIYVPPPFCAASIIEAIEAEIPLVVAIT

EGIPQQDMVKVKWHLRNQSTTRLIGPNCPGIIKPGECKMGIMPGYIHQKGRIGIVSRSGT

LTYEAVAQTTALGLGQSTVIGIGGDPFNGTNFIDCLERFTNDPETDGIIMVGEIGGSAEE

EAAEWLMAHGDPKKPVVSFIAGTTAPPGRRMGHAGAIVSGGMGTAAGKFAALEAAGVTIT

RSPARLGVTLFEEMKKYT

>contig47252 Frame-2R

MTIVGVMTKSKHCCAEILISYNLQKKLGGEDSRLLKIDKTGFPVWMLKIIQ

>contig48103 Frame-0F

MVSFLRQLLDSSDDEFPRLRRSCRTQYGKLWIVLRTISGSQILLRFTPSVNQFQTVDLTI

QCSDVADLSAVSFVALSTTRIHLITYHTDASPCA

>contig50270 Frame-1R

MRNSFAFYRNESTESPRLSDPSTSEDADASVLASLSPMSPSSANLRCNGSQVANCLDNGC

ARSFGGDCNCVASCTCNSPTLPSTPSMVPILTSSLTLTRTRPTIRDFEPRSQCAGSTMPS

ATVIKRFLLQVTLCSSLMGIEAIKALLSTMPGVRSVHLTTEASLQTPETSFQPPFADFKS

ESRKDAALCRSMENSAQLVAVRGDHEIDLEAAMASLRNLQIAKIDVVEESTTSWTRKEVV

LRVPDMMCPLNCGSAVLNAVHALEGVEAARLNFQDRQIVVRGDMLIDGIQSAISDIG

>contig50564 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61737.1|) 3e-54

MLQDDIRRLNHVLINALALEEEAFKPAIEFAFSENAFQRYVMPRIIRATKPKRVMIPWIV

EQSRVWGGSKVAKAYKDDLSFTARFLYDHVWLPYYETNIASAMKRLGNNKNNMADSDLDE

SWFGCAVM

>contig52706 Frame-1F

MPLGRYPNGSMVPASTPHHSSIGGGMSGNGIMYHSDLSSEGYDPAMTHYRKPLTQQPLAN

NVYQHQLPSSGPIPSIHTQDYGVDRRSNLGHMLSNGLAISSQSQDGYRQEYQGPSPSYPS

TMSNSVYASGPSTPSGAMTNGQFYGMGSQLNHYRSIGTMYSDTQMSPHPSTPHFPHPQLM

SYDYNLPTASKPNGGVASSSLPMHASTPS

>contig53271 Frame-0F

MTVECWTPPRLTVSGYTFRYCLSGLWRNTSGGVSCSYVGCDRRFKGDDTVGSCDVFS

>contig53415 Frame-0R

MSIGSFVEVDEALTKIHQLLVLIKSMRYVDEDIVAVLHDPTGEIEGYFHKELVEQVGPR

>contig53569 Frame-1R

MAMSTVKRSPVDIAIHFLRAAWALSTREIDVWL

>contig54069 Frame-0R

MSLHANGSAVISGTLLASERSVIDQEDTQQIVRGEILDSVQRRIDSYEKCVTAITAATTS

LQELSAHLNTMQQATQQLNAFTGGWLAVWKRPAA

>contig54771 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70513.1|) 2e-16

MAGRRATVGLSSSLYADFLAENIRLNERLEPSSRSRHSLAINAVTPSGTAIGLQSC

>contig55123 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67968.1|) 4e-27

MEAYVRDKVSILHLDASVYVEYALGLLRDEDLDVSERVSSVVAVFSGAADGLVTESVLAN

VLDEAKMTQDALKLLQDEQQQSQEEA

>contig56342 Frame-0R|Blast-F-actin-capping protein subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY62586.1|) 2e-15

MKQQIVVEDVAELPADRVTEFEKE

>contig58696 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61720.1|) 2e-08

MVLLPRVLAGLALLLGTTRGYDINVYNQCSGDLPLVHVRPGNVNTEWVASGGSTVKTIDP

>contig59264 Frame-1R

MYRLSHNVSTIPLQYAKPRAIELKYHDGTCTLAIPLPLNGFDEERVFSIPPGIFL

>contig00058 Frame-0F

MHRAWSRALARVRGRSAVFRLHTLCCSHSATPIIRGDVRSIGAVRFESSESTPSRFLSLA

DGDKIAKGEGGEEEEGDDSEVGDDQEDSEGKDGDIEVDAIPDVNKGGVEENEELDDLVME

LFLENPLRWTPQVLARKFHLSKPRVEAIIWLKRIEAELTPEEFRAKIQEAKDKANIEMEK

QSKKLADALAAGKEKEVARLKKIARQEEEALQPDYELEDYEKAALMGDDDEAFRNPEFFF

LTTSLRATHLLSDAWASTDTRTNCTQKRHWSCSDSQATIRLCHRKLLPIPSTVRARLNFD

>contig07279-0 Frame-0F0

MPCNWSIVFVVSSLAVELRRGFVLDTSSPFVAKFILNQ

>contig08249 Frame-2R

MYPHRVLALATLLACIVNGPSVASESNKPNFDTNDKAALRLRSNSAATTNADTEDRSFWR

IEKTITEKLRSKIDKQVTLIDILKKQPNEESKIIRDLKRLDKEIKPLLETYKHELKTIRE

IIQDKTMKRDSLADTLGVPKVGQFLFSKQYRKLRKISKEIKKLEERESKMKASFRRSW

>contig10367 Frame-0R

MPERERNVNRHHRKKRAAAPRTQIEYLHANYRFVIAPLDPNIAVPIWDLEALAEWSSVEQ

VLLWYDIESPQTCPICMDTFRAPKITKCGHIFCWPCILRYLSLTEKYWRRCPMCFDPVQK

GHLRSVQLQQLQLPPRVGSSVTFQFLERFKSSMFPQLRVLPSLEIKSEHAELDGSSLHIT

SATAFAACKRSRKLPNVNDADAIYSRILEATPDYLRELLRSELRDLQSIDAEFRSSGDLD

NLPFVNDAIRNITGRLSQSDDFSRGTYGFSSSTIVGGKSQKPQEDSSGDTYSFYQIADGT

YVILHPLNMKCLLKEFANQKQDEDMHDKDLETTRTVIGSVLANSKSLSFDRYHLVPEQIH

GRVLDIEHVVMDEEARKRYRFLSHLPRFCDFYICEIDLTSLLSLSTLSAFQNELKKRAKQ

RKLKFKQQNAPASSSPVFKRNADAFSLEQDGLHWPLPYEQAVAESLEELQLNNASTGEFD

VTHQNDERSFAQIMDNSGGIPALGEETLSDPRTEPVSFGASSAWGSSTSSSLPLSAWSSG

KGGKKKGSGKKGVAVFSTTQRRSYR

>contig11009 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59538.1|) 1e-26

MTKLLRGLPHIDLEKPIFAFVGAPNVG

>contig11979 Frame-2F

MLRIGILCVAAALMISDNGPCATHLGGLPKRNGGFGDNVAAERSLQPTNGEERAQEIKIN

PNTFEARTILHPYESYDDSSDSSDDKRTKYIHRRDDSSDYKRTQNRFKPSDSSDYDNKSL

RRSYQKSGVNSWNEAGNMRQHDHKNGGDSWSDNGKTGRHDNKISLDTWADKGNTQ

>contig12480 Frame-0F|Blast-60S ribosomal protein L19-1 [Phytophthora infestans T30-4](gb|EEY55600.1|) 2e-93

MVSLKLQKRLAASVLKCGKRKVWLDPNESNEIALANSRQNIRKLVKDGFVIKKPQVIHSR

ARFTKRNEAKRKGRHTGIGKRRGTANARLPFKVIWMRRIRVLRRLLRKYREAKKIDKHIY

HDLYMRSKGNQFKNKRVLMETIHKMKAERHREKTLKEQSEARKEKARLARDRKAKKVDSI

AANKE

>contig13601 Frame-1F

MLFLHSSLILKFAVCAIFLYSSICCLCHFHYMTGENEEISLWRAAQNNNISLLWQITDKK

PISEVQVLLNLPHPIKGTTPLMVAATKADGTKITRTFIEFGAHLDVADNCKYKNSALHYA

AYNNRSDQLELLLAAGANMFALNAKGHTALDVARLRGRKEAAATLTSRLQVHCDWLYLRS

KSVLGFWKRRWCVLLACNVKQTSTELCIFRGPNKAHPKAVIWQDTLAHTCTPFKSEKGNG

FELDTQIVYQNLGGRRYSRYRSSGRTHVHKPNLQPIEFLFACDSEAARDAWMDALGGQLC

GGDSTNTAISSSYMGSPHRMSRVSRDASVDATRLTGRTSPVDIINGIDAPTQATVPSLMI

TQGPYRASAPTFIEDDDGHIWGDLSWSRAVFAQESHVYPIATVITLSGDPNEPQPVLVDR

CIVCANNSRDSVCVPCGHVAGCLDCMRAVTYETSSCPVCRAHVDGVVRI

>contig14316 Frame-0F

MVKLVLCFCSLILLSSFVLVACNEHAADDEVPESNNVTLLSKEAVQGFSEERIEVPASFS

QTVAQFFGKLKGKIWHVTEQMTNLFKRIVPYWYLKFASNKPEAIRKLLKAYKVDSATSLS

DPGFLQWSALVRKVYKLDFLEANDQIFTAMIENLKPQNMVKLLADAKHNAQWTNVATRYE

DVLFNRLITVEGLKIEDMVNNFKVFRTWGEEDKTFLIRFPKFDKMKPKEKLPLIDFFFTM

AKNVKHSEFDDSLYNKVLWHLKTSNVEPNGVPDYLSISAIQGDVLEHPRMYAWESLLPID

SATSAKKYDSMYLYLKKNMDAERLEKLLTQERQDNEYGKYLAANLQEAAKRLKDPLKTKP

LNLEA

>contig17281 Frame-2F|Blast-acetyl-coenzyme A synthetase [Phytophthora infestans T30-4](gb|EEY58108.1|) 1e-136

MKHAGVQRGDTVAIYMPMIPEIAFVMLACTRIGAVHSVVFAGFSADSLRDRVLNGRSQWV

FTADEGKRGGRTLPIKKIVDHAVKGLDFVRKVFVFKRTHNPDVTLNPLIDVDMEKEVTRH

RPYCPAEFMNSEDLLFILYTSGSTGTPKGIAHTTAGYLLYTMVTAKYTFDLHEDDIFACV

ADAGWITGHSYIIYGPLANGVTTVMFESTPMYPDHGRYWDLIQRYKVTKFYTAPTAIRAL

MACGNDKIREYDLSSLKILGSVG

>contig18561 Frame-0F

MGTKNYRPPLQVLADLKLDQLSGKELLRSSVLDLWCTTVEASKDNPYPILLKKLLTTMGQ

LELLEELVAVLNQEQSFVLSSTYEKLENLIFESWVIAKQKPSAASIKEFLRLEYVPAGAF

FKMPLSQTYLSYIKYAQLNMHFLVLHSMIKHYNGVRRMIKEAHKINARLASIVISGMEDF

WKTRGILLAFNNLELSVNDLESPRFSYWVKLAYKFSQFDEAQGIVLYYLGKKNADQVQAA

TLLRKAIENTSTKIVNDLLSSVLLKYIKQKLSVHVLKGLALDKANDQLFQDKFFLYWVIA

SDGQLASAKFDPFLELYEENDLAELAFRARTTTREPVNVFADEMNKYLMSDRGPPNKRPR

MSVLDF

>contig19724 Frame-2R|Blast-2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative [Phytophthora infestans T30-4](gb|EEY66237.1|) 1e-171

MGAGLPMNKGDVAFKCNFATLKEEDDGQLIVKSRRVDRNFSAWGIDLCKFLDNMNLPEFP

DLVIATKHATEHRCGIVFRGSGLCDKITGTDPLKDNFCSLPLLSSKPLNDTPEAAYSSKA

LNVVSKAIIERLSDHPINKSREREGKPPANVVLLRGPGERIDVPAFTEMHGLTPFMVAPT

CIIAGLGMSLGFEIAIAPGATGDYHTDLCSKAKTALSWLRGNKFDFGFVHVKAVDDAGHD

RDVAKKVYFTERADEMISLLLEGLHAEFGDHDKEISIIVTGDHTTPVKYGDHTFEPVPFA

IARAGIAYERLQRFKDTGKPYQSKSGPLTDKVTQFSEVAAARGDLGRFSGDQVMKLVKSF

REFQL

>contig19791 Frame-0F|Blast-phosphatidylinositol N-acetylglucosaminyltransferase subunit C, putative [Phytophthora infestans T30-4](gb|EEY54608.1|) 3e-96

MLLGGIDVFLAIFGFAVLRACFGLPLHTWNILSSSLLFCATLSLLAPVLRTLTRSYADDT

IWALAAFLCLLHLITHDYNYINSGIGCFSGTISLNAAIFMAVMLSSRLQSNEHVFAFVLF

AIETFAMSPMFWREVKRHSERLHLMIAAALFALSSALVWQLSGLVSVLIGAFVLFLAFLC

PLWFMHVQESKSEILGPWDITHIQPEQ

>contig21200 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53546.1|) 0.0

MTPIDTSEAGVSRFRKQVSAKKTSRTMTWTLKDDLRLIDCYLEQMSCRWFVEVPLALQIK

EEHVAFRTTNISRTLISWKELGKVFKKNPSECMFRVKDLLEAPAVRARLEKTKATATQMK

NPGGIFHEKAAIMSQPRLTSLLCRALQVIFHQRSSYYSVLADALMSNWSESEVKLVWRYL

WLAGLITRTPQVVEGSDQKQRGFQVHSKVFEMKSLKISHYLMETFCQAAKYVTFVDENID

EATMMAEEYDNVFEHDIQANMPTGQAAVVLSSLVSGFSRLVPSFIKPRTQAAVIRDVQRV

ITVKGLAGHLSQQWNGVLPEDFLKDFWTVKSVFRGADVTTQARKIKMM

>contig23530 Frame-1F

MQCMWYENEVGWSQVRQKKYGLALKRFVAVKTHFDDFIDDQFDFHTYCIRKMTLRSYIQL

LRLCDGFYGREFFVNAAHGAIACYQALADAQEAKAKEEAKSAVATATMSAADKKKAKRVQ

AKARKAAFKKKNKDEDGHVKENKDENEVVKNGKIKANATPVKDDDPYGLKLVAKPPLEEA

WRFVSLLQRYAFDDAKTHLAAFDIALRKKKYLLCLQALLKLHQLPVVTTEMNTELNLRGA

VFQEELQYVKNPIVLQVIQAKKTELKM

>contig25305 Frame-2F|Blast-cystathionine beta-synthase [Phytophthora infestans T30-4](gb|EEY60543.1|) 0.0

MASPSGPHAAPSVECSSPKSCFVQQPHVHRPRQSEPKILNSILDHVGNTPLVRLNTIAKK

ASLECELLAKCEFFNAGGSVKDRIGKRMVEDAMASGRIKPGDTLIEPTSGNTGIGLALAA

ALYGFRIIITLPEKMSLEKVDMLKALGAEIIRTPTEAAWDSPESHIGVAKRLVKEIPNAH

ILDQYSNPSNPLAHYDGTAEEILEACNGHVDMVVMGVGTGGTLSGTARKIKEKCPNCIIV

GADPIGSILAEPDHLNDENRLQSYQVEGIGYDFIPNVLDRSLVDRWIKTGDQESFLLARR

LIREEGLLCGGSCGSAVAAALKAAKTLKAGQRCVVVLPDSTRNYMSKFLSDDWMYEHNYV

TDMSKSVLSSTWWAKKNVSELLLQAPVTITPDLTCIEAVDILKKEGFDNLPVVADDNSIV

GVVSEGNLIAQLMPGRVHPTDTVEKAMFKQFKQVSPQTSLYELSRIFDRDHFALVVTEQK

RIRKGGEAETKSVIFGVVTRIDLLTYITRNGVQ

>contig26564 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY61334.1|) 2e-69

MAMKDTGVGTKCYVPDSTYVWLPAQVLREEKSSDPKKPEKTVVLRVFPPPGDTNAIVESE

RVLNFNDFKVKAMLKSLQLESLPFQNENLGPKGIEDMTALNYLHEAAILYNVKKRFQQKQ

PYTYTGGICIAVNPYQWLPELYSEQMQSLYLT

>contig26678 Frame-0F|Blast-disulfide-isomerase, putative [Phytophthora infestans T30-4](gb|EEY66147.1|) 0.0

MMGSGALLLCAASLLASVQSMYSSDEDVKLLDAETFREEVLADSGVWIVEFYAAWCGHCK

EFAPEFEKAAKALKGVVNVAAIDCEEHEEFVNEFAVRGFPTIKIFGENKSQPVHFNGERT

AKGIVDAALTITRRIVKARLLDYTEKKKQKPKAEPKKASRSVRSSVITLTDETFDEKVLN

SGNIWLVEFYAPWCGHCKALAPEWEQAASNLKGFVKVAAIEGTANEQKPAEYGIEGFPTI

KLFGPNAMGPEDTATYEGERLASDITEYGLAAFDALGGNFQIKELGSASDVVDLCEGKSS

CVISILPHITEGGKKARENHLNTLQEAAKLVRGKPFRFGWMQGGEQLEFENRFELTFGYP

SLVAINLERKRYVVQRGAFTAETIGQFLERVIQGRESTVSFDLMPEITTTEPWDGKDIIL

DEIEDDDEDDDIMNEILSNVAGRDEL

>contig28311 Frame-1R|Blast-cleavage and polyadenylation specificity factor subunit 3 [Phytophthora infestans T30-4](gb|EEY53455.1|) 0.0

MSKRRLAEEAADERHIMRIMPLGAGNEVGRSCIVLKFKGKTIMLDCGVHPGYSGHGSLPF

FDGVEAEEIDLLLITHFHIDHVAALPHFTEKTNFKGRVFMTHPTKAVMQMMLRDFLRVSN

ISVDDQIYDDKDLNNCVAKVEIIDFHQEMTHNGIKFTPYNAGHVLGACMFLIEIGGVKVL

YTGDYSLENDRHLMAAELPACSPDVLIVESTYGVQVHQSVVEREGRFTGQVEAVVRRGGR

CLIPVFALGRTQELLLILDEHWRSHPDLQDIPIYFASKLAAKALRVYQTYINMMNDRIRK

QIAISNPFQFDYISSLKSMEDFDDSGPSVVMASPGMLQSGVSRQLFERWCSDKRNACLIP

GYVVEGTLAKKILSEPTEIAALDGRIIPMNCTVEYISFSAHADFVGTSGFVEKLTPPNIV

LVHGEKNEMMRLKSALNKKFNDPKIYHPSIFTPANMQEIVLEFKGEKIAKAIGKVASEQP

KNGTVISGLLVEVDSQTHLMDKEDLSTYTKLVSGIITQKQHLPFEYNSFDVLITFIRQMY

EDVVHLEKENRIVVCKQVIVTRWAVSKCATEKLVVEWTSAPTADMIADSVIALAMHAQAS

PASFKLSGQPVAACPHDHSIKTDTCAEEVDSSFKPETVETVARKDIKNNDDFASEELVAQ

TKNDTDLEKAAQELGKIDQDALNLMIVFRILKDQYGDVDLDFETNKIHVRTPSGLDAIIG

HESQEIECNDDAFKLKLHTTIRRIVGALKPIEMEIEGL

>contig28500 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65853.1|) 9e-53

MVSNIHSNTMKRSKYKQEAVMNGIAYNPATRHIFLTGKLWDSIFELELSILNSRDHGIVP

>contig28841 Frame-0F

MLTIHANSRREYDDARLILEEMKALRDKQMTITNTLRDNLQYVLSSIEETSLIARGSNPM

QASTNALDVCRRIDALYQGQQKMIPDAQGLVKNIMIHVKTIAAIKATAFERVQFTLRQIS

IAQSKIRDFENSLAVFREAISAQTKHFYELEHLEKLPESYAACLKEILRRHKYGRKFSDR

IQLMAEELAQLREDEVQHRQEFLRNFGQHLPRDFVSGLAEKPSHCEFRMRPFDQSLPMIE

DDNENAVRSPSDEFVDCEDHGSAFEMTSKVDRLQERCKELELRVSELTAELVQSKKNFLF

DGSESDSISRSDISKTSAHEGDSSCEFPLVVALAETAGGMTSSLEAERSNVVNHELAAVR

RNIAIGVDNKEATIAKLESENQQFLLNAAAFE

>contig28975 Frame-2F

MSDLMRRRKRLSESEVRFYMRQLVEGLKYLHENLVIHRDLKLGNLFLTLDMQLKIGDFGL

ATRLNNIDDRKRTMCGTPNYIAPEILSGLRGDGHSFEVDIWSTGVVMYTLLVGRPPFETN

DVKATYKRIRENQYDFPETVHISRSAQSLIRGILRSDPGARPSLDQILKHPFVADEFMPA

ALPRTALRFTPPSCKLQSYTHRHSDSEQFAKPSGGRGPLISASRKFAAQKQDDNIYAQRA

SDPGTLSSLLRSLPASSKRLLDPSKTNRLLYGPKKRSIPRSEAVVSSAPPHHVLEAAYKT

LFNFFYLQEQSRSDSKGERKLDASTSAAEIVAEAQNVKLIRIEAEEIQPIAPSRLWITQW

VDYTSKYGIGYMLSNGGSGVFFNDSTKMINSANGKIIEYIERQSNNRAASEIKARYTLDN

YDPAINKKVTLLGHFKGYLVDARAENDEADTLENQLARSFVHLLQPVDTDTNVQESNNDD

EKAMVFLKKWVKTRHAVLFQLSNGTIQFNFFDKSK

>contig29176 Frame-2F

MSVASRTRKRVHEELQSTQSPTNAVSPPRPRPEKKRRRLIISQQLQYDEPHKASGKGLIT

KQHKAQASEETPSLSAKAASTRCQHTAELASKSTLIMLQEQNEELKNVIAENAILLNRQS

KQLTSANKELEMLQKECETFKQARENEIATLKKGYENELEKVKDQAAADLAMKDEEARKN

EGVLRQECNTLKVTLDHIANDPKMPPQVRTIIELEAKIQVLKRQFKVDQESQAFQTQQQD

RPQMTPPSKKDLVELERQSSIGSPAV

>contig30206 Frame-0F

MNYAAGRTAAWGDNDSRPELQTLRGQFLRTIIILCIAGIWVVGIGGILVLWGLSLWSIGR

WVVLKTPIPFYVELFLSLMALYEGYHYATRSSHRQWPWMRQLLCHVFKQYPYFRLSVTVF

EERIENKASDTQAMQLATMASKAVEKNDLTCCVPPNDHALFAFHPHGVLSCGWSIGGVQH

GSFDKADCRWMVAESLFYFPFMRELMHWLSFASAGKTAFRTMLRTGQNVCLMPGGFEEAT

LYERGKHRVYIKQRFGFIKLALQHGYKVYPVYTFGEEYAYHTFSYLLNFRLRLNDYKLPG

VLFYGRPACFFLPRSDVDLITVVGAPLLLPRIEHPTREEVRKYHGQYVTALQALFDRYKA

VYAVDPKATLEVF

>contig31087-0 Frame-1F0

MPWKGGCVAIPKGGVSIPVFAGEN

>contig31160 Frame-1F|Blast-alcohol dehydrogenase class-3, putative [Phytophthora infestans T30-4](gb|EEY69174.1|) 0.0

MNLTCFISQPTATMSTPQSIECKAAVCWGAKEDFVLEDVVVSPPRAGEVRIKIVATGVCH

TDEYTRSGTDPEGIFPVIMGHEGAGIVESLGPNVNSVKVGDHVVPCYTPQCRNCKFCKSS

KTNLCSVIRITQGKGFMPDGTSRFTCKRNGKMLFHFMGTSTFSEYTVLPEISVAKIDPAA

PLDKVCLLGCGITTGYGAVMNTMKVEKNSTVAVFGLGAVGLAVVMGAKAAGARKIICIDI

NPRKFPIAKDFGATECVNPKDYADRPIQEVLIEMTEEEGFGGLDYTFECIGHRDTMRAAL

ECCHKGWGQSCIIGVAASGVELATRPFQLVTGRRWAGSAFGGFKSRDGVPELVDKYMKKE

LKVDEFVTHTFDLAHINEAFHAMHQGDCIRAVVYMDGVSH

>contig31304 Frame-1R

MEASVDKKQKLLPSSIATESNLHQKNGRPLKAIKFGKGEECQPVSYKTSSGSDRTGWLRP

AARLISISSFMWGFSATALNVCIVPNATGSLLIDINLSTKEQELATSLVVIGCVLSALAS

GGVGAHLGQKKVILGNNVLYIIGGAICAVATSKNELYVGRLLIGLASGVVTNTVPILLTE

ISPAESRGEITSFHQISLTIGMLFSAVMGIIFISTVPSGWRYLNAFMILPPLFQCASASF

VPESPWWLMKNRGRGACRAMLVYLRPCSQKDDIETEVQEIARVMEHRDQEPYVTWSDLLA

YKNVIITGAALVFFQAMTGINTVMLYSAKIFHFAGVSNPFFATAVVALTNVGVTTISARL

VDSCGRRPLLLAGTSIMIVSLGVLSWALLSLDNNLKVQGIVAVISVLAFVSGFAVGLGAV

VWVVLGDITPVHIRSRAFSFYMIISYVCNIIIAVYTLSAIRFLGRGSNPEKNGIAKLYLI

LSGVALVCLNYVYGLVEETYHVKTSSAEVADNEKSLLAEEEQDTLNS

>contig31454 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63414.1|) 4e-93

MSAWEQWGGKKPTGGGLLGAQEAFQSLLRSVPLSAASNASTNGKGSTASATLQQIWDSAR

DLTKHAVTTPRNIETDVAIDNLETGQSENVVHDGSFATWLLGGRHANSKSGLVLTMSWAT

RFKYFVGMAMLGMLFFAMASIFLPLIMIRPSKFALSFTLGSVCCMSALAMLKGPAAYMKG

IMQPDRLLLTSAYIVTLGCTLYSCLILGNYMLVVLSSVMQLLTLGLVAFSAFPGGQSSLK

>contig31595 Frame-2F

MFTASVGVGSSLLLEPARELLFPFPQRTSSERPRCILTLTNLSHQYDVVFRVRTRNPDAF

TVRPTHGLVMPGARVQIILSASIETCERVAVMNSQDLQCLESSELFLVQNVERGQQSWAR

EKLDFNALASLRRFWQNVPNDCITENKMVCRFSEPRGESLTKTTQDKKVYSSSMNNANVR

YSEKKSLGPSAGEHRYRNKSSTQSLNQFMPPQDQRERSRRQNSVTNGASYYKIMEPPISE

NQCEENTETWTKARPSLLYKNRISTSGLSSTIDENSFNSDTISKARPCDVMSNAMTDRRG

SLLYSITPSEVLPFHLKRATRYWGSTELCILNSSQSNCLIFKVRTSNQSGYVVQPSRGIV

SIACIQKVVVTLCAPPDAIPSDVVKREATDGFLIEVAAVSRDIYDDFMKLEKPERIKKLA

SLWSLIPSSTRETTVLAVNLHIDKSKSDRGTSKSFENGNTISQGSRRHSYKSKNDLSPSF

HQRMKGLFLSSSVPKTRESEDKLYSKHACSDPHNTEFTIPPIVASAVEGDSIHEHEAAHS

VRHGDNAVIVVSADRIDTIDFTNPKLSFFI

>contig31829 Frame-2R

MTEQTESERDAIVAWLEQNDNFLRATAFSGPPGMSRHLSDGDRHQSEQIETQALNDLAAS

VNKVLPQSRWDSKLAKQMLHRYLILFKATATQASEPGFTLSKTDIVFGIKTVEDKLNSMC

PHFIRLQMLCGMNSRMAGRKATLLDKSQETLEEKDSAKLNLIRTIKRDKTVRGTDSPTRQ

KDSFRSINRTLRGGQTNKKSAKDKTSRHDISLRSSTAKLREKTHQLGSKKKSARKKAMLA

QNSDKLQAPSTMSSKPLESIQQQQTEKADTFLEVIELLSDDEESPLVSAKETNVDNRTRP

RSLKAADNVDDESRKRKVRRVDKGSGGAKDFGENNKLSQVPDRFMKIPVRMATSRNNQSK

QIEAATPAMEHSTTASSNILIPTRAGSLKTTEMLLVRYPMCDQYAQSHLIK

>contig33672 Frame-0F

MSDKALELDQVRAALELKKSENEQREKEVERIEDYETRIEETEVMEKKCLWLKFENAKAD

VEKLKQEKISRKEVILSERRETIEPLVELLKKEQIKLEDVKIKKAEVDSEKRQFIEKIRQ

EKSRIELMESAQSQTLIDVKELRNQHHSTRRKLERLEQDIAVWRQDRENMADDADLKKEK

KELERLQREKDMEETETRSKREALARELSYIDDERRKVTSKLDKLDNEDLQRRLVLQRAD

PDCIRAADWVRNNQSRLKRKVWGPIALEMKFNEATHAKYVEDTLPKWLLGALVAECYDDY

NTILREVNNGNSDRRIKASILIVENGTCHAIHRPYSKEQINDYRDRYGMKCFLDELVTAP

QIVHEALRSHGGLHTVMVGSEQTEDIINRGGQIFSDIASSERKAAFVTPYKKYVTSVSKY

GN

>contig33913 Frame-1F

MQTHASSITPTPTLEPSSKKSRRSQVWPDSSSNYGSAEANHGSRAERREYDR

>contig33966 Frame-2F

MLVLFSYVLGRHDKARVPTCGRVAGGEG

>contig35076 Frame-0R

MFHMVNCMRVLSDQYGVVFIVTNQVTGDFTSCLDGNGMRPALGLSWSHCISQRYAFETVQ

RHLISPSHLFDSILFQSCNHTSRRSETSSTESSLLTVFASGNVHISSH

>contig35726 Frame-0F

MHLIRSVLIVVAALVAISEGKSIRGTDYGENLQQGTDANMANTIEDRRSGGIGREPYRAT

GIGILTPFMYSSDTPNLDRKREHFARKVHAAYMKMQKDNQAV

>contig36455 Frame-1R

MATRLLTLLPVAGVVAWSGNASLMRARHQSHGERNFQFITGTMNDIIMETLETGDLVFFQ

RKLTALQPLAALHTWIMRKHLRSRFDHCGWIYVDRLGRKYIVEETLNKVQCRPYSARILT

SQATEISVLTLNVE

>contig36639 Frame-1F

MPMSSIRAASFIFSIAIGYFLCDLIIIVIWPVSMQFVFIFHHIVAVVPYFINNFISCCAA

CQFGLLLFLLVELATLPLNVRGFLDARDRQDSKSYLKSIYMTYIIWGISRTALPIFLMYD

FWVYVYPSDRNHDTCFFPNFVSAHLIALFCIGVFFFVHTPEMFRITREHRRKHADDSSED

VAMNTDDVDLIEPNVDDVPSVRVNKPSSIRSLTLSLSRCKEVIVDDSYDDVELGVMPRSA

RAETAF

>contig40076 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53261.1|) 2e-26

MFDDILHLLDMAIQRNGFLFLRNLSLSRVTKIHFAMWKELLDPIINLYIHASDSNNFDSI

AYEYLSIALWALVYDNQKARALMLSKPATLQSLKRILSSQTCGTCGLKYHLRH

>contig40726 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54799.1|) 8e-26

MTERYFKQQIGDSWNITPTLQYAMERMLQAFKTHITPAQAMDLFT

>contig40753 Frame-2F

MARNASASFSTSRHSRSSQFTRRSSHPPPSNLNDAEIARKVQQSAVRVRVLLQLDSVRDE

KKTLRDVLAEFEHRLEAQIINGVTERHELRVDLLECGLNSWQDLVELQRVIMGLKRPAER

GEEQQLTARAMLSSQVPDELTLSLWFDKDSIGTVWKFTSSLMLKLRSCGILSKGLLPPRR

MMVNLAVTRMELKQLEYEAFQWEGKQSWSQIVVELISREKEEIQRAFLPYIAPNLSAQLH

YTELASILDGMLTRETDNWKPIVIIMRGIPGSGKSTLRREVENICRNLGVKFTACSADFW

FETPRGYRFDGAKLKAAHNSCRDQFSSALAGDCQTSDGRQQHVVFVDNSNTQRWEYKEYE

SIAKSSGSQVYIFEMKCVDHLMAYRMGRRNSHGVPQDKVVSMFMRWEEDRRARYFTPRFE

YPSLTRNPLSDGIAGKILYLGLFLDDASQQKLLAQIPLVHSRKFSDHVTLFYRPNKMYTR

FAELGAPFCIRGVE

>contig43455 Frame-2F

MKKIVWLLDRKHAERRELGAFVCKPVCITCLKSIKNSRLRGSSRTCKLCFGALCRSCKVM

KKLSFISPDLELTQSKLSFCVKCLHEANHLDTLEAARYQFVYGHPAYQGAYGSVGTSFMS

SLSGSIVATTPLSLRDYSFGEPEI

>contig43594 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57791.1|) 9e-21

MYHGDRVNGIALHVSYPDSVSVTLEHGGTGGMTSHFFIDHEEFITSVAVQTTKKTGRTRI

GYLKFGTNKGREYEGGKLSKDTDKLELVLCPNNTQIGGFQGRSGREVDSLGFYFTPIATT

LCP

>contig43639 Frame-0F

MEHFHELSKARRVAFDKLRTLFGPDHIDRILSQGPEILEARLEASMQP

>contig43833 Frame-0F

MPRNEACTDKDEMTVELSTKSFETSSQDLIYALDCEMCETDIGMELTRVTIVDIKGNVVY

DQLVKPQSTIINYHTEFSGISKKSLQHTKCILADVQRELTTRFLFQDTILVGHSLTSDLR

ALRLVHGTIVDTAILYPHERGFPFRTSLKYLTKTYVKKDIQMASQTG

>contig44304 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63006.1|) 1e-30

MERVFDNSKGIASAEDAETHEPGCDCCFCELTLRLSSYETVTADYIQVSTRDRNPENDAG

EDTDFQLPDFLTA

>contig46672 Frame-2R

MLLSTIERQHASRNTKLHALYAYIFWDLRRLGLLPSTEKLRLRSAPGLTRTRRCTSKHRS

SKPKVQRNQSANGCVVI

>contig46966 Frame-1F

MTLSDEISPLLSPSIECESPSQQHSNPRESFEVGFPLVVADDPTVQAIVLESKRGVSESF

CQYIGRNCAVPFTLLMSAIGAGTLAVPYTFVLVTPLQAFFVLCGVGTAMAFTANTLVEIH

VVVATASLYKDQSYRSTYQYLAKLAGGTLLAQGAGALTAFAVFGACVGCVCVVKDMAPLM

LSAISNAFNQSSFKDQQHAVVVVLWLTMLLVLLPLGCLPKISALRFSSYFGVAFSVYLVG

AVAYRALLGSIAINGHTDPSMSDTAIHVPLFWRISEVVGIYNFTFMLHLNVLPLLAQLVS

TDLLRKHENIEENIEENIVICSGVEGRVCSLSTARQNMQQYVTLSVGACIALYAVFGICA

AHIYGYQTHGNILLNLSNDPIMVVPRVA

>contig47253 Frame-0R

MVVLPSDDLFVQVLVKFVQGANLLMLYQI

>contig47503 Frame-0R

MHKCVEETDASKRQQEPLLTHEALTKSTDHIIEPYPGFIHMDAMAFGMGMCCLQVTFQAK

NVGESRHLYDHLGVLSPILLGLTAATPILKGRLADTDVRWATISASVDDRTPQELGEALD

MTDPAMKAKYANMAGNGVKRLPKSRYEGISTFICNHKQGEDPHTSTDKYNDVDVPYDEES

YKTLIDANVDRLLALHISHLFIRDPLVIYQQRLHLDNEHETDHFENIQSTNWQTVRWKPP

PPAPSNATGPHIGWRTEFRSMEIQLTDFENAAFTVFIALVSRVILTFDLNLYIPLSKVND

NMEAAHRINAVLHEKFHFRCHMAPPEVDDCGSGDGSCYLHNDPDRSELMTIAEIMLGKGS

YFPGLIPLVYAYLDYIECDEATRILVEKYMSLIRKRATGELPTAATWMRRFVRAHPDYRH

DSVVPQSTAFDLLNECQQIGEGQKQCPELLGEFEIASVRGQAAYHV

>contig50271 Frame-2F

MGRNCKTKVIKTARRKNYRPGVTSSLAPSATLAGSSATLGQRDCEQCGNNMQLDGMAKAE

MSVASIRCQICSFVAFRRSQRPCVRCTRTGCNHFCDWCGQGFHSKCAKLQNEDVSNVNGF

CCHKCEAEQSEFRTNDEETKSGDSGNDVGSRCGSCHLPFFMAGKEPDDVKIARGFKVNQA

VLVDNDEVLYNALITEVDTSGERIKIHFTRWSKSFDDWYAMDDEHINESLACDCCNDWFH

IG

>contig50749 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67844.1|) 6e-30

MGSAVQNVMRPGSREFVIVLNAVLALLFIVMLAVIYTELEDSLHVFVLLFLVIGLTVSIN

WFIIEAKNFKHTQGIPKTTQNQKTKLLAKTD

>contig52707 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67772.1|) 4e-16

MTRARSIAVWKAAHDGDEAKLQEILVESTKQFGSKLVNWKHHNHGTTPLMAAAESKHGEG

IAWQLIAAGADVNLQDNTNLRNTALHYA

>contig53568 Frame-2F

MRADLPGDTMQYLASTWLIF

>contig53847 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66659.1|) 1e-21

MLLEAMHQKNDIRKGKGSAGWSCRRDVDASDAASMKITIAIPESIRADTTWE

>contig54114 Frame-2F

MEPHVKLADPNEDTYYGRVRKTFYMLDFRTAFTKEKALQDAQRLVATHRRGDFVDPVELE

HAQYVT

>contig54770 Frame-0R|Blast-conserved oligomeric Golgi complex subunit, putative [Phytophthora infestans T30-4](gb|EEY66064.1|) 1e-16

MDAPHRRKQLEQHAALVAQLAEVKQRQQKLSDDSVIFINAPKANEKVAVQRSLQSLRELS

PKVTVLCAQTG

>contig57502 Frame-2F

MLQTRRLILTSCIHAPLQRNFLQVCSANCRLQHPCTPVIRFCSTDAANSVTAVPPAAHKH

NTSKRRKFKKNKQKTVVSAASA

>contig58558 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64078.1|) 2e-20

MSTGEEHYGNTRHAMGVSMPGMTGSAIPMPGLAKGGFRLPSMAAPGEDLTSETTFDDT

>contig59265 Frame-0F

MLALSKIIKAVVIASILIGSSSSFPMAKISSATSNDQSRHYGSEHGNGRLLRGAGIALHG

DEE

>contig01339 Frame-0R|Blast-leukotriene A-4 hydrolase-like protein [Phytophthora infestans T30-4](gb|EEY63173.1|) 0.0

MADVPALSSHSYANLHEVTFTHLNWFIALDFQAQQLKGYAEYTFHHTSPTSTSVVVLDTH

HLNILKAFVDGNETSFSLAKHEHAVFGRALIVSVPTHATTIRIDYTTTAASSGLQWLNKE

LTAGKTHPYLFTQCQAIHARTIVPCPDTPSCKFTYTATVTVPEWCTCLLSAIADSHGRHS

HNARDQTYQVSFYQSVPIPSYLLAIVAGKLESVDLSPRSRVWAEPTIVTKAAHEFAQTEA

FLQHAEEITGQEYVWQRYDLVCLPPSFPYGGMENPCLTFVTPTLLAGDRSLADVVAHEIS

HSWTGNLVTNRSWTDFWLNEGWTMWLERKIQTRIAQDPKAYDLKALLGLRDLKEAVEAFG

HDHPYTALVPNMDGIDPDDVFSSIPYEKGFNFLHYLSTVVGGQDVFETFAKAYIQAFKFQ

TITSHEFRTFFESYFIGQPDVLKTIDWEAWFYSPGMPPVANTFDTTLTCQATMLGTQMAT

RNEMDTWTSVTSTQLQKWPTSLWIVLLDTLLMKQAHARFTLPHLDAINAFTHSHLTNTRN

AELRFRWYTLLLRSGDLRSLETIVEMLQEQGRMKFVRPLFRDLCTALGPAQAETIFAECK

NLYHPIAAKMIQRDIEQSIAKTKCKKVTFASPTTPSALAQWLGVSDQVVGYAAVAAAVTT

VAVLVVSRRR

>contig07012 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64662.1|) 7e-53

MEGEDFVCINCNRMLELPLGLSTAEFICPHCLQLASVKKTSLSVLPALTTKKERLSVSSV

RSVESGASLPVDSSLSGIDVRDTKVVSCGHCDKHLIVKNGAPAVKCPSCRGVSKLSTTT

>contig12296 Frame-2F

MSTDPQSVFSGVYVPGLSPMDQPPQSDAMEEYARLMGIKVENDDPHATAYGHHPHPHDVA

KIQANAAYFENLINRDRNDAMDDGTNVTSMTLPAGIGSGMNGFLTAPMPPTAPLYNNPTS

ELAFHDGASRLYDPNSGNVFRGQSPPLPFHKGPQGVRPGMLPSEIVGSQTLPPEIISAMI

KTTPAHNFDNLSEDEKQALIKEEKSRERNRDHSRKSRLRKKEFVESLKHEVGQLQVYQQI

CEQCMDCIALVAADPSAVFLFSSAAYTRVLGYQNHQIVPRQTSFLDMVHPDHVQEVRGVF

TKLNTLGETYRFKFRIKAMNGEYFHAETTARLAEKGVVCSTRVDRVM

>contig12487 Frame-0F

MNRNEKATLNDKNTLETPVQNLKARRKMIDNEPSDRSFDSTSSNDILKRANKRPRSDSPS

QHRGLAKEKNFATTRRKALKHRPSLLLLNTNETSLSSSRRMDKNNACQPRDMAKPIVSYA

NKDKKTSNRKHLTTLNSTLSAETILSSDQSGPDDENKIGRGQRIIEEDTSMQKKSNHHAV

IESLAHQMSPASQNNSFYRYDDADASQRHQQFCLMKADKAGADDLDKVRLSKRTAISVPK

QFDSTSTLHMRTCHTNTSMIRLRPQPRIFMHESRPRTHSALPSRSTPIFSSSKGFSVESW

FKRNSMANSKN

>contig13347 Frame-0F

MPLSAAVSSHDLELGKLQTNKSWENLKIADGLKDRANTMRDLKYY

>contig13417 Frame-2R

MSNSNNGNVPPPLPSFAADGFLSSAGSPPYRRNDSHLSNQHSGDRSNEMDVMAQLASQYY

ISSRNRSFSAPIQPSALNSAWHSFSDDTTMMAAAAATATNHHLEMQNTSLRLHQPPLPQG

PPPPVLNVMVHPPLPSDNVAIGAINQAVQSLQLSNEDSGEAHNGGDTETTGAPLPATFLR

TICDQLEYYFCDENLLGDLFLLKNMNMDGYVKLELLASFGRVKRLTTDMEQVKKALELST

KLLLNEDETMVCRKEPLAPNQTYHG

>contig13606 Frame-1F

MTSPSSQGNLLPLGSEGLAMPPVGKKKKPGRTPSLIWQLLTDEPDPQRRNSATCKHCKKS

VAYYKKSEQAIRHLKKCARFQEMQHQFAFMNQFSDHLPLYNQKVLDKTPVAKRLKADHSP

SDRAATQAQMDVHLQATAALGSVLDQAVVHHAQVMNQIAMQQSLSESLIESMPLKEDFKE

NDSNNKLQKLRPFSKTQSERFDEEMAMHVFVTGMAFDAIEESHLARAMALVRPTIKLPTK

KSLETTLMMRCYEKIYKQVWGKLSSSFARVCLKREAWSNWNLYQPPTAENTYVTYLALYK

DKRFFLEVEKTIRNESPLNSILIAQDIKRMMQPIVSNISGVVTGSTEYHSRAWNMLKAEY

PTKFFYGCICHALHLAIMDIFGPPQPLESDTSRQVSSTQGPMEFPFQDLVELTINCNELL

SFFSSTHYAPKYKMFGS

>contig14122 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63918.1|) 3e-34

MLVMARDKALVFIRTCDNCECFTIENALDDRIKRATYSPDGSEVLVVGNNCKHVKIYKTP

EL

>contig14311 Frame-1F

MPRRIAGKSDKAPDNKPKEVKRVRAKKEVSTLPKKKKNVATKTHGTMKTKTTWSSRMKVR

MTATSRTKR

>contig15455 Frame-2F

MPNLVHQLARLQLGPVRERQRLSNRQINAPPININAASMHSQRISIQRSLLASLHCPSHR

VLAIRDGPRVVLNRPPGRNVHSRPVFQVSYAHTKDFFVAVDEQGVAGIVHAASGHWQSQW

MAHTNAIFDAIWTQNDSHVLTASGDFAIRIWDVENIVSRSSTPVLTLQGHDRSVKCVRQA

RDQTHVFASGGRDGKVLLWDTRTNGNPIAMLDKVHAEPHLSRDFSQSNRSMPSLKRRRQR

GASNIVPSSPSVTCVEFGENGMDLMTAGATNTIVKCWDLRQLRRGNTYAKIPEPIQEFSC

SSWEEARHGISSLMLCPGHAGRASQLLVNVLHDSIVVLDLTRTHQARPILRCYGHESSSF

YCKSSFSPQGEFIATASADGVVYIWDARLKAMTDEMLAIRRPNFNGEQRLPCVALKGHTS

DVNGVAWSSLHDLELASCSDDGTVMCW

>contig17097 Frame-1R

MYHILFQMRRKRKPVFCPLSIASVNGFKQKGIETIHAAAASTPNKRPV

>contig18412 Frame-1R|Blast-HIT domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY57253.1|) 3e-60

MTLTTYDPENIFLQIIRGEVPSYKLFETDHVLAILDAFPVVPGHALLLPKTPGFATVMDM

TPDVAANVFKELPRLAKAVQAATGASGINIIQNNGVSSGQAVFHAHIHVIPRFDGDDLLT

LPSGPKMINKADGEAMQAKIQTQI

>contig18694 Frame-2F

MPLSYRLFPVDESTGDLSYCLYAYNCKTKGANNIDVPTTHYQQTRGHKSWYQGFRYGANN

YCAPNPAEVQTYETVVASVRKGIKDNECAVDTCPGSGDVNADLSFMDNSTNQHWGINSNG

TCYPLFNSYMGSYLCDPDNTHKQCASPRDEATTPASGAMNSFKYQMDALSSNWPIHFGVY

TGYYDYQVEWVTGTNGYVRWLFQGEPLFEITTESILNVPQDADKSNPIKLMVEEPLYVIF

NVALSSSWGAKPPNPGQECRGDGKDDVDNKICDAFPMYMKIDYIRLYQDLGTDLEPDNYM

SVGCDPPSHPTKEWIEGHIEEYENDENKVIEVAGKASCKTNDDCTIGGTEARTAFKTGKC

FKQRCQCMYNSWGGPRCTTAISGSKSMESSMMSKTYGPPMEVSIAMAIVACLMSGTSVYF

AVFKLSGQSAAVLDAKRKASVKSEMAHVSEASNSRESSFTGGPQTNYRQNFV

>contig18957 Frame-0F

MTVVARQLMEVLHTTWQCYDLPLMVLAYVLNIDMDQARLDTSNNVWQWQTITTLFSTYFQ

RWFGRVIPENKVEASFDAYQHRQWPFDADTMNSFTDKMSFYTFVSDTHFEMGALCCRLFA

MTLACVDLRRFVRGVGFLPFVTQSTARRKQVEMLLHVGFATKVTNSCVFDSVLDVDNILP

DLVQANRPEDLLCRQDDWKLFAKAWRQVLVQEMASLDIARREKFQQDGTEIATKDQDVDF

ALSKLFCETLPALPAASVVDLSPHSLSKEAIQESVAL

>contig21207 Frame-1F

MYRPQRLLASRCVGSSLLRRHQTRDASTIKKLMAANRGEIATRIMRAGNELGLRTVGIFS

KEDRFTQHRYKADESYLVGADKTPVGAYLDIESIIQIAKENKIDAIHPGYGFLSENVGFA

EQCAKNGIKFVGPTPENLQRFGDKTAAREIAIEQKVPVVPGTDGPVHNLEEARAFIDSGV

GYPVIIKASMGGGGRGMRVVTCAEELEENFKRASSEALTAFGDGTVFIERYVDRPRHIEV

QILGDGQGNVVHLFHRDCSVQRRHQKVLETAPAVGLDPKTEKAMIDDAVRLTSAAKYLNA

GTVEFLVDQHGRHYFIEVNPRIQVEHTITEEITGIDLVQSQIRIAGGESFKDLGLSQEKI

KPRGHAMQCRVTTENPSTGFQPDSGVIEVFRSPGGMGIRLDDGPGFVGAHITPHYDSLLV

KVTARALDRGDCAHKLKRALSEFRVRGVTTNKSFLTNVLNHPDFIKGIVDTSFIAENPDL

LEPSSSTNRGQKMLKYIGNTIVNGPEKALGATGPPPSKIDPIIPTLPAPPASKEKSLRQI

YVEQGPEAFAKAVRVKKGLLLTDTTWRDAHQSLLATRMRTRDMLSIAPATAIAMRDAFSI

EMWGGATFDVSMRFLREDPWDRLSLLREAVPDIPFQMLLRGANAVGYTSYPDNVVYKFCE

KAQSTGMDVFRVFDSLNYLENMKLGIDAVGAAGGIIEAAMCYTGDVSDPTRGPYNLEYYL

DFVRQLVAQGIHVLAIKDMAGLLKPKAAQILITALRKEFPDLPIHVHTHDTAGTGVSSML

EAAYAGADAVDVASDAMAGTTSQPSMGAIVAALKGSEYDTGIQPEDIMEINDYWEMMRGV

YAPFESGQKSGSADVYYHEMPGGQYTNLLFQSNQLGLAGQWPAIKRAYATANRLLGDIIK

VTPSSKVVGDFAQFIVQNKLMEQEVIDQAETLSFPKSVVEYFQGYLGIPHHGFPEPLRSR

VLKGKTLPNGQEMFEGRPGAEMEPYNFDAAEKELKEKYGADKIREVDVISHAIYPDVFAD

FQTFKNEYGSMHFLDTRTFLTGLEVDTEVELEMEHGKTVFIKLVAVGGVSKKDGMRDVIF

DLNGRQRVIRVKDETAGVTSLAKAKASKLAGSVGAPMPGIVLDVRVKKGENVKAGDALLV

LSAMKMETVVTAPVSGRVVSIHAEVGDNMLGGDLLVEIDETGDHEE

>contig21782 Frame-2R

MMPSRSSGLTKARAEILSTLRDHFRDEPLARLICQSKVSKSAVTRRNARQLDRAQLDTLQ

LHNLDEIVVYTMLKLNPGAPTDIGFFQ

>contig22141 Frame-2F|Blast-amino-acid acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61292.1|) 1e-158

MRRLNVDKVRTALDDGDIVLISSLGYSASGEVFNCLSEQVASKCAVQLESAKLIYMHNGE

ELIDKRTNSAVQTLVIDQAQRYVEQARQDPEISQDFLLYLKQSIKACMNGVKRSHLVSRH

IDGGLLQELFTRDGEGLMISKYMYEGIRMATTNDIVSIMRLIQPLLDEDVLVSRDQEQIE

SNVDTFTVVERDGAIIACCTLQPYESKFAEMGCVAVDPTYRGLGKGNAMLGYIMRRASAM

GVKKLFVLTTRTAHWFLERGFVEATVNDLPPSKLAKIDLKRKSKVYICDISTDRTLDEKE

LLLQMD

>contig23256 Frame-2R

MSSDDTHWHIGACRCSECRYECAIATKSKACARRKISVSLITIVAISRSISRVVSRMNQT

CIHSK

>contig24745 Frame-0R

MNSLASSYFNGDRPSTDIAKLLSRSQTRTTRLATAMQQRRQKVSQIVQQRKQPSMLHRKD

LNAQRMDQNELQTSVSKPKKWATFSRTKFSKKEKHKPLSPIEF

>contig25434 Frame-1F|Blast-tyrosine aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY65896.1|) 2e-95

MVFGSNVFYPIATLSKTVPVIAVGGLAKQFLVPGWRVGWIIIHDRNHILQDVRTAYFKLS

QNILGANSLVQSVIPHILTPIPGSTEEQSLLDFKKQYFATLEDNAKFTLDSLAKISGLEV

VVPQGAMYAMVKLQNEVLTKIKNDLDFTQRLLKEESVFVLPGQCFGLKNYFRIVLSAPHE

VLSDAYTRLANFCCRHQ

>contig25852 Frame-1F

MVSHKKSEMDATRRKQVHFWLRFARMGVFGHFQSHPVFEGLIKSMVEMKDKERRGVGKQN

MQYSRALDAFMQSIAQRSTEAFELFASHFCGRTLRSQKIKGQSTLCRARALSDSELTTRE

LPLMLSAPQEQQFLIPSDDILSGRSLSSEESQCFMDRMLDEVRLSSVDTEMQLAGRKRTS

SRN

>contig28082 Frame-1F|Blast-geranylgeranyl transferase type-2 subunit alpha, putative [Phytophthora infestans T30-4]gb|EEY67249.1| geranylgeranyl transferase type-2 subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY67248.1|) 1e-39

MHGRVKSVEREKEEQKTDEQREEELSKVRMYHEVAGKILHMKRQHFYEPSVLPLTSHLLL

LNPEFHVLWSFRREAIDALVPTATDPKAEMHQVAKNELKLTL

>contig28846 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59918.1|) 1e-46

MGGTLSIICGLQASDSDHDLQPYQSKDCARNFDAAVNGLGRSLSSASDLSVASILSNSEQ

LVPDAYLPKDIQVLSQRRQHHGRHHRTASRSSFGYYGKNLSSGSSKVSNLSSRKLGGVRV

VRDTTVGDIPSSVNNKNNFDIKTASSSFGYSDDDDTKMETSERL

>contig29171 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65746.1|) 1e-144

MASLQPTCVSAPGKVLLVGGYLVLKEQYSGLVLSCTTRFYSQVEMKILSVNKANEAKNGR

LCFSLIVQSKQFNQCIDGRIEKMDNGCFQFRLRNESDRNPYIEETIMCAVNGIAGLQALK

INDTFRQLQNSKAGVYVTLRGDNDFYSQAQRLQDAKLSLCRANVKSLEAFAPPTIHKCGY

KKVAVKTGMGSSAALVTSLVASLVAFFVPKMQLTKNKQYLEIVHNLAQLCHCYVQRKIGS

GFDISAACFGSQQYTRFSPSLLKTCTSEKALHPEQIARCITAHTQWNTCNRVKPLRIPSS

FHLLMGDVSSGSTSVSMAQEMTKWQEKEPVKAKRMMDAIHCCNVEIEQGFAKICDLEADY

NTHVNWKELASHSREQWNTIDATIGAILSRLSQAFSHSRDLMREMGILAGVPIEPQEQTA

ILDATLTIPGVLFAGVPGAGGYDAICVLVIHDCALVAVEKLWIQWPSTHPSSIICPLLCD

IDRGQTNASSKISTLQFHSVEYLMPYTISLD

>contig30274 Frame-1F

MASTNDDASGTESRHPWGPPMHIGKVFLQGNERTRPEVFENELQVAYTAGRIGDLVRKLE

KAKEELQALDIFESINIKLDEASSGERDETDVTITVKEKSWRSLHVGATTDGNDEAGESS

LTLSNALGEAEKISLSAKYARSGSNTQCATFKKPRFWGLPLYLSAVGSNELHNHEWISSY

NEKIRSGSISISDYEGVHDLSINIGWRDLLPRRDSKIPTAYRASPSILAEAMPSTKTSLK

YVFTDDDRDNIVYPTAGGLFKYSTEIAGLVSDVKFVKAEVEGQKHVAIGPLFFGLPILNF

SISYRLGTVKSYGSEHNRPARISDRFFLGGPMSLRGFNYKGIGPRSSPEDGGVAQGDALG

GDVSYHGTASVGFPVPLPLLSALGLRGQLFANAGNLTTWDRVLDENQWMKNLVDDTRVSI

GMGLVWGTRIGRLEANYSWILKSLTH

>contig30924 Frame-1F

MVISALFLLAALALGDVGATSISDALQTLPNSGTSVVSRRLDGTFAAVKDLVATAVEGNK

LMEIFGKEKKVVGDTPSEFYEMADYAPHQDAFKTLYSHLEHLTDHDNAATDHALLLLMEK

EYGMPAVSRYVSKALTANPNSNEVKR

>contig30951 Frame-0R|Blast-COP9 signalosome complex subunit, putative [Phytophthora infestans T30-4](gb|EEY65928.1|) 1e-105

MLDTEMANDEEKDEEILVQREDSGATGGGERQIQIHPLVIVNITDHQTRQQCNSQLSQTE

ASQVIGALFGIQKGLDVDVYDSFEMKYDVIDGKIQIDKEFLTSRIQQFSQVFPGFELLGW

YTVGSKALPSDLAVHRVVMEFNESPLLMILNPESTGPSTKKKLPISLFESELHMFNGVPK

MIFAKAPFKVETSETEGIAIDHISKIAPVANASKSS

>contig31080 Frame-1F

MRPLYLDPENTTEAEKWMEAIRTHRFSLKKDEEFVEMAQQVQHAKLRVVWLEEIQRKEAD

VQKNLCVKAKTLLQKMRAIGSGHTDEDLELNADDLDDTADNMLAVLEGMEDVMITLSGKI

EQYKQGSVESLKYRRQRALSNAKCVDLPAEEEEKKLAAIRNRRKGKIQQAVSQEKHIDIV

QKT

>contig31189 Frame-1F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY61039.1|) 0.0

MKVKTISRIEKDFTQEVQSDKLKVFRNYDPALHPFERPREYTRALNAVKLERLFAKPFIG

ALDGHCDSVTALATNPKSLVAFVSGAADGEVRVWDLPRRKCVWNVYGHRGFVRGLAVTPD

GTTFYSCSEDKTIKQWALRVKEEDEGVPTALATFTSKESFLGIDHHWSQNIFATCGSKVQ

VWDPSRSTPTHEFAWGADSINSVHFNPAEASLLASTGSDRNITLYDIRLSSSMRKIVMEM

RSNALAWNPMEPMNFTVANEDHNLYTFDMRKLERAMKVHKDHVSAVMDVAYSPTGREFVT

GSYDRTIRIFTVRSTKSREVYHTRRMQRYVFR

>contig31453 Frame-0R

MTTLDSSMLTKAFKIFWHKADLRLMEQSESEAPVFAITRPKLFGGCERFLLQNPSQLEPP

TEKSIARHRFTVRHGKKRRVFQAPDNVTFNAWLSALEQALEPKKKSEHVRMQSPNTRVSY

IAIRTHSHSGMTSPGRLSPKTKMKRRGHGKKTCQVRPYTQARFFERSGFRRDPTNYKIVK

LHRPAATCSRIAMSKVEAPISDSEMKSESELEEKSSEALKEDENLVMDEIAHNQDILPRI

ATAEPDSISIGDSASCGDSISGGGKEGAESPDDLLSKTAVVPELIDRIDIERIAEKTSPE

CSSTVANATFETKTIEHDVIVTNEALSLEIDDDCGTVKHAVSVGNFPSENRSKILSKISV

VVNPQDKSDVEKPVEKRDQNVIDCKGHATIKTEAIDFEVIGIVKELLARVVEDCVTTIVP

SKSNIQASRKCYVPNSEAVKSSSTPRDCQNHWIPVDPYNSKLIWISHKRRYC

>contig32188 Frame-1R|Blast-para-aminobenzoate synthase, putative [Phytophthora infestans T30-4](gb|EEY53444.1|) 2e-78

MVASMVDELAPVSVQRDVVSKKKRRRVISLLIDNYDSYTYNIMQLLAQVNGSLNSVIVIK

NDDFGGQFVAAWDHFKAQASILAAEEDQELVTNVIVSPGPGHPSKAKDFGMCAEAIRHAP

VPVLGVCLGHQGLAHVYGGQVIQADEVMHGRTSRVVIERSDAFFAFIPNGFQVVRYHSLV

VNPSNVPEALEVLAKSQDGVIMAV

>contig33961 Frame-0R|Blast-rRNA-processing protein FCF1 [Phytophthora infestans T30-4](gb|EEY59715.1|) 1e-106

MGKAKKTRKFAAVKRMISPRDTRINSVRKAVAKLEEKKRKEAEPKQIDQVPSSMFFKYNS

ALGPPYSVILDTNFINFSIKNKLELVSAMMDCLLAKCTPCITDCVMAELEKLGHKYRVAL

RLAKDPRFERLPCTHKGTYADDCLVQRVQQHRCYVVATCDRELKRRIRKVPGVPIMYISN

RKYVIERLPEANAAKIK

>contig34568 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63892.1|) 3e-43

MASNWKRDFNCTFLQQYMKSGIIATPPHRPRELLIFLYLLVIVGIWVAAWTIGYLDFDVS

SSTREYTKGFSSTQRSFRPSRHNWVRQHPQSPYYKRSYHFDSSVSRDRAIVLCLADSIMA

MGLSLIRELRCFGNQDLVQVYHCGANELSAKSQELLLSLDNRLEMVDACSDLVHRNLFTE

NMAKKFQNWYIKLLAMYHTDVRHVMLMDADDIFLADPA

>contig34630 Frame-0R

MKPQRIILSHQLHFMEYQSPTLERSTRNPTLQIRADPVIKNSLIFVRDCWLRRGAER

>contig35721 Frame-1F

MPFPLKDSLKFLLAPSVSRILKNSECSVKSEFIVLIDIKHDEAADEVRQIPAIQQLAGNR

KRARGPPPVFDGFGSVSRALAVLTEIPESIKCPPTRLRTKPDAVVKLEREPVYMQGRYLK

FQRGLSQTPWILDGKRIGDSSVEECIGSVALSFFGGSGYKFHTAGREDVDVRMLGNGRPF

ILEILDAKKAFLNQCDYDQIQQAVNDANDGAVEILQVKSSTRDYFTGLQTGADSKKKTYC

CVVWSKNNLTKDSIKSIDSIQDLTIQQQTPVRVLHRRTLMTRPKVIHAAKCEVLNKHYML

LRLVTSAGTYVKEFVHGDRGRTNPNVSSLLVSCLTCF

>contig36184 Frame-0F

MSFHQALSASAFAGFSDELIAYFTLFCEQRELLRLSEVNSVLYVFCQEDPLWMVQCLRLH

NGDFSYHHNWKLTTFYPRDPRPLEELEKAFRPVSIRGFSSDFLYRRWLRCHLELGDAYLL

PSEEQDATIRRLQKIDIRGLSYQDYFEQYARIPFVLCNAIGKWKAMTEWTAEKLAHRFSS

DTKLRITHNLEVMSESLTMEMNFADYFKYANSQHDETPLYIFDPEFGEKMSDLLQDYNIE

DLMVFKEDFLSVTGMESRLDGNNKLRDESGKHEDRVKSIGGKTKKRDTVSKRADFRWIVI

GPQRTGASWHQDPVNTSAWNSLVKGRKRWAIYPPNVLPPGISKSESGGYFGSGMDMSSLM

WYLHVYPTLTSAQKPLEVIQEEGDTIYVPNGWWHLVLNLDNTIAVTQNFVDSHNAIMFMK

DLFEDGQDDKLAMVQHKLRATRPETYDIFRVAQIPRVNGYLSEEMFQQTFHVLEYWKPQL

KRILKRHKLLAQLNDPAAKYSAANKVKYPKMKCLTSRVNPTFAVGKRLIIKFFSQYNNNW

GEFDFETYMTPNFDVTDVIAPTFKRHKRSSLQPCELKRVMSLRYAMEESFRIEKAVYEMI

EKSTSSNCEHHPLHAMISRLYNSGHLLYLDEVDSNDEDESIWRWPYIVIEYVNNDVSLKT

VKKMGGATRKTWLNLAKWISQDFLPRLHSIPIDSEFRGVYGHDKAEWGWYVHFLLRQRKR

SISFHLTEFGLPAHLMRCLENFLPAANSDAITLELLPVKPSEVKPVLLHGDLTDENILGS

ELNDKRSNTLASSFKYHALGEEVTNLTSFLTFIGCEKYISLLVNQEEMELESLALLEEAH

LEELGIPLGPRLAILQGKQLIMGKSQACTTKREACESNGYFNCDEEWELSSSSSKCSEED

NIGT

>contig36526 Frame-2R|Blast-DNA-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY69219.1|) 0.0

MKNVPLWTCLQWSAQLMALLNGPIRRTVLVILEKMAEKYPIALFYDFMVTCKSSLNKFDV

DLHRLEVLLTNSVMEKFVAALRLLHHPELRLKEGLKEISELVEDNRTQDAHHKVTRLWKD

CFSLDRPLLGGQIGRYNREWSRKAKRDVEKIMGKDGSKMTAKSIKFAREWIMKHFGVTPG

TYGITRDMKAHLGDFAEWLEEFDHSNCSLELPGQYTSYWGPPDSSKHVKILSFDSVLGVL

ASKQLPKKLTVHCSDEKEYTFLVKGGEDLRLDQRIEQVFGVMNQIFKADPRCRDQRLCLT

TYEVFPMTQDIGLLEWVDGTLTLKGVIEAQMQVDERCIDLKSDKSKKLDLFNTIAAKAYE

SFHRKQQGASFSAKIVAPRSKDVVDQFHRVQAMIPADLLRRQLLALGLNFEAFLLVRDHF

LKSLAVFSACSYILGIGDRHLDNFLIDLSSGRVIGIDFGVSFGAGASVLP

>contig40488 Frame-2F

MKLLFPLLLNLAAVQAVVRAEGSIRYPLDADISPPIDDKKGTEDDMISDFMVALNQPFQA

SGEWLQRLLSPDKSNTEVLRIVFTENESDKNDSAPDSKRACLKALEKIHGQDPLDSVTGV

SLDLFWSIFRTGTEASCDDLETTDLVRECNVIVESAYVMELVSEGKTDLEVCDIMSVVPD

DNRADKLSCKLCKRFVQMVDEAIVQEGQEVQQVRDIIGDLCDAMSPDSKCHSFLKNYDAI

VEWLKHDTEPLVVCARIEMCLKKSDNNNEALALDLTLDDPRSTNDKAMVVAGIQENDQSC

LLCSHVASVIFHVKNVFPNQLLMMKSVLIAVCETASPESYCELMVAKYDRMVELVQLGRH

PLDVCADIEICLKKPEGGAEMVDLTLDSERTCVYCDAATTIVELVMQESPEQIDQIREYA

DIICGMLGDDSPCHKYVNQMDVVVDHLKKGVHPRDICKTLKYCSGALLDRPFELQMMRTG

SHDIAGNEGNYKLAMLKDDDLNPPRHVESCLFCSRVATVINYSNHASSEHLAIVKFIMTS

VCAFMPLKFKCDITEKYLNDMVKMDNEGKRPHEICRSLGICGGEHYGEEGASVIAYEMKS

VVAASEWPSGNGTQCSYCQLATTVAKIAIQQYGTDVSEIRAYADLICDMLGSDNPCHVYV

KEFDYVVDGIAKGMSAKAICVELQFCPALVTQPSSSEKSAFGELLNGPMVLSSDGCSFCT

EVANVIELVVVENPSLVAQIRQIADVTCSLLPIDNKCHSFMTQFDAVVDLLKLGELPNVI

CQNLMNRVADPISTTTKIAGRDVISDQNHNVVKDTCAVCSGLVTELTVAISEQPERVKVI

RETAGLICQILPADDKCYADLKIFDSALSDIKSGKQPQAICHLLKYCASTDNSGSLLSSL

LDSAGANFLSPTKLSTCRDTTLLLESLISRHDDLAVFKNKTNSICQLIPESSKCELLMNH

QDKIIESLEKHESVDAICTRIVEYEHAAGLLEQSSMCVGCLFCEYTADLLKHTMDNEKVV

REVKVTLQTLCAVLPPSAHCDALSSKFDELLSRMREGESPSEACHSVDLCDQVLSHSSSG

EENLIIHASDHGRQSTGNVMEVQ

>contig40754 Frame-1R|Blast-adenylate kinase, putative [Phytophthora infestans T30-4](gb|EEY60144.1|) 2e-58

MTEGGQVVDFHSCDFFPERWFDLVVVLRVDNTTLFDRLQKRGYSDKKVAENVECEIMEVV

LQEARDSYAPEIVQELPSRTVEDMESNIERVLM

>contig42428 Frame-0R

MPEMKWLVADMTRLREVFSPDSFDIVIDKAAMDALMCEESDVWSPSEAAIEQAAATCNGI

MSVLVPQGSFLQISFAQPHFRRRFLLGEGEQPPTSTIYGWAYSYHNIEVGLGYFFYVLKM

SR

>contig43184 Frame-2F

MCGSKARQSLYFELKSIHGSKLVHRLRMRCSRGVVNLLPLITFFTIVHVDFVVALSRTCA

I

>contig43526 Frame-2F

MMHHKLYLRSASLLRRLKIELTHTFFVKALQVDDRFLKSNASFVMAYRTIPQYLKGRRSG

KKFDTFVGSRCSQLQNCEAVFMRRNMACLCVEGPAQFKQLVSVLKTDSSPLPFN

>contig43593 Frame-0R|Blast-adenosine kinase [Phytophthora infestans T30-4](gb|EEY60546.1|) 1e-170

MTSKDLTLSIVGLGNPLLDILVDVTPEFLNKYGLKLNNAILADESHEPMFEELQTLKPAF

VAGGATQNSIRVAQWMLNKHNKTATAFFGAVGKDEHGAKLMECAKGDGVNVSYLEHANIK

TGTCAVCVHESERSLIADLSAANHFHHDHLAKPESQEIIHKGQFFYSAGFHLTVSPTAVI

TLAKHASENNKTFLLNLAAPFIVEIFKDPLMSVIPYADFVFANESEALALGKVLDWGTDI

KKIALKTAQLEKISGSRCRTVVFTQGADATIVVHQGRVHTFDVPKMETSSIVDTNGAGDA

FVGGFISRLALDLPLEQCVRAGHWAAQVVLTRSGCTFPENCDFQD

>contig43834 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54198.1|) 2e-10

MAPNQHTNAGVCIEDARSNLSLDSYEFGVMLRANSTIIKQHTEDVVIFFDW

>contig43841 Frame-1F

MSTERGIDHLQSRDVWHRFVSHVHLTVAFRPQQEKSDRTECMLHALDLRSMSIRLIKDSR

RTSEGHGNPT

>contig44080 Frame-0F

MSMETFLLQHDAANKMTPEVIQFMVLAREVVSSFPQNLLSHPHNGEPSLFWICLNLATRL

LKVDHQMQGICDAACDFLVHAMRCQPEPILERLTMFCTEIVRVALSFLGPRSRHYHVRNI

WDFLFKCLHAPEISCSIRGGFLIAVSTVVHEDGALCSCLPVETYQRMPGELRMRRQRHRF

RQYFTLLGNIANASC

>contig44167 Frame-2F

MEALTNRPTARDKETKGTTRGFSTFLRVPALSRLQKIHNVELCLYFLQEKCGTSVLKTLQ

RSTRTNDRLYGRVKVSSSGFAGLEGKVNEKRVGMLAKTIVSGHREKTLALLWTLISSFQL

QSLVDASRMRQEIATVIKRMSFHAKDCFDRQQEQAPLGCTYEHESYSLLLEWCRAVCANY

DVSIHDFTSSFADGKALCYLLHYYHPMLLLKSDVLPTTCDVKETDAESVITKELLANEQQ

HFMLVNDRIKQLGQVPVLMPQDCNSTNPPEDKIVVTFVCYLQSRLMESCSEISAASRLKR

WWQSPW

>contig44303 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59853.1|) 7e-83

MYLGYVTKSMLTQACGNITIVSDLAKCADATIIIEAIPENFEAKVNLLKTLEQYCSASTI

LATNTIHLSIDSMQLHLQHPSRFLGMRFFYPCVLISPVELTVGASTSQDTVNRLVAYLQS

LQKRPHRGPTKRVLTTKEASSLQFDTAVRGRFYHGLLEPKCHPFVADIITPQPGPPLVDS

ITTSL

>contig45951 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54941.1|) 1e-100

MLQRLGKLPRDPLLIDECGDVAAILEPTDRKTRDRVQQEIEVLLMWFLTTKSVAYMSGMA

RVVAPFFLLKMPLSTIYDCYYQYCAHFMPHFVVADTIFSDSNGVIGNPSTNSTTRGSNTS

LDDVFSSQTKSKVERSSSTESASSFLEEAKEQAD

>contig46675 Frame-2R

MAKKTTATKAQAVAGENENGGGVDSDESSSCNGLEDGAVVATTAT

>contig46961 Frame-0F

MLDSRVTRGVTLSITCWRTLELHNLVAFTLTNEAGEAACIRVDELHQCPTLNAKDLNTST

IPSLVSLLTYAIEKVLTDLIKEQNIHVIG

>contig47221 Frame-1R|Blast-cleavage induced hypothetical protein [Phytophthora infestans T30-4](gb|EEY56378.1|) 2e-17

MGVGGESSSLCADSGLTRWDRIRQTFTLNGGLVPIPPH

>contig47254 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63497.1|) 2e-68

MDHVERSHLYSELSLQPAYMSALFWVFQHGVVKQKLSATTLAFDASVEFVDVTLSVPRAS

AILTFVGCALLLLMALLVYFGGKSREAAIERHFKPHHLARILLDDEEFSHRLLKCDLLNI

GNKYLNSSELLDQFEISGLALRHRERPSDVLIVPKDQRSTVGTNHVV

>contig47571 Frame-1F|Blast-tetratricopeptide repeat protein, putative [Phytophthora infestans T30-4](gb|EEY57886.1|) 4e-64

MWVTLGDLTQEPSHYETSWRLSRQRFARAKRSLGRYYYEKRDYETAISHYKDAVLVGPMH

TGAWFTLGAIAMRIHRWALAMRAFTRVVQLEPDNGEAWGNLGSI

>contig48538 Frame-1R|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY65040.1|) 2e-36

MLLSICRDKRLDAVAAFVLVICYILKTIQPSKGRHDKSPDGKVVPKRVRYLPSKIPFLGN

SIELLMNSARMHDWITDHMLPLAGEPFMLRLPGKADLMFLSKPEHLEQVLQVQCGNFPKS

QHIHNVYFDLLGNSIVTSNGEVWKRQRRILLNLLNAQALKENVTPIVHKYVEQLRQLFEN

AA

>contig49744 Frame-2R|Blast-betaine aldehyde dehydrogenase [Phytophthora infestans T30-4](gb|EEY54272.1|) 2e-16

MSGVGRENGLAGIESWTQLKSVYVEMNEVWCPYAK

>contig49928 Frame-2R

MLEMSDDKTGNGSIPSSPTAVENTVSADLSTVTSDELSLSRSRSRNRSRGLSASNFTDDV

SKPSLRDGKRRAASVQMFKSAMDTPVEDKSGDGKYAGMSATFFEKLSSRFKRSTSPRNGI

KVTRNEVKIADGEAPIVSAFASSFERRQDVVHSKVSNERPRMYVARPPSYHEDESSDSIF

GSESSASDLSDNDMPPLPPPPPTPVQETPYLVPV

>contig50276 Frame-2F

MTKFVGSDQFTQIRRKIKLSFHLTHNNWYAFAYYLECNGALPTYTEAV

>contig50562 Frame-2F

MADDAPVASSPLSFLQTPPDSPQDNLSLSENSFSEAVLHLRLKMIDERVYDVEAALSMSV

ADFRAKVALATSVPPPRQRLIYRGKLLKDGAMLAAYRLQDGHTV

>contig50971 Frame-1R

MCEIQSTRESYKMTLWSKTALIIRLNRIR

>contig51998 Frame-0R

MDSINPVLHYLSARVDVDIVSLLLLSSKEQKDSTSTSISINALMTAIPMPLVFQHVLVSI

SSHEAKEQEVIMGIVSSMIHRRVQNQQVNASEAARICEQLLYFLSSSHVAFVTCGHDIFC

MLLMQLLTLALVSKTPSKIVTRLFFKLQALVSSTSDSILKRQVQAVEVVAFRVYLSLVTE

RNTLILGIIPRLFHDASIPLIAILATFIPFSIGIAVLENLLRVQMEPNAQHVVLIAHVLA

SIARVTVDDTSEIHKKNVGLSYKLWQFLIRQSCRKQQLSLFTTGLKVVGLFGG

>contig52285 Frame-0F

MRLETSAGTFVDENMLQASRVIRAVSDLSQV

>contig52609 Frame-0R|Blast-structural maintenance of chromosomes protein, putative [Phytophthora infestans T30-4](gb|EEY70359.1|) 2e-45

MYQAKKKELITTLRDVKGNRKVLQDLQSEMEDMQPQVIRLREQMQYVQRKQTESKATEET

MKQRFEGKSAEIEALKKDLQELEQAKAELDANQMRESNKREAQGALVLEGSRLEEYHRIK

ESVQIKTALLRNELESIVR

>contig53277 Frame-1R

MPTDQLPVAVACAQTEVSTRGALSGTSTRVYVPAYRK

>contig53840 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65737.1|) 1e-103

MSVITFFFQSVRCMDGPSFFSVAHNTLTRTVLRMRDDEQRTADAMPLGSDAIQAIMLLFA

ITLLPMLVRVRILYTFCWVAFTVLAHVAESEAALGIATSLGLSIMMGWYSLRALDRTTFL

GILQGWFGFLSKYRPFRLLANSVDLLLHMGVPLTLAFCYLPLVRLWMTAPILLFSQLWIV

FVAGGDLCLTGNDIYHIYPPRPKTFWIAVRKIEMIYNCIIPALCVCMYQAGIHEFVINCF

LKPKM

>contig54113 Frame-1F

MNAARDAVDLLQVDTFRDVDAQVFRAF

>contig54777 Frame-0R

MQERARRFQHAFKWRRITSSPLACLLPSRSPLIALYAHYGDIAIEVTSLEVSKVRKRQKI

SCEDY

>contig55125 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64663.1|) 1e-23

MSSLSLRGYSPHRGRFLLQTSLSHNSNDLCSTSLERDRIIEREIVDLQRWDRQLHSNIGS

SFQRLPTKRLRKLMTTHWVLCDLAAGWRKELQKNVRVCEDWINAAFAQLPTPHQIEFVDD

DLYAATKRQRSIARAATKNARDLQQYFSSAELVELVVHMAMMHLQTKQVTDVVWLEP

>contig56331 Frame-0R

MDKLNHGDEEVYSNFASASQTEPSMLSISCFAASMVMILYTTS

>contig57505 Frame-0F

MSLPVCARPAMFLASRIVEPSNSQIDSSTILH

>contig05464 Frame-1F

MAVSVRWQSQTEFVAYICLYMRALLYRAG

>contig06199 Frame-2F

MGKKRKCKSAPASVVESTLNDEVADVVQEQVKNQNASALAEGFAQSAAFFGKKTSYASAV

IEPGAEALEEKIDKTKKILKECKVSKMQKAKKSKKVPDLKKLTSNEISGEEKTPTIFIKK

KKSKKKHTSKTVVETEEDTEVELEDLKACRTVFVGNVSLDATPKDIKAHFSACGKVENVR

LRYLPIAGCAIDQAGNQKLMMKVCAMKKILSTAKDHCNAYVTFAEENSVAAALKLNGTTL

VHKKIRVDLSDPVLDARRSIFIGNVPFKCSDDQMLQFFQKRLKSEEEPEPIDNVRLIRDR

ESGLGKGFGYLLLRTPAVVAKALALQNLKMENRELRVQVCGKRFKNMRGEESSREKFEGL

RASAGARARIHLKRKLKINGVESGIATKRIKRAAAGKKPKPKHAARKKAKAAAAAATGN

>contig09239 Frame-2R

MKALKEVVGAKSVNSSLKKARRSSKLEPLPTIVQKFLQEFPVPAKTSLAKFFRSFSTP

>contig10787 Frame-1F

MTGLLQKFFWMKTWATLLRPIIGGNLSLLFFSSSTILF

>contig12468 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63792.1|) 4e-48

MADWSMPRELSPGSLPVNLQELAMLLVDIDLKSSSSTRYEAAKRLKELCHYDSNRRALVD

QLKEQFIMGLQAMLKDDNENIVRFAIFIILNFADDATTLNNFELPWLPETLRGIVAVSQK

ESTKQLADDLFKTINAIC

>contig12486 Frame-2R

MGDECWLQSFSNNQTLHKKNHVYEVLGDKDHSDDSDESSEEEVTVNDQCLNLSTSTGEPK

KISNGKKQPSSTSSKLKSSRSKIKDPKELEMVAKSNLETNCNGNSTKKRLRTNRPTSDMM

TSRAMEPTQNQHFESTQQQINLRVAGRHVKEKRS

>contig13346 Frame-2F

MRDLKYYGLVVPLTIFIENLLENQYFFGVCA

>contig15919 Frame-2F

MNHDFGRRRSNEGVWPALLDAAEHIFWKLQLYSIALLHLFFSTDKQWLQGTPNTHASAID

ENASVESTTLCMDPEASVVTKTKRIVFVRHAESEWNVIFNRGFTFHAIVRFVRSLGREWL

LLPTNDSILLDSPLSQRGRFQAHSLRDRVCNRPLYPIDDNTAPFYEHSPQEREESSLLRY

LFSPVPGSVVVASNLRRSIDTARLVSAARLEVPGERIHVLSCLQEIGRNLDTLAISTPHN

IQPHEVLVQGPQGEKHHEELFSVAENYGNKAILGSGRNRLFRFAQWIFKHPSSVVIVYGH

SLWFRAFCREFLPQNVNHEAKSLKIGNCHVVTFLLEEYGRGEMVQYNIQPESFQHL

>contig16059 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66695.1|) 1e-98

MVEIILDPSIRDWVVLPMIIIFGCSAMVRHYVTLLLKTEKMATVEQLLPLNTVKRAQITR

INSKFIASDAFAMRKHYFTASQKKDGMKGALREKIKSEAMNQMMNPNSMLEMMKGNMTFM

VSNFVMMGLMSYFFGGFVLAKVPFSLTQKFKTMLQRGIELNTLDVSYVSSVSWYFLVSFG

MRGFLSLILGEAS

>contig17926 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53710.1|) 1e-160

MMANEVTEAVTLTQLFEHMRLLKAVQHMIKWDITQLRTELSQAFTTVSTAPSVFLKCVHL

YTELPNKDLAEIAIWIETAVNCLKQNDHVLIIPADSQLAGSMLPLFQRLRMPLVADFALV

FRIDKDMLASFCLLLVQTRIGHAVQFLKSLTMENLVPSTVVYEAVIVQKDFRAGDVYVKG

DATKQHHYLEKLVLYSAPDKVIKKRLRMFHLEAQGFPVYYERRQKAAVRFLIYSNEYEQA

LECIAESEDLKFYACQMILKHCGVDDAATKQFLYRTGLAHQFPEVDTQTENMKTFPTLKA

LPSLDSCVSLVDVIGDSNIVLINTLDALQECAKYLLKQSIIGFDTEWKAMHFSTSQKQLP

PKCALLQMASREKAFVVDVLTLQAYGSVLMPVFRSESVLKLGFDTKGDVQVLRPFLNPRH

SFDFIMSMLVDVQAVARLFQSVHSRVDTIVETKRETNRREKNETCENSTDERIHTSTATV

WKPKCHNSSGNTTSKREDKTRLGLTAVSALYLGLSLDKRLRLSDWERRPLTHAQLQYAAL

DAHVLVQIYDKMHDNHPKEAFNAAIKRCLQKHVR

>contig18695 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68603.1|) 2e-52

MVRLKTRYLVVEVIGAPKLAIKKEDVTALIRDSIIRFYGDFASGLSQYAFQVLYFNTQTR

LTAIRCTREMCKLVEISLVFVTGIHNQDVRIRVCRVCGSSRKCRAHILKFSLERARLLNL

YATQPNFDKEVQAEIALLDT

>contig18956 Frame-2F

MVLFTALIFLKIFHWLSQSRIEFIEQSDVVSRLTHVRLVALMTILSVVDMAFVVWCSISL

LDEGPSVFILFGFEFLILTITIAATIMRYLLHIIDSRMDGAWTNKFTYLFYLELVSEITK

LVVYLVFFTLIFTLFGMPLHIVRDLWLSIKNLQRRIASYYRYRKITSNLNDRFANPTAEE

LEETDKTCIICREEMTPSTCKKLPCSHIFHINCLKMWIQRQQTCPTCRSSIPTGPAPRTG

PNNNAPTGVPAQGANAPEQQAPRFRWNAAFRRVVPPRSQPTVPTAAQVATNEPPAAAAPF

GLGYPNPYMPPMMFAPGMAAPFGYGMPGTYGMMPPFGAPPMDLLGQQQPGMDSESIQRQI

DLLQAQLAVLQASTAQFDVSHQNVATSLPHAPTPIGSVIPTEAASLSTQRSPLSSGSLSA

AHAAVQSVVNGAATTTTPIPEELEEKCRIPSTSQRGESAASAANVELTPIESKIPAAPQT

ESERRREELRQRYSRIYGSASKSSDNNEKTND

>contig19168 Frame-0F

MQIFSIAGDCHEGMYRKNHRHGMGTYLWANGDKYVGNWRVGKMHGQGTFFWKNGDSYTGE

WKKGMLHGKGKKIFVSGEIIDGTWKHNQVSGWGMKVFSSGDKYEGCFVKGEREGFGRYEW

VSGDTHEGMWYQGIMNGKGVFTSAGSSLHGSWVFGDLNGQGVQYFQCGSVYTGEYLRAQR

HGFGTLTFASGEVYEGKWHAGEVQGFGSWFSPDGKNIIGTWTNGLPSGEGVFSREHGEGD

LAADTKPSFEIGIFKSGNLMSSGEHFFMGRLAAPS

>contig19797 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59223.1|) 9e-16

MELGRVVQRLESYSYSQWQLLAMKDINASLLQTIRWIGIFAVFVILALDLSVRWLLAWYA

RRAKQLVESIMAFRGILNKFNAVYENSINVVKRAELASRGFQIGADWLPPIGRLEASDAR

NASNDECAAFTAAKIQMRCVPLRRMLRKVNDQLLRTAFAIIEEGEELDEMDN

>contig21206 Frame-2R

MRQRASSKAQRRNKQHLKDPYALTGDVYCESPTFHMGSLLTPVGMLQLMTALALGGFLLG

GALVLCVAILAVLGLVLLHCSEPRRAKHILGHNQAIHQLMALRRSVLDCSRTLSTDQSKK

YQQSQNNQIVVVPAKPTPQNVTTPALISATTVAQKRKPTHSKGDSLNNVQFTAINLPDMM

EAQELFADNNEANLEPANVHQNRSLLPLNFLVQQHCQVQPKELEPQFVLKALEIKGTQVQ

RFMKQKKHQMVLKEAESAILKGAVKKVNADASDFDAKPNAMISAMLPEEELASDLEPVDK

VSSALSSEVELPLTIFPKIKTLMEVVTGEPVMEQEVIFTRKVVLCINLRKESVKKSKKQD

LKHDLGKKAEVKPNYFPEVLPLSPIEFPPLSSIQLPQALKLQPSPGSMKSDHSTVNSMLN

PRQPFTISQSEQVGVADLRSMLDELNVMQSELDTAMTRCKVL

>contig22135 Frame-1F|Blast-alcohol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY62160.1|) 5e-33

MPSYKRLEVHTKSSDFRAATHIVETTELPKAHDNSIVVKNFYVGINATDINISNGMYTGK

QPPPFGCGLEAVGVVEDVGRHVVDLKKGDAV

>contig22140 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY59854.1|) 3e-39 NOT\_ORF

MAITIGNLLVAITFFFANTKSGWRFIAEFPIALAVLFLVLAPWIVVESPAWLLVMGKEAS

ADKELARLYGEENVRDRQNLDSARS\*TRRDIVSNLPSAM\*RLPNSIETCTFRELFSPMLI

RQLMFAVSIAGAQELTGINVVSLLVDVPETRRLQSN

>contig24744 Frame-0F

MTKFAVLLCVAVATASALEDTPVSLCRDATYTSPASRGAVCAGAGGSPAGTACPMKGDVA

TADCYDYLPSWNGSACVAPEDARCTVVNGNTWGCVLKSIGCGNVPTPCPVVSLSQAPTMD

SQSSSSITTAEDALVNALPESPNTDTLMPATPVAPVLPNSAALASIPCPLTPLPDIETAA

TFAASTSDFIDPAAPALVSALPMTTLP

>contig25435 Frame-1F

MPIGRATKGATASEIVNEFIKSPLMDTFGRRTLMEPCNMKPTIREIELQISAQDDFLAEE

LYGKAAKDGFFHGCEPAYHPQLRKEKAFKFSKPSNGGPLHTKTGRPEWEEADYDAAEPES

>contig25853 Frame-0F

MLPRKQHRLCAINRYLENTLSLLLFYNKWKQVHFKQSKKINARIYPRLTFSRMPVHLNDY

HGNQAVV

>contig25927 Frame-2F|Blast-vesicle-associated membrane protein, putative [Phytophthora infestans T30-4](gb|EEY65654.1|) 1e-96

MSIYYCVVANSYCSLAEHSNGGDKRMNEFAQKLLKKLNLAEDAVEAMEFEGKTYSYRVDN

EVAYVCVTNAAFGKSSAALFLKYINQLFDHQFGIRGKATKLKLDMNRDFAPTLKKQMETF

SSDQGAEKLQVLKKDLDHVRNSVQVNINKVLERGDKIELLVDKTDQLNSQSAAFAKSSTT

LRRHMWWENVKMNIAIGAIVA

>contig26562 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY57250.1|) 1e-79

MKCIRRVAETSTNNPLPPQKTNSRKPLCFSKKCTPAHTNYTKRNQSSRSSIAGVSSALST

AHFDARIATSDALKPLYYLMKLAEQDNMADTTALILVPSLLTLLAVFEKPGSAFVVLQDQ

TNLWLRCVCMFIGRLGGAFLAREIFTCKLRSRLRMSNEDVSETAQSTPVNGSIDGIPARL

WIQHLMLQDFHAHFWYLTAVTIVVTFGCFARIELPLRFALL

>contig28506 Frame-2F|Blast-Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily [Phytophthora infestans T30-4](gb|EEY63398.1|) 0.0

MTNVSEQTSLLANDSDVDLEYLPAIIGRGTSFPAVSPSYATSLDVIKVHDYETESDTKFL

TRELTQEQGQEPEPVALDEFWKTVTLAYPIVITYTLEYLPGLVCIVLVGHLESPDTKLYV

AAATLSTMFTNVSALCVGFGLTSALDTLCSQAYGAGKINKLGLYLQSALLVVGASLIPMF

LINWHAEKVLTLCGQDTQVAKLAGEFSRVTVFGVPFLLIYEMLRKLLQAQNVVRPMVLFA

LIGTFVNVVGGYVLTYYTSLGFHGAALSRTLGYVVLPLCLVPYFFVSGNHTKWWRGWQLQ

QAYALVPLFLRLAGPSFLMMAMEWWAYEILAVMAGNLPDGVVAVSAHAVS

>contig28973 Frame-2F

MRRLIEEDLERIQNVRMTQATKQHIVDMAQCASEAEFDVLRHALGTIDDALVSSLDEFER

SHWVKYAFWAKFRRSTFHEVTADFSVKGFERDALLPQHATVAYRTYFGTNHFKSSHPLEA

FYCYLRNVAEVLPQRREAVITRRSHELVPRRDAQLQENLQASQRCESIPCSNGLYMVRYV

GPTRLENPDTWRHVNLVECECTCHDWQDQQFPCLHAIHASALEQRRIDALYDGKAHSMET

YLTCYNTAFTVLPSNASLLSLETTLKTPLDLSYQEDASGRRKPGPRPKQKRLLEGR

>contig29589 Frame-2R

METGNMSKWNIKEGDAISAGDIVCEIETDKAVVDYEATDDMFLAKILIPEGNENVPVGQP

MMVVVDEEDSLAAFEDFKLEEASEPPAAPSHIEAKPAQKENVPMDMKAQDGPKSLETKTT

NVSEASFPPPHVAAPIAKTTASSSTPSTAFLKESWGFNMKNSATSTSLLKRQQAYIAQ

>contig29620 Frame-1F

MISKILGVKMLLNKTIVGAQSHVFWRIRSHKFQLKLINDGC

>contig30275 Frame-2R|Blast-serine palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61320.1|) 0.0

MAAEHVPWAAAILCYIQYAILITFGHLRDHAGRIFGGSRYSDSAKKGYAPLLVAFENFYT

KRIYHRLQDVFNRPVTGPPGAHIDLIERYSVDENKTLHNKDGCIQTCLNLGSYNYLGFAD

DWMNTCSKDVFPAVNQFALASTVPPMEFGTTSVHIALEKALATFIGKECALVYNMGYATN

ATSIPALMGKGTLILSDALNHTSIVNGARVSGACVGVFKHNNPKHLEKVLRTKIAEGQPR

THRPWKKIIVMIEGIYSMEGEIVRLREMVDVTKKYKAYIYVDEAHSIGALGKTGRGICEY

AGVDPSEIDILMGTFSKSFGGMGGYIAASEEIINFIRHNSSGAVYATSLSPVIAKQILTA

LNIIAGLDGSNIGRKKIASLRDNSNYFRQKLIDMGVITLGDFDSPVIPVMLYHMSKVGEF

SRQCLKRNLAVVTVGFPATPLLLARVRFCISAAHTREDMDTALVALKEVCDLCNIRFEKK

ASGYK

>contig30950 Frame-1R|Blast-COP9 signalosome complex subunit, putative [Phytophthora infestans T30-4](gb|EEY65928.1|) 1e-50

MKMLDRQVDVLLRFLYAMENGEAPLNHNLLRHISSICNQLPAMKSEHFDAAFTQEYNDAL

LVTYLATLTKGATNANTVVDRFTSTQERHHQRGTLL

>contig31081 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58775.1|) 5e-20

MDDEKPRGIIDLEYLTDVKRNADCLQRAVGGG

>contig32505 Frame-2R

MGIVISREDVSGIIFRDCEGELYGTSLRRSRASDQKD

>contig32963 Frame-2F

MSKFFLATRLKKHPLRMKTLVDATLRCGWSKLFFSSFARSLGCQSCTLVAAFYFSINVRV

NKKSATLRSPIKRMPTESRAKTFTLGNFSHVCLLKDFYKEKLNINTH

>contig33379 Frame-1F

MEGMSTYRCQLTLKDAWSAGSSSTSILQTWTSCC

>contig33960 Frame-1F

MCVSIIELLRQLCSRVCWESWTDFQGLVSLYEHLLSP

>contig35070 Frame-2R|Blast-flagellar adenylate kinase [Phytophthora infestans T30-4](gb|EEY58150.1|) 5e-93

MSSTLVKKILFVLGGPGAGKGTQCAKLVEKYGFVHLSAGDLLREERLSGSKNGELIDRMI

KEGQIVPVKITLNLLQQAMITSGCDLFLIDGFPRNFDNLQGWQEEMSADEFQVQGVLFFD

CTESIMEERLLQRGKTSGRTDDNAEAIRKRFRTYVESTMPVIEYYEKQEKVFRIDATLDP

DAVFQATAARIGPLVDK

>contig35720 Frame-0R

MFRRQIESFEESITGLRALLKEIVAHSKEYTAAGKYFGEQETALAHELIQRKYARA

>contig36592 Frame-1R

MAQEDEYFPSFLTAIQSTTKADKSTEGAPHSRVEADLLSLKSKQRLTFAESLDMNRSKQK

GVTIPENSPFSLGGSYQDGLGTRRRKCRSSQGAATSNGSRDKEVPTPPTISMLDPVELPC

GVNAEASAAYAISKAAAAKASHYPTFHSDEWGQDKQYWVTVFGFPPTARSLIRRHFQRLG

EVITLSSTTSGGNWLHIRYLTRLQAEKAISCDGTTLTNGIMVGVKKCYPSDRDANALDEG

PVSDYFDAHLRQNLGSSELEVGPTDADILLPPKRQRDICSRLLSYLFNW

>contig36840 Frame-2F|Blast-choline/Carnitine O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY67951.1|) 0.0

MAEAHQAIGVFDEHKRGVELLYSEEGIRVSFTIPPLHEIRRSVVREFFHLQRAIKRGVYP

APPFAVIMTVLVISVVVVSSPSESWWRSGPISEIVWHVGNFLMPFWYLLPTSIYVAYLAA

WTAFLGLLGLMAIQRLFLRLLLSYRGWLYLAPRQKSSVVLAWGALLKIFGGRNPLTYSFQ

DALPRLPLPSLKDTIQRYLKSVHPLLDSTEYEKVKRMAEDFVHKEGPKLQFYLYLKSWWS

SNYVTDWWEKYVYLKGRSSLMINSNYYALPGANLDFSMTKKPTALAAALVHEFLLFKQDL

DREQLPPLLIRGIVPLCMSQYQRIFSCTRIPGRETDVLKLYQNKSKHIAVFCRGRVFKLP

LFKKGQYGKLLTKFEIQRQFEWIETTALAMESASKAEENIAALTAAGRIEWAENREQFFS

SGMNKRSLEAIESAVFVVVLQNDVAKDWTLMGKDLIHGTGGNRWFDKSFNLVIYKNSVAG

INAEHAWADAPVMAHAWEEVYTKQCFANPYDADGNNSVQSENERVSTLPPCRMLLWDFST

GLHRAVLKSLEDAEKAISDFDLKVISHTDYGKGMIKNFRVSPDAFIQMALQLAYYRNSGT

ITQTYESSMTRLYRNGRTETVRPVTDESKAFVYGMENPALTGAEKLRLLQDACDVHQDLY

RKAMSGKGIDRHLFTLYCVSVGFSIESPFLTNALSRPWRLSTSQQPQQQTDNWRLVEKAL

EGTKFSIDDARCPGGGFGPVAEDGYGVSYMIAGEKMLGFHISSKKSCPTTSSKTFANDIR

QALADLKALWHSEKIETC

>contig37429 Frame-2F|Blast-13 kDa ribonucleoprotein-associated protein [Phytophthora infestans T30-4](gb|EEY69544.1|) 4e-62

MADTAVNPKAYPLADAKLTVSILDLVQQATNYKQIKKGANEATKTLNRGISEFIVMAADT

EPLEILLHLPLLCEDKNVPYVFVPSKVALGRACGVSRPVIAASITSNDASQLGSQIQSMR

EQIEQLLI

>contig39001 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66913.1|) 4e-73

MADHLQLHGSVTGVDFSKSRLGACKQLVHKYKLFKSHSEVLKWRCRLFYADGRTFNIGPK

TETMNIKGVEIILDSQEIESRASKDRLRKRKNKSA

>contig39584 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54799.1|) 1e-16 NOT\_ORF

MQLFRGEDIKVIKFGHHLTGVAKIFYNRQIEG\*WEKELTLDYAMQRLLHTFATKTTPTRN

MKPSTAPKSAS\*TWEEHYLCLVVESGACGGANNLVQDYIVHYADPAMRASMLARLNLMRS

GYLRQAEELLISRSQRIELRRRIE

>contig40489 Frame-2F|Blast-transcription elongation factor SPT5, putative [Phytophthora infestans T30-4](gb|EEY69450.1|) 0.0

MKLVPIHEMTSVLTVQVRRKPLVTGAWARMKRAGLYKEDLCKVIEILDNGARAVVKMLPR

LDPIVLAGGEQPKYKKGQRPPQKLFHANMVPGADVARRRYPSTGEMMDTFDNDFYQDGFL

IKEVNVATMLITDDVNPTLDEINRFSTVVGGDGENTAEEMLASIESDDWKNKVDLTKGDT

VRVIEGDLVNLMGVVLSTNTANDTVRVMPLHEEIKDTILDFQLKQLMKYVKVGDHIKVVS

GLYSGETGTVVAVDDGGGAPVAIVLVDSMAREIQVRVRDLQESAEISHGLDSYKGKELYD

LVALAHGDVGVIAHVGRESFTVLCQNGQSRNISDQEVQRKIVSSRTTAALDKKHNHVSVG

EMVNVLEGPFSGHSGTVKHIYRTYLFIHNNRVTTNSGMFVTRARCVVLSGSKARSDMISN

SAVPRVGAGMRQQNQRGGRFQRESDLVGQTVKVKKGRWKGYIGIVVDESDQKVKVEIHCK

AKVVDIDRLHITVAGTRDGGVIDKPRYAGTPMTGATPLPSQTPLHGSAMTPMATPLHRGM

GTPQSSGRGGDAWHVGNDDALLETQMNQEKDITHATSFGTPLEPTAPSNDMSDSRYINSA

TQMTPRSPKREGIMPVIPAANPMTPGLNPATPGLNLSTPGLQPRTPAYMMGHIPTTPGLN

PTTPAHVSAATPGIGHEPISMEPMTPGFNPTTPGLSAMTPSLNPMTPGRNTPGYSHNPMT

PGFGAATPMGRMNLAVTPAATPGMMGGTGIPMTPAFNQDSGDLLIGGLASGEVTWKMKGV

EVEVLAGESSGSVGAIISVSSGSCSVDVDGRVVTVSFNDVRPVVPEKQDSVIILSGDEAG

SRGSLIGTDASDGIVKVDGGSEIKIYAIASLAKIAQ

>contig40720 Frame-0R

MANTFVSTPSRLTNESSPRSSNSSGEARAAPIAASRFAHRRLRVVTEPKHSNKMHRTRTL

SELILLSPRTSPRITPRHKRFDMDIEVSSFFAEGEGLVDLMGSTRRFHRLSERHMIIDEE

PTLLRRNRFVSNSQLDIMDVEQPEPEVEPMEPHHSVGDVVDMLFEIHSALKSRHLGQRTA

ASALAASNLVSTLAYP

>contig41569 Frame-0R

MGKRSPVSVAEKLLAEEVFQTNPQLKLKKRKHLGKNDENPTPSLSLKAAWMDEDDAELEL

NLEDQPQLRKLRETEKDTVVDGKELNRRLKTFHQTVHGAVSWADPKNFLSDRKIEADDSD

NEDEANLIRSTGKLLEESGELLPQGSLEVARMKDANQHAPSGAVIQSVQFHPNGQVLLTA

GLDKTLHLFHVDGSMNANVENVFVEDLPMTDAKFTLDGARVVMTGPRQYYFSYDIEAGKA

TKIPGQLGRKERKRDKVIVSDSGETLVLLGSNGYLDVLSAKSYESIGTLKMNGNVFSAAF

CENDRYLLSTGSDGQIYKWDMRTRRCVFVHDDEGSLGNHALAGSNKFYAAGSKSGVVNIY

ENAGLTAKPNPRKALLHLTTRVDCLKFNATSEILAMASTDAKDSLKMVHMPSLTVFSNWP

TAHTPLHYVSAMDFSPNSGYFAVGNARGRVLLYRLTHYKST

>contig42429 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67690.1|) 2e-37

MTEYLPELNCAYKDKDYWDTRFKSEDSYDWLARYENLAGLISKYVHPSDRILMVGCGNST

FSADMYNAGYHHITNSDFSKVVVERMSAKYS

>contig43527 Frame-0R

MVHHREEFGTSFATTVKVDVRPGGKVSRYLCLPPYAVSIFSVTSNFQHCLKSIR

>contig43835 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY58105.1|) 2e-50

MSSAKEARASGDSAAFDVYSQSDALLNALHHTGKNFLVCIKPSAALENGVLDSAYVMEQI

RENHLVELMQASQSIFTVHLTYGHFFRRYKNVCGHRGTLESLLRSLSAIG

>contig44166 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55803.1|) 5e-29

MMETGQRECHNCGQGGHIRRDCPEGPSQESGGGSYSSSATCFGCGKGGHLKRECPTSAGG

GRSCHNCGEMGHIR

>contig44302 Frame-2F

MASSWYHKRPTLQSVDHCTPTYPPSVESEGALKVRKHSNFLRRKKRRPRPPTRDAELEID

ERVEQLDLDNRRSTLSSMFRDRLTSRSSRSSSDAMETLQTLMQRDKAFHMVRHGSDPLLN

DAFYASQVQLGNYVKMGWLKKQGHMWKSWKMRFFILFSDGIIAYYKNNCRKKIKGCMQLN

DGVVSVQHVDIRVAAKAYVFQIEKGFYKLLCSCSSQIEAELWVTALRSVRKAKTPWYEMN

LTVNEEKAGLNAVTKHLNKIFITDMVVAEMLVIFKEYDDDHSYVAIHNFIVDLDDAIIDR

HHLSLYQDPEIEMLPGNELVRLIRRHVEDRVFLPLYSEAYASLETEKLKATRSKVEQNLK

VLKQKAQENFGISKDVSVCNWKQAISVINMLDCMSLPTHKHEVILFAGKAITEAIARYNG

ELFEVTDDALT

>contig45950 Frame-2F|Blast-putative chitin synthase (Chitin-UDP-GlcNac-transferase) [Phytophthora infestans T30-4](gb|EEY61714.1|) 9e-16 NOT\_ORF

MHMYRKTIGLYNEDLLTIIVPALAPSATYLSTRCSFLRKEITYPQ

>contig46674 Frame-2R|Blast-polycomb-like protein [Phytophthora infestans T30-4](gb|EEY56529.1|) 3e-28

MASGTCGEVIEELHVEQQIKKLVAEATPLIKKIHAVRANAIITNNRQRIAVYLEQRFLSL

EKVYTLVGMPLHISPLEKSAA

>contig46960 Frame-0F

MKYLRLGCLWRATASKSTNMLYFSNQSPPRARPTKQMVFKELKEVAKLTFGGIAVTTALI

ASGGFVIETVKSLNPMKPPGFMVHISGDKGQTTDVHVQQLGSGDVTVLFDGGVGQTSFDW

DKVAIDVAKYATVVTIDRPGLGFSKPVVHKRTSSQVAKEYKEILENLNIDGKVVLVGHGA

GGYNMRELAQTLINTECGVKCYGIVLVDALQENLRGELESVSVAVQKSLAEMDSNGEMVL

FLARVGLIRLINVVQHAKAKLKYSPAALSYVQYFSPSPAHREGALRENQAIPETEQRFRN

STFFKAFDFPCVVLSHGKAGMFDSMKRQPGVTPTTLVDLERKWLDAQRILAETVSKRSVH

LVIDDAGHCIHHEQPEIVTKAIRVLIDDIHDDVDENSGLLSLTNSKCRKRSMLLEG

>contig47220 Frame-1R

MLTPKELHILQATVSLAIKHTSIFQDGSATSFHPTLLLLSNCADAGPNLWLHVVYQDAMT

DKTEAGFFVSLPDGTALLYSSESSRFCSCCEVAKVSDLNNSGQKETTQCIGPVGSVNFLY

CEVNNSETRARAFHPA

>contig47255 Frame-2F

MWVRLRQCSVEVTQQRQKLSGMRLVEQDANSFSKHPQALRVKVSDRGERRKSIEPSQTLG

SRLDTALHMLLHGKRLQDMLFASHTIEVCTRYSRECCHKCVQLRISSTIFEAIRGLNRSR

PHVELLHQLLLVLKNLTRYRRSADRRNMALDDSKERLEVDLRALDTLVDLLHIHRDMHHV

FVLSATVITYYLERLRFFVDTSAEAFESWNEAEKRLTGLQELLKRKLALFNATASFRRVA

WLPETSNATNLMRKMDPKTAVATIKQLTDLVHR

>contig47570 Frame-0F|Blast-DNA polymerase epsilon catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY63268.1|) 2e-59

MVTTLFKDFLASQNKFADHLLQHFYRWVSSPDSLCFDPALYAMVKRLMEKLFLQLLAEFR

RLGAQIVYADFSKLIVCTKKESLHDAKAYMNFILQTVLSNELFQVLTFTPTKCVSNLLFL

DAENYGCVLL

>contig49730 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56227.1|) 2e-25

MRLNSMFGVADSDTFSDMDLTDLPHLMRKHDVDSGTVSSGTDLQLCADDQSIEKGDAEGI

YESRLSDLLSSIQLENVQVVEDDDSASQSSNASFHIEWQSALPKPFEGKLTQDVEHAFDK

LPSLSNLLS

>contig49745 Frame-1R

MALGSCSTHCYLGVCVSIFPVNTQVCKCCLGRVVLLGP

>contig50277 Frame-1F

MLRHDRNMISRPIRTIYSSDQLVGECLTRFEGLAISASGALEVTETSSLSTDQWTLIRGA

GLAPLLHAQCDEKKVPFIAWVMPCAEGNNVPDAIAMATQLFRSLRIDLQPTKSVASMPLS

TSPTLSFAFPHSWNQLFGRSPDVSLYL

>contig50905 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61616.1|) 9e-08

MVDYWVSKERHYCKYCNVWMQSDKP

>contig50970 Frame-2R

MKFVRAHLKFKITNAFEAHLNRLKARLMCEIQSTRESYK

>contig52284 Frame-0F

MISLPNRSLLLHSANACHQDEHILIAREEKLIRGSLFEEAMCASQLRRDLLFKTS

>contig52608 Frame-0F

MVVFAKALDAYKFSATIQKRHFCITFIRGAITSKVSVHIDACGPLAEHVGMEKDVLKRQR

SH

>contig53298 Frame-1R

MREAIESGLLASALGANLGAATMRIDALKQAEEKPPIRTPLVRALTPS

>contig54776 Frame-0R

MLIGTSTGVAGYKGKKLAAIDDAVGSAEWAKSNDSLVFDCRSAFRNTRQCLLVLSDCAML

RKNWLLLST

>contig54798 Frame-1R

MREGFESLQSFYERDTCSFSKKKRMGVELDELVQQQMQVQRLRISAWAPATPLTAHSPPQ

SSRQAAQAQPAPDAPP

>contig57139 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62683.1|) 1e-125

MIRDDNNEQSKWIGLGIIIASAVLSNLGVNVQKFSHVREAVKPMFERQTYYTRPLWLIGL

VFVVLGAVGDFEALGFAPQALVAAVGGGFTVLANVFFAHLWLGQTLTATDVLGTLLIIIG

VVLSTVANEPDEQLALVELERQFVQLGFLIYIGVMTVVLGAIFGQIAAISRLPIAWNENR

YRLLPYLYATASGIFGSYSVLLAKCASILMIRTFGGENQFVYFTTYLFMGGMVCTLVLQT

DLLNRAIMAGDTLSVFPMFQCFWI

>contig57504 Frame-1R|Blast-predicted protein [Physcomitrella patens subsp. patens]gb|EDQ80476.1| predicted protein [Physcomitrella patens subsp. patens](ref|XP\_001754506.1|) 7e-21

MDNGKTLRFRGDKTDVKYADVFSGGMGMTMVVRLTGGPGATICSPFVIFQNKDCSYPICC

VPDDVPGVSYRSAKKGLMTKKVWLEWLNKPRAQQRNFPAINMPEHKRVIYVYNYG

>contig58691 Frame-0F

MEMMEIVDKRSFRLGCNYFGIGICRASLESFDLV

>contig07568 Frame-0R

MLGLNKRGYLLEKANWLMSESKSMTIVEQAAPPTPGPQEIIVL

>contig08060 Frame-2F

MLLAIRPRKRHGLALTSSLIGKNGERFFELFSSGRSNKDKHNPTTLPSHVKFRMPDLNFK

EVGSGDEEIKLTKWYVREGATVKDGTHMCEIDTPDLSFQLESGDEGFVAQL

>contig12197 Frame-1F|Blast-endomembrane protein 70-like protein, putative [Phytophthora infestans T30-4](gb|EEY69817.1|) 0.0

MPGYGPRIVAVTTAALAALRTQGFLLPGVQMTTYSKGEVLPIFVNSLKSTETLLPLDYYK

LPFCQPEKIEYKSENLGEYLTANRIQNSPYEIKFLEEQTCAVLCKQEYTDFEVQTWDDKI

KASYRVNWILDNLPATSVSSEGGLTVGFPLGSFHPDVEVVPQLNNHVKILIGYNNHPLGT

NADGSKEKGRIVDFHVIPSSFEYADKSYDKIKNRMDSCAHSSDLKQPLYVRKNKDGYMVV

YWTYSIEWVLDNDHDWRTRWDVYFDAGSGGDEVHWFSIVNALVIVLFLSGMVGMILMRSL

HRDINRYNRIPTEEERAEEREESGWKLVHADVFRPPTKQPLLFCVVIGTGCQLLGMAFVT

LFFAALGVLAPSNRGKLVIALLVCFVLLGTLAGYTSARMYKMFQGKRWQLCTILTAVLFP

GSLFALFFVLNLFTWGAGSDAAVPFGSIGVVFFLWTGISVPLVFFGAYYGFRYEPHAFPV

ATSNIPRPIPSQPWYMTHVAAALVGGILPFGAIFVELLFRTLGYGQTSITTFLAFYCLHF

SF

>contig13099 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65035.1|) 3e-18

MISYSADFKVSKVPTAPVALQVASKKAVNDASKKVSGTREFATEIRTRLEPLMGYGWHII

VGKDFAVDLR

>contig13604 Frame-0F|Blast-mannosyl-oligosaccharide glucosidase, putative [Phytophthora infestans T30-4](gb|EEY67498.1|) 0.0

MEEDGYIAREQILGQVARRQVPSEFLVQHVEHANPPSLLLALEKMLLWREKTDTDDELKT

FVRTIFPFLKRWYRWLLKTQQGPKDASFCWRGRRLNDGKLLSNTLSSGLDDYPRASHPSE

NEMHVDLLSWMICSSNIMAKLADLIGSETDVQLFQSNRAFFLDGLDLHHWNEKAQSYFDV

GEHSEDGKIEYQVAVRCRNDQGQAIDATASVAQMKAREVKCPDTHPNFMFPLGDGSGGLQ

LLPVFIPGVTKLQHVQHIGYISIFPLLLKVLPPDSPKLLALLKQMIDPLQLWSPYGLRSL

STLDQFYEQENAPGDNPYWRGAIWMNANYLALDALHYYAQSSTGSPFQAEFAAAYTKLRT

NVIANVYREFERTGYLWEQYNGDIHARHKYGQGQRCHPFSGWTALVLNIMAE

>contig14238 Frame-1F

MANPEHDHAHDHDHAHDHDHDHHHEDADSDDEIPGLEEAPDATDAEKGKHNRSEKKSRKA

MQKLGMKAIGGIIRVTIKKNKNVLFVISKPDVFKSTVSETYVIFGEAKIEDLSAQAQSMA

AQQFKAPATEAPAIDVSEAPGFGGEDDNVDVDESGIDAKDIQLVMSQAGVSKNKAISALR

SNDNDIVNAIMELTM

>contig16852 Frame-2F|Blast-aldo/keto reductase family [Phytophthora infestans T30-4](gb|EEY63915.1|) 2e-81

MSAVIRTKTLPSGAKIPVVGLGVFLSKPGPETYNAVLAALEMGYRHIDTAQYYRNEVDVG

RAIRDSKIPRNEIFVTSKVFTEPWVYEEVLKETKASNERLNLGYIDLYLLHAPCDPTTRP

DAWRALEELQAEGIVKDIGVSNFGVDHLEKLAETAKVKPAVNQVELHPWLMRPALVQYCK

DHGIFLEAYSPLVKAIKLHDPTLVEIAEEVGGTTAQVLVAFSLANDFITLPKSVNPVRLR

ENLDAASVQLKSEHVAKLAALDEYLVTGWDPIKQHAV

>contig17284 Frame-1F

MAGKQTSGDLAARPLVDASSVRLTSLRTSTDASIAPARKPKFVPKAVKRRPVEVNEKITS

ISSQRIHDTKTRPTGAGGLKSDNRERGGRGYRGGGRGRGRGRGRGIFASGKVSFVGTLSG

GSSFSGGGSTSAPRSMPSTDYSAAGGTGISVLDEELLGKNMPDIDVEEVWPPVIKSIMEP

MSLPIVRPPEPEKAGAVFCDAAGDLLVSDDSLFFFQMPTTLPLSRTVLKSRNSTDSTAED

ESVQSLEVSKEQAQKLEDGVNPDEIS

>contig17662 Frame-2F

MQKMGVGLDEKLNEASLSLFRHTTAIRADEIDSDEDGSEEEENIEEEEDDKDGEPNSGNP

TEAIVQDINGRTRRRAIFAESDGPLNSVNNEDHTDSDDDDQDDTSEEEQDEITGEQSQLR

WKETMVSRAAANFLERERSDVNLMELVYGKRQKLFKTDHDLEEEESKSDKNLQVQPSENE

DDAFFTLKLQTNSMGELSSASEKYNLINAIDCSRSNVGTNDRKDWTIPDVLESIRNRFVT

GTWKRVQRNDDVNSDEEDNGAIDPTNDDEMHGSFEDLETGEVQNGAVDVAAKGNCSDDHE

IGKNETDEQIRERLRAQKSVKRTVDEDDDVMVGGQKKVEDDEEMTEVMIEAKRLREEQAQ

RNAEEFGEEGEDMRLQLEGFRNGLYVRIEFSKIPAEFVRYYDPKNPIVVGGLPTIEDSLG

LVRMRFKKHRWHRKILKTNDPLVFSIGWRRFQSLPLYSIEDTNERHRYLKYTPEHMHCHA

TIFGPMCPPNTGVLAFQTLSTNAEGFRVSGTGVVLELDHKFSVVKKLKLIGTPSKIHKNT

AFIKGMFNTELEVAKFEGASISTVSGVRGRIKKALRGEKGDFRATFEDKILKSDLIFCRT

WVPVDPKQLYNPITSLLTNAKGSRKSSLGLMKTTYELRKEQKLAVPVNPDSLYKPIVRTE

RKFQAFKVPKKLQANLPFASKPKEDKKKGANKGYLTTRAVVLEPEEKKKYGFMLRVNTVR

RDREATRKLRQSQRNAENLKRKQREEKQFEGVHKAEKKAKYRAEGKDAAYRALKASTS

>contig18739 Frame-2R|Blast-NADH dehydrogenase [Phytophthora infestans](gb|AAN31478.1|) 9e-96

MSDTFFLSDVFRATWLAWEVHVERKVTINYPYEKGMLSPRFRGEHALRRYPSGEERCIAC

KLCESVCPAQAITIEAETRADGARRTTRYDIDMTKCIYCGFCQEACPVDAIVEGPNFEFA

TETHEELLYDKAKLLANGDKWEFEIAKNLSVEQLFR

>contig19185 Frame-2R|Blast-signal recognition particle, putative [Phytophthora infestans T30-4](gb|EEY60935.1|) 0.0

MVLAELGSKLQDALAKMNRTTVVDDEVFNVLLKEICGALLESDVQVKLVRQLRDNVKLAV

KLEDASSGMNRRRLIQKSIVDQLVQMLEPEAPPYKMKKGQSNVIMFVGLQGSGKTTSIAK

LAYFYQRKGWKTCMVCADTFRAGAFDQLKQNSTKLRIPFYGSYTEADPVRIAEEGVAQFR

AENYELILVDTSGRHKQEADLFAEMKEVSAAVQPDDVVFVMDSTIGQAVYDQARAFRDTV

NVGSVIITKLDGHAKGGGALSAVAATGSPIIFYGTGEHFMDFESFNAASFVSRLMGMGDI

RGLMEEVKTSGLFENQEELVEKFQKGVFTLRDMYKQFQSVMKMGPLGKVMSMIPGLPQGM

NDMMNAGGGEEEASKRLRRFLYMMDSMTDAELDGIVPLSESRQMRVARGSGCQMLEIDFL

LKCHKQFSSVVSRMGKSGLMKANDATLGKQMARNPNAVMQQLSKVIDPKMMAQIGGPQSM

MRIMKQMQGMDPSQLGDMTKMAQGMGLKMPF

>contig21205 Frame-0F

MPVKVATSCDASLPQQIDTKAGIDAWLLQKLRMEWSSHELGGLLTPSKLAEARASFMHLE

TPIKIRLLLSLISTRLNEANGAALKTEVDSLLQLSDEDAEEWVKVSTGIVKQFLLLKCNG

QSTDSYLHAQLEATSSKVVQAVAFSFKKHLRNSMSNVVVDDTFSLENGLLNSSLCPQSAP

SAAVHFTVIGEDEDANAKEDDVAASPVKKSLHRPLMARPAGALASSSTSSSLASSRMTSA

SKLSVGKTKNLMEMSSEIRRKADAGRFKRQRSRISMIDINEVKQIESEKAHKAEERKKQK

LAAKEKEKEEKAKEKEKEKSGAAVANLVTNAGDKAGAVTGFVAPIGANDEHVALAADIFA

MHYQSGLDESIPQYTQQQQLHSEAMTEVGDQNLSGDKYVPDGTQALLNAAFHSTQDIMKE

VVTQQNHQLSDNQLLQQQQMPQSLYQDLYRSQQPMHMHHLVSPQQQYHQGFETEDATLNS

T

>contig22136 Frame-1R|Blast-alcohol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY62160.1|) 2e-98

MAIKVPHPVPEVLPLIVSGSSASIALEQVGKMKSNETVLVTAAAGGTGQFVVQLAKLAGN

HVIGTTSSDTKAALLKSIGCDRVINYNTENVNHVLKEEYPDGVNLVFESVGGDMLQTAVN

NVAIKGRIIAFGYISCYHGEKKNFTATELVSILLKKSALLQGFFSSHYHDCYHRHMQQLL

KLIEDKQLVPGIDSIKYEGLSSIPDAVDHMYSRKNMGKIVVKLA

>contig22709 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65902.1|) 3e-30

MQQKLEEGQSSSVRVVVDLAFAPYETVRERHSLFKQLGGVYGYLKTCPLDRLISLTLVSC

TQDIADISAQHGVPSWK

>contig23254 Frame-0F

MTEYCPSTGSVLAKNSGSVTKANTDERDNPKESELICVKECERLATLAKRMITSLLEATD

LLGGIPWELVHEKHGVSLFRADAATNVPCNVHAVSRFTCNIEDVAASLITPTTASFKQMM

AMLSSDFVDGAVVHNIIMPTPAAPHRHVALKWAAFKSSGPFAKDRDLLMLEYVDMIEDVQ

GQRTAFRIMESIDTPVGLSAFAESPKYTRDLVPLIGFMYHSTKRSGELRMTYTCNFDKNG

DLPAWVANSAIQSHVEKCINGILKYTESFRVGREEIVLPQNVVPMGEQDHCRICSKKFCV

RRRRYNCLKCGDVCCSSCSSVRSTHVPEIGERQLRVCTACVIKARELSRYNKSSLEQSRA

PSLSSKSTNWLLDDKNRILGRAQSFSVSTRDTEQEITKRRSYDDLLDPVRCRLIEYKAFS

SGSCEGATANSAMGVPKANFPGRSFSDGLVMRNKALFSAKRRGSPADLAISIEAFRLHQS

RMGNTERQPEDGSDDIDNHTDDESTTSSSSGSPTFSMKRRPFAFGPMHTAHSCIHGNTES

NRDDNEGFEGAMARAKNIIIAANYANGLAQQARKLSHNRAMALQQGQEDSASTCQKNSDI

DKDFYDETEANSRNRHCHYGSDFETAGAVLFTLDDAV

>contig25559 Frame-2R

MPIVAWAVEPYMYSKCYSTTCTSLLPLQNATPVPHLLEI

>contig25924 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65651.1|) 1e-109

MNRVVQLPLSANAPPILENYTLGDVLICKANRGKLLEVEHLVKALHADVNYRNQHGCSAL

HGAAASGQLEMVQWMGKQVTVDWSAMDHDDQTALHYAAFYGHLEVVQYLVENGAPLDAPD

KFGRLAHCSAAINGHLDVVSYLLEECLSPIDINAVDEYGGTCLHWAASKGRKEVIQYLCM

KGIDIHITSYDNKTAYQIAKDKHKQKCVQFLKNWYETA

>contig26561 Frame-0F

MTSDDEFSRYKCVKLILEKVETVSWQDSLNCQMFRTKPACVIQFKESVHCSLDAF

>contig26899 Frame-2F

MKLPSGFGCETANDEAAAATANGSTADNIETCANGILRPVSRSQEYHNLPMAVAVPVSAS

NPSNATQHRKTAHNFSFRSLTGYKFIRLADYSGKPILIVNVASHCNSTTKAYMQLNELAK

RFPELVIIGCPCNQFGHQENLNGEEIYQSLRHIRPGKGFEPAFDLTEKTEVNGANAHALF

NFLRITLPYPCDRTLLDEMSAPSGVFSHPMRLIWMPVTRADVSWNFEKFLISPDGTPYKR

YSPKLDFTGLIEDIKFLCNVKLANHQEL

>contig27997 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63715.1|) 3e-95

MKTIERAHTPNRLWERVKLSRNYTKSLAQIDEQLQFWPKKLIYKNKQRLTKIHQYLMRMR

KLTLKTKPKLVVINKKIDRREKRREKKAMVAAKLDNSIEKELLERLQKGTYGDIYNFPER

EFSKVLADKGKRQTMEEESEGEEEIEYEIDEDEEEEDEVSGQVEYVEDFDEEESDLEDFA

DNFAVDDEGDSNESGSEDVDVPHVKKRQAPALPKKPRKKQKRPKGPYVEIEYEQEQETT

>contig29173 Frame-0F

MTYSLTNLFFFALSENASAPIYHLRSFCAI

>contig29779 Frame-0R

MTMYCLVRLVAVVKLFVLSWQCCDYGRNWKEQIRAG

>contig29928 Frame-2R

MRRVLTKHDEADALGTQLQENQYEKICGLKEEYGVFSNLIPENIEAVTLVANVSRKGRFK

SRLRSTTAR

>contig30203 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63907.1|) 4e-38

MLRSQVAKVATSRRLVRCFASDVKEEVAKAISTPAPIVVKKGGSSFMQRILSFGVGVAVG

ASYGLYVLSEDVEKSTQQIQKSVESLKEDMVAQNEALQKRLEALEK

>contig30319 Frame-1F

MDVPPLWLRSGWDFDVTPCVVCDKFFHLLMNRRQQLGKREK

>contig31082 Frame-0F

MTRSAVQTRTHAQKYLSKFAGRFPFDTDGMLKDHSLASTHSKNGIKCNKPNASTLSPTTS

LSSSSTAMTPASDDCASNKSWNVEEDHCIPKPGESMAMILNSPSTGALVLPTIFDQEDAA

AFPDFVQQD

>contig31301 Frame-0R

MSTSVARDEEPTSVRSTTTASTLSPSTAAVASPPLPTNHISPSKPSLDTSSATRVSGGND

NGMSRGNSDRSSPMPLVGLRAIPSGSMSLSQATTTTTTTSTRAPSLAPPSQSGGTHVATT

SAGLATKAGNNRRHLYPSQSFSSNYAGTFSPVQLPPPYHGSDAGRGTTTSSSSYNHPQLS

PGSSPSLHDHAWVGPRGLKRHLPLVYDHMNNRTNGNGPNTHVLEHRPLVSNATSSSGTQS

TVRRGPSSLSSSRSTPLLDSTYAKTSKEDPRQYEPIGEARYPRDSTRYETWTSKQLR

>contig32256 Frame-0F

MRGLMLKMEQTNEDRSTVSVVNRSPPRTVVKPTSPSSSSSSSCRSNYSAMGNRNRSVSLN

TQSSAPPCKKQRASFDEYEQATLSTLPPPKTTSYCQIDVVQEECATSEARDQISDETDAP

DIEDDHVDGFTVSNCVPPVQDDIDSSSDECDVDEVAFMNWLLDQKTAGMPAGQMLDALGL

GVSEGVAVDDDELWEAMFSMGIRLIKPTATRPREKLDTVNTLQDVASLLRSSKKIVVLAG

AGISVSCGIPDFRSENGIYS

>contig32573 Frame-0R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY53211.1|) 1e-150

MIISYGVSIAVVSSVVNALCDPLRKYLTKFMDPFMIVALRGLIQAPLFVLWAIVDSEGRL

PPLNHLFWTSVCISGCINIITSYLYNRAIQISTLSATVPFLSFTPAFLVVVAFLVLGEVP

TVSGTLGISIAVMGGIWLQGAKDEHASKELLVDTSSASKGSMYMVLVAFLWSISNAFDKI

GVQNSTPLIYGAMIQVIVAGGSYILQKMRFGGADLYLPIGQEVQIPWRYVVLAGVTSVVG

YYINLVAMQHLEISYVIAIKRSGCIWSVVMGRFLFRERNLRKKVPSILLMVFGVVCIVVG

KK

>contig32829 Frame-2R

MRLIIFQSTIVGLCVFGVALCTAKHMSGLVKCAIQSKLLTTTNISSRLHCFSRSSQGGIW

VLSIFSLQSSSFKDRTPFRHFEPIARFIERLLHSPPPHPASKMRTPKGLISKKPSRQKTC

LLQHSMSLWPTSHPRKLQLP

>contig33916 Frame-1F

MSKRTVVKWSPHDASLFAVGADNLRLFEVTTSSSLNHDYVDAVSEAAALTTQRKRAFRVV

RINAKVSQLKCLQWYPFETKPLLIATGTQSGKVFLCDFEDPRARVMREFLPKYSRPCHTV

AWNPSVSNQLAAGFEKVRSDFCTFVWDLNTSNAVGTAAGGQSVTGSSSASNIEGHVDQDG

GMERALNNRKGGNTGGGTASVGVGAGGNQFAPTDSKPVYELANSEATLALSWVPVQPTCL

ATGTGFKWLRIYDLRAKGSSPMSVVAHHKAVLGVVFDHHRPHMLATYSDAPQEPVKVWDI

RQLESSSGPIVSLYHTSRSLAQVSWCPSKPGILVTASNEEKWVSLWDITKPESGSSMLKK

PSRRRYTSEPLTSFSWQHIDLQRSRTTKGSNRKCTKKHELMAAAFPNRLLTASITGELGD

LSVHDAMPLSLSS

>contig35198 Frame-2R|Blast-pyruvate dehydrogenase kinase-like protein [Phytophthora infestans T30-4](gb|EEY57776.1|) 1e-159

MAKGVHELKMELFKSFTEKDSATTKKELGKRYLRSQEFADLSDLHSFLDAFYMSRIGIRM

LMSQHIALHEQEDGWVGCICESTSPAEIALAAIDTARHMCLRQYGDAPEVELHGHTDFSM

PFVPSHLHHMLFEVIKNSMRAVVEFHGLDTNMPPIKIVIADGEDNEDVSIKISDEGGGIP

RSSVSRIWSYLYTTADSEAFERLEAPNDFGGDSPLAGLGYGLPISRLFARYFGGDLQVIS

MEGYGTDAYLHLKRVGDASEPLP

>contig35723 Frame-1F

MTNSSAMPAKKSVCYLQELPLTRSTTEQRLDALRHRSVPKITGRKHRIPRKFVITDLLDS

SQHNRDDEGDDNSSANEVYSEDLSASSSSVRKGKTQVRGRFTITDLTPESPEALAEREDL

SVSMGATPLRAMNISRRQSSRKLSTRRPFQSAGDVRSSVGLKKGLLSQKQYPSQQESPAF

ASFQPIATDSARVVLPAQHAVFDHHLEYLEKETYEMRSVLESMVATNAQWIETLASAGLL

QAKSLPRSSGEPSIEQMAPDETLLQSRYRAIEKAYTELQANYETVCVKTERLEVKNAMLE

IRLQQQIDRSTMLRSQLDKLTQYTENLIVESSEPTLHDYSSDLNSILDEHSESHSPSADE

MTNGNGYGFTYNVVKSQQNRWDGVEEECISDTSTEGCSTRKTMSPPTSDEDNSRYCCEIE

LNATELTSSNNCGRNCDLDLMLDAQCSQLRQSLRLEDRADDVSLIESLDSMAGCPSVTKL

DSNGDDEYDGNSHIGRSDRQHLCQKSRFLKHSNSLASLNYSTVSSTSSLAGYGLHLATMA

QSKPGFFANAATSTLYGPHPESYPNVSTQQNAPQDDNTYNVLSSENLHFHDYQSLLQVAA

ERSVENVATQREFPFTISKKTTSLPGANEVSEKTRATGSLLQRLTVRRW

>contig35756 Frame-1F|Blast-scavenger mRNA-decapping enzyme DcpS, putative [Phytophthora infestans T30-4](gb|EEY57723.1|) 4e-36

MYFHYQPTYYHLHVHITHVKMTLGTFVGKAVLLEDVIYNLSVNSDHYRNATLSFVIGMMQ

HKQLLDLFHDNHIV

>contig36018 Frame-2F

MLAPWKCDQRVRSWTRWRRWLHAHRSFLCQFVLINVVCLATLKGWQSYQLYNRDLRWNLP

PMLSQGLHAFTLSLWRETQRFDPESPRGIVLPLYDDIAYLGISLILELRRLQVPLPIEIP

HCGDLRLEFQQEILMHDPDVTFYDACKRAANASTIDRPLFCADLRQCHSKFRDFNIKVLA

LVYSKFQEIMLLDADTLFFKSPMPLWDS

>contig36524 Frame-2F

MKAEDTALHYILALEHKQAALEALQHQLDDERHKSNLALSAVQEKLSHAVSEASKLSNEK

DQVNCEYASAFQQIESLQIIINTHEKEKAMLFSENQSISECLEELRDRSSGMENQCAELH

KLCDRQQAQLSTSAESIKTFTEKIEELQQLIKKQSHEGNELRNDLATAKEDCRQAAIIQA

AQLADLSSRAIKIKELMEELEANMNTIEGLTKKHNKAEGVIRDLQSAALRQQEGLKMYQG

IQFTLRDELKSLEFERLELVENLKVEQESSLDVKEKFAEAKNTWLEESQRFQKEVLALQK

RADTLSRLKMTLSSRMQELKLENENFKTVVAEKESHVQKLIDCVTDMEANIHALKASIGN

SGIIQEQLNDTVAELRSCISNLNSQLTEQQKTISKQGKELTEKLTVITGQDEMIATLKQR

LLQNETKLDQKCGDYKAELNASSGRVQDRVQLIAEKAAFAKVEEQMAEKDALNEKGEERE

TGAQQSEQLMQEIKQVEETDANLLHVTNLVVDSETTIARSVEDASSANVQGLQIALKDLQ

AKYLSAISEKAKLEEQKKQLKSYRDGAVTAQERSRSFKKTPVPQLTTATLKKAKTIAITQ

DVLVQAKRNFLAEKMKLQREIKALSKKLEMMSNEKEKLVGHQNSRQKIQHHARVKEENNR

LLEQVRQLSDDKFKLQRSLERVRLMLTEKENIDVESSSNTPLLVSPASSDLCKTSMPQQV

EQTNFERAPKATAIKAAKLTARDQPISRSVSPGPRRKRARTPAGPGWQK

>contig36591 Frame-1R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY61268.1|) 0.0

MSDLQMVTGAKCFVPDETHVWLAAEVTRDENSGDGKTRKIYCKVELPNGKLEERCVDMLS

KKTKALLAVHQLESLPYQNENVGSEGIEDMITLNYLHEAAILYNVKKRFLCELPYTYTGD

ICIAVNPYKWLPDLYAEEQHMRYLNQPKEELPPHVYATSVAAYEGMRCSEINQSILVSGE

SGAGKTETTKILMNHLATIAGGLNNSTIKKIIEVNPLLESFGNAKTVRNDNSSRFGKFTQ

LQFDLNGTLVGAKCRTYLLEKTRVIQHEAPERNYHIFYQLIDSSDVASELQLDPSKHYAY

TGNNTAQKIEGLSDEKHFNKTREALELVGLSYDDQQPLFEVLAGVLHLGEVQLLSDPTDD

EKSLISESDDGAQSTTQMLGVTWEALQTALCSRTMRAVNDVYSVPLKKELAMDCRDALAK

AIYSNVFDWLVTTINQSLADDANMANHVGVLDIFGFEHFKHNSFEQFCINFANEKLQQKF

TQDVFKTVQIEYEEEGIVWDHIEYADNQDVLNVIESRMGIISLLNEEVMRPKGNEESFMS

KVTSLHKEDMAHVIEFPRTSRTEFLIKHYAAPVMYDSVGFLEKHKDSLLPDLSELMRGSD

KPFIAKLFEPKEDPTQAVLEASGGRRKRGGALSITTVGTQFKESLTELMANINSTHVHYV

RCIKPNPIKSATVMDQSMVVSQLRCAGVIEAIRISRAAYPNRLQHTEILNKFWLFVPSGG

NTVEEKCQLLMDKLKLETPRQYQMGKTRVYFQLGVLEELEDRRKKFLDAKATFLQYTMVG

FTQRIKYLRKLEAIIKLQSVIRCVIAMRRYNTFLKGLILAQAQWRGIQGRKVAADVKCNH

YAVIIQRYMRGLVKRHRYVKMRAMVIRVQSMVRMMIQRPKYLAALDEKRREADMAYQLHK

LKAALQDEQERNAQLQRRNSVTTADSSAASSVVMADAGGMIETLTDENKKLREKNEVMKV

SMKALKAEVEKFKSDKEVSSAGNHVKLRQLQDTVREKDKRIVQLEADNKKLTEQIAKLHA

DGIVPEIKATPKKSIFRTLGSKKETKPRETVLMDSLTGSDDLNGRSSETRQSERHFPRMP

SMSVGTRFWNTNKKIENGDGHDVSEVDGEDSPTNSSTTRNTIVKSMEVGVTGAMSSIKGR

MSVVKGMYDSRSKRTNSKPEEVANKPENNALVTTASSKSAKVKPAAKPADRPVRESFNLD

ALPEVSLPVGWEAKVSRSTGRVYYVNRKHGKSQFERPTLASLKAQKLARQKSGSAD

>contig40006 Frame-1F

MEEFDRAQSQAMELLIQQCIRDENEYPSALPADPGPAAANATILDLLAQTCADANAAAQE

LSVAEVATALASAVFSTQKSLRSVGKNVNAIMQDPEQMHELCCHVKQADAKVFKAFQESQ

LLLEGQADSVNKAKQLAVSETADSMTFVVSSDEETVRNMMGFAEKMCFTMDHALSTITQD

ELALAAQLSLTITQKLLHAGQSLFTSLGDEERRKARRSHITVEEIEEELEELDQDKRKLV

ENKGQMKRAAVLRMYVEDLYYQTRAKAVDHPFVAGILTAAGLPFIGLAIPVASLVALALL

IEKYYPEHAKLTVELCSNFI

>contig40723 Frame-2F

MQTRFKLQPTALLEDLGQDTFPSLISMLNLAALTPAFIKNVVYALGKLNVGVYKYVSMGA

AGFTVAAVVIYFGFDEVLSIGQLFNSLTARVAAEVISLYAYALGLLYALTKLFSLLQRFV

LAPIVSNLNKVTTGLKLRSWMIIIIVHFVVQLVGRIKGPSSMDFINMLGLLVVASFIVFV

LHLLALGGNIEGPSDQQHMQHSVFALLLLSIFPWVGKVVYFLGIAQSPLSELSNNLLIEG

GSCVVFLSMFTYLISLSLDCMIPLPPTAFFGATSDQDSALVYENSSKKSSSCEKITAENC

PKCIFEDGGPGSIMIEFTTRATRQVVAAKSGDVVYVGPTFRVVACDCVYRFKNLRDFCGF

CIRSCRICGGGNGNFQEAAKYKDFLQDNKVESVMHALVPIIFQMSAAIQATYGLYRAYLS

YYFTIVCVLALLFYHVVLRHPIEAKRIKNKQHKKAKKRK

>contig40756-0 Frame-0F0

MASSFSSKITNVWKGAMAKYKKMLEIGYARHAADGMSVDDLEQTIRNGLMGTSTMWLSGG

MKRSLDWYSDFCVRNQYFHLLRKTDERFVPLSREAASAAETAKKAGLNAAQAARLKTGEE

EAARLAAQGGARKVVGETEELNSAETVVARREADKVGNDAIDAKAAEAAKEEAAKAAK

>contig40756-1 Frame-2R1

MVEVPIRPLRIVCSRSSTLIPSAACRAYPISNIFLYFAMAPFQTFVIFDEKELAIRFNGA

AKLSALGAPRRRTL

>contig40828 Frame-2F

MDMQSLFYQSSPSTGTGAAPSCSLLSSSVPIGSTFPTSSNLSAASFPSMQSHPAIFAHSV

GLSSTPFLQPPTLAPLRFIIPNPRASNSFGLTASSQSFSRLSVCNIVGEPEHEPLPQYSM

TLPRDRCTIETKQQQLFPSGSGMLDESNQPNKMTFKRTRLPKRSIRSTKSKARPGLRKGK

WTEEESSYATQLTCYFKEGLLPLKKGTMLRLYLSQKLNCEPMRITKKFTGEECIGKQVFR

PCNPTPESRARLLTAQLELVVLKAAFVQRLKDNHEDPPAPMDELDAFSASFDCKFQPVQL

KPRLSEDGKDGDGHAVGLLLDFFYKANRNEKQGENSAFELKNDNTIEVNKYGNTCTVKRL

SSISTSPTSNCEIDSANSPTKRMRTLSVSGCIDPGATKRSRIGSFSTITAA

>contig42088 Frame-2R|Blast-cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|EEY66756.1|) 2e-50

MRLKRGAGFSRSGTCGIGGPQSVYPKL

>contig42347 Frame-1F

MGGRGHRLDLENDSNPEYAESPVDSPVASDTVLLFTEDSGAVGGNCTKVEPPNSAPGLLT

PSLAPHAHIPSLQLPEPVLVPQTSLVRRASIHGPSAAAAVAAALADAGSQLP

>contig43836 Frame-2R

MLTFLHCAARLSLYRPQTYRPFASASLRGCMPMLALPLPIKSIRRIPLTALRGLKTSVPI

LKDPLLDDRETIRLKDLDNARIHDKPFFIKKKDPTLSEPELRTDINKAYFPGKVYRSTSR

DVVFRAMAGNTAITMLKLLAWLKTGSSAMLSEAIHSLVDTGNQAILILGLKQASGVPDKK

HQYGYGR

>contig43843 Frame-0R

MSNAQSRGLCYVHGGGGRCQREGCGSSAKKGGFCIAHGGGHRCEVTGCTSSAVSGSRCRA

HGGGRRCAVENCTSSAKTGGRCIAHGGGKRCTVNGCTSSAQRLGLCKAHGGGRRCIVDNC

ANSAVSRSRCIAHGGGKRCVFEGCSTTARRGGFCFAHGGRSTPSIACTRTKLPSPSSTFQ

TTPASVSPRSLPWSLTKERSIPALTLPPRRLLPPINVMLTANRPGIRRRSSPVPPIRKPV

LSFERKDQLSRRSFDESRRSPSQAWHCSKPAYLNFQDR

>contig44082 Frame-0F

MTEAVLYSSRRLLEAMPFLRGEIGLLTNEAMTKEQQTSVCRCMSRIACSLAIHHGRALFE

HQISTTIAHFGSDKQMHFSIEFLEFLLACSSYDDIDVVQPTLEIWFFFLDNYSFQSKVKC

QHLHATQNERVLSILSRLVSSLIDRCKYPQWFIQRQQLVSDDPDIEAITDLRREIADTLL

SLFSKWPGGLGKPAGDYVSCVKEMCLLLSDSKDIAQIDALLFLLSYMVELFDAVSSDSEP

EDDVHSIQKPEFCGMSVLLGILDCAANLPMHPLVINGVARYLRSLSTSHALQSNVYLRFS

IIISQGLQYPSSFSLAAQSLLRCSTHLSLVRYKLWHFTCNKLCLQCPGIILQLKKERL

>contig44165 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55803.1|) 4e-30

MMETGQRECHNCGQGGHIRRDCPEGPSQESGGGSYNSGATCFGCGKGGHLKRECPTSAGG

GRACHNCGGMGHIR

>contig44301 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59853.1|) 1e-10

MHEVTSGTSAYQNATAQRAAACTQVAIVGAGFLGKCIAIDLSLLGAQ

>contig44451 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60991.1|) 1e-107

MQSPLLLVLAPVGLLLGVPLGVMKEKLQKHSLKRRCLTLAPFALVSMLSLQSACILTGSY

LIGREMGASLVGVGLTGGISTGKSTVSKALREAGAVIIDADLIARQVVVPGRGAYKEIVR

YFGSQVLNEENASINRAKLGAIVFNDPMQRKKLNMLTHKYIIWEMFKQLVYQRLVCRKRL

VVLDAPLLFETKLLEYFCYPTIVVACSTKNELSRLMQRDKMTQKDAEKRIQSQMNLQDKV

AKADFVIYNDDSMNNLLLRTRKTLMLVASLV

>contig44958 Frame-1F|Blast-short chain dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY53420.1|) 1e-100

MAAKTVLITGSNRGIGLAFATHYKKEGWKVIGSARDIDGATELKKLEPWKLVTMDISSEE

SINAARKALENVPVHLLINNAGIADVKNLQSTSKADLLRHYEVNAVGPFLVTRAMLPNLR

LAVKDQGSATVAQVSSRMGSIMDNSSGGRYGYRASKAALNMITKSLAVDLEKEKICCLLL

HPGFVSTAMVNFQGNVSSSDSVKGMSKIIASAKLEDSAKMFHFDTGDVLPW

>contig45203 Frame-1R

MPLCRGKRRRDTATIGISQKKVARTALLKQNSAHIDKLP

>contig45276 Frame-1R|Blast-PREDICTED: hypothetical protein [Vitis vinifera]emb|CBI15986.3| unnamed protein product [Vitis vinifera](ref|XP\_002279568.1|) 8e-99

MAARERLCIAMCCDFFYPRLGGVEMHMWSLAQCLLQRGHKVIVLTHAVRGPSKAQTPTRR

SGVRYMTHGLKVYYLPIVPLVDNVTYLTFVNNLALFRTICIRERVQIVHGHQAASTFMHE

CLLQAKTLGLGIKTVYTDHSLYGFADAASVHLNKVIKFTLSTVDAAIGVSHTCRENLVLR

ASLAPEKVATIPNAVDTSKFTPWVTCQPNGYITVVIISRLVYRKGIDLVARAIPLVCLQN

PRVRFLIGGDGTKRLLLEEMREKYRLHDRVTLCGAVPHAHVRALLCQGHIFLNSSLTESF

CIAILEAAACGLFVVSTRVGG

>contig45953 Frame-0F

MVKIRGYSVVLGAVESALAQHPLVSTSVVLTEGDEGEDKRLIAYIVPEDWDKVPSASNLR

EFLNVKLPHYAIPSVFVQLNVLPINSASGKLDRKLMPSLEKAKKLRNESIDQSIEPKNLP

QTETEKKLALLWMDLLRLEHDNNLHRKASFFDVGGHSLLSTRLISSIRDTFGIQLTLADI

LSSPELCAIASHIDHLLLQCTNDTQSD

>contig47379 Frame-0R

MYLQFVISRPARLLAALYTVLGSSLVSRLVVSAFYSSTSRNPVGGDECFCLHEKRILKFA

LSLSTGNALFSSAQLMPGQNCHYCFESMSEPAATIIESLHNIVTVMYFIPRKCLDTKVSN

>contig47573 Frame-1R|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY68210.1|) 6e-47

MSATERLNNVARSYLMAFFVCWGSLILLTALKVSELSSVPLIAFFALQSVYDVLGVCFAV

ITLTNFHRCRKAFDFGLSLKAIDPSSIEFDDPVTIAGEGTFAV

>contig48107 Frame-0F|Blast-U3 small nucleolar RNA-associated protein, putative [Phytophthora infestans T30-4](gb|EEY64264.1|) 5e-58

MIDMFDTLVPLKIWVVAVLKSCRDAIAHLPNAVIGADKASALLEFLVALSRAEQARQWIP

EPLILTVISCLTVGQSSSCATSTTSRGIAPQILDLIIQFLDSLLDGDERLLSLRDQTEPV

TVSGQHDKLLLIPQISFVLEQFIQRFQAK

>contig49746 Frame-0F

MSASASQAETQTAGRVCSYAISSLAETKDTLILVCIGLLEALDRLQERLRLPTSIVKKLK

HRLARMVTRSSVRIKTKCLNDQELGDTVAECHLWNGAKPKDVEGVVHWMLAIFTSFQRIV

ISTTLGLCQGIYVLIMSLPGISTTCSLFNGLLQAVEDTLRLSSEEIMEAASAGGSRSESG

RSRSNYHLYHQHHRNAVSSKADENLTAVVLEYKEKECMVPTNIDRRIRRVMHFPIPLHAF

EATVRLPSGNVHAASSSSCQNRVQEENKTNFAHLSSSSPRSIPVSPMARKRVQLAFSNFS

DDVLYRARDRLRQERAATLMGDRSLCVPRFNVHDCHEDIYLSCGRHCASKLGTGMYRSVR

GSVPLQKNRFVYFEMTMQRGRTPIRGTNQSITRLETSTQAIFGSSSLFGG

>contig50429 Frame-2F|Blast-thymidylate kinase [Phytophthora infestans T30-4](gb|EEY63738.1|) 2e-97

MFQFCHRKLNKTAKSMMTRRGVFLLFEGVDRCGKTTQTTMLYDKLSASMISQSFALLHFP

DRSTVIGKSIHAYLTSSEAMDDHVIHLLFSANRWEAASKIESILTSGQHIIMDRYSFSGV

AFSAAKSGLSLDWCWAPEVGLPKPDAVIFLDLSVKLASRRTDFGEERYETTGFQEKVYRN

FHYIMRRTTPEWHVVDATGTIEQVHDKIMVIAEEAIEKFAELPLSHFDTT

>contig50678 Frame-1F|Blast-DC12 family protein [Phytophthora infestans T30-4](gb|EEY64076.1|) 3e-09

MCGRTRCTLAREEIAKAAGVAPEDFVNSEKCLTA

>contig50906 Frame-2F

MFQVNAGAISSLDVAVDLVYTVGASCRFIATLSNSSDVLATLLFPVNTTFQRKVQLSKAS

SGDGCALHISVKGVVLASFLKPTDVFDEVKKIDQQLKQLLRFNRIENVALVRAEVALAGD

RLLATSLTSENATPMRKSMLTVQQGVCADVLNVLKSEEGVKILPREVETSALDVLTRADA

DKTANCAVELEVVAMVPWSGSEAKILELLQAVEENMEIVFAGLSNATLVSVNVQLHVASK

LPNVALATLSESRATLTFNPPSYEESLGIFALVAVLLVMMMAVVVQKKRNDQHCRDRFER

ANHAAQIRRVSIRMSPDHEKQHYEGEEDSLL

>contig52287 Frame-0F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY54007.1|) 2e-07

MGGSVVSSSLWLALPTATVAAVLVYLLLPDERQRAIRGLPSPA

>contig53842 Frame-2F

MLVIAYCGLHLHRAVDVMMHQLRQKNSIKGMGELGNDFVATYLLCKHVKGNQLIQRPWSK

HRKPRARNEVAF

>contig55127 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66381.1|) 1e-32

MTGQRHEAFPAAGGIAWSKMDQQVYDLDLDNSRGHVEQYRINLTDQAAKREALIKKLRGL

NAKDLFSYPSDVTTEVDAIQQELALEKLYG

>contig55857 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65842.1|) 1e-51

MINGMPVTLHVTYGNLIYRTMVPVFAQTTVAPLKDFVNVIQTTSFGMQVVYVELNASKHL

KGITIAMGLEVDLLYQLLFELFLMHQKETNPSTITLSPLQQLDTEKNPAELKKILGSEEE

ETKKAIC

>contig56333 Frame-2R

MKISSSSRAIFRALEVETLLEGVLVMLDLPSSANLLEILASNVSWQSVLNQNHFWKKMLF

THFGGDLPPVEHLNNMIGQNIDSADEESDEEDEEELLASLQMTTRSEMTKMATFKWVKGV

PSPMVLNVACPKLTNFLRSAEQLSQFNTLVQILQGDIEKIEIIGDERVDGLAFPTDYDLK

RYPSSYYASSAIFRRAGPKLDDYVRELNIRLNAGNAIVTPAFNAGVDKLIHCVGPYRREE

HHMR

>contig56346 Frame-0R

MSIAEAENIARAESAVEAMGMRNIML

>contig56449 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57391.1|) 3e-11

MAKINAFFVCKLCKGYFRDPYTSKECLHTF

>contig56988 Frame-1F

MSLDSPSNCTYISHELAEEAVKNLALQEGYVNMRRSSKKDSSDNVKKVWLGCVHGATHQP

MVA

>contig58025-1 Frame-2R1

MSKPLVPKVKLSQKQRKITTKKEVEEKILA

>contig58995 Frame-0F

MSAKRQRALKYPLMESALMLLWFTA

>contig59329 Frame-1R

MSHPNVVKIIEALDKARKHPSVTVSLDVLKMIAFVAVVAAVTYALVYRCSIS

>contig07011 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64662.1|) 6e-12

MMRCRNCNTLLSLPAGARAYKCMKCLQTTRLS

>contig07165 Frame-0R

MARKAVGRPKKDGDHTRKPRKKKDKNAPKRALSAFMFFSNDIRDTVKKEMPDLPFLGISS

EIGRRWKQISDEDRRPYDELAAADKRRYQEEKEDYVPDPSFESSKSSRKKKDPNAPKRAL

SAYFFFCNDIRQQVRDENPNKKITEIATLSAEKWRALPDKKRAKYQKMNDEAKVKYQHQM

DVYNGQGAVEEQDEEEVEDDDEDEDED

>contig11997 Frame-1R|Blast-ribosome biogenesis regulatory protein [Phytophthora infestans T30-4](gb|EEY67367.1|) 1e-140

MVVKASEIAPVAYAVGSTSDVLKEDDLTYDLGNLAAFDTHPFSYENEKQLALHARENVQL

LMNHIFELPRVLSDMGPLAQLPPPQTILPREKPLPKPKIETKWEKFAKDKGIDKRKKSRK

VFDEAKGEWSHTWGYQRASDDMNDWAVETKAGDQADPWTKRKQEKRARVDKNTRAQANNL

KQGRGKQLGANAAIRTPTGIPLELLDTDNIKAKQRGKEGTSQALEKVQFSTASMGKFDAM

RQGEAERKVKGKRNHFLPTTGAEATERERSLNALKRVLGREEKREEEMEGWMEKEDAKDS

GKRKKKGKQLKNFTKGATKKRRMK

>contig12484 Frame-0R|Blast-ATP synthase subunit gamma, putative [Phytophthora infestans T30-4](gb|EEY62471.1|) 2e-20

MATEKQILQRITATSNIAKITKSMKMVSAAKMRGAENRMNAGRP

>contig13098 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65035.1|) 2e-18

MLYRTTSAVTSPPNKEHEALIKRSDQVCVKNEKSVVYESSMTDEMRDIVVDKTNRLYSHY

ESFKDNDAKIASAL

>contig13344 Frame-0F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY67317.1|) 0.0

MPIGLAISFVILSFFLMVESPVWLVANNQEDKARLELTRLYGAENVDVMMGWIQANDRRL

KLPSTLSSTSNCNHTEDTWTILTFQTFRKPLVIALGLTCINQLIGINAVFFYSSSILKDA

GISDSRVGLMIIDVLNIVPVPIAAYLMRTLRKRTMLFSGISAMALCCIGLTLSLVYNIGW

LSVVFLGTFVVGFGMSIGPLLWPIIAELFPDSARGAAVGICVTVRWISTLVVGIGFPYVE

EAVTNYSFVPFFVTSILSIIFIYFMVPETSNMTIDEIQNGFRSKRSSNS

>contig16853 Frame-1F

MALQSSIKSNNYNATLVSVLQIAILLFVGFYQAKYLQAYFHKKKLT

>contig17924 Frame-0F|Blast-isochorismatase, putative [Phytophthora infestans T30-4](gb|EEY62058.1|) 8e-84

MAALGPEMKRLGRLLPQASMLFVCDVQEKFRAVTFQMPTVISSTNTMVSAAKLLNLPIVV

TTQSSSRLGTTVSEITKNLEDALQVRSFDKMKFSMLVPEVEHHIINNIPERNCVLLCGIE

THVCVLQTCLDLLEKGYDVHVVSDAVSSSTSYDRSMALTRMRQSGAFITSVESSIFQLAD

DASNPEFRGISKLIKEHRLMEAGFKNTACI

>contig19184 Frame-1R

MYHENDFEVFLNPDGSRHHYYELEINCLNTIWELLLHRPYKDGHSIVNPYNLTSLRSAVF

VDGVANSPETECVRWCVEMSWSFAELQQFDKLRFTQHQLQPQLVSKVATPFVTSCDNNRS

TVTGHVWRVNFSRVQYELEVEDTTPQQYRKVPNKSEDNIVWAPTGVIDIHRPERWGYVFF

SSDTALSRGKHELADARKGFLNTRMATERVLDAVYYRQRAFYASHGGYASSMEILYTDFA

TNAQNSLDIDWSKIFPLYKLLQQYKLEFPVLSSESEFVKKQVCDEILEGRSLSYQRIKPF

PKLTNLSQEMPRSDMNALITSTYIATVRCATQRWHIRHDGCLWQTA

>contig19720 Frame-0F

MSVAFKSRHHARLAPLRRAHLHSGRATSPATEDFVNRSPYHSSKVPKLRVNDAQWISIAP

RAIGSPDLWTRDMPRVDTCKNLLSSYQSNFIQAAINPALVKKSTEKQSYVEALVLNEALK

DLDIPRECIIVSTLLGSNVLHPTDPETDERLTNEYVKLGVQMAMEELNVETLDHVVCQIP

EYLARVSKNHGELMEKLQTTCDVLESLCQDGQIQSYGFSLPSMDSAQLLLTELVEKTFTP

LSKKWVQFASLQLPQYANSGIFLLPEAVVKFQKEREMLLIGDRPLEALLSNGNPFHFATC

TSLKGEDIAGLLKSAFNLAIAIEKKYREQIRSELKQLDLPPEEDVAWAHILANQHRQFDN

LQVWKYVRETQIYPRLDATVKAFSKYEETKKLGFAYSMAMNQLLKCFTGSVELIDGDRAA

DIMNAWKEVEGLLPSDKMSIEEVAVMAALSSGIDITLLEEQLPTTSSLPFTHTFSSRQLQ

QISILAQPY

>contig19795 Frame-2F

MTKKEDFVNWGHIYLGIKAGSCLILLMWVCWDSLVVPTFHSGRRNHLIDLVRTRAYPVYR

GIGCLLLLHWLVGLSFYVWRAARINYRYIFELNPRRVQSFPQVFNDATNMAIVYLANVLL

YYKVVNGYFPEKLLHRGYYPLALFLYTFYFYAIRPWGQQFGLMRTVWEVVCSPLYPVTFF

HTFVGDYLTSTVKVTQDVSWSLCFFATKEFLQKDFVPPGVKTTALLVEAPSCAKNVYYVN

VVVPLVCVLPLWWRFLQNLRRVYDTKTWCPHLPNAAKYALTQVVVLFGLFHPLRNNNSEE

DASQVRLFVITWLILFTTSSLYAWVWDVTMDWGLGRPQFHFLGDSQMFSHKWVYYVAIVF

DLFLRFAWTLTLIPPRGATWLPLYLQPFTMVVELFRRTFWSFFRLENEHLRNTQGFRRVD

FIPLHYDHGVGELNKKSDEVEQLDFRIFTLKILAVLFTVLGLSVVAIVIER

>contig23141 Frame-1F|Blast-small ubiquitin-like modifier (SUMO), putative [Phytophthora infestans T30-4]gb|EEY55693.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55658.1|) 4e-41

MAVLTDEVPPTTTGSNDDDKKKTEAITIRVKDQSGEETFFKVKPNTRMEKIFSAYAQRKG

VPASALRFLLDGVRISGDQTPKMLELEDQDQIDCALEQVGGYWS

>contig23659 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65835.1|) 2e-85

MQSEKSRARACNSDVAKFTIVLNLPDIRFAVLTSAFDSLRHLDITLSSATSLVLATYVAC

VLAWNIVSFALGLLVQAAVFALISCFTFIGFSTLCTPKTIAAHSCFGHTEPNKRAVIAIT

ANPSLPLLSIIPSSKSVPADGAAACTAKVNKVMTSQRHVFTRTDRSRLFVNVLPGDMRRR

IDANLGKAKIRVGKAFVHVVSSKVKPCDIYVVRIDCGSQSVEREKHMNPVIMWDVTASFD

EFKKLERELKKELKTKKQFSDVKVPHLSSGAVLFKELKLTDDVLNARRARLQTFIDSLRS

HPVLSTSGSLRKFCQAY

>contig24948 Frame-2F|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ27126.1|) 4e-69

MSYLLPHLESGWAVDQAILNEGDRVVVIRFGHDHDSICMQMDEVLCGIAEDVKNYAAIYV

VDITEVPDFNTMYELYDPCTVMFFFRNKHIMIDLGTGNNNKINWAFNNKSEMIDIVETVY

RGARKGRGLVISPKDYSTKYRY

>contig25437 Frame-2F

MTCAALASFGYQAVREVAHALKAGACPYLERLELVAPFDFATESDAVFLLLHSLTDSTIK

NRKALRHLVLESTFLGDSGIKQLAEVFENHDSYYERLQTLIVRNNFMGESGCRALLESIE

WFSELEVLDLSRNILSNTDAFALADLIDDPVTDLSLWDGLNGNSKALTAEKEPFNVFGLA

GLRRLELRENFITYDGFHAITVALCARDGFWLLWMTLPKCALKRQKRWKSTRC

>contig25558 Frame-1R

MHTFSFFDARCTPDPVHSLLTSTLSTADLLAGHVQRVLHRDKPYRTIRRSTVLRTVNLRL

NTSAPLSNSFSSSDRPIPMHFCATIPPNSSTLSDSVIGNVMQRSTWNTHANSRASSTFPQ

SHHHHQHPFRQASNSIANETERTSLIHTKVPIPDALEGSAPAMSRHTGISSNRRSVTCLL

SDLEAVNNMFIGIQGTKHRVTPALQQTIVADALRKKKRHRERCRINQARYRERQLKAQTE

IEVAIVKLKFEIGQLEVKCNMAAPLPTTRTNWAFVSEYFRHFNYYISSPIIFSKTAYKFL

DTIMAPDVVVGSYFGVDAHFGCWELFALYFEDLRVDLKGLTTSAPGTLVARTTTCVSITN

NTLCRAFPHLNSDGAGGANGGVWSPLAVKLLGTKFSMRGSVVFGWDSVTNKVIRVHGQAD

MISPMLSLLGNFEDVSYVFQRALVTPDCKPIRED

>contig25851 Frame-1R

MFVRDLGGLVIVVSLTAVVAYYTELQLYAALSLGIQGVSALYAIPKQDERFYDLTGSVTF

AAVSFLAITTADAVTWREKILVAFVWLWCIRLGLFLFWRISSCGEDKRFKDIRKNTLKFL

FGLGHTRPLGVFNTAFRVTGIYSWLSRRTCIAAGYLWRLYLDNWVHNGGLCRLSKVEIST

R

>contig25990 Frame-2F|Blast-tRNA guanosine-2'-O-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65292.1|) 0.0

MPEYLVYFVHQHLNFRYPELEALLTLQKLPGIDQIVYKDLYSGKLPDPESSPLVRVQLPS

AEHAKFLSVRGILVKGVYEVWGHTPATGSYSDLVASVEAFQGPQKARILQDDKCSWRLNV

AVFGKKLSMDEQRKRRELFQNSMPFAGPVRMKNPDETFLILEELGLDQDLYQNVKPKQMF

FLRELAGSEKNRGRGGARDLVDQQTLKRRAYIGPTSMESEMALLMSNMALVQPGDLVIDP

FVGTGSVLIPCGTHGAMCYGTDIDIRVLLGTGVGVMGSGAPLNGIMSKQNDRINVTTNFR

QYGLPLPELVRADNSVSPFVTRCRGFFDAVVCDPPYGIRAGARKCGRKRQMRGDVNMSSK

QDNYIAPTQTYAAEDVMKDLLEFAAQTLREGGRLVYLLPTTYEYTDSDLPRHASLQLISN

SEQKLTKKYARRLITMMKRTPSAEVKALSQNASTAATKNPGDVSFANLREKLRKRKPGDV

E

>contig26560 Frame-2F

MQSLYLTKAREELPPHVYATSMTSYNDMKRHAINQSILVSGESGAGKTETTKILMNHLAS

IAGGLNDYTIKKIIEVNPLLESFGNAKTARNDNSSRFGKFTQLQFDDSGILVGARCRTYL

LEKTRVISHEAVERNYHIFYQLLAASESQEKWFLDEANERYEYTGANDTAQIEGMSDGKH

FQRTKTTLGLIGVTEEQQGALFEVLAGILHLGQVKLQSKNSNEESELVPDDKGAKNATTL

LGISAADLEKALCSRQIAVAGDKVTTFLKKEKAEECIGALSKAIYSNIFDWLVEIINTSL

ENDAKMRHHVGILDIFGFEHFKHNSFEQFCINYANEKLQQKFTQDVFKTVQLEYEAEGIL

WSHIDFADNQDVISIIEDRLGIISLLNDEVMRPMGNDEALVSKLSTIHKDDHEVIEFPRT

SRTQFTIKHYAGPVTYESVGFLEKHKDALLPDLSDLMRGSLKPFLRTLFTEKFVSPVVKR

RKSHSSARGARSALTVANVGTQFKDNLNELMTNIRQTKVHYVRCIKPNQVKSPTEMDQVM

VVSQLRCAGVIEAIRISRVAYPNRLLLEELMDKFWMFNVQQCDSDGDVKRRCEALMAKMH

LSSPEHYQVGLSRIYFRYGVLEKMEEKKVERLDVQARQLQHYMRGFCCRLRYLRKSRAIV

KLQSVARCVIMMHRYQSLKSAVITLQAHWRGNKGRCIALEAGKANSAIIIQKNVLRFVAR

KQFIEKRKGAVKIQAFLRMKFERPKYLRALAEKKQQADMKYQLSKLQERLHDEQRRNAEF

KKKQQSLSSADSQHSLESNGARSRGQSTTQTWMADADGIINQLNEETNRLRKKNEDQRDL

TAQLKSEVEKLKFDQTVLTANFQVKLSSFQNTIREKDKKLEAVERECVKLRELVGSDPSI

PGPRSSQKDNRSVFRRIGSKKFDDGYGNSDSNRASTAMQAALAQKSAETAQFLRQSARRM

SRGRLWRNGSTESDVEGRSSGSDIDDFSNRPSLLQEVSAAGAGAMESLKNKLTAVKEKYY

AEEGHAAPTGQDVNSQRSSIMMESSKLKAIPLPPGWEVRKSRSKGNEYYCNPMLRITQWE

HPSIDSKKQAADVRAKSGRSSSSSTGESSHRNSG

>contig27996 Frame-2F

MSVFCRDWSTSPVSDRVWAQALHAVVERRVSLRQASQDFGLQQSALHRLVRQHTLRQLRH

APSSPDSSTSPSKNDKRPLSLPTTSSCGVTSNDRYVFPQLNSLVLGQRSPNGGQLPSVVP

ITAVMTPPLFCELTPELNDEIVSVLREQFVQQYEDYKMRDGRYHR

>contig28845 Frame-1R

MQLKETQSKLQQTNADLRTSLCQILELLQLHVELPLENNHVDAFLNDNFHIVETRVKELL

ACAESEMSEVTKRRSDLCLLESEQDPDDSFKISFRRFSVNDLALFLPTSAPGSDAQRVYL

AFHLGCPHRFLSEESISSFSNDGQRYPDYVVGRIVLIDEQITTEANNPYALHLGTMFYVL

TVASLHES

>contig29622 Frame-2R

MRLTYAATDSTAIVRNPAIYSPTITLFHYFLMHSYHHSFIDEPSRSTQRSYVVIVITQTC

FRATVDVATSLIIKRAAATSSSRGSTMTKSLLDG

>contig30318 Frame-2R|Blast-pol protein [Phytophthora infestans](gb|AAV92918.1|) 6e-22

MFGMPPDHKGRTGLVVFVDRLSKMVHLAPCKTSITGKEAALLFLYHVYRLHGMPE

>contig30952 Frame-2R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY63967.1|) 4e-15

MDGFSLNISASSGTRAPVKRKNTFRAKQQAKRAKIKAKKGLKVPQKPLNQSSKGPSHLDQ

PHNGLTPRQVEVPSPQLPSNKGMAQTNSVEPLRQHEPILKPEKSLAEKEPKIEVKSVSEV

TEKQELELNVVKIKTFGTRRNPTKDNYSVEKFTQPTVQLANVLSKPLTSSSSKKIFAQHT

FESMQLAT

>contig31300 Frame-0F|Blast-peptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-4](gb|EEY58745.1|) 2e-18

MSSIYITEPNTEGKVLLLTSFGDLDVELWPQQAPKACRNFLQLCLEG

>contig31450 Frame-0R

MGNEGSTLAGPPHNCRDEDAIVGGECCGFRILGIQEKSPASQVGFVSFFDFILEANGIRL

DTRDATFMELIAKSEDRSMQLKVYNVKAQATRELELTPSRDWPGKGLLGVTIRFDSYEGA

EDQLLHVL

>contig32257 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY67682.1|) 0.0

MKSRLSVKDVQLYGAELVLAISYLHELNILYRDLKPSNVMIDAEGHIGVVDFGLSKQHIY

GSNFGVKTLSGTAEYVAPEALAQSADGTRNYGKTYDWWSLGIVIYEMLVGESPFYDENEH

TMLSRIAHSEIIFPSDFPPNAYDLVKGLLCKDPKQRLGDERMGGVDAIKRCSFFGHIDWE

KLLRREVKAHWTPKLSGETDTRYVDPEFIDEGPPSAAYDPSADSGNSQSKRFSQFSFNYN

LG

>contig32961 Frame-0F

MVPLTQVCGLAALFAAGQVKAVPIGTDVSDTGRVLTIMDESFPGYGAFREAGATSTSIPL

EKKILPGKAHGKRMDRRLELTKTADMDKLESVFGLELELDITKL

>contig33676 Frame-0R

MSLRTLSCPYVFLLMTVVADDASRRLQTYAQPSDYASLMLERVNLERRAQRLLPLCLNQK

LQKAAQRHSNDQAANNFMDHIGSDNSSASQRITDARYEWRGIAENVAAGQIDVIEVMNAW

MNSEGHRLNILGDYTMLGVAYAYTSVGPYNHFWTQNFGLSNTEECDDGSIPSSPPTFQAP

GGSVQDSKASGPSVYIMPINPPREYRGRSSSSALTPTLLVQAVAAVLTTIVLFDLRNIT

>contig33962 Frame-2R

MRTCFLIFVAGATILLSTKASNPEDDVEDRGSAIGQVRRILRPKTINYGALEPGRSNPLY

NDPRNRPTKYLKLP

>contig35678 Frame-0R

MKSNLFESGKIGLDGDSSLLLSGELPNKKMKSASRPSKPRARERKGRVSRPMKFSMDQLT

ALEAWFQQKYKPSQEEMENYLAQLNASPLRDLTKQLVDVNMTQLRRWFNKRRCLRRPPFA

LMTQQEAAKEGSKNPAILKAVLAPSSCVESVEAVLGPEVVEDATLGLEGNQSYDDSNDDS

IDNDEDDDDDDDDDDDGDDDSSDDGEHLIGAALA

>contig35722 Frame-1R|Blast-tRNA pseudouridine synthase, putative [Phytophthora infestans T30-4](gb|EEY56449.1|) 3e-07

MDGCMDLTNKLRDGLLLPDVLQVVLGLGICVRCCLRFCGIQESYFYACLSEEKIAEAFYK

FANLIEVEPRDAA

>contig35757 Frame-0F|Blast-DNA-directed RNA polymerase II 135 kDa polypeptide [Phytophthora infestans T30-4](gb|EEY60666.1|) 0.0

MSWENPIDSDTERDDPGGLGLAPGSIVSQEDAWAVISSYFEEKGLVRQQLDSFDEFIQNT

MQELVDDSRSIRINPEAQYAPGQAKANTDTIYNISFGQIYLSKPTMTEADGSTSVMFPHE

ARLRNLTYSAPLYVDVVCEKYQAPASGPANLEDMDPYDEVETPKEFIGMVPIMLRSQYCV

LTHKTDKELTELNECVYDQGGYFIINGSEKVLIAQERMSNNHVYCFRKNAASKYSWVCET

RSHVEHGVRPTSTMYVQMYQKGGGKSAITGNQIRAVIPYIRQDIPVVIIFRALGFVADRE

ILEHICYDFSDAELMERFKSSLEEAFVIQEQEVALDFIGRRGSAINVSKADRIRYAQDIL

QKEMLPHVGVEDHNETKKAYFLGYVVHKLLMCSLGRIGEDDRDHYGNKRLDLAGPLLGGL

FRVLFKKLTKDVKSFLQKCVDNGKDFNLTLAIRSRTITNGLRYSLATGNWGMQKTASKAG

VSQVLNRLTYASSLSHLRRLNTPLGREGKQAQPRQLHNTHWGMICPAETPEGQAVGLVKN

LALMAYISVGSPQAPILEFLEEWATENLEEIKPQIIPHSTKIFVNGNWVGVHREPNELIR

TLRSLRRCVDIDAEVSVIRDLMNKELRIYTDAGRVCRPLFIVEDNQLLLQKEQVVKLQNH

KITNYRWHNLLTDGVVELIDTEEEEVCMIAMEPKDVGMGSQIHTHCEIHPSMILGICASI

IPFPDHNQSPRNTYQSAMGKQAMGIYCSNFRARMDTMANVLNYPQKPLVTTRAMEYLHFR

ELPSGINAIVGIASYTGYNQEDSLIMNQSAIDRGFFRSTFYRCYIDQERNKSPHGGPGSG

GAGGANCEEFEKPSRENCLGLRHGSYHKLDNDGLVAPGTRVSGNDIIIGKTSPLPQSEDS

SLEQRHQKRDASTALRSHENGIIDSVMLTTNADGFKFTKVRFRNIRVPQIGDKFASRHGQ

KGTIGMTYRQEDMPFTVEGITPDIVVNPHAIPSRMTVGHLVECLLGKVSSQTGDEGDATP

FTDVTVQAIADTLHNLGYQKHGNEVMYSGHTGRRLTAQIFIGPTFYQRLKHMVDDKIHSR

SRGPVTMLTRQPMEGRAREGGLRMGEMERDCLISHGSANFLMDRLFANSDAYRVHVCDVC

GIIAIANLRKMTFECRTCRNKTQISQVHIPYSCKLLFQELMSMSIAPRLFTLGNPNISAK

PRLA

>contig36451 Frame-0F

MSSTWGGWGNKLNVTSIVSQGIEQVRSLREDVEKSFDNVVAGVPGVSVSQSLVESDFESQ

EQIDGTIKDLTETQNSTVDVAADKMQSEEEIVDSKAENLQLKIVKAKKSQDEADEVLFDG

DTELREEKRKPTDAACNESTTDPGQLEKEIQAKALEFKAIPTNEDIADALNVPKATTLAK

QT

>contig36590 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70675.1|) 3e-57

MEIEVLQAEKRRREPVVKHLFERTVKEDVNLKQLVEDSQKQRATQEYQLQELKVGLAMYQ

RLGLFFEPAEENRIIVKFTQIDPQDSNRVFSFRITIDPITDKYIIDSCSEVVPSLSQLVT

ELNESGDLARFIRSMRRQFKQVM

>contig36837 Frame-0F

MTPILCAACAGGTSVEMFKALVESGGDINHHVGLTGDTALHFAVKRDDQETALALLSMGG

DIMRTNGKGFRPIDCTTSTRLQFEIKRAAGTRDVMISYTHSHLEFALKVRKSLEEAHITV

WLDLMDPSGIGGGSVWREEIARGITNAAVVLCILTEDYALSEWCLKELALAKQVGTPILA

ISTEQASISEEVQVYLYTRQLVPFESAIVRINHVDANNVVYEYDEDAYRTQLRMLLDGMR

DEIEKRKEESIQRNIRRAETKPLTCSNPGAKGNPSRRLHCGMSGISTYGMDSMRFDEHML

TGSANDTMKDHLSDSHSSFVHEYDEELMMPSMLY

>contig40072 Frame-1F|Blast-salicylate hydroxylase, putative [Phytophthora infestans T30-4](gb|EEY66499.1|) 4e-64

MVSMSSCDYDIAIVGGGIAGVTLAIGLLRANIPITLYESAKAFGEIGAGVALAANAIRAM

ELISPNIKRCCDRVGTCNQSTAKKDVWFDFRKGVGTEGASVDIGASDLITSLATPAGSTY

VHRAHFLIEMVKLIPDGVVKFEKRLQDIKVCPDGNVRLKFFDGTE

>contig40199 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65900.1|) 1e-29

MTSGMSTSSKAGNFLNVLRSRCEVGNSSSQHCTPEARDSAICLLAHLDRLASDDIPAEDA

DSVQMSRCLYRSLCIDLKASTFSALYALLDDIMSRFLGILNQDMQLDTTHVIPYVLYPLL

VTIRLLKLNFFEFSRSCLAATEIGFLASSTDQGGVLYS

>contig40678 Frame-2R

MPHVSAHCRLIHARGRRIATTKVHGRQKIVRLAKLATTKSCVHVVQL

>contig40829 Frame-2R

MCVNRNVNRDPSQVDEKCRLALEGAKCLYFKKRKRVNDLKRLTPSVWDIEDLVRLAQKHR

ECAYFHAREALENAHIVFAPYNYLLDPTIRHAVGIKLKNAIIILDEAHNVEDTCRSSASV

EISMEVLEASIKAFTIVIKHGNRPKSYNALLKVLNGVHRWLHCVETNAHSILQSSNYEEK

S

>contig43451 Frame-0R|Blast-spermine synthase, putative [Phytophthora infestans T30-4](gb|EEY67514.1|) 1e-160

MTEMTKDECDKKPAMLAPAEKLFWYKEAMTEDLYMAVALKTITFEAKSSFQAMQIIETNS

FGKMLVLDGKTQSARSDEAIYHEALVHPALLNHPNPKTVYIGGGGEFATAREVLKHKSVE

KVVMVDIDELVCNMCRKEMPEWSAGAFEDPRLEVHYTDAHAFLKQYEGTFDVIIMDIADP

IEAGPGYVLYTEEFYKYASTKLNKGGYMVTQSGPGAVNNWDECFSSIYCTLKTSFNTVVP

YTVDIPSFGCVWGFNMATNVDNEDGAAVLTSIRERSIAATDALVKSRIRQRLQYLDGVSH

MGLFGLPKIVREALESETRVITVDNPVFLY

>contig43837 Frame-2F|Blast-DNA replication licensing factor MCM9 [Phytophthora infestans T30-4](gb|EEY68481.1|) 4e-86

MIEMEKEYQCCNAQCGHRFLVKSDPEQGNVLEIPKLCPSDSMGGTSCGGKKPCRSTQFLP

IGGADSSVVSDHQVIKIQEQASKLGVGSIPRSIAVVLEDDVVDTVKAGDQVVVVGTLMRT

WKPCFQGVRCNLETFINANSIQIKNASTAQVMVTEELRAEFVQFWAKHQHDPIRGRNEIV

AS

>contig44164 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55803.1|) 1e-42 NOT\_ORF

MMSNLLQRARKERVLAELPGLY

>contig44591 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58740.1|) 5e-11 NOT\_ORF

MNCEVDNFLNKLT\*IYHEVGGNDGKSLKKDKNGDDIYSLNQD\*REASSH

>contig45431 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55200.1|) 7e-26

MDNSILNAFVDFLKPSNEHLQSAAGALTPSSQESLEHYADVLPFEVFLPLPTVAHHLKDA

SASTIATKARRSQSKDTVRRSLYRKRQQAEKEALYHEIDALKTQVDTLLNMPASRTVLST

MHGPRPHELWKAIALRQRHHRQAAEEERLHLRTAITSRAALIENLHTSLRKRAHGSTISV

KEFPNAP

>contig46676 Frame-2F

MATQRTGKNECPHYSRRCHVLAECCRSWVGCRLCHDALLGDDHVIDRYAIKLMRCDLCQT

VQPIAQECIYCHENMAAYFCHFCNLLDDNGLERKVFHCTQCGIC

>contig46962 Frame-2R

MLRNAVSLLSTFICLVDKLPAFTLSICAFPSVAMVACTTFLSMLLTLPLLFASSENCTTN

AINDALIPIALDSTYTSCEIESNYTLQAIVNPSRKQTWAFCASPACRAFLNDTLTSNRLP

DCQVIIGTYDHSLTETTTFVLSHCEALHVGQSLQERAVDKDEQRSSAQSISEHIGSVLGH

SAPMEDIGAVAGALLSLL

>contig47257 Frame-1F

MDDGALRLPAQKLVSQLRASVAALMHDVSASFRLCSHDFGVLGAELVSALERDKKRERAT

INALTHERSARGKLETRLAEIQGNIRVFCRVRPMPTPLAGTSGDESEGMSPAKRRKRVQV

DSAQELSVFSPVDGALYKSFSFSRVFNEQNSQATVFKEVAPLVLSAVAGHHACVFAYGQT

GSGKTHTMQGSESDKGLYYRSGDLIYASLAQEQHMYDFQVKIQIVEIYNEDIYDLLAQPS

TSTAPIASTCTGSTVSADRSSPIAGMGCHIG

>contig47572 Frame-0F

MDAPNETSIDVSLQRLEHMRALGIGADGKLALTLLGWHLAQICSSGVSVQMAKLLLWGHT

FGCLDAMLQTTCTLSGYRDPFINFLGMTPEEQRQVNASKLAFARNKSPPALMLQSDHFVL

WKAFEAYVDVRTRSSFKTTNAFCAQYKLHRQTLEQLVSIYKQLQQELERMGVSPATQLLS

MPAAGTVATMNSIAPYLMALSIGMYPNALFSRSGGVSRNWISKEKVKVKLDGTCIVVWTA

GNVLKKNVRYGHMQDEGNEWLVYHEMMQSERTRLAKYATKLPSVLLQVLLMGCLESGKIE

AQSAENDTSKETCKWLLVLDDWIVYEFSSLDDARWIALLRKRLYAAFLRHLDHLHDNAQH

TGAKSSSVENNELKQHDKELLQALVSWVASDLHCKSNQQA

>contig47828 Frame-1R

MKTAQMRFNASTAGGTYILQLQTCWSPLLRKTRVSTIQPSDSNLNEIYMASNLFTNQN

>contig48106 Frame-0F|Blast-phosphatidylinositol kinase [Phytophthora infestans T30-4](gb|EEY59985.1|) 1e-81

MSVLGYIIGLGDRHLDNILLCVKSGDIVHIDYNVCFDKGRRLKVPEIVPFRLTPMLQDAL

GFTGVEGNFRVAFETTLRIVRSDRVREALLMLFEAFIYSPLVEWINDDRRQERSGDLKAR

LEVKVNVSLFLSRAEERRQDTISFGRQYE

>contig49048 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66384.1|) 1e-123

MKVVQFMRNSAPQLFLIAINCVLALGGALVLYVGIYTRNRGWVDVIEGYWSKFDDAVTAL

IVVGAVIIGLAGLGSLVAICRWRFGLCAYAIVMLLFLILFVIVTTAAFILWAKADDWSDT

TYPVESTEETVKDNFDQVYCYAQGQYICNEASVSEALAMFVPQLDDAMVARFENMTGGVN

SLCDDFLSNNSQLASLCNGCDTARQFENYSNIFDWAEKQCPRTNETLLFCGELLATGSFS

NIANGTAPYAQCRANFLDLIKEYSLVMGIGGLLVGIGALLIIISSCYLRRREQPTHNYAV

QDDEPISPSIEQPP

>contig49747 Frame-1F

MGRKARHSSRTGDGGAEVRLRQRQMREAQHLKEAAELTFYDDPSENESDSVQVESEDDEL

AGQEVLELDADENDETGDDEEEEDIDMDVDENPMYDADAERKKALQMDGKWGTKRKTFYS

ADTAEYELESDEEIAKDEEEAALDLQRKQNEMVDDEDLGIDGLESAGEVKEEDEEIDMVP

LDDDELVKEQLADIAQLADNGAGGSETVEQVHRDFSKMSKKDKLQIVNQSAPEFLGLVSE

LESTTKELEEVVTPAVLKLRPVRRKSRQLQMGLRYLMTRQNLLLNYSANISFYMLLRAQG

KSVADHPVLMHLLLLKKQLSKLHTIDEVVNGQLQDLLTKQLPAEQEPKFDNGLISKERKR

WSNGDLSTKQKSMKISPEERIEAERFYKQNALDQAKLKQAKKELYTHEKPVLQASSDESS

DMEGEGTKRGATYQIIKNQGLKAHKSKLNRNPRVKKRLQYRKAIIRRKGQVRDVRVGEAG

KYGGESTGIKSNLSRSRKIRN

>contig50129 Frame-0R

MSLSDQALNVKQKSFPCNVLAASGICWTKLKCLTILLEYPEGDYEPRLICDAPINNSTPQ

DLHVSSQKDFAPA

>contig50428 Frame-2F

MDGRTASYRRWLRRKLRRRHLRNAANSMKIKE

>contig50972 Frame-2R|Blast-salicylate hydroxylase, putative [Phytophthora infestans T30-4](gb|EEY66499.1|) 2e-55

MMENTDIWALFHHLPARTYTRDNMIMIGDAAHAMTPHQGSGAAMAIEDAYVLSSLLATVR

YASSLKVAFKAFEKVRMSRTQKVASTSYEAGQLYDFELPGIEDNLEKIAKNLHSRMSW

>contig52286 Frame-1F

MRKLIVAAMPSRILKQVYRTTLIPCANSYVAFGDSNC

>contig54110 Frame-2R|Blast-phosphatidylinositol kinase (PIK-K) [Phytophthora infestans T30-4](gb|EEY58119.1|) 1e-34

MLVSKTLPESKEVEKFRTFWDEKLRTAMNRLKHAAASDASRPEQDDVFHLLLKLYTHQDV

VPELYRSYDFNATEFEFYIPQLCTFLLHGNYAK

>contig58693 Frame-1F|Blast-alcohol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY68781.1|) 1e-44

MNMEVVDRHEFSPAQVVANLQQMLPPTGADVVIDTSSCSTSTG

>contig59179 Frame-0R

MRLASLLLVVFSTAAICVQHCVKAKFAAVITNTEISHHHPLISPDTKRFYLKGLNDDAQD

ERIISRAVDYM

>contig59328 Frame-1F

MENINGLIGGRIMHVLYKTIALIRKGWLESYARGECIFLVELSVAALLDWLVSIVVGP

>contig09234 Frame-1F

MRPHLKARVKDLNDRNDTSNSPTILMQSSSLSQHNFIKKKPFHSKLSNCLVSVPLLIILE

SQDSTHESNATPKNRVHTPKTA

>contig11213 Frame-1F

MLVTFVIDTSASMNQSTSSGMTLLDYAKSAVERFVKRVREPSRRYQHHFMLLSCGHDSRP

KSGTKSMESKAYDGRVRIGWDQSTNKDTFLRELKNLRATDLSDLGAALKQAFELMNQIRL

QFNWDSYALGRAPWNTNVSVCVLLTDATTLSNAEGLIQDSLTIAPSSAVGADLTFEPYRW

DQRLYTVALKLSATINGVKRQPTAPADLMALSEATGGMLYMPTSKLAVEQSIDQIISKLK

AGAVVKFKCDAMEEEVEYPVTNNIIAPIHSGKEFYWPVAEAFWLDRNTVSLPTREAHPTL

VYSCTVENAIEAATSHMLLDTLKFPADNYVLESSINPTPPRGQRWLIYVQGSKGDGRLGD

PIGMLRAPNSSPVVPSPNAILVLLPYNFPKLFTLLVEVARVYQASGQNISSVSGTWMFQA

KAMPSSWRESFSAYLSSCPLYYYAPLKKALRKYNLHDMVPEVQDSGRSYQISNLLNRLRE

QAIAESDSNNKLYSRSSRNEASGRSNMSTESLSSPNLKRDLNGTNAADATLDAVVKMSLQ

ELRAAHQKSKALFFNKNLKFQIQRSLPRVTVSQDETVPLKLAPSWLAVEEDEKHRKPIEV

MSDYESRLIKKEALRNPLAEAEPDEDTPSGLRRRQLCFNLGNPYKKSSSKMSNVYQGEAA

EEAATLGGQSPKRQRTRKRSSQLKRDKKPSKRFHRMHGSPSFRSLPGSPSQPPSSLVSSN

FSTASSPGQSESGDTETTDSSVESNYSVKAEAAQMLGIPLHDGGFVEDSDSHSFVRHIYG

ILAENWESWCTIIRLIKARSITQQEKEFVLSGLRSMKGGPTAVKTYIEQAINYSQHFRQK

VLEHQLLQLLVTVNEAVRDEPENGLRYC

>contig11972 Frame-1F

MMLNLSRSRAIRAVACPSRLSFSVSSKSSVPPTLPPPTASFKLPSQTSALTPPTSKVPSV

VTDSSRGGSLPKLLLLGLLSTPAAAAIYLKLNPEWNPAVLKDDARWIKLREAVLGEAATE

VVVAPSNRSPEYFSAVINTAMQDMGNGGELKESKKELKKEETKKDAKMKIKEEEEKKKDA

KIKDKEEKKKTKKKKDKMKEKEKDASMKDKEDEKKKEKKMKKAEKKAEKKA

>contig15459 Frame-1F|Blast-acetylornithine aminotransferase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY59010.1|) 7e-50

MLRSAKLVPRVARNSLRSFATTAESFNPDTYEKQYLASTYNPDGVRGESGLMFTHGKGSK

LYDEKGREFLDFYAGIAVSGLGHGDEDWYQSLVDNGKKVTHVSNLFHTKAPLELAKTLVD

NS

>contig16054 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55284.1|) 1e-176

MILQQMTATQRKKNTMSFNYCFVGNPGTGKTTVARLFANVLKDSRLRSSNQFVECTAQQL

KDDGAAEFRLKLKKASGGVLFIDEAYELNPVGDFKGKPIVAELLTAAEDKRDVLSIILAG

YHDDIQKKLYAYNDGLPSRFEEVVFEDFDAHELEALWDDKAQDCGWEYEQAIAKVACRRL

AKAAGRKGFGNARAVRKLFEQAVKEAMAREDFDGQLKFQTVDLLGDRPSTNPKLQAVLSE

VEEKTGWQVIKQELKNLVRVSDENYERESKGQETVQICLNRLFLGNPGTGKTTCAGFYGR

ILKALHFLSNGDVVKKTAGDFIGQNVGESQKKTAQILDMSKGKVV

>contig17725 Frame-2F|Blast-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65844.1|) 1e-74

MMITPDMVQSEAFQKDEHSEVKRLTRELEERMYDVTLNASDFSTIYAAQMMRRLYLSSRG

TVDAIKEVRLTQHIIRMLEVKPQNDNQKKRIATIREKVLQYKEKLEKLRLKDQEVILSEF

KEQSLIRLFLERILYLLVLLPLATPGLLLNFPYYFIGTFTESPFDNLTYQPSPIIGLTYR

NKVEQPCRICGIQVNV

>contig18737 Frame-2R

MVQFLKGTKRLSSRCKKLRWWRKLAACWSRRKATLTTLQKKQQSEVSQWWHNDGGQHDHR

LDGEKAKVCRTIHDGSRVCGGFTYGD

>contig19110 Frame-1F|Blast-5'-AMP-activated protein kinase subunit gamma, putative [Phytophthora infestans T30-4](gb|EEY66828.1|) 1e-23

MIFERFAACKAHRFVCLDEYSRCVGIVSLGDLFNYFLD

>contig19165 Frame-1R|Blast-phosphatidylinositol-4-phosphate 5-kinase, putative [Phytophthora infestans T30-4](gb|EEY65806.1|) 4e-19

MGNRGRRRVARLAYRRDPTGTDRVKQKGPTVHLNSLDSLIVGLSIQPAILSIRWKKPRGA

VVILYADGSRYEGNVDDARRRHGTGVQILESGSICEGEWVHGCFE

>contig19499 Frame-2F

MADADIELLLREGIEAAAKDGEYRSEERSHRSSQRKSKMRSHSRSHSRHRHRDRSRSRSR

RSRRSRHSRSRSSRRTRGSSRRDRKRSRSIERPIKKIRKSKSRSRSAIKVEREPSTSVER

AERAKQRELMELTRDHRTVFVGQLTQKVREKDLERFLSKTGKVENVLLIRDKFTNRSKGF

AYVELSNLEDVPKVLLLTGQVPDFQVFPIMIKASEAEKNFAAKKDSVMNATAMLSGPLTA

DALSAGLTGSMDGANMSAAALSAASRIYCGNLHTNITEDDLRIVFQSFGEVLSVTINRDE

MGRSKGFSFIQFSSPQEANFALSKGNGLELAGNHLRLGPVNENAMRGGNRGPGGMLDNGA

TGGRWKLEDEEGLGLSMNAQSRSALMAKLAGNDVTLFPSMAGGTGAYNPATDVTNTMAAT

AAQRAEQATALMSSTEIEGSESFCIVVKNMFDVYQEQKSGNSEWAVEIQQDVQEECTQYG

PVLHTYVDKDKQGGLVYVLFGNVSSAVAAAKKLHGRWFNKRQISVRYLSSQEYVGMFPEA

RTAVQTARTSSE

>contig21867-0 Frame-1F0

MAQTWAARRVARSSRPFRTLLTPL

>contig22707 Frame-0F

MAVLRAEPRNAAAVNSPKSHGDFFFAAACR

>contig23722 Frame-1R|Blast-hypothetical protein C56C10.11 - Caenorhabditis elegans(pir||T15851) 2e-13

MPSGVVAPIVLLLLLISRIHGFHEDPYKVLGITRSASDAEIKRAYRLLALKWHPDKNRSD

PMAKQQFMRIGAAYEKIINPIASTKPKQWRQQQ

>contig24024 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56903.1|) 2e-54

MACQLVALPKGTIQVEEISDDFYVGIVTKSLPLGPHQGG

>contig24749 Frame-0R

MKVWQDQRMQIHLQACTVLMVVLGAIDICRCSKFALMYAQAWSNLDMRKSKFLVAAISVS

VSRLVIA

>contig25557 Frame-2R

MNVHLLVLALVAALASTNAQTLGDSIVAGVELDPETYANAVADSVANITATNTATTSPST

STQEDNAEPDTAPIPTDNDSSNSGSDESEDATADGPQASAPASSDASRRLLGTCVTVLVV

AIATVL

>contig28446 Frame-0F|Blast-ribosome biogenesis protein BMS1 [Phytophthora infestans T30-4](gb|EEY64317.1|) 1e-123

METFEFLNILQVVGFPKVMGILTHLDSFKKNKSLRKTKKRLKARFWTEIYQGAKLFYFSG

ISANKYPKGEIQNLSLYISRMKFRPLTWRNSHPYLLVDRFEDVTAPDDVQRNSMVDRRVT

LYGYLRGTHLKPGMRMHIAGAGDFYMDNVTAMPDPCNMPSSTKRADGVVKKKHLTQKDTL

LYAPMSDVGNIMYDKDAMYINLSQLNYTNPDTGDIVPDEEGDQGTSGNEMSG

>contig29001 Frame-0F

MATRIADRSLSFSSGENASELSKLEITRLALAQEQKKRIDAAVARVTGKKESGKRKGLAT

SDEIFRSKKSKTVIDVGSDRAEKKNSIARRMVDRFSAMPEPELEAEVEQPIQVTTRSVST

QQFVARSMPIADLSAHAQREESPKVEERPMLKKLDIDDAEESKTEAKAANLAAEDEEEED

EEEEEKSVWDGPTTNYHVKQLGLDDNVDIYAPVVQQQYDVQRVRERAMYMPNSVESVNAV

KASADSETDSAVALNKPLHQESEERDADLRAEVDANVIQALLEEPEEFVKDPFIAIDTAW

TKRVFTYLPLFIVSIIVLVSALLFVIDRSQETFRFCEFDAENSEGSGEILMCASFLHFQS

LSKSILREIAMSMQKTVQFFFK

>contig30861 Frame-2F

MVAVEEIEENQVTSPLEQDSEVNKARAPNSSSVQQTQLKNMEEKGDITNDKQQKAEAREE

EELERQKHKMNADETCKSDKLKEAATDKKMPNMETSISKSFAKTKMDVANAAAEPSGKSK

RARALALTNLPSSTKRTKKNSDSVGDFSFARPTASSARRTAAVAKATPPAAPTRKILHNK

NSLDVVKRRPTPAPKTPVMADKKSRAQCSYTPYTGPLPPLNVQSSFAPKGSQTVFLEDRR

ATSASTKVVRKSRPA

>contig32401 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53304.1|) 1e-10

MTEQRSAPSVRASMDFNGPLNALSTSPNNRLVAVGGRD

>contig33374 Frame-1R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY56575.1|) 7e-49

MRYLDVVCVFIWDFLLLGERINCWSIVGAAIICTCAVVIALRKAHST

>contig33679 Frame-0R

MSSLIFTCILIGAQVSLQEARRIHYTSVELR

>contig35101 Frame-0R

MFGASTDSMLVSNNLKPTQLVIVNITSLCGITPFKTHMMYCTGKAAREMHHRVIAAEQAA

FDKVRVLQYSPGPMDTDMQQTLRISPTVDSELQKQFIGMKAAGKLIPPAQSSARGVKLAI

SGDYESGSHVDYYDLDM

>contig35484 Frame-1R

MSLTRKSQIVQDDIRRVKNTIRRNLAQHTETFTRSAHLSGWHHFPTKSSHLIFFTRQRTE

RIYRPLLPMLRYSRYYFIFY

>contig36081 Frame-1F

MQSPKKNYLEIAKKEKLEAPKTNNIWRFIKRPSSSNTPHTKWVFKTKSTADGDVERLNAR

LVACGNEQVFGFNYVFTFAAVMDIDSEYNSSLAAAWGVHER

>contig36162 Frame-1F

MDISTDLIELSRTPVAVVCAGIKSILDIPRTLEALETHSVPVIGYKTDQFPAFYTQDSGE

KAHLRQDTPEDIARIIYESDALLLPNGHIVAVPNSMPVPSQLVNEAIELGLQEVMTKKIH

GQAVTPFLLKRVNEITEGASLKSNIELVYNNAIVGSQIACALFHLANPVRMTPTVKAYSA

PEKKISRANTGKRVLVAGGLVLDIISSSTSSLIRGTSNIGKIKQSSGGVGRNIAECLHRL

ELDPLLVSCVGNDAPGSILLENLKQLGMQTSGVSISETKSTAVYSAILDSSGDMDAAVAD

MNGFEAIEINSISDKEIEVAELVIADGNITSSAIKELFERSSNFGIDTWFEPTSVQKAVR

VVEGGGLKFLKYMSPNLDELHAITEAIRNKQYNASVNSCSEPGDHFPLVKESAYFSMEIM

MRLKEDLITTLLSMANGDTTRSKYILVTLGRHGALIASINLCARDLNTMVDDCKFQVEIW

GQHRINNNHLISIVHHPGTQIRATNCTGAGTKLKIFNRKHC

>contig36632 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70653.1|) 3e-52

MALDLEIPGVLFNYSQLLMSLQRLDEAESVLKRALTFAHISSLSGENLELIRSALVSVSS

A

>contig37424 Frame-2R

MWMSDIGTHSKCQVMEERLESLAFCFGLNAVNQRYRERVNSDILQVLTVMLVESQLGTRN

RAYPLPVI

>contig38379 Frame-1R

MACRCQAGVLSRQDVALYYGRVMDDSCHLMSRQP

>contig39170 Frame-1R

MHLRHVCIEVPAKETALGSNRKLLAIVATSDAYKEHTYDDAMVYLHGFPDMSVHPTKVDF

ASRVSAKLAEFWVHQNDRNNIFVTFNFAGVPGSDNELRFTDKLISIEVEDMIAVCKYIRA

QLLRGNGKVHTVGLSTGAILGALLRDKHMSDTITVIAGLLDMTKGVHFDFTKNQLEQSEQ

RGWCWKEFYLVESCPLPKNVELSLDGIHSTTELTDANAPSKIFVRLNKDYIDEYYDGSLN

ILKSVSGSGLPPLLVIHGDADTDVPYANGEEIFAAAAEPKTFLSIPGANHMLSNSKHLKK

RCGRLENMSLVYDSDFNGEL

>contig39589 Frame-1F

MSTPLEVWQSIDFKIVLAITIDHWTEHRERYRHCCVVVAPSPVFDEEGLAAKVISVAFEF

RQHAHSQHMEKWQLLHLIPEQPNVYHLLLNTGTVVHVFVLLARKWSTRVRTKRSSPPKDK

TEQSFRAKHKKMTPTGLGISHFPQLPWYYSPVFPIKFQQLTEYRQQNANKLLTTEIACIC

QHLFDVERFLGEFLESFTPLQHYNLMDYDIRLVR

>contig40008 Frame-2R

MYVPCRIATRLKVSTKLVTWLSVLSECCSPDIANNVIDFVSAVCVVSTTPTYLSQIVRNE

NIQLLKTLHLEHTDFPLWSLKRSLLTLTFKVQYSRFRITLSTQNASLERHENSSLFNEPS

YRFAENFSQAPSEAVYLV

>contig40677 Frame-1R

MARIDALPKCAGQRLWASVFRQCRQLRPYAPL

>contig42086 Frame-0F

MALLSARHHGSQLLLLALIAATLVPSETLNEHKPHCADFRQYCAWNSSTSSCTFTKSMSF

VCGPRQSLEAPVSISTEFESLMDANVVSTSSFAGDSTTKELAVAGFTCHWDVAGDLHFAP

RVSVVVEGDDCLLHIGSGQMVRLGAQATLAASSLSVEASFVHLDEQAQISASYSGMFRHQ

QGLFTGTDVFGASYGGGGGQRLIANATMLTEQTTWGFFDARLQTVWNEFRGQKEAILKQS

SSGWQLASLWTTEKDDINSPAFDKALNETSSTSAYGSIVPFLLGSGSRAVIVRNNSKLIA

TVNGGGRIQIKASKDVVVMEEASIEANGGRAINGVSGGSGGSVFIAANALSVRGTIQAKG

GDAFCSADAVDRGITHCYPAGGG

>contig43016 Frame-0R|Blast-6-phosphogluconolactonase, putative [Phytophthora infestans T30-4](gb|EEY55014.1|) 1e-105

MDVRVSSSPDEVGTAVAKLIFSLSKQAIATHDRFTIALSGGSLPKILSKGLQAIKDTVDF

SKWYVFFADERCVPLDDDDSNYKACKSALFDSISVPPKQIYTINTFFLNPEAVAVDYTRK

LANIWGSDVLPRFDLILLGMGPDGHTCSLFPGHPLLKESIMFVAPINDSPKPPLQRITLT

FPVLNNAAHVAFVATGANKAELIPHMVGIEKRTPPLPAANVKPKNGIVYWFIDKDAAAKL

>contig43081 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56530.1|) 2e-39

MLQNLRGLGGRRLINWRSAQRCLSVEQHKQTVLRLESGACGLPHPQKRATGGEDAWFISG

NTVGVADGVGGWARKGIDSGEYSRALMSSAKLTVKASSEMATPLHVLTSAHRSAQCLGSS

TACIIQLEESSLRAINLGDSGFLLCRLQPDKVEEGVSRWQVIHETPSQCHYFNCPYQLGF

GANGDK

>contig43838 Frame-1R

MIHDNKASEAEVKRFVRLRI

>contig44822 Frame-2F|Blast-DNA-directed RNA polymerase II subunit J [Phytophthora infestans T30-4](gb|EEY68824.1|) 1e-17

MNAPSRSDSYLLPEGAQKVAYEKDTKISNAGKFTILREDHTVGNLIR

>contig45483 Frame-2R

MKAKSFAQNLYILDYAIEFLLAGCTSSSSDTSYALFEFEVRVVLPTMKQFEVDLPSLQII

IAENSLLRSKMDETELTNSQQQAARA

>contig47401 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55595.1|) 2e-15 NOT\_ORF

MHI\*RLVHGLQIVDAAFVVSAFYFCLDFGDTLNEFANY

>contig48109 Frame-0R

MNETAPTSICNFVPVKSSENIPVTNLFAISLGNDFIGSGKFILPNEGANGLRIDCKDFGA

ALWRQHAVVITTGFQSMLSLTNPAAEDAHRRNVAFAMCEASFWNITPLLLEATNISTMSS

CDVTDPSPRYFDGSAMLIKLSSDAVSPGFWMYEVGLYIWSKRKGSPLSRVFRVAGGPTTA

L

>contig49047 Frame-2F

MQTSPPYWRKDHTLSYSSNRSKTIYWTRKTKYRQEQLLPICAYTCDIQSNYRQNYRYSDT

ASHLICRQRCHAVHIHAD

>contig49748 Frame-0F

MAQTPSPHEQSVLKAHGGQGFSKGHDAKPSREKGLRRQKKFGLGVYADLLFPPNINGTSR

TAVLVMMGAWSRYMTLQSFKNKSAAMVNKHAQEYVVWGERQAGRGIEKIVQSEFEMAESK

RFPIQMILSDKGSEFVSKETAAW

>contig49924 Frame-1F|Blast-ethanolamine-phosphate cytidylyltransferase, putative [Phytophthora infestans T30-4](gb|EEY66711.1|) 4e-74

MSEALVSRAVRYVHELLHSPAANDIMVHVHQALARIGFPEPYPDAERLAIALLTGIFTLL

AYFVLFGKRHRRRRKVLQNELDKAYRKVQELQDNMALMEVEEREAPPKEQIRIWMDGAFD

MMHYGHMNAFRQARSLGTYLVVGVNDDESITA

>contig50427 Frame-0F

MSSSQSMNVTILLFACCVLLNKVCRVSTVVRTGSWTKHRDST

>contig50896 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63623.1|) 1e-19

MTRTWRRSLPDTTLALLRGRRGTISQLQCIQLASQMHKHLQLLWQSYHLLAKDHLFPELN

EIRAMLLELQERGEMALKYKHTLLSKLQGG

>contig50908 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61616.1|) 2e-83

MANLRAPNRLKQKTPPPPPRRDQDQPRPIARPPLLGATKPSSHSYATLLHQVPHREHEYP

PVEIQVPIKEDENDQGVYAVRGSVYLDGRKHSEQLGTGSACQIWVEDVEEWIDALVEHVT

VQDDSKYDAKLSTLYSHVFTSETSSYDIFWREFKAYSGA

>contig51279 Frame-1R

MGDVFASTSNVVDRVGNTIGAVGFVKMPSNEADVADVREAVLAKFFRRMLLIYPFQIVPN

RLHVLDLDDTV

>contig51994 Frame-1F

MTPLCCESPACLNTVMYVVQDFMALCATSMQKSCHRPAAKIANF

>contig52670-0 Frame-0F0

MVMTTVFAILVVVSALLLVEAQQDGCRCKRTMKGREHLHPTRNSLPILSLDETQELEQLP

K

>contig52670-1 Frame-2F1

MPVQTNHERSRTSASNAKLAPHLVTRRNTRARAAPET

>contig53563 Frame-1R

MPLQSLFPLFLSYHAVVFMRNEHVSIASILRSKNTRL

>contig53930 Frame-2R

MSTSQNLLSVGHDAAGRRKSKRRNGFRYEHYRKQL

>contig55129 Frame-2R|Blast-malonyl CoA-acyl carrier protein transacylase, putative [Phytophthora infestans T30-4](gb|EEY62333.1|) 1e-50

MSIAVLQVLQHEMELPPVQFVLGHSLGEYTALVAADSIKFADAARLVHVRGLAMQRAVAP

GVGSMAALMPVRAEDALSLCHEASASTGKVCQIANYNSNQQIVISGDARAVDAAIARAKS

TRV

>contig55244 Frame-1F

MTSLLSYTTASICQCKVIPVSSMLPVHPPLLFVKLYLDELHAQ

>contig55859 Frame-2R

MKRLVGIGDTTSSMSSYSSSAQSSILIDP

>contig56241 Frame-0R

MVNSPNVGNSGTPILYQIYKVRCATKLKNQTLRCLRRKLKCAPRSCSLTSSCA

>contig56447 Frame-2F

MSSKSFGYNLDKSPNTTPEKFVTSRDND

>contig56911 Frame-1F|Blast-phosphoglycerate kinase [Phytophthora infestans](gb|AAN31474.1|) 4e-63

MAKLSINDVDVKGKRVLIRVDFNVPFAQDGSISNTQRIDAALPTIQHVLDNGAKAVILMS

HLGRPEGKFTTKDSLASVAVAVEQKLGQKVTFLKDCVGPDVEAACACPAEGSVLLLENLR

FHVEEEGKGTDDKGNKTKASAEAV

>contig56986 Frame-0R

MEIDDYALVYKSILTESCVVTLGSGRSKKP

>contig58975 Frame-1F|Blast-proteasome subunit beta type-3, putative [Phytophthora infestans T30-4](gb|EEY54548.1|) 2e-38

MMTQDFVVAGTMEEALYGMCESMYKPDMEEEDLFETLSQCLLSACNRDALSGWGAVVHII

TPKGITSKKLQSRQD

>contig02120 Frame-1R

MFASRLLSQVQQQLQVASVTELDVQILLANYRKLPEVSLPTPLDDAMIMFDYLVQQENVS

PENIILAGDSAGGGLVLATLLRLRRARREMPLAAMCNCPYVDLSADVAISEHCFISKSMI

DAIRDFCVQETPRTSWGESAMLQTDLRGLPPLFIQAAEFDILHPQSLALAANAQSDGVLV

ELNMNEHMPHVFTLFPHFMMPQSSVGITTFAAFITRRLTTYRVPVQQPQAAPAF

>contig05338 Frame-0R

MIWLLAVALSCALLSTLLAAYLQLGNPTRETIFWIGIIPGISLFITGILGSVSLVLWQKY

YLQLDNGDCLSITVAATIIAYVAAISMVIRWRWPGICAIPNEQQALGSRSISNQYLPHCS

RRRGSITATTRRSAPALDLESVVTPLDR

>contig11003 Frame-0R|Blast-CDP-alcohol phosphatidyltransferase, putative [Phytophthora infestans T30-4](gb|EEY59537.1|) 1e-36

MIISHMCKIPFTPQLRVIIPFGLVIVNAYGPAVGFFSQPLIPPIVASSTYVIFIVLVYLH

FVTGVVKDICDFLDIFLFKLSPAKKETDKSK

>contig12464 Frame-0F

MEQLTKHLANLSGEDTGMSTTQQSSSEDKGKMTSGHSEKTSSSGGSSKPKSEFADLEAKI

LELRKKQRAVVDTLSKAAQSGDTKLAKECQRKRNKIKEELKEAQDELHRLKTKGKPSTRG

DSSSKDKKEEEAPTTLSRQPSSQHNKKAKQDASNASNADAKGADSTSTSGSTRGKMPMLS

GFLDKGPTEWADRGIISGMKAMRGSRERWCVITPDGFLKYYKRRGDSVVRGEINLADKSF

EVVCEDLRHGNEFVLSTDEQQSHFFTKTSQELNNWVKTLRAANNYLLKMAAPAQSPVRSK

DKQATRKQDVDDSHLDGLVDSLPEEDEQFYGRATLGF

>contig13096 Frame-2F|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY60765.1|) 1e-102

MIANANMPSQQACFHIINKYMQLMTRENDPKENERVLATLETTLSTRTALLRAGESSGGN

LVADALKIELAADVGFINGGFIRGDKEYGATSKITVGILKHEMPFPRPAVLVRIKASDLR

DALLEHLSKYPQQSGSHPHVSGLQVTVEMHETSFKITKMAFATDELIDLEQELLVATSKF

VADGGDGCSSWLKGEIVRVGCQIPEVVANFLVKKKVVAYGEHESRITIVE

>contig18736 Frame-1R

MPVLIDSLSKCVTVCLSCILHSRNHPDEIRRGELGISTRRRDIINKTFIIYDE

>contig19111 Frame-1F

MSHDGYYASSRDDTAPPAPHNITSNFHDLSDSNAMNAPNGLLSRTYITMPLQLQGDEDQS

MSDSERPKSSSALNLSQASVLDIVKEGKRVIATFLKETQCYDVIKNSGKVVVFDVKIPIN

LAFFALVEHDIKSVPIWDAEQGKFVGMFTATDFVNILRHFYIRGSPMNELAEHSIASWRA

IPQSLSMAPTREEMVSVTPEHNLYEVCQTLQLNRLHRLPVLDPTQISVLSVITHSGILEY

LVATFREQRRLFDQPIFDLGIGVYSGFVTVPEDMPLIRVLHTLVERRVSAVPIVDSGGVV

VNIYCVSNVTELVKDRSLTQLDMPVGEILRIQAAEG

>contig19861 Frame-0F

MFSNPTMKKEVLAGWAASELPLYKVQAKLSNFGIDDKTKVSDMLKFNQFCLDKYISARWD

SRKLNDFDRYFQDVDKKAISSDIVQVARKDFHMTEDDLTALLKSTKADLSSHLFVSLTKL

NREFDKPKDKNTLLRELQNLNDDSNTHL

>contig20630 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61370.1|) 0.0

MSAVIPSIGLSFLHNANSNMVEVAYLSMQRLGLLYSCAGGSSEVVFSLGNLQMDNQMEHQ

VVLGPKVHQVKEGVSVRLRDRWRSFVRYRYRGIFQELDPNSVSVLQFRMLWNASCHAGEF

THYELIEFILQELEISTDEKFVVNLIRVFQGLEGLTTYHGFETIVNTQLDYAGSGDSSVL

GSSVHSDEQSTRSNVLAFTPMDDVGSGVYIEELSIETIRIQFSMELHGGRYIKTLGPSGR

RLAVYLPESNVKDFRLYLTKLTFTHLYEPQASVVEKVVRRYSQQAVILVLRGLHTVSVYA

NPFRIVYRLGHGIVELIRLPARGLASGSPLELISGAYLGVRSLAMNTISASYEIVAGATG

IVGAILTPFVPESRRKAFEDDLVAFQRAVIEEVDAFDAAEERTMTKTIVRKPRQFDSSSV

GLLTVYGPGSVPLEEQERIDHRAVVLLQLWWRRRRRATLLLAEARRLCPKVKDKKHVLRS

YVCVLQ

>contig22250 Frame-1R

MSILRRLEQCSDSESSLQNVTTRGHAKMRLCNGIPLHEYYFC

>contig22863 Frame-1F

MGFNATDSEAPECAIKYRLVEAEEVSNKSHASFSSRANRSKRKGRLNWCQYPHDSEAAPE

GDAFQAILVNSSSSDVRTRKLHQQGRRGSRSGGKFSGRREYRDSKGSYVNGVYVPNVDTR

VTAQWAKNQIEFYFTSDNLVRDIFLRQHMDVEGYVPLAFVGSFQAVYAVHQDYESLIEAM

KHSETLELDEANEKVRLRNGWEKWVWPNIEGGYGVPRYIKVTEGENIVAGKMV

>contig23723 Frame-2F|Blast-DnaJ and TPR domain protein [Aspergillus flavus NRRL3357]gb|EED47073.1| DnaJ and TPR domain protein [Aspergillus flavus NRRL3357](ref|XP\_002383253.1|) 1e-13

MPSGVVAPIVLLLLLISRIHGFHEDPYKVLGITRSASDAEIKRAYRLLALKWHPDKNRDD

PMAKQQFMRIGAAYETLINPIASTKPQQWRQQQ

>contig24410 Frame-2R|Blast-glycosyltransferase UGT88A8 [Hieracium pilosella](gb|ACB56924.1|) 0.0

MGTIILYPSPGMGHLISMVELGKLILKHYPSYSIVVLTLIPSFNTGTTATYVRRISTTYP

AIAFHHLPDIPLDPLLYPSMEAIIFDLIRLSNPNVNNALQSISQSSKVTVFIIDLFCTPA

MSLADKLNIPVYYFFTSGACCLAQFLYFPTIHRTTNESFKDMNRPIHSPGLPPIPSSEMI

SPLLDRTTTDYSDFLEFCEHFPKSAGIIGNTFDSLEPKAIKAITDGLCVPDLPTPPLYSV

GPLVAPGEDSQHECLNWLDLQPSRSVVYLCFGSLGLFSADQLKEIATGLEMSGQRFLWVV

RSPPSHNQADRFLPPPEPDLDLLLPQGFLDRTKDRGLVVKKWAPQVAVLSHESVGGFVTH

CGWNSVLEAVRVGVPMVAWPLYAEQRFNKVVLVEEMGLALPMDESDGGRVAATEVEKRVR

QLMEAEEGKAVREVAMARKLDAARAMEDDGSSRVALSKLVESW

>contig24748 Frame-0R

MVYDERHSDTKDAQQKTFDAAASGASTCPVDSNRSAEPFVEAEIKSTTLSFRNVFALRRL

RRKRVPVISVTSLYNRLQTSGVVLVDCRKVIEFAAGHLPNALHCPQLNSKAHLSVISCVG

QVAQTVSDVLEITDNAKLRDKLKFRDLMEVVIIGGNHNGSSLLYRLDWGYRFAKMLADEG

RVFSVRFLAQGFPAFAEKYKFMLVASPLWMPIEKANKLTSSAHTLNPSPGTHFPNEIIDE

FLYLGNFWQANSAEVVDALQISHIINMGAITDQRNKFKNVQYLDVAIKDKVDVDIAQEFG

RTVKFIQKVAAENGRVLIHCVQGVSRSSTICIWYVMLKTKCTLSAAYSHVLKCRPLIFPN

RGFMVQLIANERELYGDQSVMEDELELLQNGLLSPVDRSGSALCRTFLP

>contig25439 Frame-2F

MRRHSLWGGCPLVRMPLSGRYYIYILQRLLIS

>contig26672 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56097.1|) 2e-36

MSSSSALGDPSSSGTTCPMQVSSMTFEDLQWTRDGRILSISSQNGCLHNFIILNSVLQTS

FFHPKSPFAALFKPIAPWTLVFTIGFMAVAILLVISFRFNVSCWDVIRAMTGFIEVL

>contig27514 Frame-0F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY54564.1|) 3e-81

MDLKLKTPRFEAVESLVIEQLGIRTFPLVDMKRQRTNFKLSLSAQLIEGRILLVVSSPIK

LVNRLTTEPCCGASSERSDVAIASGNWNTATKSRICCASVAISCVRGSCAACGE

>contig28447 Frame-0F

MPTPCASVRSNEDHSQQKNTGHTFFSESQYSSYPYLVQVTLNSVSFVHRGTHVVERRFVF

PGRVLQAVLTEFVVSSSESEQPNGSWASLNMQGASRKSRLQHHLCVLVRSDCLSVFTASG

DAFEVALPFQATRLFSMSGKGLLLERSSSLPLSPSSKRFGDATTVALARKYRRASTSNRG

DGDRYRYSNADKYSLLRPRYFTLRRPLDEVKPVVLSTVADTNEKTFIVDSALEAVNVLED

ATSLILVTFNRSEQAFCVFRINMFQKLSSGLTPKLRLLNEPTRMKQRSKCNLEEVQVPIE

PDWVATLWWKSPFLGPRSSDSMLSSPTPSLLITLPVTVVTKTS

>contig29000 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57569.1|) 2e-97

MGNRRRIRNMLTVSDGYWGFVHQKRFYRWLYASLTFFAIFAVVVAFFDVGAGTSHAASFV

ASKYTQGQLDENQRLLQWMYIYYPTPFAFAWFLVYFAKFFFCWKIKRLRKARNYKYNLML

ASLVIAIFYAVGLKFVLRMSLYSGPKLRSAFVIGLCELGLVSIEVFDERKERKERHQKKR

LLREQYAAEEPTHRRRADNPDNALPQWPGNGDEFILV

>contig29109 Frame-2F|Blast-thioredoxin-like protein [Phytophthora infestans T30-4](gb|EEY66345.1|) 7e-95

MELRPRTEATIIAAMMAFKELHKVERDQEYKISILVCPSERSQGDEEKLVDTDVLCHVGL

LPPLRSDLVKLQVAGLPRHNAAAKDSAWVKERKVIYDKMASDMEEVILMDPATRHLLEGS

QTNFYTIRDGTVYTADTKILKGTVRSLVLDICVKKNIPLKLSPPSLDDVEEWQGCFISST

SRLVMGAKSLTYEHPHTMESLTRSFLAHPILDQLTTAVHDLIISRSTE

>contig29585 Frame-2F

MFADSEQHCLLRQSYMGTDLEDSRLLFRVVAPTSQNPFTFIGVKWGRQTYGRFSQPRDFV

FLEATGIIQDASGDSVSYGIRQSTDLSEVLTLPRSHHVRRGHLSVCQTFANQNPLMAGST

RHSVEMFSRAFLQMDGDVLVNVAASAFAEKLMAFASTMECATAYKLTWRMRQCFHSTRSE

ANMDLANGFCT

>contig29927 Frame-0F

MPSKHAKPQEANPSAKIVILSVNDVYDMIPNENGHGGIAEFATLLEQQKATIPADATLLV

TLNGDFLSGSELAERFKGAHMIEIMNHLQIEYVVLGNHEFDFGAEELKLRMGESSAKWFG

SNVLHASSNALFDGIVDTEIISLNDGLKLGIFGVCTEETPTLSFPGPGIKFDDVVTTSRR

CVDELQAQGADFILALTHVSIAIDQKLARHVPGIDVILGGHDH

>contig30293 Frame-1R

MMKENELDGRLFTVRKRTDEEQKEEDEDQAAFQSKHSREKEMAPEEFLEHYLTSEGWKDK

METIPHYEDIVKEDDEDAEELKNAEEFEHSYNFRFEEQGSNVIQTYTRQVEDTMRREDDA

RKRKRAERKERKALERQKKEEELRRLKNLKQAEIEQKLEKVARLMGGSDSTNGLKPEDLE

GDFDPVEYDKRMHAVFDEQYYKEDDEMVKPTWDEEEDKELFGGLPVDLEEDTVEMGSEIV

DEQNEEEEEEDIQLKKMTIEEMERAKQQYMDELYGLDYEDLIGEMKCRFKYRQVQNNDFG

LTVDEIMAADDKDLKQLVSLKRLAPYADTEYSVDRKRLRNLKKSIRKVQEEKKRRKSKQE

PSKDTETQIVELSKKKRKRSKLKKEKTNDSEAIEEADDKEAKQMNEEEKQDSTEPVVDNV

SKESEKKKRRSKKKKNGEKKSTYASTGLSTSRLESYKL

>contig31184 Frame-2F

MADSPDAQDALASFMNITGAESDSAVQFLELTNWSLHEAINLFMESGRPSHRAAFAGSPR

SAARSTNASSQPVPAASMDIDAATAAAIASAYGEEEDLVRAPDPSKRQRLVESEMDLSRP

LRHLRDQSRDFAAESIAAMTAGSISTAFGQLNAVDTPSHAYGADGASIERTRDLSTLFHP

PTSIIYQGTYADARTHAKNEGKWLLVNIQDEIVFASHMLNRDTWSDDVVQNLVASGFVFW

QNYSGSEHGKKFCSLYQIDHNSLPVVIIIDPRTGEIRQHWTGFHEPQDMTEKLSDFCCMR

AVDTPMTEQ

>contig31823 Frame-1R|Blast-phosphatidylserine synthase, putative [Phytophthora infestans T30-4](gb|EEY63057.1|) 0.0 NOT\_ORF

MAAGSTRSSLRQRKVHAPSACTVQDEHNDRVDAHVSSEKRFKSRPESWTYNTFRATHGSD

VEGLLLFPEQPRQIFVLLIVVVAFSYYSFTHDSQDAVQNVRNALFAAIGIFLVYCFLQTR

DGLMMRPHPGVWRVVHGCSVVYLLLLAAMLVQNRESAIKGMQFLFPEVGSRPRTSIVAKL

QCDMNFEVCNPIIKGSNDRLKIMKL\*HL\*SLTRGMTSIWFLAHMTGWWGKMCMFRDWRFC

WMLSIAFELLELAFQFVIPDFQECWWDSVLLDLLGANILGMCLGRVTLWMLESKEYDWPG

RRGKKMGYIRLALNQFTPFRWEEYHWEVFSSFHRFAAILFAFIMCLVSELNAFFMLTTLR

IPKESRFNSYRLFLVFLLGIPAAAEYYEFITNPACWRLGQNAWMILSIATFEVLVWVKFS

ANGELFTKPPPPMVMYPILAFFVMFSVWMLLFFRKEKQRPGLQRSRTQVLSWSYLDVLFW

ASFAPFLFLASQWA

>contig32185-0 Frame-2F0

MTTDKKAARDLKLLISFVAMIFVGLGNKIFQKLANCFV

>contig33919 Frame-1R

MIPRSQFYSCIQSDWHEYTCNDFPQQSGLDCAILHLPSFHIASSFSASSLLLIIYTQSNY

LGHYNRQCQNATIYLSYGRLSSRQ

>contig35100 Frame-2R|Blast-sepiapterin reductase, putative [Phytophthora infestans T30-4](gb|EEY59412.1|) 5e-11

MEWKMKATASELRCFVESVDLSNSSDYASKMDKLRLQVSKQSYDRVYVVHNAGSLGKLGL

VQECASSIIELSN

>contig35676 Frame-0F

MQKMQRTNEQLNGLLQHLLQRLNGLENDKDTSATRHEFTQPVSFKASTSIAQSQARTLPS

IAIPPTSTSLNGPQQALLQLRQGHQPQGTPRELLTPRTPGSSSLYLRPVQSLMVKLSPTS

RPTPSPRPYINTPSYTQPHQEQHPRKQQRWHLPQSPRTAKQSPIKRTRLDSTTSVSKTHS

KIGLRSPEDVAVRELSRIASEIRADLLACITARVTGFLRVHCDQTDPTREADADAVATAV

GSDIRQKLALLQPSSSSSDPMLLDVETTCMYRVEILKFISRELQRAVQDAVDKRMPAFER

LKQRSAKDRSLLALLVQKAQKALEHQMHSETAAISTGRR

>contig36017 Frame-1F

MIFGLLDIMSNFGTLQLNPDLFGPEVNIIFNAAYVNQAMISNEFEVVGKFLQCMKLFGNT

KSAESQNMIESCERYLLFKHLPDGSWCKINGSTVDQYKATVTCSKALLAPAFRGFGPVSS

EFLRFLEKWARSTSPKLPSTAVSGAKQPADMSNLKVLASGATVKLSTRTRLKRLEAMYQR

LAAPKGGNSSLEFLMTDRMKQLLKLKKNEAQPEQGKSVETNYSSSQNEMAQHVENVVASK

GSDTSVAVEEGTADGMTDSEDLKSDHPSTSHDRCNSRVPGQDDDDMLTSMSLHEDLEIFD

GLQFEDGGGIIDVSFQSLVPHGEADNGNRTHSVEGYNGTDAPGQDEDETMDEQMIDDDED

EIESSEAREGGDHQGAAADETADTVNAMSDFPEM

>contig37010 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69627.1|) 8e-43

MDRAPTPRSLVPQFAYAKKILSAASINCIELPGVEADDIIATYAAQYTAAGFDVLVVSND

NDFLQLVHDGVTEEADLDTSTDRTIEVPATIVEIYQP

>contig37425 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63945.1|) 1e-18

MKDPFFEEDSNDFDDLYGHLRPSVSTSASRPQSRNNDGSTALRTSTNSYTSAYSSVASSS

VASKSYARERTGSWASNVTDVAATGQRGKRRSRHGKPR

>contig39171 Frame-0F

MKLLQAKLLHDEFQFSQADIIAVIGLSMASMLMEKFASQATSLAMACKNRLLLSINQAKS

LFTTRDYENLRVVELYERSIGDENSNLTRLQALLQITDNTNSSTLWTRLGLATIDSEGFQ

MSRCLTQLMRSNAKTVPFCDESVERNYFNALLGLLKANSLGEDGFCLDAQKLIRAQPWNP

HAYILAGTSILKRSNLAAKIDSHDITLRQLLRLLQIGLLNARGNEFCVAQLYLLISYCYV

MLGEQAEAIANSTQALNRIEAGKEKATVNETVNTDLLEARLLSISNPNKAIKKYLNIIKS

VSAAAAPCSNRIFPILIELGGHYEQWQLSNAAITVWKFLASITSTKSARSTADKNESSAS

TCLSSDGYLATCFFANLRLALVHGKRNQLKSARKHIKVAQALAETGEDLRPSTVAAFVES

IFSN

>contig40485 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56857.1|) 1e-78

MVERLNAPYLSLGDAARVWHEHCRIGVGVREWDAVGRLQTISLWNLIRSVFSSIVIDIVE

LRPHLPDGAMILTKWRIQGEIASTDLLARVCASEDCPATMRIALLQFSRPI

>contig40759 Frame-1F

MADFEAAIAFLQKEGGKSPEESYFSVFKLAEHQVHCPCGELYCSETCKQAAYAQHHALLC

PRSEARETAMGLFLNHTLVTNEIFQLAAKVVAKVLLVYIATHDMAQARGAVDMFCKLP

>contig42087 Frame-2F

MGGDDCSQSLGNLFARFLHLKLSKWGRETVSDGEEE

>contig43017 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66773.1|) 1e-113

MTTLVVGKNLPGSRNGEFFAWEETAGGRVAETGGAFEVEQLIQRLIRADPTALSQIYDVP

DDHDTYLWQYEHLRQVMKELNVLVARLDGSCTNDSCPVMKATDEWVFLCAAHKSPKECCA

FEYIVHTMDNVNTLLTSSRVFPSRVSISSNATQYFQSVSRRLYRIFSHTFFHHPEVFQEF

EDKSYLCHRFVYFALHFCLIPKSLLIIPDIG

>contig43163 Frame-2F

MSAGFLRKSSRTLSGRLTVSDLGLFHNEDDDQNPEMEPYQALRASRLNTKKQLKDSYEDN

VMKVLPTRSQSQR

>contig45190 Frame-1R|Blast-dolichyl-phosphate beta-glucosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62508.1|) 2e-25

MHGFHMIVSTLCIENVRDTQCGFKLFDRTAARVLFAPLHIERWAFDVELLYLAASRTSKS

>contig45293 Frame-2R|Blast-hypothetical protein [Vitis vinifera](emb|CAN76565.1|) 1e-08

MVDANPTRGPIYIDVYEVQSDNIALLENTSTQGQPNAHDYQSTVGSLLYVVRYTGSDIAF

AVRKATRRTNKLQLHDWKLVKHIKRNACNKARYEARCRNEREIISC

>contig46375 Frame-1F

MIFAIYIQLQRRDGTAERLFFTTRCGLMYLENTLAHCFMISHLYPRDSPARSLK

>contig46919 Frame-1R

MTNARDWQLLPLRLIAVCVRMSRTNSGLLMGIESRRCRPNADTLHLGAKWQNELIYLSRG

DDRAIHWPSRFLYAKHKQI

>contig47376 Frame-0R

MSWFHHQTHSPPLTTRAAARKLIAHWTARKRSMSLPPKDCVKTEKFCLKKADGCVITKTV

RTTTHTKTSRTGELVTTIEVETTTDAETNDVAEKRIVESDSTLETTLEIAKMSNSSCAEN

MAISFAKQDDSAHDETMKTEVFHSEKKDGSIVTKT

>contig47400 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60199.1|) 5e-29 NOT\_ORF

MGCVDLDPLKEPPTIWYCPACQEEDCANISENRTWCCPD\*TNVYLFE\*SVIYGDMILHVL

IILL

>contig48108 Frame-0F

MLNNGQQVEAVIRVESKAQAREKKKQNRWEPALEMMQKLLQASGAMAQVDLSELNEDERM

QQERDVALMRCDRLELLLYRMICRFEEYKEVTFDPNRNKYGRLPQRKPSKMLAPRISMLP

TPKRFGGAVRSHHQDNQEYFKDDEVSAVARVAAEKRERELQKVVAEQKHQIEELLQRCKK

PRRRMICFGMNCVSFLSGSTVVEDEHQRASETPLVDSAQDIEGEEVDTPILEASTVPSEE

MQGMQELLNVYRSLFDDVTELMYTKRPMLCSPPSPKSGSSVITDSNSTTYASGDDDETGD

DCFSIDGCNASEDGDAGVNDTYREARRVNALSSRLGRKLDQYQDAIQRLEKELITTQDEL

ETSSAATKFAEFQLQQLRSLTADEETKETLELQKKLEDLEDIMRSQRDQLALALNGKVTE

DALA

>contig49046 Frame-2R

MSWTCGQCTLVNAKESAASCEACNTVRVLQCPTCKGDIKYGKRLHVNGSCYHPDCFCCSK

CKRPLPHQFKVVNGRNYHPECTPPPITTTITKTAVTGKRVVQSGNRINIANVKKNCASEH

GKAHLSEGWHCASCTFLNDNDLAPTCGACEAIRIMQCPGCNGEIKYGQRVNVNGKAYHPD

CFRCAACHASFKTSQFQVKEGEYYHQECYKELYYPRCDVCEEIISCQPGTQKISYKVMTF

GGQKFCAEHESCDRCYSCQRVEPIIAARQFHKLSDGRKICHDCCDYMVHDTIEARSVVKE

VWAFMHEIGIDLPEIPVYLVESSILDEQCNAHRKTKTLMHGNKPTKSHVTRGLCLSEVSQ

IQHMVRTGKHAVPRVTSI

>contig49749 Frame-2F

MRPSRSHHRCRCFSSIAKVISQYRIGSSVEYFRNCSYTSLITSFSSSFYKRLVFDKRICW

SLFFLATLAALARTCIPIRPFVFHSRLSSNLIL

>contig50743 Frame-1R

MEADKAMAMGTSAFATEVETSAPPTTSQIVAFSFRNPFHDALRDSTRRFPIAGKSIRIDQ

AWQSDGRGGTALGFGASVYDAAIALSLYIADHPHLVKGKRVIELGCGPGLVGIVAAHFEP

KHVVITDGDPASVALTRHNIRLNDVSEEICTTDKYLWGDLKHHLVEEHDS

>contig50800 Frame-0F

MACCDDQQSQSKSKGKAISNANPASLLDDFNVILHPTSYRGLYFEKSPINILSLCGQTCN

PPFKW

>contig50909 Frame-0F

MRLPSVRHSKCYVDDHVHFSTYDEQAALSNA

>contig51995 Frame-2R

MLGEQMVKTPMVMPMQWPTLSIIVIVGPSTLYISVTVTSNLKSTSLDSVVCVTNRANLFN

A

>contig52288 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59832.1|) 7e-93

MVDATILAPLPFMLGFCTLSELQQLAQVSKAVSKICEFEWRLRTIASFGELRFTTCSWRR

CFLLRSRFQRKKAFKHVTARIYLMNNRGETRYFSIARGTPLMCSRERAVVYSHCKRMFDL

SLRINRSIQEISALIDMISVEETRELLSEHINLMTSVASLRGSLNFESELFSIFPAPVLL

DTNSLLRVTHTFEDENDAEFLQSSLMMMQVWASIDG

>contig52671 Frame-2F

MTEKFKLSKEMLHHAKVQWCAAIASQKALEECNRLAQVEVSRLTQLLDCNVAACDGTDAK

DKQRRVRLESEKSSKWTEETAPFAAPPGDINSPLIKCLLDHWTTDKSKCMVLTDWLHNSI

RGTGRATPMRLTNLSSEVTAGFLQLLVPIMRERHNVSVSIYRRDNLHVLTDLVLQTNHSH

LSASTFEPQVVITREDPGKSAEPQLDSVLCRSRDTCGGSILLKGEAKFLYG

>contig53294 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62223.1|) 1e-24

MSDTSATLWESELLRARQWIAGNNKNKQHEHDRIYQCVKAHIGYNDHQRSLQSDMVVSDD

EDHRALDFLGDLNAADISILLQAEAEVSLPRADVAVPVESHVQDRLIPLDMPP

>contig53931 Frame-1F|Blast-anaphase-promoting complex subunit, putative [Phytophthora infestans T30-4](gb|EEY68460.1|) 7e-29

MHEMAEQNIAAQLRCATHDLRVRGLKQATKFAAELLLGMSSGAPIWQSAMPNRSDEANEK

IESFAEADRFEAAKACFDLGEYLRAHHLLSFSELWCNCDETDAYCSPTQKTCFLKYYSLY

L

>contig53944 Frame-2F

MRPLALPAWNHRASNSLHYGDLHRFLSASDEQKVLAVMRTQQGQYLTSDDVRYAVRSIVS

QG

>contig55245 Frame-0F|Blast-putative chitin synthase (Chitin-UDP-GlcNac-transferase) [Phytophthora infestans T30-4](gb|EEY61714.1|) 7e-15

MLTYLKAIGQYYKDLLTINSAGIGAQCHLFEHTLQLSAKVKLPTLKDRMG

>contig55858 Frame-0F

MVKIKGQLTTHGKIAIPSNQSSFSFF

>contig56349 Frame-1F

MSTANVLGLVCSPLGVLRNDWTPLNTPYTPQLMKLHLKRHEAYDEQDEFTMSALVSNLLR

QSSRRSFLRCSRFKKF

>contig56910 Frame-2F

MTVKTGLSSSKSASAEHLVILNSNGLTPTTASFGASIANIEVNGVFFNVFKRVNEGVAQY

IYVPN

>contig57135 Frame-2F|Blast-Rab8 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY69822.1|) 3e-10

MSSRVSNESKDDAAAQSRRRSCSFSAYEPPKRLSTTDALLEEDVESMAKRAA

>contig59177 Frame-0F|Blast-programmed cell death protein, putative [Phytophthora infestans T30-4](gb|EEY62221.1|) 1e-40

MNSLEEGGEANGAAMASLLAYLVTNEVVSTGQLVKGFQRFQFVLNDVALDIPNAAKLFQD

IVADGIRDGILPKNFDANAVKK

>contig59326 Frame-0F

MKDNVMLDTEHSYTETDNLKFITFRVWKEAVELVLQWREQDYKAFWLLLAQFHRMIPVDN

NGMDLSGPL

>contig05706 Frame-2F

MVAKDPYLLRTLPLYPCVRKVSRHQTFRYQCKVKWYLSVLVKGAPLQHSDHRVSRFFVWM

IRLKRSSTAVGSFGSNLLAL

>contig06196 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57090.1|) 9e-19

MGKWKLTFVHDVMDLLAVDRSKKSFDEEGNHFNKEMLLNRLIEWLYKPQITK

>contig07168 Frame-0R|Blast-glutaryl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY57306.1|) 7e-63

MVKRNSCGKAIEIARNARDMLGGNGVSDEYHVIRHVVNLEAVNTYEGTHDVHALILGRAI

TGLPSFVPRMAP

>contig10502 Frame-0R

MLHLGWLTIMSGIALLVSGIEEASKFKANAQEHGLMIRFTSLTADQERRLAEERSIGASL

VDKLTELVDAFQDSAIGRFVKRFRVTNKNSTNLGENAGQVVNVYEAGTVSSKPLQSEPFR

KWANSINNYL

>contig11000 Frame-1F

MSEESSTEEVPVSIPRRATKTSIAIDQEDRRAVSRK

>contig12298 Frame-0F

MSSFAFQRASKRVVLITAGAITVSGLTIVSAKEPKRLVTPITCDDGSTISPYETPTRAAQ

LQRLKREQFDVLVIGGGATGSGCALDAATRGLNTAVVEANDFAAGTSGRSTKLIHGGIRY

LETAFLKFDYLALKLVYEALEERAFFLSAAPYMNRPLPIMIPIYKWWEVPYMWVGAKAYD

IVAGSQRFVPRSYYINAEEAMFQFPMLRKEGLKGAIVYYDGQMNDTRMNVSIALTATQNG

ATIANYVEVLQLLKDEDGKVQGAHVRDTLTGDEWNIKAHAVVNATGPFTDTIRQMDDSTK

DKICVPAAGVHAVLPDHFSPHRMGLIVPKTSDGRVLFFLPWENGTLAGTTDSQSDVTMLP

SPTTNEVDFIIDEANRYLAKNVTRNDVKSAWSGIRPLVKDPRHANGSTAAISREHVVEVS

ASNLVTIAGGKWTTYRRMAQDAINKLVETVPELQTKAFPCKTKDVGIIGADRVGEVCNKK

FDKITVTLREKYNLDKDIAEHLMRNYGTRALQVAEIEKSGFLDRKPSDHPRRLHPKYPYL

EAEVVFAVRQEYALKATDVLGRRMRLAFIDSKVSTELIPRVVHMMGELLGWSKARREQEV

VECKEYLKTMHN

>contig13482 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60272.1|) 2e-95

MRFRGLLLLRLSLHVCVALLLTIHSSQLGSSLHYLQRAAANEWVRLLFYVDVVKKIAPDE

TMVETLPHFLLEVEEMIAANANDEFFAGGFAARASALPVGLLFTINETRQHLHGVVRNYI

RLADVALDSFLVYSNNTRSQLPPPLLTVRSSVNDDTSESLFSITNESVSSQWPPALRLGS

ETARQQDTRHFFDTLDAMEMKMVVGMRQKAKEKEKTGKTEMLYEWTVVMRYDLLNQGHLE

VTMNYALSYVPLLDRQRTIGERRMPPVLSDTGVVFDWLTLTTIGL

>contig13701 Frame-0F

MSWAKYHLSLFDNGKECLTNGEELHSDDAVPPTSTIPRITFPQATNKVDKFETPAKRVGS

FQDSVTPLVSPQTVSMTPALTVEASVPKFEKTGKFQFTLPRCTKEDTHNDVDGEDIRLRF

VFSPPLALREPPAKVLSYKIKANTGAAAAFSFVPSSPKLQSTEWVSQPVKAKESAMKSVV

DKPVALVEAGTTGRVLAVNNCGSVNPLAKFMQLKPGQWKCPGCSVLNEGTNDKCPCCETV

KPSASARVKAGLTPPNASHSVSSSDFSFGSSKDAPKVVEKPTGGAITASGFSFGIPTVDK

KIADKSAGSAPFSGFSFGVSAADIAKTAEKPALESTKSTNGGFSFTAPIAPIAVLETSSV

STSSSANVSRPSPSISFEFSKPANMVDETALEPSSATMKTVFAPSFSFGVPLASSAPTLT

AVSNESTVDASSASINDKSNKAKRKAFETEEPEKHAASPFTCGVSATPTTALKPSNVSAS

KFEAPKPSDVSTSKFEAPKPSNVSAFKFEPKPSNGAGFNFGAAPGPFQESSANLERPKKR

LAPFAAADDLSSESSIQAFAAKSALKPPQVPVKNTTVSILSAPSFSFGGKAGSTNNDKMN

ESTTSLFSVGGDTSTEKAAKVNLNNTVPLMPEFTFGSSSATPAPKSSGQVVTKAPANSFN

SFPANSASAHVPGSSANFSFGQSSTATSTGCAPAFNASPAAPSTSAFENKSSVQLSNASC

TLSKSSAPAFTFNSSSPADTTFGLASTSGSAFGKQLSNTSSFGSTSTAFGSSSAFGSGSS

SGGFGSSTIAVPAAAAAFASLTPAASAFSIGASSQIAAPGARPAGQPAFSFGASAPSGFG

GAPAASSGFGSSAPSGGLNAAHNGFRSSSPAPAFGTQTPSTFSNILPPPTTTFGAPPFGA

PAPCGFGSGPAGSGFRTPSPTSAFGAVPASAFTPGPAFGAAPTAGAFGALPSAGAFGAPP

ADGGFNMGAAPQHARGRRILKAKTRPRRTS

>contig15916 Frame-2R|Blast-60S ribosomal protein L4 [Phytophthora infestans T30-4](gb|EEY53349.1|) 0.0

MASAAASRPVVSVLSLDGETTTVCSQLVLPAVFIAPIRPDVVNFVHTNMAKNRRQAYGVS

REAGHQHSAESWGTGRAVSRIPRIQGGGNQSSGQAAFGNMCRGGRMFAPTRIWRKWHRKI

NVNQRRFAVASALAASAVPALVMARGHRIEKIPEIPLVLDDSVEATQKTAQAMKILAKIG

ADVEVEKVKDSKKITTGRGKSRNRRYTTRRGPLIVFANANGLEKAFRNIPGVELAHVDRL

NLLLLAPGGHLGRFIIWTKSAFQKLDKLYGTYSKKSEFKADYQLPRHLMNNANLGRLINS

DEIQSVVRAGKYQKHRRFQKKNPLKNLGAMVKLNPYTLVARRAELRAEALRAEKKAAVSS

KKRKNTCKTDPKRKAQSRALFAKNSAD

>contig16056 Frame-2F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY70558.1|) 0.0

MLADRVASGGAGVHLEGLVEVNGQPRDLRTFHSVMNYVSEDMAFLGAFTVLETLQIGAGL

SLPGHMPPVQREARVQNVIDAMGLRSCSNARVGDVFHKGISTGQRKRLGIALELLSDPAL

LLLDEPTSGLDSSSARGVMQYIERLCQEGGKNVVCTIHQPSSSIYGMLTNLIILSCGELI

YSGPTNAAIAHFFAMGYVCPMYTNPAEYFVHLVNTNFHDGLKLEPFLRALKESAEPQRLR

ADVVRDRSRRDNLANPELLKAMQPWPMDQFVVLVKRNLTNNWRHPGVFWVRVLMYVLLSL

MVGTMYLSSNRGITETSMVSLLFYVQAFLVFMSVAALPALLEHRTVMEREMRSYALSLTG

YTMSNLLAALPGILLISVLASSIVVFLARVYSFPTFLLNLTLSLVAAESLMHLLGA

>contig17002 Frame-1R|Blast-phosphatidate cytidylyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56488.1|) 4e-47

MKYVLTNIFNGLFWFLFPVSLVICNDCFAFFCGKLFGRKFIKTPFLRLSPNKTWEGFIGA

FICTVIYAFFSSAFISK

>contig17727 Frame-2F

MLRLMTKNYLSLMINILSKIFQIQQLMVALRELDSVKPK

>contig17929 Frame-2F|Blast-hypothetical protein OsJ\_19422 [Oryza sativa Japonica Group](gb|EEE64570.1|) 6e-19

MYQKETTDGLGFQHEVRPYIMDLNSTNSTFLNGFKIEGSR

>contig18164 Frame-0F

MKKNLMKAKSLTDVFKLLKGEKEFFDKQDLPLFVKISEKTFDQRGGHDRYGVDVLLTQIG

AETLAKMNAHGLSSKDALVVEACKQIVNGLYRKWFDKGLDLHEIKQKIIGSVDWNAYRQF

YGSLFETSRFVKLKASHPAE

>contig18238 Frame-0F|Blast-inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY59677.1|) 0.0

MSVGASTRVAGVLLTIAGLWIPCTAFPDTFAYKCENQKCLYTTETSGAVYTDPVDCVKAC

RTSNLRNVDEGSDLSDVANMRLASSLNGTCSNCSLVVMSHYNFPQMLKTFDLTPESVAAP

SCNFSCEVLLNTPALWALEGTSSNCFAGNEDTDVECARDGNATIMALDADALSEFMIVSN

SYQFIVDHVTTRVGPGTFSEETTLTVKFDGTGCLASSRSAGQQAFQLTLVSDSYELIGMF

SNTAMEAENSMIMSSTPVTIRVTSGAVLSAGAFFLLRVASDNEEQFGHMIDNVTTAFMVL

PDSDSGGPIDLELFVGASNISFTIPDSFAGSIQNGDTINIMFERLENPDNTSVAIDKVYL

SAYQGLASAVDNSPIRFYTLDDASRSLKAAALDIVTVIVYGACFLFSLVIIRWHGLPLTV

STLWTDLVAIAALFSFAAATGGYLVWVIQPSKAYVHWYTAQYFFNNAMILSLCFHWATVL

SFKWFKKLTFTSPVVVAYVLINTCVLAFIIVVSIAAADKLECVYDVKSTSCSSEEECALS

IAAEGRVIRTAIEECNMEPFYLAFGTGFIVYTLMLMVLGCMVMSRGRTLMLNEDPSDARI

RKSLTIFYVIIATTCVLYVSAQVIYIAQYVTHKGEENQLSDIVWYTFVVWLPHSLPPLLL

LFLQWNPSTETFRHDEAPSLDHSSKEDVFNYTPRSSGSSSHMPYSKLLRDRLSMGDSLLN

NDEPGSRLRIIVRLKLPASFDRACFVSLDFYSSKETITSSNTLNTISTAAAWKCIGTTEP

VGVAGETESVLTNGSTHAIFPFVAVLEVPVIGPASKTLLRFMVHASTLGKRETSATGLDR

STSSPNSQDSSSNPQLSFQMTMFHPVLEFVTS

>contig18568 Frame-0F|Blast-ER degradation-enhancing alpha-mannosidase-like protein [Phytophthora infestans T30-4](gb|EEY55417.1|) 0.0

MAYLSRLTGDSRFEERAKQAVVALWKRRSGLNLLGSAIDVGSGRWIYSHGGIGAGLDSFY

EYLLKYYLISGDSQWLVMFNASYHAVETHVNHDDVYFEVDMHGGKNHVRARRVSALQAFW

PGLQVLAGDVSGAIRSHEHLFPLWNDYGAMPELVDLAPSGSLLSGKRGTVTSWARTSPLR

PELIESTYHLYQATRDHKYLKMGRKMLRDLRRVSEVPCGFAAVGNIHTLDVEDRMDSFFL

SETAKYLYLLFSDDLSVIVPAPIARSRNNGSTTVL

>contig18670 Frame-0F

MKKKRFDKCAQLQSDIDVFKKKRAKFPTAKKALTPSASPKKPELSVKPLKKPEPPVKPTS

PLSSVNEAPVAKKSVLQSTTVAPPSNMDRNGIPPARETSVLAPNSSPAALPGDKRPALEI

PPVAAVPALLASPVVVPPSQARPVMLPPTQAPPVALSPLQASPMTSPPLMPSPVQAPSML

PLVQALDEPPAPLIDCILPQELPTSQLSRRPPAIYHGPAPSLRGGESVTMTPM

>contig18735 Frame-1F

MEGRRTVSTNSENVWLKGKRQELWSTLHQRLIATPLFNGKVRKEKDSDNDEHQDVVPDND

MNNNRLKHRVRCRSNYDARGRCRNLDLENTTFLSPAQKAGCYGYIKRRYTIALAFASNDA

TDDIREPSNISPAEESDVIGSNWEFTKLKNGVQLFKSKRSQCEVRGSTRVNASVKNVMSL

LSTGASTQAFADAQKIIFGADQVIEAKVLASCADSTTSRYFHCGLKYQAMKNPFGTAPLD

LVFLDYTDVKTTSEGKLLGFRILESIRIPALQPAFKYLRASIRCEVYTVVETDTPGVVDV

TFASHLDPKSKCASIKRSQWLDLACARLGNIRSYAEKT

>contig21209 Frame-2F|Blast-elicitin-like protein RAL1A [Phytophthora ramorum](gb|ABB55957.1|) 4e-34

MRLAYIASTAAFFATADAATTCNVTSLQKLLMDPSVKPCAMESGYAVTSLSTPTEDQMTK

MCSSTACQTVLTQVQTLAPTECNLGAFALYADLVTPLNSYCESSGLSIDKSSVPSDELAL

TDTSNDSDPLATVKPSMLDSADQTTTPRKAALSPKSSTAPLKATSPKSEVDDDDGLSSDS

SSSTSQNDTMQDSNFDISGASFISISATAAVAAFVLNFF

>contig21991 Frame-2R

MIVSKSKRLRSFRYMANHSAAPLSSSKPNAHPPLQTSRTRFSTHASASSGSFQSPSTTSL

STFDPKVPHFMAPRLQFETNKTPNAINRSHFALDLHTWTFLNHGAFGASTHEAIKAVEYW

HSQANKQPLKFHDRDLFPLLMQSIEALATFLEVSNPKELVLLPNATSGLHAVLASILQSR

LAKAKTVVLFSTRYDAVRAILQSLQDTHEPHVHVHEEELSLSDSYDDNKVLDKLEKAFKA

VEASGRSVTLVVVDHITSTTAVLMPLQAIIERCHSRGQGVPVLVDGAHGPLNIP

>contig23258 Frame-0F|Blast-threonine dehydratase, putative [Phytophthora infestans T30-4](gb|EEY54393.1|) 1e-51

MFRCGFHSRAAKPFWVRPDSQDYLREVLESRVYDVATQTPLHLASALSQSMPGNCRLYLK

REDMQPTFSFNLRGAYNKIANLTLAQRKKGIVACAAGGHLEAVAYASAHLNVDAVVVAPT

GMTQNISSCIKSKISILEHG

>contig23720 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY61608.1|) 5e-19

MENYHILERIGVGSFGKVYRGRRKYSGHIVALKFVTKQGKSARDLKNLRQE

>contig25555 Frame-0F|Blast-serine/threonine protein phosphatase 2A [Phytophthora infestans T30-4](gb|EEY70034.1|) 0.0

MASMAANGSTKLGELPALEDVPSGERMRLFRQKLKLCSVLYDFTDMRKHVREKEAKRNAL

LQIVEYISAGKVAWDPSIVADLLECVGSNIFRHLGRSSNMSTISATGNTEAAPEEDEPML

EPSWPHMQLVYEILLRFVLSKEVDSRTAKEYFSKKFMIRLLNLFDSEDPRERDYLKTILH

RIYGKSMALRSFIRRSINDMFYTFVYETDSLHGVGELLEILGSIINGFALPLKPEHQNFL

ERALIPLHTAANLAMFHQQLAYCTTQFVEKDPQTAEPIIMGLLKYWPVTASAKEILFLNE

LEEIIEMIKMQQFAGVMRPLFLRLSHAVCSSHFQVSQRALYLWNNEALVRLVSARRAEIL

PLIFGALYRNCENHWHSTVQTLTYNVLKLFMEMDSQLFDQCSAQFEEREG

>contig26257 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55358.1|) 5e-47

MGAFAECLEEKERVKACYSDWFQKLWGGSLERSKCEQETEDYRNCVQDVMKNRKEEGKRK

LNLDDENDWMDQMKDKTHGAADEAKSRARNAQNRVYDEKENAKSSLRSKASDVTSKVQDT

AESWVDSVKGFTKKADKKARKYADDQDNKARKYADDQDNKARKYAEDHK

>contig26671 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56097.1|) 3e-40

MSSSSALGDPSSSGTCPMQVPSMTFEDLEWTRDGRILSISSQNGCLHNFIILNSVLQTSF

FHPKSPFAALLKPIAPWTLVFTIVFMVVAILLVISLRFNVSCWDVIRAMTGFIEVL

>contig27517 Frame-2F

MSILWGRLQNGNACSSNTVMDDDVYKLRQPLISSDNANDCDGSTEDNEFGGLHPRWLEFD

VSTATRRTRRRRKDEEDLGERVKEFSINVGPLKLLRSAGSWLVLLSTASNFLVPRNPRTL

LSTQIPTPRRKLEGMDEATERALAVLALLTIACSLLLLLVVYTQAT

>contig27562 Frame-2R

MYQYWLSYPFSFQRQNSAPCHCPSLSFPSLYNHQQHFLSVALSEHGNTRRMTRFLLQSSI

KTSVFIHLLAQQQRDRK

>contig28031 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65279.1|) 1e-124

MQVVWAIRLGSFLLIRVLKRGKDERFDEMRANCMAFFGFWVYQILWVFSVSLPVILANSC

GSQVDGGFGKARDITGLIVWAFGAIVEVTADASKSAFHDVPQNKRKLLRSGVWKYSRHPN

YFGEILCWVGVTIVASANFGSNRGETWFYYVSCISPIFTFLVLIFLSGVPLAEDRYDERF

GLDSDYIDYKKSTSPLIMLPPAIYRALPDLIKRWCFFELRRYSRKLREASNYETIP

>contig28444 Frame-1R

MRDDLFLKRRHALHRSISFATASAALPFSCSTCWTTEMVLFPITTASTNTPKSAYSAAES

ACIDPSTPWRSSAPFLREQLWQHCCTA

>contig28750 Frame-1R|Blast-PREDICTED: hypothetical protein [Rattus norvegicus](ref|XP\_002729692.1|) 7e-08

MKREKRDKKKKKKKKKKDKHKREHGHDDEMDESSGKKRKRC

>contig29003 Frame-1F

MLMSDLDMSTEAGGCDGSEPLDEVDCKLLQLGLRIILPTPKTDVKGDTTPCNVVQGNLED

DLIFADAIIDPIYSIPEELEVVTAYDLTLFERAQAADIFSFGCLVAELYTRSPIFSRRSL

EQYLTAYARHQTQCQATAPEQSSWISRYVSVSRKKMSTNQRLWWNHAVSNRLAGLPLNLK

NGVLDMLHPDPRQRLFLVSQIDGFEWIQARQLDSCQSSQENQCVLSTLPPHAVHAAPSAW

FPHDMMVVYMFLKKLHTVPDQNWHARLTLTRQLLPSLTSLSELHFRVAMPELVRFFRARS

HTESIRVECVTAAVVFLLPEMARQLGRDQARAELLSDVVRLYEKNDLAPLYRCCLAAPKV

VLSVLQAFGAATILDTFVPVILEWLVPPTAADVDVTLQSSMTPDSIHPAPLPPFAAESAA

LAAVTCGELSSPLMLGPSLTVKYVLPALLNQLGRAKSRWTHLAESKPLRRTDRKVSIASG

GGHGQDTEPEASDFHLTFLLKAKLYESHHVADAVLQICREVGEYAVIHLLLPRLFDVLPK

LVTLAEKIASVRIEGVPEELGREIYVLLRMLRHVVRTLNDPAALHDLLSRRARSNLMDLL

AQTSPPFLSPRVATAVIAAATASKRHFNDSLPPTKTSRFTKKVLQSFNGLKDADHRNLRA

FTVVGLSRTIAAVCQKLGPDAVVSDSTVVNGLNRFLKRCSDVYAELEVSNFQWDLASELM

SELCVPLRLVLGKEMFSRTFPIVAGSSVLQLLLLPLGNPEASGRNHEARSSSRHLSALDD

RLGKSQQMLLNPDERADQIRTEDEPTLKNTLFHTDTTTPEEYTTYPPELLRTAYHAVRLH

AVRATSFLRIPSTLLVGSGSTATHWESALNNELICLQEARRERKVGTPADERPNADAVWL

RPRVVQPFDTRYEDLNTTASPLKTSWALVAEIRQSLKAHSSAISCISVDLEEEIVLTGSR

HGSYRVWRLRT

>contig29586 Frame-2R|Blast-trafficking protein particle complex subunit 2, putative [Phytophthora infestans T30-4](gb|EEY55507.1|) 2e-64

MFVVVGSKEPLYKMEMRVRREDIAHVDEFVLHAALDLVDELMWTTPAMALKVVDRFNDQL

VSAFVTASGVKFLLLHETRNDDTIKAFFHEVHELYVKLLMNPFYEYDTPIFSEVFDARVK

TLARRYL

>contig29924 Frame-1F

MTFIKDVRYPKRIPRPMVRLGQVVLAFILFFLEGLAQPMEPKLEYGAQDSMKIASSPIDS

AAVRFVAFERADADHNGVIDQHEFAAFTDAIKGALESFVGAFSADTGAPIAAAWIPSTRP

TLHLEGSPKFWSGFVSGILTIWATEIGDKTFFIAAILSMKKDRIVVFAGAIGALIIMTIL

SVVMGMVATKFLPPDLTHYLGGVLFIIFGVKMLIDAREMNAAGPSDELNEVEEELMGKKN

EDAVRVEEGNGKTDDLTDGMLKVISQTFLMTFLAEWGDRSQIATVTLSATKDAFGVTLGA

ILGHSMCTGIAVVGGKFLASRISERTVTLVGGILFVLFALHSFVTGPSVST

>contig30315 Frame-1F

MLSAFYSRLLEENDDCAYYFDSSGKRLKEANFYRVELFDDYFMRWERSQKKCNEPAPSPI

KSLEMECFSTSSTVASECDCWASTDSLFPWVQQVPVLRRCSSLQSVVTKVEMHRTNTGPY

LQKATYNAIAQQSQSTP

>contig31187 Frame-1F|Blast-40S ribosomal protein S18 [Phytophthora infestans T30-4](gb|EEY65702.1|) 4e-81

MVCKKAEVDVSKRAGELTNDEIERVVAIIQNPLQFKIPVWFLNRQKDFKTGKHSQVVANN

LQGKWREDYERLKKIYAHRGLRHWWGLKVRGQHTKTTGRRGRTVGILGGK

>contig31521 Frame-2F

MLLPAFKGHSQATKRGTEATVGFETATLASKRIKVKSNIVPQSQLRSRSIRGKKRRQVSD

YGATLKTEASPIITDLPPLPFTTLDVDTEKNKSKEATSTRQFETEVTRRCEFCKKASNIC

VMMHCLACRRLYHASCFVHAFKPYVDNQTPLWDQLARLQLQVPEHRGNFFHCLSCKAAFM

DFYESGGYMWDCTCPTCVQPE

>contig32186 Frame-0R|Blast-calcium-binding atopy-related autoantigen-like protein [Phytophthora infestans T30-4](gb|EEY56604.1|) 1e-30

MHTRKDSGFNEPRDIGALHFIERIKECIDTTI

>contig35194 Frame-2F|Blast-trimethyllysine dioxygenase, putative [Phytophthora infestans T30-4](gb|EEY68209.1|) 2e-65

MHPETQQRQLDTASIPLNMPLQRLDVTDAGNMVVIDWDAPVRGTMCERSKYHAKWLREHA

YAFEGGTAEDKATAPYPKLYRQPRLTTKKLWAGADFKLPTYDFAKSVSNIEPLMRDLYMY

GLVQVVGT

>contig35486 Frame-0F

MNALKVQAHKTETTVPLTGSGKLPLLPAKKDAVIVIRAKKRKLIEKETETELKKSPRKWD

NSGGKNGQMPAHLSTIETLKNDQKPVVAVMIQHTQKAPLATRLLEDYSSSSDEETEIIRN

KVR

>contig36014 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66462.1|) 1e-120

MRIREVTRCSDIVYAAQRSEGYEMSRFGSYLSALSELEKKDSDMKQLAEIAGDHFETVSN

IYQDQLDKLLSLYVSIVRYQAGKVDAVKTVMHNRESAIYEVQQANASMQRNKERFAAARA

SSGAAASAMRAEQKIASAEDRMNQAKEQVQFIANSLKVESRRMDTGKAAKFKTALLSLAN

LELEYHV

>contig37013 Frame-0F|Blast-adenylate kinase, putative [Phytophthora infestans T30-4](gb|EEY63456.1|) 1e-106

MTSKSLKIMFLGAPGAGKGTYASRIAPMLQIPTISTGDLVRFEIKNGTQLGARIKSYNNS

GALVPDQIILDMMETRLAQADAKRGFILDGFPRNVPQAKAFQNVTDLDLVVNINLPQWIL

TDKISGRRVCTKCGSGYNVAYINKGAYQMPPLLPKTEGVCDSCGAAALVQRPDDTPETVK

QRLEVYNRETAPLIDFYTQLGNLRTFDVKKGLADLDQLVGLIEKELHP

>contig37426 Frame-2R

MRVLGYDLNLLRSQVEGMPDCGSQADSQTASPSSLVICHV

>contig38896 Frame-2F

MQSLFHGVREYLTPVLTESSFEDKGLLTPEEFVKAGDLLVYKCPTWRWESGEPNLRRAYL

PADKQYLITHNVPCRRRVTSLEENYQTEEVVEGEDEWVATSSKTTGTSLAASCVTDLSEE

MDTMTIKESNSSKYSKRGILEAIVDEHFMPTAVAGSTPVLRNLSSFEDDDNLIEDDEAAL

STYVVAQEPDDFNDAILRTRTYDVSITYDKYYQTPRVWLFGYDERNSPLTGDEMFQDIMQ

DYANRTVTMELHPHRNALIHASIHPCQHGAVMKRILANLKMRPVDSIESNEDDTKRIRCD

QYLFVFLKFIQSVVPTIDYDYTIEVHAKQ

>contig39107 Frame-2F

MGMAVCVWDDSADSEITSLVAQAFQASATEQESKMAGMEDECKRWTELSAKVIENEEIAD

ESYLDEEEFGEIEVDEETDCNEEALNEAKVNRSASIIKLSGGDTSIQMDDTASLPAQVRD

EAEEQAVDANDAFPISISFSSLTSESFINFEDSQSLAQESNTNSEEVDDNPERGSSSEDS

TVSTRHLDIDAHEFCSRDMLHSVLFELNVTMLELAYFKGQEQAIVPHSPDVALIVLEGIF

AVSLEETCWADLSETRADFIAEFFAHHGETHGGFTRVQLEKLKVLPIYVNIRNVPCAIEG

SENFFLIPPNFNVTDIPLPVDAQHCFLKSNPRLNTFYKELGVEEMSDSKLLIYILPMFCN

LQEEQRNQVLDILLLKWQSLRDSAELKAVLKKTALFRNDDSNDSRYRIASSYHDPQNNVL

ATIFAGIRGKFPAQRYQTPEWLNLMSEIGLQTEVTVDIYVECAQRIDGQCSGKQALSIDD

EHLLTTLHQFFVQNVDKFDRSRSFFERIISLSFVPAVVYDKVANSSLDDVVDVSLDQGYF

TSRLVVRRYLDCAIPDDEALVFSTTPIMSTVALPPRVLFSRLGIKSPPPKDQVVNHLFTI

TRGDRAMSFHAITWQFFLPMDKVFQAIFKFLQENWEEFGTDIQQRLANAAIIPVGSTLVK

GSRLFFHLREHLAPLLFEVPRVYGAYDSLFRHLGSKDAPQVSDYIRLLRDLKAECCSHPL

NLNELIATVRAIDLLVAAMAESNYRLSLEEKSSIFLPSNSAVMQSMLMMVYNDSASLCAS

ISLTELHVVHPRITTKCCKILEVPGITQIVTEELNGDLPLEVVVSDEIAHYNSVLTSQQF

ADGMRKIITAQQQKTSSYDAMRFNIDYEDLNERIVNLVHYEIKCVVELNTRFIAKLKYLD

RIVDVSKPTHQDSLSFLDQANRRIYITLQTVKGRMRSSYLVAQCVNQLLGRILQDCSVLE

CILTCDEVEIPEILNAWYSEDPLLITDKLRGVLGQPLCEVDGANVELAPLRSCQPGELVA

VEDENGNLCYAKILKKAPEDAVGINRYEVTVNSSSTRWMSATQLYFFRSSRMRSSASELS

GRRVMDHASNFTDDNVALPSSVVPISPVDQGSELVSEMSVPKASGPTIPPANILSAVNDL

LSRLNVTLDSSVEDLMAKNIQLQHRLKLAEASRRAAATQIEKVLRDKKEIQDSLVCAVCL

ENQVNRVLIPCGHIYCASCVQQLPRPSCPICRQNIVSSSTFHVPS

>contig40103 Frame-2F|Blast-acyl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY65023.1|) 5e-88

MGRSIVLGPEVFNCSAPDSGNMEILMRFGTLEQKHEWLVPLLDGTIRSCFAMTEKRVASS

DATNIETSIVRDDKRQGVCD

>contig43014 Frame-2R

MEHEMQVFLQQHQVQLMEAQVPEHLWPIAFYKLKNEVFDAGNYFFLARDEDGDLHAVVRD

DVDLAPIQPQSDEALFLVDHAWTFIADKMREQLKALPSLLERMKLLLQIEEMASEELVKT

VADRVWRYANTYRLGNVKPEDATTIWYVMDEVGSAIEHGKVPNVRMAPFYYGPSQCAFSL

FWTIEPIEGGNFLSRDYFLKYALDAPMHTALLAALFYEPGKDNTPFQKELQEVVADRAQN

YTLEFARAQLQAIVSLNSDKPPDSAKTITSDSLSTIVAGSNPIRIYSELELLHQNLTHSR

FKLVDNEEEAQVVWTTRHIKDYPKYTTNENVLIINQFPNERLLTCKDLLYEMCKL

>contig43160 Frame-1R

MVVFSTARKNSKDFKILCLTLLKSEHRNAFKVARKMQHDPPW

>contig43955 Frame-2F

MQQREAWHLLPGGDEKILELLHMGLDGAKAFANGKVWAFMDYVAWKNLEKVFYTEKQL

>contig44187 Frame-0F|Blast-methionine-R-sulfoxide reductase [Phytophthora infestans T30-4](gb|EEY60936.1|) 9e-67

MSKWVCSLRSLSAKRLGPSSIAFAKSPAYLSIVLTNKMSSSSSDAVTLSDEEWKQRLTPM

QYQVLRLKSTERAGTGEYNKHKDSGVYVCAGCKSPVYTSSTKFDSGCGWPAFYDAIPGAI

KTVPDVDGHRIEIVCAKCGGHMGHVFKGEGFKTPTDERHCVNSVSLAFHAGEVPSQ

>contig45104 Frame-0F

MRSQTCIEFLHIMKEFSESSCGASETVQRVDSLVSQDEQLLRLFPLSRTNEEDEAARRLR

RALENEDEGMITRIAARDDDKELDAQDELQRWMDLDLGDLDHHMDVFHYQHPQPLALNDN

SAADNAKSVALVSQIVTPTASPSMKRGVNGFLQQKVCQASAKTAKIATECLRESSAVNVC

QRPNFSRQNKSVTASPNGINDVSLDLDLSSATLSSGSPLKRAKMLRSNNSHALRVSVSLN

QAETDDEGAAGEDEEGNVWGMESDDHEHDLLSSIDHAVLCDRENRFLQWNLEGAQHQDQQ

IGNRSIGGMSIATNSVLRDFKVVHSPRSLHQAGGKIMAPSPTSSKSPSNVDIVEDWNSLD

FGTFQNRTVSHILSSCLHKRKLHHPYKNQVQLVNFSVPCSGDTSSRRVAVPHPHQLGGSL

ATSLAFGGQQNGGGGDDGSPISGYVPLLASGHESNMAARSPGKGEKKDVEEARRTQAAYD

TQDAGNVCRSRRDVY

>contig45193 Frame-2R|Blast-DNA polymerase epsilon catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY63268.1|) 6e-84

MNGSTKTISYPCVMLNADVNTKFTNQQYHELDAISGKYTTHSECSILFEVDGPYKAMVLP

ASTEEGRLLKKRYAVFNFDHSLAELKGFELKRRGELQLIKAFQSQVFECFLDGANLEECY

ASVAKCANRWLDVIDARGKSMDTDELMALITENKSMSGKLA

>contig45481 Frame-1R|Blast-Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, putative [Phytophthora infestans T30-4](gb|EEY57699.1|) 1e-146

MRFLSALSRPNLCQALPNRRYASKSNREHIVDWMTSPSKIINLKSTQFETLSLGFANRDA

TSGVLHLKLNRPKVVNAMNMQMWIDLSKAFEMVERDLSVKAVVVSGEGRGFTSGMDLDVF

AQMQTVAMEESCDGRKREKLMRTIKKFQNVISAPEKCRVPVISAVHGPCIGAGVDFITAC

DLCYSDVSAVFSVKEVDLAIIADVGTLQRLPKLIGERPAKELAFTGRDFDGLEAEKLGLV

LKALPNKEKLMKYVENLAMTIAQKSPLTIRGIKKTIHYQREHSTMDSLEQIRYHNAAVLY

SDDLAQAVGAVMSKTDPKFRND

>contig47403 Frame-2F|Blast-Ca2 :Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4](gb|EEY66466.1|) 2e-59

MMSVLVALPAPCDASPFVANMTLGPLGIDYVHIHNCLLADLPLLSFLLLLLWLGCLFYFL

GSTADGYFSPTLASISDRLQVSHDVAGVTFLAFGNGAPDIFSAIAAYSSGVGETGVNELL

GGAMFISTVVVGGV

>contig47494 Frame-1F

MCTVFTLMRRERPDDRGDFFRLPSALLVEFLDLRDAINLLNSSRCMRYDSIMTVTALEKT

RYAQHFHQKCAADWWHLTQAWRASEHMVESDWDGENDANSADLWNDCHVRTAAGKELTYW

KDTVRDTPQWQHVPLLSIIDFMVTKLLPQSYISFKYAATVYTARPVIVRLHPPEKKMKKE

DGQDAEEKNVARTITGALGAQNGKLTSLFGLHWENMVVDTNTGKVACAVCQLYADEVKKY

QTKVAEMVSDWKKAVNAELPGWKEKGMHQMEIDRRTYEMREDMIPYSGYFTSNVARRHGD

IIIRHICSYWTTVDHLKINTLGYRDASQLVAALTSDIRKQCQHFLKIKQAMTNAFPRVAR

IRYEVDQPEHPTSSLLWQVEAVTELVAGVSPSGFLCGMLFIEKSV

>contig47825 Frame-0F

MAIITSLLLLIPSAIAVATASIVSNAGLPTDWCRNGPAPMTKYTAYNNAFNTDVKQCSVV

TRQDGQK

>contig49045 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64541.1|) 2e-22

MMECDGSKKRTYESRLRKFYMHQLKMDTSPVYGDGFREAYEAYKRVNSLQRMFDTIRQDG

LFP

>contig50124 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60792.1|) 2e-26

MEPPPKRSRSSQHIHSGSQKTKWQSSSSCTTTARGNVLHMTAKTLSKKSHQLVPDRPVAV

SQQTMVEIDRFQQSCELWQKRLIALQNKLEEKVEKVEFNQVDVSLRDVVKSVETESLQYE

LNETQEQLQWVTWMHHNAALCIKEYSTQRQSLEDFEAVEKQLLYDRIVELETQLAHPQAL

EG

>contig50425-1 Frame-2R1

MSSEREENHLSSAVFARKSCSSLASTSSSTSSFFSLIL

>contig50674 Frame-0R

MIFLACARHVALNSSSDAYVRSSCKRQNTCFAILCWAAYVYSK

>contig51776 Frame-2F

MIFNHLVADREKLFTSPLLRVWANYIDLLLQKPSVTADVKASAILKDVMFATKLEDASHQ

AVTIAGNTVHVVEHCTIQSTQFLRWQRQNLSPDDIKHILLSSYDEELHMQALVQIERKVW

NAYKTFCQTPGTMEAYHDLNWKLDTNFVYHELNIRKPSFFDTEQYNSWFKDLARFAEREH

QNVNDIDLTAFRRWYSDEELLLLLTSPDNINNSQSQTLLKHLIATWVHENEGPAPVSFIK

LLIEEQEKSSALPLLQVWANYNNLVGEGKGNLYVWIFLEDLALARLLQEQFQLYNALVGV

ELQATQFSRWMKIGFNADSIRSRLRDANIFEMHPQREIDENLIAAYSTYIALSTHHDFI

>contig51996 Frame-0R|Blast-multicopper oxidase, putative [Phytophthora infestans T30-4](gb|EEY66763.1|) 9e-27

MGFKHFTAIVMALKALNVESTAADCITYDWRITSIYSEYDGVYIPSLGINDRPADKAIIE

VTLGQEVEVHVTNQIHEPTCLHWHG

>contig53279 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54377.1|) 2e-18

MQSLLALSHRRTVIFIANERRALEVREE

>contig53561 Frame-1R

MLQELGFWCSKDEVFYRDSLSTDRPNPLRLVDNLWFAKIDASQLRIIKLYLTQAHVESYE

LAYSFCRFNCQLALDQPSVMGACTMTDGVYCWPEGYWHYINHHHVKPPHDFLSHVMQRFS

AMADVTRKARREMKLLLWDDEELKAIEMPQAMQDWITSYTTIKMVTEDK

>contig53932 Frame-2F

MPDECASGTLYATFSRTLSAVYAGTPIVVLLRCRRVRSVSSRQVIQRPRDELLVNHVDGR

TPADGSRICCGVAGHALQHRGFGRDCNNFDN

>contig53947 Frame-0F

MQVIDGMSHEDKDVGFSGNKVTLLNLVSLVLDLVSATSFKSWSKKRKLCLALFSAATINS

SDLFSHQLTDLVLSWLEKIEAMQALMIELGLQESDLEQRRLADGKGKQSVAVVLLNEVEV

VVDLLYQEKNDSHFVIRLLQRGFHLSQVRLNDATEDEKETMSKFVTSFLQQIIQLSVEEI

AK

>contig54779 Frame-1R|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY54703.1|) 1e-102

MAQSLESHRSKFFTFEDAKISFTLICCICGIGTLAMPSNFARAGPVYGTFAMLFMAFANI

YATVALSRVILVAPPSVKTFSDVGDWVLGRTGRYLVNVSQLLVCLLLPCAFLVLGSTLLD

VLFPNAFSQIFWIIFMAITAIPACLIPTLKAAASMSFIGCMGTITADIVGVSVLVWEMRG

HPTAPSPDISLHQVLTAFGNLSLAYGVAV

>contig54797 Frame-0R

MLKKPRDICSLHRSSLLISLCTPLAYARLFCSKSLQLLILDPTCT

>contig56913-0 Frame-0F0

MTSRFLHRITATEMTMEACGRRCTTVALSEGMLLLD

>contig57136 Frame-0F|Blast-Rab8 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY69822.1|) 3e-09

MSSHFSNESKDDAAAQSRRRSCSFSAYEPPKRLSTTDALLEEDVESMAKRAA

>contig58029 Frame-2F

MAQEPMSSPRMRRPSASSERSTRPVTSSVGADGRIVLTPTELHDGNGSYGHLSSPPYGSI

SQSQPQ

>contig58977 Frame-0F|Blast-predicted protein [Physcomitrella patens subsp. patens]gb|EDQ58468.1| predicted protein [Physcomitrella patens subsp. patens](ref|XP\_001776774.1|) 3e-07

MNMPEHKCVIYVDNYGEHNDGLEVQDYMDRIGASMRKLIACETDKVQPCDSFVISKIKEW

TTL

>contig59174 Frame-0R

MATGKFLMKHITIEGEVTYNGAPANQLIRRLPL

>contig03433 Frame-1R

MEDSTPESVDLECGIATCSLSRRQMERDLIMSFDSRDLGRHEAWFLIETKWLDAWMRYVM

GDDEMTALRPGPVKNDTLFDRIEFHVRDNLLATKDYRGVNPQVYALYSELYGTDNATPIA

RWILDLYASPVMIDDISEMLRVPRLKARSVVAEMNEELQRYEQKNLQGLQTRIVASESWL

RRCCCQCEFLVPCLNRLLGGGPTYKSEKDSTWCYCWKRKREKQKRTIESEETSISDDFSD

DETQGLLG

>contig06197 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53231.1|) 6e-41

MTNDTQTTVALIVNPNMDATNTALVSDSLAMSTSLGGRVRKTTQTFTFSQATSDEPEVFS

PPLGTGVKLRDMEFVAKNIEALGKKELDMIKQLYSIMYGRRFQQKNVKLIKDHILDFSGI

VAQDER

>contig07169 Frame-0F|Blast-C2 domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY63775.1|) 5e-61

MYAVHVTLIKAVDLPSADFNGKSDPYVVFQLANTTRKSSTIPANLNPEWDPEETFAFIAD

DPQTAVLDVSVFDHDRISKDDMIGFCNLPLAPLMDKAESEVLMYELEVPAALAKQKRKSA

IMLEIKLEKED

>contig09967 Frame-1F

MYDTFVQHTSDGLLEEETFLEALEELLSMTDTRHLMENNVFLEKMLDFFRSFLSEKSSTV

DAYEIAAGLSLLTWGSKSDKLASAFHFFDVESKGSLNRQQLWRFLRSVLITLLHVSPPLG

ALLEQRHGSWAALVDLGEEEIVD

>contig12466 Frame-1F

MGVLALCVPFVLGDYAVGYFQSKMISKATESMQAALLNIILRQDTQFFAERSEGDLNNLF

SSDVARVNALWQAVFWNLLNPLLAVIFGFGYALYMDVSIGVMSFAFTAMLLSSGPQGFAA

QRSKEFGSRNAYVAAEFQNAVGCEKVVRAYAIQDPLITRFKKTCALLRKSQFSKDFWSSI

VQIYIESAMYIFVAVMTASLAMKVWHKELSSGEFFGFITLLSRVSNPVTVLGGFMRVAIG

NASSLQRVDDIIVGLGSSSTDKNDGDKDMPSLPKMSQDLRVEKLAFKYDKASENYVLNDV

TATIPRGSYTCVVGPSGCGKSTLLACLMQFQDADGGCIRLDGHDIFNFSKKSFMDQTAVV

FQDGGILNGTIYDNIRYGNISATKADCEESARLAECHFIKNLKDGFETVVGQHATCNLSG

GQAQRICLARALCRRPSLLLLDEATSALDPETEASIVATLERLSSKMNMTIISVTHRLST

ALNADQILVLNAGRVAEEGRYEALVQKGGLFFEMVHKVEKPEEEVNFAPLETSDLISMAM

SRRRGTVPPRRNPDTIGAAGEEPKEMLDSALALQQFTKNLSSRVVHDAGDGLRTAGTTSW

YRYGNRNSRRSRKASDDGMTARRSGNNTEGAGTRWPSTHNELRGGATSGANEEDP

>contig12488 Frame-0F

MKNVFAPIAIALAAVVPTINATSYACEAGLLNYNFFDVNSQATAPNTVCSSVTENSETAI

HWTSSFNVVDPNAIHQAPSALVKTKFAPVAIDTIHEAYAKFSFETPDPKDNCTAAIMRIN

TKRSKDGSASFVHVVFLATYNVAQAVSPSMKWFTTVFVSGNHFDVYMEKVDDLTTFTYIP

SQNVMNFVGNVLDFLNCLPKDSTTFPLDLHSIEAGFEMYAGRSYFNGNLEAKIIKLA

>contig13348 Frame-2F|Blast-cytosol aminopeptidase, putative [Phytophthora infestans T30-4](gb|EEY68382.1|) 1e-172

MEKVALASADLPNMSVRVLQQEDLEKEGMNMFLSVGQAGVCPPRLVILEYHGNPNSDTKI

ALIGKGITFDTGGLNLKPTGAIEDMHTDMCGSAAVLGAIRAASRRNLRVNIVGALALAEN

AIGSKAVKPLTIVKSHLGITVENNNTDAEGRLVLGDAMSYVQKEFKPKTVIDVATLTGAC

IVALGQHCAGLFSNSDDLADKLTEVGTECHERCWRLPIHPEHTAALKGSQSDSRSTGRTR

YGGASTAAAFLQQFVYEGVDWAHLDIAGPSNYSSAKSYFPKGATGFGVQLLYAYLKKIEE

Q

>contig13700 Frame-1F

MRGQMMGKFEMRLIYSSGHAIQEDCPHEVAKAISCLSSRCVRAVSGNICGPDRIISQPIN

DLALAERLAKARAMVPTEGICSAVDLQKLLPK

>contig16057 Frame-0R

MKDTMALMDGAFIRQECMIGTQLEEPPPVDVEKTQLQPPRVEIVDSSDSGSNSDNLGAQP

VGARIGMSLQAILSGEVDDFIKLGRVLI

>contig17003 Frame-0F

MALRKRRSDSDSVSKHAHAVVATPPPGIGGLTKFMTRVIVGFAMIGGFIAILYCGHMYVW

GLVVALQTLLFRELVNVRYRAAAEKNIPWFRSVQWMWFVVALIYNYGDSLGAFIESSKIR

FVPPAIAHYLRYHTWVSFSYVRHALCHVRLESQERLLQIPDG

>contig17098 Frame-1F|Blast-40S ribosomal protein S5-2 [Phytophthora infestans T30-4](gb|EEY55393.1|) 1e-103

MAEVATEVKLFNKWSYDDISVAADISLEDYIAVKGKAATFLPHTAQRYQKKRFRKAQCPI

TERLVNALMRKGRNSGKKLKATRIVKHTLEIIHLLTDKNPLQVVVDAVIKSGPREDSTRV

GSAGVVRRQGVDVSPFRRVNQALYLIATGAREASFRNVKTIAECLADELINASKGSSNSY

AIKKKDEIERVAKANR

>contig17726 Frame-2F|Blast-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65844.1|) 2e-49

MLAVGLPLLLYSHIRVLEESRSIAENVFFLFRISAYAEQVAALQKERETLAREVHALVTT

YVDAKFLLALHKSIASSPVNRRLRHRASSTSDTLLER

>contig18958-0 Frame-0F0

MKLALFPLRHFYFFHSALVFPNHSPPRNPHHLNSFVNFSSTFSSVFFQKLYISLRFAASG

IFVSAFFS

>contig19113 Frame-2F

MNTVRCVQGSLPVAPQKTRMKQHLVVRRLVHGVNLCLGNWNEF

>contig19188 Frame-0R

MIVEEEEFALTEHSSALPTYIAMSQEIDDTQELVAAFMDIVQKWPNQKNYGNPKDSYMEL

FDGCILYLVGFPSQLHTLLQRVLRIGMGTIYHDMVIHQVTHIIGSTSLHERKTLEAMRAH

AMAANAFDTVSFVSARWVIDSIKCQTLQPEELYPIEFHPHSVLNAKTVLNTQQIESDPIT

SVNKTQTTTQAPLETLVPMKQKTDAINPLFPGYAFLLLCRDPNDTFVIQPLLEKLRGPQS

KAEALALAAIDFAHIDPTHFSFITHAVVCTGAVFNEPAARTMQDQIHHLQRHLRSTQCHV

THKSDKLSQSSQQRMLQFVSDLWVHCSLTAHTKLSFASHELFHVSALRPRALFTCILPIA

GFQDVIASTSVYLDVEKLVVMELLRLAGARVTRRLSPHNTHLVCRKPIGMKFAKAIEWGL

HVVTARWVVASLLHGKRLSEDLPELQLGDQN

>contig19863 Frame-1R

MKTALFTTVISAFALISAPARASPIDIRRKLILGGSVVKGHEKPYMVGLRSSETGKIFCG

GALVSSTHVLAASRCTMKDIRWASIGSHTRSGNNDGELLKVMSVMNHPNYSLNIEFSHDF

ALLELERPSSFAPVKLAAADDSDFKEGAMATAIGFGLTSEGGVMSEKLQRVNLPLLRDDE

CEKSVRIDDSMVCAGGVISADVCDGDTGGPLVLEAANGHGNDVLMGVVSWSRNNACGRGP

YYPGVYARVSRARKWIDSLATKSCFISGK

>contig20805 Frame-2R

MTCQSSAGALGFFSPVKKYI

>contig21293 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57766.1|) 0.0

MRGLRPTKIKVWKQDKRPTVILSRRLPRAIGLVAFMVEQKVKLMKWAPSWIKIDAKQLFL

TDIVGNEWYGGTIRNWVGPTIGTPKDTACYRKYKPFDSKRDCPLGYSNDDDDCIAQCPMA

YPVRCALECIPQNDDCALAILTKIAAVASVAFNAATAGVFVSVKNLYTGAKRIYMCAAEV

INVIRQLIYYIRYTQTTVPQGEIEQLLTLSYQSNVVLTDLPIAIYTCLGIKPPKTLVWSG

FVVIAVQTIVKQVIVYGEEIIASAKNVIDLIQNSTSVENSMSSVTELDDFITANTSCGYE

LKKLTDRVIFTVSDIRNKTPNAAIDDVRVTVSKSSMVFNDVPRITNNCMKEMLKTKTKQA

AFETRDLLRKTMEVIIDQLVDTGTTDMGKDVAEEQQLLESANFGLVVLGGLDPTGIVYMA

SQFVQPICGPSGFIGDIDDGNLYDALGMMTVDEAFVGSYGTWTKVGDGVVRIIFESTDRE

DVTVVIHSGGNDYADVDVAAGDTVTWEASVPELQDKTLYLDRWRPGLFGLPGSGGGSLLL

WIPRAEEGGHLTLHARINVS

>contig21730 Frame-0R

MSGGNSTESESEAYASLSNISAAQPQKEREIDEVMDFLKFSVKPSASFGGTILFRFKDKD

DPEPKTTYAVEVSDMRKVTTRKNVNAREERPTCEVTLSMDDFLWIYSGKASSTDLAKLFY

AGRVVISGYAFRTVSRFAQSFDFSSEKWLNFYAKREMEQTMNGSSRSFSAENSPTDPVSL

SKDHWYFYTTNLLHISKLRRLLWETSLVSLFGKKIVLESISRSSTPKIICDRCNVILSAI

GISNLMWTTYKHPTSSLIQSDQLYYKHDLRADLEKFLNPCTKQSSKVTNSILMNKSEQTA

EIVFDFLSEEFVDAVKLSAKERQQRRHRRRVDFGDAGMAQLDKLVKVIGKGGHSNLKRDN

CSKYVPAPEVLLHGFRVNVAVIMDALKEKAFGRKALHKIPAPEMAWLMRNRRSGSMVISD

CSNSRGDLKNEANLALPASTLPSFPQSIIVEVNRAKIARNRKRFALPRQRIKAKIATFSR

ELVSQRNPVTSHLDEHLVFSDYL

>contig22252 Frame-2R

MALSPKAESGSSSNSEDEFDLGGSSVPYNNEELNKETSRSTCIDAKLDGRTKSIDKGDLF

NGQNEKKIGMTTNLLPKNEEKDKEIEDLFGSDYDSEEEEFKASGVKESPARDTGRTTDDL

FGDENTDRTLSKSGDVDSRYATTIWLPRTPKAPSTTTYFITKMPNILRLVPEPYTNDSIR

AEMDNPSDEMLYRNYVRWRYKRDTVSGRVVVHETTKVPLRESNTKLVQWEDGTFTMFVGK

EALTLSRQKLSNSFLFVNEMASDSPEFQDTHDVVIGQESVLECHARVKEKFTIRPMTTAS

KSHKSLTMSMRAKHNKSVQKMKEYISELDGEREQEQRVKITDEKLRLQNRKKARQGYEFD

RERSSRMDAQFLEEGFDAMEYDDEEHVGAIKEQFGKRKSVVGIVRKPGVRRPVPGGGFDE

YRSNQRQSALKREADKSESDNDTGGDDGQEEDEEDEMVIQSHKKRRTVEEEDSE

>contig22982 Frame-1R|Blast-hypothetical protein PITG\_04380 [Phytophthora infestans T30-4](gb|EEY67363.1|) 1e-35

MPNGDENYRNMEAQQQFDQRRADDLARQDALLDQIHGGVVGLKNHAHAINDEVLEQNVMI

DDISNRMDTATHDIAREEQTARDVNARKK

>contig23259 Frame-0F|Blast-threonine dehydratase, putative [Phytophthora infestans T30-4](gb|EEY54393.1|) 6e-71

MEILKETAGDRPAAIFTPVGGGGLIAGLAAYVKEVAPEVKVIGVEAEGANLLEMSLKEGL

PVVVQSVNRFTEEVGIRSIGVENFRLCKDLVDEVITVSTDEICSAIKDVFGDTRSLVEPN

>contig23538 Frame-0F

MSYKNRRGGFGGRSRGNRGGRGGYAGGRGSFGSGPSVGNEVCRRFMDGGKCEFEQTSGGR

PCRYPHFVKTIGETRGHSGSIKDVVMWAERQQLFTCAADASIKLWDCATWQEITTISVQD

ALPPSVSSVSNGSGGRGDSRDKSAQREGVVALVLCGPFLFAGFEGRFPANPKVSVGMMRG

WNLENPQVPPFEFSASDMMPC

>contig23721 Frame-0R

MNLHAQSVEMQSAWQKQFKSTSAPFVVSLSYKGQKISLLPSRQKSYDGREALEKEVRSWL

LRLSGGEISQNVSSLERFE

>contig24485 Frame-2F|Blast-DNA damage-binding protein, putative [Phytophthora infestans T30-4](gb|EEY61436.1|) 0.0

MCPFDSESFPECLALSSEDELLIGTVDDIQKLHIQTFPLHEWARRIAHDSESHTLGVLTV

TFTIDESGEEVDQGFVRLFDDQTFEVLHSYRLDPFETPCSVVVCPFATDAGSASYLVVGT

AYIHEEEAEPHQGRILVFAITGIHGERKLHLVTEKEVKGAVYCLNAFNGKVLAGVNSKAQ

LYKWSENPDNEKELVSECGHYGHTLVLYMESRGDFIVVGDLMKSISLLSYKPIDGTIEEI

AKDLNSNWMSAVGILDDDTYIGSETDFNLFTVQRNSGAASDEERGRLETVGEFHLGEFVN

RFRYGSLVMQNHTITSSTPASFVASGLEQMGQPNQLIATKSVPCHESMLFGTVSGMIGVV

MPITKDHYTFLLRVQQALTVIVKGVGGFSHKGWRTFENRRSVSEARNFIDGDLVESFLDL

PKLEMTKVVDKLNSDGILNGAEQCTVEELTRRIEEFAQLH

>contig26256 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57652.1|) 5e-83

MRGKTVVGTRLHWHNHSQHDPIEVDRVLNQVRAFCLHAATYSDGGILIAVGLPEAFVSSI

PAPQSPYRKDFVLSAFTHSVREFMVKLQSELAAGNLVGKVVIIPMLHWGKFVPALNAIVG

TAADRFPEAETLLLQSMEINVHANSVEALHLHFDSKEDLVVGAALPGHAFHPNSASQPIQ

LSGLTSPWNTLALWNLESLIKIGFALMGDALRLEVDGIGSAAG

>contig26670 Frame-1R|Blast-DNA repair protein RAD50, putative [Phytophthora infestans T30-4](gb|EEY58381.1|) 1e-139

MRRTEAREALRVQRSELQECQGDLQVFHAKCRQVLENEVDVLEQQAQTLNNQILQLKQRE

DTTITSLENLAPQMKMAEKNLSENEIVKRQIQDNLDYRDLEKELTTIRREVQDLGDRVGH

LPPLKDVNDRVASASAALNAAEHLSAVMKGKRQQLMENIRECKAQLLKPALKDVDEKYRQ

KLIQFETTQMAVADLDRYYKALDESLLQYHSKKVDEINTIIRSLWQMTYKGQDIDTIELV

SGQQDGAVSKAARSYDYRVMMNKAGAAIEMRGRCSAGQKVLAALVIRLALAETFCLNCGI

LALDEPTTNLDTENKFGLAQAITDILNARSQQQNFQLVCITHDEEFVQMLSRTQAMEGTR

PEFYWRIARENIGGNRFVSKIERHEWEDGI

>contig26894 Frame-2F

MEGQFIARARWTASLPSTTPHAYRDSSSI

>contig26911 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67170.1|) 2e-38

MHAIVLRVAEEADCVEKLLLQRCEENVARQKADLASTQQLELEKFEIQIARESEERKRKL

LEMKREELSRAFVKDLQTYQMRVTPCEGGSTTALDLQEEDWKQESLDEVELVVMANSDQL

EAFYESEHEDEEKQLVLNKIEKWTESRIPGDKCDAESTVDEKEIIGMAERSKDF

>contig27563 Frame-2F

MNEIYVQVNETKTFVRTICDLLHLK

>contig28030 Frame-2F

MRRATFDGAFGNPTNIQIQSDEERRSESHYTSVFDDAESIYSRNMVFQNVHKWFGVDEFL

LLSRSPLEFSNETTTMAAINDIETLEGSREKRCDEGGDVMADIQVDLNEAGMMLSALTMA

LNNCNCTMPAFVPVNEPSRGTWMGSAVPGATGNVSMAFETDSVPEVNPNQSCISGLLDFF

RAKLQLSPQFEEACQMEADEARDVALGILVSASFGYSWNPKDVPREIPTPDKSYLLAWRT

IESQLAKNDQHQIEQITTKLFKPNKSIPLFGTCDNPLDGMDLTVIWPQLREGAYVDNVVH

STLDPKSAPQWILTVRFQELVSENERKPQLPLSKQLANLVQVYSNSRELNKDILVSELAP

PMPGAFKTYKPLAALTASKLSGANEVPANQASTIIPESIPAARGAAVVLGHAISSIVSAA

TRKGSDFEEIRRIIAELFGKEQGHANDDSRNVTCGIKVSGDSLLATLPSSILHGAPLGEL

VSILATRMAQLHSINSMSLLWVEFVKALRERWFQQQMLPLMSRSISGGGDD

>contig28445 Frame-1F

MRIDYISLLVTATIVTNANSARLRSFPIDTNEPISGETQDLTNQENNAWHNDDERMLPIT

SADKYASAPLLPFLNKAGHEEGSVMTRISQGLKTLVKWMAQLLEPNIKGELANVNTLAQS

LNEVAGKSHPQYIYVKGLVNDLVQKEGATKVAQALLDDNQYTTVGAKEVWKMLMKDAELP

VENIEHMLRKKGYLDLADLDLLIALMEAKGDKRNEILKLVKSDAYKKAKKDAEVDHENFI

KVISHRSLPHMQ

>contig28751 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70365.1|) 1e-102

MKRKKKHHEKRGSSLESTRSKMARSTIITDVRKRLFRGAQLGDLKLLRRSIRMAKTHLGD

AFAYELYSDPVMVFGIFGLATKNPMHVAAYQGNIAAMELLVHAHFQVNALDKVSRVRFST

GDLFWYLASYLIPKPVVSADELCCSVFKTTLVTPLHCAVSTGRLAAVQWLIAHGANVNLC

SKSSHRCESRLPPLFVADHPDIVHELLRARANHLAIPDPGHMNTITVL

>contig29774 Frame-0F

MPHECKFHNWNERFKLLFHAEKALPPSETFRTAGIAVHGPDGRIQVDVAEEDEIDLNALR

RQSQSTFDEEDDLGLERPRCPPQLTICILIVGTRGDVQPFVAIARRLQQDGHRVRLATHA

IYRDLVTSNQVEFYPLGGDPKELAAYMVKTGGHLIPTKVETIQKDLPRNLQMIDEILQST

WPAVTAPDPEGGGLNIKGPVFRAQAIISNPVTYGHIHVAERLGVPLHIMFPQPWVPTTAF

PHP

>contig29925 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57817.1|) 2e-93

MSSSCVVPVSPVAALKRARGADDDLCLLKVNKHASDSSPHSPRAVAAAMLAQRQQQILRH

YQMQQQQTRRDESVSPFVLACGNIRYAITFIQNSRRHALALCLQNQWERALTVLEKIERA

NDKISRQRRTKVREQANANVDRIFDASAMPTQLPQVPSPTKACKPKRSVRFCEEVEVAVI

EDVDRSPAPMPVLMRDEILVLRASRPIPLRNFSEFWSASL

>contig30480 Frame-2R

MARGNSATTYLPVSTHTTIDEAKLALHAQDEFEYVTAYNYGAYSNGKVFRCISHEACSRR

LRIVEKVKDEAEIPVTFQLAVAGKHGARMTNRKRKGIDLSIKGEVDGLLTKGVSLKKCRL

SLQVKYADQPALLSKIPDVHKLKNRLLTLKKNGWEIPKATNTMTPNTVGCVKSAELDNSS

DSETELSSLVEDDTHNYHPDEDSHSRLGIEVGNEFDKNKLMKEFAAVPGRPVFWCIVKRT

DFLSNKSDEIVTEWITGQVTGWQARNNEPIKWMVLFTDGEKRPYELEELVSEIREAAQLG

LNVTGRNCLL

>contig32187 Frame-1F|Blast-calcium-binding atopy-related autoantigen-like protein [Phytophthora infestans T30-4](gb|EEY56604.1|) 6e-67

MFFRTLLAIPERQFKLAFRMFDADNNGKLDHREFKQVMELMRLRTPAGRRDRRLHDNDVP

LFKNHFGELGTKSLLYGDFCSFRRELQREMMRIQ

>contig32824 Frame-0R|Blast-pyrophosphate-energized vacuolar membrane proton pump, putative [Phytophthora infestans T30-4](gb|EEY69386.1|) 0.0

MAEAFEVYAYIVTAGLFGILFAAYLFWEVSKVKVTRRGDSYALLSTEVRHQTADRLFEIY

CAIQEGARAFLLAEYTLCFAFIIVFGAVVLVLTSFVNKDGKQFDWLFGILNATAFAVGGL

TSMAAGYLGMMVAVYSNARTTVSAMKEGARGWRDAFNTAFRAGAVMGFGLSSIALLVLFI

LIKSFETQYPLATDHKKLFEAISGYGLGGSSIAMFGRVGGGIYTKAADVGADLAGKVVQN

IPEDDPRNPATIADNVGDNVGDVAGMGSDLFGSLAEATCACLVISTQSPEIISAGWPAVL

FPLVITATGIFVSAIVSFLATHVSPVKKEKDVELVLKVQLFVSTLLMTVFIIPVALWLLP

STFSIGASFQVTPIRAFYCVAIGLWGGCIVGFVTEYFTSHSYSPVREVAQACETGAATNI

IYGLALGYQSAIIPITIISIAVYIGFSTAGMYGVALAALGFLGTLATCLAIDVYGPICDN

AGGIAEMAELPAEVRDKTDALDAAGNTTAAIGKGFAIGSAALVSLALFGGFVTRIEEESI

NILSPITFAGLFMGAMLPYWFTAMTMKSVGVAAMEMVKEVKHQFATIPGLLEGLPGHGPP

NHARCIKISTDASLREMIPPGLLVMLSPIIAGTFFGVHAVSGLLVGSLTSGVQLAISQSN

TGGAWDNAKKFVEKGCVSIEDKDGKLIVQGKGSSIHKAAVIGDTVGDPLKDTSGPALNIL

MKLMAIISLVFGDFFKSINDGRGLFNVPGDVASAAVAAPIVEPATAPHL

>contig34567 Frame-2R

MSTPLDRAMNSRPWIRTLPTTSEFEHSLILRQPSDIQHYFLKNCSQPTQLLPSIGSISPA

NTTTPSRFPLAPSTLLNPVKLEYCNFEGCANFSKMQGYCHDHIHGQPAPFFPSPVESPFV

QTTNMPLLSLVLPSPESQSPYLPTLKSVVNTGNNECQSA

>contig35487 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61177.1|) 7e-16

MDAPSWHPANQNANAAQRDVAPPRTTYVIVDTSTEEERQMVAASEENVVLGGGRGLLDPS

DRLYLVEQTQLKLQAQSMEELERQN

>contig36082 Frame-1R

MWQVIYLCSLAASLAQAQTSQENETCIMSDSNLCPVDDLTPSALDSSILIYPGGATRCAF

DDFSDPNVSYTTNSTYFFQVFPASSTTKLMLYFQGGGACVDELTCAFSLQCMFETFSANA

KPLSHGVLNRSNEENSFNDYNIVHLPYCTGDLHIGNSVKSDRSSGLDALLNMPECLGRNM

TLHQNGYNNTKAVLDWAVENYPDTDEIIITGYSAGALGAQMLSALVADTWQVNENDIRYS

VLSDSYVGVLHKDEAGGKILSYYGSCDVDLKLTDSLQDQCEESSLSFIDIVTHMILYTPS

AQWLFLQSMYDQVQRYFYQLVKDGILGYPFPDLISGEDFYTKVTAIMDEYKNISDNISTF

EVNNSQHVFMTDNEYYDNVIRTPGGDSLGDYLEKWLVANSSVDDDASTSASSGGGDTNQS

AAIHLQHALLLTFIVIIAMLVQ

>contig36631 Frame-0R

MFERSIICWKPQWRWRKDAITENEQTYSNLLSVWRLFIHNIIRDWRNYMLIQISLVYGTR

GAFILLCVLIGYS

>contig36954 Frame-2F

MEQGICAAILMERAALCDVRARQPKFRKYGFRMVMAGHVYNTLGHEKHSARCYSLARAIY

DCSGWFLVEDHINFMLTQQANKLNDRMATIILFLKLIGTGRNSASQQEAMLYDFGLMVKE

FLATERADASPSSLSSNGPVCITGSNGGVKRLLVRDLRMPELDEKSTVVFAATNAIGIDR

SIDGNNLEAEMWRDLGQMMDNQQLLHQYMAAGEQTEAKSWYAPLHLYAGYRNKKNAVIPQ

PENYVKGEQIFVEFVMKNALSCAVDVEDIHLFGTFESAGEAIVFDVPESLEPDEQRVEIN

SVNLQLLPCSEERVRLAVCPHICGRLKLTGVRWSICGGDVQGEHAFNLPGPLLNDTRAHR

EARARAPNMSLIANVVESMPWLGVEIKVVPTESFVGELIKLKALLINAGTASLHNLQVCC

TDLQLCTSKSGTVEDLCGYVGANGHVVDLSKVVLAPGEREEVTIWARGLVAGRHLAALLF

KYTTKPVSHIPSLSRTVKIKLDLDLLPCIDVSYSIEPNFSARGEYILGITVSNQRRDHHA

TTNVLGSVVRLEELLCVSNSWSVENLSRMASQKSTEVRDSLHLGFSEASTSYFRVVRRRG

NYAEASEWCKLSLTSSLESNELSANLPIQQFLCLENAAALVRIGGAEMSDSSGGKRSGGF

RTIQSVRRENKALKNAAVGDGNDATSQQEPQPTSKDALLSHLGTDGHLVLVWSTEYSSEV

SCHRAIGQINLTAVKILPLMHETSCPLTVTLKYKDSIKLHESAFPVSKSKHRMAELDIMM

QICNDSAPNSTPLDVTIELLHPEEAQASIPKLSALTKLHSVTHSGASPPHGSPPRFFWTG

ITKKQIERFAANSQVTIQLKACFMASGIYNLNRFRFVVNAATSRQLTNVFMLPADYLVYV

KDPQTDQTSMQLDTKQPFDELIAPVLS

>contig39173 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64699.1|) 7e-53

MSEDEFVVLLEHAGILETSDENDMEFMVETVLFDWLERDGVQLFTTQMTAAKREQSDADL

VVGGSASTGPTATATATTLVGEARTRMAGHILSRLLERGWIAPIEFDYDDDETEEWKIKL

YTPRLRTNEAYRIYIEKDP

>contig39807 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58226.1|) 0.0

MLLDQPIELWRGRAADAALLGASSSISKDGKRQILLTSAQDVREICISTRKCINHWAFRA

GSAHALTVAATRHPHSRVFFGVSGAPGVNASKKARQARRQETNKTTILPANEALAVWHDT

DLDVAKWRRLPLQATAQAFAILTHSKLKDEVVIVFQDGSFASYNEDLVKGLQRNDAKVAT

SVEIFDEDDANDQKESVVWSCLETDNRSPLKGALFLSILMQKTNQKTTNHLDLLVYQVTI

PDASKRLSVTLGAVLLIRHRVNLPDNEEYSSCAFHAESFSYSFIGAAGCWQSLRLSRDAL

TNALTLVGSQEMPNLTSVDATSSEPVHKKRKLQRDSTSAPGFLVSGIGNFTYLVSMSFDS

SLKLTGWDSKFAVPVSKTEIDLKRDKDDEDNVVIGRSSNDGIGKPVRLVSVAAGDALLAL

YERGAFLVHVREKTLDAVECFGCNGIDCFDFIRNFEGTGNA

>contig40102 Frame-2F

MRLNCREIFRPLYRCFTKTRKSPFIHLDDAPTAWPDVLAYADGASRGNPGRSGCGALLLD

PCTGQVLASESKFVGNLETNNVAEYHGLILVLQLAQRHRATHVRVHMDSQLIVRQMLGQY

RVKAA

>contig42085 Frame-2F|Blast-methionine aminopeptidase, putative [Phytophthora infestans T30-4](gb|EEY59637.1|) 1e-173

MSIVPKHIQCPDYAETGIPVSEQQASKSIPVYTPEQIAGIREACRLGREVLDIAGNALRP

GVTGDEIDKIVHQACLERGCYPSPLNYFHFPKSVCISVNEVICHGIPDSRPFEDGDIVNL

DVTVYKNGYHGDLNDTFLVGTVDEDGVRLVNTAFESLAAASKLVRPGTMFRELGKHIAAV

ANAQDFSVVKTYCGHGIGSLFHCSPNIPHYAKNKAVGIMKPGMIFTIEPMINMGTWRDKT

WPDDWTAVTQDGMRSAQFEHTFLVTETGYEILTARDNEPVMEWDLAKVHRP

>contig44186 Frame-2R

MGDITDMMAASSLRDYAGDTPLKRVRSAIDGCIRHKQKLQPGRLFRAATFTKGQTT

>contig44821 Frame-0R|Blast-ubiquitin carboxyl-terminal hydrolase, putative [Phytophthora infestans T30-4](gb|EEY56259.1|) 5e-43

MARDEGEMRFTILALAKTKIE

>contig44955 Frame-2R

MAKLWENFEDAKRIVIEDKVPQILGTKFSDNCPEVRAAAAYALGTLVGFQCEFNAGGKHD

DTSRLKKIIHQRAHSDILVALELLRGCQDGSPLVRRECVLALANVILHSYHQSRFEFIAK

HFKNQPAKAPSIKVEDKAAVIALSSKQMSLHCISNVFVDEVLSNEIGVDAEIYAQIWHV

>contig45192 Frame-2F

MARFRDDSRHRSRDRRRSPSFERRNAKSCSRSSHRHRHSHSSSRNSSTSHCSRYPSRSTD

LLFAPHSSDSERESTRSRNSLLGLDKLAVEKRQHATNRSPTRSKLVA

>contig45291 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58717.1|) 9e-75

MEPPNLLPHVDELVMEYLLFRGFTKSFQVFSAEHKRDRTRGFDVEQIISQLLVCVQTYQI

ATVLETWQFLTARFFNHLDASYALTLQQLETSLLRLYVVNAIKCGHRERAAEFFQLQADK

LNASVDAGAGGSDSWSRWFILPYIEHPENDAYFQIFFGQPW

>contig47187 Frame-1R|Blast-dihydroxyacetone kinase, putative [Phytophthora infestans T30-4](gb|EEY69770.1|) 3e-76

MTKTKQLVRESHTIVDDMMVGIALSHPHLVLEPIQRVLLHRNYLTIRERQVTIISGGGSG

HEPAHAGYIGEGMLTGVVCGAVFASPSSQQVLTAIRLAAGPHGCLIVVKNYTGDRLNFGL

AVEQAKAEGFKCDMVIVGEDVAVVNPNTGRRGLSGTVFVHKLVGAAAKLGS

>contig47402 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57197.1|) 1e-101 NOT\_ORF

MSLELPTVISHLSTWLTSVELCALRALNSSFSTTISRYTWELTVSNISSSKVMSQLSVLF

PHVWCLRVLDSFYKDLMAIQSLIPWLDRSQELRELELARIYCVSGFHLHLSAKQLTKVVI

RQCYQMQEPALVAPKIETLVIEHCPMTRFHPDTHLPQLKKLLLSSRNFTALHSRILVEEM

HLRSPALMDLSFAGCSRLEEVTIEAEEIPALRRLDCSGCPMLSRVHVTSKLLKNLNLSCN

DSLQCVVLNVESMENLDLSFLKNLTNLSISSPSLRRLNLQGCCRLQRDTISINLSKLHSA

KLHGTTLKARDF\*IEAVIVSDINP

>contig49044 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64541.1|) 2e-11

MYGLPYDLTAAVLAHEATHAFIKLSDKYPNSLSP

>contig49642 Frame-0F

MLLVYDCLFHAGSLFDHVSDLLNRLMK

>contig50125 Frame-2R

MRAESLVITWISLCAFMLLTDPRLWIVVISSIAFSMVRVLIVPLTFAEVKAFRALSTFSR

LLFCNTLVSMLHSIISSLLAILALLTSHSLNGDYVNAATTGEFLATSVSAGYFAYDLGDY

VLNGLNVKAPVIIVHHVVVLSCYISALTKTVGLPLLSLALFCELHSIFMHARKLLTMSNF

SVRQSLLLRWVWRSQWIMFSTARVFSHLIVAVLTYQARLLFAQQLHFAIAFGGMIVINLL

NIQLFLDVRKAWQKDYAPAMASFSAPVLKTC

>contig50279 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53216.1|) 3e-49 NOT\_ORF

MKVTLENGINASAGCGKPCFAEFDNILQELRRCEERKQQQSVEVTSATTKQKILRDHLQQ

SMT\*LV\*DRKHTNTDSAE\*VAQAELAAARASKLKLCEEIGTLKQAKEHQNKQLETYEFDL

QFARETHASMTKKLKDLETSTWTIKQQYIQSLASRIKSSVQVLRQLNVTHPATFNVDATE

SCSEPGQANQKKRKRVLGDEISEQQVLHTVYQPEESSIEVAM

>contig50675 Frame-1F

MCINNMVGGWTHQKQLSVAISTMEVEFASGSQVASNLRGLNELLGQADADAREKSSQYQN

NTGVRLARRAKHIAVHSSSSMITAENK

>contig51997 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69476.1|) 6e-55

MDPRIKPFTQLSPLSSLPPQQNFAQGLEASNVAAASSSGGYVSLSHLKSPEIRFRKKLVP

GGPHACGDLKRRRLHLHSQNADDMDSDQRKPSAKKQLALALSGALGFKRFFVGVGSGVIG

TLGRIGCESLDSVDTAEDQDGSDSSDTDEDRRSSECANTHNSNLLKMLSSGGS

>contig53278 Frame-2F|Blast-crossover junction endonuclease MUS81-like protein [Phytophthora infestans T30-4](gb|EEY65333.1|) 5e-13

MSSKALLKRLIDTGYDGNSVKMRACLTSLCGT

>contig53296 Frame-1R

MLKLKFSNCKFMNKFVAYAFRTNYSVNDIVFYMKVIETRASYGTCTLQMELDLGNIVFLI

FFTIDAFAAFVYAELKQSHFQINSGG

>contig53560 Frame-2R

MSSVESDEESIGTFEHNKLNISRMNEKDAGSSLGQQGAQNDEISSSSANSSEGDMSLSDA

KSSNYKTIIAPPHVSLGQDVSVSQSRQKLHGAPRYLSTKTSISKGISAP

>contig53946 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58312.1|) 6e-19

MCLMHEKPIVLPPIGTLFVSSRPPTPAFMICASEEQREQHEEVMARYFGVPLANGIRKTV

TKNEDTANMRTPTSVQPCSGFPHSSPV

>contig54778 Frame-0R

MTLVALILPDDALGEIRTGSATVYIACYFSAVQ

>contig54796 Frame-0F

MTGSETLEPGPLVDHNGIVMLINDPAKCRTIKNRRAAYPLPAYATALVLLADFSKA

>contig56242 Frame-0R

MHVSWSLAVKLRMNLFYFTS

>contig58550 Frame-2F

MKPSSYFNGQESVSLYSYILNFRLCGRIVDFCPRSCSGCSGFCSHSG

>contig58976-0 Frame-2F0

MPEHKRVIYVDNYGRHNDGLEVQDYLNRIGG

>contig58998 Frame-0R

MERPNSRLSQRLEVILFFHLVTRRPTRTKADPKMSVML

>contig59041 Frame-1R

MLSDGLLLLISLGGLGTTILLLFFLLGFFARTKKLAHEDHAEVVRGERGGLAALRKRKER

KKRNAGREENIAPAEAVQAAQNEAVAATEDDNVEP

>contig00057 Frame-0F|Blast-NADH dehydrogenase subunit 4 [Phytophthora sojae]gb|ABG54058.1| NADH dehydrogenase subunit 4 [Phytophthora sojae](ref|YP\_001165397.1|) 0.0

MGSSPIFRPFYNLDKSLMFNKYILPLLLFLPFISIITLFFSKNEKFIKNFSIFMSFFIFL

VSLPLWILFDKSTSNFQYLFKIEWIDQFNINFYLGLDGISLFFIILTTFLIPICMLISYE

IINKNIKEYFILYFILEFCLIISFSVLDILVFYIFFESVLIPMFLIIGIWGSRERKIKAS

YLFFMYTLAGSLFMFIAIIHLFLTVGTTDYQILYYSNFNFSYEKLYFLAFFLTFAVKVPM

LPFHVWLPEAHVEAPTAGSVLLAGILLKLGSYGMIRFLVPLFPKATIYFTPYVLVLCLIS

IIYASLTAIRQTDLKRIIAYASVAHMNFIVLGIFSLTIQGLEGSIIQMISHGLVSSGLFF

SIGCLYDRYHTRFIDYYGGLAHTMPLFCIALFIYVLANMSIPGSSSFVGEILILTGIFED

NTTTAIFATIGMFLGGVYSLLFYNRICYGNIKNMYLNIYYDLTYREFLIHLILIINIFLL

GLYPKIFESCMHESVSKILIHIDFSYFF

>contig07333 Frame-2R

MDIGPMVGSNLQTSDPRAPYPGNYWFSYPGSCAQKMRADKTDKCRTQYPGGLCGIGIRPD

GDNCNFSYKILGFLNIDDLVGITTMGYRNYRDFCKDGGVEFKATNTGNGFKMEQAIDFWK

HPEDENANFNRTFTMVNMYNELAASTTNMVPLPSIDTLTSANPKCNENSATCANAPNGCR

RELYSQICFVCSVFGPDCSGPSSFPELQLPVNPMEDNGSSMS

>contig08246 Frame-1R

MSCVLALLAHNVFVKKCLLATQFWVSSSSKDRKTH

>contig08880 Frame-0F

MPKDYETNLFSQMIESALFRSTTLEEELNHEGHELRNDYSYFDVKLLRNWAGPGHWKFPA

VRKVHMKKLIKDEVEKDGLVGIEEDEIAMKAEMYETVTDRVRKASAVSVEKKTVATVDFF

GEKPDFSRLEAPKSALSLEVTKGVIKKQVENALDLVLPVDTHIELGLFFRHFLKEKMRFF

RKRGGMESSYRDNPLMNEVKFKDSYSDNGDYQDRKEPFAYNEDTGGFEPDYDEDDESPVE

ADDHGTEALYSVENLVQANRVVEKIGVHYERFAKRVDVKKLKSSIWDHLEKKVIPSGTND

TGNEPSTNDSGKRPFDCLHETGGDEIFETSFENVVENVANKV

>contig11217 Frame-1F

MVSPSSIKTRIRHDSFQESPQSAFTHIPAPIKTPPGRLTARRDDLRIQVSKKMAAAAPRV

SRNTIIPTVVHLPLTPASPIALRDIRNQQESLKTILQHKHDEEKVLKQQQEEWMRTNTFH

PNDHCRHVSDSLKALPLNLKDQGLDDTKDEAWALEAPVLLRTISLGGAEPSIMTPTFTAR

NDNTTDRLQHNKLKNRRKTTPLVLNLDQLRQLERETMHVENKLKVYSSTESIASTASTVI

TCHRRITSSVSSESARSVDLCDFVGYEDDSEDMTTSYRMADFEDSDELVGHAREQQTSAF

KSTCLPRASSVYGSLSPLLSSNSSNTRFGSPRRCRSKTYTASRSSNIHDLIAEGDASLRS

SRVWNFKKEYVK

>contig13484 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60272.1|) 3e-82

MKNAKPSYHAGKGTIMLALRNELRCNFWFWLVLALNLATVACLLTTWRHAYEHSLNDMLC

FTYAICCALQWLCLIRYLQENARFQILGLTLKRGLPRVIQFLVGVFPIFVGFVLFGTVMF

GSRVPRFQSASTTATTLFSVANGDEIHDTFNDVAYTPWIGQIYVYSYMILFSYVVLMVCI

GLIEDAFFSAVFPDIW

>contig14319 Frame-2R

MAGTVGYIAPEVISSHVYSEAADVFGAGVILYILLVGRPPFYGDSEVEVLSKTARGDYSF

DPKVWKHVSESAKQLVARMLEMHAQDRITVKEVLAHPWITRQGSTRSSESDEERGLTTSM

ITRLQQFSLDRKSQNMGSFMASMLLDDNEADFQTLVDEKTIELVIRQLSVEGNNRLPLDG

AHVILKGIGLSPYMDEKAFVQFLDQNHDGFIDASDFCASVRAVRNHHQSFAKIVFSAIQK

INFEDKSDLNVEDIKAPALTRQHFAKAFDKLECPKSLAEVFYKCMDENLDAKSLDNSSMP

AVSSWSVNEDEFAALLTQFSFLGMLFMQTAKANVISIVKTHSGNDMPCISEDMSSSRSKK

>contig14386 Frame-1F

MTVSTSATKEKPLSTKERNETSQAPENDEETSQSSENEDESTGDQEGTEDDGAMESNNES

EEGKDDEDGEKED

>contig15910 Frame-0F

MVEMGQSIVLVLEKSVVSELQSDVPGTVRAHIGLSGWLLEPVDSGCSTLVTYITNLDMKG

WIGPATRASFLLARLECVSVLSEYVNQAHLSGSELGFGGNLDDEGDFNSQSSGYEDACKG

NDGLGDLADGQSSALFHPKTYMRGMMPLPSGGLKLIDKEIAKKQGGVVKDVIKSAGAKIL

EGKSAVSLSLPVRIFEPRTNLERICDLMLYAPTFLNVAATQDNVLERFKYVLTFAVAGLH

HSIGQLKPFNPIVGETFQSTLNDGTDVSCEHTSHHPPISNFQFTGDKYTIAGFVLWHASM

SVKSNAMLNTNKGPVRVTFPDTELLQGTTIEYNLPYLQIGGLLWGDRTVDILGTMLFEDK

TNHLQCELRLNPDAKSGMGGMFSSSKTPTDSLRGVILDTSVSPPRELGDVSGSWLRDLVV

DNQTYWSMHKYPSGYMVPYPEDKMLPSDSRFREDLHSLAVGDLDESQEWKVKLEVLQRAD

RKLRLDGRRPTHWSFNVASGH

>contig16050 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60308.1|) 5e-18

MGFCFWTIVFISWVLLFQMKWKDFGWQSLVMVVPEEDVNLGW

>contig16858 Frame-0R

MKRELANGKLCARGTVVIGGKSLYLETRDCVNDASDSKSSDQ

>contig17721 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62533.1|) 1e-119

MQCNAFDSGVFLHNAMFNHDCNPNCVKFTPDNAGPDGGVSEVRVVRPIAKGEQLTISYLY

PREQCRENRQNALWKQFGFRCCCEFCKRGDSVLSLPLPQISLDGSASTKSCILDLEKVLV

EAEGLIKLHPERAAEALSAALETLSDALAIVAHDHLICMRIHKLVADSCDLLLREKTDRV

CEYSILFLRSSYELLELQRTYLNPDHIDLARTLNDVSQGIQLLLSYDSKVLLAEFPEWKD

FRHASIVESQYRNKYRRLKEMYE

>contig19864 Frame-1R

MTEMKGHDETIGIPKSIEKIVSLEELSALESLAFKSLVEKERQTVSQLKQNKYEMDVDGL

LAAGRIGAQATENKTAGRMMKKLESMLSNLEVEIEQVDRHVGDRLNLLDRDSDGVLSAEE

LRDAVMTILRKANTQEDVEWVISLIDEDNDGKIALEELVAWIAKCRESLEATGRIALQEP

TDVEAGVESEKMDKSEKAEKAKVKRGNSRKKKEMDREVGNV

>contig20059 Frame-2R

MGPGFSFTLLIFTLLTYYNELSSAAVLSSTHSTSTDIASSRSIVRIARRYLRETAAMEGQ

ELEKNLGFDQTIKNVKKPSLPQKVYENVLEYLGRMNGKSKRDKFFVIATLLLLPFGIFYV

CNR

>contig20895 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53391.1|) 3e-39

MNGKVRDLYKRFLLVGRDYPMGLSYVREKTKTAFYQNRNLTDPVAIKKAIKHGRWMVREL

VGVIQLKKYRMLNSRYTPEELREKLRDIENRRVVDNIGQKHIGVNDNDA

>contig21056 Frame-0F

MKTLVASFTIALMLLALPTSVNAHGQLIFPVPRLITQQYRAKCGALDGAGDQELQYAPVE

LLKAREQADRPSAPTFNMMNGCRGTIYEPNNTVTPLVAGSPFQVEWFIQAPHPGTMVLSI

VKPSTDSNGTITYVSVSKLLTIDPFAVSSADKTNTLATVPTNVTECETPGKCALQFYWHS

DLASQTYPTCADITVTKSTGFTAQESETIAPTPDSPAVLNATPESTSPAELSTPPSTTSP

AEGFSAVKPLDTTTSTPAMPLMVNKNCKVGRGTARARN

>contig21737 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57512.1|) 0.0

MQTWEAFGASLAIVASIVSNLGVNIQKYSHSSEALQPVHKRRPYVRRPVWWIGLLLVIFG

SLGDFAAFGFATQSLVAALGGGATLVANVVTAQCINKERLYMTDVGGVLFVIIGVIMIAC

IAEPNVEYPLPELELRFVRTPFVVYITCVGVCTVSMLATIKGSLANRLKNQVYWSNKRQK

KLLKEFELRLQRLEQRLLDVEVKVLQVATSSAQLPSGLIHPSAISKELRDLIDSTNAEEA

QAVEEAATHGSHVSYYYAICSGIVGAMTVLLAKCSAIMIALTLKGANQFQYGLTYMFLGG

MFVSILIQTHFLNMATALGNIMTVFPIFQACWITFSVVGGAVFYQNEDIPISTIDKVVYA

VAILFIAIGVAFLVQHTSSLSDNSSLKRAKKAISDTEINEMLLSVDASMKLPLLSTETRE

NSDILRLYA

>contig22703 Frame-0F

MRAIPQRITCKKRRQSMHAMKREPL

>contig22866 Frame-2F|Blast-NADP-specific glutamate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY53988.1|) 1e-12

MYKLHDRVAATAEDFNAASDLHVGSNITAFMSVAAAMFRQGAV

>contig22912 Frame-1F|Blast-protein phosphatase 2C, putative [Phytophthora infestans T30-4](gb|EEY57130.1|) 1e-10

MSVVIIKFPGAKLGPGGGVAKIREDRARVEKLNQKTTGGSNRKDDGGLAAAQSALNLS

>contig23652 Frame-1R

MLHSKKSDCESDLSKFRKIVKGYEKAKLKLEKKMESLVGIQHSFDKELAVRQEEIQKLQT

RIDNQELSAHDMEQIGQERMRLTEQLHQVFARQLEFQKRIKNDENRAAEIRDDLDAQIHK

YINTCKQLKIIPNTAKYSLNFDYMLELDPDLQELEAVQKLTHYLKTEVRQAALTLKQNRI

ACANAGLDMALVQDNKLQQCDNELNNEIQLEKKQEAKVKKYVEQMPKQREKQAENLRRKT

AAIEEVEKTITNITNEDNLTEEESMSRQRLTDIKKL

>contig24020 Frame-0F

MLTKTQQNAIVTNLLTRSDVFSTYEGGDEATALDNQDEGGECDEDSIVLDEKFDPLALEQ

PAIEIKLESTGRCTDIDLSYGVSDDSFALNSLPSLSPSDFTNALAESFDSSDNLKGSFEV

ETDTQENVVDFEDSDNFGDFKNFEAPAGVSTWHSYSSSPPVHNSPVTKAGSHSFKTFAGT

NTAVAEDAFADFDHNDDFGEFNEAGDCEQTATNNKNFANFQQSGSQTFGEDDGFGDFGPA

VPPTSVVSPTPSISSAPLLSKSDWSSFFQEALAIEPFPTCLEIEPDDTNEDDEVNGEENI

SLEFVQDLHHSLWKEYVANAAGHQLAKSLSASDLSHDGDRVSLDRKTARPSKYLKYVLAE

KIQEASRQNGIFPHGSQRHKLYVEHAVSDDADRMRVALNELQEALFHCSVNDAMMRIAKQ

AALSAKAKIAEQAAQQHASSRGGSLFSTTRQLLSRSGGSTGVPGFGSNGHEKGSHVSADT

PTGASAQKLARLALTSSRDDSATSHLGISARDEIGSVGSDRTGHSSGSDSEIVKSAGDSR

TKSQNLISSNGGLMRKFQDRFPFASSKHRPRFVSLRRERQSSEEVRKMELHLDAINGGLD

EVKWKCAMFLYDMDEVAHVAPSQIQILSYPSKQLLTGKTDRSALMKLVKPHTIWTVDIGA

NHSDMLNDW

>contig24482 Frame-2R|Blast-argininosuccinate synthase [Phytophthora infestans T30-4](gb|EEY69175.1|) 0.0

MSVEAQPGDKVVLAYSGGLDTSIILKWLTNKGFEVICYCANVGQHGEDYEKVRAKAMSLG

AKKVYIEDLREEFVNNYVFEAVKANAIYESRYLLGTSLARPVIAKKQVEIAQAEGAKYVA

HGATGKGNDQVRFELCAQALDAQLKTIAPWRDAEFIKTFKGRADLIQYAKEQNIPIDATP

KAPYSVDENLYHTSYEAGMLEDPMTSPMIEMFKMTVDPKVAPDTSEQIQVRFEKGIPVGV

TNLTAKTAEITGALDLFLELNKLAGKHGVGRIDIVENRFVGIKSRGCYETPGGTILRHAH

LDLEGLCMDREVMKVRDSLSAKFAEFCYNGFWFAPEMEFVRHAIDFSQQNITGFVNLELY

KGNVTVIGRFSDEALYSADLASMDQEGGGALFDYNPADAQGFIRINATRLKAWRCRPQPK

I

>contig26989 Frame-1F

MSMDRSQEDDYEEKREEALGLEADNWPRILDYELSDRSSSRVPAARTADVQLTSFTLPDW

SSFSSGRALKGLGPENNVTKIGRKRGESNASNATTVIEGSITASYVGSVRDVEIKTIASA

VVGEIEEEPWENLFGASSTLNSSTVDESMPSILGFDEESSESSDKYKEKMMKPRKNARKF

NDQLRLARSRPLSLRINEEETMTGMSCVTPVSFAKLERKPSLLPPGPPRLSSASMLLRHR

SSDNVLTACGKTDDLPPMHRTSYRYDPKCEMEGNESAKIKRRNDRKLHKARSVASIDTSI

LRTEPENFDCSRSIASPPATSLNQIKTLAARMKQKRKQNSNGSIEFVAMARTQSDATGSA

SPAREAAREPRTPKKKKETTTLSGVAALRARFEK

>contig27511 Frame-1R

MSKSGTKPLVIMKALKASGQTCRVIGEIFYNIRKQEQQHLLTGRTPLEALLDTLGEEDVY

HAFERNSTRQLSNLF

>contig28037 Frame-1R

MSFNPETTQTQTTTKKRVTSTTNNAYVYTSTSGEETKLDLKDGANTRPHARKVKGSIITS

NFTQSSSIFVFEYTSEGVGALEPTEIFVPYIHFPGGYRVTASDGHCTIEKHEGYDIVKHE

HGSHARKHRLVVEKSKKVAARYSWFAWTGHSNIPVYVALGIAIVAPYLSFK

>contig29773 Frame-1F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 5e-92

MDGQIGVDSELDVGSNFYFTVVVRLLDDMEVKGLLYAANELLSDESGAGSPRANTLNVNS

NDSAGSVNAGKIMIPTQARILVAEDNEFNWEVVKCFLQEADHLLQWEVNGRDALKAYMEN

STKFDLVFMDCEMPVMDGYTATKAIRQFELDNDLPRIPILGLTAYAMSGDRQKCLVAGMD

EFMVKPISKSSLLKAIRQWMRVRYLGPKARTPLVAELDDHSRKCSKEATLAASAPIGALY

SPSSSIGRGGDEDRVPTSYPTCPTPRQSFDSEAGEIDTFNNTSKVGLRLAPASRHMQQLD

LARAISNLELDDP

>contig29922 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56655.1|) 5e-24

MHCAMVQVAKALANTGAMLSPRALAKLKAQVQSMLRCLKFSNDAWDVGVMLTTESHVQTL

NRKFRERNTPTDILSFPFHK

>contig30959 Frame-1F

MYMPLSETEPMLMSPSADKTHRLSPSSAITPRRLEASSAKCNDAFFAVVFVANVVILSLV

AIWKGVPAIQKEFSHDENDDQFQGNSATLTMIGLLCAVGTVLSLAWIKLLMTYAASMIRV

ALWLNVGMVVSFAMSTFAVNVWAALFLLFLAALNVWYIMAVENRIAFASANIQAACAGLK

EHSSIFAVAFLLVLQQLVWMFLWGVACVGLHQLFLETDPNCDRELDLASRGRNHGGLCVG

FPAYVTLFYMLVSLYWGQQVLQNILTCTTAGVIATWWYHPNGTKATTGALYRSITTSFGS

ICFGSLLVAVLQALRTMAEMAKRRARGNNESGLACFACIAECILSCLAGVMEYINHWAYV

YVGVYGHTFRTSGKAVMDLFRTRGWTAVINDDLTSSALSFGAMGVGIVTSCVGLLMVHFL

PMDYFTALGSQMAVYSTMALIGFIVGLSMAMILAHVIIAALHTIFVCFAEDPVAFNRNHP

KEYEDLVAGWRQFHGDVLLTAYRDSI

>contig31088 Frame-0R

MTFSPAKTGIDTPPFGIATHPPFQGIQKSAVIL

>contig31527 Frame-2F|Blast-Mitochondrial Protein Translocase (MPT) Family [Phytophthora infestans T30-4](gb|EEY66230.1|) 4e-39

MSQREFERKMEEHIEEMRVTQTIAYFSRTVELCFTDCVHAFRSKKLDDKETSCVNNCSEK

FLRHTMRSSVRLQESYAEIMQQQEQQK

>contig32180 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66154.1|) 3e-28

MIQQNHQLQMQDFQIALSVASGHSMDVDEIECVLTNLIFKGYIKGYMSHTKKILVVSKTD

PFPSIVSVSS

>contig33370 Frame-2F

MAIGETQVLEHRALLPTVVIKTEDQPHKLLGISCVALSAVCFSLTSTLIKFNTYFMTSME

AIFWRSFVAMVLNYACIRYSGKTLYVAPADRAMLLCRCVAGFSSISFAFYAVSQMVLADA

STLIFTSPVFTFLL

>contig33969 Frame-1R

MLGDSESLYLSTLEIWRGYVVAANIPGATNNHAKEYVDYVPFLGAMRSDLANLLRDKTAS

LLRTDPLHKFIWFMDRAVKNQTLEIAQLHELLGFIGRLRTSDLPPNKKIRKKPGNEEEEE

NFEVVLGPPPVDELLVVLDKIAKIDARMIFAEPVPDDVPNYREIIKDPMDISTMRRRVKR

GKYKTLDAFVADFNLMIRNCMTFNPDTTVFYKEGKRIGKRGNELIERNATALRGEPQRIR

TKKRRKTGNGTTNEALSMLTSSGVVTIKDFGDVDQSGMIPEGMCDEQLADVALVVSDPPV

KQLVCEAIMKNLVVCWHRKDLPTDNLICRALVQLLQIGNPFGVRRMIRKQDFVLRVPQVV

TMRVVLPLLMRSMVTFRV

>contig35105 Frame-0F|Blast-sepiapterin reductase, putative [Phytophthora infestans T30-4](gb|EEY59412.1|) 2e-11

MEWTMKATASELQCFVKSVDLSNSSDYASKMDELRLQVSKQNYDRVYVVHNAGSLGKLGL

VQECASSLIELSQ

>contig36636 Frame-0R

MMHLLTNNNWNGAGDVGARRPASDEAVKNLGSFSADQASTVEVAIIVEGIKGEVIAIPGN

FGPCESLQEKKMVIADPFDGASAFHNFSELKEK

>contig37420 Frame-1R

MEAQHQWWTICQKTVFSDPRLVLVAMYGLGLLIVDGERPGYHTRLKVLEEMCRFS

>contig38670 Frame-1R

MRKIDDLDQKLYRAFKTGLYLAVSVNAEVSTGSTHNQAVQYTEITTE

>contig39101 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69518.1|) 8e-59

MFEAGLRHSRFIREAQAIGFHYHCGSVWPRFFDTRLIDGGLLILSRYPIVKRDQFVFSQG

SGSDGICAKGVLYARIQLSPAVSDFFHVFTTHTQAGDNRNEYTIRLTQLEEMHRFIATTI

QSDPQVPILITG

>contig39800 Frame-1R|Blast-ribosomal RNA methyltransferase nop2-like protein [Phytophthora infestans T30-4](gb|EEY64209.1|) 1e-159

MRLNIANNEPYHLSTEGEMERNGEGYDNMSDPAEVHQRIKDVVEVLSHFNSRREPGRSRV

DYIETLATDLAGYFGYNRELIDLFLQMFSPAECVDFVEANEQPRPLVIRTNTLKARRRDL

AQALIQRGVNLDPLAKWSKVGLKIYDSPVPIGATPEYLAGHYMLQSASSICAVMALAPQM

NERILDMACAPGGKTTYIAQLMKNTGTIIANDLKKQRLKATVANLHRLGV

>contig40079 Frame-0R

MNSSCLSKPYVLYKVAHLLFEFIRARSCNFSRQSRFCRRIDLFDYFFCCFSMGWWRPKVL

KRLCLAVLCRLSRNKLSNLIHSSAC

>contig40105 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53160.1|) 1e-159

MFFASGFTETDRRATCVGSEENDILRDLLLDNEFISPRQLPPTPAKHYEDSNSSSNPTTT

NGLLKHSSHQVDVSFSQICFDNSPHLTRLQPLSSRSCASFLLPNQSPLSASVTNAIVSPP

RVFVQEFACFPQQFFQDNYTIDSDMRCAKDEDSTVSFFNSCLPPAPLPMLTMPPFKKQKL

STVLTSTIAERKQLRCKYPNCPNLRRSAGFCNRHSGKMCSILGCNKSALSRGKCPEHGGG

SRCKNDGCSKFAQTRGLCKSHGGGRQCNISGCSKNAHQNRLCRSHGGGKRCHFFGCPKWA

QRSGYCCAHTKVSVTDALKPSGGSQHSLPNNSAINSLSPASSRCIPPTSVSSPILLSPHR

LFSLIP

>contig40480 Frame-1F

MMHQPSSYLWHLASNTSGYERVPNILRRRHTMSVCLAVEAYNSASENYRSRLCPTGFNHN

RRIPMALRNETWNTAIPLADGSPMEKDPPVYFGNYKPIEAKLALNPDIKGSDDVHFVFTT

SCEQYQDWQSEALAQSFARVGQRGALTRIVSGCSDTILKDLVRRTRKSSPHLRIHVTRDF

SSIPMLQTDNSKGENASFPDAYVPYNKPFGLRDWLATANPPVREKLLVVLDPDFLFLRTF

AVNSGGRVTTAKGVDSGDYEHDAEVIEGMRQYKRFFVYAGSRDNVSDTVVDGAAVAQRWT

KYLKSLAFINSSAICPECANVSETDALEYYSVGPPYALTRTDLMEMVDDYCNMTLLKREQ

NREYWMNEMLGYSLAAAKHNIKHTAFDNLALSKKSDDYTGFIKMVKGNPCEDPVIPLIPS

EAPPLLHGCHLYEMVDDRGLNWIYYKQLMPNNLFACDSWLLATPPASIWSIAKRSHDEHK

MLEAFGLCTSIKVINQALVDFKTKMCPDGFNQNRRLRLVKKFREDLLEVGKVHKPWQDAA

DENAREGA

>contig40822 Frame-1F

MVWINEDVILAAFTRESEAHTCMYLYAYARNQLTTESVLAKFVIPLQSKEESFWSMELDK

QHVFGWSLRYVWWFQVLVTGSIKDETIAVTLELQRQIKFPSWVVEAQRQEPGTLHIAILP

REFTQFVPTTQQQQLVPLEPTEDETHWLTDFVNRLVHGQIPEQYVPDQVLPRFIVLSTNG

DVIVWDPENRSQRLVCSNISTMTRLIVTSQSCAVWPTSCRLLFGLYGPDGMHLYLPLLDG

VYLTQTKTFEHDFKRLETFLACHDPLRAKTYEIEFGTAPATAELYEDVMREYGIELDLFR

RGTTNGLKSLQDGYMNQRGCVMSVDDPSGKYSMLQFDVDVQVLGIEPTFGLLVGISQDVY

GPSGVVLPC

>contig41560 Frame-0F|Blast-signal peptidase complex subunit 3, putative [Phytophthora infestans T30-4](gb|EEY54545.1|) 9e-81

MHSIWTRANNVFFTSLMALAIMCTLTSISTFLHESNPVVRRLEMTELHSLRNYRDKTDRA

TLSFNLDADLSSVFNWNVKQLFVYVMADFESASNVRNQVVIWDTIVQTKEAASLLQFQNE

SVKYFLADQHDELRGANVTLRLEWDIMPVCGRLFIHSSDNEFAFKLPDAYHGKVVKARGH

F

>contig42082 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60173.1|) 1e-123

MSDVDISMQQECVIADAGATTKELSPHHSAADNFGIPLRFQSLGEMPSMARFRSDSVATE

PRLSVCSTSGTVYESVVVVGHMYGSDNVVYYLLEVRSWEMPLEGYVVRRRYNDFCKFHAE

LTQYMPSQRLRSRSSIDFGLTYSSLLCNPLIKAVPETSPLWSPVLTDDGRGSHQRKDSWI

SENSSTSQPSVEESTNNTKSHSPKLQTEEFRPHGGDSSYNNDAMLPLNAVKFNLTGRPWL

PPMPSGGVLTMFTTRNALIHYRIQHFNHILAAVMSDKSSDVARLLMNFIQEKPGTQAQTY

THLSEYALIDIPLNVERHARRRAMSIGKRQPQE

>contig42420 Frame-1F

MNPDLMNVLSMRQKEMSYHQLALAGRLAPVVANPLKSPVLQSQESVLGLQKATYEQFGFT

WRWIVEVATHFALQRQTAHFANQYAQVLLRRRAAASLHENFTFGHGSDVRHMQKQLRVLG

LSCVFMAAKIEEVHPPKAAEFMAFLAERGCVQLAAEDLARLEVDYVVELQWNLHPTTPYA

WLLFMVAGGSADLRPLDTMGDFVNPARNASGTKELFVNAIRLVDIALLDYQAIEYWPSVL

AGAALLLVDPALDFMFVAQFLQLDPNVLWECKSWLYAMAYGVCDLEAASTHAKDRWIKVP

TEELLFIQSQVVVPSHLACGLLGSDNLLNLYSAGMNTPLGKGYGLDTCPSPCSPSDNYAM

VATALACMCKGSYHTCSGGETPGPRVYHFKYGWQEIETGLMTEPYFGNLYEQHMQYP

>contig43012 Frame-1R

MSARGQSFRSHHHSSRGQLSSRGQHSSRGQQSSSGLNSSRGLASSRGPSSSRGQSARRGT

AMSVSSVSSRPSTVPLDEYVASFSGPGSSASSSRRQRSADLNAMRKDVDVDDVETDCVAC

NTYSLTSNCQQFDPSASGALTSSSLAMMQSYVNFSDSIVSSVSRKSTMEQKDNTFSSVMG

VARAGKCGGYGSSPQAKTSIFSNDSNCSYDDESNNWFKHRSTAAFSTEDPEREMYEAEGQ

SYELGPFGVTKSAFSRDSVDSYDFHSTNKLATSHLVFSDKGGSDDGSFRLLNRRGTDSSN

HSSNMLSNQSVLSTLSDDSFTYDVDKSRSASDYPNSLTF

>contig43166 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY61544.1|) 8e-83

MCQFIQLCLEILPRWRSALAGLGTIKTFFLGGWLVAMNCLGGLWMIEWSARHFNLKVTLL

SDLTNYQWEIFGMALLVGWIAWFLAITCFTFHNVTECDSNRKALVGFFERLKFTFAVGQG

IVFCRACLHPHMGFVHAQLELTIINLLLPS

>contig44088 Frame-1R

MLTSRNTALSLGLITRAQKLMLSLSAFCIASSKDGSSSTTCEYVMDSYMRSSVNAFTTKF

RLHREIYQYESGYML

>contig45313 Frame-1F

MNAVRAVRMLYATGVLFIRFDRNYTQIKCVTRIVLVLIL

>contig46370 Frame-2R

MCISADAVLVVPQGTTKVCKPKTCQPCLPVRITGSRVLVRDIHVTSPQRLQYVIYATSFK

RFFTRILPFSSESKRQNPHYIGSFFIVIALLVETLLKLLLY

>contig46969 Frame-0R

MEDAVKNLHDHELVAFGAENEKNDAPTSAAPAEIESADCQNLAKGATKAQRKREAKRKQS

QERRERIEESNKNIVSKRQMEADSIRAQLARHGLTIKDIPSDGHCMYHAVADQIKQKNLT

IADRAMEFQYLRKLTSEYMLAHSDEFLPFVALDESSGSPTKEFSTYCDRVANTADWGGQL

ELRALACALRTPIEIFSAESDVIVMG

>contig47180 Frame-1F

MLTIRCPLPVFLRRRILRQPGTRRLRVGDSPITRRNRRSGDHVGRTWHTARRRQRTYLQR

TGPWPPTSEGERLRAIARSGRLCHGALTAPDAPLPTQSPACSPLLRGESARRRRRGRQLR

PLLPRVQQVGGQSSQHRDGHSNIRSG

>contig47823 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64772.1|) 2e-21

MTTKRLHKKQSLPVGSLPPQVAWLDGISMSVSSLISKQRTSHQADYVLTVTCQNHIGAES

SIWHLVRSFDEFRFFRKR

>contig48530 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53277.1|) 2e-55

MRSTQIDNALSMKRERSTSFSSVTGRSVAFCRPNHNLAMLQKRLRDGSFLNKSNVALESN

QYEATSNTNTCIYGGGAVGHQKSTTPTSPAMSPPATLMKFADFFVDPSNVPPSEAATVAE

EMAADFFSEVSIMYDMLSDITAPTAEGRAVNELMQRLHNVLRAIDNRRIDSEGSNLLAQF

ANVRSLYNGLIRVFIFLYQRYYRTFVVLEVSELLTASWQRLLAFVVEYRILDETFVWKVY

DYVAQIIGSLR

>contig49739 Frame-2F

MVMPLIVFCTFCHFCQGYRLRAQTHLLRCMSALCHSCQDYRLRAQTHLVTLHERFMPFLS

RLPPQGTNASIKFLINIF

>contig50423 Frame-2F

MTSAQEALVMKKPLICIPFLGDQLDVAARVVDSRAGLMLDKNSLSGLFIHAALTELRTNA

SYKDAARKVGVLLIRGGGTARAIDVIDAALQVGFDHLVTPEMTMPWHRAALLDVGALYIA

LVCLLVVFLRVTSLLLYHLVFISLHHYKENTSLCPASLIEAQNEICEDEGEGSSDSSQSV

I

>contig50672 Frame-0F

MNEVTESHTNKTSATTDGHMTAVTTTTTSVTTSTTTESTVVSALADVIHTLRLIPEFGGQ

GISYWTELQRLYVASETSTRAFINTAAQALLAESSSAEAKASIAFEAVIDLRTWLQSLEI

GVAPSKLVLDRVFFSMPLLVLTQCANYLHFLENANVSHESVVKNATAAMGHSQGVVSAVI

FSLAKTDQDFMDISVSMLRFMFWQGLRAQEAYDCCLKHYQQDGKVVENASAMLVVRGLLP

EPIMGAIQAIKHRTKSPDLHLSLINSSNMINVTGFPSSLSLLEQALENLFAKPEVS

>contig50979 Frame-0F

MGRCSMLAAVNGKMFNARGCEHVPVAGVRLMKITLYLVLVLEDRKVDAPRRPRSGLLKEA

DKNALIQARDGMACDTRMNEIASINPKKDDVPFRRCRNLFRSKVPLTGRS

>contig51990 Frame-2F

MMTKAEAVFSALALSSARNDPLLQGLPSASLSTLSVAVSVTDTATYMNARWLKGVPSV

>contig52601 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57883.1|) 1e-36

MIPLVMGGAVVGTVLSKLLPSYLLSLLFVVLLILGSFRTVSKGITMYRTEMNTAKIMKAC

KIDETP

>contig54791 Frame-2R|Blast-transcriptional repressor TUP1-like protein [Phytophthora infestans T30-4](gb|EEY59397.1|) 1e-86

MLDQVKAEYEATIQQLNMAKMEQLEMERKIQSQVVEMDQIQQSLKALESNHRRIRQQYEE

DMLRMRRQLETGQVQQQQQQQQVPPPQQPMSVKLPAKRSRALPSGGSMQDDSVSLMSNLV

AAATSSGRAGSTSTQQRGNGSSPVRVVPVQPASRSLQQLGQQPSQLPPPPQGGSSNPPSQ

LNPLDPSSTNTTPSSRRMP

>contig55510 Frame-1F

MSDELLPCLVCDEPLPADPMARCLTDCSHEFCLSCLCRDLALNKNRCPGCDAQVKQVTQL

VSPKQNTPKPAFVRFCNAVYTLNVSIWAVDNPTIILAALFDLDHAKLIHQGKVLKKGDVW

PGSVVQLVGTRKGILQEAAARDLVYSFCHDWLQRAKQVLCSPLSIIFDFFRSLFGNVPEQ

QRRGERGYAPLPTRNAISTSIFREPGRVASPEHINLL

>contig55925 Frame-0R

MRRERAAIKDSLRSLSHVSTEQMKKWARLT

>contig56245 Frame-1F

MPKGSRPVIVSVMHQATLVIFLTMLLITDLLFLNDSDFKYEPDYKVRKDRVVVSRICPDF

TFYFT

>contig56915-0 Frame-1F0

MKESSDGIDFFPFAITHSHDRHTDFDRQRRNLARMTTLK

>contig56915-1 Frame-0R1

MAMCDCKRKKIDAVTRFFHCRLF

>contig57130 Frame-1R

MVIRNSSLPKVRTSSSRRLFFPFKCQFRR

>contig57938 Frame-2R|Blast-eukaryotic peptide chain release factor subunit 1 [Phytophthora infestans T30-4](gb|EEY60208.1|) 8e-22

MATPTAADDQVELFKVKKLIKSLQAARGYVTHRFNVSTSFSRSILITPSLTSNGTSMISL

IIPPKQQIPLVAKMLSDEMGTASNIKSRV

>contig58904 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58324.1|) 2e-22

MTPTAVATSLTRDNIKFLAIARATDKVIIASYLHTSNGKPVRGAEVEINTFRAMLGKVLR

APTWQAQVTPNVR

>contig58971 Frame-1R

MLDRSLESFSDDYEAVTSETKRIWFLMSTICQRCFELR

>contig59046 Frame-2R

MIVMEALWVAREVIEYCQEHRIRRCILICGVGHHSINGKPRILTALQLSLQRRQIAFREL

NGIVTVFPLRSISSS

>contig59323 Frame-0F|Blast-dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichyl-alpha-1, 6-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58713.1|) 6e-12

MNEREVPQSVHIDIPAAMTGVSRFGEEFPAW

>contig06191 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53087.1|) 1e-149

MVFMSIRNYLSRELLAACFFVMLLSSTLDQYPGEVDPLPYNCDYELHTREQEARYNKTQQ

LIRNTKLFEPPQIERLFLDQALGAEDMAVSQDGIAYVGLTDGRIASFDAAANRLGNFSRT

GRHVPGCGASDMEGICGRPLGLIFASATPFSTFMNRIPSSKPFPGDQVLLIADAYKGVFL

FDANGKRTLLFSRTKEEKLNYFNGIAVVHATGEVYVSASSQRFQRNQTVLDFLERNPTGS

LVHFDPRTKQVRIVAKNLGYPNGLTLDQKRLGLLVALSFQSKIVRFDFLTKQMTDFAFLP

GDPDNISIEKIGLGTKEKEVLMVAMVSHNDGSIIHQMRESVKVRKLLSLLPTWVTMSLVH

KVGFFASVDLDTGDINFVYEASQGQTPMVSGVRRFGDHIYLLSWARSYLTRIPAALLQ

>contig07563 Frame-1F

MTKMPTLRHNWRGEEVRQGRGGEEKLCDDYAVRNGLLCISLETTLLIHALSSS

>contig07916 Frame-0R

MSSNPRSRLNGLFQDAATTGGGNDALRYTAPREPIMKPQQQPPAAASAVSSSPAASTVVY

STMVSLYQYDASERKYVQLGGATAGTKAAVGCVIVGAETSYTLLFYNAAKHHLCTLPLKF

STFNPTLQAKSYVNFYDDHSQNWSIKFPNDSQVAEFMRHVFLAKLHVEIWGLDKSVTKTH

PSALIQDDLVFVKPELPAVTTGDTVAVAFQAWRVVGNASSLPTDVVTKYPPFETATTKNE

LRKFRLGDATERFKALDEGILGMKKGGKRILVAPPGKTNGHEWYLFEIELLKTKSSASRP

KATLKNTQEASKESVMESTHSPSQHSNRHSMSTPIPARHHLESFETPRDLVPYQRRSVSQ

QRNKP

>contig08247 Frame-0F

MFQRFSLRLAVVFLIIGCGSALEAIDTNSETFGTQHSTDMNQPSAAISSNTRSLRLLKAN

AVGLKGLKGIIHSILTQKKNLSKFEVEELRTSTLGATQKKYGG

>contig11007 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59538.1|) 2e-32

MKFWRAPVSESNRIADPIKRAKNHTSRCINMLLGKLSEITRQVSLSFPVLNRLHPFEREV

VLLTLGQGVFENHILCLRKAYAALHNTG

>contig13117 Frame-2R

MRVFRILTAASFAAVASASCDPSKWQPPYDGNYKTSSRVAPDKLNVHLIAHSHDDPGWLI

SVDQYYVQRVQYILDTAVEELLRNPDRQFMFVEQSFFQRWWHEQGFEVRSMVKQLVKEGR

LDLTVNGGWCMHDEATPHYIAMIDQTAYGHQLLMDEFGISPRIGWQIDPFGHSATQGSLL

SQGVGFDALYFARIDYQDYANRKKNKELEFIWRPSKSRGKASQVFTGEIIDHYCPPSKFD

FGENANEIQDDAALHDYDVCDEVEDFVKNAKMRGDASKGNHVFIPMGCDFQYDNSRHWFK

NMDKIIHYVNQDGRINVLYSNLSYYTDLKRKEGLTWSIKTDDFLPYGSARNDYWSGFFTS

RPTLKRFARVSNTLLQQVRQLNAVYQSHHSAQLVALQRAVALVQHHDGLSGTEKQSVTND

YVLRLYDGIVKAEKELNEVLFVIGEKESYHFCIMTNTSVCDVSTQNKNFEVLVHNALAHT

SIQTLTVPIMHNSAAVTVLSDDAKVRDQNVYVAIPVHPETLVAPYSLVFSAELKPLSSYR

FLVKQEDLNDEQVSAETHAFNDNVVVLENSLIRAEINKTTGLIVNLANKKKNIQIPLSLD

VAYYQAYQGDGAKSGAYVFRPDGNKTYPITDNKHDGGARDTAGVTMVNLQTSAGARTSVP

RVAFKISSWVTLEYRVNDDDEFLEIEWTVGPIPIDDNKGKEVILRFDSLNSIASDATLYT

DSNGLEFMKRVRNHRDTWNLTLHDNEEMVAANYFPITTGAYIKDAKHQLNVVTDRAQGAA

SLVDGQVEVMVHRRLLADDSKGVSENLNETESVYDFASKQHVTKGLSVRGSFFINVDSAE

DGMRSIRSKMESQFFRPLSIYRKSVPSEVEAKVPWLLVGEFPENVGLTTLSELTKQCLMV

RLTHLYALDEHLTLSKPVTVDFSTLFTVRKMVVSVVTELVLTGTKEMVAEDKGFDMQWQT

IDDANNLSTRSLPVKGTSVTLQAIEVRAFRVCFAKATENQAVVDGRKVESWDEADNSLST

ALQGLAEIIAIE

>contig16051 Frame-2R|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ27027.1|) 5e-22

MYSRFVSRCASSRTSPSSIFAHWTLLSDIRHSSSTAILAERRDVELKESELSESFVKGSG

KGGQKINKVRNCVLLTHVPTGLQVQCQKTRSLDGNRRAARKLLQQKLDDHVNGESSKRSL

KIDRLRRKKANRSAKSKKKYTNSVDMKLKEKEQAEGIASNAVTKSDEEPDSDSGNENESN

DNYVDWDLKDSKVRFSRLALVAVATAHTRLR

>contig16859 Frame-1F|Blast-3-phosphoinositide-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66101.1|) 9e-77

MHIFRRKSVLHLPGIYPRFFKSISRGRCLYARNHNYIGLTHELQNHWTENFFFMQLSGPK

LGQASAQAEVDNRGGSSWLVESEAFLGAIKILNSQRPAFVVICGNFVNATPSQKFYGAQV

AAFQEMLNHLSPQIHLVFAAAANEYYNRNELKIYQEYFGDAHFSF

>contig17005 Frame-0R|Blast-phosphatidate cytidylyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56488.1|) 2e-58

MDRMDCQLITNCFTTVYFNTFI

>contig20634 Frame-2R

MDDNSTALKFFQLCESFAPTKIKFKRYVAHSLKVLTTTKTFYRVRRNGCSTVYK

>contig21862 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58320.1|) 3e-90

MTGRVINPYQTVISAITRVFELFDDDDCIPAFGFGGYPERPLAERYFPFVKGRGCELDEV

LQQYFAIASTMELNATASFVPVIDEAIKMATNTGRYHILIIITNGHIDDPNMARRAIVQA

SEYPISIVMIGVGDGPWTTMREFDDQLPERRFDNFQFVNYNTIPRGNLDNPDGGFAMQAL

MEIPEQYNKILELGLIKKQHISRAKYQI

>contig22867 Frame-0F|Blast-NADP-specific glutamate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY53988.1|) 0.0

MWCCVNLSYTTISSKPSMSNSVKHASTMVLTMSSLARYTQPFGPAMARASSSLMSDVHGT

THGKKHWKNKPLFRRGGDKRFRNGQEAADMLMDEVIRRDPNQAEYVQAVQNFVNSVVPVF

DRYPKYAWVMKTLMEPERVIQFRVPWIDDEGSSRVTRGFRVQFSSALGPYMGGLRFHPDT

THATAKFLGFETIFRNALAGSYGGAHGGADFNPMDKSESEIMRFCQSYMTELANYIGPHT

DVPTSGVGVGPQEIGYMFGQYKRLRQLHPGGTEGILSGGAYHYPQVTGYGVAYFANRILE

SRGETFAGKRCLISGSGTVALNVAQKLLDLGAIPVGLSDNFGFVVEDQGFTRKNLDELKR

IKKERNARLGAYIMASTTANYHPSEEGRLWETPCDYAFPCAIQNDMDADAVRMLIKNGCK

GIFEGANFPCTDEAINIVKQHGLSFGPNKAANGGSFALINKNLGASTQLSDDDLDKIVK

>contig24021 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57770.1|) 3e-23

MSRWAALEAVAFLLALFVPAFGTSTAETVAQRIANDDDIELSKVFGGHSGYAFSDMANIR

LEQTLSAITIRGAKRIDAISINIKTPVEKTWSHGGHGGTENTLALEKDEYIVSMVIHWGR

KHSRKSIFYLKFTT

>contig25202 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56538.1|) 1e-111

MLGSIKLEKKSVLGRRKGVLTVNPSTLEDDIPTEYRVEISETPLKLKVFSLDGSGRMAIE

GTVKNSCSIMAQHNDQYSKMCKQRLIKSMVKTRIVQPLEDLPRVKKARIQFTIEKADAEG

DEDDADSKLLDRLDRKIKMSKDELKNLVFHHFEEREYWPLKELNYHCRQPESLLKEILKE

ICVYHRKGPNKSCYELKPQYKDGVSLNT

>contig25448 Frame-2F

MYGTTTVGAFTAHVYGFRSGGVRQMREELEKLQARLVKAAQASSDLTMDALERKYNELKW

HIERRLEVAFCQAMSALVTCFQQTLYVHTHDNRPHPLKASGIEYLEMLTRVGFLFSVESL

LSTYGNELGMLGDTEAAVKELGRVQIKLRPVKSPRAATFRVSITSGSSGFVIELPIITRR

ASEFPDRSMHRVPGQDAVSGAIYLSLLTPEQRMRAKFLFQKPIRVIPVIFSQGLNEMQTV

ANTVGKASLQKDINAENMGKLEAYVKSFAEWVTKKQVRDVALTPIYDADDLDRIQTSLVA

LKVSIQLSGRSKRMSILSLSSSIARCVGGGRVTMCKSAKDRTSMSITLEEAKLLVHAHGL

LADDMDAFTDLLRTYGVRRENARKNIGKAQYCFSALQNYMLPQDYQCPPGTGGGSRAYS

>contig26676 Frame-1F

MAMFGQSLDGRPYDSFSQKETSLFSHNSPSSSLVKTLHNKESSIALHTSTKWLRDEDERL

RVAVARFGGKNWKMIAESLGNGRTDVQCLHRWNKVLKPGLIKGPWTPEEDRILTSLITRY

GVGKIRWCDLALHLPGRIGKQCRERWCNHLDSRIRKGQWASEEDDMVFRWQQKLGNKWSE

IAKLLPGRTENAVKNRFNSAARRKWLMNQENKTVSTSLVPSTSQTYRPATTRDGNAFNFR

SS

>contig26892 Frame-2F|Blast-Chloride Channel (ClC) Family [Phytophthora infestans T30-4](gb|EEY62942.1|) 2e-89

MLWTSMDLESLDYDLFESVVNKSGMGFKYRDGQEKNRLIYARWFLTLLTGIITALVAVFM

LFFTTLLFSLKHHLLEYTIHRELTKHVLFGTTFWSFVAFNLGLVMISATMTVFGELVAAG

SGISEVKTTLNGMKIPHLLRLRTFCCKVIGTVCSVAGGLPLGKEGPMIHSGAIVAAGLSQ

GKSSTVGYDT

>contig27510-0 Frame-2F0

MKTFPQVAQLALLITSVVIGVYLLFQNAPKAK

>contig27565-0 Frame-0F0

METRDLDNGKGLNFVVEKRKGTTSNTDTLDIVGVR

>contig27679 Frame-2R

MERQLMDLRQTNVQNNTAMCRHIARPDADGTNNSIPMSMRVTKHHT

>contig28757 Frame-0R|Blast-DNA-directed RNA polymerase I subunit RPA1, putative [Phytophthora infestans T30-4](gb|EEY66296.1|) 1e-50

MSVFGVYGISVDPRHLSLLADYMTAQGSYMPLNRMGINNKGSSMQQITFETSMKFLSQAA

LGGLVDKLESPSARLVLGQPPRVGTGSFSLLHPITL

>contig29581 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61289.1|) 3e-48

MWRRALACSAPVLRSSHPISGSLKALCRPSFANLPSTFLPIGHLLLRRPSGRCCGVATRS

HDDNDMPVPSANYSNFATTAAELSGAPGVQGSGDKFVMVYTCSICETRSAKTISKHAYYK

GVVLVRCPGCENLHLVADRLGWFEDNGIDVESILKQKGEKVRFATAEDVLELTENGILGP

>contig30297 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56431.1|) 9e-34

MVRMAFATGGLLIEPHRGDIDPKVHSAACTRLTCVVRADFKGLMPRYLAESIVYRQVLEI

ETIRLRVEAKRNDVPSEWV

>contig30958 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69668.1|) 0.0

MASADDATATLAEQLRLERKKLTLFRRPLSVLYHFSIVLVQFFKWLALRVQRSRATRFVL

IPLLILWLVASSYDGPHRHLVIIFNEGVKFIVWWVGLGVLSSVGLGTGMHSGVLFLFPHI

FLVVQGAQECKSLDFDSHHHMWLHPFEANCNNVPDVSTVTFALIFWKVFIPCMLWGAGTA

IGEIPPYALSRAAKLAGQRNEEFMEIAESKSTFNLMNSMKDWMIGFLQKHGFWGVLLMSA

WPNMAFDLCGICCGHFLMPFWTFFGATLIGKALIKVNIQAAFFITIFTDSHLKWVEALIG

RATPEQWGLGSRVSEFLLECREKFHKAQVKAAAEQAGTVATSSGSLVSQLGSFIMVAFIA

YFAISCIEQFAQQHAAEEDDEKIRKQK

>contig31526 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66231.1|) 4e-28

MQNQIIKDQDQQLDLISHGVSNLRNYSLTVKDETDLHVRLLDEIDADVSRVTDGLESEGA

RAARV

>contig31953 Frame-2F

MRRILLLSLALTFKLVRTQEHRFPKLHGPQSPHLPQHRHTTTITTPCLSSPYRTQQVI

>contig32404 Frame-2R

MDEVERSSVETMYLTEALAELYTITEQYDHALRIYLSQGAFCSNKEFVFKLILEHQLWSL

VAKKVVNLVQIDTILAIRMLVNQTEHLKIRDIVMQLENEPKMLHLYLHELVLHRFSEYNA

EIYASLHEKQVTLYAKYAPDLLLPFLQTSNYVPLEKAYAYCRDHTPPLWDSMIYILGRMG

HHKTALDLILNQRGDMNRAIQYVQDHDHGLWDYVIDLSLTSQENVEELLKFASQHKIDPI

QLIRKIPNDMSLSNLKAKLMAIIANYRMQHQLCIGSRKVFDNDRIELLHRQIRAHKHGRR

VAALTMCAICHDQLRAFSRSTESIHVCVFECGHCYHFVCLEDKMRMWRSSESSNLSRALG

CFVCDHSTRAYARTSTLNEKINAFPPRNARGVSEKQLQRAKDTLLQMASRAE

>contig32493 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60002.1|) 1e-91

MEALMEWFCGESTPMAGDHPEVGLTRDLVAAVKFLATMETKEVELIRRRTENNHWQMWQL

SFDDSPATYRRNFFGVRGLNQILDAKLKWKVINFRGSDQDIADVELEGFMKRKIYFGEGP

NTTSPANLSALLAKSFSKSSSSNLPALITEDDIMHLDDLPTYSGTLSTEESQYLMSYLTV

PYARLPLVLSFFSSRERV

>contig32578 Frame-1F|Blast-glucose transporter, putative [Phytophthora infestans T30-4](gb|EEY59860.1|) 1e-30

MAEYTEGTTPKDGGAIVFNETNKAAARLIKPKAILYTTALLSWMQPFQSGWSTSQMNLSQ

FDDADDCDARPVAKDTCL

>contig34561 Frame-1R|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY67697.1|) 0.0

MDNLIPYNNFTAADILKYGALSARTENNEAIDVVCHNTYPGKDTMWKEYTLLHYTPFDPT

TKRTIAKLKDNRTGEIFRAVKGAPQVVLDMDVNADSMRVEVEGRIDEFASRGYRGLGVGI

SRSGDVPMEECEWKMIGLLPLFDPPRHDTADTVKQAIALGISVKMVTGDQKAIAVETCRQ

LGMPTNILDTSFFNTAPPPGLNLAQMIYDTDGFAQVFPEHKFEIVKHLQSLDKVVGMTGD

GVNDAPALAQADIGIAVDDATDAARAAADIVLVSPGLSVIITAIRMSREIFLRMKNYAMY

SIAMTVRIVFTFGILTVAWNWYFPPILVVILAILNDGTILTISKDNVVASPYPDSWKLKE

VFISSITFGLWLT

>contig34639 Frame-1F|Blast-hypothetical protein PITG\_18705 [Phytophthora infestans T30-4](gb|EEY68804.1|) 3e-06 NOT\_ORF

MPIRQPPSATCTTQSKLLYFN\*SVTQRTYKRIEVVQATHTTRYLGYDVETGEIVNINCFF

CLQMIQRRLLTATKVARAVKNRSWFSIPSSSRQFCFFFLRLLYSG

>contig35078 Frame-0F

MLAKDDGSFATHPLKPIVEKIFESSAKKELDTFELNYVFKPSTERTSDEKQTDAILKSLR

NSKYFRNAFLNAKLHQRAVETPSTDPMLRMWVAVVWAHSRKKTLNDKSFSKFFTGVTGLT

DKVLNEKKLFSKHEFSEDKYKIYLEEDIFTLAEKDEETIVRLLPIDLAKILYGEMGDDWV

SKYLVAARINVGPEFYKKFKEILELIDDNI

>contig35104 Frame-0F|Blast-phosphoinositide 3-kinase regulatory subunit [Phytophthora infestans T30-4](gb|EEY53006.1|) 1e-106

MGNAAPRAQPQSVLDSASQYRTFLMDYTPRSMDMMFGSLIGDGKFLKSISCKCDEGHLVV

KIYRKYDERESLTSAEVALRRLALAFSVELQPNVIPYADFQLSSKYNVAFMVRQYFASNL

YDRICSRPFLTMIEKKWIAFQILRALEQSHSKGICHGDIKQENVMVTSWNWVFLTDFAPF

KPTYIPEDDPAD

>contig35672 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66007.1|) 1e-111

MDDDVKSAASAMNDRSADLDFEVSVFGTDELENGIISPRVKDYLIGAKAAALGEDGKPIR

PTGACGCFSLAFYQPYFNVDTSDIQQRLMRALLPFKKDPAFSELALESPDAYGPFWLSVT

LIFFLASCSNAASFLDYEGNRNDWSYDFSRLASACTLVEIFLLGLPTLIWLVGKYFQVPM

TLLFLLCLYGYSSLMFIPAAILCISPVDAVDWIVMLIAMAWSLYFLLSNLWRVIGEHLTK

EKMLPVLAIISGAHLVWAALMKLLFF

>contig35823 Frame-2F|Blast-DNA-directed RNA polymerase III largest subunit [Phytophthora infestans T30-4](gb|EEY54825.1|) 1e-110

MGIPGVDGLRTTSNHIVEVEKTLGIEAARELISSEVNYIMSAYGIGIDRRHLMLLSDIMT

FKGEVLGITRFGIAKMKESVLMLASFEKTTDHLFDAAVHSRTDAIVGVSECIIMGIPIPI

GTGIFQLLRQVDKPRVQQRRPLLLQL

>contig36013 Frame-1F

MALTRASVAAGRMQAASRCPFMHALPTARAALLPNIAQLAKLCPHMSSIMAAAAASGPTS

SQAHATSTTSDATLKRIAEIKKKVQQQKAKQLGVPKPYSSAVAQFPTTPTRQTRVGGLSA

SQYENGFAQTIETIKREGRYRLFADLERKRGKFPRATHHEVSGKTKEVVAWCSNDYLSMG

QNPKVISAMQEYLMKSGAGSGGTRNISGTNHNHVLLERDLANLHQQEAALLFTSCYVAND

SVISTLTKIFPDLIMFSDSLNHASMIQGIRNSGAQKFVYKHNDMIDLEEKLRLADPKAPK

LILFESVNSMEGTVAPLHEICDLADKYGAMTFNDEVHAVGLYGNRGAGVAERDHCLDRIT

MVTGTLAKGYGIMGGYVAGNAALVDAMRSCASGFIFSSSMPPMLAAGARASVNHLMESQV

ERMAMHTRSQELKIKLVDAGFPLLPSVSHIIPLMVCDAVKVKEASRILMEKYHIYVQPIN

FPTVPRGEERLRLTPLPTHTDAMVEDLMTALEDVWTTLDLPRHYVANGEYLPKVEWTNSP

LGFDEEFMMQSAEVACAA

>contig36084 Frame-2F

MRSTRKTLEKDGASLGNKKLMSKYFSSYHAPIKDKTFDDQSDVSKDVLMRDTR

>contig36637 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53082.1|) 9e-10

MLMGARVTKMPCQVQIVTDNW

>contig36952 Frame-2F

MVARPQSDSKGHYSPEVCDVCESAIAGLRYEDCHLDLCVACSRARHVSSLHLTRGRFRFY

RQTDLNRGIKESPSTNSLPNLPTAEELRYSPQTTIGVPRDFDDALAHSLRALSFATDEES

CVDSATPSASMVKTTTSLALAEKQSHSFSNSLMLGDTDHWRTPTKTAELIDLYDAMKTNF

ASRHVVLRCVAGAFDASDVCRVVDRLSSFGSVASMCCELSTKGLLFCTFYDLMNAVAAVE

RWPTNSEILCFCLPYELPDDINSATLLLRFARSRSSASMAAELHHICASFGRVASVLQPD

MQVAKFIVEYSDSRVLPAALNGLPGAFHATMPPTVARTTPPTLDFSKLQLFLDCLNKVAI

THSRVARPRPNSFSSSTTSLLTSPTSSVASSLNASYLDGAGNISPMASAASVKHPGELTS

PVLTPQDEQHIWATPVPRARSNSSSAYLGGMLSSSNFGNPAYPHRFTFPSSSALSGRAVR

HTSFWTTPLLQSLGNHVSSRAEQCQHSYYANNEQQSTAVSMRGCYSNNDRVTRMSPANCG

HVCCSSTRSTAGRHDQGTGEFSLSIEKVASGEDRRTTLMIRNIPNKYTQHMLLAEINRNH

LGNYDFFYLPIDFKNKCNMGYAFINFIEALHIERFHKEFDGQKWTNFNSEKVCAISYARL

QGKQAMVARFQNSSLLDKHESYRPLVFSSFGSNRGKPEPFPVSNQIAQRKPLHPSGMSRV

DDNGGSYVNHQTYSQAFLQQPQQHSYSQQFLELRQHPLTPSLASNVHFGMQVLPSHYIPM

YQQNEAQLASPLVCDAGMPSNDTR

>contig37014 Frame-1R

MARVKYPMAGWRQSAREESNRLKKIFRGAHWPVRPTGTSRYRDRLFSGRNKSFVNSFRTP

HPKHPRRAATEMPSFSMCATSSTFNVEHPLHTPSASPFHPSFTLSPSTLTASPSQLTSPT

ISYSRARTAPAVSPIKRTR

>contig39801 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61881.1|) 0.0 NOT\_ORF

MSSLEVETFLLRLRYEEMRFTTSKPNVVTYTTLIRGVGLSDKVNVELCLDFLTEAQDSGA

FDEALFLEALESSARRKCRVTAKRVLAKIAKHSPKLRKDERFVHAMSNVTRVLDHNELPP

VLDDWVKSGVVSLDERDCILKVQIEMGASSADDTKTLGCLGQQTSQSVRKAVVYHDIN\*L

IERIQSCAIVTVNDFETLIHQCRKRKWKEDVSVIFEAMRDLATKGWQPANGDDRKPIPPQ

PHLRPTSKTYVSIVDAYMCCDDEGLAWQVVQKMDNLPNITRDLPLYRKFVRGAYLLNKCD

HIAELIAQAHIDKIAFTQRMGIEIARMFGHRHEEGFDILVHDIPVGESSVMAKRQIFLEE

LVKSCAYKKNLLGAEKTLRAMLKHGYDRSATTESALFICCIQHDSISEALSMLEHLQKFS

LMMSVPVYDSMLREFYFKYTRRGDIFDESSRKV

>contig40104 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56945.1|) 2e-70

MDVWALGIVLYVILCGTHPFDPTNEATDFELQERIRKGTFDCQSPRWKCLSPLARDLIQR

MLTVDPVQRISASQVLQHEWLTSL

>contig40481 Frame-2F

MATKGEHEKPEALDDEHQPIFKKVRLDEDAKVTEDVKRVKIYEDSSPPFESGAHVDVVTT

TLSASPVTEQDTGLNKSDTDPVEVKPNITGSAYGGFSAFSGKSAFAAFTSPDNVDGFSTK

ATSALASDSVQVALKEPSTFDKFTPLSVNSATSSSTNGFASFQSESPVTFASFAASQPAT

DDGFGAMASSASATDFLDAEVAKKVEPVVPALTEAELANGEEGEQILVEKRTKLFKLVEK

DYTEVGIGPLRVLDAKDTEADKVTARIVMRRESYPHGPGTKLLMNASLGSCLLCEKKTEK

TMLLTVLEAIEDPEADKKFTTVTYLMRYGNPNDLDAVIVRIQAHMHLPTASDSSS

>contig40728 Frame-2R

MIHALRASQCSFKSTKILSADQDTEAALRQEA

>contig40823 Frame-2F

MNSVLFLEWLQWFNRRMGRRQVLLIMDNCPAHVPIDSLPELANVKILYLPPNTTSRIQPC

DAGIIRTLKAFYRKIFNRNLLRALELDETLDNVEAHKKVDVLQAMVWAVEAWNMVTKKTI

RNYFNHCKIRTSSLNIQVPARATEPPA

>contig41639 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60022.1|) 7e-40

MFPKYFSATWEWLQYVNENHVQHSLQLLSINDANLRPAVLLELPLAPQVHTHKSRDLALL

TLKDSTALESWRTVEQKFKLQPLT

>contig42421 Frame-2R

MAEVEDRKPTENVDEEQTEQVQLSEGDIETNWDEVIETFDGMDLREDLLRGIYAYGFEKP

SAIQQRAVKPILLGHDCIAQAQSGTGKTATFAVSILQKIDINLKETQALILAPTRELAQQ

IVKVVVAIGDYMSVQVHACVGGTAVRDDIRTLQQGVHIVVGTPGRVGDMINRRALRTDEV

KMFVLDEADEMLSRGFKDQIYEVFRFLPEKVQVALFSATMPLDVLEVTHRFMREPIRILV

KRDELTLEGIKQFFIAIDREEWKFDTLCDLYETLTITQAIIYCNTRRKVDWLTEKMQSKD

FTVSAMHGDMEQRERDIIMREFRSGSSRVLITTDLLARGIDVQQVSLVINYDLPTNRENY

IHRIGRSGRFGRKGVAINFLTHNDVRYLRDIEQFYNTQIDEMPMNVADLI

>contig43013 Frame-0F|Blast-ubulin-tyrosine ligase-like protein [Phytophthora infestans T30-4](gb|EEY64890.1|) 1e-129

MASEFPELIARFIQCDLIAHKNGDEDDEGNYWICKPWNMARSIDTCIAQNAPHLARLAET

GPKIACKYIHRPLLIDQRKFDLRFLVMVKSTEPLELYLSGVYWLRIANEEFSMDSFEDFE

KHFTVMNYSGFSVRIMQNSEFVERFDTEYPSEDWATVYNKICSSIKQLFEYATAQPPPFG

LGRCSKSRALYGVDVMLSWEVDEKTGDESVCPIILETNFQPDCGRACKYFPHFFNDLMNV

LVLDRPDETVHGCTRL

>contig43952 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63830.1|) 2e-73

MKDLLKRAQNGEMLENQKGENEDDDAEEDDDNYTAKDMDVIKRDLGGNIIRDRSTAVGDG

EVMNDLKLGAGSADGRGADVSATGKALAAAIGSVTGKRKE

>contig44526 Frame-1F|Blast-myb-like DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY58333.1|) 5e-23

MQAQFGNCWAKITSQLPGRTDNAVKNHWHSSLKTQANRARGVCEDESSKRSKLKKKANKV

KSSRLATNQPVWSAIEEAGLSEASVCAVEDMSMDASPVTSAESPMVEYLAHVCDFLDSPV

IQDEGLGSLSPDAVSSVDNLDLYAYAYSYQDGVTRAQAVIDNILDPMGMDTCSDNSFPAL

SLPDDYSCRTTDHSKSDLVEAWGVRNDDNGSCSIRDELLEDSAPPAPAPSELDELLFGML

HDVCEDDTMPLTTGMESSDLILSAPLGEIARVYKRPQQATEWDSCVSHPSPTAAALAEIA

FDSTSLTTNLSMNSTDESLLQCKDEVMFEKHDDMFDEGGYTSRISSLPSLLDVGV

>contig44827 Frame-2R

MYWQWSIHPRSQHELMPIIRLSILEGTRTKRRNKRQERDWKISIRTSSWYECLKMSFLIF

RRSLSSRRLFSIARCLSTTPFAGTHHTIFY

>contig45297 Frame-2F

MSSSASICVLATFKHVIDSNYTEESAVRTIYLQPPIGLISVIYNFGEAMEKASNLANCCI

QLIKRELILRERTDNRGIHAQTSLRHFC

>contig45312 Frame-1R

MKVENPLFHVESSVLQLWQSVVKFSAKPLLCQGVESDIALARDSRRVSVAKNGLVSSNMT

SEEKDTHIAFNDMCKLVQPDSAALYKLPTSSRVQVIALANWELAPTFALDEHLGIEFPNA

SADRLLNKCNPFLSGKRRGDSVDLTSEAQTVSTDSSVVPERDVDELDIVKEEEDNTSEEF

ELLKTDGGNAWKAKDQGIFSTHPEGVVASLANQFESRSNQRPGSGAEKHPSHWMCIGYGR

YVKQRQRDYTRSFKSVLVQ

>contig45486 Frame-1F

MFYSQIILAKKGPLGKIWLAAHWDKKLNKQQIFTADIRSSVQSIVDPQVPLALRVTGHLL

LGVVRIYSRKVKYLYSDCSEALVKIKLAFRPGVVDLPTNNQQASSHAINVSNFGEFEAEV

TYSIETAVIPSLEEWIAASSQTTARRQDITLADPLDQTSKLNAFAERDMIALEDSFGGGE

GDWQAFDLDDNGGSSMLQSSTVSDIEVAREADVLRLPLDESMEAREKAMNQSSIAMEEEQ

AVFTYNDASFDIPAEATMDSIDASTPALDISTDLKDSIVGSSRTSLDAALGNLEVEALRS

TKKRKIVRDTVTELTSAFVKQGMEDTSDITCIRDPVSYMAENKWEVQKQKADLFTRPCLS

SMADELLQMFEMTMRQRKFPFKTKQEESTEAEDVELTRRMSATSRLSTTSTGLDVTTGSC

DASMLHDVDDGRQQYDLADMGPTHEERIDDGFPFDDVGNPFEPEDHPELNDSTVDIELGA

VNDIRSDAKEDAATSAHHKWHPHTVKVMKVLRQSLGDKEEVTYKQLTKKTRDRRTAAALF

FELLQLKTLDYIDVKQAAPYSDITISRATRFVEHIPAISQDVR

>contig46371 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61913.1|) 2e-50

MATQTDRTNDNLCKGVRNALAPCGKKVIPKLLPALLKDDVCCAQISDFIELLNIVVPADK

SMETFLVNELIDGFNSFMCSKKRGT

>contig47181 Frame-1F

MLLLRQAHRDLLKCLPLLVFFCVPIVGNAAPLLGYQFPKQLLPWQFWRPDQRTQFLQENV

EARSKTYPTLMKLLQQIKHKDDTLQEMLAIANKSGSDGLRPTQVVELVPFFEGPAALSAL

SSEHIHVLAEGSALFPSFALLNRLLLKTQLEKRLSRRMEALSVDDQQLLTGGVDDLSLSE

LEFACHERGIVTQYG

>contig47493 Frame-0F|Blast-PLAC8 family protein [Phytophthora infestans T30-4](gb|EEY54306.1|) 8e-81

MDTELQSTRAQFSEVTASAPSTAGHVNKVHYLSSPSSAHDLDTPRGAEYIGGDGIPTGAW

ASGLFDCFDNLMPNCFMVTFCPCVALAQLTTRLGISSYKVALSLLLLAALVQLAMIVLAL

ATAKEGHNAYNKTYTYPSDPHDKEVNGVYLVIALALQGLLIGYIWRLRVRTRSRFQLPGS

ALTDCISSWFCSCCAIAQLRTHVRCYQPGSCTLAAPDVLQAYPGKSYAV

>contig47578 Frame-0F

MLLRFADRFNLALARRHGRNAGKKLQVAYFSSDDDWRISDDDFDEGPDKIIDKSRRDSLP

QRQIMPEAARKSRFMIVSPENRGKVRRRLLDEFKKDGITLADPDQPGQYLTPDAGILRDI

RAMNKESDEMEFADEEEEGELNLGRMGMLRQIVHVDQVQKVTTQERIVNFRALVVVGNMR

GVAGYAVGKGSSPPLAILRGTKLAMKRFTYIDRFDNRTLYHEVHGKWNSCTLFLRPAPKD

KGLTVSDTVACVLDCFGITDIVSKTHGQRNPFTVVKATFDALSKHETAEEIALRTGHSLV

ELSTLARMRNL

>contig48531 Frame-1F

MELLAKIEKLVRTDEKRIGQWDDFKQWLKEFGPFDVVIDAANVGYCNQNFDGGGFDYAQI

NLMVQHYELQKKKVLIVLHERRTSDEQVPAKHRKQVAQWRKSHTMFNCQHGNNDDWYWLY

AAVKLGGRTLLVSNDEMRDHHFQMIHNRAFHRWKERHQVHYQVHGWRVTVEEPLPYSARP

QRVGNNWHFPSADVSDKDSTDTPRVVDCKWLCVKQD

>contig49738 Frame-0R

MTSDLWLSIPSTAHTCQFHGYYPCQKCTNNLRHA

>contig50422 Frame-2R|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY57627.1|) 3e-86

MESSSEDEESIISLRKELRTKKQELKRMQDEFDEYTQSSHELELELEQELSRVEKRNIQL

LSKNQYLERDLQLSRTKLEEVLDQTRQFEDELQATRAELQTAVQALRKMEQQQDDLETQV

RVLQATESDLRHKVEREMEEKVFLLSDQEELQHEHELATERFRTEIMDLKSELFAVQQKV

EDATTASETLSGNDSMAT

>contig50673 Frame-1R

MACSGVVTNSKKDYEVESERIASNTYDSAHDGRGLLASWSNNSNKKDDGDSSEDTSSSEI

VAKSTRTQYRRRYQRVIKTSGGYKTGQMP

>contig52709 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58799.1|) 1e-48

MEEKEMHSYVDHVLAICRDTANNTSRMPTLSEADILQDAKDITRDELLINGEHIAGKKGY

DAVVDALQRELELILARQVGKVPEETPMAVSNALQSVAMAVLHASNRTESGGSSYELLAK

LLSTHTSDRVLLRPASARAAPLQVQMDVGPYIESVPGCTYETWAFGLRIQLIAVTWYLVC

DAFDPCKELYEMETTFCNRLAFPVGLTPFYPLDSMRKDPG

>contig53290 Frame-0R

MHLSPMGDADNVVPNVKPKGQRRYTYDIRRDHPAGTFWYHPHSHGNSNSQLNGMMAGALI

VVDRPRDFPADLMAMEDLVLLLQALCIENCLNPRDNLQEAIENKQSSHHRRLESGAGVWN

TDLRIVEDDADVPLNDTSLPTVFVNGQY

>contig53849 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66787.1|) 3e-26

MSSSDLAAAIDQAYKAESLKLATITALEGQINAIREAKFNPEKKSSDSQLDPQTTILEKS

FDVWDSPRVSAEVSISSGSDSIYEELYTVSDDSVSFTLVKL

>contig54790-0 Frame-1F0

MTSMKRAYEVDVDEARSKRTRRSRWGIDDVEDATDDKERTYASPKALNDIVKRLSSVVQE

KRA

>contig54790-1 Frame-1R1

MSFNAFGLAYVLSLSSVASSTSSIPQRERRVRLLRASSTSTSYARFIDVMPILSILL

>contig55241 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69475.1|) 3e-09

MHCASRISYMGEKISLCCCFVEMNIFEEHVLLPLMQEDYRGNISSITNDAIYIKLISGQK

VRILLPYIKHRRYEL

>contig56244 Frame-0R

MRATGNFPFPNFILEVAYKNEGLRALRAKLLRWIDP

>contig56338 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65793.1|) 2e-16 NOT\_ORF

MQ\*LSDKDCREFNRLLRKTANPSMPFIELYFQTLDSLIELPAFGKDGFVNIYRLQKMSEL

ALEILHDNLLLTL

>contig56983-0 Frame-1F0

MQFQSEMCATKIDIKHAGIWRSIASSPIPEVTDAFTL

>contig58556 Frame-0R

MMQRYVRAKRITEATRLQSCVHSELVEGI

>contig58699 Frame-2F

MPRRRSRSRSRSRSRNPCFHRSSRSRSPSRHHYCHRS

>contig58905 Frame-2R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY62818.1|) 4e-08 NOT\_ORF

MNLMKVLEITFAN\*AVFCREHMSNYDGPLPDSLSL\*FADVPYSIADDPP

>contig58970 Frame-0R

MSASRPESSSKVSNMHRSFAPCDATI

>contig08244 Frame-1F

MSVTGYPPISTGLVSGFTLELEDTVAVPREFSLTDVSAARLRCYHQQCDQRLATTMLRFQ

AHQARSWPRESDLEHWKLLRERRDICVYRHKTRQAQTSTVQAIGTLHGAFDDVMNGLYAD

STRTAQILQKLLSPLALNARVLQVEKSQSETKPYQFAGIVSMAVKVRGLLFCRPREFVCF

KKMAIVQDEMGDDVGVLVWHSIDELIEEVAVTTYGTSTASRPFVRGFLSLAVVFKRVGDD

RVTMFAYGHFNPKGHLTQRKSDQCIAEWLLSMSNAVQSGQAKNLSRLILRPSTKQNNAIH

ESSKSQGRCGICARALFFWDAPRSCRGCWQLCCRVCRVQRPIFCAHSHASATVLSGPCIE

TFCLACVGTALPTSALIHARLLQRLAKKRKRTPPGLRSTLATSSTTDGSAMAFIERDSSD

LSSISALSSRDSEKYQHHRLSLDARAKTRENKPRLPLDECVEMPILEVLAHYQHQRRDSA

SEGSSNASLRSYTSADLAPTSTLPLQLGRYPSGHSLLAHNPSFYHSRVRLPESGNQMGVP

RGLSCLPTPSSFWLPRESTLVKKSVEALPMLGDEYYQRLLQSYLLHMSSSHSLASVLSMS

SHNGQSQAAFKLPMSLSLQ

>contig09232 Frame-0F

MDCEYPVAIKDDEDKPWIVSAPTTCLVTDLQQHLWRVARTFPLCKSFLETTNETGKTAVQ

VCYRRHHDAIWTPLERAFVMPGTSLHGSMATLGERHGTSHGRLADFQLESRGNEYLYQLL

LESRFMSKSREVDWRHGRFYSDIQANTWRFTLEKGQLLDALDTDKKWYESRVVELQKGAI

KVHYRGWTSKWDEWLDRMSPRLAPLYTNVPRWREFQRGDHVLVGKNVVSKTFPEWRVAQV

TSVTKGMANTSLQIELEVDGMTQCMDAQDELLCPVGTHKAVNGSRFVTSPNAVSPFASVD

DQFERHEVMGRGRPEFAGVVGLTNLGNTCFLNSMLQCLINTAPLRAYFLQKDTKTGHLFF

STELNRTNPLGMKGMMAVVFATLVRKMWSQEYTTVTPRKFKAIIGQYAPQFAGYQQHDSQ

ELMNFVLDGLHEDLNRVHSKPSTTLVEHNGRSDADVANDAWHQYLRRNDSVIVDNFMGQL

RSHVTCSNPTCGHESITFDPFMSLSVPIPAYETKTIQVQLYWANGNLPTKYAMTL

>contig10955 Frame-2F|Blast-60S ribosomal protein L13, putative [Phytophthora infestans T30-4](gb|EEY68387.1|) 1e-105

MVKHNNVIPNGHFHKYWESRIKTWFDQASKKKTRRLRRKAKAAAVAPRPAAGLLRPAVHC

PTIKYGSKVRAGKGFTLEELKEAGINRKQALSIGIAVDFRRTNKSVESLQANVHRLKAYK

AKLVVFPRKSNKPKNGDAASEDVKNAVQHAGPILPIKSLSVKSTTAFITPEMKENSVFTQ

LRVARADKRIFGKQAKRLADKKEKK

>contig14384 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY61027.1|) 4e-53

MHDADIVHGDLTTSNMMLSSDNATHVTLIDFGLATSQPLPEDKAVDLYVMERAFASTHVN

SEILVANVLRAYRAKSRRADAIFQKLSQVRLRGRKRTMIG

>contig15912 Frame-0F

MGWFRRKKERRKIGVEEKLEDDVVPPLLTVSPELTTMITAVQEMQWKPPVTLMLLGVMYL

LHVQVKRTPSVVLSFALCPSNVIANKEIGTVLVAPFIHGEELYLYQSMVSFLYKGFELER

RFGSIGFSLVLIYFIVLTQTLIVFIAHYVS

>contig16052 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60308.1|) 4e-29

MVRKESVADTPVLEETQRMEQPVETNNRGNFTRNLNKEADESVARKMFLGGLALLPWLHL

VNVIFYRKQFIDPTIDAKVT

>contig17723 Frame-2F|Blast-actin-related protein 2/3 complex subunit, putative [Phytophthora infestans T30-4](gb|EEY62532.1|) 0.0

MVAGGDANLFRLASGISCHAWNKDRSKLAICPNSNEIWIYAGCHTPDPAQWRKEAVLTEH

DMLVCGLDWSPVHDQIVSCSHDRSAFVWKYEATYRQWKPLLVVLRITRAATNVKWSPDGK

KFAVSSGAKCVSVCYYQAAENWWVSKIIKKHKSTVTDLDWHPNSQLLVTACTDLKCRVLS

AHIHDIDGSPDAGPFEALPPFGEPLAEFDNANAWVNAVAWSPKGNCLAFAGQGSSIHIVH

FGAPGECPTVQSIRFLQLPLMRIMFLSNSAIVGVGYEFNPMLFARDANKFWSFSEFVDKR

STESAVKKNTGGFSAARSLFESKVMRGQSSDATQHDKNMLW

>contig18731 Frame-1R|Blast-trafficking protein particle complex subunit 3 [Phytophthora infestans T30-4](gb|EEY62001.1|) 3e-65

MFLGINVDVSQWNATNTACSLLIYDNPLTEFVELPPSAYGVLWYSNVLCGVLRGALEMVQ

MRVETKFVKDVLQGDEVSEIRVELKGMIEETMGDEYKEDV

>contig19163 Frame-1F

MTQTKDALKKDPNQSQWVQLLVHLIQADETNGKQWQFHAKTKLNAFCKDPAHLSSILHLD

PTFSFTVLELEDKVKADDAHFLQWFQNFLQNDVNTKAHHNELYYLLFKN

>contig19866 Frame-2F

MPTLAPRRLKQCRVTSHASIRSESNGPEQDEAAPESNLSSYRLASTTTDKAETLNNEKPV

LTPVQKSEGTEKAPVKLRSSAGFAAYCSFSARKYKAVHDETEGLSGFLEYRKLNGLWRPF

LFQTTGHQLMLYRIHSTHQVLIMTTDIHCASKIALDEENSESTRLLRLEINGTLITLRAV

THAAALYWVT

>contig20167 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66087.1|) 1e-35

MSLSYRTHLQSEDANDDGKALMTLNQFLATHTSEDNKSFKDLQECAVKDHQRRYHWAFED

VEEKGDPKLHLLTSGMWITKEQRKIADKICAPKG

>contig20637 Frame-0F

METSWKEEKTHAMDAVLGPLEALKLATGSSTEPPAWAKPFPTPAVSSIETHDVDLTPNLG

GFNPFGLGFEGTSRSDDVWGPSSPSERHLHSTSLTTSAMAESVTTSSSFASIDAIFSQRN

KSSEALAGLLGVTLSPNPLAQSGVLVPPLKDAHTSRFSFANPSDSGIPPPSARYELLNGT

TVINGPPFSGFEASGDLQGVPSSSSGCISTEHSVFSPLQTPQHVSPRPLRDPIPNDLKSQ

YIAFK

>contig21296 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY66249.1|) 1e-125 NOT\_ORF

MTKIGILDIYGFEVFDKNGFEQFCINYVNEKLQQIFIELTLKSEQEEYAREGIEWAPIPF

FNNKVVCDLIEARRPTSGIFLILDDTIKTMHSRQGGSVDANFLEKVSGIHGSHPHFSKRG

KTFEIKHYAGDVQYSIDGFGDANKDHLSKDIALIISETSNKLMLYVFPKEIDLNDRRMAN

TAGYKIRSQCEALVTALMDCTPHYVRCIKSND\*KQPNKLD

>contig21681 Frame-2F

MALYGAIPVLVAPNKKNTVGMFWNNPSETFVDIWSNHVTNSKTSHWLSESGVFDLFLLTG

PSSADLFSQFTLLTGRAPLPPLFALGYHQCRWNYKNEADVARVDAGFDEHLIPYDVLWLD

IEHTDGKRYFTWDKHAFPTPLHMQESIARTGRKMVTIVDPHIKVSQSKDSEPYYIHTEAQ

ELGVFIKDEQGNDFNGWCWPGESSYVDFTSPKARAWWRHQFRYENYQGSSKHLFTWNDMN

EPSVFNGPEVSMRKGCSSIAGVEHREWHNLYGTLFQRSTMEGQLVRQQPPPMPLSAFAEE

LTLTSTMERPFVLSRAFSAGSQRYGAVWTGDNTAEWGHLRYATKMLLSMSVSGLTFVGAD

VGGFFGNPSAELFTRWNQAAVYQPFFRGHAHHDSARREPWVFGEPTTSIVRAAIRQRYAL

LPYIYTLFYTCYVQGMPVMRPLWLHYPEEPQSFSEEDEFLLGEALLVKPIVEDGARVTHV

FLPSQNGPDKTIWYQVTNNYKPFIGGKTYENVPAPLDVIPVFHRGGTILPRKQRVRRSSA

LMHSDPLTLVVALDQHFEACGELYVDDERSLAAELEGESTIVKFQQTKEGLRSRAAAATA

GGRPYTSRMWVERIEIYGFRTEANLPKQVLVGERALDLQYDVVTDRLVLRKPQMLVTDDW

DLHFVYDQALE

>contig21735 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58147.1|) 6e-80

MILGELEMAGRVTKVRVEKTVPGKFPHRFSVSAAEVVRVEGRRMKLSEPRVTEFAAPTND

LMKEWANSLHLWRRMSWKDNVKFFDSSSEISQTEEHETLQLQLHAVKTIRGRSMSGNKFR

TPFVSIMQGQPSPTIKKLRQMIMQTGSTACTSTA

>contig21788 Frame-0F

MADANDNTNELQHQSDEICSDGDAAEIVDVFHDPQPLTVQSLPYVKCRESASAIFSFDSA

ARHRTSLTSKSTAHTYKSSSGNTEQMLASLSYSVPSTTMVTNTPRGRPAVDVIATYMNTC

DQRTVKTDLMRARAHFASPRGTVNVVCILATNAC

>contig21928 Frame-0F

MRSTKCYFAVTIVLFYVALLARSSFVHIKLHSSYVRHRSEQLQILEMAKIIDWTGRGLNS

WSQVERNLTSAVDNLNVSDNALGEIVFTQTFENLQTLACSNASISQIKLNGTFLKKLSAS

RNRLASFRDTVLVASIKEL

>contig22051 Frame-0F

MKPPTSAMTPIIANALSCDSMMSFI

>contig22608 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62946.1|) 7e-16

MKTWVRESAKRTRQPHFGPALNYSVNLSLLDSALQVAFVQLNCDDESKAFLD

>contig22701 Frame-1F

MSFALLRRRPKRTTITEGSTLSGETRNDSCPLLGEHEELKCNVQPVRIQNVRRIDNGIYV

HSPKESVVMRMQRRKNRIVQRVLVACRLADPSRDQT

>contig23148 Frame-2F

MWKEWLLVLAQSMSRTQVTENLIQAELLRVEIDQTSEGFSVPQQQAIDRVLCELLTSILP

PPSPEYVAFVFKIIHDGRTANSMAQRRILEIIQTLLSLNEPCTSATDTPVVRDLDQDLSC

LQKLAQIPDYAAKSHALDEWKGATGVKWWESLLDFASSIDPEVASRALLLVSKTPFPSLE

DPKWQYRCLRKLCTLFFSLLQQYRTHFVNDTKPDESTNCQSIQERVLRLKIVLFRVVATD

GGIAQNSSSVFTMFASFWLDALLSITSATSIPTHFPIRETTRTDTKFENERPLLRSERTS

SSKCTNLQSSQVITKVPDVALVYRKTLDSSWTREMQGARICSVYATDLFDQIILSTNPVT

SILYQTGDDSRRLQMDANDQLERRLNVVIQMLLERVVPCCGIPNDEIYKDLLPNRSSFDM

DLRIEQYLNHFPAFLPLLRTIVNASMVVNSSQVLRLVPIIKAALIVLLGHWNSVKGDLSL

ENLDVPPYMRNANQLTLSCNLMRLLQATKWLPTPLSQAAELLPLTTPLDIRSILFSCWFY

LSDHPPRIESCAPTPVTSAVASPISSGSSPIGFPFSGMSTGDSLSNLGNPPLEFYLIPLR

KALHRNIHKIGAKYPLFMC

>contig23650 Frame-1F

MRRTTLGPVSSSQLNTRFPALRHPSTRVSNPSKINGVTERQSIGVVSRRVSTAAGNNARR

PPIGPRASVNPRQSIGNTRRNSTYSSRGSVSSRSGSRVLDPRPVTDRSFLTNCVRTLVEF

LSEHMYDQTLPPALLRRGPSKKDFCHMILFLFKLVDSSFEFGTKFEEDVVTQFRNLRYPI

HISKTSLSAVGTPHTWPTLLLSISWLIELLT

>contig24941 Frame-0F

MPSAGRRHIRLSILLRSSGRGPVHHKTFTSAAKLGLPDSMDLYA

>contig25201 Frame-2R

MRDTRSTISIEASAPPQRLRSFRSSPRNPPLSPPTASTRDSSRQPLPTKPRPSVKLEKTA

ANQEQAPSTNVASTVVKKNNNKEDASVTLTEYERKRIENIQRNLAFMQQMGVATATIEAR

TAIQPAVNSPHTSATKRSTFTRKKPFTQPVRKSRRLEGKEVEMARNDFIDQMEIKNDRNV

AMKPPSQWHDVMDTNDHKSQEFLQNLTNSLNDENDTTPMVAPPRDLVDYTLATDDIMKVT

PERIYSLAFLPRSDRIVIACGDKVGHIALWTRSENAHLETDTNLALYRPHTNPVTQLIFS

NTKTLVSSSFDGTIRAFDLHAATTSILYETTDNAGITSLVRSGIAAESYYASSDDGSVRV

IDPRTSLTSRYQLHEKKINTVHQHTNLN

>contig25551 Frame-0F

MSVHLPPSTYLRATRIRLGSRS

>contig25858 Frame-2F|Blast-U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein, putative [Phytophthora infestans T30-4](gb|EEY59391.1|) 2e-17

MRRSRSSSLDSLGRRRRRKASPARRPRRSSSSSSRSRSRSSSHRHRSSRRSRSRSYGRKR

SRRSRNRSHGRNRDRRRRNHSHSRSMSDSPVRRPRSPF

>contig26226 Frame-0F

MVISATDAQQHIEASVLRTAEMFALANTSHEYVPSKKARVRTKLNDTYLMDSFILMQKIK

TTAGAIDSTSSVIEASTRAHPSCAGALTETAMNGHTVPSIPVISIDRKNLASAENYSFVH

KVAEEAEKELALKKRKTAAAKSNDTSSAIVNYKKQTESAAQLGASAITRRRSTEVPKPQW

HAPWKLKRVIAGHLGWVRSISVDPTNDWFVTGSADRTIKVWDLASGQLKLTLTGHINAIR

GLEVSSRHPYLFSAGEDKKVLCWDLECNKVIRSYHGHLSGVFSLKVHPTLDILVTGGRDA

VARVWDMRTKNQIHVLSGHQSTVWTIETQATDPQIITGSSDSTIKLWDLAAGKVMTTLTN

HKKSVRAITKSPTDHTFMSGAADNMKKWEAKEGRFLRNFSKHNAIINSISINQDGVMSSC

GDNGSMRFWDYQTGYCFQSHTTKAQPGSLDSETGIFASTFDRTGLRFITCEADKTIKMWQ

EDSSASEESHAIDMDQWTKDFTAPKRY

>contig26675 Frame-1F

MHAHSNLSKPSPKRSLSCAGLDDLEALLHGVDSGNRKRRQSFSQNALNDTAPSASPASQS

QHDSTASSSLRHIELPIVNEKPTSSDNHELVESQYPDHAQINEHNRHPNDSNCPENQLQD

LDG

>contig26891 Frame-1R

MSATFTLAFFLSGMNDNLSWGTLGSHTGSFSFGPFASSTYQIWELPLFILMGIGGGLQGA

LFNGLNTRLARIRSRWIRAPGVAWLEALLVSMLVSSILFSTPFLLGKCYNLPKTHAIELL

NGAPSKAFAFGMEKLSKENSACICENCTSILMDNAECYQADETMAYPYRKELVRFYCPIG

QYNDLASLMLTGGEIAIKHLFHAPPDSFSVRNLVVFWLVMLVLACITYGLKIPSGLFVPA

LLIGAAYGRLWTRVINFVTSLYNLKTVDPRLYGLVGSLAMLGGVTRMTISLTVIILECTG

NVEFGLPLILTSFFARWVGNYYNEGIYDIHIHLRHVPFLDWNPPLRGFFLRVKHIMTAHP

KTLRTVERAGVIFDLLLSTKHNAFPVIVEDPTFGSHFFAGIILRKQLNVLLSHRDFSFEK

PKPFHRQPHPASCYSDKKRSESFRRSQSSDVEASGRTRIDQKLLESPLAHNYCLSYQDME

VHYPRYPIPSLMHKDFRAAVHAGRVAGDEFYTLQEEDRALWVDLTPYMNQTPYVIQEEAP

FVRAYRIFRSAGLRHLVVVNRHNNVRGIITRRELEEEHCTRCFRLA

>contig26914 Frame-0R

MKVRIYCEVFSQDFPSFSSSKGLQKDFAIYRYLTLN

>contig27513 Frame-1F|Blast-phosphatidate cytidylyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56459.1|) 1e-118

MAVDWGRRVLTVLMGVPTALWLLSSSVGMLLLTTTVCCLTLVEYTNTISPQIVAQPMAAN

LKQPHRVLLISTGAVLCVGAWSGDKLLYDTLSFGATLAIITIHIATTTKMNQTAMLQLLL

DLFALIYIVNGFSHAILLRYSSKKYGYGLQILGLCCAWVCDTGALIAGTFMGHVKLAPLV

SPGKTLLGAIAGVVSSVAMALAIFFLSSHYSAVLPWTYDILPPAHVAPLIHQVMLGTVLG

ILCIVGDLVESFVKRVAGVKDSGVFFPGHGGLLDRMDSFLFIAPYLYFHSQYFVPAL

>contig28088 Frame-0F|Blast-lipoxygenase [Prunus dulcis](emb|CAB94852.1|) 3e-59

MFHKTEDAAMMEDGKKMITGRVVLQKKNVLDFNDLGASVLDRLHEVFGGNISFQLISAIH

PEHESSEGRLKGKLGNPAILEDWITTITPLTVEDTEYEVSFEWDDKIGVPGAFLVKNRHH

SEFYLKTLTLHDVPGHGHVHFVCNSWVYPSKYYLKDRIFFANKAYLPGETPELLGPYREE

>contig28754 Frame-0F

MSGRVDIIKVSLEEPVMQILPLNEHLGLISERMQDKVRNYNTRNPSYRLESRKKMKNKKS

KKNGHALSGDVNREVMQPKNAVSPDAFQLLVWVNYLRSMCAPGENVGILAAQGIGEPSTQ

MTLNTFHLAGHGAANVTLGIPRLREIIMTASQNMSTPMMTIPLRKDVNSSKAQEVEQRLN

RISLFELISNTNGVCVKDYFRCSENGILWVHDYQIRLTFFQHQEIKRVFGLSADKVNSAI

GHGFVGKLLSLISREVKKNSVAVSASANNSTVKTHSGVSSKLRNEDDDDDDDEQGTLRFG

SLGEVQGYGEMDEEDEKIRQAQMEDDSDNDFDNEPLGRTSSKDAKLSKVGSAESSFKTES

RTQLKAALVNEMDNLHVPNSVLKSPYFVYCGRKKNENFVELHLRFPTHFKTLLMVPLVEK

VAKQVLVHHCPGISRCYLINHRIGASLAEKPCVQTEGLNFQEIW

>contig28978 Frame-0R

MSNALKSDMLRSTSISKNETNLVCVILGDRCQLHVLYLTPSTFIVKIRSCKQIKVSRCNL

IAKVALKSTDIVRTIIKGDTTQHRQE

>contig29007 Frame-0F

MKQKRYHEFIIGQLCLLLCSSYRADDGKVNLIDSHYACLDEKTTFRLILRGNGHLYKVEG

KIKADEANIEAEDRRTWKCRSVFPHPANDVLLHLTMTGGLSYRPFKQPLREVLSSVLTTT

M

>contig29771 Frame-0F

MGNIIRNSAILIWLELAWSHNVDPYQVLLLELITSRDAHYVDIAKIAAAPYEGEGIRAVA

LNLEMALAHHWYKEDLKDEAVFAILGLDKLTETDVIKSPFCETWFYYYYLKNFYSSVGNI

KMLKSYFKDDIFVLILFASVKRNDDLENAVYPLMEEALISKNIDPVQLFRIFCLDEARGQ

LFENLFFKFWAKYVKSVYPDVNPAKIMVNIMVNAGYSINTLEEIIGRVIHASSRELESSV

PLLRNAEFAPDLWAVVLEAKQKQ

>contig31183 Frame-0F

MVPCLATRVAVSLPEALDPQLDHFAPQDDSKLNILLRALRRMPLLFSNRHWGFYQSLCFP

IAQNLRLALSAEQWLETLSQGPPLELGLPILSQDLFYLCVAICCSMLTTKADIMLTIRSL

CVLYMAQVLIQLARMEAEDDDDCHEEDAKKHCANSGDGGSPEQIEEMQRGLERLMARLAH

EAGVACVDQSDMPIGRRPAPQGRQLELLFKSSCLAFMRQVTLLCRAFFRGEQDPDASWSA

NFVGSLRLSTSYHGMCQQLGIPRIVQLIADENLVDYLLRAARELRTRPSSAAVSKELQFR

YQQRGHADHLRIELEKFVSKEGQQGDWAAREALIARSNLRKIPKLPFRLEPDTQQGKRLF

HFANIRLVKLPSAYTDLHSEVLGKSKCKQTWNTVENPAICLVCEQILCAGTECCRRRSDG

MGACTYHASTCGAGVGLFFLMRSSSVLLIFGPRSSYFGSPYLDMFGEEDINVRRGRPLHL

SAKRMKALQVLYASHQLANEVARNRRTSDQYIRNNYY

>contig31309 Frame-1F

MSTLTSTDMGELKRPTTRVHAPPGGGSSWSFGSDPIPVSAGRKRINEPQIQAHNDTKMES

PRAAPAPVVAQAPRMPSTSGVIRIALLKTSSDAELVDRIVQNCFAKLESQIVSTETFTVA

SLEQLPYAANKLTSFGGFDAVICCGFLNTQEPHFPALSTSLTQSFMDISIKNVRPVVRAV

FMGEPRVASVKIKGGWGTECADNIVPLVQLGGCIGSQ

>contig31525 Frame-0F

MTLCCYSSTVVKTSQMEELRPESAVFSAQQQRLRNSYSSPMRPSQYTRAPGDAARAIAVP

RETTIRLNRDRASIEQVLLGRRWLFHSVSPLFHFRRDQLSEYAHDLVKTMRAAALRAYGQ

QFGYNVSIHDTNTIVAFQISEVRDQRQSRATKKTVAQKEFPGRTGSFVLYFSTDKEQYEG

RERKKVLLQSGDEELMRWVCSWLQRHFQCLVSSRCVRMHPLSLKKLARSWVVASLLAEEE

RPVSIIMNSNKQESVENSIGSCTAPLLLHYRATNEMDVVRTYTMIVPWAMLHRLFQQTKD

GPDGTCTSTYIPELIELVERLYLGCLPFDLSTYKIERVEMKYAAIDHDGGLEFYSTDLVQ

TVFFSLLELLAVPTVALTFHPETIF

>contig32371 Frame-0F

MVDSFQPECVFVAPTTALCRFFVLGKCRYGSRCTFSHELPAQVSECADNETENLSAAASL

VNCPFYLRGNCKYGEYCRLKHNPALLPDGKAVNFSHSASIIGKAETFAALSSGAAIHIEA

AVNQQDFTCGICFDDIVQSGKHFGLLRCDHCFCLECLRSWRQSKDMELEVIRACPACRLP

SDFIVPSLIFVAGEEKDKVVEAYKSHLALRECKYFTGLLGSCPFGPRCFYAHRDSEGQDV

KHLDCLKRSPKPRRRRNGLRIGNAAQHILQRHDHLFHFFDVPDWDGDDLGEDLDFLDV

>contig32968 Frame-0F|Blast-acyl-CoA-binding domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY61823.1|) 2e-07

MTPLHYAASCEHEALARLLVKCLLL

>contig33372 Frame-0F

MPQSSPVAASSSIDPWESSTVLSTTTFTIADSVNTDENEVVTAEFSVDLADGQTWAVNFF

ECAAENDLECLEEILDSGRVRVNDVDVDGFTALMVAAAEGHRDVVRTLLKRGADVRIQTH

ELRSTALHFAAKNGDAVIVAALCECDASMIDCWNSNGDTPLIWACIEGRVEAVKVFLKYG

ADVTALNQYGASTLLCAVMVGEDPEEVEEIDEQRAEILTMLLATKKVLVNFQDPEGSTAM

HLAMSCGYLACIKTLLANGADITLRNVIGQTALEEALDVWKEEREPCIAYVRGIWQQLEE

EAAARMMAMLEIEDKADKRKTGGNSVLTSKKSKKKNKKVKRKAIKQP

>contig35190 Frame-1F

MKRRELSSSQEGYHALVTNT

>contig36010 Frame-0F

MATGYDGNFGIAQRGSTAAYLTNASDRYKIPFLQREIRDKLNTSA

>contig36164 Frame-2R

MTIYWLAMHGDPWQVYVNCAWLQGGKGRGLPPVVKGQGPAKKGAGSKSVLAITPSNEMEK

VAKEADGMNGSENETREETEPPSIEASPAKCSRRRE

>contig37422 Frame-2F

MLSPSESCRRIIPSPSEEAVKVVWYERHTAARQRDAGESV

>contig39176 Frame-2R

MARKWLSVCIKTGFNTFVYKLLAAD

>contig41562 Frame-2R|Blast-exonuclease 1, putative [Phytophthora infestans T30-4](gb|EEY69991.1|) 2e-78

MGANFILGRVKRRGSLDELMEVECHVRERVDFLMKDVLYFHNGRIDSWVRLGKTMKFLYH

AATDAFAAVLGRHRRVEAYRWYTAEVLNAESGHELESPQKYCESRLASFEHVVLKWNLFQ

RIKEWKETNGTNEGHHDSKALSSKNESIGGTIDAQPVSRQIPVEEFATMYITQVIEFARR

CFNMAAQLAKEASTTQKTEVQKYNEKDFTHV

>contig43010 Frame-1F

MPHDRVSRAVKRLLRPFHRHDSHAAVDDVYLKHQRGSLMSSTTNTSSLCSKSPSSSDSSN

LARSVFTLKTDGDGIPHTVLMPPTLLRQLRALVEQTNALTSSDHRASHKKP

>contig43458 Frame-0R

MDGFLQPSSSANDDGEMVNDAVTMEISDFADSKQADALFSEKLCPSVGEIAVDGEVDGHG

KSFSVTKLDDIERRHYLNRLLSIEEDMQEARCEVQHRIDTMKRIVDLMDPMEQLSEYLAL

RQKARKEDDVDIVEDLVLCAKRMTNKEDSEVAMVGAFFFLRDRQQTRTRGMTAMLPVLAP

MMVIFNKSVGCNNALAGEG

>contig43599 Frame-1R|Blast-ATP-dependent protease hslV [Phytophthora infestans T30-4](gb|EEY64142.1|) 5e-88

MVKCRWATLWSSQTRKRCGASVEHIVAGFAGSTADAFTLIERLEAKLDEYPGQLTRSCVE

LAKAWRTDKYLRRLEAILIVSDVKQSYTLTGNGDVLEPHDGIIGIGSGGTYALAAARALI

DQDLDAETIGRKAMKIAADICVYTNENVVVEVLEEGKDEVIKSTKD

>contig43634 Frame-2F

MQGGSVYYMRLLCMKPVSIKAIIY

>contig44525 Frame-2R

MQQTPNSSCADAPNASYELLSLDGALHDFQLDYSSLQFAICVVGYVANSEPNKQIKSILR

QKENAGHIESNGHIFSDNYRVACESEPSSTEVLTPSFVSCQACVLVA

>contig44950 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53975.1|) 9e-50

MQRSLVDVDHRSTVQDFDGDFSLSSPVFVRNFIRNVQDVDRVLLHLMTATASIKENSDSA

ANQFFFGTSTSLASTAGSPKITSFHPVFNIIGELTTALWHRWFFVERFEILSIVNSDVFV

GVFYRNEVHGAMEHSNTG

>contig45197 Frame-0R

MELLSAKEKDQSFREVDFLAKLKHPNVVEYMENFVVDDVLHIVMAYCDGGDLSRKIKEQQ

KLREQITGPDSDPADPRGYFPITQVLDWFVQMAMAIRYLHGQRVLHRDLKTNNVFLTTEN

VVKLGDFGIAKTLDSTLDQAKTVVGTPYYMSPEVCESKPYSYASDVWSLGCVLYEMLSLR

HAFDAPNILMLILKIVQQDFAPVPPHYDAEVSNLLRILLDKNPERRPSMEDIFAIPYIRR

HMQGLIASGGSFRVRALTFEARRPQQNSASETGRRRLNSKNMLARRSSVEKRKTHLVAPS

TTSRAASVAPIQWMPIKSPNEEAAGPDRYNELDLA

>contig45294 Frame-2F

MPLKEYDSSWHRQDRSSSVATTSTSFSSTSGRQLADALFSSHGPTRAQALAIVRQVVQHV

TSDTTPSNLCVNTSMRCSEGPENDIVDKYLEARWHLSRIATTSYTNHKDVRIPTNRTRSY

SSSPLDHGMPRRRCNTSGHQRDNLNENTTNIRLDSIRTKLETELDLDDEMYSAALNAICQ

V

>contig45438 Frame-0R

MHYLSPHMSGISPDTWPVALQGPVKVAPQSELEEKVLTSKRFWATSLLVGPLGSRSFVEK

HPVNTSPFLMRTFASGHVELILLDAPIRPHWQSNRQLATAVVDRYIPALLLECLNLGFDD

SGGKLVLERDAADPRLVYCLHSTGVHVININWVSALASGKQFTSLPKSSVR

>contig45867 Frame-2R

MLKSLRSDYDVSSKDSSDLSWLDHSSSLSNDKYSTTGEVSKILPEDDDSSSDDSSMLKNI

SNLIGNYSHPIDESVDTSKSVNDLLELEDCSSASDDDQLIKAVSKLQISNDAMGSKTPTY

SKDLSHLGDSSSLNLDAYAIAGKPLSGAREEDNYPSGDEYLSNYKTSLIGKENVPDSRFS

KELLWLDDSSSLPFEKYSSTGKSSKDLLDDDNTVSGGVYLSNEKTSLFDDKNGKSSKDLS

WLDDSSSLPFDKYSATGKSSKDLPDDDNTISGDDICQTTKTSY

>contig47968 Frame-0F

MFSLFWGLWNYLFSKAELHLLIVGLDDAGKTTLLEQLKGIFGKKPGIPLDKIPPTVGLNI

ARVDIRRSRVIFWDLGGQERLRAIWNKYYSESHGIVFVIDSANIERFQEAKTTL

>contig48532 Frame-1F

MAEVVHEQRSTSSAEALTSCCPLKSNDAEHERRIGEAPIKKEFLKPKPAQKPIVIEIESN

KEHQALNREDSKK

>contig49041 Frame-2R

MRIRDYALEFAFSVVSWRIAPYTKPFDQKAVDIRRPFRSDFVTDFEILLKRSVGILETL

>contig49647 Frame-0F|Blast-hypothetical protein PITG\_05283 [Phytophthora infestans T30-4](gb|EEY69099.1|) 1e-12 NOT\_ORF

MKLSPVKIILVLALH\*KVPSRHGD

>contig50120 Frame-0F|Blast-N-acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69879.1|) 1e-45

MKSLYQTSDWGYDANAKRSELFEAEARYLLVIDANESLVGFVHFRFVDDDGALVLYLFEI

QLAAITQRQGVGKFLMQLLLLVARKHG

>contig50421 Frame-2F|Blast-acetyltransferase (GNAT) family protein, putative [Phytophthora infestans T30-4](gb|EEY58913.1|) 1e-39

MAKSKSSSAANTNAVVFSKYQGEKQLAELVKLIDKDLSEPYSIFTYRYFLYNWPQLSILA

RVQQKLVGVIICRQEPLGATPEETGDDGLNARKD

>contig50568 Frame-1F

MLFYAGSIRSMGEVHDGDATMDFMPQERERGITIGAAAISFPWREHHINLIDTPGHVDFT

IEVERAVRVLDGAVAVLDGVSGVEAQTETVWEQADRYKLPRIVFINKLDRDGASFDRSCE

SIKTRFGVQTLCVQLPIGEEAGFQRLLDLVDMQLIRWIDKDGKQIQRLPLLPSGRGEMAE

LYQKAFQGRQRLIECASNFDDELGELFLMDQAIDSKSLKAALRRITVQRGMASQVVVTLC

GSALKNKGVQPL

>contig50807 Frame-0R

MDGQASDAEPPPSLQAQYHRLQPSPNSADTSSERTAFNPSKYFHRNQTVEVLSRHPAGAS

GLLIDRPNSDLFRTLTSSQLLNVRQRLLNDGASSRTELLTRLGTASTPTTASNAGYFRRF

HRNLPRPLRFRQNTRSTTRY

>contig51992 Frame-0F

MTLKTAMIVEVLRDFDYSVRVNLANSSVCGDRIASVILKLRLTNSQGLER

>contig52603 Frame-0R|Blast-phosphatidylinositol kinase (PIK-L1) [Phytophthora infestans T30-4](gb|EEY63188.1|) 1e-125

MIKGDTGDEIDTILLSLRTLSCFDFSGSFCLMPFVRDCVALYLKNPDARIRKQAVITGSK

LLLPSLDTSNSAVMSPWRHVKKRGPTGRVIDLVLTQLLQVGISDMDVGVRRSVVESLDPR

FDELLVQETHLRLVFLFLNDECAIIRESAMQLLERLAPRNPAFVMPSLRRVIIQLITELQ

HTSDMRMREESTRLLGHLVRGAQHLVDPYVVRILEVLLPILVRGNAPLTMAVLVTLGELA

LVSRTQIAAYERYLFPL

>contig52676 Frame-0F

MAFPIEFKWPNALLDDFYHHLCYGDGARSCNSRTFAEIISAFCTWYLNLL

>contig53293 Frame-1R

MRYRVALAHQTLTNATTRPLKPFTGSLRRSTMSMQFGRTFVDRKSIIRTDVTPAQMKEAT

EVLQTPIGNRKRKRRAIMQPLNALSPQVKITDKSDSTNDTKDMEIWRRP

>contig53936 Frame-2F

MGLCSSKSIATTEVVPFVAPDRCAFEAEVNEANNGINEMLMDRVHEASVNKSKALVVGTK

VLLRYPENAVTQYSPALLQKISHSADDIPISSTYHRVHSAEVAMQEEKRQEEVRREAEQR

ALEVREYNSALQIASTDF

>contig58906-0 Frame-0R0

MKYLVRYYRLTIYEPREMTPSQAKK

>contig59044 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63793.1|) 5e-06

MSLACIALKNDEFSCSRRCDGQGDVQFVLSGAISTFAAWVKHAVLFILIPLAAAISFSSF

FEVPNAEKTD

>contig06276-0 Frame-2F0

MHNHKSITVDGGRPPSALIQSQVGLHLILNHLLPDFFFFIISLSKN

>contig06276-1 Frame-1R1

MMKKKKSGSRWLRMRCSPTCDWIKAEGGRPPSTVMDLWLCIIVA

>contig08069 Frame-0F

MYQVGKQGAIVLLCCINLLNYIDRGIIPGAPEKFNHFITKTLDVSVVRQSVYFGLLTSAF

IATYSIFSIVFGYFALTHRPFRIIALGMSVWVIAVAICGMAQATQSYYVLILGRLISGVG

EASFQCTATPFINRHAPPAKRSLYLGIYLASITVGTAFGYIYGSMFASSGSGWAGAYFVE

GIIMTGFIVCCLTVVPDELNQIPIKEMERDEIEHKQSLAAVVLSTPDDEEKIHSTAFQED

KDRSPSIEKLSFIDEWQAIFTCVPFMLIILGHAAYTFSLAAMSTFSPAIFIGLRLFEDET

TVSLIFGGLVAITGTIGTPLGGLLVDYLAKMKPDEVGRRCMVSVKALFYFMVAAVSFGLI

MVAVTSMRVLCLIFLTLCLFSMCALTVPETIAVLELFPESRRSMAVAANTLVIHVLGDVP

SPIILGAIKDSWAPDCGTVEINGEAELNPDCSHDHVGLRNVLLFAVIWLAWGVMFWGAAM

IVLKRKQKLETRCVVRRSPIDNTL

>contig09233 Frame-1R

MRWFFFLMKLCCKRLEDCMRMVGEFDVSFRSFKSSTRVLRSGRIQSGLFYSVRCL

>contig11478 Frame-1F

MLEMLRTQNPGLTRRFPLESAFNFEDYTAQELLDIVEWNCAKRCLTCPHDVAEALLKKLA

LQKTQPHFGNAGAVEQLLKQAAGQAMRRPMVNGMTVLTLEDIGMDASVNTPKKDPISLLN

DLYRMDAIKEQLIQLQNQLLVADREGSSLPQVGHFVFRGSPGTGKTTVARVMAEILHGMG

VLASTKLVETSGLDLTGQYIGQTKEKVTQKLGDAKGGLLFIDEAYMLGTGTYGEEAMTTL

VAAMTDPSYVGMVIIVAGYPKDMDEMLDRNVGLKSRFTRFIDFADWEAQDAVAFLGKQAE

TENFEVTSQAVASIHETFVELKTLSDFGNGRDAVQMWKTLLQCRSQRVVNEPEEERTITD

RDAEQAGEILIAARRGGGVLGKNIVSTEDPLQLLDHLYRMDQIRDQLSRLRMEMVVAKRE

GTARPNVGHFVFRGSPGTGKTTVARVMAQILHAMGALASTKLVETSGLGLTGEYLGQTKK

KVTEKLVEAKGGLLFIDEAYELGKGQYGEEAMTTLVAAMTDPKYMGLVLVIAGYPKDMDV

MLNRNAGLKSRFTRFINFPDWEAEDGVAFLQGKADSDEMKLGRGSKEILYQLFMKLKKLE

GFGNGRDADHVWKELLQSRAQRVFNASEDVRCITAEDAVMARDLVLAARRPPDGPLLTQK

VVSSERVQSQNQEASLLPECLSEMMEWQEATMTLEEDVEEEEVAETEETPTIDALEDEAS

CNCERDPGVSDEDWEELERAKAMYAAHLKSLKQARDEAKLAEERRRVAAIQEKIRQICPC

PAGFQWFKNGSGWRCGGGSHFVSDAQLNSQFTC

>contig11544 Frame-0F

MMMRSVIKRMPRQVGVPIVISPRLINKCPAILHHFLIDKQSKQRSARLALSIQQFNVCFS

TCTSDNKANRHEFQAETRQLLDIVTHSIYTDKEVFIRELISNASDALEKIRHLQSTGAAI

EDAELEPEIVITTDEAAATLTIEDTGVGMSKDELVENLGTIARSGSKAFLEQLKENSPNE

SGDALSGIIGKFGVGFYSAFMVADKVEVFSKSAHSGQNSHLWRSDGSGSYEIVETNDVTR

GSKIVIHLKDSCKEFGTKAKVESIIRRYSNFVSFPIVLDGDTVNTVQALWTKSETEVADA

EYTEFYKFIANAFDEPAYRIVFKADAPIELKTLFFIGSSHTEKFGYARLEPGVSLYSRKV

LIERNSADILPDWLRFVRGVVDSEDLPLSLSREKMQDSRLIHKIREVLTRRIIRFLERES

SKDSEKFEKFFSEFGQFIKEGICTDFVNKDALAKLLRFESSHVDNSKLTTLDEYVSRCPP

DQNELYYLCAPSRALAESSPYFEAFKKMNKEVLFVYSPIDDFVMTNVAEFNGRKVISAEH

AKFDVDSDDNTSEKKLSIDEQKLFSAWFKLSLENSVKEVKYTSRLTDSPAIIVDHESASI

RKMMQMVNERAGKDQASLAKNVLEINPNHSIIVDLNSLREKNPSLAKKVARQIYINATVA

AGLVEDGRAILNGLNETLAELLEQSLKE

>contig12462 Frame-0R

MTSCVGSQNVFEANSFKNVVMASHAASCKDLDDEMSSSDLRQNKTEDLNFDAAKDAASTS

QFFIPTEEVPDAQEVNYHQVNPMFESSEPADVVFFTLYEAMQALDIKFSCGPDWTMDAYA

VIAAEELSFKVLLQRLAIKSTICVDFILISGDELKFLGLTDSIRKSCRSIDKDMTGIPD

>contig13704 Frame-1F

MTESSGYNDVWVNYFDSKEDVKLSNDD

>contig16053 Frame-1F

MINNKSRASSAKERSVFVGNIPYDVTEDMLKEIFSEAGAVINFRLVTDRESGKPKGYGFC

EYADGATALSAMRNLNGYEVSGRNLRVDFADGGDKSSSVDRKRHDANTHTQRIGVNIAAG

NFRNGGAEGMITGEMAINAIESAITRLGPIKLYDMLLQLKEHARQKPDVTKSILMANPAL

THAIVQSFKTLQITIPSSTETQPVLLAPPSTITQPPPVATRMMPLPPRPPMGGPMGSGIL

GMAPPGTGPAKPGGGTRWSARPGPLTTQASNVAMNGRPGAVLPSTSPMHTQAQIGLIPTP

AGSNGPPSSNLAHPNRDPRRAGRDPRLAKRPFPGEQYGLMPTPGDNDLSKRVKVSESPSP

GPYDAIAELAR

>contig17007 Frame-1R|Blast-phosphatidate cytidylyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56488.1|) 6e-30

MDRMDCQLITNCFTTVYFNTFIWYAVDEMRKLGRY

>contig17722-1 Frame-1R1

MLLSTIRICYGCKIDVYVLAQYRLLIFLL

>contig17757-0 Frame-0F0

MWGNYRVQTSLGRVKVQPSGVPKPRANDIDQSS

>contig17757-1 Frame-0R1

MTIGRCHSREVWAHQTAVLLLVLVTFELDSFPTFYQPG

>contig19728 Frame-2R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY54766.1|) 1e-138

MFLLKKNFLHFNNSLSPHELPFIKITMATNLSTSVAPPVELRRLNFAFAKVTIGGHLVSH

LQHDPASPDATPDDDWVLRDVSLSLPPGRRVLVVGGNGAGKSTLLSILAGKHLTADDTAL

VFGRDSFRDTTLNCIRTFVSADWGQRAVAFATHAMAYSADMAVEEMMTAMQKQYPARRKQ

LLQVLRINPKWRLHRLSDGQRRRVQLFLALLRPSQLILLDEVLGMLDIISRENVLGFLKT

ESDLRQATVVLATHIFDGTDKWASDVLYIRRGTLGFYGSIEECTDGRTVPMFQVVERWLR

QELEEDDRIEQEAIGVGGDFDLSNAQNRAGGYAAGRLGGGDIDLL

>contig21341 Frame-2R

MMSSHYLVNLITSNTIFAKAITLDVVALGIPVLEADGEALTKIQTLAFHQSYQLLPRRKG

VLQKKFLIYIVASCGFF

>contig21789 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56454.1|) 1e-120

MMSKDGSAEWGWFADIDSSSESWGGDGSIHSLRRRLSADLGLIDVGNLHVLGDEQSNTRI

TAAHKTFTIITEGNSKVVSATVSIPKFRIVQSRSGADRHAQYLITLMLGKELYADWRRYS

EFGELVKTLDDLRYTRTQEAWAGIETRWFNRLEPSYLHQKCITLENFIRELMYESSEPTV

LINFLGGYLGKVNTRPTDPVAYRPGAQLPKELRPPQPQHERELFEKMWAENFQRSHVEYS

YNDERNCQAECEHAAVR

>contig21860 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54801.1|) 1e-119

MHRNDRSGVVLHCCHVRSLQILHHVRPHKSMAFYQQIGESNTSLTTFCQLEWNRLGYDMD

ILAMRLQLVEYLAQTVGGDTLTAEYLLLVLLSHVYARADLSTPLGNLSLNLFLTMSSIRV

QTADFVNTMHMTLSSLMPMVGRVDLTINTLNTTTFVPYKDYECDVLRSGVLQVANGTTLL

VNETGLSTGQLNEQGVKNIGALQSLMDKMVLPYDFQYYSKDFPQDVAVITLSEGKSIVPA

IVSLPVVGTGNCTTFKRPTEELLECFRLFLCVLRSFNVTIGNEEAEMAEKHYVKCRKSKQ

NVSIDDLHRWLRLARLVALSRGEGHISSNSWDAMLQLETQRLSRLPINKAT

>contig21929 Frame-1F

MVRTDVIGDLTSLGLLNQRARILVVGDGNFSYSRALMRANSARIKASEINVTVTSLDAES

QLVKMYPNSRAILDELRSSGINIRHGVDATKLESLSFKNDTQRNKFDRVVFNFPHYVANG

GGNKNISNKIHRHRQLLVAFFASASQVLTRDGQIWVTLCAGQGGTKLEMKPRTEGNTWQI

IQCAAAAKLVLQDAHFFPMEALTALGYYSVGYQSREKAFWTEGGITHVFCHEARGHKSCF

PITWRRGISFWITDEALFTQDRLVDVLHEHFPLETMDLAISLLDEYRCKNSGRKSVTYRL

DISSPVMALSRERINALVQTALYAIDSSEFGACRTT

>contig22609 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62946.1|) 3e-93

MCLIVNNIVADLIVLLCVIPTISMLNVLDRADKPLTMLRAIREMLDPREGLFLLAVVLPF

SAFVEQGTRRMEPNEKLPMQGGLCAEGASFEVAASLLLRNVLLPAGFKLRHFSRVPYLCR

GDIQQPYYVLSDAIFVLEVDSQFDIRPSLEN

>contig23725 Frame-2F

MTMADIVHMNGPVRVAVDRNNAPTPDLSVADVLLYGEKTLETFSLDAVSGFRRPYLSSAA

SSHMTKEILFGRSEFMTRAVPSQNASFARCFKIAEYFLDFAEQARCLYEDSDHNAAPEIY

VLTKDSNSAVNDKGPSIVAFDPWTSELLWAFEVPDFDVLAVYGISTAHGSIFYKWKVDGP

SSTGFFRPKTPLDASIKSLDQEQNQIYADFREKTASADGRRQRMQKSDADKQLIQVRSRN

WDTTESEFKLRKLGDNYFLGASEDNSLVGYDSNQATHNVPTFHRGQSDDIHNLHESMDPR

RRRSIFWEPIVNDGERGVFITYTHVVAMGLAVATCGILLAWGCYVKGLSASLAQTAIKTM

DRSQFFRSHVHRLIVERPGEEDITISSVISNSFMVNALSVDGQVPLLEDSEPVNAFLAQV

NFQVIESMLMKKFSRLAAAEAAAVLINGGHSDPTQKLIECDRTHVSSSSLSPMKTIVSRG

FSSSSSTVRISSQKPTLAVSEMLSLSYSEDSSFMEKDFSGIYEVEMLPMGMIGVDNASAA

FNHTFDNERFEQADLNDDISVGEDSAETVIGAKTMSSSGDSTTGSCCSNNDSCISHALEN

SDGYGMTFAPDDNNTDEKSRDIRSSSQDLSASSSADSGISSNDEEVLFPFVCQSRFVNEF

EELSAIGKGGFGQVMLAENRLDGRKYAIKRVGLNLKTQTSKTLQKFLREVKILALLDHTN

IVRYYQAWLEKVEEGTPKTYEASAKSEMGSAGGHMEARSTNILAPISELDFSENQRQIET

FYSNGSVTGDNDGGFDWDRGSSSGIGDDCGWKEEDLIVRNKPRAKSALSPLSPLYMSRSL

GAPGDELDSSLSALDYCDHWLYIQMQYCAGRNLADYLAVPTQPME

>contig24023 Frame-1F

MAQYGIEGEFSGWVYKQGSLVKNWKKRFMVLNGRQLTYYNASNVTPDVKAKGSFQVITVE

LSTAIQNGLLVHGRGGRVLKLYTASAEATSAWYNMILNATTASAQQFVAAPPDRFSTHSA

TKSASMGNESELLERLESLPLSEDGSKQVTHSGWLKKEGARIKSWKRRYFVLRSNALSYF

DSEDTGTAAKGYGHVRAVEVNAIVTFGLDILFDSGRVLRVSAKTSGDMETWLCQLSDAIE

ATFKELNDVRQSLAVFSSYRASLTGKVAPSRMNFHQGVILYDGTNTRPKTRHSIAAVPSK

PRGSIAETPEMSQRRTAQAKQFSLYDSYSSSDMSSQSCSPGSYDHMNLFTRSNEHRHDMG

HTLSSSDSTFFDSDDEFGSEDSEGDWI

>contig25998 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53952.1|) 1e-152

MDLEDFGKFQTLNIRRAERRFHEMTFEKELQPSLITLNSLLAVYANALRLRSAEVFMKET

FARYNFKPNKFSYRSMMQMYVRAKRTTDAEQLLDCIRSEISCGDLEADDATFGFLVDHYA

RKRLMRRALTTLEEADALGIQLQEKHYKKIRALTEKYGVFSDLIPENPNAVLLAGSRHQL

MEKRRVREQVLQYNSKIGKRYLLPSTF

>contig26227 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64066.1|) 6e-52

MVKTYCEPNKAAAKAASHEVTESDLAVTHEYQILEERSMADFEWLFVKLGELTNPKALPF

FPEKRTPRNEREKV

>contig26568 Frame-1R

MRRTGHLKKRHDYTRHLRINTIFTKVHECDVFFCRQVVRF

>contig26674 Frame-1F

MGGKTILLYDLTERENALELAFQARYGKIVSYQWFGHGYIVAGFSSGYVVIISTHLKHIG

QEQYCVKFHEQSLREIVYNEANEVVATCGDNCIKVVRMSDWKEIAVEYLDSDA

>contig26890 Frame-2R

MQTTATRLLRELKVRQSLLHHIKSS

>contig27567 Frame-2F

MNELTPNQSAPQPSQATAQSRGITMPYAAYAGASAVNTNFAVADRVKSFQSVPRGTNLST

AKYQPRPQQLQQLSEYHAASYALQKSPADTRSGKFDYANQSYSLHPAQPQQSYVAPYGYS

TYAQNYGNTGDFQHQHHPAHQHQQHYHSGYAQVETNALG

>contig29583 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61307.1|) 2e-33

MKDYTPTLTDDFDPTRIVDDWNDSLEKAMVESEEPHPLPWVSPDLQQKKTLWDSELKNVE

LEEEIVIDDLNYLPPPENLPRDAVAHDDHDILLEDLLSVNVETLCSE

>contig31308 Frame-0F|Blast-glucose-6-phosphate isomerase [Phytophthora mirabilis](gb|AAP51063.1|) 0.0

MINDTPAWKALAEHVAEIKETNLRELLTDDARNTSMRVEQQNIYLDYSRQNATSKTLDLL

FELANSAKLKEKLKAIASGEHVNATEDRAVMHMALRAPKTQKILVDGHDVVPDVHKVLDA

IRAFSTNVRDGKFVGVTGKPLQNVISVGIGGSYLGPEFVFEALRHEPIAKASAQGRNLRF

LANVDPVDVARAINGLNPEETLVVIVSKTFTTAETMLNARTLRKWLVDDLTTKGSSETDA

VAKHMVAASSAVPLVQQFGIDRANIFGFWDWVGGRFSVTSAVGILPLALQYGFDIVEHFL

EGAHAMDNHLLQTPLRENLPVIMGLLGVWNSSFLGHSSRALLPYSQALMRFAAHIQQVDM

ESNGKRVTMEGDTLPFEAGEINFGEPGTNGQHSFYQLIHQGRVVPCDFLGFCESQNPIQL

AGESVSNHDELMSNFFAQPDALAYGKSIDDLIAEGVPENLRTHKFFPGNRPSISLLFKKL

DAYSTGQLLALYEHRTIVQGAIWGLNSFDQWGVELGKVLAKQVRRQLNASRMENQPIKGF

NSATTSILETYLAYKA

>contig31524 Frame-1F

MYLDEFVTLACQIATTSAEGKELLMFQCLGLRLINVLIKKFASARDPEVTTGDAYLLDPY

RAQLSSAIRHAFKQVHVEQLPLSATIEREIGEEKHFYAPLLLEAHGIAGACISAHITQDR

VALGRILRAVKTSDYGHAHFIGDELTRISLSLANLASVGELLTSSITKAIDQNDIDDDEH

QAVASSPFVKAMTSELSESIEYLLNCWIDSTFAYSVAMQEYAHYAHLETTNDASLIIDKA

ILLPALQMPLPLYSAAKTSATATSTFKDLCALYKRYWPKIVNAMAIFMVFLSNSILKSDP

QEGTISKWTTILLSSAIFHIRANTRDRMEAEDELRAVLRSVPLLLRAFVENASTEALSTN

FPMLFTVSLNTLKLASKRCCGLAQVVALETIFECLKS

>contig32183 Frame-0R

MHNYPAFLNLLTTFVYIPISFAYILPMIKYGKAITWDHQNIPKHRFAIMGGLDSIAGTLQ

VFAATHLGGSLIILLGQAAIPMSMVISRLLLKAKYSSFQYLGAVVVTLGLLIVLGSGDSS

SSSSANSHVIVIWSIVMIFSCIPMCLSSVYKEKMLGEVELDAVYLNGWVAVYQLLCAIPL

TFPAAMVGNHPISPRELPENLYDGLLCT

>contig32491 Frame-0F

MVATDNKSECGFMEEEDNRTTLMPFKPYQIKSLLFRQCLAEFLGTMVLVMFGDGVVAQVV

LSEGTKGEYLSICLGWGLGVLFGIYVAGGVSGAHLNPAVTTTLALYGRMEWRKAPCYILA

QFCGAFVAATVVGIIYFPMFTVIDPDMTSTQGIFATYPYSDDVPVGTCFLTEVVGTALLL

GGLFAIGDELNKPASPYSQPGAVALLVVAIGMCFGMNSGFAINPARDFGPRLFTWLAGWG

SQVFTLGDSYFWVPIIGPLLGGPIGAGIYVCVIEHHHPRNVRHPFESHAFIA

>contig32969 Frame-2R

MSLLHSWSIFYKDAEVDLLVMINWRVWLDAFSNGVSPSMSLISTNAPYVT

>contig35670 Frame-0F

MTRNGHVSTKLRDLSLHPTH

>contig36011 Frame-1R

MTRSVLLNLLHVPTKEDPMVDNHHGSFHVDPYHGSSKSMDDKSRLRKLTSLSYLGGKLRI

MFQRELRDTILCEDELLPRANKRNLYEIIHCNDKTTSPRFDPLIELSDSVRLAEKDEPSK

AQRSCTNCSKCFQRELSRFDQYCGLDCKTAHRMRQASHYLA

>contig36165-0 Frame-2F0

MRSSGVSDSSIPVRCTSSIFPGKMQRSGRNLLETLIFILKSCNQTLACGLWCFVQ

>contig36165-1 Frame-1R1

MKINVSNKLRPDRCILPGKIEEVHLTGMDESDTPEERIKIQPRAYFSFNKKTSKIFD

>contig36635 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53082.1|) 2e-19

MFHTPCLHEWLQIGNSCPICRVEITAKGNANHQNSRHSQSAQQRGDFAWSEWFS

>contig40670 Frame-1R|Blast-predicted protein [Nematostella vectensis]gb|EDO49629.1| predicted protein [Nematostella vectensis](ref|XP\_001641692.1|) 8e-44

MEHHDVKTLEGGLETRYSKFHLVDLAGSERVRRTNSEGARFREGVNINRGLLALGNVINA

LSERSRTSSTTVHIPYRDSKLTRLLQDSLGGNSKTLMIACISPADVNFEETSSTLRYASR

TRNIENRAVINKEWSAENEVLYLKQQLEIV

>contig40821 Frame-0F|Blast-predicted protein [Phaeodactylum tricornutum CCAP 1055/1]gb|EEC43453.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1](ref|XP\_002185006.1|) 3e-08

MIADCLGKKVILEAGAIESTSRGLAVLIGTYLNLHTLNESKMFPTEISCLELSQPDATAH

AAYLEARCHQESLYRKMY

>contig42081 Frame-2F|Blast-tetraacyldisaccharide 4'-kinase, putative [Phytophthora infestans T30-4](gb|EEY66436.1|) 4e-26

MKTLKALVNTERNCIVAASRMKVVGLVSAHTLLSGEMQEANSDIATPKRRLLLTDKIGAV

LCGVGNPKSVIKVVEKVARWAQLEIKAYPDHHNFTLQDANDIIKWVGALQWQRNESVILV

TTEKDF

>contig42423 Frame-0R

MVRGDMNSQFYGRKVTPNDILSGQVAPPLGSCDVLFDAICRASTQQGLGSRRLTMSSHTN

IFGSGNRADYAADHAAAARASFAENPAPMLSGSNRELQLVSSSGTHRSLPPATSMPLDPK

DPRLQRYSSYKSERELYAQFEQRKSGVISTESKHTHPTNPTLTYKSYPAPAPNMSYTAPP

EAQAMYNSFVAPAAPKRPVPSLPPSAKGAEMKQIYSDVISVVQSKCPYANVQVFKDNCRL

FGQDAMSLDAFFSYLLSICSHSQMKELVPQLVRLLPTQDKRERLWTMYVRETLLIKI

>contig43086 Frame-0F|Blast-N-acetylglucosamine-1-phosphotransferase subunits alpha/beta, putative [Phytophthora infestans T30-4](gb|EEY58113.1|) 1e-42

MFLYFNDDVFLGAPVRPEDFVSQAGVQKAYFAWEIPLCADRCFEKSLGNGMCDQECNVTA

CDFDMGDCGCDVDPLTGSVECNSEKVANLLEHAAKP

>contig43165 Frame-1R|Blast-elongation factor P, putative [Phytophthora infestans T30-4](gb|EEY65750.1|) 9e-98

MLRRAITQVTRAVVPSRCNGVRFATINGNQVRAGMALEIDGKVYRVGKNQFVKPGKGGAY

VQAELKEIKTGSKINRRFRAAETVNKAPLGPDELFQFLYYTGDRLVIMHCGTFEQMEIPR

DLFSGRKLDFLQEGMTLSLQIIKNEVLWANMPEFVTLQVSKTTPKGVADTALSVKNATLE

NGAVVKVPLFIDIGNKIKVSTEDGAYVDKL

>contig43598 Frame-2F

MSRSFTGCLHAATFACLGRFASIARILSSAKALAHGPTSSLWLLLATAILMHYRSTTSDT

DATCSDQSEWTKIRRFGDGASHCRRWRITKCTRQAILLATV

>contig43635 Frame-2R|Blast-phosphatidylinositol 4-phosphate 5-kinase (PIPK-D11/GPCR-PIPK) [Phytophthora infestans T30-4](gb|EEY64612.1|) 1e-112

MNKLFFAWQLTALISGVLASGVMLFYFTKSARVRVHPGSMFMCIFMSTTIASLMRVGLHT

WFLLLTSKDDGGPIPATISRVAIEQLGHDAGALEAYAAFFFWGYLFFSTSATLWYLMLAL

DLIFSLSNPFLPFHTDNIKHHIVAWPISLLYCLVFRYVLGYIQFSEVATVVLYYNLPAYL

VLLYIGGALIQSRRRIRILESHAHATTERMAKRILPFLAIFAAHTIVAFVIFLVQLGTEF

GSLTIDALDQLSLVLESLILFALFCHNAGIFKASRSKVSNEFNASPLDA

>contig44458 Frame-2R

MKDDVEEREGYCDPVNLSCLNDDIINMVNRQHAETISPQELLAIRQLRQEKDEAFYAFQQ

KFLTTTVASLPEVEQRRILKEPTHSVEFRRLQ

>contig44825 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64596.1|) 3e-24 NOT\_ORF

MLFTERSLKPLAS\*LEAVCYARTNNFYETRSIYMIKASTLDTRFSCVLVF

>contig44951 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60444.1|) 3e-43

MHWHAHTVQCLAYGHKGQSLVSGGEECVLVSWDIESGRRTYVPRLSSSIHTILIGPDTSN

YVVELADHTLFQYNTVTRVQTWYVQGLGPAGTRVQTSLPTRQLVFDPMTSAIVLHTASST

GILQLYEPYSNRVCERIHLSERNHVTRTDFEKLPKFQALITCISATGQVLVTLSSPLTAP

QGEHQTLRFYTRRVDGSFVVQTAIDAPHG

>contig45196 Frame-0F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY64990.1|) 5e-09

MSHLRPPEAKDNSFFDSTLIVIGITAASLVLLALIIWFLCWRRGRHRVNRSSNSHSQSTE

SMDFVLTSDLMAIVADGSR

>contig45310 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66338.1|) 4e-14

MSQFQPSSPGIMRSITTRAADATISRTPRTKRDRNNSKKLRKGDDGKKSLLEAIFSKKKS

PSRNNR

>contig45439 Frame-0R

MYWYGYDVHKRPILWVRAMLKDWQTMSSRRTEEVRAHVYMVEMGCRRFMPPGVTTFTIVT

DSSGLGLAQVDYQLMQQLLEVCVNNFPDRIGLVHAGPLTRMLKLITSWLWPLLPIRLRGK

ISLLNDCAKELAKHMATDLIPLHMGGTAIHKLREPQVDSLKTHDIMEVSYMIQQQARCME

EIIDR

>contig45866 Frame-1R

MVQMGLREAHFGALLQNELHVSRFVEYFFRPAKAVEKLENTMPLTSTPELWLVFRDEGKS

LRQYLYEKLEILSGADGGGHSGAGVVLQPSRFWEKLRTDVSGESVLREIMRQLLVGVASL

HARGITHRDIKPSNILVFIPPSLSSSTINPPMPLVKLADFGSAVDDYTLKNLYRMKAAST

ASAGPSQAEETREYQPPEVLFSETGQPYDYTAPEAYDLWSVGVVFLEIVLGSPHVFLISP

RERAKVDVVLNAQQRLRRKRQSNEAGWRTKAYLLHVLTHDFCIFQPGPQQLRSLFDTYAL

VSESCHFGRFNRTVIERDPLKKGLQDMWGLDLIWRLLQWHPKDRITATKALEHAFFQGAY

VCNDSGRQFATKDELLLHERYLKVQKARDSIFASVVRPRYELPDRFTCPQCGRIFSTAHS

CELHAHARRHMTNSSFCTFEASKITTAIRSETKAIDLPKPRHSRVSMALFQGRKKY

>contig47491 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56549.1|) 2e-20

MLSSNARIVTYLNREGDLAVFSSLKAILTPEPLDLVKRLRYAKDMLQQMVRTTEQIR

>contig47820 Frame-0F

MTSEATPLQLRSTSLQYKVDVWRREEARKRDLTRGGIFLLLLCALSVFIMHVTEFLVDDE

ESDSAGRHVQTRNMAQDKLVNITSEVFCGLIPDDSGYIELPNIDERFFYWFFKSRRQPDT

DPLVLWLTRRPVSSSLQALLTENGPCQVLPDLSTRINPYSWTNESNVLWLDLPTSGSTYA

DEDTAEISEMKVGENVYCFLQRFFAKHPELAMRDLFITGESYGGHYVPVVSHYVWKRSKE

ITDIPKVINLKGISIGNSLFQAAIQMPHYLNMAINNSYNIALVDAAELNTMKEALPECVS

RLKQCPQNLTACRAGEDFCMKELLNPMLMADRNPFDIRLPYQNDDIDIKGDNMSYVSRYL

NSPKIQTALNLDLKHSDALQECNLNRYSAFIKSANPAEPIDSYVADLLNDDVRVLVYAGD

ADLVSNWFGSEVWTLALKWKDRDGFNAANVTSFITKNGVNAGAVRSLKKLFTFLRVYSSG

HFVVKDQPAVALDILNRFLRDEDF

>contig48533 Frame-2F

MTTDESPVRTGPKPAKINMLFSFSDSRVVGCIEVNLTLRTRHTRRPTKVLAFSSAVVGAP

MRRIMTIYRDHGDASVRFAPTYSFKKETRY

>contig49040 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61468.1|) 2e-06

MEPRPALALFPKRQREDIMSLFTAQSPQSCDQLPQFLPSHELKFGLAPVARDKATSHITL

VLCR

>contig49923 Frame-2R

MSNEVVIEDLVTLGICRYFIAGLPFHLYTSTYAAMLGYVVFCKIFTTCILGQ

>contig50420 Frame-2R|Blast-sepiapterin reductase, putative [Phytophthora infestans T30-4](gb|EEY59412.1|) 8e-14

MKAAGKLIPPAQSSARGVKLAISGDYESGSHVDYYDLDV

>contig50745 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67845.1|) 6e-72

MDALRWQKQKLLDPQTGQPTESSPGSDSSYWLCSSLSYQERLIGCVTCFLLGFLLSLGST

FRLAKLVHGNPAPFSIAYTIGNVLSISCTTFFVGPWKQIQTMFHIKRRESAVVYVVFIFV

TLALCFMPHIHHRMVFVMMSLLVQFTALVWYSLSYV

>contig50806 Frame-1R

MRKMAPSRARMNVLEGHPSQFTKI

>contig52602 Frame-2F

MHTGHGYLQPQTPYNYCGNALNLMSGFMPMKRGPNTERACEHVQHELG

>contig53418 Frame-2R

MTPYQEALDAHKGRCAVAVSALQAGKCVLRTTAICAVSRTCGWCFTFQVALQRCTGCRKA

RYCSRTCQQRDWSEHRHECSAWCSIPADSISPTVLLVTRLAARLFFSSSVTQIEKYRVLR

LRHHMADHAKLKLKQFHEMTQLVLLLLSRYTVGKEKPVMTFQKL

>contig53564-0 Frame-0F0

MTTPIALPTLSPMTCLCKMFSMKNSPVKTTAACR

>contig56440-1 Frame-0R1

MFSSAGAAPFKPWEKPQVAGAQDDLMY

>contig56916 Frame-2R

MAMCDCKRKKFDAVTRFFHCKLN

>contig58248 Frame-0R|Blast-dihydrolipoamide succinyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64480.1|) 9e-10

MIDKERQKILYRDNVDMSVAASTPKSLV

>contig58972 Frame-0R|Blast-unknown [Glycine max](gb|ACU14313.1|) 4e-07

MTRGPNILVTGTPGTGKTSMCQQLAERSQLLTHLNVGDLIKE

>contig59171 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61493.1|) 1e-09

MLLSLMGGVHPRMIAMVPDSKVSNEKK

>contig59320 Frame-1F|Blast-RNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY60449.1|) 7e-27

MSGKYIGNRPVKLSKSKWEDRNLDVA

>contig02514 Frame-2R|Blast-O-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY57684.1|) 1e-102

MECCPSSSLLKAATFEVDDAIAESIAFVTTYMRAVESRREDRIINDPFAEPLTREQQSKI

EKFMVEILSEISSDLPNTIAIRTRYLDEALHHRDPRIKQIVILGAGLDARAYRLNSLRGS

HVLEIDQSGALFEYKAKVMAELHAPLVAQSVDCITSNLVEADLEANLMGHDFNPTMPTFW

AMEGVISSMERPNILELLKAIDHLSAPGSAFWADIPGQIVVADKELGNVAMKYGEDNPMS

GVFCEISWTMDMQASLKNAGKHFARNWTPPLSSTSGQTIPFSFVVGKKPL

>contig05528 Frame-2F|Blast-actin-related protein 2/3 complex subunit 3, putative [Phytophthora infestans T30-4](gb|EEY54896.1|) 1e-09

MFPLGGLVRAPSNANEAGTDVTIFF

>contig15114-0 Frame-1R0

MPNLVPLELYAKFWINQQARVACENKQTLRIS

>contig15114-1 Frame-2R1

MPNFGSINKLALRVRISRLYGLV

>contig15305 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56132.1|) 4e-91

MALHRSFQTARRFPLQSFLRSMHVLIHLQVSAASYSVPSTSTRVVPNVTDNAIHTLFERA

IAQRHPTQALQCLAQLHTSPGAPLLQKLAILLARQKKTSRHDVLRAFEILRGVYRLPCLK

PDDYTKLASIYVLDACVRHSMLDHAMELYDEALNQAVVLDLPAYDGLLKALVKQKRMEEA

MDVLRALVRGEDLCPMETTFVPVLIKLIETREYDEAINVLQQGQTRGVVFTSTTFHPLLT

LAEEDTVSTDSLIKFLSFIEDAWEECKDFDVEEYEDDLND

>contig15370 Frame-0F

MRRFAPSLAESDYKLVQFKEITTNFRYKRTLSSRTRQEMQQQDRHGYSVLKMPQEIVASS

GRLQCLVGPSNTPTWFIRLQHVPNAYVQVSQKGLENPATFKPHTSLELLPLNEKAIQIFG

RFYYRVVVSMELCSAPDLLAQGNALHLLKKKNVEEIIESHETYQCPHSSVTFVKLAYEEG

WLVETLLSGIPVLERLATEPAREDGKFFYIVQIPVGVRVAPHIMAQRTGQGFPLHSIVEG

TQRFTPPQSRITYVRVEGKGWLFETTMDGQLVLERMEVPSARHVARQFYRVLKDVTVLSM

PIGKMEMEGGLLSVSTPRKRLKNTLIECSERLVPAVNVPCALNVVEMGFLKLRHDAGWIC

EREFLPPYRRVLLQVHGHAKTQQKLVMYRVLQPVFLRSAPDLECPRLPGVALLTPGTVFE

SSLQYTPPESRITYVKVA

>contig16296 Frame-2F

MMRGFKKIYTVRKATMLRRTRCNRYLVVLMAHRVI

>contig16946 Frame-0R

MWTQEEHEKFLEAMEKYPAGPWKVIAAFIGTKTTRQTMTHAQKYRQKISRWRRGLRHKGR

KQAGEDGLLHTEGELLQEYSVKENRFQSIEYVSSDEMAGSYSRVNTNANVSVSPARSLTG

VPGHKAPPNELFRLAELASVEVIKKEPVAVPSLPMPSSPLDVEMADMSSPVVTKEYPQEI

IARGSVEFSEKIRKMEWGTSQSGYILPYRDWSMQKTEVRLSPLRVTPSGPTFSTRKFGGV

LSAITEMSYQNAQNRLPLPLSSAPMFSSMRVAEADAQKLPQQATAFRLPPLNVVSTHAPR

VYSIPPLRSKIDPSVLNGRVYYTSSN

>contig17422 Frame-0R

MTWMLLSVAFCASVCHSPGPVDPLKPLFPEMPS

>contig17497 Frame-2F

MLALQAPPPSERALAVLPPPPPPPFDENEANIQVESSIDDLVSDDGVPKAPETKTLSDFA

QEVTKWTLHSDRDLHSYLKRFSADLFARTKDLDDSVRNIALEADSAHVRLKNTLNAFLLL

SNNQFIENRVYDEEQEDFMITDGSSVELRTQQEENEHERTEPNNGGMETKENTKATAASI

VNKYRSALEMGFEAMKLFVMMDEEEDDERDASSPFETVLDIYNERPLPFIIGTRDFLEDD

TLGLGAAPEEDFESDSSDASSDSSSSFESDSTSDSNSSSDTRRSISRDDRSSSDEVVSVS

RYRMHSDESDTSGLFGHVVRDEVSLRERVDSDDESDTSGLFGRFLESKAQSSRGVVLNDS

DESESMRENDKDVVKSRNKRGSRRGREDVLPLFQASTPYRNSPFLDSSDDESVATFSKQS

HRNKSNVANSLDFSSSDDDEGFKPERLESTRSTEVALAQGFRLPPMNERTSRRSKAGSVA

SSDSDAESTTSGLFGRPVLEPKRMAPVAVVDYSRADDSSEDDKTKDLFASVKAKPWTPKM

ASATPRQLVSRRSSGSSSSDNESKEEGVLNAPPTALASRSQPVQQRPLSGLLNGNESDDS

TGSGGLFGIRQSSSSNVPVSKLSREVPHTLSDSDSDDEGLFGATTTASKPTIVLPVVKKS

TPLQTKSTDVQSESSDSDDSGLFGAPNAHTEFKPQPLTASMPAIMPPRPMMNQTSVSDNS

DDSSDDDGGLFGTAASKPARNSTELNTVSNPVATSVLPIVQPPLPSAIGRMQVASSDSDS

DWESDGDLFGSSTLK

>contig20415 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63977.1|) 4e-57

MKNSTKALFRMQRWLFVFSASRLIGIAASRATFVLWPQHINATLSLSISPDNSPFVEASH

GGVLSTFDTKFDTKSKVALDPLIDAIEIKWKPATDVHSSTFNRFLASSSRFDGINAVGIH

LHVDLRKGVRWIEMNTTFHKRIEENVRKVLDNIVPSVQILPNFLKDFLAKSFCNHATWKS

SNSPERIFHEDASKSQTLCYSSSFPFWPENDNSSFFHNLFQKSNANTGIVKHSITERALL

EAHRNLRTCRQEPIIAALKLSRRETSPATLEATFFGSYIVRFCRSGAADRTAVQVRRSTS

DNFFVTPIISKHNIYELEYAWLQRKGKAVSVESVLTTPIEVQVTQPVAAALMHAAIIGEG

FHRRYVIDVKVLKHEGCGKATRNNTILLRVPISNTAYIDLDELRRMERFNELKLVSFTKH

IEIERPSPVSAQHVIVLEFP

>contig20460 Frame-0R

MPPRVALVLSLFCAVVTCGLADYGPKDSVTILTDKNFKKEVLQSPDYWLVEFYAPWCGHC

KTLEPEYKAAAKKLKKHARLGVVDATKHQQLAQKYQIKGFPTIKEFGATKKRPQDYRGGR

TTSEIVQYVMNSPEAKKLGVSSASVVTLEIEKAHAFFNQKLPSAVFFGSPKKGKKSAKVP

SWLSEVAESFSEGKKKRKQPKVQLAFVPGSDTKMLSHFELTEDQLPTVMYVYPSSQKYVV

SDVSKLDKAAATKFIGDALANTEVAEKDEMLPIVSSFPSPGVATKKPIVALKALDATLVR

NCVAKRGKMCVVVAKADIKLVRALAKKYRRDPFLFLSSKVDDPTYHSLSNFLGVKTAEVI

VVKPGRKVKYSALTDASDERAISEFLDKLIDGSNPLSLPSGDLTILEAALSGSPDDATNH

EEL

>contig23836 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64117.1|) 2e-28 NOT\_ORF

MELYFANIDELLEREEMPTEYQKYKSLIYCSDCKRKSITYFHFVNHT

>contig24345 Frame-1F

MDGPARPQTKVNVEDFDLLKVLGKGSFGKVMMVRKKDTKMIYAMKTLRKAALVKRNQLLH

TKTERSILQSIKHPYLTSLTYAFQTPDKLYLVMDYCGGGELFFWLKKDRRFSQQKARLFA

AEIILALQELHKHDIIYRDLKPENILLDLEGHIRLTDFGLSKEAVTGAGATGGTKTFCGT

PEYLAPEILENKGHGKAVDWWSLGTLIYEMLTGLPPFYDQNMQRMYDKILNAPLRFPSFM

SAEAKDLLTGLLTRKVSDRLGSGPSDAEEIKSHPFFKGIDWDAVFRKEVLPEFKPPNRLG

SMDTSNFDVEFTAEKPVDSVVTTTMSETQRNKAQFPGFTYNADTIDEDHKGN

>contig25621 Frame-1R

MVVSVTRFTDYSPHWTQRLITKTHCFVHGIYENQNAELAAQL

>contig27177 Frame-0F|Blast-Amino Acid-Polyamine-Organocation (APC) Family [Phytophthora infestans T30-4](gb|EEY57666.1|) 1e-154

MPMGIHGVIAGAGVVFFAYLGFDMVACLAEEVNDPQHTLPRGIIGSLLISMAIYVGVSLV

VTGMAPVDILGNEVPLVNAFAFHNLPWAGCVVSFGSIFGLTTAAFTCLMGQPRIYYQMAK

DGLLPSFFAKLNHRTQVPMASTIFSGVLVAIIAFVFDLTFLANVISCGTLQVFTFVNAGV

LLLRMRPSLSSVNVIYRVLLFVVSCFALSLSFVLEFSWVIQGVLFVLVVVSYVYINQLGK

LSERTGTFLCPLVPFVPCMGIIANVHMMVSIPVEGWIGVLIWLGMGLIVYLSYGIRNSVL

SDPYILYPLI

>contig27887 Frame-0R

MLAVHVYYTDRHCFIRCNKTSFFLTTPMLEPAKTTALT

>contig29434 Frame-2R|Blast-copine-like protein [Phytophthora infestans T30-4](gb|EEY70665.1|) 2e-13

MKGIHPRAPLQRQGTSYLVRSSISNGMADGWM

>contig31736 Frame-0R|Blast-protein arginine N-methyltransferase 1 [Phytophthora infestans T30-4](gb|EEY66477.1|) 1e-170

MSSAPRVANESVPAEMTSKDYYFDSYSHFGIHEEMLKDTVRTKAYMNAILQSKHLFKDKV

VLDVGCGTGILSMFAAKAGAKHVYGVDCSSILTQARMIVQANGYADQITLLQGKMEDLTL

PVDKVDIIISEWMGYFLLYESMLDTVLYARDKYLVPHGLMFPDHATLYIGAIEDGDYKSE

KLNFWDNVYGFDMSCIKEIAKVEPLVDTVSSDALLTDVCPIFDIDLTSVTKEELTFSSTF

QLTAFRQDFCHALVAYFDCTFSATHKMLSLSTGPKAEYTHWKQTVFYLEGELACHPGELI

EGELTCKPNATNPRDLDIAINVRFDGEKWVLQSSA

>contig33868 Frame-2F

MMAMEVNHSLVDKDFDRYVLAANGIAKHAIPLPVAALMPLDAEQSLLKAKRVSRLNYNAL

TVDPFLCQSLAANVAYFVNGEYQLMQIIDCKINGAKLTKICNFPILTTRLENVSIHVAGK

GMIVYSDGQGSLYYVKADSIASDAKWQILYECQPLGVIPLLLLNAVNDEENHKIYAVGAE

CVSTNEANELFRLHIFQVSSQMALKSENKVDISFLEFEHKVTGLAEVSELPINILCNKTD

MVFLVKGECHLLAPAKDRSFESLDVFNKSMPIQRRQEKEVLNDPDMNMLYSMFPRAGIGY

HGENVRPTKTSELASLDLKIPLRDRFQKSSSSLSSFYTPHEGSSNFIKSNDHERSNSPQN

QPLKVPTTDTLLGGFEECDSGDPDAKAHLLLVNLSSQAVVQQQRAINCREFQFLCPGAPV

LDIPSTLLFRNDVHGLMYELKIASNQVVLNHVATFPAFGFVQASKQDTKLMSFHPAGSFA

CIGEFTRRIFIYQNDDLETENKAHTCKQHIVEFGNQELLGLQITNNDTLLVLT

>contig34047 Frame-1F

MGGKSTLLRQTCILTLMAQIGSFVPASRCRLSPVDRIFTRIGASDRILAGQSTLFVELAE

TATILNHATSHSLVILDELGRGTSTFDGTAIAYSVVEYLLSEVQCRTMFATHYHSLVEEY

ADNDNVSLGHMGCIVDSENERKVTFLYKLEEGMCPKSYGINVAMLAKLPNEVIECAAKKS

EQFERSLKANTELESVRLAQKVRELLAEGDADIEKLRQLWEYARSITLYARN

>contig34223 Frame-0F

MRITDQSASPCLPSSVNQIYLLFRSKNTLHRCECSHSSYLVY

>contig34494 Frame-1R|Blast-PREDICTED: similar to conserved hypothetical protein [Nasonia vitripennis](ref|XP\_001603407.1|) 4e-09

MTDCAVAILVASPLDFEATYALVHDAQHIDFLQQVCRIHGSLEENLTRRPPRLRLALEEV

VVGVQKGFLRLESALENNDRDDHSKVINSIVERAVRTLVGADTDCEDFDDDFKWKLSLQR

RERLQVFHDLWKKGYIVTFGSKFGADFLIYKDTPKHAHAVALIVVKGFEEEFARVDIVSF

CRIAKMVKKQLVFASVRSLKERECESERADKNLDSVLDVTSSDVVYVSLTHALLVSRQDE

NGDTI

>contig34937 Frame-2F|Blast-DNA repair protein RAD51 [Phytophthora infestans T30-4](gb|EEY63552.1|) 1e-103

MLKAAREMVNVGFTTAADVLESRRDLITLSTGSNAVDELLKGGVETGSITEIFGEFRTGK

TQLCHQLCVTCQLPVDRGGGEGKALFIDTEGTFRPQRLQAIAERYGLDGASVLDNVAFAR

AYNSEHQVQLLSQASAMMAESRFALVIVDSATALFRTDYTGRGELAARQQELAKFLRALT

KMADEFGVAVVITN

>contig34982 Frame-2F

MFRATASCGLMKMMRNRQLEALVSVSDWHCLGLSLQDASEDVRRQFLKKLTSHLMKQSVQ

YPHKYLSYLALAATDANTSIKRQARIVLKNAVERMRRVFTALSEISSQEHDSSTTALMVP

EYALPYVLHIVAHHPTFPSKLVETTSMEMLLYSTEWSDQLMYLNFFLDGLVSSNAAAADN

IAFLLQILTKLTHCHDSKAPNDLSIYALIDTTAVLLKKKIKNQSNLKPFPGKIFLPKHLY

GLGRPSTLVTPGGGKEPEASDSLPVRPSRLSASLSPIKPIDFAAHFMKIQSPPGSSLKSS

FKKRKRSLLSIDDNENCEMNELNEDVGNIANSATNAIAIRGRRQSVLGQTRPKKRTFADS

SSDSEVEIEYQESGLAPLPRHSIASHVSITDPIVEEKEEVELHKVSKNR

>contig35390 Frame-2R|Blast-myb-like DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY56170.1|) 3e-24

MRTETSGRAKAAVQSDAGQTHL

>contig35534 Frame-1R

MKHKGTQSREKHSFSGVSVNLVLMVAMHRSLMMSFFKARTTSQSFSKRGVKSSIGLGGTA

NRVSKLHASLKIQRF

>contig35901 Frame-1R|Blast-nucleolar protein 6, putative [Phytophthora infestans T30-4](gb|EEY54789.1|) 2e-36

MVFTGKQSNEYGSISIDVTIEMPEKCFVPKDFGNYRYFDKRNLYLGVVALALESST

>contig36229 Frame-0F

MPKTDKEIRHAKRKAAMDRQERRIKKKLKKEDKEYELEFGTEFDVAAPVDSDEEAVINAE

ARMDSNDELTAEKKALIRSGMGAALDSTNSAEKIEVVAAGEEPDENALPIYDERKYDSDH

EEYDAEDRAKTLALASMMIHKSKAKDLIDASYNRYAWNDSEALPDWFVDDEEKHNRPQIP

IPKHVMAQMKERFMEMATKPVKKVAEARGRKNRLKMKKLKAAKKQATDIANLPDMSTREK

LKAIDRAMKGARLKKESKVYVVSTRGGAKTAGGKKAGKGKVKIVDPRMKSDKRNAELRAK

RGKKPLPSFMFKRLDLSGR

>contig37248 Frame-0R

MSCDPVKNQASERDNLAISKRS

>contig37554 Frame-2R

MVAETLTSQYRSLCNRHHTQESDFKLVILRSTDLVPQVMTSFGKSASIRHGSTTSQAVVQ

LRVGDLYWKQHGPYGWTLGQVTAFDLKQQCATFVLLNESTGERLDPLDEKAPLPTEHQLD

LRQVPLYAANPL

>contig37730 Frame-1R

MHAQISFGAKSRFSLKYRKTSYFPVNLTRMRSILHHRMQLSSNYKHYSNFSRISP

>contig38025 Frame-2R

MPQLDEVLIESASDVEYDVVWSEGPLGCELKQRNGLPAVKSVTGTGVTPSVAQIAAGDIL

VSINGLRTEEIGFKSTVTLMMRATKPVYLRFHRGGPRQSSSAGRSSNDLPPNYRGRVSNR

RTCQEKLDGGDGGSLESKQYTVLWREGPLGLQIRTSSKGFVVVARLTGAGAPNVHEVVKP

GDMFLRIAGVDVDSLGIAGAFEMLQTVQKPVVLVFQRRGRTSNRSNLRNRHHGLPAPAPV

PSSSAVPSFRQLREEEAAAAAAGIYRTHSAGHMPIQPRHPSHGGSLKQYGSGYDHLDNYT

ASDDGMSQQSFDYSGDSPRSSASRRNPGNLANVDGTFTENWLPDQPSAFPHDAINEAKDD

EDTFPSESRDESPSLAALVPPPSYMDVFTASGRAKDVDSMVPPSARSMDLQNLHDDEAGG

DEYFGGQLERPPPFEAHSDYGPLPPPIKHYEAPRPSAEETSSLLGQPSRLQELRRQYIES

ERQRNMLQNGSATMVSTYSDIDDSGLVVRHSSDGARHINKQPPQLPLPELWVRWSEGPLG

ITFKRKNGQIVVSRLTGSGYSPGLTQLRPGDWLVSFNNQSTSNLRLGDTMELLKRLPKPV

DMCFVVQ

>contig38050 Frame-2F|Blast-short/branched chain specific acyl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY64823.1|) 0.0

MLASKLILGRAAKASVAGAARWRSSITSARDSLPSPPIPLTVLTEEEKMFKDSVSRFAAG

VVQPQVRSMDEAGEMTPEVIKGLFDNGLMSVEIPMEYGGVGASFMSLILTIEELSRVDAS

VGLLCDLQNTVVSNVFQGFGTEEQRQEYLPRLSTNTVGSFCLTEPEAGSDAFSLKTTADI

SADASYYTLNGEKMWISNVAHADVFLVMATVDPSIGYKGITCFIVERGLPGLSYGPPENK

LGLNASSTCSVILEDVKIPREKVLGKVGQGYAIAIGKLNEGRIGIAAQQLGIAEGAYRHA

LPYLFERKQFGRVIGDFQAMQHQYADLAVDIESARLLVYNAARLKDAGHEFVKASCMAKL

HASRVAERTSSKCIELMGGIGFSKQLLAEKYYRDCKVGSIYGGTSNVQLSTIARLIKQEL

L

>contig38292 Frame-2F

MMNRVISSDTYAKWQKAVSLRSIEHYQSVLELKLLTEELPWYGLSSLTWKQLLNKPPGVK

LAKWHHGADFQRVINYNADLVKLARNYKSTTSIVKTFDEKLSMMPPDIRKYVEGVLALAE

QVIVRGIP

>contig38483 Frame-0R|Blast-tRNA pseudouridine synthase A, putative [Phytophthora infestans T30-4](gb|EEY65684.1|) 1e-21

MYPSTSCRYCLHVAYYGTGYIGWQRQQRGIRCIYDQGSVQEVIEAAVTEVSGSGQRVNVT

GVSRTDAGTHALY

>contig38700 Frame-2F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY53198.1|) 0.0

MWCVKQKSISPRNFKKSIGKFNEAFRGNDQQDAQELLAFLLSGLSEDLNRIHDKPYIEQP

DSDGRYDGDLADEWWRNHLRREVSIIVALFTGQYKSLLTCSVCGFKSARFEPFTFLQVPL

PEPKHNTVTVQVMLANGVTPMKVSVRLSISATIFDLKHELMKMCHEEFNLPEVSESDIKL

CEFSGCMILSFKADNRRIGQIRSIDRLVAFQLEPLGPEMYEATRHRRPSFVQAVGSGGIK

SDDDDHSNFYEKLAKGVLVDFRMRTQSQDYIPAVVLEPPAAHADYDDQSVVRVRLCRTED

EMKVPLNRLRPRQARLLYIPLLSRKLSYSAVYFKNPFRPVPFGSPNLLRLCPEMTSGLQL

YQQVWERVNKYVGPNATPPTEWQENESQNLDLLVTNNIDSVFAGLKDTSESISSKCGFLL

RRVENKGLTDSRSSWLTRSFGFTIPCTSERLDILEDEAIAIDWDLSVFQNREMMDKMKHV

ENHDSVARNEAIDKGPVPLKHCLDAFTSEEKISEGFCSSCKQHQEMTKKLEIWRLPPVMV

VHLKRFQYTQTYRRKLASLVEFPIHDLDLSCCVAPHDEIPEKYPMKKRRNSLGGVANPAR

KLFKLRSRGECTTSNVSTPPTITEEISPRVVMNKREENLSESANIIIEENPEGSKLPAEA

PEKASDVLLSTTKEHCSTVTDSEFAFTSPTESDIEAAAEAAAVRNRVRRGYTNSNLDQSR

CLETKYNLYGVVNHQGALGGGHYTAYAKNFVDDQWYYYDDERVRVVEDQQVVSPSAYLLF

YLRSDMDDVLVKDLFPKNLKPGKITDEDIERFVEDGDDHRCNIM

>contig39413 Frame-0R|Blast-RNA binding protein, putative [Phytophthora infestans T30-4](gb|EEY68406.1|) 1e-146

MTLEDTEKKLNMSLDQIVHERQAEATAAENKDFPVGKAKSTKRADRIAQSNPYQSKHGHH

DDDEEMDQKAPSSCRVYVGNLSWSVKWQDLKDHMEAAGSVEIATILEWNGRSKGCGVVTY

ATEEAAQNAIASLNDTELGGRKIFVREDRESQSVSAVKPKRGFRVYVGNLSWTVKWQELK

DHMKQVGTVVHADVLELSNGRSKGCGLVEYSTEEEAALAISELNNTELEGRLIFVREDRE

PEGGSISKFVKRASAPPRVNGDGRQLYVGNLPWDTNWQQLKDLFRTVGDVERADIAEYSD

GRSRGFGIIRFTNAADACQAIEQLNGLEVEGRMIEVRLDKME

>contig41982 Frame-2F|Blast-U11/U12 small nuclear ribonucleoprotein 35 kDa protein, putative [Phytophthora infestans T30-4](gb|EEY53620.1|) 3e-18

MKGWKPRRLGGGLGGKKESGQLRFGGRNQPFKPPPRQC

>contig42554 Frame-1F|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69238.1|) 1e-118

MDHHCPWVNNCVGLGNHKFFLLFIFYVFALSTYTLTLVFFRYAKCINESCPTYGAIRVVC

LIMEAVLFGLFTMCMMCDQYSVITTGTTQIDRLKGETTDNLGLHEVFGGLDCKFSLHWLL

PINIWFPASVKNQVLGYMLEHELLLSEDEASEVDAFLDNDTSLKIATTMTTETLEGGWSV

EKRIPTCEASDIV

>contig42730 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70334.1|) 7e-75

MDGCDKRAQSNGLCKGHGGGARCNFVGCSKSSQGGGFCRAHGGGKRCMHKGCEKGTQRNG

FCYLHGGVRSCSIDGCEKKDRGNGKCFFHGGGRKCQAPMCFHTIRRGTYCDLHNGKFPK

>contig42745 Frame-0F

MEKHQLLTLCRVKYLSLRVLRLASSSCVLAAGPVIQASNASPAAS

>contig42811 Frame-0F

MITKHNKHQRRHATRLNFLRIDGSTNQQDRFRKIAEFNDLEEDVDLIMISTKAGGEGINL

CAGNRIIMFDVCWNPCNDSQSMCRSYRFGQTKPVFVYRFVTMGTMEKKVYDLQIRKEGVA

KRIVDEKTTERKFMTSELQTYFSIEDFYKSLLHAQGKVANDGKRAVQAIPQEDDVLKSIL

EAMRERATPLYDLPSANGHTSAASRQADKGCIIDWFEQETMFEEDLDQQCTPAEQREILE

TNDYFKAVRGLRRKGVLHMNRQGLLMKYCEKCRASNEIYPTKLTNVPVPVSIECNYCKQT

MATAGAVPPSELPAASHLFMQRIPGIPVPAPGLIPSITFVPPGSAIPAKPFAPRSVGSTP

TAARNGGRNLPSHLQTLQDQEKLTYKERFDMLMRRKAEQQQ

>contig43351 Frame-2F

MSILLPILKVQRIRHSAEASAIGASRCTWLAQVLERDSVSLTFIGNVEDNQACR

>contig44299 Frame-2F

MANMHKTTTTSSSSSCVPIMAGFVRVEEDGKKQCKRSLSASSPYSVATLEGRASSKSKVF

SRWLYGTLRGDTLLLYWRRIDYKRKMPPLDSLTLHMQPAKPNESVFGFDQECLYVRVKDS

GRVVALRIHKRKEIVRWVTALYYQSIGNERVEENEESNTNWHRTLSIGAPERDPRKKSVS

FLDEPSVWVLPEEAYDPADLFYSTDDYEKFLMERPSSLCSLISVVYSKTAAKLRVSRKR

>contig45061 Frame-0F

MPAVDEPSRSSHRPPMDPPTRSRSAAGRSHLTAAPQHQVQATGTGSLRAS

>contig46200 Frame-2F

MLREPPHGVFDPLSFSRSQYESQSNSSSLLGCVQ

>contig46550 Frame-0F

MYQHVLQETKLEFDLLYGAFAWHTLFSDTALLDEVLGRKYRNTNSICGQCHTDREMMYIH

TGGTSGNATMVSRYLCNS

>contig47690 Frame-0R

MDAVDQTMTEPDPAPSAVDQTNFDSSQSI

>contig48093 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56915.1|) 1e-171

MDEQYLSNLNELDANALAIRVAQLATEMKHRSKWEAVRLLESLRRMEEDVQKKSAHVLRR

QDELHKELLARELRLQQEVLSRQSRDEMDALKKQYADDLARNVSQQRASLLSEVQRTFAR

ESKAIEDRYDERLKEVTEKMQKVLTEERAKRVQELQQYRAELRALGMVLDSSSTYEAFSH

RVHKTSMAALALSDRVEAAAPLQSEVRALRKAAKSDPFIETAVNSLSQEAIEIGAPSVGQ

LQERFKAVKSVGHRTALIPENSGIVGQAFGTALSLLMIPPGGPIEGNDVDAVFSRADFAV

QAGNLEKAVDEMKALSGIPAQISQDWITAAESRLAVEQTAKVIKAHVALLAASCS

>contig48282 Frame-1R

MWTVLVENSLFGGNNAENSAPTSHERQGLALKLFELVAPKLPESTLYSILTPRLVRCLYH

NSVAKRNYLHEAAHHCLKSFATTA

>contig48758 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70505.1|) 5e-41 NOT\_ORF

MARQQRKKARVHGVAARSKSSVSHLNDPVQVDALGAAAVAATFGDDAASTVDKEAENEPN

ALQNYSRGQRKRLKRRAAFMRKMGIVSRVAQDQQQHAKAAEDGVFAGLSELESSLLQATD

RKKTKLVKKKPLSGRQRQKLAVRELV\*LKAVQTH

>contig48923-1 Frame-1R1

MAPDPCRNARDRLEHHQQQQQQHRSNLVYDHRLIPSSKHPLNDPEEELGLSPS

>contig49124 Frame-0R

MYMANLLRRAASAAPRCLSSQPQAIIRRRYLQSDRFFSQVSFTFIDGEGERKTVKAEEGQ

TLLDVAQENDLDLEGACGGELACSTCHLVFEKRFFDKLPTISEEEEDMLDLAWGLTDT

>contig49854 Frame-2R

MLAPLVAEIKRVMIERVQTAEALDGVAFPCQVYRNPRLHKLFQIVYQLCKVRGYKTVVKL

LPHEVSDFEPTVQLLQSQDRSDYSTWEMRYVLLLWLSMLCLVPFHLTTIDSSFTSDNTTG

TILLVSNIITLCKGYLCDPGATQVAAAVCLSRLLSRP

>contig50001 Frame-0R

MNDPELLRQGMEAMRNPAAMRELMRSQDTALRNIESHPEGFNALRRMYHDVQEPLMDAAA

SGTPAPRGPAFTMPGVAGGNSTASTTPSQPASVTNPVGSINPWATPAASTNTAANPWSAA

GMNSLGDMGGLGNLGGNPEMMAQMMQSPLFQAALSQVSSNPTQFISQMEAMNPQMAAVMN

ANPQMRQMMSNPEFLRQAMNPNNLQAMMQMQNAMNQLRSSGLMPGLDTMNSGAVAGGADT

TRASNPSTMNPFAMFGDFNGAGFNTAANTSVSNPAEVYASQLTQLSDMGFTNQEQNIRAL

QATMGNVQAAVDRLLSGTI

>contig50395 Frame-2R|Blast-charged multivesicular body protein 1b-2 [Phytophthora infestans T30-4](gb|EEY68594.1|) 5e-80

MMNIFSRKNKLEDELFNMKFTAKMLMRNFKKCEKNQVAQKAKLKKAIEQGNMEGAKIYAQ

NAIREKNQALSYLQLSSRMDAVAARVQTAISMGHLKANMSGVVNGMDMVMESMNVENISQ

TMDQFEKHFEDMDVRSAYMEGAMSSNTSLSTPADQVDDLIQMVADENG

>contig51091 Frame-0R

MVQVGLPVAVVEHKMRMDGVDVSWLQGPPTRPKVIVITEDDRVAHRQKYHKYFQMLRMGL

PRGAVEQKMRMAGIDPMELHGPCLARTISSNAPPKALKRKNSIRKKLHWEGKKHRT

>contig51327 Frame-0R

MVNSEAEDDYGDGSDIDRSSNGVISDQEARNVEVLDEVVVESNDGVIIGDNQLDRFDRSM

SYDQMLDTKRVQLGVAPTP

>contig51392 Frame-1F

MLLYRTHISRHRSECISYHSKRDIGANKWEAAASNRPLLKLVGFAQYNCPIQGLVPSLLA

PRQTNIMTSFCCAS

>contig51518 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65649.1|) 3e-21

MNAILTTPRSLPSQVLLRTEVEALCSRLSSSAAYSRILREMEDSMRGTHLLFIYNAESL

>contig51675 Frame-0R

MINHGDTGAHIQAQDFSAILRMISCK

>contig52313 Frame-0F

MLQLEYDHRESTPKSVAKELSALHSWRPLKESTCLGLIHDSFLDIKAFSTSADFVSTGLK

LCGWQEWRKLVGKNVNFMFHKSFATDCSEELATRSWAMRAVQDQVSRYFGQSLEVQVEVL

QRLKNDVV

>contig52388 Frame-2F

MMKSIRKILGGGDIGVQRQVREARNQASNEKAKRMHWTLLNMVRSMICASRLSLSFWLSM

HIYFQSQPDKRNQIRALPMEVLTKRASRMNSLAKRSQVDVIIGRGSQTVIS

>contig52443 Frame-0F

MYRQVAAIGRLDLLLERRRLSNLVQIRRTEWVADHARKACAVCAKLFSLRRRKHHCRNCG

EVVCGSCAPNREIDSDADAIINVRICTACVVQSRKGSHAQKSRAVEVMSFTDTFSLPDAS

YSTPSTMICRTAINNKTELITRQKALSSGSSTFSISNDSPGSVQLSEASRL

>contig53026 Frame-1F

MINLRVRCVDDGCELLVERHGANEHSIQVAELKEIVLQQRRQLSDCKRVITPTNTQPLNL

EDCFVLFRGQI

>contig53642 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65536.1|) 4e-56

MLKLPGNGMGVHPLIYGAQRVFVHDHCAIASPLCFNRDGKWYNVTREIRRGRSLVCVACS

RRGATIGCTVSACPASYHWKCAINLGWSVDQLHFYCPDHQGRRTQRLW

>contig54342 Frame-1R

MSVPPFHGADEGMLFHDDFQHLTSFEWEALRRHTDIASITKSVDAMRKDTPERLQRIAIL

HQPQTRRFASASFNSAVATR

>contig54526-2 Frame-2F2

MRHCRRVNLVVQAQDWKDLRSKRAGFKSVEQLQIISKTAADYF

>contig54812 Frame-1R|Blast-MMS19 nucleotide excision repair protein [Phytophthora infestans T30-4](gb|EEY67788.1|) 6e-69

MFRLDAPLAPAIEAFVHPGNDDSVQKTGLNAVVMQIHRQVTIEALIEALGTHLTSSDNKV

RSRATLLLAEVLTRLPEMHLSLSSVELLLDFFADRLADFSSGSACLRALLALETHHAAQI

QSPLKTVVIILKIGSTLHIPQLGQAMRKMCFDLMHLALGQPPVIDLLLDLAPASQDVQ

>contig56111 Frame-0F

MHIIFHRNNFQVFLRTITKAFSRPLQKMLFGILKSI

>contig57040 Frame-1F|Blast-hypothetical protein PITG\_08805 [Phytophthora infestans T30-4](gb|EEY56044.1|) 2e-26

MKKGQFQLSLERQQKKETLRFQMTSDERVATVVGGSNVHIRTLQSAKIEPMNKLDVLLLT

VKAYDSTEVIRELYKNNRHVLKNDALCVLLQNGPGEVPEIGDEDSKRVDTQKWHFANGVT

YVGGRVVEFGTVLTSGLEGGMTYLAPFQNFKIKASNDFYENRRFQNKCNASIEKLAQLFI

AAGLRCKILERNEMKGMLWRKLIINAAINPLASILNASNSVMT

>contig57264 Frame-1R

MITSWRTKVKSSESLSHCHEAGSCL

>contig57358 Frame-1F|Blast-26S protease regulatory subunit 6A-A [Phytophthora infestans T30-4](gb|EEY61489.1|) 5e-08

MTSLLSRGDVQVCVEAGMLALRRESNVIKHEDFMEGIAVVSA

>contig03602 Frame-2F|Blast-sulfatase-like protein [Phytophthora infestans T30-4](gb|EEY70229.1|) 1e-115 NOT\_ORF

MFKGDARAERIERYMKVRYFTDLELGKFMDRMEQEGIFNDTIVILAGDHGQAPEVQVVNS

HEESVTRVPLAIIAEGRLGDAVGKVFDDVAVHYDLLNTIADITGLPKDGFVQDGVGRSLK

RKIPSGQRVVYANDPTRKMAVMRGHQRLHYDAVADAMFLHDTELDYFMSLNLLPLLSDKE

REDWVNMREDGRQITAYYKKRWDENCLLAVTCKD

>contig04687 Frame-1F

MTGFVNKTHYQIDEHVDSNEDFADAHRLNDEKAEKQEHQDMRLSAAYRSSEESIEPNSEL

MEHQSKNASSTSPLSKNLIELEAQEQEHRFSSRLSKEYKNRPSTPPRRQSIESLEHSKAN

RSGFNTPPRRLSGSKVSQPHGQSEKVGNFDSSRALSPQPHRQSGEQVSSSPRRQSEEYVD

SEYKRRLSASLNRKSEEFIEFEYNSEPARSPPRQSEDFVDHDKDKELAALPRRQSEESYE

SEYERVSIASPPRQSEKSVEYENETELTALHDCQSEDSVESEYERELATSLHRKSEESVE

YEYKRGISSSPRQSEEYADYEYERERSSMPYRQSEDSAESEYERGFTSLPRRPSEDSVEY

EYERKLNALPSRFSEESVESSYEEELSDMPQRPSKDSVKYEYNRESGALPNRLSEESVES

EYEEGELLLMLHGQSEGFVKHEYENEPVDTIHGFSKESADEHNVKHSNAETTPSSELSKD

VSRTKSPDEQEDFLARRAHDNLTSENHKVVGAVSEGLGHENDRASILSSESEPEDVEALY

RSSEDQTATSALKFHFSNSQLAPGEGGGAVDEFLAESYNTVSRSKFLAQVDEHEEYTRSP

RDPSSFPPAVTDDHGTTRMSTSSDRIDGMTSSSRMSNVSVLDEELLNRPTIELFDLIRAN

RIKPSTDEMESSDMMHDLETSHLRRMEELNRIAVDQLGNRISSLNEDMLGSALKPVRVRQ

PDCHSARDDMQWCSSSLMEEVQTKHEVDMDKLHRRIRELEAECRESFASVLTREEMNLSE

FDSDDDGKLCGLQSQSSRPSFNPHSSYMCASDLSASTISEHMSDDESEVPPLPAHTLLQQ

ITRLRHLQQKMNQVEDKDTKEYRERLKEQYRELRSIQANGARHERVSLGIEMPSEENWV

>contig07440 Frame-2R

MTCCHPGCHVRFDSTGKRQHHCRNCGGSVCSDHSPRFALLPHLQTDHAVRLCMGCFRVQR

FVLWLVMLLQRLNIVQTEEGRIAKPVLSKADEEELEALFVISGDDDYGISDVIQVLHLHR

HGCDEAYAYAVSKLLELSASNLADFEFFLPQIFHMWLTMDWTNNNVKAALLIRVICYATQ

LHIRLATAIYWLIRAAIDDSCGWGFGQSELYVPEFLYWKMSMCKLLMINLEMQIYQDDWT

FKTDKDLPASIEQSAIVNCLFERLVVIVHNTTKVGAPLGVVCNAVDNSSIPSEFLISSNA

LFHDIFRHNMVERQIFTNQIQFIGELCELTERLRLSAPHERKMTFKGELQKLKLYDGAFC

PLGSCGDTLQQFLAISKDEGTVFTTRARAPALIFFEVAKLITEYEINPWLHGYRSRTFSN

RSNNVNDLKKSNNVNVRAPFVASKMARNAIEMATSSDIAQVIAQDTFSGDEDEQDNADPI

ENSNRPDNLGDDELSAYCEDDSENEEQRDCVFSGPSPSLVALTRASACKKKLSRRGRSGS

LISSTSKSLDFLIASCADTINIRRKRSNSEGSGFGDQENSQNFNFGLTLSGIENFSDDQL

ISMAQSMEISMLEMHSCGSGIFTGKQIVEWMTNNEIVSDKAHALWLGSELLRCGALIKTS

SYQIVDGFKATDETYQLRGNLSIMFRSTDCPTISKKSFQSAKESDLNFTDRESSLTCTLS

HLRLKAQSLKVNNANLADAVDSSLATNIALRSFAKDPILLQDYAAGSSDERRSVVSNIQH

DSLILKFEPELAITAMNSVEQAMQQYVLPLEGVPNIAQLSADLHVLKEQINIAYEYVIDK

RRRLHVAVESAFGESFEEKKERLRNKSLFTAEKEAKNWDCVAFIVKSNDDLRQEVLCQQI

IRQLQDIFQSSDLPLRLLPYEIIATSASTGLIELVKNAVSLDSLKKKDNYTTLAAHFVKT

YGQVDSIPYKSAMTNFVRSTAAYSLACYFLQIKDRHNGNIMIDSDGHVVHIDFGFILGIA

PGGRFSLETAPFKLTGEMVDAMGGTQSDYFKAFVIFLIQGFLALQ

>contig15115 Frame-0R

MAFPTEFKWTNALLDDFYHHLCDGDGALSCDNRTFAEINLLFARGISIRSMHRHAQPRAP

RALCQILNQSTSARCVRE

>contig15304 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67334.1|) 4e-96

MGARKHMEDAHTIIQDLCIEPLSRLGLHPQSFFAVYDGHGGNEASSFLSDVLHHSLITAF

FMHTSELKPLLTMTIEELQSIIMKRLTNAFERTDEEFLRTSDRPQAGSTATTVFVAGKYL

FVANVGDSRTVLSRNGTAERLSNDHKPSRTDEAQRIRETGGFVIHGRIMGELAVSRAFGD

APFKSFDLVEPLVDDIDTKARNEYNSQELPVNPNDILKGPLVIPTPEFTVTELTDECEFV

MLASDGLYDVLKDQEAVDFVRRKLVELKDVQRAVEALIEYAIFHQRSTDNVTCVVVMFKE

AKEIVWQSSS

>contig16406 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65974.1|) 8e-27

MEVVASEEYQSLLKRFEDAEAISRGLKFQLEKEQHEKKYLRKELTALQETVGVKTAAETA

ASVGFLPDMPLVEPRGGVSNQEDTEAAIGS

>contig20780 Frame-2F|Blast-phosphate carrier protein, putative [Phytophthora infestans T30-4]gb|EEY69488.1| Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY66591.1|) 0.0

MSSFFPSIAALNPAIPSVNAAKVRPNSILATSAAKWDARLSHDPIHDNAYYGKCMIGGIL

SCGLTHTGITPLDVVKCNMQVNSAKYNGLMPGLKTIASEEGSGALFKGWAPTAIGYSAQG

MCKFGFYEFFKDLYSSMAGEENAYKYRGAIYLAGSASAEFFADMALCPMEMVKVKVQTSP

AGTFPTEFGAAVSAMKANSAETRFPFGSLVPLWSRQIPYTMAKFFFFEKVVEAFYTYVFT

EPKSSYPKSTQLGVTFASGYLAGVICAIVSHPADSVVSLMGKSENKGKGFGQIASETGLF

NLATKGLGTRIIMIGTLTGAQWWIYDTFKTVMGMGTSGGAAPKKH

>contig23468 Frame-2R

MYVVALGISRLDSNAWKATIATRNETSIGLQARVEYCREMHDVTYICHSDRVFQVCEPLT

AVVRLSRVGSRVFVSIVLTCNPFESIELKDYNILLEPNAILTIHNDRNGSLRGSKVQVQD

CVAFAFTLASTPTTKDDVQLNVTCSFVLSFYYTNDLNCLKTMQVAVPIHEIQGTGYQIKV

QQLVQHENQDEKSGIRVSDVLVYQVDVCEEESLWPQDHRDNVSTIELYLDTSSEVDWILL

GKQHEGFTLDFGGHFCTQKRLVPTRSGSLRFPAFRLEKNGQAIASSRVYCPQKTRRVLVQ

DN

>contig24331 Frame-1F

MFASNFMSIVLKKNNTMFKSGVAYARNRLTEIQDEAKVARLQLKELHVSFDHVQKKIKRQ

HQRVENLEQRQMTGRDFVERIVCFFTCSAADQLHRVSW

>contig25620 Frame-1F

MTVYEKLQALVLAENNKLDKPTVGSGSPKEEGQVPDDDEDEGEDDSYEISWDGGSLGLLF

KANANGQPVIRRVNKKGAATGLQYARAGDVLLALNGVSVSATPFSEVIEALKNPEFPVKL

DFRPLKLSDLASAASSATTKWGLSRPNSSI

>contig27176 Frame-1F|Blast-26S protease regulatory subunit S10B [Phytophthora infestans T30-4](gb|EEY57667.1|) 0.0

MATEDERMQVLAAYKAKVMEHREMESRVKSMRENVKALVNDYNKTEDDLKALQSVGQIIG

EVLRQLDEDRFIVKASSGPRYVVGCRAKVDKTKLKSGTRVALDMTTLTIMRYLPREVDPT

VYHMLKEDAGNVSFSSIGGLNEQIRELREVIELPLTNPELFFRVGIKPPKGVLLYGPPGT

GKTLLARALACNINATFLKVVASAIVDKYIGESARVIREMFGYARDHQPCVIFMDEIDAI

GGSRYSEGTSADREIQRTLMELLNQLDGFDALGQVKMVMATNRPDILDPALLRPGRLDRK

IEIPLPNEASRMDILKIHSGPITKKGEIDYESIVKLTDGFNGADMRNVCTEAGMFAIRAD

REYVVEEDFMKAARKLSETKKLESKMDYSKV

>contig27886 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70312.1|) 3e-18

MACKRVAIGGTFACDDTLAVPLLHLINHAVWNVDVDVQWLRYGSLTDFNEWSTAVLYPAR

PVDLVLLLIRLSDLEVMHPELQNRFVKGDTYDRANVQADGGTEQLMRYLGRYDSIPSAVP

LVVHLCPCPPTSASRFKALECMVRLKAQALKRVSVQTSGHVLSLFKQQYSTEYYDAVSDK

RQHSPYTQAMLNVLSLLLCRQICQLFRAA

>contig31737-0 Frame-1F0

MDREIVSITDSVPSALCRITPPPRFVIMHASVRLHLLQ

>contig31737-1 Frame-0R1

MTNRGGGVIRQRADGTESVIETISRSIPMPFSSVVSLEGTLICRHDY

>contig34495 Frame-1R|Blast-Folate-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4](gb|EEY63901.1|) 0.0

MAPNSSGQNVHDLQRLSVLSLANDSFTKDANVSYNHSKTPGEAQELYEGGAIRPGGMPNL

LSRDHIGLIFQYAAVGVVYGMLPGTIYPLMQQYLNGSGAQVAAAKELVVLPWSFKVFYGI

TSDCFPIFGYRRRPYMLIGWAICIAMLLSMALMPIGSPYYTVASDRNVDVADYTPEMEAR

MNYNAPSQGAKYVILMFFAAFGYVLSDVCSDSIVCELAQQEPIAKRGKTQSTIYTVRTTL

VILGELLVGFCFNGEEYGGSFDFSLSFPQLMMVMVVLTTPAVPLTWFFIREDKVKRLDFG

KYIHELWEMLCKRVVYQVIAHHFFAGIFMSISYTASSPIQSYLVGVSPINNTINDVLGHL

CFMTGIMVTSKYGLQWNWRVMIVVTGIVVIVVDCSVALITIWDIFRNQWFWLGPPIAVMI

PSGVAWIIAMFVTVEIAGIGNEGAVYGLMTTVGNLAAPFGMTITLLINGPFDITNARVQG

DDYSIRMDITYTIIISYVMTILSWGFLVLLPPQKKETQELARTGGSSKVFGG

>contig35391 Frame-2F

MASTKRQRIDLLIERGNLLANQETSSEPPDSPQSCATAPLYSPRRSSWTSQEDDKLRKLV

HQLGPSKWSEIAKQFPLRDRKRCRERYVNHLAPSLLPVLSAWSFEDDERLLQLQRTIGFK

WAKIAEKMDGKSAASVKNRSLLLARRESDKQYTVRKALPQRWLKTENEKLRHLVATHGAK

NWLFIASQLPRRTDVQCIQQWYRIVDDKVVKGKGMWTPSEDRLLIEKVIEHGRKWT

>contig36228 Frame-1R|Blast-rRNA methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58054.1|) 0.0

MVKRKKHDKDKYYNLAKQQGYRARSAFKLIQLNKKYDFLSTAKVCIDLCAAPGGWCQVAA

KYMPASSIILGIDLLPIRPIRGVKTFQCDITSARCRQIIKQEMQSWQADVVLCDGAPNVG

AEYSKDAYVQNELALIALKLAVDVMGRGGTFVSKVFRSQDYNALLWVFKQLFKKVSATKP

LSSRNESAEIFVVCEQFLAPHSIDPKLFDPKYVFDQVDTQEKSITIFHPKFGDRKRHREG

YDEGLGVTLTNECSVSQFIDAHDPIRLLTDTTSVKFLPEDDVYRDHVNTSDEIVTCLSDL

KVLGKGDFKSLLKWRSRMVKYKEELLKAEKVEEVNDEENLFSKSLSVK

>contig36350 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66653.1|) 4e-45

MAQLQSARNDQEYTALSELFKEFMNDIYFHFQDAFEEETEFTGKEIVMAIRKILKQNTMA

ILAKLEEFYEQQALQRQGR

>contig38226 Frame-0F

MQRCHNFETEELLTARRADGSAAKLLVRFKETPRKWKEEIVDLLRTKELQAVLKYVLLSG

GETGREMLKPFNMAQVSTRVFWSIAHMYNGDVAAGLAYLVPEVDWAFIDTRTRTMSEKAM

EAKANEEEYKSWKQRKHGKTNGDPTLLADVESPPETKLAISDVTSADMNEEIDVGRESSS

PKREESVSTPALSATRATPSSLRSAAANAALIRLDRSAQTKAVISAFLKDNKLTQKSVPN

EGDTDEVSEDEIEDATTVYCDACKKARILSSEEAENADLDKDPWTCINLRKAGRSGGCGS

TDDEVAQITGAAAAKWLQTAGITTRRELADASVNATVHFLLNPLDPSVRMVQERLNKLID

EARLDEVNDWMADIISEADILQRLELQKLGTPADLIATPTDLILAAVGFRSDISIELVRT

WQNCAKSLVSKHSWLTEWRTL

>contig38419 Frame-0R|Blast-tyrosine phosphatase, putative [Phytophthora infestans T30-4](gb|EEY53181.1|) 3e-39

MRKMENWSLTSIIDEYCRFAGPRMRLLDQQFIEYFTPTIQYDERQKPKWLSTKV

>contig38482 Frame-0F|Blast-tRNA pseudouridine synthase A, putative [Phytophthora infestans T30-4](gb|EEY65684.1|) 1e-94

MTLIEFKDRVNAKLDTDRVVVLGVTVPTTSPSRIRSRCKKYIYYLQQGHRPDLKLGKYSW

FLGRRIDIEQIRQALKFIEGTHDFRPFSKGLSKPMYENISTTRTIISTKVVVRRNVDFSL

NPKICGSGKILDSTNSYNDLRSAADSKVASADAHNEQMMERGEGGTAVHFICIEIVANGF

LRHMVRRIIGTLRPIGEGNQQPVQMQRVLDGSVQPGPSAPTKGLWLHRTWLTQDEYDVDC

AGNLKTAT

>contig38701 Frame-0F

MKRSQSYGVLVIEGILALIAWLAMVRGGLSMHVHDLMGGILLISSAGACYLSVCHILLSL

PGAKYVGELLLDRSNPCSWPREKRRLFLEVCMWMASVLSLYTASHSGWIAIGAGAIAAAV

LACISDFLAAFLHLLETKLDFQQTRGIGGMLWLKVALSYGSVGYIVSDTGQKLHDFVFGL

EATQQQVQSVDQLVFNYLLISLVGASLVIASELLLLCAPTRRAGIILQNRIVEARKNWEQ

HLLRSLIEVSGTCGATILYYSTTKDMLLSLQVGTCCGVLLILSSELDASVGRSRFIRLSS

PHAAVEMPADHWVKLIPVAVMMLYFMYQIFAAIVRGGNVLLIYLAAMMCFIAVAAISLTG

LALSGKKTSLVDMACIERRLAARICVGLITIIAPKVSGGLSGVVFSCVLSLFCIAFSRDC

WDNIESSEEATVANVIPLCPVQPVLSTISAASKANASLSDVTQSWPVRALSFVKERHSAF

YKRIKWAFVGTIIVSALDICSTLFAVICQDKVSLSLSQYSAINVGISASVGYLTSPAPYE

LHPAELLKIGLKQFKNKWVLFPLHMFVETLVFIGVFLGTCAASSTVFSSITLATLSGIVV

SIGGHWICSRLHLTIATQMRMQLTATCALLFCVLMIAYASMVSLLSIYQYFDSIEAAFCL

ASLAGIVFLAASELFLLWEPTREVGLLLQRRVTNASENWQLEPLRSFLELFTWFAIICGS

FAMYNDLVLALQLGTFCGIAVTLSGEYFRKNRFKLIPWGKCFLADDEVIAAPTSSIESAT

GSAVARNRARPLPVMLFFAYIGSGTFHWIFENMRSLEVTVLLATIAGISFLCFADMLVIF

KPTRWAGVILQDRFINVKQNWHEYPVRSFVEIGCFLGVIYGSYAIYHDLVVAVQVGTLSG

MLVTLGGEQLRICARASPLNEEKDEVEKTQILPLPVMSLLGLFGAVAFNMIYTHLRSIEV

AFVFATTSGVIFALVGDMFVIWKPTRKVGMILQERVLFARSNFATHTSRSWLEVASLCSG

WYMSYEFLWPRDLLIAIQFGTTTGIVMCVCGELTIEYVAETERRLLASVSARLRQDPQKG

SLFLKLPYEVKVEVAHFLSAEDLLVARATCHKINNLLKAE

>contig39342 Frame-1R

MGKGATLLLAPSRRHCCCLVSYSGLCKNIFKYEYTCQPSFKFRMELRFRGKKSAKDSSIG

FWLCEGRKKRHVIVEKSQSLASVAPQWELSHILENKNMHFMNESAGTVVPYDTAIGEFIS

ERDVVRLCSRKELDALQEKFATRDQEVAAEMMYPKAATPISAAL

>contig39412 Frame-1F|Blast-V-type proton ATPase subunit H, putative [Phytophthora infestans T30-4](gb|EEY58149.1|) 0.0

MSGNGSLDVALAREEALHRFRDINWATYTRAGGFSLEKTEIAALKDLESVIQPTFDGTMN

TKVVDEFLSVSGSLVGSALLKLVKNVTELTVLRYCLARMEELLPDGLRLHKRMVYFVSEG

STVDAAPFLRMIRNDTGYSQYAASHVLALFLTIRPCQEDAEALCQWAIQALKTGALPSST

SDASRSNVTRAAVASLMVLLRNEKLRVVFVKLGGVPAYGT

>contig41495 Frame-1F|Blast-methionine aminopeptidase, putative [Phytophthora infestans T30-4](gb|EEY60896.1|) 1e-118

MRRSFHRLANRQPVVASRQTPSRTVPQCITRPPYAANGSMSDMKPFIPILDSKEQQRLRA

ACALARAIREFAEPLCQPGVTTEDIDRLVHEEIVRHGAYPSPLNYGGFPKALCASVNEIV

VHGIPDCRPLEDGDIVNIDISVFLEGFHGDTSKTFLVGDVDEAGRHLVNVTDQALLGAIK

HCCLPLKRFASIGDFIQDLAEQEGLGVVREYTGHGIGKEFHCLPFILHHRNNEPGKMLPG

MAFTVEPVLTEGNSQVGPKIV

>contig41936 Frame-1F|Blast-G protein beta subunit 1 [Phytophthora sojae](gb|ACH68456.1|) 0.0

MVDAAELKKKCESLKETIEKTRDAKSNGGFHSINASASAKAIPAAPQCRRLLKGHFGKIY

AMQWGGVCSSLVSASQDGKLIVWNAQTTSKIRAIPLRSSWVMTCAFEQKHSNMVACGGLD

NLCSIFHLSRAPVMRATKELAAHDGYLSCCRFIDETSIVTSSGDSNCVLWDVESGEVKTT

FREHSSDVMSVSINPHNPSMFLSGSCDTTAKVWDIRTGKTTHTFHGHESDINSVDFFPSG

NALGTGSDDSSCRLFDLRAYGELNNFSNDKILCGITSVSFSKSGRFVFAGYDDYNCYCWD

VLSTTGAHVYQLEGHESRVSCLGVDPAGQALCTGSWDTLLKIWA

>contig41983 Frame-1F

MVLEKFEERLKSGLQMPVGVTHLQFTGHQRLVVGYTDSSLCAFDLASSAILCCIPNAWTT

SVITSLETPRYPPP

>contig42249 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53801.1|) 6e-07

MAGNEFGRSPFDAISLSPADQNELRTLVKTILDANFTRYGQFAGVDPRAWKLSRGKDGMQ

IYSSRNEPCQALPTNE

>contig42731 Frame-2R|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY54394.1|) 1e-139

MSAGATSRAIRDGSALNKVLYLLLSSVDIFGPVIFAQAAIVVSDIINNDPSSINHVHASG

LAEAFLKTLTRWDIAELYPARMLLPPSSELLTAVPTVLNSLCLTTAHAEKVFKFEPLMHL

LDIFALPQFTEDDCKDYCFHSDTAAVVGTGIFELMRHVPSFQNAAIQAVIHALKKIIRFG

EESYSSTIPTLSQSVGDKVDGILVRMTTHVADLLEPLLTKPEYAAYFADLGGIQLLLALY

QIMLPSTSSFLKSALP

>contig42744 Frame-0F

MKYQITDNGNNARPAQALNGR

>contig44298 Frame-1F|Blast-CRN domain-containing protein-containing protein [Phytophthora infestans T30-4](gb|EEY64621.1|) 3e-12

MIRRVWFYLADEAGNRAWSVDRVNLSDDAKVFQLQDAVKEKYSDSCLAGVAVCELRVYAN

SAAFARGQKLPTPSSPLSALGIDDDNPLVVQVSDTND

>contig45060 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55202.1|) 9e-08

MADSTFLDDIVGFLHNDDDLNASGGDMLPSLDKEDSVLSTSDAQIPLQ

>contig46119 Frame-2F|Blast-histidinol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY62863.1|) 0.0

MALLKQITPADVASFAYDPVDVSALKDAKLIVHDVRTKGEQALKHHAMRLGDIPSENTPL

LLCLSDLANAYNMLPLKEQQVLKRTMHRIQVFAQAQRNSITNFQQRIEGGFAGQDVAPMA

VAGCYAPGGRYPLPSSVLMTAVTARVAGVKTVVVASPRPAPATLAAAYLAGVDYFLSAGG

AQAIAAMAYGIGGIPSCDIIVGPGNKWVTAAKSLVYGKCAIDMLAGPSECLVIADESADA

TIIAADLLAQAEHDPAAIPILVTPSVNLIETVNQQLVLQLETLSTNAIATKSLQNGFAVV

CPDMATCVSVSDTVAPEHLEIMTKNAQEVATQVSNYGGLFINSRAAEVFGDYGAGPNHVL

PTGGTAKYTGGLSVHTFLRIRTWMRIDDAVASQSLVRDSALLARIEGLEGHARAAEKRL

>contig46201 Frame-0F

MVATGVFVLAAKGVVVTIRNSTVFVLPSSDLATQTLLQSEVLQEKDGEAKAAENDDDVKT

KATQRKPPANRITAAELLCPQGSAILALLLIVDERRLVHYELNLKTKSLVLKASRSVPRS

ATCMTVGHVKLSNKEIKYVIIVGQKTGEAVAMPFPDISRDLKTLLGHTTSMITDIAVNYH

SSLLLTADRDEKLRVSRFPNAAIIESYCLGHAASVTKIACSIVTPELVVSTSMDNTLKLW

QMSTGTLLASEVLLFNVEVSLEPLDFNADNDNTGRLAAKSLINVSLAICPKTNIVAVLVN

YEFLRLFSIVVANEVSTLSELEISSEDVKTLLAGEPCELLFTENEMLAVSYKKNPFLQLF

TISASDKNCKLSPVHVAPTAFDEFRNVASNIGLVVYD

>contig46274 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53256.1|) 7e-18

MCLFHGGGYRCTMEGYNTGARGTSGLCAKHGG

>contig46490-0 Frame-1F0

MSEALMKPSTIILNNIKRENRRRNSQSYKSGKG

>contig46490-1 Frame-0R1

MIVDGFMRASDILQFSEAAATASVSSASCLDWGNAKAPMPAA

>contig46524 Frame-2R

MLVSYSHHHEGAIVYKALSRAAPNTLFMGGTSSGGVFESAIPSAPGSELSGESKQHSDKR

SNNATVGLWGIYDPEGSYAILNADLDRESPREAARRCLLDGMVMLAIEPEESPDFVWTVV

GGRDSTSDVNGEEEQIMRAVNEIVDCSYSVVGGSSSRHAASRRGFATQLCSEGGDVGCVT

KHGACFAICCPSVEVSQALFTCYDATASTFSVTKAIGRDLFALDDKPALETLNEATHGLL

TEMTQRPEKFNLESSLLPAFYPLARERRSAVPRGLKRNSSRYQMLQPEASVSDLSLHLGA

EVRLGERLRMMTLSPQSVSSRVRRGLRDAIRVSIPTMNNQDVIGCFLSIGISYDRILQGD

LDEVADATGRAFPRGALLLSVSHGQLGVMTGGNEAIYANSMLTALIITNRKKAQKFNP

>contig46726 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56954.1|) 2e-18

MQPEELGKLGFHEEGMKKTWTDQTNEGRKESEGFVAGMGIKKSRYDK

>contig48009 Frame-2F

MLYLAIQVRWTDCLEYKMKLIKYKQLQ

>contig48236 Frame-1F|Blast-RCC1 and BTB domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY57867.1|) 1e-15

MDVACGNEQTVFLFDSGDVYACGYND

>contig48759 Frame-2R|Blast-sphingosine kinase, putative [Phytophthora infestans T30-4](gb|EEY53016.1|) 2e-57

MDKYLAKHWPHSSVSVSCRVYASKRRADEYKRLRLTAEGIQLSTVGPSSATDVIPWLSIL

GASESTRSIRHRFLSVYEGSEIDEEKEFIVYGCVFKPESAGYGGLLGALHLLAKTVLPAV

FSASKPGNERMLVQWVFRCNDEDGDAVARRTVKAIRFL

>contig49125 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56475.1|) 2e-24

MTRLQHTATLTVVCVAFAFLFFAICVPAYQLQGPSKASPISLRTHTSVGSITAGCVLCRD

SGNCSVAMNDLSSGVFCGDLHAPAETQPCCCPYFTECLVNGMTSSCKCAGPSFQERVSET

KSADDTEPLRRKHVTLKMDDPMENQMSISTEILLHLSAYLALVVIAVYVDHWVECFRDVR

RNQMVTYSESVEVKLLRFRQRFGLRLSESQTNTKSEDDRPLLASESRCGFNSNFDCTDVE

ENYVRNNADKATCPIDAL

>contig49381 Frame-1F

MRTSDRKMVDEGILRLEILLNEIRCDVHEGAENTGAADRFAIQRRIGIYPRVNFAFLTSL

LASNSFEADLRARNPFVKIATSHLIEELSLLLFTCSRIIHLNRTIQAASTLVEYLSSLTS

QYADDYSRKIKITCQASRDLAGIL

>contig49855 Frame-1R

MGEYYHCYSQVLMQLTLLSALQWATVKDSVNDATKVAHVQAQDHIFVKVTIDCSVDFFGR

VVVTQCCLTI

>contig50000 Frame-1F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68035.1|) 2e-41

MSTSSVGLFEFELVDFCGTTRNSASPLFRHSLLSGHIDLEPESLSEAILSSYYGISLSLN

ELSLGITPEQYTTCLGIAYENFREISRVVTDDTYPLCAACGGLHFVTDY

>contig50394 Frame-2F

MLKPTIVQAKRCPSRVAYAVQLLGMKREVPDTSEDKGVSFYKRIDDDIVVGITTGHWTTN

FFACFNGLVSNAFMATICPCVSLAQIARRLGIVPYFTALLFFLLLCSLELVAVALTIQQF

ISVVILHHNVYYSYFHAHRLEENRSAINLVFVTDFLLAHMVFATALLVLRKQIRSQFQIP

GTTRNDILSVTCCPCFSIAQMASHLRCDRPNSCILRPVDVLPRYQ

>contig51090 Frame-2R

MMDREHAICSMHFRPTINRVSCVRSRNKQCNWLMVSHSSRPSGMTSTLRKTSR

>contig51151 Frame-2R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY53382.1|) 2e-91

MCLELIEQRFGGIFSLLDEECVVPKGSDAGFARKLYQRLQDHCSFSATRTEQADFAFQVH

HYAGHVRYQTEGFCEKNKDQFNAELYDVLGQTRDSHLRELFIFFRTSESVESQLGPPKLR

RRSSALAAVGIGSQFKQQLASLLEVVQQTQRHYIRCIKPNDEGASGQFDRAKVSSQLRYG

GVLKAVEIMRQSFP

>contig51601 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66065.1|) 9e-35

MDSIYTSLCRVASFAALDIELIVNRSLSRKSKSKGMSATTTATVLVSQYQKRLHYFREEA

SVDEVFLLLQDVGIISNPAGFIDCAISLLSGAHSKSPETGGA

>contig51674 Frame-2F

MESASNLLQLVQDARSGAQGLIMLEDDLIGRIKNASEQLLCAGLCTISPESSAIAVCHVT

AEVMAFLVEYRPLTEHSKWHKRVLVLETAVASAVAGLVDSNEADLENETRDLNNMVERLF

RMLWKTSDSSQSLSNKAAIMTKLCMLLGLSWLSYDRMGSEKRVENLLILCSDLCAERETT

IKLAKWPLFLLG

>contig52811 Frame-0F|Blast-predicted protein [Populus trichocarpa]gb|EEE93633.1| predicted protein [Populus trichocarpa](ref|XP\_002306637.1|) 8e-06

MLMEEKLAIDEENYKLGTTIELLQSKIDLLMKKKAELEGASIGSAERASQLEEQVADAKD

EIITLKAELNRFNEIQQSLEESVSSLQEEKGKLELEFNKTKSQLREELGLSVENAKSLQA

QMVQSI

>contig53027 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69970.1|) 2e-17

MLHVLNAAYRAPWFVVYLAAGIGVMVNLMDEACSTALAVCKLYPHFSFAETLGEEISMHT

TLVPLVR

>contig55072 Frame-0R

MDEEMAESESDRNAALNLSNHLRQQLYKKMHSSAYRSKLPQRECLPIASFKTQIVEMLQN

HDVMLISGETGCGKSTQVPQFLLKDLLLSRLGGARGQILCTQPRR

>contig56525-0 Frame-2F0

MARQNLFIKMRRTNLCAWNWLQVTRRFSSKADRSKQVLRPIHFEHDKN

>contig57041 Frame-2F

MIPIIFAMRNCSVFRSKVRSICSLSRLENV

>contig57265 Frame-1F

MQTSETSTDTSSTSSLSSIPCDMIQSLSLSSDTTLDGDACSAVQIDLVLEMTATFDADGY

QLPSLVTRIEVQRALETCDGDVSRAVDEVLNLVAIKTYSQQDQQIQHERRQWQQEHGKLP

LAELCSGLGLEKDSSFMKALQHLPESERDELLATNGAFVQQLLLSLEDSEVGSETDTEHP

LQYLLELYPDYKADVVEDVLDCHGYDVDKAAEALYNLRALHHVQSFAAVVSADARDAAEK

SFSCTTGPEEDTLEGFPKLSDASKMQQKKHKKLPRRRQKIQQAPHYRPPPKPLPKRVQYP

ALPTRGHTVKSTVKSTFNAWDHQHTPNRAESSIATQLKLERLEKMLPTIDRSVVQTTFFL

NGCNSDTTEAALREVYNLPLVERQIPSPVLREEAEIDYIPIKRKSQRSGDWTLVSSKHKV

NASREALSKRYCDVLASFRHGQHIVAVDRIRDLSIARREHREAQRQWAHDYFLAHEGQV

>contig57359 Frame-2R

MTQDGAIKSIQEPAPIPRGRERPPGSRNKENTRTRRELCAFESRVLRAKYN

>contig04510 Frame-0F

MIGKTLKKRRWCELRQPIFVDREALDTATEMAECFSKADAARREGDREHALVHAFYALQA

LRIDLIMKESSTAAALRLACRHYYEGIDEEDRVKIIGGDNRSSSHDEPIKTTNSEDVEFY

LKKVGVATTANSRRKDEILKLLSDIEQDNSPCQESVMLARGWLALNTIEALESIPDEDRY

FHPSRYVLAQIVYWLSHFYVDLEKLQIKSGKVCALLAALQYRRSRDKVMGPCDAAARALK

EMAPIFDKRRPQVVAIWISEYIPMAKKFEELNQRQLKYDYYRLKYWRFYIALLVENSANG

RLKEVESWVLACKEEHDVIAMMLGIVLEARGTVLRRRLQEFVNTDFENPDISNTVKDVER

LLKLLAKTYTYFLEVLNAQQRLNHVVEHCELVMENAELFMVSVFVMGVVHYSNEVALLEE

DSELLDQDFFGNVTVILNALRRNELPPRIYDAHNRCAWKAYLNAAHSFCEDKWPERSGKS

KPSKKQSRSKAAVSLGLLTEAQV

>contig09166-0 Frame-2F0

MVEALYRYNRNQRMREMADAGTTDTMTHVAQPPPLS

>contig14418 Frame-2R|Blast-N(6)-adenine-specific DNA methyltransferase 2, putative [Phytophthora infestans T30-4](gb|EEY53906.1|) 5e-56

MEPPHLSQDCLKKYSDTLRWLAKDVESVPHKKDRVVCPSAFINSKQLRKEMKAELGFTPS

GFYPGFQSKLSNHLLTYTNYKSERFGPCKEPDEENNA

>contig15307 Frame-0F|Blast-fructokinase, putative [Phytophthora infestans T30-4](gb|EEY56250.1|) 1e-158

MHRFAGVEVGGTTWVVAIAEDHPENILEKFEVDTTTPTETIGAVLGWLKERKFDSIGIAS

FGPVDLNKKSPTYGYITSTPKPNWGNVDVVGAFKRAFPSTPIAFDTDVNAPALYEVAYGG

HGDISSAVYITVGTGVGVGVCTNGNAIHGFMHPEGGHIVVPPAPQDIKTGFKGVCPFHGD

CVEGMVAAGSIAERTGVDRRELASITDDDPVWETIAHYLANLCVNVTFITSPDVIVIGGG

IARREKLFHLIREKFLARVNKYGQQPPVEKYIRASFHPAIGLVSSLHLARLELQ

>contig17420 Frame-2F|Blast-T-complex protein 1 subunit eta [Phytophthora infestans T30-4](gb|EEY57222.1|) 0.0

MNGMMQPQIILLKEGTDTSQGKAQLISNINACQAVMEAVRTTLGPRGMDKLIHAGGKTTI

SNDGATIMNLLDVVHPAAKTLVDISLSQDAEVGDGTTSVVLLGAEFMRLAKPFIEESMHP

QMIIKSFRNAGQLAVQKIKEIEVHVAKTDEIGRRQMLERVGGTALNSKLIARHKHFFSPM

IVDAILSLDEGLDISMVGIKKVPGGSVTDSFLVQGVAFKKTFSYAGFEQQPKTFVSPKIL

LLNVELELKSEKENAEVRLDDPSKYQSIVDAEWNIIYEKLDLCVKSGAQIILSKLPVGDL

ATQYFADRGLFCAGRVAQDDMERTQRATGGVVQTSVHDMKPSVLGSCGRFEERQVGNERY

NIFMECAEAKSATIVLRGGAEQFIEEAHRSVHDALMVVKRALASSTVVAGGGAIEMEISR

HLRQFARTIEGKAQLLVNAYAKAFEIIPRQIAENAGHDATDILNHLRQKHFKDPKGGKWF

GVDIATGGICDTYESHVWEPAANKINSIAAATEAACLILSVDETVRNPKSEQPQGGGPSG

SAPMSAAMGGQGMRGVMGGGRGGPSGMGRGVRAFRGKGGA

>contig17554 Frame-0R|Blast-gephyrin-like protein [Phytophthora infestans T30-4](gb|EEY60213.1|) 8e-64

MTDMSRPAMAHALQQLEQIQVNVVIDKVVPDDLDQIQNVVKDWVDSDLVDLILTSGGTGF

SPRDITPEAIKALLDKDIPGFPIAMLESSLKITAKAVLSRLVAGIRKKTLIVTLPGKPTA

ITENLSAIASVLPHALCLVRDVPHEHHRTSM

>contig19260 Frame-1F|Blast-metalloprotease family M48X, putative [Phytophthora infestans T30-4](gb|EEY59998.1|) 1e-75

MKWTFHVIESEEPNAFCLPGGKVFVHSGLFKILSNEDTLAAVMFHEAAHGLARHGAEKIS

FSLLVYGLLTLVFPDYGQLSDLIIKLAVDLPFSRKLELEADSIGLRLMAQACYDPRASIL

MNTSLGQVEKKSRFKYFSTHPPSDERVQALR

>contig19314 Frame-2F|Blast-serine/threonine-protein phosphatase 6 regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY61995.1|) 3e-62

MAVAKGFSLGYMGHLHRMCNMILTMLDELRSSTNEEGSLNDMRHADTVLELFEADNVTWK

KWEDMSTNVLAPLYEAERLPLGGVMLPLESDDPYSVMGFNQNDELLNAQFAEMLGASGFD

AENTNEFETEVDGTFTDTPMLP

>contig19585 Frame-1F|Blast-U3 small nucleolar ribonucleoprotein, putative [Phytophthora infestans T30-4](gb|EEY64073.1|) 1e-144

MDKAAEEEEDDVALDDNENDEDEEEEDSEMEEDSDAETAENLKYADFFHNENDTQDEKDG

GEEEEEELNDVKKHGKENEMEYVGIEREQLEKESFNDDEDVAERGVLSTHQRQRQRLQKE

IQVLEQEAIGEKPWLLKGEVRAAVRTENSLLEAVLDYDRPVKAAPVITEEVSIALEDMIK

KRILEDDYDDVVRKFAGNENELKQKLVDISMEKSNEGLGEIYEKEYMKTAMGFEADDESK

QDQDAIDVMFKSLCWKLDALSNYHFTPKPAVKELQVKPAVPAIAMEEVIPIGVSDANLKA

PEEVYEKKRKRGEAVLQSKEEMTQKERKALRNAKKHTRRKEKRQRECDERLVAKLNPGLG

NKYEKKKMLESIASAKNITTGKQI

>contig20462 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58485.1|) 8e-07

MKALDEKLAKLAHARDDEGSLSILSVKVRDDKD

>contig22323 Frame-0F|Blast-calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type, putative [Phytophthora infestans T30-4](gb|EEY62297.1|) 7e-59

MAFIYITTMEMLRAYTARSFTQSVCKDLFSNKWMQLAAVGSMVLTLSVTTIPMVNDDLFG

FAYIQWYEWMFAMVFAVTMVALGETLKLVYRRRDRVKLRRAAEATYAGMAEEIQNLRMRL

QQLEIRVKVEPNHVPEVLSHTERSLTGLMTS

>contig23834 Frame-2F

MCNQINPTTLCEFEKKRRYDANARDPIGTCERR

>contig27830 Frame-2F|Blast-proliferation-associated protein, metalloprotease family M24X, putative [Phytophthora infestans T30-4](gb|EEY59870.1|) 0.0

MPSDDEYSGSDASDVEVDVPTPAEAIEDCSNSDVVTKYKLAAEIAQSALQGVLTQLEAGK

DVVEVCKFGDLVVQQRCAAIFKSKKVDKGLAFPTSISVNEILCHYSPLANESMILQAGDW

VKIDLGCHLDGYIAVVAHTAIVPTEGSAATAEFPELHGAEADVLQCAHDAVEVCARLIKP

GNTNVQVTEALTKLEQSYGVKSLQGTLMHQLKRFVIDGNKIIAQKVDVENRTPKVTFEPH

EVYTIDVCYTTGSDKPIHSERRTTVFKRQVDKQYRLKMKASRYVFKEINTKFPTLPFTIR

AFSDESQARMGVVECVKHDLLQSYPILEGRAGDKVAHFKVTVLLLPNGTTKITGMPFPSD

KVHSEKTVDEDCAKILATSLKKKNKKKKKKTIA

>contig27885 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70313.1|) 4e-32

MEWSFEGVTCHGVYKPEANVAILNFCLQESMVTITYRVLDAN

>contig32036 Frame-0F|Blast-signal peptidase complex catalytic subunit SEC11A, putative [Phytophthora infestans T30-4](gb|EEY67703.1|) 1e-46

MLQQQVDEIKRLWANKRQLAHQALNLALVVLTALVIWKGLMTFTRSESPVVVVLSGSMEP

AFQRGDILYLENTKSQLEVGDIVVYKVKGRDIPIVHRVLELHE

>contig32692 Frame-1F

MEFVFTKRFPTLAVAKVMQKAWENEMNWQGAQVVKYDVQRLVMLQKINSHAYVLGRDVQS

PDKAPVFRTSLLRYRMATSGHFDSLRGVANDKHSSHFYATGVVIGTQSVAPIETTGHKMV

WDTRESSACVVWPELAHSIEMLQIVDARTGENQYVHVRWGGQTNYGSAFDARRNAADMVT

TLLRWELATIAPAIELMPTGKAPVVDASLSVDDCFMATKD

>contig33181 Frame-0F

MRSWTLLAAATAMTFDVVTASGVVSVYTINEPAFGTCRLQGISDSSDNFNYYASVPRRDY

SLNSACARCITVTRDDNPAVSTTAYVLDVCDGCDSGSLGLAASSMVALNISTTDTSTIVS

YQFSDCPTSFMSGNIRACLMEGASASYVPLQYYNSQKVITSVTIEEVPATRTSSSFLYSA

NSGSSSRTWYENVRFSVTSDDGETLSSTLSFPGTSGCAASNVQFNSASTANGVRAGNDTS

SSNGAIIGGVVGGVAAVLLIVGSIILIRRRKNADKDLDGPEKDMENQYLSPKAKTKTIGV

VNSTFTDDFDDNQHPASPTVDYAESFSPAASAKTRIPDVITHKALKEPSALIAPAPVVSA

AVAVYSPSSSASSHRSSGVYSNHSSLEHSPSVDSMNSAPTYAFSNPMATTSPRHSNIKAA

LTLSAPIVPPSNTYFQQEDVDENRTSFDIDDMRESEARATLTDRSSRLQTPFVPYSAADP

YTIAMTSPERNVRATSFRRPSFKQNSMRASGRDFGRDTNDSIMSEADSYSLSAPRQGNQS

ILSNDGVSNSLDEDKNLVRADSSESADADTMTDSARDGFTSIQQNWDPTLSQSSTGSNGG

YSRESLNILGYPYSKRSGR

>contig34221 Frame-2R|Blast-nuclear migration protein nudC-like protein [Phytophthora infestans T30-4](gb|EEY57584.1|) 2e-55 NOT\_ORF

MKLMQGIRAKNLHCQIESTKLRVTLNNDPTKLLLYGEFSDTIRPNESVWSVESAKTLSIS

LEKIKPTWWASA\*KSDPEIDTSQVDCRRNIQDYDEATQGAIRKAVYDQCLQQMSGGLPPT

PKMQMLQEAKNTPGLRHSSQNQIDFF

>contig34496 Frame-0F

MKEARRSFLAARKWQMVFALCGRDQESRDEIRREAYVLAQEMLSNDQPQRDHTKDLILAV

SRIYIEYCNDINEAIALLVVHHEWTEALRLSYLHQRNDLIESDIEPGALQCFDDVLDELE

VKEREYCKYWKRYSTIREQKRLFKLHGIDGSRWEFDKNQGRDGTEGGSIHSGVSSAIDSA

LSYASASSVGSHNSAASIGNFAMQSLSMATASHFYATHALGDACKNAGLNAKRGRRERRK

RMKEGSAEEEAYVAQQLLELRPNEALVREVTGLLEILVVLGYVPRAQKLQTQLARFEHFV

AENQGLERDSSRDNDAKNGDALESRMYSPWRLEALQD

>contig34980 Frame-0F

MSAWFNAGQDAKATTTDTSDIESVRTNLTSISVGDHEHDVTPLKSTNVVATNPPRGYSQH

LDFQEITLGRMIGEGAFGKVHEGKWRGKSVAVKLLICQDLRRDILHEFQSEVEIMSVLRH

PNICRLLGACMDPPHRALVVELLQRGSLWGVLRMNRKSIDQDMRTRFIYDTAKGMAYLHH

FERPILHRDLKSPNLLVDKNFNIKLSDFGLARVKAHVQTMTGNCGTVQWMAPEVLGNQKY

TEKADVFSFAIVIWEIVTGECPYDGMSQIQAALGVLNRNLRPNIPKDCPPFFSRLMKACW

NRQPELRPSFPHIVNAFRTHQSAI

>contig35378 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58092.1|) 5e-32

MNGHKRQVTKLQAINDEEEEVVTLSDVIQHNDQMTEAANAVLGDASDTHCSYPMGYMRQA

VFACMTCTPDARENPQTRAGVCLACTYHCHQDHELVELYTKRAFRCDCGNETFLP

>contig35536 Frame-0F|Blast-hormone-sensitive lipase, putative [Phytophthora infestans T30-4](gb|EEY58722.1|) 2e-85

MGAAVCIRCIQDGIDLPSGNVFMFPALNLHLSPSPSRFLHQNDPVLPRGILELALTLYYP

SHGHSNQYKHNIHDPCVSPGLAEDSLLEKFPPTSLVVGDLDPLLDDSVDFYTRLSFLKVP

STLKIYPGLSHGFLIYGDLVPEAQTAIDETCERLQNYIRLR

>contig36353 Frame-0R|Blast-D-Tyr-tRNA(Tyr) deacylase [Phytophthora infestans T30-4](gb|EEY61053.1|) 4e-10

MEVSIVNDGPVTMQLNSKDRKLAKV

>contig37747 Frame-1R|Blast-tRNA pseudouridine synthase A, putative [Phytophthora infestans T30-4](gb|EEY67733.1|) 1e-98 NOT\_ORF

MRTVQEVIEDAIQRTTGETALPRLRFASRTDAGVHAIGQVIVIASRCIEPDRIFRDSLNT

RLPQDIVCHSVVWMSEAEADFDPCSNAKRKCYEYTILAGGLRPVFSRRNVWHI\*RPLDLA

KMQEAIDYFMAPPAAKDFSSFTPQKSDDEERNNVCVLSAIRLYSDKPLSAIRLYSDKPSD

KIEAQYQEDVATRIRLVFEGNRFRYKMVRNLVGTIIDVGLGRLKSEDIPAIVAA

>contig37813 Frame-1F|Blast-TATA-box-binding protein [Phytophthora infestans T30-4](gb|EEY53626.1|) 2e-14 NOT\_ORF

MKTLLDLKTIALHARNAEYNPKVLQFM\*TGDGFEAKSNSLNSHLIVS\*RFSAVIMRLRDP

KTTALIFGSG

>contig38948 Frame-1F

MYALLYLSTTSPIWESLNTSSVSSRLLLSSRFSFVKFDEKFRASIINKAGCHWVAEDSKL

IQWLFLLKFHSDTRVAAIMSSLWQFAIINSATDMTTKGKQKLLRLSWNSRFQFSLGRLES

ARNFKYRKAACLALVDLLSCAEADDIREDFVRLWKTSSRAVDDVMETVAISGVKLYRCLG

ELSLRVAASDAQCCLQLLKFLVEHGIVSKSTTCRALSINILLRLVKALKASDMQEYLAPL

LLKLLEYLSSLEMPEFQYAQYHVDKKDQLERLRISISQAGPIGQLLELTTTRLIELTESP

VRIQVVAELSRGIANLLKFGVGLNTRVGTANFVVRLANELSFELRKCNAANLLLRGVLMP

YVRSKTAAENDQYGDAESRYGDKSANNEIQRTDGYLTATKGLTDGLAIQSYCRAAAHLCP

LVDASAVRDYVHSGVFAFNNMSSRATRPSSMSSNDNNDKELDGKAATSSAMGGAYTSRYL

LICALATTELVKKVPPIADASTVVTNDLHNHWYCTHVFPAAFVGRFAASDTLKSLWTAIL

DELPPSVLYASRSLDSVLQAIA

>contig39600 Frame-1F

MPFQEIHFGIPELSMYILPHSQRFGFKRFFPLKFNYECETSAHYDRKAHVWIVNVQLSRR

LLRSLER

>contig40903 Frame-2F

MDDVSLKQKQTDDKELDNLMFDGEKEEMSVKKNLSQYHDVDSDGEASAKSGDRSSVSNVL

PVDKLKNGANTASKVLGQTFSMFKEKSGAALEAAKSSNAGKTIAGGLNSAANASQEKYGK

LKETGAFKKSSNLASGAYERTSFVASGALEKARAASSTGLEKAKTTAAAGIETIKSKTGS

KKGGE

>contig41935 Frame-0F

MNLIRAMFVAALVACTRNGVHAKASEADLVTLLTTNSEIVTSQRLLRTSAEPDDNDERAI

NIPFITNYNQRTRIKAPLKELK

>contig41980 Frame-2R

MLKSLTRKIKPVETLLNTSEGVAFVFAIREMKATESEGYSEAVGVFRKTFEADVLEKMMK

NANSDDTIVAGFIDAYIELMGVKIA

>contig43353 Frame-2R

MIPRQGGRCGHEFWFLMSSIS

>contig44734 Frame-2F

MLSSRVNNHGRSLYMQFLSSSFCLNLNDALGARPIVNRNTQRSRALTS

>contig44789 Frame-1R|Blast-prefoldin subunit 2, putative [Phytophthora infestans T30-4](gb|EEY55520.1|) 3e-47

MSEPITEQQVVATYKGLRAEVRQMAEKISELEVEVLEHDRVIQTLNDLPKDRKAYRMVGG

VLVERTVQEVLPAVTANRDGIAQVLAQLNGNIGQKEKAADEWQRKYKIQVQQ

>contig45063 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58471.1|) 5e-94

MSYYSADSPKMGEAEHYNEVVEETSKAVSQFNQVTRTIAQKMTLFGTPQDSRANHQQLTE

LTDRGNKLASKISRRLQELDKGAKAASGRARKTQVAKLSMDYKNQLKSFEETCQKLLAAE

RAAVSNLRQSSLSFRSDDEQKPAGFDGYNEDQIYAQVNVTSYNEDDLIRREEDILKINQQ

LHEVNAAYREVDGLVQDQGELVVEIENNADTAQENTEAALRNVREADMKRGFCKCSKTKL

ICFGLFALMIAAAAIAVATSVA

>contig45658 Frame-1F|Blast-nuclear mitotic apparatus protein, putative [Phytophthora infestans T30-4](gb|EEY54191.1|) 1e-110

MVERDSAVRNVNFISKNEENMMLEMTTLRLDNTNLLKLMESMRRMEAGREERNRCEVETL

VKKVSTLEIKLQNAFEKFDSKEAISGAQVLAAAREKQAVLAELTKLKEAQSQLKEQYARA

EEQKIAYESKSALLEKETTHLREQLRKGASTAASDSVAALEVQLRDTQLEVQALLISRKT

LAEYVTKYKALAEASDKSLAELSMASEKWKQSETEKMRALETSRELLSEELEKVRAELLK

HDTENIRLREELDQTKQTHL

>contig45733 Frame-0F

MQQLPLVVMLMCDPQGKLPQ

>contig46181 Frame-1F|Blast-branchpoint-bridging protein, putative [Phytophthora infestans T30-4](gb|EEY69167.1|) 6e-41

MIEKDPNRSPSPPPQYDSNGKRTNTREVRMKDALEKRRREIIDELMKTNPLFRPPADYTR

QKLHRKIYIPIREFPSYNF

>contig46202 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69842.1|) 3e-47

MTSSGTIESANHNGLVVRGTHTELHGDCHVSPHKHISFIDSMTAGQLDEHIRSLRFNFVA

TFPSRSSRID

>contig46277 Frame-0F

MALIADDVCASPSCRTTEPRLLPWRAKIASVSH

>contig46790 Frame-0F

MVSLFRSNKKGMTLRPRVRRSTPLIDLGLAVILGAVTGVYIFTDSMQRWQVSEGEFMAAK

NKKAIQDTQTLIERDETHQR

>contig47692 Frame-0F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 5e-36

MKDQRHLWQWLGPANYLYHYARELKAVIYSLSELLIKDAKWVWRQEHQNAYDEIRLGSRQ

RPSSAARRSGTPRV

>contig48235 Frame-1F

MATNHRLATPAFALSHATCHDEGEDDDQAGVYSFGQ

>contig48280 Frame-2R|Blast-XTP3-transactivated gene A protein [Phytophthora infestans T30-4](gb|EEY54276.1|) 4e-15 NOT\_ORF

MPVY\*ILMCGFKLNDHMVSDWTAREKEHLGEEIS

>contig49368 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68140.1|) 1e-36

MGYVRELQLSESSLRNQLVRTKQHTEDELSQSVSRVQELERTMMEVERDRMLALRKLKEQ

EKLIRTLAAKLKEAEISPTNFSTSTGIDELPPINEEGSFDADTENAEKSVPAPVPPDHTK

SPHELLEQKPIPTDSHNQLSNLTQAVQLASPRSPNRPLWDPWASGGATSMKNLPPVFSIG

STSVVQAASQSASDAQPPATSTALKAARGYELQSVLISPRQNQGQAEVAEANFRAYQIKL

QGSFNEMLAPEGIDSEPYVGA

>contig49382 Frame-0F

MDWEDNDWIEENASAAPTCDDDQDSTEPHVLSNQSTSKVKEEASLLWSQELPPHIRSLMA

RVTSCDPPTYVMRAMHKNLLDEISKGDPYYYLRPATPSKEALTFSSSASSLMCEFGCRGV

SAIKWERKLVSQIGSRIKSFDIVAYSLARRSGETICNRRKLNSMIRKVHLFGMQLHSFIS

HLYCVKGHGTCKEVDSLSTALNRSHFERKMSVYKSKLKLEVPHQHVLQQPNSAKEVPQEL

LHDTFEFFPELLLCVDIWGYNYRESLYKRHDQTSVFQSQRLDSSAVFPLAFCSEVETLAF

DFEHDSNGLLRVICDELLTIVCLWNDFTWTDEFTTVNIDRIVMFETKSMACILKILDVYG

NHLQALWAVHLLDEPEQLHDIHMTQLNAYYSDRSHGSVRTRVAGKGPSNGTSTIDGLVAN

EIIEQRLAETYWSRKVSLRSFEHDAVDDDMEGSNLMSALLSSVEAIPSWNKQTRDSLMLR

WSDVY

>contig49438 Frame-0R|Blast-hypothetical protein OsJ\_16521 [Oryza sativa Japonica Group](gb|EEE61853.1|) 9e-12

MTPSFENAAFALNVGGLSDLVDSDSGIHVILRIA

>contig49856 Frame-1R

MPLSPKKTMSHRPIELVFLNSGEIRAREECPPELALPELPQELDGSKTEARGCHSEGYTS

DEEQSDASPQSATRKQVKKGSRPQNRRQAGARQQLEQSASPPVSISNGSSVSESMHTASI

TNDAKKATSRKVYKARRHQNRG

>contig50397 Frame-1R|Blast-cyclin-L1, putative [Phytophthora infestans T30-4](gb|EEY68422.1|) 4e-77

MVARPVPVHVVLPTSSLSRSPSNEDGVNPDIEVLHRFFGCELIQEAGVLLRLPQVVMATA

QTLLQRFYYRKSLRQFDAFRVAFSCLFLAAKVEENPTRIKDVIGVFYAMFRRRKWQRSTV

AQQLIDLDGTTFNQWRMWLIMVERQVLIDLGFSIYSVTEHPHKYVL

>contig51152 Frame-2F

MPVLTRGLKDRAGDAKKKAALIVGSMCAMINNTKDLVPYLETVLPNLQMQLTDPIPEVRA

VAAKALGKLANGLGHHYFAEMLIGLLAALKNDAVGPVERSGAAQGLCEILVALGLERVDR

VMHNEIFPLARHPKFSLREGVLWIMAFLPPALGKQFSVFLREALPIVVAGISDEAESVRD

VAMHSGHVIVNAHALSHTRDLLPSLEAGLFDDSWRIRQSSVMLLGDLMFRISGTRAIAIV

SEECDDDEENFGSAAGDRAIIKLLGMRRRNEILASLYMIRSDTSAVVR

>contig51325 Frame-2F

MTQIVSDESSLPRVGLEGPSLCKNSLTKCVAACLKNNNVATP

>contig51581 Frame-0F

MRVEKHPSSGAEEYERMTWHKEAQAQSPQSSQAHVEKAGCCRQLPKVSSINGIFAAHQVS

QPIQSHLKARNPKVFLVREDTLQEHELFSIGAPANTTFTSPMHKWFQRLPQQLQPYSFGS

KAENSHQEMKSSQSTSNFCTNDF

>contig51602 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67081.1|) 2e-63

MVVTRARDVAREEIEADPKYRRIFFPTQARERASDDYLHTRMLAQLSGSTRDNTNVFCHM

SIGSRRPEHAVREHFQRCA

>contig51848 Frame-1F

MRLFEGDKNEQSSSTVIGKMHSSTNVHEISGIGLKPCNCRSLFLHLCEVLKSWVSITIGS

ACTLLAVTLLLRLRAAADVHYRWHRSRTYTARTFRCSLVSPAPICSRS

>contig52441 Frame-2F

MPNNKMSSSAIGRRVRESLSPKASPHVTQLVVRPT

>contig52812 Frame-2F

MAHFDLVCPRRITTIGPTSASSSKECQWTWHR

>contig52867 Frame-0R

MQEGMPSIKQKLFTLKPRLVPEKVAIDMNWSI

>contig52979 Frame-0R

MTSIHLSILSCSEEEEIQDYFDENWCEEKYFVEPLRSSGYCSSNNAESTSILGSFSAFRQ

NTNTMRARLSSSDAHFSQTSAILSSQRFKIPVSWQRESVTWK

>contig53024 Frame-0F

MGKGPRRVWHLRISDRKRYSTTICCSFRNTWNGLIVRAILEMQM

>contig54599 Frame-0F

MEYEVVYISSRVCPAKLNIADEADSLNRPA

>contig56038 Frame-2F|Blast-autophagy-related protein, putative [Phytophthora infestans T30-4](gb|EEY64085.1|) 6e-89

MLYCTSLVALVGAGEQPAFSPRRLRVWNTKTGAAICDFNFVTAVLAVRMNRQRLVTVLER

QIYIFDINTMKVLETLDTSLNYKALCVLSPHENGHLAFPSGAAPGEIVLYDAIDLSVLNA

FQAHRTAPVAMAFNAQG

>contig57037 Frame-1F|Blast-nucleotide-binding protein 1 [Phytophthora infestans T30-4](gb|EEY59030.1|) 1e-116

MVTSIPSNANEECVGPQSEQAGKADGCTGCPNQSVCASGAARQPDTAASDVKQRLAGIKH

KLLVLSGKGGVGKSTIACQLAFALAGQGFQVGLLDVDITGPSVPRMLGLLGQEVHQSAAG

WSPVYVDDNLGVMSIGFMLPNADDAIIWRGPKKSGIIKQFLVDVQWGELDYLIIDTPPGT

SDEHISIVQYMKEADLDGAVVVTTPQEVALSDVRKELNFCLRLKLRCLASSKI

>contig57266-0 Frame-1F0

MSLTPEQISRAPAKNQLYVL

>contig57266-1 Frame-2F1

MSFTTVQRSMYSKSERSKYFFWHSNPIT

>contig57491 Frame-2R

MGQQEVTFGGLLLLVSVATTCVYESALVQSIKSFEEGRSVVKELLKPQVEECHEGQLIHF

SGLITTNATLKQKSRDVDEIGVRQSPFVMDPVFGIAAKGVRLYRRVEMLQWVETSHTSTS

STPEDEDQRFDTDRERIYMYDLQWREGHIDSSAFDDISHRNPPIEAWTYKSLVIQGTDLV

VGEFSLSEELLDQIQRRDAVPLDALKRRVMANLLDQQHGEEWNEKMVANVTVEKDFFYFR

NEIRNLVVGDQRVYFEVTPNYPVTVCAKQRGNKVEPYTTSAGDSLLLLEDGIMTADELFD

LKSYSKVQKIRFFRLFATVLGFMGFLVLRNPLIERFRPLVTIQQHLLAGSMGAALTFSVV

GAHWLLYRPLWTMALTLCGWTPLIVLFLFFFNKNERKSQ

>contig57859-0 Frame-0F0

MQSFPDNSVLAKTIVDALFTLSP

>contig57859-1 Frame-2R1

MVLASTELSGKDCISLSVKLPNTASSSS

>contig00821 Frame-2F|Blast-DNA repair protein radA [Phytophthora infestans T30-4](gb|EEY54403.1|) 7e-28

MWSKLRAHLMSAGPTQRKRNTLTFVRSFANSLDAFQCQNCGQSFIKWLGQCSACSQWGSV

APLKQSEPHFRQIKAEPYARNKSKLMVAWSKTDQTAFEKPNHYAERINEVKLNTIVERIE

LPERE

>contig04511 Frame-2R|Blast-phosphoglucomutase [Phytophthora infestans T30-4](gb|EEY67584.1|) 0.0

MAQFDAFRTKMQGAGLSTEAVKAFEYSYEALVSGETGMIAESSIKPADSIPYLENATDSI

RESVKADPALLKETVVLKLNGGLGTSMGLDKAKSLLTVKGDDTFLDIMAKQIVELRIKHK

SHVRFVMMNSFSTSADTLEYLQKYPEMVEDDTLELLQNKVPKVDAATMEPAVYAANPSKE

WCPPGHGDLYASLAGSGKLKKLLADGVKYMFVSNSDNLGATLDLDLLTYFAQSDKPFLME

CCERTESDKKGGHLAMRTTDGRLILRESAQCASEDEKEFQNITKHRYFNTNNLWIRLDKL

QEELLKQDGVIRLPMIKNSKTVDPKDSSSTPVFQLETAMGAAIECFDGAGAVCVPRTRFA

PVKKCDDLILLRSDAYVITEDYRPVIAPEREGVAPIVSLDSKTFKLVQQLEAAVRGNVPS

LINCSRLKITGDVGFAPGVVFEGIVEVVNKSAEQKTVLAGTYKDTTVDLTEQKGLGKLKV

VTVKTAPFHDQKPGTSGLRKKTKVFISDNYLQNFVASVFEALPAKDLNGGTLVVSGDGRY

FNKEAIQIIIKMAVAYGVDRLWIGKDGLLSTPCVSAVVREREGGSVAFGAFILSASHNPG

GPNEDFGIKYNCENGGPAPEKVTNEVFALSKVITSYKVAADFPSIDVSKIGVTTVDADDG

SRTITIEVFDSAEHHVSLLKQIFEFHAIKKLVSRSDFTFVVDSMSGVNGPYARRVFVDEL

GCDESCLLNATPMEDFNGCHADPNLTYAKSLIQAMGVDAKGLPVPNQKQDPPSFGAAWDG

DADRNMILGSRFFVTPSDSLAIIAANCTVIPFFKNGLRGVARSMPTSGAVDLVAKKLNVP

FFEVPTGWKFFGNLMDSNVVFGKEDYTPFICGEESFGTGSNHIREKDGMWAVLSWLSILA

SKQVEGAPLVTVEDIVRDHWKKFGRNYYCRYDYENVDKAAAESMFADMVKFDGIVGKEIN

GFKVKKADEFEYVDPVDGSVSSQQGIRYLFEGGSRVVFRLSGTGVAGATVRMYVEKYEEP

TGNLEENAAVALEKLINVGLQLSDLVKKTGRKEPTVIT

>contig04898 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58085.1|) 1e-70

MADIAAIINLVNTFALSYSLEDGDKSVKTLLALFTEDATFFEELVGGTCTGTGEIEAALQ

ELSQLKFLADTRHLPSGHVVELLFSEKATVTSHTTVFWKCTPVMVVTWSDVVVKCDGKWK

FLKRAADAVQKNLEMIGEMQLRGKKQYAHKDEA

>contig05066 Frame-1F

MPLRFLATPAYTATYPHACHAAKVPLRHFKPVRRNSVTSRHPTKTETPVLVTRPGLCRFP

CQHSRRPSRQ

>contig05178 Frame-0F

MALGRSYWELPSELKAQVKTPTLNALREWDPETAERKYGAAKDFLGADDEEIRKRREVAL

AKSRTETLEAQAASIKLSLEERMASIAQKRKAMEVQTSEPRQLNPNAESSNEYLKLVRQL

QQNNDSEEGTGGKWLVR

>contig14419 Frame-2F|Blast-N(6)-adenine-specific DNA methyltransferase 2, putative [Phytophthora infestans T30-4](gb|EEY53906.1|) 7e-40

MDSNMNELLPNELLANELSTETLAALQAHLQETHKEENPFVSEDFRLSQFWYDEQTGRSL

AKEAIEHSSNELKIAFVSTPAAYRDFLKIQSEVTDNRKQARMAENVYIFEFDRRFGAKYG

K

>contig15399 Frame-1R|Blast-glutamyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY69415.1|) 3e-41

MKAKYIDEGTAELVAEIHANLCSLSDQDFTPNIITKSIKAIAKKRNLGLKKMLMPIRYYL

TGMDVGASLGDTITLLGRETVLRRLKLK

>contig16295 Frame-1F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY57647.1|) 1e-180

MAEKSKFTMRWLVLFLSCVLMIGNYYCFDNPAALKSQLQQHFSNIPKERYEYFFSLLYTL

YSIPNIFLPFFGGVLVDRFGARAMLLAFSAAILMGQLVFATGCSLSNFEMMLFGRVVFGI

GGESLGVAQGTLVASWFENSELALALGINLSVARLGSVINNELSPLVAQASGVSMALWVG

FAMCVVSFFSMVLLIPIDKRAEMLTKRNNRKDEAMTAKSIHFSDIKHFRPAFWLLSLSCL

VVYGCVIPFNNVASSLLMERDFFKEPPMPCRRCGKGLYLEEIDCKAIVSGCPRVPPYGWP

LPLLSANCTIKKPFDQWNCSTSPPLIPKEKINCDDIAWKFGPLTKAYCAAEIDAAERAAT

PMSVPYIISATISPFLGFVADRIGLRAVLAFVAP

>contig16660 Frame-2R

MDEKYLKKRKRQLQKLRAILQHASDERDKGAINEALARAERKQMSAALHDDIQRAHNVLN

DLAAAEDQRSRDCLEPLSNGNVASLTSPIKPSKSPSLAIRPIAYGQALQAAEQQQQQLKI

CQKLLEEKEAEIISLRRLVAQTESCVQEDVTSKEARSQAKAAGLASYVIQLRTQFPVQKA

CARQAEALIEWIGPSDTADSVRQQVLSFVQRIITAQFPLAAAPLFFATGSYPMKTYLPGS

DLDICLLVPQALETSWYYIVMQALCVAGGSGGAGTVLDLGHMGRSGEASGTSSPSAPHTA

SGSSSGSLLLTNTVRNVTFINADVRVVKCTIDNISVDLTANRVGALGAVRLLDAMSTRVG

RKNLFKKSLILIKAWCAHESSSFVQTATAETGGLNIPLGLSSLPQTVMGASHGGFSTYAV

NTIVMALFNEHGDALIHPLQALYLFLDRLAEFPWHESALSLHGAVSLCRLATIPANEYTH

FKYKPHCAKLDAKDIEAIRDALCDEFGAFDAMLTSQKGNSFPVRVCNIVDPLDEKNNLAR

SVSAEGFPVLKRAFRLARDQLAALLKNNLEPGSAHLLDEDGSKVFFAQCWHLYGRGDGWR

PDLLTHPRQTWHGMALSSSIKKNKTTSRHPATSALGTIDEDEGRRWESLLPSVDASAMNA

LLFQHQQLQQQAVAAAAYHHGSTIAYQQPYYNPLQHTPSSPQPTGVPTRTIDNVA

>contig17494 Frame-1F

MMHPLLTCDEYNPLDANLDELEEPGTNYLQDFIVASHSTQSDTPLSHSNGYTSEESDYSV

ITPSDEQNYDEMSSLRAVSTSELVDVVGDLSTSDLTDVNPLQQMAVAGKGKGKTSKYRGV

TQTSKSSWGAKYSAKRIMNTCKTPEEAARAYDDYLKTNFPQKFAKFANFCDKCSKFVNPL

GLSQFRTECECFATPQEGISSPEPTSVVKMGNFFSHQTPTIKKPAPSLVPPTAPSPVGRP

LTISTSTSLNLKETSGLLLDHAITTADKEDPCAKSRRSSNLFVELHNFSFTNDTEQFFAE

SFTDVVKMTADLSNTAMISEQQLQACAKQAKLPIAVISSALDSFTSEDNLDQIIKEIGYS

HSVVRNTSTEGRINFDSFGSFAATNCSSSSSSGNASEISPMSTIQVDPIMSNSEGYYGDE

LDEMTKYFMLENDDAAIFQQEIQASSANLQQRSTTMTQKLFYKKNHSLDFGFDDIMTRKS

SCSGVVESDVKIEDTEMMNNCLTTSMHAHAGVNMPIGTAIIEIQTHFLEKYWRNDRKNIQ

CFPCCPEHGDYYRVRIENLQHLCKGVCRAPVKAHVSVPAHLGMSLELDNLLLLARCNSTF

SRNVSLTEQQLFSAAEMKILQGISAVGVIKSLAPLANCMEGVQFDVTFHPDVWKFEFDLP

KKRRHLLSTSAAPPPHGPDTSIAEDPFAAEFLYFFEVDVFHSRDKQTFERLGHSESVSFQ

IGNTRTLLRQRNKIEEVISRGESLPNANDSDILANADELPEKKRVKVTSCRQEAPSSSSS

SENNPGSPVEMCSPQDFNEKVESDSSFLFFEGQESSLYFYNAKTDVWKDLDNNCDDQRKI

FTFNYLSLVSPNHKNRNALTTNSRGATVLSTEPDLNFRPGL

>contig23888 Frame-0F|Blast-CAAX prenyl protease 1 [Phytophthora infestans T30-4](gb|EEY60189.1|) 0.0

MSDLSWWQVPYYTEPGWRPSVPSVPYFQGALVFMTLVYLFETYLDVRQHRKLHDKQFPKP

LTEAIKGLGSYRIAPKDEKDAVSKQTEAVAEKLKEDTDVPTTEKTLLAATQEKFDKSRAY

GLDQSTFGFVSGVYKQVEATAFLLLGYLPFMWMISGKALVALNLDASNEIYRALMLLTLT

NIRETLVEIPFGLYSTFVVEARHGFNKQTLGLFFMDKIKNFALFIVIGYPVTAALIYVIR

WGGAYFYMYVWAFLFVFSVVMMTLYPVLIMPLFNKFTPLDQSELRTRIEALAASLNFPLT

KLFVTDGSKRSSHSNAYFFGFFKSKRIVLFDTLLEQATHDEIVAILGHELGHWKLWHTAQ

GFVIQQMYILASFYVFGLCMNDAELFASFGFAGDSAKPIIIGFLLFSQTVWAPVEHVLSF

LITLNTRKNEFEADAFAVDLGHDIPLKSGLTKLAIENLSNMNPDHLYSAYHYSHPPLVER

LNAITARAKKSQ

>contig24827 Frame-2R

MDVKMGTRSYEHNAPIEKIAYEKSKFPLQEKVGLRIQGMKVYQHTKKGYVEFDKSFGRGI

VSLEQLVYAFRCYFPADDTTKKIALLQTFLHRLGQIKEWFDEQQSTEFIASSFLFLYDGD

MSSANGSKADIRLIDFAHVTMPVSPKRDEGLRTGIATLISSFQTLLHEARTKQDCSINCA

EAPDAS

>contig25622 Frame-2F

MVVETLKLSTKLTALDLSGCINVDDTDLKILHDLDHLKSLQLVGCCKVTDVGVNSLLQLT

QLEKLHLGRCQHITDKAFESFADSFPKLRELDVAYCRLSERAMQSIGRVKRLEKLVIRGC

QAISDDGIRALAQLTSLMYFDARYCRKIHSVPHEWTHLQFLLLGHTAFAESDVTILQSLT

NLQELELCKCHIKTRGLELISRLTCLQRLELEETALTDSALVKICSSASRLEALFSNTEI

GDGGAAGLEKLKELRILRLDTLGITDLALAHISFLSQLERLDLFGANITDNGLIHLILLS

KLQELTICGGNISDRGVGYISKLTSLTTLNLSQNRNIRAKSLYYLRSLTNLRCLNLSNTG

ISAESLRYLSPLKALQSLSVYGCSLSQNHIDGLRELLPELKRLRCT

>contig26771 Frame-2F

MMYPTWWWTASPNEDEEIVQCCCSHRRSREPWRSRAAIFL

>contig27048 Frame-2F

MRAVPPKDKMDIFLKSALTLDAEIVGPILEDCLLDDQWTVVSKALATIDALLKTDGCEEF

EEYFSENYSEIESCAKSEKAAVRDRAIKVLNHLDISTDVRGSSSNSDLSKKSKPSSHRMQ

PAAGEADLLGAFDDTTSAGDGGSLFSGLQTGAVSQQSAQEYSQPAGTAQKMTDMFGGLQL

QSSTEGTASAPEPSQSAAPAPVAAVSTAPSAPVLTASTNKTMVLDPLLEPVPVAPVMNQG

FGGPMNMNMMNFSTPQQMAQMQQMQQMQYMQQMQQMQQMQQMQYMQQMQQMQGMGGNPGG

SQVIGAAMTPTGYIAKTIQEPTEGLASDSGFGFIKKKDDSFNFVKDAMKNG

>contig27174 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63058.1|) 4e-71

MRVSKKLCAGTIDGKIMPKNYGQQKFKLRKKSLWDANEAARRISELEGLTIAMWTEARMR

KPSFLTLSSTCTLKNRRHGDDESDVVVSPPSPGLSCSPASTLTVLKQEKFPIIYLNLSNL

KHYSGRGDTSDSDPASKDSDSDAEPVRLDGESLQAA

>contig27884 Frame-2R

MKKMLDDLNLKKRRIQEEITELKEQEKLYAEAKRKVQHRITEIRSLRKAIIRLDDKIAEG

ENKVYSLKSELAQDVSAKEEAIVRKLRNQVSKQAQQIKQCLLLIRDLYKACVRETCLSLQ

LGTQQVRVDFTEKHLTQIESTFRGLREAYKLAKERLLTVAKEAMLLKHKAEKDAPWDSYE

ERFNQLPDDLDELLGKIENNKAALECFRGDKSIREVYERVIKEIQDDEANMADLESFVNH

GEEKINRIKVKWHADLKEVVQNIDTSFRSFFKDIGCVGEILLDDEDPDVAKWGIERRAQF

RKNTKLSTMNAEEQSGGEKSVGTIMYLMALQSLTKCPFRVVDEINQGMDVYNERKVFQRI

TKSSCGSKLPQYFLITPKLITGLTYHRDTKVLVILNGPYNNIRQELWDPDKFIERHAKRK

GKGAIAGSCKKRIRA

>contig29802 Frame-2R|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY57302.1|) 0.0

MASFKLVTGDLIRLIEAPHEKQHGALARLGGLEGIAAALNVTPREGLDSNNAADLAQREE

CFGKNYVPPPKAKNFLELMWDAFQDITIIVLTISGFISIILSATVGDHPETGWVEGACII

LAVVVVTIVTAMNDYQKEAQFRALNAVKEDEKIKVIRNGQPAEVSKWSLVVGDIVRVDLG

DIIPADGIVFDEKEIKMDESAMTGESDLLSKTAENPFLLSGTKVMEGVGKMLVVCVGENS

QAGIIKSLINGNRPGAAAAGGSDSKSIKNFEAPDDQIYIEIETPKNVSVLEDRTKKEDDG

EEESQSPLEGKLYNLTVFIGKLGTLVALLVFVIMSIRFSIDTFGRDNKPWKSGYISDYLN

FFIIAITVLVVAIPEGLPLAVTIALAYSVKKMLVDNNLVRHLDACETMGSATTICSDKTG

TLTTNRMTVMQLWIGGHEYSSAADGMGALSDATREALCVGIAVNSTAEILPPKVENGQPE

HTGNKTECALLQYIRDGGVEYPDIRMNNEVIHMLTFSSAKKRMS

>contig30732 Frame-2F

MDQVQQVQQAQISLEDHNEEGNNITINDTSPCIFDSPLPMAPTNTETQSLPMLDCFSARS

SSIDDDMPPEYSPATTPIGQAKREGGLSEPFTQMALAREPKFSPDKRKLCCVEGCKSQAR

AFNRCKRHGGSKRCSSIGCTKSVQSRGLCIRHGGGSRCQEPGCTRASQSHGRCKMHGGGR

PCVVVGCEKKAHLKRLCRRHGGGAKCCVAGCDKWAQRQGMCMTHSKVVTTQPQATGIVDE

SGFNRSPPQPFAPDSSPSLRIFDSDV

>contig31735 Frame-0R|Blast-cystathionine gamma-synthase, putative [Phytophthora infestans T30-4](gb|EEY67429.1|) 0.0

MSLSPQRLGMSLPPHDMNAISVSMPRWEDIVSYEEGDSEVLNVMACGYPRFFRHPFVVTL

QITIQNHFFANDDVNYWEIMILPTFDVAERLRNFLLTSNSDAIKREEVSVHVVLTAVHLV

RFPRQINVTAKQFWQHSGEIISSRHAERLLAVIKSSGELKAPAVAQTNSHLALRQRVAEL

YLPTADAGKVSLYPAGMSAIFSTVRLLQKIQGNDCKSILVGFPYVDTLKILSRKEWCAQG

VHFFATCGEKEMQQVEAIVAKEKVLGIWTEFPSNPLLSLADLKRLAKCAHDNGVVLVVDD

TVGSFNVNPMKHGCADLVVTSLSKIFSGSCNVMGGSVVLNPDSPLIHQLEAVFDPENDSF

IVEDDVNVLLEQSKDLCKRVAKANTSTAAIVQKLQRHPLVKDVFYPTFGDSKKLYDPFLN

SLYDNEKPQYGPLISIVLYGGIESAKAFYNALTIAKGPSLGTNFTLCCPYAQLAHYNELD

FVESFGVDRNIIRISIGQEDPDVLWTDFEQAFATAEAA

>contig32679 Frame-1R

MANFKSLKKHTRTKSSTSFSMQPAFQPV

>contig32693 Frame-2R

MSISQQNTEENTQTCEDTPILCLMRLVLHPEVDKAVTAFQKNALEKSGLYRIEMQMLTPR

VSLGRDNYVGIFDQKNSGVDPVKLSRTHCIIETAVDPATHQYAVFITDKSTNGIRIDGVQ

VIKNKKYKLCDGQKISLLSSRQGNVLLGYMVEDPHVRCQDEGLKQQVEMDSQDNTQQGPN

IQEYTLGVLFSAPLVGKDIHGKYHPIAELDVKREYSILQKSLMEASKFAKRPVDLNAHGL

GTVSRRYECPRHISVVSKFANTDTFRAMVTLGCRALHFSGHGDENHLYFEDGMGLVHPIL

HKGLQELFSAGGGGELTLRLVFVSACSSAPLAHAFVACGIPHVIGVRSNQKIEDYAAIEF

TRAFYLALATGKPVGASFTIAQQSVAKSPNIRGPMAVAEKFMLLPEDGDHTEIIFPLAAV

ESTSRVNLEPIKTKHYPKLWFDDLPAMCQGFCNRSIEVYKICLALMMTQSRITRLVTICG

EEGIGKTAVAHAVANYVGPRITSEGGVRIFSIAKLAQDVVDDHVGIMRRNMNIANGRCRV

LSRLETMVSDHLKQHKARIEFNGQQMLLIMDGCDYLLRNDTRRDRFRAFLSEILTNNASL

KIVLTARTSLCVDGAVRGHGERLYTLSKFDMKKATIMLVSLMSRPIRVDELKLSCASTSA

DKLERIASHPALRATKGIPKRIADLAGRLNEMTMDKIPVDESVLSLIEC

>contig33180 Frame-1F

MKQNKYVRAAERKANESQTQGESDEEASEADKSLEQHRQVPSYRSRTKQRENWTNAEQQG

SKPLRTVSGGKMYFEEQLDEIKRVHEQTRQREQDAKVAV

>contig33203 Frame-1F|Blast-Der1-like family, putative [Phytophthora infestans T30-4](gb|EEY68036.1|) 1e-36

MAGSIEAWYYGLPYVTRFYLSVCFGSTLLSTLGFLNPQSLYLDFDLVWQRFHLWRLTTCF

MYIGGFSFPFLMQLMIL

>contig34044-1 Frame-2R1

MLGLSKFCLKISTRTCKIPSSIDLYPSISYMT

>contig34220 Frame-2F|Blast-ribosome biogenesis protein NEP1, putative [Phytophthora infestans T30-4](gb|EEY57583.1|) 5e-46

MSAIKEEVNRRQVIVILEQAALETVKTSKGYQLLNCDDHKGLHKKLNRDASQSRPDILHQ

ELMALLDSPLNKAGYLKMYIRSTKGVLIEVSSQMRVPRTYKRFAGLM

>contig34981 Frame-0R

MGGPWVRSQSPLGFDKDSATSSDSLRHVNANYPLRHSLDCELSLQTDVIQSRPLNFMGRR

KLDAGSSHEGNHQGYRDFKLVKEHTSSAESLKNQDGLRTILSQESPQNQNQDRDNSTAIL

RLAKGDGESGGSSTHSLDVSGSEYSGAGSNNTTFSRRSMVTKIKTDLGDLTPVRWEKVVI

VQVSVQGFREMMSQAKDFMEDAKLLYEHTVLSRLASEYGGQEILSHSRSGLFVIAFASEF

HAAKWCLSLQLSLVYAAWNDKLLKQFDDMKEILVTTTGKTKKNMLLYRGFRVRMVIHTAD

PDVNPELSLCEAVKWTKTVSEYAHGGQIVLSDSVWDRLKEQLVQLGNPVVEDLGGHAVLG

DEVLLMLLLPRDLELRRFPTLKSPQQLSLGMRDAPSAHKPVTMVFTFIEGARPLVRCHAE

ELADRIKTLCMVARELLKKHNGYECQELQGDFMLAFFTTATAILWCGEFQLRIRQKFCEW

DLENENQELRFSMSMGIETGVPASVSPHKTSGRADYFGNIVNQTARIAKAAHGGQVLIGG

DAWSAFCTAQATCPSQQIIAIAEKIKDIPGFTVFHFKAHGYYSFKGISKPIGLIEAIPID

VQSPVLSLELVTLIRGRTPKSKRIDDAALANQAKTTVSDVPSELVRLRHGGEQPNNSIRE

TEFDLNLSWDDSIFVFEDIDEEEMEDKEFGRGSASQMVYGSVALAMRNSTLNHSRLMAQL

RLSGMEGSNTRSERGSANAIGSEDMNRV

>contig35393 Frame-2F|Blast-myb-like DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY56170.1|) 7e-10

MRTETSGRAKAAVQSDAGQTHL

>contig35537 Frame-1F|Blast-hormone-sensitive lipase, putative [Phytophthora infestans T30-4](gb|EEY58722.1|) 1e-129

MGWQVFGESRLARLMTNFQCPKLPVFEKQYVATDGSSSHTKRDNASDIGIYLFSARPVNS

VKAGTWTDASTPLTSRMVACGLPSTRPVILYIHGGGFFGRFIAKDIKNLKNWACVLGAVI

VYVDYGLAPETHYPHSMNQCFTIYKWLLNDGLGFSPSKIALFGESAG

>contig35902 Frame-0F|Blast-phosphatidylinositol-3-phosphate 5-kinase [Phytophthora infestans T30-4](gb|EEY69411.1|) 1e-120

MPDHLCKVCYDCSAAFFLFRRRHHCRLCGQIFCHECSNYFIDGTFHGFPGYVRVCAFCFE

FANAALKNEMKPKKHQRLSIESPNGNETSNESVSSHLNKAAPYQHNCEVAFTRPSPLIFG

YSESLNDNSLLLSPVDSDLRDQPDVKQHEDSRIITIDSANSVETSESLIMKRNNCPQART

RKRHYSAELLKIIECGGLMENKAIAQIKGNEELPHEIKKLSVSEKIQKENAACLRTKAQS

RREAALDKCSKTPMSRFATVSNDRSQI

>contig37746 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67883.1|) 6e-32

MVLTAQIPFNTSVADAKQACPSQCRNHKLIANNQTIRRADARAIHRVRLCYRDEAYRQRA

EERTKNLIVDASSPTNSSTSVLLAKKALKYRKVYDRITNVNVNDPKFDVFEFLGVDWCKS

TTTNSSGYV

>contig37812 Frame-0F

MQHNVEDETNNADELQPPPEDHPLLVQEEGKSSSHHIHVKATKALVASKILFLDGVRGLA

ALLVFAQHVPEYLKNINVGAVAVDSFFVLSSFLLTWLFMKKSLRLVHERAGLRKWLYVLA

DYFCKRFFRVYPLFAITCVVLWFMDVDSRRHYYLGDNPTAFDLFKTLTFEFHSRYFVFWT

LPLEISYYFCIPVFVYGTIVLRRLWWIAYLPAYYWVISQGWTEYRTSHTGLLPHIPTFLA

GSMAAVIFVKLDTWIKARKFQFQWFHTLVLRAIELTALGLFLSVVFRGLFFVWIHENVAP

KSPGFPFTSVLLTILLVCELLLPSPLSRMMEWNFLRFWGKVSFSVYLLHGFVIYNERLNF

QTDYYCRLFSRLGMLALLTTASYQLVEYPSQLLARRISKTLDEQEAKASMTMPVLCTFAS

SEGSKGLGAGVIK

>contig37939 Frame-0R

MVLSMWLLEILERLSLKFFFKGDELMLIQSSHLLCTQIGRRKATSILAKKFGVTVANRHD

QIVSTLGARFLKCHSSSVSYCSAINLPLKEKLLTCTRLVTIRDLQIYGEKRLQLTNKSGP

DLVKVSLIRIPANDLHWCLLLGGIRGNIDIGDLEVFDRTGSIALRLNGGNSGVSLCNEHG

MYLFRKFEFEIEKSSQSQEVQLEENVPMIYSLACSADNVEIVRLHDDETISGPLEGIKMA

VSENIEEVIIMVTRLDAVPHSSIRSIGILNQYRFLHGIIYPVGNACSTDQFLKSVYTADI

LVNTQIHDWFIQKGG

>contig38026 Frame-2F|Blast-unknown [Picea sitchensis](gb|ABK23920.1|) 5e-11

MDVLLVTLFVQAGLLISSYFWLVYLVIPGYLLYHGGRMVLKYVFTPNSIDENDPALLKKK

EKAERKAARPKFRSGRR

>contig38053 Frame-2R

MVQLFVVARELARIYGPDFVQNISAFLTFKPSMDGQFFELCFFAKLFYGGVECFKSVRME

RYFYMINEACRRSVLLPYRPTMEDRSKEWTVPRLWNQGGYDAVYEEKSIDNTGIPTVRIR

IVQITRAEKHSFKYQYFASLLRNLTESLQSHRVQPVEVYFVVPIKELSIFKPKIDT

>contig38224 Frame-0R

MAILQILAILLFGNSNLPRNNKEAICFPIFTRPREAMGTPFPKEAILPCRAIVQPISELS

SHEATLDVRPTSPTPRRDNKLPSWMQTS

>contig38291 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56468.1|) 5e-11

MHEVAFFKESVFNLRGDISFVKHRERMSRD

>contig38703 Frame-0R

MLGHARRRRSTLLKHLFSSAAIADAVLTREFIYASLYAKEAGYFTTQHREVLHTPAQGID

FGNLWGAGEYRSVLAQLYKESPEAWLTPVEIFAPHYSHALARYMLNSPFLRQELVIFEIG

GGSGSNALHILNYLKEHMPDVYARTKYTLIEISPVMAKRQHKCVTTVHPHQCTVINQDIL

TFADTHAPVSSHCFFLALEVLDNLPHDKVTIKNGKWFETVVKMQSDVGIPVLEEAIRPLN

DMLIRQTLHYFGCELPLHVSYKNKSGLAQRVRHMLGKESPALTSAFIPTGAMQLLNTLRS

AFPQHHLIAADFDSLPAPNLNELSDVKAIKHPLSPTATSAGALFAGNAPLVASKVTG

>contig39340 Frame-0F

MLSKTLVLLGLCVDLQMVNARGIAMGMGPRRRLGSYKNIDHHPYKNDHGYKMDSNDKGYD

YPYYRRRLEEKDIKSTESSDYGYGKDDYDHKGYKHD

>contig39601 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55853.1|) 1e-106

MVIRGADPLSYGFVIPRPISAFLADTCTAALYSVYIMALGYWATIILRGAAVTDKPPKLV

CLESIAIAVVWTFQILYDMCLFLSKGFNPEGLVYMQLTVSACMLGIISTVFLIYGLRVLS

RLQQYERQMKLRMPSIQSDRMMSNRSFDLNISEDEEDPPVTQSRKACRRQQEGHTTKIKK

ILFVVETCSFIVVAAQMYMAIDRTNDVSVELLCANGHRCETVHCRVNVLHVFQVMCIWVI

LWTFRKIQKKAVVPRPHASRAVGSSGLA

>contig39708 Frame-1R

MSRSGCLARYRSYDPTSAAHFDSMLAAFHSADLSSTTGQVFPSDALSTAIQHPRDYVLLV

LSSPLPLPSPKLGAVYAAWDEESYWSSSPDDSPNPAETIKTPASSSSATLSGLMPPATSI

IGACGDNPVPV

>contig41934 Frame-0F|Blast-histone H3 [Phytophthora infestans T30-4]gb|EEY69440.1| histone, putative [Phytophthora infestans T30-4](gb|EEY66013.1|) 1e-68

MARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTE

LLIRKLPFQRLVREIAQDFKTDLRFQGSAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI

MPKDIQLARRIRGERS

>contig41981 Frame-0F

MIRKAGTIMDDHVPDVAKLFTSHLKMNMRESGVEARISKYSMDFDRLTDEHRISTWVIRG

SANDVTGRQRMKMRATSC

>contig42733 Frame-1R

MTRLYVNDAIKYLRCKFDNRMMR

>contig42746 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54952.1|) 3e-85

MHKAQEDSAEVVFNGWMSALRLLQDDDKRVRAKARHAVLYALLNATEKPAFHVDSSQSDA

AILPVAINFIASLFVKTKDGAKNLSNVLMKLIDANSVLQAYTGAAGAKALDWNDLYRRIF

ESESNNYFAEQDVVAQNWIIALLIRAGSESERIQSLHALILTAVECVLTTLIHDAQACLD

KKNQWLGGILYFPNVFARLFGLLAAAVAILTSSLHQLSTELFSLANKVRELAREALQFYG

KDDGMHPFLIRALELLASNQENGLTTQGAEPVRDLLYLTPDWAA

>contig43352 Frame-2R|Blast-DNA repair protein RAD5, SWI/SNF-related matrix-associated actin-dependent regulator of chromatin, putative [Phytophthora infestans T30-4](gb|EEY55917.1|) 4e-71

MIHGAKESSLAALATPLNLKIESPALQLNTRDLDTLFSECLGGNELQQSMNDLDFDPADD

LTQYFKAFKLRDHQKQALRWMLWRENQLRYGACEQDRYDSMWEEHHFLSNIAYYVNPFEK

VASLSRPKSPLPCLSGILVDDMGMGKTMMMLSLVAYQKYIREEQSAMVNDNYLGRVNAKL

SGKSLVICPLSLLHQWKNEAQERFRAKTLSVYVYYGDDRDEK

>contig44788 Frame-0F

MLPLPMTLKSRRRNARTRRTRCIRFIQANGFETVTL

>contig46203 Frame-0F|Blast-lariat debranching enzyme B [Phytophthora infestans T30-4](gb|EEY62947.1|) 4e-97

MVRVAVVGCAHGMLDDIYATVNFVNQMNSGTPIELLLCCGDFECMRNMRDLDSMACPPKY

RALHAFHRYYAKEKTAPVLTIFVGGNHEASGYLQELHYGGWVAPNIFYLGAAGVINVAGL

RIAGLSGIYKQQHYTMGHFESQPFDENTMRSVYHIRELEVFQLSHVQELDKTPVNAFLSH

DWPRGIEQHG

>contig46276 Frame-1F|Blast-proteasome subunit beta type-3, putative [Phytophthora infestans T30-4](gb|EEY54548.1|) 2e-38

MMTQDFVVAGTMEEALYGMCESMYKPDMEEEDLFETLSQCLLSACNRDALSGWGAVVHII

TPKGITSKKLQSRQD

>contig46526 Frame-0F

MEKRSVEQDYEASIKKIDTSSTILSSKRPKRQAVVR

>contig48281 Frame-2F

MMAWSEEQQPRTDNGEWPDTELLELVNLSPSEDTDERAQHGASNIQSNASQSVGGLTYSA

SCPSFSGLEESSTFTVAEAGENGFMSPSQEPLEPMGNTSFPSNKSYNMLLQFQQEYQNSS

HRQFPHQQAMRQPNNLMPQQISGARRGFHGSQSFTNLPSMETEYKRLHPNSKRKMEPERW

LKLQRHKSFDSSTSESEASIVNTNVIIDNALCSSSYIQDQLLNEPPESDTIGFSIDDVPN

SNGLGLPSVGCGSASGYVDYNYPETHLPQHQSEFHMQFGSKVDGKSSAFVPAEVEPESEL

DLLLSETEQANLFDAIRDFDAPSTRDSIDALSL

>contig49369 Frame-2F

MSNAELTKIGRMDDQMADNAQKSTKDDLEHPDKDEATVDASKMYSTPMNLEEYWFECDTR

SKPLVLLELLSDFADSLSIVFTASVNATHRLARLLQLYSSHPERIREFSSSLSQKQRSSL

VADCKTGRVETVVCSDAMARGMDLEEVANVVNYDVPSFVKTYIHRVGRTARAGRHGRCVT

LVKMGQLKGMLRMLKKADVNKLKPYPLQQEHMKTLVPRYTEALQQLKDTLEAEKTGKILT

TSIPRKFNVYLHESNTSDDMFNVKSKEKVISTDKKRTLAVLNAQLERNLARRKILKQ

>contig49383 Frame-2F

MVVSARSIPIKHSVFDLWCLGDHRLTPRVEFAGHQASSVLSRSAMWSEADGTSIVASWSQ

DVEKVTLWNPATHGEIKGFEPEFSSVANAAMPVVDIQHAVAMNNWSSGTALYGTMTARQL

CIYSR

>contig49512 Frame-0R

MGNFNTCAILMNDDKSSHFSSSSYPNGKCALLDEKRVPTPREKSDLSTLNPKKRPRRVVD

SSTTCVPEQRHCRYANKRCLHPRAVKRTGGLHTFCAMHRANANRNQRRLDMRKRMARQAL

KVEATDIHSHSSTVTLKQQHDVVQDTTAQLPRRNFNTNFEPFYEPTPLQEEDIATLVMLF

LPRQGATFEREFGTSLVLATPNEWVSTASSGSNDHILPSSRI

>contig49857 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56930.1|) 2e-14

MELNALPPLSPTMEQAFYEAFADMSDLEKRNNVSFFKQKPPNNALQSKDVASALTPHLEP

RKRVELPLCQLSPRLFKCHSITTNSDLKRARRSAIEKKSRQRRNEHLRRMRDQVRKLETI

IRQGFEGYPSCTPNDAII

>contig51391 Frame-1F

MSKFRVVQLTHEALKVQCKVDDFEEWGAPALDRSQYLCKEELQRAMAFSQQGSIFWALVD

TMEDSELVAGQTVIYCHCESHRFDCAVRHGSGEIKRGFSHHIGSVFTLPQYRNKGLASFF

MKEVANQLKLLPGALVSILYSDIGPTFYDKLGWKLYPSISAILDVEHPVNANAGSNYKAE

LVALTLDDKLDDILKADNTRLVEELSSNRFKKQEAFAILPTRDSIEWQFCIGVHYATAHK

NSELPYYCGVKIHEDAFLIWRHNFKESTLNVLRARFPEKRDNFVNVIHLLLNEAVKEARK

FNLQKIAIW

>contig51676 Frame-1R

MMPLVNSSKHALMRSRHPGADIFDPLPSKGSGGRGIGRTQNAIKHMKPCLLIHPGAKITH

FLQECGIIR

>contig51849 Frame-0F|Blast-PREDICTED: hypothetical protein [Nasonia vitripennis](ref|XP\_001599751.1|) 8e-11 NOT\_ORF

MQEVIWLSLLLKDIACEKEMATTKIEDNHGCIALAKNPVFLTRTKHIDINLHFFREKDDK

AGSSFERQWKHKDLPRPSKSLFSKLQADSIVALTCGLLCAVKRFGQ

>contig52008 Frame-0R

MVRWEPKEERDEEDQEHLRKRKAEDVRLEYPCAACTERPRMIPINYV

>contig52866 Frame-1R

MQYQLRKEKHKQEQPRALTTRQARRSSRRWSITLYAGEPRETTHRWKRREIRLASTRRFV

ASVFVIGQRSAHLKCMMTMCASQIWRYELSGRLASRLMPTTARSQRTDERPCALSMPTSG

AWRYFY

>contig52978 Frame-2F

MTNPRLGSRSLVNRIGLYRSDATMGMTNTRIAKVAKLRISLHLSSKFAFAHSSLRSSA

>contig53641 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62486.1|) 2e-06 NOT\_ORF

MQRDIHSNLRTKDWEISIVDIKTGGCFRKTTFLEHFINRLLLIDIIPSFCCPHNSHSEEL

LNDTKIFKLKHLHVGIKLIKTFHICASNKQVIRQTPFS

>contig53775 Frame-1R|Blast-zygote-specific protein [Chlamydomonas reinhardtii]gb|AAB21907.1| cysteine-rich protein [Chlamydomonas reinhardtii]gb|EDP01443.1| zygote-specific protein [Chlamydomonas reinhardtii](ref|XP\_001695656.1|) 9e-18

MMKKLSTALVLSAFVLAITKVTAGPLAYGICQAGCNAIAVACYAAAGAKFGTVTAGVGTA

PAIVGCNSALGACMVKCVAAGFLPIP

>contig54341 Frame-2R

MTLNEATSCSSAERVISPKKKAKAEDFYASSALSKWAAVNIVGMQKH

>contig54811 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60688.1|) 4e-26

MEVVVHSCAQRTDEKTAIAVANAYTWELPAKTWFRVSQTQDLEERRARLELSLETLLLQK

NREICNLPLLRDFLMLDVFGLQVTQQNNHEIAAHFE

>contig55070 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64506.1|) 9e-39

MSASAGINSGDEVNIFVDLDHRHTRGSDFETHNGRKLLIALGVTTMTRTEIFRATRGLAV

TRLVRLCPDAP

>contig56769 Frame-1F|Blast-PREDICTED: hypothetical protein [Mus musculus](ref|XP\_001003060.2|) 2e-10

MIPESFEETAEMNVLPPIPLGEPLLEPMPQSIQEPAETNLLFLPSLPFPPLPLPPLPSLP

LPFPPLPFSMADDSPVTLPSASPNSRRLRSH

>contig56783 Frame-0F

MHYLLLLSLHWLSSLQDAHVGF

>contig57267 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY66867.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58787.1|) 9e-18

MASASAAQAEMVASLIGEKVLKALDQKEQKLDETIKKLEEADEDELERLRERR

>contig57858 Frame-2R

MILQFKSEMFHLLLSNFSTLWVSNRLNVSIS

>contig59496 Frame-2F

MLSLFTMSKAFMKSSSTISNNSSWILWSSCYTVFEGCQHEHN

>contig03108 Frame-1R

MSTRNGYRIQRISRDNIWPLAKSTLTGLVKARKTSQKLCSSLRWQGPDGIQLGISGSIAS

>contig08505 Frame-0R

MIFLIRLSTTVFPPFRGTTNTRVIYHWHVLGLKTPNNEPINNCYTEPAIRTNHLPTNVFV

SLFCSYPEMWPITYQV

>contig09331 Frame-1R

MKLAIKATMSSCQLRKKQQQKQSPPSSPWVLNYKKQPARKWS

>contig09890 Frame-2R

MRRASPDFTSELNVFIHLFGYGRRYEGAIHDFKFITHMRKVSTELSRRVRCSLVLISSYS

FLLRRSRVRPVAIKT

>contig12612 Frame-0F

MIWYNCKLNTWYKNTTNSVLGSIKTCSSRLMLAYQPTERWVHCSWI

>contig12973 Frame-1F

MSCLRHPNIVQFIGASWDNASNLCIVMEYLENGDMHSCLHSRIGKRFTWADPLLQMAIDV

VQGMLYLHSQERPVVHRDLKSVNILCSATFGCKVGDFGLSRRYQKGIDALTTLVGTPFWL

APEIIRSERYGPEADVYSFGIVLTELETRETPYYDLEETGLKVLMRVAHKGLRPSVPSSC

LPARRKLIQDCLCDIPNHRPTFLQVLCRLQGPVRLEIEGFAALQPELGHRVRYQERRSL

>contig14481 Frame-0F|Blast-predicted protein [Phaeodactylum tricornutum CCAP 1055/1]gb|EEC46688.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1](ref|XP\_002181474.1|) 2e-10

MDAWLPQASYPCGNFSDTSS

>contig15301 Frame-0F

MANEPLLLSTGTDNSIKMWIFDHVHGGTARLLKSREGHCAPPTRIRYYGNNTLATMADGA

DGTCCQILSAGQDRAFRVFHTAREQQSREMSQGPVLKKARHFNVRVETLKLPPIVQFAAI

ETRARDWANVVTCHENKVGAYVWRFEHRAIGKKVLQQYDPRNHVVSGSVEDLRRKKTQAT

SVAISSCGNYALVGSLGGSIFRYNMQSGETRGSYPVAATPKAPIIQSLVLPGTDLSTLQD

DEAAKTAVNAHTGPVSAVAVDALNTTLVSAGIDGVLKFWGFQKHELRDEIDVGSPISQME

LHRDSNLLGVACDDQVLRLYDVATHKLVRRFAGHSHRVTDMTFSSDARWLFSSSADASLR

IWDLPTGKCVDWMRFHKPVTGLAVSPTGEFLATTHVAHVGIFLWANRSFFTDVFFDAEPT

APILMDLPVSLNEVDNTDQLGVGTERNPQVLMSTEALDLMKTVEKKEEREPSDPLDASLI

TLSTAPRAFWQSLFNLELIKKRNKPIEPPKAPDKAPFFLQTARKDDVQPTFVPLAAEKKT

DVDKDMDIWDAGDENDSWDIDDGEAPEDDEVIVSSSRILKSEGMVTSRCKLATLLAEAVK

KKNEKDLTFACYRDVGSYMQSLSASAVDVEMSTLCMGHFDEDGKKLLGWFLDFLRMEMKS

HRDFQVLQAYLNRFLKLHEDLLVANPALLAQVDELGVVQQQQWQHLQKLLHNNLCLVQ

>contig15640 Frame-2R

MLHLCCCLFVACGKYYPPLRLFNGHLQTLFFAFDESGPL

>contig15749 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58752.1|) 1e-161

MIKSTFLVYFRATKPEDAGDSGQCEQQNSSKYLNLRKCKIKLINGDSAGYVLCIKPETGK

GALYFAADTEKDRSSFASKAVAVQHRVLSLKNFTTLKLLGRGHYGRVILALNDADRQLYA

IKEMKLGQVKSKVVFGERAVMEWVGNHPFIMELDYALARGRSVFLISKFMQGGDLFLHMQ

NNGGNFCEEAVRFYAAELLLALEYMHNMCIIHRDIKPENVLLDGEGHIKLADMGLAKRME

TRAGRTKTICGTDSYLPPEIVGRYPDGHGLPVDLWQFGCILFELQAGYPPF

>contig15824 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69848.1|) 6e-67

MEESIVASSGVKTKGSDSNSLEADKTVDQCSHERGSVKVVDNVRTCVCVSDWTHPPECNQ

WPLWKWLVTIAGGLATLFSIALSIRAFLQNRHKKNK

>contig17358 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70004.1|) 5e-40

MTLASDNGQLDPQLYTMIALEHTRYCAFYAKLSNGASNSWISRTTALDFYRKSSLPEAQV

QELYARIKEQHLLRDNDRMNETEFVMGMHLIVCITKRNLVSIPPTFPSYLFPLLNLTPER

LREDPFLAPFPEISKAS

>contig17426 Frame-2F|Blast-peptidyl-prolyl cis-trans isomerase E, putative [Phytophthora infestans T30-4](gb|EEY65819.1|) 2e-17

MDDSELFGKTLRVTIAKPDRPKLGSNRP

>contig17552 Frame-0R

MCDCHDRVATPRESSYALVSVDAAIALVLEHSQPREIITIEAYEADGFVLAESVYSP

>contig19312 Frame-0F|Blast-serine/threonine-protein phosphatase 6 regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY61995.1|) 1e-172

MSLFSAMADDSSVWAQGSSLFNLSSPLNDLLEKDIFTLEQVLQEDELVQEVKTRNTKLID

FLSQEATVLELVNYVVRTSEDPTDAVRTLKYPYMSCEVICCDITSITETLVSASNGFLIE

TLFTLVYQSTPLNPRLAGYFEKIMTMLMVRKPHEMTMLLNKHSEQLLRGFTHHIASFSIA

ELLKRLLQPYQNDYMDDCMEFPGLSLNGPSPPSWCGNEDDEGMSGSETQTTPKNKTLTWQ

SDILVVDLLMAIVADSHAENDAQTHAAEVLVDIIHSGSHIQSTEPTSPVSSSAPVSFVLL

EYLESQRMVEKLVSLAIPSNDTSLTGKSSMLGAMAILSALLSRATNAQYTCATEIVPPVV

ACLVEKMPDLCEVLTASNLDIETIRNQRHEQVPRLGFRRLKTVHVVGLLVQSKYHAVDRA

FQAYPVISCCLDLFFQFELVNLLHTEVETMVVGILESGS

>contig20200 Frame-2F

MTNAVNNSLKILNSEAASLRPERWTTKKVAYADTIKRRKSLGALQKRLSSQLDTPSEKRR

KSMPVGLLRRQKQQTLENGSVISGKLDRNLSQSKKKLLSDILQRATMISQRQNIFLETSL

TSQAQSGEDNTKSDAISDTIKQLQAEPFVLESFSSVKSSSVEAFMDRKTKTVMNEFKTRG

NLGDVIRKAIRKRKRDLTLLRSHDQHLLPQQSSQSLHSSNGVMECVQDRAWIKVHLKRRC

AAMPHLLLYECQMHDYEVRKLKNAPRAFKEKNMIVKAFFDLRDAGYPKLSDGILLKIYDP

LYLVAEQLAAGSTREPTYFLLGTQLAESLNDS

>contig20785 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63842.1|) 3e-90

MDIRRLLHNPDDGGWFIIGETKSEFELNEFRRSLKRNAIINTHLVNCTISHENLGANFAN

TEHKMKVQWTKCTSVLCHPKGNNQNKLGNACKPRICPVQVRMSTCQLTFAGIICQAYQHL

SDEQDSAEPLQTSVTEEMKSHIVRVLQRNPEVKPMTIYKELTALHQQGVFGADPMPTKIQ

LRNALTYLRNRKPKLL

>contig26776 Frame-0F

MDDTMRRNAKIERDMLREVRHPFVASLLFAFQNEDKVYMGMEFYNGGDLRHHLTMNQNNE

LKLTAGRIKLYAAELVAGLAHLHSLDIIYRDLKPENILIQKDGHIVLVDFGLSTYARHDE

NMKAHSLAGSPEYISPEVLAAANPKKGDPLALYDKTCDWWSLGILIFEMYVGRTPFKDDN

KAIMYRNIAEGFLYIPPELPEDVQSLVLV

>contig27173 Frame-0R|Blast-fumarylacetoacetate (FAA) hydrolase, putative [Phytophthora infestans T30-4](gb|EEY66444.1|) 1e-137

MFYTKSSMLTMRCLRSSVRPLHFHSTNASCRMLSSMPRVDGKATVLTRFLDENGAVRCGQ

RMEDGSTALLVEDDDPLGTLCFTGRTATIRKILAPVVPSQILGIGLNYRKHAKETNKPEP

KFPVLFTKGVNSLQHPEEPIIIPRIASEPPEVDYECELAVVLNKNACNVTEEEALMYVGG

YTCANDITARRWQGVKGGGQWCRAKTFDTFCPLGPVLVMPEIIPDPQTLALATYLNGKQV

QKSNTGDMIFSVARLISQLSQDCSLPKGTVILTGTPEGVGVARNPPLYLAPGDMLEIEIE

HIGRLVNPVESASAL

>contig27883 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70313.1|) 7e-25

MSTVSTNVMRYDVPNGDFCAYLKGFWKRNLEWHRFGGGFQHLRSTNNVVLIEEDLDAARQ

PNTQ

>contig29294 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61671.1|) 1e-32

MAQLEASMAKLSGDMTEGRKQMARLPAGCKTLTTEFWTPVAIVENVYILPGIPSMVRAML

TANEKYFVGVPIFRAIV

>contig31732 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54036.1|) 1e-106

MGAVLNQLAHIHDDIDAYIRSSSELLAKKREMYAKQGELANSSCAEAIEEPVVKKQRIEM

AMPSDHMVKVERIAAAEAATEAAGVNAIYEVFVSDLPWGTTREADVLSYFGIAGAVLSVQ

MPTMADGSTVGVAVVRFAALEGMTLALRMDGYPFNGKNIRVAVHKSA

>contig33169 Frame-0R|Blast-polycomb protein, putative [Phytophthora infestans T30-4](gb|EEY68889.1|) 4e-22

MCEPAVQPLSSKESPLSNTTAADVITPPSLLPRLRKKGYKYSSYSREDHGNALYCVTFCD

VLPIYERIFAVAGGNR

>contig33204 Frame-0F

MLFPAIRVWKYLPDVTNEEEKRLSLKNDESRRLGIQSLQDGQEFLVPGTTSRLTTVYTPG

HCNDHVCFVLDTMDEWSGPILFSGDCILGFGSCLFDSLIDLMASLAKLDMYKASTIYPGH

GPIVLEASAKIQEYRTHRQEREKEILQVLKNQPNATVWEIVKQLYEPLPYSLIMAASQAI

RKHLDKLVQENRINELRPA

>contig33521 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66966.1|) 1e-27

MRSSLYKAYPRRLLAPNRRQKAKESSLIRPQALSRQEVRQNKQSSGIVHSPTRTVNPTAR

GMSSKKHRFSLLRFFKLKDENVNTTKEAHIQPMPLPTEILTRKRNGSVMVSGKRVPFMHD

TQKRRRKFTKPLPSIFEDRPFVTGNSSLEAYRRRAYYSAAKEKNKR

>contig33688 Frame-0F

MANRELLDERQPLLGPPGSSGARTAALSPSTESASAQWRRAIHHGEQHRRQCTDVVFLGV

FATYWIGMVALAMTAFSKESSVSFAQEIKSGVDFQGRACGARQFVYFPDYKTNPDFGFCV

DSCPLRSGELLTVQLPVKSNTKEVNGLQELQQVHFTSYATHHWAYVCAPAEVNSEQVMIR

QLQDSFGRFVGALGNCWQVFLIATAVALSTAGLYLVLLRYCGCVSVFLSTVAIESTLVYS

SYRLLHAASDTVSYGNDPVMLSSLQISAVVLCCAVILFFLYAAVNLSRLLLAGTFISHAA

RALSELKRLLVLPFIAYVLLLLLFAWGIFVTICLFGAGDTFTRVATIQATVPSSFQIETE

SFQVSMELRWLVVYHLWGMYWSVTFVLALCEMITATAISLWYFSPENRITGRKEFQEADP

VSYAAITTIKYHLGTLALSSSSVAPVEHIRSFLLYLEHKNEYDANALTEFVAKCCCCCSC

CFRHCLKYICKEAVYVSAIQGTNFYTSGKLAYTLISSNLLRVGALSRIGHASVLLGKLIV

CTTTGLITWVLLDD

>contig34043 Frame-1R|Blast-protein enhancer of rudimentary [Phytophthora infestans T30-4](gb|EEY55861.1|) 7e-34

MDGVVKMYEAKLKQLNPSLKNITYDIQDLYTYIDSLTDLSALVLDLETKTYLPCGKEWIK

KKVFQVLKNQAG

>contig34986 Frame-2R

MGSTLRDVAALEGYEAVEVHGRNQLPEIGRCVSLRIPLLMETLLYCRDELLFANRFIGCF

QPSTRVPCISVRDVGYAAAEVLVNTKRKYESVYRLTGGNHASCSPDEIAQTLTELLKREI

KYRKLSDAEYLQVMKEKDVPEQAAQGTVGLRIFLEEASNSEAIRDDMPHSRQAPREAERP

RSLHVLDAFRSSSNFRLLTKRDRMSPHEWLERHATTMFAGSPHTQVQIFIVGSSDALFLE

VNNVVTSLITAPSALKTREVGASNLLLGRSSGTNSVQDAKVTVCTVKSAPGGSRRAKPLD

TSGPSTMYQL

>contig37239 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY66548.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62034.1|) 1e-164

MGATEAGWSKQETLKAFQDAGNLKFLEHINLSNTDKCSETAPVYIFYIRGLQCARDTRLA

YHIWANYAGRHQFHLFTGQPKNDCINATIYIYVADLDATEKSLASVADELKGTKFSIKRV

NRGFTSTIDYPLEMWHELFDANDHDHLEVTDPYGNKLCINVTPRNYNSINSSLGKTLPMT

NGVAEMPQGFPFMLYPCRPGIAQGISRFFEYYLGAKTVVTKKNGNVELYRTSVFCGPVQS

IIFDEQESETNSKGEYDGHHLCIHIDRFQEFYDKAYQDSMQWNNVRFFDRCDTWFEANRD

QQYRILHLVDPIDKTFLMSFELEIRSAQHFRYLIHRSD

>contig37741 Frame-2F

MAAGADSEIINATDDPSAAQQAMIKLNFSSDSDSDFLSPSERERHSAGSAYSPNHGMFTT

KSVAISEAGISSPDAACLHLQENLERVNEIGRGASGVVHKAIHIPTLKVVAVKDVPVYGR

GQRRQMVRELHALYSNLVPMADNESPNSQHPAPNSNSSKPNPRPSPYIVSFYDAFVDRPK

NSICMVMEYMNTGSLQDIVLRGGCQNEKVIARLANGVLHGLAHIHNKRMVHRDIKPHNLL

TNRKGDVKISDFGLARTLNDNFTSTKTFVGTLLYMAPERIGGGDYSYPADIWSFGLALTS

VALGRYPLPTQDGFFGLVDYVSNEHCLKLPIESFSDECRSFLDQCLIVNPNERPSAETLL

QHPFLDKYTSEQTVAEWKLFIDKINLCEERNTELESLSEAVYRHMYEHSVKISHLPQSDF

GVSFVSQATPTFSRRQISLQPVQK

>contig38021 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65139.1|) 3e-09

MVNKLAENVRPFSLDVRRGMYDDGKMYLSVVNTVR

>contig38223-0 Frame-2F0

MTLLSPINLLRSLSVIVGLMLFVVACIGFKTLNFSVDSVESQAQLGCLCFLGVCFGLLLA

FGETTWELFFFFFGFMRYRLGRACIFALSGTMTAILGKTRGQQCNCHDNLILIIEG

>contig38223-1 Frame-1R1

MVPLKAKIHARPSRYRMKPKKKKKSSHVVSPNASKRPKHTPRKQRHPNCAWLSTESTEKL

SVLKPIHATTKSMRPTMTLRERNKLIGESNVMTRD

>contig38296 Frame-2F

MSLSRTPRYRTPRMLCAVFFILVAVCAKSSYGHNVSVSSRDSQHIALKSDEHATIPKDVE

AMRRLRVAMTTDVVMHGGIVGKLKELLPNNDISNPFSKTRPSKTVTNSYGFNDVVMLDRT

>contig38469 Frame-2R

MAWQEEKKALLATIRSHEQKATLLAKRFKLLQQTLQEQQKLLNRYQIALRSFQTAYSKNR

KKTSNDITSVDSATDDKQQDLAALAWVKKKSVDLTEQPSIVKNSMTATVEKQAKEKKADM

TFPLQDSAKRTSRLAPTWAEEKQRDYKKPKRQQARKLAATSANKENVEMKQAAVKPKHFA

YVEVVRNQDERKALPAHDCVDCKKYFDALGEFSAIDAAQYKTKCSRHRARFEPYQTPDDF

WRLSFPDSEPEIN

>contig38487 Frame-2F|Blast-ubiquitin, putative [Phytophthora infestans T30-4](gb|EEY56642.1|) 1e-84

MQIFVKTLTGKTITLDVEPSDCIENVKQKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYN

IQKESTLHLVLRLRGGGKKRKKKQYTKPKKIKHKHRKVKLAVLKYYKVDDNGKIQRLKKE

CPAPQCGAGVFMATHFDRHYCGKCHVTYKFQSEDSA

>contig38704 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54092.1|) 1e-105

MKKKKRRREVDDYASVDEVEPESQISMDLSREMQPIDYAVTYFKFLFKREMKRDVGESED

VCFCCKDGGNVIECDWKGINNAFARCPKVYHEECLGYSVPDGKTWVCPRHRCQDCGIIAR

NSCRFCVTSYCDEHLPEEVTRLGSATKDIATSTYIMCNRCMRQIHVALKQKKIRPDFYSK

LTRQWTHKQ

>contig38771 Frame-2F|Blast-putative dolichyl-phosphate beta-glucosyltransferase [Phytophthora infestans T30-4](gb|EEY53237.1|) 2e-52

MILPSAALSLALMVMTMCIVLGVIMLIAWICAPIFEAKRRAEELEPMQEASFQDPTDYKH

LPFGSLGDEKAEVALTVVIPAYNEEHRIRVTIEDTVAFFEAKKESNSSFSYEIIIVDDCS

SDRTVNIVMQAVKKYSVTRIRLLQLQHNHGKGGAIRKGVMRARGERVLFADADNATKIQD

YDKLATAMDEVATSHGVVVCGSRAHLEEQAIAKRNALRNLLMHGFHMIVSTLC

>contig39578 Frame-0R

MVRREMTGFNLDEEKDEGHFDDDGNYVWSKEAKKVQEDAWLENISRQQMGAANSAKNRRE

IRDEQVEETMTIEESTKILAMLLGPRENVLHALKRIGSKKPSRIRPGEKRKQAQWSESEL

AQTAEEKEQFEQITEAADFLMRLGKVDVYVRTKEDFHREEKRLVHGRRENKSFEIECKNE

EILPKQENFWEYKAADGQIYGPYPTSNFLAWQQQGYFKGDKAVDMRQLQMSDYNSEKLKV

KRDEFPFEHDLLNDFEDSEDKAINVDTRVEKAGEIPWRRSDTIDFFAYS

>contig40394 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58240.1|) 6e-86

MSFTGLRFFLSLKLTVSVVQLNVPTSERCEPTRRKRVAYKHIYEDKTFSIGIFILPPGVA

IPLHDHPGMSVISRMLYGSLHFKSYDLVKDNAIYSGSKQPARLCVEKIITAPYTMEVLPE

SGNLHELIGGDDIGCAFLDIITPPYDVEEGRNCTYFRVVDSISSQHTENEKLWLLEKHEP

QDFVVVTETYCGPHISSTLN

>contig41128 Frame-0F

MRVEFAAPSPSDSTTAYTLDMGAQAAASSSTESATPVVSVQPKNLRRGNTFTGANEEEQR

NIISLR

>contig41227 Frame-0F

MGSPRINSSFSSPMINGGSYVNPNISAAAELQRARERTNARIMHQQKMASFSYGQHLNVS

ADNYELAGGNLGETQLYWERIRTLKAAYSDKLHTALRALAHNTAPRNSVYSVKAQSMMQN

IGLVLNILNEQPTNIQPRKFDILNSIERFMQMSVIPIVQKVLSSTESISSASPSAGVRTA

FSSPKADHNIGMDTTSKQETGTPCNSSQSFLYEKDTPEVSTYEVESKNDLDNSSPTMKTS

RQLVHELKAVNNGSAINDKAGFDPSDFVLSKADKEILSSQTLVDQDPITTPQEFCTSSLP

ALDSHLSASTETQLSSVSPPGNAQDVTNNKVMENNVDDTLNAFSELADMDFDDPVAIVNN

SSKVLRKRELEDV

>contig42239 Frame-1F

MAHHSRLEPLVIAQALPVKFASILSCHRSTSCKVIMRITFIRFRENRGLSTAGSIVSNIL

HI

>contig45735 Frame-0F

MLAQRQLPAHFMGMHYSLQESCKSHAFASPTKTLARIDYVTMLAAAAASKYSKFCVTCKK

IGLRLRSHRKN

>contig46169 Frame-1F

MVPLIKHNITMLIRSTMEYNGHGTYISGRPRLHARETCTTSLENLAIIEARTRILQDGSN

KYCDENIGARITKILEELQIPVWLSIRGAHGQAMSVVIPRS

>contig46723-0 Frame-0F0

MKSADEVDIAKQPAVKVVSTVVSIVAAAFLSGG

>contig47030 Frame-1R|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY54007.1|) 2e-78

MNTIFRDVIGGGITAVDGNQWRTQRKILSRLMTTRAFRESVFQCVHDYTLILGRFLSASA

KNGVPIDFADLMHRFSFDVFTNIAFGLQANSVEGKNHTQCIEAIGTITRNIEVRLSSPDW

LWKCKRALKLG

>contig48097 Frame-0R

MGKVRDLDVKSINSQYFDDKSSAWFADKTYNRSIIMACCSTQNEESSLSSLSPSNTSSAR

SNSPLQETKGGEERESLNLIGVDVTSSIDSEVQSETKTSMSSSLDDEMEVEVVERVDRAL

IDLRHLRTMAGAERVVQAVEEEEVRMMRESLAALDYKDVRLVELSPNEDSDSDYDFLSDR

SASFPLMEEDEDDVIEILGDSSMTVSTARQVVSSPRKEIPINDGTLEHILFRSPRENITI

DQRLQEQEVLLKRLVMAANSSAGYKPPSIRSQQ

>contig48233 Frame-1F|Blast-RCC1 and BTB domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY57867.1|) 2e-74

MGTTGQAPILRFSPGLSSLHIERVFSGNGSEHVAALSENGLLYTAGYNMRGQLGLGHSNI

VTKASLVEELAGQRVVDVACSFFHTAIIMENGDLYACGYNEYGQLGMADHNSQSLPRPVD

YFYRHPVLAIGCGRHYTIASLRDGGVVAFGKNDYGQLGLHCTSGPVFNPTLLAPP

>contig48286 Frame-1F|Blast-anaphase-promoting complex subunit, putative [Phytophthora infestans T30-4](gb|EEY66226.1|) 3e-19

MNSKLSFMNEYLEIVFAGLHMLCEEFKLSITHFQHHLHLAKLLLTMALRLELHPFISYYE

EDNRILQGRTKSAENHVGMKKFLKSERDGLLCFAAHGSVPDILLWLQDKMATKPPTIQDF

STLFDRVVQSSVCSYRQKVSPLRRTQAVCQIFKLIYPSLDESMSQVQTTQLNAFKLIMYL

TQDSVGKKISLDDLPVGLSIVIIQIIHQVKLHPPNFFTEDICEFVGR

>contig48444 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60248.1|) 2e-30

MEDELIAQRDAAIAVTKELQRQLQMHRIEMEKTFERRTLNAERLRLHAEEKLRRAVEDRD

WSENCCRQLLALALFLGCGGAAVGWALGLLVLLVSGEPLVGFLLVLPGMAVGTLLGLAVA

KAKIHVESRRRNSRYRDARRHFEVERAINSGVGEQDDALEPLQSVPGMADVADENSRYAE

QDRRRNGAEEMPVARGTASLLGRSWKAAWVMLYASKDIAAGLYHGGDYVRGIFEHKHEKK

P

>contig48660 Frame-0F

MQMENNDDAMDIVIQGMILHSLVKDSLPVKSLSHRLDRW

>contig48927 Frame-2F|Blast-DNA repair protein XRCC3 [Phytophthora infestans T30-4](gb|EEY60741.1|) 1e-50

MKGVRSHQPLVPKESFHFSDASLRVEQVMVTAFTLWQSRSSHSVVLPSGCDSIDSLLQGG

FRSGIVTEICGEASAGKTQLCLQLLLQCCLPRSLGGLESTACYVCTEGVGSMKRLHDLAQ

VYAKRYNTAVLSSGTKRKHDDTLLSASGSDFLDGYFYRKALCRERPNGSRGLCCMTIALS

SKSN

>contig49850 Frame-1R|Blast-glycine dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63500.1|) 1e-40

MRLQRILSIRRGTLLRAATARAMATSSGYAPSDGFLQRHLGVSSAKDITAMLSTVGFDTI

EDLVSATVPAEIRLTEPLNLPPPLSESAALAKLKTLATKNQTLKSFIGMGFHDTITPA

>contig51121 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61439.1|) 4e-21

MSPKRTRTSYQSALSDNVRPGGSTTMDVLIRWMRTSGNVKRWRTEPRAPLIREVVDMMQA

EGLAHRQP

>contig51154 Frame-0F

MRVHVLKVVLGSPQNMHQNHHHHMISRSNLSTHLLWGGKLSSIIACLCRGVVE

>contig51396 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64249.1|) 4e-62

MKRQCLQESSPHSMKLSPSRIGVNLSRRDRQDMAVIFEGVVYRFYATEFLRQEVLLLTND

ELLFYRSYASNAEKKSVVLTH

>contig51569 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61885.1|) 6e-44

MRYVKLAVEAGHDSQAAEEEIDLRLEQRITQLRASVDPNELVKEVDRVRAQSYLADAAVN

TFTRPNNVQSCIAASFSVPTTAEQQG

>contig52278 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64180.1|) 1e-43

MFPPHMIVTVEDTSCIARKMAANAEGRRHFAIGKGAAVAVKFSGILNDKSEPPTPAIVEE

DLNSGTPCTTTGLWKYLYAYSFLKPITPEDIEQRLALEDPNVFSSDMESFNGALNTAKEC

ERHEGIVSVQSVDDKFK

>contig52317 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY69207.1|) 4e-19

MDDSRDDLALVRHEGGKFISQPVQRSFTTEDLPNAKSFVSISDATLETKKRSSSDIFESS

RM

>contig52447 Frame-0F

MYEELKERKIKPDLVTFITMMHAVYHGEIGAIDQKKVKTILVGMAMMGMSFVPFINYEEY

MMTTLFCGSLVGSMGLAAYMNPDGVLRALYPNTDELRNDTVIEAFFRRLREEDHCGRSIY

LWREMIKYNVPADPRVYDILVRTCVRKRHPELAYEAVLEEKLPLVDREGRFVLSLHTTLS

LLQSLLAQRRENMANTLYDAARSHNVFDTVFDEKSRVYVYDMRPFLSEQLRSYIIIKLMD

ELRSKTDLSKGEVPIPSVQFLIYHGYELLDRLDADNASLRTLFSMDDMTRVDAEKHSATS

GRYYFWIAIPSERL

>contig52814 Frame-0F|Blast-PNS1-like protein [Phytophthora infestans T30-4](gb|EEY67718.1|) 7e-59

MTASRRAYQLFKSKGWSAIVNDELMGCMFWLSNFIIGFVTACIGVQTIGSIYSIRVAIYA

YPHGFVAFFCFLGGFSINYVLMAVVASAVTTIFVLWAEDPHIWQLSRPKHYETLHEAWLQ

NYPDEYNYGYGKQGSISICDCTPCPI

>contig52861 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65234.1|) 2e-16

MTAADDARHLELCANELRELGAAIGSCRFRTPSSHLSIPLQTSESTSKRRKLVSTSPSKT

SRSLFSLV

>contig53022 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63828.1|) 3e-10

MQTRRKRIVRNDRSRSDSFISSFDANKIAIASPTIASIKKRARRQCSRPNCIKVDAGGGF

CVAHGGGK

>contig53646 Frame-2R

MHKNRFCFQISTSEYDEADHKVKIGTNQHKALRNQKRNNHVAVRPHKTNFSPLKQAVSRF

GDAVSRRRESVIPSGGPSIVSDQMNLLISPSPAQIAPSLSPNASNTNGVATNHETEWILC

ALTIQEEVAWRVAIQGSADKALHRMRRSRVTDFPGSLAQSGILSLNLNLPPNNIRSSMSV

VSSLGCNGTFGRRRMS

>contig53772 Frame-0F

MLVGYDSRLLEPLQCGSSSISARRCNGTCTMSAFCFEPPSDPIGESSSNACFVSY

>contig54346 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53300.1|) 8e-22

MEANVSMMRLLSVLKYWIKESTFIEQDLVC

>contig54522 Frame-1R

METSNSPNIWADSIFPLLMKDSICCCIILALYCVAIRVLASAVSLSSRHRCNLFARRFLD

VSISELY

>contig54908 Frame-1R

MLERIREMRDDLSSLTMSKQRHSRESGSMASSTAECFKTLTDAVPGSSRSQKEGTFSNSR

DLIDVDFINSSNQFTLLCPKTLVHQCRTRTSSCVHQDAGENSYLDASAADISSVSSSPRY

SFKTKKSMQKVAARERSCWHSHRV

>contig55077 Frame-2F|Blast-inositol polyphosphate 5-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY59786.1|) 2e-12

MAARGLGSSTAVLPSSPVAMASSLGPPACNSICKLESVGSPPGSTASSTASQSVNGKYYN

PVVM

>contig55099 Frame-0F

MIEYLEVAMQRCYQDDDAFARRKERFSAR

>contig55451 Frame-1R

MEAPTMLPQLDEAIAFLQAEITALRSGANDANLVAQAVAVAAGELPLPEPQFAPLLALWK

PSTSSFATELAALVDQFNAAQRREQEHLIKTTEMIASLPIVHSALQHVRGQRTRPRTRPR

RRFEDPDVGHTSPLASDGTASSHAEIDRKEENSNAAVEIISAHDVAKEASEEEHRGTVIK

QAKERNPEKEEAEAALAGLQALRQSMLLDVLSKIVSVAKSKDVDPAMF

>contig57497 Frame-2F

MKPSSYFNGQELVSLYRYILNFRLCGRIVDFCPRSCSGCWGFGSHSGAIFSR

>contig57686 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59785.1|) 1e-79

MSTLLPNSIKQIKCYQELLVLVWKLLDENTEFLHYVLKRADVNQLVVPLLFLMYEGRQEP

AKVGMIHICTFILLLLSGERDFGVNLNKPFNNHLPLDLPPFSGNHADLLIVCLHKVIVTG

YEKLNSVYNCFL

>contig00892 Frame-2F

MGPRPPADSGTPTGAYALLSQPSPLEDKNNDDDVLGSDVVDVHVVDSPTEWSHDKATSKA

LEISNCDNVDYRIIHLNAPEKNAAFSYCSNLVITSRFTLSNFLPKLLFYEFSKLANAYFL

IISIMQTIKPISNTGGFPASLPALSIIVLIDMFFACLEDYKRHQADHIANNLPCQKFQLE

TNTFAIVKWHTLQVGDVVKVGNRDAVPADLVILGAYEPDVSNPAGICYVETKSLDGETNL

KLRQGLEATYPLLVTDASVATLVGTISCETPNNFIHRFSGSIALQDGTKEVISTNAIVLR

GSTIRNTDYIYGVVVNTGPDTKIMRASSSEPMKWSNMEKRLNKQILYICVLMIALCLSGA

ILSTVWNAQNLDQDRNDAAWYLYDGASVAVKSPVGNFMIMVLYYFLLLNSFIPVSLYVSM

TSVKFMQAYFMNNDLAMYHDESDTPCQVRTMSLNEELGQIDYLFTDKTGTLTCNIMEFRK

CSINGVAYGYGETEVGVAAKKRQGLDTTNVVASDTLSPTLTDRVVQVPFVNYQDDALVDA

LAQKHSVQALAIDAFFEHLAICHTVMPERTTDKKLRLSASSPDEQALVAAAACFGFKFIG

RGPGKAMVEYFSCVDEEAAMECNQPVETHDVGTYQVLEVLEFNSTRKRMSVIVQGPRGNV

TLYCKGADTVLYERLRPTMDANVLQTRDLTLQHMEQFASEGLRTLAIGATDVSQNVFHAW

KRRYRCASNDMRQIELRRQGLANDIDRLMEEIETNLEILGATAIEDRLQAQVPETIYKLR

QAAIKIWMLTGDKEETAINIAFACRLLATEIEQIVLSADSHATIEAICTELQLYALEKHD

DEEMATSTATADGRGRNARTSGRKRLTRIESRAERPSREVALVIDGETLEVALEECPELL

LNVAEQCVAVIACRVSPAQKAQLVRLVRDHKPHVRTLAIGDGANDVSMIQAAHVGVGISG

QEGMQAANSSDYAIAQFRFLSRLLLVHGRWNYVRMGKLILYIFYKNVILNLTQFWYMFYT

GYSGQKFFLEWGLQGYNLLFTALPIILVSTFEQDVPAGLAHAYPLLYRIGQENTNFNTKV

VWAWITSCIWESLIICFGVVHGMQYLVTRADTPTMWVYGSTSFTIVLIVVTLKLCLHQQM

WWAFHYVVYGTSFMLWIGTAALISSGDSISSSYWNGVFSNTFRIDAFWLVVPLIVVAALS

RDFMWKGYTRMFRPSYKHLAQEVHAFHLTHLASQLLTFPPAQELPENARMRPNDRVRTTA

SIGTASGDDMSVTKPVVSSVLMPSRPLTSRLHSRRSTTRGSAFSYDAESVMVESYLATDG

YARDTRRTKTIFKRHASRGSLAFQRLPSVDDESVDSAGRTRRSRHGSVNGLSQRILGPDR

RRRGFEARALSSDDAQQLLRQNSPTRRPLRQSAVTPT

>contig03383 Frame-1R

MIRTSKVAFVHVILVKSAIERCQLHIIWYSCSDSLPPCKFLCDAKQNGSNEDAFRSSNVV

>contig04409 Frame-2R|Blast-receptor kinase, putative [Phytophthora infestans T30-4](gb|EEY65021.1|) 3e-06 NOT\_ORF

MRFFSSNDSAHMA\*MLVLSLSYLTTRSTRRLKQILALRHGKCEGYQIV

>contig04683 Frame-2F

MSNSHLLPKIVQDIEKVEATIKLTDAISSRPLVVVLDSLNALIQQTSLQQVLLFLRQLRG

HAVIGSIIARFNAGAESSGAAQALAAQATAVVLVETRSSLRSYPLLSQERKREIPKNMHG

LVLLVRQKKNGRSSESIEYFQVSFNKVQFLTITDEKRPSVSTGAAKRVNPA

>contig05060 Frame-1F

MKDAEEERRALTLQEGDLDHIVDDLSDEERAKALDLDTIVRQEQETEDRHQVKEVMRNVK

EGFGRNRRAFSSVRLHSEARGRFNLDDLVAADGSKLEAARLGLLASDEEFSDEELHGEYH

EKEMDEDEEAEMERILRERFRNQPQIYVTSSESESDNEDMETKDYNRPEIESDEARERQQ

IKLFSDRARMNRRMQRMKDLERQEAIETGEMDLKKRASLGGMDEEDSHELLQLRNRTDSD

AEQHKMIAGCSIRGRFDSYRAMASKSQASSSFRRVLGHCKLFGADSNGGAGSLKSFVFTS

FGSEKPLEEDESVKEKVCFGKSQSRGGLKRRNELSGPGPN

>contig10192 Frame-2F

MTVPSLRLEPSKATVGTDIRVVGNDAAEKLAIASGTLARLDRDAPNYGFNSYNDFNTFYL

QASSSTTGGSSGSPVLNHDGDAIALNAGGKIGTSASFYLPLDRVKRAFDLIREGKSVPRG

TIQTIFNYKPFDEVRRLGVDPVTEKLVRTTHPLGTGMLTVAETIPGGPSSKKLQPGDVLI

RVNGKLITQFVPLEAILDDSVGSEVELQLERSGESITLKVEVQDLHSVTPSRFIEIGGAV

INPLSYQQARNHAMRPGSPYVADPGYFLQRSRIGRGAIIHSVNGIDTPDLETLKHYLKQC

KDRDRIVVKFSKLTDKSEKVEVVHVDRRWFPFCEYVRDDRLGTWHCEHFSPPSDAHDIKA

SNSLSQDEPIGSTTTLPGKNPVENKLARSLVTVDFDRPFSVNSLSTSNYRGTGLVIDAVK

GLVVVDRNTVTDSMGDAMVTFASTIMVPAHVVFVHPVHNFAIVQYDPKLIGSTPIESCQV

ASKPLMPSDPVWLVGLMSSIGRSGHSDLVSRETIVSGVKWIGLPMPNPPRYQEHNLEMVS

LQDVVGTEGGVICSENGEVSAFWASFSFQQQRRSSKTESQFNRGIPIDLVMESAASLMRG

ATPEIYDLGVDFEHLSLAKARELGLGQALAEILEKNAPDRRTILTVARRWGGTEAQDVLK

NGDILVAVDGKIVTSIREVERCTQKPEVQLTIVRDGQESQLEVKTLFMERTDIKRIIFWQ

GLLLQAPPLSVSAQRSISLDDGIYVSCRYSGSPAARYGPPPTSRIKEIDGIKITSIDEFL

RVVTEKSANDSVCIKYADLSGKEHLSTLKLEPKYWPTSELVYKSGEWHRRQH

>contig12613 Frame-1R

MTDYPNDILLRNIKANITRNAHLLGTGRHEVRGHLWGSDTIELLKCLEDSDSANELRQIV

STPTRSARFDVAIVAECLWLHDMHQDLLKSINACLSTDG

>contig15111 Frame-2F

MKTNRSIVCKNKSQCVAFKSQYICHEEPRQARKLGQY

>contig15300 Frame-2F

MRPLFESVKYLHRLGIVHRDLKPENILCGEALTDVTIADFGLSK

>contig15641 Frame-2R|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY63359.1|) 2e-96

MQMPDGGIVSLDWALLHDEKVPNLVQDLNASASSTWLQDVNPTQRTMILLPGLTGGSAEN

YIRKTIAKLHDLNWQCVVLNARGCANTPLTTPQLFCSAYTEDLRFVLQQLGTQYQFAHEA

SVATGFSMGSNVLVKYLGEDGYQTNLSGAISIGNPFDLTICSANFGNSFINRMTYDKVLT

KNLCELFFEK

>contig15825 Frame-2R

MRKSRRVFGPGYYYVGVIDILQTWTLQKRMERFWKVTVQQKDGNGLSAMDPIRYQRRFEA

KLREIISIPKQYFRTEPRVGMAASVQRLSPVLQAAAAFEAAMETRRDEARNRNDSSTSGV

SSTVVDGGDLEQAGRNPEPILLPFNQRLISTNSMPSQRSLTDYIV

>contig17359 Frame-2F

MVLPAVIEEKLNELEEEVKLYKFETCQLQERKKSFERQVKKLALEQDNFARYQQEQRVLL

KQIWEQERNKMKKEEKLQKQQCMLRINATVAHAGCSEVELLKAQIAEMQLDATSRERDLK

AGNDTLRQRVAILEKENLELRDEYTFLKQIRLEQWEEHKYLIKERQRAFDPAINLKIPLC

LANKAIFALRPRLMEQVIGSYEGGVFFVKMAHAAILMMKSKK

>contig19313 Frame-0R

MNADMVVLLALSGLLFVGALTILLFFCRVQRDRESLVFIQETVDVYREELNDSFNEQALW

RCGVCKFLNHPERKLCDLCQTLRGAGRVVTDSKKHTSSTGPSSHSKNNGNSALVRRMSAI

GESETFSSGQVDNAIGGSLERPSGDFMKLLTG

>contig20465 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58485.1|) 2e-95

MVIFGNLFVLYIIFRDPVYLETRFAGFSGGITALLVAFMKPMPFATTFLLPGVPLRLYPL

VACVIFCLSTLAGVFFIAVPAVSSMLISAGPFAILGGYFGWYYLRFLNKNRDHTVGDVSD

EFALVVLLPDFCTPVVGPLANFCFSVTKLCGFFNNRVTHKPTMLPILTEIKDDPIAERR

>contig22324 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60163.1|) 2e-26

MTNLRDFLGSRLEVMYECMYTRHLTQKRKIWQDGFLSLYASRRLVLYADDEGKAGKAIEE

AKFGLSDWDRKEEGPFQTS

>contig23833 Frame-2R

MPYKSAERLQKELAAQKARAEALNYLHITGSGPSQRELVQQQQLRERQAANAVSAVAQRR

VAPPPASDTPDPRVRDNTLHVIALRRAQDLEKKQQNNNAMESYWVESKATTNEVLPIGWQ

IVVDPASGDLYYWN

>contig24151 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60120.1|) 2e-38

MIHMDAVVNDLLFPATEKSPVEYGLSGLTLTPQNTPKMEGTAAVTLRWVVLYRYNLLPHD

PVILQDLEILRPCFNGDL

>contig24638 Frame-2F

MTTTRADFLLEWLNPRTPLCDSTVENSVTPERMIRPDHRMDITALCTTADEEGPMASEDR

PSVSEMFMAPTFLPIYPRSSRVNDRMQLSLRFEATATGMLSSKKRSRRLSNSERGKMYRS

RRKSYVQTLEEQVDQLKDEVHELLLDDRSRQQLTKTCQIQWQLMGTSFATVVKEYFSLFK

YGVRVTEQRGTSNGPQEQIALSTRQALFLKRLMHPNVVFASSYGVQELLNQWQK

>contig25624 Frame-0R|Blast-NADH-cytochrome b5 reductase [Phytophthora infestans T30-4](gb|EEY63523.1|) 1e-158

MDSLLTLVDGDYRVLLGIALVAGTTIFMFLKRMKPRELVHVTLQAPSTPGDSPPTVHLAL

VEKQTLSHDTRQFRFALPSEQHVLGLPVGQHISLRYLDDEGKLVMRSYTPVSSDDTKGYV

DLVIKVYFKNVHPKFPDGGKMSQHLESLSIGDTIEVSGPKGKLTYMGKGEIHIKHRVRDV

VPEIRKAAKIGMIAGGTGITPMLQVVRRALQDPEDKTEFYLLFANQTEADILCRDEIEAM

AANHGNVKIWYTVDKASDGWQYSTGFVSADMIKQHLPPASSDVQIFMCGPPPMLKFAVLP

ALEELGFQPHQHFSF

>contig26063 Frame-1F

MLDYVSRQYRWYKLEFGLTMLSWWEVSIFNCFLLLVTSVTGYYIYNAGSHIAAFLN

>contig27356 Frame-0R

MSTLCWSRVVHLGVTALFLHVKMLFLAALKVLVLLLFLLVLRRHLELAPNFKLQFASLHV

LHNLSDRRVGRTAFRLANINQLNKLNWLN

>contig27882 Frame-1R

MIKEAYKHSLGNQAIRASKNNLNSGTCHRGDDATFFSPLSFTVDEACFDAWDAQTSQRNL

LRNWSKVLEPLREFFACNLPCKFGSGIENNFAQPVIDNFMHVYSIGTNAFLTFQLLRSFA

LSAAFFFFYNNKTAFTSPAICAEHTCTSLNWTL

>contig29295 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61671.1|) 1e-38

MLSFKQAAGRVPRKVPLLPHRRCWLEQSHTFLSCMMSTLQIAPQAAVCVIANEVLTGKTL

DTNSHWIAKFLFRRGIDLKRVVVIPDEEEAIMSTVKELSQSVGPSGYVFTTGGIGPTHDD

ITYESV

>contig29431 Frame-0F

MGRRNRWDSDSDSSNERTSKRKQKLSKKLPPTSTTISIPNIKDSIISNASTSPLDMASPR

HNFYLLGCRSVDSYARIGKIDEGTYGVVSKARDKETGDIVALKQVKMSASASQEGFPITA

LRETNVLLALDHPNIIQVREMVVGSTPDKIFMVMEYAENDLKHVMQTKMKAPWLQSEVKY

LLH

>contig31733 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60310.1|) 1e-171

MSFLPMLRHAGREWSVFMRQPVLPRHSKQVHSWLRHVTLLRALLFACAVFLCWGYTQLLV

RYGSISPIATVLFTTAYNGRSVSDVPPPSPPWRPPFRVVVSLTTTPNRLKNVMDSVRSLL

TQHLIPDQIYVNIPIGPMKRHPDKLYDDTEIPSELIQLYPRVRVHRCVDDGPATKLLGAL

RQETNASTLIVTLDDDFVYPPALVASLAWEAIAKPEDALGVCGWGMLPLWHQVGVVPAYV

PYFMRPNGRYVDILQACCGNAYRRGFFTDIKALADIPSICVTVDDVWIAGYLRTIEHRKS

AVISKRLDPVDPQWKKDEAQSSERQMTLSSFNHEKMVHYKCVQALEEKFQHKWIRNYEAQ

T

>contig32695 Frame-2R

MEFEAERKDLYEQIQKAEATNANLTVVVKTLNQEREKYKHQKDELKILYTKFSLAMDSVS

EKTMRLEELQEELQHALESSRRVETDKKKLEMQVVELQEMTNRQLGEQKQMCEELTSLKR

QYEEVQAQLLHQNEVASKFETEVANLKIRNETLEKEHAQRPHQSVGEPSNENDYSPFGRD

RVLVKQVAEKEALQMFLLRYYSVAEEKCSLLREKVRELEARNAPV

>contig33186 Frame-1F|Blast-charged multivesicular body protein 5, putative [Phytophthora infestans T30-4](gb|EEY61243.1|) 4e-53

MKGIFAKKKPEAPAINISDAGEKVHARISVLNSKIEQLDEELRRHREQMKKVRGPAVSSI

KQRAIQTLKQKKMFEAQRDNLQAQSFNIEQAAFAIDTSRDAVTTVAAMKSAIVQLKVETQ

NINVSELEDLQDDMADLLEDMNEIQDTMGRSYG

>contig33205 Frame-0F

MIFPKFASQKRLSKRLINLIPTIQTMVSKFKVCPVEKLAKELVPVNAGFRKFMTDNPKIK

RKTAEW

>contig33520 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66966.1|) 1e-25

MSSKKHRFSLLRFFKLKDENVNTTKEAHIQPMPLPTEILTRKRNGSVMVSGKRVPFMHDT

QKRRRKFTKPLPSIFEDRPFVTGNTSLEAYRRRAYYSDAKEKTKR

>contig33689 Frame-0R|Blast-choline transporter-like protein [Phytophthora infestans T30-4]gb|EEY62350.1| choline transporter-like protein [Phytophthora infestans T30-4](gb|EEY60882.1|) 1e-31

MLFSYSVAQAFMTIYETSINMLLMCFTLDENLHGGRGNSAHASASLIRSVDDHLRPKWQT

AL

>contig33722 Frame-2F|Blast-ubiquitin-like protein/ribosomal protein [Phytophthora infestans]gb|EEY52907.1| ubiquitin-like protein/ribosomal protein [Phytophthora infestans T30-4](gb|AAY43412.1|) 1e-06

MRFVCVCLSFYNSRSRQHFDLSHLCVLVDSTCNENAALVNLSIRLRGGGKVHGSLARAGK

VKVRLLKFL

>contig34042 Frame-2F

MAVISNLMRRLQQRLMQVKDERIKICVEVLAGIKVVKLKAWENSFGQRVMNFRDEELARL

RTYVLARSGSNTIFSFVPALVTVVTFTAYVLLGHTLDVGTALTSLALFNILRFPLFMLPQ

VLNNVVEASVSFDRLRSFFLAEERIRVSESGLTDVGIVVKDADFKWDTAPPIDGKLISDG

TIAEPTLRHINFSAKQGELHAIVGHVGCGKSTLLAGMLGDARCSSGSVALRGKVAYVSQQ

PFIQNATVRDNITCGLPFEAEKYEEALRVSSLKRDLRTLTAGDRTEIGEKGINLSGGQRT

RVAVARAVYQDADIYLLDDILSAVDSHVGADIFNECIKKTLKDKLVVLVTHSLSFVNQCD

EIAVIAEGRIVEQGTYKSLMTEKKLLAQMVSNYKKGDEEERPLSVKEEVSEIKNDEKVTT

TRRRRSSEGHMSRNSRLSSQSNESQGDVDDEGQLMVEEDQSVGDVSWSVYRVWIDAFGGI

FAAFVVVLGFFIAQALTLSATLWISYWSEQAAKYPGSQMYYVYVYMVINLVYAVLLFLRV

TLLYVGSLHASRLLFSKLLSQVLRAPTSFFDTTPLGRIVNRMSKDIYTLDESIPGTLVAL

LNTVVAVLFSLITVSAVTPTFMVILVPVLVGYYSSQRYFIKTSRELQRLDSVSRSPIFAL

LSETLDGLSTIRAFGIEQSFIRHNNYLLDKNQRAYFLNFTINCWLALRLEFVGTCIAAAA

ALSAVVAHDTKSAQNPAFAGLVGVSLTYAFTVTQSLNWTVRMVSQLQTQMVSVERIETYT

KMPTEAPLTSSVHAKPASDWPSTGAIAFNGVDLRYRPGLPRVLRGLTFSVNGKEKIGVVG

RTGAGKSSLIVALMRLVELDAGSIVIDGVNVSKIGLHDLRSSIAIIPQDPVLFSGTVRSN

LDPFDRFSDDQLWTSVKRASLQNAVASLDDVVDEKGSNFSVGERQLLSIARALLKRSKVI

LMDEATASIDPETDRKIQLSIREEFQDCTTLTIAHRINTILDSNRILVMEKGSVAEFGPP

MELQSKPNGIFKSLVDAWRQSSNNEEAKV

>contig34129 Frame-2F

MENPLPSILPKPTGLRKSSSTRSLASLADVQALILAQDEEEQAHRRRKSLSKPPRHGSMP

MYAKILLQLWQRELQCNNVDLMSDFFYDLQGTEEQGVQLVSHMQALGFNITEAQFLAMHR

CSIYSVLLRAL

>contig34226 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56206.1|) 0.0

MFKPLRGQSAFSYKTDSICIGAGRFLRCVLVPTLRSAGSAVVVAQTRGTSFSSACADADG

LYEVDTIQNDGSVQTEVVEVEAVGSLGDAEGRAAFMQLPAKLPKIKFIGFGVTESGINTG

SLAIVDLTELLYNCFLKLPNNVISVINTDNLPKNGDTIRKLVLETEWNGQPCDLALFRAY

VASKVHFHNTMVDRLTSHRENDPLVPLTEPWPVKTLVIEDLEGVLDINVLSTLPGVHIRT

TAGQLEQDHLLKLSIANAVHSSMVYLLALSRVKTTCEITKYPEVRQFLDLLYVKDIAPSL

KLRGISDEEAQHTYDEWIRRIEHKHFGLDNFWVGQNAMLKYGVRLFSSVEANVTRNESYH

PSVFMAFVTAVILRYLTPTQSDSRKEGSDKPEVFVGAMDAIQSRSLIYSVTDKTWPYANG

LAANVSTGKYEFLDGEHGQTAKTLWKASQ

>contig34491 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69288.1|) 0.0

MADNAEHTTGYGSIPSQVRMGIGSISPPLSPLMLRVNKEKNALKGWEFPGWGGNTSIVAS

DNELSEIQAHLSMDHPKLSEWLATAICGNDILSSCLYVSGLVASKAGKLAPLALAIVAGI

LYLYRFIYGEVLNAVPLNGGSYNVLLNTTSKRVAAMAASLAILSYIATGVVSGTSACNYL

VSHVPSLQIVPATIGLLCLFAVLSIIGITESAVVALVIFITHTATLTVLCLLSVIYIVKD

DFQTLNANFNTDFPNINLAGDIISGNSLTAIFFGTSTAMLGISGFETSSQFIEEQAEGVF

SKTLRNMWWGVAIFNPLISFLSLGVLPLNGPGGIVDKKETVLAEMGYKVAGEKLQLIVSL

DAFIVLSGAVLTAYVGVVGLIRRLASDRVLPDFLLHVNRARGTNHYIIISYFIVATSLVL

ILYGDTETLSGVYTYAFLGLMTLFGTGCMLLKFKRAEIPRTVIAPWWSCILGVSMVLIAF

LGNLLGDPTILTYFSLYFIAVLSLVYIMFERTFLLRICLYCMRQLCPSQRNDTDNETYSL

RTGARGGQTIARVIREINEPAVFFFCKTANLNIINKAILYVRNNEQTRTLYFVHCHPRGT

AVPEGFKETVSMFDHVYLKIKLNFLSVEGPFGPAMVEWISRKYSQPKNLMFIKQPDHDFA

HTIASLGGVRVITG

>contig34987 Frame-0F

MSIGCDPKSHPSKEWIDGHLNEYVDDDNPHKVVAGKAFCRVDDDCTIGGILGKTLLKTGK

CVKKRCECTYSSSWGGPRCTTAVSSSSSSSITTKSLMTNSYGPPFGMAIGVAIMTVFCSF

LAIMRSATKEKKTDILLKKQSKTAAGSSTRSNDGLVKNDGDRQSHGNNSTNGRPRDNYSQ

NFV

>contig35531 Frame-0F

MVDILVSNFSDPETAVRTLSARSIAVLLSLAIKNCKTDSIFKRIFSLCRHPGAMQRSSAA

LSISCFLRSLNEEDGNTFSQCA

>contig35904 Frame-0R

MADAERHLQSAPHQRLDLDPSRLTTFPVPGFLASIV

>contig36354 Frame-1F

MRGSQGGLDLSKQEEMQITINVSELGHEDVRIATYKSLEIHSTIAELMIFANSTVAHRLM

QYYPTHAFLRHHPSPSGDRFTELVELAKARDVIIDATNNFTLQQSLAAAEKSNSMDSKTM

ALFKSLAVRVMTEAAYVSSGEVVAADIAMANGDDTRIAHYGLGLQYYTHFTSPIRRYADV

IVHRQLLASIKWSWNCKSTSQRSAVSISTTLALPRALVPSVLSPQDDEDYLDNLLSSINN

QLLVSTSATAATNDVTTNKDNMFTPKELVSLAQHLNEKHRQAKLAARACDELFLALYFST

HTVKVPAIITALKENGFIVFVPKYDIRAPVYLRDKNCVVQMNPLILGVPVTDTDPATGVF

AGTECIRQIPQAHLILTDSDREMLEVVASGDKRTMFQRLDEVEVQVSCDLAASGARVPQL

QLLLINRATSTLPKHVASSRSELDRFVQTKSEMANKAS

>contig37814 Frame-1F|Blast-TATA-box-binding protein [Phytophthora infestans T30-4](gb|EEY53626.1|) 2e-11

MVIKEATESRRSSSRAVKDRQLALVEKPETNLQSVGARELQVEDDWEERLDLHVKVM

>contig38020 Frame-2F|Blast-seryl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY65929.1|) 0.0

MPIDINSLRPERGGDPDAVRADQKKRNIDVAIVNKVIELDEQWRKKQGEVETISMNMNAL

QQEIKKLSKAKEDFKAISDERKQLAASLPEKKKEVEALKELVERELPKIGNTVDPSVPIS

NNEEDNVIVKTWGKTIKREGLHFHHEVLHRIDGYEPERGVQVAGHRAYFLTGYGFLLEQA

LMAYASAFLMKAQYKMLKPPFFMNKDCMAAVAQLDDFDEQLYKVIGEDEKYLIATSEQPI

CGYHKGEWITESSLPLRYGGFSTCFRKEAGSHGKDTWGIFRVHQFDKIEQFCITDPESST

AMHEEMIRHAEEFYQSLNLPYRVVNIVSGELNNAAVKKYDLEAWFPAYKEYRELVSASNC

TDFQSRAMEIRCGVKKENQREKKYVHMLNSTLCASTRTVCCILENYQDENGVKVPKVLVP

FMGGVTYLPFTRDVKVNAQAVKMQKAAKKKGDKV

>contig38222 Frame-0R

MAILQILAILLFGNSNLPRSNKEVICLPIFTRPTEAMGTPFPKEAILPSRAIVQPLSELP

SHEGTLDVRPTSPTPRRDNKLPSWMQTS

>contig38297 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56468.1|) 2e-11

MSMITNVVLVGIAFGQVVYIRSMLESGF

>contig38770 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57608.1|) 5e-06 NOT\_ORF

MYSASRAILLKKPLGLGAVEEPV\*RSKKPRRIFTSCDSGINSPNFMSWHSASPDSKLLKL

CNKFPSIIFIVLLQLISLRSEVELTVGD

>contig39346 Frame-0F

MASPNNSIIVLDDSSDEEPAPAPKNQSVESSIDHIKSGCVNSPIKPSKEPKKSSKILSWA

QNRGVNVKDASLDNGMDSDDACNRLMPCNEVEVHLSKPRSYVNESNDSEIVAAEATTQLY

SDHKSGHVHADVKPSSDLQVQQLKIERPQVKTHSTFMPRTTTPQVSTGAKRKAAEAIVSP

A

>contig39416 Frame-1F|Blast-V-type proton ATPase subunit H, putative [Phytophthora infestans T30-4](gb|EEY58149.1|) 2e-31

MTMKLMTHENAEVQKQALQCVSKMMVNKWG

>contig39607 Frame-0R|Blast-hypothetical protein [Gallus gallus](emb|CAH65335.1|) 8e-07 NOT\_ORF

MNKRGPTMKMTQQMRILAVKAMKAR

>contig40395 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53117.1|) 2e-74

MSKEGFLLVHDEGRRSHIYYCVLGEGKMQYYTKRDRGVMVREVILSRSRLKVRGMTDADG

RGCPYSFSVRLQRSRIRDGRVLVYGSPVVLVMSAPTWGERKDWGNAIHAWQRNYWGEPQH

KALGLALDELEVFFDTQYKVLQMMLQTAV

>contig40904 Frame-0F

MCFSDDVTLVGAACDDASFRVWRNDDQPLGTATGSVYHGSTATDEDERMAVLRGHSSAVY

GASFSPDNRFALTASADSTVRLWSLAAKSQVVIYRSHHGAPVWDVTFAPLGYYFATCSMD

RTARVWSTDHMTPLRVFAGHLSDVDCVRFHPNHNYVATGSSDKTVRLWDVQSGKCVRVFT

GHFQGVQCLAFSHNGRYLASSGDDQYINIWDLQAGKRLETLMGHKATVTSLDFSRESTIL

ASGGMDSTVRLWDMKALTEKPTTFTSLPGAIKALHVRSACTRRSRFIKPVPMIRPGGRHE

MPSSRFLLKTLRSKHTPVYRVHFTPRNLLLAGGIFQPKVES

>contig41226 Frame-1R

MWLNEDEPAPHTGIGSDYRMQMQELRMSMALMAPSVPKAPGFSALVSPAYIRQLLVAIGI

AGVQ

>contig41491 Frame-0F

MKINVSLLEVPQFVTGIPAALLTYGELRKHHVRVFVSLRDVSSTSSDVMRSFMPIAVSML

GTREDGSINFELGGFYNDRTSTYNVLYT

>contig41932 Frame-0F

MPSLIDTPAKTSNKLKVKLRKSDFPVRKVCFGGVEAEDLVDENGLPRDGYNYSQHMKEMG

QGKFYSATSRFDAGEEARSLSRKVDLPEGALPSIDEQDRMLDAITLTTNVMDEDLREALG

NDEAFEELDDNFVIQAAEENVDQEDVDDFDYEAHIAKLMDAASGVRPMHRGNITDSEDSE

DDDNDIRASKQDSVGMAIDRDEAQQALDELFEKTLAEEYDDELLGELEEHDPETRGKETL

EGCLLAAVVEDYVMVQQDLADAEGKLGNPLRSGNHLKQVLKECEADRHAYEYDENADTED

EVEPEEPIARAEREEKELQELFERNRYLQREEREKWDCETIVSTYSTMDNHPTVLREEDA

SLCKK

>contig41987 Frame-0R|Blast-branchpoint-bridging protein, putative [Phytophthora infestans T30-4](gb|EEY69167.1|) 2e-56

MAGNDANGFEAFIATVDDGKLNKADINIVDKFSYEEQQEKEVMMKNYHYPMKQWFSQQPR

LETKYGAFPLFWQELKIWKPYREVLKAFIKSTDHGEDANGTDETANGPNNRDHAKIKKCN

SAEVAKEQPKKRRKSRWGDPVESAVDDNCEKRKKKSRWAPASSTSSVMVGLLAQNQQQMV

SLRLELE

>contig42551 Frame-1R|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69238.1|) 3e-37

MPSLDERKRPAECGTGFNVRTWCNMDPCGIVCATISWFLVLYAECTVVGVVVYPWMGLSL

LGLLHIAIFTGLCFMALVSHGKGCNNHFRKQVHS

>contig42735 Frame-0F

MNFIAALVFAASTCAYVNATFTVASSTTEARISSLNHVSHARQWTINAATARDSLNSIDL

DLAGRVYVSYASSLPRGVLGYVHVLGDSKSVVNAVTVSNGDADDDDDDDENEGDLHVVMS

TSAEATRGYLLTEIVVASSGIVSKLKSTRSAQVVVQDGVLLTSSATEEVQIKASGSSAVY

VAAPSATVSVRVFQLEAKGHWKATDYCRESNSDGQSATRSREYGQDFDPFVVGRDGLP

>contig42740 Frame-2F

MTTLFAVKRAFERGIKPRFSLLTASVTEVSARPKHLRRPSSQLSLNLNAAHGPTGTPVGL

GRPTLQRRKPALATCEMLFERFTIYETPSTYFMVCSDRHYSQFRMLELSRLVDRPQKLEE

VLTEEKKIYNWEEMEAQLQFLAELARVRGTGALQRAFSAVAIVGCIRFLRGYYFIFVTQR

RKIGNIGGNSIYGISATQQLNVSRPEDDRSAWTHLNRWFNPSPEEEAEARYLGLFHFLDL

TKDFYFSYSYDITHTLQHNMTTEHSEPAEMFTWNFYLTQELRTCLSGNAAADLVVPLVLG

CYEQRKCSVFGRLVSIVLLARRSRHFAGTRYLKRGVADTGKAANDVETEQIIEDESMGPG

KFSSFVQHRGSIPVFWSQETSATLPKPPIVLNRVDPTYTATQKHFADLFTRYGSPIVALN

LVKQSEKKEREVIVGNEYMNAVEYLNSFMPPKHR

>contig44733 Frame-1R

MVSQTSFSGVRADYFNDWQLEKARLSDVDASSESSIHTVDEALDFEELNHLEATDSSCID

QHSDDEYNECSGGVSGLPLVCSNCGVSFFSLQIHDDQMDCYCSGECKWSVIMYREMDMRM

FAMRRPMRRYSILDTMRLSTNFHENYDYEEHEFSLTSSSKSGNSTSTSSCS

>contig45064 Frame-2F

MQSEPDIRQPWPLNRCFYPLGRDGRLLRQCKRATIQFVFIKPIFAALSLLMLACGKYHTL

AYQLILAVVYNISYTLALYGLYVFYLATRHILQPFNPVLKFFAVKSVVFLTFWQNRLLDF

IPGITNEQAFAWKDFILCVEMVLFACLHLLAFNSSQFKRNLDRLPDSEVLNNMKEVLSLS

DILADAYHNFMPFYRDYMLQRGGESTDRGRKDMSSDDSPTHMAHNNAQVPRFVIDDEDEM

EEIGLGRRHQWRQLVYQLMSFRSLDCPI

>contig46205 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60452.1|) 8e-95

MAGDTNVVNIFECDGNFSFLHQTHRFTFKIYSDNSLRVDIELIVFPDQFNSRDPTIGFDQ

ETTISEEFDDYDDNVDAMTIASIPIDDMARIEFERAQIEAENDIMTTLSAFDGRALIELP

MKGPQDPMSSLSYMVHFKIIQWSRSSQRVWSQIIKCVGRLSRDQGMSGWFLDVSESMDEA

QDFRLKPVDYRVEIIKNPLYPLTPGHYEMQGITIAENAFVYECAVSLTLQANGMVYGTSR

ELPFAQECPLTGMWSRSHLKYLLEYKMLGNRHAYIYCGIPFSSSLQGTWQNSELLVLKDL

LDEVSIQAECGVVELQLIQAVRVWSEGYHKDYPMTFKECVKLLLLASCRNSILPNHLWSS

VIVYCGYDWFSPS

>contig46494 Frame-1R

MGYGIEEDELDDEIVRPIDKHISTTLRATQSNIASNYAHQFMSNHSITEESDRSLSFGSD

GELSID

>contig46722 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69733.1|) 3e-24

MTKQKKALEEEEKTLDKLLSTKKSIEPKKLSRLEQKVALEQYLKPTTAAWKALLGVTLVS

ITGCCVLVGGATAAIGVTNMTDLLQRLQQSSKQASLQLEVKKLRESKG

>contig46818 Frame-0F

MLLGDFIELRTDISLDKSKSGVSRDESLGVAMEAILSTISECINFADFGASQTQRGVQQI

PADGIHSFVTVLKTSGHANRMLASQVLIQVSKEQSLILLLAKEETFVKEIMWMLDNGDST

IASEILCGLCSTVSNQNLNGSFRGGKSNHAHEQVLKLLYELQVFDLVLKKLN

>contig48078 Frame-0R

MQYKVVTKFGEKHALILRLELYTLWKAQGLRGEDLFLKLELDKIIYNITKTQQYLIWHEY

MNMLSHENVLKAEFDIITSIFKDGNSWASLFGFSEHTSNPLVAYFLKATLDFCCYKKRQR

TMSSNCSRSAGMIKNCLATHYFQSGRHIYKSHLEVHLAKCIKKQWTSYQKVA

>contig48287 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65994.1|) 9e-78

MHFAHDAAADAPRYFSFKDYLSETEAATFFELTHSEQVEKVTQYLNFLSQQPNSAQFTTS

PKASISFAKLRDGCANDEFCNEQGTNNTPDEALLNQLLEGRTRSGFGAFGTEVGFLPQMN

LSLAVAATVEMIGHTYIVEHNKSGVVKSSMLNSRSFFFYWCHAEKQKLIDIREKLAARQI

SLKVRQKHWQRITIVVDRVMCDDCIQFAECFARYEKVSICIQDPDVVRIFSPCSS

>contig48445 Frame-2F

MNVEGINSFQLRRCHKNMFLKRLSGYSLSIENVNRHVDGWHEKLPKNKSLMLLGADIAVV

NQ

>contig48661 Frame-0F|Blast-transcription initiation factor IIB, putative [Phytophthora infestans T30-4](gb|EEY62976.1|) 2e-34

MIAHTVAQKADRLELSNGQPPVAVAASVIYLVAAYTNAKRSIQEISDVTMIGEKSMKRVC

KELNKSRVVLFEGVVMT

>contig48728 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60667.1|) 3e-17

MSSLACIQWIRNELEMHGDLQELNPPLVDTTSLCEFVTDGRALCLLTNVV

>contig49385 Frame-2R

MKYANRLRRLKKIAQAVHRRPSLSPCTAYVVDASSTMAT

>contig49514 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55034.1|) 4e-92

MSFPYFVDESEVDYVLQAVHFVANHGYKLLPQYELNCRTGVWRSLSRVDAPFPDKKRLFD

MRIEDTNNVQLLSITESIPDITAHRERNLQLAMKLANRSIRKAASSHFHQKVKLSNSNEG

LRWFAYPEEAVAAYQEFGGKPPLSEEISGPCQPQRYFDAAINHIWDGVPTLARKKRHPVA

LMTQMLVAQYVPGHSSLYILDMPSN

>contig50390 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68374.1|) 1e-115

MLLMPMARVLVVLVATNAIFSQLPCATVDATGDASMPRSFSAMTSNGQSFNRSKSSFESV

KDDDIVVGTIRIDNEDAETHRNVDGSKKLWESSHNNVGAHSSGHSGTLALVNAALKLGSV

LNATSTIEQTYVNWLGNPYGSIYSSRACWRKAHIAKMCPLGYNSKLGMCWTQCPYSYPLE

CGLECIRQNDDCGTAVFYKVAVVVQTAISLSAWSIYGDMEKWDKGVKVAIKCIKYMISII

KSLVRYIRYIKVYNPEATKDKILSILYQIDNVIIDLPVTVAYCIGKRASDDIKFVDTVLT

TAEYLLYDIISNGDFIISTWKEFMRFMKKLALGDSAASLTGEEIKALKSALKSNTTCGYD

LKRLLDRTWMTVAELRLLHPEMSEDEIRVTVSQSNLMLNDIPI

>contig51155 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60641.1|) 1e-29

MVTDASGGDEADDCEPKQLLLSQDHVKYEILGVTRVNGIVMYHIYAFQSVTSEQPMSTAK

RYSQFISLAEQLRALKVPAARDLPELPKCTVGTFLRGRRNKKTIEHRQIAFEAFLHYVAQ

HQELHECVIFHQFITT

>contig51322 Frame-0F

MYEKDSLRDAGNVDLSFSQILEVRSTLQRRRQTSVVAETQLSRPVNPFPRQNASQSYSSI

EANYDKEDKGPSAYGMLDSVYEGSEDILEESADDIRRGSLQHCIDSSRTEDQDWINRDDG

HVGPDMYRFVQPRRLSSWVQDDAVFACFKCHTVFSLLIRKHHCRACGRIFCSVCSSQRVI

IPGDYEVTPVSPTYNSLTTNATDLIGNISWYLTSYSTPDTVAELEMRTSSALTDSETFTP

ANQHETFFKDVQRLQELKIISNFTPNRSKSASSLSNASASTTQSSMPRPDGSVLQRVCDD

CACALQQRRRHYNTVKVFELCAFNLQELRT

>contig51397 Frame-1F

MVLNLFEDLMLTTLINYANAQLKIDSKLFVAVALLYHYGDDLSDMVKLALANPKYLEKAL

YIETGLAFSTTNLLRLLECKSTDLFRLSDPSMRMIFYYAKQSKARFGDNTLDFFETLSLW

YNTNSKHELAIQWTQEQSTEEAEKLAKEIRKYATELDSKAKENAAVSKPATVASSPLTAS

PSRQHADAPLVNQIGMDKPLKTTIHPEGLLARIGRLFKEWWTKLLNMLTSL

>contig51568 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66804.1|) 1e-43

MLGCAVDAAVLCNIHTKESNKPHQYLGMKWVCLQSSTLSRKRDMCFLEYLVYTKDLQGRN

VGVRITLPLDLKECPPLPDKLKTRRTHSHTVTIVRPMREISDAS

>contig51670 Frame-1R

MIQLSCKVKDGLPDYLLVKCPIYWHKRSRTPLFFCRRTNGATHSLLCALALLFSIAN

>contig52446 Frame-0R|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY60954.1|) 3e-30

MTNGKRRITEVMKTLDIKRRYIIKRLTAMHNVRFAYPTSAFYV

>contig52815 Frame-0F|Blast-polyprotein [Agaricus bisporus var. bisporus](gb|ACZ04926.1|) 7e-10 NOT\_ORF

MKSDETAKLDEDNQGAIAMAKYSEF\*KRTKHVGIRYHYVRGRVEDGEFVLQYFSTKEMKA

DMLTKPIPYCSGFMFSP

>contig52860-0 Frame-0F0

MVLLAASKIHQGEKNPSDSAPSADASRTLEEKHLEQLVLDGDASYRNINLDQVDPDNY

>contig53023 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64785.1|) 1e-15

MLTTSPPSHHRLGHRVTMDPRRAYMELVALDKQLLDQLRTNPLDAKDANALRCRLMDAAT

RLVDSHPSFA

>contig54523 Frame-2F|Blast-anaphase-promoting complex subunit 7, putative [Phytophthora infestans T30-4](gb|EEY63812.1|) 6e-07

MAALPQNSYVSEAALAFAKLATAKGTSPEAFAAIKTPFILNL

>contig54909 Frame-2R|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 6e-09 NOT\_ORF

MASQAHVFEFGMREGMTRYCLTRDDPFFWRKHLPPRCARTIS\*YLRI\*APSRWNTDHRIQ

SRWRLTSSNFCLTVCTKWQPTDLLSLPIKRQLCR

>contig55098 Frame-1F|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56806.1|) 1e-33

MFTCARQNNLAQFIQLVAQYGDELAREQRDPQGHTIAHWAAQKADGEFLTYLHSIGAPID

TPSTDEKVQLHPIHWACAA

>contig56114 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54425.1|) 3e-34

MMALSSVTAFVEYLKLQAQQYSVLMPIFALALARFIHLRLRGPLDQLNLHRALRSQLTIE

SKHFEHDNAVSPRLIIPLAEEWHIVTEDGAKAHSLVYYPTVTPDTHRLLVLVIPGNPGVP

FYYLPLM

>contig57030 Frame-2F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY53859.1|) 2e-10

MLELVCAVIGVKAVFPVDIDEKKIVGALKDAIKAKIPSKVKCDASDLELYLARKGDAWLS

E

>contig57496 Frame-1R

MLLRTNATRASNVIHLRFHIIFNTRVKRYSEVINCHAFEKHYV

>contig58703 Frame-1R

MDTLHPPVYICLRRKIDFVAEKPMELDG

>contig01258 Frame-1F

MRVKGHDKFTTINAVTPIHDTVLSSSNQMIKAIEPLVNEVVTPAANNGSVPYKKTNIVSN

AINSTAKAVIDTVATPLAPAVKAFALKEADSAIHPTTHVTSPVMKAVTPI

>contig02776 Frame-0F|Blast-elongation factor Tu [Granulibacter bethesdensis CGDNIH1]sp|Q0BUQ2.1|EFTU\_GRABC RecName: Full=Elongation factor Tu; Short=EF-Tugb|ABI61450.1| protein translation elongation factor Tu (EF-TU) [Granulibacter bethesdensis CGDNIH1](ref|YP\_744373.1|) 1e-178

MASLRKLVASSATIARSSKRFMATFDRTKPHLNVGTIGHVDHGKTTLTAAITKVLSETGG

ATFTSYADIDKAPEERARGITISTAHVEYETEKRHYAHVDCPGHADYVKNMITGAAQMDG

GILVVSAGDGPMPQTREHILLARQVGVPALVVFLNKVDQVDDEELLELVEMEIRELLEAY

DFPADDIPVVQGSALAAVEGRDHDIGRDAVRKLMDEVDAYIPDPVRDFEKPFLMPVEDVF

SISGRGTVVSGRVEQGVINTGDEVELVGLKPSFKTTCTGVEMFKKSLDRGQAGDNVGLLL

RGLKRDEVLRGQVLCKPGTINPHTKFEAEVYVLKKEEGGRHTPFFSNYRPQFFFRTADVT

GNILLKQGTEMVMPGDNTAIDIELIHPIALDAGMKFSIREGGRTIGAGVVSKVAV

>contig09162 Frame-0F

MYIALLNRQHPTGLNPTSGKGGLVASTSATNSRNFKWSSMQLWEIWKELSFAYTKTCFEF

TAAGMIK

>contig09795 Frame-0F|Blast-pectinesterase, putative [Phytophthora infestans T30-4](gb|EEY69622.1|) 1e-107

MKVYVLPLVALASLAINASATSVANECSGPGAPPHPPIMEDPASSPESCSGEHARTTPPA

GAIVVDITGKYEGSVKTLTEAIANIPDTTEVTTVFVFPGVYEEQVVVEKIKSPLVIQGYT

CDTMKYSANQVTVTQAKAQAHVPAEITDNRNFLTSTMGFKSQSGVKVYNLNVANTAGKIE

KDGQAVAVYVDNTDYGFYACNFTGFQDTVCANKGRELFVKSYIRGAVDFVFGQRAMAWFE

SCDIEAISKGYITGNGNQNETVVSEFVFNKARVFGSKSKSTMLGRPWREYARVVFQECEL

SDVVDPKGWSAWDDKM

>contig09892 Frame-2F|Blast-Putative beta-1,4-galactosyltransferase [Phytophthora infestans T30-4](gb|EEY53624.1|) 5e-36

MKSKRFASSRETDFHTSEKRQRQACSVPWLETNKVVELRCNFRDTPEKTELPQLSRCSTT

DTKRVAVLVPFRDSYPTQKRRAHLDEFVPYLTNFLQRHCSLNRATFHIFIIEQSLDSRKF

NRGKLLNAGFDIARNDYDIFIFHDVDLLPG

>contig12368-0 Frame-2F0

MKTMAVRFCLRSKKWPEEALRMMTSDGTKEPIRNLTDSLSKYRQKREGLHTILRFAMEAE

DIITRDIVWHIKQVLFRRY

>contig12368-1 Frame-2R1

MSSASIAKRRIVCRPSRFWRYFDKESVRLRIGSFVPSEVIILKASSGHFLDLKQNRTAIV

FISGKCSASVSTPSNFSNDVSTKLCAS

>contig12610 Frame-2F|Blast-CDP-alcohol phosphatidyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64290.1|) 7e-36

MTMVSILQMGTTWKTVVFVLSGHFVFIFATWE

>contig15642 Frame-0R|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY63359.1|) 8e-55

MWTIDPIAEFAEAVRLKKTTVDA

>contig17491 Frame-1F|Blast-cAMP-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY63920.1|) 1e-167

MASFLVVTTSHKFGTPLDSTQFDIGVTLGTGSFGRVRFATHKATNTYWAIKILKKADIVR

LQQVEHMLSEKRILVSLDHPFIVNLAGTYQDPRYLYMVLEYVVGGEFFTHLRKAGRFNTN

TAKFYAAQVVSIFEYMHQQDFIYRDLKPENLLLDSNGYIKITDFGFAKRVAFKTYTLCGT

PEYIAPEVLLNKGHGKGVDWWTLGILLFEMLAGQPPFYDDDPMGIYQLVLSGKISFPRHF

DRSAKGLIKRLLTADLTKRYGCLKNGVEDIKKHKFFSGMNWEDLLARKEAAPILPRVSRA

NDTSNFDKYPDSFEEAIVPVYNGIDPFAEF

>contig17859 Frame-0R

MRFAFVWLVVMIAASVAASDTTDSTRKALATKEIATSVVAKPSAHQRRRLGWSSHVSEWA

SKMGEKPFIQKSKALYRKFRPAKLKKTTTQRPDVPLYAQSGTIPIPKKSSVSEPGMFTAT

KLDDPPVLPLASIPVVEPIKPPVSMSASVPDVKPIEPPRSKHKVRFDLSDKNPEENAVRT

PMKRPVSALTPV

>contig19581 Frame-1F

MDLLGFGVPSAELSFVLKGDEEREKFKLPRLDETKSGKSIELPLFRDDEKICGILTVKVG

AGKHLEHA

>contig20466 Frame-0R

MEPPPPPPPPTSSGPRGQMQAFKSVTPAYIRSSGRDASMNKLQVDGLSSCSPSLQVD

>contig23830 Frame-2R

MKRMVLSEEMADVVFLWPLQEPSNDRTFKRLPAHKAILLQVEYFRTMFMGGFSEGQLTQE

AGNDFSTRTVHEIPLYYMHRDGVSLNAFKDLLRWIYTGCFELLRANLEPKTIMDLYVGAS

LVGLTVLAYRCELQLVELLPQLDVDSLQAVEDFGERFNARRLHTICQQMLQTQQHKGGL

>contig24152 Frame-0R

MRDKRSLLPWRKAKEALDKLAIFVATICIVGGHVEGFREGGFVAIEEQGPIRFGVLSGIT

RDPRTANLLAKVVVTVSVDDPVSPLIPAKLSSQMFSLSKLHVVERIPPMIHMFDDFDNIL

ITLSSLIAKSSSDYDEDATHCDLEQPNNRSANQTLRNHLIAYKQQIQWRAAKAIASLLMQ

MSSLSLTLSSIDSQFVSNLATLISSENCIARASKLKSSSLETATNLQKRWMCVKQRQVFL

ETEEILNSALDQYELNICHQVVAKLTGENVLSWEMGAIQSPRQKVGHTSPVKNGIQRQQS

DLLGDESVLPFGTWGVLIPLPPLTDSEHSIGTSGHSAIDYKPFPLTASIVRVGRAADACD

LLVNDRSVSGRHFHLRRLRNGMELEEARFELQDFSKNGTIVDGVRIHGSSAPITTGSRIS

LILSRGGLVTYEFQARTAASVGRQMPLSDIYTTQNSEDLNIMVPGQEYQLSQVTFPAFLP

RSPAEIQNRGSGHSAATEGLGNGRRRDTLTQSLRVITSIAESDVPRAIVSPNPAVDSPRP

GGYNSPRSSLLQPPGTPVARLHSSSVFASTIPSGILSPASHQQRESSSPNNSAGLFSPRS

SSGNVGSMLRISLGRDSVNRESLLQRMSNSRPDKLPKTRIDCLGLICQSNESLAVQEMQA

LAFRLHARTQDAQLVVSVIECEEALRISSGKIEEAFAALLQSRSSNSRNFAIVVRHLARI

LGRSESVCAKAFHQANNDVSDALRYILSSKEGDLESSRHYDALGVYDDQNGRKPSAGYQS

MIDDNPSYALLESSALCPSVPQRLKSPVRPHVKEYANMKTTSFKSNLTLWSECNSSFDDD

VRQMNAFEVELESGVLSKRLAAIHARQIVLQIVRLLKTASQTEEVPLQDLSNLLVLRPLI

SALYAPGHANTSVSHEAASALHQQTISCTSGKMQEILSRMVENVMMQSPVETMARNLCMT

QNISIFQRSIDHAMEQLSRSGWTGMARLFELLVESENAVKTHPGEDRNDQTTSNTLEDLT

FDTILHIISRTHAVPAVARSYDSFNTQKLDGSFPKGPLQLSCGLQVIVVNTYERLWSIPS

PDPLRKHRHKWRKRVATKGNTDYEWMKATADSTVTLWRPKGPPALNSSITWFGLGDVAKC

GNGAPDAPMLLISDYQQDGLLAPPVRYDRMDISGKGLPRNADSYPDFQRKQLRSIWWPVA

PSGYAALGCIAGSKEDPFKPPDISWTCCVREDLVKRLKSLSCVWCATSLSSTGGGDIEHS

TVIKNERKDSRPV

>contig24822 Frame-0R

MLETASSKAALPAMLTYRWPTLGVANATIAISLSYLRIGFRDRRAKKRESHNKAQEILHL

ELNT

>contig29432 Frame-2F|Blast-copine-like protein [Phytophthora infestans T30-4](gb|EEY70665.1|) 0.0

MQEAQTKGWKEVGQTETINNTANPVFVKTFQVDFFFEEVQRLRVEVFDRDSPSEKLSDHD

FLGCVEITMGQLMASKGQSAVLQVLQNDKKRGHVHYLSGHVIIDAEEVKSCADIVHVRFS

ATKLDNKDGWFGASDPFLNIYRLRDAKSDPLAETSWILVWRSEVIMNNCNPKWRHATIGV

QTLCNGELSRLLKIECMDWERSGMHQFIGSCTVKTIELVTGELRSINLINRERQLRKGKR

YKNSGVLVVEQIELQKQHTFAEFLRGGCEVSLIVGIDYTASNGNPSDPLSLHYLGGNYQG

QMNDYQAAIAATGAILEPYDSDKHFPVYGFGGLVNGVADHCFPLTFDPSQPEVDGLGGIL

KAYSDSFQFVHLHGPTKFAPLVHQASAISRAFSAPAEQGGHGNLKYFVLLIITDGAIMDM

QETIDELVQASTLPLSIVIVAVGNADFTAMSALDADGKVLIDSRRQRAARDIVQFVPFNQ

FRSNPARLA

>contig30737 Frame-2R

MVMKRSSTQLIDAALEAVFQQGMTRVGEEQE

>contig31208 Frame-2F|Blast-hypothetical protein [Vitis vinifera](emb|CAN71077.1|) 7e-25

MCQQFEWRIEKDLPTATYFVRAYVYDSGDEEIGYGQTTNDKKISNLFKIQGISGRHPSID

IASICFSVFAILSLVGFFLLEKRQSKAKK

>contig32032 Frame-0F

MCLAEQGPLDWLVPFIPPVLRVNCETRAKIKCKVAHLVSKETVRSIGFEILACWRYLAVF

SVIFSVWMAGLFYIYDNEREFAMAYIITSGFALIGCHLLIGDEGRSSGISAYSVFNRGTL

RMMGSLSAEQFENEIRHRNPENSNPHLIAEVIQEHHDELNDEGDIELVAAIKLSLQEYKR

ADRRIRRTSHRRE

>contig33497 Frame-0F|Blast-AP-2 complex subunit beta, putative [Phytophthora infestans T30-4](gb|EEY70462.1|) 0.0

MRSKFFFCKYNDPIYVKMEKLEIIIRLVTERNIEQVLLEFKEYATEVDVEFVRRSVRAIG

RCAVKLERAAEKCINVLLELIQTKVNYIVQEAIIVIKDIFRKYPNQYESIIATLCENLES

LDEPEAKASMIWIVGEYAERIDNADELLESFMDAFDDETAQVQLQLLTATVKLFLKRPNE

TQEMVTKVLHKATEESDNPDLRDRGYIYWRLLSANPEAAHAVVLAEKPVINDDTFALEPS

VLDELIGKISTLSSVYHKLPSAFVVRSNVSELREHHQEDDEINEKEDESLSDQRADKDRT

QPSESVVDLLDMGDLSMTGSVFTAPASVASSGNLVDIFGDIAAPLAPIAASAGTLASLKK

ILMTAQQGKGLQMTGAFTRRNGTFVLDVDFENQSSAPIEGVSIQFNKSTFGVVPLQTTVT

FAQLLGPGQCMNQVVPMGVSPQFVNAAVAPNLTLQVAIKNNSSNEVVYFQSELDLSAIFT

EAGSMASTAFITMWQTIAEANEHYFSVTTGACSADDVSERLKRSNVFNVAKRPLYGKEVA

YFSIKTMTNVVALFELTFDSSGTTKVCLKLEQQVFSAIFQETMERLLA

>contig33523 Frame-1F|Blast-cysteine protease family [Phytophthora infestans T30-4](gb|EEY66445.1|) 6e-55

MPSYSKQQLVSCEEKNYGCNGGDPVYALEHIRDNGICTESSYPYQSVKTTTTGACLKSCI

PAKSGISEIVKLSPGNESALLNALEKQPVIVSVVSNCVAWKQYKSGIVSSCDVQAVDHTV

LAVGFDSATIKIKNSWGTDWGEDGYVRISRNSKGMGTCGVLTDMSYPKL

>contig33556 Frame-2R|Blast-negative elongation factor, putative [Phytophthora infestans T30-4](gb|EEY61455.1|) 1e-178

MVLSSLLDRVFNPSDSISPAFLQNCVYLLAYAASTKDDRSLLQTGVQDSLNQVQVDKNGV

DATKKALVEASVICKSDHTLGYNMNQSGVVDKLISVMAVPVVSLGVLHWLEVILTSPGFF

SSTPLHICFPSLLQILKASIKLHVAQWPISFEVLVTSLRLHPDINPVKALELKRETLRCM

VFMITSGYVLPVLEFVLTNTLELDQALLRNFITMLLARIAPPFSHKFVVALTKILTHPKV

QTAIKTCPPESRMKLRDFVNFCEKNLNMLASDQLHLLTAIQDGKD

>contig33721 Frame-2R

MLQAVSLSSDHWPLMFITQRIRHTQCNVVNTTSSSLNLHD

>contig34041 Frame-2R|Blast-croquemort-like mating protein M82, putative [Phytophthora infestans T30-4](gb|EEY60216.1|) 1e-78

MLNATNAEDYLARNAKLQVKEVGPYVYRRREIKLNVTLANDASTVTYKMYTYHTYEPEKS

CPGCSELDESVSFDAGYLSVIAATGGEWNFLASLASQSFAVNATITELQTLLAAQGEQLM

RWLNGLNSLHPGAMRNVTDNARILRVLTTGPDAIADLNLSTFAFNGLFVKRTARQWALGY

PSLLTGFVLGANYINNCQPR

>contig34492 Frame-0R|Blast-glutathione reductase [Phytophthora infestans T30-4](gb|EEY62182.1|) 0.0

MNSKMIYDYMVIGGGSGGMASARRAASFGAKVLIVERGREFNGMGLGGTCVNFGCVPKKV

MFNLAAHVEHLNRNKDYSINTATKEFAFGDFDWANMKTKRDAYIKRLNGIYARNLGNAKV

DHVQGIAKLVAKDKIEVAGHVYTGKHVLVAPGGIPNVSDLPGKEHVIDSDDFFKLEHQPQ

NVAVVGAGYIAVELAGIFNVLKSNTTLFCRYDQVLRKFDPIVRDLVNTEMEKAGVTFVRQ

MRVVRVEKQENGQLTLVVTINGEEARFSGFDAILYAVGRIPRTQDLGLEQIGVKLSEGGF

IEVDAQENTSVPGVYAIGDATVTGWELTPVAIAAGRRLADRLFGGEKDACLNYHQIPTVI

FSHPPIGTIGYTEPEAIAKYGQENVKVYTSTFVNLLHSMADPERKGKTAMKLVTVGERET

VVGVHVAGEGADEMMQGFGVAVKMNATKADFDNIVAIHPTAAEELVTMAPWGMIKDKIVV

APEPARPAPMEEK

>contig34931 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57911.1|) 5e-37

MSKLMNYRFRENFMEGCSLGNLLLAALTDLQGGFDRAIASISDILNINGSVLPATLGITE

LCAELTDGSVVVSEVNVRNPYMPDEDVHSNSTAKETP

>contig35396 Frame-2F|Blast-tetrahydrofolate dehydrogenase [Phytophthora infestans T30-4](gb|EEY68099.1|) 7e-18

MTDASVGGVKLNASTIADPFSSAVRHYIDDAMGGVGPKLVGLLAHGDPAAKKYAEWTG

>contig35907 Frame-1R

MPPDDSKTLEEALFSLNNCEESIPWTFGADSWANLEVNACTGELEMDFELPVLTEQSLSI

VNLTPPSQLITPQLQPCMEPIQLSCVDNCSISSAIKSLSPPTSINTRKRAKQTRKHSNRA

RDLRREELVYLRQKVTDLQLQLNQRRSKPKLETASTPCLSSSVALQGRQSNVA

>contig37736 Frame-2F

MEVMMELTSYDDEENDEFHEVIEEGVDLLEDETYKPAVPPTMSFSVNEMEVITNREGRTG

SLSKFLEDADSYRRRSLPSYPEEQRFVGSMNHKKMTLGAFLSMQIDPVLEILEDTDSDIR

LWLMQSDTVKEVLTEFVTPPVLHGEPHEEYGYYKKHFLCSEIIMKLYTGEDDLYESFSSD

SSSGSTAATAVFGCQEPADIDKWEHLYAIFKNPIPLDEMQLLFFSKALVRLHDGFCLEEG

YVTNVLKRFLPVVIPHLYSNTIKYMLTLILQSYESVHPITGRNDAMEIAAQLLAEATRVD

PSKPQNLALVENTTNLLVDMLQANQADRLGAFSRREGGVYLSKYFVRDQFGTIRGFESMT

HGYHNFLQYMLLEEFSKQLQIVDELFTNASNELAIISDQKFTEVSSVLNIHVVAELLALC

QKLLNEGVETDDDSNQAHGAEAQMFGYSNFSSEQYANSPHDSVNGTSMYNLSSLPRGHVL

WAYVLDIARRTCGTFVSQLNKGLPSSVEVSVAKYLNNLVLLRDIGMDEALHKGGLIQAYL

TILEKRSSFDMLIIHIVPAIALILRDGDASRAKNCPLTKDLFGVDIKIPENILTLLLRAR

IDIPSLHIYAAILHDVIDEVFLSKAP

>contig37817 Frame-0F|Blast-TATA-box-binding protein [Phytophthora infestans T30-4](gb|EEY53626.1|) 2e-38

MYPVLLQYRKVTAPPSLSTGKPGYDDGEDLERLEPGTNV

>contig38197 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63726.1|) 2e-44

MMTSALAWQILPLMMGLYAKVSAQRVPRRLPGFTLGKGSADAGVQLESFVDLLCPDSKSA

YPGLKKIVEHYEADEFRVRFVLFPLPYHQHAYTTAEAAFAITTSLGDKTFTTWLETIYAN

QA

>contig38221 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67763.1|) 1e-169

MSNTNMRTAPMKKVSTLGKRKKSIDADDVKTIMKKDEFDPNQFYVSLTSHAEQFGVEPIR

IRWGQREPEVRGPIIGTNRHHKYRNAIGAHGGSYCIYRGLAVASGAIVNSAKPDLSETTP

AAKIGPHPSWADPEKMVTIDPFGACVVEAFPEFYKKGYDIRPTIAVTKAHMDFPEIHEAV

RLGRLKPDGKVLTKSSQLVITKAAIDPVWYLPGVAKRFNTTESNLRQQIFQETNGMYPEL

VTRNDLKVFLPPIGGLTIYIFGSVEAISDPSKKLAVRVHDECNGSDVFGSDICTCRPYLA

HGIEVCVQTAQEGG

>contig39415 Frame-1R

MTQPQSLGHSTLTNQSTTYRIPRIINDNTTSRRNEGSKR

>contig40396 Frame-0F

MTPRRRPANRRGPRSAEHLKLSSPHLLYPQANSLKSSLRLKNVKMGRLSSPHEKTPSKVD

GEDASDTSTTTSFSSEGDTTSFLHNAQQLQRKNTASVERYSSVPLKTRFSRRNRRTVDAS

NPLRCPLLGRRSLNKRQNIETSKLDLILSARPAAAATAAACAEAAENEKKRNK

>contig40532 Frame-1F

MTCITLFNAISQVISSLRKCVQEITQY

>contig41225 Frame-2F

MLDRFFIKRIPTDGLAKFRVKSMVLAGTLRSKSISETERYSSAGLGHDSSDLCISSSWLR

NGE

>contig41492 Frame-0F

MVIGIILLKVYLQCRSDEDPKQFFWCGQIKKHSRRALNFELASMRVNVDKAFTS

>contig41931 Frame-2R|Blast-putative methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY53044.1|) 7e-92

MAGAGNSQLSEAMVNDGYEKLMNVDVSEVVVKQMATKYEDRAEQLQWQTMNMCSLDFADE

TYDAVVDKGTMDSILCGEGSTTNVAKMCQEIHRVLKPNGLYFIVSYGAPENRLSYLENQE

LHWKVEVHTVPKPIVSAVQVPEGDAKAVHYIYVCQKENKAE

>contig42817 Frame-1R

MASDTRLTFESLKADQEDEHFCRRISLESEEAEEIGSIARANSMHADDEGPHATMVENAQ

VVEVAPISEAQATMVAQHDIQRRKFELENEHHERKTIPSVADSSTYKHQLFQQMQDLHHV

VESTYQVARANTEAAFKERDSGRTSKASPKRTMKTLRSVRTFSQPFAFAVVGLRSTRAMT

VSGDK

>contig44019 Frame-2F

MLRDICMDFIPYHVHLRWRRLSVVSKQHDHINDNFDFFRMMRRTVINSA

>contig44208 Frame-2F

MLWTYALVLRYFNGDYKQDTTEAAFLLLDYCRVLSEDARYESLEHVCFACLEKQNTEGFN

ANLVALEDTQHILRSNVFLLDAISDIQALLQQCLQELACGGKAPKEGKAALKKLAAVQKK

VSFYLTWA

>contig45067 Frame-2R

MISSHSNEEYELKTCSLIGQQVPSELEVVHCICVVDDPFTKNCSSQTKYSCCDSATKML

>contig46497 Frame-1R|Blast-pre-mRNA-processing factor, putative [Phytophthora infestans T30-4](gb|EEY56427.1|) 5e-62

MIDRIIQLAIKSLQKHQVVMNREMWLKEAEACEQADAPLTCAAIVRASLDVGVDPEDRKR

TWMDDAENSINRGALLTAKAIYAAALKVFPGKKSLWLRAVALEKQVQEGKSPESVEQLLQ

KA

>contig46556 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66991.1|) 1e-15 NOT\_ORF

MNAREAVTSNAIAYDKQIQTCHLCSNLKMLRELLPPRRCDYVRCRANYFEPN\*ISWHYNY

SL\*CRRWRCQFCTLKLPMLGARKGPFKKLKGNSR

>contig48095 Frame-0F|Blast-isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase, putative [Phytophthora infestans T30-4](gb|EEY66594.1|) 7e-39

MDHILFVQGEVPMENVNKNEVEHVEFVSRENLPALLSDSTRKLSPWFHLIGSNLLPRWWD

DLDAVLKHDHMNRQIHDYR

>contig48284 Frame-1R

MNDNSTENSESDSRTEGSEQPWRLERQHARTNRRHFVGGYEHTTNDLDGNFIQPEGNPEE

LPKDVIRCTGLRLEKTTDGLMKQLQDIFAQQQKHIATFHEEQKQVDQMLANLPAISLSGL

NDLYRKVATLDNVFLTKILVNAGEDAMDTIARTLDRRENLPSAFDQLDREIGDWKDELKE

CSQWIHNIREIVEDAFTQRKAQIPRGQLEQTESSCDSSYSSDNDDAYHNFNEADKAYKVD

ERESNTPKQKRHHDFVLKNDVRRPSLAKARNQT

>contig49852 Frame-1R

MSFELATPPRSRDTSNCDCILFPTRKRGAVDSGTLSSMLDANFTSKLHREALKLVVIARP

LGAAPVIVKLGSSRYSNHQVAPLRA

>contig51097 Frame-2F

MQEYNQHPLADNPNEQCQHRAHKQQSHEQQRQLSQHGLQAQHQDYVNSSFGAASMNPGAV

SQHIQMQPEHVQRKQQQYNPQQYQQQQHQQQTMYNSQQLSQQNPQQQINAYGLKPPQPIP

FDNASVEERATHLLAACESCLGVTRVPGVDMTFRRIMERKCSLCGGMLVMPQEVMEMLIL

YGHFVPEFVAVTLILGTMVLHPSLRADFIAAAMNDLLIPLQTDFVYDVAVPKRQEGLGMS

LRIYQGNLVVRGFIDFKNNQESPSVAARIIAVDDVLVAINKKSITSWTFEKSISMLARAA

SPVYLTFRRRQPVMLL

>contig51321 Frame-1F

MALSHCEERRERLESEEEKPLVQSMDEVDMNLDKQEEMEAFTSSHMMWPLLEPTLASSKI

YLMSLADAAKALIATAFTFPLHRMKTKVLYTSRATMTEVQRVFQRHAYKARPVRLSRVDA

LREQCGREFWRIAYWPRPHTQQFLECAVEFMKDAETAVETSAAVGGDISKSALVLPVSQR

FEDLTDITPI

>contig51394 Frame-1F

MTTKGANNAIIYVISYCGPAFRSGTHCFSFMKRNNFFAWQTACDA

>contig51585 Frame-0F

MIVVGVLLALAIVLISAAHVPIYEEHSTSASLVPVNISKASALPSQVHVALAGEVEVRSY

LTTEASNRMPSEIRLGMTISWATGLKTATSLVRYGVSKDNLSTSQQTEGSCEQYNFCYYT

SPWLHHVTISGDKLTPNTNYYYQCGDEDGGWSAVYSFKTAVPVGTESSQTFGIVGDLGQT

QYSMQTIHHLQGYHSNMSAIICAGDLSYADSEQYRWDRWGELIEPLIARMPWMVAAGNHE

MEVPCQLGVSEFVAYQTRFRMPYVESEKLQIRNLYYGFRVGLVHFIVLTPYVDSIRTSLQ

YKWVQQEFLRVDRTLTPWLVVIMHGPWYNSNTAHQDIEPHLIMKENMEDVLYRHKVDVVV

AGHVHAYERSHPVYKEQIVQNGPIYVVLGDAGNREGLAPMYYDPQPAWSAFRQADYGYSL

LNVINRTHAVMQWFEDQEEGDAVLHDTVVLTTSEYRSS

>contig51606 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66726.1|) 2e-30

MGMEMHDVTRHQESSHFVGNASANLRGTPYEISRSTPQQSVPTPPPTSFYGGEGQMHSQD

IFSSQGLSGPSRQLPDHHHHIFGSELQQQQQSDQARTMAGQDFIMNRTYRAINDDHDLQH

SNMEQSDHNDVNLGDWQ

>contig51673 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69864.1|) 4e-44

MALLRRVVRGDFQAKEYPATMARMFEWTPDECVPEFYLDARIFTSLHHDEMEDLEFPPWG

DTTNTNAAVAFVTWHRKMLESDRVSSQLHLWIDLNFGAALSGDA

>contig52104 Frame-2F

MANIDKNGAGDCVVAAHVDVDALTDIVYSDLDEQNDYVDDDILSFSSPPSSHALHVAQYL

SFSINLVTCGDV

>contig52799 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55524.1|) 1e-101

MDNTIRLWALSHGEEERVNNEDTWEGERLSSNPGATVTAELVHSFVGHGDSIKGMAMRVR

PQASVYQLVSWSKDQELRLWHVDGPQLEACGFDTASYLADVALSEGHNNSARQQLNAQRL

LHAEFAEMHAHHSKYSLSALKTDFMPLVVPKSAVPLRTDEYTLDGNDGSLQALMALEEEL

TKGEESHSQSACSEDEGLMCGIRDKNYEHLNDIAGASDCGANTSGARALPCPRISGAAFS

GPNMLLVF

>contig54344 Frame-2F

MVEQEQVSYCRMIMRGLATEAAVNDTKVPEAAESWCTTMLDQCWNDIYRLYPRYFEPCL

>contig55075 Frame-2F|Blast-adenosylmethionine-8-amino-7-oxononanoate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY69924.1|) 2e-36

MSEPLGPWFVDHHTVFDEITMGLWSFHKTRLESFKHMQERAEQVFWWPFTQHKKAGSLSI

IDSAHGDEFSVYRSTSNTLEPLFDACASW

>contig56117 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64425.1|) 8e-44

MSIVATLESQAQKTYYLVDKKPFFKHFYPKDVAILAVRSVATQSLLVANAYVASLDLEYQ

DEESSEDEFEDVDAVIGHNAEFVPPSIDEFCIASAQIFGKSLSITTCVRSLEEVALCFCH

PRIVSKFIKG

>contig57684 Frame-0R

MTSAGSCGQYELLQSNSRSARYH

>contig58609 Frame-1R|Blast-peptidase, putative [Phytophthora infestans T30-4](gb|EEY65781.1|) 4e-06

MYRTLFAIVLQSRSHVPTSHLFRSLILFP

>contig08506 Frame-2R

MSANPFQARTKASALKTTFGQSSGYGSQPPLPPGGVMGYPDNGFGKHPPLAKASPPLARD

YSGSLKSGYPFGQTMDSRRKMSNSSSTPFGSAASEQNSVSVSPTLANAHVMFGSSTNGDR

KATSQDSGFAHNNSASISESITASEHGIIVKTTHFGADKRRKNSFPIKSGRNGLGIPITM

SSSVTSFGGNGLDAQLRNQQNASQVMSAVHATKSNGSVDSGGGKLKGFNTCTTFGSAPNG

IGVKTFSTSENSSSHEPVIHTAFGDKRRHSALQIGSETSVIKTNKIVSPMELRASGFEKL

PPGRGKQTQGFKKERREIIAQNLSRPKKDLQIPFGPNADKEVNIQKKSSKKDTARKTRHK

REKERVASIIGDEPSNLPVPSSVSFRDDSSKA

>contig09163 Frame-2R

MEQSVPEAAVRQQRRSPESKVLPEEHGECLVAMKDPLLRSLLDEYMQEMSNSNNQIEKEQ

SFAQREHDENVLFSNQLIKPTPGFVIKTTWDNSQKIFINVCSNPTIEPSYNYFHGSRNQP

FKTSWKIPYLVGPERVELDHRGHQVPTFDVCFHPHVLEYAQTRVGYQDLVVQTCLEAIEA

DLRVSRHAAKAVLLRQYIVLQGVSYKSGTPTQCNVHHTTSLKHLTTISKKQSNNNTKAKD

LPTSASILSVQNKHNFINLSTPQESSPNAFQSLQETTKKSQPNPLNHVHPAIKLHIPRYQ

THETNTCVTYLVQVAHIIESSVQLSFPSSSSLTLVFQASKNHPYQLDIALSFRSINSTQV

HVASENLALLLFKTSTVQPNDST

>contig09332 Frame-2R

MLRLAKNEPLFRCESENFEKRAISYQNASSHTSGVFFFLAKSDSRFASVSYSSRFNHLHS

ARSSVRDTLGLVVIAMSLNDDHEDLSDGEHEELLFPVEDLDVVHSPRLHSKGSHVFYSVD

GVDIERPGNPMAAILEHREAIDRKKRERDEEADEFNPDGAEESPIATRVFSHKCKRKTFE

LPTAPARVIRPVAKRFKAYGFDRSITAPACFIDKRLRYETTEEAKLELEKEDLDLPLRAA

SIAVPDSFQPILWPGDAALSHKFGKDRSHSCSSSSSSKSWASGLGLFCRRSLDVSSPLRV

RLND

>contig12369 Frame-1F

MVTTSARVNEEINPTTSRKLSQHLLRLITQEVMSPNPKEVVREVQTPVRFRWRQAISWTS

TPGILHKNIRHVASQKSHRVSACNQNEAGIENRATGSAECEQQYYDEPQDNVKTGSRSDR

SSILSKANTTGSDNLYDLSSSNNKPALSGLRQAKSSAIYPTSSASPLKVLQSSVCDLSLS

QLKRAALFQELCEFSASDDAHITFFPEYFSDEELRIVQNVAQNLQLGCQVVEKTVAVYKP

IVGHLQECVSQYTSPANDMFVNVHQLARQGKASFFAK

>contig13928 Frame-2R

MGASKPQFPYVSGLSAFARNFFAEKASCYLTKKLHNY

>contig14482 Frame-0F

MLIIYVGEVYTGEPTKALRSGTKKQSGRNPFLLSSRSYQLN

>contig16350 Frame-2F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY57528.1|) 2e-39

MPHCGKALYQNVLACNWGLQLHHVVIIGNSFTAYADRVLARVEREQLLLVRVLPYVNETA

LSCGVARTHDDFRHYEAAFNDLSVHAFRPFHALHNDKHDNAFKTAFVAELKNSHIISSIT

PIASQRM

>contig17551 Frame-0F

MMDGYAVVAADGIGTYPVVERIAAGDVPTTVVTSGQVSYITTGSCVPEGADAVVRVEDTQ

SGDNNPSRHETRVTITQSVPPGQNIRFIGSDIGLNEELLSVFQVISAVEIGLLATAGIGH

VQVYRKPLVGVLSTGTELVHASPNKTTCGQIRDSNRPMLLSLLRQWGVSTMDLGVFHDEK

AQLHNALKAAVINHDVVITTGGVSMGEFDLIKPLLEEMGTIHFGRLFMKPGKPTTFATVT

INGKKKLVFALPGNPVSAFTTCHLIVRPALKRLAGFLVEDCGFPRINAQLTHSIRLDAAR

PEYHRARVEWGTQGFLATSTGVQLSSRLLSCRNANALLCLPTGIEMKKGAIVAAFILDTS

FKNASSLVYDPKEDPFKGSCC

>contig17858 Frame-0F

MTGFYTRPVFMHILMLLSFDGIGFPRKCRPRHAFIIEDERLERAMAVWNLL

>contig19311 Frame-2R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY61994.1|) 1e-129

MVRHVMDQRELQRGEGPIALVLVPTRELAHQTYMYVKKFLTSYGASCAAIYGGAGKWEQV

QTLKKGVEVIVATPGRLIEMIRKKVVKMTRVTFVVLDEADRMFEMGFEPQLRSVMGQIRP

DRQTLMFSATFRRPLQTLALEVLSNPIKVTIGQVGQANEDICQFAIVLPTHGAKWPWLVA

HMPQFVNDGRLLIFANSKNGCEELATNLRTAWPTAPARCLHGDKTQQERMEALHKFKQGD

CRVLVATDVAARGLDVKKY

>contig19669 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63468.1|) 0.0

MYFFTEAVLEEQEKQRQHVDPLLPSIVEKKKNAANVLLTSITVYFPLFLLLILVYETLRP

RIPHVYAPKNHADFPESKQRKFLSWIPALWRIDEAQVAETCGLDAWVLLRFIQLGRKVAL

LCVLCSLALFPMYFFTEAVLEEQEKQRQHVDPLLPSIVEEKKNATNAYITSVVLLMLDKQ

VETGNSTLKRLSSDGKLKLDVVDRLTIANVGKDDWRLYFTVLVAYLISIYVMRLLLWEYT

IYRKRRHEFLVRKHPQQYSVVISDLPDAQRRPQTLEAYLNYLFPDSVHSVYIGVECTELE

ELLKKRQGLVYELYVATKKLQAAQVTRKDHEGIVRPKVWIPRRFCGLCRAGKQVDAVDHY

TKELQHLEADIVRVRDEILQHQSAVIEADEYTTNKQYEATKAVVRRSLCTLEELAVKLQM

TKRSVVNPRWTDETLPLLHSSVSVPMRPNVMRSCAFVSFRSIRSAQAAQQLLQVENPRRM

IVRPAPNIRDVQWKNFGLPHKLRAKWKLVSIGISLLIGLFWTVPTAFVASMSSVDELQHL

FPWLRGLLTTYPWLLIALQQTAPLVYSVMNGLANVIFKLLSTQEGHLSISEVEASRFTKL

CFFQAFQMFFVSALAGSVITEFLLILNQPRLIFFFLGNTIASQSMMFITFIITQICVDMA

LFLLRLAPLAISAMYHLVAPMHAKLPTPRDWMGLCPINYQTDLDTPINLAQQYLVFLFVV

VFAPIAPLVGYFGAMFFVVSEVAYKRYFFFINSSSWAATNSMGVFWPPLYSFVIAALVIA

QCTLIGLLTLKSAGYIPLSLTAMLPFITLVFHWYAVDLSQLERAAENLPLDQCCDIDEER

KNISFEFLNGVYQQPAMIEAFQSSSILLHDFDKNKGAAVEITHGEVSALGITPTRTALKA

TSHQTSLAELNRDLKDDGKMNA

>contig22326 Frame-2F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY64147.1|) 1e-76

MFEVPVLVATNVLSRGIDLLNVQNVVVYDLPKTIPDYIHLIGRTGRADDVSGRVLTLLNT

TDRPLFRDLVPLLRQMNASVPVEMYREINLKHAKEKAQSSQIVMSEAKRAFRIRMQMTDD

FNTQALDWKEWKHQNPKRRRIGP

>contig26061 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63982.1|) 5e-61

MATKGVWQLKQVTIRYCQHSGSSRYVRQLLADERFHKFVEENPQVQFETELKGARHPILV

GDYITNQRKVADVKNQEIPFILKQLERLRNSSGRKMTLIKKPVFSKRPTIQGIWQPDLEF

PKFEISDHA

>contig26128 Frame-2R|Blast-protein phosphatase 2 [Phytophthora infestans T30-4](gb|EEY66111.1|) 0.0

MTATVSEDNSLYPIAILVDELKHEDVQLRLNSIRQIRIIAEALGPERTQNELLPFMNDSL

DDEDEVLLVMAEELGDFMDEIGGPAHAYLLLKPLESLATVDEACVRDMAVRSICKVVEAM

DSGHVAEHFIPVLRRLVTRDWFTSRIASCNLFQVGYAHVSADIQAELRGMFGQLCRDDTP

MVRKAASAALGGFASVIDGPNASGEMLSLFLALATDRQDSVRIHMIDNAVALACRVSADA

LQTRVLPKIFEMARDSSWRVRWSVANRFPEICEALSVETINLTFCDSVVSLLEDNEAEVR

TAATSKILGIAKHLQPVRIVEKLVPCFQRLSRDMSDHVRSALASVVMNIAPYLGKDFTIE

HLLPLFLLLLNDQNSEVRLNVISNLEEGNAIIGIELLSQSLLPAIVHLAEDHQWRIRLAI

IEYVPLLAAQLGCEYFEEQLSELCMAWLVDNVFSIREAATINLKKLTEHFGVDWARTSVV

PRIVTMHSNANFLHRLTSLYAMKVLSEAMNPETIRTLLIPLVVELAQDPVPNIRFNVAKT

LEVLGSKVDAEIREATVTPCLSALQQDGDTDVVYFAQRALAKLG

>contig26379 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58384.1|) 1e-19

MGPSFAVLPNMTSIFPLPEDYFPLLPLSKKEAQCYLEWGNSLLQATIDAYHRDQFDSLEV

RERQWKPIKQKNNLTV

>contig27170 Frame-2R

MDASLKETKYDVLLVGTGMVEAILAGALARIGKRVLHLDQNDYYGSNYASFSLAQFLRWT

KNETITPQPLSDEETIDHTPNATVDNSTHRFLPMQYSFECHLLDEKFRSIDVKETLLQKS

SSFSMDVNPRLLLASEQVVETLITSGVGRYLEFAAIERTYVHLPSVNKIKKEFSGNLDTV

WHVPCSKKDVFQSKLLQMGEKRQLMKFLQFVADYGDTHILHADVKTKNERSLALGRALPR

PQNKTSAATNTVAIATLFDEPFHKVLHEYFHLSEKLQHVIVYCVGLATLPATTTQFSGRQ

GLAAVYRYVTSIGRFATTAFLTPLYGISELAQSFCRLSAVYGGLYVLRAPIDAFVLNTVT

HDLSGVRCTDGSVLRATHVVVNRSYLDCLNLTRTATPRGCGDVLRGVFILDASLRQGVTR

LMLVIPPDDTEFHNPCAIQMVQLDHNAFACPEGYYLVQLAMPLPLPWQQQKERQLTLMQN

VIRRLILSSEAEKRKEDGEEVDFDWNDRVAWRAIFTMDHFIAEDTSLSTDVHLPTNAWVC

ETKVKGANEIFPLEMHLESASANARAIFEALCPGADFLPKSASAEQAELGEQEGEEDAVL

RAAQKLVHETFIAGNCAQEGSSG

>contig27835 Frame-1F

MQINCLDWLSRVFRGYQRALQYAAKGLESNQLLLLHLQKDHWKGLNLHNFLVSLELGKIN

FSMYENRLFQFWVEFACVRNQEANAVQILVKKAMIDYLNYINPDFALNEVQLELLDINKP

KNIMLNAAANLFTRLRLHKASSLRKGKWLCWINFTKGSEARARYVLGIHQFPILQELIME

WKTSEKLALQKFAKELVAYNHEKSPPN

>contig31731 Frame-2F

MKTIYIIHTKHVRYSIGSSYSKPRGYRSVKNTEKGVSRQHTSRTSLLHRPSFVLSRLNTK

ILKVYWLHRIIDFT

>contig32033 Frame-0F|Blast-UDP-N-acetylglucosamine-peptide N-acetylglucosaminyltransferase, putative [Phytophthora infestans T30-4](gb|EEY67702.1|) 0.0

MAARLMPQFAAAHSNIGSVLKEQGKLDLALAHYQQAITIDPNFADAYSNMGNVFKDLCRL

KEAIQCYSTAIRLKPHFPDAFSNLASAYKDGGRLEEAITCYRKALALRPHFPDAFANYFH

SMVFICDWRTRQQDTETLQRFVDEQLQINDVLPAVQPFHALVYPLSMQRFLDISRRYAER

AKLNVSLVELPPMRFQTKQASERIRIGYVSSDLGNHPLAHLMQSVFGMHDKTKFQVFCYA

TSPDDGSSWRKQISESVENFVDICALSNGDAARTIHADGIHILVNLNGYTKGARNEIFAL

RPAPVQVSYMGFCGTLGADYIQYMVGDATVVPREYRRYFTEKQIHMPHSYFVNDHKQSAR

DVLETDKCPTRADYGVPADKFVFCNFNQVYKIDPVTFTTWMNILKRVPNSILWLLRFPPI

AEANIRAEARARGLEDQARLFFTNVAPKEEHLKRGYLADLFLDTPECNAHTTGCDILWGG

TPMVTMAKDRMATRVASSLLRAANMSELITNSLEEYEELAVALATDVDRHQALRRRLEGE

RLTCPLFDTQRWVRNLETGLSMAWERHEGGLMPDHIDVPDVNDLEAAKSEDRQLTKAIE

>contig33207 Frame-0R

MVVSYRRATIEVHAEREALEAFRIEAIALQNIRSKADEQSNGNITASLRCKYPPLQVLDR

REMVWQNRMLWEGKHSDIMTSSKQLAILYYFVQFLNASSYGVSLQQLSETCRAQVVDNVA

LSGNLWEKDIMGGIASLSWTFLEPRQGGKKELQRHRKNDEKADVDNENLRNLISICSGLA

GWLTLDIANLTLYQRVFQSYSISLLEKSKVRAGYVEIIRLMCELIDCFVDWSEEQNGSSS

ASLPCLCEDIMAAVFQYSHLKPLRPVLMAVLLSNRMFGMHEFVAQLRAQYLIQQRYTVPR

RYVETWQNENQMSVFDGLWVFDGNKSQITPISKTRAAEYSLGSILAFLRELAQINICPLN

SQSLEIRSNWNICSAQIEKRKSSTRSQSGLILVLDNRQRIYGNLPSGISSAISLGGHQYG

DYCGKLISPNSFEVEMCSWPANCSRPCQALRWKLHVNKKTDRRGRQYEKSQSGISVNVVV

EEGVWQTNTSNQVLDFHVLPFKSKIESVEAWYPIFEIVGLYNHIC

>contig33795 Frame-0R

MLKPRYNRLTNLARALQRPQVAIPSRAFIVPLLKSASPQIIFHRYFSFVPLDSDDGEQKQ

KNRPSFAIAAAFEGHEDLEEEDGLDQSYVHTPDVKKPCDERVRALTEQFRLGMEKKKVWM

QSLVAQNRYAAVVKCVADCYAPLYVAMGLEGKCPLLMVTNDKNRNHHESETEFKPQRFDD

MLTKTTEQEALALLVIAKQSLLALTIVEHREKLAEELARRSNAGIGVMVPGSNVMEDRNV

LTLGSHLRMFYSWSMSAYAFCGQAYYPKVLEMYKRAQDAGLYVTANMNVQYLSVLIKQRH

YDKLFDFYKEVVRENLPTSVYFYRQMVFAVSVAHNIELLDALLDDMRIKGFKLREVDYLR

AIRTYDLKYFLKAKHQHKTTQKHNNYRKMHEHEAMLTTPTDSYEMCVKRFREQDDNPERY

KELVEAAKSVVAIFDAMVNIDGLAPRHGDLFSRVITACVYAQEYNLVPDLLALHAEYVDE

KLHPAGVRMAVNAYLLLEEPAKAWTLIFETDVNLERDRAALISNIFDYMCAKKLGADIIS

LMRDVDNLKLQGVFTQSLIKKIVPALCRSIDSVKDEELLAIMSQFDSVFRLFTSEHHFGV

FLRECCHNRRIAAVKTALEQWIALSDNKRPLSGSVGVKILKAFEDKSDWASMAETFELIN

FSKEIHTDNCEAIVTLVTQAYDGLGQSERIKQAKQVLDMTKKRPDH

>contig34224 Frame-2R

MGFLSGQAQQKVLESFQKYFMKGLNDTCDGSGITTVEQAQNKPSKKSESTHNGVRCFCCE

KGDKSG

>contig34493 Frame-2F|Blast-beta-secretase, putative [Phytophthora infestans T30-4](gb|EEY54529.1|) 1e-125

MRYPVSTLVAMTTALQSLPTTMAVLQQKLYGLPSGLAYYVEINIGSPVYSSSSSPSSINS

FNLLVDTGSANTAVVTAQCCALTNEKVFSCQASSTCVDEGASISVRYISSSWTGEKVRDT

FSGQGLGLIESMPFAQILVEDNFVTVGYDGIIGLGYESIASPSDETSMPYFDVVSTRNGL

NDVFSMQMCGTLQALSLRNVSTEDTSFLYAGELLLGGTEGPNGQTYHQGDIVFTPLVHER

FYNVIVTDIGANGQSLGIDCESINSPRAIVDSGSSNVAFPSSVYTAVIAELRAQVAQVAS

MDDSFFSDDSTCCSNECDPGNLNSFLYRLPGLTISLALENNESQQMTFTIP

>contig34985 Frame-0R

MTVKKNCMRLMTGKGGVTSRHFPSQLMFGRLCDRRPIAQHLVNRHGPTTMSLSVQRFGVR

LTVFTTATLDDKCHAIVN

>contig37553 Frame-1R|Blast-cell 5A endo-1,4-betaglucanase, putative [Phytophthora infestans T30-4](gb|EEY55029.1|) 0.0

MASRNRRKIKDGLEDDNVLVSDDGQVGNPKKYPDMGCELPDYQSKNGQIFAVSKNGTEVP

VGIKGLNWFGMETGLAIPFGLWENMDNGTSVYEVAAFMARNKFNSVRLPLCIKHILSDVA

PDKSLINLNTNRAINITTYMTTIQTIVEALGYRHISIMISLHTLDPKKSGGAWFSETLGV

TEDDFLSAVDILTKNLCKSKYWNILGLDLKNEPHECTWGGSDPDWSKGATLIGNRMLEGC

PNWMAFVEGIASKGTITLNGQTDTYFDWWGGGLADAGANMITFDIANKLVWAPHYYNTGV

SPAWYLY

>contig37742 Frame-2F

MSVDHSCVCVGQVWPYYPAAFSRMNLFHWVCVADYQFLCQTADVVKYQVMLSSSEGSSNN

LRVACHYNSIVS

>contig37816 Frame-1R

MLQRQLTKFHTIDLAPLQFSMALNRSNHKQKSVGQKSIIN

>contig38022 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65139.1|) 1e-23 NOT\_ORF

MLNHSDRMLLQRMMVAQFIF\*TKLRC\*\*ISLIHMLSLLQAAGAMEDQEVRHLASQLTGKD

MTASDVDQMVNKLAENVRPFSLDVRRGMYDDGKMYLSVVNT

>contig38220 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67763.1|) 2e-41

MPDALHWLGIKKIDKFVSMSDMKYDAIVKSG

>contig38484 Frame-0F

MEASLTPHFRDAGFNENESDVCGGMEPSAYAVTFFIDRYMGDVRCAAVIFALLAASIAAA

VAVAVATYTEDSLTVCAAVGCFSGMLCACFAPTPGDGVSILVQEGALTMTAMNSIIVNYT

GSELELAIVDYLFVALVGWVIIVISRIIASKKLLKCLLMVALDTTALLHVTIVMMEIVHY

VNHPLANTLPHEFSAFIVTIACAESGHYLFSAVTTQWLRYNFDRWIITYPRVYAALDLIV

SVMLSAAGMSIWMQWIYAMHLSTWSAVALIGAAALSYAGRSIMTLTYETAMVLPWYCSTF

TVWNNGMMELLNPFLVGWIIFNPYIKNSFEA

>contig38707 Frame-2F|Blast-calcium/calmodulin-dependent protein kinase II [Phytophthora infestans T30-4](gb|EEY66907.1|) 0.0

MKLLDRSGWKRVDVSVPPGPLGLIVSTSPIGESHVIVDGFRPVGNSAEPGALERQGEIGP

NSLLLGVNDHDFTDSAVGWSFEKIREILVSTSGTERIVRFLVPPPPPTVQFEEIAAHECD

KRFAEMYALGKELGSGTFSVVREAILKLTGEKFAVKCIKRAQLTADDLEALVAEVKILRE

MQHPHIVKLYDVYQEDTYFFLVTEYMPGGELFDRIVKKNFYSEREARDLVKVLLETIAFC

HDADVVHRDLKPENLLLSSADDDADIKLADFGFAKKAIESTEAGLSTACGTPGYVAPEIL

MSKPYGKEVDIWSIGVITYILLCGYPPFHHNNQGMLFRLIKAGSYEFDSPYWDEVSAEAK

DLIGKMLVLLPEERWTARQLLEHPWIAEDVVKDVQLTTALQELRKFNARRKFRAAVSTVK

ATISLTKVLTLGGSPRSNKDSEEEEEEQTESAPAPLNSPINATAAPPSPP

>contig39098 Frame-1R

MRQMVALLLVTLTSFIAESVQLTIVCTSSADCLNGDTCVAGDSAIPIQTCVAGAVCGGTS

SGNCPSDTTSGQLACIQRNSIYQCVSIERCDQYFGGASCSGGCSASGVACSGQGTCNLVS

TDANGRPGFSCSCNEGFSGDKCEDVSRTDFDSSTTSRTTSNAMDSSFDAASQDFSLLTSS

SQARSTSTTSNVADPGSVANSEVDLTDSVSSRSGSPSGSSFV

>contig40533 Frame-2F

MVTISPCCAVLTFRYKLSQLTSTPLFGLSNMIVSNKASLLNDDY

>contig41493 Frame-2F|Blast-thioredoxin-like protein [Phytophthora infestans T30-4](gb|EEY70088.1|) 1e-177

MQSRAALLALAAFVFATHFVQANLVALNEASFDHQTSSGVWFIKFYAPWCGHCQKLAPTI

QDLSKASEDVHVAKVDCTSERSICERFSVGSYPTLKVVTDGKSYDYNGPRDVDAMLTFST

EGYKKDFGEIVLSYAEFVEKRKAAAAEHEENERKSAVVHLNTTSFEEQVLAGKNPWLIKF

YAPWCGHCKRLAPTWTKLSRTLKEKNSNVFVAKVDCTVHRRVCSRFGVSGYPSLLYINDA

QVYRYKGGRSVPALLDFVESGWKTAESTGPIPEEGFFSKIIDMTIEWATEHTVLAVLAGI

LVIAIVVAVLVALLDYWLGADDVAQYKKALDEKEAEQDGGNALPPKVASVAETKKNGSKP

KDE

>contig41930 Frame-1R

MWPCRIAPFDRTMNCSLVSLLSLIE

>contig42737 Frame-2F

MPNFSTGSAAQSRHLTAESSAPRYSANSSPSSIRARDYLELPNSVKNVLKRQIAAAVEDV

LDSMMREGTADNYWRAKMCKDGITYYEDRESVTKKQSRFCCVDSTEASVEKVINLFVVSD

TDMMLQRCRFMYDNLLDARLLNVLEYATEEHPLRSTYIRYTAFKARTLQRHHRDMCVVVS

TDVIKYPDGSTIGYCVWDSLNLTDISQLDVPKGFVRTRMFRSGYFVQNTGQPGALSKIAY

IIGIETGGLAPRLTTRYYVPRFADVLSRVIALLHRQQLDPSTFVHQSLWTNKYQVDFCQC

CSKHFGAVKLLGLRRYNCMSCGDAICHACHHIEELRIAGARNMTVGVCVGCITATTRKGT

ARLSRLSSWRTSSISSSFVSSTKSSPM

>contig42816 Frame-2F

MPAASPPCVCSLSRLYSRYAVSDLRRISKTWSRAEKDSFRFKLGSLIFQN

>contig44731 Frame-1F

MSVDESKDRINMFSHLYGISLRPTKK

>contig45066 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62998.1|) 6e-81

MLTTAMLCIVVLAYQVATRSPEMTQMLIGIPANMLSIATAASPLLQLKHILRRKDASCLP

LGMSAMNVVGGTIWSTYGIMLKDPLVICPNMFALTMGTIQVYLILRYPGGKEISAASFKE

KPSLPTKPATKITPRHKEKITCSE

>contig46184 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64066.1|) 3e-11

MTFIVHSYGIFHSAKDEKDKVPLELVELHAQFIKI

>contig46207 Frame-0F

MACRDTAPRVRSLWLTRHYEPLCPKAFTDFQSRALRR

>contig46272 Frame-2R

MQRIYNSLNLLVESTPFLAMPGSMAECQPSVQFDNRFLIKNPTQFALDKRHRIYRHQQVI

KRL

>contig47033 Frame-2F|Blast-animal inward rectifier K channel (IRK-C) family protein [Phytophthora infestans T30-4](gb|EEY69106.1|) 0.0 NOT\_ORF

MSGVDQPLLSLASGSGAASWQMQPTQQIRFLDRCGRFKQSLGRFKFVDNKCF\*AILQRLI

F\*YSVYRKGGEWRKIYWDDPFHTLINTRTSRIVWGVSIAYFFVILLFALAYLNVSMRHPT

CHVGLSSIIDAYIFSLETIMTIGYGAPTNDIFYGGCTSMATLLTLESFAGIILDSVCIGI

FYARFARANQRANTIIFSNSAVIRKIRGQYYFMFQTCERRKHQLVEAHVRLYAVRHEAED

DAAGPSEVMFQCHQMRVQQPDDDCGAMLLMVLPQVVVHRIDQWSPLFPPECLQRDCEDSK

TCTNYPDPSQRQVDIDNGNRDGGLADNFNFCKAPTKMQIINHLRKSGLEVIVILEGIDSS

TSNTMQARNSYTDEDIVWDATFERCVMKTSKGLCIDFDRFHLLKP

>contig47697 Frame-1R|Blast-6 snRNA-associated Sm-like protein, putative [Phytophthora infestans T30-4](gb|EEY62423.1|) 8e-45

MIFYSFFKTLVGKEVAVELKNDVALMGVLDSVDQYLNIKLLNVSVVESDKFPQLMNMKNC

FIRGSSIRYVQIPAGEVDTELLQDAARREATANKQT

>contig48094 Frame-1R|Blast-isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase, putative [Phytophthora infestans T30-4](gb|EEY66594.1|) 2e-61

MKASWWTTKLPARKAAVVHAANIATFGSAGRMAFEEIIANADAQQLQFMKEKIVQVDEHD

NVIGPISKKDAHLHSGVLHRAFSVFVFNSKKELLIQKRASKKITFPSFWANSCCSHPLFT

EGELEDGVGIKRAAIRKLEHELGIPNSTFAINDLAFVSTVMY

>contig48230 Frame-1R

MGSVELDVRKEAAWAISNATTRGSSEQIQYLVQQGCIPPLVKLLDVKDSRLINVALDALN

NILQVGEAETSLTDTNNRMARYIEEADGIDLIQNLQFHQEQEIYEKAMRIICDYFDGEDE

DDFDITPDMDYNAHEFTFGVSASAGGDVPFKC

>contig48285 Frame-2R

MYCALLPAARRISFSCIKRKINRLITSESFLELDCIPHAESFCRRNFPPTSLRNNHR

>contig48432 Frame-1F

MKGDTELRQDKELHCEEIAGIEQLYEILAPECLKYQNIISLAASQLKTMISRADQEQGNH

EQQEK

>contig50006 Frame-1F

MSQWILPASARCPNFPPQASSMSLSFWIFYAFKVATAWRERVFALPH

>contig51096 Frame-0R

MVANGETSPLLPLHAAHDSSSFRVPLHSHHEPPSLRANFLSRITFSWLGPLLLQGAARPL

ESQDLWPLALEDDAAQVANSLRDAVFDARNTSRSLWIPILRVFGSNMYIAGGCKLAGDCF

GFVGPICINALIKYVDDPNAAMFVSSYYGYILSGFLFIASILQSLCLHQHHHLVIREAIR

VRSA

>contig51607 Frame-2F|Blast-tripeptidyl-peptidase, putative [Phytophthora infestans T30-4](gb|EEY67424.1|) 9e-29

MKSFPTASLLPKQETLADRFLDQYPDYDGRDAIVAIFDTGVDPGAIGLQMTPDGRPKIID

IVDATGAG

>contig52314 Frame-2F

MGKENKVLLKRVMRHKEDVRAAGIWCVPVLSMA

>contig52444 Frame-2F

MLKVAYDMHDYAGMFVLAVDIGEASVRLAMRSDPKALKLLKEAVENFDYALQIVSK

>contig52798 Frame-1R

MFAESHTDIVHHCGVASFQRHCRCATELFLGNWWERPFFYNLIPPKSE

>contig53771 Frame-1F

MLVRVNGKQHKFTISNVYFAEGLAHNLLSYCELKKKEVVLSFTKGQRHLKQACDDISVSQ

VMKSNNVLTIHAATVSQPIVMCDVVYAAVKQTIEKL

>contig54271 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64436.1|) 2e-28

MHASRLLFNPKKPLELWWRHKHGER

>contig57494 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY59728.1|) 2e-34

MDLKFHLDRQTGALSRIIDRGSRSIDFVLRALAFRVVPTVLEIGLVSTIMTTSFGLPYAG

VTLGTLTT

>contig01014 Frame-1R

MYQPGPSSDQQHPEVESPPTEHPNLLDVPQNPPMTPETDPNQTDAPVTQAPNLLDPPTSP

PDEKPTEQPNLFEVPPTSAPEHEGPDVVQQIPPNYPESEAPAHPDSSAPSSADTPLTSSP

MPSNPPVTESPLIVQPEVV

>contig05555 Frame-2F|Blast-omega-3 fatty acid desaturase, endoplasmic reticulum, putative [Phytophthora infestans T30-4](gb|EEY56525.1|) 1e-180

MVAKQPYVFPTLTEIKRSLPIECFEASVPLSLYYTVRSLVFSALLTFGLKYARALPIVQN

FWALDVAFCASYILCQGIVFWGFFTVGHDAGHGAFSRYQLLNFVVGTLMHSLILTPFESW

KLTHRHHHKNTGNIDRDEIFYPQRKATEHPLSRNLILGLGAAWFVYLVEGFPPRKVNHYN

PFEPLFSRQVSAVVVSLLAQFFVASFSIYLCFQLGFKTVALYYYAPILIFGSMLVITTFL

HHNDDETLWYADSEWTYVKGNLSSVDRSYGALIDNLSHNIGTHQIHHLFPIIPHYKLNQA

TAAFRKAFPELVRKSDEPILKAFYHVGRLYANHGVVDADAKQFTLKEAKAATEAAAKTKA

T

>contig12366 Frame-1F

MKEFHTVSFFQNDYWKLWAITVLLEFGEGERLKKLFDAMLQTYGSKRLLFELARSKNKTF

LEIPLLSMKKWMVETYAKDEQPSISKYLQRQHSSE

>contig12843 Frame-2F

MPKNHEVGSGVTTEQLFANLLNSSEHLVAKLSRDGSNNGDDAGDVTIPHRGRPP

>contig15392 Frame-0F

MCRDGTSSARQRRLRISKPAVSLPYHENDLSASVQQLYVLRAENCELHRILQMTDQHTRS

EPTSRVAVYAYFFVTGCSALRARKRLKEMEI

>contig15730 Frame-1R

MEKDCKAISLGEKAIRQVVDSCMDQMKSIFVEVARSASVLDQTFSDQFGQPVVDIPKSPF

IASIEAGSHTSGRWPNKSTDSVVKCSSHNEPCAVRTVRKDGPNKGRKFYSCQRSQTDNSC

GYFLWQDEAKEILGAADLSAPKCTGHDTRCVLRDTRKPGPNQNREFYTCSVQGSDSCGYF

EWKDEMKPLLSRPAPVSIQPSAGGGDNKKPTCGCGLPSVLLTCKKGSNKGRTFCKCPNPQ

ASQCDFFQWMT

>contig18311 Frame-1F

MKPNPFGSTSATTFLPAATSSTRPRLSSDTLSSTLNKDERFEKLDDEKPTKRTLDFGDTS

AFDVKANTVVFEKAKGFPLAGPVKPAKDIPSSRMEGQLWKLILDFDQSLQRVNQSVTNVL

STDQEFASKTLSKVDNLRAELLDLCNEIDSFDESRDQIEKDVLYVIGSDGDVHEQLEYGR

EILDSFNDEGLKRTLDEQPLDERSKEARELLKKKLSEVDKCCMELSRHIISLKLSADKTG

VVSCAHLFRILKQTFDKSKLQYNKACELADQIEKLSLHSDCTHQTNRVSGASGCKGAASS

IVSKTSMMETILATEKRNQDVRCHFLSLCNNVIKPRDVFLTPRRTSASPTASRSASSSLR

VEATSKLMPKTQLRVTSPMSTPKEFLKTISFKNEKSEPGSKLLSLAEAMTPKKEPVKLVS

TPQPSVSVGTALQRPSLGTSATEPKPSMTSKSNNLNTIRQANDSTTSVLKAFVDKDKNKT

TLSPVPTFGTRSPGNKCKADTKTAPLFSLGGKDLKSMTSILPSVAAACAPNYKMLLQEFY

KVHNPVKTESVVEKTLTTYKGREEALFTKVFTSYLPNSTPEDVKTYINGGPVPPKSDVAT

PKSHAGPAAKTSFTDFNALTKPSSTSAATTSPFQASQSSFNLSSTAIKPTGFNVLASDAT

KPASMPSFSTTSSPFGKPPVDYRQKLVAFYQQHNPDKLSSVDATLQKYKGKEDQLFQNLA

TKYKIQDINTGLSASTSASPFGTPSPFAASGTSNFMAVKPSPSASPFGTPAPTSSPFGVS

SGSGFSTFQSTSESPFNAPPTLTPMVSSFPGCVNYREKLTAFYQQYNPAKLSAVEATLEK

YKGREDQLFQMLEQKYVKKTTGNFGVSSTSAFNNATRFGTTSAFGSASATPAFGSASTLG

APSAFNAPSAGFGMASRMGGGFVPVATSHAVPSAGFSAFGAQQPTFGQATTQASGFGNAA

NTGGFGFGTGATSNGFNQSAAFSSSSFTQMR

>contig18386 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65943.1|) 1e-138

MGIKKRHGNDRRRVRGLPGQVPAARERRHVRQKEIELRAVIVHLRALKRDGNVAAVEDLD

ECFREVRRLAITPYGLTSNEFRRSLWPFLLGHHTLASSSVEDPKAFEKTYVTDHRDAEQL

EKDVERSLWHYDVVQGLKESERYAKRRALTQVILTVLSANDDLFYFQGYHDIVSVFLLTL

GYSTSTFHAVETVSQTYQREPMRSGFEIVMATTRLLFPLLDAADEQLFQHLRASSVEPYF

ALPWIITWFSHQLTRFGDVARLYDVFLVTHPLFSLYVSAGVVLEAREKILRCERDFGTMH

GMLSNLPQSMNLEKVIARGLVLFHQLPPQQLIQQYELDAAMR

>contig18841 Frame-0R

MAMNGPKMKAGTPRAGVNVGGGSSTGRAIFAVCGGFAGAYYGFYLQSKYIEERRV

>contig20969 Frame-1F

MEKYSRWADLTTGINPFVPQRRRFTSNWPITILQIASGSFLVLLRIPFLAVLVVALVVVN

LVVSILAIIPLFGRLFKRIIEWLLCSLLLLVFGVISSEESANTRRLGIVAAKARSSQGST

RVGPGDVLICNHTSFLEILYLSKRFSPVFLFATMKKGDDGKTGHVCGLLEALYRSIAMPV

NTNCYQSTRTIADVVRRASGPVVVFPEGARSNGKAVLSFMPVLQSLPVKTRVHLVAFRYE

FNRFSPSQAAGDAWPHLFWIAFHLYHSMCVTVLNARELHVDDLTPIKVSGNKTRMKQDRT

TLSLDQVEKLRLLLATMLRTKTVDLDLEDFRTFNNYWKHVNKGGRQPASCFTDRKAPHEH

ARWAKR

>contig24635 Frame-2F

MRKLEEKGLPSYSLATLLAGFFEFYATQFDFARQVVTVRSPETRILKLALWGSRKAKSWR

MSIQDPLEIDRDIGCVLQFKGQMKIIGEFRRAHEMLMLGKSFSEEICAVAKAKGNAANAK

QGARMEAATSRKPTIKDKLPASGSQCHQEKQEADKQKCSYIIFLQSADVELTEAAIKTLF

KTFQKSLQILNVTEAAPLDRGVDSKCANKQWKVELLTQKLPRAFSQRTHIDWKASDGRMG

RVWVHHQASIATPLCQSFLSSKHATSSCPSGDDNKGAGAGEKGTNRDAHRRHVLHLNISS

SATKKDHRKKSQQQNGAVHDTRIKSFIFDTGDQVSGRGNNRSGNKRAQVGTDTVVRRVEL

IETEKSTSCSTPIDKSTNPPIKMTQKKRRQQQRAYKKKTHVKEGTNNGAAL

>contig26376 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70536.1|) 2e-51

MGGRAIPHKSTENDGLVEFQSCASGIPYSQFGKTPDSRFYECELNHADTAFKTGDGIFKS

TVRPLKWFECLL

>contig27043 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70443.1|) 0.0

MSTLESLVLDDKEYVELLRKLISVSEKVQNAPSLGLIPQENLVSDFLLTELKPYLGLELS

VERVEFVPGRGNVIIKYAPLSTSSEKTLALVGAHMDVVPANPEGWERDPFTLTVEGDKLY

GRGTTDCLGHVALLTMLFRELAKQKVQTAMQIVCVLIASEENGEIEGVGVEKLMESGKLD

FIKNGPVFWVDCSDSQPCIGTAGASTWTLKATGKLFHSGLPNLGINGLELAMDAMTKIQA

FFYQEFGPLEKENEYNYSCPSTMKPTRMESSVNGLNQIPSWAKIAGDVRLSPFYDMDTMI

ATMTAFVDNLNANVTSLEGHRGPVSKYALPDENCKGKIELIFDKNYYEGIACSLDSIGYK

ALHAAITTVLGEAKPFSISG

>contig28271 Frame-0R

MLSAASRFSAAALSHCAASRCRVACANPALQHRTFFGLRELFFGSTNSSEINSKDTKTDK

PKQQLKPTSLSHSEAPNVDKETFVRSLDVTSYSVKKVAKLADGAVLASCGRTVLLTTVVS

GDYNGDLSSSGRPAIRDFLPLTVDFRVKSHAVGLIPDNQNRREYTGNDEEVLQSRVMDRA

IRPLFPRDYCENTQVLATVQSYDPNNDPLVVAVNSTSAALSISDIPWNGPIGCVRVVEID

G

>contig30652 Frame-2R

MSFQHFVGEENPQESQALGEFILYLGSHPTPANSRSL

>contig31017 Frame-0F|Blast-T-complex protein 1 subunit delta [Phytophthora infestans T30-4](gb|EEY58178.1|) 0.0

MAKPVELANREELINCVNTSLSSKVISEYTDRLSPIAVDAVLNVIDIATATNVDLNTVRV

VKQLGGTIDDSELVEGLVFSKGFDKTAAAGAPTTIENAKIALIQFCLSAPKADMESNVVI

NDYAAMDRILREERKYILNLCKKVKKSGVNVLLIQKSILRDATNDLSLHFLAKMGIRVIT

DIERNDIEHIATTLGCLPVANIEYLTPEKLGTAGLVQEETVGGHKVVKMTEIVNPGKTMS

ILVRGSNKLVLEEAERSLHDALCVVRSLVKKRFLICGGGAPEIQVAQKLGIYGRSLEGTA

SYCLQAFADAMEIVPYTLAENAGLHPIAIVTELRAKHAQGHTSMGINVRKGATSDMYELN

VLQPLLVNTSEISLATECVRMILKIDDIVMVR

>contig31206 Frame-1R

MKGCPRLYIKSQVEVTPANHLDVIYWHQDMPTQAAQNVLDQLCAYDTRNPLANCYFLEVS

ESFERL

>contig32672 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56709.1|) 1e-93

MRYKRDNKQLALAVEDAKKRLEQHEAQANMDSQDPVAKDLKMEMDKVRQLHAKLEAVRQH

RLVVEEESKALFNQVVEKKADLKFKSKKKMETALSEVDAKIKTLKEEQASVSKSLAQKPE

GDALRKINARRNDIRSELGALKERRTMLLAEKRKQEGVEL

>contig33110 Frame-2R|Blast-casein kinase II subunit beta [Phytophthora infestans T30-4](gb|EEY70111.1|) 2e-32 NOT\_ORF

MTHPQLVMPPPTQTYVPRVYGYKIHSSSEYYTGKKKISSVREREKYREVMTLIDRMKGRP

NGEQ\*AR

>contig34124 Frame-2F

MSSKRIDSRKWDQHGTSLRAHHGSKFRQHSIVDKLASEWTQALSRSHENPTLPLASFELR

AFSPLWLSSVTNN

>contig35909 Frame-1F

MSSLRVRTKNKVLMAFGALKPSTNAAYELAFSDFEATLQRLTTLNSALKSYAGSLQLYHG

AANSVLDAVHSLMSSDAGSINLQQQTAGLAERQQVAVDACVASANVEIVALQETYSRLER

EVILPLKGWLHYAHRLRNKVTTFQEQKALYDHYARKVAGLQESHEKRLAMRKVDKTKQIQ

RRIRNEHKLVASTQAYTRLSDVVIRELRAFVLTRDTALVPLLERILRGRVLYAERQMEAA

NHLRTFIQDSVEDKDGGVLSHFANMAL

>contig37235 Frame-0F|Blast-calcineurin-like phosphoesterase [Phytophthora infestans T30-4](gb|EEY65132.1|) 1e-120

MITCFESMPLAARLDTVHGSFLVVHGGLSPDIQYVEDINGQVNRFMEPAPNGALCDLLWS

DPAKGEIQELEWVPNRTRGCSFTFNESACREFLKRNNLLAIIRAHELEEDGYKEHFRQNL

DRSEVEADENLVLPAVVTVFSAPEYCNTNHNVGATLKIPWEKQNGRLLQYQQHKRSHYAE

NKYNHPSEEKAVKDFLVNNLPFLPIEFYDLVNLCRQMRLSLERTASNSSCGNELNSKQSA

ISP

>contig38058 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62332.1|) 1e-18

MGMLGGPIVLYLGLNNVPETDSDVFAREEALKKRTE

>contig38410 Frame-2R|Blast-NhaC Na:H antiporter (NhaC) family protein [Phytophthora infestans T30-4](gb|EEY66397.1|) 1e-102

MANGSVTTLDVDGNFRSQLSIFIKQLRIDSYGKHTLTTTIWEEPTHQSLTESSETNKSDT

ISLKSPAPLRYRETHTTTVVVSPGWISLLPPLVTLILSAVLGQVTVSMLAGIWCGATIVS

NGDPFSAFLRTFDYYWVNAFKVDDHAGVLLFTLVLGGTIGVVQKGGGGHGLAIVAKKYMT

SSLRMQLSTWLLCLLIFFDDYSCILIVGSSLRQVLSQTGVSREKFAAIIHAVGVCLPSM

>contig39480 Frame-1F

MGLVKHDEYAGINFIRHFSVSVLPVHIRVDGALLYQILPLLMHSKIYRSTSINVATTKKK

LTDYGDSNNVKVTRAAHSQILLKALNESLEIPVKVLDAAQKEGIFFSEQTTAMTTPTKAT

FLGNSYQRQIQNQHALVDNDIQRYSPAIVGNFEAISAKDEQMKLYFEEFQIDPIRATVSF

SFGDGVNAITESHLSPLPSYAAALNDSSSSQESSVITVGPLRLILNAIGTSLTKIANAPF

HLKPLHIHNTFVQPDALAMRLVSHYQSEALRQAYVILGSVDVLGNPMIAWKNMRNGFQDL

ISEPAHGLSQRSPKAFAYGVGRGSLSLLRGSVYTFLDFNTRILTAFSLGLSEACLKLDDY

TGYPATRHIFQGIVQGISGVVVAPIHSFEVNGARGVLPGLIAGALGVMLKPLLGLSL

>contig39574 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61284.1|) 1e-44

MLENMLLIGGTAMIPGLAQRIVAEVREALRHDSDFASSTSAVDRVELVQICFPRNMLAWV

GGSVYAATENAKKSAITALDYNNSNGITIPDWLTVADEEY

>contig39703 Frame-1R

MFRFLPSKKYIGSSLAADFVDKRQRDLGNYIMSILHSCPL

>contig40372 Frame-1R|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY68188.1|) 0.0

MTSTCPWGVHASEPTKPQLRMQDLIDEALALRLHEAEVNAIQREIDPECQSSVFSNLQRN

KDQREQERSKDLFNADSFEVLVEASGETVVAPSVLTRTFTASDGAAALARARVSGSLSME

DAAYGAGTGKGFTSFRESQRRQLKSQKKGFGSGRIEAESHATTNGVMDERTTILLQKMIN

KGDLDEVHGCVQSGKEAHVYFAMGTDSDTIKPVQLAVKIFRTTLNEFGNRHEYVTGDRRF

DLNFQKKDVRRQLKAWTDKEYRNLCRAAKCNIRAPTPVVCKEHVLVMQFVGTDGWPEPTL

KDVLLDMSPKQQARVYADILQATRTLYQRAHLVHGDLSEYNILFAQREKRIWLIDFGQAI

DRSHPETEKLLRRDLHTINQFFQRGQLLEASADEVGLLSDEEAYEYIVNDSTNELFAKYP

LLAQLLDIMTDDVILTDKEKTRFENALIKEQLHDNANTVLFKEEQTIELQKLVDTDTSDK

FSEKVVDIP

>contig40398 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57637.1|) 4e-12

MIAPSIAATPPLTEFLLSLS

>contig41124 Frame-2F

MEGCTFKAKNQALEARVSSTASDVIELKEKLQHKDEEVSNLVRSLTEIQRFNASVSTKVE

ADKKELADKVEQFQKAIRLLEQKDLSSSTIVRDLRMQLDLEIQSRKE

>contig42240 Frame-1F

MFLQNQIHDLEQDTARQEGKARTEILYLRQKWQDAMVRVDLLGQSVSEA

>contig42738 Frame-2F

MAARDVVTMNTAFVQKIYHQALLLVERLGPGGENWTMRLFSDVLFHPIPLQALGIFSDEA

VASRMSRTLVPIYQALVNATSEQEVHSKHLFTGTSCTDKFSCHLRLPLEEHAYISSNLPL

PSFWMVSPLSNIEYNSSNSGNSINENPSRAQHNEIKLIVSATCRFLFEFERVAPSMTFLA

SKADFRPEDKLFHVMHVFFAGS

>contig42819 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66488.1|) 2e-51

MVAITQHRQDGRASNELRPFAAEQGALFRADGSARMSHGSSTVLAAVYGPGQARNWRTEK

EDKATLDVSFKLEKGILTSKEKEYEQILRETFTPIVLTDTFPRAVISIVVQVIEDNGS

>contig43359 Frame-2R

MASDEAEHQRVSELFARVVGNSKPFVSGSLSIDESTESAAVQLVWGGTDLVNSVTHKYQT

HHHVSALYQPQPNVIATGFPRIDNSDCTSVSPSGKYFVTLKLEKTQNDGAPEGLFCVFEK

HRFVSSFKAPKTLHGAIYLGEREGGIVWSNDEKTIAYVAEKKIEAAVAFYTNVNTKGAEK

KGSVGAKFQYCGDWGEQYEGKKTASIFLATLATGTIHEVKNVPEHLTCADVAFVPGDDEL

VFAAIEVDKPKRLGIIYCFNRPQTLYHVFLDKKDPTKNVVQRLVLDFQDEDDTDIGSMRS

PRFAPDGKQLAFLATRDIATHGTCSFLCVTNWASKKTSTVIPIVEEPDASELDVAKRFNG

LFVTSLHRKAWSSDARFIFIETHVGSRVLWKYVEVASKELVSPAYVEGSKVAVEVVVDRS

HDYYVVLVMSPIRPASVFLVHVDPTTGTYIRPPICIADQQEATTFIKQWKVYSIPSSVSD

GPAAAKTKPEMPHVLQNLLLSSVASTTDYEATVLLPSSVPSQDGYPVILDL

>contig44206 Frame-0F

MKQWNSPEKLFQLKLQDARDTLFENPFLPFWDHFMENIHKESDTPDVENHYFAMLMIILN

NGYDEPYLERLLAQVRNSDMTINSIILSQNASIAKALQEQLWEWNFKTSEEVFQLLGLDQ

TYYDPRLSKMYPYWLSYHANLNSKLPENRQILANDVIAKCALEVPSDLL

>contig44783 Frame-1R

MLRLNIFSMAADVVFHVESNHSYLDRNNEGPSEISALKTSKKGTS

>contig45739 Frame-0R

MQDAIKKKLDQRVIEGETPTAKRVRLSPPMLPQLSKMPVSSSLPPLLPLRTVSVSTSVKD

SLGHLTASVTVKRSAQELLDLRRKYLGDIVMVIQELKVVLTYGPGSAYFDAPVQPSVVLK

LVRTVQTLEKLRALLVMDPSRLRRVSLAQLDTVEQQIKTNLLPLATLLRSFDNEAYCECA

VPVGGSNVKIVQGYNYDCDTETMLSPSRATVTPLRRHDWHFLSIALSLQL

>contig46815 Frame-0R|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 4e-55

MGMVGIGQDITVRMAQEKEKNRMIHSANAPIFGVDRDGHVNIWNLKVAEVTQFSSDEVMG

QDLVNGFVAEDYRDEVRLNLQKALDGRPTGNFDFPLITKTGRRVEILLNATP

>contig47672 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68750.1|) 0.0

MTPSAPIVWLLYVSVALVLLLLSAWLVHFAQPRRGASSSLAAGANSSTLSVAPITVSSRF

VNAISILALYISLLCLFTAPVDVYLLENALPYVPSSTRALRTMYQVYFAALGLYSFVGAP

LAYNYAKQTAIAHLTLNFAARARLYAALKRTGSYLLGLSLVLIMLMVVLLSGKPASSDID

WLRPLLKFSSDFETFLRLMGGILALTGIYLWLFVCSRGLASVPLVGLLMEDHSIDENMTT

FEILLQENSMETHATKQTRETILQRYAVEQQMSGADKERLVQLKMRENLLKERREVLNAN

LQKFALSGNLSCWKIPIGVLLMILSLLIVVSILMTSIDKVAHSKFERGFLLNRPKILNPM

DLLLVLASRVFPLDYLVFSVLFVYFFTISLVVLKRHGLQILCFRLGRLQPRLTSSTTVAM

LSPVMMQLAIGGLFALLTLAPQYATFGHQNFADNEGRIVPCTLQEASKAAAAAAKSGGPP

NHCRLTQLASFYNGLAVELPMFGTAFFAGQFLFAAAFVPWIAHAYCMAKKLDDPIDSKRQ

RLLDDY

>contig47698 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64387.1|) 1e-100

MRLTQEEMPRFLKSDVYLKMLIDTEVRPRKIPMERLLQQPRAAHYFLFFLMQSRQHFELY

FWLHVEYVLKHLLDINKYELFWRLACVLVDKAQNNSQAITLATKNDLYLTVVSRRFDDDV

QSQQPVAEALFMKAQEEICIKLLSSWYEQFITSDLYKVALQDPLIYFDLVESREFPP

>contig48075 Frame-2F

MKSVKSMWPIRIGRSRSLGNHHVNGQEGGPSKRLENIERPHFIVEKSVTPQTPTTDTELH

WTLNEHEAELDGMNPLKSPTSSASITVSNSSSMDSMAPTLPITVNTCHSASSQYVDSPRM

FSFPPP

>contig48750 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65519.1|) 5e-06

MTKTTEFMVAMTCDGCSSACTRILTKIEG

>contig50009 Frame-2F

MIVHPAVRRLLGLWLIECSDRARGSVSDFCMHWLACVQRPESDGLHVEAEWTLLSQAVNA

FVCAGYALDAMPLLLVLPIKRELMPRFFELLKKLALDSKHASMLQLHAELVIAWQESHRK

>contig50302 Frame-0R|Blast-guanylate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY62385.1|) 0.0

MSAEATFLEEAVPLITFSEKEDQLKVNHEAVDFLRRIEGPVAVIAMAGLYRTGKSSMLNW

LLDRQSGFRVGPTIERCTRGIWLWGQPQKHTMHNGDDVWVLMLDTEGIGGLEASQQYDAR

IFSLATLLCSKLIYNSQGSVDEKAISGLSFVANLAKHIKVSASAEEGGTSDGADVRQLHS

FFPSFLWVVRDFTLELVDEDGDSITSRDYLERALADQPRTPANTERNRLRAMMKDFFRDR

DCVTLVRPVHDEVKLQQVDALPIEELRPEFQQQLRDVKEIIYGNTLKPKILQGKPLNGSM

FAGLLQAYVAAINSGGVPVITSAWEGVTVSECHKAMSTAAEAFDTNLAALDLPLDDDDLY

QAIKDAEKKAVTQYRAAAMGNSASKLEADLLTRMEDHKATCLRDNAVKSKEMCDRLLQVL

YAEQIQPKLASSNDKTGSVTDIQQFTLKWQELPG

>contig51284 Frame-2R|Blast-predicted protein [Ostreococcus lucimarinus CCE9901]gb|ABO97520.1| predicted protein [Ostreococcus lucimarinus CCE9901](ref|XP\_001419227.1|) 4e-07

MCMKVECSSCHKATWKGCGQHIDTALVGVKAEDRCPNWKTGKH

>contig52274 Frame-0R|Blast-autophagy-related protein, putative [Phytophthora infestans T30-4](gb|EEY54259.1|) 2e-16

MMPSASLESFSQLNQSMYSS

>contig52797 Frame-1F|Blast-anaphase-promoting complex subunit, putative [Phytophthora infestans T30-4](gb|EEY65802.1|) 3e-19

MEAALVSQVQRYLDIFVYNNALFLAERLVAHHPSEENALLLATCYYRTGKIAQAAAILSG

AK

>contig52973 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56656.1|) 6e-42

MTIEVLRSHPENVSALGKRRRLQESTNQRVEAPEACNQSAVSADEAVSSDDTEYESSKDR

TSLRRSLQCAECREHFHFAAELVTHSQQTHHRPFRCQYKDCDKCYSKREHLTRHVNAVHI

RGVHQSLEERKPFNCELCKARFTYNHGLTRHLKRSHHNVNRPFECTA

>contig53093 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53794.1|) 3e-09 NOT\_ORF

MFAERASDFQWSEDVKVDVLAFDAGIRNMHQQRCVLAYCSFEKGRHRVTSNLSDGLLQRD

Q

>contig53167 Frame-0F

MPTLHEHVPFCPFLFAFMPKNVSARSRPSTTRLASSCPALPLHPPFFSCMNRSLTHCTST

SCRRCASSSRRYDCLLFLN

>contig53336 Frame-0F|Blast-bifunctional aspartokinase/homoserine dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY60186.1|) 9e-26

MTLEKFVVHKFGGTSVGSADCFAKVADIVLGTEGSRIAVVVSAIGGKPKVTDLLISLLEL

AKQRHTSKCNEVL

>contig54467 Frame-2R

MEERKTRRLRLLDGYVYRQFNSSRKLSSEC

>contig54636 Frame-2R|Blast-bystin [Phytophthora infestans T30-4](gb|EEY57827.1|) 1e-34

MKPLLKQHFHHQITPEIRRELFNEM

>contig54904 Frame-2R

MGRLRDDSKAITAYWWVCFSARTFACITMHVHDASLIACHNWLAGRSWNHTNFKYNLRWY

NRYEPKMTSEYRHQFIPQHRDLKFLMIHIVPFCT

>contig55428 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64471.1|) 3e-32 NOT\_ORF

MARFSEGYEVMCPNSWYKCMYSCMLKDLESHSIFDLVV\*SIRQVLETLDHVVEGTMTDFY

SYDVVCPNDVLGCKETCARVNLAAHLATCPVKGMSWEKEWEEP

>contig56032 Frame-0F|Blast-cAMP-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY54121.1|) 0.0

MFRKKTTSHSLDEKGGPINAISPAAPVETTRMRRSFALNDFNLLATLGTGTFGRVRLVQL

KDVGSFHALKILKKSEILRLQQLHHIKCEVEILSRIQHPFVVNYLGHFQDERRLYLVLEY

VQGGELFSYLRRQGRFQEHVACYYASQLVTALSYLHAQHIIYRDLKPENLLITADGYLKI

TDFGFAKIVEDKTWTLCGTPEYLAPEIIQSKGHGKSVDWWALGVLIYEMLAGYPPFYDEN

PFGIYQKILDGKVDYPKHMDSKAKDLIKKLLLQDRTKRLGCLRGGSDDVKKHKYFSKVDW

DAVLARTDAPPYLPPVRGPGDHSHFDEYPDSPMDDSVILYGEDRTAFNVFDQF

>contig57325 Frame-2R

MLRSKLMLYYEAQAEPFSGSSFLSTALSRFLSISADGMYTRLDSAQSASLQVNHTKHIRH

AELLTMVILRWPISRVMS

>contig57350 Frame-0R

MQTLSLCHSSNQPYRRNSFSFPMS

>contig58881 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61043.1|) 2e-08

MTETQFVELADKTLHDIQSWLDGIEEMLDDSDIMY

>contig03332 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61119.1|) 1e-121

MDREGLFIQRVSVFRKKPKAIVIAKDDLLAASLSSQSTTSVVVHFMLPGRGKGDQRLMRR

YGTVTLRFSNESVTHAFQQGVQLLVKWLARVPEHVTRRIKVVINPHSGRRRGRQIWDHWQ

PLLAYANIECDVEETQYSGHARDIGAALDLEAKYEAIVFVGGDGTVNEFMNGVFTREEQV

WRTLVATTPVSLICAGTDNAFGKGVGTPTHASSVYCIIKRKIRPLDVMTCQASNEDGTNR

LEFACTGVSYGIGSDIAVESEATRWLGVHRYLYLKVKRGLLAPHQHEAKISYVLSDTVPV

DPVTGDQVLRTYYEIKDDTAANQHHVERCNIYDDSDPSMKQWKGDAEAIFHPASAAKYAD

KWQSFTSKLTSAGGSNVYFETKYSHPSDGNMDLIYSRKGTIMQTAEIAVRYLSNTFLKSE

LVGYHKVKAMVIEPIVQDVLNVDGEVFAGPGPFRIEVVPQLLCVLSEK

>contig04391 Frame-0F|Blast-cyclin-dependent kinase, putative [Phytophthora infestans T30-4](gb|EEY63935.1|) 1e-142

MDRQHFFDDTEIKCVMKQLLDVMKYMHSIDIIHRDIKCSNLLMTRDHLLKVADFGLARSL

RGDQLFTNKVVTLWYRPPELLLGATSYDASIDMWSIGCVFAELYIGHPIFQGKSELEQIT

KIFDVCGTPTTESWPDYKFLTHSSTFVPEKPKPSASS

>contig04405 Frame-0F

MPSAKTARPTADAAGTRSTKRVRVSHVSRRNEKDASGSISDDDEVSATVTSACKVPKFLR

SLYAILQTEDPHIISWVQNKDLKPNSVTAFHILEMKHFEREILPKYFKHQKFASFQRQLN

NFGFRKWTKTQSSGVCTFSHNCFPPDLSTANQSRMPIREQWRQKSTQVLPAPSSLESDMS

LKRNMLGKTSAPRKRPAVVRVPAYCVPDASLLADMYHSPNANASPENNGFRPNRSHQPPA

KKLARPNLAMKPDVPEPYHGLEAFCDESFKQFLLPPLQPHHLVATTSRNAIRPPSFSRPS

ESGSSGLNGFRFSGAHPSSCHHLAFSADLTYNSTGPKPYEIKNSDVSLTAYPSVVSNVTM

GNAMADAAALQGAFLEPWIWDAQVSSSNFEVESFSLEYDNKSEFDGKDELNWQEGTSNNA

FLGAHAMSCSIPSKEVCQRQECDVASSVEDFGLDNLLFVE

>contig04786 Frame-0F|Blast-urease, putative [Phytophthora infestans T30-4](gb|EEY58029.1|) 1e-180

MDRKQAYGHRLNIAAGTAVRFEPGDQKTVSIVPIGGHRIISGGNNVATGVVDESRVDAIV

AKAVTKGFHHRVLDSKNLPRHVTQSGFHMCTMPRSVYAQTYGPTTGDIIRLGDTDLFICV

ENDLTTYGDECKFGGGKVIREGMGQASGRNASQVVDTIITNALIIDYTGIYKADIGIKNG

MIVAIGKGGNPDVMDNVTTNLIVGVNTEVIAGEGLLLTAGGVDTHVHFICPQLCTEALSS

GVTTLVGGGTGPATGTKATTCTPGPAHLKLMLLATDAMPLNIGLTSKGNTSVQNGLQETI

DAGAIGMKLHEDWGTTPAAIDTCLEVAELNDIQVTIHTDTLNESSCIEHTLEAFQGRTIH

TYHSEGAG

>contig06959 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69724.1|) 1e-130

MTDEEHPNGIIVTDEMELIREHPEYLTLSEEPMATSRKLLPPSMESSLVVGTANTSMMNT

PLVTDAGSEAESQTDGRASVQRSPVFAPTPSPRLSPMELLPPRTSQENNDMDDEKEVDLL

EDDILDGMDTKVASSAHPKAYLTDPAYLKLLPIRDRLHKSMRDAERDMSELSAKVDANSN

IIVKNRFKQMLETANHQRTEIARELDKVVAEITTFESR

>contig07710 Frame-2F

MTTLKIVWKEKEDMRRVQLAAVHQALTSLDGRSFVNTNDLRFRDLRDYAFLVFPELQTAE

LLLYYIDDDNEQVRITNDAELDEAFRLMRELAIVAGKEAKNAVCKILVVSRPLANVVATP

LPPPSETMLASQQKKKMLGLFVDLGKIVGNWEATAEYQTLKKDLLSLLHEPGCQEAMMEI

MANPRFATLFTTVTEEVQKHTTFVECFAAVAGTDDLENVAKILLAKCPYARVQVERVLQQ

VQDRHNAQLMSTSDYFENISMDETKQDLGPVLAVFEGDVTCPDGTVVLPGEAFDKVWKLR

NGGSNKWPIGAMLSCVGGDKMQAPDSVLIPSVSPGKSIDVSLRMVAPMKAGRYTGYWRLS

TPDGNRFGQRLWVDINVMEPEEPFVSVVESKEVPIEAPKIVMEEEKRADSVQTNGDDTPW

AVLHQVLADMGFMDHARNEALLTQHNGDLDAVISGLLSSC

>contig12367 Frame-0R

MYDLWRPTRSVTCNIFTKSFEKFRKKIQFFSFELRKCVVKGRSAVSDSFFSGDSMQPQEH

PKDPV

>contig12842 Frame-2F

MLRKSSVLVPKPWKRDVLEGVSTIRNEPQTLVVPSTLEIEKKPFSRGDLDEHEQVSLKTP

LLGRHHVVVLQIEKAVQKYMEMYKEHLELRSSVRSRELYDLLFAVEAIWMFGLKSPVLKR

LHERDSTNLNGDVVHTPPMSPEGENVGFVERMSCGSFETSDVDTNVDESGVLYWDFLAID

RPGADELNRHWRFVIEECPECCASDSFVSPRGIQWILGALAKGMLGTFMAEICTHSDMLE

LFYDPLAVVYDCHQMDTIVRSLLQVDAYKICLDEFLVRNIKEYEAPLVWPPRSWHTSVVR

VLERVYEIERYVAMNGWVKGAEKPWPDLPSSEWIWEDEWTLENVHEEMGEGSDSEPLRSA

WTYAKTLDDDFHCIKKKGDLVRRREWKRQRFQLPPVLTVASPPLSPQAFQLPSPVAFSNG

YTRAKTVKQRFMKHDATKKETGMIAKGKMPQKKKRSTSFEKKGQLDSPSMLSECEDLPPV

STKLSAYVRARATIPSLRRAVSNRSVISSMSEVQSPSTRLSGTDDLMTGYEHDDDEEEIR

CFGCLKSFAVLQVRGKTCQLCHQRVCTSCLQGFAFLVYPPPLDTSKKANVCDNCYNHLVQ

KYRLRIEAHVGKVGNENSDLRGSSISNPSNGNSFLHQNFYNLPSPTSSNNKGDNSAPLFR

QSISPLSPSGESTLYEITVKVKEDNAYAWSVLKTFHDFVLLEENLIGKAKKQEEKWGQEC

QHCHWKGVDYTEMNAIYPMLRTVAIATLTYEKRLYMLEQFLQQLLACDTLCQSRSVQNFL

LLANAYGTPKTATNLSTSGWDNSNDHLIFPVAGTQGNATGSATLGTNGNVSVVDKSKKGR

WSAMDANSKETKMQVLQKIEVSLFAVLSELFEFDGIGVVRRQIFAMTRSFIKAFLGASHF

RMLERQFLSFTDPKKLSGWIRHLRECVFPSDVSNEPSPSPPDLHVLRKDCLEAILASFPS

KALSLFGDTACENAALKLHEFLQHEVFVKNLLFSITDEVLLHLFPDSTTYKGKKVPTSTT

KSVVAAT

>contig14413 Frame-2R

MELHVRACSARNLLIKQTFGKQDPFCTIKLRGKSFKTRVHDNGHKTPVWNEVFVLSVVDP

QLDELFIEVKDKNFTSSTLIGDCRLPVSMFTNSNGSVVDQWYPLKNGSKSAGEINLRVQL

RGPGMQAARAAIASTTNALQQSAYPYPQQTSYTDVQQYPAASAYPGPNPYPASGAYPAPN

AYPTPSAYPASNAYPAASMPSKSGAVASNASAPAHPQQSYYQQPPQQYSQPMPPPYYAQP

PPPQYAQQPDYYPPPPQQPAYGYPPPVPVAYATGPPVMNAYSAASYGQSHHGSSQGHGGG

GLSSKFGGGGLSSKFGGGGHSGKFGGGSSRSGGMSGGQMAMGIGAGVLGGMLLGEALDDV

FD

>contig18387 Frame-0F

MTTFYPREAAENATNNIHNMCTRPRHGVPRYTTCGSPYGELIVVDILEARDLAIESTSAP

LFGVTMQLGSMSRKSNSTARSSSIVNERFVFWVPSTPLIDRRTLDIFVHSGDERDLGEVH

FSLAMPVNETFGDWFPLVCRADGLKHGTLKVAMRRLVLTSLPMVKAAKTLDEQTSCLSLR

DCKAYGALLPELQSTFPRSELETSSFTKEQNISSKIVRLIGFQDVQRTVF

>contig18840 Frame-2R

MPVPFKLITAVAIAFLLIGSSASPPMAKTSLAVTTNQGRHYESKEVDGRPLRGAERALSL

NQEERGRFSLLNKFRKLFKRKPKKKLTRTE

>contig19465 Frame-1R

MATLLDSTMEEVSPETHSSKNLRILHSADPETDAPEDEDDDEDFNFNAPSYYDLKNPALE

RRYVNNADGYFSSPTRSAATSKGSPLTTEISCTSSISEPALGVTLDASNEIAGSTQLVNG

KQDENMEEINMLDTTMPGIEDVETVLNLLDDREESFKEVFRHYASSSQSSATSSYLLHDL

DTSTHSSIHAGHFSPLNSHASSSSTSMRANSDSIAKSRFRAANTAVSSNLMQPTQSYSRR

IQAEQMLRQELYVEDAPVENKPSRVTRPRSPKLRTKTRTTHSSDASRMSSTSRELLKIQE

ERLLLQLEKLKIREFHEKIRVQRPPTNVHQRSTKQLTIPQTPHFQVDNRIRRVQSGPDTS

ESGHVQNQPPIAAEKLLTRDYSKPFPPYRESRLALTTPRSPKLHTATRAAHRPPPAPVPD

KKVKAAVSRVNGSLTQPMTPQLETRRRAAQHRRPIKVIDQDAEELAKKFHAKPLNKSILE

PKLYTRYAPAKSDGKSCLAAPRAAPSAFSASCLSSADRSASVLSEAERHRKEREQRLKTR

QAGQATQQLKSAPRPIRRPLIAETPPLKSIQLHRKYQEKFSRKIEIEEKEKEKQRQFKAN

PIRVASTPAKFECSSKPLTEVKPFELPGEQYLNQAHARLEQKRRDEEERLKALGTFRAKP

MPVFESDLVQIVASTKPLTQTESPMLATKRRAAERAAFEAAEKERRAREEAFRQQREEQE

RQLKDEEIKRLRREEMVFHARPVPDGNTF

>contig23330 Frame-1R

MNKIIQHKNYIFVLTFSLFTMESILTAYRSSSDDCASASSESEEECPTSTLLAKRKRSDE

PHFVRAFPHVDGNWPSHVRLEFPVNPEFRELAKCTIDRAQKLVGDAITVVPFKELGLHKS

ISAGGNKYLHVSLSRPFVLCYNQINNFVDSLRAALKWRQ

>contig24641 Frame-0R|Blast-carbon catabolite repressor protein, putative [Phytophthora infestans T30-4](gb|EEY61326.1|) 8e-23

MPFAGLRVHPPQVLEGFSKTALPNCQFLSDHVPLCLDFSFKPSAL

>contig26126-0 Frame-0F0

MEAQWPPCLLPTPFCLYCFSDIHTILNSISIRTSHCRAPKARHLSIIGKVALFLWNKAIL

GCCFSRNAKTQPPSEHVRPIRAITINCKLIFNPRDVPSERLSN

>contig26126-1 Frame-2R1

MARIGRTCSEGGCVLAFLEKQHPKIALFHRNKATFPIMDKWRALGARQCEVLIEIEFSIV

WMSEKQYKQNGVGKRHGGHCASISPDATISLNIDAVLYFLFP

>contig27965 Frame-1F

MARNNLITINQSLSRRNVLISDPASRKAVSAYDSDRLESDDQTHMALSLLAKMERSCQKE

RELSQQEENFASSVATADSSAVLFQTAVDAVEAALVQCATHDRREALTALLLRAKLVQAQ

KVPANTSFCRERAYVLTALQVQLQELGRNYSNISHVHELVYRVCQSVSRFQDEPLEDNNS

SHSQVRDTEYAHHDWAFDQKYVDDTEMCGRFREIALHVYENDACVGSDLIGCKTTEELMQ

PFSNQREDDNSNCKPAETKLIEADHKSKQGSKRALAVVTSKFCDLLPIVTGNVIIKRVEV

PQLPRRSHGCSSREPHSESSTRLTSLFKNGGQTSRRRFEFPEKELLQFLEDEAMASGSLK

SPGMRRRNSHTSKITCAVPLRRKSFIMKRTALKSSSFIEVHPLTIKTNVASNTNSSNFQS

PQKSTKQHFAIARRKSMSAFEAVVPRSFSPSTRRKNNGASALNQPSLALYSRRKSVPRLS

INTLNASFTSSPPSPASMTHTQMVLRVRAREGVPELVIAKKPVRCIVWHWNHRCIRVPFM

RAANVIDLGPIQHGL

>contig33164 Frame-0F|Blast-40S ribosomal protein S14 [Phytophthora infestans T30-4](gb|EEY55094.1|) 5e-77

MSKKTATKEVEEVVRVGPTLKEGEQVFGVAHIFASFNDTFVHVTDLSGRETIVRVTGGMK

VKADRDEASPYAAMLAAQDVAAKCKEVGVTALHIKIRATGGNRTKTPGPGAQSALRALAR

NGLKIGRIEDVTPIPTDSTRRKGGRRGRRL

>contig36220 Frame-2R|Blast-malate dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY60864.1|) 1e-165 NOT\_ORF

MNFRLPSSVAATLRRAYSTSSGQQKVAVLGAAGGIGQPMSLLLKDCDHIKHLSLFDVVHT

PGVAADIGHINTHAKVTGHVGMDQVAEALEGANVVVIPAGVPRKPGMTRDDLFNTNAGIV

QSLAAAAAKHCPDAMMLIIANPVNSTVPIVAETFKKAGVYNPKRLFGVTTLDIVRAATFV

ADNQKWDPRTTNVKVIGGHAGTTILPLLSQLQGAKFSDEDIAILTRRIQFGGDEVVQAKN

GTGSATLSMAYAGARFTTRLLDAMNGAKDIVECSYTQNDVTPLSFFSTPVTLGPNGVEAV

HHFGELSTVEKANF\*EMLVTLEAQIQKGVEFAKH

>contig36358 Frame-0R|Blast-D-Tyr-tRNA(Tyr) deacylase [Phytophthora infestans T30-4](gb|EEY61053.1|) 2e-09

MEVSIVNDGPVTMQLNSKDRKLA

>contig37241 Frame-0F

MICDGFFYDNLQLHTTKVRPCLKRQELCDPRRYAQEQDILNRKECCLNQYNWPNLNNVLR

AQAVPSLESLCLLKKLTNDG

>contig37933 Frame-1F

MPMRRYVKCLSAHRLAPPGTEPNKLTSRPFTRSFSSCDTSMRSIRLFRPTRRSSSRCCIF

P

>contig38198 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63726.1|) 2e-70

MTGYGGTDVDNQARESWKYSCSRGISGTPMYMLNGVPFEAGANWTVEQWFEVIDPLVKAN

NVAIKVKSDLQEWKNVHLSGTPRGLPDRDVTHLLRAGEWATSSSVCKNNIGREKACEFAP

GRVMCCHINEACILRDGCVMLE

>contig39096 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57771.1|) 3e-23

MANIRLEQTLSAITIRGAKRIDAISINIKTPVEKTWSHGGHGGTENTLALEKDEYIISMV

IHWGRKHSRKSIFYLKFTTSSGNTVAAG

>contig39481 Frame-1F

MTEFGEVHPVIQSAWFVFPLDRIQHSFDFTFVSSSGDFFIKMFVLHNFRS

>contig39575 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61284.1|) 6e-06

MSSDKSVLVLELGARYIRCGISGERSPQCVEYCQ

>contig39702-0 Frame-1F0

MGLTPQMLPDVKRVGEHTDPVSLQFSRARSRMWRFMSRNESIISSRTS

>contig40399 Frame-2R

MPKAVITSKAAITPYVVPVAPSMAESSRQQLVKSTKSSKSVRFASTKECRTQLDSHYPTP

HVARNVPQNGSTSRRFTIDEVELYFSEDRPNFPMSSQDYAVHKTAKRVTFVLC

>contig43220 Frame-0F|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY59568.1|) 2e-76

MSVWLVSVPNEGNTTSETTFLSLKAETASNRHDYADCLRVELPSDLLVGTLDSLMALSDE

LNRVDMLIESVVRKIERQFHDLSKGDQVLTIDGVPVERYLSFFSWDEAKHPHRRPLPEIV

SIIQSSVGKIEEELKQLGSRYSEKKQQLVGLQRKKG

>contig44016 Frame-2F

MKVLGCLESIIQACGAHIVSFCRQIIAILPALWENESDASNLVRGKVLQLMAKLLSSVNE

VPSGEEAGGVEALPRMCVQVIRYATDVLNPDAVFLIEGGLQLWKVTLEVSTMYTEELHVL

FGSALRLMKRDCEHIVLVLNLLERYLLLGNIQFWQAYHAPISQLFLIVFANVKAEASLLI

ASVAERIIKTIPTNQLATFSPVVKTMAESCINYKRGRANQERDSVIGGYLSVVARLMVTS

LDFSLNTCCNDLAVLLELANVMLRLFYTVGSSSLTPLQRKVWALALLSTLTLKEHSFLDK

TGQILDLCAEVIDEEQEITAAVDSDKSGGQVGVFCYKQQPIEQDACILALDLKSFVCKQL

NALASN

>contig44207 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68462.1|) 1e-121

MGRRSGNQLADVLLKRLCTKEMVAWKLPCFTSSEVSHLCQRLRRLMEKDDVMRCKCTGKC

RNARCACVKAGLVCGVQCKCVLCANPFIPMAREGIDIQLVVSDKCMMQHLSKIKDMQELL

DSTISYECCEEGGGVVQVKHTVENGFACPYCDTQFTYSWCNNRLCPDSKKPRRHCAKCRR

CGDHRNLHCDLCNHCYFAGVANSFRCSCQLAGSGNGAKTRAVVPNPVIRETGLIKRDQKD

GQKCELKHYDAASNGCARMD

>contig44782 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54283.1|) 6e-33

MSDTKLQNAVDKMVDRLDRTFLRGMQREGYLCAAKVFENKSWSSDQLSAAVERCQMPTQQ

LNQLMQQEMQNFQNRIQR

>contig46111 Frame-1F

MRIVLSVPLRHSWKPPMNCFFDESIGSQIELFARELRPYWTSVGYEVLKFQAVDLFQSAT

SVVRAT

>contig46209 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61095.1|) 2e-57

MAFMTAGRRMSCTADLLEDLDMPSNVAKTHHEVGVNLMCQGEFCEAIVALQRSVKLDETI

SVTWLDLAKALDGEGNDRESAEEAVRRALELEPSSIGALSLLGKLLHLRGDHDDAILVFR

QVLELQCPGSGHR

>contig46685 Frame-0F

MLRRLGCGAQFKQFVPPLKSSSSVDENGNMDDVVTRKHQSTRGGTSLSVKRLPFLSFLVM

EPERRAQQVRLQFKSPCGEGGRTQESNRLLITRTLGMRRRWGSVVSKPMMRHDLPPIEVC

DEEIETSFDKNSAAAEIEPLVVTSKVDAPPPLVLWRSKTDPEAIVVVPEIVGKFLRPHQR

EGVQFMYDCVNRVKDFEGEGCILADDMGLGKTLQSIALMYTMLVTGMDMKPTVNRAIVVC

PTSLVKNWDDEIIKWLHGRVKTVALYEAKRETVIKGINQFIEGSKRPRPGFSAQVLIISY

ETFRMHAPKFAATTECCDLLICDEAHRLKNASSQINKALSSLACRKRVLLSGTPMQNDLE

EFFAMVEFTNPNILGTPSEFRKNYLGPILTGREPDSTDRERQVAQSCSAMLCEIVNQFIL

RRGNTLNAKHLPPKLMQVVCCPLSPLQKQLYNHFLSSSAFRDMMKNSCTNVLSSITALKK

LCNHPL

>contig47673 Frame-2F

MTVENQAISEECTRLQHSEHSRFQSTKNMKQTIRGIERERDTLQIELDDLRHTYRSLIQE

HEGMQKARREVSVLQEELATVNESLRKQVATLENQLEVLREKNSKLACESAAYRDQVSFL

TEKLQTNKEKEDDLRDRLQQIENELDAQKQVATEISAQRYGAQAENAAVSQRIIHLEAKL

SNSKYEMKTLQDKLHAEQAQRRSLEEVASNLRQKIANNETIISRFEKQRNAMAQEIQALH

QRRLSASNSVMEMSDFNHSPSSINPSSHTSTQDGNGGKSVQNCSSSRSPSVSPASNVTGS

SPDSAQKAS

>contig48724 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY69921.1|) 1e-80

MKDLLMVDAVDEAHVVDELVMRYRHGHVYMFLGPVLIAMNPYKMLCQPNGDSIYAPNMID

EFQGKELHVCDPHPFALAENAYSNLMRFGLDQSVLITGESGSGKTETSKHVMRYLTTVST

RFRAKSAVIANRRMSVAQRKVVDDMTSHVTDVLWGSNPVLEAFGN

>contig49389 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY69399.1|) 2e-64

MSTVGIQPDLQRTIFRLVACVLHLGNIEFIENAKNESEIAHPEDVKHLAELMMVTSDELD

FALTKRTMSAGARGSVAEISLTAVESAKSRNGLAKDMFSKIFDWLVFQINKSTANVG

>contig50008 Frame-1F

MRTVATLSAALGVAYQSSFGIRASICDKCGERPVRVKGIYGSFCVPRQQCDGFLSGTNDK

PFFCPRAGQRNLDGGVTLAQDSCCAVVDSIRGTLGCVQKEENSQTACLMPPKWPREQHYV

RVGRKRGRSRTLKSAVTSEAIFTIPVSLRGTLTPTMNGAAAKSAILTKAAQTMAPVIPAV

SNASLAPIQVSLAASEGSELTPSDFVGTNDVLQDEAQATQQESSDTAQVPTYMQEYLDIS

TAAVGPVISIPGASTAGPRTGDCADMTESPDVTAPAPVIAYERPALVLASVAAEVSREPP

SALLLTSPPTTNILVLINSTMEPIALADNTSPAKISAIDVAAPIAVTEVPCDIQESVKIA

TQSPQVTNATPALDYFAAAPATADALKATMPPLLSENSAIDVVNNDAASLTANLT

>contig51098 Frame-2F

MRRNACVLCLRVILNIVMLAIDLRSELLDNQITITDACAYMSCCMRNRRYVARRSASSEW

LNSYAAI

>contig51609 Frame-1F

MVSMLNMNMRDMYGGDGVSSLMDPHHHSVHTSSPVSPPRQRTVKKAHTTYHHYFAFKESA

MDPALGNPRKLLARLNALGIPPLPPDLGALRLSDGSPYSIYNYASSPYCLLGGSSIGSST

NGISGHERGGSGLPSVTSASVPIGSGAYSPGGGNTFTVAVAAAAAINGGVTP

>contig52819 Frame-1R|Blast-Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4](gb|EEY60470.1|) 6e-91

MLLHELPHEIGDFAILLQSGFTRREAMASQLLTAIGAMIGTIIGLLIEGAGDSSSVWISP

FTAGGFIYIACTSVMPQLLEDCSLAQSLKEAGALCVGIGLMALIALNEL

>contig53166 Frame-2F|Blast-importin alpha-2 subunit [Phytophthora infestans T30-4](gb|EEY61401.1|) 2e-69

MQFEAAWALTNIASGTTEHTKVVIRHGAVELLCALLLSSNEDVCEQAIWALGNIAGDSPQ

CRDFVLAAGAMMPLLAMLRRSSGKLPILRNATWTLSNFCRGKPRPEFELVSPALEVLPHL

IHSRD

>contig53337 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58332.1|) 7e-18

MQKLLLPIICSRLTTIMFSQVVKQTATKMSVAGRRGISHSAKRMSGEGEHHQHLVFEGDF

NKRVVLGLTLLV

>contig54592 Frame-2F|Blast-tRNA pseudouridine synthase D (TruD), putative [Phytophthora infestans T30-4](gb|EEY58382.1|) 7e-10

MELFVNKVAGQLLGLFNANKRAMLMRQKMENVEQLQVAIARVCGTALAKKLREFVQDVIF

TQEKKEKQP

>contig54905 Frame-2R

MFIGFDVPPVIDPVVVNSDSNTDVLMTLNPATAAQQIDKLQAKSCATCTQLHSRNLLPAS

ASSKLHRATDLPILKTGSSCYALAFIHD

>contig55094 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66208.1|) 8e-55

MVPPSLNQECHICLEDLQQELAAVPCGHVFHHICIIQALQVNKQCPICRRCTSDADIIAL

YFDVPSSCTAPNGDLQKNRISPSSGDNVVLGSRVKTLMEHIERQNKHQERIAHELRHLRS

QSEQLLHDKETLIQRIRVLEATRIELLTKVARYQIQVSHQAEAARRVILNQ

>contig56033 Frame-2F|Blast-mitochondrial 2-oxoglutarate/malate carrier protein, putative [Phytophthora infestans T30-4](gb|EEY67662.1|) 4e-35

MHDGVQTHILASMVAGLVATTACAPADVVRTRLMHMRDHEYTSATDCFVKIIKYEGLRGL

YKGWVPAYMRLGPQTLLT

>contig57049 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65074.1|) 1e-51

MTDWMPLFEKLQHFSNESEEIAVSIVLDDVSTIKWWFGEAALLDFVRCCKTLTHEKNGWC

KCRV

>contig57401 Frame-1F|Blast-aminoacylase, metalloprotease family M20A, putative [Phytophthora infestans T30-4](gb|EEY64299.1|) 5e-13

MTWKDPVERFLELLRLRTVSAEGPSGSYNECARWLRKYIEE

>contig58606 Frame-2R

MPTSGGLASFSRRLRRNLGVQ

>contig58880 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63999.1|) 1e-50

MFPSNDGYHSSTHAATRDSSDNLLGHTAIGDFHLHSVCSDGKLKPSEVVAKAATNGVSYM

SLTDHDTMSGVNEAIIAAQKLGVFVIPGVEISAEVKGGEN

>contig59403 Frame-2F

MIYFFKMVLFLYLLRDPVFASVTKPAVEK

>contig05496 Frame-2F|Blast-phosphoribosylformylglycinamidine synthase [Phytophthora infestans T30-4](gb|EEY59422.1|) 0.0

MFSAGLGQLDSRHCSKGDPEIQMYVVKVGGPCYRIGMGGGAASSRIQAKQTAELDFNAVQ

RGDAEMECKLNKVIRACCDLGALNPIVSIHDQGAGGNGNVLKEIVAMNRSSNETGDLNRG

GARYDVRKILVGDETLSVLEIWGAEYQENDAILLRPEHIQLFDQICTREKCPYAVLGQVT

GDGHVVLQDSMDQSTPVDLDLDLVLGKMPQKIFFDTTKTETLLELSFPIDITLRDALDRV

LRLVSVGSKRFLTTKVDRSVSGLIAQQ

>contig11145 Frame-0R

MHTRPRSQFLPVKLRPTEPSCKPLFADLTKTQIIVLRLKRSRKKDKPNALSKQVATNETT

DKYQITAEVAGLVTEKYVCEGMADFQYFTARSFYPSNMDTNALNTVLDPMEVANPVKTNP

IAIHSHPLSTPSPQQQQLQRCLRPYLVVNNETQLEMIPEVFSKVDLPLKYEFRQKSGYRP

TT

>contig12364 Frame-1R

MPARRPSLYFILTSCRSRATEAFSAQSTQSAEPIVLPSPSTSWNHASRDIFAANSRMPVK

KTFCEITLQEVKCYRSFLIHASSIRYFLY

>contig12768 Frame-1R

MDGLPAFFANGSVDDTKYESLLADLRAHDLLGPVESGAQASEGGTSSLFFNDAFSAVFMG

TFESESVAKSSRAPPGLAPPSEDLKWARGQQKFSRLEEQFHGSKADTINLNERALPPGLS

LEDTELDESQIPGLKGLGLDDDDTGAVQLLPPQAPPPLPPRELMPPIPPTPPANAYTAPP

LPPQTMAFRPPLMYVPPHPPGVYPSSLPQYRHGSPLPQAYGYTNGVPVPMQMPVLAFQMM

TPRDIQFVIQQQMKWLRSSDPFSDDYYFHHFMQKRTRTNIVGRSSIPLPSWKLQHVKSID

PRDVQREVKSRNWEAEYHVLGRNAKSSLYRPKQLLNLATSRASPIKSEESDRCTHVNPSP

LNDASSMTAESSSEATSSSLSVRNSTRSPGAQTVALEAQGAKVLRMTETANRRSVFDNAT

WTLRMQIDRGMHCLLSLQEARHLLDARGIHVQQFHCMKKEDMDPPLAALRLRTTSLLMEL

AGLVGVKGHTIEDKGKPRCDVVQVEKMLSVKKGKVLVSRALPLLYPSARFVLLPYLVDLL

LAARAVAGRLLDKKDPEDDRLCQTLVLLLLYVPPAPSATLLTEWLQRAVSGHTVESLSLV

LHNRAKAEALQALLKCGGAAIQQLAETDGSDVKSVKERWEYHQNVFVQLATAMTRSE

>contig13275 Frame-0R

MGGNGGYGGISSYGGGLGGYGGGHGGGYGGGYGGGYGGYGNMSRLGMGGMMGGASGDLNS

GSLGWLSNINQMVSSIGQITELLGMNAEALNFCITSFIHFIERIRAMCAGIATMLAPRPV

FPPGHPRHGEPPISEEEEKIRRRRVRIFQFMVSMFLLTALYKGVRWITRLSIRTRPKMLV

APSTDVMTCDLESIFQRTVGVKHFNNQINK

>contig13503 Frame-2R

MHSLDQLERCAELKKLAWLLKTSQPTLTNSQESGSCAECFRSFGRWPHRAERQCSVCDDH

VCTSCIKYRHMRFALPDRLKIIRSKLAFCGRCVRRANETSPLTVATFDAMEHDDEFDLNT

IESSSPLLSHGSKWGSQYLDDLAMTILGDL

>contig15390 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66972.1|) 0.0

MKRQETESPTILHRKKRRGRRKSKAERLTRSISEIYTNDGLTKLLEGSSSCEWDAAQSLA

QHIGTPDARATVVRVILMERAAPRAAAHYAKRLNFRGDELLTAILPTLMMSPPPPLLLAQ

FLVELDEDLLATDERLKRFLWPWLLLSLENKKEGAAVKAAVNLLLHPTLLEGSKTEEKRE

RGRRLERALVVNCLKTGQLLHLVPIHSRAFVGQLSSVFSPHPENEHVAMEFAENVDDELQ

RRLEVACRVQDCLRLLWPDARVLVFGSSVTGLLSRSENVEVNSSDVDLCALLPSALLFRQ

NTASLVTDVKEHLSLYLVPDENEVITAVTGARIPIVHFFDPRTSLPCDLCVNNVPAIWNT

RLLRWFLHGGVKATPFERKQLAHVRQLCKWLRYWRQVKKRVVAGALSSYGLVLLAIYFLQ

RVNILPVIDCSAHATEDEATLRTLSDKIIDEKLDAVDKVFVNAKDHESTCHHWQDLRQRF

FYFYTCEFDYEHTVVSIRTKEIMLKTSKGWSRQKNNRLCVEDPIEIDRDLGGLCSKRSLG

RLRCAFAHAWIVLSDFMKTKSVVGVDPDLEADLVASWMYEDENLS

>contig17114 Frame-0F

MTCVALDEDKRPSPGLPKLLDPLNFHYVKNHQAIAAQRKELAAQWRAVQEQVNQMPHVSI

DMIQSLDYGRSLEVLISERIIEVQNLFLPKHLNQNNTIFGGKVLT

>contig17428 Frame-0R

MDVQSFYASLVAELGAESTSTFVHTLARLVPDDDRRKELVEYNADQRRASGINGQEMVVA

NQNSSLSNAFRRNSSMTSASDGTPSKGILNNRYADHPNCDVCNVRFDVTKRRHQCRKCGH

YICSSCCPVRLLVPPEIVIEGAKKYDPSLPQRVCLQCAPQLHLLQDELVAKYSQSQIDNL

HDARGRFHIPFSSSLNKECCNAADIIGNFFRSDWGSSADRAVPVTFLQKAHGLAIMTVLK

AGFLVSGKIGTGLVVAKLSDGSWSAPSAIGTFGLSGGFELGGEIVEVMIILGSEGAVKVF

HKPQVNLGAGLDLTVGPYGRVADAAAAASTSGLNANYSYSHSKGLFAGISLQGAILAARS

DLNRKFYGRDLQPSELLSGFVAQPTAGRPLYEAIDNAMRGVENHKEVKLRRSSLMGPCRL

CNCPMFQAHTAQVWNKKCKTCNHAH

>contig18313 Frame-0R

MHTGHFQLPSWAVNFEKTAAISSFDFILIDLHDKSKFSSSSDSGSSFRNIQCKYHATKSS

>contig19268 Frame-1F|Blast-chorismate mutase, putative [Phytophthora infestans T30-4](gb|EEY61001.1|) 0.0

MKESTSAAFGGLRGKYTTFDGSLLDFMLLETEKLHALARRYTSPDENAFFPHLLPEPILP

IVEYPRVLRPNRINVNSQIMIVYQEKILPGLTAPTSNDSVFGSTATADIAVLQALSKRIH

FGKFIAEAKFQAEMERYTKLILANNVLGIMEALTNIAVENKVLERVKLKASTYGQDPDAP

ATSNGKYRKVDPQLISDLYRDFVMPLTKEVQVQYLLQRVTHPSIAVAGVKGSSSWLAALA

HFGGKSLDENQLFSTESISTVFYDVNANRAAYGVLPIENSHSGMIKETQAQLMRSSLKVS

AEILLIRSIIFAAKDMQLGMQQNVTKIFCPTDSDARLLAQAEQYWPHAEIVSVAHVSDAA

SRAFSEASTVAVTTIGAAESHGLKRIDMSHALASEVACVESESFIRFVVVSKGYPAATGK

DKSCLSMEIKHEVGSLLKALDVWKKHGINLSSLESIYSQEQSGYDFFVQIDGHIDDENVR

LAVKELQSVCVVKHLGSYPVAKRLIRS

>contig19466 Frame-2F

MLSRLDFSYYSTLHLNQRAGVPSATGGQAGMYLENPQYGGPAVHPGAQQSQPTKSMVMGT

GGIPANSAAPANTTPQAVIKPGGGTVGVSGDMLAEYWRQHAALKAKYHDDVEKVHSAFKK

YVDHMKGHDETEQKKKLRYLLSYVQLCASILNEDKTTNPPRKIEELDKVYKYIVKIVNPY

LKKLRTETDKRSFTLNTSSQNLAGVNLSAQNPAASSTGIPASIESNAASGHTSNGANGSM

LVQQNQQNMSLQQKQQQYLLQQRQQQMQQQQQRMQAQARQHQMMQHQQILQQQQKAVTPP

NRAHVSVPQADPRKPPNHLQNSQPTSHSQQKQQHLAQAQHAQRAQQAHTNQQQSAHSHSQ

QPASQQSQQSRQLSQQSQHSQPQSQAQQQDQQLQGQPHSQQPQQQQNSAPPPSRADPSSL

SLDESLYGGMDSSGLLQMPSNLATSSSLSGFMNFPNDLSPTHFSSMDLLDMDGFMGHDNS

NSSSGPGQNNNNSTGGNNNAHSGDGSDSDLMFMEAL

>contig23333 Frame-2R

MRVHVVLLYLTLYGVITTLALHASDELSPNSLSNRFLRVDSTVHEIASFKGPSDRSTEAR

STTPFRTFYQNTLYGFAKSLHLKPKWTLSLSYLLREHDETNMVRRFTEYLTHHHQFSFKV

KEKLIKKLVNKLRHHHELTNLKAILLKLQDEPKSSAAAALLLQRIHHIEK

>contig24642 Frame-1F|Blast-carbon catabolite repressor protein, putative [Phytophthora infestans T30-4](gb|EEY61326.1|) 1e-164

MPPKRRMLATATEARLTPRLRQLGVFRVLTYNVLAEIYATRQMYPYCPVWALNWSFRREL

LKRELQSYNADILCLQEVQGDHFKTFFAPLMDEWGYEGWYLKKARESMGLEGKVDGCALF

FKRSRFILKERYPVDFNELANNFLSQVQTEYDLKYQGPSMAAREKYLATLNKMRQRLLRD

NVAQIAVLEVVPTSNEVVLRKSQSGPLMCIANVHIFSNPKFPDVKMWQTSMLEKQLERVT

LRRNLPTILCGDFNSEPTSAVYEFMTQNHVSLHHPDIQYAPSQLANIYASLDLEQHIGFA

SAYASIFGAEPEYTNYTG

>contig26374 Frame-1R|Blast-transcriptional adapter 2-alpha, putative [Phytophthora infestans T30-4](gb|EEY69130.1|) 0.0

MKTKLCLNCQKDLTRNIRITCAECHSQPPFDLCVECFAVGIELGEHKRNHKYMVSDCLAF

PIVFEPDTPDNATILPAPVGTNAAALPGAGNETVNIAWMADEELLLLEGIEMFGLGNWKD

IAEHVVTKSSKKCEQHYLTAYLGWKNLLPRFIDDDLTNSEKEKNKDSTQVGIEDKSETFD

HAAKGSSGERHGPSQLAGYMPLRGDFDVEYDNEAEVILADMEFSDTDHPSERELKLKVIQ

IYNQKLAKRIERKKLSLSEVYWTINCISILRGSDRKRNANCWLRCGHLHDFRRLKSTIIL

>contig27041 Frame-1R|Blast-predicted protein [Micromonas sp. RCC299]gb|ACO63014.1| predicted protein [Micromonas sp. RCC299](ref|XP\_002501756.1|) 1e-10

MQRSGFDLTLVGFGKSSVYHGDNEYCLLSDMKKAMQILALTIAHCDGSLK

>contig27711 Frame-0R|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY69166.1|) 2e-82

MLSTTESTSNVSTDSVLALELDPYTFENRQALITSRRVNRYLCSRPDVVKLHSQKMPLIP

CNKQKLRRQIIFQTSPTLTLKFLGVLGSGTFACVFLANIVDEAKNTIHTKAVKIEKERQN

LAWEFYITSKIKEKVRIKNGPTEDKIPLPDFTGLHLFPNGALLIMNKGQNGTLFDVLNCY

KQCGIQFPEVLAVFYGIKMLRCIELLHAAKVLHGDIKPDNWLMIRGSLASEFSMDIHDTR

MDKDFQAGDLYLIDYGRSIDLSLYPKGTVFKGNCHAKGFQCVEMLTQRPWTHQIDTFAFC

GTMHCLLFGEYMKIKLRQTSNGSTYWGIDRQFKRYWKVDLWKTLFHELLNISSCTLQPSL

SNLRRRLKNYFVSDRGRHQELHDQLCRQERILLKSTIF

>contig27838 Frame-0R

MKFNIELPINPEKESDRGHLHFQMWDRDAIYDDCLADAVVDLTSFLKLASKTRQVVNVFA

KPKPIRIRGLNDIRRGESSHRPEYSATEDARYAARARSPSPHPGEVVLSIEEFESDKKPL

LSTKEVSNYDEAEAASKYADAEMENAQSLVKSFMHRLGMGDDPEDASWLTMTTRDSRTGE

RAHAGELLVSVEIIPKHQADVRAAGLGRGEPNNFPFLPEPADRLHLSAMWNPCNVLKALM

GPKYFQSFASFFLCSVFVLLVLMIGPLINVLLTLFELVPNPFGLICFFFSLGLLMGIPVY

LLYRCRRAILRVADIDSTSKSCNHKTKAHRTLR

>contig30650-1 Frame-0R1

MRKITMSTIAYRMFVDDTFTFERKSSS

>contig32670 Frame-2F|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY54401.1|) 0.0

MVVTVGVTDPELTSVVLYSTLPWPMRLGFLPFLFFYVTAVYLNVFCPEGDVISWIFGALC

VFLHMLALLSAEWSVDVRCWMTCARLKIVEQNEHRKVLAKVKPSLPMLPKQLCDCHVVSK

DTITKNTGPTVWFSFQNLKFYLFDDIEAINSSGTSHFRRLDFPVDRSLESYLQSNGINSD

EELQQARDRWGRNEFELSVPNFTDLLKEQLVAPFFVFQVFCMLLWCLDEYMYYSVMTLFM

LIIFECTVVKQRQQNVDTLLHMRNAPQPCLVYRLGRWTRILSDDLVPGDICSTCNNEGAT

RVPCDLLLLRGNCIVNEAMLPGESIPLRKESVEKSIVDEVSKLKALEVDTSSSMQHKRHA

LYGGTKILQHSVAASKDLLKISSPPDGGCIGFVLKTGFGTTQGSLMRTILYSSQRVTANN

LEAMWFIVLLLNFAFAAAAFVLSQGMNDPTRDQFKLFLHCIMIITSVVPPELPMELSLAV

TNSLIALTNHSIFCTEPFRIPSAGRIDICCFDKTGTLTS

>contig33817 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59726.1|) 1e-78

MSDIHEETKAMADLCRSHGTLWKLEERLRTVFHSRFVNLHVDTLKQRLTIATEKLWPTRA

LVLTDAFHSTDDLCDALIASCFVPWYLARRGTSVFRGEYHVDGGLRTLVPEVSGYVKVCA

FHSHILRRNDCAISPSIDPDFPFTMMQLVRFALSPPHVKVLDQLFELGQKSAYIWAKN

>contig34229 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56206.1|) 0.0

MLWGINELLTYHYLVAEFLQTSRMQVEEFNSYAKEQQAVIIWQHLFIDRSPVSEACRGVL

TTLHLLGLDHLVAKRDIAAIQNWFKQQDPEEYVDTVFRLSGLKYAVMTNIPFEPKEACHW

LGDPATNTPPPAWSRKYFRSALRVDQVLLGDWASIGPTLDVFKLPHTLAGVRGVLEKWID

IMKPEYFMASVPIFFEYSDENALESTSDTLPSGYELLTKVLLPLAEKKNLPIALKFDSVR

PINARYGVAGDGVKPSNVDILINLCNDFPRVKFLATFLSRVNQHEVTVTANKFPNLHLYG

CWWYCNNPSIIEELTRMRIEILGTAFTSQHSDARVLDQLIYKWSHSRDVIGEVLVDMYQ

>contig37242 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58446.1|) 5e-29

MHRNFLDAAVLCVFNKDSFDRNDRGVSYEFAGIKWLA

>contig38489 Frame-1R

MQAVLLRASTRACVRRSAIAVEARNHKFLSVIHLKHTALPTVLVEIRYASTANVRNKFAW

AETDIAPPSPGRGILGRSANIDVTKSQNPFQRFYWLWKMLGFLNEDDRLFRHSSAVFQSC

MNHTAQPDYYRALGLPQSFRAQQAILMAHVWLVHRRLALEGEKGKIMQELVFDRLWEETV

VRIRYLNISELTVNKYLAQVQQICFNACIAYDKGLKEGPRYFQTAVAQHLLENESTEGLR

IASIMAEHMKRELKNLEKVDAKYIMLGTIPWTPLPETHAKIRPTDVDDVVLIGQRFGNWR

SALDNRGKLYFWNITTRYSIWDRPTGDKLHEGEMSK

>contig38940 Frame-0F|Blast-diacylglycerol O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY66276.1|) 0.0

MDASQLNRRTIQSSPKSIVELDDEDKAIAAVPVEHMSARGVFLLAMTIASFGAFTLFVLA

ELMHHHPRFLLTCVLQSNTHAAAQWALQLIVPSTSAAAWFPISISHAPTEMFQIVSAAPP

LTPTLSFIKKIARGIRYNYMFAIYQSIGWTLYILFVGQQFFCSNFSKISNFQFCLPGSRS

GQAVAAFISEVLIISSVLTLDKRRDRNLQRRRDRFVVQLNNFNNMLLLVGATMLALASEY

MRLHPSPSGSSVGYPLATGIGSFALFVTALFNTYGLGGVLSTKDGWKFYQPFMGGARFVL

IQIMSWTCFGAGAALQVVYLLSLTVVELELFVGAMAVAGSLYIMAEIGMMISLLVFKKST

QSLERLDKIAQADNLISEETAKEMKRTATKKTFDLASIDSSSMQYFLLTLHKRLRDFADE

CLGVIVVGGLANVQYAPNALVCVVFAATTNLSPAGVAFYGILTTCVEFGIVVSRSIATHL

YIKDSKNGLLEEVNRYNVKYVLPQIITGCIPAVATYNHYINERAAFVPVLLITIFIYIYE

LTYRGNPQQTGCRERASWVKGRSILFETVKRYFSGTIIRMAPLDPKKRYVLCFHPHGIMP

ISIMWLQFTAQWRQLFPNFYAHILTASILHQIPLARDLLHFYGSREVSRTVFANTLRQNE

SVLVVPGGQAEMLHQQSAKNEVRVYTHHKGFIRLAIEHGVPLVPVLSFKEGELMDNVQAP

ILQRWFIEKLAFPFPHFPYGRGLLPIPRKIDIPIVVGEPLIVPHIKKPTQDDIDKVHSKY

FAVLQEMFDKYKDEVGCSNFKLVYI

>contig41229 Frame-1F

MDNRLTVDNFVAKSMDKNLLNSAKEFESSLYATKTYLDLTLYRDERMTPQLYKKFKETNG

DINWLGHQLLGKRQWEKVSIEDQESIANVLLHAALFRIYEKADDPEEAIQSFLRHKEGTE

TIRTVIRENLATDKDLRLF

>contig41988 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55687.1|) 1e-32

MGGDQNFCRTSTRANTTLGRVHKRQVQRQFRPGGQ

>contig42237 Frame-2R|Blast-centromere/kinetochore protein, putative [Phytophthora infestans T30-4](gb|EEY58042.1|) 4e-64

MTSLDSLTRKLEETHDEIIEVQREVIDAIRSFYGSSSSISADEAVKIAAQWDSSHTFPID

DDDSTASNLQEKMRRLNVALLDAVDHLQLNEAGEMAPEAQLLLSLTQQERLKTKIQQSKS

MLTILEQLMEFDRLLGDEDDAIDHQSFLTRAEGVVEAERLLHELIQVDQIDTTLEKPSTI

IRFLKLRFVSKKNCLLSDLKRYFNNT

>contig42242 Frame-2R|Blast-hypothetical protein PITG\_19522 [Phytophthora infestans T30-4](gb|EEY70231.1|) 1e-12 NOT\_ORF

MQHGRNQNLKAVFDGHSQKQRYAE\*LTLTWTPIEQQQYSSLLNRVAKPAKLFLHLIRRRY

A

>contig44293 Frame-1F

MTETTPSATGIAENKAAFFHIFQISNSGWPGPSEQKFLQTINPAGDTNQELLPEEAQGLK

NLLLSASSRNQYSRFSFFKLKRVVVPPVKIPPELATPNATNIIVAGSRIPMTKDMWTRHR

VRMLRRLPRCIDEVDAW

>contig46112 Frame-0F|Blast-N-acetyltransferase 10 [Phytophthora infestans T30-4](gb|EEY52909.1|) 1e-112

MVKKKVDTRVRTLLENCIKENFRSFVVLVGDHGKDQVMNLHYIMSKAAVKARPRVLWCYK

KELGFSTHRQKRMRQIKKKQQRGLYETCENDTFELFISSTDIRWCYYKETHKVLGSTYGM

CVLQDFEAITPNIMARTIETVEGGGVVVMLLRTMDSLKQLYTMSMDVHTRFRTESHQDVV

ARFNERFILSFASCERCIVLDDELNVLPISKHT

>contig46167 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62218.1|) 4e-09

MRTILLAKVDYTRTDYLVQAEHLAISLKRTNCNLEERKFLAVKLLF

>contig46686 Frame-2F

MPNPADLKISIEDLSSSTISLEDSGKTFLPRLSINSVLPPLAIHLSRTSYLGIVALLIEN

FGADALQNDSSIPLESKHSTKLRSRRPAVMYTYLQPD

>contig48077 Frame-0R

MGVISQAATRRQRRKTVESTTSASSSRPSSPSHTASPPVGDKRSSPDDGSPSDNASAAAS

EGTSPRKRLKVAASTPKQMDIITDRVTFRVLLHESEQSHVPKLERTLFTTSAKLKIRHLK

KHLAAMLKLKRYDNMCIVLPTINCTLSGLSETAKARKSVAIRQDLQCDQELEDFLRLKDI

YEQYGMGMAWELQLLYHFSPGTIVHGLAQFVAARTKSVEVRDHE

>contig48727 Frame-1F

MHPSTQSMMARQMHAGATTDASTKSTGMGMDWMESTEAVIDTVWNLSGHVTIFTAVGWTL

FGHHTLAQAFRRIHLLCYEDSATTEEIALIVSQLAMASLTQAKGDVPVHEQALNFLVDVA

DQAERRFLLNDMLYQRNLHRLFFLWALQRGEVTRAQVHIRAILALSPP

>contig48752 Frame-2R|Blast-hypothetical protein PITG\_16835 [Phytophthora infestans T30-4](gb|EEY65214.1|) 7e-08 NOT\_ORF

MLARLKLTRINYLRQAEELAHFAQSMEIDLRGKHIGRDVVNAVHNES\*DARKIRLDGRKD

RQRVHKFTTVGSQGT

>contig49430 Frame-1F

MFYDQSRHNILLMLPNKKIVKTAADHSGAC

>contig50300 Frame-1F

MSVSPSASEATVGARWPVKSGGMLGLHSHRDWCRRQCYTATTFQGYGRLRLAPPPLSGGG

LGDGFVSVVRKMLADASECTAIIS

>contig51567 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65904.1|) 2e-10

MAQLLRAAANGNLDKVIELRNDWGFQNKKGDSVLHVAVAEDQLKIVQHLVSNGAMLNLQD

KKRRFTPLMLALAQQPPCFEEIFQALLKGKS

>contig52108 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58190.1|) 2e-09

MSDPDRDAVMADPEPVASESSIASSPSISSHLLSLAAAGNLSSLPNDVATTESFETLDDL

VTPFLPLLTRL

>contig52319 Frame-1F|Blast-mitogen-activated protein kinase, putative [Phytophthora infestans T30-4](gb|EEY68793.1|) 9e-94

MQTLTLLGSPVYVDLRILYEAWGCIAARRGNFALLLPSLHPNIMLTSNYPPSVPIAGEYH

GHSGMLAFFANLHGSMDIIQYGVQHVARCEDLAVVSGRETILSADSGRRFRHLWKHELRF

EADGRISHINILADKIAAAIAF

>contig52382 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69403.1|) 4e-64

MVNFGDEFQLGRWFNNSSCSSSSAHATDSEDCDAANSMDDAVAPSSSGNVAECYICHVPN

PEFMSTNSVKKAPPVPVCSVSCEAKYLDMKGMRPSSDSRNADPTQCFMCQAFNPEYSISS

RGIVTPVCSKECEKAFLRRKKQR

>contig52795 Frame-0R

MLCTFKRKTHFSQHALCEYQSFKLVCAFILYSNLRPCRNDRAFAADMLSN

>contig53091 Frame-0R

MSSKLKVALSRLTSMTKSLMAPQLGFPVCFSTVGKRYRYSEQTKTVFHQFI

>contig53165 Frame-0F|Blast-DNA repair endonuclease XPF, putative [Phytophthora infestans T30-4](gb|EEY59646.1|) 2e-99

MVKDERTCAQLREFLSLGAQEMMRRRFGHYLLQKEAALLQKGSSMMSLGLEQRLLLEAAA

KLRVDELYAEKVTAIDAEGKKTLSRSMKRKREASSQSSYSDVQTHATDVSCFGLSTTELE

AITTAQAKYELESKSKAFLNRQPRVASGRRSQSGGTPNLLLEVVNPMDSVVLCTYEQATQ

HGCGASAFLDDMMPSCIVLYDPDMAFIREVEVFHASHVSSLEIYFLMYDESTE

>contig53648 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69344.1|) 4e-48

MARGSTQYSAPELVTKAESLVDQCQPELALQFYEKALQQDPGNASLLDSIGELSTELDNP

ERARSAFRQSVQISPSQNPAKYFYLAQLVTGTEAEQYTTQGIAFLEQELQQHAETHNPEV

ISIKKK

>contig54818 Frame-0F

MSAAMTSEDDDARLNERMSKARSELSELQKIMTKDNSDLSLHEGNGPASRTRSRSSNAQY

DSKRPPSMDIDYHLSPSLVPGETMMWQKEIVEGGRLDRMRIAELSNEQLRPATEKEAAAS

SFARRHKILMKQDKASMNSRRTTPKDLRDCSTDYVQQALNFDNGTADDEDEAASLTSQKS

II

>contig54906 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62219.1|) 3e-55

MGCCAPQATESAQLLRSPAPNMLLHGSCGPAWFRQLSAEVQHGVHSLLHGITLFVAYMLM

LVSMTYDFTLLLWVITGYVLGYYIFGERREVSH

>contig58353 Frame-2F

MSNRVESKIQEMSDRVESKIQKMSDREERVESK

>contig58605 Frame-0R

MKFSNLVRTRNREQIDFRIVSGEISGECKDDGQPLPLNTMREILSRVPPDSKVHLVVTRA

LQNRYFKEGTYATFVREHNLPAMDVYRISDESTLEAIVGMENHELHKVQCMDDGSTRLC

>contig58883 Frame-1F

MMKESLDIAMSKRLCVVLKRHMPQLEMRVLINRGLDDTEELMKRMSMVKAVC

>contig03107 Frame-0F|Blast-mar5 transposase [synthetic construct](gb|ACV32571.1|) 4e-08

MQFRAEKFRSRLLKYRFAWVDIVEPTTTRQTVPKAKKLTPIQRRSVFEFSLECCVGGHLP

YGTINDAVIRFAITRKVVAAIWQQGRHFVNDGSVAADFTSRNVGKVGRKRKAITQADIES

IPKEQRGNIRSTAAALNIGVATAINCLEKG

>contig12365-0 Frame-0F0

MLVYDESRLLELLQCWFLTEFRSTLRRYLYDD

>contig12365-1 Frame-0R1

MNSIGRNLDIRTWHIAGISLEICS

>contig15746 Frame-2F

MIYTGASEVIANEIGDLGDGGQILVTKRVADWLVMYEDLVAIDFVVEKVGEYSIPQIKAK

LEVYQVLPEVLTGRKKMFSSTLKKRRATTASSLYSVASSNRSRLSSNAGQLPLPEQRRRM

SRPHALATPPDPGPVQGGLSRFGRVQRSFWRTDHGSFYTRATSM

>contig17854 Frame-2R

MESGTCVPLDDPLSGRFRVILDLFMVVALAIALAFILVRVTSSGARSLRSSNSPSASPQA

LRNSKGTKRASSVRDRLEHETRLRLPRRSTYYSMPFFADTVANKQEFVDSFVELGEASLD

GWLLIKKGVQRGNHWKKRYVVLDARARIKYYTNVDAARRNFNVKGSLAVHAVKPADPFEF

GANTLEIRGTLGGTYFFRAEDDMAARSWLCVLTMRAIQGRVPGRIDSVLSAAVVMPNPTF

LSNSAPPVVSSSSLKLHPVAESNETGYNRLSVAGALKHASNSDDTSAETRLKSHSFELVV

QDMTYDKDAALRQFYVVAKFKSELHDYSSVPVGQTSPKPRGEKGEKNAVIKWNEKLTWHF

QDHLCFECPECRALGATSGAFCGLPDILVLHVYEIHLRYLTTKIGELSLSLRELLGFTGM

RTAQFTCAWPVTSARDAILGELLLSFKYAVDKAGGAELMPFLVTSADEREFVGEFPLHPA

LPSAFAFYQTFLANHTSDRMKEYYKERGDTEVEVGDWTKSKEYGGQVRVMSCRSPTNASI

GPSHTMTTTTDHVPFDDNSLDESAKLVMQSKVVMHDIPYGDCFSVEKLTVVERVASSDGS

PGKLVAKIYLGVPFSKGCMFKSKIISATREAMASSSRLYFTL

>contig24636 Frame-1R

MQMPSRRYNPREEPYCTGGLTDACWMGDDKGDAPITAGFHTIHPFAQSKPKSG

>contig27839 Frame-0F|Blast-mitogen-activated protein kinase kinase kinase, putative [Phytophthora infestans T30-4](gb|EEY59283.1|) 1e-153

MGSHRSANHFCINMEYVPGGSIASMLNQFDAFNEDLIRIFTRQIVHGVVYLHEMGIIHRD

IKGANVLVNEQGVSKLADFGCSKQIPAILTTSLEESLRSIRGSIPWMAPEVVKQTGHGYK

ADIWSIGATVIEMATAKHPWPHCHNGLAAMYTIAMATAPPPLPDHLSLEAKSFLQRCLCV

DPN

>contig28272 Frame-1R

MMADVSITYLPPYTFPSASPLKNLTEERHYCRRVSSSWRPPVVTCAYFIYK

>contig30651 Frame-1F

MINSRAVSHQSSIAFLVLRTCDAVIRRSQSLTRPTSFFLEISLRYKPFR

>contig33166 Frame-0R

MKIEIAGALLLAASLPAKPLANVVGANSGEPQEAVTSNTMAAEVNMERVQKLTEGAVFAE

TFDFDELDGSRWFKSLHEKYANQDISLADRTLPASLPKNDRCLVLNKPARHYGLAVLLNE

PLKIDESDSRKEMVVQYEVKLQIGLDCGGAYVKLLRHDEENKNLSSFSDSTPFVLMFGPD

KCGQSDKVHLIFTHKNPVSGVYEEKHMMEAPRIKTDRDTHLYTAVIRDDNTFEVFVDQKS

VKSGSLFENFLPSVIPEKEIDDPEDFKPDDWVNEKKIRDSSAVKPDDWDEEAPAQIRDEN

AVKPDDWLDNEPVLINDPDVSKPEDWVDEDDGEFVIPQISNPKCSEVSGCGEWSRPLKAN

PAYKGKFYAPYIPNPAYKGEWKPRKIPNSNYFDDEHPARLDPIGALAVEVWTMTEGIAFD

NFWLGNDLKKAQEFAEQTWSPKHAAEVKENEEATNIFKANDDASLLDTIKIFIADLAAYA

GLSSRLFIGSVGGLFVLLTGFYMCCASRKPIQTAVSKKEDSGAENDEGEDAKVPSSEDKA

KTTRQRKKVPKVD

>contig33188 Frame-0R

MRYMYGDAFVDGRTLFTFPKHSGHTGQYNHIPTTFPPVVIVSSNQVACVENPADPSSSSG

KDCRFLLFRVRRKAETSS

>contig33863 Frame-0R

MAPARLPSVDQAETNALQAATGLKSVGAKLVCIDFDATFVTVHTGGLWSGTPMALRTHVR

RFFELLVPLLCENGINVAIVTFSPQVQLIRNVLKLCFSSEVAAQLVVRGDDRTWTLTHDQ

TKTFVPLWQTNGRHLDRKFKLPFLISAALEVQHRSGGDVVICNRDTVLVDDDVVNIRVAN

DSGVVGVFFDPGERNEESFCKRIQELHHSETSTPSYKTPSKKPIAGSTIKLVARERKLKF

PSRARRRLGIATSTSSGRNTSSFSMCTPSPVMKLKCSVDMGKPRSKRASRMLRNYSKEMD

LSSVSKSSTFTVAEVSTNATI

>contig34127 Frame-0R

MEFSCSRGSGKAALDSDVLNLSLASWKNDAGVRSCSGSGKCSSHICVPSGGANRQVCCAW

DIPDPIGFRPTGLVSDKNLVSNIAIVRISIAGGDSLKGMLASGSENEDGELLVSVYQRDT

PAVDPSQVFLWIIAGATVLVGSYKAAAYERTKAQLKAALIAADTTSSDAIAQARFAYEEH

NEQATTFEWLGLKSWLATTFLLLGIGLLALLPIVNVVVVMVALFGIASVFATFQTVWQPL

VRCLSGQIFLKHPWRDVVWQWRGFLVPAQWSFGDLLALALSVTTAFLWFLTRFWSIAWIF

QDILGVCFCLMLLRTARLPNLKVATVLLGFVFIYEVFIYFVLPFISEESIMIKAVEDGTQ

RISDGVSNAYCLRYPTDVKHDCRSESMPTQLRVPTVLDWRSGSSILGLGNIVLPGLLLVF

CARYDYATRGQLFGRLAPRHGKAFGQPLFGNVLHVSGRTSIAANRDLEMLGAELENSQHM

SRRGLFCLLLWGYTIGLVFANIAILKTGHGQPTLMYLIPCTLGLLVTVGWRRGILNKLWE

GPPELYPGYGRCHSISTRGGLDIFDATRLRGLSSGTGKAVMSGIVLQQQRSVSGSYASED

TPKSQGT

>contig34228 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56205.1|) 0.0

MFTPLQGSHFAPNTCAVCIGSGRFMRAVLVPVFRQLNYGVIIAQTRGTSFASACAAAKGE

YEVDTIDSNGHVLTAVYKLEAVGSLGTPEGRAAFLELPSKLPQLKYVGFGVTEAGLQSNS

QVIKDLAEFLLATYTSIRGNNLSLINTDNFPNNGNHIKKLVLELDWVKSDDLTAFRAYLN

TMVHFHNTMVDRITNHRANDSLVPLTEPLPAKILAIEDLHGVLEAGSFHNVPGVFVRAKK

SEIAKDYLLKFSLGNAVNSAMVYLLALSRQRTANQYHQFPIISEYLDLLFEKDILPTLLA

GHVADQEARSFYTEWLVRMKHPYFGLDNFWVSQNALLRVHVRLLNSVNVNVANDVKYQPS

SFMAFAIAVALRFLTPSQNDARHEASTIFVGQMDPINDNTPLYSITDETWNYDSGLTANV

STGKYIFDDGENGRASRLLWSASQR

>contig34989 Frame-2R

MFKTNIHAATKRPSSDNVDLVEVIKSAMPPKKSIVVFVRFSRVQITESLKACNPRIRV

>contig36222 Frame-0F|Blast-Folate-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4](gb|EEY58118.1|) 0.0

MAGTMLYNTFLTNISFRTIFLVAQICLALVSLVDVILVTRANLTVGIPDKAFVLGDHVVA

EVIGRLKTMPIMVLCAKLCPRGIEGTLFALLMSISNLSYSVSEFWGAFVCEWMGIDKDEY

EMLWLAIVLRSALKVVPIGFLFLIPSTDPQEIIDQLDLGSPVHRTLDAETDQSGTIRKDQ

QVETCSPSESKLAKGSAVPIV

>contig37243 Frame-2R

MEQRALMQLAILASMATVTAFVALTLYLKRTAADTKRPRVPSSASKPPQKTLVCQSADSN

IVIAASLVEHDATLATEKYKSGDFSGAVKLYSVAISKCEKQQPLDIRNLKVMYSNRAAAY

EKLQDHENVVEDCTKALLLEKRHLKSYLRRAKARACSGDLRGSLVDYVCLLVISEENQEQ

VDENLVQEISRIHSTITAKEIEDARQNKQNPIRYLPDQFFVTSYFSSFHPSDDENDFLAE

KPSEEYTSELEALDTNESTRYQRGLLLTKRGLALKKVKNYDLAAKDLDAACKLVDPENEA

YYTAQIENGTFYHLRGEFDVARNAFEKALAVKPYSIFAKIRMGGLCFDQKNLTKALEWFD

EALSEKPECSTAYFHRGQLHSIDLLPDESSNELSMATALSDLEKCISIAPDFSMAYIQLG

VSHARNGNFQGAVEYLMTAARITPEVPEIYNYIGETYMQMLQAPGSPVDLNSVEEMFLKA

IELDPTYPMGYINQGNMLVQKGTEYGHQALMLFEKAVEMCPRSKFAYCHLAQVYMAMQDY

SRAIEQIDKAVAFAFSKDELNELFAIRVTAETHQKASGLLQ

>contig38299 Frame-1F|Blast-5'-3' exoribonuclease 1, putative [Phytophthora infestans T30-4](gb|EEY67074.1|) 1e-111

MKIDPLWAQLEIFFSGSEVPGEGEHKIVEFIRHRKMAADYESNLRHCMYGSDADLMLLGL

MTHEPHFTLVRETVVWGGSFKKVAVKHIEEQQWQLVHLSLFREYLMLEMRVEAPWNGERM

LDDFILLTFLLGNDFIPHSPTL

>contig38387 Frame-2F|Blast-peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 [Phytophthora infestans T30-4](gb|EEY57286.1|) 3e-25

MSSTAKDLPRGWKEVQSKSRPGKFYFLHIKSGEKTWKLSHVHAKEREIRHRGSSDPKKRG

LIDSSVGPKSL

>contig39348 Frame-0R

MHTLFMLLMNTCLGDKVSQHNQVGAILAAVMHDIEHVGLTNDFLIKTNHPIAQKYLTEAP

MESKHTDLALQAVLDPRFNILSKMSSIQQEQILEVICKSISATALIYQPELLAEVDGTTA

DEWKMLEDVVLPQRLQVRALRIAMHVSDISQTMKPFANHQTWVYRLNDELYNQGELDMRE

QWGVSPSYCFRDQCTYEGFLSSQLSFLRNMALPAVMMLNNIPWMDVNELVNGIEKNILQW

EQLAIFI

>contig39418 Frame-2F

MTHQDIRHALDVVSLTAYIHAQLGVSHGSIASIFQFRHGQSNPTYLLTMATSNAKYVLRK

KPPGQILPSAHAVEREYRVLRALEHMEVPVPRAVILCEDLTILGTPFYLMEYVHGRIFHD

PSLPGVKPMHRFAMYSSVLDALVHLHALDYKKLGLTDFGRPEKYCQRVVTRWSQQIQKNK

KIFTHANIPENPRLIELQNWLNQHIETALQATDDRTSLVHGDFRIDNVLFHATEPRVVAI

LDWELCTIG

>contig41750 Frame-0R

MFSFRYPRRSCIADEYISILFGTGLTDLWIIRLYFQT

>contig45651 Frame-0F

MDQIASWKWIIKSFPRLHVRFAKDKVAAAATVFPNNLLKIKSNLFGEKAFQEWVTLVRRS

IKGPTDEADGIITAVLVRKFGNVRAIQLVMEGASTTNSVNAQWLLLLENYFVQANVNLPK

LLEDIFRMSNQVLDEKMLGFVIKVGSVKQHNQDAAYVAINDFMKSKQLSVELHKLEGDVK

TYGIKWYDLKKAYRNAMSDSKTNANVAPIDRLMKLADSSNFQVARPPGWKIANNYAQSSE

NLEVLRIAIQAILKNEGADAHKAKVFAIGTLKHIGLKWEENNFDIGKMLKTMVGTKGNTD

ELLQTPQAWAVIHAVTAAHMAKVEQMIRDAMKNASGRSIEKAVLDARTRAKPEGVKKAVQ

IFLDTFGHAKISTMLTNSGETNAIVKEFNTAFRKLHPVPVQK

>contig46166 Frame-1F

MINTIEITSQNGPSSSAFTKQDYLGPVTLVTFSSSGSLLYVGVGPTIFLYATTTSEFLGK

HDVFTRGILHGCDIVLHAASESFVGAFFGQKRVSCFQQLPQNPDAARSHEQLAVLGTSKV

FCDWVFDVQLLTSEITAIEDENLLVAVGLAHNLVQIWDPVRNSILRTAQCAERCILYSLA

FHGRSLDELIVASGTVFQQILLWNPMEITND

>contig46188 Frame-1F

MWRLLYAMFITAFGICLICLVVLGHIVQDNSIANNGIKGLESTSQGLLA

>contig46816 Frame-2R

MVAGEIKRLLRGVAAISISAPHTVLARTSCTHTIPANLSLAKEKFVPPPRVITATQEVKK

TASGDIELKLLSLNNDAQAVGTVIMNGGVFGAPDRVDILQRVVRWQLACRRAGTNKTKTR

SEVSSSTRKPWKQKGSGRARVGDIRAPQWRGGYRVHGPVLRDFSYNLPKKVRAMGLRVAL

STKLREGKLAVVDSLSIDVTKTKDMKKLLSSRGWNHALFVGGKDVESSFVMATRNIPYVD

TIPQNKINVYSILQKDLLIITKDAVNYLEERLHIE

>contig46863 Frame-2R|Blast-triosephosphate isomerase [Phytophthora infestans T30-4](gb|EEY59956.1|) 1e-112

MTRTCLIGGNWKCNGTLQSVKDMCAMLNKVEFNTEKVEVVVAPSVLHLNLAKSLFKKRIA

LAAQNVSLTGTGAYTGEIAAEQYLDFGIGWTITGHSERRTYYGETDEIVAQKTKRALDLG

LKVIFCIGEALEERKAGKTLDVLIRQMDALLNIVKESDWARIVIAYEPVWAIGTGVVATP

AQAQQAHKDLRAWIASKVSVAVAESIRIIYGGSVNDNNCEELIALADVDGFLVGGASLKP

EFEKIIRSAS

>contig47671 Frame-0R|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY54028.1|) 4e-12

MGLSWFYIKLILLTGIGWAMDSMETFVFTYCAELIRKDISQSSRQASFLGGAVFVGSFVG

SFLFGSLADKFGRRPIFMATLVLFLA

>contig48003 Frame-0F|Blast-lamin-like protein [Phytophthora infestans T30-4](gb|EEY63232.1|) 3e-16

MTTELSPIKSKRMEEKASLQQLNSRLEMYVLGVNELEGAKNAAERELETIRQRMQQDLDS

VRTRLTKELEETRKYELEVSCSMMSLSR

>contig48076 Frame-0R

MVGNASSTAEAWGSYRKNARHSVHNRVQLRRHLNEFKLLKAGNILEHFLKFDALCMSIQA

TGQ

>contig48098 Frame-2R

MAIPSPLNTQKLTPFDVPYYWTNVANTPSLHWAYPDVNIAKALGGCGIHNAMLYIRALPS

DLERWNMKNWTWE

>contig48289 Frame-0R|Blast-U3 small nucleolar RNA-associated protein, putative [Phytophthora infestans T30-4](gb|EEY66389.1|) 1e-173

MAASGDYKRLVLKKFPATIEVDTCEDSYWKKFHAPQELQQVGPVTHIDVSPVTPHHVAIT

SSTRIHLYSTTTNEIIKTFSRFRDVVYSGTFRSDGKLLVAGGEASHVQVLDIKTRAILRS

FKGHTAATRSTRFSSDNVHVLSCSDDKTARYWDLPTGKPLALLGEHSDYVRSSGANPSSH

NIWATGSYDHTVKLWDLRTSDQTVSKSSMSLNHGAPVEACMIMPGGSLLLSAGGNSIKVW

DILSGGRILHSFSSHQKTITCLGLDGSGTRLMSGSLDGHLKIYDLKTYELAHGFKYNSGV

LAFGMSPTNSHLFAGTVDGVLAVRRRTIKRV

>contig51399 Frame-1F|Blast-polycomb protein EZH2, putative [Phytophthora infestans T30-4](gb|EEY61878.1|) 2e-37

MCWKNENIQPMTALLTSLSAAEIGLIRKLRGTMGDNTCLLSAIVGSISCITVRELIKKQS

KDMLVVEGDNFRRKGCRARNWKQGRRAGGSNHELFQRTRMHRLQDRGTENHEYQPCMHEG

MCDSTGCSCMKRDHMCEKACACSR

>contig51566 Frame-1F

MDVDETKYMGPAESKVSEVTTPFAWEQHARLARLQLVEKRAIMQSDGNGATQSDGQIMQS

DGDGATQSDG

>contig52000 Frame-1F

MALTPANMKARKEETMLLKAGIRRLSLHTEGLMQCCNVLERNTLEQKEYMETLTAEIERL

TSLVNLEKNRHMKGSLPGLELEDLHGDESLSRPSSDSGTASTSSSQNIFSRLPRQESERQ

RHDLQQAMQEDSSLSAYVQNILKKATEKIEDKWRTRFAEQFVEHEQALAQERERSSASVL

SSSRLVTETLHGKDDELKAIQELNIKLNQQIRQLDLDLDATRSERDFFKQQMEDDDDRSS

SAHSF

>contig52277 Frame-2R

MTESRAGMKWHASTDTWNPNGITRALRSIALLENSTTEDAMIFSICPRDDEVLEEIR

>contig52383 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65996.1|) 2e-06

MRMLTSTTKRRKIHLEWRSYLRQVSNPVHEVSDNKALILKLELCAILPDAPIEYTRLSYS

NKKDAYGEGDAHTFYHVS

>contig52794 Frame-1F

MTKITPCAFGAPLLASCSICAGRYGLSMCS

>contig53090 Frame-2F|Blast-carbohydrate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY58600.1|) 6e-46

MIALIFLAAIVAGTYADKYFTGDGTAYTLGQTSAGNCNMMSALNFATTEYAALNNEQWDG

LQNCGRCAQVSCDDDRCDDTSKTIVVQILDRCPECKYGDLDLSPSVFTAL

>contig53164 Frame-2F

MPLRHHNDGRCPCGSLQTSHRESRTDSGSACQLASGQLSAEGQPGDGLCNGALRLALFQY

KSTRRGRLLLR

>contig53335 Frame-1F

MTSNNQILYNDCCRYVNSLTRLNVRNEHLRSNPAYLLKLRMRLAACKSELDVSVHSYHQA

FGAYND

>contig54349 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59599.1|) 1e-12

MNWVSSSLELAGSLLESVDQQAALTLAGSEEEEQEQEPEMTASKTLEKTTLNTVFTQQHG

KFAMEEANVTIDGPAPT

>contig54590 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59011.1|) 3e-18

MRDLQRTYRSVLRCIQQENLHCVAVVSISTGNMGLPVDRAAWVALCAIQRYIRSVPWTAT

IAIVCYDADAFAAYTKSKTEVLSQFNAEALRAFPT

>contig55078 Frame-0R|Blast-elongation factor G, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY55935.1|) 1e-36

MDSMELEREKGITIQSAATYCSWKDSNINIIDTPV

>contig55096 Frame-1F

MTDSRRVFVQLASVQDSRASLRAPVMAFIMPTDTRLSVVNEFLMSCNDDDIEVEERPPGL

LEDCVILLAASLQRIADPTSCEDGKQYILCMSAEDAERLQKQQFEDSSASSVTGMYETRD

SVVLTDQLESLEELD

>contig56761 Frame-2F

MILKLVNDPMRARECGITLAMANKMKATRSAMEFLDTMTDTERMASITTAWNDWLKDYIA

RIQDEFNPASDVLRRERMLQVNPLFILRNHVAQSAIDFALHGEYDKVQHIFQLVTNPYKE

PVNESDFVYAVPQDSSVTPLCVSCSS

>contig57326 Frame-1F|Blast-putative elicitin protein SOJ5 [Phytophthora sojae](gb|ABB56000.1|) 2e-18

MNSNIAFIAAALAFVASVNGDGQKCSFMEETMALARMAPLYNNEDLKQCSQKSGFSMMDS

KTMPTPEQKAAMCATNECHAFIGAVGGMNPPHCILKIPGGGLEVDVSQMCGTFEKDCA

>contig57353 Frame-1F

MELGEDDDICAFEATLSFLEECAIDTFSSADLSDLLVTSDVSSSFQLGEQPSQFSSLSGR

PCYLPDHLAREALKVASPCITSTVQANPDRACNNLRFELAFLHK

>contig57689 Frame-0F|Blast-transcription initiation factor TFIID subunit, putative [Phytophthora infestans T30-4](gb|EEY63035.1|) 2e-09

MAEAAQLEAFLAALTQYTPTIPDELIDFYLQRVGFVTN

>contig58604 Frame-2R

MKFGDLVRSKNCDKIDFRIASGEISGECKDHGQPLPLQTMKEILSRVPVESKVHLVVTRK

LQKKYFTREERYATFVREQNLSPINVYRISGGSTLHKIVGMENQELQKVQCMDDGSTRLC

D

>contig58882 Frame-0R

MLRRVASSSLRRASRNASKTCCNASTTCCHATSCRLYQQRLNVPTVEPQWCSLQTAQFST

DVPV

>contig59401 Frame-1F|Blast-TFIIH basal transcription factor complex helicase subunit [Phytophthora infestans T30-4](gb|EEY64472.1|) 1e-06 NOT\_ORF

MCVHPRVMAHVDREDVHANVAR

>contig00655 Frame-1F

MTAKVSVKWGKQVFPDVEVDKTSNVSVFKAQLYALTFVPVERQKLMSKAWKGMLKDDMDL

SKLEKLVDGAGVMLMGSAEVVQKPTEPIVFIEDMTVNDIAASGTVYPAGIVNLGNTCYMN

ATLQCLRPVKELREALKEHSGGVSADLASNFTTALRDMYGQLDGSLDSITPSMFVSILRR

AYPQFAQQSPRSGGFMQQDSEEFLSTLFATLQQTLTRPAGGLKSLAPTSNMVDALFGFEM

DETIECTESGMEAAVVKKEKALKLVCNITISTNHLSEGINIGLEGTIEKHSDVLGKNAVW

KKTLRMNRLPKYLCVQFMRFYWKTTPESRDHTGVKCKMLRPISFPMTLDVYDFCSDELKA

SMKIYRDKNAEKILNELKDTVEKSNEDESKVEEEDTMDGLTEEEIAALETARALSLGAKS

PGVELPIDFQGNYELYAILTHKGRSADSGHYMAWVRHQGDDWYCYDDDDVSPCKTEDIMK

LKGGGDWHMAYLAFYRATK

>contig01010 Frame-0F

MKLHLSFVLAAFGFVLNGGANALNVVMPGSNYDPYLSDSPGAIDVCKSAADVDADLRALQ

PYVVTIRTVMNMKCDTKFILQSAKALNVSVYLVLALTTVSPTFEEGKMKLQELMSSEFFS

IVSGISVGNNAIHEKILDMSTAFQNLETIRKMLREQNRTLPVTMTEDPETYDNSNLAAMV

DTISVSVSPFLDGVGVNQAVSDILRRLQSVRASGQRLNKPVVLVQIGWASGGGEESQNLQ

ATPEAQAAFLSNLHQVCSALKIPYSYYTAFDRRIQGVPEVQHHFGLFQEDRTLKSSIQNL

VIPMRTSLHIKNERSNLYLYEFLDGLYMKSVSTDPLETVRSNWYYDTTTQLVRSVGSDKC

LALYQYVSGGYPTMATCSPMDGNLKWIYDSNTRLLQHASQNLCLNTDMAMGYSLTVYACA

PGNPKQEWIIENI

>contig03100 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58763.1|) 9e-18 NOT\_ORF

MVQEKLNRLINRAELAVKFSAHNFDQLELDLYTNVINACSQ

>contig03742 Frame-0F

MFAILTSHDRHTRSNSYFPQRFCN

>contig05069 Frame-1F

MPTLTMSLHEGQKTPVHRPNCFSISDILLSNPPLKTLPTSERPKLQVKKRGRRRLLQDEE

QRKARRKAQCKLNQRRYRARQRGIISTLMLETEGLNGHFQDLHDYREFLRHYFLRDTAST

WTIWNDPRPLLVAKHLVRAFRSGFALHSYELSNLQESFVRLVCAPDLITQGATTDGVEAL

LLQLKRYTSYHGTLEIRSSHVNIVHTPVMDRQANEEKLTWIVAIRGAMRLRISRDTLMLV

YPHVLRHHDRIAQRIVGQTIEPEFLTTLYFDTRGKVTKFDQHVDFAGAFIQLLNSMDDVV

TLLDGALISSFSELGVDNKSTKESALPLGCKQLSLKFILL

>contig05807 Frame-0R|Blast-calcium-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63061.1|) 2e-21

MKTFASCLNHVFYNLDQDHDGYVTVLNVATLPLFQTTDE

>contig06778 Frame-0F|Blast-hypothetical protein PITG\_01705 [Phytophthora infestans T30-4](gb|EEY61408.1|) 3e-06

MALGKFIRYYLDREPMVVISCAIGAVGV

>contig07715 Frame-2R

MSYLSYHIRIRHLIKLAISLCKNHNFDVYEKLNNLSVNWTYIPNFTLLSIQDILLNCRLV

STYLLLLAVQFSKEHDSCHISLQSQQESLYVTEYVHDVLALHDCEFVFLVLRISYKSCAI

>contig12533 Frame-0F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY54229.1|) 0.0

MKGFLQCLGLCDAIEHTCIALEVMDCKLSDYLRRYGVNSGGSKHRRYTLSFDDTKAMLKK

ICLPMMTLHDDINVAHGDLACRNILMRTPPEGYEKSWEPDIKLSDFGRIKLPSDEPKILD

SSFSFHKNCDVGAFGREILYRLLVGEIVPKEHMEIRSLHKLLQDVTVTQIPKAAETRLGP

YYALFMRCTAWGVRPTFCEIYKHLDDLEYFKSSENGLFPLKPTGIPDPTFMSPIAETSRY

KALTSSSSRATARDTPTGHPHRSVGSKSRLLGSKNVAEVIVPGLSKPVNWLKTRSVGVQR

NAAPQALTPIAHPMLLTKKRKTPPSAGGGAGASRRSLQILNQIQHRTIEKGRKSK

>contig13592 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65535.1|) 7e-10

MAGNRHSALWNLALQLLVGLLVMPYLYKNEAV

>contig17112 Frame-2F

MKLPTLLLPIVVANPAHRVHDLPGLNQADVPFAHFAGQLELPSPTHEKLFYWYAQSRRSP

EKDPFVLWLNGGPGCASSQGFFTENGPFVAKRDGNVGLNPYGWNARANIVWVDSPSGVGF

SKPLQAATGYYNDDIVADRLRLFLSVFLTTYPELRDRAFYVTGESYAGMYIPYLVERLVT

NPLEGVTLKGFAIGNPLTDMGIDGNAYMEYYYTHALISHGDYLRLLDYCDHNIAQCMFTD

VNCTAHCEKAVVQAHEAADVGEFNHYYIYGDLCRNNQRTAVHAPALHQRLETIRTHRGVV

GPCAGDYTKTLLNRADVQEALHLEGQLPVQWMACHPFISHNYDRTFSSLDKYRTLLGNNL

TILIYSGDADSVVNFIGTQRWITEDKGLALRPVSPWRAWLGPDAQIAGYHQDFERGLTFK

TVKGAGHMVPAVRPLHALHLFDCFLFGDEKCTNISYPAEFDEREDAREPRS

>contig17185 Frame-1R

MSLMNIAGTQSVEDPEYRYKMPRLLAKIEGRGNGIKTLVVNCADIATSLHRSTAEVCKFF

GCELGAQSKYDDKTDRAIVNGAFEAGLMQQHLTKYIEGFVLCPGCRLPETKYKFKGQLIF

HKCYACGAVEPVDMNHKLTTFIFKEHTAAKRSSKDEKKKKDKKKDKKDKKIGSDDPEDEV

GTKKKKEKKEKKDKKDKKDKKKRHSKDKSLDKEPLGSEDDEVVWHTDLSAEAVAARAAEA

EAIEAAAAAAMASAAAAEEVVATLDNLRVDDENALDLAVSNLQRFLTTSSSPPEVFDELC

RQQINSALPVTDRLVIFFRSALTEAILTSNQVSKYAPVFAKLMEGHHSQYQLLALAEHFC

AVKYPTLLSAYPIVLKLLYDQDLLEEECLVAWASKGIRKEYAHWEVTEEVAGQLQTLLQP

FIEWLANAEEESEESDDES

>contig18315 Frame-0F

MASTDAAALEAVLKAALSTLYESTVSKPQEKKAADAFLRSFQLTPAALDVCASLLDQSLR

NGITESLSSESVPPIFFSAQTLAIKMRREPLTSNFEAGVWAKRIITWLSCDVRLPRVVVT

QLLLAFVATLPRLQAQDIKLFDSYGKDKNTCQLYAVVRDFYAQFNGKSVVGYALYHLIKN

NATHATLAEFLLLLIEEVDFLAERSARRRMQDEVNAWVSTVLDQLLPQLMHDASNQAGDT

YSNRVETQGTVLRALTSWLRYGTISSQVILRNPLLHSLVDFIARDELFDVSIDLAVQLVT

SYTHDTVVLQWITPRFLALRGAFHTAAAVDDVSTCLSLCRLFTEMGEACLELVVAGNTDQ

VRFVDLLLDCMSFTDADVADVTISFWFQLLEMLRRRETLAMEEQLKPRLARLATLSMEKL

QFQDDFTRLPIDKQQNIKAFRQEVGDLLRDCCHLLGVDAVLQHCVNELNQACQTPIQARR

WEAVEARLYCFRSIAREVEKNTTNALDALISSLFHHLPQFADHPAICYTSCLIVARYAAW

LCNHPTSLSILVSFLTTCVTKSAQDAQYGAWEVARAAAAAVRALAIDCWSILGHDIVAFY

LQIEQSNGMSVEDQVLILEGICAGVASSKDRAQILSVLDQVMKGIGQRLTALVASSQAIS

QVHIASNDLLRLLCLYEYLDVIQIPQEKPPLVMLTEQLWPLLNQLLSLYRGHDELVESIC

RCYKRILRSCGHGITPLVPQLADNLVTFYKAEPKSSYLYTASMVLKFLTPSSSADLDSLF

GRLLFTLIEATTPIFASASDMEARPDVIEEFFYLMERAVRCTPQVLTAPLSSDSVSGPLL

TRALSFAVSALAIFHNDANKSVLCFLENVYAKSGTGTTLVSLCAVNLAGYEENTKKLVHC

LLQGVVLGTMSTSRVDADYGSIAGLLAQIATVHGLELQQWIAEWFEIATAGTFATAAVYF

ITLDEAQEFQKELFSATSERAFRRTVRHFGKLCASRNTTLTDCER

>contig18382 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY67981.1|) 1e-110

MAAFKAPPLSAFFRKEEDNLVTQGLTDVHGVAMFHSLYDVGDLVGRGAFSLVYLCRRKET

QQIFAVKVINKALCVKKKTLRDEITVLLRVKHANIISLEEVYESDQELLLVMERVTGGEL

FDRIVRVGVYSERQAAEIVTNVLQAVDYLHSCHILHRDIKPENILLASGDSSEVKLSDFG

IAKILEDEDDGARSRGRAYTSCGTDYYVG

>contig19033 Frame-2F

MSLAIQVQPQPLLLFPPMTALLLLLVSVLFRHRTIYDHLYFLFFF

>contig20301 Frame-1R

MTLLSKYSARLQRSMTHDVEDTSRREGETKRNHDRSFSRRRNEDQEEDAPIDYDQLPGVN

VDFKAGRCEDENSDSRGCDRKSSRQEKHGRTRSRSRDRLATSKKPRRSNQRLRSRSRQRS

QSPAKSKITRGLSNEERNISGSASIKEKVSLPREVHVKESAFDTLALTNRRAFLYGPKKS

SVLNVSRSEQPLKNQGSDVETTSSLRLQSLGSLLPKREAKYENDTSELNKLAAKALRAQM

MGKTALFHKLTDELNELEAKLE

>contig20419 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63977.1|) 9e-10

MERFNELKLVSFTKHIEIERPSPVSAQHVIVLEFPMSGIPAGSCIILLIVITNS

>contig21575 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68785.1|) 2e-08

MFDDLIKLLRSPRWVNSPIARRFGYSLELSYAEDEF

>contig23335 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66028.1|) 1e-24

MSAVNTVSSTATSSSVMETSGPARSALVIDGSYAMIGARDLGGKIDYIKLRAALEEQAST

QFGDCWFFDQNPSAQRI

>contig24631 Frame-1F

MPLSISFYHNKRGDNAANSFMSVALHDREKVKHKMALPCEFYRNIWGPTEEEDAALRRRA

RSIKSGKCPASAASRKFKKRVATGHLVDISQVAHCVTTMSNFRADYGEEAEKARLINIWD

DRSLALGLETVVDKTANSSTAHSDHCPSTAETEPERMMSPIGSRVKRITEVSCEDSDEDV

TSFASSSILNRQRPGELKRAKTPEVIFPNAFKNGKTKTASDRKELFFHSDPVPPPSSRNG

SVVFSAIFSEKRDWSWSVKFLLGIHEPIRHALFVMDRFLQQSQIQSKPVASHTLALESHV

AEFFDWFKTYFVEYLLCQHEVKAAVLLPMLNLPAATKQQILDVYHGIRQMLSQIQQLERA

LCVSGACSASSWLLRLQVLQTEIRQLNRTLHSALNKEETTLHAAMSAAFTERAFRSHIMP

RIFRAIRSKRVVVPWIVERSKIWGGELEQRSLQSMLPFSAKFMYRKVWRPYFMSNVAVAM

KNLNEFDCSEDSNSCSSSAFNERNGEMCSVM

>contig27047 Frame-1F

MSETDRFDSMLLTIAQSQRGIEPLLDTVFSFLRRKTDFFSGAEAQVIENTILKCVRKQAA

LAEKDEFTKKQKEAEKRRKEELADLKKRQKKHDKVKEDKNPPRFEEISDSDEMQISTLEQ

TMPIKASTSKDVDEEGDEESGPSLVGNGGRTEKYVWTQTLQEAQVNFAVPAGTKSRQVDV

EIRAGKLRVGLRGENTFVDGNLYNKVKVDDSFWTLEDGNRICVYLQKDNQMEWWKTIIQG

DPEIDTQKVQPENSKLNDLDADTRQTVEKMMFDQRQKAMGLPTSDDMQKQEMLQKFMAQH

PEMDFSKAKMN

>contig28275 Frame-1F

MLTVEDQQRKQQIQDLVACSDQDGETNVSLPYRFHFFKQPAQDMVVSHSSKMKVTRQLAG

KERKFEINYIAKHNTNGSNAGPDLPLEDVWSCRFEHTPALIMTMRDKVKAEIVYFEVTVV

EWNTTTTFRNMFALGFSSLSFPLEGVPVGSNVDGSRSYAFAPASGQIRCADDPKVDRWRW

VESASTSTIASGDIIGCGLCLGTQELFICKNGQLFGTAFSSISRPHQLHPTISINSDCKL

LVNLGTTTTKPAKHANFSYRFCSFECNNIMSAFEWFEPLSQVYGVMKALMNPARLNEVTV

GDEFSVNSVLESQLPDEFMLSADTFLSRISEDACIRVESSHPYDMEFQESLVKIPLATSI

RVHLDVQSDTASSHCLQIVQGGSMDGDLVEATLGEVELRAFTGACGGQEVTVIGDSFVWR

FPVQSNFQCRVDRVRKGPYLKLEMRDTRMSLVRDKGWQTAIGVARFDCGVHIWEVCIAFV

TASSNIFLGIARRDVRLDSYLGKDSRGWGWIGNRALWHNGSKQRGTYGDKFKTGDIIRLT

LDLRRGTLSYTLNGRDLGVAFGPGGTGPKLEGIFYPAFALYNQRDSIELIGGHRVENGGL

EQGLLRTESGLASEDDSYYSEDEEELDGYAGSDAGVDDDSVPNFRMESAIFLREMGFPME

WCVFALRQCNDNPEQAADFILANADTLETLIRDENVALARRTRQRLLMHEQVLASFENAE

SGDANDAAVIPPPPPMEQITDAISPAKDFTYKEAATTYFKPSNGDARWGIAFTAVPEYSI

TGRRLLAIKYEAKLHRLHASQHIFNDARDRALVQLVNEICEARAEALQSCDPLRMTPEEF

VLTEAQIHAFPVLRGVPLEALQRRFLVLRNFNCRLQTSLAFIDFSASDEQSLLARGARTL

RGLVFQHVKLAWWLGVLREQQAPAAARPEIEVDRTRAHDALELSERGDALASEAGERDSV

FAQTFTQLHGLQPALLRGADRAFKVQFLGEFGDDFGGLYRECLAHLSSELQTIKPLLPLL

RPCPNALMSMGENRELFVPNANLRTSARRVQMAEFLGKLAGVAIRTKTPLDLNLPSAVWK

SLVGQQVERHDIEAIHDGCFQVMDTIANLDSHGITEAMFEEIVDANFTVLSSARETVQLV

PGGKHLHVTWNDRDDYARAVESYRLTEFAPVCEDIVRGMATILPVPTLGILSWHELRTLV

CGKASVDVALLQRRTIYGDGCHATDPHIGYFWDVLTNFTEEQKSSFLRFVWGRSRLPTHA

ADFTQDFKIAGLPKAAGRADMYLPLAHTCFFSIDLPAYTCKEVMHDKLLYAITHCQSIDA

DNTTVAQRAGQGIN

>contig29276 Frame-2F

MKTSELRVDLAVKVARFRSNYVNFNTRSYNGHIPAPTIKVCPGDRLILTLTNLLEAGSNN

NTN

>contig30656 Frame-2R|Blast-choline/Carnitine O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69430.1|) 1e-157

MKQRMELSLHGQGCHRWFDKLQVIVQPDGHLTINFEHSFSDGTIWNRWLHECWHDMRHSD

SGFTPLKEMPEYFGASKPEKLNWKLSNNLIEDVRKAECHFGDFAGILNSECLIYTGFAKR

ECKKWQLSPDGIAQMALQLAFYRTHGKIAPTYESCSTRQFHHGRTETIRSATPAAEAFVN

SVETGMAVTTQRELLVAAIKNHVEIAKIAQKGLGVDRHLTALNSIATEYGIRSNFLTSSV

RAESTHFRISSSNVTMPLLQYFSFGAVVPHGYGVGYLLHSKSINLCLTHYKDSRISNGKE

MKKALKSSLDTIRAIVESF

>contig31202 Frame-2F

MDHLRKNISDLRQEELKYDQHIKTVSQSIRQLYEEDAFDKGSFENFCYVTHDDMRRQESF

ADQSVMAIKAPPGTTLEVPDPDEGMEAGERRFQIFLKSTEGPVDVYLVRRLDEKQIDSNS

DLTKNSVPFTEPLSPEPPLDEQNSYDSDSGIFKLAPLK

>contig33114 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64003.1|) 4e-12

MTRQPSSRAWVSVPCENPSVAPCPRSLHVCAVRKDSLYIFG

>contig33864 Frame-1F

MESPRDSSSRRHVSKFMANTNPPSSPHHNNYLNASVSEPVSPLMLAATRTALLPTKTELQ

LPTLRSDYGATSTGSSTLKLLSELERSWAMFAATWRVVDLFAGLQIWQEQPREYDSTSEP

LNSVLLSTTSAGLVTFLAGHIGGGGFIVSLLLTMVVVTAALWTLSNARVKAAVPSFKTLQ

VVDGSPSSIFMYLMCINNYRVWDASVERAEVVHTIDDHSDIIHIVYKPVWIWPIWLAPRD

LCLLRYWRRADDGSYIICMQSALHPECPPMHGRVRANCNGGGFVISPSVTQVDETTSMVT

NVVHMDPRGWEGNVLQRLNIMHIYLRPQVLSLTGLRDVMEARKYVCPNVPGEFSAVLAAT

IEEQHTIATVQTSGSGGVSGFAQENTSQLDEFPSNVPRAMWAEPDGAAMMVRGPDYLVDR

RKIPSQSPYFRLVGMDLFESTEAIEHIASRPDNSVQSELRRHEEQGTDMPFTFVINFVVP

GTPRINLVLYYQIPSPSVLMDGSPSSELMADFLDGSEEFRNERFKLIPCIVEGSFIVRQA

VGSTPALIGKKLRQPYYRGKQYFELDVDIGSSAVANRVVGLVSGYTKKLVIDMGFVLEGQ

NPDELPERLFGTCRLVHIDLGVAKKLT

>contig34757 Frame-2F

MESSSSSAAAAAATTSASTPSSSSAQPFKSTIATSTTASASHMADSDPQTDPDDFEGSKA

IAVPRCSTWFAMDKINPIEKRMLPEFFTNHASKTAELYLKYRNYMVHAYRQQPGVYLTAT

ACRRNLAGDACAILRVHEFLTHWGLINFHVPPHAMPPTVHSNYALKTVESTALNCEKGPV

AMLVAATQTNNRHANVPLACEACGAPRNPDDSFFELPKEIKTKWMSHGATTSATPMVSSS

IHGKSSESKEVTIHGFALRPGSGICEECYIRGAYPEGYEASDFVLMPQLGGTSVSKTAQW

SLNETNALLEAVSSTRKDASGDEHGNCDWNYVASKVGTKTAEECLLHFLELPMLEEMLPR

HGKQLQQWSQEGIRPYYPGSALNAPVLDLVALVEGIDPAVAQAAAYAAISAIQRLHLKPI

DSDIKVETTQLVTPASSTLLDAAADAVVTSAETAGIKSTIKSEDSVGDTNVVMEDVTSAT

DSAGPHPAGKAEQPSVSKELLAVTEEIANA

>contig37231 Frame-0F

MAIAPTQCRKVIMDAEVPKHKVLARIRSRCHRHKSATPKRVHSASSPHRETRSDELYHVS

QQKPQLGHCRYDQPHKPARPVYDCCITEVMMLKAQLHRGNSRFRKRFHRFVMKRMIVPPV

TIPKAIAEQRGSKQFVGGQRVPFTRGMWESEKLRQYRRLHTLPVLHEV

>contig38779 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56458.1|) 6e-59

MELRTQYLLLIFVFGMIAKGMVKSTLGSNLSILLLVCVSIYYWRTKQKEKSVYDDIARQQ

AEVAAKLSALHGIGDGKVTDLSMAMRSTSFKLSESEAGVITDRVRRYSSKLGGSRKDRQK

FLRRNSKSKKVATVSKDDHTELADTKDVKVPLIGNTSLSDNKASELGKKGHAIGSIVEEA

V

>contig39484 Frame-0R

MADKNHRDKNRVRNLHHRRGNEISPSVISLRCTLAIKANRSFEAIGMTLMKLTNEVEQKS

IPMAELIPAYDVNSALMYVYKPNTIPR

>contig39570 Frame-1R

MRQCRLDYFSACCRVYLRCIFSVSTLTIDKMPDGVCTSLPYRKGQVHVFESYPKQMRLTS

LVSGSTKRLISEFFFIYH

>contig39707 Frame-1F

MEDMAWKCTTAFVLGAATHYLVSIYLHSDDTFKSNPKISEKNCNNTENTRSDDLSRSPSN

SSDDWEGEDSVSWVPHKMVMCVRTDLKMGKGKIAAQCCHATLGAYKRALKRAPDAIRSWE

TLGQAKVCLKIDSEAELMALAEKAAEHGLVNYVVIDAGRTQIAPDSKTVLSIGPAPLKAI

DEVTGHLKLM

>contig40538 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68374.1|) 8e-90

MTTVQGAFNNSDGMWTKVGDGTVTITFKSIDVKDVAVNIKSGGDKIAEVPIPAGKTVVWK

STVAVLGGKTLYLDRWRPGFLNLPGTGGGSLRLWVPRSALGGTLQLTAFLNANE

>contig42231-0 Frame-1F0

MRLQKLKESIRRAHDIAQTSQERLGSDDPARESILQEV

>contig42749 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54952.1|) 1e-34

MAGPDAARINVLIRAEVVAIIDVVMHFYAYDVSSVHDMLLTDAARKAFVQTTEDIQAEVE

RQLLQRCALHRAAALVLSTRPGMYALDRSLVSTWFCLWTASTSINLFNGVVKEFLVSNVL

QIRKKAIKQFAHKLTVTDLT

>contig43225 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55976.1|) 2e-24

MENEEGLTAAQVAARNKYEDIVCLLG

>contig44295 Frame-0F

MASHSHRWLKSSVTRPRAIFGTPIKQYSNHCDWRVFSGIQPTGTPHLGNYCGALANWVAL

QGATNLERDIVASPTVPTLRNVTRLYSVVDLHALTVPYNPQRMPSQVHSMVAALLGTGLD

PTCNIIFRQSDVPAHAELAWLLSCVTPLGRVHRMTQFKQKAAIARTETSLGLLAYPVLMA

ADILLYRATHVPVGDDQQQHLELTRTIATTFNNRFQSPGKEVLLKPRPYTTTQSKTLVRI

MSLRNPRKKMSKSDTSALSRIELTDSADDIRKKIRKATTDAIHGISYDCQERPGISNLLA

IASAVTGYSVVHLEAEYANYSTGTFKDCVADAVIAKMCPIGERIKQYEADVEYVDKVLKD

GAAKASELAAATMKDVKKVMGLSRSAESN

>contig45656 Frame-0R|Blast-hypothetical protein PITG\_03285 [Phytophthora infestans T30-4](gb|EEY65761.1|) 2e-06

MVRLVEAAGIHSVVKWNLRASMIQTGTFLDRQTIQLIYSIRILHSQALVSLENWWLCLTV

RVHQNSVTTFSFPLTELLMRGEQSIVLDPDLLAQHDQGIMWVSSSIAFCSSRQKNVNHEY

HKVIGIDIKDAQHESNLAFVIPLLQNRRFLFAQLSQPIEEEMPISKVAIHAAFRQNHEPF

MPTGRKAVDGKAHTSVLWHGAQWWDALAEYAYSSPQFAKLWSFAVSD

>contig46161 Frame-1F

MDASPAPLPHVNLVVRNVYSPSQSLALTIDPKTLVSELKRRLSVEFVSAPAISDQKLIFG

GKICRDDEPLEVLLSKLQEKDPKDGENREEPVVIHLLVSSTRGVELNALSQRDAMAQDSP

RPTVGAVQHSPLSNLQPEDPVLLQHPHLMNPQTQQHQNYFRQSVLMQQQAMVLHQIQYLQ

MMLMQQQQAAPMPNAQQNLFGAQHAALYGNFYGMMHQQMLHARPAVAT

>contig47676 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62979.1|) 0.0

MLKVVSQCAWSCDSQWLFAGCEEKGTRHARLCVWNVAAATLVSIFKFQGVITALSAHPCN

AELLLVSYWNSCPEVFNIVTGEKVGLVNMPLENTDVVPLTSQINSRHPVLASCARYGHSG

KRIYCATSKSTLAIFDATTLECLDSFKLHVLIQFVDLCVNLREDAMLVTSSKGIHEFVMN

PIDLKDESLTILEDHSIGLREVALHSTGAVRAPWAICCFSETEEFVVGTPVVRHRHVGEN

GLFTWHRAGVGNKTTAQHNVGVKDGVLALAWDRSRHSVLAVSTSGTLHVLEEHFSTTWPG

AMYPPGFRLITDNELHLQVYDADAQERQREKDKLTEAAKAAPVDVFCVLNPIEEFKKESD

IVDAAFVANEGDKPCYISAIPITYYHRRHC

>contig48004 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55710.1|) 3e-56

MPVATPRQAVRRKRMELILQKALDVSVHAASLVDLRACLESECQGDEELLSAFFPSSTLE

PTKHDTSDEVSAQAVLSLRQKVETLFQWLCETHDVDAELLELEDVIHQAEERRLRQVEEK

QPKKQENESNNAVKNNTNESVQENKLSPEAQIRVERLRAKQQEQKELEALVHELEAKNKE

LEKDVEDNRRVAIADVQRM

>contig48668 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62725.1|) 8e-12

MAKYTHPKETLSSVKLSTFHEAALIREAETIVRETIHANEAFLQVGSRFLPSDWRFVRSR

QGLDVYCQRSDSKSNIYPR

>contig49128 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67355.1|) 7e-26

MKVHSGLQLQVLALYKKALQTAKYKDSDTQRYIRDRFRNDVRAVERKDFAVIEHMLRKGE

RDLKMLSRVKAAQFASVNRTTSDATPRID

>contig49436 Frame-1F

MELGFEFRRDLEQLVHDDVLCSRRALQRINFRPGVLASAEPVDIFLQQRTKKKLARALRS

LCDDYGISLALSKEALAYTNSLEDALNFLALQYTSGELPSTLRVLPKALQGADDVDKSAG

ELRAEVNTIPQNDAAICIEQKPPITVEDISTAHVMVERREEIKQQKQE

>contig50306 Frame-0R|Blast-Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4](gb|EEY59634.1|) 2e-36

MVNLAFAVTTPVGVGIGILIRNSYSSSSKTALWIEGSLSCVAGGILLYTGIVELLTYNMT

TNGQFLARPTLQRFTLYISMWMGAGAMALIGKWA

>contig51514 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58346.1|) 2e-38

MLLSHTRENLQQVNEFLAEAKVMASMD

>contig51561 Frame-1F

MPALEVFGRRSRVVGSDDLFFPALLLFLHQLPLTLVCILFSCLWRGCSSTSLNDRGLPFW

YMLGA

>contig51846 Frame-1R

MEAQIADVGVGRGSTRTFIVRTEQADEEHLLKKYTIITSLRNLL

>contig55091 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68982.1|) 3e-13

MTLESHVFAAALGALIPSLLLILQMEKLWAQELPPQCSGVLDSIF

>contig57268 Frame-2F|Blast-glutaminyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY68531.1|) 0.0

MASYSVTATALEARRIEMARNTPEQLAEHHRIMQGKVRTRFPPEPNGYLHVGHAKSMNMN

FFEAFEKLGVPLDKRETYFRYDDTNPDAESTEYIDAIANNVLWLGYTPTKETYSSQYFQE

LYELALKLIRKGKAYVCHQSKADIEASRIALQQFHSTTGEKNEQNVPEAAMSPFRLRSVA

DNLAEFEKMRIGLYGEGEACLRMKMDLTSPNPNMWDHVAYRIKFVPHPHIGDKWCIYPTY

DYTHCIVDSLEHIDYSICTLEFETRRESYYWLLHELDLYKPSVYEFARLSMTYTVLSKRK

LLRLVASKKVRGWDDPRMSTLNGLRRRGFTPEIIKQFCKVIGVTRVQSTIQIERLYSVAR

DILGDSSKRVMAVLDPVELIIENFDDAPDKSALLLRVPNYPQDVDRDDGNAYHQVPLTKT

IFLDRSDVRLEDSKDFYGLAPNKQVRLKYAFPFTCSKLQTDASGRVITILGQMDWHALTK

PKGVLSWVPANSPTVEVRVYSHLFTVPELPSDVKDWEAFVDSKHSERVYTSARVDPESYA

KNLDQIVQFERIGYFVMDKDSTEDKRVFNQIVALRESGGEAASSTKKVGASTSRKDSQMQ

QLALKMEKMKLPPVDMFKKQPELYSQFDAEGLPTHDAAGEVLTKNQRKKLKKEQDKQKKQ

YDAYIATNKA

>contig57321 Frame-2F

MTNNEPSEHLCDRHSEALHLAALTKSLDDGHVDMAAHWLELLVLSRTVNPSNQPEKSQTS

SRHRRLKTLANAVAQMLDDCDKYKHDNQFVLTPGIADRTATTSFELSYAQLQMFALQQLQ

PSSTAYNVVRALYFPTTPFNKVIVKSTIHALVAKHEILRTCFAVNTDGQPRQFVHPLSH

>contig57471 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54599.1|) 1e-39

MTITGITRLIERHPNHSKFTKIHISGHLVTDETIKAIMAKCRKLHSFSVGYCAITDEALI

ALLKKRESISRLYLHWNVAITDQFLRFLASGARNLQELNLCGVKSISADAIVATIHAKMG

AQSELLDPNMLQLGNDENHVPERKRLKKIDFRYTSMTKEAAAAVKELYPELMVT

>contig57857 Frame-0F

MGSVSKHWCQRPSCWRVMLTDSAGWHYRHFWVGFCTSWASGHKMGESNYLEALRQAGIWS

FHS

>contig58355 Frame-2F

MVCAAHTTLPTSWSDASASTADSQMTLLSWLQLYDSKLVYSLLMGILAVLAAFTGIVVVA

MKLDFLHVLILAIAAWLTTLLLYYLGATPFISTNRRFGNNEMLLSFICVFMPTCFTLTAT

YSEDRAARMAYASKVRAERINTSLKLDLSVKQTGLENRNAMTRDEEEMLKQALWASGHKM

KLLQTVAIPFADLKLKELLAKTHNGEVLVGEYYQTNVIVKRLAQSCLTADGLATFKRQIE

LLACLRHPNIVLFIGATFDNLSNVGLVMEYLERGDVLSLLRSSIALTWSDPLLKIATDVA

QGVSYLHNCDPPLVHRDLKSSNLLCTPTYSCKVSDFGESKQQLPPGNLFSTIVGTPYWLA

PEILREERYDTQVDCYSFGVILVELETRREPYHDVLKEFSTIDIMMGVS

>contig58812 Frame-2R|Blast-catalase [Phytophthora infestans T30-4](gb|EEY62821.1|) 4e-28

MLQGRLFSYQDTQRYRLGVHYNQLPVNRPLFEPQTYQRDGLM

>contig58885 Frame-2F

MEFVEALPCGHSFHAQCINKWLAYRRVCPVDRQPVG

>contig03101 Frame-1F

MINDLRQNILSTKKLPMTSPTPLGMGIGATAGAAAGAAVTTNKNSPHLHSVASSLSSCLD

GMLPDNLRNDSAAFQQHFAHQKTRLQTEKNFWRFGLNYLFETLKQHKDWYGRNQQFVQLR

KDFKRSESHVATIKNFVAESVSELDLEAGLRGAELEGRVGAYKVMFEVTKIVSKLSRPLV

KLQILKPNESSLSVYCDTFVLDIVLSGGEGSLESASLTTVEKG

>contig06779 Frame-1F

MRWGLKPLLLRNAVSLLATSRLGSRSSARRESTSRFFRRDGLVSYHVSWTRYNY

>contig08698 Frame-0F

MFDWRYVYTTAQILLPLLSVCFDLISFRVKSAVFAFFFRSSPTTRKGNCVCLSARRRLWD

TYSGMLSMLVLALDVRVPGIKTLYETMYLHRGREADDSRTTVVFPVDMEMNTMPVRQYPL

>contig10484 Frame-2R

MLIENNSELTDSRQHGSTIKSSVYKMFEDKVLRQESTAESVPRKPEAKAIFGMKNTYRSL

TLLPTARKVRKQFEAKVVMAESFPVQPYDFIPVIEFLSTTGEHMKNLDEFFRMKLPPGFP

VKFELPMMFTVRVAYTFQKIVLNPLLDPEMFEIPNDYHEVFTLDEVRS

>contig12532 Frame-2F

MGLLSTYRYIFYLAGITVRSVVVKSLPINSHNLRPFIHCQHKC

>contig13593 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65535.1|) 5e-94

MHRAQKYPHDLVEDLENGQIIDASLHEQGQQPMRQALDEELLWMLLLAAVSECVTTCFVP

GYSLLSSGLNVSGTALNWIGPFLDGATYGYEDQLHGAEMPLVCVHFRSAFLGVFTSFSFM

VDHAGDLSGISFGAGPIYICISTLGGCCFFYLGYQVAFAKWIKPLAGYASKALHKIVHKV

SLLKSLVTFVGVTTLRAALGSHGFVRDPKDPQFIGRLPVADGEELLLGIFMSCSAVLLSN

YVSTFFPREPPQLRNAASPGGGPFIDWGCLCCNLLASFLAGLAYQLSRILSSDMTKTLLA

MKFVSSFCGSLSGFS

>contig14488 Frame-1R

MQQERESAELCLNGCGFFGAPGSGGMCSVCWKKTMSDRQAVVASPRATERKVEVAAVLET

VAPTAADVIDNSMAAVKEEAVEQAPLEKLVQKNKKRCWECKKKVGLTAIECRCSHVFCNS

HRFEDQHNCTFDFKTADRVELARRNPGGGEFSKLDKL

>contig15308 Frame-1R

MIRMLLLAVALPVATVNGAIVNHLAKRTFDLTKHVVREYTEYHFSDASAEVKTYDVAFPR

ALETHLAHVSARCGKSSCEIVAAAKEHAGIATTPEDTALYTVQLKNTVSKGEKGIVKITA

YYTRVLTPYPAEISQKEDQLVLFETSHLIKSPFVTKTQTTKLKLPSGKVESIRAADPILR

KGSVVTLGPYTNVESFATASGLSVHYKNHVPFMTVTKLTREIEVSMWGRVSFEEVYDMQH

TGAKLKGGFSRLDYVQLQQHGASFHEMHAHLPKNSVNVYYRDQIGNISTSRLRPASPSGS

YQDLEFKPRFPLFGGWKSQWYLGYSVPLYSVLTHSGNKFKLEADFSTPVQGASVDDLTVK

IVLPEGATNVQVNVPFSLDSLSETTRQTYLDTPAIGRHVVILEKKNVVAAHNVPFEVTFD

FPAYYMMHEPLLLVSAFLAVFVICMLLSRLDISIVHKSVNKKKT

>contig17184 Frame-0F

MMATLSSSMGLVGDPTRNKGVEEDGDYEELIPPENFAMIEKGLYR

>contig18383 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY67981.1|) 2e-30

MLCGFPPFSEDENGLESVYLKIRSGALDFPHPYWTNVSDG

>contig19032 Frame-2R|Blast-ubiquitin activating enzyme, E1 family, putative [Phytophthora infestans T30-4](gb|EEY69455.1|) 0.0

MSSHVVTAGDVRETADGVQNLVHVTDSTMEVDQISTASIDEGLYSRQLYVMGHEAQLRMG

ASNVLVVGLNGLGVEIAKNVILAGVKAVTLHDDTPANMLDLASQFYLAEADIGKPRAAAS

VKKLAELNPYVPVRCHSGEITEDFLLDFRVVVVVNMPLKDAKRLNAICRKNSIAFISAEA

RGVFGAVFCDFGNEFVVSDVDGVEPVACLVSSISNFAPPLVTVSDEMRHNLASGDLVSFR

EVTGFPFLNDSEPRKVMVTGPFTFTFEITYDAENKLFEQGLPSTGGYVTKVKQPIVTKFK

SLEDALAAPGEFFVNDFSKLGRSELLHVAFQALDAFQEKHHGGYPKPGCMEEASEVFTLA

SDINRKAAFKNEFFVENFDTDDSKTIIQALAAGSTGVIAPMAAFLGGIVGQEVLKACSGK

FTPIQQFFYFDAVECLPDALRNENSGEFAPTGSRYDGQIVVFGRELQNKIEKLSMFLVGA

GAIGCEMLKNWAMMGVASNKSGAIYITDMDTIEKSNLNRQFLFRSEDVQQAKSSVAARAI

KEMNPDINVQAYVSRVGAESESKFNDDFFESLSGVCTALDNVEARLYMDQRCLFYGLPMF

ESGTLGTKGNTQIVVPHKTENYGASRDPPEKSIPICTLKNFPNAIEHTLQWARDWFEGEF

FQAPLDVQRYLSGPELLNELNEQQNTRAETLSRLKSSLLDDRPLSYNDCISWARFKFEEL

FSNQIKQLLYNFPLDQLTTLGTPFWSGPKRPPTPLIFDVKDPLHMDFIVSVANSRAKIYG

LEGHSNRDAFAKVLSEIPVPEFSPRKGIKIAASDAELKEGSDASRSDGGESQYHSILQEL

PQPASLAGFCMYTIEFDKDDDSHMEVVVSVSNLRARSYRIPEEDMHKSRLIAGKIIPAIA

TTTALVTGLVCFEFMKVFQDKPVNHYKNGFVNLALPLITFAEPVKPKFTKTMLKGKEYKW

TAWDRLEVDRGDMTLKDFLAWFKEEYDAEVSMLSYGVTILYAMYSAKSRSKERMAMKISD

LVRTVTKKSIDKNLKYLILEVCAMDSEGEDVELPYVRYHYTQ

>contig23464 Frame-2F

MRLTCFVLTTSTLTFVAAAVPCSEQSLHQGATMLLNAHTDAELGGVGAGKRGDVGFQYLK

PAEALLAAQALAHDDFDLAAAQVFRILEYQKPDGLLPHLVYGPSVSSELRWIPSNRTFFP

GPAFWQQSSIEQRRKVHSASEFETSTISAPPVAADVVWEIFQLAPYDSMVGGKATAVQFL

CHVYEPLRKLQKHLFSTRNGTAPDSLLLTRHPWETFSSLSPHWIAFLADLKTAPDYDTIV

SSIPEEASARFAEGASAIYSAKDAVRNLYEPMIYLASQARHDEALFESISSAKSGIEAAP

FGVKDVEFNALVLRSSRGLENIGRVLIEHSFACKKFALTPKEVLNDIKESHVLIQKLEGA

LIGNNNTQGLWNTSADFFADSSRVSWTSLHSLREFLPAYAVELDSIKKCV

>contig24159 Frame-2R

MKPHRMKLAHHLVVNYDLYRKMDIFEPHIASAEEIKTFHAPDYIDFLQRISPTNQKDLAS

ELQKYNLGELTDCPVFDGIFDFCQIYSGGTLDAVSRLNHGQCDIAINWAGGLHHAKKSEG

SGFCYVNDIVLGILELLKYHPRVLYIDIDVHHGDGVEEAFYVTDRVMTVSFHKYGDFFPG

TGDIKDIGTKNGKYYAVNFPLLSGMNDASYESVFKPVIQKVMERFALRLSCFSVVQTR

>contig24630 Frame-2F|Blast-hypothetical protein PITG\_16925 [Phytophthora infestans T30-4](gb|EEY65282.1|) 4e-15

MAITCGDIPRLICSIIIPPVGVFFQVGCTKDLAINCLLTLL

>contig24829 Frame-1F

MPLEVLASEKLDTSLSAFTNAPQAFEALLNAPRRAELSRQRPFVAFEHQTIELCPAFRTT

PEPIVLLSPRHDASVSSILRHRSASTSLLTSEEVPSAVASKKKKKVSFLQKAPRNELETS

VKKPCECQGVKRTDTIKTMPSPIHAICRRAERQALKHLLSFYFGADLLKLVNSICACGRS

PLEVACEVGDLYIVKMLLKRHADPNSGSFT

>contig27961 Frame-0R

MHWYVLRAYYSKYLVSWMTLADIPVNVNALRCIT

>contig28274 Frame-1F|Blast-succinyl CoA transferase, putative [Phytophthora infestans T30-4](gb|EEY59065.1|) 0.0

MVSSYVGENALFERLYLSGELEVELTPQGTLAERIRAGGSGIPAFYTPTAYGTIIQEGGF

AIKLKPDGSIDIPSASREVRAFHGRQYVMEEGITGDFALVKAWKGDTDGNLVFRGTARNF

NMDAAKAGRITIAEVEELVPPGQIYPDQVHVPGIYVQRIFKAKTNEKRIERLTLATTTNS

PYQLSRDRERIIRRAAKELQDGMYVNLGIGLPTLASNYIPSGVKVVLQSENGLLGMGPYP

MEGDQDPDLINAGKETVTYLPGSSTFSSSESFAMIRGGHVHLTILGALQVAENGDLANWI

IPGKMVKGMGGAMDLVGSGNRVVVTMEHNTKNGAMKILQNCSLPLTGKSVVNTIITELGV

FDVLPGKGLELVEIASTTTLEKIYAR

>contig29277 Frame-0F

MSRKGDMDDAIDFNVSYQFAQLRDGDNH

>contig31012 Frame-0F|Blast-T-complex protein 1 subunit delta [Phytophthora infestans T30-4](gb|EEY58178.1|) 3e-48

MAIPATIARPMGETLRGKQKEKDVRMSNIIAAKAIANAIRTSLGPRGMDKMIQQGSGEVI

ISNDGATILSQMQVYHPTAKMLVDLSKSQDIEAGDGTTSVCII

>contig35377 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58092.1|) 2e-26

MVQCIICEDWLHEEHIFENLDQNVECSP

>contig37230 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53566.1|) 8e-12

MSVFLLKESRPTDSLICRMGRNRKGRQCGGYSSKKERFVLLNHWQQEVAKVSHKNAQ

>contig37559 Frame-1F

MLLRTRMSRRSTRAKTRRCLDGRERDWNQKNLPSQCLVTPSFARSDS

>contig38381 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY60753.1|) 0.0

MMAVENKSTRASPANLAYGSEIITPEIHSTMLKPENIDTRPRVQPTYILYTSAMLAFVLP

LQYGWSTSQLNLRKFNNFEDCNAWPVAEGTCIMFPGHTKFQWTVVVNAWIVGGMFGSFFV

GKLADRFGRKQVLIYNCFFVIVGAIVMAAVSNLWLFAFGRFLAGIASGATTGNVGSYINE

ISPPHLRSLLGAGLHSSNTIGIVLVATTFFYMDFENGWRYIAAFPIVLAAIFLSMSPFIM

VESPVWLLMKGRRNDAEAALTRLYGAENVSTALEWIESKRKVDLELQSSTWSENGNEVVR

SGKGAPFSELISPVLRRQFIIVIGVACMQKITGINTVFYYSSDLFHQAGLDNVLFNTIII

DIVNMLPALVSGVLAARFGNRTMLLWGLAGMFFSAVGITLALWFSWSTMTILIVASYVTA

YGLSIGPLMYVVLSDIFPDYARATVSSIGVMVSWLSNLIVGVGYPYISSALGNLAYLPFT

VLLALSFVFVYMLLPETSGKTNEEIQDEFRAIRQRKRRGAK

>contig38415 Frame-0F

MEEEMKSDVAPTSVSCEEKRFEIKKWNAVALWSWDIVVDNCAICRNHIMDLCIECQANQA

SATSEECTVAWGVC

>contig38947 Frame-2F|Blast-60S ribosomal protein L27 [Phytophthora infestans T30-4](gb|EEY65720.1|) 3e-71

MSKAKLKKRTKVKPFVKYVNYNHIMPTRYVADIDLKKVLDDEVLANPESRIESRKTIKKV

FEERYLNQAACKSEKKAAGVSFFFKKLRF

>contig39706 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY54351.1|) 1e-145

MRIAYSSLYFTRVLSKGAFGEVWLAQLENRQVAVKRILNEKKNDEKEIECFGAEIKLMAS

FSHPKIVEFLGVSWSSMQDVCAVTEYMGKGDLYGFLKRRQGQLNWRDHKIFLAEDVADAL

GYLHGLSPKVIHRDLKSKNILLDDSFRAKLSDFGISRERSVEDTMTAGVGTIYWTAPEVL

MGKKYTEKADIYSFGIVMSELESHAVPYSDKRDNAGKKLQGMKIVQMVIRRNLRPTFSPE

CPSLVKELADRCLDSDPDVR

>contig41121 Frame-0R

MESYSSRIPRSKPVVAYLAKHYRMESSSVKTASLYPHSSSDGNSKTMLDITGTFFTFHTM

RFILILEKYE

>contig42230 Frame-0F|Blast-hypothetical protein PITG\_19106 [Phytophthora infestans T30-4](gb|EEY68731.1|) 3e-07

MICSSALKLQFSKFLDQELFLAYIDDWSAKRDT

>contig42245 Frame-1R|Blast-RNA pseudouridine synthase, putative [Phytophthora infestans T30-4](gb|EEY67704.1|) 6e-75 NOT\_ORF

MGLTQHMMPVVR\*RQFSERSLIK\*CLMLAQGRLDYNTEGLLLLTNNGDYARELEHPKTGV

TRVYRAFVRGNVTESKLQELKRGPLIEGVKYRPMKVTVQSTDKKDSWLRVQVAEGKNREV

RKALAHVRLIVKQLIRVQYGPYRLADLPAGAVLAVRAKSLDKPQARTSDDE

>contig43224 Frame-2R

MSRIPLLLSNLFLRASSDYIICSNSLQTLLNVSLPARSCHTQY

>contig44294 Frame-1F|Blast-delta-1-pyrroline-5-carboxylate synthetase, putative [Phytophthora infestans T30-4](gb|EEY64385.1|) 1e-145

MVSYSNEPEKRDGGRNLRRARTILIKIGTEIVQSPEGLLAMGQIGNIVEQIAVLHMRGHS

IILVSSGSVPIGKMVLHRQFLLSGSMQSHLGGQVDKNAQFYEKACAAAGQSGLQSLYEML

FSQYHLACSQVLASDADFREPQVRVNLKRAMRSLLDVGIIPVINENDVITHRTTPLIVED

KIAWDNDSLAALFAQEMIVDLMVLLTDVDGIYTGSKDNRKLITRFHRGDKQVIARESRVG

AIGQKDKLYSCIRAVNSGAVHAAVVAKAEQGVLLRIVNGERVGTLFVSDGEPIGDAKMEH

QYIDPLYSSIAPQVGNAASKL

>contig44786 Frame-2R

MRYAGCERSTEAVNGDRGSELAKKLGLRIGSIADEEITEFVLRLVIRCLGDSEQVFNALK

SELNFSQAYTAYSELKKLYESRQQAKVRLDWVTTLCHDGLNAQNSNISGFVKLLDKSNLL

KGNCTLSWRLLSPTWSLKSSIIDSLEGDTAVSSTSLGLRSTELYNELVDVFSSSFCRVCY

LYNCHEHGGDHPQPARRVDPNYPQLELMARHATTIRSSLEVALSTDDV

>contig45657 Frame-2R

MNLLMGLRRFLGLGLLSAVLRFFTGVSSSSSSSSSGMSSSDASSSSERLRSSSSSLDDIV

ASRFRPLQCAPSNVNINSQLMD

>contig46810 Frame-2F

MNLSSLCIEKMEAKENSAETHCLAAGQGYCFLGRCRSCCCSYRHHFRIESAI

>contig46865 Frame-2F

MDLLTNSLPSDPTSTDANSSPSQKPLLPSGPLNPVTEPKPGP

>contig47039 Frame-1R

MISEAAHSECVRLLDLLTNSRVQESWSWVFMMPVNIPGYDKVIKKPMDLGTIKKNLGIKP

SRCRFKSHEKFARDVRLVFQNALLYNKDDQDVKGSVYAAAQHLRRVFETAYAKAIENVFR

ADDAAKAAHREAKEEKRKAECGDATRVDGEGAVISNLSPSHNHQSSSSSHHSSHRHRSRS

DGEDGRKQKHKHSKKEKKSKKSKQKSRDRDREHRHGSSSTGERKKKYHQSELDRSIASSL

NDKAMSVSILKAPVPPPSLPSSSALMLQQEV

>contig48005 Frame-0R

MLSSLHDNLPLRDIINFNVDTLLRQIDGYLADSVVKKRRKKMNKHKHRKRKKALRMRTKK

N

>contig48438 Frame-2F

MDYSLENESDTHDQTLHSTLMLTEDGSSLTEQIIPDYFTSDGLRTRTLDSCNDEPVLAGS

GGEEQKCMSKGKPQEVEDVDVLSNAPVNHSLAPIAQSGLTRNILEGISACTWEMALSVLL

VILAIVYFMWFNI

>contig49367 Frame-1R

MASYLQELIDQTISVITNDGRNIIVQRMDSSNAVACSDIYCAYDCLM

>contig49437 Frame-2F

MASWISSASVPSGATSGREMSFTSMVESAAAANEWAQDIKVAPEGRGVWSPDEHRLFVEG

IKIFPSGPWKDIASHVGTRTARQTMTHAQKYRQKIARRLRNLRKDGNHRLPFLMNQSSRF

DALQSSEELFNDSILATSMAIAAEEELDLLDETSEGSASPSITNNANSYQKHLPLAIDFS

STEANPYHLDGPPFEPSDIEFDKCIDFLIETFHRET

>contig51678 Frame-0R

MTKEASLNLGHQPGLLRSLGDLQQLQTTAIYIAGDCSSLVRRRLRRQPPRASTLAASFWF

TRVIPDTVLIRIWTVVPGRGNIAVRSFPRRAAGRDTQQEWSFDKGSKTVA

>contig51847 Frame-1F

MVEARLNDRGRIASIFSRAAALERLVEHRILHARRHHLVKARRQTIGNVLILVRLSHLRG

VGCQNASRCPIADTLEDRIVSREDLIRSNTSTSGISCDELIKVRERVVEDQNRCRAETIY

SQIYLSSRASTSRCVSLQHCPLS

>contig52006 Frame-0R

MRCHVSCIAELSVVRNSFGHQDIHCRTIAYDYVTRVILESCFVMCLVIYELQNL

>contig52385 Frame-2R

MQHRQKGFHFSFCSERQHTTVKTQRSIMTNVATLIRKLFRKDSSEVIGHSGVRGMQLRLR

KAVAMGKFRQVAKLLDLGASPVWIEDETHLQRHRYAGPCRLNALLLACQRGDEEVLSLML

DVLLAEPQVLAHFSSAMYCLVIRHNHWKAFQQLQQRGVPMAAPSLKSSSDIRDSISSTQL

V

>contig52868 Frame-1R

MLIFCNWCALWPQIYMGNLHVCLSSCNLWCFLVVKRK

>contig52976 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64511.1|) 5e-69

MDMTTYEKLSACGEFRVLGNLFFQHGQYQRAAYHYNKALVYFEYMFPDTDAEEAQADALK

LKLLLNFTACRLKTMHLDDAIRHATQALEIDQESVKTLYRRAQAYRLKDEFELAQNDIDH

AIKLSTSTGTTQSVHATLLQELKLLQAKKLAYKLRTKQLSASMFGTADKARNPEKK

>contig53096 Frame-0F

MCKLRCAAVRLTAVRRSRDVARLCSASPIRTRWPWSSAKR

>contig53333 Frame-1R

MCFARKLSVINVLLLDMHAVKQSLRHLGLLYILSISKFIVGYNPEKLLV

>contig54596 Frame-1F|Blast-DNA mismatch repair protein, putative [Phytophthora infestans T30-4](gb|EEY60963.1|) 7e-24

MTTPAPRIQRLSTEVINRIAAGEVVHRPANAVKELLENALDAGATHVTVTVSQGGLTLLQ

VQDNGRGI

>contig54633 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67179.1|) 8e-38

MQAGELLSPQDTQVLFESIEPPLVNPVFVYTDIQQSSDLWGVGDGLIMQKATEIHDNILR

SLLMKYRGYE

>contig56037 Frame-1R

MRDACGIFHVNFFERSDDLTWCDKHFV

>contig57269 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY70002.1|) 1e-14

MKEVHVVERLRQRVLLEMFNLDPVAAPKPSQATWPRWTEEDTETVQLRVLSLNA

>contig57470 Frame-0R|Blast-geranylgeranyl pyrophosphate synthetase [Phytophthora infestans T30-4](gb|EEY59925.1|) 2e-60

MQAFSNCSLDFTPLVNALAVYFQIRDDYVNLLDEVYMENKSFCEDLTEGKFSFPLIVAIR

ENPQDSRLLSILKQRTKSASMKQYAVQYLRETGAVKLTLEKLKPYRTRNS

>contig57856 Frame-0R

MTSTPARKRSRTRPRDSLDNEDEDRVLDAMLMELGIPRQRPIHPSPRRSPFEIIELLTPS

PPAKKTKEPRDDGAAVVDLTTPPSVPHLPPSTSNHYIQTAQKAP

>contig58152-0 Frame-1F0

MSTFKLKMGFFNVRHVEASEATSMLRVSFPR

>contig58152-1 Frame-1R1

MDVASEASTWRTLKNPIFSLNVDISSFRRSRITKTQRLRF

>contig58813 Frame-0F|Blast-catalase [Phytophthora infestans T30-4](gb|EEY62821.1|) 1e-18

MAGRERLTDNIASSLVNASEPVQTRAIENLKV

>contig58884-0 Frame-0F0

MRDWHSRHNRATVCVHLKWLTSRHRVATGHVHGLRRLLRVHLRYNNWK

>contig58884-2 Frame-1R2

MDPKKPPKTVDVPGCYPMATGQPFQVDAYGRPIVTAMPVSHGNV

>contig03740 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64005.1|) 1e-128

MANRPSLEMNEFNFVTKEWAVVAADGVAPCQRRSHSAVVYKDSLFVFGGYDGDRRLNDFY

SYNFLTQTWTNVFVNAGHQPTSRYGHAAVVYDNAMYVFGGSDSHYGRDSASSRNSSDYGR

SESGRHVNDMYSFNLETNTWSSLRVTGEVPYPREGASMVVYKESCLLYGGYDHDLGYLSD

VHVYHFETRVWTCLETKGQAPLGCHRPLVTLLNNSLVTFGGQTDPNLYMLDLETNTWDTV

AYAGLSPKSNSPAGCMNDNDLVILSEQNNVLGFQQLHLPEKEEQAMTREELDSDEDGSAV

AHLRSLVNNPLMSDVTFMVEGEPIYSHKSLCVRCHFFEAMLTREMKESTAREIEITDVSR

ATFLAFLEYIYTDRIAVAGADLEELFIAAD

>contig04688 Frame-2F

MEDFLLHRCVTSDVSKATNINSHATSSLWQTKGRAECIVVQENRQAHGASRIILEAMLKL

VLRST

>contig05492 Frame-2R

MQASIVTSTRVACTALRRPYKRQIDCVHMHRSVLSLIMRRKSSSAHEVARTWTTANSDST

DEFEPRIEYVKTRRLAEADWSIRAKNMIPRSTVEKPYELAPLTLGLDDLLGNTVKLCKSS

RSYMSDEDVEKWLETFEIPTEQLAKCSTSEEVQEMRRRYARQLRLECSVYEMAMDKYSAS

QEKVRQIGRTTETNAAKDLIRKWIPETEKYVKVEQQKIKNGKHSTDSNIYGPALMLLDHA

VLAATGMNIMLNMCLMESKGPKFIKLALAMGKAVQEEIISKKEESTKRYNGDEEKFFLQV

SQKIKLESLKVRMKNYIDTVGGWDKRLQLKVGAAVVDCIQRTCYVPNAFGEVSTPELCAA

RGLPAPEPAFLHNYVFDRNRRAGVIQIHQRIADTVLATNPDANVLPWTARYLPMLVPPRP

WVDVVNGGYLKLRTKIMRQRDSAWQMDCVQRGDMDGILKALNLMADVPWVINREVLDVVL

QIWENGGNFGDLPTRKDVPLPDPESPEFANDPTLYQKNVRKIEQLNREFHSLRCDTLYKL

QVAEEFKDEPELYFPYNMDFRGRVYPIPPNLNHLGSDLSRSLLIFKDRKPLGEHGLRWMK

IHLANVFGVDKCSFDERVEFANAHMDKVVASAKNPLGQDDCAWWKGADYPFLALGVCFEL

RRAIESPDPTKYLSNIPIHQDGSCNGLQHYAALGRDLCGGAQVNLVPAGRPSDVYMGVAT

QVMAKVEHDAAQDVPSPDEVRAMILNTPVNDSTESCAQRAKLRHLLDRAQRKKCAQFLQG

IITRKVVKQTVMTSVYGVTYIGARKQISARLHETFLTKGHIMDDKLEDAIYHASCYCAEL

TIGSMGDLFNSARGIMSWLARCAAKVGESGQPMSWITPLGLPVVQPYRSKATKQVRTKVQ

HVLMVDNEGQPVSIGRQKSAFPPNFVHSLDSTHMMLTARRCLEDDKISFAAVHDSYWTHA

CSVDTMNRRLREEFVNLYEQPLLEDLLTELHLRFPDMAFDDVPQLGDLDLRSVLDSLYFF

N

>contig12618 Frame-1R

MKSTWLALVLMLLEAHALAKETLNAFNEPTSDLSLLLKHRNECALLGFDVEALDCRLCDT

LASFLAPVAAKAQTNGAKAVQKVTQECHECCSDLSKVFEAEGRRFYKAVLAVNQYRLKRY

PKVANFLEHQAKQIKRLEVEEANLRLPMLLFYDKVGEKVEEISVAHWDENSILEFIERKL

LPDDEAEEAVVEVEVDATNL

>contig13271 Frame-2F

MDNSMDTPSSTEAQENAAHGNTDIKVIVMNYGKWKDAKALEDVLRKEGVSFVKVQKARHL

SFGFVHFHSTQERLEMLPKLHAIQWQGEFLEVKEALPKKSMQPIHRPPSPPQDDKSTLKT

PLNTTLSRNVCDVVTPWASIPYEHQLQLKETAMKKVLIKIVRHTRKEFHKKQKRVVQDHQ

NIARKKRKLHAKKALENNATMPLETSMNTTQSQLESTVTIPSWLASPGALYLVANNVLYS

RLHESEKPWTRVSDALNIIAITSWNSNLIAIKSTNELVALKQDTLQHFSWESIGHGPLDC

LPFSIVSIQGILVLCTTTGHLFKHTLSLPFDSNEWKCIGNVSQGARLGVHHRFLYACTNH

NWQRASIHETQLDSLVFEPVQVPVLQPVLGISSHNHTLLLLTPTTLEYVTQDKEPSITSI

PLQLPNMETLTFAGLTSHTNLCCTMDSIHASPVIQGYRNKCDFSFGYDEWNQPCLGFRLG

LFRHGSVIVSKPYDCIHVSIEMKAVCLEMQALVDSTKIPVYNVESKTGVWRVLTVRQSTK

TRELMLLIQVNFTGYTDKERAGMKTQVRECFTNSKTASFQVTSIYIQEYHGHSTPSDHDP

IEHVYGKFKLEEELLHKRFVISQRRFFKSIHAEPRRSTL

>contig13921 Frame-1F

MKQQNLHVLKETQLTDRSLKQGTKCKRCQTATPSFYEPGQFLCQRIYVVPTMKSPGVNIP

LTLIHRRNLKYNGQNPTLLIGYGAYGTNLEADFELEHLSLIERGWVIALAHVRGGGELGL

QWYHSGKKLQKCHSFEDYVSCTQHLFDIGVTNPKRLAGKGVSAGGLIMGYVANAYPQLYQ

ALIMKVPFVDILATMEDATLPLTIHEYDEWGDPREKQVREYIRSYAPCENVVDNQVYPAM

FVTGSINDQRVQFWEPAKWMYQMRKVQSLLPKRDKRLMMLKMTQDEGHFGGGGRLEQLEE

SAMEIAFLYQALKLPISHK

>contig16683 Frame-2F

MLRLIYLTTAIVLLLIQGACAQTRFLGALCGGNGPTNFYTDEGDYKKLTGVMFRSGKRID

RVGLFYDGSKEPKAFGGTGGVWRQLKFENGEYVKSLHLHSILYKGGYRISYIKFITNKER

VLEGGIKTDNITISTPEKNYRLAGLSGTHGNEVNSLQAVWYIR

>contig17110 Frame-0F|Blast-N-acetyltransferase 5 [Phytophthora infestans T30-4](gb|EEY66623.1|) 5e-72

MGYIMGKAEGQGTDWHGHVTAVTVAPEFRRLGLAKKLMEYLENVSVELYDGYFVDLFVRV

SNSLAIAMYEKFGYVVYRRVLGYYSSAEDKEDAFDMRKALPRDVQKKSIIPLSYCVTPDE

L

>contig18317 Frame-1R|Blast-mitochondrial inner membrane protease subunit 1, putative [Phytophthora infestans T30-4](gb|EEY53724.1|) 2e-59

MRAALRETSTVIAWLARFGGVSFCLTQLVDTIKCSGPSMLPTLNQNGDILLLDKFSPKLW

KLQPGEVVIAKSVSDPRRTVCKRIIADEGETVCVRTRLSSSEVEFHKIPKGHVWLEGDNK

HDSHDSRYYGPVPRALLEGRVLMRVSY

>contig19462 Frame-0F|Blast-transcription factor Dp-1 [Phytophthora infestans T30-4](gb|EEY54594.1|) 1e-117

MKVCQKVEEKHVTSYNEVADELVLEFVTMRPNDSVYDEKNIRRRVYDALNVLMAMDIISK

ERKEIRWKGLPSNLQHDTEMLMAERNERMKSVKQKKQHLQDLLVQQVAMKNLLKRNAERK

RKECEDSAGATIVRDEGRVFLPFIAVNTSKDTVIQCEMSEDRQDIFFNFSAPFEIHDDAD

ILQKLNLHKATYASLKHMVPGNLLSYLPAECELKSEE

>contig20376 Frame-1F

MPSISGDAAKPLDNLSHEKMQQLKEISERRGVLYIARVPPFMKPEKLRHLLGKYGTLNRI

YLVPEDKSLHKKRVTGGGNRRIQYTEGWIEFQDKKVAKRVAKMLNTTQIGGRKRDYYHDD

LWNLKYLKGFKWDHLTEKVAYENRIRDQKLRMEIAQAKKENEGYLERVEKSKVIERMEER

NSSKKREGEAIHSTLQRVHRTFYQKTPTSSKDLQSIGDEELEKVFRARSKNKKRRVA

>contig23337 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55359.1|) 1e-134

MPPTGRSIRNMMRGSSSSEGSGLSDENEIQMQGWMRKQKETLRSWARRYFTLNGKVLTYF

DSEDTSRGARGVLEFVDVAALTTEKNGLSLHLVNGKEVRLIADTHVAYAAWLAVLSAAVK

KPRTNKTPTSKEGWAHCLTDDDVWTRFFVVIKNDSFSCYESEDDDAELALSGLIRAVDDW

DGKRFGVVCSLNRSRTIKLCFDSAEEKMSWFLTLEFSVSYGAARMKKETSVKNNISDHNP

VVRAESSKSDDGAAAAEDDDGVWI

>contig23838 Frame-2R

MTKDYRDFFTGAIINLNDPMCVEDDDNSIRQSPQELGRIYHKKMT

>contig25124 Frame-2F

MFTLAGTAFHSTKIPEIRSESCYLMGRGCHAQGRYKDAYSYYFNAGRLWPKFVLPWFGLA

QMYYERKELTKAASYLEKANKAYPENVEILSLLADVYGKLGKKEGAVGLLRRVVELEPGN

VEALIGTAELLHASPERKDRIIAISSYIAAEKVMNNASERVPMEVYVNLGVLQQRVGKTA

DAIKCFKKALRQIIDENSSTEESKSKEGDASEDLDVKPTAEKVTILYNMGRVYEEMGDRE

QAKTLYNTILEAFPNYTDCLLRLGCMLRDRGQDSEAIKMFDKVLEVNPTCAEASLLQGNI

HLKKREWVFAQKKYEKVMGMPGLKNDPYAFLSMGNIFMSNLGEKNRYTKNMSLSEVYYKK

TLASHPRNIYAANGLGIMIAEKGNFELAKQIFSQVREASPDMPDAWINLAHIFVAEERYQ

EAIQLYTVSLTKCYQGQDLEVLLYLAKAFYESKIFTKCIATLSCGLHMYPNDMRLWYNTG

LAQEDYAVLTLGQETTIARSAGGNNVPQHRTMADVQRAISDLKRAQRIFRFLLQQAEAVN

TSGFNEKKKHHNNLPFDKEKVSDHEKFCGDTLTKASYHLEFERQKEEKRRLEIEAQRMLL

REYEERVAREQEEVRVQEEDLRKRHEGIRLKQDERLKKLHEGWSVREREEEEKKVVKKKS

GKKRKKTEDQDGGFIDDGEDELEEDGDNTMSIEDMKNRNATMKRLVEKRNKRARGGSDLE

NGKEDSTGLFGSDSSDDEQASAIANDG

>contig26068 Frame-1F

MEEKSGLDQLFSDELEPICDLPPCDIDHLDEILLCLTSSYPNIRSMVQLKLADKDGAYIV

RLLDLFDVSELDADKSILHKLFKVFYAMLELCNRRLIEILLNEANFISVVGVFGYNPGLI

REMDFRTVLEGDGGFREVIPITDQNVVERVHMNFRIQVIKDNVLSRLLPDGCVLLLEYMM

NENNFHILSFISETEIYWKAIKKLVSNEAKRLEGLGLLKAIINMVRVTKPLDRPHSRDAF

AVQPLFSALVDNLFGDGELYAAFAAVLGLSDSNSGEAAIVMDILTVLVVYQSPEKLRSYL

ATEGKCIPAPASDKDRITWTVESSLFTALLVVFERDETLRIQVVNLLREIFSVPLGQDDK

FLSVLYPNYMHWLLQPLKTHAFIRDASAMFNLQDSIMELLTFCTENHGYRVKYLFGRQPV

ATYAAKMLRSHNKLFVIHGVKFIRACAVRAEAFFSRFLIQNDLFTPMLANLEIGKPNNGA

LCSAIFEVLSLIEKTNLTSLIEHVFTKFYEIYKEECSLVFEAIRARYDGKSGLEDAAMTR

APKPQLVRSSSFDAEEELYFESDSDVAESSPGFAKNCLSEEEVSCQNRPRSVKLVDYDDD

ELAVGEKLDIPIDLVAMKATRYTENEEEREFKLPVRAKVDEADTNLFLGGSSLISQKKSS

ALQ

>contig27179 Frame-0F|Blast-peptidylprolyl isomerase [Phytophthora infestans T30-4](gb|EEY68840.1|) 1e-125

MVHKESAIINDYAAESLIESNNIETLQTSSFIVKKGNAAANEDRDSGKLQLSHSTSGKCS

SSFTSSVIAPVTENAITLASEQELLQRRWQTVRKLKKKGLVQLETTFGKINLEVDCDFVP

QTADNFLSLCQRKYYDGVLFHRVIRGFMMQGGDPTGTGRGGESIYKKPFRDEIDDRLTHN

SRGVLSMANSGPGTNKSQFLSLSMHARIWTKNTRFLAGLLEEWTY

>contig27889 Frame-1F|Blast-Mitochondrial Protein Translocase (MPT) Family [Phytophthora infestans T30-4](gb|EEY60531.1|) 1e-169

MLGEPLNRSPVNTGSLVLFIRPILVCLICLTVIMGSAPSKNECASSKIYSVLATSVTPDE

DLPVYMQQVEQIEKDQSKLPNPGLYENAPNELKGPVSPDVFDGFRFDFTRILGQSCSTSH

SFLLGTPMIPGGLYQFGANVVMGNPMDPPTFLMSKITPDGYLDARWNQKLSNNWKMRAKA

QLKNEEHGSQALADFDYTGDDFTWNMKISNGPLFGVSYLQSVMPNLALGVEAYYHGKHRK

VISAYAGKWTDRDWVGMATYGAMGTLQLAYLRKVGHRIRYGSELVYNHASGEAQTTCGVE

MDLGQTRFVSSVDSTYRVATSIESRVLPNFVLSLSAEGFPLKDDFKFGYGAQLSF

>contig28277 Frame-1R

MSGRDKAMYKNFNLIKNKCCPVKRTIYLVAMSSSHYARMCEGRLKISYNFYVTATNL

>contig29274 Frame-0R

MKLPIKKFRVKKIIANRLQDCFVYSSFQLLRIQ

>contig30654 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65225.1|) 3e-11 NOT\_ORF

MAVVQAIVGTTLEGPDKSLELSTASLKRGIKQTGFIHLEDQLTHYHRVNALQYVYRGWTA

MTRG\*SLSHFR\*FLANYTSSPSERDALVTNDTWGEERHIRHSGHLLAT\*HLCRPKNRATP

SGLAL\*EDWPNGATSERKAGGNSSGTPHAAIADLVNEPGDKSKIIDQAKHPIVLRFLGNQ

FSYFVHHARQNVSSTTPELIITAQRSAAHIGRTAKNQRNNASHTGRDGAAKWRRIPQVIK

>contig31200 Frame-1F

MEHGSVRELLRASATDADAVRQYLQLIESDELNGLLDGITPRDCSNKGKKKLDFVVQEEW

LPLVHLLVHCETTRLRAASRIIQVLRQGSPSELESMQLLTEINLGYSKALDELHEIKHLK

VQHLVKRRKLLEEIHVVLEIVSSFLEEVVRDAKPSTSKVLPQLLGLVPYFIGMSGELSDE

IRISDKLAKLLELPWSCQTVPRLLDVLVENSALMSREGWQMLQENVERMVTTSPEIAGET

MNSVIRECILVANVTNEYKWIDIARYLLTQLPVHLRQEAEFNLQMSFNQTPRIVTLVCQS

IRCSKEFESSKVDRVEASSGVKDIEGGTLYLKADWRDLYLLLHSLQASKPILHHRILSSR

VATEASVFAEIEELASWIVLREFKAFFHTAANDLLTKRGMETTKKHVFAQVELLLHFGGK

QTYSREWKALLLMDIVFFWIEQCNSTKDVDKVRTLNFPLLLLFMQAIFETAPETRSEMLS

SLFERSFTGNTKEDC

>contig31297 Frame-2F

MSAHSSDICGINVTELYLNDPGNNQEPAGYVLCSDMGNTCIKNTCSCRRAAHAEVDGSTK

YFGVCIILQQGKECVASGDEYLTCAVSSGTNMLNENSVATSNPSTNTKAITESNTKPLTS

ESSSPDDVMATEARTAASSATLSTTITVVIIVVAVVFVALLSWVVRSFCKRRSSKDSKFA

SRRNRNGPNTSADATSPTYITGTSSTTPPFPAFDRRAREIQSPTSKSRGGRGGRGAPSVH

DSSSGRDRRNQDIDAYLAQGGSRDVTRDSRNQRNPEIDAPFLPLGPRREPTSGRGRRNPE

TDSSVTPLGRREPTSGQGRQNSGYDADGFRSFKEPALQREPTSGRGQADAMRSQPRDQRN

KQNQPSRPVEKIATEPSGGTVYTGRNTYDRVAQFAQLAAFEAPPPLPPRPQKPIQPVPMA

NLVSKNTRAPQPARPARTVPKCSAFHVPDNPSPTYHDILSPKTARSLAPSIASQATTVVA

AGRNRPTPLQQNRRPPYTNAPSSYYQPGLTHQNNTNAESHGLSLNDSNYDESDYGNSRYN

ESNYRGKYKGQTNYDDSFVSEVSSMAWSEASGLSEDSYYRAVPTSTAR

>contig33682 Frame-1F

MSLLIFGSSKFCQSRKDVAVITAVHKAYTHSRLVIYKNCSKPEAHSTTRSSTFDNV

>contig34049 Frame-1R

MSDLTLIDLPGTMDKRILPQVRQLVDQYVKQEQTMIIADVPANNNNAQSRDYTSSARGMS

QRVAVVTKLDLLDAEKASLELLLIKNKKMFLGYHAVNGRKQRELTTGTHLWGIPT

>contig34939 Frame-2R|Blast-DNA repair protein RAD51 [Phytophthora infestans T30-4](gb|EEY63552.1|) 2e-32

MTANPDSGMFAKDPLQPIGGNIMAHASCTRLRLRKGRGENRVMKVVDSPILPESEAIYSI

TEQGIQDELN

>contig36227 Frame-0F

MKHYQKMINPDDVSCIYIFYFQSLCAIPHPCYLFRVRSVPLLSCQTWGKASWIAIMSDWF

SKFFGISRSCNPLCILHLAYANHCILFKLLD

>contig38416 Frame-2F

MGKAYTPPQWTGKSIRKLSLHRRRVNLWNWGYGLEHLPFLCLYAFALYHCFLTIGEPYAQ

AMREREEIGLDTNAIFSSGAEDGGLAASMLARGSVREVPSTMPVLQPSMVNQDTSADGPP

LPNPFLPGIVPLLYLLATLMAHGLMVLFQIWSVQFRAFIKYTPVSTLDAATCIMVVPRSF

KGSSCIVEIVRPPHGKPYFVFQKHKYVAEDDDNNKSSIVFQN

>contig38463 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59121.1|) 6e-31

MFKKLEIPVLCGLLGAPCAMIVSKSIATPSLFAMHPASNAFAYLICFPVGIFVMQERKSV

TTFQTRELMLKIHMSFLILGMLLLSAGGAAAFMTKNAYGKDHFTSTHSWLAGATAVLCTL

NMVVGLTFTFGGKKTSWQWKNAGHRIGGLLAFFGGGCSVMLGIYSGSWGDLHLGEKVQRK

MATSVAAAYLLLFLKLMSSKFSSISVHKSK

>contig39705 Frame-1R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60837.1|) 1e-21

MWVAKRIKGSVICRSIEYFQPLSCRCVVYFSSSSAFLPMSGMLVGSFSVEQKKRLTIDVE

VVANPSILFIVELMSGLDGGSALNFMHGVQSIVCTGQPCCLQSISRVILSLNSLTGMHGV

L

>contig41122 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61881.1|) 2e-46

MKVGLHKDGTRDKEAIERAFAYVEWLVLLASKGDVSRNIPQLPMLQPSYALNTIITASQR

AGSVKEAQRAF

>contig41939 Frame-0F

MRLALFSTVFFGTLLASTKASQERFPCRPACAKGETCKLQKVLCVTTPCYPIATCVPNET

IKPACTKICSKNELCQIDSATSAQYCLNPCAFTLCGANTTCEIEQVQCIRAPCPSTVVCK

PIETDPSLC

>contig42233 Frame-0R

MWCLTLMVWITRDWKMFIKSHARHLSSRPSLSSSMSTNNSKFKLALCQIAVGDDKQKNIA

LATAAVTEAATNAAQVVSLPECWNSPYSTASFPQYAESIPETKANLNENDHPSTFALSQL

AAKFQIYLVGGSIPEKDTADKFYNTSVIFSPEGEILGKHRKVHLFDIDVPGKITFKESDT

LSPGDSVTLFDTPYCKIGVGICYDIRFPELSMLMKKHGAKVLLFPGAFNLTTGPAHWELL

QRARAVDNQLYVAATSPARGPEGGYQAWGHSSVISPWGEVVATCGHGESIVYGEVNLEKV

EEMRNNIPTSNQTRSDLYELVHKQSA

>contig42246 Frame-0F

MQSTLLRFDQYVASADAAKQKRVQKALDVLRSAIDIFGLDGVCLSFNGGKDSTVLLHLLR

IVLAKRVLEEAQPMHSKKNLASPRTPLVDLLPDDELETRVQAQLQDIPVMYFDSYDQFLE

VRAFTEKCTKMYALNCHVYKCSFVEGV

>contig44011 Frame-1F

MQSDRGVAVAANECTPPEYSTLSSNCYGVCSSSLCVNYASSNTKDMNKDSSEANFFSQGC

STSNIPSCKLNVTSGDCQLQCLVTSWKSPQWTLTIAQPQSDKTDTALFRKIDELALPPTL

QNLTIVGATSSSQIIVPISFAPDALRSGTALQQVVISDVNVGDLKTNIFPDSLHTLIIQR

SKLTQFDPRGLRVFNLLSTL

>contig45654 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57206.1|) 3e-32

MEKEPAAQAHSCIMSQVKASNVESPTKVAGVVSTAEQIQALHMTTNDALLILSSDTGGAL

RVPVTGVGLDVGESCSTVESNSLLDQDVQVKSFDGEKKKLGRPSHPAWQYFIRGEKRNHF

HYNAYCSFCHGNGVKFMAVRGVSGNMIRHLQECKHCPADVVAQLKLVCARKDADNFSKRH

LMYTRG

>contig48006 Frame-0R

MRTTFFLTVVIAMFCACITAIETLEGPTTTGREPNIADATPTVVARALRGAVAFNEDRLD

LEGLTNSVATLFDGALHEINPELVRTAKALTP

>contig49434 Frame-0F|Blast-apoptosis-inducing factor 1, putative [Phytophthora infestans T30-4](gb|EEY59276.1|) 1e-13

MFMMWRSWIRSPFPAAALAAGISTLSLSSSNDPVPSPSDVPLEGPDALSPPGPPSAGGEK

LHLARRFTRRK

>contig51329 Frame-1R

MAISTTFSSGEILSSLARHSYVIPATGMPQSMPPRMNHMPISSAHVVNNAHQKRSPFLCG

YPSKKCWSWRVEKRNGELHKFCEYHRQKANTNQRRMEQRRKNGHAVPTRAKGSGGSRRSH

KVMGDVKQEVIIKADHSAAIPKSITHPKAVDISPTIDKSSSPRGIDCFGNNSAVIDDAAV

YSWMDAELDIGIGIDVAVDHLMIGTPVFDMEPSDKPVDLFEEDLYFLEHFINEISNSTV

>contig51516 Frame-1R

MLTNVDTLYSEALGLYDLDLVQSVATHSQRDPKEYVSFLDHVASLSSTLWRKYTIDVHLK

RYPQALDHIAALLEETKAHDEAKRSQLHQMALSLIQQGELYDQAMTRFFNTPRDTDRVFR

QTILRLKGEYLHVHKQYEAAG

>contig51844 Frame-0F

MSFCFLVHKPSLQFFCCLDCCLNFHLKLLLRPWLTAWCRVTLYFVTSQQQLGPLCILLVP

LKCTVARDTQLLLRFLRYKKWRSTYWWHRHLNCAINSHMLHSENRNIFRRMFSFFK

>contig52005 Frame-0F

MDSEDERDWEELKRLGGVAHCARKYPEAAEYYRQSIEALDSLLYYNLIHLSSAIRTDKAK

LHANRAASLLMLMQMTEAMHECRRSIEVDETYACAYLRLGRIQVLLGDTAHAQSNLKTAR

HLMVEQGGETKMRDQADFASLLKMETTIKKLTALEGEIMWYVANGDYNQALVHTEKALQL

APRSRKLQIQKGQILLYQRKFDQIVKFCNANIEKHQATQRNLSRTADNGAETSRSATSLM

VEKITILGIELGLLWATSWHYQNKVEQAVEVLNALEMVAPCSSHVIQLKRQWQDMKQLKH

NGNDHFKRGDYQEAVRFYSEAVQIDSAHQEFCAIIYCNRAAAQMGLGRYHTAILDCNEAL

QRKPTYPRALLRRARCHVALEMYHEAVKDFERYLREQPKDVATADVCREKNEAKAAIAKA

RIEASRREAAKKRAEREQHQRRQNCGDDSSRDESRFHDKFRRGSNGSNETNSRHQSSRAG

GRTSFMISKTQRRTHYDVLGIAKKATSDQIKKAYRTLALVYHPDKAKTATHADLFKEMTA

AYNVLCDEQARLKYDRELMYNRFGNFYED

>contig52272 Frame-2F

METLPSTRIDGISVSMNHQHEDNYRTQHSINEYYSQEKAETDEVPQQEPAVLTNIATSLS

NRAAESRRIRFWRTENRQQLIDCTRSCCVRSLSMQQQPLDGNLAQDFESEAAEIRTLIAQ

TAELWSVVDQAEHHNRLESLWYPAQRTSAACSEDES

>contig52791 Frame-2R

MRQFSTLLTLLLSASPASARLVHYEWDITRLTNTALFDGVLGKFGYG

>contig52975 Frame-2R

MSNQTEVHRHHDRTLNCCGTTLSHYDAGQQCDTTRVHSMAACSRAATRSCGNPVRFGAHP

ALTRIVQHWVGEHRWRPRRGVMQKIIARRQQRQG

>contig53330 Frame-2F|Blast-histone-lysine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62225.1|) 3e-71

MLSPSLEEALRIKYVKSIFHIAKGLRLDREDATSAILALNRYFTFHAMPMEVDVYAATML

HLFLKAHARKVPWIAFVKEVYTAKHGSSAAERLTAASPELSALKRHLVKAESELLEGLRY

DVSSEDPYALLDSLTTHKSSKKLAVLSHKGNFYQFAARSSSS

>contig54278 Frame-2F

MGIKKWLGLGASQSAVFGNKADDPPSHQQLQVSKSHRRHTTYDMQSCNESTNQRAQLHNR

PSYKGKQEVRFLPDEKANYQLELSSEGSNVSVGVDDDYALPPALPT

>contig54461 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54511.1|) 3e-22

MTVPVIVVDDHHHCLPEIHLAIRQRRLPFSQIHVLHVDAHPDLSFSAATKTDVIFEPEIL

YD

>contig54595 Frame-0F

MAVTKQKIQELCSHSPRSARMREKRQSQSLQLARQTVEMLRNIRSMYTSPSR

>contig54902-0 Frame-0F0

MRSRPTTLRLDNRLQHYPRRWN

>contig55093 Frame-1F|Blast-transcription factor, putative [Phytophthora infestans T30-4](gb|EEY61664.1|) 5e-77

MLADLYITLKKYQEAIDVINHLHARYASSQDPDQLEGDPGGLPLDIAVKYGICHLFKRDF

ATADSMFTHLFAQDVDVFGDLYLDVADAYIALGDRDREAA

>contig56034 Frame-1F|Blast-elongation factor 2 [Phytophthora infestans T30-4](gb|EEY57133.1|) 0.0

MVNFTVDQMREIMDYTKNIRNMSVIAHVDHGKSTLTDSLVSKAGIISAKHAGEARFTDTR

ADEQERCITIKSTGISMFFEYDMDAGEQATADAIAKDNIVEAPSDEAVVINKNSYLINLI

DSPGHVDFSSEVTAALRVTDGALVVVDCIEGVCVQTETVLRQSISERVKPVLMVNKVDRA

LLELHLEPEDCYQSFTRAIETVNVVIATYFDEKLGDVQVYPEKGTVAFGSGLHQWGFTLK

KFARLYSKKFGIAEDKMMQKLWGDWYFDAANKKWTSKNNAEGTLKRAFCQFIMDPIIKMF

DAIMNDKKAKFEKMMKAVGVELKSDEKELTGKPLLKRVMQRWLPAADAVLEMIVVHLPSP

VTAQRYRVDTLYEGPQDDECAEAIRKCDVNGPLVMYISKMVPTSDKGRFYAFGRVFAGKV

ATGQKVRMLGPNYVPGKKTDLWVKNIQRTVIMMGRYVEQTPDIPAGNTCALVGVDQYLLK

SGTITTSETGHTIRTMKFSVSPVVRVAVEPKTASDLPKLVEGMKRLSKSDPMVLCYTEES

GEHIIAGAGELHLEICLKDLQEEFMGTTVKISEPVVSYRETITGNSSKTCLSKSPNKHNR

LFCEASPLGDELTQEIEEGKDEVTPRHDFKLRARYLADNHGWDVTDARKIWGYGPDGTGA

NLFVDATKGISYLNEIKESVLGGFNWATKDGVLCEEVVRGMRVNLLDVVLHADAIHRGMG

QILPTTRRVVYACQLVSEPALMEPVFLADIQVPQDAVGGVYGVLTRRRGHVFAEEQRPGT

PMMQLKAYLPVNESFGFTADLRQATGGKAFPQCVFDHYQTVGGDPTDLGNMAGKLVNGVR

LRKGLNPDVPPLDRFYDRL

>contig57406 Frame-2R

MLLPGGCLLDYGAGCPQVAIIEWMSACGYLRRDAAIAASAIPTLTSNEHLQLAEMALQWH

SPLPKNYENWKLAWVDSIKGVC

>contig57855 Frame-0F

MADHRMLAAQREAKRGYTTCRSCGFTNFVRVVHCALCGLPRLSSNVLKTTNARLDLNIIE

NPTLPHAFKRYEWTRGFKSLNNIVWHRRPIDGCEFSPAYVLRFDRRPETEPEPETKASKQ

RERSLSTGYDPYAGVQFELLDVSDVDALQFPLPPSCVANLSDTKEMRRQMALDHALLDFP

TKYQHLMTSANVVLHEAEKKSSPSSSVSINQDFLIQELVQYLATFQNESLNGIDSSVHEI

PNEINSEKDLCQLRGESLVWLNETLVDPRSGLLSCTHHSDRAFYINSQSNDVLGVDHLQH

FYAAGRFIGRALLEGMVLRFHLCPPLLKMMLGAPISFSDLEYLDAEMYRHLTWLLDHDGA

TLLELDFTVTLRHQAQTRTVELIPTGRNIQVNDDNKFEFADRKFRFMMFESVAPQLASFL

QGFYEIVPQHVLLPFDYKELDYLLCSSEEISVYDWQKHTHVALEFRREVTWFWDVVKEMS

SEYRRRLMRMVTGSSRVPLIGFQGLISHDGQLCKFTLIDASDRQCFRSQVGSNTLELPFF

ETKKELRTALYAALCDKSADCDFEAL

>contig03741 Frame-1F

MFAILTSHDCHIRSNSLFPQRFC

>contig06412 Frame-2F

MGVPAFYRWVQEKYPKCVVDCIESHAVVLEGERHFELTDTTGPNPNGFEADNLYIDMNGL

IHPCAHPEQGDAPKTEEEMYRRVMAYVDRLVAAVRPRRVLYLAIDGVAPRAKMNQQRARR

FRAAQEAEQRMEVEKEALEYMSALGHQVPAKQEKAWDSNVITPGTTFMAKLAKHLRFYIR

DRVNNSVAWKRIKVILSDAGVPGEGEHKLMEYVRVQRSQPEYDPNQHHVLHGLDADLIML

GLATHEVHFSILREEVLFGKQKYERERQKEQQMVLDANGTALKRKRGEDFEEHASELIAS

DLKPLQYLHIATLREYLQLEFAPLSTVLPFVYDFERIVDDFVFLCFFVGNDFLPHLPSLD

IRDGALDFLILIYAKLLPAMGGYLTEGGHVNLSRVDVILAEVGQVEDIIFQRRALKQSEN

ERRRKSYLSNEKKDQIAANAAKDSAVEIVKKRRIDKETIAAEKKYGGMTPEEAMKARVKE

SVEKKLEQYREEVQDVVRLGEPGWKARYYSDKLKADDIEVGGGRERVFHAYIEGLCWVMQ

YYYTGCASWQWFYPFHYAPFASDLRNIDQFKIQFQKGLPFHPFEQLMGVFPAGSAHAVPK

PYRWLMSDPKSPIIDFYPKEIPVDPNGKAMPWLWVVLLPFIDETRLLDAMKEPNEKLTEA

EMKRNARFGKEVIFFHTKCPVTSHCPTAEVTEALVIPNLSQSFNGRLHYIETLYFPIGSV

VPSPEKAQKHLMDIPNNQCYSFQYRLPPTRPHYSKILDGAKLPPSVLLTDNDRQIVIPFF

GKANINIVDLAGDASNHTNVRINSMARQSGRGRGFGNRGGRGPQRYPSQSNPRFRNDNLN

VNRYGTHPPVQQYNQYLASGYGNWGSQEPRNKHGQYSDSYHQFSEGQSSYGRPSNEYRGG

GFHPNAGREHYNGHGFQGGFGGRGRGAVYQPTFGGSRQPSHAYPSDRFVATPSAPPVPRG

LEALKAGLRSMHQQRQNHPDEAKTSRYDR

>contig09538 Frame-0F|Blast-alcohol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY68781.1|) 5e-50

MTTLEKTVGMDSDLEPSAIFNEMLRIVRKCGHVSIVSDYRRSMESFPIGHVAMKGVTISA

GRPPAQKYYPQVFEAIESGELDPSVLISHRLALEELPEAYSRIAKKDGNFLKVFVAPHEM

RSKA

>contig10198 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60757.1|) 6e-33 NOT\_ORF

MM\*DEDTLYVGTELFEPKIWGTLTYKNSTMYHENDFEAFF

>contig12163 Frame-2F

MGLARLVFVLSPAKTLDLSSPRFSQCSQPRLLSHAHELIERLQKLSQSQIKSLFGVSDSL

AKLNYDRFQHFETSESVTKHIIASATLKQAVLAFSGPAYQGLEASTLSESDLEFAQTHLR

ILCGLYGILRPLDLIQPYRLEMGQKLATKRGKDLYEFWGDTIVSELDALFRKQEAIDGKT

ATRVLINVASQEYFKSLPSVALQTANISVVECIFKDDGKIKSVYAKRARGLMCRYLIQNR

VDSIEDLKGFHTEGYSYSSSGSSQKKLVFVRSGAAQKAAMQKIESTSAIERHTATSLSKL

DCDSILIKRKKEKTIGQPLRRSLRKKRKIED

>contig13920 Frame-0F|Blast-WD domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY60691.1|) 0.0

MSFGQPASTGGYLNPNNDYTIGEAISDGIQDLTWSPTSNVLVSGSWDNYVRCWEVQQQGT

QFNSVAKAQIAHEGPVLCTAFSGDGSTVFSGSCDKTAKMWVLNGPAQGQQIAAHDAPIRS

IAPIPEANCVATGSWDKTIKYWDTRSPTAMATVQLSERCYAMDAKHPLLVVATADRQIHV

FDIRQPSQIYKSIPSNLKFQTRTIACFPDASGFAIGSVEGRCAIQHVEEKDKRNDFAFKC

HRDGADIYPVSSIAFHPFGTFATTGGDGTFCFWDKDARQKLKSFNKCNQSITTGRFNARG

DIFAYALSYDWSMGVEKYNPSQPSVIRLHSVAEAEVKQKKKP

>contig16408 Frame-2R|Blast-hypothetical protein DDB\_G0279697 [Dictyostelium discoideum AX4]gb|EAL67623.1| hypothetical protein DDB\_G0279697 [Dictyostelium discoideum AX4](ref|XP\_641605.1|) 1e-11

MLNKRKEVLRLYRTIIRTTRMFPHRNEQGQLWSSVLHKNARMEIEQNRYETDAETISKRI

IFGWQCVQEVQQK

>contig16949 Frame-2R

MRVGDYLVVVFIAWIATCFSFSSANNVAQVSEQGEGKQLLKGSGLSITIKTGVNSEERRL

GGVYKSTASKLASIVKFSWNRILSPVLESASHLF

>contig17559 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61494.1|) 5e-81

MLLSLMGGVHPRMIAMVPDSKVSNEMKAQGVLVIQPSIALANIATRMALLDLKMAEALSN

EISTTSELSTASYFLRAESHDVTDMRMEGRRLAFGHNVVNHHSVDYDRLAEALRSEHLPM

PPPPSRVAMFGTSSAAGFDPFHQERNASNFFVMHDDRDDHDEIVVDAPYGPYSSRGNSMV

SRHESSMHLGSSRLRYCDMYKSR

>contig19319 Frame-0R|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY53844.1|) 0.0

MDFTARRDHIPYVNFEDVRLFNALEKPCTDDKANREAEFFLHLSLCQTVIPEVIEDSSEV

RFSASSPDEQALVSGAKYFGFSFESRGLGIARVRVKRPEMISRYANGATSPNTLMEFKIL

DVLEFTSDRKRMSVVVQYPNGEYWVLTKGADNVIYPMLAKEKSDPEILKETMRHLEVFGD

DGLRTLTIAQRRVDEKEYLNWSERFKKANASLEEIGKRKNGEANEIDKLMTEIERDLELL

GATAIEDKLQTNVPSCIANLMRAGMRVWMLTGDKQETAINISYACQLMDNDMQQFVFNCN

LYPTKDAIFTQLSEANAQIQQQSGRHAVVIDGECLELTLEDDRCQYEFLALAMACDAVVC

CRVSPSQKAEVVTLVRTTDRKVRTLAIGDGANDVAMIQRAHVGVGISGQEGMQAVNSSDY

AIGQFYFLEKLLLHHGRLNYKRVSTLVGYMFYKNIVMVMAQYFYMFCTGTSGQKFYGELA

FQLYNVLYTAMPIIVLGVFDYDVPFEVSRHFPELYLVGPRMELFNNYTFFKWICSAAYES

AVIFVFVIYAFNENYSNAGSAPMVQYGLLAFTMVVLIANIKLCMVQMSWSVYSIFVWTAG

IIGYLPFTPIFSSYWVALFSTEYGSFQNTLGQETYWLVIPVCLVVALIRHFTWTAIRRRF

YPDPWQIVQEQYVLHKGKRSMEHDGMARIDVEAGIPVVNGGMHGNETAYINSSSPDYGHN

>contig20302 Frame-0F

MLATRAKLPAAKEAFQVIECVQNNQVVLVCGATGCGKTTQIPQFILDDYITRGVGGECSI

ICTQPRRIAALGVATRVAQERCEAIGDVVGYQIRLEAKKSSHTRLLFCTTGVLLRRLLHD

RQLADISHVIVDEVHERNVDTDFLLSILRDLLPQRPAMRVILMSATMNADLFVTYFTSKK

TSPCPVVTIPGFTYPVAIHFIDTILEDTQYKVPTHLLKAKKVKKVNGDTHEKKAPFEMTF

RELAAHIDDTQLDYDLIVHLVQYLVTTKSRTHGAILIFLPGTAEIKRLIQMLTHGDEMLS

SKIWALPL

>contig20377 Frame-2F

MYAVATSGNFRHKMTLPMHSTVLDGASVELRFVHIQPQLHPLFETQHNLFRSFLFYPLMK

EEHSKMQVANAKLAVEEAAEVDFSVKIPLQLLRVCQYELLQMYEKWKLRYNYNRKKNCFF

ENDAEALNFGHDVFRVQVVSGRELKLRSIDAAASSESETTIELEVRPSRTSGFSMGSVVA

GRGGLVNRIKAAKWGGSNGPSSFSSNDADASDSGGEANNSVHPFVVVKFEDGLVGNQEYT

VGKTNTEYDSTNPIWSTNKNAGTKCPHGKPNVKYQTSQQLKSRVVVSPVNALKQFVFYRP

SLPDQPLAGWLLFQVFNEHYSYMSGIENELIGEVMIPL

>contig21576 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68785.1|) 0.0

MYVFGGYNDGNCHNDIYAFDLMRHDWVHIETPNGISPDGRASHAWCSSTDNSKLYLFGGS

GPHWGQSNMGKLLQFNIRDKEWTIVEAEGTNPPPGYGQSLCAIDNKLYLFGGTSGHVYVN

DLYVFDELTKIWKKEETRGNCPSPRYKHQVAVIGNRMFVVGGGLYDPPKGFIDTYYLDVD

TLEWQRIECGGDIPKSRIAHTISQFSSDPSRLIMFGGRDDSGARQNELSELNVQTGEWRI

YNDKEGLLPDARDFHSTVAYNEHIFVFGGSNGVERNNDVYRYTTLHQPSTLLVLAMQTLH

QNLDDIHKNDLDLLPFELRLGVENINPDVKCTWNPTWFRPDEEMHDSEALVM

>contig23884 Frame-1F|Blast-T-complex protein 1 subunit gamma [Phytophthora infestans T30-4](gb|EEY66501.1|) 0.0

MMQAPVMVLNTNTKRETGRTAQLGNIEAAKAVSDIVRTTLGPRSMLKMLLDPMGGIVMTN

DGNAILREVDVMHPAAKSMIELSRAQDEEVGDGTTSVIILAGELLVVAEPFLSHQVHPTV

IIRGFKRALEASLVVAKTLARPIDTANQDDMRQLVQSSIGTKFSPRVGNLVSDLALTAVL

TVARTSASGQKEVDVKRYAKVEKIPGGELEDSRVLRGVMFNKDVTHSKMRRRIENPRVLL

LDCPLEYKKGESQTNVELTNDQDWNTLLRLEEEFIENLCAQVVAMKPDVVITEKGVSDLA

QHYFVKAGITAFRRLRKTDNNRVARATGATIVSRTDEIQESDIGTKCGLFEVRKLGDEYF

AFFEECQDPGACSILLRGGSKDVLNEIERNLQDAMQVARNVVFEPLLLPGGGATEMRLAH

ELKQRADAIEGIEQFAFRAVGEALEVIPRTLLQNCGADVVRVMTALRAKQAETNESHGID

GVTGKVTPSEVLGVWEPYQVKTQTIKTAVEAACMLLRIDDIVSGLAKKKN

>contig27714 Frame-2F

MSMYGVSLNALYYPDSRPNMFLVDKHCSKTVDAVKTERCCSQARDSPKALMLKLPLDIRE

SSYHSACRDFQRRHSFWRDTETHGQTLSFCARYGADRSYQIIVFATRSQYSAVIIYIGAH

SSAFLRQSVGFFLHEEVPSYFDTTFPISIRRNSSSCCAAYVI

>contig29275 Frame-1F

MQLVNASDPRLFQILSQCPDVDLYTPSKVRGYGYCEDAAAYTKYLKARMLPAWVLKRQFY

HESRKRMVMYHEICPKTPMLFFNHYWDNVPFLSEWPATKSLYLMPNIEMYEIEREHLSRA

DVILCKTAVCTIYVNLWFAQEGNPRGTVVMYTRHTTSNIAMVYESQLSPRERRAKKAKDF

SKVKFLHAAGKSVQKGTNEVIDCWLSRPNLPQLELRMGQKLYDTVYKDNYDRKLRDSPNV

ILHTGRVEPDEFGRIISDATYFMCPSYQEGYGHYINQARASRALIFTTDVPPMNELITPS

SGILIKAKRTAHDRHFLGGLDPRNHSLRNVVGYAAEIQNTSICGAVAKMLLFTTPEERAR

RADKALQHYYFDTVFFAHKMKELRAMASLKDFYNPATGRITAT

>contig31010 Frame-1F

MAPKPKRESFSTRGRHFLITGIALLTCAAIVAEVAKATENAMDSDFHRRLREQTKMNGFK

YPEERVSIPSGAIRSVETQVPGSWSTLYQTIQSQAFALNTELEKLVCVYILGMDPRVYAA

KVFKSIVKGFRPDNYYQSKYYMDLFTHFQKYFPDDVNLAKAVFNLPHFRDDPSLEAAATD

MQTRVVSKFVSNGKKGELIQILESVYDTKWKDFNVDESSPISLLQDHHDGVYKTKRLGDE

AD

>contig31739 Frame-2R

MFTSTTEISNRPLPGPLKPSNVSSQSTIAHCSSVQSSGDYGMDGARKEPPRGGMGFGISL

EKVNRCKRYRSISGKMAAIKSLGDKGLISNVDRGHLKDLLLNDDSPQLQEALDTYKNTGD

FQAVKDLLLREINNPSSKRNSGDWLSESFVNEIALNLIPSPQATKREHMPLQKDFNLGRI

NDVSAALNAPTNAFAYQTSQSASIKDTSYAQSSPDAFNYYSSLRSLEAPAAAGSFLSINR

FPTEISILNGYSSSPMMTQQYHQPQFSTSNMYAPQINQPLRDGAYMKRDFESDSAQNLRG

MDSLAGTLNGYSSQQDFSMNQVPYPANVIYQSQQPLNSLTPASLNDFGCNIYMQQPQYAL

NRYGYGSMQPDTGYNFYAAGYGFDKAQLRAGPGGKWTTAPPMPSYPPACSKEEKKDKISR

WLKKRENRNWSNKPSYPVRHSIAKNRKRGEDGRFITKARLAEMAAEEAAMDVGNEIKPQT

ASPPPSSSGDAAGFATSQKNMLPITSVP

>contig31784 Frame-1R|Blast-peptide deformylase, putative [Phytophthora infestans T30-4](gb|EEY59432.1|) 4e-79

MIQNMPEDDADLDNLEYQEVVNPKIVKMSKATTRDFEGCLSVPGYQGIVKRAEVIQVQYE

NNQGRKVEETLKDFPARIFQHELDHLNGVMYLDRMEAGSLMHNEEFEAMEWTDLQKLLLQ

GPPTIPPLMTPTYTTPNGKKRPQNTGL

>contig34938 Frame-0R

MRKHFTDQTKICFAACNIRSFSFKYPIRSRPLLPHRLTLHP

>contig37232 Frame-2F

MASRSHRRRSSPLMEHRWSHNAFDDRSPSPPRQVNPLYRPEPEAWVSRAGGVYMPRK

>contig37247 Frame-2R

MLVISHTSTIVRRAGSRALSCSRCRRETILLDLAKGHPPRSCLLGMVDARAGIRRNSSYT

SRIACPPSPLADIPRALLSIERGLTALSHIVRSFDILRAST

>contig38383 Frame-0F|Blast-transcriptional repressor TUP1-like protein [Phytophthora infestans T30-4](gb|EEY59397.1|) 0.0

MSYQESERPAAEMHQSMDHQSVVCCVRFSSDGTMMASGCHKTAQVFDVKTGDRKFLVSRP

AGSGHTPTSQTNTAANEPDDAYVRAVCFSPDCTKLVAGMPQNTIRIWDIASNEEGPAMTG

HESEIYSLDYVNDLIVSGSGDRKVRLWDARNGQCKKIFGNESGGPSDGVTSVALSPDGRL

LAAASLDKVVRIWDTETAQLLDRLEGHSDSVYSIAFSPDGKNVISGSLDRNIMLWDVCAQ

GRTTTRPRMLFQGHKDFVLSVAYTPDGRWLMSGSKDRSVVFWDPRSSRSVLTLTGYRNSV

ISVASSPASPYFATGSGDCFAVIWKYQCQTF

>contig38462 Frame-1F

MRQVFNQYFQNGVTLNRLTCTTPPPFAEDPDAGVDGSRRSFSEDDAYSVNWLTLKAQPKL

GTVENHRDFTLVCYQDVFSRHESGVLERVGRGTARARSNTLNYQPQSRLVGAHVLSSVNF

QDVPELPIPECTDRLHFRNSGFVIEETSEPNVMRLSLLLSLLPTKATLKYARKYQRWLQN

LACCVGNLALVLRPEVTLHCMSKLSWKQSDHCFMCLKMFRTFRRRHHCRFCGEAVCSACS

SMANMSGYEVKDGSGNALTESSALNLVSSQSGGPISTEFSQTGDVCTPTEGSRDSRYTRN

FREARGCNTCVADLRHGLTASAVLRMRHNSGSGCHGNVEYVNYFSGDSSTLASSRNGRSA

SNCDEDSIVYDNFEDGNYERRLGTIATYIPSEGGPGALVEGNGLYSISTQGPAELADIFP

VLSEELQDKFPSVDEVAPPRFRTVSDPDQLRRMRNVSDPEMPQRLKEKHSMVSMSTTSSS

FSRSSNDKYLNDNASQYSRGTNYSAMSDGLSAGDLSRDPDILAIAGLSMKLRPSDDYEIA

SVRRRPMPYYYDFEPQVSHVLEDYDRERKAVINEEDREDLDGRYLSNPWPGGTNAESQYR

SDIATSRDGLVIPQSNSVSPVDVFRPADVLRHRSQTTGSLTWNSAATSLVKESDTNCNKV

IDSSSRSTIGIGKLVGPNEASNSSSGSGHNSTSKMTYQPHSVMPADVAAVTAISANITQL

DHVKPRNNIETPLAARSGTAGHRLPPSIPEGPSTWGLDDLIPLTQPIQVPANFIVFSDSK

RESIFTRADDGQDMIPLRL

>contig39573 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61284.1|) 9e-55

MLVNPSRRRFVVCEDLLLPRVFRETLLCILFDSFKAAAVTLVPSMVAVLYATANHTALVI

DCGWMETRLLPVYKGIPLPYLYETVPIGSRNCCNVIQQELNVLHDQPTGNSKRVMPVTET

LAEDILERACFAQQI

>contig39704 Frame-2F

MQSVETSFPQLQPLQRLSSGESLQGDFSVEVIGSQESLDLDSGKFYT

>contig41123 Frame-2F

MRKGRSRVAHSSHIAPKSSSTSMDKAEIGLVTIPKEIFTDNSASHTDSSLKPLASSNGLQ

GSLKVTSMKNQTAARLKHANTSNTKKIVQCQNESDTMAHESPRQNAMSAELSSSSESEKE

NEYFDSRQRDEVDSLFSRMIDSAAREQWELVEVGRLIRLFAAEWDFEQTKTARFLLDTCP

ELVNVEFLEGLGVNLSANQLVQVFEAGSGTAGVLMNKLASAVENGHLSVCDPSFVEALER

RVAMMESNGEVLELLYPLLESLSSVRDVGALIKQLCAHWQLERKSALVQQILLSRVFDDL

DGNQDEICLDLPELAGKLDFPSRLDQEDVDEKGNLKGFVEDSDSDGDAEFIEKDEIDSED

GESDSDEGMEIHGRSRGCNHFIEDEADVGEEDEIEVENERDHHDHGSSSSSDSD

>contig42232 Frame-2F|Blast-hypothetical protein PITG\_19106 [Phytophthora infestans T30-4](gb|EEY68731.1|) 2e-60

MTTVAGLVREFETLLVHKYRFALSDIVLCLQTAVQDLHNVQRALIMATASILPSNAIFVD

PLTYISSRLERLVMLVPYFLGERELTILLSALQEFNQLSSGLETFPKLHQSMESLSSHTK

TLKIAVARGAARCMLLTKKRDYLTKFLDKAVQVLQNSHSRRVEKYQYAIEQFTVDYKLAL

QDEHLQQVKQLHFDIQTIETSMSAMLLPHFEICRAITTANAHMQPVESTFTTSECRDIDA

FVQSAAKFKSGEISIHSALEDAAKFLTRLTLFERAAN

>contig42247 Frame-1R

MAKLLIIATAVLAFSLALGEALDRDKLHEVMASVHGNHNYTVHYDDVEENRQELKCYGNL

TREINPVCGSNGKRYTNLSMFNFRKCMMKVQEDEEIQVTDMEFCKDAELEDMAPNMKYIS

>contig44296 Frame-2R

MTAAPSIQLLHESPFTDSFCWLLRGNGCIEGRSQGAAATRIVTLKQGEDGLRWFLEGRIP

ELKTAQLPQ

>contig44739 Frame-0F

MQKKTRSNTNLCINQISAKAFSSSDTSRRKYLEKTRTLLQEAKYTCKIDSLASEIDAVLA

KADRLLSKSTGASGLGAKICSYTGSNESPKFSQLLDDMTEASLFDNCSNISGVLWKRG

>contig48007 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65370.1|) 2e-72

MFPSLTEKKYERWLKDLVVPHCSVVSRCMEHERSRLPPPRQLKNQQFHALVSLPFGRDFV

DMFFKQISYYRYFGEDKENRELLRMYFEKVSTTGMTDENWAQELTPVDLHYVVGCSAEIL

QEAARLYGP

>contig48072 Frame-2R

MFSYLAEKLNVKNLGELIAPTLTPEQEFHASIEHGLRDKFMFMLDDQKIDPNAKNTAGNL

PIHTAAYFGRVDFLEILLARNVDVNVMCPRENSPLHFAAAQSRDDAVKFLVSHGANPALR

NRSGRTPYDVASGDNIRQFLLPLQFRHEDPREAATMLPPGITPSVDPTAPRPVIAPPPLS

GDCSVMQSPPMGMPQQQTLQTNLYAAATHSAIPRGGLTRFARPKDYRPIQADGFGSSVGN

EELTAKFGNTREIKVTAPPPNMTVLSTSTINDTEAAETAASAAIPGVNPYASAYAHQTQS

GKFEANFGYASAASNAAIGPPQFKIFNPKLADTSATSGSTSVAHGHPVTGAPATPQFVAQ

NSASQ

>contig48238 Frame-1F

MSPPKEKDPVRLPSIRVMMDRDTSPCSSTGLYPIHKHYNDSYKQLHDIPIVSHPESYAAE

LSNRLVASAVNTQPRKICRQVKADMTKRNSHAKLCGIKDCRKRAKAGGCCIAHGGGLRCS

ESECKKHAVSLGLCISHGGGKRCNVKECHNASRKNGVCWTHGGKRQCKIDGCNKGPKSGG

FCWSHGGRMRKDGDMF

>contig50305 Frame-2R

MYDLFEAYYMLQGAVAINDDSRDEQNHETCLVFKIYGDDKLLWQSEQISESCQIEFFEVV

IKDVRMLELKVSCLGSNFCAHAVWVDPFLHPVKEWACSKCSFVCKGCSKLCTLCRNGIRP

ESISLAAAADTKLVIPAVYTDV

>contig51283 Frame-2R

MTSPPQQQSIKNDGVCSKPTPYTLAQRDQLAKSSRHAMPSATTNTTHFSLNSPIKSFYSK

RAKEEVKPDNSLLQTTRR

>contig51328 Frame-0R

MDHNREEIDSSEFSDGQRDGIVMVVYPKLVPSAYAAIKTLRSVLGCKLPIEIWYSSDEMD

LTSDITKPLNALASENPTLMRFQEITIESHNNVFGAKIAAIYHSHFARLLFLDADNMPSR

DPTFLFNSREFLDHGAVFWPDLWHPNRTIFNIHNKSLLWELLDMPFIDMFEQESGQLLID

RRRHTQALELVMFYSFHKPNFFTSMQLVHGDKDLFRLAWLTLEAPFHMIQTPPALAGKFI

NNTFCGLTMA

>contig52004 Frame-0R

MAELYAEVAEEERRLQRGPSQRQYWDRKTFTSFAEQQRAMERSSTLYIGNLSFFTSEAQI

YELFSRVGFVKRVIMGLDRFKKTPCGFCFVEYSKHTEADACAQFLSETKLDNRVVRCEMD

GGFREGRQFGRGLSGGQVRDDRRSKDDYDAGRGGYGRGDDATADGHHFRRSAHVKRPRDD

ALTDEQPSSRQRRPDSPSDKNDEDEDSKFRENDDLGAE

>contig52273 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59251.1|) 4e-31

MDMKIAVCTTDDRQPTIDTLKHLAVFDMVDALACGDDGLPAKPAGEQIWTICQKLSVEPH

NTIMVGDTSTDMLLGKNAGCGLSVGVLGGASSLDDLAEDADVLVPSIDRVIKVLFQYGQQ

AQRFREK

>contig52387 Frame-1F

MGWSFDTESELSSAPATPIKRVSMNSLSKNDNLPSLSPSRSETRARQVSISSPAERNSGY

RSARIEKEVLLKMGVDPSMLSEIQHVLDVLAADEVEKLRVETLRRHEEAACAASLVVPEP

ANEAEQNSLMSIGCAFGNDEKEEKRDAVSNGSDEISSSSPIDHPVWHENQLREALRRRHG

HAEAVAGQREMDEHRIREM

>contig52790 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58623.1|) 1e-100

MKSGDSDTTVSATVASRTEPIVAYVICQLTTFVFSDRLDRWEPLLVLLKSELFDAAIKVL

ENIVPVLSRRDEMKNDLISQPDGSVTHSEKNEEAASSDESKTEAGALLSDNAIAVELDYE

VEVCMAAMQALSTDELLSLLDSLHEFSYINTDELHRMQEVLKKGYIGGWESTAKARILAK

LRFVRECSRYLHPVVLPALINECFPQSSPVFVTTSALYHGAISWISSTLGGENSTGALSP

S

>contig53094 Frame-1R

MDMHMETSANFLEDMEAFIEPSYRNRPQSELKKMVANQLWAQYNGRVVEASHVEVSTTPS

TPRSYERV

>contig53331 Frame-2F

MSSDTMALPINCSPAAYEPIAPPVNSYVSSSTTNKAITPNRQLGELLRSVDPKYCFQPAV

EELLLDMASDFVQDVVEFSSKLTKHRRSTTLEPRDLQLCLAKNHGISLAGVLPAGSLRPM

GQDLLVRARPAKNSIHMRRVAMKRRSLILTKNKLKAV

>contig54460 Frame-2R

MSKILQRVHLLGRFYLNKWQYDATKWLDDVWFGRSNRPRVASVAFMITHSTRQKLLAAGF

PSSVIRMLQPTTAQKIIADNIMYDQFKELQEQHQEEQAERARRTSEQMETQKNALAMAKV

KQVEERMAPSAALVIHQTSVAAEKDENK

>contig54631 Frame-2F|Blast-alpha-1,3-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY57731.1|) 2e-14

MALALATALYVIVASGIILLIVVGWAFLHGLSCVIPRAVRPSKGTELLRVGFLHPDLGIG

GAENLVV

>contig54903 Frame-2R

MAFMVSGKTAKHVDDGAQLLHSLVVSTEQKLRKIEKENTKGGQRDDCLQDMTEGSSRQEK

RNHRLTSQQSTQRYAMN

>contig56035 Frame-2F

MHLKYFVAILAVNLRAVSALDLIEQGLIDPSRRWPEPFRSFPANQLVDESHGALRTSRDL

AQDDDNETRMISLTSMRAPITKSVANAQKGPMRNAVFDIVAERISQLEHSLANKDTVVAK

NAEKFFDKSTAETNPVAETSTAAKARSSVAETSDAAHVKPVGFSHDKPSGIEYRGDDEVA

LFFAINYELGPISTDENICFYADYNIYYNLKSKTEDVIFDRALFDKIDPAYLYQQFRRFA

SIDENNQLIWKEYITPEALGENAHAAFTKALKNVKRDNWEHHFDSIVRVLRFLKLIEENQ

GTADPYVEHAMDILSSWSINIDNLDDTVESLIGLKTLRPEIHRILEDKRLKIKKNMEIEN

NMKAKKAKKKEAKKTKKVADANQKKKGN

>contig57357 Frame-1R|Blast-26S protease regulatory subunit 6A-A [Phytophthora infestans T30-4](gb|EEY61489.1|) 2e-12

MLALRRESNVIKHEDFMEGIAVVSAKKKTSLQYYA

>contig57854 Frame-0R|Blast-COP9 signalosome complex subunit, putative [Phytophthora infestans T30-4](gb|EEY56325.1|) 1e-175

MFRESLAAIYMDEEEYIEAAKALAAINLESSTRQYTDVEKTEKYVKIAELYLQEDETVDA

ENFINRASRFIHNIEDWALKLRFQVSYARILDSKRKFLDAALRYYEFSQSKPDEVDPDDL

LELLRKAVTCAILASAGPQRSRLLGTLYKDERVKNSEHVAILEKMYMEQLIRRPELVQFE

KSLLPHQKAMLSNGFTVLENAFLEHNLLAASRVYISISLAELGKLLEIEPANAERVAATM

IGEDRMKGKIDQHLSFLEFEKTDDEVLTAFDTRISSVCFNVNQCAEQIEQLYPDLVRAAT

TMTAS

>contig58150 Frame-0F

MLFQSKNGCRRNEYKKLLDMPSLPGKTGYSISLRSLTSLSSASLPISINCDA

>contig58356 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67655.1|) 6e-18

MEMQRETIRSGVFKPGHRLPTMTLEEYADQEMTSAIERQKKEQ

>contig58886 Frame-2R

MMRRIAPASRRLFSTAMADTDVV

>contig04479 Frame-1F

MLGLIYSTTVTVLLLVQCSNAAVIRDTPFGGAGSKCQKAKDPSRTVTGLMVCAGKRVDKI

GVYYQGVNEPETLGGPGGECHNYMLGKDEYFNSYDAYAGLRNGKWRIFYVQFNTNKGNQL

VGGTKTTKKAYTTPYKYKLAGIEGCYGDEVDKINGVWNPI

>contig04813 Frame-0R

MSTEKVPFAIKRFGMLNLELTDAEFLILFALTKRDVEFEDKVFLIAEKILLSKKFDPVDL

FYFFDLNLVGFKLFESLFFKFWAKFVKSVCHPDLNPAEEMINIMENANYSIDYLEEIIGR

VIYTPSHELESSIPLSRNAEFAPELWAVVEAKQKQKKNAGYVV

>contig09322 Frame-1R

MTKYTLATSTLLIAFAVIVSAHDGEDHSQATDDDVSTECESNVSTSFIDTIDNSSYFNTC

VEGTTFNVTSVFDALNFTEPEFLTFCNSSTCLEPIHRLMGSVDCLITYMGEPRDLSDEIS

KLHDECHEVLDAANLTMNMDGESTAGGATNNTGSTTPEDGTASNPATLIITLGSVISATV

IAA

>contig09689 Frame-2R

MDLMKVLSLRCVPPLQSDLLISVALQLLHRLPEDLLYEIARHPFANPDAPTSLPFHPKTI

SAIAKQVQNRQQSQTRDF

>contig12964 Frame-1F

MTVDVHGANDCVEQIVWPMPVLEVIFDRVRGSSRYFSSDSFKGFCQFAVAVWC

>contig13853 Frame-1F|Blast-Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily [Phytophthora infestans T30-4](gb|EEY59454.1|) 1e-55 NOT\_ORF

MCYLGYGLEVSFTTFCRFSLSTISTMFLGRMGPRELAAGALANIWTGGIQVLIFGVAVSI

CTLGGQAYGAQNYRLVGVWLQFALLFLSLLSMPVMISFFYVDHILSVVTEDQTILALADT

YARLLAPSVLPQAIY\*ALRQYLH

>contig15312 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58420.1|) 1e-161

MSHHQDNVAMAAPIASSPASIETIKVTIKSDTMAFTLETTPQESVAGVKAAYQESGKNVN

FILLLHKGKELPDEKTLAELGITDGDVLVHIEAAHQPFQPLNYRLLAESIKNRRKHEDTN

MQMLKEDNIWAAGSDGTVHRLGMEKSIVSRSQHKSVPLPFGSKHAGKSRAFFNQLSVRVN

GCSFHVLPSMEGRWNGELITVPLQDEGSQVCSSDLVFRDDEGVWSQRQSRTTMSGLTSMQ

HMWIKAVSDGILKIETDDPTLRDSEITMQELGLNVIITTATSKRTGRPLMVETITGIDSS

RRLRTIQRFDESGAFRSVYVMNEVRVVDAVSGAMEKYDNVF

>contig15631 Frame-2R

MACRTRSRLMSVFSIRPKVRSTSFDAASSSEFVSMVERALKQLRLIIYPNGLLKQRRVLT

NMKGFMFYPAFGVFFLMAVAKRKGLIKRQCEEKAENERNALNC

>contig16344 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69058.1|) 8e-20

MAFPSIFQSLKNAIRQELILESFRY

>contig16605 Frame-1F

MSFCNENSFIGSLFFYDIRSVETVDL

>contig17484 Frame-2R

MNLLRQNAVRQGLNNSSRIPIFYKYISCLLSLTFVLNRQKAINSLLLSRHDFLSKIRS

>contig18306 Frame-0F

MILRTRVLLPRRFILVESLSFQDHFLGPILGPYVITTPLHKTKNLL

>contig19323 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY69268.1|) 6e-22 NOT\_ORF

MHGYFYDD\*CVYLELEYAPYGELYKKACQRKMLFRRCGCTLCGSSC

>contig23898 Frame-2R

MSDGLELGLDLKGLDHEPKALKVDAAQLTEAISNILKDADLEKLSRRMIRNQLEEDFHSD

LSSYKDVINATILAIIEQQQTHEDESEPDPSDEEIGHEERTPRKPAAAVKKKATPKKRKR

KSEDDQPRKPVAAVKKKATPKKRKRKSEDD

>contig24851 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67611.1|) 3e-51

MSGRRCLGRMDWTRLRKQPQLYAMDASAEGCTDFSRGNIKHTNSATETYRRVINLQSAAL

HRGIFNCAANAAKTTPAFLMMLCQVSPLAVALALSILSLLASNVGAHQTMMVPKPAYVSD

DKETRHNPVAFLENQNFSTQLDFQDYMKKNKYSSLRDFMDNAKYTPAEGADFSCGFTKSD

APPEPIPKSCSVRSSGYTHDGPCALYLDDVKIYEKANCHTDIPGKEIQVDYSSCKGTCML

RWYWLGIRTLKNIVSWQVYKICVPLKRDPKDEICGAGDGTGQR

>contig25117 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57050.1|) 1e-37

MLIGADVVCWPMLVKPILQTVKYL

>contig26053 Frame-1R|Blast-peroxisome biogenesis factor, putative [Phytophthora infestans T30-4](gb|EEY70091.1|) 5e-22

MFAGFAKARNTSFSVAEADVSASSELLKSHLIHQRTALA

>contig27335 Frame-0R

MACGKLVKMLLHTKVTRYLEFRTQ

>contig27919 Frame-0F|Blast-PLAC8 family protein [Phytophthora infestans T30-4](gb|EEY54312.1|) 1e-58

MVTFCPCVTQAQVSTRLGMAPYWFALVTLFILVLLTGGTVHLILFVWVWKARALTRERFQ

IPGGCFRDCCASLFCPCCTLAQIATHIKSYQPGSCDFGPPDTLPPYSRT

>contig29247 Frame-0F|Blast-ER lumen protein retaining receptor [Phytophthora infestans T30-4](gb|EEY69550.1|) 4e-96

MKLLFLVFSGALVYVIRFKEPFRGTYDKSHDAFLHFKFAVLPCAVLALVFNEKFEVLEIL

WTFSIYLEAVAIIPQLILLQRHGEVENLTSNYVVLLGAYRGCYVINWIYRAATETSYHFI

WLMFIAGMVQSALYVDFFYYYASSKYYGKKMTLPS

>contig29441-1 Frame-0R1

MRWFIFSKTRFSACSLKIREVSRILITFAVTASSFENTAELWQIADDRSKEHL

>contig30667 Frame-1F

MERSTNTKSIGLSHLEVRQRRALLAKIAKLEARGAILPSDARTLRSQVHESSSGHWKAVE

VRLQQLACNWNPYQDGTRVTSNPFPLNKKKYQEVDYYQLLELEKDDTLTTEDFKRQFRKL

ALQMHPDKKRANRKQVRNSEDEKGEADNVSLDSTQFARLRLAYETLSDHKRRSEYDTKLL

GIASPQQIGKVIKNQVKLEASTDFASLEWMARVKHKMDVMAQIPGWAKLLSLHSAELRFE

TGEPCTGKDCGKIVSMDRDLECLGSLRRRVYICLLHKYIHSCDESCTSLYDDAEFDRRVC

QMRAYWLIQNWIFDQFQVKALQRQKLTPLQTTANPQQVEVSATEILKHEDGRNHCASLNE

SRIVSTVSEFEERDIHLGDHNTRFQIENVAECKSPGCRTSFQYLEEGIYACRRHGTPHIC

TFEQCNQQEVQAGTYICWVSGKRYGCERVQAGTDVRTRRLVFLSAPGEENAVEMEVPVML

PLGKATEYLLMGDSPLSNYGIVSSLSPPPPPDEKAWNKQLCVASGVLEVRPDDCQLPKRD

LRKKLKRDHEPEQNLSSVRRRLHDRFLSKFQRSNTTSFFVFLNLPRAVAILPKVVLELEQ

FACSSSDDEHVPHSAAIDEKNLLQITVSSHCTVNYIKCWIEEITEQQLSIWDQQIYWGDT

LIGEETNEMNLSEHGISAGCTLELRLHDDCPLLLSTWNGKSAASGRCGGAFMEYSTVQIS

KEAAEDLDELQEEYEIVTAAEEQAFQEYRIKRKRKKLELSGAIKHSEVLRYDNAKSEPRL

LGMIRKRIQDVDDRTLKRHVLSTDAQQEQSSQKEDLLFIEDEELVKGEHEQVSTEIKAMR

SVSMNAQPLGIFG

>contig31286 Frame-2F|Blast-Annexin (Annexin) Family [Phytophthora infestans T30-4](gb|EEY59586.1|) 2e-32

MNCLACVTILIVCTVRLALQPDVAIAILFERTMRGLGTDEKGLSAAVIRYHGMQPHVELL

YENLYGRSLEERIRTETDANYGDLLVSLLHIPIDMCDALKTIAIVEKL

>contig32647 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57280.1|) 9e-63

MDPFIIGIIKKRRFTALSKTFPELIEIAKQITSKEIPESMWIATDCAEIPKAALTHSIQS

SLKDLEDFIESIVVTDMNKQLIMGLPKTQTNVLRARFKLHGGSKKLNILQALQLIFALVD

AVGATTKLSSNAKHSANKRRLKIKQAADAVALDQENEVARYQAKRIEKKQKEYESLSYEE

QQKIDAKNEKRAARKRFNRKK

>contig38032 Frame-1F

MGNDLTKLKRQQPRALNYEPQNGPIPASDALMQIIPDQFTSLSEVTQALRRSGLGSCNLI

VGIDCTKSNDW

>contig38087 Frame-2F|Blast-DNA polymerase zeta catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY64210.1|) 9e-44

MDAEELRVEAVVVDYYMRSPLPTGSIEYLPDSPCYQHAHEVPIVRVFGATPAGQKALVHV

HGIFPYFYFNAENDPDFEDPERLRKLLPQLAKDIETANALNQQQRQQTDKYATDSSKSSK

IIAKMLIVQGTPFYGYHLRSKLFVQIFLYNPRAVPYVVRLLESGSIGDRHFQPYESHIPF

LLQ

>contig38490 Frame-1F

MRMSPRSHNTRSREAAGETSITAGLSPENLLANRALQVERNGRDELIKQDKSSPSSASDV

AMLHNSVSFCALCCDLEPFGDAPLFLCPSCDQKYPTQQALGRVCMA

>contig39400 Frame-1F

MHWWLTYDDDATLPNAVLKELRVHLRKSTRSAMNRVREDSQQLLLGDNTAALNDEFGLKS

IYHEWKAFMKLALQDDV

>contig39509 Frame-0F

MAAHVPREVLSLDWIFPIQYERDWVVSWQPEFCHESMSMAVLICGVYCALCFIGRRIMRD

FKPFQLKGPLALWNLGLAVFSAIGASRTVPFLLINIYKYGIYDSVCAPPTPNYGRGPAAL

WIVLFIFSKVPELADTVFIVLRKKPLIFLHWYHHITVLLFCWHAFGTRSASGIYFIAMNY

SVHAVMYFYYFLTACGYRPRWARLVTIFQLSQMGVGVAVCGLNVYYMKHGYACSVDPESL

KWGIIMYSSYFALFLKFFVERYLLRSAKKAAVAPAKKAQ

>contig39783 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY65284.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54655.1|) 3e-58

MSTYVAQGIAYILVHPPLWRMTFRLVLLTILVGTTTVFVLLAAAMYPQEQALYGAGLSRT

WAWLLAIMLCLVESFIIVMIYTFVCLARCQDKVFEYVMREQGHVELVSNQRKHASWTRIC

TSCCRISVLLRYGLLVVTIPLNIVPV

>contig40347-0 Frame-1F0

MSLYIPFLANPGALCICRSSIFTQYYRLDHSLEEILALTIAYVHPGSDFILYNRQRHEKV

IDRSSFKSVAVELRSADS

>contig40541 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65208.1|) 1e-112

MLYDIPTVTNNCMEQMTIESDEATAYKTRDMLRKTYGVMVDDLIDNGKSDNGTTLTAKQY

ARVVADKAFMIIVTLCYIDFTRISGTLSEFIETICGPTQLVGEIDDGTDPNTLGLRVVGD

AFKGSGLSWKRKGDGVIRITFVSTDTKHVTINIISGGDKYDEKNVPPGKNVTWISSVKEL

GGKTLYINRWRPGFLGLPSTGGGTIKLWVPRASEGGHLDITAKLNVNN

>contig41054 Frame-0R|Blast-probable adenosine deaminase, putative [Phytophthora infestans T30-4](gb|EEY58771.1|) 0.0

MSSTNFRQYPKNETFADEFLRFVPKTDLHCHLDGCLRPQTLIDLATEQGVTLPTYDAERL

NRELFKEKYDSLEEYLACFSYASAVLRKSEALERVSYEQACDQFTVGVRYFETRFAPQII

AIPGELPLENVLRSVNYGLQRATDEYNAKDLDVVSGLAPRFAYGIIVCAMRYFTPAAGPY

YKQFCEVHRHVEPHRLYGLASMALITQAYATKLEHGVPIVALDIAGAERGFPAHDHVEAF

AFAHKKFMHKTVHAGEGYGPESIFEAITDLHAERIGHALNLFRHDTIEKINLDEEQRQMY

CHNLVQYLGNSRTCLEVCLSSNLQTTPDMQLDARNHPLRDMLKNKLAVSLCTDNCTVSHT

NMLQEVRLACDAFELSPHELRQILLTGFKRSFMPGDYTYKRAYTHHVIDYYDHLIKKFDI

NDTSTSKSC

>contig41159 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68232.1|) 1e-06

MKVLLMKYIEKDDSLLCTSQLSASE

>contig42752 Frame-2R

MASETTPLRAGQYTSDAQKRKRIVGITGIVVVLAAVIFVLWLSLSGHNSESRDVKGQDIP

KPEPALRTKIPVAIELPTEAPTEKPAESVPKAAAANHPPAVGPSSTALPAPAAKLVSVPP

RVPGPPVEAALYQLAQ

>contig43236 Frame-2F

MGLQLKRGEQGSSLRDKYMDKLNQLKEKKQQESVARYEEAENGTTSEGLSTWLVNDGANE

VLSYSDLRGFFKAVIPPKDPLQNDEYLQFQKE

>contig44798 Frame-1F

MHKGRLSGPYKSIDLHQIGPVTSIALFPRPITPTTETDGRTWQCNVLVTCAIGQAVVYED

IYSTSDQDQKSEMLMDSDSFDSILAGITADIDLDGVAELILGTDNQVTLAYKRNADKNSS

QDAVSDLSHEVAAVESNQTFTPTSFDSSHNIWSDTETENQGNTFTGNFVDSKTEVAAIAS

TSVGFEDIWGDLQSFMAGH

>contig45667 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64310.1|) 2e-73

MTTADISVLHTEQALWRAFDACLAVIIDQERRCAREGNRKFQTDQLAARSRALAFRTLKR

HTTEDSIAAATTSINEGLPGRKPCHEVESLDEELRREPPYFLRYLPNDEEAMLEELRHLA

SNVKYPHENQVYAAPSLRCYSDLLKQYYRVLDSQGFVDPPPLAFF

>contig47041 Frame-0F|Blast-putative transient receptor potential channel [Xenopus laevis]emb|CAE09056.1| putative transient receptor potential channel [Xenopus laevis](ref|NP\_001089174.1|) 2e-06

MNTGHVVLLKQLVEGTMGSNWIQNLRLSNGWTPLHLAASQTNFALVRYLLVECGCNPLLM

SPNGRTAFDFAVEIDRESRVSSLLREHIKQRAFWER

>contig48080 Frame-2R

MLHRVWRHRSEIFKAEVLSWADFGYNPALWVQYSALGTIQRCK

>contig48189 Frame-0F

MRPFPLSRLYDVGTRNLNYLDAQPSSKFSSVMGRLRVMLAISWVLAAYATNAVKLSEGTK

FDGVVSSRGNRLLVGKGMDMSLVDNNYTPAQVTTNEERSIGGVWPTSKGLVLLSDPSVVG

PAKPFDGGMKTYKRSNVAYQSGAKMTRANAVFIVQAGGTLKNVIIAGG

>contig48422 Frame-0R

MALIASVIQEWYLWLSFWFWN

>contig48497 Frame-2R|Blast-nucleolar protein, putative [Phytophthora infestans T30-4](gb|EEY66010.1|) 2e-40

MFLSDYFEKKPLHVRKEEKGQLFNSNLFSRKKMLKIMEKQSDPFSFGKDLAICKYVDSKR

ENFHDEACNGQASSRQVARLLDSGYSCQFYQPQRYADGLYELNAAL

>contig50382 Frame-2F

MVHSCEDMPRWDDEMFHVEYPSMYNELLVNGYYLTYLIPYIANSSAPHEIADPLTLVWHL

ADRLVVEHDEKWAQLCLQCLRLIITRHPTRFTSELPTQYVLSVLRNHANHSPAFLRECFR

YLNTAIMLTYKAPSKIFCRNCTSVARSILQVLADPNLAAPIVGPLEVERDAAEDTLHFVE

PEDDRIAIVN

>contig51187 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62433.1|) 2e-56

MLMDANKFEDALALVALHERCENIINADNIHRQIWTKYREQAGRRIDGVEGVLMHHELQN

IVLLSTISQENLHYKQRSEFLEALDHLRAISDKRWVIQECLTLIADDSSASMKKILDLAW

DAWVTLNGVNDGGAQLLQEKAKLQRFFYRLETLRLFLCEEAGVQPTSLAAAQLFEGTSYA

LFRALP

>contig51590 Frame-1R

MFSVQTQSLPVWTSIQESKIIKPGAIASNGEDPLYLSGEETDSDSDRGSDTLSREDQHLM

PNFIQLHLAHMHKKTYHRGRAGFVMSHSSPVSIPARTRKHVATSAKRWIWDEDDEDDEED

NCNQFSCCAHHSSQRQSSMAKATAKSVADDGAMKDLIFELEL

>contig51877 Frame-1F

MHFSLSSHSSLVCRSLSAYSVPCYKHTKISVYQSRDESKSNLYQNLDAFTQDLIQVLCFF

NIRHQSLFFLKQQTFFTVESLFVLKNALLLALLILVVRFKITISFPCIDY

>contig52018 Frame-1F

MSMRLSSSHVPPSRLANSNASLAFTLDHLENSIARAGQVIELSASDELERGRWFSQQAQT

EPIPWPGR

>contig52209 Frame-1R

MALLAVLLLASIVATPCTAISAADSISSAVVNVKNSEAAFYVSSAAAEGWGESLEAQKLK

DGASHAYYPLVYNVTGLVNGFGCTSKEMLLKESSNGSLAASNLSSASLLG

>contig52300 Frame-2F

MEDGIFFYWYAVALIRNGIECDATAALDKCIQCDYKPASCLYLQAIVQLQASDYHAARNQ

LQRLIELDFTQPSSMFNYALLMERMSNFSAEQQMLKYILEFHGNGISGIAAAQESAAQVN

TVNTLCAFDDQANFTALFPSRRRNVTVTMVHRHAALAAMENGCWLESKYHFEEYLSSVYG

LDDSDAFRVARDYVYVLLQSKLPSLALRESEQYLLSYDASNAASDSDKEVTLLL

>contig52425 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63028.1|) 8e-78

MRACSKAGRVSWAYNIMERLQVAGLVPDRASFTILMNTAIAEGDLDKAFEVFHLMRSHVT

EPDEVAFSCLINGFAREGRVERAMNLFEDLLECGLTPSLVTFNTLMNACAKSHYYAHKAI

DFYYEMQELYDYTPDIYSYTTVLHACAKHG

>contig53743 Frame-1F|Blast-deoxyhypusine synthase, putative [Phytophthora infestans T30-4](gb|EEY58052.1|) 4e-25

MSASLDANDSKVPKVAQNAVLVRSENLEGKSAQVRGYDFNEGVNYEKLLQSYLTMGYQGT

NLGEAIEE

>contig54243 Frame-1R|Blast-Cullin family protein, putative [Phytophthora infestans T30-4](gb|EEY70364.1|) 3e-30

MLLRALNDQWVDHQVVMTMVRDILMYMDRTYVTQKRKLPVYDNGLYLFRDIIIHHNSVRE

RLRGCLLGSI

>contig55015 Frame-0R

MATTTGTTGELLDFQLDNADIQFEEDDDADWGEM

>contig55604-0 Frame-2F0

MASSPRSRSPSRPNASSRSSSRSSSPTPSSLKATPSTRIAVRVENLTRNVQADHLREI

>contig55604-1 Frame-1R1

MRVDGVAFKDDGVGEDDREDEREDALGRDGERERGEEAMTCGGY

>contig55778 Frame-1F

MYLDNCGGHNSSEILNAALAKTRTKLT

>contig57097 Frame-2R

MRPSSAIRLIGVALLIVNYSSSLATQDTHSATVATVASSDPVESIELVSTTTRSVRSLQT

EDDDPSNESGLTEEARGILATLTDSLGKKLNLHNGAVPTTSRVSKDLTSKPEELLPSIAK

KAL

>contig57848 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56987.1|) 4e-12

MTDKCPEDLSFHTEQLDSDSDVNSPLTAVSEEMRCQYSSKRCENERTHKKSGGLHKFCAM

HREKANRNQMRLDQRRRVVKQQQKDMHRQQQARQMQTLLRYSPSAMAAGQNFCFNRTQRS

PVGFMRSSANGRPISPSNMMINMKAMHIQKGMSTGYQSPQLKLSPELPLFDQHDLDILEA

LLFSSDEEQQDAAPAKHCNTSQLFCAPSIVNV

>contig59482 Frame-0F

MPNSMLPVWQSWSYIGPLWLHG

>contig01572 Frame-0R

MAALSGAVGPASFGPPQISPSSTSTTPGYSHASVTPGYAFAGMSQQTRHARRLYVGGIGE

IAEPEITAFFNDVIDRALEEKQPGGSVVSVYINRERHFAFVELRTIELTTACMNLDGVSY

HGQPLKIRRPNDYNPVTVPTELGPIPQLNLAALGIVSTTVSDGPGKIFVGGLPYHLNEEQ

VKELLQAFGPLRSFHLVKELSSNLSKGYGFCEYLDVSVTDAACMGLNDMRLGDKTLTVRR

AMSQENAKAVANAAGNVNTGLEMGLDPSQAAMQAMTLAGITGVPLGVPTRVIVLLNMVTR

DELEDDDEYADIVDDIKGECERFGRVVSLLLPRPRDGIVSAVGKVFIEFQDVASAQGAAT

ELHGRGFSNRIVSVEFMPEELYARREIS

>contig04478 Frame-0F

MVCSGDRVDTIGVFYQGVNEPETLGGPGGKCHNYTLGQDEYFNRIEASADFRNFERRIFF

VRFETNKGNKLEGGTKSGRVGVSSRSNHKLAGIEGCYGNDVDSITPIWISI

>contig08940 Frame-1F

MVFIQTPETFFELEKLRERKLGSFVMRIQKAWKKYFGRRHLLQLSHDITKLYTSNNKQRQ

CVSIYRPFDGDYLRDSALREAVMGIIQYYCDSEKIVFMDTIKKICSIAGVSPDGSPAVEV

ERIFIITDHYLYLMEKRTWQPLIDPKSSWVPPLVYLRRRLRLTAIQEIVMSTLADPYFIL

KVHQEPLLPEPDKSNWMDNKSTMVCLATGKKFGLFNRRHHCRFTGKLYCNDVCKQLEVVP

DLGFYTPVRVYDKVIGLMSTEMPEDQLLSSEKKTEIAVTLVDAIRSLASIVTPITFNDSV

RLRQATCAGLSRTPQQQIQFVSCGHDKITGDLTTMQINVAPGVPDEYIRKRRKREKARRK

KLELQREEELAIRAQRQEQRSYEREAERNRRVAEKKAKKLAEKEARKHAVTSKKKSAKAL

MGSARKFGENVKDSSARGGVGDELAAILARRRGT

>contig09323 Frame-0R

MATYTLATLTLFVAFAVIVTAHEGEDHSETTIDLSNECASNVSTSFIDTIDNSSYFSTCV

EGTTFNVTSVFDVLNFTEPEFLTFCNSSTCLEPIHRLMGSVDCFITYLGAPRNLSDEISK

LHDECHEVLDAANLTMNMDGDSDAMDNSDSTPPGANASNSPTLLITLGSIMSATVIAAFL

V

>contig11757 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58463.1|) 4e-65

MVLFAVIAGAAALASASLAAPIFPEPKPLPYDGSFNDLTVANIADKYHTFTFNMRNKKEN

AKVEKYVKIDQKARVPAYNNDTGVAYIAVDDTSIFKNQTNFRRSELSQFIKTNPKGKTFI

RASFMKEDEFLNPRQWQMFQAESLIFQIGVDASVEPPQVIYYNNHEWVPKWQTDFKTKTW

YNFGVAISKDPKGDNHGWSCTPAWETTNSN

>contig12095 Frame-0F|Blast-serine protease family S09X, putative [Phytophthora infestans T30-4](gb|EEY70124.1|) 1e-10

MYSRTDIDSSKIVVFGRSLGGAVSIYLAEKESSRV

>contig15160 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63766.1|) 1e-145

MEDLTEEELNEPMSQMDKARLSSDIKVLPQDKINRVLQIIAEAVPVAKLANENDEVELDI

NAFDTRCLRMLEGYVRENGIGRKRKRPTKKSKMQPAEKRLKSAKVAALNIRHRKEELKNQ

LAAIDREALKGLRTGETGDRRPDQDVPMTEVDADTEIGALKRSGETSSDSFSSSSELSDS

DSGSDSDSDSEDEGGVPLERSSPIASASSLSHVDHSTSSHSADAANKIRDEQLSSLEPLR

VENRGAWSMLAKKENPDGTPLIGKSYGSSQSTSSLWLSARSMEQIKQQKIQQKEKERTDE

LEAQNRRKIEQREKEKEREQAERRKQELEQAAKIAEEKCVREERGREAKLARIAQLAMVR

EKLARDDDVELHDATLSEDLDAFSSSSFL

>contig18307 Frame-1F

MEWMKTHRKPVEVQHRAIQCSFKEVEQDTFASIEFNQLKKKHSVSPYHKRRTKKLFQSKR

LSLAPITCTKAPTAFDKANNTCAEINSSATKIVSKVREDAGVSICTTLIKVMWFRHSPLP

IRNE

>contig18857 Frame-1R

MIIDWFLIFNFILVHHTTINFVNRTPRCNYPEILCQVETQNKKTLLAKFWRIGINLLTCY

ATLG

>contig19322-1 Frame-2R1

MQKLRLKLISSCEDLSNGRSMQIALA

>contig19418 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59232.1|) 1e-140

MRRHLQTRLQRSHWAAFSVSKGLNLDGILSKKLRATAKELSDEMVPALKVLSESLGLLRH

SIVLKNWNASDWLVGLSVLAQYKTQLRANEARNDYTKMPAVMEKELLTKLLRYVRMCDAV

YAPSDAAFCEEANILQSQVLRSHSGGVVSPRCVIVADHEHRELVLVVRGTASLLDFCTDL

CLQNEPFLNGQGHRGMVHAATWLVRHLRDDLVKFSERYIDYKVVATGHSLGAAVAALSTM

QLKDSFPKIHCFAFGTPACVTRELAASSYDLVTSVVNGYDCVPRLHQHSLMELQEEIRQF

NWRSALRDMVVEVYRKQKLAVEKHQRAKLNELQSALWNVKGPLKLKQRTNNAMAKLNEVK

TLALNNIASEVDALLSDKLHAAYSIITMDKSLLKHDSYLKKLLKLKEGDSLWQQRISDSF

IALERLVPVVNKPEELDNVLAEVKKVLYNTVEGTKTLLKQRGDGS

>contig20384 Frame-0F|Blast-coatomer subunit zeta-1, putative [Phytophthora infestans T30-4](gb|EEY57872.1|) 2e-17 NOT\_ORF

MDRHVMLDNIELVLLTFDEVVDGG\*DHFIDSSCSITHLVPSQRIILEVDTPSIANRVLMR

VRAFQYLLDCNLFLMNTLDHFFFNF

>contig22416 Frame-0R

MLRIKYRTERLDIFDLWRCLDLRLRCLTTGLWPRMISQWRGWSPCADEEALDLHPLLKRF

WRPLHEH

>contig23327 Frame-1R

MSANIVEADASGDDENDGDDEAILDFTQTDYAIQMSQVETYSSESDSVEGESKLFKEPTK

PKALHKLSDKALDELTAKLVRYMVYKGGLKLPIKFPDITKDVFPQFKNVSRYFFYYAKQK

LEVVFGYRVVHVDDSISKEMYLVLNNASSQEHLLLMNKNGRAATRGFLMMVLGLLWCAPS

RQLSE

>contig23802 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67255.1|) 1e-117

MQLLHCKWPSALEGLVPSVKTSVAIGLKPQVLFRGIRVRMGIHDTNVGEEGNLIRQTHRV

TGRALYIGASEYIGREIGDVGFGGQILVSKRVALWLESSTNVARVRTPFRLDYYGRHSVA

QLDLDH

>contig23899 Frame-0R

MTSSPSPETDKMHTPVAESARYNDQTVLNFDSSASEKLKDEGCSSVFTDRHGHPLVKFFK

WYVTRKQRIFLISGLVIIVFVVILLIIVLAILPALIKHNVDSVQLAINYLDVKSIPNATS

LSVDLSVNVQHDIGISASTDDITAWLLYGGVAFGSVIIPGLDIKTGKQDYNVTVDGTLML

TDVGAFNSMAATLLDDTETLLGTTATVTAHALGMTFNDLALRRTLHLKGFNMLRDPAPVV

NYINWFGCSNDVYQMDINVTLTNPSVMGLNGIGALNLSLYYGNSYLGYAESMKPDLGLPR

GESVQILRATVPQDTKALSSMALGVAGGSAHFYITGDNPYSIKYTQFQDAIGHVNMSIIY

TDGLAKLGFNTSCDKLSHLA

>contig24850 Frame-1F|Blast-polysaccharide lyase, putative [Phytophthora infestans T30-4](gb|EEY62246.1|) 3e-90

MLQAFKAIASLVVASTTVAGLPVPDGTWPKSTGLVSFDEPYVVKSGETYDGKMQTFDRSN

IKCEGQKESGAETSVFKLEPGATLRNCIIGKNQMEGVHCFEHDCIVENVWWDDVCEDAFT

IKGGKASSVTKILGGGARYADDKVFQHNSVGTVVIDGFFAQDFGKLYRSCGTCSTNPAQR

FLKLSNVYADLTIIKAKRVDPNVSIVMMNENYKDEA

>contig26052 Frame-1R

MQRKTVAIVAVARSDTSIHKVLRACSLFDRPIHVACPDAERREVLIREMLQLKVDDAILP

DKDSHQVVVDPVIDFGLLSSKTEGYSLRDLSSATDRAFHQMLKRHAYSEPSKSSKVICTL

RQHDFIEGIENFQPTALLGVDLFKSSVKWSDVGGLHQVRLILKDTLELPTRYAKLYDNTP

IKLPAGLLLYGPPGCGKTLLASAVANECGLNFISVKGPEVLNKYIGASEEAIRDLFKRAG

LAAPSILFLDEFDSIAPRRGADNTGVTDRLVNQLLTFLDGVEARKGVYVLAATSRPDMID

PALLRPGRLDKYLYCGFPNEAERLDILRVVSKGMNLSKEAAEYLSDIAKAPKSDNFTGAD

LQAV

>contig27334 Frame-2R|Blast-rab GDP dissociation inhibitor alpha [Phytophthora infestans T30-4](gb|EEY66313.1|) 0.0

MAEKSKKDLAWLPLGAVALADGEYDVIVLGTGLKECILSGLLAVNGKKVLVVDRNPYYGG

ECASPNLTNLYKKFKPEQDPRTDLGADRDYNVDLVPKFIMACGKLVKMLLHTKVTRYLEF

KNVDGSYVVKGGRTHKVPATGEEALRSSLMGMFEKRKFRKLIMYIYNYEEGDPKTYEGID

LFKQPMSDLFEKFGVDANTQSFMGHAMALMRDESYHQRPAIETVRAIKLYAYSLERYGKS

PYIYPLYGLGGLPESFSRLCAINGGTFMLNRAVDEILTDKDGRAWGIKCDNEVAKAKLVI

GDPSYFPKEKMRKIGVAVRSIFVLNHPIPSTNDAESLQIIIPAAQANRKNDIYVAVVSSA

HCVAPQGIYIAIVSTLVETSMPLQELESGVKLLGPFLERFDAITDMFEPVGNGKKDNCFI

SSSYDPTSHFETTSEDVLDLYKRITGEELDMNINADSTDVDQ

>contig27341 Frame-2R

MQFKHIKPLNEPLLSAPMSLGKVLCSLYANTLDFFCNSSAKARWVGNSSRHRNLLSNLTK

>contig28267 Frame-1R|Blast-adenine phosphoribosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY59064.1|) 9e-85

MSKLNFDDPKIKKQVLADLAGTIPIVPFKGVEFFDIGGLLANPEKLQLTFDLLVHLVSPF

RDQVDAIGCFDARGFLFGPFLGAFFQKRVFMLRKPDKMPSVSDIIEYFKEYKGDNSDGSN

SLSIQTYAVNTGDRVLLIDDLLATGGTCEAGIRLVQQAGASVTICIFVIEISELNGRLRA

IKASTNEKTQILSMLTS

>contig31287 Frame-2F|Blast-Annexin (Annexin) Family [Phytophthora infestans T30-4](gb|EEY59586.1|) 2e-52

MQHIFPRHAHNVFHGVPLMYPREIDDACERIRDATDGLGVDEKILVNVLTSLSASDRSLL

IYRYKDLYREELKDTLSRETVGNFRFLLLLLTMPLPEVEAFVLNVATSGSSTKERLLYP

>contig37906 Frame-1F

MVGSPHYVAPEVLSNARYGYDGRKADMWSIGVILYGLLVGSLPFGRELTTCPRYLKFSEW

LRSLPCDSHTNKLVYDSNSYQSGSPTSLSKSQVPDMALTYSTISASRALMRNNSNCISNT

NSNVGWCSSLASGTTSSSLGPEGSNGITNRRSVVFPTWFFPVTLSPRAAFLLASLLHPDP

NKRISCEEACKSSWVLEV

>contig38033 Frame-1R

MTGTKSNDWSGKRTFGGRCLHEVDDLSARNPYEDVIETIGRTLQDFDEDNVVPVYGFGDE

LTCDRAVFTFSEQGQAGLPLETIRSRYREVVHNVVMAGPTSFAPIINEAVNIVNRSGNFH

ILVIIADGQVTRSVDIPPHAVSKNEKETIDAITFASNFPLSIVMVGVGDGPWDSMIYFDN

HLLHRKFDNFQFVEYHKITSQFSDPQMKETQFALQTLMEVPGQYQKIKSMNYLDRGSHRA

RADLPRVEVFPPPQSIGLVHHNSNHHVQRQAQARNAVISTSSLQPDQAKPRSMSRKDTSH

TSTGLTPQHRSLRAEDELKRLQESLLCSICEERKKDAVFQCGH

>contig38491 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69137.1|) 6e-22

MLAIKRPRRAAVTEDSLDPRVMTERQQLAFLLRATAPSDDSASSSESNSTSDSEEDDEPS

YRRQPSKRIKTRPAR

>contig39290 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64346.1|) 1e-94

MKRKGVKVAPYICNVVINVCSKADDPAVYQSRALEVYQDMRGTSPSIKQKKKKADSDEPM

YSAIIKLCSKARDFDACKMIVAEMEAAKVEPKLRTFGPLLQAYSDAGNLNKSMWVYEKLV

SYKLELSEDDYVALLRVCSLAGHAKHFYAILECFIDDIWQPSLSTWDVLTDWFNSEAARV

NGHKWRVTHGTVSTQGVC

>contig39324 Frame-1F|Blast-ATBET10 (Arabidopsis thaliana BROMODOMAIN AND EXTRATERMINAL DOMAIN PROTEIN 10); DNA bindinggb|AAL15293.1| AT3g01770/F28J7\_10 [Arabidopsis thaliana]gb|AAM20580.1| unknown protein [Arabidopsis thaliana]gb|AAM91306.1| unknown protein [Arabidopsis thaliana](ref|NP\_566151.1|) 1e-12

MDLSTIAEKLAAFEYKMHGDFIRDVRLTFENAISYNRADKERAEWSVYSAAAHMLSVVDD

LWGDVTLEVTEKTRRRNLLRKERLNDPKRKRSDDLESKMQKSHQPTSEAESHHQSDQKSR

AEESVGSSTFVKTLDKCASLTRNNATSTSVVGTIVVGGARGSSEDATYSEATRVKLQLMP

S

>contig39474 Frame-2R

MCPTDRVSTEKVFSKLKQLLIEVAEDVFNCLGDFNSNLSAFDSRHEKLFSGNTSTFYLKS

YIQTARDTTLELRNVAHQIAECSQPSQPEIDAACNAMHATVNSLNELARMACQFDKESLN

LNGLSVVAGSLEAKASSTIKNDTNTTGKDLTSIRNKRSESEALRASDTVEEVVAMAFGHC

FGKFRALQHQVATSEKALSPLFAGRVNELVAESCAP

>contig40540 Frame-0R

MEIKRSSEQLSRAAQRKRRKQKKSENKDIGQWDRCMFVVVRKRRYCNIARVAGSLFCGNH

LPESDAVVSNKSQKFKATLRRRVPCPVDKAHTVYEFDLAKHVLICNRAKDADVMKKLPYY

IHNINSGANCSDTEQKAALNNSADNTEEKESEHSALSAKEQQSMIGKLQIINFLNLRNRI

EAIYASCVGDLALEKLHHNCCDKLLENKAKAGASKCVLRHIEQQSSIIGHMNRVKLFNDP

TAAFVELGAGRGMLSLAVAQMLPDSLYVLIDRAHTRGKADRYIGGDVNRINSSKKSASTL

RAKIDIRHLNFAGIKEILNKPIICMSKHLCGVATDLSLRAIAQTLHNPRIDRANVTEGTC

VSNSLQGLAIALCCHHVCVWDDYINPRFFQEHGISPEEFNLLCSMSSWATCGMGLDGDAV

EHMLGI

>contig41158 Frame-0F|Blast-elongator complex protein, putative [Phytophthora infestans T30-4](gb|EEY66437.1|) 3e-40

MMSFRRKSPTSNIPQRNGTKPFLHGQTLVTSGLNELDMTLGGGLLLRTLNLVETTTLISA

QDASSLDLSSRASDALSIDLLRYFVAEGVVDREQRVALVAPDAAGFINLQLPLELSLAQS

QVKQQLADKED

>contig42520 Frame-2F

MTTSYLIRAGLDFYVSKSEFSNDFGTFLSRIWTAEDNKNLDLTIGDLAALLANIDESFTA

HPLCPILVNCLEYKANAKLDRFEEGLINKAQNRKELTSTEEWTDKLLTAQRSSS

>contig42906 Frame-1R

MRLLPKSSGIRPLMNLSNAIGHTKVSVNKSLEALHRVLTFEMERQPERLVGASVQNIDEI

HARLKPLIRQITQCSRCAERRSDYRDIPMAYGVTVDVERCFDTIRPRKLYQMLKKALQED

EYLIRKHWVGHQVTPLTLADHDETLPSASLYFKLERPAYPSGELLGFDEVAARSKIKNTM

LVDGVLYDYLKKSTALGLLKEHLSTNVVHINGHEFVQRCGIPQGSVISTILCNIYYAHFE

RHVLRKRFPKVCEPISVSCCQHEELFRYTDDFMFITTDLNRAHQFLKVMQEGHHDYGCFV

NVAKSQTNFAVQNENNQTAISSPKEYLAWCGMLIELKNFQVYVNYEKLGCSLMQGSIPIN

ETKAIRKYFVTKVISSVRQRWHALYFDPELQSHDSIIINLFQMLLIIAHRFFVLVDMLPF

VNKEMHFFYRAMHRIFTKMTKSIHRSLEQKLKNTELVSATQSSKRVYEAQKDQVWTVGLY

AFRLTIQAKQKRANVRHVGKKIDWQKLLNVICTEQDNFKKRAKRTQGTAVLDLEWLLQDH

RNKRVLQQSL

>contig43237 Frame-1F

MKLAKAAAQQLKGVIIEFDVLCSSLLGKSEIEMRCNVAAEKKHQEIKEHLSPSLFDLKSI

KSMLVSDVRSLLKDLNEDSTGKPWVAKERLQNTLQGLPNQFLKRITGFDEQEKAASVEND

TNSASLAPARMKQQNHEV

>contig44287 Frame-1F

MASLMSRCRSFWLASLAILACYLSFSKVYSEKNFIKVPLYKHQESAQLSDRLARQQIRAQ

RRALEESAATFDNVSVGVLALSESHLGVGFGTHYAELYLGIPAQRASVIVDTGSFFTALP

CSTCVNCGSHTDGFFNISKSMTAKYVACKDFQYCTSCENNRCILS

>contig44702 Frame-2F

MRNLTLEQTAVVAFASPGDIARELTKINEDSDYDYILDCQPTAQKSGLALALSNGKMQLR

NLETLSLLHEFQAHSSAINEVYTSPSSPFQLATCSSDHCVKLWDTRTALPAMVVPVGREV

WSLSIGCGETLLATGTDELALFYDVRTGTLLNQYGESHVDAITKVRFHPMQQNFVVTASE

DGVVCFFDCRIPEKEDTIESIFNVESAVTTVGFFGPERENIFCLTGSETLDLWNIWTAER

LHHYDTIRDDCNKYGFKTDYFIDCVYDDQSNELFLLAGNHEGNMNAVTISKDGRVQHATA

LHGGHKACVRCLYYNPE

>contig46191 Frame-1F|Blast-bifunctional folD protein [Phytophthora infestans T30-4](gb|EEY66137.1|) 6e-06 NOT\_ORF

MACRR\*GIRFDSFLFDKSVSQVAASADAREIP

>contig46533 Frame-2R

MKRNFGSLNLVALDLSSPFQKDAESADYSLSDRFSAINPSAEDCSMDPDASDCSGDENVG

FPMERLSADMQSASELLRVEDIDLHDTMPELTLPVRSRTPPPQNKKCDAQASSVLYPSVT

ELSHDLHDYHHVELNALRCLNLKVMLSNTKPNYSCPGVNGRTKAALLPIHHPSLQSA

>contig46586 Frame-1F

MRDLDCVKLHCIWTRHTKMTMLHVNMIARQCNHHEARGEKVFGSARVTQLRVKPSCIPKT

KTWICKAMSIGFVIIHKKCVVSIKRNNASMLLCRGEKKSASKRDSSRGRCQ

>contig47040 Frame-1F|Blast-DNA-directed RNA polymerase II largest subunit [Phytophthora infestans T30-4](gb|EEY59052.1|) 1e-18

MASTQFSYSSARLRRVKYLQFGVFSPEEIRAMSVTKQTKVNDRIIPDG

>contig48081 Frame-1R

MCNALYKYCPDVKYTEPTGGYFLWLHLPDNMHAEQLLKEAVSHHGVAFTPGTRCSLGTDD

EDVSNVALTNCARLSFAFYSEEEISTGIQRLCAAVALQSRNSN

>contig48225 Frame-0F

MLQSITNIYAQTNQHRQASNKNRLLAPVSTSFLLDAPLYVLPSCGLANDSGQLYSKECER

KVKSGLFCPRVSHKTFKRRSKI

>contig48423 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58089.1|) 1e-152

MQHETSEVALLTFGLVADVQYADVDDGWDFHHTSKRYYRNALPQLQAAVAEWLREAKSGT

KLRFAVNLGDLIDGKNRPASTSRQALARTKAAWKPFVDTVGPVHHLVGNHELYNFSAAVI

QHELLYHPPTPVNVTSPVSYYDFQVSEAPNYRFIVLNCYGLSILGRETSDPVYQEAMGLL

RRVNPNENFNSPVGLVAEQRRFVAFNGAVDQVQMQWLEATLMKATEAREHVVIFTHIPIH

PSSSPTPSSLLWNYPEVLDLIQRHACVRVVFSGHSHVDGYVYACEGVHNKGVHYVVCDAI

LETPPSETAHALVHVYDNKLVVEGYGKIPTRELCFPVNA

>contig48496 Frame-0R

MLAACLFTIFRQISSSKCAIEAFYCLHIAYTSTAKDLTTLKAATYCMSVTDILPTFLSTA

SDQAAI

>contig48944 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65045.1|) 4e-23

MSSENAVLSRAVHGGSYRFVQRLLTFSANSFVLRKLHLNVTGAVTVRLELTLASIFFLRD

GFRLAFLRM

>contig49356 Frame-0F

MADIAEIQRLIRLGETYEVCLTNHLRSEYALHDPLAFYCMLRSRNPAPFAGFYLANPMNH

FQTLDRHLKAGRMVDTYAVCCSSPERFLHMKANGWMESKPIKGTRPRGLNPESEKTIIAE

LANCEKDRAENMMIADLVRNDFGVVARVGSVHVPCLMGVETYA

>contig49820 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65151.1|) 4e-83

MWDLRVKQHSVSIKSAHLSSTLSLDFNPNKPYMLASGGDDGKIKFWDLRFAQKPVLAMNA

HSHWVYSVRYHPLHDQLVLSGSSDATLALWRVSSISSSPFVDLDELDLMDETAGEAAVA

>contig50336 Frame-0F

MRAPSNSMRRVRVRTSHHRESSEKVVDSMALQRNLVSDATDALEVTFCAVQRVRDRYFVL

LCTTSSWRLFRLDGFCAARESCSPVQLMMDPNKDAAQLTGVRFFHLFKFPTDVGSVDAMG

ALFVTNRSCLLAEDDNEYVTSEAEINDNNGHEDITVLSLDTQQVMHKLPPSPSLILDIQT

NATIAAVLCETLEVFLYDLATFQLQFSILAASPAMALGPRWLAYPGITQSITTMQANEQD

QMYFGREDSDSDYDDVSMDALLTGGITVDARNESHSSSPAYTAIDVAQNVASGLYYLSEV

GRATIAP

>contig52019 Frame-2R

MKRLRIQKPAITRKLDQSVSINTSTYLPTSKLEGHAMNSTECSARGNILAQDKLSGNETI

GDTIHECVNLERIQDCDESSKPKALVGLLTGSHSTDVITAESEATVSQLKASISLKEAKA

KACS

>contig52082 Frame-2F

MAFRQQNAKFRRWPWFRAYTVFTHARFRQAPAPAAYARFEPLPLLNSSVLSTPVGSKSLL

DGSRSLSQRPA

>contig52301 Frame-0F

MLPSLHSWVASAKLEQFHAKATSKSLQVEQAGHHHRQGLPAWPQQIRSRYCSPLPTSAAA

NHLRSLRLNSSHCLC

>contig52374 Frame-2F

MKTPTIAMMAAMLLVGASADVMTNTSLTSESTAATNASTTPGCFEVSVENDATYCIQGPI

CSGPALRPAGSLCPVRGDVATADCFGNLPSYSAQGICALPMDALCHIGKTGAWSCVIPTS

GNFSNENTSAADGMMNATMTSNTTATITNTTVSTDTTKILGCTEVSVENDATYCIQGPVC

SGTAANPAGSLCPVRG

>contig52424 Frame-1F

MPECFNIALLHWAAYHVVLAPSILTLTDVLRRKWQIFTDTTRLARSLS

>contig52451 Frame-0F|Blast-alpha-tubulin, putative [Phytophthora infestans T30-4](gb|EEY54333.1|) 2e-07

MREILSIHLGQGGIQTGNSCWELYCL

>contig52590 Frame-1F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY65546.1|) 1e-108

MQFLGALLLSCTQQLSGINAVFYYSSNIFSDAGISDSRVGTLIIDFINIWPAIFTGVLTL

RFGNRNMILWGIAGMAFMSIGMTVAFLVDVSVLSIVFTALYVIVFGVTLGPLVWVMTADM

FPDSVRASASSICIAVNWLCNLIVGVGYPYLADAFDDWSYMPFTVLLAIFFILSLKLVPE

TAGKTNEEIQVEYEERR

>contig52969 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66701.1|) 6e-83

MSGWFKGQHVAIKMLLPENRKNMKLLNSFLEEVKLMSNLEHPRIVRFIGVAWDSLSDLCL

LTEFMEGGDLRALLMSYEAQNLPVGFNATKVTIALHLAHALTYLHSLDPPVLHRDLKSKN

ILLSLSLDARLSDFGVSRENVDKTMTAGVGTSRWMAPEVMMGERY

>contig53742 Frame-0F

MFRRMSFSIAHRMVQQRVQAHVSCLSKNHSNSSERVLFVSRTAAAAGLQDLLPFPVSAAA

LRDFKA

>contig54512 Frame-2F

MHNREPIYLHRDLKASNILVTADWTAKIADFGIARIATNYSVNKQQKSMQSLHESVNIGN

GAASELMTTFAGTWRWNAPEIMKDPNECRFNREADVYSFGVSLWEILTNGAIPFGNVDFD

HQVRLLVAAGERPLLPSA

>contig54978 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54011.1|) 1e-31

MWPPAAKLSHLRGTLVLLEVVAMMCSVMHNTDPDANSSTVRTWMAERAQFCL

>contig55061 Frame-2F|Blast-hypothetical protein [Monosiga brevicollis MX1]gb|EDQ85523.1| predicted protein [Monosiga brevicollis MX1](ref|XP\_001749714.1|) 2e-15

MFMFFRSLYFKDFVERERERERERERERERERERERERERERERERERERERERE

>contig55380 Frame-0R

MTSRSISMRLAPLIELIASVERAFAAVTKRQINDAFLALQR

>contig57023 Frame-1F|Blast-predicted protein [Micromonas pusilla CCMP1545](gb|EEH56938.1|) 2e-13

MSDEEKEAIQAWIEANNRNKYGDLVTTMYLGGTPLFDESTGMKLDLYDYILSRHRDRPWL

EENVTCAENIGDDTKDV

>contig57096 Frame-1R

MMGSDYLDRVKEMIYSGKNKIPDSSSDISL

>contig58347 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69058.1|) 3e-56

MSAGTRVRRDAATNSSFVVRIWRWVKIQFWHVFYGQNEWQRLCRPTGAEIDEDERIVRFR

TELALSNKMEQTCNMVFDKVPFSVEAMLHDIAIRANLDESDIALMANVRACLRQCNFVNK

VYARAYALKSEGYSSLNRDHEEMLDQLWTNLKPNVRREGGRITKEWGEIGFQGTDPMSDF

RGMGLFSLVQLNHFTKEYKVESK

>contig09320 Frame-2R|Blast-diacylglycerol O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY54102.1|) 1e-146

MAFNPAIVEQEKDNSAMRATQKTECPFVYETPGYFAEDSRVPLWAQVIVTDLFSFLTTHY

NFYGVPFLFLFHYMYTIGYGYIPAALIAMYLPFFLNGAQKTAKGNLWLAIRSTRIWGLST

KYLGIKLIREQALDCNKKYIFGYHPHGILVLSRVSTYGGNWEKVFPGISTRALGASTMFY

VPLGREFCLWLGGVDASRSTADKVLNDGTSIVVYPGGVPEIFKTDPKSKVNELVLKNRLG

FIKLAMRHGAELVPSFVFGEKWLYNMWNPPQSVINFFRKTLKIPLIFFWGKFMWMPKQPP

KGKRFGVVYGKTIPTKLTANPSESEIRAVHTLYVAEIKRIFSQYKKDFGYDDDETLLII

>contig12096 Frame-1R|Blast-serine protease family S09X, putative [Phytophthora infestans T30-4](gb|EEY70124.1|) 8e-67

MIDSPSLVPWLLSVVYTGGALCVGAAFLLYMYQDQLLYFPTIPGTPKLTRDNPPGYRNPG

EFSIEYEDLTISCKDGVKINAWLMKQKEYTTRPTFIFFHGNAGNIGYRLPNAVRIFRKVK

VNVLLVDYRGFGHSEGNPTEEGIKLDA

>contig12359 Frame-2R

MLATSAQFKIRNDDLLLDECLVPFWSFSDLQLIGAHREWPKQEIKERYFYSGGNLRDFTS

LKKKSTYRAAKSVDRAMGEVNVDGAKLLNTQVGTLSGQQIDRIRMTGLNASGERDTGEEF

LEKYQNRKDWVYVITSEYALRQLGKIVMPKYYEELYSKGIMLGDDGLMGIAFENYVHTMA

RDRNKIELRMRAYDRQQVREHTYVALELEAKSFCNDGKTATECDEVHKAICEVD

>contig12621 Frame-1R

MDKALLTRATSKDDTPTPGYLYGEIARMTQHSYETCTKVQDYLISRVKNKHHFIKYKALQ

VIKHVCREGRVDFKREMQKHIPIIKECLQVRGVPDPLKGDEYYRRVREAAKEVLDAIYDT

DNTPGLSGMGMSARIQGVGINPSDHGSGNSGWSSKIWGGKNANDSSLPPPPMAGPPIGGY

NGGAPPGAPYGYPTDSLPGNNNGPQPYGGHPPYGQQQPDYSHQGSYGGSGGANPPYGGVP

PNQYGGAAPPYHDQKFSGIGNPMYQDPRADEKGFFKGLKEKVASKYSKSDKSTFGSGPPG

SSNPPEGWSFATNRGPTGGTYGPSPAPYNPEEPYRPTGFAGGGYRPGGYGQDTRESASSQ

LRENLDGDRKKGRVGGAWSDADAPSAGGASGMPQSSGQESRAQSFNGSARDVRSYTRNSD

YDYDEKRREA

>contig13851 Frame-2F|Blast-Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily [Phytophthora infestans T30-4](gb|EEY59454.1|) 3e-72

MTSLTCPPAPAPAQNYVDKSSSPLISSGKSRQLVEPDAQQKIDTVPPFHEEAWAIWGMGW

QVSITTFCRMSLSTISTMFLGQLGPRELAAGALANIWTGGIQVLIFGVAVSICTLCGQAY

GAQNYRLVGVWLQLAILFLSLLSVPVMISFFYVDHILSVVTEDPTILALADTYAKLLAPS

VLPQAIYCALRQYLQAQEIVQPATIISIISVAASLSSNYFF

>contig15758 Frame-1R

MSLLSPKTCDEDVKRCAFPCSNLDVLSKRSIIYLSEKANLGLLITNVLFSKAFFLFSIAL

GSEIDSWRNRYQQRVNEWESKYNMRQA

>contig16698 Frame-2R

MRELLRTHPIYATDTPLKYSTYIYTAYQRRGTVSSCNLCQHTFFRRQLTTQESVAYCRQT

LLKAAKHY

>contig17561 Frame-1F

MVILSAGILFMESAFFYSDMDFLCQLGIALMFGSISVLGSPATVMAIKIELNSVGPFTSL

MLGATMTAEFIVLISFSVSRIVSSIYCAKLNVSMLNLFYTMSIVGSNVLVGVILAGVTLL

IFKLPGGESPHDDHSHDHKLDDNAAYCNQNTTKKESGTMTQPKMDTNTDFSIDDLHPPSS

SSCLSPQAVLSFKGFLWLSMGYMFYISSGLVAEATAAAFGLSWEIKFEALLVLMIASCVA

GHHTGIRHDMHVILDTAAPYFFLPFFVMTGASLKLDQVVAAIPLMSLYVILRYLAIFLAC

YFGGRYVLKLTPRQYNNLWLTMTPQAGVALGLANEVQAMSDEQWAADFSATIVAAVVVNQ

IVGPVLCAMGLGRAGETLQDRLKAGGVHDPKEKLESLEKGGFDRSMMPQHDRLSVVTGNG

PAGPFDLSRRMSMDPRGNAMALNKVRNAVVIGDDEVAFEIALGLSLYGARVNVPLLDKKR

TSKWQVMNEAILQRAAKGDLITYKNTLQDQESARAMSSA

>contig19321 Frame-0F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY61201.1|) 0.0

MIFSKKKTFYKDLRTSAMIGSYWNKVPGSPEVRAQCIEAFCELKGFHLLLSTLELLMQNH

TEGDELEATMDSEDIQILLQALLEFRTSVPESICTKISVLIMTYYTRIPDSVLKKESSDA

VGAVVDIVRRLVDAGVVPSEAINALWLGITERYVQSTSLPLRLFGLEQINQIVNCVRASR

ALPPRYFVRNAGTAAVNGVYVLKTNSTSATYVLRQHETGQVFTLFCCTMKSGLKWWFISE

ADKMQPGSDQDIDYYQHQSQYEEYLPPTHNWIPTGKGEVPPPELIAESVQEEGAEDCTQL

DYILSAWVVEKKILEAIFGDRIHREIVSRSALLVKYLAEANKLDTHSVDVIWHSCIQKDQ

TLVHEIHNLLIATVPFLSN

>contig20318 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55888.1|) 4e-50

MSSDDEGVLFRANALDIVKSWMPGGDEELNENKVQQQLEKRPQRNPVTLYRPTSASSGMS

LPSLTRPNTVNVNTDAVQINCDREMKQKLLRKARGSREDESVMAELNMKLQREEVEDDEE

KRLIISKTHDNKESMKRKRTTHDELLDKLRQEAAQKKAKNLKRKLQLQRKKLQQQKEISA

>contig23801 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68699.1|) 3e-31

MKHDSASPPPTALSFEEADVLLSISDAFIQEAVQMSRHYIGCSRHPSAIDATRWKRVAHV

RDLTMYQERRGRARLGTKRKLGSRLAETDFPDDQTKLLPATL

>contig24628 Frame-1F

MMIPSKREIFSVGCLVAAKIARSHELWIMARVVKFNFDSNTYEVEDVDSGDDESDDDAPR

RHYIVSWQQAVRLPGDTLPEGEWIQYAVNERVMAMYPNTTSFFRSTIRVPNPKGAPYVIL

KFDEDEDEHGLVPDRKVPFRFVAPLEPWHQK

>contig29245 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69549.1|) 5e-33

MLKQINVRLRGVVLNKANPKKMDMIQDYYSRALKRWDIPLVGCIPNRQDLSSPTIADYAK

LLNSGLVA

>contig33530 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68297.1|) 1e-151

MINVQNPKVLLRQYRQFLEAAFGHLKMGLDQYDDPVFLRLRYRCRNVFLQELISHLAGNF

EVFRRVYSVDCCQFSGYIGTVDGQREQSQFFLTPRALIAVRIKTKYTKEFEYRMIEEITE

ATAIPEAFMLLRKSRLHFIYSDHKYEIINGMRALAGYIGIHLCLNSQSLLPTQQMEQQFD

QSALESNEYFDVQRPTGRNGFTHLRKKKLCFVNGTIIEFTSGFNKVYELKKLRRIVVPRL

EGNVVQGVVVLEFADSCRVAYVPYDFDKFQAALYDGYNYVGNYNVSLSREFTNLNPRMSP

KALLKVKQEKLLYLNQDGLYIPAHAALERKIEKFCGEGVTIRSVLIKIIFSFESLNMNVE

VEDFTDKSMRGA

>contig33808 Frame-1R|Blast-glutamyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY69415.1|) 3e-52

MLLDPFYMRIQMQLSRLQSRVLLWPKALNLRRCTKSVSERKASDFAVRVRYAPSPTGYLH

LGGLRTALFNYLFAKRTGGQFILRIEDTDKTRQVEGSVEALVKSLKWCGIEEDEGPNAGG

PYGPYIQSRRLAIYKEAAEKLV

>contig33897 Frame-0F

MLNVCPIRENITFNDREYSAELLHYIKIKSPLNDPDSFTKHPKIVKSWCISILANIPWNL

W

>contig35543 Frame-1R

MAEEDAEFNKEVDVATSSFSVPFFFRFECRKLTGSRKIRCNSADTFTLDSNMLRENFSIA

KYEGLQEDGIDQEQHSSPSSRRKEFDVFLESLLTNQEQHKPFESADIMQIAELYSKVPYG

RI

>contig37523 Frame-2F|Blast-hydroxymethylglutaryl-CoA lyase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY58132.1|) 2e-60

MIMKMPGAAMARMSRSLTMNSVTSSTPAKVQLMGYPSFVKLVEVGPRDGLQNEKIIVSTD

DKVKLIDMLSETGLSAIEATSFVSPKWVPQMADNADVLNRITRKKGVSYSVLAPNIKGFD

NAVAAGAEEVAIFGAASEAFSQKNINCSIEESLQRFRPVCEKAAIVGVRVR

>contig39327 Frame-1F

MSDKGKASPKTKKVVRSKTPPPSGSSKGSGWLSGLSSFIVTKMNPEAKVAKLGVQMEAYY

DEEAKRWVFPGEASTAEPTKPSAPPTGPMPGSAPGSSATGIPPVGTNSAPSSMRSGPVPS

DDPLAALMAPPPSHNLMKKDPLAAMMAPPSRPGYYNARRGSATSHKPPRPQFAVFKPSAA

SVGAPED

>contig39352 Frame-1F

MIRCALCNVIEVTATSRMNLGFAHIKKYLAILEECFVNPNESVRDAAIAAFGAFTAQYCR

KVFQKDISVHVKYMQEIIPRYINCGIMILLKENSKHGRVPNPNVTARRGFLQAVGIATKE

LIQPCIVKVLDAVIQSTLVQEQQSETEDPGSRVAAVQALVNLCSRPPAELDICGMEGIVV

QTLVQCIQRDYRLDERGDVGSWVRKEAMKGLEKLMLGESSDAQDQHGLFIGASVLTDYGV

GIIVDKLSARKLKSGERSESNPVCYVKFEKPVLGYYYFSPNGVGLIHARKLIVNTSRPQR

SVEKSILDFDARMKFAIGHTNSDLGLATPFVRRLSPDLVGSVVGALAKQLAEKLDSIRNT

AGKVLFRLLHSTHPRVDGIPNRLQLEEIFPSRLVINWSRPHDTFPLVVKMMEIPDFMEEI

AAGLVISVGGLTESVVKASKESLFNWMRTHLRAQKIGLLERFGLFLVTLLSRHHLNDRIA

IPLMKTLALLLESNLFRFLFPKRLLSTSSRISCSDFGERLYAVLRHGVQRCSSIPKLSAA

ISVLIGLLPSDPKTETKTLRALVLFLGHKFPKIRTLTAEKLYTRLLLHDEVIDTNKCDTV

VQVLTDTAWDASISQVRSARDKLLQVLGMDIPPKKTPLPLKTQAIQGAQNYQELIKETGY

>contig41232 Frame-1F|Blast-animal inward rectifier K channel (IRK-C) family protein [Phytophthora infestans T30-4](gb|EEY64136.1|) 1e-118

MSVEVEDTPRFLRIVPVHIPKSFSFMRIYQSALHVGWPRIIVVFVLSFLVINLCFGLLYF

LDVTHLVAYDEINVTDFELAFYMSVHTLATIGYGSIAPMSNALYMNVIVFIESMVGIVTV

TIITGIAWSKFARPRAHIHFSSKMTISTIYGHRCLVFRAANTRHSGEVHENFFRIGVILT

NRRTGLRQMYDVPLVTAEWPSIKLPATLIHVINENSPFYKFHSIDDLSQSRVAALRCSRD

LIPPFPKMFMRAKCTFGTTLHTTCALRTLL

>contig42523 Frame-0R|Blast-beta-glucan synthesis-associated protein, putative [Phytophthora infestans T30-4](gb|EEY59096.1|) 8e-84

MIEEPMYVIFNVAMSSKWGAQPPNPKNPCRGDGLDPVANAICDAFPMHLKIDYIRVYQDL

SPRSIMSIGCDPKSHPTRQWILDHLNEYEDEENKFVEVRGKAFCHTDADCSIQLAQTERE

NDSIGNRNRITTIVTGRCVNKRCECVSKSWAGPRCITPNKSSMNSYGPPVALAACIGSLL

LLLGITSCLGIWC

>contig45665 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54214.1|) 1e-137

MRSKKDEIYGLTMRVGRALCNAACVLTDLLLSTKHANKSVLVLGHPGSGKTTLIRDVARC

VSETMENVCIIDTSNEIGGDGLVPHECIGWARRMMVPSLEAQARVMVECVQNHTVETLIV

DEIGRKAEVLAASTVRQRGPRLIASAHGDFRALIKNPDLKGLVGGSQQVIVGDKEAKTSS

QGKLQSQRAGNPIFDVIVELDHVCRGRCQIIWDVAKAVDNMLEGNDYAVEIRRWEKSTVG

VQVLGDIAT

>contig46192 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59392.1|) 3e-77

MERMRSPHVPLMALHGSVDGTLDDCMYGCVAATDVAWMLRSSHIHDGLDDARILATFQRP

NRIDPCRFLNLKWFAKEHPVLLTGIVQQRDFVIVEFSGFSLNATGERVGFMFNALSSDA

>contig46260 Frame-0F

MYTPFYVPVDPVAVPNYYLIVKRPMDLSTIRDKLNDKEYTCFEQFMDDIQLIVRNANVFN

PKRCRTRHIAHAAGTMKDNILSYAHRFRIRQGYDLFAKCREVTKRLRAHPQMYGEFGQRF

LESVKRQRQTLEIPHVRTSARLRGVKAPEISLNTAIFKASARSCKPSSNEAFMRDEVTIL

AEVEAKRMKKNTDMKLEPDQQWFTEKGDEVGIAKSENKAFLASDCSENINSKCDEANVEN

GMDEETFAEGDRIFVSSRTHPGINREGGAGVVQSHNRDGSYNVKYILGGSEKSVSVKYIK

RLTDDAIMESVKTQRSVVNDSTNADSVRFIQDEERMDETDYFDELLWPLLKEEGWKRDDK

FDII

>contig46530 Frame-2R

MIRMRVRWHYLLQYLLQEYTHALAAFCVIFSTFAHGDAHRGVPVDNYRVSSVRDVKSLKW

HV

>contig46897 Frame-0F|Blast-splicing factor 3B subunit, putative [Phytophthora infestans T30-4](gb|EEY54061.1|) 9e-48

MTEKDDNVGVSLSSTGQFDRDIYGSGPSNQFEGYSATVTEEGDDTEPEARADDHHSRATK

ANASDGLIDESYDPFADTRDANGSGLVNTRIVDRENAYRKRRFERMLSPERGDAFGGKTP

A

>contig48068 Frame-1R

MRAIVFVTAAIVLISACDDVWASEAVARMEERSVYPLSLFDQLKFLLCGLPPVKMFKDNA

ASALLPLKSSVFADIHLTWWERIEALFLPDYLKRFFMSYASLDWYFASWYDCLSADEITN

QLKEKYPGKARFIDKIVKA

>contig48613 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62433.1|) 1e-140

MSLFFSTDLDSKRFSNDANYRTETILILATQKESFLLSRQLASKHGIDEYDCVLAYIKHC

LLYATGSSRMDRRDQLDQAFMIEETDILEEALQKPNSFGDFLLTRKTVGEPSLYETIDGT

DHVGALLILRMVLECSKRLRLNGEVAKEESSQELSILLVSKPIVERITLLFLCLKKLKDI

GDSLDDVDAVDLKLIGAASTTTELLTPLGSTRTDPQIIIANRNVAVEAVRPLMTNKTIKL

VTKILRKLHRVTPSAMVMIYMNDLLNGIWKEHQSSVDSSGSLSANVAVYAYKSCVPCRLV

LSNEHLMLFHCLFLKRSVGAPLPKVVEHLDLNEEFYGQQFIGLQRFGALLVPQNRVV

>contig48738 Frame-1R

MSQIASQTTAIATIKVKDKTTDEKLQRRRLQFKLHQRRHRAKQKQKVTMLDCEVQSLTAE

VKTLHHERCKLVMQHNWFSSRGTAGGGPARVAMEYFRLFQVSAYPLHLDQQERFLRATMT

SETAGPDYLGVDTIITQ

>contig48947 Frame-0F|Blast-histone-lysine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69457.1|) 5e-18

MQKSPRHKRAAWNNDPCVTPVSTMKFVDETGNECCDINDKNGSVNCKRAILNEVIHASKE

SRCANDNFYRNIQGEQQVDVYDITSEKWLAAQILRKDSEGYIVEFVGWNTKCVVK

>contig49355 Frame-1F

MGNLTNLQKRQLCIKFSRQKMTQQELCHWAKREFQLTHLPHQSTISKILARSEELTQMAP

RDLSARRKGLVTHPELDTALCNWVLCARHNGLKISGDIIKSQARSLALQLGIASTMSFSN

GWLGGFKKRYNIRLGSAAAAMDSGSSVMLASHITSREQLQSVARVYDPRDVYSM

>contig49405 Frame-2F|Blast-26S protease regulatory subunit 6A-A [Phytophthora infestans T30-4](gb|EEY61489.1|) 0.0

MSGLESSEIWGADEELDPEILLMSNDELRQRIRLLDNDIRIMRSDIQRINHESNSQRERI

KENNEKVKLNKQLPYLVANVVEILELEDDDDEQDGAATDVDAARKGKSAVIKTSTRQTIF

LPIPGLVDSTTLIPNDLVGVNKDSYLILEKLPCEYDSRVKAMEVDEKPTEEYSDIGGLDK

QIQELVEAVVLPMTHKEKFDAIGIMPPKGVLLHGPPGTGKTLLARACAKQTDAIFLKLAA

PQLVQMFIGDGAKLVRDAFELAKEKCQDQQRGGAIIFIDELDAIGTKRFGGEQSGDREVQ

RTMLELLNQLDGFTSNTKIKVIAATNRPDVLDPALLRSGRLDRKIELPHPTEEARARILQ

IHSRKMNVDIEDTNFDELARSTDDFNGAQLKAV

>contig49823 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53794.1|) 2e-14

MIRKVGSVTLQLSAGGKTHTVKLTEVYFAVGLAHVLISYGKLDAKGYVLGRRGTQRLLET

RDEKC

>contig50380 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64889.1|) 6e-21

MQMRTTTPASSPWRLPSSHTLTQIQTYLNEQLKHVVALSSTLVHRDTGPKYGTRMFLTNE

KEAEDDIDRVCTLDLARIWKFLAV

>contig51130 Frame-2F|Blast-cAMP-dependent protein kinase regulatory subunit [Phytophthora infestans T30-4](gb|EEY64141.1|) 4e-65

MTDAEGVQQELQYYLHKKGINTLFMNLVESLLLAKPDNPIQHIIHYLRTNYPEEAIVRHI

GGSKDENPATSPRIQYHSDESESEDEDDGGDDVSEISAHVPPLRILAKGRRTSVSAETID

PLSAKHFERVMYPKSTKEREGIRRMVAENILFKSLDEKQMILCSMPCFP

>contig51185 Frame-0F

MGPSASKQRRLYRPFNAGEFTVAWLTFKGDAVEDKEQRYVAKKEGLLSSKLLRGLFGAVI

MQSFEEIQGEYISKEAFVCTLALFYEGNTDDRISYIFTMHKIILSGENKTGEGYIDEKDY

LFLLNYLGEYLPVPKQLYAAFEECLLPMAGMLSNSKFITWARQYPDVVQFLAIYLPPSPV

PESLTSAVRAMPNEGFLETSDLNNSPSCQIEPNRSLYSSSFDFIGGEDSGDEDSDGLYDS

DHLTEVEMSQSSYRDGTTLMNGHDELTNTLKEADAVVQGEDIECTGNSSQSGQRVD

>contig51336 Frame-1R|Blast-fidgetin-like protein [Phytophthora infestans T30-4](gb|EEY54210.1|) 9e-23

MVDNDAGNVVYDLLRARKDSNNAEMHKEMLRALSFVHSDRDSAHVLQRLHAATFCL

>contig51578 Frame-0R

MMRLTFSPRRLLPRDNADRAS

>contig51592 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65544.1|) 3e-30

MFRVKDKKGGGRKRRDVEVENDHEAAVASQNDNLISGFDSVSSSSAVEVESELQELVKLR

QGRFRPVKSAMSFSSKSTTVRTSGSSSSRSTAAVSVDTNGLLSFDDEEHQNKQKQRKMRP

NLVVSSSVEVEIEEQVPGKYSAQMLTSLRSEQRVLLSHKKEEVTEDTAMQME

>contig52302 Frame-1F

MWRPFGLLYVFQVVSLSVTFEAISNVKAADVSILSSTSSSSSNANGGWHMKAVTSIQARV

QGDAPIWNDKARMWLSQYGDTIEAAYRNNLDTV

>contig52452 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60257.1|) 4e-55

MTILDVLADGAAPEPSLRHTMAHSRDVAIAVATEKKLQLKQVALTLLTLVIRRQEFDALL

VAVGHGGCESHKPLEDSRHGRSRLSRRLSRQSRRSTARQSNGPASAILSSQLKKSKHKSA

VRICDSVHHYLELHESTFQYAYETLHGPIESSNSHT

>contig52870 Frame-0F

MLMHDIPTKDEVSIDFAPYFEIPLCCISPQLQYGESFTHHLAAGKNFLVNLSEPVETLLR

SLLFSMNDDFTAFGIDTAEHRVSFFLGSKEEGYDARRATLNKYVLHRL

>contig53011 Frame-2F|Blast-26S proteasome non-ATPase regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY55095.1|) 9e-24

MAECEYEAVVKAKHAIEAEIEAIVAELSSGNNPGTDGPLVDAEGFPRADIDVYRVRHLRH

SLACKRTDYQ

>contig53741 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70357.1|) 1e-15

MELDVVVCSTSGKPILRHRVFTPDPNSSLDDDDSSSSSFTSSLQGLLSFVSCTQHEELLE

LVTAGCRCVFQ

>contig54241 Frame-1R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY56413.1|) 2e-39

MSVHHVIMFDFPKSAVNYVHRAGRTGRAKEKGLVTSLVTKHDLTLAMSIENSKRSKSTIK

ELREDASANYLTAQSSQHPTSAVRVREKQSPALSQCFNRGTKKMRNHKIRSSRLFR

>contig54511 Frame-2F|Blast-acetyltransferase, GNAT family protein [Trichomonas vaginalis G3]gb|EAY16197.1| acetyltransferase, GNAT family protein [Trichomonas vaginalis G3](ref|XP\_001328420.1|) 2e-08

MTDGKVTACLSVLMKLIKYKEGNISPAAPFLQPVDLSHFPDYRVKVPNRMHLYGVQKKLH

RGSYATMDAFAYDMRLIFSNCFVYNSDVILSKIMRNHAVTLLKLFESQFMKIGGSWPGVP

DRWKCHQIIHEILAHRTAGQV

>contig55017 Frame-1R

MLGASRGYKTLLTMPDITATEKVQMMKTMGAQVLLLPTTSMSDKENHFFHVAQRLGRETP

NAYCPNQFDNIANIEGTL

>contig55062 Frame-0R

MVLADDGTHEHESADLNTMGCS

>contig55088 Frame-1F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY58749.1|) 9e-37

MRAKSIQNKAVVNEQRSVAEYEALLAAAEKEVAKQQTYIIALEARL

>contig55383 Frame-1F

MNDATETLETILDALHSDTLNHMLLLRHTRVPQTAHQPLRKTEDMSVSLRHDAIVCEPQC

VAHRLFQMNLMELTICP

>contig55606 Frame-2R

MVYLDDFFLLCNWICRDCHFQIASICAFKYADCCLLKDHIFANVM

>contig57095 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62310.1|) 1e-07

MIDDLLTKDIPALMCSLPMHTRGNSDGKEITES

>contig57213 Frame-1R

MGAHYMFLANMLHLDSRIYLHGSKKGIICDAPLGFIVLATPDNTKTYIPAGGTVSNTMEV

FHTFLWPLRLDVHVAANVSTKRIREMIQDMDQLLFWDPVVVLAPDGSATLDVRRTSSVVS

ASSPRERHSALGYAEASEFRTKLLFDENQQEMDRIVRRARGNEGYIALEPNKRWVVQLRT

FVQAKQKIHFRQVRAAVSEMNH

>contig57338 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59513.1|) 7e-15

MAECVEGVHRFTSEERMRLLEGAGVSEGMILRFSRETSIINCSRRQ

>contig57482 Frame-0R

MVYVDMNVRATTRVSSEELFR

>contig58344 Frame-0R

MTSKWAHLSVEKLTLRSYGKKKQRKYSQYNSSTPHRLENMIFSMVTKEKK

>contig58731 Frame-0R

MFVSHPAGGEYSILCCLLWRPCSSHACRRRSSFLNPYRSNQVAITTSMMFNK

>contig58829 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60740.1|) 8e-36

MDYTYASSPSSTCSSSFSSSPPSKFSDGSCYSAAYGYIPPQSRRGFASDKMFVTCGGQMV

SFMVGV

>contig09112 Frame-0R|Blast-phosphate acetyltransferase [Phytophthora infestans T30-4](gb|EEY62816.1|) 0.0

MLGLMVSRLPGILPNVSAIVLTNGSYPHSNTQEILQGVEALDQTGLSIPIFTVPEDTFTT

AYKFSKVSTDILPTSQLKSDRSKQLFDDFVETQLLIGELNEGMVVNRSPKQFQHFLFRKA

RAVQRHIVLAEGEDIRILQAADQILRQNLAKVTILGPPDVIERHAKSLALDLSRANIVRT

ADSPLLKTYVSRYYQKRKHKGVTRESARDAVLEETCFGTLMVDSGDADGMVSGACHTTAH

TIRPALQLIKTAPNRPIVSSVFFMCLDDGIRIYGDCAVNTDPSASELAQIAVTSAESAEA

FGLIPKVALLSYATGDSNTGPIIDKVREATKLAQALRPDLDIYGPIQYDAAVDKSIAKTK

LKAIPSGARVGGQANVLIFPDLNTGNNTYKAVQQSTGCIAMGPMLQGLCKPVNDLSRGAT

VKDIVTTVAITAIQA

>contig10187 Frame-2F|Blast-pro-apoptotic serine protease, putative [Phytophthora infestans T30-4](gb|EEY65688.1|) 1e-47

MWNTRAMVARRSSLSRSRTHAKSAQVIVQCPRSLQILPFRLPRFFSTSSSASSSNTKSAQ

MVVAALTVAGTGYLLVATGRQSEQEKQQRDLEIAHERKLSARLAAELVTAEANQHKSDWK

ATLERVVPAIVSLKLNSPKFFDTESPGNGSATGFVVDADKGIILTNRHVVGPGPI

>contig12097 Frame-2R

MVDALMPFLTIIKPLVLRIGWNSELAIQKLRQPILFIAGMQDELVPHSHMEKLHSLATSS

KRAVWYPVPGGSHNDSWLRGGDKYYSEIRQFLDTLISGSVCLEIDGSSSISYSEDENSIP

SMLQQPILGSLLQTE

>contig13515 Frame-0F

MTMLVDPLSRGGARADQDYLCMELALTLIRNLLAVPNEDLSYVTSTTSYYNHLQEDLVHS

LHEESVYEMVLLFSQDIDSAEHRDWNLLIMEIICLTLECSQPDFVAAFAKKQLAREQSKR

PDGQETILSTSLRDNSKSRSTQNAGEDLLAKLKNETKSSTQSHSTSRRHTNFGGVLRTVG

PTGRMAVVSDFSKTICGQVPEVAKKPVSLRRRKKSTAPAQDISEIFGGKGIVNETDERLM

SILQSICDAILAKSYAQLTDSLKAEFRRGSDKLIFTDRLQYFFLVGFLLKYHRLKVQALK

SHYKHQLKAAQKQAELQSALNVSAILVPIPKKPDYHENSVLSTLDMFSFNFVLQSIENYA

ATKYYFGMTLSVQLLAEMMAYLAELATSDDLRFQRIADSVQHKIFYERDFLDRLPVLLKF

WSPGLFSKAYEVDVVTLTHLVFKVLDSQGTIKVLSRRKAFLDKKCKKIEVINGEPKSGDI

ADDRSTDEENTEKQTQLVMEMQRKEADFDVRKYFSSMVSADTIRMYCSILSNYRENSPSV

NHYIHSFFYRLKHFKIQQEEWTMQPMLFNIHALLLFNTMLQDTHIRHLPDFKTFLDFIRG

VVRDFFTFADKNNLLFVEVFLR

>contig13850 Frame-0F

MYSAWDTFDVEKELALVDQQEQSEARQKQQCKLLQAKDSVETLATRKAQQSADILAAQAA

VAALKAKKRHRTYPNAKSDALADAIKVEKLKTQAQLFAQKHQLLQEILENRRQGDSALAE

EKKEANVFFKNALAAIQKLEKLVPELLQDEKKHESFELLDKNAPECKEKPSYGDKSCHRE

KEPKAKRTEGLPKANDLVAIITMFYTDVYMGIGTCDLKQGRLAAATEAFKEVLVRDDEHV

MAWLQRGQAFEEMNALLVAMLHYNRIMSLDSEHEKGKEFLERVKSRLLTEGDAR

>contig17128 Frame-2R|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY66304.1|) 1e-140

MEIPNIHSMRESMKKLRNLCSSTSCDNLRWLGSVEDTKWLVYIRQLLKSSLHVAQLLRLG

ESVLLHCSHGWDRTSQIASLAQIFVDPFYRSWKGIQVLIEKEWLTFGHPFHLRHSHGEKA

DTQESPIFIQFLDCLSQLIRIFPSYFEFNEGLLLMLAEALHSCRFGTFLFDCKKHRQEAN

LKYRTPSVWTWVNGFRSQLVEQTYLPEQVLNPPLTGLLKRVVLWDAMFMRWSGQPLVQDA

LISESIVYDNTQRIPTWKLPQNTVCALNAALNLKYREVRLIQTLEGRVAALEEQLRKEKK

S

>contig22414 Frame-1F

MQPPCPSFYCQLHLTFTRSTNPFFKRKHGRLRL

>contig23475 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54585.1|) 0.0

MAGSMYTKMTSSGSSLIVNSRTISRELESKIAASIAGVIRSHDVCKLTTKLVRQAVEKEV

RVSLTNHKEVLKRLMHQELRKLKAKKAAQRAAPEPWKYALRRKSILKGLNCVYHMGRNSS

NFPSWGLHAIQSLYDLQAVESVDILRQSALYARLFGALWLKADRHADWAVGTIPTPTQLV

HAIAAIHVIERLGISHARRVELLDFCSQSPPVYGASDLLGWDPAESTPSVAYKAGASIYE

LLTSALVLWHHAHALGISLGYTLPQLLQHLLLVYPYKGPGDLSPQVYEDQVHFVTSLVLV

LTNQGRLRCETELLPHEYFFLRHNIINHLAHQDVALLGETMRALRCFEGSDDLVQVRRGM

AYLLLTQREDGSWATEGTQNDPQQCYFMTMQAVWALSEPQRLGFAPAFLEATPILELHLN

ADIHNPGNIPVESSDGSAIDGNERDVSIEVAAATAAALSVNEDVSTQVAFLQGVLNQNGN

VKNVSAALAIHILSTLADMVLTVEILKSTGVGRTINKLRKHATTTVAKAATQLVAKWKKD

LL

>contig24351 Frame-2F

MPLPSSCQHRTKLSGTCDCHKQQLHESIPLIG

>contig25114 Frame-2F

MESAWKQGSDEEDTWVLALEKELELTG

>contig26348 Frame-2F

MTSLELKVQIATMTSAQLEQQFQARIAQAKEAARLASIAAAARSEQASHAQPFATIPSVP

GLPYYPTSIPPVSSKFTEPLVIKNIPLDIKNRIDRLVEFVARNGAAFETTAKQREMNNPD

FAFLKPGGLYSDYYEARKRQVCGTQSLPGAPHMKFSSSLPPQALTTSPNSFPVVST

>contig27336 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66319.1|) 1e-84 NOT\_ORF

MAPACHPTGATAVAYSSIHQLLITGGSGGALNIFDLRQRRFLHSISNAHETSIKTIVMHP

TGECVLSGSAGGDVKIWSLPIFREVAFLGKVHVKPSFLGGAATNFLGDAASNVAINMTNS

SWGVTDAFAYKDSFLTCGTDGSVQRLLIPSLGTHL

>contig28265 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66797.1|) 4e-39

MIAAQVVAAGFVRRGAWKLRQCYCGRATAVLLLLLGVVVLSSMLLEELASTLLHFFQNKF

ELSGSANALRWGYDSTVIELKGQPLQRILPSQYPNGAANKFLCDLPSLRFQCDLDKELGC

KAYPQLFPSAALFENWKPESTKHVPATIFNSLCHFNVSDHVE

>contig31238 Frame-2F|Blast-carbohydrate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY54796.1|) 1e-142

MASNLVAYVQNLLPHTALPDLSNEIKKRDWTPVVAAIVSNLPQLLALEAETDVEGAFVLL

FDVVLVIPSAQEAALQILRVLKSESKASAILRLRVAVALFNKAKTLPKVQLQALLDVLTL

AQSSDNVELVAPYLMQVEALVDTQKLCMEDRRALLLAAADVLEQANEKLKVLTYLEKYLA

TYEKGQQNKQQALRAVQIVLQNPVATFLSRVDLAANCVVQESLQGEEILELLDIVSTKTL

KEFQTFQHKAGSVFTDNKLNEAELTDTMRLFTLCTLPTGFHEIPYADVAISLDVNEEDIE

QWVVRATTAGVVHAKIDQLARTVTISRSLQRRFGIEQWKEIHVKLQLYKKNVGSLLNIVR

NARRAQEQQ

>contig36288 Frame-2R

MIKLVKKYGTRHWTIIGTKLPGRNGKQCRERWHNQLNPAIRKEPWTLEEECMLKDLHDTF

GNKWAEIAKKLPGRTDNAIKNHWNSSNRRRKRGMTMAPSYSRHVNLEKAQTASVETNNFC

SFNRHGNNMALLNLTTLHLPLAIPAAQLGSPPSALCWTPTELTDYRLNTMFKRPLQANGA

SVHPTTTIEPRKYKVASDHALVIHGKRLLDTATGMPSHVKSKAMTMRKGDPSLEILANAA

LLQSIGNSA

>contig37229 Frame-2R|Blast-GTP-binding protein, putative [Phytophthora infestans T30-4](gb|EEY60136.1|) 1e-101

MVHFDVQTNKTFMLNLVDTPGHVDFSYEVNRSLSACEGVLLLVDCSQGIQAQTLATYYAA

KERHLAIVPILTKIDMPHAQIDESILNLSSLLNIDPDDVLLTSAKSGDGIEKILPAIVQR

LPPPVQCHRQAPLRC

>contig38479 Frame-0F|Blast-DNA-directed RNA polymerase I subunit RPA1, putative [Phytophthora infestans T30-4](gb|EEY66296.1|) 1e-127 NOT\_ORF

MDSATDQTILRHEVAEVAFGFYSDDEIRDLSVKQISSRLSFDALNNPVLGGLYDPSLGPV

DYNVICPTCRQTQKECPGHLGHIELPVPVYNPVLFSQMLTLLKRKCFTCHKFRQAGARSR

VLRVKILLLDNGYVNEAAQLGELLEQRNGIEDEPSQRTIQRQQAILDEYERLALSRRSCS

NNGKINLLCPLPRFAEVTREKLTTDFLKSIKNKC\*NCGAISPAVRQDAHAKIFLKGLSAR

SRKVNRSKNQAVTSALDTIRGSVSDYNDDLASGNVSYTNDGFV

>contig38493 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57361.1|) 3e-44

MLDYGEQPRWASQPLVLSPRSSQDPLSTFLHADLKAWHPRTKRAASEALPRSKGQSGSNI

HSTKHISADSREDGDRKERLSTPNEHENGETNEKNQTGNESTGNALLYFWKRFVPHAKYQ

VNHVTVMYSISFYPWKMEPHCYYSHPEAAANWMPDTSSPRCQICLVSFTLTRRRHHCRLC

GHLVCANCSPDRTYLPFLGSAPSQHRLIKDGAP

>contig38761 Frame-1R|Blast-calcium-dependent protein 4 [Phytophthora sojae](gb|ACH68461.1|) 2e-19 NOT\_ORF

MTLKMVD\*YARLRCMHSE\*FRSAA\*SDKDSREDIQKGFNLFDNDQTGKISLRNLKRVAKE

\*NKTMTDTELLEMIENS

>contig38974 Frame-0F

MTDTWQPQPALLNEVVTLLQAYMVPDNQVQRESYQRLQQFQKNLEFNLYLVHLLCAHAEP

NVRQLAGLLLKRNIKARDAEVVLSSAETEVLAVIRAQTLRMLADPSPPIRNVASSIVTTF

VSQYTFLDEWPELMPALYLLLEQQDENAVAGAFSALVKICEDSAAKLENSPSRPLNMLVP

KLLQYFHHKNETFRRDALECLNHVLVFMPVGLVVQMENFLAGISLLTQDVSNEVRKLVCK

SIVILLEVGVQYLVPHLNSIIQFILRANQDEDDDVAIEACEFWSSFCDLREFNDIKTILQ

PYLPQIVPLLFQRMVYSEEDLINFEAEEQNQNENVPDRPEDIKPIFHRKTALSHEGGGLH

VDEDDDDDDDDDDDDDSLLEWNLRRCSAASLDNLANGFGNDILPTLLPLLQDRLAQEQSW

PLVESGILALGAIADGCYNGITPHL

>contig39403 Frame-1F

MNSHGIVNRNELRPLRPPRIPVPTASLYTNFRNLNALNSPRNVDALRFRRAAGVLLLIFC

LSMAIGLMHVISLSHQMLARLETHHMQQQLYNQPHTQSRGVVGGVLQRVHEDEAANVLIA

FSDGPHLQKLAEAVGIGVQSIVGNDTQSLRMRRLENASFIDDVLWADAVILGTHVINANV

EPKMTKFMGNWSFAEDLSRKVGAVFVTSGGFSAGEELTMVNLLHSLMIFRMIIVGGEHWT

SAFGASAIVGEGPFRPATLKSQDFPSVCYPTDPDSIHNLFKDKAIGLGERVASIATQLRR

AYMDLSKRNS

>contig41057 Frame-1F|Blast-dihydroxy-acid dehydratase, putative [Phytophthora infestans T30-4](gb|EEY61521.1|) 0.0

MLSKTMKRSVASSPMRKTLLHRTFTATGDLTSKSDNNVRINRYSATVTQSKARGASQAML

YATGMTEEDMDKPQVGIASMWWEGNPCNMHLLDLAGEVKKGVNAAGLVGLRFNTIGVSDG

ISMGTDGMSYSLQSRDLIADSIETVMGGQWYDANICIPGCDKNMPGCVIAMARVNRPSLM

VYGGTIRAGCSSKGESLDVVSAFQAYGEYIAGRITEEERHDIIRNACPGAGACGGMYTAN

TMATAIETLGLSLPFSSSYPADSSEKQNECLEAGEAIKLLLEKDIKPLDILSRKAFENAI

TVIMVLGGSTNAVLHLIAIARAAGIPLTIDDFERISERVPFLADLKPSGKFVMEDIHRVG

GTPAVLKYLMNQGLIDGDCITVTGKTLAENLENVADLSDNHEIIHPVDRPLKSSGHLRIL

RGDLAPEGSVAKITGKEGLVFTGTAKVYDCEEDMMAGLEAGEITKGSVVIIRYEGPKGGP

GMPEMLTPTSAIMGAGLGKDVAMLTDGRFSGGSHGFIIGHITPEAQVGGPIALVKNGDKI

TIDAEKNRIDLVEV

>contig41246 Frame-1F

MYCGDDVEAVVGDVGIGLSKFGMAGEDTPQMVIPSMVGRRAPPSKDVVLGDLWHRHDLEV

LWLPQVRNTDFIEHIWTHAFKSLRVEPTSHPIIASVASCFANDAACSAASGDREKYMEIM

FETFQVPAFYMAKDAMLDAFAFGRSLALVAEIGAGASRVVPVYEGYALEKPAQYSSVGCN

QMSDYLEHLVVTRKPNPITLRPRGTFIRKMNVLTGALESSALTEELTTPPVMPLSYLKFL

RSDLIRNMREAVCVMSETPLKLDCEGSPGQATLSCSEILNFKEQQYELPDGQKVVLGKER

YEVPELLLHPKNFVGAMVNNEEHAGAAAKVEVKGLHTMIHDAVKLCDADLRRDMLTNIVL

CGGGSLTPGVTERLHAEVTRMVPSTFKVRLTTVTKIERQFSVFIGGSILASLGSFQQMWI

SKQEYDEIGAATLCADRFS

>contig42522 Frame-0R

MSRETATSPSERLRQLNANERVDIVNKPSTLRSDELLSSIELHDKRKSCPPKPATKFPSP

ASDENAAEEVQLSMVQRFSHWVEHLRATFGTAFLVLTTVVYVVQGFSSFTALAINYFFKD

NLGLQPTE

>contig42751 Frame-0R|Blast-kinetochore protein NUF2-like protein [Phytophthora infestans T30-4](gb|EEY69125.1|) 1e-175

MAQSMSSSSGAGVYSFPLLKPREIFACLRDMRVPVSEDEIRACDVGAVRKVLEAFIESIM

GITREDMAQIAFPGLPTLTYPELHSESVPELTFYRTAQRLLGASGVDDFGLRDVLYPTPK

RVRRQLSALINFGKFRDERLVTFSKITSQTDELLAQKKALQEENTVLKRELDQLLEEQKA

EEPARLQLQDEVSSLEKEINVLNKQQAVMRVETDELKGKRAKMEDDVSSVRFNKVEAEET

IEKLKVLIVTSPDRVRRELKAIGATLEKAKDDLHELEEKHAAVIEFIEIYERAEKELART

FTLLHEIEKEMQTCKEVKHQVKSTSKRIHELQFRTAETITRRQRLEKLLELKTRELSRHI

EEARAKDVIASKVLESARNELAKLQLVHNEVRQRITLNTEASRKIELQIMEEESQYQKEL

KDLEQMYTRLHQAAKYYNEQVISAIRTS

>contig43235 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61437.1|) 3e-26

MPEDKAIPNHTAHYHLTHLCDYQHLIENY

>contig43288 Frame-1F

MAFVAAAVAFVAVVVAAVALVYVRQKLVGEKTKVVEDTIENASQEEDEGSDQDAKLDGPS

IAPPTPTVVAERMAKTPIAAMKATVAGTIIGAERSFENNSGMEPFSEV

>contig44285 Frame-2R|Blast-aspartyl protease family A01B, putative [Phytophthora infestans T30-4](gb|EEY64098.1|) 7e-53

MWQAELIDELVWVGGSTTTSITMEGIIKTFGFRYPVGCQTKETGLFITQKENGIMGLGRR

RPTLLNYMIEAGRVTQNIFTLCLSSYGGHLVLGGVDYSHHTSDVGYTPMLSEKAGHYTVY

VKELRINNLRLAINAHTINSGL

>contig44700 Frame-0R|Blast-carbohydrate esterase, putative [Phytophthora infestans T30-4](gb|EEY55007.1|) 1e-109

MVPFAAILEAHEALVVSSTLQVVGVCLITTACAFLMSVYLLPRWLLRLLEWNSHPSVLWS

VRTSSLVCSLTIDDVPSASTSAILDILLEYNAKATFFIISSRIPGNEEVLRRIVREGHTL

ANHLTEDRASILDELHVFDQKLQECDRSISKFQPAIPEETLTADSSEMQDLLLEEIARDI

FAAGFSNGEENRKTSRPKVKWMRPASGWFTTPMREITARHGYRICLGSVYPHDAQIRSEL

LNSMYLQTRTKCGSVIIVHDRSWTIGVLKTALPVLTRKFKLVSLDELVAYNEPHPR

>contig46179 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54249.1|) 0.0

MKQRSFGMEVARPIRYWKYSHSPLGLSQLLQEREVRGNSRVIDAACQGHGSLVRRLQCDA

VLNGHGGCVNSLQWNESGQLLASGSDDHKVIIWRYDQRKQQQVIESGHTLNIFAVCFVPG

TDDHVLASGAMDNDVRIHYAPFRDDSSKAFRVHRNRVKDIGSSWAVPQIFWTAAEDGLVY

QFDLRALPRSREASEGPDTSGVLVNLGKDRNGRELRGMGISIHPLDPTKMALACGDFYTR

MYDRRMLRVQGHISSARNAGTTDPVEVFAPPHLHLDVFSDHKAQKAHDRRHGTSIQFSSD

GTELLANYHSDHIYLFKVGSNEAVVFQKDNISEPQIQPMAWLNGAHMDEPFVPLDLQLEA

LQTLLEQGKDALRVDQYTQALKSLNLACGARCVTQLTASQLKELHSICAKVTWDDHGMQI

PFWPLCIARKRWSLIRMTGTWN

>contig46193 Frame-1F|Blast-RAC family serine/threonine-protein kinase [Phytophthora infestans T30-4](gb|EEY67999.1|) 5e-58

MKVEECGLDGDGKSLMVKGSETLKSKHSGAIITQLWSHRIRFGPYGRILRFRVDVDVASA

TGNWKSFGVKNPYSELSDASIRSNRSLSISMKDFTVYNV

>contig46261 Frame-2R

MNSALQCFVHSPVFREYFLSNRFEADVNKKNLLGSRGAVAAAFAQLQGSVWRERTQGYKV

PDRFRHEFIRVRRHFEETRQYDAHEFMVALLDCLHEDLNQGRRSIADDDAIQLMSSRCLA

FNLKRHSPGREIANLDNPEATQLYFDEDQGNAAWRQYTSVNSSVVVDLFHGQMRNETICG

SCGERKCTFDPNLFFSLPIPELNFIRVEVSILMQARTLPNGPSDEYDPEMALQAVQRGFW

LRRGSNVKTLCDRIAAVYGRGRGNQFLLVEVHRHRIGRIVEGDEVVNNLMIVASGSLVAY

ERAWTLAEIPSIPVSVLEYFSGNFPCNASDDAKPISDKEIKSFVDLRVGSRVVVRDH

>contig46809 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55514.1|) 2e-22

MNRVELEEVLEAEERLNKEGNTSVRQQWDFDQQH

>contig46896 Frame-0F|Blast-formin-homology 2 domain-containing protein [Phytophthora infestans T30-4](gb|EEY69903.1|) 1e-65

MHASSHSRASIGSRISMVSDDAFAREAQCGVCTKSFNILRRRHHCRSCHIAVCKECGQKA

IDRKKPERTRPQWYCMGCLDEDATLDITGSRQSVSKRRSLSTSASFGPSSAPQVTNLTSS

TKFCIECGYELPPRVKFCIECGTSVRPQVKSPVSADVKTVGVDRG

>contig47644 Frame-2R

MFFTNAKQYDSIAPTVASQRCTLPSQLR

>contig48069 Frame-2R

MNHSSKNCKNSRIKSQPDSQYGPNSRPPAPYVGEHWRKTSSGRFVPLTLRELTVRSLCAK

LLTIDHDVLQPSFLPSEVAASTLQWLRQHAVLDKPQFQTLVPFLLMEWNT

>contig48421 Frame-0R|Blast-homoserine kinase, putative [Phytophthora infestans T30-4](gb|EEY63720.1|) 0.0

MPRNLKVQCKNRIPFARGLGSSSAGIVGGIIAGLALAGIRLPVHGREDLLQLASEIEGHP

DNVAPAIYGGLQIGIFADNRWYSSRVQIPDGLQCIVFIPDSTGPTSVARAILPTDVPRKD

AVFNIGRAAIFVNAFRSGNLSELRYATQDMLHQPQRGAAQYPHLKPLMTAAMGAGAHGCF

LSGAGPTVLAITSGRAGDIFTQHLAERQQNKVANAMREAAAAMGVLGCVFITNPDHRGAF

IVRAEPQFSDRSVARYEGDIADL

>contig48494 Frame-1F

MLAVAPRAVEIKSTGSRLSSTSLGSTALKNSTGNAKSSHFNVAASPVGNGLLSLQAHCKS

AVAL

>contig49354 Frame-1F|Blast-predicted protein [Populus trichocarpa]gb|EEE98989.1| predicted protein [Populus trichocarpa](ref|XP\_002320674.1|) 8e-11

MSTSRLSVRGDGDRGIFVAGLSEHIVQSVDQASKLLR

>contig50381 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70357.1|) 2e-14

MELDVVVCSTSGKPILRHRVFTPDPNSSLDDDDISSSSFTSSLQGLLSFVSCTQHEELLE

LVTAGCRCV

>contig51131 Frame-1R

MRLSSCCAGHLLELFASRPNGKGLATAVTRAKSSNEVVAINAVAEMAIIKYELTAAAIAG

LAVTGNKRAREIGN

>contig51337 Frame-0R

MEAPVEAPACSMLTEMVREVFRLLDFRVAFKMALMLLIIGQDTPIDRIAMLVLLSIISYL

HITGIFAKIYEVYNRRRGANDSANLNGAVAAAGAAIVTQYGDLTRILQISADGGLACDIK

YFLAGFFLSLVPAWRPQPIHGAVPVVDNAIPNDVPLQGI

>contig51579 Frame-0F

MALKRGRSSSLIHDARSAKRGCSETIDRFLQLDAEPTEGITCTGTLTNTVITATDSDMPI

VEKNATLNAAAAIPSGTDTIETEK

>contig51874 Frame-1F

MKLNITRSTSESMTGRCNSLGNNHELSNVRTQKTTFSNDASKQQLGWVIVLDFVTKRVMA

NFSCHATALVNLSLDHSGLLLATSSTKGQNLHVYRLAPPLQSVARQSKGVSVGKNGTLQC

Q

>contig52080 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56431.1|) 6e-56

MKVYYATLSQNGLQRLINANDANGAGWTAYKSNQGVKVLRKTSSHFVCPSGSLVSENDRL

VEMKGHVIIQATPKEVFDYLRSLEISDLTALRRKSVDDKTTIRRVEPLDDSNAVLYREHS

KLSLWPAWLVKPRDSCDL

>contig52376 Frame-1F|Blast-puromycin-sensitive aminopeptidase, putative [Phytophthora infestans T30-4](gb|EEY64340.1|) 2e-23

MDKPFARLPTCVTPTKYFLDYVVDLDRCRFEVKERVLLSVSHATRTITCHALELYVFDVS

VSI

>contig52453 Frame-2F

MRNNQERSRQQCRQEPQFTQEQLVCERNILVGIDDTLQQETTPDSPSSYTIQVESNNIES

NLGIVPVEDPEVAEQKFRELWKLSFPSMGLIERTALLKIKRPEILMDVMLGMSSLACGAL

TLPEFNQRLVELGYADSDRQAVISMLNTAQAS

>contig53010 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63485.1|) 8e-54

MDMDEEEVLRKAARAGIRLLEDNKALNDEVLALREQVVVLECERPKLRAHLETQTIEMAS

VVENRKNLLIETSALHSKLEAKSVLVKNLLEKENQLKIRLAEAEAAKRLVENQVFELQTE

LEQLKMHVAKAEALERNYTISNPATAYDLNEACGITYMDYEKLQHR

>contig53308 Frame-1F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY61535.1|) 9e-24

MTSAILSGPCCICMNLDDEQGTFLVQCIRCSICVHVKCYGVSIEGGDATSWLCQACEYAT

SAPSPP

>contig57021 Frame-0R

MYTHASPAPSDVPLNKRPCHMKVSSSSRAIFRALEVETLLEGVLVMLDLPSSANLLEILA

SNVLWQSVLNQNHFWKKMLFTHFGGDLPPVEHLNNVIGQNIDSDDEDSDEEESDEEEEEE

ELLASTQMATRSETTQMATFKWVKGVPSPMVLNVACPMLTNFLRSAEQLYQFNTLVQILQ

GDIEKIEIIGDERVDGLAFPTGYDLKQYRSSYYASSAIFRRAGPKLDDHVRELKIRLKAG

NAIVTPAFDAGVDKLIHCVGPYQYDGHHMRTLQQTYWSMLRCVQQEKLHCVAVASISTGA

KRLPVIGAAWVALCAIQRYIRSVPWTATVAIVCHSARAYSAYTKSKAKVMSRFNAKYLRT

SPTRDWY

>contig57212 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70533.1|) 3e-31

MVPCPSCSADVSHSCSCSQCGTKLVRTSSIQSTYAVKNSSLTRRNTSKDRIKKKKQKDKE

RVTTIASDQAKDKIITPPAASGDEAAMIYKKMLAAVRGANQDHDEVVRAFKADCKLYGQG

QLRSRVFYERLSTYFGSELMLAHMLPELVRLIAHDQKRRKLMKVHAKSKQTGGFTSPTTS

NVRSSNNPPPLLHTD

>contig57339 Frame-2F|Blast-putative endo-1,3;1,4-beta-glucanase [Phytophthora infestans](gb|AAM18486.1|AF494017\_1) 1e-119

MSCCPVTAEPACEQADHIGAMKKAGTTNIYVTGPVSSSAGVIVYPDVFGLDSGRTKADAD

TLGKLGYAVVVVDIANGDYLPDMNGFDDWLKKYTFAEHFGPRIQDAVNYLKGEVGVEHII

SYGMCWGAWVGAVQTTQTDPIVIGHVSFHPAWIVENKLKGAGAVNNLAAAVKVPQLLMPA

GDDPEELKPGGSVYNILKAREDIGSNSDVVLFADQKHGWVHRGDMNDAATKTSVMKAWHT

AVKFIQTNCPV

>contig58730 Frame-1F|Blast-putative 3-isopropylmalate dehydratase large subunit [Hyaloperonospora parasitica](gb|AAY58912.1|) 1e-32

MSTEFGGIAGVFQADDITQRVLTER

>contig59481 Frame-2R

MFIPSDKPLSVCWLAKRSVTKLHLTHL

>contig06983 Frame-1F

MKVLVWFRRDVRMHDNLALHAALQQIKNTSGKGDVELIPLYILHRPQLLRCGVHRFQFVL

ESVADLAKSFQDRGSPLLIAKGDGLKVLECLLPAWGITHLFFDGACEPFGIERDNQVLDV

AKTLNIQTHVTNGYNLYDLKKVITSHSNQAPKTYRSFLKAIGNQSKPNEPIPAPEKLPSP

LRNPTELYQNVLNYWNDSNQSNQSQKNKNKKLIEDIGGPKHDFTLPDLQHFQFTPPEKHS

FIYGGEEIALEMLKKFCADETRVAKFEKPKTSPAATPPSPSTTVLSPYLHLGCLSPRTFY

HTVQAILQRHSNVTKPPTSLLGQLLWRDFYHCHGQANPYFDKMEESPTCLQINWRYHLIP

EKKEDWSADDKLARSQFEAWRDGKTGFPWIDAIMIQLKEEGWMHHLARHAVACFLTRGDL

YISWIRGLEVFQERLIDHDWSVNAGNWLWLSSSYFFTAYFRVYSPISFGKKYDPEGLLIK

KYIPALKKFPAKYIYEPWKAPESIQRSAGCRIGTDYPAPIVEHPKAKKKCLEGLKMSYAN

HEYGTFPTAKDTRRSTKRQREDSENGE

>contig09520 Frame-0F

MAEDADAQAQAQLLFSEIQRQHEARSALRTANSRANVSTVRAQIATLKLKSDIKRSSAFV

KKLRGLSEASADSLLRDAAELNLTRYVSECVAALADAPLKLADLGAAVKVASLLHQRYED

FSPGMVRALVSSFESSYAQDDKNKMLKRRLLLRLLCELYLAGVFDDVYIIAHIIQRVAKR

EPIGVKKNRGMTATTNSSTSSQQLEVPLLVSFAKSVGIEFLGIQPRKFKEMINKYANDTG

MQHLVVTQSQLVPEQVQQECRRCYIEAYDMICKFYLAQHAMFLKADARNEKEEANRGEVT

DEHVQELRNAKLLFEKLQTSVNALADALDRQVPLLPIEKKDDGSGNGGILVYEGENGIRH

LHRDSPFDDEATRSFYEDLPDLLELVPAVVLGLTEADVVELKKKKEKGTEEEAEMEVTDE

VEAIDEEGEDTIREECELDGTKDVGDKDEGEKKRKDETREASGGSCNTMTAPLSGATTSY

HHQLDAFFASLEDLVNRDRCDKAAVEFCYRNSRATRNRLVKALFAVPRTHLELLAYYSRL

VATLQSVLKEDIGGELVEMLVSEFHGLMKRRNQFRLESKIKNIRFLAELVKFRICPPNTG

FRCLQKCFQDFQGHNVHVATTFLENCGRFLYCSKHTHGRTVNCLSVMMKLKAAKHLDPQL

ETLVENAYYMCKPPARVQRQVKEHDPLYLYLLKVLYQDLNGSNINKVVKTLRRYPWHEHT

TCPMVLKALLKVTKGKVMQMKWICEVIKGLSRYHDDVLVLLVDDVLEYIRYSLELNDYRD

HQRSLGYIKLLGELYNAGVVSMNVVVETLYLLINHSHDVLTLPQYSSDKLSALQLLEMKK

RFLLVPDMRYDPRVPSEVDGPFEVFRIRLVSALIETCNGSSGNTLGIGSNHTSSNERGIS

RPRLGRFMIFFQRYLFSKVDVPMETEFVVYDLFELLASHLKDQFLKFETWDQVDRAVHEV

LQGDLEEAERRLLKKNTALLMATNGLESVLEDQALSQPGEDDEEFLDDDEEDTEEDDDDE

EEHDDEEHGEGGEQGDDEENDDENDDEDEEYDEEDEQLIIHDRIPQSEEDEEFEKAFKVM

MHGTTDTRKPLVRVNVDKMAIPAVVKSSVAPTLGGLHGLPQALERNGPFDGVVFRVLRRG

NKGKVEARHVIVPEASSLAQHSHRQENAGKKEQSELKRLVLQNMERDDFLSEGMGPLDGM

PAFGPSLPRANGNHSHQATMVQGNDSRTGFGIGSEWNNAEFGLRRGKGYRGTK

>contig11752 Frame-2F

MKTGFATFISHPKYPLQGHL

>contig13938 Frame-0F

MNKNDAEEPLKFYALLKNSFNDFKIINMIKAAAGYDASSTLDLVTKNAQMEDWVKRFSLK

KVFEMYKLKDVRTDLLTHPEFIDWMQFRTKYVKKYPESQNEYLHVLVEHFDEPYLMQLLL

TDTRSLTSKSNKSIIETVLLDLRKHLAKQLATAEHDVEKVFKMLNLHLSDEAIFSVDSQR

GSSIAPSLLE

>contig14621 Frame-1R

MSVKCKLATRLNRLNLLVSLVLLACSKIATVAVAYSVEANRRFRALPSFEATTRSQRNEE

RAAVKTLSKFIRFKKSAAQKLFEEEALLSYLGKLKHKMMFAKVENDLLRDQKWWIEAEGV

ALNELMRDAKTFDVNSRNFQHLAFVVNHIASKMPRIDIRKIFLRYVENLGEAKAATIFLK

GEVTLPKYAFERGVLESLLTKNEVSPADAFRFLAPRDLTDVQFTVERLELWTTHCDPLLG

ENRYNVLAKLLLDRYDETKLVSTLNISKRQSATIDSVLSAVELGRAANAK

>contig14795 Frame-2F

MPVNLEISSSKRFYRRYGGGRLPYKVSALLASLFLAIEHVHGQLSSTSLRLLKTTLPQVQ

NHEPLHRALAQKKEISSYICNNKDSFLGVGNTECLNENLDTAIFLLSVIILVSLFLDRLV

HHIRAAIKCPQLALIVDRIFEEVMILGFISMVIFTINTSGAIDSLDLNDLTAYEQLHFYE

FFHYIVFLTVVYFIAIVLLLLFIGTVAPKLVWEIQQQHADHRRESISDIHDDTYASRRPS

DRDERQSQSRESRVRKFSFYSSGSTYLDDSEQTGTTPHDDYEDTARGVQPSRVHRSVRTP

TRPRSGSGMDLVMGSLAYSLLLQRYQSEGWWAHLNVCRQWNLYKSFEILAYNICQNRSGY

IYKNPKEMQRLFGVEPPLERSMEDDQSDDSNDDDEPMTYARYHILCMRNLLYHMTNIPLR

VFVVLIVLCLLPSIFPDQDHWIFLSVGIFLLFLNVLIFVKVLQILRGIVDDRLHIITSRE

IQSRLTHVSKRPRPRHRLRGSVDDDIDEENDVMDDRRRKALMRFKTAALAVRALIRMQMS

ALCHRQLHHHNDRFWFQSPKFLLRLFQLATIGQAFYLVWLSLVEINSVRDSSPGEGGGPE

FLVIMIVLPILALFVITPLTMPSLVLVMSLTGIYVELNAKNQKGTSHAKKHNTPKDLETH

IQTHTRLIRRSFLRSSHSEHGGGGYRTPNTPPLEPRRSSLAPEMAPPSQQNLVPSPSEMF

LRVYDSPANARRHSYRAGASIGRDHPLGRWKSNSRSGDSFCSASGEDNERNSFNLAAFQL

MSSPMTTTNEEYFPPTSGNSFSSTTSSAYKSPRDSKMDKNSSIPSKSWSQANVEPDIQGY

NERESLHEQGMTPRDPSFKSFCSKYGGYPDA

>contig15316 Frame-0F|Blast-protein RER1A [Phytophthora infestans T30-4](gb|EEY65383.1|) 5e-80

MDAESDGPLLPHSQNEEFRPFTRRVPEFQFWYSTFKATVVSLLMTLSSAFDVPVFWPILL

VYFAVLFALTMKRQIKHMWKHNYVPWDHGKQV

>contig15635 Frame-1F

MALITVVYLQSRNTHEKKDTTKKRRRLASGDIVKNDDESACADLYKAAYDQLEQEMKDAG

LEGSLPMSFGGGSKFLTSRQRKMRNDNQDEDINKAEEKQAVEIEIRSPDIAVVDKIRVIY

NSDGEEASRVIEQVEAIEPIEPEVERICEAKHANSRKKKKKKKKKIK

>contig16032 Frame-2F

MPTPFVAGALVVRREKRRRRKVNEVSISKRRPRRGFKFSDSKGEDARIGPAEATPVGKRK

AGKPVKENTFVFRVRKDEEKDVSTKHAMDAVAVSAALRAKQEKEARAEMRRLVRQKKHEE

MSREALNEEEMKRKKLSADQVLLYHMVQRQVKRELRKVRKEFLSSAARRDIMQLSEFSLQ

TMKQELISFMAEHPPGNFAIEIANPENSRICAAIKTCEQQMKSLEEEETLWIKIKASIEK

DEASASSDATVSETRSPLCELKVTQSLDILQRSVLQQLGSTTEQLALLDASMVTVNRLIV

EAEIKKAQLFNIYHDSAFKGYGNVAQPKESLRSLLELPSRGELP

>contig16674 Frame-0R|Blast-casein kinase II subunit, putative [Phytophthora infestans T30-4](gb|EEY57633.1|) 7e-37

MSRARVYCDVNEARPREYWDYETLNVAWGDQDNYEVIRKIGRGKYSEVFEGYNVANNSRC

VIKILKPVKKKKIK

>contig17053 Frame-0F|Blast-peptidase family U48, putative [Phytophthora infestans T30-4](gb|EEY66429.1|) 5e-57

MPLLMTSALFLGSLLANALRLLHVSRQFHSNGFWFAIKNSALYYSITHERLPSLRTYVMG

PLTEEFVFRSCMVPLLVCADFTVKQIVLGGPLIFG

>contig17703 Frame-2F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY54396.1|) 0.0

MDAEVFASLPSDMQAEIVAQSAPEIHESASALSGAATAEASGPISESMSQMDLDMANSTF

DRETLEALPPDIRAEVLENERHEREAAARAETADTSLAQEMDNASFVASLAPELREEILI

TCDEAFLHTLSSQVRAEAMVLRERAAFRTATYRDRSRGPEGRASGGGEAEMDNLLNRPSL

RRMLTSLSPERESSSRRRSRFYYDELGGGRRSNRRDYRQESDGSKTRKGFLRVAKDEEET

LSERIFDDRCVRGLLRLLFMTESVIQNRVFQRLLANMCLYPLTRRSIRRNMLQLISLPLS

QPLTPADEKDNDDDGSGKIQFPPSRMFGCGIDGNRVITGSAVPAEVVNRMLHVLVTLAKY

NLRFAVELLEPHGMRHTPNEENQPVKVELNTSEECGAAVLIDMLSLPVVFRNDTNLDALL

ELLELVFSPLERLHQQSDEEEGKREMEEGDASAMVSGDECVKVPAVMLNETRMGDIVSVL

SMDLCTAQMQERTLAVLKLLNYVTGNRELGIHAIISHASTLAHIDQYKDRKLSAGSTTYE

SSAVLPSAQDELKLLRLLHSLSDVCESTVEFAECCQTIGLDSLWNALSLSLTEARAKGGI

DDPDNVSASDGTINASFTSSAAGLEHQTPAIEDVENTVIEGTSAGASCAMAALLARFLPL

VEAFFVVNARDAASMSLRVPDLSEREETMVAALRLGGFEGAGATALKDEKEQKSPTKNLL

NRNMSSISSFSEASETKRLASFVESNRILLNLLVREKPLLLDTSLAALIKLSRCRAYLAF

DNKRTYFHSYMKRLRQAALRNHGGGSSSVRIPVRRDHIFEDSYYALRMRSGSELRRKLHI

SFTGEEGIDAGGVTREWYMILAREMFNPNYVLFTSAADSPTFQPNPLSYVNKDHLSYFEF

VGKVLGKAVADGQLLDAHFTRSFYKHILQLPITYHDMEAIDPEYYRNLHSILDNSIVDLG

LDLTFSAEQSNFGKVEIVDLIPNGQNVPVTDDNKMEYVKLVTHHRMATGIRQQIDAFLKG

FHQLVPPELIAIFNENELELLISGMPEIDIDDLKANTEYANYKPTDSVIRWFWNVLYAFT

HEERALFLQFVTGTSKVPLEGFKALEGMRGTQKFNIHKAFGNISALPSAHTCFNQLDLPE

YESEEKLKQCLLLAVREGSEGFGFG

>contig17848 Frame-0F

MKTRRRSLVLFGLLSLQLQRLGASVNEHFVLIQKGNASTIPSGVTLLPLELSSVAASELL

TTKRVLRSVTFDSYVTDAEWTLNSWSAPLSQMRLQERGTAYKIQVDFRLTNAPEMSISKL

LVLADPTPLESVELSLSFGKNALANMPSLVQVHVDGMNTTFEDQWLPAGVDLNQLIFDRA

TVHKFKLGASVSIRQVIIRNSTLSFPTAVLDLMPAVKTLVLEYNTIMGPIELTADKYSQL

TNISDLRLIGNVEIMARNASSSCIKKEIIGDLTICIVKEMTSPSYSLYAGSDDSASSNKH

STGPLETQATGNSDSPRSALSITAIVVGCACTVIIAVFLSFFRRFKRKASKFVDERLAFT

NRDENLLAGHRNEPGMEHAILKRANILAAMDLCKDQTTLYKKIGVQGLWLGEYKDTKVVA

LKFIPREINMVIEELNAILSSYVPLRHNHIVAFVGCSWTEREEFLIVVEHMSKGNLRTVL

ADNSIELSWSQRLQMSKDICSGLNFIRSLQGSKLSRNLTARSVLVDSQLTCKLDIFDYAL

SLRTNFVPLRSYGLGDIASRAPELLKGDEMTAAAEVYALGVIFCEISSRQILFEHLLEER

GSTLADIFIATEVVAQRLTPSLAEDVPADYRELIFRCLSYEPSERPNVAEIFKIISK

>contig19327 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68404.1|) 1e-63

MYADKQTIDPDDIRLAISSRLNHHYAQVPPRELMMELADKRNCIPLPPISNEYGVRLPPV

QYQIVTKESDRQDAKAPNTPRLGGVTSFAVGLRAESIRPPMHPRVEGSRNKRYARRPIPI

NLNSNM

>contig20381 Frame-2R

MEKPVLALGQRLLRRKASTIVASSRSVPHSYVSCCRIALNFGTRSFSGGRDDKAFPRVVS

EHTLFENRWIRLKRILFLNAHGLKRNWTGIERTSTYPEASFGESKGFITKLEKQSQDAQE

KCDAVVVFPFLLKQGAPTRVVLIRQFRPPVGQWVLELPAGLIDAQELPEVAAMRELKEET

GYVGSRVLHMGPPMVNDQGVTNGKCRLVLVEVMAEKQQAPLIQQLEPDEIIHVVHAPLQG

>contig20406 Frame-2F

MTVEMEASEATMMSPISSKSTAPEPLRLSEIESAHLCPAGRMKMEELFRQWLNLDGTKEM

IQNMVVDLRQGKELNLDTLLATVNVVSSGADSPSRSPKRPPNYQLGLLSPGSAGSPSSRK

RHQHLVSLFGDELHSALVSGAAAESAQTDEAVALVSPYDDVDMSTGETEATENAQKAFQV

KNQEETIAADQLVHADADEIMEEEEEHEQEKQPPLKSQKAEETTDNLARETLKHAQIPQF

YSPGENRRGRLRGLSTDAMMRKAVDIEARFREFPEGMKVEDFVAITKDLCGFPSFFNAPF

FRRILATCRVVDETTRKCEDACSSGSPTSADGGVAPQRILKDVFKNYWMREMAPCDSVER

FFRVVKQPKSDFIERDDFAPFLHELLKYHPGLEFLGGTPEFQEKYALTVVVRIFYSVDRD

SSGRITLRKLRRSNLISAFNTVDEEEDINKVNSYFSYEHFYVLYCKFWELDTDHDFLLSP

DDLVRYGGHALTRIIVDRIFERGRRPFARFQTLTAEEKKKMSYEDFIYFMLSEEDKANAV

SIRYWFELIDTNDDGVLRADEMRVFYRDQIHRMECLGHEVVPFEDILCQLSDLLHPEKEG

EFYHKDFIRPDKIRVSGVFFNVLFNLSKFIEFEQRDPFLLRQQLAEPELTDWDRYARAEY

ARLAMEEESRDEDTAMDIDTMDGWYVSDEQEEEASEGTANAAGTEGRTVEAPF

>contig20617 Frame-1F|Blast-TATA-box-binding protein, putative [Phytophthora infestans T30-4](gb|EEY59714.1|) 6e-77

MATVPPLHIKNFVCSANLGMRFDLTNLLVKSHRRAELVPKKNCILMKLHNPKATAMLFSN

GKLVCTGADTEEDIKNVARRFTHVIQKMDFPNVNLIDFKIQNVVGTCDLGFRVLVEALAF

AYSESCTYEPELYPALIYRLEEPQVKVLVFVSGKVVFTDSKEPQELYTACEVIFPILSQF

KDLKPIDCAIIPESYGSYGLNGKAG

>contig20998 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68244.1|) 1e-100

MSRGWEKKAIDTLIKMKKVEKIKEEVTELTDFISNEEELYYYGAPDNFKADVTETLFSEA

NYSFLDVTKDGLKTETNLCNGERPAPPKTCTYFLQGLCSYGNTCFYAHSLPEEIVSEEER

LATDEEFRLSQGLECGICYEIILNKGEQFGMLSGCNHSFCLTCVRNWPNSEDHPKQTVRQ

CPACGKETKFIIPTSRMVYNPNRKKVLMDVYRKELNGIPCRHFDGGRKTCPFGTSCYYAH

RSPDGFQALRQARTVVDEDGQNIQFRQSRQDIFLKQSEVTEELSR

>contig21319 Frame-2F

MRLAAALSALLLHAVPTAAQESTQDVYITPSLSASNNVTGLPGGNEICGSTRVRKPWASL

TAQEQALYLEATEMAIADGGVSAFADIAADSLSQAQGQYSCAFLSWHRRLLIAYEAYLRD

LDTRFACLTLPYYDVHTAYVRTINGECTNIWECSDIFLALGGAGNVSAQVSVLADDSVNA

TGVALIGAPYSNSC

>contig21562 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60283.1|) 6e-85

MGDANGLVTYEEYYVLVHLLQIPKEHFDVAFAMFDLDEDGSVDKAEFCAVIEKLLQAMSP

REEEERIAISAENTLPRLTKSLFGLFGKTITAIELEVTLDKLRKQILKAEFDLYATVHPL

TKQQTVSVHDFALTLISGHDPKKLPPYLDRVQALNACDDVVTWDEFCTFHFNVQHNLPDI

KLAFELTGADEITE

>contig22413 Frame-0F

MLRRGIAGNARFTFLARQGSWTGRRRIWSTPWLQLEAAENCETKAAS

>contig22624 Frame-1R

MRVDVMEHPLRPHYPNIANFLSKTRFFLQKLRDRAHHNF

>contig22840 Frame-1F

MLQTFGSKMAWLRHIVMLNTRRDKVRYSRSLQREVGPEVAAIIKQAKFRIRSSAELYECR

ARCFRIKAKMEERGFPF

>contig23322 Frame-2R|Blast-iron-sulfur cluster scaffold protein Nfu-like protein [Phytophthora infestans T30-4](gb|EEY55950.1|) 1e-53

MIKELLEQRIRPSVQDDGGDIFYKGFDEKTGMVSVQLAGSCAGCPSSSVTLKHGVENMLK

HYIPEVRGIEEWVDEELNTVNEKEFRSFEEKLRAAGIPTD

>contig23609 Frame-1F

MNTGQRTFSFCGSPEYLSPEMVSKTGHGLETDMWSFGCFIYELLTGSPPFQCEDMHRLFR

LIQQGRVWYPPYLSGYVISLLKGLLCVNPASRLTVAQAMNHPFFTLALNWDEVLQRKILP

PMVPMCHGRDCTDNFDDDYTNAPVSLLKLQSLDLHKRLSCGDCAGTGDLFDDF

>contig24437 Frame-1R|Blast-hypothetical protein PITG\_02637 [Phytophthora infestans T30-4](gb|EEY64109.1|) 5e-19

MVDIAGTAADHFLLFHVCEIVSIHVNGRQEEGSQSKRNEHKEKDIRLRVGLLKR

>contig24855 Frame-1F|Blast-serine protease family S08A, putative [Phytophthora infestans T30-4](gb|EEY68685.1|) 3e-15

MQVCFLSLVLAAIVQTSASSVIIDQRGLEFVSQDAFCAYHCSSVHVAVAYRHLSATSECV

PRNCDTYLRTHPPERRLPA

>contig25113 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57044.1|) 2e-37

MSGPDMANPQLAHQRKEWIRKRTHEVMRDGHEADGFESDLFECRNCGSSRTRYRQWRRKA

VVDRTRIIVICLRCPYRWEL

>contig25324 Frame-1F

MVSKKVLIIGVVVAIAAIGVIAGILVATSSSSSEATNESSNPTSANSDTPLSRATNSSKS

GIRSNTTKSSGGPLITSDPTSAKFTLCAFALGDWGTTIYQDSCCTRAKTYNKYDVNAMDV

VASIMNTHAGAVDVKPQCILGHGDNFYWTGIDSEADRDTRFTTTFEKKYNGDNIATIPFI

NVAGNHDYGGASFVCSDGKQTVECNDADELVAGLENKFKWQQEYVSPNDNRWILKDHFYV

HTIEDKDSGVSIDIFNVDTGDADVHAAMQVCCQCFGYSKGIKNACKGVSRGHKYCAGGNN

EMYDACFAKFEEWGADSRKQLAEKAATSTATWKIVNSHYSPHAHYDEAGMKEWFDVLQGL

GIHAWIYGHTHGEKHDYSESLGMHFIENGAGGGIQMEAASGLTAYAEAYAKNVWTYSGDE

YGFFSIDASTEWLKLQYHTADDSWSFGSNMEETKAGGASTKHCWYVPADGSEGQACTT

>contig26057 Frame-2F

MAFAHAVETLRPMRSVSPVTATAPMRHSGSVGPSSVRDRTVVVFDWDDTLCPSSWLHVQD

LLPKYRGDQRIVKREQREVLFLIDAHVARLLQKAVAYGPVFIVTAAEKGWIEASAALYLP

TVKSMLALADIHIVSARSWYEQNFGLGGDSATWKQEVMELIARKCFTNGTAQQFGARPYL

QNFAPQSAFFNLVSIGDSMAERDACFAAVQNVCQTFAKTLKFIEHPSAEEVLQQVELTHD

SFEQVCGWHNNLDLRLSREQLDELRGSPI

>contig26505 Frame-0R|Blast-short chain dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY53420.1|) 2e-77

MLITLDTSSEDSINAASKALENVPIHLLINNAGIMTEHNLQSTTKADLLRQYEVNAVGPF

LMTRAMLPNLQLAVKDQGLAKVAQVTSRMGSIMDNNSGGYYGYRASKTALNMITKSLAVD

LGKEKICCLLLHPGYVNTAMVQFSGSVSPADSVKGMAKIIAGAKLEDSAKMFHFEKGDVL

PW

>contig27331 Frame-0F|Blast-hypothetical protein SORBIDRAFT\_06g024850 [Sorghum bicolor]gb|EES12626.1| hypothetical protein SORBIDRAFT\_06g024850 [Sorghum bicolor](ref|XP\_002448298.1|) 3e-22 NOT\_ORF

MGALEPNRLKF\*MDRFNAFEDPDIPKSL

>contig28419 Frame-0F

MVKFTYAFPSSPGGTHDRSTKLIYLNQGVGTRSDSPAFCTRWHKDRIT

>contig28770 Frame-0F|Blast-pre-mRNA-processing factor 39, putative [Phytophthora infestans T30-4](gb|EEY59701.1|) 0.0

METPNDPSGDAAAAAVEKTPLDKLMEVVEANPLDFNSWVSLLALVQSESATPREIVEETY

DRFLLEFPLCYGYWNKYAQYEYRLASRTREDGLATIATLEEAKQKAREVYERGVAAVRYS

VDMWMKYCEFLIHTLLCHVDETRPVLDRAVEACGGDPMAGPLWELYIHLETVNNDMPRLN

NVFKRIMHQPLRNLEDFWEKYNQFVLAQALNALATIEEQKALASDGEELMDEGLLRVKIV

NAIEAVKNKTMEENNRRQAFEANIDRSYFHVTPVAETAMKNWHAYLDFEETEGNNERCQA

LYERCLISCANYEEIWLRYASWNETVHGFAAAEAIFLRAMTIFLKHRASIYLEYAAFLEA

HNELQKAQDTYMKVIFEKAPKLAEAYLLYCNFERRRGDIEMAKAWYERAMEAVENEVEVF

AYVATSYAVFLKQTGSETASVRAVFQRAVQKYSESVLLWLNYIHFEINAGGKPTDLVKRI

GGVYELALEDHCNLSMEEKNDLWFQYVEFLVNNETSIAQVREARKREFQWKLKNSQPRNR

TIKVIHFQRDGDRNMIGYNSNVDVGMKRSRYTAPQTSAVLVTPTAAATTAIPAVVATDTA

AATTASAYFQDYRVIISSLLSSAPHVRLHLYLLLVWTGLRMSS

>contig28921 Frame-1F

METHEDHVFLGNEAKFQALEHKLAQTRARGETKFKGMSARASALSADQEAWETNRLLTSG

VVLSGRVETEFDDEVDSRVQVMVHNTKPPFLDGRVAFTTQVEMVATVKDPTCDMAICARK

GSELLREVREQRERNKMRKRFWEVGGSRMGDAIGIKKDEGSDEEEEKDEKESYKHDSQFA

THLKKQKAVSVFAKTRTLRQQREFLPIYQCRQELLQVIRENQIVVIVGETGSGKTTQLTQ

YLYEEGYAQFGMIGCTQPRRVAAMSVAQRVSEEMDVILGDEVGYAIRFEDLTSDKTIIKY

MTEGVLLRESLRESDLDSYSCVIMDEAHERALNTDVLFGILRKVVQRRSDFKLVVTSATL

DANKFANFFGGVPMFTIPGRTFHVETRYAKSPSEDYVDAAVKQVMQIHLSHPQGDILVFM

TGQEDIEATCYVLADRMGKLDGAMPLMVLPMYSQLPADLQAKIFDASDIRKCIVSTNIAE

TSLTVDGIK

>contig29328 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53024.1|) 0.0

MAMKTTWNRSDLEAVNKRIPYQLRVHIYQGRRLPPADSNGLLDPFLVVRCMGEEKLTSKK

KKTRDPLWYETLHFDVNLPELQYAPQVMLRVMDYDDFDSNDFVGLVALNLSEAVIRSSDQ

VAGEHQPSLPDPHWHRIMFQEPGDCEGEILASLELIRKQFPDETVRRAPSIVPRNRKAFL

EITVLGLRNLEPYQFMPIQLPFVEFVLGGKDHAAQEMITEKSKRPSGSNPNFLQRIVKEV

ELPENAHFAPRLNIIVKDTRLGGFQTPIIGSASIEMSSKIPWSRHYRPPQTDALAEIEME

SADEWGDDAPLLGKAARRNDSPVTEFAD

>contig29979 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62783.1|) 3e-29

MPTFLLPVTRHSLSFATSFLRSVLNSSISRQDKIQFIISSQSRDLERSLRFRFPSLMASH

EHEALPDWSNQNDMKEALRQCSGAILAASGCEDNALNCPGLLSREWLQC

>contig30098 Frame-1F|Blast-putative cytoplasmic catalase [Phytophthora nicotianae](gb|ABX61043.1|) 4e-11

MAPPTICTTSNGAPMPRYGLTASVTAGSTGPILLEDFQFI

>contig30461 Frame-2F

MHRASKVILKTNALGHPDFGAYNKCNFLLKFPLSAPQESKLSQRSIIKVTPHISWKEICL

TFEKATDLRPVVHDNGLGLHPFGSTLCYPLTPGCTFEVMKNGFIASVTLSIRN

>contig30663 Frame-2F

MYVELGRRVTYARNKSLHFIADCG

>contig31707 Frame-0R

MTESDLPEGDWQCNECKKPSRFDAYSAAVASERNLLDKCLKVVACLKSHPFSKPFLSPVE

NVPLYTRVVKQPMDLSKIETKLKLGAYVSDSNRVASELDITH

>contig31909 Frame-0F

MGFNNTRRAIPFLLLSIREVAFSFFLIFLSGSYYAKPLSC

>contig32427 Frame-1F|Blast-carbonic anhydrase, putative [Phytophthora infestans T30-4](gb|EEY58063.1|) 1e-150

MADATVVAPPYPRGSNTTKEECFHSSESIQHLLDNNKKWREELMQRDSSLFDRTAEDQHP

PYLWIGCSDSRVPAEEITGLDPGEMFCHRNVANLVVTNDINVLSVVQYAVESLNVKDIIV

CGHYGCGGVKAAMENKHIGILDTWLQTVRDVHREHKKELDALPTEKARYRRTVELNVKQQ

CLNIFKMNVVQHRLGRRDQPIIHGLVYDVKTGKLKELKVDYSGYYANLVAVDNLHAFPDG

EPTISLAHRRRNAILDLADGLENEPGIVRTRYMARMLKREADLFSPEEVDEAIETIKSRV

NDADDSLINVKHLIAHFAPLEAQIID

>contig34050 Frame-0R

MASSSDVITNNMLQHPPPIVWRVAHADNQDTLARARLPNASFETETDFQRMKSQHLDWSN

RTGTPFLSTFSDKSNAECWGRKLLDTSDVWIYSIDTKGLIVFPTDTDELLIFGGVPNNNI

GVEEEIHNLEKGDLMMDETPIVGDEQALDDLCYDHAINPCDLVHNDRTGLNYQPDDDAGM

EEDEDWIDFAEYQMDH

>contig34234 Frame-0F

MQETAHVSTVTLLLGSDARKLVLVPGIPLQELMQCVTAGFHIVNKTPVAVRHATSNVLYP

LSLLCRSPDLFENATLHLVLESEQILPHDYGRKSSKHRHRVLHSRKRGARAHSTPDRRNS

HVLSTSYDAAANDASKAQIMKDEPNVDLDLDLSDFELPQLVNVFTQACPTGALDRLTFDR

CLEKILSQSGRYDSQARKMFTRLFSIFEAESFQKDIVDVADFLGGVSVFACGERDEKIQL

TFELYDMDGDGFITMEEMTKYFMAVFLVIGNSSPDLFQPTNINPAELGRVTAKQCFAEST

LNEEGKLSYEAFREWYLESGPTQLVTTKFSQDGGPKSRENVVHSEGFDLATLREVTGLAA

VSAAEFFSMFSVLLRKSDDTKQVLTRAEFKKCFSDMLEILNREHSSRIATFLDQVYDAFD

EDGSDMIDLVELSSGLSVLCGGSVEDKITATFKIIDTNDDGYITQQEMQTYLASTYNVMY

VTSPALRTTVGVDAKALAYFTS

>contig34739 Frame-2F

MDWVRHFLNQCGSWFHLKFGSDVEDIYSVCLWLEKISNGELDVTATPLVQTPVITVANHS

LIENSRFKGNGLTLGTRLFLLELHFDRLSSQLVRGRKLRKIRKLVDFRIAQAQKLLFEYA

WLEDSEDGISCLNVIEFLRLLWLIARMYERCESPRMALHYFIKCREKMSEHMEADDDNNI

FFRVNMPNQKVSNVITMAALAEKISGLRFSDVCSEARRYFGARNYDQVVSILLGHYFPLS

QSPRMNDFLYEFETVLDDVQKCDCIIGKTLFEMLLESIDQSPNFSEKDTYLLLLTILYHV

IEFLDRLDATSKLDSTDEMVD

>contig35127 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62218.1|) 7e-06 NOT\_ORF

MFEYFLASFQNEFNCRIHVLRTDGEGKYEVVSLFCKQTG\*DVKEQKRALPQLKGKSERMN

RSLQHGAI

>contig35343 Frame-1F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY70221.1|) 1e-10

MPIQKEQLVTKKKSFREALKVCTHPHVDDPDNADKLPCGANLMLRVLSCVTTCTLVGNQG

AQVFLEIPFGHGDIILHC

>contig35897 Frame-2F

MSARLVRMLEVALIRGKGAKVNAFIPRPAPFRALSNAAHATASKTDGFYVSKKAVKTTLL

VGAALSAGLYYMKAQENADWKKLKLLLGRSQMSLEKGDIEQFKKVQEKAYGFLKKKFPD

>contig37648-1 Frame-0R1

MLDVRENGAGEVQAETKLRGVNALDSIQIVGFTKKSYSFANTLPLQFTFRSGCDVNRF

>contig37756 Frame-2F

MAADFGIAYEKKGGNKATGCAGEMFCSQKALQERCKQFAMQRGFQLFVSGSSTRANNGGN

VKYRCKKLHGQQFFDQTTPINQLQCPFYINGYGKNAQWKVTRACYLHNHYKFIGWRVVAA

PLPATIPEPSTTTSLSTASLVSPNVTETKNVSTTTLKLALPIDATESCAQRLKSQRNTTM

SMKALCRIVSNDVSIDPIASTLPYLDGKAIRRILLRQGHTINHMMASRIKRHLHDEHLAK

VRLSFQYLSSYLHLVAEKNPGSFYRVETRACDGVFTRALFIPYATLQAVPYCRPIVSLDR

LTPS

>contig37903 Frame-2R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY54023.1|) 7e-10

MSLTDTHSLDKPMRATIEYANGKTLMAQGPLAMHEHVSFRMEKALG

>contig38230 Frame-2R

MRCHILTLFLVALSAVGTVVTGDTEHGDVAIGVDSDLVVDEDTLQVQEETADDAVPAQEV

DPRLTAEVMEKIISKMSGKCQTQVRGSIMDPSKISDRCRNEVARRVQRYLKRLEEEEKGE

TVEKEKKQTKKHKRSSRTSKKKSRAQREAAKAEVEYQKTLQTILAFVATLTAIAVGAIFF

INRKLKAAGMYFPDPEAKASCCN

>contig39088 Frame-1R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY53362.1|) 2e-15

MKKRSRISRHLTGLFRKKRRDNNANLSSQTTSFVELSSSKLNTEATQLDRFQVNETELTD

YSSIQVTLTNLEWVWLQVLQLKKTERLFSAALLLDRLEVFFTDMKSDTTPLLNATVYQRV

KDSMCAH

>contig39123 Frame-2F

MGVTGLLPMLKSVTDMVHVSKYAGKTVGIDVSDWLYKGAYSCPVDLVLGKPTDACGTNYP

PFKLLSFNLTPKRAPVLGTSTFRCSISSSFRRMTSSQL

>contig39295 Frame-2F

MSIQLLLNADESGTEHVFWSDEEIANLVFSDHNGLHANGKAEEEETNPG

>contig39404 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61938.1|) 5e-15

MQFISEDEIDRVNDIPLAQIASPPSSGSNTSADHLSGSDDDVWDNCTFCGCLFHSRADLI

AHIRDTHGEILHRVSIPGTFCTRCGTRRVDGSCTRCNLAA

>contig39769 Frame-0F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68035.1|) 1e-107

MRRVRRPRVFGRYNELKCYKEADTIAYELLKRVGGDRLSGEKIIFYNEIVQLVSAADLTR

AARDRRRSGNIGSGKPKSSDSTRARTNSLRIALQEDDERRRAAGETLDAGPGERSSRKLR

YEVTFHKKLLGLDLETDFYCENVTIKVMDERRMSKVKIQGHIAPGQQVLQKGDCLIGVGG

VDVRGIGFHETLALLRGTPRPITVQFESAEELMQEVSTPTANYSSHSETEGQAKRRISVA

GPGCASDAMDMPGKQLKVQLAHWLIVTEQRVLYINVGSYTKPVVEWMTPLRYIYRVEWQK

SAAQISLHLSVGVDSLPMGPRLQPSLKALDGHERDMNVFLDVMWHSFRSTTAEQQELWPS

DTSLNGYLLKKGGFSTVRRWFVLSRNCLYYFSSRKQLRGIIPLGNVRLEMDGGDTLCLRI

TNAIRSQPLVTLQLDSGQVVERVQSEVVLVAAAPQELEMWHSSLAHAAGKGMRHSRGTRY

FNPTAASRLEIGTQETPDFVVSPLAEALQKTVEVFNTKLPQ

>contig39862 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61155.1|) 4e-89

MMRAIALKTFETELGKLMSGNDRTLKCSHSSLLALVDELLENHVDALTQLAVEHPELLIQ

EITTSVANEKNSLNVTGRISSSELTDALRTKAPSRYLNILEQIFKNAISRQETVRSAILF

CLSTIGEAAMPSAKRIATSESVALVDVDRISVHFVPDQVLVLRFLAFVLQMFSTLEPLSL

KEEIQDDEKDLQHAKAAVAAEMMRLCIRLRSCLSDPETYDKDRCVETTLCDLFETISLEP

VACSMLPSWVQDYVKIHCLPKSSRLRRILENLYNQTLGLLYQNDLICPQQMLTEYENNAS

EGFEPMQWNLENNLAVIVVLLSLPRAS

>contig40790 Frame-0F

MNTAIPAALTNIPAKVNCRWSLASQT

>contig41234 Frame-1F

MLKGSLSSNETQPIVPNLGTAVAPSRIQSHRLSSTFFPCGMHPDNLAPVADNGGDDGGRK

DLLHQSIGEEHDETSGAYHAGPFHGKHSELNSYFRGIPDAEDLPAPEEISPAFAKDSEEL

VAVIGPFFTRCVFSNLWKHRVAAIRKVTMDMKLYDVDSTRLLDVCSRLAQIGVQDCIAQV

TLSAFELLDRMLSFSARVR

>contig42442 Frame-0R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY69304.1|) 2e-37

MISEECALQAYRSQESCYMFFYTKFQRSGDENGKENLLVNRVNAPDENEKNFSHQQQGSS

INELRAFL

>contig42756 Frame-0R

MRHPLLLSKLSSHVSKGQWCQQLRPITRRC

>contig43401 Frame-1F|Blast-glutamine amidotransferase subunit pdxT, putative [Phytophthora infestans T30-4](gb|EEY63668.1|) 2e-90

MIMLSQHAKHVEDGGQTLIGGLNVEVSRNFFGAQVHSFEMLISGPPGFDTEPYNAVFIRA

PAIISVDEEIEVLSRVVNAKPADGSDPVDVIVAARKENILVTAFHPEITTDARWHQYFIE

TIVLPRV

>contig43474 Frame-1R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY65715.1|) 8e-90 NOT\_ORF

MAFDAAGAANLEQFTLLAKNARGRACQALIQQVLSNKKLFVFRELLDMPSVEALKDSEYK

DQYELLRIFCFGTYNDYVERKAELPELTPLQINKLRKLTAVSLAHKFKNIPYDTMSQHLG

LTTVREVEDIFIDTIYSGLIQGKLDQKSRCFVVKYAVGRDTCHEDIDDMIQKLMKWKAQS

AKAREKIHTILTLAKKQEEDERTREITINSKMAARANERGKSFASSSSNFRSGVDFASYA

EAGTRRGSSSKQRIHSMGRKGRM\*ILIDKF\*Q\*NQWVRRSYRFFSTTLILSNYIASNEMH

TLDLHSSSMPTFFDQHHGAQRKRPMQSHYIDHIQRSKKYHHRAAISEKSSITALQRSR

>contig44116 Frame-2F|Blast-protein transporter Sec61 subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY68018.1|) 0.0

MRFLHLIRPVMCVLPEVEQPDRKIPFREKVLWTIITLFIFLVCCQIPLYGIQTSKSSDPL

YWMRVILASNRGTLMELGISPIVTSGLVMQLLAGSKMIEVDQSLKEDRALFSGAQKLFGI

LITLGEAVAYVVSGMYGNISDIGAFNAILIIVQLLCAGVLVIILDEMLQKGYGLGSGISL

FIATNICENIVWKAFSPTTINTGRGTEFEGAIIALFHLLITRSDKLRALKEAFYRQNLPN

ITNLLATMFVFIVVIYFQGFRIDLPVKYQKLRGQQGTYPIKLFYTSNMPIILQTALVSNL

YFISQLLYRKFSGNFLVRLLGVWQDVEGNAGQTVPVGGLAYYMSAPSNLAQILYDPIRFV

IYVVFILGSCALFSKTWIEISGSSARDVAKQLRDQQMVMKGHRDSSIVHVLNRYIPTAAA

FGGMCIGALSMVADLLGAIGSGTGILLAVTIIYQYFETFAREQAEMPLSGLFGF

>contig44365 Frame-1F

MLPLSSSKLATRASRSLFSKATAMPSVALSEHFPSVPQTQPQTAAAAKLTTSTAVLGLKL

GSDDRAASVATIGFQLNTGARDENDDTAGLSQLFAKMAFRATQSRSDLRLYRDIEAIGGV

VSTQAGRDFVRYSVSVLPDQLESAAGILAETTLSPRFALYDVDEQKKVVQAEFDRISADA

SASLVEGVHAAAFYDDMTLGRPLVSTENIDALSCEALLAYHNTYVNTSNAALISVGVSHN

TLTDLANSYFSSLTKGDQAASVTAKYVGGETRVKKARNYTHVALGLPTVGRDSADFGASQ

VLHALLRLRLKNKKASAFLSSYSDIALIGLSGHATPPEAGALIDSFVFELKKAALSPATQ

DELTAAKTAAALESVELYNTQAGALSRVGIFVSSSTVPASPLQLVETVTAAKLQELAHKA

MKAVPSVSAIGMLSTVPHVDVIARKLL

>contig44707 Frame-1R

METMKEIAVNVNGKGAMQMVTTLYPMKDGQVPAGRDVVFTTGEDGLLYVTDLTTESSVYE

SEVCEGFVPTFAVTPEQRHILIVSDDDNTVASYSFPPNCQLHQLLRRSTVSIRQITCSKT

FVVIVDEEPVVRILMRCNTEQVILAEGATGIIKSVVLDPQEKYLCVSSEDTTVRIFALDA

EHQRATVAKSFKIKHKDIRNDDVLLHCAWQPGLTGKLLAVPVDQGILELFERDSWISKGR

LMLPIGKSIASDLDIVDFSPNGQYVAAITCAKEVFIWELKTQRVLRSFRIDYPALGLQFA

PQNNALVLYHTGGKLAFVKEVIPAGYTPPQHLVGEFSAAMPSIQSSSKKVQVSSYVEDEA

VENRKHEKNNDEFDDFDDENEARVEAIKASFGFGTAAKDLQNPDESITLLTTKDTTSNQS

FNALSRTIMEPFQPGSALNNSGNSAPSLLAWTLEGEIEVLRG

>contig44800 Frame-1F|Blast-thymidine kinase [Phytophthora infestans T30-4](gb|EEY61441.1|) 5e-65

MRVEVRGCLQLILGPMYSGKSTELIRRIRRYQHAKLECLVIKYLFDTNHSEEILSTHDKV

FIEAMPVQTLAEVRPFLKEIDVIGIDEGQFYPDLVEFCLSVADMGKVVIVAALDATLEQK

AFNNVVEVDP

>contig45414 Frame-1F

MLSRTGRISLPTPLRPNDVQIYRKSPLARTLDFPRCTLDQRLRTDQAGTV

>contig46194 Frame-0R

MVHRLDQETSGLLVVALTKSAAQTLSAQFRKRLVQKVYMARVHGWMNDAVKGSESLQCVR

VPMEKHPTKPLVQRVVVDREIDPSSSLWTITEYCVQSRMIDAGEDKLEEGRKSTIVELRP

YTGKTHQLRLHMQHLGHPILGDSLYSPDLVYHRASRLCLHAIKLSFAHPVTNVWMSFQSP

LPKAFFLPDGNKSIHQRPESTGSTCANTMPSVI

>contig46266 Frame-0F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY70104.1|) 1e-29

MVQFAKKLAAAERPEWKGHYLEYKQLKKKLREVSDAKREETRNEQEKFKHALDSEVERVV

LFFLTKQGEFATALQ

>contig46583 Frame-1R

MRVFEAETYECTACVKTFRDTILNDMDNLNKVNVEFELLRDSRKNILATVAAEGAFLMSR

AWIKSYKTHLQALHKVLSHAAFTCAKSAVKTSDDGLSMWQKPINEDITCFHGNLTLQKRL

YRPVSTATWSYFRAKFSYRVEFAQSTTQPCAKCEIDENTNKECLL

>contig46891 Frame-2F|Blast-ubiquitin activating enzyme, E1 family, putative [Phytophthora infestans T30-4](gb|EEY67711.1|) 0.0

MTSPSVSPPSPSLAHKKIKLSLSLATASSNCAMTTNSLHSVRGNQRHWDLLRVLSHRTAY

PAETSFESIGEFDPTAARETLGFLQEECRVLIIGAGGLGCELLKNVTLSGFTKVDIIDMD

TIDVSNLNRQFLFRVADVGKSKAECAAAFVRKRMGVSATTSMDITPHFKKVQDMDADFYR

QFHIILSGLDNIEARRYVNSVVVSLAEVNDDGEVDPSTIIPLIDGGTEGLRGQARVILPR

ITSCFECSLETFPPQKSFPLCTIAETPRQPAHCIAYAFLVLWPRAFPEQTLDKDSPEHMQ

WVYQTAKERAEQFGIAGVTYSLTLGVVKNIIPAVASTNAIVSAMCVNEALKVMSYCSRVM

NNYHMHMGATGCYSHTFQYDRKMDCVVCSSQQKTLHVDPDAMTLQQLIDELCGTNFRLLK

PSITSARANLFMQGPPVLRAATSPNLLKLLRELVKDRETLTITDAAFVGDMALSLELIFL

PETPSGVVTAIAS

>contig47290 Frame-2R|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY55799.1|) 2e-27

MRVPSKDEVATELTPLISTSAPRSRSSSSSGAPLLSPGYAASSPSNSVFSPFRKTDDLKD

GLKALAPSHSLSVSGRISEQDENEPQSEDEEATESECAFFASPAKVLGSACVKGD

>contig47643 Frame-1R

MMLLCTATALLLLWTVHARLLYTLFPTLLIASIISFLLVNFLLVVFLLVIFLLVVFLLFI

VLLVIILLVIIFVLFVVIFSVILVIFFVVLVIILSDLLVTIIIFLLGFIIFVLVIIIFVL

LAIIVAILLVIIVAILLVIIVAILLVILLVILLVILLVVIVVILLVVIVVILLV

>contig47728 Frame-1F

MTTKRRRPRSRSFSENKVHVKKAKLNHKAQSLIKPWSQCGAFVASVLHFHALQTCSSSAA

VADVLEWLGDAIIGELVGRCLLSQFHRAPLSARVFRNLRLAIVTNRNLAKVYDAMGYKRR

HQKNSVYHPTVNLKQRADVVEAIVGELVLKLHQCNANVNTNRVHLDTLLATMLQCHFDEQ

IQAAKEKGD

>contig47931 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57361.1|) 1e-19

MSSAWLKQWLQYVRVDTTTSDALMANMRPSGERNRRGTRQSRKNRIVRPRRPGPVSNYEL

LRFVGGELVARDGLQQSRGNHRGGDYRVVSQEVWLSFLEIYGGGPSIQVQCNGQSRGTEP

QVSSIRPQWIITELDDSIPALATSLTDNDYASNSRQRGGRMRFLPSEVKTYRNHSPYSMV

RTRSEPTSCLISAPFVSLAENRTTLV

>contig48220 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY54382.1|) 9e-16

MEEIEALVDLAFRSTYASNARLTFEQFCRWCETTPGVTDFLMSALPIEDQATRDGGSNSH

GCIVTSV

>contig48358 Frame-0R

MVASLCKEDSIDVLMLSEMAFTGYVFKTKADVTAMAEMAGKGRTFWWCRRQARRLRCIVT

CGYVEKEGELLYNSMLVVSPDGELMCNPRKKFLYETDKSWATPGDDFLTWHCPWLNKVIS

FGICMDINPNDFKSPFCAFEFGTNVVEKQSDLVLFACAWTDFDDHDEEPFPTLSYWAERL

SPITRALKNGEYNKSNCHYLCSNRIGLENGTFFVGASCV

>contig48552 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63426.1|) 1e-145

MTLSGPVKQQLEAARGYVYPTNGALVPMSAKKGIVNKHLANGYRHRSAKLWAFLGHRLAV

IKTVKPRKRLLEVVAKDDLADVLDAINTGADLSAKNSLGQSPVYIAAMNGFHLILTLLLE

RGANANEVALDGTSPLHVACENNHNQAVKTLLRYKARVDVVANDGFTPLHHAAKQGHTEI

VAILLSSRAKFDLPIRNSSTTALLLASVAGHSYVVEQLLDAGADPQVEDAEGNTPLHFTS

RDGNYRATYLLLTAGADPDMPNENQETAFDMAEKQGHSHVQYLLDTNGMGLDGQTVDDMD

SACVQDSRLSESLARNRPEIAEIIVKLHMKY

>contig48941 Frame-1R

MELHVIMTDRSTIPLLLTLSLRLMRLLQKNTWR

>contig50179 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58779.1|) 7e-18 NOT\_ORF

MLKNVVNCDQSCRAANNTMERVIKMGSVELSTIVDDKEVIVYLPEIY\*C\*ASF\*YYDQQC

QFEERGVYLDREGKRSYMVH

>contig50386 Frame-1F

MADESPRIYAASAPLRPFLDDKKLPLDPSTSRKRRVDVLGSLSPAIRAPSSSLNSPSLLA

ISGSPSVLQMFTADTCSSNRNTGFSLLSSTSALSSSWQTRSARDLEREPELHNVGNLPAK

RLKETPFALP

>contig50531 Frame-2F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY54564.1|) 1e-122

MSFIDRVNKLQKETWAHFQHKSLVSAFPSEEETELESDDEDLLTYFVPPKDEDQEGAVDL

TAMTGRKVYIASGEISPVRVIVSFIRDKSNSSQREGFWLSNLKLQIDNACVTLEGYRVSH

ALATQESLGAAIVRFYEQVVKSQALHLIDSIQVTSLVTSMVTGGVTSLVSTLRGKADPAA

AAGALAPGLLTSSVNENTSFGAPFKYERLSNNDIMQKHSQAFSACRSSALFLRQVRHLVY

DWDANHTGLEARGCVVLASHQQFAPVISGQYTA

>contig50544 Frame-0F

MVAGTPELELLTPPTQAALPSSPSKLTSATLVYSLDGQYLFQRQAHVLRVLNASTGRVLH

ECVRENSQQTVSALALHPTTPHELFAAYDDHTVILWDVLQQKIKTERHVPGPVHWMASSR

TCPSVLFLVIQLDAQTWQLIEFNHQNPTRPRVVYQHSTLAFQTAAFQSYVTASSDVTEPG

DLLVLLAGSKHIALWYPTHLTNNKSTTPRAYTLYKHKHRYAVTSIALHPTQREFA

>contig50629 Frame-2F

MVVAAELQTALKSIMPDHLQTILLADSVDISSSPIELQSVQKLAEVLPFADDPELQAQLN

DVISIVKAL

>contig51068 Frame-2F

MTRRDKKLIGSSSLEAFVQDTEQRFPSTLGIGQEYS

>contig51136 Frame-0F

MPLFVTIASDKSAQDLHKALLLQTARFWKGFPAGSGSTDSNHREDLTLPYQVHVVNLDDL

CSERGEPLPMDSSSLLQYFTSRSVVALDWSKSCDYFSSAERAPDDVPPDVAEAALEDPDL

RALLEENHS

>contig51183 Frame-0F|Blast-anthranilate phosphoribosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65373.1|) 1e-127

MTMKLSTLLAKLTLREDLTDAEATFAVQQIASEKASVNPVAVGVFLALLAAKGESAAEVA

AFANFMRSEAVNIPIPHGLATLDIVGTGGDGANTVNISTAAAVLAASCGALVCKHGNRSV

SSRSGSADVLEELGVPMLKPDKVVPCLESARIAFMYAPYFHPAMRFVAPVRKAMGVRSIF

NVLGPLLNPARCKRVVVGVYTPTLLDVFGQVLLALGVEHGLVVHCAGLDELNSMGMADIV

EIRLGAEMPCRRYQLDPRAVGVPAVTLDGLKGGNATENAAMIRKVFLGG

>contig51594 Frame-2F|Blast-ATPase AFG2 protein [Phytophthora infestans T30-4](gb|EEY58411.1|) 3e-94

MGIRPPKGVLLYGPPGCSKTLAAKALATESSMNFIAIKGPELFSKWVGESEQQVRDIFRK

ARAASPTVVFFDEIDALASTRGSGGSSGTTDRVLSQLLTELDGLEPLKRVLVVAATNRPD

LLDPALMRPGRIDRALYVSPPDVSA

>contig51666 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58409.1|) 3e-32

MPLDKESTDTSRFSSRSTTSTTSSSLYQEENDSEQYRMSLFARLLQVSNQAEATYHFTQK

QSLVANSVLQRNR

>contig51712 Frame-2R|Blast-cleft lip and palate transmembrane family protein [Phytophthora infestans T30-4](gb|EEY65260.1|) 4e-46

MLPQLVINYRLKSVAHLQWRLLIYRALNTFIDDLFAFVIKMPTLHRISCFRDDIVFVVYL

YQRWIYPVDTKRLGDDADGTPIVSDSTNKPHSE

>contig52069-0 Frame-1F0

MERRQRADDADGRCRRSRSFSPVSSRLRYQLRRRHTRPSSQSRTPHRRRRRVAKDAHEHE

TRSRSRVRS

>contig52069-1 Frame-2F1

MTRMDDVGAVVASVPCPHGFVTSCVDVIHVLLLSPEPRTDVGAVLPRTHTNMKLAVEAAS

AL

>contig52304 Frame-0F

MQSLATALTHNKSLEELTLGQNKVGSAGVLHLAAAFATGQVVLSTLELGKNGVDQEGAIG

LARSLCGTNHLQNLYMDHNPLGDVGASAFGALLAQNTELRVLDLSYTQMSLLGLRELSVV

GLARSRILLCLLLDGHDWASTQYMKKNQHPSLNGASLATKGANNYAASCIVGAINANVHS

VLFKLTGVDLSLAVAMPTSSTIENRRSSD

>contig52595 Frame-2R

MFAKQVLTSNAKLLGRIECPVPLQCLKFDTFEAEVNEISTFLSQKRQSSATIQATVLCPS

NADVHRIAMGFRNQGLSIQIPNPSFAATTNARGGFIHLFDEPGV

>contig52919 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60956.1|) 1e-40 NOT\_ORF

MERATWLEQLQRHGVVFYAHPRHHRLPWAVADEVSNAAIRTTLSRLSFKLHKRQLAVALR

PLMQRLEAATRTDRWQRAVAHQRPSQVWKHAHGLTEYQVWTCYRIASKQLNLYNENRNDD

NSCRAHQACREV\*ETLAHIFWDCPKARSCWAKLIGHWTGETVADLFGTCQYLGSANRQAP

AISPRLRHRLHQRFTDDAVAGVRVWKRIWFLMSTSCLTHLWQERNDAVFRGVLTTASHSV

TRFWETGIRQLLA

>contig53178 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58303.1|) 2e-09

MVFDEHVEAKKVSESSVCDFYDRVFRSPIYAEHHRVCCNVGFHSSEGTYIDPSTAAITAA

SDSADSYIQLHQGDRCQ

>contig53206 Frame-0R|Blast-sporangia induced predicted protein [Phytophthora infestans T30-4](gb|EEY57562.1|) 7e-16

MDKSVGISAVADASCMSGGPGCTPHGDQCRFCRESETSQALHLTLCSEVQVARSFGTESA

GKTQSKNGSPSSDESVNIVATSMPTTLEESTITCLSL

>contig54081 Frame-0R|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY53479.1|) 6e-46

MNEQQLAKPKCKIYIHYGSRTKMFLPTVFKELCDKNPNIYKLGTPIADCSHAMILEKPA

>contig54175 Frame-2F|Blast-DNA-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY69219.1|) 8e-54

MLTAGHISKLRVQVSDHTIEDGILLVMTSKTTPLYTLAAEVGGLYLQTTRQIDTDAFMCK

LKSLIIKAYDEEDFGRFLAILRYASLDQANIIDSVMLQRVSFVLPRAILVDAWALFAIDI

INHACRNDAVVKDIFTHVQ

>contig54706 Frame-2F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY59230.1|) 7e-32

MLLPLLHFRVATLHADLRGRLEDRFTAIASLRFGIQAYNSQLAVWEPVLEDFEV

>contig56753 Frame-0F

MKHITTKEHITTKEQLISSYKPLPTLQTTAVVVQPEGVFQGESHPR

>contig57026 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69549.1|) 7e-31 NOT\_ORF

MSPVIFPDGFTRDFIDGKVTSQQLMNSI\*AAHKNLIEQSDFLICEGTGHTGVGSICELSN

AQVA

>contig57152 Frame-1F|Blast-6,7-dimethyl-8-ribityllumazine synthase [Phytophthora infestans T30-4](gb|EEY66511.1|) 4e-17

MKQDAKSTLSCRKTNGKGLRVAIVHTKWNAEVVNSLVSAAKSELLRSGVSESDLVIADV

>contig58892 Frame-0R

MPNQCSEVLEQHRSTSLDDVQPRFATILEV

>contig01150 Frame-0R

MQYSHMGQMHLVVRRPVDATKALKSKPLVVLNNFTASNDHIKLMNVTFQHMFPAIDVQSV

ALSECRRVVLFHYESASDTVEFRQYVIRASPLGLSKSVKTIVNAKIPNLNKLEDISEYVL

GNGAGIGSASESEVDDEAAHVTLPDSFRGRGNQKAEKSAVRLTEIGPRLTLSLIKVERGI

CEGDVLYHAYKTKSPEEAAKAKAKHEAAVALKRQRREEQETNVAKKQEIQDAKKQRKADR

KRQRDANEDDFDETTAKKPHCEDVNDVEYYRQEVGEEPETYMFPEITKTNKQTLKPNDAH

VQKPSEVANSNQKHRFLRPQTKAPKGKVIRQRQPKSTL

>contig03462 Frame-2F|Blast-cellulose synthase 4 [Phytophthora infestans]gb|EEY65337.1| cellulose synthase 4 [Phytophthora infestans T30-4](gb|ABP96905.1|) 0.0

MCRKCNRVVSRRQTNQFIGVSGDDYSDNVSVNQVGYVQTPQYFEDCLQLRLGDPCGHRNS

TFFDSAQTGMDGYDCASFAGTNAIFRREALDSVCGIQYGSLTEDAYTGKMMVDKGWKGYY

FRKDLEGEEADRIRLAEGAVPESVAAALAQRKRWAKGNFQIFLRNKKSLVDPEWIPPTVE

LPPKRKINKFMKWVIFMNLTVYPIGSFPAIFFFYITGYFLYTGQAPIYTSGLRLLMALVP

KIVAQSILSALSNRTVDNDDVLRSQQTWFSYAFVHVMAVFETIYWKITGKEAAWANTGAL

SGNSIMEVPNLLVFLSMVFGMIWNTVRYFAGYNNAATTHGTPLYFASLFLGGFLASQLGP

MVRMSLQTYFGWSHKSLTDQGNIVGNFWLAFVLIILCIWVYVETPNHSIFG

>contig04799 Frame-2R

MCQLYLKNKQTLASRKSDSMSSFLPCTSKIHKKKRLLLFISKSAYYSSAVLLDRPVGHPS

>contig05763 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56052.1|) 8e-13

MKTHVDEVFAFDRTVSRLLEVKCVCVVYSFR

>contig06339 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61946.1|) 2e-66

MDKVMEYKDKISAKLERYDKIVELEKQTGIDKFYIFCVVTVLVGIILFVVGGEDLVVGLV

GFIYPAYMSFKAINTPGTGDDTQWLTYWVVYSFFNLTESVTDLVLSWMPFYFFFKVGFLV

WTYHPSTHGSKLIYNTL

>contig08944 Frame-1R|Blast-ras-related GTP-binding protein, putative [Phytophthora infestans T30-4](gb|EEY61255.1|) 1e-149

MKKKVLLMGKSGSGKTSMRSIIFANYLARDTMRLGPTLDVEHSHVRFLGNLVLNLWDCGG

QDAFYENYFESQRDHIFRSVELLIYVFDIESREVDKDMAHFDSCVEAIDQNSSNAKVFVL

IHKMDLVPEDQRERVFYQKKETILERTGQLPTVCFGTSIWDETLYRAWSSIVYSLIPNMQ

DLEKHLNSFCSICSADEVVLFERATFLVISHATHTSHRDIHRFEKISNIIKQFKLSCSKT

QAQFQGMEVRNSNFTAFIDFFTANTYIMIIMSDDSIQPANVHLNIKAARPVFEEHVQQTS

>contig10181 Frame-2R|Blast-Folate-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4](gb|EEY60971.1|) 0.0

MADETKISIFMERPSGKCNDQNDSTFAHHLTPAKPPTFELEDTVLRDGKLLTLLSGECIG

LFSQYAGVGFLTGIIPGVIYPILQGYLNAEGTTVVSATVLVQIPWCYKMFFGVISDCFPI

LGYRRRPYMVLGWVFCIAILLIMAAMTTPDPYYGDSTMHRINEIDWTEAQINSINFHAPS

SASKYVVPMMLASFGYLMCEVAADAMVVEYAQREPIEKRGRIQTAVYAIKTSFTAIGASV

IAIFMNGEEYAGSFSFSLSFQELMLITGLICTPLIFFSWILLHENRVTKNGSFMEYMASF

WGLLQKRAIYQIVAYKFFSGVFNSFNIVSSSNIKLYWVHATPFNNSFMTIVGTIFYAITL

ALTGKYGLHWNWRTITIVTMCGALSIDAFMTMFTVWNVVRNQWFWLGVPMIEYLPDGIRF

MIATYVVVELAEPGHEGALYGLLTATTNLTTPFGRSMAKIVNGQFHVWLKDIQSDTTLVR

RDVTITIWMCYGMKLLSLAFLPLLPRQRAETQELKRTGGTSQVMGIVTAGYLAFAIVWAT

MVNLLSIYASTMCWKVTGGCAPK

>contig12091 Frame-0F

MVFKFTSTGGNIPNEILSRALKTTTHNYIQPNTNRSKRKSFAPIILEKLSKKKSKRGKKN

KIFSDEDEDESDSDDNYSGPKILAEEKPARRSGRNVGKAKKKYVEEKLDFELSDEEKSVK

PKEKEIPKGPQIDKVVSVRFHKETSADTGVSMEFLIKWKDTSYLHVTWLHVREVEEFGQH

AVQRMKRHLQKNCRQVEDARETVVVGEEKDLSSYFSDSYVEVDRIINAKDVEEPEESNPY

LVHLHKKEFGDESVVPMKKGVKYLVKWRDMSYVDCTWEWEDQLTDDRKIAAYHRYNHPPI

INGAHPATFADIRPEPNTWAKYQESPIYNNQNNLRSYQLEGLNWLTFCWYNRRNCILADE

MGLGKTVQATSILEHLRQREFIRGPFLVVAPLATLGNWKREIEMWTSMNCVVYHDSEGGS

DIRSFIREQEFHFASEAHRRRGIYKFNVLVTSYQTLMMDAEFLEPIHWRYIVIDEAHKLK

NREAKLLQVLHGFTWDSCLLMTGTPLQNGVFELWCLLNFIEPDKFPSQQEFYDEFGDLNT

AEQVAQLHEQLRPYMLRRVKEDVEKSIPPKEETIVDVELTTMQKKYYRAIFERNRQFLNA

GASGTVANLVNVEMELRKCCNHPFLIRGVEDKECAGFDDLMRMKVLTQASGKTVLLDKLL

TKFHQEKKKVLIFSQFKIMLDIIEDMCHLRGYSMERLDGSVRGNSRQAAIDRFNNPGSDT

FAFLLSTRAGGVGINLIAASVVILFDSDWNPQNDLQAVARCHRIGQTQSVNIYRLVTKKT

YEAQMFEIASKKLGMHHAVFETGGVRNEFDGEDDSSGNMMSLMSLDREKVEMMIRYGAYA

IMGEEDDQDPENRAINELDIDHLLSNSRTIRYDPTKPGEVGGDEEISGDGSSNLKTAPVS

QSSALSFSKATFTSESADTTIDFNDEKFWEKVLGPKPVQVLMTKVQEGWLKTASQEDVKG

FLLQLRELARAVVKERQRGKSLADADQVLAILIELKVTGCVIKGVVNVREIAADWLQVIE

RPRRRRSHNIGDELMYLEFLDGPKDKPLKVKKGGARRKRIQSFNGRNKDHKPYKIDDEDL

AEYDADLSKRKKVARQGSSAKMSSGLSPGGRSLSGIYISVKRPKGNEDFGVVKVLSKMNR

VQKMLDQSSDDANSPISSAKNEEPAQLHMDDDGERASGSDIEEHLSGSEGEEHLSGSDEE

EEEEDAYEDEEPETKRGRPRKIMKSGGKFRKASKLIIDPQEDEEMWCRVCFSDQGFLDDP

IVQCEKCSVAVHQYCYGIGSVPEKDDPWFCDFCAELDNLRADATCELCPLKRPKSAFKKT

VEGNWVHVVCALWAPGVQFSDVERMSGVRHVAAAAEELKGSICAICEKESGCVKCMRGGC

STYFHPLCGRETRGAYDMFMKEGGQLQAFCQKHRTHRKRS

>contig12626 Frame-2F

MMHCTPSDEAMNASGSLIMENVRFSASKVALITGLHDYGDVTEEFLNCVYQNRQETLEQD

AEKLQLRLVSKDEELELLVQKSGTEAASQVRAALRWAKEKSIPARVGVAQRLLTGVDKRL

NEAQKGKKLAIVEVQEARKLLAEKIHTSVGTRNESLALKAYERQIGSPVRLTNERFYFLT

FPRPGKQTEQETIVDYTLLSGQGQRSFAFKRQSKRLLQPAKTAIFEESKMPSDGFFSICG

MVDGIADVLTISADDEWEISPVVVEVKNRMRRFRTPPPIYDQIQVAVYMKMLGVEHGDLV

QCIYGDDPHPSIQVSRVSLGISPLCLSDSSSGQVRDIWSEMIVPRLYAFAAAVEKMRANE

SLRLSFLIGTGEERRTILRAECNFL

>contig13131 Frame-2F|Blast-40S ribosomal protein S26, putative [Phytophthora infestans T30-4](gb|EEY60916.1|) 2e-54

MTVKRRNHGRNKKGRGHVKRVHCVSTAKLIPKDKAIKRFVVRNIVDQSAIRDLKEASVYE

SYALPKIYIKNYYCVEAAIHQRIVRGRSIEARKSRAPPPRRFAPKRT

>contig14105 Frame-1R

MQCPSSFLDGAYSSSYTSSNKKFSSIINSQSERSSRCLLLFLTHQNRAIAYFFFIVFIVV

RSSHLKKLP

>contig14268 Frame-2F

MAGRPSAQLPNAAPSTTSSIFSKMLGSKRKLQQFDGFASDDEDTIEWKDASIQTHKNIDD

AESLHEISRREVRMDRENQNDSDTESECLLDEDEENKEEDKKGSYNPMTSVASQLVSSED

FAPVSGLSGINLPLQIAAEYSKFDHHGKRRGYHGKLHAIVLTWPRCIRATEIIHSGDMVW

CCPDSICGFSREGELVKVTAVRKTRRELVVSLRNGTETTVLIDRVRRLNEYLIRKGVVRL

RSLYNG

>contig14422 Frame-1F

MSATSYGLLKQGSTGECRQKNCKKEIPKCLSHKRLLLPSGSSFFFRFTGSSHLSVWSRSK

AKIEISDSGERKSCSTYLPIEVTCSDFATDSSHQLPVWLTAAQCCICCVHLICSFKRSAA

GCLSKLPKSLEFLDLGDTYSRDDYTVLMKIMRPDNTLYTSQRPAIRKRNAI

>contig14655 Frame-0R

MSTLSAFVVTYWAVGIFVVDLHQSFKERSSISNERILTLDSVPPWGVLFD

>contig15209 Frame-0R

MAEFIDTPPSDTIVSINASDQPLQLTTSVLSLETGKRAASEAFDGDSGEDFKDSETTLDD

VLMSLSDKKRKLLDDELPDVDDNEEFTHQAEEVDTDLTLGLVAGESGETTDATGLGVAIQ

NDGHYHHFEHKRSEAEESDHAIDIVDVDDEDESVGSIQESLNSQEPFQDDETTTRALLRA

ENQREARVLLQQLDDAVRSKLCLLALQKYGEELFYGHEDARDGILVAACAQDAVLSLVRD

ATQARERSERGSSATVPVELDDKTKQEATTKTRTK

>contig15317 Frame-0F

MVKVEHRKIFKQLEVDSTKLLSLILRFGFDNHGSPQHEDAIACHHAFI

>contig15634 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58019.1|) 2e-90

MIKYRTAQDEWNHLKAITGAIHLLQTIQDDELNGLLASCQAEYESRRVGLAANGDEPEEY

PRTDVIVPVQRKLFKAIEAGPFQHFLLQNGYQLLIERIIGAIA

>contig16675 Frame-2F|Blast-casein kinase II subunit, putative [Phytophthora infestans T30-4](gb|EEY57633.1|) 1e-158

MHRDVKPHNVMIDHEKRQLRLIDWGLAEFYHPGREYNVRVASRYFKGPELLVDMQEYDYS

LDMWSMGCMFAAMIFRKEPFFHGHDNCDQLVKIAKVKGTDELFDYLTTYDLELDPQYDGI

LGTHTKKPWEKFVTQDNKHLVSPEAIDFLDGLLRYDHQERLTAKEAMQHAYFQPVRDAAE

QKLRGNAHHTDEITSVSDSSA

>contig17849 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53537.1|) 6e-49

MKPVLYILAESAVMFDNSWSIGMEGVFDRYRFGAKRERIEDTKDTTSCSNAIVFTATAPP

IFVKRRKIKEPEGVAESQSSCKWQERWHAVCDDCFQKYRPCVHFPESRLRLLIVGHNPSD

HAWKTGYSYSNPTNRMWMLLTGNFPPQSWKGIVPSSAKIMDQNILPHTLGVGFTSIGLE

>contig18138 Frame-2F|Blast-myb-like DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY56798.1|) 1e-93

MSLPTAPQYSTPKPSVGVGMWTEEEHARFLEGVKLFSSGPWKRVAAYVGTRNVRQTMTHA

QKYRLKAARRLREAQRKQAAARHGLANAHRGSETEDNMVLVSRSLQTPSPTGGLGLGSYS

KMRLPCSCIEKECPHMDDASKIYMSIADAIEILDSKSCGAASSAGSPVSTDENLGNSWLH

IDAYDPVIKSQAFDNDDLIPLDSASSDCDEYPTLEDCASELLELLF

>contig18651 Frame-0F|Blast-transcription initiation factor TFIID subunit, putative [Phytophthora infestans T30-4](gb|EEY64604.1|) 2e-31

MMSSLAASTSHEATTAHPVVPLMQEQSISSRVLPVAARQSGEISVKNDAMASVMDELLLK

YLQTRGYHVSKLEAYHSEATEDERRRVLGEQAARIENASIDTYAQQMGLTTEACTANH

>contig18927 Frame-2R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY55551.1|) 1e-168

MELFLPVLLSTALLLLANLDSFSDDWRSGWLTSEAANLAANNTLICSGLAVWGLEAIGGP

SSTMASFYTGSQAVLGLFFLVSYIKFVSTTTTTMVMEKENKLREVMKIMGLSGATLLGSW

LLTTAVLATPLAFAIAAELKYGNVFPTTEYATLVFLFWSLSVAITAFSYSITPFFNQSRS

AAIASVLLWLILFFPYYAVQSAETNAPRYWAALCPPTAFALAVDEMLRRAQLGTGFAYSA

GLLEDPVTVPSAFRLSLFLIFDSVILMGLG

>contig19326 Frame-1F

MACEKETEKEKVLETKLKQLLLCNPMAVEELLNPVEEDESAQPELNDQEILDAVQEEEGN

EGACLIYPRKPTVLPTSYSAAFRLKFAVLKKFFLYKLYLASRLSYKLATIERPRWTSNPT

I

>contig19887 Frame-2F

MLSEGSLRTAASSGISLSGRGSILAQVEIAKANNELLQECGALTVFVDRLQRSIHAFRGL

NFQHLDLDQVDALINDLQQDMVLVYLLIVFNSHKENAVFDRQLMMIGTMGPSFSLLSILD

CLSQLNVLPGFPIKRLLLLFYEWFSAVMGNFNELGALKRYRRERSDIDPSILKDDAANVL

HCKTLKPYCDTIQVDMQDPYYLQKKNFAKKREAIHNKYLHRANYELKCQESTEANSATKP

LNTLDDEWEVRVETLYQLLLPCMRDHITFFGNLVTLSCGSALNARDKQTFFTRRGDQYGM

SDFSAPNGENNDNQFWKWILREKAIVLDVSNLIILLVYKHFRASHACKGEYFMQFFLEAN

VLATLTKFMNKDVSTYLQVPRQDSDEAKMGFYGLDKELDKCNIRFEDDLNEFSIQSTRTI

TSILRVLQKLTKRKPNLIKNALCRGQTIVWLK

>contig20146 Frame-1F

MSNKQASSSFYKAPNRQPYFAETAVFPPLPRLPPPDVFHETESTRKAPSACIARPRRFGT

KITNLQNARDVDSFVLKIENKLPPSIASNGPQRYSHTKQPLSPLIKQPSAAENTPVGNHE

KTPVLSAKKKTIALQENAENSCLQIPGRDHQSRKLPDWSPIKPPLQPGRSIWSIDPDELS

ELELEMAAITKDLADSAQKVTYAEASKCALPGCGGRRASQPQVKENLPRSYKRYYGLPII

PSYAPFC

>contig20616 Frame-1F

MPNAPGHDIWEQGIFPTAVVDVTGAGDSFNSGSSHGRRIVETLMMPCVAAVQQLRGQLPR

SEHVHFLLLRRRTKVKIFSSKNSNSERRYYECHLAAASNEATILCNLSIRSHVSGIFLAD

LLNILLKG

>contig21318 Frame-0F

MLVVLFALYMALIEEERVVLFRRQPQSACSLLYLDAKERTFWRMHPANYDTLKLYEQNLR

GAKLCLDGFRKDDIMSHFGVLEPFQLLATSAQYETKGGESTVTCECLVPFWSLSDLKLIG

AHRKLSKHMIKNMYFYSGGSMRAFLSDQTGAKKVVDDAIRKVDPNIADRLITQHGSTSDK

QIDHIRMTGIRANDHRDLNKYTSSSDWVSEVTSEYALRILGKIVKPTYYEEMWF

>contig22412 Frame-2F

MLRRGIAGNARFTFIARQGSWPGRRRIWSTPRLLSEAAENCETKAAP

>contig23323-0 Frame-0F0

MDFFASNEEVMSDEPIITVRDKRRHYYLASSEPFIAADR

>contig23323-1 Frame-0R1

MPTFISYCYNGLVRHYFFIRGKKIHN

>contig23473 Frame-1F

MEAKTMQFVTQFARAVYLQWSHSLEHAKFWDDHAFLHAMLEEAVAKLPDGKLKSQLAHDL

EPLVTRLASSLRELHVRERLHEKEQSFNVPLNEIGTEIALTQAATAPVGDKKRKLADVLA

LDTDITLMNNQNYDAKQLVQRFALIAARRYESPKEQQHKRGFVLRRLAACVQQQMASWPC

HWCCSKESDGWKEVQELRVLLESIARQDVVALASILYWKEEKDRDSLMAPWTKFYRPDES

NELTQVVYEDEIAKIYGALLTLAIDFPIVNKELKEATSSESSDDEVSGMYRESKLKLLEP

GTQAQETTRQVLFAAQLRQREGYKNQQWLVSVLSFRHRLLTLKTNTFKLEGTNSDELDRR

AMLECLGHVYSRTFANVALFDQVKQNLSVEKAAEQDLALFEAAVCLRYAATFMRVERKSS

LPALTTAMAHLAGIPVPLSFMTWLEHEQVSHPVSVLEKATQRLWTKCCGQNRMMNILLSS

TNVTTEALSLIQTSYEDFVRQLAKGHFPKSPSVVDIEALAASVQEATSDLFYVDTGGNED

KERGKTKKKKSFKKKKQRNNKKNVAVANSKRS

>contig24436 Frame-1R

MPSGHATTAIGLFMWILLESLLGVGYQWKVVKKVAVCVGITLLFVPVPYSRIYLGDHTRL

QVVIGCINGVLFGLFYFFVLRYGLGRRLSVATKRINEGRFHFLHMVNDFHVDRRYLLDSQ

FNVEDQQFVRSDVGQT

>contig25325 Frame-1F

MGMANFNKNIFVGTGGSEGINFSHFIGAVYGMERMMGRADNPLRRILNYASTHFLQKFPL

IYVQTVIGRGEQGNLVTRGIFIGDDEECFMKAAELSLEVNFELLDAPIQKVVVYLDPEEF

KSTWLGNKSIYRTRMAIADDGELIVLAPGVARFGEDKRIDELIRKYGYRTTPEVLAHLNA

NRDLMKNLSAVAHLIHGSSENRFRITYCPGYLTREEIEGVGFNYGDLKEQSAKYPVDQLK

DGWNVDTKGERFFYISNPALGLWAYRGRFEDASTGTMSPSVSAKTSLSTSADTTEACLDI

GVGGGPFKHT

>contig25776 Frame-2R|Blast-DAHP synthase [Phytophthora infestans T30-4](gb|EEY61462.1|) 0.0

MQNERLIKRQRLQDRNVVAITPLVPPACILEELPVTSEVHELVDATRENVTRILHGHDDR

LVVIVGPCSIHDVDAALEYAKRLKSLASDLKGELLVIMRTYFEKPRTTVGWKGLINDPDL

DQSFNINKGIRVARKLLLDINSMGLPVGLEFLDTISPQFTSDLISWGAIGARTTESQLHR

ELTSGLSMPVGFKNGTGGNTKVAIDAVVASSQPHNFLGLNEHGLASIVRTKGNKNCHVIL

RGGSDGPNYEQKFIDEAAGMLQKVTQPCKIMVDCSHGNSRKLHTNQPKVVDYLAGIVAEG

NKNVLGVMIESNLVEGNQSLGDDPSKLVYGQSITDACISWESTVTTLKELASAVMKRRNE

DTAILTNN

>contig25800 Frame-1R

MHVWNLASVLAVLTLSQQVAAKGSGSKDRPGNCKDTEDCKTKGYECVALQTTRAGTETVK

QCLPKEQDSDVCSGQYPGLCPSFSSWKTPYNQISSVCTYKPADKCVNGDESSAGSKGGVI

CVGGAKDPDGKTFDAIYGCADFDTSELELLFGEEGANDLAAELGTAPAIIEDCLSTNATS

NSTLLCSGQGTCVPDAMGSLTYNCRCNIGYSGNFCEFIDSNKCQLPGQCATGVCNLDTQE

CECAAGTTGDQCSECDAKSSEACNGKGMCSNSVCKCEEGWEGLQCTKESAVKKSAKSTKK

ATTETTSGGTMLSAYSFGSITMSLAVLLAAIFFN

>contig26139 Frame-1R

MARSTSVFLGGYKARSTIPWQRILSRWRQIRWIISSICITTLWVQRNRVVNEHTSVTLEG

CVQNFKLHFSAVTSVGNAGC

>contig27028 Frame-2F

MGRLSGLTKEQKLAIFRQSEKKPEWNQKQLGQWAAKTFELRNVPSQSSISVALRQAGKER

SPNTKRPSVLVKSKVTKFPQ

>contig28418 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58735.1|) 8e-12

MEIMSLEDASKEVALPSTISPSDHLPLLCKFHIKKVLF

>contig28771 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60637.1|) 1e-51

MFNMAKIETLEPAMSEMVAKTDNKQLSHQISIDGINAESQFAPIMGAPIFKEKTSGFALR

FLPGEVCINEYGVAFYNFDGSNPADPTQENHVCKRYSEFKKMHAVISRFMSSENNLRIKD

EDKFQTYPSLPPMPRANAVTCLLGRGNEKVVKEREEQFVKILNAIAAHPIAFQNKTFTNF

IS

>contig28920 Frame-0F|Blast-endonuclease III-like, HhH-GPD superfamily base excision DNA repair enzyme, putative [Phytophthora infestans T30-4](gb|EEY57975.1|) 2e-73

MSMPLRLVSIFTLSKHTVMRLRSHAALVSDAYLDDDLVNGVDSKTVDSVKQKIKVEFGQE

VPTQHPGHRRKIDDNAVTVKIELTPTKKAKKKIAMKTERVIRQEPSNWRELFQGIEQMRA

KKDAEVDKFGCESFSTERFPPHVNRFHVLISAMLSSQTKDPVNAAAMTRLIKHGLTVESM

LEIDQEKLARLIRPVGFFNLKAKYIKQTASLLLKQAETEGLKLVDIPNSYEALIALPGVG

PKMATLVMTYAWGNTMGICVDTHVHRISNRLQ

>contig28955 Frame-0F

MARSNKQTNSLAVVVCAAMLAGMTMWARSRKQRAKLLRKQLTNLRFDVSVPEIKAETERI

LARMKRVDDEIAALQPSAVKFESSAQKLIDLDHEMLSRVTNVTFLGQVSDDKAIRDACTK

AYETIEDYAVQRSMRADVYKAIRTLYKSQCYQDLDSITQRYVCRLVQDFERNGLQLPEEK

RKELQSWKQKLSKLEIQFQQNLSEETINIKFSDDDLKGVSDDFIAALQKNDDGMYMITLS

YPTVFPILNTCTIESTRKAVEFAFNRRCISTNVAILEEMLKIRHKAAVALGFDNHASYVL

EHRMAKTPEDVNKFLNDLNSQLEPLAKKDLDDLLKLKKADCERNRWKFDGKINMWDFRFY

MDQYLKKHCLIDTEEIREYFPLAHVTAELLSMYQEILSLKFEEISQPHVWHKDVRMFKVS

DARLGTVGNLVGYFYLDLFPRAGKYGHAACFTLQQSCTNSAGVREYPVAAMVANFNAPTN

LKPSLLSHDEVVTFFHEFGHVMHCLCSEVAIPRFAGTRVEQDFVEAPSQMLENWCWEKES

LQRLSSHNKTNAKLSDEYIARLISTKNVTAGLSNKRQLLFAMFDQSIHSRPNSDTAHLLK

QLQKDIMLIDMTPDTNFAASFNHLACGYDAQYYGYMWSEVFSMDMFMSRFKKEGLMNSKT

GLAYRELILARGGSIDACVMLEDFLGRAPNQDAFLRSKGLTSC

>contig29444 Frame-0F

MTEEGMKTDGAVATEVLHATALKSGRKQVKRVIGDDLDDVIMPCEIFDTREAFLLYCQNN

HCQFDQIRRAKHSSMMVLYHLFNQGTTGFTFSCSSCKTTLLQGNRWNCSICPVFNLCDVC

HGKTKHEHQLHLFKVVSIPRPGNEVSNETVSTKVKGIVSKAGGAAGMRAIKRETGTVDLK

RAKQFQTQKSGGTRKRKLQQSSPVASVDVAPAVKREVVASDSLSSTATSASYGTSVDTDG

SKKRRIHNIDPQLLLQLEHASSCAVMNCTFFNCNRMQAMLQHGAICEQRLAGPCVLCKRI

IGLLSAHARQCSKEYASCKVPRCADIRRHFLAQVQARQQHQGGGSSARSDGGATVMEEMK

DSVT

>contig30662 Frame-0F

MNCNRIERLLCRPNHRNFKRCHWLNQCTLSFSRSKLRERGSRLVAQYLHQTFSSLQATSS

PQHKCTEAQKCTHVLTKNIC

>contig31283 Frame-1R

MSTLERLVSSLNARKPHVKVVAVVTGGGISAAESLFIPGSSSTMLHFAVPYSRASLQSYL

SSVPSLSQKIEFCSAETSERMALAAWKHGKEILRQEADADNKQMTLISALKRFRASFGIA

CTAALATNYSKVGPHECFLSVCHAEAASKNNNILLPQFRTYHLLLDKSLGRSRIEEDQIV

GRWLIYFLAKAANVDPDICNSFYDELKSARSGADSVVKVSSDRDITHSNDPLRDIKSNKS

EQLVSVAFLPDDSQHSADGSNPIIAVQEFDFRGLILPGSFNPVHQGHIGLARAAQQLVKA

RTGVEYPVAFELAIANVDKGAIDMRTVSTRVAQFSGKNALGLGAWPVLVTNAALFQQKSD

QFPGCIFVIGTDTAIRIVSKNYYSMDEHKIVLALSYIARNGCSFVVAGRFDQKFENRFIS

AEETLNKHVPPVFRHIFVPLPESSFRNDISSSTIRARVATI

>contig31801 Frame-2F

MNNGERIRQSPTDVESMMKRSSYKELIKRRGKRGRLNKKQWRHDKAASQPVKRGGKTSL

>contig32044 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55691.1|) 4e-42

MSALVKERPPNPIEWLAAYLIKNNPQNSSSGSEVK

>contig32945 Frame-1F

MEPLRKKRCLRDEKLLPSFHEVFPCASRLQATLETESRPTSTLFSGLLPLSTSYKHLDET

TEDAQIASSNEILTAFDSLDTEALTLSRVESQCGYGNKKCFKPRALKTNGSLHTLCHFHR

ERSVRNQRTFDHKKRRHQAIATETVNNQ

>contig33195 Frame-0R|Blast-ubiquitin-conjugating enzyme E2, putative [Phytophthora infestans T30-4](gb|EEY54779.1|) 1e-104

MASVMATKRLRKEYLAMQRKPVEYIQAVPLETNILEWHYVITGTTGSPYEGGFYHGKLKF

PPEYPMKPPSVMMITPNGRFKTNQRLCLSMSDFHPETWNPMWSVSSILTGLYSFMLENQT

TLGSISTTDGQKRKYAMASLETNCSNATFRKLFPDLVALQEEREKNQELLRQSSVNGLVA

PSFASTKTASGPENAGTIEDWSSTVYLIGSVAIVATFAAYWLS

>contig33469 Frame-0R|Blast-ubiquitin-activating enzyme (E1), putative [Phytophthora infestans T30-4](gb|EEY62529.1|) 0.0

MVTSTDLIKLTAAFGVGVATALVLQFAYQVALQRSNTRRVAIKSGEKSPHGTDAAAQELL

KEQMSRVASYFGPEGFEKIKNAFVLVVGLGGVGSHAAHMLARSGVGKMRLIDFDNVTLSS

LNRHAVATRSDVGLPKVVVMKRHLLEVVPDCRIEDMAVMFEADSADELLEGTPTFVLDCI

DDVKTKCALLEAVTRKGLKVITATGAGAKADPTRLHIGTLKDAVRDPLATKIRYFLKKKE

VLSSDITTIFSSEKSVCKLLPLDAVQARNPEEFGNLENFRIRVIPVLGTMPALFGQSMAA

YVLCDLAGQKIYPEAVARLSRDQRNKLHQKLQQREHVLFHEGRKIELGKDEVEFIYQEIW

QGRSSVSRTRNGGHDRLYLARWRTDRPLYPDNVVYLTTKELSTLDKTGLLGFDPDVVARI

DKRLSEFGSWIAPS

>contig33582 Frame-1R

MELCRDHENLVAGFGIADDMHWQDVASDMNLLIERRKQGPLTITRTFGTVQGDFRRFINF

FSSETSEELFAWNQFFFGYAVDAVALCNLSAENLDKHATLGIKWTCMQPSVLMRKRDECF

LEYIVFQKDGQGRDAAVIVRKPINIPECPPLPNELKTKREKITTVMVVRESDTCSDETQL

FMISKCDHKGLSASTKYCKKLLRALKNVSLSADAKRIATNICSPRCLEHPSGTDEPSGMN

ESIRPWVPTSVHRGCKSCSRPFRAGRRRRFCHRCGGVFCTKCIVQRAGIRHEKNTVGSCK

SMASQRTFRVAQAHFCMLCVDICREGAMEAIQDQADTVRSSVASCKSSPVHRRSSIDSLT

QPRSSKSSTPTSSVPHSFISHQADVPRHSATWSEENRNSWWSENESDACSWNSGSSRFSS

ISRNCSGAPTVRSSFSSEYSISRNSFMAVQSLETSCEIDTSQIDHCIDERSSIYEVIDTK

DMMPESELQKQLQSQQSSLANSNDSQFTSDTVRNRYTSTPMAPIFLPTTSRRTRSAALNE

NAIPPKSLNQCIAEQNELLQQVLSASRGFTPNLRPSASQSINEFDDIPDDGVYEL

>contig34051 Frame-0F|Blast-pre-mRNA-splicing factor SYF1-like protein [Phytophthora infestans T30-4](gb|EEY57316.1|) 0.0

MVLHFAAYLEENKYFEESFRTFERGLALFPKFPHAGDLWQTYLTQFVKRYAGSKVERTRD

LFEQAICAAPDKSVHLYYEMYADFEEQHGMLRNVMTIYERASDAVPDNEKLSIYNKFVKK

AQKFFGVARVRDVYEKGIGKLPDKYVSPLSLKFAQLETKLGEFDRARAIYSHASQFCDPR

HHEKTFWKLWHEFEVSHGSEHTFLEMLRIKRSVVAQYSQVNYVTSEFAPQHDDSSKIAGM

VAASVPASTRAVAGDAMAALEAQLDAAPADEQDTTEKRKGQTNENQMERNVRQKQVVEVA

NEEEIDLDDEEGEEA

>contig35229 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54011.1|) 1e-110

MEPPSPRDSIDATAEELLHPLEARVLDLSQELTQTDVDAPALSDDEVITKLNMIAETLEE

VETSFRRERSSPYRRDGHLIGNLLQVLEQNEDFYPMLEGKLSDLSVNRVKAATCRLLLAT

VPVNSRAIVRVLDDDDEMLERVCGFATDPDPGLRCYATGLLSVGLRDRSVADTVVNNDTP

LKLLKRARMFASKLERERQQAVKYIQDHLRLVASRHKKTNNSSGNGNTKATTP

>contig36475 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58024.1|) 5e-24

MANLTYSHPRTYGKDSRHCRVCKTTRGLIRKYHLNMCRRCFRERATDIGFVKYR

>contig37443 Frame-2F

MIPLQSVRDAMAVEEKKVFDGDDGAEGDGIGTHDLKSHQVVTSFTLVDWFDVHSLSTDEV

SGQIQVRINILLANPIARPDSDHVANYASDSLLSIPRRQRQAVDCAPPSADGLIEQEIPL

SFLYPHVLHIRKQIANVTSMIRLTEHLVEEKNTFKSSLHKKRADIQGIPTNLHISYFRIF

RRFGSDTRSLTEDLVQVNCNNTHNSILNLAQSSSMQEHMAAPEIHATVTCGAPTAHAMGL

SDCGLREMELEMHNFHTALEKLKPQVVETPIGEKDCYIPEDSPNFFFPPMDDENDAEVED

EARNSDSGNLSESPASSGSNSIVAAAPVTPVETAPKRKPSKYSVMARKAAAARVKALPTN

RFVKKKNSRQLDQNNNDEKAANYANYPSLRAEPEENRDPRTSLKYAVQLLCRLEMLRSDY

YLRKSVAVSQSVSSLVTCFMAELDLCLQERNDKVLDQLAKVGFLVGWESLISSHGKELCM

ISDAWVAIKCLETFSFELCEGADMEVLVKKELDVGYIIKISIPSSQFALLPFSLRDGGLI

SVTSVLFTQGINEMQSLANMVGHSGVSIQRKINSTSFRTISEYYNRFTERCGIGMSEISV

GSHPDEILRNLRLSVESENSASKNTCILLHAADAVRSLNGGRITYCKSGKDRTAMSTTLE

QARLLVQRKRHVLQEIESGSATEYGPLEEVKDVANIMREFGVRIHVAKKNVGRFKYSFNS

LQRKLFPEIYRPPISTIQDMVTSVTARDS

>contig37524 Frame-2F

MSSEGVSGFLAAATVTAAMASLALLQKKRAAAYKPKNRKAIDQSRSSTYSAPKNGFTGVL

LDPSEGYELFAIDYSMHVQIRQKVIHKFLQTHPEAEKSAAAILLHGGVEVDRYDTDIQYN

FHQESFFQYLFGVREPGCAGLVDLTTRKAVLFVPRLSDEWELWCGDRKPLAYFKAHYKVD

EIFYIDEIAAVLAEKLQTEKIYVLHGTNTDSGLETTTTSTFEGIANFEVDQIALHPVLVE

CRVIKTEKELELLRFVNKLSSRAHTQVMKTIRPGKMEFHAESDFLHYVYSNGGARFHAYT

CICGSGHNASALHYGHSGAPNNKLLEDGDLFLNDMGGELHGYTSDITCTWPVNGFFSTDQ

RMIYEGVLKAHDAVMAAIKPGVSYVDMHLLSHRVLTQHLLEFGLFQNGTVDELMDHEISA

YFYPHGLGHFMGLDTHDVGGIPIGYERSTKKILAKLRCVRNLEKNMVLTIEPGCYFIEAQ

IQAVLANRVTAAFINQEMLSRYRCTGGVRIESDVVVTATGVECMSQVPRKVEDIEATMQK

N

>contig37757 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61450.1|) 1e-70

MTLEKHTYALFDNRYLHAGYYVNVKNSSVLRQSFMDKKIDVALLNADLIAGPLQVHAAAM

RALQSDASKSLTTRSLHAELVFNMSGSRNVSESFKRFGISEKTTSIVVCVFDADEAKLKE

VEANVEGMQVPFKELGASLTHQDNQLIKKAYKISEQELTQSSLVDAATCRIATKSYSK

>contig38037 Frame-1F

MIDSWSEAVSTPLIQDIFTRKALSSSSMRQPQPYPS

>contig38972 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70589.1|) 1e-112

MITRGCEYIRARSQHLDLMKPQLMDHRYEDANGNFCCERFEFFHFTGVQSMRQVFEAIKY

FMLNMEITISEALGHTTVREDYDAVDAKTSLWNYRLLSTDTHGVTSEVNKVALTEYFDEL

FEMEGKPCAVVLTDCVDVDDMYPYNPHERVRRDICATTLLTEVRRSKCSGKSLKAIERQD

NSCVPDANFAPRARDEQSSDDEEELVIVMQRVALLTLHRPAFPITKSALRSLKEGIASWG

EIEVQSIRRAVEA

>contig39089 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58399.1|) 1e-103

MSTYKETVLTAGVARLSELPQRIAHVQALVQQHTSDHTPSMLRAKFALEVLADPATVGSN

GDVQALLAIVGDEVLQLLHTTQQLQLWIQLQVPKVEDGNNFGVEVQKYAFMHLKEAQVMW

QKTWDSLAEYSAARATAVEKCHTKATSESSTTTTVTSSKGGKDGDEEKSVTATVEKECKA

GTKAAEDAIAAVVELDVKWYFNLLRALEGVRDQYAVTEDVIVKNQSKIELPRGKNDRAGF

NMF

>contig39294 Frame-0F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY65040.1|) 0.0

MFIAKPEHLEAVLKTQIDIFPKSEYIHDVFRDVLGDGIVVTNGETWRRQRNVFVGLFSSR

ALHEHMTPIVQKYLVQLVAILLDAAASNKCLDVFDLLQRYTFDVFGEIGFGATLHSMDGA

CQPFAKAMDEAQYLAGKRFKQPMWFWKLRRWLNVGDEKTLKAHICVMNEHVMAMIADAIA

RRRYRAKNKPTNGSTAPFDKDIVSIVLDKMESSENAVDLIEIRNIAIASIIAGRNTTSDC

MGWLFHLLSQNPNAEAKLRTELWTKIKPLRTDKHYIPTAAEVNRVPYLEACIREVLRLYP

PAPLITTHCIEDTQFLDGTFVPANTDIGIALFSCGRLTSVWGDDALEFKPERFLDNETGK

IIPMTATKFAA

>contig39320 Frame-2F

MRSRGLARQSRRISITFCRQIYLMKVLRLGCNTLSISSKPTAPYDKLFNN

>contig39405 Frame-0F

MGFCLSKCLPDGDMAAELEAELDETSHSYVQQSTEQSTFGTTSLLAADEVVCLDVIGEGP

SGVIYKGSYRGSVVAVKKMKMISFPSKPSARENVEMELEVEATRMGSLRHPNTVLFMGAC

LQEDYFCIVSEYCTRGSLFNVLHAPKVSASGRNRQKRSDLEAFSTAALSNTNNAPGVVAK

KKTNLKWSLRIRLALGAARGLLYLHSADPPLVHGQLKSTNILVDDSWNAKLADFGTQRVA

EAVGFDRSRMNTIDERSALLRWTAPELLKLGEERVLKGAFPSDTPSPQAVDIFSFGLIMW

ELTTGELPYRDMHTNVEIGAYVLSGCRPIMKPGQCNLNWAELMARCWSHNPTRRPSAAEI

VSSLESISKADAIAQSAKKEARVVNSNRADYRFAENPRSRSKGPSKFKSNVRVVV

>contig40229 Frame-1R

MCPTPPLDWHYTHWQYKASDGGMPDKSTLSDAVAIADFDPPPPIISTSSVSSALSQSTNT

RMSGSTKNYSLASFSKIAGLDASQKGTPPSEFTKGGLTMASVREHDSDSSAADSEKES

>contig40342 Frame-0R

MLLLPLQEGSVLMTLCVYYGALMLLLELILPLVFQRRVRIEIPRLIPSAQANPLSSQEFQ

KQRRALRQKLIALQRALAETPRLLPQKKRRRAGSSAMQSAASPLKSPVSLMRPKSSRKSS

EMKRTSYRAQEMKSDGYRRQNFGQKNILGTQSSMAISDLRTTTSHSGFSFYDVDEDKKLD

AKRAEKKKVKPKLHTHLAAEKESPVFAERKPIRLVKDVDGGEYSEAVTSYKAFIEARRIN

TGSALPSSALHFFPGTITQASVMNCESLVVSSFSEESKRTPKMPQLAQTQNEQKTDEGIK

EIEVSEQRGPLSDFQAFCTSFVQGNSTAELQAMKHSELSDGDVSASQQSFKKYKRSQDIK

KSVEHFRRVGKTLEFQSLDNYSHDDVSETDEQKISDIMATQLFLEKRTYDQAFGSFNDMN

RPEEKTPRITRRISFSDEVEALAASSPEKGDGEHLVKKCKHVRAFGMPDEEDEEAEWRES

LAFQSHLADW

>contig40878 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY52981.1|) 1e-76

MDHVLGELHGHTDVLRFVVGFLSFYDWLWLSSCNRLLASSDLRRFVLSQSVFRVPPPPIV

KGDSMREDQVAASYYADSFLRHMKPEALCCITSVLVPRTGMHLLNLLCAFSSLRSLRLWD

YPYCTEANSNEINEDAEINVAALLQLLPNLQELNVAGTEVSLSELFEMNALYGPEKHVIT

PTNWSLHTLNLSESGVTDLAPLAMVPQLQSLSVRRTNVSSLEVLETLPHLRVLDISETKI

IEFSFLKCLTQLER

>contig41235 Frame-2R

MLAQGPASIIGDCVRRLHFSEEAIRTFGRFSRDVGRCCGGAQWLLDRRLGQTTIIIKFIN

YGTFR

>contig41240 Frame-2F

MDRTKRIVDDFQVLSETEWQRLRRVGLQLTPDANSKESFCFQNVPSSDGLSVRVLRLLRE

SQYGTTEIQTWMDAAMRREHGECSSKLAAEKTPPRQNIVTAGKISPEEMQKRRHISFDDE

AQKVESEYKTDGMRLRSLMRSLSPRRKEQNAFKISTSLLESGSACYFFNSERHDQLDTSG

DSEEFKKNMSDAPSLFLDSKVVSLDALNEVDSDDMDRYNNQIILKRDIFQKFGLCVGENQ

RTGNASYHEAFRSAATILKCFFEWAAKRAFAMVQNYLEALFETLTDRDFCDYDLLWTEEE

GYHRWTMFGEPRGWRQRG

>contig41921 Frame-1R

MSESDRLNGIVETAAQAFINVSEVPEPLEAEQAVQRKNEIATACQSLLNEKMLGAQLMTL

RLPPVQAQFSNEELLSRLDANNDDGMTYEQDQEFLCGILKNVESSLHINITPLSTDLLAV

MTVSTALESRSSGSNGSLLKGSGMAEAGSLDDRSSMGNGSFS

>contig42119 Frame-0R

METLRRLASSVFDVHRGSLNDTRLPDARSLDITFVADRLAVMGTPSNAPTDKKRNVVNVD

DLAQFLDAHHRNHFMVFNLNALLYTLNNEHESVADKLHEQLLEFNWERDGMKAHTPPLDL

IYRICYALHAWILLDPQHIALVNCQSGKTRSGVVVACYLLFARLVNDPMDAFVEFYKKRW

DMKSLTSEVLRKKTPPSIQRFLTSFHELLKQEMPINDNPLLLKAVIFRQLPVELQPCVQI

WDDYKLVYCTNTSEGETHGEAPVLDWNEEDGFFAILWENGIELDGGFSILCSFGANYDNV

DDMDASSKVLFRYANSTFCLAPGLVTLKKQDLDLMKQYEHGFDGDLFSVDLVLHENSAKK

PPSFVGRNLTGNNAVRQGLIEMTKHHVILPDPAMHSKLIRIGFSDTPATFALQCSQNAPN

LALDLLHTKGFSRFFAQEAADVAATERQESSILNHETTICTKNSQQTAGNERGKCKAITT

RENLSVSTNSNDHATPTNEYTTKKHLLIEGKAASSLATMSALIVRSSHNTLNSAIDVVTN

APGPPKLEIKSAMPSDLFLASRPTEAVGLSVESGEDTKCAALKSGASFKAIQSCLLKDGA

NLSALLPIHLCENCTSNSGDMSSAPIASETKLKNREEYARYFRMLRMGCPREAVKQKMLM

DGLDPVILEHGSNSTYKMGKDRTAITQSVPESSNDKEYTNSSTTEDKVVPVSDVLMKDYK

IYSKYYKMRK

>contig42649 Frame-0R|Blast-SCO1 family protein [Phytophthora infestans T30-4](gb|EEY55526.1|) 2e-43

MQTYKADFHPKLKMLTGTRDQVADIAKAYRVYFSKADENEDDDDDYLVDHSIVMYLVGPD

GDFLDFFTQTARVDDIASKIKT

>contig43475 Frame-0F|Blast-WD domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY69409.1|) 1e-81

MRVFDLRSLDSSTIVYKTACETPLLRLAWNKRDDHFIATFADDSTKISVIDLRRPIYPMA

ELDQHKAGINSMSWSPHSRYDLCSAGEDCTAIVYDICTQLTRSGKNPAGPSYTLLKSVEP

INQIQWSPTEPNCIALCDEKFLHIVQM

>contig43611 Frame-2F

MDLLEVDDEVAMPQSDLKAKMSLETESKSAVSDETDSTLRRGRAPANADTVNSKWFEELV

RHPTPHFDLNSPEVAYLLRAWTIDMKKWRYLRRWLLQVVQTKGPLPDAFSHGCRIASIVA

>contig44009 Frame-0R

MSPTSLSKRSTRAMSSSYPTDPMLPQSALTQAAAAAAAAMPFNLGNSDLSDPNDFPVQLP

LSPTLMRNLGDRSYDKRKGAAMELENLIKQLQENAASIEFHQHHQLSHDSSSNSTDILTS

STTEVLAQTNPSRQRIPAIIELLGNDFACSSNANHRKGGLIGLAATAIGLMHDAHWYLEK

LLPPVLHCFDDPESRVRYY

>contig44908 Frame-2F

MEFVEALPCGHTFHAQCINKWLAYRRVCPVDRQPVC

>contig45099 Frame-1F

MSKYFHYLVRLLEDKGDEAGKDAQIVSRCLELCFAGSAVVGDLFDNETRINRLLWVATLV

RQPDIFIYDHSKCWDMFLTNNAFYALMELMLISLQAEGDATTVQRGVSELSQLVTLIMKR

NELAYFNTIFKRIAVLPHNSEECFLNTLSQVEASMAIKNSDNDLCSAVIHALLNSVTLGY

GVRLLARYPMLVAAAPLQTYHTIIELHVLSERQKHELVQILEIVDTNVWTTYKESVSATS

SVSFAPQLAAILQLEMDTLSPAMSQEQYETWETKCQQYNNETTLHRPSKIEKTRIDEGFV

CRTTSPPRPKCDAKFPVLLDETSIACRSFEYRNSDWGGEVQLHDSTCGTCELPVIILSDD

NNSLDVVLLSCGHAFHKQCLEDQACPNCLEDNLSTVGCFKV

>contig45662 Frame-0R

MAGNETQAKNRDKISASEKLVPPLYMYFINVRGTLAISTACVNAKDAKRSANERWRDILE

ALNKMNIHSTMYSSNGNQNLTRNLAASQSTLTRAPASAQSKKSNLILCSDDEMDDDDDEY

DNYSDGMDGDDWYPRGLKLVKDANDGLDQFENALKMNYDERGESDPSDDAKFRAAIRSLF

TPTDDLCAGIHKLRASLKYRGAEKKQIVSNVTATIKMERLREGIFEVVVDVNNVVRYKAS

EALKSDACNAAVDGMLNKLNKIRSTWAQLLHFLDIKSLAYVSP

>contig46195 Frame-2F

MTSEEVSYDDDSAKSSTSQAPAARSWNKVNLSEQNTIFDSNLASQMKGKALANTRKCKRL

RLNDSCERFQSKKCVKKPKQTPLTQKIEAKDVFDHFRLYSGCSQRDSKASENETILCEKS

YLHATIPAAHHRRPQGLETAHMHPTKKFTMSTHNDDEDGRKNNTRRCN

>contig46469 Frame-1F

MVDVANGEALDSPSRTDTYFSAQSPFLGLVFPMLESAISNLDLSTEAIDGMHKYLVVRNT

RSGLQARLALRNDSVFFSVVIDETLSTPGASSIDLLDHGVCAGRRPTLLVTIQPQSAAVF

QVKPDVAALRKFHQLWDQSIKEHVTLYNIKQFAEHYQVTLCFTCSVASFYIPPNISESYP

ISALEDVVAKFLQNYEHTWKWLMSYYEKTLVATMRSTSQSSLVEVLNKFENALDLVSPLS

PRNLVPAATKVFDEAEGVEMTPSRDDLHQLVQSYRALYFDFYYITDELVWYGVRGNAVRH

SLALADLAYGVVFNHEVFRSFLSVVGIENDAVALPRLLLPWVCQLEHFLSFFPDNQEATQ

PLRLIYDQLRKFEAN

>contig46731 Frame-1R|Blast-chromosome segregation protein, putative [Phytophthora infestans T30-4](gb|EEY67985.1|) 7e-83

MHIKQVVMCGFRSYKDQVAVEPFSMQHNVVIGRNGTGKSNFFNAIRFGLLTSRFANLRPE

ERQALLHEGSGKHVMSAYVEIIFDNSDGRLPVDDSEVALRRTIGVKKDEFFLNRKHITKS

DVVHLLESAGFSRSNPYYIVQQGKVNALAVMRERERLDLLKEV

>contig46890 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68217.1|) 1e-56

MQFKRWFQFELGWDGELQSLRHRRWFVGAQTRDGLLRPFIARDKAASFEIIDANEIDAQS

FVMAATFINSEDCEHPALIQRADSAPELDKVADDESEDGHQ

>contig47044 Frame-2R|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY69908.1|) 1e-109

MALALEQGQYLLKGIQAFYREELHNRARKSDEAAIGNISKAEASFESSVCSSGVIVEDGG

RAVRTRETSYQYAAVNCGIFDGKASWIFRLDTDTQDDEMTCFGAATLPVTVNGYDSSPSL

WMLRGYNGNLYARGHKVSRTIGKVHPGDIVQVDIDMAEGTLAYKINGTDYGVVFTDLAGQ

EVHPAVSFYGSGKVISLLGVTRWDCPALIPAGIDPVFLSNLREHHFFVGYGTLGKGGQLG

>contig48085 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68428.1|) 1e-113

MHVTTLQPSLSPQSFRRRATVGNDGDMHHHHTSHASIERPPLASNKVDVQILKKLSASVS

HFEGPRTNLSFVVSVDTLIPGRRAFSDERASCQLVARSFDDFRRFRKSLLTRVGSLHDPA

LLLMGRRGKCHCEGINKCPFDVTRSFLERLKFKRMPFISLSENEADLTKRQLEMNNFLHI

IFAILHRMQHGSWHSECLFLQDVMVFLEVEESFSQQMELLLRSKNRYMSLDGWKAHTLQT

FGFGIGI

>contig48221 Frame-0F

MMRWNFIIVIIVATSAVGVIGEDTSTVQTESKKSSTLPAHHYLKGRKAAIMTTATDDEER

VFAENFASLKTGFAKSLAKIRQKYRSIDEFLKDNPVIKKEIIVAIVLLTLIVASPIVVNW

FYPA

>contig48427 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69089.1|) 2e-23

MTIYDPPHLSFLFAMMLTAVAFVLRSYPAVMHLEESLRVISIFIGPSPNLIFSEACQFGS

IRLLDWIWSISCTTPSTRLRGWSLTDYLRSDANYHNWQFSKSLYVAVSRDDLTMVKWLFA

HFSGCEASEHAVDVAMSKGYLKVLFYLWIHRSRRL

>contig48492 Frame-2R

MERSIAELPTDSDVPPLVLKPEPILVPRQNSSLPGQVIDLTLEDDSHDDDDDDDDDDDDD

DGIDDDNEDESMGFGKGVDEHIMPVIVSSPASDDAKQIYLGDARNESAVAVQSPLEDVSH

DVADGGRC

>contig48935 Frame-1F

MTRESQDEDAEMMQQEEPEEQRDDMDDFQGEDDDDASGSKRRLFRFKPAYDVLLVREVIR

DFPWAAGYGRTRSAWMAVATRVQTVLESNKGVIFSRGSTLDHAIVKRRVDMLLEAYRKNE

LSTLRGSGTPEEFDMRYKLIAILTRVVDEQTLNKGAMREKRVQSALQDALRSLEELDVSA

NLAGSQPIGFTSSAAAPLSSSLMPIAPAPASTSTVTSRASPSLSPSSQSPTIKQQAQQND

AKRPLRTSSMPVAALIQDTKRSRVERTGDTISNYEERKLRLQERRVALEEERLYWDKQKA

EQEGKERQALLDLLRAQGSLLTELVRTTKESPNTLDL

>contig48940 Frame-1R

MSNTFLRQCCSQIDAHVKRDSLSSSLSSSNFAHKSVLNILGSLHGILRASVLAAAAWATF

SSIKIIGEYSRSSTRMFYLGTYRPNPGDLLSLLAQINGTYGKTKVY

>contig49352 Frame-1F

MQQERRCVVRPIEKSIMLQVRTQDVRTSCQNDESSKLTPLIVESVESDDSNIHKILAELF

ADLECKKQSFNREEEAFRHGAEQLNGLKEEHAELLRKLELYKRRQKERLGMQKMLVDLKQ

ENGDCERVQDIESDSESDSDHKNRDCRSSSSYRGRRR

>contig49666 Frame-2F|Blast-bloom syndrome protein [Phytophthora infestans T30-4](gb|EEY56970.1|) 4e-43

MVDDLRQWIMQTRENLRKVREECDDASLEGDVPDFMQKRRTELEMELEQLNKRYRECKGT

TTNTSLCQSKSPVQPRGQSIQVQECTTPIKTSSSSCLNPLCSCGITTIEARVHHGANANR

LYYRCSTCGFHSWVDAESSTHKDNFAVTK

>contig49781 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68733.1|) 2e-35

MAYLLDNYQHDWVNYTFEGHSLLSVATSNGHYDCVRVLLAHQIATKRSLEAAIALARRNW

QAHILVLLTSYLAELDYVLQQDSQSSQAANSRINANKVIELRRSTYRGSITDTVGSDFDD

EFRRSSLESVTSPTNHINSIEDLNHT

>contig50545 Frame-1F

MRESKIFATLRRTLRLFQPLSSHTVDSFNLQTVSTQATAFSCYKLVPGNTAKCGNAAVAM

SGALAVAVALTNEAQSEQKKDVIERSGSNPIQNVTMLLRLYEQIDQNMSVFAARMLEDLE

KTIEMEKQANDGKVVSSPEQRALNMSIAFESTLRKVQDAVFRNNYVTQEQVREAMQQLIA

GT

>contig50761 Frame-2F

MSSRGSNKQMALPRGFGARDDSVKTGPSGRPAAFGVAARQARTGAPGAPASSSASRRSPV

VVSSKKPQSLTPVAIAIPSLDDETLENIGKKAKSIAEEYALIADLKEAEACLAELQKEYK

QHEDVNRIFAFGILKNAIDAKAEIRKKMMELLYQLSLRTHALSFVSIRYAIKKTIELCSD

LWCDVPKLHEYMSDFVVHFIMESTTTGVSLDWMLGSCLQAVDIIALRELVDGGFLAAVIG

EILKTFEIRRCCQSKEGIE

>contig50826 Frame-1F

MNSLGLEYASDDENDLISRPPTSTHSVAASQSVIDSSNAKELADSSQDRPNLVYAPTKAS

EPAWSDAPFNAEDEEALLLQAGIPPAVTSQTGNCDVQHRIERFLRVQRERGQDFQTTLQD

KKEVRNPYILEKVVEYFGIDELQSNFASDVFDPHGLPLHEFADVLALEQKKRADARAHRQ

LQQQGGADPRKIRFVSS

>contig51069 Frame-1F|Blast-anaphase-promoting complex subunit, putative [Phytophthora infestans T30-4](gb|EEY68460.1|) 0.0

MQRQGSNPYLKELYLALSMAYQQNSLDGFGLYLYAVILKRLGYSTSTGSTQDSTTTPICM

KTRHRADIVEEQKRQQYHGSANDKRTKFDSAATTLTFDVTTRFILIESIRRYPWNWSAWM

ELAAHSPFTSSEEEIILAASCPWMYQLFQAHVLLDQQQNDAARQVLMSLEEHFPQSSYLL

AQQALTSYHIRDFDQSQEQFQRLAERDPHRMENMDVYSNVLYVKEDKTELSRLAHRALKV

EKYRPETCCIIGNYYSIKNKHDRAIIYFHRALKLDPNFLSAWTLIGHEYIEMKNISAAIE

AYRHAVDLSARDYRAWYGLGQAYEILNMFLYSIYYYRKSVAIRPYDARMWCALGGCYEKL

SKVDEALACFHRAVNNQDREGIASFHLGRLNAARGQQHEAAKFYLIHLGLRSTVTSALQD

ESGKSKASGSHHTSNNQKEEFVLFCSSSGNIRIDTPQALSATLYLAYYFKQ

>contig51137 Frame-0R|Blast-importin-like protein [Phytophthora infestans T30-4](gb|EEY65606.1|) 3e-84

MCEVDEDVTWIQKFDDPETFTEANDSDTSISDAGAAAIDRLSSSLGGNAVLPVAIPVIKS

FLRDGDWRKRRAGLYAICLLGEGAKTLMTRELDNVVSMVLPFLSDQNPRVQYAALHSIGQ

LAEDFGEVEKGRNFQAKFHAVIIPALTALIQNEQTVMRTRALAAS

>contig51182 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65784.1|) 7e-18

MAVQANMSASMVNKSYNSGGKSTNNAKKRSAEGHGDYIKKSFVDQKLAKKQRKMQRPHYE

MVTRAKQI

>contig51331-0 Frame-1F0

MLILLHGSLIMCRNGATANGASLSDSNLGICLKSCGDRVVQLSTRSLNIAISSDEISLTK

SY

>contig51331-1 Frame-1R1

MPRLLSDKDAPFAVAPLRHIIKLPCKSINMLATDHLRLIFEWNNLQDIISSL

>contig51667 Frame-1R

MPLGEKLGRPFELLSLIGRKRKDEHHEHHQHHSGAVARAYANAIGSTTSGYTNSHSHNSH

HSGTSSRFYPGVKYERITPVTTCARVVQYERLTPGSVSAIPSSGVTSSLPLPQTYEAAAR

EAAFPKSDMMPSAGSCSFRSAPSPALSSLPSPGMLTPLINTSNGPSTSACRSPLAETLRP

LRPPRLAQNFVSPAQPPIGPIVAPSAP

>contig51713 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57789.1|) 2e-30

MTMPFLRPRQDSNEPEKSLKEVEVASKQKKIQDEIDAGMREPVAGMVYGLYDPKKPDASP

RISVNSVLNDTINDENLADQDAKIPLFGDGGASWRAKMLKHAEAKARASGVALKEIVQER

>contig52420 Frame-0R

MAMGSIPTSMNPTAVAGEGGASMQPAGAQMVASGADWRIQLTREHRANLIAKIYNEMVRV

SADPVPGIKLWMNVSWYELTLYKESRTQEEYINKIFTRLKSLRAQHTDMNAVMAAQT

>contig52697 Frame-0R

MQGILSQTIDTNAPHRSHTKRPD

>contig52877 Frame-0R

MVYHAARLHSGRDHEPSSAVDHNPALNLYKPTANVVVFSRRHRKH

>contig53016 Frame-1F

MSTNDDTNASVPDAKFDLTNSLAPFMDLHFMFPLIDFLSSSELYDEAQLMAAKLALLKPT

NMADFAVEIHQTLHGSEDMPEEFDARRSEILDALSFAKSECSLMLELIENEEKIMQLQSE

NLLNANYLEQNEGITPAVLGGLYKYAKLQYECGNYQDCLTYLTYYGVLIPNSSE

>contig53179 Frame-1F

MKVLHLLLCTALAISRVSGATIRATASSPAAASPTTLTETSTAPLTATSTETVTT

>contig53207 Frame-2R

MCYMNCHFNNKRKKNIAGPTRLHKSLARSQSLCCWDGQCHYVIGKR

>contig53474 Frame-1F|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY66927.1|) 1e-123

MPTTNGKSAFFTVEDTKASFNLFCCVCGIGSLAMPSNFARAGPVYASIALASMIFANTYA

TLKLSKVMLVAPSSVKTYGDLGEWALGKWGRTLTVISQMGVCLLVPCAFLILGSTLLNVL

FPNSFSQVFWIIFMAIMVIPMCLIPTLKESAGMAFAGCMGTVIADIIAVSVLQWNMSGHG

PIPAPDISVHQILTCFGNLALAYGAAIVVPDLQREHSQPQRMPRVVLITILFISGFFVAI

GLLGYTAG

>contig53580 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53567.1|) 4e-54

MPPKHRVRYVALDYSRLSGPKQKGLNVLHSLDKVAVWALTQTGFFCSAPKRLISQNGNRR

KAQAFFPSPPSEPWDAFLTSSNFQSKGESSQESTSTESSQSPTLSRNSGDWLEQRGILRT

>contig54080 Frame-0F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY58155.1|) 2e-58

MDAQIVITLLILAFISCSIVYDVELSPQGRKLHSRGYRWRRLQNWLPMGVAYAAFYMARY

NVSAGNVSWVRNQLGYTSVYMGWVLSAGSWAYAISSPITGKITDCIGGRNGMIVACIGAA

ICNLALGSTYLWNDSFLMKQ

>contig54246 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65793.1|) 1e-48

MVKFLISMGADANLCNGKGRRPLHVVKQSIDMASIIQSLIDAGADIDATENHGFTPLMFM

CFTVSLEGSATLLALGADVHRI

>contig54479 Frame-1F

MMLYLIEEFVRASCLTSLFKDEASFGVPCCKYKFAQFYVLVRCVLLLSRSAADV

>contig54707 Frame-0R

MTRLIFIQASCMNSGLAEVVTSDVRITGLNYGSTATVGGS

>contig55384 Frame-0R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY67294.1|) 8e-14

MSSASYEKDSDCIARSGIDVLAYYSMDSSRNARSDCLILLSLSVVSFFIGYVALSLRWRW

YKSTA

>contig56266 Frame-1F

MAARNLVRFLKSAEVSFSSFDRQATG

>contig56288 Frame-1R

MERREDLPQRFLYFLWFRKRIILLTRAQATTENVSPRT

>contig56381 Frame-2F

MKYRDPFCNISQSIADKIGVNLHRQQNHPLHIIKTKIERYFDDQNRLH

>contig56693 Frame-1F|Blast-ATP synthase subunit gamma, putative [Phytophthora infestans T30-4](gb|EEY62471.1|) 8e-28

MVMMILVKNSAPVLKTVGQQARGMATEKQILQRITATSNIAKITKSMKMVSAAKMRGAEN

RMNAGRP

>contig57027 Frame-1R|Blast-GPI-anchored wall transfer protein 1, putative [Phytophthora infestans T30-4](gb|EEY61363.1|) 1e-30

MLWVMAQSLSLIALYSGIQIVCMLPRMPLLCRGVNNNQLFVFIVANLMTGAINLSMHTIN

SSPEVSCGVLLTYMLIISVVATMLQHVNIRIKL

>contig57153 Frame-0F|Blast-6,7-dimethyl-8-ribityllumazine synthase [Phytophthora infestans T30-4](gb|EEY66511.1|) 1e-16

MKQDAKSTLSCRKTNGKGLRVAIVHAKWNAEVVNSLVSAAKSELLCSGVSESDLVIADV

>contig57485-0 Frame-0F0

MRADCGRQSQKRLRTNFHCCQLGQHYNRSLGCTGCMGSIPR

>contig57485-1 Frame-0R1

MLPQLATVEIRTQPLLRLPPAICAHKCRDNLSTILVTSNTTFQSRYICC

>contig58619 Frame-1R|Blast-phosphoglycerate kinase [Phytophthora infestans](gb|AAN31474.1|) 3e-74

MVGVNLPIRAAGFLLDKELVYFAKALDAPQHPFVSILGGAKVADKIQLIMNMLDKVDEMV

IGGGMAYTFKKVINNMEIGDSLFDAEGAKIVPEIVEKAKKKGVTLHLPVDFVIADKFAGD

AATKIC

>contig58893-0 Frame-1F0

MPPFKQQAAPAPASETDSEDSSPKQFDMTFIDETTPTVTPVNNST

>contig58893-1 Frame-1R1

MNVMSNCLGELSSESVSDAGAGAACCLNGGIKSIERLSLDLIS

>contig58952 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62772.1|) 4e-20

MTGLFTWEIAPAMMTRNVQSLSEVHSKQPNYELEDKVALNEALTPQAELKLSTSMTLHRP

TG

>contig59230 Frame-2F

MCIRLSAKCFIYNAQTMKSWGRFDEIRSMQRRRRFSIKMISILVHNRLQFR

>contig59245 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65833.1|) 2e-20

MVEGVELTDGVVRSFSVARNFAPHEDESPNVLVLSLDFHRDGERCVTSRGDGVMSMINCI

S

>contig59487 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69693.1|) 1e-09

MDLMGINKEEMTHPHRHIIIHRSTQQPMKWHCTFIDFEKCLPTRKPKNVTQLCQ

>contig00727 Frame-1F

MTLITSSSAAPYSSLHELPSPLLECSIQDSGYLSENNQTQSSRLSGKSTPSSHDTVVPNY

DHFINPCLLSWHDLSYVVPCPTSATNRHGHQTILDKVSGRSAPGDLTAIIGPSGSGKTTL

VDLLAD

>contig02589 Frame-1R

MARKGKTKAPVKPASSSDSSSSSSDEAPQKKSVVAKAAVKKPVDSDSSDSSSEEEKDVSK

KEIATKSVVKQESSSSDSSSSEEEEKVPAKKATPTKKAVTKKESSDSSSDSSSEEEAAPA

KKATPVKTTVTKEESSNSSSDSSSDEEEVPKKAPASSKKPVAKSESSDSSSSSDEDEPKQ

KAATKAVPVSKKTSESSSDSESSETDTKKATKKPSTTKKDSSSSSSDSSSSSEETPLVAK

KRKNSDTVNESNKVHKHENGDAAAVANPQQALEVFIAGLPWSATEDELQEHFSGCGQVTG

ARIPLQNGRSSGTAFVTFSTPEAVEAALAMDGQDFGGRWMKIRTAEKKNMFEEKPEGCTS

VFIGNLAWDVDENSIRETFGECGEIVNCRLATDRETGEFRGFGHVDFDSTEAVDAAILLA

GSYVNGRAIRVNYAKSRDNNMG

>contig04316 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53884.1|) 1e-95

MLWSYFVLMPTVAFASANGFFKGEGTAYTLGNVSSGNCNFMYDPGVNGNYAALNNDQWDS

TRNCGRCAQVSCDDDRCSDKITTEVVYLLDRCPECKQGDLDLSPSVFKKLTGSDPSRYNI

KWQFVDCPVKGNVQYCTKSGSSSSWLAIQPTNFANGVASFKIENQDVTMVDSCYYYLLAN

GANVNMDAVNVEMTSISGETITDTLKLEVDKCIEGTMNFNGGETHQSSNDPKPSELPPTI

APAPVTPTYPVVPPITPEVTPPESNPIQVPPVSTTDFVPTPDIVPTPEQVPTTPVPVLTP

ELVPSLETVPASESVPTTPVAAPPTPEQTDAYNTFDLIGASNTNYKAGLVTLADVPASDV

SVLQSNEGDVGHTYPGPNLLPESLNLANNQAEKGPELTVGPLNSEKPINLLTEHLGSNQY

DAGNVQVPGDSGLSSQDQTQQLPVIPGSGNYKAGTVLSDVPVQMELPVLLSEDGKSKTSV

LLSNDDIDMPNNQQNDKANPLKTEQV

>contig05885 Frame-2F

MVADGKEAILNGKVAVLRDYIASFSKENEVDTILREQLTIVFGGEKNLVSILAKLYSSAL

GNRSAFLEIKPALPIIESIQLSVFDKWLKEGLSLNQVWSLIVSGRNKGQDLSIGEYSVFK

AYANAFLDRQMTLKSDKFVLYSVKDISAAPEATFLDYYDLVLDMSLLDGERLFFLLDRVG

ASSFVFEPDFYRKLQGFDKTGDLPGLITEAIAAKEKTFKLLNTNGEAIKTAKKRGTFDVV

TPEAKKINHLQNKWKQDMSFLLKAKHVASSAKARSSGLKY

>contig07159 Frame-1F|Blast-glutaryl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY57306.1|) 1e-138

MLATKSLFLSAARRHALGAIRSMSNDMSAFNWRDPLLLEHQLTDEEIMIQKSSIDYCQGK

LLPRIVKDNRNGKFDRSIMNELGEMGFLGPTIQGYGCAGVGYVSYGLIANAVEQVDSAYR

SAMSVQSSLVMHPIYKFGSDAQKEKYLPRLATGELIGCFGLTEPNHGSDPGSMETRAKRK

GGKFVLNGSKNWITNAPIADVFLVWAKDDEGDIRGFILEKEFSGLSAPYIEGKATLMASA

TGMIFLEDVEVPVENMLPKVKGLKGPFTCLNSARYGISWGALGAA

>contig08684 Frame-1F

MSHKTNECVERPRKIGAWKTNMDLKKDEVVVDVRSEKFGKLTFDAKRDQWLGYDPKDHLK

TVERYEKIDAARKKLRADEINKKLKESADKNKEKKVRNKGQNREGDLSNSDSGSDYESDM

ESEDEEFRDHDEGTMFTERVARQGGVGGAQMKTTVRNLRIREDTAKYLRNLNPNSAYYDP

KTRSMRDNPNPELNPEDTTFIGDNMTRFTGDAQKLASAQLFAWEAYSKGTDIHPLANPSQ

AEFLKKQYEERKALLEKEKSSKILEKYGGQEHLEAPPKELLLAQTEHYVEYSRDGHVVKG

RERASARSKYVEDSFENNHTQIWGSWFDRTAMLWGYACCHSKVRKSYCTGEAGIQAADES

YIANSERPMLNVSEQVEPKKADESGIIRKRSEMYGENIAPELDEKKLKQAIKKAVKEKKK

QLEQNDKQHRKYNSMGNFEVNAEEMEAYKLLKSRDDDPMRNVQDNDELLDVEESGKGKRL

RR

>contig08749 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63266.1|) 3e-44

MSFSSFYSVVNAIKDKSVEAINTLSSDLEDFKSVVREDVAELTDTVRQNMQEGRLSIERR

DDNESNQDKELDTADDTSIEPSSEDTDKDPLMLLRNSLFSFDVTSSLHSVSNSVQDSLTS

VQGSWSSVGSKLTSINVSSSLGSLEAMGSKLLNSADEFLGTLAGETAYNEDDDIS

>contig11624 Frame-0R|Blast-glutamine-dependent NAD(+) synthetase, putative [Phytophthora infestans T30-4](gb|EEY69301.1|) 5e-75

MMSNDSSKKLAFLIFSQRQDLTDDFDFKMQVKNVPSRKRIILLSKNQQPSFKKGMSALVT

VATCNLNQWALDFDGNLKRIIISIRKAKVLGARYRVGPELEVCGYGCEDHFLEQDTFYHC

WQSLETILRLDITNDILCDIGMPVMHNGVRYNCRVFCLNQRILLIRPKLSLADDGNYREK

RWFTTWKPHLDKNHSRRLDKFVLPA

>contig11952 Frame-2F|Blast-fatty-acid-CoA ligase, putative [Phytophthora infestans T30-4](gb|EEY59449.1|) 0.0

MSSLIVDTMGDVAFEVMAAASLAAVASLAAIGVHCTKRQNGRAHAMTPASKKTRMKSRDK

AVEHTHPVLVANNVAINMEPVILALQRRASSTKWCHKLVYTFLDDLGREMVNLSLKDVDR

AARKVAAILQRDAHVKKGDRVVLCFPPGLDFALAFWGCLYAGVVGIPVYPPYPGTLSTDL

PKFNRLIEDSGAAIVLTNTTYYLASKMATVKGYFSLSRTSWPAHLQWITTDNLSDSLVLQ

YNEQDAMSLTHHDVAFFQYSSGSTSAPKAVMITHGNLKAQLKTWESIEPSDTMVSWLPSY

HDMGLVGFIITPCVFAARCVSMSPISFIKDPTLWMRTASKYMATHVCAPNFGYALVARKT

SDKQAAEMDLSTLKQTICAAEPIRPDSLAAFTAKFRVSGFNPHSFNCGYGLAEVTLVCTG

QDPPQLPTILSLNKHILETQRRAEVYTPSGTKPVATDVLQLVGCGKPMPTFNVAIVDADT

KVVLDEQVVGEVWVQGPSVALGYWNRPEYTKAMFHAQVAGTKSMKKAHLRTGDMGFFFHG

ELFITGRLKDLIILRGRNVCPQDIEASVETAHENVRPGCSAAFSIEKGDEEALVVVAEIK

NGTSLPIMKDICREIITRVLSEHQIKCEAIVLLRQKTIPKTTSGKIQRSVSKTRFLDGTL

EKPLFDYRSTTGNVSITSSSASSNTVISKAATLSRELKTPDEILTWLLEHVADEMAPLPI

ANEKKKSNDTLNDSVRTGKTDPHTPWAMFGMDSVAIVGLSSDLSEFLGCIVSPSVFFMYD

TPFKLANAPGLASGELTSVQNENDTSSHCAIPSVHSIDEIDASCFEIENFPEVQRLFQQM

HEFEQEGLIVPFLETLTPEKRQMVNFNTYNYLGNASDAVVAAASKAGIDKYGTTMSSSPI

VGQTQLNVDLENALCEFFHAEACILFVGGWVSNVTTIDTIVSKGDLILCDALNHDSCVSG

QRLSGATILPFPHNDTKALERMLASLRTTYRRVLIVVEGVYSMDGDIPDIPELIRLKKKY

KAILFLDEAHSFGTMGSTGRGICEHFDVNPHDIDIRMGTLSKALGSVGGFILGSKALVQY

LKHCAGGFVFSVGLAPACGAAALASLELMTQSASRTVTLQERSGLFYDLCQEHKVPIRKS

TYRGAPVVVVMIGSTIATAQASEYLASRKINVKPIVYPAVEEGKCRLRFFLSALHTPKEL

NETVKALTMYLSESAASKVATSAALESTVEMKRNGLKTTSDGVTIVKKRKTRKKKRSSVS

NKAKV

>contig13639 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66271.1|) 7e-10

MLEGGSWKAGRTIAKEKRTDGGPPIKIISDGTVF

>contig13855 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61882.1|) 8e-48

MFYHYLSWAITFKVTSWAITITRFVCFSLNITYGTFMLYSLVMMMAGEALMFFTC

>contig14285 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60881.1|) 0.0

MATSPCCSQSELQLNAFETTTFRNSKSEPVLQLPQPTDKPLQNVAAPAYALDHLLHVHDH

LIESPRTASSSSLVSGESSRATAQFRNHNPLRCDHNRTIISSSENVAITKHNLSPRTSPL

PPLAEIDTSSSSTLLDKFLNRHGTSMPETLKRNPPTIIEDERLQALNVVVMNSNLPPPPF

ANMYACESCREDIGSLLSKGRHHCRNCGGSFCAECSTKVICVPYQAYVTRGALRVCDGCY

HRIQNFHKQVKSTNVTWSGLQPPAISDLVKTLELSDNEEPVSIFNCALFLETTPYYGHLV

LTRRRLCFLSYVDAIKRKVAYAQILSLLKPQFYYISGLQVKTKHKETFFLAEFNGLRDTC

FLRLDQLIRAYQEASKITSIGPGKSPSSTQLRKEALDRRRSYKLITEHLGSSTSGCGAIL

HPSLSSSPLSTVGFIDFEQDDDKDLALREIIEGDSNTDDNKSTASDEEPFEPLPLDPFLS

KMTVLLDCDMRADVKRVFDLLWTDGPGREFLHASLEKARDIDIDIESWQVMNHDDTALMS

AIQNGFEISKEKDYTLYRIVRSQHPPKTSFPGLPPYAGCTRTQRFRLDASSNGGDKWDRF

VITEVNRMSKIPFCDYFEVEMRYVFSRDGNNYCHVQVGLVVNFLKPTWFKTQINSSTRSE

SKEAVEAWAKQAIEFLETQRNRIIPLTPTVKALVGTDCLFVSESDESRNLYKIQISTDGQ

VQIVLNPT

>contig14872 Frame-1F|Blast-phosphatidate cytidylyltransferase, putative [Phytophthora infestans T30-4](gb|EEY55709.1|) 9e-94

MVIFLVFRFATSRNHAEAFLTFALDVVGLIYIIGTLSVLVAFVDDERRPLYRKLLIALLY

VVWASDTGAYLTGKLLALVNYPYYHPLAAHLSKNKDYEGTVGAIGFGIVAMVVTSNQLEL

PGSFGAKVLFTVVAVIIGRIGDLFESLLKRAAGVKDSGTLIPGHGGVLDRIDALMFATLV

FSRYYASVL

>contig15314 Frame-2R

MNGGSVRLRESPPCMTWTGRLNCRY

>contig15448 Frame-1F

MKFFICSAIALAAAASAENAPEPTCISGQYQDGPYYFISSVPAPPARSCLSMTANRSTAI

SWNVDFSLPGIVDDTYWSESHVSLSLPSVKMEYLQTATVKFEYTSFQDKDLSAIAHITML

LQANVFDRGSLVVVMLCQSGPDPTWLGIFKKEVQVDGVSYSLFEGYVNTMLFQTFVPKSC

TTAYIGNTKAFLNQLGLSSSHRLATIRAGFMIRSGVDAVLNVNNHYMTYTAAVDPSARMF

R

>contig16603 Frame-2R

MADEVDYESDTAMAVEEEEVKPKKTKRTIRGRGSGSAAMDAARYPAESGVFDKLKPSRDH

STALRSVEGWLLFVTGVHEEAQEEDVMDVFGEDSQVKDLHLNLDRRSGFVKGYALVEFEH

FEDAKAAMERMDGEKILGQTIHVDWAFRMEAEKRGGRRSTRR

>contig16676 Frame-1R

MLADAREYHNKCVQISQIVRYSRKFVLSRNATLFRKLASNHVFGISLEFRDVQFTHDQGH

DDHSGRHGIYVAYGFNKIPISESHRKKKKLDSLVVFLADTVVVLAN

>contig16975 Frame-2F|Blast-ribosomal protein L23, putative [Phytophthora infestans T30-4](gb|EEY55586.1|) 1e-45

MVWNRVKFPNMAVTFMGKNARTRLRDNQYVFRVEPHHTKHDIKEYLTKIYDLPVAKVNTM

NYEGKFKRAFRGRYVYKEKDWKKAIVTLKE

>contig18300 Frame-2R

MWHALLTLLKSFVGTGILFLPDGFRSGGVLFSPLCLMFIAAMTLYAMLRLLQCRELVGGT

YGHIGFLAYGAWGRRMVQISIIMMQAGFCCTYVIFVAQNLAQVVSFVGYSVHPSVLILSQ

IAVYIPLSWIRYISYFSISNLLADVFILYGVAFILGNSMMLLATQGPAQDVHLFNENDYP

VFIGTSIFTFEGIGLVLPTQSSLNQARQKRFPSLLAWTVVGLLCFYSLFAGINYLAFGNS

IAPMVTSSLPRNGWSSSVQFGYAFAQLLSYPLFLFPAVNIMEEMLGFPKRASGRKVAKNF

FRAIAVLVTVCIAYFGQDRLDLFVSIVGAFCCVPLSLVYPPLFYLKLTPHSTWMDKIVDS

FVIIIGVLTFFYVTYSNLQSWSN

>contig18559 Frame-1F

MVTFKMDGSTTYCYYISQKYSEEELVKYQVLEEKQENLCPITIRVDVANNLEKNALIPLR

YTATVDTSFADPNFEFPTPIVRVPVPDYLLEHTNASAELSGQATYDVAVANVVICDWRSC

DIFLKSSKSSSYYSSRNNPTNFNDKVAVFGSEELVVPKDGKYTGYVHIVINVGGNSRADF

VTFFPVQIGDVAGTAPNSIATDGTTTYCWTAKDVSVFDPSVSGDLTIRSDDYCPGSMSMS

LSSSEVFVGETIGIEWKVDISDTSADDSTLIAEISKTDAIRNPRSNLYSIVPVAVFSGCQ

RNLVGANCSTYTGEESTTFSIAEFDDMNLTSNAVSYLTSYTFTSSGLYTMFGRVAMAAVD

GERLDMAIYSSVTVSVIGGSGDSYVFLYVGIGIGAVILLIGLLFCYMKKRSINNVSTKAI

PFRQPVRGFDRSSVYTLASSNFLSHKKPATVQGTDMSGDYSTSNSGPSYLAVNAANSGVF

SDTIRVGPDQMAESRQSGGSFSLNPYDRASFADLNENVANSRPSDTSKFSFQSGYDDETD

WEYDNKQVRCPDRDSNFSDFSADPGTSLPLSSTFDMNRGTNMPILEEDYLDEPQGLNPP

>contig18652 Frame-1F

MDWICNSLDMYRNELHAVAFPIFVHCFLELVAKGFVEPGRLFFHRYASDHTRLHLEELRT

LSLVFRTQQLHDNEYVREVLHSKFNVELSLLSFELLNTFLSQARLFLLLSIVNARVNLVV

TSNQPGLQVSELQGTDRVWNNLELRTNPASGFKTSDDLAL

>contig19325 Frame-2F

MVQAVANNQFTLSGCVVALDRFATWVHDLPLAANKSKSFGIDLLSLFESNRCVTGSDVFP

VIQDLLPNSIVDAVKTLISKACLHVPMKYADGCNFTRPVSLVDWNYNAPPVKQAKNHQGS

KDKDTSAINKFQPVSTDATLNASVAIKTFAWHALVSPTITFVLSVALLLSTGNH

>contig19488 Frame-0F

MTKDTWCYLLKSSVRYRVTFRATCYVSKVSSWLIVMTSDGIKLVLLQGTITMHAAFECQR

SRVAKALQNMLYWTWLLAVTVSGLAIVHAMFLLAHDVVMIRKTYQTRLSIDRMGSKTTKS

KVLDNTGTSITLRLDAMELAAFTPNPRVEMRAVSQLVEQRSKDGSTSACSKNGIRQEHQD

GIGTKKPLLRDVKAHVPPMETSSHVVATKLTGLNDSKHSVSSYNESLIQTIVESSLERVD

SQEPRNSSSKTRTRLESFTTGLNSSRSNRVLWNTTDQTTSLPQVSCQTKGFMRKRGRTRE

DKKVVPSKPLNQAEEAFEAFKSVSTRWRSEDWQRNLSNASCGGSDWSEWLSFHNPNTVVT

DIEVTRETKDCSFACRDNATKAYGAKSQLPIDPFAASAPVATSTTSSTMDRKAPPGFTAA

DAQPLETRAAFEHFRHNSGFTTASPLASTSRSFGNYSVFTSSLPLSGPALPSTRDENMTL

GNVGRIGSGRSKVFRGLGSPTMK

>contig19884 Frame-0F

MTDRRLSFIVPSDATALPPVEVLIFGQSNDLESLTPVKRDSHFRGQKQNFFFKRVLHLVL

YSGFVDIRAYKEVLRKVSLMWEKVVIMAYAWTITDYAKTDNLYTTDKLYRLHPRGHYLAE

GAYKEVY

>contig20299 Frame-2R

MARGPKDILAQPLVSFELQAPAHITSIVCVPVGEGIENCFAVLDQSNRVYILSLMSLNLI

WETECDNFVSRSFFDVSYGGELVLRMHWAR

>contig20383 Frame-2F|Blast-coatomer subunit zeta-1, putative [Phytophthora infestans T30-4](gb|EEY57872.1|) 1e-75

MVKVASPSVKAIFILDSDGNRVCAKYYDKSYPTQKEQLALEKKIYAKTKSFTSRQEADIV

LIEKIVSVHRCGSDTIMHVIGSASENELILLSVLGSAFDTVGNLLKGRMDRHVMLDNIEL

VLLTFDEVVDGGIILEVDTPSIANRVLMRGIDNEVPMAELTIS

>contig21072 Frame-0F

MSADLFADWKKEEETIGEPRGHGGGGVYDSPYGAAADTHGGDRSSNDDFDFETVGDEAKA

KHKEEEKPMFELREHGLKVSRRKGFTLCCMGVGNGIFAMGSQEGMLLRCTTEATDSSGTI

EEIMIEPRVAMSNVFIDPTGAHVLVSMENGSNFYLPTSSTRPKKIIKAQAMQFTSVAWDR

QSGSPEASEAILIGTDSGAVYEAEFDGGKEKSFTKVYQISNQGPIAGIGFEHWTLPSGDL

RYYVMLTTSASGKRPTRMFQFIGGGPGGLKTMFKEYTSPEKLRFQELPGDIPLAELWFFS

KQERERAKGFGILTGEGVYHGDFVFGLSSTMENVTSSTGLLMYPGKPEKATSSKKAWTPP

ISMAVTPYHVVLLYPRQVQVVSKLSSVVVMEEAFDSRVGTVRRIAVDETFHTVWIYSDRR

ILEVVVTEEDRNVWKLLLSKAVMGNGDDRDFEQALGVCRNGWERQRVLTAQADKLFEKGA

YDRAAVLYAKTTRSFEEVALKFLEKETRDSLLLFLLQKLKSLGLDEKTQKTVLCSWIVEL

FLDKFNVLKGSAQDVDAHANLLFEFKQFLQDQKSHLDPATTFNLISSHGRPDELVFYATL

IEDYEKVITYHVDRGEYGAAIELLRSVETSKVEELWYKYSPELIIHKPKEVYEAWLEAAS

LNPTRLIPSIVRHVHQKSSTGGDQTANSSKTRSVLDMAIRFLKFAIKQGNRDPTIHNYLL

FLLAKHPDERLLISFLRKTHNGKHLFDIAFALRLCTQNEKNRACIYIYSAMGLFQDAVEK

ALQVDVKIAKEMASMPEDDETRKKLWTLIAKHTIDAGGEIKDAMNILKESDLLKIEDILP

FFPDFVLINEFKKEICESLEIYNDRIEQLKEEMQDYTQSAELIRTDMQKLRKRCAVVSGN

QRCELTGQNILGKEFYVFPCSHAFHAGALRQEMQKHLNSFQRQTVKQLIQKLTELSTEMP

TRTNFFHRPLSTFPFLNLSSSEKEVMTPGIDGASVAATAKAKNAAKEQSIAQEREMVQQK

LDEIIASECIFCGEVMIKSIHSPFITPEDEANEGSEWTI

>contig21274 Frame-0F

MLRAFGSKMAWLRQIAKLDNRRKQTQRTRIAYEQVGQEFATFMKKTKLINRDEDDLDECR

ERYFTLKAKVKEHGLPFQPTAFSCKIYINDGIGSVEEVIQSVADTIT

>contig21560 Frame-0R

MQDPVHWKMSELACAVKYRLLAADFSSGYKDGLVAHIGVSCEYVAPIVDRAFALHPMYRI

KTEDGDEVPDL

>contig21678 Frame-2F

MVSCLLVICLMERTTYSLIMEAKKVASAKVQIC

>contig21906 Frame-0F

MTCVPGSVITTNHSPASNLNHQPDSRKALRYMDVYRKGLTGKAAEYAVRKYK

>contig22411 Frame-1R|Blast-DNA mismatch repair protein mutS, putative [Phytophthora infestans T30-4](gb|EEY62876.1|) 1e-123

MLTPTENNYLAALYYSPSHWGLAWADVSTGEFISTTSTRDKLASALLRCRPKEILLPNDF

NPLNHDHASSCIPKDAIEFVQTILPSTCVRTYRHESCFTNLPPSCPQTPVFRTLQASEQA

AAIAILDYVSFTNRSTSVLIRYPLHLESSDHMLLDASAWKSLELVKHANGSKTATLLHTI

DATVTPGGARLLATHLASPILNLKLLTQRLDAVSYLYTQETLLVQIRKELLQICDMERTL

QRLRRHVGTPKDLKTIATTITHATWLRDLVYTHERLRSSRIPTFPVKEPHNCRIYSIRVA

TILWHKTPFVQSLPIPCLRSMLRFTTSTLVYRQKQDLSNPDIRHYWTSGKHLSTPITHVL

PSVPSRQNTRNCITRHDYACGITPIKAFSSNFLMQNMFKCLHHHVV

>contig22842 Frame-0F

MSDERNDSATEPLLFGQSNLFKALHGRGAATPLEVVENHVTSCPVHAKQLGCTPLIFKNV

SENESLVASKSPGRNRNPSQDVALCDAYATRLSIVPSKGSIRGSVFNLAGATLGAGALSL

PYAVAVSGLGFAVAQLVLAAVLTIYTIRLLIRAEQITKLKCYEDLAMFCFGRKMTIFVEV

NILIFCFGIAVAYLVTLGDLITPLVKLCFGVQSIFAHRWVLMTIVSGTIMLPLSLLKDIS

SLQFSSIVGVLSIVFLVVAVAIRSLMYTSANGIPVDISWTINLSRGPNFMLSVPIVMFAF

TCQVNVFSIYTELQRPCIRRMNKVVDRATLISFLIYLCIGGVAYLAFGPQLVDPKYKGNI

LLSFPPNDTLIAISRAAITLTVAVAFPLNIFPCRFTIDMMFFANSEVSRLRHIAVTSGLV

LLALLLAILCPSINIVFGIIGGTCSTVVCFCFPAAFIMHLEDGPLLGPNKIGPLLLFIGA

>contig23113 Frame-0F

MKCALLSSLAAAGAVCIAVTATECELNSIENTLRSNSTIGASMGPAQMKCKEDTGVDIFA

ISDFPTKATALKIQKSDKGCNVVINLVNVYANTDAQCTIEINGINVTYGRLISDFLDGKI

GNETDTSSDSSNEIATISSESESGSTSSSSSDQIITSGASTKVLSLTTCGAITAIAFALR

>contig23948 Frame-1R|Blast-DNA replication complex GINS protein PSF1 [Phytophthora infestans T30-4](gb|EEY57519.1|) 3e-36

MANFELDLSSDLKPPKELYIEVRVLRDCGELMTESGLVNLEVHSQHFLRRVDVEQLIRQG

LLEQIKR

>contig25326 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55513.1|) 2e-22

MAEELKIATLPDTDNTSLKCAARILAHECADVNIAFMRCKQRDENPRSCLVQGEKVTAAV

LKT

>contig26868 Frame-2F

MCNKWLYFPLWLSIVLVNKRYIVLGRLTDHITFTPDLNPVFKGQCYTDEAGLTSFRGYQH

LKHYLAELSEVSNE

>contig26932 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY70511.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55065.1|) 7e-74

MLLLWLCMLAIPTTLAQGDFASLDPEAALIAEDPHFTPYHDKPRKVDADAHYAPRERTVE

KFDFDPSEGLTFFVASKSSECFFQDIKLNNDDLSGAYVVSSADSHIDLEVKNPEGVTIFH

RLDDAEGEYRIEPKQVGVYQLCFQNSDSDGKLVTHVIHTLKSQHPVEKEHVSLLAKYASH

VDVRLGELESELRLQLIRTNRHIKMEKNMNKRVTFYGTLECAVYLIVCFFQVYYIKRLL

>contig27333 Frame-1F

MNQFKFNYYEIIYNYAPQDFSAQTPPVNEPM

>contig27449 Frame-2F|Blast-unnamed protein product [Vitis vinifera](emb|CBI21868.1|) 5e-14 NOT\_ORF

MAGHIGCRRMIKEKKGRALELISAGVSCTSGMNTFYCYKIANCGKILVAIDERKQFFMRK

VVKLRK

>contig27584 Frame-1F

MSLKVEFDHQSKRVSVTPDKTMFQVLAEAQDHFSLSDSRQYQLLHRSKRIDLSIPFRLTG

ISNNACLEIKELEGVDVLQQVRVCVQLRDGKRVQASFENDATLEHILTYFKLLPAYQQFC

LGFLRREIELHAFATTTLRELGISSGSAMFRVQAIDGLAISRPPINNKLSKLSGQLSIAP

IHDHVTVANSVASSALAPEALCQTLTPESASEIQVNETAPAISSYHALQLLRDRNFDAVS

RNTVTTLMKIVTNILSELEDEKVRSIKLSNTAFNRLVGQVEGGLEFLKSIGFMVNEQAQM

LVLTSKPSDKKVLEEGFRLLNIEADDLNISLNKRPAIRQSETNIEFDVYKTRITRVQMQP

RGPSPTEALVGALRSNHDQLVGHDPPPRSTVITLRGRPTSDMLESLTEGKISEGNDVLLQ

VQSLKAWRNEMEKKKNFRTQAMRELDKLKRKKVFRTALIRVQFPDQAVLQATFHANETIQ

DVMDHVTDCMSNQFKTSKFYLYLSPPAQKLNATKTLTELNMVPAALTYLSWTKMPHAEMA

NVGFYFRDDL

>contig27988 Frame-2R

MVQHSFMDQFSVSLPNLVDPANDRGKNRSRSRSYGAMAASVGLSHKQMIEIGELFGFHRE

DDLQNNLNAPIDPRDMPRVAEVYLPLNELSDDEGIGSYDEISPDAAILEKKLISPIFSPI

TTSSRSLVGDTGTLADSSCNPIKPTSWSATCSGSDEIKDNARASLIREFNMLNDWKPTQS

VMTARSRFSSDGEFLAIAKLGNNQIDIWCANPAAFSRVSTIQLPARLISLNWLGPGPKKQ

LLACTIEHGETMLWDSDGQEVISCPPNEDNLQIQQLMCARGAPIAACLFTSRDEEDNALQ

QILVLHGGMEEPMQDYMPMEDKQLTCIAWNNEGNVLITGSRTGEIEFIDVIRPERIHRCS

LISCKDGTHIDGGNLAAICLSPDGESMLSVHERCNLVREWSVASILAAVASPVDAANDSR

GSIVNVTPSLTRTYEMDKPLSSISAEVDSTIRFCDVANYFIVADSSSLHVFKRGEKHAIS

SLLPNQAAIADLDWHPTLHLCCSANQDGAISLWNFKAADN

>contig28923 Frame-0F

MDALQVSPISQQNANQRSGRAGRTGPGVAYRLYTQRQFVNELLEAQIPEIQRTNLGYVVL

LLKSLGVSNLLEFDFMDPPPQDNIINSMYQLWVLGALDNTGELTQIGKKMVVFPLDPPLA

KMLLFSEQLGCSMEVLTVVSMLSVPSVFFRPKDREEESDTAREKFFVPESDHLTLLNVYQ

QWESNRYSAQWCSDHFIHAKGLRKAREVREQLIDIMKQQRVRLLSCEGRWDVIRKAICSA

YFYNSAQIKGIGEYVNMLTGMPCNLHPSAALFGLGYTPDFVVYHELIYTSKEYMQCATAV

EGEWLAELGPMFFSVKESFQSRILKRMKEKKEAAEMENEMEASLHAKEEAKADSKINSLA

NLQHKKQRMTVAGPGCPEPPAIIPTGAARRLPRPRRFGF

>contig28956 Frame-2F

MLNRRIPCSWCEVKYCSRCCEDKFVPGFGSWRVCSLCQSLPCLIDPRRKDRSATNHTSPT

AAAHERCSVFIRPTADDDDPVCLGDFEIVKLVGRGACGRVKLVRKKHGYDEGVFYAMKAI

RKKLVIQRGLVEATNAERRILDRIKHPYVATLCYAFQTEAKLYLLSKYYAGGNLLDQMRL

ARRFSEDRTRLYTAEVALALRHLHENDIIYRDLKLENVLVDSDGHVALTDFGMSKENMPD

KGRTTTFVGTYQMMAPEVFSGKSYSRAVDWWALGVMVYEMIDGRTPFNAKTNRLIKERIV

NVDLKFSPRFTEDAKDFVSRLLTKNEAKRLGSGAHGFQQIKRHPWFKGLDWDSVEQKEAL

FEGQYALMEQHAKEYRTDDIFETYMNTSEVPIDTPESAKSSNDELFNDFAFNYMDGPEQE

QRDVPEPDEEGDEEQPLSPLSPKDSIGLGTPTSLPRSHNEGKISTFLSTTASEFDLSLLR

PDQATDFGLSACSSMSYDGTEDEAAELVVRLDDLLETSSDEEDAETDDKNLSSPTTQPVS

PSSNEDTDLELVTSNGKIVNNVAAKNITA

>contig29447 Frame-2F

MLFENKVGLSTDEVIKKLKGDKAQLDIDDFGILYQYIKVAKPEEMKKFAKLVLNEFKGKD

AEANAFRFLFNIPVTSELTLAMQKQYIKLQFIEANSVVRLLAKSRDKMLEKDNLGSLVGF

IKVYNTMTKRGSDFETNKVNAAKLLEDNF

>contig30416 Frame-2R|Blast-tRNA pseudouridine synthase B, putative [Phytophthora infestans T30-4](gb|EEY68894.1|) 3e-26

MIKSGFLNVHKPAGLTSHQCVAAMRKVFDTRHVGHGGTLDPMATGVLTVAVGRATRFLQY

LTTDKEYRGIIR

>contig30845 Frame-0F

MLIKRIITYLQNPFASRSEGFLYAGIVFITGVAQSFLLRNYFFHCFEAGMRVRSAICSAV

YNKSLVLSAAARQKKTTGEITNLMSIDAQRLQDLSLYLNSVWFSIFQIVVACYLLWQQIG

LATIAGVAVILLVLPIAAGLSKLMRRLQLNLMAVKDERIKICNEVLAGIKVVKMQAWEHS

FTKRVLEYRSEELKKLRSYIYARSGSKTLFLAIPSFVTVASFYAYVLLGHTLDVGTALTS

LALFNILRFPLFLLPQVINAVVEASVSIDRLSSYFQETEREKVGHGDLDSVGICVEAADF

MWDTAPSNLLSSDALKSVEQDNLLKKESILGTDAKMKDGGRPVLRQITINAQPGDLIAVV

GHVGAGKSTLLSGILGDARCGRGKVSLFGSVAYVSQQPFIQNATLRENICFGLPFNETKY

AEALRVSSLVKDLSALPGGDRTEIGEKGINLSGGQRTRVALARAVYQDADIYLLDDILSA

VDSHVGHDIFVDCIKTCLKDKLVILITHNLSFLSECDKIVMLENGVIREVGPYQDLMEKA

GGFLLNFVGKHEVQEPQSIETDDEVPDIELEQSDDTDPAHHSLDRRLSRLSVHSNRSSSE

VDVDVQLITDEDRSVGDVSWHIYKTWIVAFGGMCAGLVVISMFIAAQSLDLMSTCWLSYW

SEQSRINGYDNEASAKKSQMFYVYIYMALNLVFVVALYIRAIILYKGGLRASKSLFQDLF

ARILRAPISFFDTTPTGRIVNRLSKDVYVVDENIPATWSMLLNISFSLLMTLVTISYATP

PFMIILFPVLVGYYSSQRYFIKSSRELQRLDSISRSPVFALLSETLDGIPTIRAYRAETR

FSTKNEEMIDRNQRAYFLNFAVNCWLALRLEFAGTLIATFAAIFAVLAHSSDPERGAASA

GLAGVALTYAFSVTQPLNWSVRMLSQLQTQMVSVERIKSYTNMDTEAELSSVGKLPPAQE

WPLAGTIEFRNVNLRYRPGLPRVLRNLSLSIRSQEKIGIVGRTGAGKSSLVVALMRLVEL

DSGSIVIDGLDIGTIGLHELRNKISIIPQDPVLFSGTVRSNVDPFDQFTDEQIWTSLRRG

HLAHIVSALDSPVDEKGSNFSVGERQLLCIARALLKRSRIILMDEATASIDVETDRKIQH

SIREEFRDCTCLTIAHRINTILDADRILVMDHGAVGEFDTPKALQLKEDGLFKELVEHWK

NEGK

>contig31280 Frame-1F|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ32573.1|) 2e-13

MKNPWLQEMTASEPLTFEEEVAMQSSWRADAK

>contig31705 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68286.1|) 9e-15

MWSNCKLFNDDGSGITRAADILSAGFERLFRESIQPH

>contig32047 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68748.1|) 1e-32

MLQSLVALCVARLAMGATQHSLLSILRRLPEELALTLLANMIASKTLTDDRLATFFMISR

RVLNLSGCCSIRNSILRQIPFRCPAL

>contig32292 Frame-2F

MYYMHPITAPSTATLVKSIAPELLLGANEIVSDGPSSGSKGPVIESASLASEITFAFVDT

FGDKLSPPASAIDENS

>contig32933 Frame-1F|Blast-syntaxin 6 [Phytophthora infestans](gb|AAM12665.1|AF404749\_1) 4e-33

MHAKLRAYLEAQGSPAADDLPSLTHQMEGAIATAEKSVKFLEDTIVMVEANRSKFEHIDA

AEISCRKEFVATIRKDLQTLLNEISSDTIQSQIRKLEH

>contig33039 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69362.1|) 1e-53

MAGFSVVWNVVLSPYLLHEKVSSHDLKGSTIILFGCALVGVSGSHNTPTHHSAELFALFK

SRIFIEYAFFVVCGAIVLTWMLSSYEKKSGWRRFAFGALSGLIGGNLFFLK

>contig34052 Frame-1R

MQRLAFAAQSKGAFGVREYLQDNRQVAPDILHELSIFVEVEDGEITDDDREYSKLGICLE

QHSLRVQRDIWSALASGASPSTEAAMSLAKAFLQVTAMPRRYETDAVCLTLAEMVLGVEE

SRKKKKNLPKNSAFRRRMRRLTLNQVDFSLHEFEAENMPKALSSEICSMTPITAYFRVKK

RFKAETLDTSATLKPMQQNSRDKLPISTQTG

>contig34243 Frame-2F

MFARAASELQMLQDFHEFIRQMRNYYEQPPCVTFEGLANAVAEILKEFVYKIQLVEQQIY

ATTAKDSRPWSGMTMRQPTLLGIYGGLREVFNMISWLKGILMECFQGLSNRHWHEVKRAA

RAKCVLDALYDMMIVEYVESTAAISSTKNDGSRFDLLLHLFIGTLNPLLDLLNRTVFERG

HLKTIQWEDELFFVESNSASTYTSSIGTQNQTFQEGLKSLAPYEIDRSLVPKFILSVIPL

LNEAVASRQLKNRLMQHKQYSPIDFLSNSKQPKLCWSKLLTDELEMKMGRRKHRNFSRSG

VSMRNTEVDSSSSQATMFKCVPFNKTMEQCLNLHLENKCRELNGEITDTFRRTMD

>contig35341 Frame-1F

MESKREDDEEEVKESAQEADATDSSRIRPSLTAMLKTKYVDELAKMDQRSGRWQHMEEGE

LYSQKELLREFVRGLEIAQAEQETRMNKIRALEVENHRLRQVVKTTGDDVKEATDVGDVD

DVVARGLFTS

>contig35688 Frame-0R

MQRQRPTLHRLVDAELEMYPSTHRFEQEPLRIHNDIECKAHCKRKWFDSSKIQRSWWWHI

QRRPEQNCWMSRRDRIFKRSKNWIVYALAIWIAVATKPLLGIAALTQQTQVIARCLSWAN

NTCVFLPMKPVQFGGLYLARQTVCKADLSVAVLQIDWESPDGGRGSVNSLLVNGVELLQA

PVYPSQAYIMANYPYCNDMFNIFPPLKNGMIGPDGRKSIISEITSRDLPISIHFNWKGPH

EIQPVCSITGVSIAGYAEININLEAQDDSDCPGWDSASLTPCFSNGKCGCAANDFSQRTC

SCVVGYAEPDCRDCASGFFGDQCKQTCEPCLNDGHCDSGLMGTGTCTCLQGFNPETRCAT

CLPGYFGDKCTRCPDCNFPHGNCDDGLMGSGRCSCAVGFDAEKNCMECMNSFFGASCEPC

KPCDGGKCNYGLLGDGKCVCSEGFSSDSRCLECDFGFYGPSCTPCRTCNNHGRCNDTYTG

DGMCICDEGYTSASRCS

>contig35895 Frame-0R

MAIGASHERTDHFSQAIPFYQEALENIALEKRFIHREDLRIVMLDRLGQCYKKV

>contig36612 Frame-0R

MCTWQKEKYNSEIVEYYLIRDAWDKFQEIWREIMYVRSSMDRQDTAFWKCNSSTC

>contig37358 Frame-0R

MVSPGRVAVSPNSSFVLVDVDNTFSPNETTLLRNRTNPSHVSPGPRRPYPPTPTVRSHDD

TTMRNEHERHATNRLDSVSNLFPMPGNNNVFTTSANILPTREASILIDTDVQQAAAAQDA

SHRLPTQQPTTSSILLPITTESKGEVYLHNRNTHSTNPSNRQDMLENDLRGFLCTPRDYV

RSHQSILAGLPPLRPVERSARCAQRIRKSASWLWRQLHRWQFRQNIASIWKRMMPNWDSY

VLIVVFIMALVSIPLAVFVAKIVSDATPHRVHLVVQCALPGRTEYYTASTLYLAGVLVPA

MNNLVILIVSLWIGFLCSRSRARMLRSNPC

>contig37440 Frame-0R

MDQLIPVINKLQDVFSAIGQSPINLPQIVVIGSQSSGKSSVLENIVGKDFLPRGSGIVTR

RPLILQLYNRSSISVEMENDTAEEWGEFLHLPGQKFVDFNEIRREIEKETDRITGKNKGI

SNETINLKIYSHHVLNLTLVDLPGITKVPVGDQPINIEEQIRDMCSEFITNPNSLILAVT

SANTDLANSDALKMAREIDPEGKRTIGVLTKLDLMDDGTDAMDMLQGRVIPLKKGYVGVI

NRSQADINSQLSIRDSLVKEQNFFKTHPAYRPVASKMGTQYLSKTLNTILMHHIRDCLPD

IKSKISSMISDLDKDLEEMGSPTEAMTPTEMGGCLLNLLSHFSSNFMNSLDGRNHQLVDM

DELYGGARINYIFNEIFSKSLREVNPFDGLSDEDIRTTIRNANGPRQSLFVPEVSFELLA

KRQIGRLEQPGLQCVDLVFDELQRVTSQCETIELTRFPELRNRVMEVVNGLLRASLIPTQ

AMIQNLIRIELAYVNTNHPDFIGGSRAVAQLMEKMQRETMVSAGAPSNIHDSRHVGQVPK

QSAVSTIHSGTAEDKHEGNALMSFFGGSRKKSGLDVPASSKVAVVKLPQVPVRMRQGDDP

TDRERIETEIIKSLLASYFDIVRKNFLDLVPKAIMCFMVGNSKECIQNELVSSLYREDKL

TELLAETGDIAARRSNCDEMRTLLHRALEIVNEVRDFNTFK

>contig37901 Frame-0F

MTTQWIQDACYSTYQPVTTSPDKTTHACRFIHNQCNKELFTTEYLRSNKASGHKNLRCFP

HCCGGHNPKSFCGSGLVVECFLAKYQLVLGRFEEVAKQQSTKSKILPTVDTSLGRCSLVI

NREYARQELFDDVKMPDQPFGRWFRGAVVPNTSGLGTCFLLNGNRQSWHYGWQSSRLNCK

NLHVFKVYVFDASANGNVNTLTCVASIASPAFRISSSRKARKTFRSPVSQSLVLQAPSTA

MAEAMTSPQNVHRIDELLENGNETATTHEAALYATAQPQRPLCGFLPGQQDPARRERKRL

TRSASLKTDYFSTISFPTLPQQQTMHHSLYFKQPQRLSLSATHPPPHIETLHESRASMPS

LPGVDSFLTGSGSMDGNRSFHSRRSSLAALPVPLSASRTLSRHHQSPGPLLTPITGMMQL

RLESQSPFASCVAH

>contig38034 Frame-0R

MTIIKDTLDLKSSDDKMVRRDHSGTFSVKHGLPRIVLTKENLSLGSSGSNDASDIKTSAA

KVVTPTEKRAPKLLCSTKEEKLGCENFNLVTSEGQLEARRRKRKRNNSSASGDISQASAK

MLFECSCQLLKTQSLEYDVRARELANRCTMQAKKIKDWETRVHNLKRELKEYADEWTPTK

SASGATIEENAATLEASTEQVAAAASIGGINSSLSPAVSVAEAKLRKELHKRTQK

>contig38764 Frame-2F

MDGQELLTIPSAWPQKCQLRSLLECLQPLSNRLLWSRMDSMTNGRLSSSQAPKPS

>contig39121 Frame-1F

MRFLLSTFRPSKVVLLLDFYHRAT

>contig39279 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56246.1|) 5e-67

MKLNGDVSTSMMYGSALHAAVAAFATYLAQAQRHGKITEEIKTLAAAKATKAFEQSWSQD

GYGLFASEEQAFVVYERGLNALNEFMGMHFWDTQLKEIVCVEQAFSFHVSEANVELRGVW

DRVDLVLNPIGDGTSSFVVKEFKSNMGGTQRNMQKLAIDSLQLKLYMYALRQVYGETPNG

ATLQQIGGYQSDRIKTESSPKVAIEKGFVPFSDKVEQEA

>contig40341 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69120.1|) 1e-06

MASISSPMLVTHGLVRWSPSSHCIAAANGNSLIIRDARSLQIVQRYFA

>contig40547 Frame-1F|Blast-metalloprotease family M67A, putative [Phytophthora infestans T30-4](gb|EEY66643.1|) 6e-96

MDPGSEIELRTIIENAHLEVVGWYHSHPAFAPDPSIRDIENQTSYQQLFQRPYASKDEDS

ASKPLEPFIGLIVGTYDTRRSSPVSLFRYFHTRGEKVSGGARREIYMPYEFIPARRHFRT

VLKDEQRERRQLYPMYCSVLKHFQLELSATKLQPPTDIKALPEQIKTVGSSLFLVNAHRP

VRKRKQSSDTAGGHFVKKAKGRRPTLSSSAVKSRTFLTSRDLNQHHPAADEGIITAESEA

KIVNKSTNLSIEEIHCDVSCPGTDKIKVEIVSSDCAQDISIHTETARIDPNQADLQESKK

FADNLTFQAGTALKNVCNKRIQILKESSNGSGGNEYCQKNANLAQCKTLSQSITSRAGSD

VKHAAIKPNAMAGLTPIYRSVLQHLPA

>contig40688-0 Frame-1F0

MNWILFVASNPFPCMADLVEADAVGSFDLNATGKAEQLRQDGNEAFRRREFLKAKDLYTE

AILLQSGHSVLYGNRSAANH

>contig40688-1 Frame-1R1

MASVYRSLALRNSRRLNASFPSWRNCSAFPVAFRSKEPTASASTRSAIHGKGLDATNNIQ

FMSLNLFNS

>contig41236 Frame-2R

MVYRFDDCDSRICKYSVYILVEHFSAPHIMIEDTRTAFRIIRHLSNLAQNFIHVVNSHAR

ELIATICHQKRDTHPRMWL

>contig41243 Frame-2R|Blast-pyruvate dehydrogenase E1 component subunit beta [Phytophthora infestans T30-4](gb|EEY68780.1|) 0.0

MALRRVLTTSNVYRTAFSSLRRNMATVADEMTVRDALNTAMDEELARDDEVFLMGEEVAE

YNGAYKVSKGLWEKYGDKRIIDTPITEQGFTGLAIGAAYHNTKPIVEFMTFNFAMQAIDQ

IINSAAKQFYMSNGNIHVPIVFRGSNGPAAGVAAQHSQCYAAWYGSVPGLKVVAPYDSED

ARGLLKAAIRDPNPVVVLENELLYGVSYPVSKEAQDKDFLIEIGKAKIMKQGKDVTIVAF

SRMVGEALQAAAILGKEGIDAEVINLRSIRPFDRQAIVNSVKKTNRIVSIEEGWGQHGIG

AEIAGILMETEAFDYLDAPLERVTGTDVPMPYADNLEKLCLPQIEDILAAAKRTLARKL

>contig42901 Frame-2R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY61071.1|) 7e-42

MTQMLLQRVPPVLIIRLQRFRQLSWGGCTEKVDTPVTFPCGNDELLDISMNTFCQEDTKR

VNYELVAVCAHLGHSIDSGHYIAYVRHRGPWRDAASSEQWLRIDDENVRVIETTKLRNET

LTAAYLLFYSQVPLK

>contig43142 Frame-0R

MKRVTVPTPVGGGEMHVQLSPEAWVPQRRLWRITVDSKEFRKNEGLQSLRSFVKAQGNLG

TLLRQDPAATVLPAFLDIHPGQRVLDLCGGGDHRAPIVEEYLCLVSTGLETALKTNLLVI

NERDATAAASAVRNLTRTLPLARDLIVTVHKPEEFPVPEIPEALFDRIICCAPCSGDGLI

RKLPEKWRTWSPEQGLAFHPSQLGLTDHAMTLLRIGGTLLYSTRSLNPIENEAVVAEIIR

RSKGALELVDTNTILEGLKRSHGRTKWTVLDLASWSEAPEDERHRLRPSMWPPSSEECNE

MHLNRCVRLLPHQNDTHGLFLAVIRKVRATQKAALTIGPALPPKSKPMLRNYAMKKIQAK

AEKAFSSFTSIDQESLASIQSFFALCSKPTFLIRAGMARLKRAVHVVTPALADLVTRELR

GRL

>contig43403 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54302.1|) 9e-10

MSGRPYARNPHATACSGPRDLEAILPHSFRIEAPMHRRDAKSKAIR

>contig43519 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68376.1|) 1e-176

MSEESASLQKIIVCGGKGVGKSTFCRYLVNRLLSEFKIVAFLDTDLGQSELNPSGLVALH

TLTTPLLGPGFSHMKNPIRSFYCGNTNPGNDPLYYLKAVKSLLRLCDLKWANKWSGTSDN

GSSGGRQCVPLVINTDGWIKSMGHDLLCNIIQESNPDHVVQLVAATKNKQFEIPTEGTWQ

IHAVPPWDPIGLTQSPRSSKELRKYRLHSYFLSRIRCDLPRTLLQNLHVLSEKNRIDSSI

YCAYAQLPPFVVSFDRVDVAFAGSSVAPSQLLFSLNACVVGLCVNPNYKPIKDDKTKPRM

GPPRIVLQPAHAPCLGIGIIRAVDATKRQLFLLSPLPLSIVKNVNLLIRSSIPLDDIILS

AREAAQTPYVVTDV

>contig44367 Frame-2F

MDASPPTELQLGAAYGRYLHWRSPSSPPAESAAGDANIKPFLASLCALVVQFEATAREDL

RVGFAPAIDDMNDAAGTGRPKKPNFEWKYEVAVGMSGNTELVWRKSASGRHKEVDLARVF

TGRACSVQEFVPYWAVVNLKSGSMSFGIGKQVGQDVLSTIQDSDFVRVTYIAFTTWDSPV

SIRSIQVDGVYDGQTEALEATDVAAYPLPRPIIRADPLGEQDLLSPEQRQQYEAECEVSK

RRAERFKAPFAPPDIKNYLDSRDVRKLQRTGAIVARFRTGIDITSQEEQMKRQERMKRFD

TPQFASNYTSETVKALEEGMTQDEWVEQQHDQHKLRARAQKFGLSAEEDRTQIVIASLKP

ASEKVRRERCDVKTMASGGTVLIRDDALHMYSLDDDFQQVRTTDVKRYFTGFAPAYIEWF

NDSSCTIVFNDTFTAERALVALAQEITPQKRKDAKTEALNAVGEDVDMVDVEEPAHDPVI

AMKDREETIDVLDVEFNRSHWFLGTPISSSQLQTRSKKWRVLLRRATDDDFPPEKIPKKG

MYHARSSQIQDSRNSRRRADPEHKSSSRRRGANSRAHPYGDFREDRRGEEPSGSRLRRDE

KKTDRNTGKASNRIHVNADGSINIVRNSQAASTGFAKEILVNKKSEPHLAGA

>contig44389 Frame-1F

MSTFAAISKQDFMLSGVSSRPAQERKVLPPLDRPPSHRYASKRCEPASYASETSKKKLVP

VASIVTSFVKLDTQRQTFEKSHTAAATRVDICATFMQKICRKNSTPRWPHRLFCGSWKRC

SSIQKFTQRSDSELQRHSYNHHLQKQKAKVETIPRSL

>contig44705 Frame-2R

MGPFAETPKGCGACGCCGGAGGSFCSIVALTKGASNRVVGSLRWTNERLVTSGGLPTSRG

SFFMAYKNEGPN

>contig44802 Frame-0R

MTAGDIEADNKSSHSTGTDAQVNVKADDECKDSAGAEVSVNANAADVVTSLMKNKPIIAK

EALKFENGKEAQESVIDVCVRTDDVPCKIEINQGSSEFSLKVKSLQQEVSGKFRREQELR

EAIEFCLAQWQRIEWPAELNSMFFKPTITTMLGASSVIKSELMKSNFDHDEKKSNIVSSL

SVMDELKRIMIDLTQDQVAPVPPPVEPTTLVLYHPVFINHQTPKNHPECPERIDRVVNIL

NSLIKRHRETLKLDRLSMSPDELCPPETTLLMVHSPTYFRQLKERSIEAGLQPASSPSAS

ASSPSSRALVFESDSGISDEPSSCGDRRKKGRTLLAGAFGAASLEQNGIELDTFVSSKSW

DVARAAAGTVCHAVDQVVRKEYHNAVCLVRPPGHHVGRHGRPQNAPSSGFCLLNNVVIGA

THARLYPWIRKIAVLDWDIHHGNGTEELLQDDPDAFFASIHLYSSGKYFPGTGKSCETGN

RVNVALENTGAGSGSMAFRAALELKVLPAMRAFHPDIIFISAGFDGHRDDIIGGVAAVNN

PNVPAGYVEEDYAWATLEVLKLAADVCDGRIVSVLEGGYDVRCETNSLAKSVAAHVAAIA

AYEAARRMSGASVSINVEMKDEEPSAFSGLNTSPLGDIGIKSEHETETKPVSLLEKLLST

DLDNANVIDDEDHDDEISQGSPSGEDENIDMEDENTGEEEDDTNATMADAAKLSDHENGA

MDVDDC

>contig45416 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54349.1|) 1e-06

MGPSVKKHLQPNYYEVLGVERSASPDKIKAAYRKL

>contig45661-0 Frame-0F0

MLHRTITKQNNCRYKCLLCASESVVEACGI

>contig46039 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY64036.1|) 1e-19

MGAPRSWQYLVDCLRDPPRSDFAFVPHQYILAPLELSQASNHSVDDASTPILSRPEYCQK

KRPRQRNS

>contig46196 Frame-0F

MWEQNRQSLRQDPQPVHSLVIPSSSTHLQL

>contig46264 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69902.1|) 5e-11

MLLTFLEKLPLGQGGKVFVGTSICLAICAYPVIRK

>contig46310 Frame-1F

MVEEKPAARMREMVLDNMIREKRVWVQQAIAMTSTEIQVALKLIQASGRVRIVCDKVTSG

SKRCGARQIWCLQKYYN

>contig46732 Frame-2F|Blast-Phosphatidylinositol-3-phosphate5- kinase (Fab-like; PIPK-A1) [Phytophthora infestans T30-4](gb|EEY53276.1|) 2e-81

MRKEACRYAFDLKTNGTLPSTSLGQSDENRNMLRMLRSSTRNNVDHSFVDENQFQSAVRF

SCKSYYAMQFHALRKLYYGGDRNYVESLCNCQQWNAAGGKSG

>contig47292 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70109.1|) 2e-33

MADYTNIDIFQHLLPVHEAINEKVLL

>contig47641 Frame-1F

MASAVSADGTHSLLKTHSSASISLNGDATKGAGNKVISAVDADPMTLVEVQEAARAQSEW

TKLVAFDEGGKILFSNVKPLDGEIAGFIKLFNKREDAMASGIVLLGEQYDVH

>contig48424 Frame-0R

MFAAHEVNECTFKSLCAKQRLQIVPRFPSGSNDSKYLLDDESRRGLVRLGAVGRRYAVVA

L

>contig48491 Frame-2F

MDNRLDDNQTDMPLPIPFIKIDVECAHNTLQADQGIGCGILTIWRPSEDLLAGELREGAE

YFASSLTISWKIDNGRGQDASLRLSSTKHSKFEKIRDEEILANSEVPSLSKRQQVCVSIQ

RATKDYRANYEEGRNERRPTIDVCVCVVLVAAREIQNIPLSVLAQQTENTLLDPDVRPHE

TRYVEHIFVTDQSCHLMSIRLSSTEVHLPKNSSFVFRRGGKNLWKEGAVLCLRG

>contig48943 Frame-2R

MSIPIALILTNAALAMKVVTLQMLTDPFALEHSTNACVKAAYRYASSMDVADPTGF

>contig49157 Frame-0F|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY61338.1|) 1e-121

MVVKLRPLDVEAEVPTAVYALDLQRVSQLLRIPETELLASFHADPTRSEIQGVIVDAGEN

VPFETVGHDVVYSSDQAPMDAHNNVHAHSHVASLPSKPSGPAALLLTPTSRPSSVRQVLL

TAAVRPSHLNATERPKCLIQLGQQTIISHILTQLYAAGIERVVVSVAVAGGQIMAAVKQT

PFYTKMKIEFLDLGQTNDDGHARSILAARSFFPGPEPFLIHTADHIFDKSVISKLSAYPL

DKAAACVLVETDIAELSGLPATIVKVKINEAQHNIVHISRDLANYNGIDAGLFLSSVRIF

DALQTLALTPRYFSLAEALNSFTSTASNGSSCLT

>contig49782 Frame-1F

MSMVEHGSTSASDLNGLIARHSSLSQPPAMNSDVGQIRHQFPVERQLVNSSEELEMEDSD

DEEETQIPV

>contig49827 Frame-1F

MEGCFVACLLISIPCMFLYFVLLGFHLWLMVLGYGTYEWMLRRRKDQRVKMKINPTDATS

TQEIESQDCNISVVKVCEMNSEQRERELTVL

>contig50384 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54342.1|) 7e-07

MLQQPDASRPLGSHHVSSLKGVNMLSPVISDGQATRVHAARKSDFLTMSPA

>contig50825 Frame-0R

MQPRPLQEAVLVTIYLEGHDSAVASTKVHRSRYFRRGILIFNHSEFVVLGHLAFLVRRA

>contig51134 Frame-2F|Blast-snRNA-activating protein complex subunit 3, putative [Phytophthora infestans T30-4](gb|EEY54329.1|) 2e-33

MSFEALFPPLLPTDNSTQEDYSSVDISVDEILLPPLEKAVDNGIYRALRRWNEGDLAVTD

KALSYPERIKKYQRVAALALQGDGAFDAEEDAIDNAVIESHEERLGVDRATVVAKQKAAT

AA

>contig51181 Frame-0R

MATTSSSCVIDDCFVVESDEHGYNFDAANRSWSMQVRLGHMQPLVNMQPLVTPNQT

>contig51268 Frame-2R|Blast-rRNA biogenesis protein rrp5 [Phytophthora infestans T30-4](gb|EEY64678.1|) 1e-64

MDIRVETHKQTGKVRALVSIVDVDCIDEKAGHAHPFDKYS

>contig51596 Frame-1R

MGEKVKLGEFSICIWKCVIYLKFVVWSAA

>contig51664 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY60675.1|) 1e-113

MQKYGYAVDWWSLGVFLYEMLTGAHPFFDNNREVMVRKIMTPGSIAAMMPPEMPPEAVSL

ISGLLTFNPSARLGSRGAQELRDHPFFTGISWEGLMRHEVTPPWHPVVQNELDVGNFDAE

FTSEPVVDSVCTHQSMVLNSTFTDFTFNPSISESMGKR

>contig51871 Frame-0R|Blast-transcription initiation factor TFIID subunit 1, putative [Phytophthora infestans T30-4](gb|EEY64028.1|) 1e-39

MTKPRNYRWELEDVSIRKQKVESVEEKVPETLLCPLNKELLDDSWVAAIGWKSTQDMPES

KLVLDDNDASLIYSVSEMEDVRPTLRIPERKLGAA

>contig52085 Frame-0F

MVALPSAYLGDCIQCIGRFGSHAKDVNISLTAVNELWTVADVLGKPMKTNVTTSRHDQWG

V

>contig52306 Frame-2R

MADVYNYLSLSNEMVTVAIMLGMASTAAHCRHKRTHQSTTAKPDTSNEGSPASPLANESD

EIAPLDHFYSVPFELESSDKTPLLETGLELALERSVSKMLCLHVPSLLPSPFGGFSVPAS

TQIAALLGLGILYQGTGFRLMTELLLTEIARSPTSAQFVENLSNAGLSNVSFDQIESYAL

AAGMALGLITLGRGQTTIGDPGLAD

>contig52597 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58430.1|) 3e-10

MRGLRTSLSCHAIRLMTRTCPMGAYNRPVHEEFEFSDE

>contig52874 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66080.1|) 2e-28

MTVSEAPSAELLVEDVRQLWVLACLLAQNKLTMQTAQCLYPLCAVECSTRTPDEQGILLQ

ANVLLAEISIVACSNSKKADDRDLWMRRVTQTEKCIHSAESAIVRGISCSADTELRLIKA

KFLLQQQVKAKRSLKDRRILEILCDGLKCCAIAENAKSQLFADFRSYFSVKLKACLVKMH

ATTFMSKYSKDGSDSCNFANNLRYIRNAL

>contig53583 Frame-0R

MCLYWKKDGEDLVVVGVYVDDLLATGTNAAAVDRLFDSLTSLSIKDLGLVSKILGAKDDA

LLIRRRQSVTFFVGTD

>contig53745 Frame-0F

MDGGNESPPASPPSPLSPARPAPRYLSRDTINSPPSISIPVSAASARDEGRPRSPMSASV

SAISASAVSATDMTGRYGFAEMSASIDATPAPRYLGRYEDAADDAESGHDDVEAELRRMA

QRQLPRGDLGRREWRLDGFQSQQRPERSNMEGAPSSPSSSSMASIRSSRSGIPTPMQTAL

PQPPPSPPNS

>contig54177 Frame-1R|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 2e-08

MVYSHTVFSYATWMTFATTFVYIFCEVYIALLDQLLT

>contig55066 Frame-0F

MQELKTPISSYKSVISPISIPETPLNGHASEKTKVQQLQDRLAAQELLVQEL

>contig55138 Frame-0R

MIRSRISYRVQHTFRDLRDIKSGSATHAVASNNKKWNEMHAIVCQNYSRGELRCSNINHD

GGITPSRIRSHMLA

>contig55387 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54218.1|) 5e-46

MAKSPNCGKRCSLHLEHSNLHKCDVAVHACGAKCSAQNCRGQCVLNIEEPHTAHKCVEIR

CTQQCVMDGCNEICG

>contig55602 Frame-0F

MQSVNARTHSSRSTRDSASNTYAAWNRIFY

>contig55905 Frame-1F|Blast-RecName: Full=Autophagy-related protein 8; AltName: Full=Autophagy-related ubiquitin-like modifier ATG8; Flags: Precursorgb|AAN31480.1| microtubial binding protein [Phytophthora infestans]gb|EEY65864.1| autophagy-related protein, putative [Phytophthora infestans T30-4](sp|Q8H715.1|ATG8\_PHYIN) 3e-60

MSSFKKEHPFEKRQAEAQRIRSKYPDRIPVICEKADRSDIPDIDKKKYLVPADLTVGQFV

YVIRKRIKLSPEKAIFIFINNVLPPTAALMSNIYEEQKDVDGFLYITYSGENTFGQ

>contig56935 Frame-2F|Blast-nucleolar protein, putative [Phytophthora infestans T30-4](gb|EEY63521.1|) 0.0

MAMNTAKPPTSAPSTKKRRVASSPPVPLVVQHDISPNDVQPALEFLSRTDIHSATKARML

FTWLLYPVTPEEFYSKYWEQRPLVIKRNYASYYDGWFSKDEVDRILKTHTLEYGTDLDVT

KYVDGTRHTLNPAGTATAKQVWKHFDEGCSVRLLCPQKFSDNVWKLLTTLEDEWGCMAGA

NSYLTPQGTQGFAPHFDDIEAFLLQTEGSKHWKIYQPSNDSHTLPRYPSGNFTPDELSKP

TLEVDLEEGDLLYFPRGFIHEARAHTEKHSLHLTVSTGQQNSMGNFLEVLLPQALASAIN

TNVELRRSLPRDYLEYMGVMHSDRQGDSDRQAFANKLKNALKMVLGNAMGMLDAASDQMA

KNFLMDRLPPALEDDEENCT

>contig57217 Frame-0R

MVGTRSLRPASCVPSSASRRALDIPPPMLDRSLESFSDDYEAVTSE

>contig57486 Frame-1F

MLSCKTFLEIFAVAVALSTYTDNAARAHAAECEMTYGENTVPVETNPASTTPFVPNIAAD

TASSTVASVEGTVAE

>contig57518 Frame-2F|Blast-hypothetical protein PITG\_07336 [Phytophthora infestans T30-4](gb|EEY53646.1|) 3e-17

MCKTLKGQRNARQFSSPPRSTIEGAGVGQHNGGALIPKATHFSRPSMRPLAKNNAIDASS

PSMRISMANSNRLGTPHLSQRPNAGMFDRFLRPPIGGALRSSAQPLGGSRTRIIRPKTPL

QASQRIGFLSR

>contig58458 Frame-2F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY54050.1|) 1e-07

MFDAEILTRSILQVPRQVQLNTELHETFAKYGNYPTSENL

>contig58890 Frame-0F

MVVAANFLSLPRISCIYSSISPSGSSISPNSHLRSIK

>contig58951 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66835.1|) 4e-10

MDGVVVLETQFSKSFMLHIMNSIDYPALCHTTK

>contig59549 Frame-1R

MRLPVQMRKIKIAILTVICVKKG

>contig03460 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66166.1|) 1e-108

MQRVLPKLVWWMNSFTRSRGVDTLEPALLEMPDRERVKKIVCSAALTFILTECGKLFTLG

ANGYGQCGIGEEGVSVQLPTHVRFDGDKVVDIASGYQHGLAVTENGTVFCWGKGERGQLG

FGSGNTDAPQELIALKGKRIVKVDAGFNYSCAITEDGELYVWGKLLNPKGMSEANGDQIT

PRLVQTSDAVKLSKCSHFHTSFIT

>contig05628 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65850.1|) 0.0

MELVMHNFVALGKRIQECMTVSEKSLDFCIAGFVRAISECGQAFIVYFVDYTLDMRPGSL

VYEFLNEVLFFTSLNNVDVSNETMEFWIAFRTYISGKHEQRMHVFETFISRLLVILIERT

RYPEGFEAFPEAAMDRFFIYRSKVRNVFRALATVTAASEDKFIVDAINAILQQYEAYDSG

MILPPNWWQQTEVYVHALSALSKFIREEDTNLVPRLFENLSRKNPSHRALSRTVTIFLGV

AGHWFARNPEYLNTYAFRIISNGFESQDDSSYLPSQRRQQDHVGAVALRKLTFRCGSHFF

NPLWMDALVNLYRVNFVAVRGSSQTHLTGDNLKLIAESICHILATVSYKDASLIVHEIGI

IIFAGLVDQHSQVHTKDESSIECICDSLDHLTVLATKIPVQMAQEIPHPFLSLLQKHWNV

METILRVYGCCKEVAGQLCTLLVGVFESLRSQALELASAIMPDLIEQFAKSHNASYLCVI

KSIIACTGDDEATAKSLERVMIIVCKNSMRKLAADGSSHEHSGLSIALFALVITCGTHHP

STLARSNQLEDVLTLALHTLKSQDFEAGAATLDLLLELGSLYGQIVRTPSNLLQGPEFAG

KLLLHKQIQMLLFERDMQYHVLIALFNAAAGGMAVNLIDKIAEVVRSCWNYYGRQRSESL

ISRLLSDSNFLGSHVSARARTDFFINISTPLCVENPRKFKRVFWAFCDHFKRNLAISAKL

SQEI

>contig06070 Frame-2F

MEVRLIEIAMCVILEAASLSSVVLMMKIFKNYNFQHVM

>contig08685 Frame-0R|Blast-RecName: Full=Phosphomannomutase; AltName: Full=LePMMgb|ABD97872.1| phosphomannomutase [Solanum lycopersicum](sp|Q1W377.1|PMM\_SOLLC) 2e-70

MFSRLKKLRESITIGVVGGSDLIKQKEQLGDNVINNFDYSFSENGLVAYHNGQLVGETDL

KSKYTNLQINKLVNFCLRYIAELDIPVKRGTFVEFRMGMINVSPVGRNCSQKERDEFEKY

DSIYKIRETFVEKLRAEFSEYDLTFSIGGQISFDVFPMGWDKTFCLRYLDAKDYDEIHFF

GDKTH

>contig09325 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60119.1|) 3e-38

MIVNNIVSTELTASHGMVHIDAVTDDALYPVTGTAASRFSICGLVLTPRREQVTRKLVAV

TLRWMVVYRYKMVPCDPAIEEEIKNIRPLLNGDLLTASVCSYLKQQKHA

>contig11319 Frame-0F

MALRSLRQAPRALCKVSPRSGSMHTRTTDRIASIGSTSTSSESMLPLICVRNAATTHGEL

DVLLPLPGVKGLTRLGLTDATTSVQDFINAIKANDTSLKTVEIATLDGTKLARTVRLSEL

TSMSFCVRLNHISVLVESDAAAMDSRRVREENVAFATVKAEIEKKSQLILPLPEFYRMCH

NAGAEEKVATKWLRELQRRNLVVHFDRSRNPQLENALILRPY

>contig11751 Frame-0F

MTLNNFALTHLLIHPERLGTQKYVQAKKIPGALIVTPDWIIKCARSWLRVSEQDFLADDW

KAICRKKDLHKQKDDASESSKGITLCEGEAAQNSCKNNDGKQPPLLVDTPENSLPAQEGT

NAKRGKQVTFAKATDDSGNSLNKVDTAGKPKTVRRSRVVCRPHDALGTRAHAAGVVATGG

TFDFLSKIKATKRENSRPIVNTKPAENDSSRPSRRASSPKNIDDAFLRLLNAEQREQEIE

RKRKHWSTNIKDQLVSRRTHEDYKRSSANSIYGDKRMRKTPREQLNGEEKE

>contig12246 Frame-0F|Blast-lectin, putative [Phytophthora infestans T30-4](gb|EEY65859.1|) 0.0

MYLSPLLLVCEAALFALFQPSPSNAKRLDYVSFEKPFDKIDEEGLRQVGENFEYGGDTAV

NRHFARLTPDRQSKRGYIWGKQKLLVKDFAVVFTFRISGQAQSLFGDGLALWLTTSEFVR

GDNHGFTGEFKGFGILFDTFVNQEHSGGHKDVTFFENDGTKTLDQLNDMEKLGCMAPGIR

VHEKNAAFNPSLNMSRAKITYTQADQHVTISIDADASGNWVKCHDQRVNIAGDWISDAYV

GVSASTGGLADNHDVISVNVYDDVIDSLVDRQDQKHRDAVDKSLEGLLNNGTNDEKMQLI

KRKYTHLLEEFEFKLNALKESTENTILKLKQQGIKDEENIRKLEAWANGAVVERVQSSVS

VVRDHMDSRLKESVMETAAQSSGWKTPFFIVLLIIAGLTAVGYQKYQALRKTHFL

>contig13638 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66271.1|) 5e-74

MTVKVTYLRSLPSVRDSCHRVFSLAKQNELPNFLVVESKIPALAEYVLGIIRQSYPTPNE

AKVPFHSRWRHFESGNPQRVANLLSSWNCDKLEKARRLLDLALVSVLLDAGAGPTWKYQE

PGTLEYYTRSEGLGIASFHMFVSGEFSADSKEEPHRVDATALTSLADDAIAKAFQV

>contig14420 Frame-2F|Blast-N(6)-adenine-specific DNA methyltransferase 2, putative [Phytophthora infestans T30-4](gb|EEY53906.1|) 1e-39

MDSNMNELLPNELLANELSTETLAALQAHLQETHKEDNAFVSEDFRLSQFWYDEQTGRSL

AKEAIEHSSNGLKIAFVSTPAAYRDFLKIQSEVTDNRKQARMAENVYIFEFDRRFGAKYG

E

>contig15188 Frame-2F|Blast-mitochondrial Rho GTPase, putative [Phytophthora infestans T30-4](gb|EEY66275.1|) 2e-90

MTAARAGEANVAHKNLPLKPQVVRIEVLGDEKVGKTSLICSLVSRRFSEKVPSVLLNVQI

PAEESDENVIVSITDTSSRISDMVRVTMATKRSDAILLVYDLTRPETFQRLRRWLDCIAK

SKEIPVVLVANKVDINAVTPTTDAPYAKQVLHLVNTYPFVVSEVECSAKNFTQVAQAFFF

AQKAVLYPVAPLYNVKTR

>contig15636 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53369.1|) 1e-126

MGPLFLLFLSDLNDNGTYWFQPCELVQPAIYRGFQRAPRRSRLLEIRVGSEPYWNDLMNP

FRQNQLFYIDYLPTLMRYDGGGNSSALLAGPNCLNQKLLDVVFQTNLYTMKTRRKNRIVH

YNTVRQVLDYLASYDFSYPLFLYIVSGVHAFNNRLWCPFCDKAEVPVMHYFNETATDSAV

MLRIVAAREPRQWFEEDNDFTGKEFSENVVVFDGVPFLGYVGRNHTSKKIHVTEYVYGPD

RHDLLQKFFQRQASGLAVEA

>contig16031 Frame-2F

MGEEMCCGCTSLNADDEYDMGMHVAAIFIVFIVAGTGSMVPIISRMIPQSKANSVIMESV

SAFSYGVVVATALIHMISEGIEKLSSECLGPIVEEYESWGLAIVMITLLIMHLIECESTV

FFGDEGSAHGHGPSNGEDTVILGENLPSPHSVNHPYQKKSMDEGDGSSKLSRKIATLIFE

AGVIFHSVIIGVNLGVASGPGFKTLLAALSFHQFFEGIAIGSSALKTVESKSKLLTVNFA

FALTTPAGLGFGILVRNSYSKSSTTALWVEGVLACVAGGILLYTGIVELMTYNMTTNGQF

MSRPTAQRFTLYFSMWAGAGVMALLGKWA

>contig16343 Frame-0F

MDVVEGPMLRSTSEEMASPPNSNGTDKMDVSNKLRMDVMRYMSKGIMRSIEMAQAVERNA

FRSSSSAEYTGSANTDAAIDGGGGYSSVSYKDYTHVESMGVVVVGEKGGTMLSFRDCAPK

IFHRIRAQFNINQDFYRESFDPLRILSEHGSEGKSGNIFYFTANKQFMVKSVPKEEFDTL

RAILPNYHEYLQSNPNSMLGRYFGCHSISLPIGKRRMYFVVMQNLFNEGPVDQRYDLKGN

RDRRQAVSAATMEGLIEIAKNRKAIDHLLMDIDFLKISPGIFLSYTKTAFLQDQLCSDFV

FLASRGIIDYSILLGVRYEKSQPSRSHQNAIMSHDEKEVYYIGIVDMLQRYNWRWTVQRW

LLGCFLCKDTHDVSAVPANEYASRLANFVHDKLFDIQGNARSRVKSSHDESKFTNDSGYN

SESSRVSSLASSPYSFMSVAILEPKGVPAMDILRMPVHSNVADLPGLELSSLSPSGAYSS

VCESP

>contig16718 Frame-0R

MCLSFIHGLSGCRRLLMRYRFIPDRARLKYTGRVPHHAHINDLGGWCRSPLSVITGDKGA

CQSLICDWVERPVICSY

>contig18437 Frame-2F

MTTSTTLREVASYSLSLLGAHLVSQESEALVSRRVRQIAPKQESQIKQLLST

>contig19140 Frame-2F

MTTPPLLKTRTKDPLESPWRKHMGDDQWVPDVSVDRCMLCRTDFGFWIRRHHCRRCGAVV

CDSCSGSRTKFINKVIAPNKMAKEDCRVCDACVRLIDEKLAQGVSRRFGKDKVDALATGV

DNGKQEYTEAIPLGPDKGGNRTVMTIGKY

>contig19489 Frame-1F

MHASFEKYQSCEACGDSKLYCSETIRKIYQWTLRNYCRMMTEIATILQSITQKVCRFEVI

PREVGLASCSYKMITLEGPTLLPVD

>contig19885 Frame-2F|Blast-serine/threonine-protein phosphatase PP2A catalytic subunit [Phytophthora infestans T30-4](gb|EEY53092.1|) 0.0

MSSTPFDLSIDTLDTWCEKLLGCNPLTENEVMQLCSKAKEVLVQESNVQPVRCPVTVCGD

VHGQFHDLMELFRIGGHAPDTNYLFMGDYVDRGYYSVETVTLLVCLKVRYKDRIFILRGN

HESRQITQVYGFYDECLRKYGSPNVWRYFTDVFDYLPLTAVVENQIFCLHGGLSPSIDTL

DYIRGFDRLQEVPHEGAMCDLLWSDPDDRSGWGISPRGAGYTFGQDISDQFNHANGLTLI

ARAHQLVMEGYNWSHKCNVVTIFSAPNYCYRCGNEAAIMEVDEQMQYTFLQFDPAPRRGE

PHVSRRTPDYFL

>contig19948 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66723.1|) 0.0

MRSDFIGGAIAVASAFMSIFGVNLQKYSHDKEELRAVPRPYTMRPIWWVGMVCVVSASLG

DFLALGFAPQTLVASLGGGSTILGNCLMSHFWLKQSLYLTDIVGVAFVSLGVVVLAAASE

EDEGHYKMEQIYTLMEALPFILYALITTAFSMTLFMRARRSKAPALRVASNDKDDPRVDD

VQEKKREIALKQKIVDEPLALEEPPRSKGAMMSPFPSPIFGDHLSLAAIDKEEDDTLDEI

VLSKLKIGRYDASKIEKHTLIIDPKLPLYWAAISGTIGGQSVLLAKCVVELISSSVSGDN

QFQYFGTYVLCAGMAATLLTQTHTLNLATMCGDTMSSYPVFQGFWITMSNISGVVFFQQA

HNFTRFQWIMFPAAILLVAVGIILVSKHEKFGNFVKYSIAMPISLSSPRQHDIVAQSFVF

RVSTPQKAYEDDYASTSESSDSSDEYLRRTLEVV

>contig20298 Frame-0R

MSQDTDLLAATLLRELPPHDQPRRSVSIKKKSAFNTYGRCGTPDYLAPEIILGLPHGPPV

DYWALGIILYEMLVGFPPFNDDTVDAIFHNIIERQILWPDGEKCLSPEAMDLIDRLLDPN

VATRMSWEGIQFHPFFKGINWETILESIPPFVPTLEGPNDTSYFNNRNLTDIFRDDEDSD

DPFCLERQNLIDSGPESDEQGLGLIDLTEGEMKEGANNTGSQHSSATAGAAWTSDELDRE

DGAHDKCVIELEDNNSHFRFPSGMYGNPEESSLSDAFRSFSFTNMTALAAASHAEAEMIT

DSEQQAVETTSGPSILI

>contig21275 Frame-0F

MVSCIKAQRSCILADEMGLGKTVQIVSLIEHFKSEESIRGPFLIVVPLSTIQHWRREIES

WTDLNVCVYHDIGDRSTKFTAKDMRAVIRNQEWYYPGLGNSIFKFHILLTTFETLLADFE

EFEHIHWRLVVVDEAHRLKSTGSRVLKMMRVLHVDRKVLLTGTPLQNNTQELWVLLNYLE

PVKFASLEDFNQNFGRLHSQEQVIRLQQLLAPFILRRVKEDVEKSIPPKEETIISVELTT

LQKQYYRAIYDKNKSFLYRGTKNGLPTLNNIQLQLRKCCNHPFLIKGVEERELEELGNNP

SPTQVIEKTIECSGKMVLVSKLIPKLKRDGHKILIFSQFLKQLDLLERYCEANSFVFERL

DGSTGGSVRQTAIDRFSRPHSKSFIFLLSTKAGGVGINLIAADTVIIFDSDWNPMNDLQA

QSRCHRIGQKKSVQIYRLVTHNTYESEMFDRASRKLGLEHAVLGTASFNENSQITKPSAE

QLVELLKRGAYALQEDGDTASKEFAERDIETILKKNARVMVVGGAANVTKGTDEASSKQK

KSFVQANKRKSLGGMAVDRSSFVAEGASGELSVDDPNFWEKVLPGAVSVEMLSLKLEDGS

AVNSRQSKIKFISNLDIALTSLVADMSSGNNVDEGRTENRDIQHEYDIAIQVLNTVSSKY

RDEFSTDQLDIVKGYLTKIEKSRVRSCRLAPSRTNLFQDEDFGTPRKKRKRRPTADCSDD

EAYGDTIAKKKGNKRRGRPPKHSQNQNLTSPVLLGQGGIINGSDDLCILCGDGGLILLCD

GPCHRSFHLECVGIKDEPNDEQWLCPDCAEGRHMCLICKQVGEMGVEFGVTQCSVAKCGR

FYHKGCLAENPHVEWVGRKRFRCPSHFCHACTKPSPALATTTTKKTEDDKSRIVSCIHCA

QAFHPACIPSADKFVLLSMNLMLCANHLSLEKARGAASRTAISERHPEARHGGTLLAKVA

AQQRLDNPQFIPFTDNEPNLTKTLSSKRKRARSSKMLSSSLSKKSKSINSIAKDKVCALC

HGENVMGKGADGSDVVRLLSAPTELDSTSADVAIEGPFIEAPVRLKYAEKPNESVHVHLN

CAVHSPEVYVKADGLIMNLPKAIKRGRQLKCTSCHQFGATVGCIVAKCRRNYHLRCAVES

GGEIDRTTYSLRCKSHIVACQEPSRVCLCDASEDDRKLSLVCSSCCTKFHAKCVNMSERQ

ATRTAKSWVCSVCKDSALAKPVISTQGSAAAKKEAPKNKSSLSIELGKRTTRVASKMTSN

GQVPANEFNGISSIKRKKNKKNRLSMRRNKSRSKTNGTNHGISPHVEASSESGVSTDE

>contig21561 Frame-0F

MLGAPAFGRLLVRQSVSVLGLTALGVVATITGRDTEMHSLGEKGLVVVVNSRDSDDKSTR

LGAGRRLILKQRSKHQAQ

>contig21972 Frame-2F|Blast-anaphase-promoting complex subunit, putative [Phytophthora infestans T30-4](gb|EEY69744.1|) 0.0 NOT\_ORF

MSGVLRVDRELLWRKLFAFDHEPEDDPSTEFLCNSDRLCNVIQTAVARGRHEPLRQMLLQ

RLGYWLRSDVVPPFWSFFDQLLAEYAHNSNSRRGHRQFALLCAQQLMLALQFAEDAFSHC

VQIASLFDDHVQLRNKQQRMLQELQLHFRLRLFDDLRLVEKFEELLLIFFTMSFHRFRGK

EKAQVFDARPIRQSLMQLNWFHLAEPVLLKVLHSQIKKEVLSICGEVYDELLLAEVERWA

HSDLVPWLENVLETTNTTILKKWREELSRQVVQEFASLRITQLFEMIKEFPDSVPALEDL

RQCIDQTQQHRELVYEFRQALQSRLLQPGANTSAILDLYVSTIKVVPF\*N\*\*IVKLLDAV

RW\*AFRLLDPKGVMLEALSGPIKEVMKVVATTDGLRC\*EVLILFGF\*YLRKRKDTVRCIV

QSLTDDQSGDLFDELRRNNMRLIPYDDDSDDDEVKSGDVTWISVALLNYNLTNSMQDVSP

DSWEPDPIEADPTKTSLSRSSEDILKILVR\*\*ASNLSFQQTFDPSVCFFCLKVNIYGSRE

LFVNEYRMMLADKLLQNRDFNTDRDVQTLELLKLRFGEDSLQQCEIMVRDIDDSKRLNPN

VQSIIQNSAATAGSKTGTQVACARVDATIVSQQFWPPLQGEVFTLHPKLMHDLNAFKDAY

HVLRNPRALVWSPSLGSIQLSIELENEEREFTVSPLQATIILYFEAQR

>contig22274 Frame-1F|Blast-exonuclease 1, putative [Phytophthora infestans T30-4](gb|EEY59632.1|) 2e-19

MTHTPQIALVFIDAKSTIVKFHYAPFPAMGISGLLPVLKSITEAKSIETYQGHTLAIDGY

CWLHRAAYTCSQEICLGQETD

>contig22627 Frame-1R|Blast-unnamed protein product [Sordaria macrospora](emb|CBI55114.1|) 3e-09

MTYHRKPGFPRSLGNTMVKAGSDEDLDEK

>contig22843 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58840.1|) 1e-131

MARPQDLLPDWLVNHHVSGGIAPPEHIHLCAWDDKFTPSGCDERPGKIVCNFPRDHAGAL

AIIDDAISEETASQLYKSAVKATVWGVYVPISDLFPKRVQKEGPTIKLDELKDPVAFRQA

LARRAVQEFLIEKDDGQTISQNDWNMTHGVAVWVIASDCDDATAYHLDYAEQVRYETNVI

FPPIYGATLHVSPFYDASETDAASLGREMSAMQGGALYVNSIGLGHYAMYGYKTRKHVHR

LSTDELEMQSNTEAGWRRVSYRYRRGILCDGEFPHFSGRVRKLPTEGTFLLESGYHYPVK

RVVVGFNLFPSEIGACVARFPEHSNAFNRYVKLMQAAVKQTTFPSTPSAASVNGNWTLES

VRANPKQAAFLKLLARKVRKSQIQKAADQDSKQKVPSQQGLGM

>contig23112 Frame-1F|Blast-GTP-binding protein, putative [Phytophthora infestans T30-4](gb|EEY60136.1|) 1e-153

MKVTTLTPLPGFQEARSMVFASMYPTDDSSFDELRVAVEKLVMNDASVTIVQETSGALGM

GFRCGFLGLLHMEVFHQRLSDEQGIQVMVTAPMVPYRIMDSKKVQRTVETPGAFPALTKE

FDIFEPMVEASILTPSSYLGPVLALANDKRGIQTNLVYLEDTRVLVTVHLPWQEVVTNFY

NELKTISSGYATLNYFEIAPQKSDIVKVDVMLNGKVLDALSFVCHRSRATLSGRQLCQKL

KRVIDRQQFEISIQAALGGKIFAKERIPPFRKDVLIKSGKTVGGGDSTRKKKLLAKQKQG

KRRMRTVSNVQLSQDAFWSVLSK

>contig23321 Frame-0F|Blast-iron-sulfur cluster scaffold protein Nfu-like protein [Phytophthora infestans T30-4](gb|EEY55950.1|) 6e-46

MFLRSRHHLSTLARRCAAISSVTRSVHVLSKTKRCNVSLKSRNMSPFLARSGALRSMFIQ

TESTPNPQSVKFLPGRAVLDDRFTTGVDFTPTSEEVRRSPLAKKLFQVEGITRVFFSKDF

ISITKSEDEDWDGLNAEIFAVIMDFFASNEEVMSDEPIIT

>contig23471 Frame-0F

MSKFMSSHTMLEIVACAGISEAYLTRQSVLILNDLGIDEDVFMELQEEYLSELRSLIASD

DGAYFELKAVLPPSLIWWIDVLARKLEVKIMTDEYLSSLARTVYHYRLANTVMRARVPIS

KGRTLMGVADFTGALDYGEVFVQYTETDEDTGTESYVAIDNVDVAVHRSPCHHPGDIRVL

RCKADVPLQLRQLKDCIVFPCKGPRPHPDECTGGDLDGDMFVVIWDERLIPSRTKVHEPM

AFDEDNGEDIGPRVKEYHESTDDAGLVDFYIHSIQDDILGVASNAHLALCDSSNDGSLDE

NAKILARICSKQVDSLRAEKDLEIVRNLAPKSYPDFMQNKEKPSYPSKKVLGKMYRRCKA

IFDSTMTKGVSQMPIRDDTFLISGYTEYIQSATMLYHQYKLRLRALLLMSGAQTEAELAT

GMIVEPQSEYKADYFRFGEQCKHSFYVLQSSFRSQFDFNISTLAPGENLKFAAACYFVSY

DDSDATTRSLSFPWIVIDLLTTIKTSNADRVQYKMWTPVRLSAFAQTIPKLQLCMLAEIA

TITEELLADLFDRLVAVSSLRSEMPGNLQKKEFNLILFGSSGLLTFEKQSDLDVMVCCTS

TRGSLKAIAKALEGSHGNINVKDNIRVPLLSFSFQQWSVEMCKFSSGPVKTRLFRTYMEE

YLFFWPCVYFLVRWGKCVGLIRRRSGGGLDMFSPTGFIWLFIRFCTEQNFVQPISVGTIT

LKEILQDNEIDKEISFWTELLTRLVSGGEEESSTLSAADVLLSFFAYYANLSNPDCAYGF

TDPLDPENDTQLESDAVTLFRSECHIALHQLVIEQGDIKYLLTHRKEQTSRITLSHALST

RIHEAKDFFSRKFLFETKADSSTRLIFTLHPNLLRSDLYVAEIIGPGDAVQRIEDHIRMI

EQELGARMPFRSNKNFHHEGSSLLLFEGAESQQEKIGFQDYFGGRHVEHNNIRLHQAHLI

CFMNGRQWYEHASVTFCAKFIQQMIKLSRYEHLNPGVAKAKAYVRFGHHYLINLPRSFDE

ESIMLASIKKLEDEFERGRTARELYESVLIAKQKQRAHADNLKECDGAAEENFDEEQGGW

NCCDHSEEDDDRYEKEGGGGGEMKQRRHPRRPRMQLQSANTVAQGDKGVTHSFYSMIESQ

HAPWTKVYAETRLELTSIEEFDSYQVSIVHQSFEYNIRLTNDLQLIKVSTRPSRWFSATL

KMRQELDDESQTMDSTPDVRFYVSTTEDMPKTDNLFVKLAECCKTAPDGRGIIEFCDETR

AKVRISRHLLEAGESPACIGTIRHVRGTKYYNSVTELQLSLMHIREFGIPDRNPEDGFMS

IRDKVEAEFSLPPLTPERRLLPAFARKFLATGMQFVDFLRTKSDLECVKGTDWP

>contig23949 Frame-2F

MVLFSLGKSIGRKSKQFYQWRVGMHEFSPLLDREGTINSVFSRILGQLFRPLTTAMSDDF

PSHLKRDLGLFDFFCSRTISLVNRKTCSDSASSSRASSSHTKTNSCLSASSASTPPPAPT

SSILSVEAHTISSHTYTVLDSMDSLITVASADSINNNDHLSDDDNDSDSDDGTAHELTDT

DLGSAISKYEIVRELGRGATAIVQLGRLRGGDELVALKVFKTSLLKKMREVKRVGRRMVV

STALDKVQVEIAIMKKLHHPYLLNLLEVFDDDSETLVLMLEYASSGQVMQWFPEEKIYKR

TFEKKKSNCFSEEELRICVRQLLLGLEYLHENNICHRDLKPENILMGRDGTFKIADFGVA

HFFEDDKKKDTGEDIIIAGVPHRKGYVSTTAGTYAFMGPETLKGGEYSAYAADIWALGIS

LHALAFGTIPFYDPDVVTLFEMIEKNPVELDNKDNASEGLVELLKGLLKKDPDKRWSLQT

CKEHPWVLEGLSDQERQEYIETSYEAVNVGPEDLACAVTRLTSLNVILRVKLGANKWKHK

AMRTLEKRRKSLQDGLSGLDKSLQSSVVSAPRSTELESKSLASHMLAMKQLQI

>contig24041 Frame-0F

MTYPPQHTNGLGPQGMMINPFLMFPMMGPQAMNMMGMPIQMPMGINVNAMNSMNGANAMN

NASGLTGMNYTNGMHDLSGTPLSMHLQLQMQFQMQMAQMAQMNGMGLHGMSMPSGFANLP

MSLNMQIPLNVQHQINPQSGLANDANTTSEYSMGMFSTEGKLPKPNGANEAFGGGSGFVS

IAKKPDEPGVSSILKSLMTEEAKKKEKKLERNRDSARESRKKQQTYVETLENGIKRLQIN

REFVRSYQWGISSPGFSFLTCPNSLQMIDWKNRINVVTGQTEAFASIQNPANFWSLMQLN

RQRRTLAMQHEDRERAVWKCFVYVGRQLNGLRTRVLQMQMLRS

>contig24355 Frame-0R

MHELTRDIPSCRNWAGHGCNGANRYKVTISRAKRRIA

>contig24434 Frame-2R|Blast-Phosphatidylinositol kinase (PIK-L2) [Phytophthora infestans T30-4](gb|EEY59643.1|) 1e-135 NOT\_ORF

MAIMYICKSQQKRMRQHLDKIIPAFLYALEKVNRSLRKFLFEQLCDLVQIVEEQIQPHLD

HVALLSIVNSYWDEHLEEVLNLVKKLANSLGENFRAYLPDLVPQMLRVIRTERDNHVRPR

TLLV\*RLLFRLGACWMGICT

>contig24759 Frame-0R

MTLQNASSKFSPSQLDVLHVVILSCCALSLLGCLYILRHHYMSARLPSGVSMVQKMVVVL

SIMDAGLTFPKMFGHLIQDATVFCYAQAFSLHVFGLMSVFWNTSIAHCFYRKIVHKDSEA

RLKSRFKVYVLLAIVPAVADSVALGAARMFGSATFYCWVESRMVRFWSFYLFVVVAIFYI

CVILWVTHTRMSRLFQNANVDAQESWALITSKLRIYIAAFIVLWIPSIIFRLFDNQLGSA

TFSVALLMQVTVCSQGLTTAIIYGGLLTKLYQILSCKPSIPLTHKCVASPSFPTMESGTT

YAHVKHYRKPANLFVSTFNMGEAQVTPVELTKWIPRGHDIYVIGLQECLHLSTTRSLIRQ

HLEGTLSNLLDHQSSAYHQFDREIGRKTTALGYHGHIAITVFIKSFDVGSGAFYMPPVVQ

QEVNVGKSLVLGRASNKGAVGFAFRYYDTSFAFVACHLASDPKGKSNVRRRNRDSQDLLK

NLHLNLEDVGFEFPFVHHHSFVLGDLNYRLTRRHATAETILELVSKVKQCENASVSRRKQ

QATLHREFLDKRSSPMRLGSPFNHESYRGSERESNPYDVSLLERNVKSTSFDFVSSNTSS

TSARYSGDCELLDDDQFGWDKVLAHDELHANLREGYVFYGFQEAPIAFPPTFRRKRKAAL

NLDAANWTSEDLAKCFTTAIKGHGTRVPSYTDRILFLFPV

>contig25110 Frame-2F|Blast-hypothetical protein PITG\_01004 [Phytophthora infestans T30-4](gb|EEY58348.1|) 8e-17

MISPLKDIVVATVLGVGAGMVWNRYKDSELDRTTRFYKWYDAQDAQTKRLNTDE

>contig25327 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55512.1|) 2e-32

MTLLFAEGSKTTELSDTRLREILQDTLQKLESQRGAKFDRAVIVPPDFTRFHSKAGLLSQ

YAYEYLQDKVVDVLPALGTHDPMSDDEICKMFGDIPKYLFRVHDW

>contig25918 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61186.1|) 1e-144

MYMSEATTVRWISDAEVSVCYSCQLLFDWLRRKHHCRYCGHVFCELCTPQCSLIREHLIL

ADPERKYLAVNAHKPQRVCNECYTRLEPEQKELRSAMSYAVQQIEVVESGPQSLFNSPYS

FSLQDEIRKATYSVKNLTAQGVIKDQSLPLPLLVRAKGIAFLTVIKMGFVFSGRFGSGLV

IAKLPDGRWSAPSAIGTAGVGWGPQIGGEITEFVIILNTQQSVDAFCASGHVNLGAELGI

AAGPVGRVASGALEASTYMEMTPCYSYSHSKGLFAGISLEGSVILSRPDINRLFYGKAVT

VSSLLEGVEPPPVAAAPLYRIICAAMESSGTEAVK

>contig26933 Frame-1R

MHQMLQRVVLATLTDSSTYLARLAELGVAEIRFLEARDVNETCIPKVLVLDILRHAMDFS

RDNLQQLEAFMPPINLVLKEICAFIDYHQHISTIEDFAARNCFSDSESDCESIVSGGDVG

NGAKLENSVIVSSQVALSGQDTVAPIMASRNPIYSLKPCKASENYQPLTSALLVVHVVEL

LNVVVLSANDRIDKRLSQLHFAPSLVRIFEKYPEANILHCRLVKLYLNLLNRPRTSERVS

NPLLLSLFRSRESILEFILHKLDVKVVNHAYDAHLAIIGVKLAQICNSPKLQQKLICQFC

NNLKGWNEFAASLVANHHQQMYALDASLLASQTAVSSAFRMRNVNNNNTDMKQLFTRLSS

SVRKYL

>contig27163 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64068.1|) 1e-59

MLPAWRNGFLAAFADKQGQLDSKVQMLTLNVIEDWYMKFVSGSITRGLQERTPKELHATT

FAHFGRCDDFRTPMALDNSFVGYVHLVDGKGRIRWIAGGPATPLELDRLKNMTRQLLAQS

TQRLQG

>contig27332 Frame-0F

MTDLCDHKEAESRCEMFFEKAMNFDIGLPEPTQALANLRLVQQRKEEADVLLEDTYRRLN

EMCDVESLPSLDFRTATGKMLIEVERYEQACDILEGVMQEDDENAELWFLVGTCYRAMDD

LPNALEFFEKCLAMLSKLKKELGDEFHLHDQLESIIEVIDAIKASIASYPPELDSDGEES

ADCDADGVGQQDVEME

>contig27989 Frame-1R

MVATPRFHVTQDATWVFVHIHVPFVRVSEMEFDVDGQAFTFYCKPYLLKLHFPHEVKDDE

LAKAVYDPNKDNGTIVVHLPKMVPGVDFPDLDMLTTLLQPRRPLFDRTRQNHSQAPCIEV

LESSSTDLHNSLQEHNSDQRNAFIDTAPVQKTTGAANVQSDSSLLRLEKNVAISENDNSM

LLDTESSGVRVTAVMPTYGFNNAYSDFFRVWHGEVSEILSLPDPDETPLKDRSMLRESAE

EQMFSIERYLLDVADQDDDMYYQLAMKYVPFWREYPVTPLPVSPLNIHNGIQSLSLDNKN

PLKPLSVNATETPFSFTDKEQELLRRLPKKEFLLFEHSEDEKIVLGGLVDILIGFVYDQL

TTQGDSGVESAWTVSIISPTLSWLDSNADLRAVVRTTVRRMITFPFLRQYDLAIRCLQEA

SELLKRGKRVVLRALFALYQIFEKSETQYLLNALYLQDYCVWIQSVNDERLLRGSIELDT

RIAAFSKKETHWALDELERSVLELDYASASSSADDSDEDSSSEDGTSETTIGTQEI

>contig28179 Frame-2R

MWAAKLPTEAARLYECCAAMTTFMKEIGVAVDGGKDSLSMAAQVHQTNVKTPGTLVITMY

ALTEDVNVKVTPNLVRTTDTSFLYLVDVGKGANRLGGSALAHVYGQVGNDCPDIDDVPLF

QRAFQVIQTSLSKGYLLAGHDRSDGGLIVTLLEMAFAGNCGFNVEISSTKTGIVTMHDVL

QTLFAEEIGFVVQVAADHVMEILSLFQASNVPLVKLGNVTTDGVIRVAMNGELVLLDQMI

DLRDVWEATSFELEKQQCNPECVAKEQASLRTRTGPRYTLSYVPHATPARQLNTRHLHRI

AILREEGSNGEREMCAAFYAAGFEVWDVTMSDLVANRLTLDERFRGIAFVGGFTFADVFG

SAKGWAGVVKYHSNVFHQFAAFRARTDTFSFGACNGCQFMTLLGWVDHVDASLLETLTHT

PAQPRFIRNTSGRHESRFVSVQIQETNAVMLQGMVGSTLGVWVSHGEGRVHFPHPLIQDK

YVSSGAAAIRYVDDLNGITEEYPFNPNGSVEGIAGLVSSDGRHLCLMPHPERCFLKYQWP

YWPQAFQDVEESPWMQLFQNAKTFCEQN

>contig28922 Frame-1F|Blast-pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 [Phytophthora infestans T30-4](gb|EEY69080.1|) 4e-10

MGKLDGAMPLMVLPMYSQLPADLQAKIFDASDI

>contig28957-0 Frame-0F0

MKMIPSSALTRLTAEGVMSFGHHNCLRFVKGTTVDQVPKKKTMRSTYFYVEEYKAYKSET

>contig28957-1 Frame-0R1

MTPSAVRRVRALDGIIFIVVELFIPASQMNAYRLKDPLRSTKKRE

>contig29024 Frame-2F

MKTVKRQVKGHEELTAATDPGALFGRVDVSGHITKELLDDMKNETDKVAWKKRAEAIDRV

QAICEGAGCAIELTRPVQDVLRSLKARLNDANANLKVKATNVIAVVATSVGPEIAKMSKF

LGASLIAGVADNKKTMQLAAVQALNKWVFHNHTTNSNCVESLLPSLSDGLMNPVGRAELL

GWAVEHLQRCEKVDLSCMVVPTIQCMMDKSSEAREKAQLLLIEVMKSVGKDVVLTTGCRD

IKPAAMRALKPLLQKVCDVVETFEGPAQSSEASKLFSEPNVMSPAARSAISGAIGGSGLR

RRASPSASGNTPSKSRLARPSSTRTSSNLAPPVQSSAKVAPSLKISNNKPARIAKGHLNK

WIFESTSLSDMKMRKSEIEVEWKPFLSPEFHAKLFAPSLEKGMLSAMDELTLCIAHHPDE

IISLLDLVLKWCTLRVVDNNVQALAKLLEVFVKLLEMLKDTKYQLDDVEAAILLPYLLQE

CGQSKPRFRVRFRDVMKLIVDVYNPEQYVVYLMECFNGSKNMKSRCECIDMVEYIVSVHG

YHVIGRKCIKEVGKYVVAHEKELRESAISALVAVYSRTENRNADKFFRFAGITTQQGVDL

LTARLKHLPAHNVSIEPSASLKNDATEREVSQQPRTGFGFGFGRASVMAPPAPTNVSGPS

FTNAVKVGQPFQEHAFDSGVQHDKEDPFDNDVDMSQPRNEVRDEDAPSAVIEELLLRPIE

KLINSSKGLYKQGLLPTRKVAMH

>contig30417 Frame-0R|Blast-DNA topoisomerase, putative [Phytophthora infestans T30-4](gb|EEY68895.1|) 1e-142

MRVFRARFSALIPLDISHAVQNLSEPNEKLSLAVDARSEIDLRIGAAFTRFQTMRIHSRF

PALKQESGVISYGPCQFPTLGFVVERFLKIQNL

>contig31115 Frame-2R|Blast-regulatory-associated protein of mTOR [Phytophthora infestans T30-4](gb|EEY69298.1|) 8e-97

MGHLDASFIERIPGKLTDRKTPLGELNWIFTAITDTIAWNMLPRKLFQKLFRQDLLVASL

FRNFLLAERIMKSEGCSPCSLPVLPPTHHHSLWRSWDLAAEVCLHQLYKCTYPYPNVDMT

FQPSRFFAEQLTAFEVWLRFGSSDSPPPQQLPMVL

>contig31649 Frame-0R

MDISIPRANGCFLLVVETRDVPIVVLFFVGVSFFQIAYVSGSHMRPSRFKSYLISPLATN

SHNFLSTYSDSSSFPLLFFHLQLVFSRIPYYHNRNVSPKQLVLYQRL

>contig32046 Frame-2F

MDITDKAFTTELSDQRNGFYAMGRALRAIDLTQSNITDFTLFALAKHCRYLEKVKLGHCS

EITDVGIEALVSSCSHLRELDLTNCALISDRGVGMIGAYCQRLERLNLSWCLNITDKSVL

CISRGCKNLQEVLLVWCTQLTDASIDAFLSNDESTWLNNLKLNFSGCKGISAVRIENVCK

KGLDIVGG

>contig32932 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57399.1|) 1e-32

MLDELTVEVDEAQERMNFVVARLSTLLKTKDTCQLGLILFLVAVLTVMVFLVVYT

>contig33265-0 Frame-2F0

MHFRKVCRSKVEYNSSLAGPTKTNKFACARAHL

>contig33580 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66388.1|) 1e-119

MRRLTTAGSLMILVNIAFIVAGAILLRYKLTLEDSGWDDALVGTDYESVAVTATTVIQLL

GIGAMALGLLGIVGAIVQNRLVLLLYSVVMVVATSAFGVLVGTAFAFKNKAKVWEEAAFP

ANDQENELAKTFNEVYCYAEGYYFCNSATAEEAYITFFPDASTTLISVLPKITGIVSLCA

QPVAMIDGLSTVCEACNMASQFTRYDKILTWAENKCPRNLITGHWCASFLATGAADSIYE

GTPYGQCRNIFLDVVIDWSNSLAIAGLFVAISAAVIVVLACFSRRSKSFSKSENLPKNNL

FWK

>contig34237 Frame-1F

MVRIREPQRFPLGTRVANPLEGRTGEITAFDADSGLYTLVYNDNHHDILTAIQTEQFIIR

TSINDATEQISTINTVDPNQFLGVTVTKSSKSYDGKLLTTSGHVTQYFADIQRYRVLFSD

GLYSDMTLEEV

>contig34242 Frame-2F

MLLSCGKYFLPTDASSTGVVAFTKKSPLMIKMSSCLFVSLLKVFAQSSIPAKILMVLGMQ

ARLA

>contig34408 Frame-2R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY65777.1|) 0.0

MTASPVVITNPMLDLPVASKPPNLDYLSDVMFASLDISANSKRAIVEDLKYERLTHVQNE

TFALILDGRDVLAKAKTGNGKTIAFLLPVIENLVKQGPSLEVIPVLAISPTRELALQIAT

EAKRLTKFHDLKTACLVGGVPIKKDERTLTSTVPIDILVATPGRLLDHIKQNTGSIATRL

GQSSVLILDEADRLLDMGFRKEVMRIIEYLPKERQTLLFSATLPASTKELKKVALRRDFV

FIDTIDENEADTNVQTEQEFIVCRMDDVIPMVETILREHMKLPAYKVMIFFPTARSAQFM

AQLFQTAGFPGVLAIHSRKSQAVRTKTAEAFRKGHKVMMFSSDVSARGVDYPDVSLVLQV

GLTDRDQYIHRLGRTARAGMTGKGVLVLAEFEKPLLNNLVDLPLTQSKTFTSKKLVQSDL

STLKVMKNLKTYCELEKSAQQSYQAWLGFYNSNVKRLKIDTVELVRLAAEYSRIIGLKEV

PKLEKKTLRKMGLLGVAGIESSAYTRETGNGRNTGGSNGRYSGGNSEGYERR

>contig34923 Frame-0F

MMVLTADSCSAGLRVELSQRADRPWQSLDSSFGSSSHLERMTSYSYSPSYCSLRDDVCHQ

SQTLRLLLPVPCSREVSCYCHRVHQRASVSHQQLNPAPYHRHLYNVLACRCLCAFSTALQ

PPVYPSFVDSA

>contig35793 Frame-0F

MFFENNFIATMKKASNLHAANAISVVGNSMAIPPRMSASNGVSLAGMSQLNQRNLSHVRS

AAYKPTLPMVGSSVVLPNAGTATIVSNTAGEGALQLSGRWSLDREDSDSTNDYLEAMGLP

LIARQAADKLDLMVIISQTPGDFMITRRTRIFTETKQLKFGQEVNVKNNLITVTGNASQI

ETVTQLASFRGILTDIRTLDPRGRMHVELTLTLPDKPVVIINRYFKKTSDSTSLENLPAF

DMSLETSGDVKRKR

>contig36477 Frame-2F|Blast-DNA-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY69219.1|) 1e-110

MENENMILCNSIDVDNRSFRRAVTERILQALLRSTSMSLHDTSLVGKIEDFCSYLTVHSS

DWANQFQKTVDLILLNLKQCLDHVDSSETFDKQSETISSLSLFGSKVLCAGIAGFPEADK

HAEMFALIASKVLDHGNGAPHDRLVIAAALKGAAACGWRITDIFLKPYDRQKYAFIYSDM

THVIASLAVWKRCASELASLSLDNDFVVNAFLDILRQVTSFKVYTPRSADWDMFTKTLLP

NAKHFVDSLDAFKANTQRALSNLQVLYYILELWLHCSASFIQALCIDPILDIQNAVTRLL

KERGCSYLVKANSLRLLRLLGP

>contig36518 Frame-2F

MNFLQPLDKGTLDFIHVMKRNSIIKTEAAGENSKVIVTQAGSTENVDPRLVEDLYSALSN

EVMDTGTTESICNREPSANLFPLLTPAFVGIVEEEVYTDPDASLRHIYSRIYQKLRRSKL

LVPTSKVVSCYVDFFRNRFKESLQGFVHSRMLLRYERFIVNFLRHQLALGALEITEDFIK

VAADEMKRVLPSPHPHFPNEKAVEETMRLYVPKLLRQRRLQLIELKKTLQPVLKKLVYVD

ENLFVDAAYTVCCQSVYLFVLTRADIGKVLQRMMPVHYFGVLEKMRPSVIHLLTTHEFRG

DCDTAEDILKKLKRNKPALQEIKALLWIERYEAMGGFGNRDEEKDGSRNDCGSGDKRECD

SDASSSSKLHQQ

>contig36613 Frame-1F

MVDAEVQKCKDRELKEQEKCHAAIERKEQERERQEAKDMKEKEKRNREQAEKENKKTLSS

KRQKRFLAFFEATPSCRVETSDTGVETTGNYVTEYKADVNECMSSVIHRMDAAIEFLGDG

SPRSCGFKEDSVVSILSSLKKKHDADSMSHGWSARRQRDHTRGVMKLLQFHENNRPAYYG

TYSTQTSVFRGGRRPFAQSSKLDYSVDSDDEWEEDESGESLSDDEIDGEESDEDNLDYGD

QWLAYEDEVDYMDGVESEEDAMDRVDGSLSPSKHKLPSQLLKKRVKVKSVKPAKLEPQIV

GPFWSTFDENSEGLEHPFLGMMGEVLCDPVFESTLMRKAREYEEECERQVAVQQEQPRKI

KEQEKFKTVKAKQTTPEKTKQAVKMPETVPGQLAVSKKSKRMAKKSKSVKTTAKLSASLP

NVVNSTAVAMSSLLSSKPQIDSFFKKVEESVPVSLTSQQHEFELKQAKVEDESIRNTSLN

>contig37034 Frame-2F

MATTVHIDTPRRMKRDLARALLDPQSQGVAAYVQECVHSTSIGVDATFVFLLKVIEELDD

AIEEFLPIPPNKELLPHENEVELGTLLSAASLTIRYVTEKQAMALLLQRYCDAFRKVLEY

REWSHKCFYGLKAVALMGSTRVLESFGTQVVAGDVIKLLRFLFTLFKNENIGNNDQRLLR

LNVLLRPSCEFVTVALQTHVVARKIIFFEVLPQMLQLLTRIDADQQNVVVTEEVQVDLAA

TVAVLLDAAFPCPLPNPFALLSLPAFVEEMEADETKLIDDNAVFSSTTQVISKVADGEED

QDSVNVIVEELEKNCCKALYSWLKMRSRRMVAAPTLAIAYRVVASVSDKTFSATSLTAPL

FEISNALKNVKLTAREDFDYMNALLESIRDIYLYQHTLVASTIECAFEVMSTVMSRLETA

LAAFPVKHSTERRSAKAACSTIRHTLVEAFLAWLHHPNAANLLLSQIDFLHNVAGTLADP

RVYGDVLATLRTSNVPEARVEYATGRQLTVVTLSEAINQLDRYSKSTVNRIVSGLTRFAA

ACCEDMYPLANELVLPLLPAMLDGSQWGKFLRLRTEAIATILIGCAQSDDFRVENHPWIG

DFISFLLDPIVSSENVHSFIILNGLIRTNSKLLEHVASFCVANPRTVSQTLHEPIARWPL

YEEDIDLVVISLELIDALLCVNSLRESVDVDIFYATLLQLSDNAASEKLDVISIACKQVV

ATLG

>contig37755 Frame-0F

MKIPNSPVLVITRNPNHMASKQPLLHELAS

>contig38369 Frame-1F|Blast-Poly(A) polymerase, putative [Phytophthora infestans T30-4](gb|EEY62302.1|) 2e-22

MTAEAKILSWDELPEFVFPSGRKSAEIERAQFTTNLQKMGFTFGNTSLFQPFCDVNRCTS

SGKWRGGYGPRKYTGGPRKQRRDYQNAQQSQGG

>contig38538 Frame-0R|Blast-COP9 signalosome complex subunit 1, putative [Phytophthora infestans T30-4](gb|EEY57774.1|) 6e-11

MATLEGFDMEAYAAKYSGRNRIERLLFLTKTSPALEAEATRA

>contig38765 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63950.1|) 4e-12

MNPIVFTAEACRVWTGPSGTPLHAIEDAEQHQFDIIPFSVHVWLEPQSNTAAIVKDSS

>contig38970 Frame-0F|Blast-methylmalonate semialdehyde dehydrogenase [acylating], putative [Phytophthora infestans T30-4](gb|EEY63363.1|) 0.0

MSSKQLKASNSLVAQNLINGSFVAPSEGKYIDVISPSTGHVIGKCALSSSADVELAVAKG

REAFSEWRHFTVKARAAILLQLHALILQHQDELADLVVHESGKNRTEALASVLKANETLE

YACSLPQLIQGRTLQVSRGITCHDVREPVGVVACIVPFNFPIMVPMWTIPIAVALGNCVI

LKPSEKVPMTMTRVAELFLQAGIPKGVFQIINGTIDPVLSLCDHANIAAITFVGSSRVAQ

SIARRCRAIDKRVLALGGAKNHLVVLPDAAIEETAKDIVSSYAGCAGQRCMAASVLLLVG

DCHVVLENVIDKSKALIRGTKAGQVGALIDAVSKARVLQYINEAEAAGAQVLVDGRAWAT

ESPGFWVGPTILLHFKATDVAMKEEIFGPVLSVYQVTLFDEALAIENDNEYGNAAAIYTS

NGAHAEYFQTRFRAGMIGVNIGIPVPREPFSFGGMYGTRSKFGDMDITGDGCIEFFSTRR

KITSKWSTTRNLQDVANFSGQM

>contig39322 Frame-2F

MTPYRHVDIASNRITRTEGWVSGKKKENSRSISVINTCNSMTVTSATVRYL

>contig39357 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69971.1|) 1e-103

MDYAEGKRYKGQWLGTVRHGATKDSTSLELRKQVSAAQQTIDPSSFLCQWQPNKEPIDSI

QWGGAFGKVCGHNEVVMHELRAFYPQEVLNTKVCSKLFPAPGNQGFDGCLEYLRYACIHH

RTSMTLWDAEFFLFLSSNGRVTWSKKHQLLSLSLASLQCLVPALRRWTAACEGRMPPNAV

LRAIQLCCQLGSGAKKSSDGKLSLKILKRIMSFV

>contig39928 Frame-2F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY66415.1|) 1e-128

MYKQAAIKWWAIKSGSLASKSSDFYVLEYIGIETSGGDIVACYFFQESLAEVGGMPHIQG

NNLERSQFDALICKFERTSSPDYKDDFVTISIAFQRPPPLVSLFRSNPAVEMVIQLARGL

RDLLEDPPELQEISVVKTSAWVKDKERRFCVLCNKRFSPIFRRRHHCRTCGEVICWACSS

TIRVPSISFTHNDTGKQVLSRHQPSIRVCSKCVVSHHRSKSGRDLNHL

>contig40124 Frame-1R|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY64900.1|) 3e-41

MTTIFGQELSPGMAMLVYIFLVMALLILCGSIWYYWSYARKIERFLARDNENNNMMRHHL

VDSFLQRGEEEWPCSICFHDNHPGKT

>contig40340 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69120.1|) 1e-129

MMWSASGQFLALGSYDEHLRVLSHVTLKPIADFDHEQIATSRLHTSHLAIDFEERYADVD

VMDRPRGRRVAVSQRSSSLLSNSLQAASAAAQAAGEKKQCDICFVKREPPFSVRTITCDP

>contig40689 Frame-2F

MSAFEQKVEAPDKYWQYLLFACEPYETVAFKIPNDDIDKSEGKFFSNWDKDGKMFMLQLT

FAVGEAAKKQPVPPPPRPQLRYL

>contig41053 Frame-0R

MASDDEDAVYASILANIQRSERREKLQRVVRREYRSISRRLRHVIASWEALRQLQMASEQ

LRPSGDWLPTTLQTQLQSIQKLRHRLEVALSQVGTNAIKNHSGKRRKRLRDQEKVATLEM

VEMEMKEPLQKTRRCTCGAIPDSIEKIKMVASMYENKELLVKNLEDLDVEACTENGKSVD

TQTSTTEDIPYTNSIDFVQPQAEIINIDTIPAVEGRMGAHACESELLDTKATVIKEECFE

SQSTHDPMCETDELPCGLMRINRNDAVRIKGEPMPLPEPIFQEACSHIMSDAARPNLIES

PLELNGFESTDSEETTEGMARTFVKELAYELEVPDSDFEDA

>contig41237 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67179.1|) 2e-89

MVVGLTQPLETTTDVSNSLLSYQYSRLGVFAVLHFKVSSDALITTLLVFGDCALFAVATW

SFPLAYELGLIATRSMDRGVGKEKEQIRWYLWRVWMVIGAFAIVETTLAAVRRGYTGYTQ

RCLLAVYVVQFTSFLYMVWNLIRLKCGGRKFEHVQGQFVPSPIYQRLSRI

>contig41242 Frame-0R

MRWHRTLPLLHLLIASLLFLIAHNLLYLIFAMSYYACGMWSLPQNE

>contig41408 Frame-0F|Blast-type VI secretion system Vgr family protein [Burkholderia ambifaria MC40-6]gb|ACB65495.1| type VI secretion system Vgr family protein [Burkholderia ambifaria MC40-6](ref|YP\_001809711.1|) 3e-22

MPLAEETPPTSETPPTSETPPTSETPPTSETPPTSETPPTSETPPMEEMPPMEEMPPMEP

YGNTATKSSSCIRRRN

>contig41923 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61813.1|) 9e-29

MAMLHVSAEITGYDTVGDHTEFIIEISWNGGVWRVSRRFSDFDQLHSRLVRRFGDLIEVT

LPEKQWFGR

>contig42526 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70403.1|) 2e-07

MKLEHELQKIQGDLSIASKEIVEKQGFQHQITSRSRRFVGFVHDRTTTQLHANKVDSLLK

HKATIETALKRQQHLLVVATPALSALPVVQTLDNKSMDKPVKKSTVVAIAPVTFTSDSNK

LLNPVSHDECKTSERVCSGSTTEKRPMVSSSGTIHKKEELNVLKRRRVAGPAMPIKPVQI

ESINRELIGRNAGV

>contig42755 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67174.1|) 5e-32

MYIQWIEDCRAKGDSIEELLRLYELAQADYWSVSLTLQYLNLIKEHQDTAALDMAMEKAQ

TTMGTHFTRGHEVWARCREL

>contig43477 Frame-2R|Blast-WD domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY69409.1|) 1e-06

MRFAGVDIGTYFKLVSSKILTLLV

>contig43613 Frame-1R

MRVQPVLIQLRKSSSTGKHHVVRWRRHPKTGAETLPEEAQQLKEKIMRLHQSKRTRFSLS

YMRKRVVPPVEIPKEINSQCALSAIVAGRNVPLTRCMWDNTKRKKRHHMEQIAESYPLR

>contig44115 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56376.1|) 2e-48

MEEHKQVAAIKEKAEKDAQAKREQDRLNDRKKREAELARRRQQKLKEMRAGLEKKRAMLA

AEAKSRLETNAAMALTSAASAPLPSHHKHRGLSSATEADYLTANIKPLQKAMSKPVSKPI

PSQPPPIASRTAPKPAPKLLSSSESVSSLAHMKPISKSHTPEIITYEMSDNIESSDSGS

>contig44366 Frame-1R

MVDCNPSCFDIEAPYGSTIERSNLEPRQATELGSNVILTTYRATCTAVPRCQYIFWL

>contig44704 Frame-2F|Blast-serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' gamma, putative [Phytophthora infestans T30-4](gb|EEY59248.1|) 0.0

MLENPLDKYSEYTTEEQLWGLLSACYDLLLKAIEHIDKLEKHVRKEFFPLRFIAQLVALF

KTPSFKERQMLKGVLHRLYYKLTQRRSAIRKEIANTFYEYIYETSNHYGVAELLEILGSI

VNGFACPIKHEHVVLLEKALIPLHSTPAFISYHQQLAYCMIQYVSKDHTLFTPIVRGLLK

YWPVGNSFKEVIFIVEFEEMLEHVLAETDFDTVALKLARRLGQCMVSDQFQVAERAISCW

SSPVCMRIMNEYEKLGQSMFTMIKPFLNRAVADHWNTLIQQKGQETYIMYYNMGYDSDEI

ATSPPLLISDGKGLDSSAKTEESDPDEETTTSNEANLSMSVRLSASSAVEPLDVVISDEE

EETSYSSS

>contig45417 Frame-0R

MGTGELNTTLAVKPVATDNSSLTTERDEPADFSIRIGERELGCSWGWGLSWSRLVVAAKL

R

>contig45844 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58482.1|) 0.0

MKQNVATGDRRRHLFKRYRDCFTGMEAVDWMLEQMEAKSVAEAVRKGQGLMSHHYIEKVE

KETKFEYNKKRFYRFTATTPEFVQAVERPLPCATLDLPLSAAARRRALAALIGGFVADAA

STSLNGVSHPEKTIPNLLRLDFDPAFCGLYDTAHGNDKKGSRTRMESSTGFEARILLQCI

SRRGHIHGSQLAKDAYWGFKNDHRLLSASSRSFIKRVHSGKGWPHCAVKCRSIDVLSLIP

IVVALYAGTNQLFTKVDELVKVFYVGTRVRDAALVAAFVLEQVILGASVLQAMRMSIRTE

RLSVKQRKVIFKAFTKSQLPSYEAIQKFGNRGSLPGGFHAVLQPLFVLNDYPTAVRENII

GGGRTCRRAMFIGACFAAQDGLEAIPEGWIQKTQYFDFIEADASSLVGRREAQGSFTEED

EEDQLAAYVDYLPRSSMSSSRQMDHLDLSRRSSNNLAASLTGVNGETADVASDVPPENLL

SSSHRSSNPVRRRSNSYASSGG

>contig46733 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54011.1|) 4e-44

MRQAFCRPHFFQNSILAQAASSPRVASRVISSDALQRLPINARLSGNTDAAAMSARSKLD

DIITHYLREQHRQCANPVTTVPPFKVLGKGSQHRCPDPPATTLSNLSICSRLMRRSRTGC

RVGTSAFSSSSYAN

>contig47046 Frame-0F

MECLDDATVVSVKADAVRCRWQRYKCLETLNNWETLEAEISIAT

>contig47293 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57010.1|) 9e-08

MDVLESREAVLRAKVLGTSPSHTNAAPLVDRLRTLYSQLNHLCAATTGSVKLREL

>contig48223-0 Frame-0R0

MWPRLTAALQIMLRHCPTIIKIATMPPPVALSTSIEYGRRVVQTVRRPPGHCLHTKNIVC

QQVEISTILLNFALERAAHGHLLT

>contig48858 Frame-0F

MNEALAASPTGPLVVNTSPLADVESMTPQSNEDDDSRSETSSEVSMGSGRPERRRGTRKR

VSMACSDHQDLAARMKKALSVESFSESMIGADVVLCVQYNEHHPGCSGNTSARNGSNVGI

VRRFYA

>contig49156 Frame-1F

MGVDKSTSSESFRMLKEVLRSTNIKEDEEAILITRMCVDPQHVEEFERLLRMILKSTHSV

GHVSTCVVRPPPEKFTYTSIVKYSGLQSMRQIYPSTIESGADFYKLLAARDSLLVEPPTY

QIEAGFGTWIESDGNTKPMRGDDSEEDENMVYQSVPGPCCNDSCENPHGLNVRASFVAPT

KDFQL

>contig49291 Frame-1R

MVGQIARPSTQRGRLRRLLAQLKRARDVQGDQ

>contig49664 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68023.1|) 1e-96

MAGILKATHKTQAGFHGCSALMHILPQNIINLLETCSSSAFTDVFCEGEISPVVIWSDSM

RNHLQTLCQAHLQDYAEVLKEDVLRDWSFCPMAPVAYKELNDEIWCGGVYLGQYCKHDDF

VIAEPSEFMERLISEWRVEVSRQSTSIDNAQALQILGLANRTSEEYPDVTLRAGFKEKAR

ALVRSNVSANEYAESLEKLKEAYRVLTCLRPT

>contig49783 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62407.1|) 1e-117

MTAQKAYLTSARQKVLARCADPTKGEATEQELRELIKADAMVQQLRERHALVVQKLDEKI

AIAAQSYDIVDHHIRRLDRDLESYSALLKANGEYQEESRPHRKKQKVAAAMTVHQASQNH

LVPQVNVRSKHNTNTGNVKEKSATPLVLRASSSGTSSSRKRSTSETSAALPAADASPVVL

ASEDLPIDPNEPIYCSCRRVSFGQMVGCDNDDCKYEWFHFGCVGLTDQPAGKWYCQDCKV

QLGIK

>contig50194 Frame-1F

MTRVATTQVQTATSQVSPTATLLLQSENSKHTATDASSQKQLGELNINSSFARIVHQTDR

YGKPQPILTSFRPAFRVGSSAMKLRGSFRNIFANIWSIQGHQEEQQDIPKSKVMVSSSAR

GNSIELRPSLLPPLSPGDSNKKCLVLDLDETLVHASFQLTDHYDFLIPVHIDGMSYQVYV

CKRPGADDFLIEMAKYYEIVVYTASISKYADPLLDQLDPKGVIRHRLYREDCVQYEGNYV

KDLSLLDRDISQTIIIDNSPAAYIFHPRNAIGCSSFIDDLEDCELKSIARFLTQCQDVED

VRDHLQKWDATF

>contig50248 Frame-0R

MTISRFIIYKRKKGRLASLQLHPLVKRWSALFF

>contig50385 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59668.1|) 1e-38

MYWQRDASNAHCWTKVYGVLDNEFLWLFKGNHSSRTMFLQIAVSSVEVSGQRQLRLVDPN

NEILDIWL

>contig50532 Frame-2F

MQRYTLPQSSREFYRRNEPYKDTTSRYGGIVEAGSATTPLLPGGTFGANMSISQTRHQL

>contig51180 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59893.1|) 5e-60

MSKLRFSVAAYSSEDAVFRACELNKQAEITKGYMTDKNCPYPQDLVLQLQDGLCRVSQMQ

LLSHQSHIATKIELFVSKKQSYEGDTTRFTRLGFLTLKTNIENNYKARELKTVHIEQEAI

LLKLRIHTCHINERNLYNQVGFITINLYGQPLGLLPCHSRSKSVSNMP

>contig51333 Frame-1R

MMASSAATSAINVALRVSCGSLPISLCEPSVCVDVAEDLTILVALGRQIFIVGAQDDLEI

VSQTPASLRVVVDTESVKLEDEEHIAHIKWLDRELFCVGYTTGVVRIFNRLGKLVFEQKL

HDVAVHRLDVNRNEATLMVPRRANVLLSSELNMEGELWVLYADSTVAIIQISEVFTKLDS

VMFGPAHVSKFRKYLLREQKDIVAAMPCGPVRPTIFQSHSRLGVYTVVSTGSDPYFAFYQ

AGNDQNSIIHLAHIATAIVSKAAG

>contig51665 Frame-0R

MLKHSGSRVTAILYTIIDKEMARHRDDYPPPTTLSATRKESKKLSWLPAIPTTGPVIVLL

AVATLLASVLRRR

>contig51711 Frame-2F

MDATAATKLAANRIMTDSSSDQNLYDVLEISISGIEVQILDGRSSEVASHVFRARAYSGK

KSPRHYLLEKTSLAFSFYMSVTPDDPSIPLLKLHGGVDSINLNLSATSFRSLVQLLLSFG

DNFSAHAQRLCHRSSVIVAEVASQPLTRFISPTRPSKPRLARMTSSNIKAGVTALSSSES

SGIHVAASEHSP

>contig52084 Frame-2F

MKYLLCLVVTIAFLGSTNSVTYPQVSPGTCLGCVCPPPAGLTRIPHCRPCCQGTPAPFS

>contig52307 Frame-1F|Blast-DNA repair and recombination protein radA, putative [Phytophthora infestans T30-4](gb|EEY68784.1|) 1e-11

MTTTTRTSDSDEEEYDNLRSYEPIDLLQDAGINATDIFKLKKDGFATIGQLF

>contig52457 Frame-2F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY70256.1|) 5e-38

MNLATIDANRILELFYVIHYSWAAPVQLIIGLSLLLQYLGIASFAGVFMMVILLPTSAAL

SSRAALISKRMLQCTDKRLKFLT

>contig52596 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66339.1|) 1e-172

MTDIQGLYSSLPKYTSSNVVALLMTAIKAETDPTNQQMMMWIMVVAIQQEAAFWTNGLAS

SRNSQVPFTILLICSIISKSQKYKPPVLFTAFECLRHLSLICEEIFFHHANSVVHLLNAC

CDFISTSAPVLRSRSAPFYLDSLMAAAYHCIIEWIVAAPLLLSKQQVVAKIIATIVDGNE

RFQSLSPNTTNMAVREAAQKLVNMLMKQHVSHTSDGSSIGPHSSGLTEKSVLEQCCSVDD

LNNIYRHCRFFSVNKNSILTVIEKPANGAQSGEAVLIMRDA

>contig52620 Frame-0R

MNLVSEFSETLQQQRDRQRDRQELRRRQKALMKDLP

>contig53014 Frame-0F|Blast-cleavage induced hypothetical protein [Phytophthora infestans T30-4](gb|EEY67665.1|) 4e-43

MGGEELALETQLLLQKAAQITQRAGIESVLESASVLPHESELEAATNALLAKLRKKKDLC

SAQHQQSNQQRLKNPNCLSLINKSGLLSPQQVLKLPVAIPAIGASRKKRDLLVKLRTQAI

QQKADSLAKAFGYANHEEHIRAIDDDEAESLRASEHPKQHKQQESQEQQESQEQHEQESQ

EQHEQHEQEQHEQHEQPNTSSILAMSVAENDEHSSDVEMNPN

>contig53498 Frame-2F

MIRDNLSNIYVLVTGITLPACCLPSFANTGSVYLSSRLLLAQNLRVHSLAGLICLVWKCL

KSSTTSSDLHSQWIPQHHICVAEPASSDKALSLLLHKSSFETDNPCVALWTSKSDSMGRF

TVAKQCIHTGERAIQAAAFAVIVRESVVPKRCHWCFAMLRQKALQCAACKFARYCSRACL

D

>contig53582 Frame-0R|Blast-transcription initiation factor TFIID subunit 1, putative [Phytophthora infestans T30-4](gb|EEY64028.1|) 9e-58

MELASMLHDGALQSPKLPTDVPASSNDETSSLYKTSASSPALDDASSPQKKAHTESINFA

ALYKRSSRGGDVIATLRALEKELKEISIRHRAQQQQKSSVSDVTVLRYAPDQQQQLLTTQ

EAGGAENAAGKEKTIQPQFPRAAEAKGKPMRRFLASSETPFAIMAATTERRNGLIDMEEE

SDAQYHKVQQLSWEDDIIWGIDFNTAAKQDME

>contig53744 Frame-1R

MWLRRSCLRSIVHDRSFARYGSKSVLSRAFSMDYSAVTARNIRNVAIVAHVDHGKTTLVD

QLLKHGGNQLSNERVMDSIDLERERGITIMSKCTRVEYNGHVLNIVDTPGHADFGGEVER

ILSMVDGVVLVVDATEGPMPQTKFVLTKALQRGLKPLVVVNKVDRDSSRLDGSVENELFD

MFVALDADDDQLEFPVLYASAKQGWAVHDLDNTDEPHDSMMPLL

>contig54176 Frame-1F

MLRVLRPAVSLQVRAFAQPLLLFNGARSLRTARGGTRRQKDHIARIAKLEAMAQEREYAQ

>contig55067 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55997.1|) 1e-50

MDNFNQALRINFLEERLLRMKQGTDFSSEDLESELAQLRIALEERDHELRQRNFSMIRAT

EAIDMLTAQLHEAQAAAAQAKDEAQREADAQLHQMIKERGG

>contig55386 Frame-0F|Blast-CDK5 regulatory subunit-associated protein 1 [Phytophthora infestans T30-4](gb|EEY55916.1|) 6e-07

MLSAIRRDLIARSSSSLAVVRCRSNSSHAQAKQMQIHRSRLPIAGPSLGDFLQASDPEC

>contig55904 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69289.1|) 2e-29

MIRKLFHVPVVLRDSRTFFSGLRSRVTVIASDEAYSHIAKEGTGRKAIVYFTAKWCPPCK

IIGPIYDELSVNYKAIDFAKLDVDDLHETTSKAGVR

>contig56000 Frame-2F

MDQSNFTIQLANSLMPRSLSQTLGFYECPEKTSILATVQDDYDFADEWNEQEKFQCRNSC

PDKRSLFSTSRWKCRLKSLSFTRSKGSALSKQFTVGDSTRQAISHLRHSMIDISSHTLGL

LKDSMPVRHRYSEADISRYGDIMDQFRSETPPGKDFYEESINKEAQETFHTQVADPIVNL

RES

>contig56383 Frame-0R|Blast-TATA-box-binding protein [Phytophthora infestans T30-4](gb|EEY53626.1|) 5e-33

MKTLLDLKTIALHARNAEYNPKRFSAVIMRLRDPKTTALIFGSGKIVITGATSEDSCRLA

ARKFTRVIQ

>contig56556 Frame-0F|Blast-actin-related protein 2/3 complex subunit 3, putative [Phytophthora infestans T30-4](gb|EEY54896.1|) 1e-59

MPAYHSTFNELQLQEACGCAILPIKTRTRGPAPPAPEGQDDIVDEILTLFRANVLFTNFE

IKGNADRVLIYGTLFVHLCLKKLERCTRKAEATRILHQTAVDTFAIPGDAMFPLGGLVRA

PSN

>contig56691 Frame-0R

MPTNMSKFQLVQTAKFSVLHPIKGAKPMKPIVGAKKAAAPAKKEAPKKAIPTKVEEDNDD

DDDLFGDDDDEDDEAAKALAAKRAEAAKSAKKEKKKPIERSQVVIEVKPWEAETDLEELA

KKIKALVVEGLTWGEGHKLVPVAFGIKKLLVQCVIVDELVLLDDITESIEAIEDYVQSVD

IASMNKL

>contig57151 Frame-0R

MLAPFIETRAAVGLSLRAHNVVFT

>contig57216 Frame-1R

MPSKPLARVPRVPGLLEELVAFLQVQQQSREVRYDFDETDLPSVVGDDCLLVLCNTKSRG

RHKGISSMNPRSASKLLGSTRCSIQRRPHSHTYYSSHPYRSLNAVVYLI

>contig57519 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60157.1|) 1e-45

MNSEELPFAPRETSNSLQQQLSSYHERQRNKQRRHHHSILFGRIIVGFVAALLLTLLLVA

LWWPAPRNMRAIKVQTLLDIYEKERNFSGVVQLSYNGETSGSRPWAVPMYHSNNQ

>contig58459 Frame-0F

MEAMTRDLLACEKAVLFFCSY

>contig58950 Frame-0R

MGEKVELGKLSICKRKCVVYIIFVVWRQKFRFHLVFLQINQTPLTLLIF

>contig59063 Frame-0F

MKAKQWNKFVCILTLHLSADVWIQPQYARHRYQEEDSHSHSKEL

>contig59232 Frame-1R

MFAKFYLPNQRQPLFLPISYSACCRVFGFSLRELGFYPHTVVASKIIPNK

>contig59485 Frame-0F

MPMLLHKQIVFKRAFLLQYL

>contig00729 Frame-1F|Blast-transient receptor potential Ca2 channel (TRP-CC) family protein [Phytophthora infestans T30-4](gb|EEY70343.1|) 1e-121

MTQSNKALAVVRKRLYKATRQGNLREMCDILDYAEAAGLTTATHGFPRTTYAPSTLFLGL

FAQSRKNPVHLAAYHGNIPALELLVARGFDVTVMDKFSRVRFSTGDLFWYFARYFVARPG

GDSGGSEEESVASLFRSTLVTPLHCAVSTGQLDAVRWLLGHGASPHTLAR

>contig02046 Frame-1F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY64568.1|) 1e-28

MWPNFLSTHFPIRWQDITSFLLPTTMKLFLPTFFASVAFLSNFGVESLNVKLSGINYTVQ

KGPAWVELSEKCKTLAEVEQDLEAIKKYTNKIRIPYSPECNQADLVLPAAKKVGLQVELG

IWTAKGRECMDQEKKMLTRLIDSGA

>contig07038 Frame-1F

MAPSEDAKAVDLAPVGAAASVDESEPSAATTRSPSTRKVKTTAGVKKDEANVKVAPKAKK

AKAKPASASKNAVENGPSYFELIVHAIKELKERNGSSRQAIAKVVEAKKDNYASHHLNKA

LRTAVEGGKLIQIKGSYKLSPELRKSPSSSNKGMKVTDSSTKSIKKIAKVSKQSVLGKKS

ALKKVAAKKKPVKKTPTKKLSAKKPSTKKLTTKKTASKKAASKKPSTKKVSAKSAKKIVK

KTAKK

>contig07157 Frame-1F

MFRKLAVCTAVLGAVLSNEALAMRQGGPSMVSPGGNNQDENSFRPTPLATTPTASNPTPD

NHFKDCNPNFPKDIGETDAPIPAVTLPETTSAPPPPPPVTPTMAPSVIQTDALATKNDGI

ADESSAHQANTQSGTASTSHTGSFVGVGVVGLIAAVAMVGTVASRMKKAREADAALATPG

DSNIHIEIRRTPTGGSTIL

>contig08747 Frame-2F

MFGFMPPAPQEHMMRAGVLSRGIVSEIVTQGPEKYTSTTARVKLLESNGVGLEKLDIPIG

LGASDAQIRQQMPPGWKPGDPVDLPLDALLHYMGRSFFTEHGITLPESWKTGDSVPTEVM

EILRQKLKLPEQRTALYEDEVVDDVESLRKKRKLEEGKGNEGVAESNSSSESSDSEEEGP

KTLSLSLSSSEEESDDSD

>contig09807 Frame-0F|Blast-pectinesterase, putative [Phytophthora infestans T30-4](gb|EEY69622.1|) 6e-11

MSDILGKGHEKYWWVDTKFF

>contig10759 Frame-2R|Blast-conserved hypothetical protein [Ricinus communis]gb|EEF32450.1| conserved hypothetical protein [Ricinus communis](ref|XP\_002529942.1|) 1e-33

MIEVILNDRLGKKIRVKCNEDDTVGDLKKLVAAQVGTRPEKIRIQKWYTIYKDHITLEDY

EIHDGMGLELYYT

>contig11154 Frame-0R|Blast-TATA-box-binding protein [Phytophthora infestans T30-4](gb|EEY69721.1|) 4e-32

MLRPKCTMLIFISGKLVITGC

>contig11419 Frame-0F

MDSRVDLLPISQHALNPEQAAAAATAAVTKGGGGGNSVDGSRSKPFSRNRQVAFSTVGTP

DYIAPEVLAQKGYGKECDWWSMGVILYECLVGYPPFYADEPVQTCRKIVNWRKSFGFPPE

AIARLSPQCMDFVRLLICNAENRLGTGSVEEIKRHAWFQGIDWSTLRSMRAPYIPPGGGL

QFDYVLKQLQINDPNKSGPQYQELVQQITSNFDEFTEPCELPVPPLIETPGTGLAPPATP

INLMLCSSSERGAGGIDTGEMPPAFGPDGKPVTFNKFIGYTYKRKATVRMALDDGLFESA

PARALETALLHTDISSHVNGDESSKLNIATVAIGDAAQVHLDGKTDYC

>contig11851 Frame-2R

MNTAALGDINEKNEAFDESNNQVLTNDVATGDNCAKSYQLGDIHPPALKLNIEAKTASSV

NKILYSESSSKSKIVPSEKGLFSCRRMIKDTRSSYYLPQQMPEFKYTSQDRG

>contig12249 Frame-1F

MLLYQSVQNKENSYNCAPMMQGLPTLYMQACC

>contig13264 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60120.1|) 3e-25

MDPLIDLASSFRPPSCQVEPTEEITLKPIELLPKDVPRPRGRPRISKTPRSAKSSSSSAT

HELRRLRAQVASMESKLHALQSQWTRSLPNTRLLAMAQHTASKKREVAMTEAAHETLQNR

LLQQQLCLATLQTALYQSPLHSSGV

>contig14210 Frame-1F|Blast-eukaryotic translation initiation factor 2 subunit beta [Phytophthora infestans T30-4](gb|EEY62989.1|) 1e-123

MADVAEKQELPPIDDAVVAPPTVPDDVAAMFDLKKKKKKSKKVKKEKKEKSEDADESTEA

TPDASSVLVQDLATYSYKDELLARIMAKLHENNPELTDRKRHTMKPPQLMRVGTKKTLWV

NFQEICQMMHRSPEHVLQFTLAELGTEGSIDGNQRLVIRGRYVPKYIESLLRKYITEYVS

CQMCRSPNTTLTRDSVSRLYFVHCQDCGSSRSVAAIRSGFHAATRADRRAARK

>contig15187 Frame-0F

MDTLLEYLSSEVPSGVAPDRSGMFLEGFIYLWWLFIDRNRPESGWQVLRSLGYSNELHLR

IPPKRLRLPPHEEDQSAQLTAQAVEFLTRLFRQFDANKDNNIAENEIEAIFSICEDECAP

WTTCSAISSPLLFEKTLVGDTLALSLSAWLACWSYVAQENPQKLVETLFYLGYNDKLVPA

VEFLKSRTVTRNAMKIERNVVSCYVYGSSESEIDYFIRSFVGGAELAIDKDQIIISRSIG

AVPDGDKMRYLFITQAISDNELETKADVILFILNPKNESSVTFVEELDQKLPASIPRVVI

SIKPEKGNPKLLEKVKEGIEKAGSCHFVDGRVECAIDAECAIDATLQLHPTSLKCYESHC

IKDEVACALVACALRPPKNARLKSSGIWLPSRKTGLFVVGLATAAFAVYVAKPEKSKGIV

GDFIARFRR

>contig15446 Frame-1R

MQWNVPISENNLYDALIQQARP

>contig15639 Frame-1F

MGNVISGLASRPTLALLLVCVGHKAFSHIIFSRFLRWYIAETPRLVYKATDGNKKLLSHC

HTI

>contig15752 Frame-0F

MESEEQHLRKSREVTLSGGSSPLCGRELVTNNDNAATAAKRNSGLYEKEVSEYVDDDYLL

ALTFQREEEELSRGSRSILPSASRHSLQLDKGNCDISSTKVPARVKGDESRFTNESESLS

SAAYRQAIHMSEEELELQRQTERNYQEKKWQEDALTRQYHQEQERLRKQQRVRGGQRRTS

SELANCIIT

>contig16717 Frame-1R|Blast-RL11A, ribosomal protein 11A 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335]gb|EED93306.1| RL11A, ribosomal protein 11A 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335](ref|XP\_002289769.1|) 3e-52

MDFYVVLKRPGARVARRKIQQSRVGHSHRLTKDDAINWFQTKFEGIVLDAARN

>contig19411 Frame-2R|Blast-myb-like DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY62627.1|) 2e-52

MEEHARFLEGLELFPSGPWKEIAAHVGTRSTRQTMTHAQKYREKNARRKCGLRSSITESR

SRKRQREHESSVEAASPSSVVKKQNSIPSIVSARKGIDPMDFHKCFVPWPLGQNYVYQMV

SIPQTEYSNVAVGSSISDPRFLSEEEVKYILEAASVLSPVAHGRIG

>contig19653 Frame-2R

MEANRLTANLLTQATDVLKNGQLMHQNEKNRMSSCQSSSTTAPSSETSVHHESEIETESL

KATTPKTTPFLAVVPKESSDASRPLSSLPKLPKLQPTAPDRCVVPNCCDYFTSPHPHYPK

EVVGRAPKVDESFQTNPLPTDLAESKETT

>contig19947 Frame-2R

MTTHRSLSETFLLLFMSSGLELLDAEQREDAMVVAADLEKCYTQLVGKKLLTGSTKKEAN

EAEQESVLVLTDLLLSLLSQDSSAMREIVTQVFRSLLPLLNRECLTTMINVLLSTREGNV

EHEDEGDEFAPITEAEDVEQEQDVSLSSDALSDAVRKDEKLLALHGEDLALAAFVGQVKI

RSQRKKDLKRARLQTMHFQLRVVDLLQVFASQRPEQSKSAIEKHDALVLSLVAPLFCVLT

QVETADSKQLVLRDRIQAVLLHKVLRVKDKLPCSESAQMEALNALRQLVELFRTTPMDKD

HSGKVASAAVVYLVRVVCTGKAEIEVLPIVHTAVFDAFTKKRSRFPRASFQDLLTKAPIV

GARLLLEPLVAVAAATNNKENADVSVARTAVDEFSQFEVFRLLTLLLRGASKLPVSADML

NSINGVCDTLKSALVRRLAPDSVHHLKAKRLKIVLLFALQIVKFWRTLEDQRAHETDVRD

VVAAVQAVNFKSPVIKNLIKHVSESADVPLVVRNGFETDKKEDEENELTRKAKPSKKKRK

RSITLE

>contig20680 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56911.1|) 1e-97

MCGTNEYMPPEMIRRKAYNKAVDWWALGALIYEMVTGYPPFRHKNRKKLHHKILNEKLLL

PKWLGADTHSILKQLLERNVDKRLGSGKSTMFQVKGVQAIKKHAFFKSIDWGLLEQKTVQ

PPILLNVVSNTDTTYFSEEFTTLDVGPRSRAGSSSANSDSKKLFARFSWVADDALSFADI

VRGSTVKEDLTAVAADGVPKVVLSETLDASY

>contig21896 Frame-1F|Blast-serine protease family S08A, putative [Phytophthora infestans T30-4](gb|EEY60762.1|) 1e-139

MSKETPDTADKVGHGTHTMGTAVGGNGIGIAPEATWITARAFDVWGAAKKSDFLVAAQWV

LCPTKRDGSKVNCSLGADVITNSYGVDRSTPEYSHWTWLQPVIDTWRAAGVYPVFASGNT

NGFLCGSIYYPGSQEDTIAVGALIGGFSLWGASGKGPSLDNACREQNLNGLTSSFRNNYV

IKPDFVAPGVGIRSAMSVKDHAFTRFTGTSMATPHVAGAIALLLSISYLPEERLKIKPPP

YKVLLQSLSNTTTRGLSKPFLVPSKCGNISYQDYPNNIYGWGLVNVCEAA

>contig22930 Frame-1R

MRSQTLKNIARWLLRCVQARDPRTSLTRQMWAFEAKLAFVKMSGRMWSYVKTLDVTFSQH

LWSLFEDLFVNLASTILKNTLMDSYDAATLNMY

>contig23267 Frame-0F|Blast-threonine dehydratase, putative [Phytophthora infestans T30-4](gb|EEY54393.1|) 9e-40

MDSDCDNEARICLSIQTKTDNEFAGVVKAINERGDMRASNLVSNELAKSHLRHLVGGRPE

NVTNERLFRLEFPERPGALKDFLEALG

>contig23670 Frame-1F|Blast-lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, putative [Phytophthora infestans T30-4](gb|EEY57866.1|) 2e-35

MVPQVAIGAIGRILKRPRYDAEDNVVPVRLMNISWSGDHRVIDGATMARFSNQWKAYLEA

PVSMLTELS

>contig23946 Frame-2F

MEAISELLGVQTDAAVAVTSAVAVT

>contig24244 Frame-2F

MVVERDSLLLRIQLRNIVAWIEKDPAKALEEIADAAAQQELAVASARAAADTQAMSMPQP

LKLPPSSYIEQTKLPQATLAYPDSPSPPPSPPVAELPCVEGATGILEEEEDEDFPASFGA

PPPSWNEHENTFNAEVSGEALNAFLNDGSNSEEDDPLPVGNSNLTNEDQEEYDEPFPDTP

QSPKCIQSCSSAKACNDCVAGSASEPIEVNDDDSDDTLEQDKPSSLPPPPPSSHSPRPPP

PHSPPPPISPPSHSLPSDHHHPSSPTIMTPQSPRLAPPVTPSLLKETKKWGPIDLSRYHP

YIAMAQRINGCLEKLA

>contig25063 Frame-2F

MVFTAGLSGIKTPWGCSGEYDYRQEHYSSHGNSGVVSLRHSTNHYTSDSVHQTGKSYSSN

NAGDGPEKTRDRKSWFPRFKSNWLGTFRSKQMFFCCECAVPPTSNGSLSSHVCRYKGAEG

KHCRCGKDQWHLAKTVEETEYNRRMEVSKALGGMRYDEAVQRLRSMGQSELDFKPLDAVA

NVGMTTQARETALLAMSSPPSSSSNPPKRARSVSGGPLLTKMYPLSQGTKPELPYVSSVI

SHVYGYENVSKHYGVYPSGYHHNNYIEGMQLSEHSEEHEHLTTVPFGDEECIGELLQGIL

EDDSRFATVSSAGLCFKPNQCARGGSYWVLYRSPGYTLPGGPTEAYDEHASIRGDPHDGR

CRTGIL

>contig25261 Frame-0F

MYQIGNRRFIANRCCVNLLIKRHRSVWCERTI

>contig25878 Frame-1F

MVEVVEMEMHDLNERIDKRQVEFEEKKQELKKMQKRLELATLHELWKEAKHLRTALHKIE

KHKSEGDAASDGMDFRSSAILLIQAEYDACMLQVESFEKKYDVSDPAKDEPVEEEDDHDD

ELIDGDENDRSDHVLRSSLIGRTTDGSALDGNVEDLEDSSSALKAIEAQLYELESKIEIA

TENEEYELAARLDEKIEILKERQQAIKVSNPVTDACENSVDEADEEDEEESMRDDLSDDE

DEMEEEYGHEEMVSPRIEEEKVLSFETNEVEAVMLKEQVETSIENKKNGSVPSHQEELQS

MREEERYSGSQLEAGDSSVTVPHKFKGQIDEITCSSAAEAVDSRMLEHILPQQSTHTSKA

LFGGLQMSPNAVTNATEVLISKPNDESLEREVEASATSEIFSPTSSNMKDSFFGNPDLLT

QQASQLAHSASPFLFNGLHMSGGLSVSPLSSSVLKNVLSEDGERNVDASLIETNASASDD

VFGGLQLSSSVVTDTLMNATRAFEVEELPLNGATSSDCAPKEIPTDMFGGLKLSSSAPSV

PMTASSETFGDSKLCNSVVTARSVSFAKESLKEEVDGVKRDEEGTRMSIHELTEHETEGL

CAEAETTMTIYEASADDTQVLNGQVEDTRKHDATQL

>contig25892 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58514.1|) 1e-167

MNSVCIVSENHEEGSALVNVEAGARLGWLYTNLDSLGGYNFNAGSCPSVGIGGHISGGGY

GMVSRQYGLAADQTYEMRVVLYNGTVVTASSFENSDLFWAMRGGGAGSFGIVTLYTIKVY

KVPKVTVFSLLFDVAVRGQVIRSYMDYFLTADSKITTLLSIDVRSARIVGQYLGSQMELD

TMLNESGILIDGGLRRIDRRDNCSQLAVKAYIWAGTCDDLSSLTVPTHLTLKDKSYIKIK

GGYSNSKIDDNGILTALNWIDKLPNTSSTFLQFEAYGGVFTTQKNDMTPWAHRNAMWSVQ

IVGDAITAEPENSPSNEWIRGIANALDKYLDGGNYQNYCDLDLGSDFGQRYWGAENFGRL

RQIKAHYDPLNIFHSAQSIPLPS

>contig26509 Frame-2F|Blast-COP9 signalosome complex subunit, putative [Phytophthora infestans T30-4](gb|EEY63010.1|) 7e-13

MISPKPIHSVCRTSSRILDLDRLNTLSKAVLHLEQNTLLKLP

>contig26866 Frame-2F|Blast-isoamyl acetate-hydrolyzing esterase 1 [Phytophthora infestans T30-4](gb|EEY53786.1|) 1e-111

MSQTLSCDRRPVFYFIGDSITEYGSDPEKCGFITILQNHYVRSIDCVNRGLSGYNSKWVR

EHGMPIYAKELQSQYSASFVTVFLGANDAALEHGNSHEQYVSLEDYRANLQKILRTVQPL

LAPQGQVLLITPPCIIDSVRHNDRSNASSAKYAKVCVELAAAENVHVVDLHTYFNKTFPD

EEVRKTFFVDGLHFSEKGNKEVGKLLIITINSMFSEEELNRFNKWQLPDWHQFVPHEEEA

>contig27775 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70136.1|) 4e-32

MADDDIKQAFQALCGDYGELLDEAAHVTQSADERIGLALFKIDEACAAADNLRLDAQQVQ

QQLLGELLSNCHELENIFLQINLI

>contig28042 Frame-2F

MSAGGKKRPRADLLSSLDAIFSSVTQPKASKYTALASSQSMSKGIVQQAYQHSKRKRVNK

KRQLGSTTQESTNEANKKEENNEKQPKKNDLLYEKLDLDLLAIGLKDCSLQSQIKLFSKP

HAYHETLKSYLEAVTKGSKASSTAVDSLKNKVLSLDNPFKNTAADTTKKAIARASLKQTH

KLISARQRRKLGLHVLGKEMSYCHAEQLHRIWTGYVSQVIESDIATVQPVVEEEQRRRNA

KLQTKFKYLDLSGCRA

>contig28877 Frame-1F

MRIPCNCRSCLTVSPSVSTTNKNKAWREGNLVECPSCNGVYPYMKLTL

>contig29449 Frame-2F

MYMIGEGPGVVDCRTKVEPVLIVMLLHPTEPHGVPAQRKLAKDH

>contig29786 Frame-1F

MELARVDEANPWLLNTAKKSTRRKKSRKNAKKRLPETDVGAAIESLSREVQKETDAKVTK

RKREEIHKTVKNAEATKKQKQEAKVAGQDELVRRAFEFVAEDDDELAHEKNRLAEQEVDV

KKGAEIAKLVGMSGWGSWAGDGVRVSKRQLLREQTATKIAKDAKQTALANRKDARLERVL

INEKKDKKAARFTVKDVPYPFTCRQEYEAAMRNPLGSDWNTSVVTNVLTAPKVMTRAGTT

IIPLVLSKDDRKMAIKELSLKRKAKF

>contig29900 Frame-1F

MKRSLVRILDLPPENLIQSGKKYINFKEYKHSITYPIIWSNLSIDADATQVESAPQARRE

ELRSLNASFDNESRPSPCYNRFHQINEVSLS

>contig30094 Frame-2F

MGDDKQNTIDTSIKETHDSQDHDSSTIRSKGVASNDLSVNSGDGGTIGLKSFRQPGTVTD

INTSSATFDTLGTCSIIAIVGVVVGIVCLVLFYAISSRKTHTDANKDSPLPCNYKTGALS

VARLSQAFMPNTFSTKCSTDPSMESVVVPPYMSSRKDGNERTMNYNTTIAPTYCDQGGG

>contig30371 Frame-0F|Blast-ser/thr kinase [Phytophthora infestans T30-4](gb|EEY57890.1|) 5e-74

MIVEDLTSSRDNFDNIVQYYQAWTENGFFFMQMELCEGGTLQDFIMMRNRQILPENYLWS

IIRDVTGGLKVLADHNIVHLDIKPENIFITGDGRLKIGDFGMAGKVMTSTITTGMLSNLE

GDAKYMAKELLSSADRRPSADIFCLG

>contig30418 Frame-1R

MVTIGALSEAAREIVGSGCAYVSTTIKEELNERNVVDTNDKAIAEAAERADQTSNDEVEP

DKKRKKIRAAHYTQQLISRDLLEKCTFFTELRRLVFLYIAIVFHDCRGIDGIDKMKNSNI

LTDAEYDELHACGSEQKRDVKDKESYRAIIRRTPHKLRATITQLWLKRLVQVATRRGHLT

LPNSNNLQLKIAQLPNLYTTVFTIANVPIPFNYMQYLQFLLVGYMLLYTFVIVPNSGLYT

PIWVFLWGTFLFMADEIAMEIECPFGLDANDIDLEARLLQIEEELTVLIRSQYYFMTGGT

SLAHISEKANVDNWGQSPNSELYLKPTTPGSFSFHQGRLSPSNMSLVQQDSLPEINEYTA

LIHDPVDYQKREMDKYGSAYIVA

>contig31439 Frame-2F|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY62010.1|) 2e-11

MDESDVYVREEGDRPVEHSPRGRYIRFDIRLGTGA

>contig31905 Frame-0R

MHRYYYPCYSRGSRQCVARESTELRLRLDRLLLDQRSTWNNKTGVTSVSIRLLFNSPSIA

HLTNPLIVRNELKSLVVIPRTATPIQTCRTKTTRLRPRF

>contig32386 Frame-2F|Blast-glycosyltransferase [Phytophthora infestans T30-4](gb|EEY68934.1|) 0.0

MQCGKGRDVALSQISMFEGKLANGAGETSLAREAHRMGQFMDFFRLNSMYYSHTGFYFAT

WMTIVTTFVYMYCKVYLALAGVQQQIVFDMNSTAVIADNIENNFDGRVFRDLKSVLNTQF

YIQAGTFLMLPLMCVYFGEGGFVRGMTRFIDMIITLGPAFFVFQVGTTMHYFDNNIVHGG

AKYQATGRGFKISRETLVLLYKAYASSHYRKAWELIGLCLVYMAFGNFYICQTDASANDN

TFASDYCDTAQGYGVQTFSVWFISILWVVGPFMFNSDGLDFRKTKVDINQWCMWMFAPED

YKDDDPANTGGWIGWWKGDLEQLHNSNMISRVTVIIRECRHFLLMFYVATLETSDVMYVA

YSFGAAVVSVVLLGFFHAIGMSMRSIKPVTRAMLYLGTMVFLVVAYFLASKIVMDWTFKY

AMSLFFAYVAALYGINECFRMWSFRHSSIAGIAVFQQLQFLFDFIFCTGMIIPLVVMSCI

PFLNVIQTRMMYNEGFSKVMSASSQYAFSLAAFMGVLGGIGVGWLFNLLSTLEQSASFAS

YVVTYDGVMDGNLGDGTTTFVLYGSCVMGTIIAGFLNFFMGRRLAIVAGGLFSTLGMVAV

SANDDLRSMLLMPGICLLGLSCGILLPSLAIYIFEISTKEMRGKSVLLLGIGFVSGSLLG

SIFASVNQLGWIWQTFAACIVIALVAPVVNVFPESPYWVLDRKGWEACEACLVILRRKPD

VQEELKVMREEETVDEAGAGSFKFLVCLALMLVSSLTTGFLNAFISYKGASEYTDQDHLF

VNAMALQVSGAIIAIFFIDKLDHKSILFGTLIPIAICAGILGFNEKSEFLGASESSGVYV

SLVVMLMYFFMGLGTSSALWSACVGMFTSRSRASSTTFLFAIFFVA

>contig32841 Frame-2F|Blast-structural maintenance of chromosomes protein 4, putative [Phytophthora infestans T30-4](gb|EEY67708.1|) 1e-160

MAIEGVDATALTAAMKKKVMDTMRTEEEIKAATEMEAFASDAQAVNTEQTTSKAQPVATE

MIETLTPSAQEAPLAADTPAVITPLKAARVKRLMITKMQLENFKSYAGKIEIGPFHKCFS

AVVGPNGSGKSNVIDALLFVFGKRASKLRLKKVSELVHRSANFPNLDMATVSVFFQEIID

TDDKTTRSIDNEENYTVVPNSSFRVTRTATKSNVSKYFVNDRASTFTEVTELLQDKGIDL

DNNRFLILQGEVEQIAMMKSKGTDGTNEDGLLEYLEDIIGSNVYVEPTERVWNEVEQCNE

VRGEKVNRVKLVEKEKTHLEGPRAEALEYLRKEKEVYMKTNILYQLWIQEASKNRQLCES

KRDELQVKYKAEQARMDKNREELQSVEAIYQRVKSEHDEVAKQLDEAKAE

>contig32948 Frame-0F

MVKKVCLLKAVVLRRRLGYYPLSRLPTSPDEALLATYCAACFGSFSLLRKKYYCRLCSHY

TCRKCSDLHDVEITVGLIERHRVCVSCVLRVGTCVFTMPSFPPLTSPTVSDEDWVSARAQ

LPLDEFDTPMMDQDASEDIEDVELVHTNQVGKLAGFVSNLLHSKQDKKREFQKKELAVRQ

KQRLQLTIDDLNSWASGPTYESTGTPKESISLLDSFCTSNSSASWSSPSPTEA

>contig33037 Frame-1F

MRYPLGLKGLAHRSDFGHLGLSKCCCADSHCWRLLRQWQPRLTKCSRSASFKLSLRRYAL

SPRYQGLKAFFLMFG

>contig33172 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66616.1|) 9e-08

MATSPVHSSGHDSLLKYSKITLNTALTTAPVMPSLSDNLLQRV

>contig33198 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63172.1|) 1e-84

MPSLNQLLCPGPMENLRKSAFDNNFDTETSEAYVKHKSRRCSFPACQKTAKRGGRCISHG

GGNKCTKVGCTTSVVSRGLCVAHGGGKRCQTHGCSKSAQSGGFCWVHGGGKKCGYQGCSK

RAQSGGACIAHGGGKRCRIDMCNKVVQYDGLCVGHGGFRRCAEEKCNRRAMANNYCQQHG

GSSICLLQHCCKRAVRGGLCSLHKTKTLVPSPTSRQVPSKDQWHDRLNVDERVMSFSSDS

RASCATETVMTRSPSPVRSIAQMTSADASRALGYSALLNADIQLPHLKSLRSTRPSLLAQ

HSSFNHEKQHRQPPNVMPLLPSIHVLQDYQRRVSFTEKPLYITQGLTNLSPSISSDFQHM

ILQDRYKHSYPTMMDNQEGYNAHNYYA

>contig33802 Frame-0F

MPLKNVVATALAALMALHDVGAAFYVPGVAPESWSAGETVRLNVNKITSTKTLVPYEYYY

LPFCKPASTSEQQENLGEIMAGDAIMNSLYNMQMEKDAICQVLCKPMKYTPKESKAFIDM

IQNEYYVQWVVDNLPVLYRDPTDLQQAGSFKRGFPVGEVDENGKYLLYNHVRIIISVSPD

PYAEPSDGPKWRIVGFEVVPTSIQHSFENEPLPGQELDSNTCGKFVNVEEVSQGRYQYLD

PDNETTVLYTYDVQFVKSNIVWEERWDRIISSKSSNDQIHWFSIINSLMIVLFLTGMIAM

IMLRTLHRDIARYNEVQTTEEAQEESGWKLCHGDVFRPPQYSPMLFSVVVGTGVQVCAMS

ASTMVIALLGLLSPANRGSLLTTLLLLFVFMGSFAGYYSSRTYKMFNGKDWKNNTILTAV

LYPGLLFIIFFLLNLVLWGKASSQAVPFGTLFALLVLWFGISVPLVFLGSYFGFKAAAIE

HPVRTNQIARQIPEQVWYLSSPFSILVGGILPFGAVFIELFFIMSALWLHQIYYVFGFLF

IVLLILVATCAEVTVVMCYFQLCAEDYRWWWRSFLTSGSAAVYLFLYSFLYFSTKLNITA

FVSGILYFGYMFLISVTFFFLTGTIGYFACLWFIRKIYGSIKID

>contig34151 Frame-0F|Blast-alanine aminotransferase 2 [Phytophthora infestans T30-4](gb|EEY66057.1|) 0.0

MLIRDENDVILAPIPQYPLYSAAIAINGGTLVGYYLDEINAWGLDVKEMGRAVKEARDAG

KTVRAMAVINPGNPTGQCLSEQSIQEIIIFCQKEHILVMADEVYQENVYAQGKRFFSFKK

VLRDMGKEYDNVELISFHSTSKGFTGECGRRGGYMELVNIHESVKDQFYKLMSVNLCSNI

EGQLMVGMMTNPPQPGDASYKRYREQRDGTLQSLKRRAMKLVEAFNKLEGVTCNETEGSM

YTFPNLMLPLKAVEAAKEANMAPDAFYCTQMLDMTGIVVVPGSGFGQKEGTWHFRTTILP

PEAAVDDVIEKMATFHAKFMDMYR

>contig34238 Frame-1F

MVDNTFGLAWSCPLCTYLNADTTRKRCEMCDSARPELPKRVRNFPQWLPQPMKYVKHESN

MKGVPLKPWLDPQDEIDNSENEDIASVNSSALCIFKTNQFNKSNSNASKTAAAKSRKGLW

IDFYAPETAGDLCVSKKKVQEMYQWFEQNALARSGVIQKRLLFVCGPPGSGKSTAVRCIA

RKLNVLIKEWEDNSAAGKLKFERMPHVPVEDNFSEFMYRSSAYAALPISTSRPPYFADSD

RRLACSQRESDYIRVSSVSSRQIVLVESFSLAWSNDSLLYEEKLKRIYQRVIASAGGSQY

PIVCIYSASRGRKVDLDYLSKKFSHEVMNSPLTSVIYINGVTSAQLKKQLVCVAEQENFK

CKPSVIHNIIDRCNGDMRYALNMLQFLQNLNLKTCQIEPANASMQRAQGANALKVSMNSS

ELQCHTRDFFLSDFHVVGKLLHGKVARDKFAQLSSSKRDASNFDYDQIFDRCAMPLNRVL

ELVHENSIAYFLEVEDLAEALELMSLCEVIIAKSYNGANCLKVSKRSRDVAQAVLMHTVA

VANNNPAPKAFRPILRPRTYSATQRIVTRRKDMLHATRGEQSGLQFAFTGDVFAFEVEPF

LSIMDRVSNSSTIPNAGGGTNGTESLLKENLDEIENSADEW

>contig34357 Frame-1F

MPLRRWSQSKRHSLVPNLHLLIVRCQAHCCHLQTVGSSHICKWLYATCHSYCSKAEQ

>contig34735 Frame-2R

MDSSWGGVAFEMMTYVAEECPGATIVVLGNDWSYPMTADYDDAIFRVASDCTKVEARKQI

NVASSVALLSEVSQLLVPLAMSLSSLPRTAFSHLGVDRSNCADVSTIVATALELALSAHR

GKPVYDLLEGFRPGMKVAELAASFPVATDPTQLLRHLNASFTNVNDSNNSIQDPFHNCSV

FPALHQADRLHKTYYRRLSFRGFSYNSSLRSAIDSFAVSPQDITLRWSNTSPLAIPVSYR

FPTLQTLSIDGISQLALTSKTGIYLSSLAQSAIRSNKRILYEFTRTGMSPDALEELNSTL

ATLSDKYAS

>contig35686 Frame-1R

MSKSLKNFISVQEFLQNGNTADQFRLFCLQYKYRANLVYSQDRIRDAEAMIARLRGFVQS

AVTYGENLHEASSSVSKQYQIKRCEQIDLNLLTML

>contig35800 Frame-1F

MKTSTPPLLVLSEQDSELLCELAETLTVHNIQQYNTLIKTKEGFADCRRWKELRRKDGVR

IYRERNRHNGLPNTPSLLLLGTINGTLDDVMYGAVASTDEAIRLKSTCTLDGVIDSKVLH

ELVHPTMDDPFHHIGVKWRLYNNQRDYISLDTTGIAHTVKRERIGYVISHSVAFAQIPG

>contig36492 Frame-2R

MTIFAQIYVDGNDKVTAFIVERASGSVTKNKLGTRGFNTCQVFFDN

>contig37114 Frame-0F

MEWIQVEIRSVGTRLQLTWEKRVSIIRLIALRSLSTVGQNRHAFDATLFDESVRGILSLP

LPGVLPFLPLLLGPSTSRFREKVLMDINVKVKTENDVQQQILLLKKHWAEALLDLSLTCS

VTAEVDASENDTNDTTEQDNPYGRAYSIDASKTG

>contig37222 Frame-2R

MSDDGKLTEECIPKSGSDLSQQQPLLQQQLQQQQLQLQLLQFQQQQLQGLANQNMSPAEV

AAFQQQQLALFMMPMFPLMMPMQQQNMSISTTAGTSACEETSTEAATTSEETIESASTSA

TGGDVSPSYQTATAESLGLTPPFVGTDGFGMLTGAPNTLLNIEEMPKRKRGRPPKKDVAA

RVKADAEKSLKQSFPMWGYGLPMSLLPGFSGMMPGMSNPGAVVKDHSAMDDQTIKEEDGG

SDHPTKMAKKKQRGTG

>contig37529 Frame-2R|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY54484.1|) 2e-87

MSGVFVSVALGLMLLKLYTWVVVIRPHSSNVLNIISFFLITLMFWSYARAMFPRPSNRRP

SNSTEQIRRYCERCDANKADYVHHCSVCQRCVYRMDHHCPWTGNCVGWSNKKFFLLFLIY

TSMSCLVFFIMASNLVWDARFHQYEALLTFSWFMTLSVGLLLLGYFLFHLWLLRIGKTTL

EFLAGDEGEFMDIAFMQNVKVYFGQDVWTWW

>contig38537 Frame-2R|Blast-COP9 signalosome complex subunit 1, putative [Phytophthora infestans T30-4](gb|EEY57774.1|) 1e-178

MGLYAELLGDKATDEASYIENVKHTSAQQYERLEQELNSYKSTMIKESIRMGHDDLGNFY

YELGDLPAALKSFAQARDYCTTDKHIIEMCLNVSKVALHMGHFGHVTNYLTKLEHVSTSQ

SDVILKSKIASAFGLVALHDKKYHTAASKFIECSAEIGASYNEVLHAEDIALYGGICALA

SFTREELKEKVINNSSFKAFLELLPWLRELISAFYSSNYASCLQALEKMKPELQLDLYLS

EHVEILCKEIRNRGIIQYFFPYLSVDLHQMAQTFSTSTADLEIEICELIAAERLHARMDS

YQKILYAYHPNQRAATYDRAFEVGRTYAAESRNLLLRMSLLQNNVIIRDA

>contig39084 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63526.1|) 1e-128

MVNAVRSQLKLGPDIAVSLVQTDSVRQHEIQPHRTLGECTIGAGPEHPVLVLQTRVVQFD

KKKCSTYIKLQDDNSRAVQVAEGCGSVLGNCDVNCGVKYWEVELISARFGEGMFVGVAAP

DLALDNSVVGSGVCWGIICATGHKFHETIECYADPLKDGDIVGVLLDKELGRLSFFVNGR

NLGVAFRGIQARNLCPMFSLTFVGQQIKLRPTALPPMP

>contig39408 Frame-1F

MQFDYNGHERVVGYQSRQLKPAIELSDPRQGTVGYAVRSRQNPE

>contig39501 Frame-0R

MAPHSSTCRSVLAVPRALVSQNKRRFQQDGFDLDLAYVHPRIIVMGYPAVGMEFLFRNPR

SEVQQLLDERHDGNYFVYNFCDESKRSYASSVFAGRVKHFPIEDHNVPSFQTMTTFCEEA

AAWLYENENHVVVLHCKAGKGRAGMMACMLLLRMGFSSSAIEAIELYNRERVHDRCGLTV

QSQKKWVNYYAALLAQNAASLSAIQEPAFVIKKLAMVNTLTAAKPSTLRLRIFTLRLDEH

TKVLLHQQSGSNEFYLHEKVRGCVLLEFYRERVNGCLRAKHFKIWFHTGFLNPDSKTGRI

VFSRLEMDCRDKRYRLLPAAFELEMTVMRLDHKYEEA

>contig40549 Frame-2R

MLQQKYLMLAQLDLVYFRRVAREQSRHDDEHGFWTSLASHSMDVIGALQQLLSTPGFVAV

ISELLHHDNSLVRKKAMQLFNERLQEDCDALTFGEALLFIDMLDEFDAILRNTQGLENSA

NIQTALLSVDILARYFAADHAKRFQHILPTIITYLEQDVSNSPFMTLHLSGCAFVCLSSI

CRAAGPMVLPLLPKFFPRLLSGIEYCTSSANSIRGIKSVLQCLLKALEVFTDKIPQFLGP

QLPAVIRALLTPSLLSSAPMNAEVLLSVDCCFLNLCNHVELRQLLPVLFGAYENVLTLKS

DTSVTRLFAVVGTVVSNLGSSSVRKHLPSFARFFVTALDARRVHLSKLEDLEEVEEVMLN

CFVQFILKLSEKQLKPLFFKLVEWVQARIKSSDKLGDISRRISFFKLVVKLSERLRGIFV

PYYAHILELLTLALRESCKSVMQKPPRSFENNESEDDDFFTSNDEPAAKRAKTRSISAAD

MEAERNCNVLLLTTAVRALDGCFVHDNDGFTEKDRFDMVLAPLVDVLDVLKYDATMREFV

LETVAPCLANLAWAAKSDILWKPLHYAVLMKSRGECALVRLAALVTVEKCYQVIGDEFLA

MLPESIPFLAEFMEDTNDEVEKTCHRVIKQIEDISGESLDQYLTT

>contig40611 Frame-1F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY65780.1|) 9e-35

MSKTELVKTGALYSQLIGLEKVPLLQRKTLRAMGLMGTEGIIPATSTPNRVKGRDNNAGE

TRVPSRTNGSSYSSLQNRKKGKKGNFRNEPGQAFNGKKMKPYRDVHTHEGNSSD

>contig40800 Frame-1F

MTANQVHSGSNIFRFDDNVQFMTRELRPLLEAHREALVKRCGEAWKSHFHVTIAY

>contig41238 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67179.1|) 2e-09

MWTSLALTFISVSCAATGITSFTLWRSWDLQVSSVRWLFFIF

>contig42529 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY53343.1|) 8e-17

MALLPRTPKVEYARLRNLGKRVKVYSKRLRRIWPRIASFLTPRDIFSVFSTCHQLQRLLD

NDRV

>contig42644 Frame-0F|Blast-SCO1 family protein [Phytophthora infestans T30-4](gb|EEY55526.1|) 3e-15

MASRSILAMKTLSRAQKARSHASRRMLSNVPDLIKRTEKFGPITWSGLALAGIVGGGAVY

YYYSEKDRLQTQ

>contig43045 Frame-2F

MSRRQALHMSSERRHTHTGVNVSAMATVPLNCARRLSLDQTAIASTIYCEGYVHLKRRNM

LPWNTRFLVLSNSHLQIFPTKQDACLRCNILETLEIVSGRIAPKHELGIELTTTEGRELL

GRVLCRADQTQWISAFYQLAMRSVVRRVKSESMDVEGTAMLVDKRRVSFFKSVQVRTIPT

VPTEQVSKLFYSKKDVQKFSEQASSLFSRTEDAMSLVFRKPWRKQVI

>contig43478 Frame-0F|Blast-WD domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY69409.1|) 2e-55

MAASQRSILCDRPFITYPTRDRLYGLCWRPDLSSLRIAATTFIPGEYANKIEIFHPTANQ

NEVVSALEIDHPYPPTKIMWSPASLSSHVELLATTADFLRLWTITDSSIELHMRFA

>contig43492 Frame-1R|Blast-predicted protein [Nematostella vectensis]gb|EDO45823.1| predicted protein [Nematostella vectensis](ref|XP\_001637886.1|) 8e-06

MNYITDFHVSEFPTSLRILRLAGNPFVKHMPAYAHLFFERLPNIMQVDQYRRPLSHSLTK

VHPVDESAMNVAKSPLVFSSANDQKSDLLGEQEVATPIFNLTDYEKQHNDRIAKWKLQLT

TLTSRT

>contig44004 Frame-2F|Blast-Sulfate Permease (SulP) Family [Phytophthora infestans T30-4](gb|EEY55885.1|) 0.0

MYFSHTITPAPAIALQYTALEAIDAKLTVCEQYDASIGFGIRRIARNLRRHIHTPQLSTK

NTLRSLQSNVKDSTQYYWQNLVIFQREVLCGVAAMLLMIPETVAFSYAANLDPLNGLYAT

GFLGLSVSLFGGVPATIAGAAGAVAMVMPTITSGTGSLAYLTYEERLQHLFVAVTIAGIM

ELSFGILKLSKLFAMIPRTAHIGFLNGLALMMFLSQKTTIQVCKDDIMRFGECEIAGKLE

YMSVSSPTTWVTISLVFTTMVIMHFFPRTPYIGHLIPPTLLATVIGVGFEFGINRPFLGY

NVRTIGDTSPLNGSLPTFAIPKFGNVQDWGVVLSTAASIMAVGLFESLMTLQSVVDLKKE

QLSQTATRKECIAQGIGNVLCGLFSGMGGCSMIAQSNGNILNGARHRLSSFMGG

>contig44233 Frame-1R

MQMVGLGGDKMKDEWEWPADCKAQREMESHLRCEICGDFFHGPVLLACSHTFCSACVRRF

LQSKGANGCCPSCKQPCTSRDLVPNRALEQVTLLFENSKQELLKRLQGITVPSSATCTSN

AERGKIKKMKHTPERMPLMSYSVMRDKEVRKLLDSINIRIPTKNRDEIIQIHK

>contig44369 Frame-2F

MAIHELSVVDLFVLHVTQKLRFLRALLETSKLTIEVMYGVVKAVRGEGAKDPENLKLLLQ

IAKLRPYTISWSNVLDYFVLEDFHDLARRCSVYGNCVHYGYSMNWSTQVYGASLIDYNPK

QCKEFIDTVLNVALGIPDSSNSIASSFNFHQAFKMDGLDKLVNYPFRENPLNSTGYALAH

IYKQHWIDFFLEKGQLSAAAAHRLGSFCTSTNSGLKKGT

>contig44387 Frame-2F

MALTTKSAFRPCQNEGADAYYNRIAAHLQTDMQASRNTSYSAKSLTPSYIQNILAQVE

>contig44439 Frame-0F

MFCAVPGCNKRYASRSAIRFLCLNHLPNDQVSKNRQNLIACVNENEGLVSRAMV

>contig44552 Frame-1F

MKETREDLNVAERKMHPIHTIFTPYEVKCIRWNPMNEDEIACSFTNRNEIYVFDLRKFPD

KPYKVLKSLTQPSSGYNDFVYLHPIEITMPNSRHSKKPNIKQENIIAGDMDGAIRMWDAR

YPLRPVFSFLAGSLPINALVLSPNKQLIVCGNEAGMLMTYDIKHKVIPAFGSKPVPQRKA

SFNILDMIKPYLSAALLESVLLSSRYGSPGIISMRLVPESEAHVLCQLRNDWVVVLDYLN

GSIFKLYTLNRK

>contig45120 Frame-0R|Blast-aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY67916.1|) 4e-33

MTRVDEKLSRALARRRTIGTLRTLQIPDEQFLRAADFYSNDYLGFAHSQPLKQLVTKRQK

ELQRCHTRMLGATGSRLISGNSELFMETEAKLAALYNR

>contig45155 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56320.1|) 9e-31

MAAMGCENAGVLDAFSDFSASSDSDEEVLHVMDPSDPRAHRAALSIVQSTRAKNTKPSPS

QKSSRWDFDNDVGEPISVDSNATYSKREADIVINENDATEVSKPKVGVTCPSGPRRGS

>contig45418 Frame-0R

MFIQLQFPHRPGFPVQVTLEGQLMWREFFYCYACGTPNF

>contig46037 Frame-2F

MNMKRRRRRQSKLSQEEMKIARDAFYNEATNNLQVVGARPRHIIGSAIFENDDAD

>contig46198 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55822.1|) 2e-81

MNKMETTLKIMEPIQHDFKALLATDHVIYVQSCREIFSSSFYPLSDSEVRALIANGNSAD

DWSNVRKVDAHIPLETSRVHQNSFHSRVVFGQFSDSFQHDVDGIPFPCGVYNSTLSNVVV

LDNALVKDTQVLRNVLVAARASVIHCGSVTGPKEKSMVSCSNGNLIHVGVELGGRDLRIL

ADLPFALGSAVVTTRENIEFLKAYDSFVEKYVAAVQAPMAIIASNARVRGCFRVHETFVG

DY

>contig46464 Frame-2R|Blast-dynactin subunit 5, putative [Phytophthora infestans T30-4](gb|EEY58087.1|) 2e-88

MNPFVEAAEKQFDPKTYIHTTTGNKISRMCTLAGAQNIHLRGKTIVDSGAIVRADLARVS

LGKQCIIRERCVIKPPTRIVSTGLAFIPIKVGDYVYIGEDSVVEAAMIGSCVQIGKNCVI

GKRVIIRDCCRIEENSVVPADSVIPPFSRIGGVPGKYLEDMPEATQELYISQISRYFDNF

TPRTN

>contig46802 Frame-2R

MHRGSGIYQDSDERALCKSGNTSGTEQPYDAYDYTA

>contig47311 Frame-0R

MIDFYPKALEGTDVQTKFGSGIVIDLRPADAIYTVRLHDPQPAGKSNVVFVHESDLHRSR

KIAVTAANVRDKLKIMAQWRFGERIVVAHQHHAEEPNSAGI

>contig47841 Frame-1F

MIGRHRVVDELLFFSIPNSRLLSQIGYFDKNNVVPVAPRKTDC

>contig48062 Frame-1F|Blast-L-aspartate oxidase, putative [Phytophthora infestans T30-4](gb|EEY65025.1|) 3e-87

MTQLELLAQPMLSAPFSALESCVKANFTIPRHRLTGSSSLRRASVATANYDTIECKALIL

GCGVAGNAAALRLANQGVNVTILAAADDPNHCATYYAQGGIIYKSEDDTPALLSSDVHRA

GAGVCDDVAVQKLAVEGPGRVEELLLDVAKVPFTRKDDGELALTLEASHNRARILYKADH

TGRAISTSMIQAVREHPNILLLPGRS

>contig48116 Frame-2R

MPNLGIAQSAQFSAIDTAVKRLQCACRELQLSSLPRVMTGRENERDEIYTALRSSIEHQS

AGGPIYISGLPGAGKTSIVKEVIRTLEKQRDNAKLCEFAWVEVNGLHMPRPDVAYSVLWK

ALQPSKTNKQEPQPLRASMSAARLCEILQREFNSSSSTRPMLLVLLDEMDFMLAGKNQVL

YNLLEWQTSASAKLILIGIANTMDLPERMPAKIRSRLGGHRITFPAYTRAQLENIIKQRL

FQLDIFSDEAIQICAKTLAHQSGDVRQALSLCRKSAEVCLHRLTKLERSTAANAKDELFV

TGEDLHVAQQAMSVSAPMSRLGACSKFECTFLIALQMEARSIATRGISKRGVELEAVIER

FAILCKTHSFEPIPRLRALLFICDELERSGIINQIAIRTSRYPLLELRCSHQELLDVFIM

HPVG

>contig48181 Frame-1R

MRIYVLHHNVDRGDWQRRCTLLRHEVTHYRRDQMVVKSENLISHSLKAIHLNI

>contig48732 Frame-1F

MISTAQVRWSGKRFLSIRRSFNKWGMLYLFPPPPHLRISFMQD

>contig49685 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54879.1|) 4e-20

MLVLVGDETGLLKSIVLETKEQRILSNREHPQARSRGIQRLCWSSDGRDASYCENNVVLA

RANGIVESYE

>contig49829 Frame-0F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY70221.1|) 9e-20

MADSLNYVQRLWVFAAPPISTPGKEQQQLLKSYLHKCADNIRSGLLVETSMTFIERVVDG

LSVKAKLASTMSGD

>contig50100 Frame-1F

MMEGDTVQRHVHLDTDSEIDEIKRRQKVNLSQATVYAATDGLIKEDSSAVQTDEACNSSS

ILGDEKKNSSILSAPMTSAPNANENTVALKNSDKKDNDPCLQKTSTNSHAISKAIDVTDS

SELR

>contig50175 Frame-0R

MAFIFSTCAVAAALSLVTAQPSFIYKFDASLAAGIDGSIIVKYASADSSTATITANLDFS

GVDQSKIAAFDGNCTEAVTSWKWHIHTKWNSTQTSDSYKQCSKAATDNHYDP

>contig50441 Frame-2F|Blast-exosome complex exonuclease RRP43, putative [Phytophthora infestans T30-4](gb|EEY54228.1|) 7e-26

MSSAAFSISYTTEGQLCGMHKAGGSTVMPDVLEQCMLIAKQNAVALARLVSRAL

>contig50650 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59076.1|) 5e-53

MSKYFRKPQSQSKWLIMTSKENGEGGHLAVLKRSDGEFVYVLGSKNTHLVAQSIEDIAKT

HEIQTKDGNNSQFFAADLIATAIFKMLLALEPAKQKLLCEFLWQTRTTASFEVLCPRHQH

VQLLDYISDDTPVFYGL

>contig51064 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67581.1|) 1e-12

MTMLVHRSRRSIWQIAVRATNCQSQSALWCMPRSFLAQFATMSPRAVSLKNDDVSAAAES

EGPPMSCKLTTSTIVSNPMNAHSTVWEYAASITNRSRMNDRTKCPAEIDRVSFRMLLAEG

MRHGRVSATLRQKILNFQIFDSYWSDQELVMIVHALTKINRCDMALKVLFHQIKEP

>contig51437 Frame-0F

MAIPSQTFSTRRFACRSRDILALLRRLCVSRC

>contig51598 Frame-2F

MMYQPRMFHKLHFDQLFGSISLTFCFSPHQNL

>contig53174 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62398.1|) 1e-19

MLGVYFLGLVLFDELTSFKNGKTRTKKPLKMKRRRRRSSVEQRQRASLSVSTRKAKSPCC

AVESSAPPSPHTSQ

>contig53479 Frame-0F

MMLFVALVMVCIQIGWAVLWVLGSLGILFHRNGLKLERTCMATKCELIFNSTATLGVLCV

ILFIYFWITCVFRNIIGVTTAGTIAAWMNPINTSCITMKAWLRA

>contig54012 Frame-0R

MCDDFNARTRPRRRSRSSNAILISSIHSKTAEFKATADCSDGSVLTSEVTELRRCASADL

DGRERRLSRSSFLPFSQSDGLCALPRFLMMDIDAARQSIDGLSRAMSLDEDNVSDGGRLT

RNMLEDSTGEAERYKRASSLDASPPLPPDSTISAEEVIRESMASAHSLSFYRDKDDMSLS

HQIRSAGA

>contig54474 Frame-1R|Blast-rRNA biogenesis protein rrp5 [Phytophthora infestans T30-4](gb|EEY64678.1|) 8e-54

MQKKFRSSKQTWIQSLQYLVRHNQFAEAAETLQRSLKSLAAHKHLPVILKYGQLLYGQSE

LDKART

>contig54580 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57231.1|) 2e-54

MEQSILLDKMGAAQLTHRRQTLSELLQQAGHYSAHVRQHALQGIKELANQATAANLRANA

SVLLERFLPSLQDDEAIVREAAVQAWKAMLP

>contig54603 Frame-2F

MTMRRRRRNSLLLSCLTLLLYKYDTNAAKADYSIDLTGIASGTAYTLTVNIGTLGSSSDN

N

>contig55068 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY57349.1|) 6e-25

MREQQSETYTKVETLTKKNLSLVAELRNMRDERDKQRQEVQNQLEQLKLAHADVQGK

>contig55389 Frame-1F

MVLVALSAAFTIIITFIDQATDTMRVQVAIKTAMFSSLIKSTSVDSSSTSTSVCSDTPTS

V

>contig56421 Frame-1F

MANSSHLNKMSEDSQNQISCDFPVPEYKNPHLSTNNTYGKATAP

>contig56559 Frame-1F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY67459.1|) 7e-21

MARESIVLLMNNDSALPLKKKASVFLTG

>contig56814 Frame-1R

MLSTLGGAMLEYFLQKEIGGLRCFQSEPIPVNGVYI

>contig57219 Frame-1R

MTTEPEWPVVPLLSDPMSVLCLKAEYVGNPNTNFMYGIEFLNKRYEALRRVRGDGNCFFR

GFIFALCEQLLPSKSNDTNAALRNRIQQLIQASKSDLVAIGYSDVAIDAFWETFVDYLAA

METRSHAELVQDFQTEGGESEYLVWYMRLLTAGYMKKHVDTFHPFIEGLYPGQTVAEFCS

AEVEPMGKECDQPQIVALTEALQVGVKIEYLDGSAGPGENLQNYVCSPYEKKTNKSMPVI

ITLLYRPGHYEILYP

>contig57332 Frame-2F

MDENKHQKKKPNPTKELFDGLRKVEQELRDKKDKENLDDNVSW

>contig57840 Frame-0F|Blast-peroxisome assembly protein, putative [Phytophthora infestans T30-4](gb|EEY68846.1|) 6e-07

MEQQLRRGKDHQSDVPSLIGSDRIPLFTSRRTFQQLDRLVSTIRSKCAWIENDVFPA

>contig58144 Frame-0R

MRNSKTKSKRCHPSFPPASICHHAHKLQAPRALFAHLQSLWDRYISV

>contig58229 Frame-0F|Blast-metalloprotease family M48X, putative [Phytophthora infestans T30-4](gb|EEY59998.1|) 2e-20

MNVSYRRKDWERMPFKFKALFVVSASALGLYVVSHVETMPLTNRRRIMLLSRKYEEQLGE

QAYREIMSNGRLLPKSHP

>contig58614 Frame-1R

MTRQSSGTFKAREAILLGMGLFFIAYCLVVNVYFNASMHEPLLTPLQTTDETLTE

>contig58823 Frame-2R

MTRATREFFTSDSYAAKGTV

>contig59341 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61418.1|) 3e-09

MTEDETSTVAMRRLAEVVLYAEFDLTKGSTLRGSYPTRFAHYS

>contig00728 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65259.1|) 3e-67

MAENKSKAKTKMREKEAVAETVSPVDATKDVESTGMAASISYGSLLLNDSSQKDSKPKTR

HGQSVRGIQNLLKKAERNAQRLEELKKTEKGKETIKAKGWDTALQQAAGQVVLDDPKLLR

AKLKRKEKSKTKSTKEWKERTAKQEVSKKERQKKKMASSLGRNKRSDGKAIEKKGRKGPR

AGFEGKKGDAFLNSNKTGGKVVGNNSAGSLKH

>contig05626 Frame-0F

MEQCDRFLLHYFSTINDIYPHYEVLFADLRFLFDELLSLRDFYRHFLASYSSIGPELQRR

KQVDANIYQF

>contig07156 Frame-0F

MTTKPMCVYMEDQAIEAITKMLEGRFKHLPVLGSDGIPQGMLDISKCLYDAITCLEKVQQ

STEAAATEFSRELGSASNLQRLLGPMMEKMVRPTVGDALDGELMPPVIRLHTTAAHAAKL

MASTKKAAIVLNDEHELCGMVTTKDLLRKVVAKGLYADTTTVEDVMTVDPDLMGPHMSIL

NGLRALHDAGQLVMPVLADDGEILGMADVLCLSYGQFQTTSGGTSKTDWRQFWHTAMNLQ

EEVAGGAYGGHDDNDARSVGTIEEFERDEYHVNDSMSTPTASAVGLNPTRHYSNSLGAYA

ELGESVSVVSGANTTPSALIATTLDDHVFVFKVSDAIQEHFYRIVCPFHALQGLVEHICF

QMKIPEHDQVQLKYKDDEGDWAVLTSDESLVEAVQMAQRFGWKRLVVV

>contig08049 Frame-1F|Blast-hypothetical protein SORBIDRAFT\_04g004420 [Sorghum bicolor]gb|EES04574.1| hypothetical protein SORBIDRAFT\_04g004420 [Sorghum bicolor](ref|XP\_002451598.1|) 5e-38

MSPMDGAPEEFDQTIFSVNPDTRTIGSYESLALNLVKDQQRKRSYTDTANFTLRCGVCQI

GVIGQKEAVEHAQATGHVNFQEYK

>contig08746 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63314.1|) 9e-11

MFGFMPPAPQEHMMRAGVLSRGIVSEIVTQGA

>contig09617 Frame-0F

MRHFSHLLKPRPWLVAALPAALGVTYVSKQQEKSRCKSFIPTSEFLYEPLSEDRASKDSI

EFNTKAPLSKRMEALILRVQDEICAGIEAIDGKTFHEDSWEREGHGGGGRSRILQDGNVF

EKAGVGVSIIHGTLPPAAIKEMTQPGKDLKEGVALPFYACGVSLVMHPHNPMAPTIHMNY

RYFEVETGYNDAQGKAKTIGWFGGGTDLTPSYLFEDDARHFHAVYKTQLDKRDLSLYPAW

KEACDKYFYIPHRQECRGIGGFFFDDLTDTSEEHFQLIRQCANSMLDAYVPILNKRKDMP

FTPQQKEWQQMRRGRYVEFNIMYDRGTKFGLLTPGSRVESILMSLPLTARWEYMNIPAPG

SWEEKTLQILKHPVNWLDVPALDLETLSTKELL

>contig09806 Frame-0R|Blast-pectinesterase, putative [Phytophthora infestans T30-4](gb|EEY56128.1|) 2e-12

MSEILGEGLANYWWVDTKYF

>contig10758 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64653.1|) 1e-107

MLLFIYGEIGHFDAMRALFERESIAFPLNIAHYEAAMDYCADARDELAGSVTSLKLFEKL

RSRSFIRPSGHTYLRTLQSCLRLERLEPAQSSAVKSTGQIILDDVREHGFQKAVLGELAK

QVAFAVKQVKSNDEQAVRRKEPSPSVGDTGAISPEELARIALFCHRHGLPIKTKLVSSLL

ILHQHLPAMIAKELTFIQRSLEEGLGVVVAPGSQIREKEMTSTRIRKTKKTGDSQAKRVP

ASFALKFGQRHPRRKSYEAAVRAATDSRWGVLLEPIVADKD

>contig11317 Frame-2F

MYCVWDVYSWDVMEPITYFIGFTAVLGNSFYHTITKKDPTYSNIWQKRYLHRVDVLSKQR

KHDPMEMKKLQACIMDLRNDISMLLQWENNKQVP

>contig14109 Frame-2F

MLCRLLQVRGARAVPTTTYRSLLQPTYCLRTDIKRWRSYGTSTTVSAATNESTTEIEATD

VDPMDRQP

>contig15638 Frame-1F|Blast-trimethylguanosine synthase [Phytophthora infestans T30-4](gb|EEY53306.1|) 3e-95

MTCKQVIAIDIDPEKIRMAQHNAAIYGVAHKIEFIVGNSIDIIPQLKADAIFLSPPWGGV

KYNRKQFNLKDMVVEGISGLDLFAKARLVTKNIAYYLPRGTPIQDLEELTPGEPVECESI

FLNQQLKVKTFYYGDLVQLEKSIEEAALSTLKWVFRKFQ

>contig15753 Frame-2F

MDEIYAVKKTQFLGKPVSFVCQNGNGPCPLLAIANVLLLRGYLSLDKVVEPLGYVSAFNL

MQLVRRRLIDTNPPLTNTSELQRLTQEKTLEDVAELLPTMLVGLDVNVRFHRITDFEYTV

VCAAFDMLDIVMVHGWLLDEQDEKTMKVVGNKSYNELIERLVDYRALLMAEEANAKQAAE

FSSLDTAVRQDGDEGAEVALQLSPLATQTIGFETLSIDANSTHATSTSNCVQSPHSVMSQ

TSPTKSPSQQTVETMMKERHISDADALDTANTLLEEGPILEEFFNLTANQLTYYGLVRLH

EGIRERQLCVFFRNNHFSTLFK

>contig16244 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69156.1|) 4e-50

MQSEEDASAYGLKALATVVFDVDSGPKLSEIYPPTCELSEAAKKSLAYLSLPHCSNLNEG

DTQYTVRFKDRTDDSELLFGFVLFRQLKDESQVRGYSQKALIIVSTKPFLDLYDRALRLI

GPIFFKIGAQVLAAVYNDIKL

>contig18141 Frame-2F|Blast-acetyl-CoA carboxylase, putative [Phytophthora infestans T30-4](gb|EEY68805.1|) 0.0

MVVLVGAVCCAYQASNALQEEYVSQIERGQLPHSNLLDQQESLELIYEGIKYNIKACRSG

PIQFTLFCNGSYVQVEIRTLSDGGFLVLLNGKSHVAYATKEAQGLRLVVDSHTCVFTKEY

DPTRLVTNTAGKLARYLVDDGASLRRGMPYAEIEVMKMYMPLLTPEAGVIRLLKSEGAVL

APGDCIATMELDDPSCVKKSDVFMGKLPSSDSTNGNSTKSVHKMRKSLAVLKSVLQGYYT

PDDLMQKALNDLFQLLLEPLLPVDEIKEALSSLAGRIPLDVFAKITDKIQTYKKSLVEKP

PATHEFNVADVVEILDDHQKTLDTDRKCSDFEASVATLRSIATKYKHGLISGEEAVLTDL

INEYFTVETVYANSPNIEDVVMALRQQNSSDLNKVFSIARSHKALESKNKLLLQLLAQMS

RGSAVAP

>contig19410 Frame-0R

MSATPKGKWGTFKTSSRLKKLVIGRRLSFYCRHAVLPEEK

>contig20502 Frame-0F

MVGLCLPTCSSPASISKKGASNSINSILFRQSEERARVKSLSEKRHNFYGSVAIYCFVTA

KRRTCNIHRVMLRFVPFDYFFRQNYMTTQFYMRGDW

>contig20681 Frame-0F|Blast-tetrahydrofolate dehydrogenase [Phytophthora infestans T30-4](gb|EEY68099.1|) 1e-165

MTDASVGGVKLNASTIADPFSSAVRHYIDDAMGGVGPKLVGLLAHGDPAAKKYAEWTGKA

CARDGIQYELREVPKDDLLEALTTANHDSNVHGILVYYPCFGAFPSFFGGTMDDFLRDSI

SIKKDVEGLGQFYRGNLYRNIRYVDDDETQKCVLPCTPLAIVKILEHIGIYDKSKPEGNH

LAGVNITVINRSDIVGRPLAAMLANDGADVYSADIDSLYLFRRGKLIPSEETQETACKKS

RVIITGVPVKSYKLPLEWVSENTVIINVASFKNVDETELLKIKGVQYVPLVGKVTVAMLE

RNLLRLYENFHYKPKKVWQ

>contig21897 Frame-0R

MSSRLAVVTCAAIRRRHNSKLMEKFNLTTLNDGKNPFVVSSNQLLKGSKEPQQCIAEKVL

STVPLRVKKITDELQEKPLLAKL

>contig22030 Frame-1F

MPPKTLRRRTHAVAQLEKKDDLIQPQRVRSYESDKEMVAAAPEPPRQFSNGVWANDRYMR

RKNREYLNEVKAAQEAIEAEQMSIQERAEMISKKDKRVILSRDLEIGGKFPGKVSVINEE

VVIRKEAMGKQQQEAIESKVETEERSILPELVTPDTNVVGQGLEKDFTSDTFSNVKTTSG

LIADMSTCIGSMHSPIEQNMHPRSEIDPTLDKSAPPVILAMKPTKSVARG

>contig22629 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68764.1|) 3e-28

MVAKEAVDCRADIPPMLSQEERNALQITTRCRQRWGACHNREAMPQDSAKVIEEFVTQCA

WLKERELALECLYDGNFNVPKAAKLLRQARRERYKLRRNQDKILPLNDFKKALATYGKKF

HLV

>contig22931-0 Frame-0R0

MSSLFASTGLVCYTGLALQLMIG

>contig23392 Frame-0F

MAISIVPAISPLLLDESLPVREQAKKAIDIFIGIVLNEAVQIKIRDELKVKECELRHDVG

NGDHIGDSDEIRAPLTFISGSQSSSGYATSLSAWATSAVATNVNKLIGSGGASSSIAQSS

ATVLSSQVDDFLAEDGWGNRNVIDDLDELKHASSVPGLTLLAKRGSSLTPASSTENLVSG

SLKPSTYSSVSRDAGKTYKSLTENDLFPSSSLAINCKSAWENDGWGGDDDLNLDAMAPQA

KISNTHAQNGIGGLGSSISAKRSAITHSTERNKANADAPEKATARSKNLGAIKLMSADDS

KADEWNWDF

>contig23604 Frame-1R

MVPFKATLLIQLTAVIVLSEVLTASVRAHSAISVHVRVHRAEKYLPPSLQDAALSNKSSQ

EEPNKEREGERSGKSEKNNVAHNVNNYFGAKNTKDRKKPVLNDSQEKPAKERQTEETVVE

YERGSVKILSEKKLKGETFHGMKVATFNEKNVTSMFSEAKFSSADPKKHILFADANNPVF

VVCGIIGGLAAIIGVAGLVINRHYPNEMNLESILSNSNLDIDIEASIRSTIEEQGDSDVS

NNDQGDSESDVADCEGDGKNAFPVTIAHISEY

>contig23671 Frame-1R

MRTLLLHTRYLGQRLATSHRKFYAGTMVRFPEIPFKLADIGEGIAEVEVLQWFVKCGEKV

QQFQNVCEVQSDKATVEITSRFDGVVTKVHYDVGEMAKVGSTLIDIDVNEATAATTLVGR

NKRALTPRTIPKMTASEPFQSMQGLTPLAAPAHVPLRIAIAPRRFDGDPKLLTSPSVRRL

AKEHRIDLSDVEGTGPQRRILKGDLLNYIKTRAAQPSQPLSNSTRHETAAILAPEENTWK

GTSLQQNVVVPLTSFQKMMVKSMNAALQIPHFGYSDEIQMDALYELRKKMAPLAETRGVK

LSFMPFILKAASLALKHYPILNAVVSECETTITLVAAHNISVAMDTPTGLIVPNVKNVQD

KSILEIAKELTRLQSLAFTGKLAPSDIAGGTIS

>contig23947 Frame-0F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY70003.1|) 0.0

MYAIPGRPAIIVLSSPELFKDVLVTQANVFLRGPVARSISFDIFGNGMVISDGDPWFYHR

KTASHLFSMQRMREAMETTVCDLLSTFVDVLNVYAKRRESFSMKKELSHFTMDAIGKIGF

GIDMETLKDTLDRADDHEFLTAFNEGSVAFGVRIQSPLWLWKVKKYLRIGWEKILMDNLQ

IMNAFISNVIVDSMNRKAALAAQGKEMEAKDLVSMFLEKRLKETENIQMEDDDATIMRDM

VMTFVFAGKDSTAHSMGWFIVNMNRYPNVLRKIREEIYRVVPGLITGEIKVPTHAQLESL

VYLEATIKENIRLHPSTGFIVREAMQDTTLIDGTFIQKGQSIMMSSYCNARNRKTWGDDC

LEFKPERMMDAQTGKLRVFSPYVFSGFGSGQHVCIGQKFALMEIKLAMATLFSKFDITTV

DDPWSFTYEFSLTIPVKGPLNVQVTPFMGLAPPAA

>contig24858 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69806.1|) 1e-139

MATLRPYHTLLLLVEKGEILQKLPVDHARQLEIVVKTVNPLKSFQDIALESSVPIHQVFR

LAAHLVYWGFGRIVDAITLYNVYQVTANANVYVGSPLAVEFRRTFEPYELSEVLSTFSGS

RRIGEYMKTLSTAKKTEYIHMLLWLLQHRFIVQLHRYVYFMIPSDGEDVTDRSYSAGKLV

FCDDGVEFTKRNGGKPCQDRSFTTTGSSCKSGADFGSNSGGEQGG

>contig25062 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY65268.1|) 0.0

MKHIARLSRDGKNVVCTIHQPSSFVYNLFTNVIVLARGQTVYSGPCSSLLPHFASSGFPC

PSYVNIAEFVVNLVNTDFEHHVDVWKLVLAYEEGIVKQQLVDQLAVDRETFKNVLEIELQ

ASSAMRQFQVLLYRNTLNNLRNPGIYWIRVLMYFCLSFMVGTMYLSSNHELTEEDLVPML

FYVQAFLVFMSVAVLPFFIEQRAVFARERANSSLSVVSYVCANFLAALPGIFVIAVMSTC

LVVWLANLQAFEYFLLNLFLSLVVAESMMHVIGAAAPHYITGIAVGAGIFGMFMLCEGFM

VPSSSIPTFWKWGYYIAFHTYSFESFVFKQFEHSTSESGKAILIKYGMEHVDVMQNMLYL

VAFVAGFEVLFMAILWKFHTGRR

>contig25260 Frame-0F

MVFEHSRDATVGSINLQRQVCGFISNANY

>contig25329 Frame-1F

MHGNYEPPPEIPKRPRDCFI

>contig25794 Frame-0R

MTWSVSTRAAIATIDTLLNQYAVGSNTSPDAVFIVWKELSRIGSKLPRTKANISKEDDLQ

QFQRLIEIDIASQTKLNLHS

>contig26135 Frame-0R|Blast-tRNA pseudouridine synthase B, putative [Phytophthora infestans T30-4](gb|EEY68894.1|) 3e-31

MLQTIESMLQHLPYAQLQLQTVQHWLNGGAVTISVQDVKFVDYKISNTLSFQPIRIYQSS

SPVLLGVAEAIFQAQHDKYILKKRLFI

>contig26342 Frame-0R

MIAIIVCIAVKVAIFAGISSVRGHGNFVKPAVVFTDGYVMNGFSATLDNEIWGLYNHDKY

GHGVNATLTFFINVFPFKGYNSLGALIVENQEVLDAGVDAECGRTVFKESKRSELPRSEL

EFSGFTHPGPCEIWCDQAKVVFAYDCQTEYPGVPAKIPYDHAKCVHANRMTIYWLALHGD

PWQVYTNCAWLQGGKGRGSPPVEKGQNTLKKGGGSNLALAITPFNEMDTIAPELDGKLKG

EDDVLEKTTEPPSVEIISAKCMRRRE

>contig26867 Frame-0R

MVADILRSFIQLADDLILTAATQHCAISPFNVAIPDLSRSWVLTSRILAFKRSDNATSAI

FTGGTRTNAADVSLSFKKAKSKVDILKDPGRYQHPALSV

>contig28043 Frame-0F

MAWTCTACDFAANEDGQEACVACGSERPEEEHQDTADETMQPTDNGALEVVVIELPAKEK

LGVKLMPPKDGVISHGLAIDNINNPLLENKVQAGDLIVAIGGQSVDGMGFSDAIDLIRKL

PRPLAISFEIDEVRRQEVVREKFQQNQDDDLDTQLTTYAVVFDNGPMGLNLEEAVRYGID

GAVVRALKGQAKTSGMISVGDIVYKVNETDVLCIPYLEVMNVLRNAAAPKTLQFVPKDKL

ADVQRVNSRHSESFRLRESTSHVKQKLMNNPRIVKDDGHDGDDTQSIAQLILDNQGATIK

KGRMYKQGRVMRNWKSRYFVLSVSKVEYFKSPSSTTSRGEMSFLDHRSTVRSLPGTGDVV

CRSPNVTAEFLLELRVDDRRMVMACTSESDKKGWMDAIKLAIDASKTVNRTQNLDESLRE

AKALRTQRTESLSLDGTFLERNAGGRLSQFNYEAFSTPVIHVGVLSATNLTKSGSSVNAL

CEVTVGAETFKTSVVKNQRSPVWKQDNSASFEVPNNDMVVEIRIFNEHLFRATELVATLS

IPLKSLPNMQKTTKRYPLALGSRSAGAVLTLSLEYVNKQKAYEEDQERGRLGDDLNSNGM

MNERDEMVKIKAEAQMAADEATHHAARAQEEAHMLLEQSRQKAEAAMAAAREEQREGKAA

VEKAMAEAARAKEEAEKQLAEARRAQEEAQKLIEANRRIQESDVQGPSIYAAYRRMVQDG

HSNEDVKKKMQEDGVDEMGIVAFFDGINSYDEKIRALQAEVEKLKRSRSMRQKDEPRAQD

MLANLDISSDQVKLLRRLLKLEKQLQQAGIAVAADIPYEEAMAKVREISKRMQEIGSADV

THPDPAIQKQLREEYYRLEQDMEKYNTALMLTDEYAAEEARKEREWEEENYEENVKALRA

IRRMMPVDVKKMSEADLQTVKSSTGKTLSREIARKYKRTNVLELLRMDPADIAKNHPSLL

DNLRVTGLTVTERRALHMHLRDIAETWKAQQGEEMTKKKYEWFKTLKETFKTVVNSYNKH

VKQYEP

>contig28876 Frame-2R|Blast-chromosome segregation protein, putative [Phytophthora infestans T30-4](gb|EEY67985.1|) 1e-180

MIMIGADPSQISSADGGDSSRKSNVETYSGVQIKVNFRGEGDSYLMQQLSGGQKALVALA

FIFAIQRVDPAPFYLFDEIDQALDSTHRAAVAALIHRQAHSKENPAQFITSTFRPELVNI

ADKCYGIGHQNKISNVYSMTKEESLDFISNIMTEEEGVKGS

>contig29552 Frame-1F

MSMGLHSAREELGLPNVSSSLGMNPSGYLNSDIGHPLAGLPKPMSLSPRTFGMEDFRDFC

GPVGTFKTGLTPRVFSTGLTPRTGFTPRFTTGFTPRINISGLSQGSNAPPTESSSAYLNR

HGGVYSPRSAIDAKNNKISPSGYTPKDVSGAKVPMRFPGAFSGNSPPKMSMTDHFKQEQQ

ASHQSHMQHMEQMHHQMNHGPHHPVQMSHPGLSNMNMNMYDYMNRPTMQLPTNTRLSATA

SSEHGSDQEDMDERRRMKNRERVRKCRKRKQDRLNFLEDRTAE

>contig29901 Frame-1R

MQQLEMPPSVIDIYLERHPVDRKYYPNFHAPKEKTIWMMQNVEFFDRHELENPTVGVMIV

KNRIGLKKVLEYRLRHQLSYSVFYAKHTSRDVYQPAIKRDWTSFLHLAGWSPFKNTRVIL

QAWALHPEWPHLVLRVIKASLCEWIEEQFGPKESWRLLNVDYTCGSVPAEEKDRLQNEMG

LHLCPSETEGFGHYINEARSVGALIVTSNVPPMNELVDEKNGILIGEPHAWWWQTKGDLF

MPLALVTVADIERSVEKILLLSIEERQRMGRRSRSRFLEDRVYFLNAMAVLEESLCQDEI

QIKKLKPYLY

>contig30095 Frame-2F|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY59113.1|) 1e-171

MVSPLLTAMISSSVMILPVVVMVSGCAFFFIKGLEGSRILPTKRIVASDSELNAFMTKAL

QPLVDRYKPTWWTNSHIQCILTFVVPQSPITYKRDILVLNDGGQASLDWALESSVTMNEP

LQHDSPIVIILHGLVGCSESMRSLCAEALKHGYRPVVFNKRGHGGLKLSTPKLQAFGCVQ

DLMEAIAYVERTFPKSELFGVGSSAGAGLLSSYLCELGDKSRLRAGVLISPGYNAFDLFC

GGKINPVYNFLMTFTLKTFLLRHKSELDQVVNVAGALRAKSIREFDEHVYMKMHGYPDLE

AYWKINNPMRDVDNLKMPFLCINALDDPVCTKDTIPYHEFRRKPNAMLLETPEGSHCAFF

EGNFFQLKSWCNEVAMTYLDRLREFHAASGLDTSSSSS

>contig30154 Frame-0F

MEDEEFGEDVLVTTRGDGLSIKEEIKTKESRAEWEVSKVSAIKAEKKDEIEDEDEELYGG

VSIKLNATASSQAEAEIAALAAAMTDTETCKTNDDAPVDSDDDDEDVAIVLNTDQSSSKP

TLRFTGGGNRYVRGSHAGSQHNGPGTSNVSAMVGSQPEDLDKPEADGMDDMAIFGGRRTA

FDVDIDLLEDRPWRKPGIDISDYFNYGFDEHTWREYATRQLRLRRELAVEKSREQASRQA

VNAANQQLVRDRDAKVQGQDGKGVPLRGLPGHASTEGDNEIGEWGGHVVPLMGNLPPRGS

NFMGGLPPRGWHPSMGPPPAFMGQQDWTGPPMGGAPWGPGPGRGPPWMAGPNAGRGNGHG

>contig31005 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61360.1|) 7e-88

MYELVALREMCKGFVLKYAHEVFCDPQIVRLPEKILLELIPQDELQIRELALMEALVMWG

ESRVANTNKSVCELLADMMEFVRFPTMSVSDLYGKVRPLVNEGVIREHLLTEALFNHLKW

GSQTGIAAKRAKPRALTASLRKRKRVSFTQHVTFETTLEGHGEV

>contig31386 Frame-0F

MHLTAIQEKMNCSNNAATHLRKLNKELREIFETYGNHLDEEEENVLQKKRFALLNFSLKQ

SQELIEEMESAQNLMATPAAVQNYMARIERLEKLLSELKQENESLRKHLEKAELNLAVFE

KRLGRGEFNIETTKIMHLAVNPTRELLESKTKTSDAEQLRQENEMLRARLCKLTEGDDSA

ATIADDDKLTTMTSYETVEGLKKLNQRLKQVFGDQIRQYREAVYLLTGYKVDLRKSNGIE

MLRLRSVYAEHDDDELLVRMEADGSLELLESDFCSQINQRVFAYLTACRSFPAFLSTLTL

HLFEKQTFQGN

>contig32152 Frame-1F

MPNTSFSRQTFFLVGSLREQTDR

>contig32387 Frame-1F

MQEKLQPQFHQNQLHTTRDRRMFQTHFDREPRRSKTQDMQTLELIRMYEAQQDQFDVEIN

HLRAQLDALTNELRDLNNTIARQPLAARQDESPMWEQDTNHNSSYAVHSFDDMLVEQLEA

ARQEQEIIATQLRDREAQRIQKMVTMEQNLVTARERIQELEHEKTHGIQNATSRFKCHRN

DCIPLVESQTKANPSQTQQYGAFT

>contig33036 Frame-2R|Blast-1,3-beta-glucanosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62229.1|) 4e-50

MGCNSRVQGLCAAIVLCTVIAVSSTTAWVAPIITKGNKFFNSVTGSEFRLKGIAYYPRPN

DGEMANVSNYDWTTDEHEAIWKPHLKSHEGPRCKYDSSLLGGPKQVS

>contig33465 Frame-0R

MSDPSDHDALRVVSDTASSATPSFFNSDDQGPECYMTSSIAERPYFSDSGAQRRDPDSFS

SSKPHLESLNGHNASRFKSSVFSSNSKNINYGA

>contig33667 Frame-2R

MRKPVITSHLLPTLVIPESDRILLQELATTLVQHNLNEYFNMCVTTDGRPEREAWIPTRK

TKRIRIYRERPHAFKQAIPSLLLLGRVAGKLDDVMYGVVTPTDESLKIKSSCIHDGVVDS

KVLQELVSPSVEDPFHHVSLQWRQ

>contig34150 Frame-0F

MFVGSTSIQNSDNAAVVVGNDAHVMSFFIQSLHRMNEHKLVVTFFEAYDRDRILWLQEHR

LREAANDYSTDGQGTDDSISELNKKFTPSLKALELPRVAHSCYIQSLAALKHQKKILRLF

DNENYQLNKMCRTTLNLSVLLHACHSERNGELARKAIDTITIQSPLAVIPLSCYELAIRA

NLLDRKHHERELLAAVHLAKALHNDGGYLLKPDIWSGLIKVSLKRNRPDLALEIFKSYPN

HRISEYQTNFRQVLRVACRTPDRTALEMMQFCWAPYINDLANKAIMLERKAYQDAISLKN

LNAKELLLGDIALITSIPAWKNNVEADLLNMMLWEMLKHSHAMPSIVEVLNVMETTRSKG

RTAVLRSVVVAQIDHDMAQNEILSRTAVERSLEFWKEHPSVLDSPGFLVRLLLDKCLEHR

WDDECEFLVDYMLELGLYRIPFITIIKMMKDFENRGRFEANARIGQKLLQRLSETNRQKL

YDRFLRVLSDELLSPRAIRQS

>contig34356 Frame-1F

MPVLLPYFIGFHQSSLLQYFHSHYPCKFYLSRIDSHSAKRSLKIFRDVTRVLLDIRTKMK

GDC

>contig34741 Frame-2R|Blast-ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY57180.1|) 0.0

MKKSRQTFAVGASDLLTDVNAFEAWRHVVQRGKRNGVDEKTFCQTHFLSQRGLWELSKLK

RHFRGLVAQLGFISATESSRDERMTLEQLATMSAILYAGLAPNLVHAELPSVAYGPQRAI

FRERDQNLVVMHPSSINYKVATFHASSFLTYAVKLHTSQVYLPASSLVCPLAVCLFSHTF

ELLPQLRQKDKDGNETIGVRVNDWIMLQNSFRSAALLQELRHTLHEIVDTSFQTPPYARE

DKSETSEQQAKRTTLVDVLRKLLVAEYEERDPKKSLSCQLKLGGNFLEST

>contig36031 Frame-2F|Blast-isocitrate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY70199.1|) 0.0

MDIKKISVENPIVELDGDEMTRVIWKDIREKLILPFVDLQIEYYDLGIKHRDITNDEVTI

EAARAIKRHNVGIKCATITPDEDRVKEFRLKKMWPSPNGTLRNELGGTVFREPIVCKNIP

KLVPGWKDPIIIGRHAFGDQYKAVDFVANEPGTFQMTFTPSRSRSEIKTYHVYDFKGLDG

GVGLGMYNTSESITGFAKACFEYALERKMPLYMSTKNTILKHYDGRFKEIFQKTYEDTYE

AQFKAIGAWYEHRLIDDMVAQCLKSTGGFVWACKNYDGDVQSDILAQGFGSLGLMTSVLL

TPDGKTLEAEAAHGTVTRHFRVHQKGGETSTNSIASIFAWSRGLMHRAKLDRNSQLKAFC

EELETCVIDSVEAGQMTKDLALLIHGSTLKRENYLDTFQFIDSIATNLRARLGARSSV

>contig36516 Frame-1F

MAVTEEKDVAVMARQIAKVTQREGWTSDTSVVPDMQRLLGKLTTLKVDKDLLQRTKIGAA

VNKLKKHEDEIVRGYSQSLTKKWKSQVGIASSSSSGPIKTQWVPSPSPPKQIDPGDRKRL

ESARKRLQEGYATERARRDSRTVQVLSGPIAKKRKGTRVSTLPSRSSIGRAQLVQRRPLS

SVKYRAASAPPVPRRVMPTTRVQQREIRPASSVTHMSAEERHRQRQQKYRVLSGHVGKDT

DRGRQERHRIQSSNKFVDQRVRPDSRPSSSSPSKSGSVPRTSPPSIDARKAMLNKMFPRV

CGVGTASTYGSASGGTKKKSSAAASKRDVNYTEGQREVLSWLKGLTVDMSEYALAFFENG

FDSVKLSKHD

>contig36930 Frame-0F

MLNVFRSFGLVVVVSSTSGTARSLTSVSSGSRCPADYLWCIVHPLLPRT

>contig37115 Frame-2R|Blast-succinate semialdehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY61278.1|) 0.0

MSPKIRCFMAHSTLRRCYHAKVRNKSLIQSTGFINGNWVESHSNQHFIVTDPSTDKEIAH

VANMGRAETNEAISAALTAQKKWRRTTAAARSTLLKKWYAAIVAHTEDLAVIASVESGKP

LPEAKGEVAYAAGFIDFFAHEIMHSNGFLPSTSAPDHKIMAIKEPVGVCGIITPWNFPIA

MITRKLGPCLASGCTAVVKPAAETPLSALALAKLAEDVGFPAGVLNVLPSCNDMASEVGG

ALTSSHEVRKISFTGSTQVGKLLMEQSAATMKRLSLELGGNAPFIVFEDADLDKALDGLI

ASKFRNTGQTCVCSNRMFIHASIYDAFAAKLVERVKKLKMGLPHEDGVRLGPLISPIAFA

KTSGLVNDAVAKGAVALVGGQSSDIGRNYYEATVLTDVNATMQIWSEEAFGPIVPLIKFS

TEDDVIRMANDTESGLAGYFFSQDLSRMWRLAAALECGMIGVNTGLISNVQAPFGGVKQS

GLGREGSFMGLDEYQETKMVCVGGLDLGDTHKFD

>contig38165 Frame-0R|Blast-dolichol-phosphate mannosyltransferase [Phytophthora infestans T30-4](gb|EEY56408.1|) 2e-60

MNAIQGLGYVFQMEILVRARQRQYSIAEVPITFVDRIYGESKLGAGEIVAYLKGLLNLFL

TT

>contig38367 Frame-2F

MNSSVQVSQSTYSVIYEELWRARYLAEIAVGISKPIPSAALVRNSSETDITPAVVCMTTS

VPSCDSTFRTQEAIDDKNAWDELFQRSNFFIRYGSYLVFNFKADSENAMLKWGKFVQSRL

RKLVDNLQHMSPVSRVHALPCYYSQTSDSEGHGFGSCMFIGIEFYYHEQDGIPPKDDPEV

KTTLEQTIRFFLATDLQQMEDKQS

>contig38499 Frame-2F|Blast-medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY56335.1|) 2e-67

MMQATSLRQAARLLRLPSTRTFALAQHVDDSKFSAFSFKLSDDQREFQQLARKFAREEMI

PKEKHYDQTMEYPHEIFKKAWELGLTNSHVPEKFGGLGLGTLDGCIIGEELAYGCTGMAT

AMEANGLATAPLLVAGSDEQNGKYLSRL

>contig39926 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68450.1|) 1e-64

MRSAVKVKVIRSATGNARSRRYTAPIGTVLKDSSEAIVCARAILKQHKTFLRNLNDAIYT

FHSPLIEGSVGQHTRHSLDHIQKPLEILATLEKGCNENMVRYDIRERHTPVEKDRHVAIE

LIAQLETMLCATPQKYLSYPVRAVFMLSTDRSEVQFESTFNRELAFAVHHCIHHNALSKV

LLAYHFPNQTIPEDFGMAPSTANFNQEIEDECE

>contig40610 Frame-1F

MSSSPRQTRRSSRIDRSSSADLTPSSSSLFRRFQGKKNNAKTLNDSLASSLPPPRHSHRH

LLSRDRKRSTVIYYSGNLVNGFDESKLTTANTSKDVTALTDGEMSDDELPGEDRFDGDAK

MP

>contig40801 Frame-0F|Blast-Resistance-Nodulation-Cell Division (RND) Superfamily [Phytophthora infestans T30-4](gb|EEY58756.1|) 4e-62

MLILSAMGSSKLPLGLKQELAVPVDFYLHEYFQKQTALGEAGPPAYLVFDGHLDYTDATV

QQGINLLLDELAGSGTIH

>contig41741 Frame-0F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 4e-08

MSIFPPSPKPEMSIDHTAFPHVTGIEWQALHRLAAVSGEFSVSSLLSLATPSRQQLSSMS

SWTASFGYY

>contig42357 Frame-0F|Blast-RecName: Full=Ras-like GTP-binding protein YPT1gb|AAB40355.1| ras related protein PiYpt1 [Phytophthora infestans]gb|EEY65863.1| Rab1 family GTPase (PiYpt1) [Phytophthora infestans T30-4](sp|Q01890.1|YPT1\_PHYIN) 1e-110

MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ

IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLHEIDRYACENVNKLLVG

NKSDLTAKRVVSTDAAKEFAESLGIEFLETSAKNAANVEKAFMMMAAQIKKRMANAPVAP

KAGVKLTPGQQVPSNGGSKCC

>contig42528 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY53343.1|) 2e-56

MVWINVPLVLTLCFLSIWSYTSASADVKKLTEIPIAQLRGATNDIYQPSRVHPMKTFVLG

TDLLLFIAVVILGVGDASDQALYTVGVLVVLEATAMVAQLVTWSSPLEIVHSFLVLSILI

FNIAVGIKERNKSLRDVAAFVSNY

>contig42645 Frame-1R

MQMENNDDAIDVVIQGMNLHSLVKDSFPVKSLSHRLDRWATRCMKLVHCELFQIMKLNAK

ICDLGNACWTSKRFTDDIQTRQYRCPEVILHKGYDTSADIWSMACFIFELLTGDLLFDPK

SGRNFNRDEDHLAQMIELLGRMPKSLSDSPLGRREFFNRKGHLKHIRNLKFWSLQQVLVE

KYHFVRQEAECLASFLEPMLRFDPSKRATARECLAHPWLAHVDKPDEQRTNSNKKKAM

>contig43031 Frame-2F

MKHGMVFPHPSAALSHSPSGQSLGKSQSTISGSEVTAHGPAAIPMSTSFVMTQAPELGRM

MTNAQPSWVPDHQRKVCFVCFKSFGIVRRHRHHCRMCGEVMCSRCMITLPLVAPPSSAPC

LDGVVNETVGAENSQPHQLDERPLSVLLKQPAKKSLEETRSNGYPAVNNVKLCKKCMFCI

RQERKGTMRGATNFYAAPTMIKQFPLVLQGSLADNLGLQPGPMRGFFPGGRYAADDELLL

SADRGV

>contig43493 Frame-0F

MLLLDHQWKGNASLSTKLAGEIELVAELPLPGNSCTAPFARLLLGHSFTCMTLLVAVKKY

EAALQVAETTISSWISHLLQFSGLDAKLASSFSDRTFRMLWKIAAAVDGAKLETDVPSKA

IRFRMVSLSFLLKCSSYTSVYFIQQVHRVGVQHERVMKRSLEGLNEIYRFYHESANHLSS

SRPL

>contig43790 Frame-2R|Blast-type II inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY56403.1|) 2e-30

MRLYGVRRRNVFMNTRADKFAFNEMQRKMLPECYKPPAGTYKSGKT

>contig43930 Frame-1F

MGFCGECGSYLAPDLQGAFCPECGEAIPGAAPNASAPSRHVQFALASEADDSIQSREAAA

IVPQREEAERQAQEARDRAEAMRLSAQNAILDYEAQQKAVLERESARIQQELEAQRQQHL

QVAQAARERRELAERLAQEKLAKAERLRAEAQAAQELMKKEEAKRLAKDKQREEARRLRE

EQARREENRRKAEDEARQAFEVKQQEEQLRQEAMRLSTLSVSSTSSNTSTTAPTTASNSC

VGCRSALKPTQKFCLQCGTKVAAALSLNSKTLSAAPSSSGIQPLSLPLTNSSVSVASATS

SVLISGDHKCTSCQTTLKATQKFCLKCGTKVSQAAPPPRAPSPASSVSSASSFSASDSLV

AALSACVKCSQPLKSAQKFCLLCGTKVTVAASTPNLSASFSSSSSSYTSVPLPAPIPTTG

SWSSPASQPNLKNCPTCSKGCKSTAKFCVGCGFNYAKSDEEEVARNIEAARQRQQQLRDR

ELQQRSQASLMANQAAQAYQPSW

>contig44232 Frame-0F|Blast-F-box protein, putative [Phytophthora infestans T30-4](gb|EEY65520.1|) 1e-131

MIRHTKDSISEVLPKPIRRTVYINPTPSEYAQYNGVAAAVRANLVITNMDPKTPGEKHPD

SLLNPINRKDAMRVVSNLRSACCGGSAVKVSLAEWSRLDTINMLSALNVSGENMGIVIEY

LRKVQFRGNVTQCGCCKRKLQLLMIIPCGHLCCADCVEDRMKSVGPSCYRCSAVFDREAF

QRLQPGFEFEMVEAETPNINIPQNGHNGRRDNPIQHFTNQNERPNVAGQDRRIRARNQRG

HDGNDQNTPRLPRRALDLTRDIHFIDASKAFYAATRIKELEKEFLHRRMNSSGRSRQ

>contig44368 Frame-0F

MHPNPLGGSSPGNSLILERYRPAGLRSEISTPSDCLLFTNVKCSFAIPEDSSGFIPRAES

L

>contig44438 Frame-1F|Blast-sporangia induced conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70121.1|) 9e-21

MCVRFVTPSYWLNEAPDDKSFTVEISSVTIMNGVAKFAISVLQFVNGELAVNTLDHRYSE

FDKLAVKLEEKIPALQIRRLLPPKTFFRYRSANFLERRAAYLQQFLERVLCLHFPGVLDQ

NIPLTAEPHVRDFLKLPSVEWVVVSKGAKICALLS

>contig44904 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63623.1|) 6e-38

MLQLDTHLQMPRKRRKSTKGYSTTEDALLAHGIKRFGTQANAWAAIQTHFLPTKTTANLR

HRYKYLLSPKLGFNAIKAWHCKSQPLHNHKSWL

>contig45121 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY58651.1|) 1e-130

MMLLMGGVSFGSMINFCSVHTVVVTLSQRESLERRGVFQADYLVVRAAGQITARLFVFLI

QNVVRKVEILLLLIVLMSLSVISIVVVITSLDEPLAYLKESLRFKCESYWKVTKQKAVWK

ILVFIASFAFFLNFSFPVVSNAFRQWTDTNDSASWLLSTSLNDLFMIVTVLLYRWRYRNM

LWRRLFAVAPTMTIIPQGLMAVFAIPNLCRRSFIYILLNGVTGISYGIMALMVLVPVTEI

IEEGSEGGVVGLALSFGTIFKVFASTLLTSIQRISYFPSNDVVDTTHRRWSIAVLVSITI

FAYSLAY

>contig45419 Frame-1F

MPSNNLSLIPSTHDKENNVAESSSRYGQFDQISRRSRQPRRIPEVIVIEEDEDDDDVSDD

LGDESVYEEVDGARAPPDVVLDEEDTMQSPNVIAVYPPETRSLNTNGEEIIDVLENESDV

RTGLLLYFCLGGAPDLDVYWTHCFTQLNSEECVDLPRVFRFQRQYVFLQCFPLHLTQCIL

QAMASNGQSGCKKIKSRISEAITATQLRDNFDDVVTTTRLSWIKALNIYLTEQAQSSDES

LSEGLVLSLNPAALSCSLDEDVAISAWRRRQGYVLWNLVRTLHYGP

>contig46173 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY65306.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62378.1|) 1e-51

MDLFLGILNNDRELKTSRIPRNCLWRTLPRPSCRAVCKKNNLVEFALVGISNCILDATLQ

QQFTKSDGVEIVTPYILEVSLERVPTTSSERNVTVSAVTIAYFLLNLSALAKITIERLKA

KMQALQSHCTVPISNTADCSGKSYLIKYQT

>contig46465 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55504.1|) 1e-124

MTDFSSPPDPVKLAKQLVADAAAAMAASLGVAPFITIVDRAIIENASGARALSRGLRELS

VEFLKHPLRFVGKREFHLIFGLYTATYVTANVVDSVCEYAETDNQMPKFFGVTAVNMSLC

IAKDRAFARMFGVIAPGAFPLASIGLFAIRDSLTCGASFNAPKVLAKTIEEKGVMERSGA

NTFAQLLCPAAVQFVSTPLHLLGLDLYNNKGHAIGRRVNFIQREYVKSVLARVGRIGPAF

GIGGVGNNYFRNTLRATLD

>contig46667 Frame-2F

MSARRRARRDRCSTYAPPTKPAEQTRESKLDDASSAAQRETSDFNRRDVIVSRVQVSRIL

SSTLKSPIYLGASFLAPNYVIAES

>contig46803 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70656.1|) 2e-57

MSMVSMQKGFDRRRCVLLMDGSAIGCYQRNLHETHIVMLAPSSHTYTYIQPDGTCSRHLT

PTALSRHRPIVIDTLNLRNTLTHHAPYVHKKILQLETMRYQRRNNAHRATWPCLKGKTKV

SRLYNDQDKCFEMQSIEGAAKVQLHVSGKVVNVQYSVEVKTSDADG

>contig47840 Frame-0F

MRFAVLRLRADSDEDTRRLAEKALFARPMPSADVLAEWLKGEISRKDWKVTIHDSRLAES

CIRFCVEILKFSNDNGYSDDASADRAYIVEFIFDTLLCHAQLEESSALNSSSVYETAASA

LVEVCGFDARSVSAVFASHIKEVFDVVALSQDCTYFSNISTIVFCSCRAGSFNVKQIVAE

IVKVGLRKLEVGTCEENQLQGALYILGSAMRYVGENAMLVNAATSEEMELFLLCFQKMAN

FLESKIQAGSNFASYPKSETAQKDYMRLLRSSMDSVGLSGTLKGFLMSPDGNKWSHVKVQ

TLASIKCVVEWNLESVHIDEYLNSMLVALKRVAIENYGRMVSGLPGITSSTKVLSCHEGF

LHALLGLKNATSFEMLFEVGECLVALGTHDVKETFAAVRTTKFDNYAENRAAIIFERVLS

EHAGSRQIKVRRSATIWLLCMCAAGLGPSSGLMSIMSWRSVFESPAYSRLLLEAHEFFVT

MLDDAQDIVKESAVKGLAYMRMHAPTSEMAAQFSDMLYRRLRCFRAFTSN

>contig48355 Frame-1F|Blast-exportin-5-like protein [Phytophthora infestans T30-4](gb|EEY54314.1|) 4e-65

MDLQLYQQVLHAVQTSHSPLAPPSDRQAAYAFCENFKNRSDCALYALKMYRSPRGSDTLE

RHTCQHFALHVLEHHVLTNWRTLPVEEQQNMRTELVDLLLREPQSDDADDPVFLREKKVS

LVAQVAKRQFPQRWPELMPELLQLWQTGNYRQVEFVLLLLRSLA

>contig48618 Frame-0F|Blast-RNA pseudouridine synthase, putative [Phytophthora infestans T30-4](gb|EEY67704.1|) 1e-22

MIRIKRLVQVCGFVGSRRGLLTIKKFSRPDKKQAQANILSPPTLVTVQPSESDAKASTVR

LAKRIAMSGLCSRREAEKRIQSFDVTVNGHVVFDVATSVDSEYDVVAVDGRVLPKTQQVK

IWMAHKLKG

>contig48733 Frame-1F|Blast-nucleolar protein 6, putative [Phytophthora infestans T30-4](gb|EEY54789.1|) 7e-39

MNSVSMLWKSFNTFAKTLRDLESLPLKISDVLPVHSAFRATSLFPAQPHPLAYSKGEHVD

AVPMA

>contig48856 Frame-2R

MNVQAIMQVEDTVARMMPVLEGALAFDAVNVVHMAQQASENYNLSQKSLLEDENVDDDTL

TTEEEQKIMAAQMKVRTWRNSVLTLTLALELVAQLAAVENDNDDEEEWKSDDEDAMEEYA

ASHMENHGAMSGTSTIVSKYLENSRVFPYCVVILQGLVSTPQLSTKRIAKDFEKMRIRVC

NAVNNLLLSVSWEVLGEEVVPQIFRNLCALYGNFSRETEAPVAGDFTLVSSATNDLEVAV

TAAMLSAVRRSTLEKRHLAVAAEDANLIVTCAAHGRSAESRLN

>contig48939 Frame-1F

MVKDELSRFQVQLCSDIAFEEFYIAAPVHWTIQLWKHWVHLSDEDVETFLNEAEEYDTDS

KKEFEARFAAWHALVARISLKPATFWSYTRMKALLNPHIISTLPLTNDCAHVQPRKRRRT

GTATAQGVCPRQLECSLDVLLLPDVMERVCSYL

>contig49020 Frame-1F

MHQMISVASKSAWSKAQLQAKIHQLHLQIIKVGSLPAPKTGIATSITVHAELISLCQTRQ

FSEELGKLLKSCVIAISHDVKVALEQCMLGANKKIL

>contig49828 Frame-2F

MIGTLETPVSLTANVTKLASDQTIRAAIALREWDGINETNAGMTGDAFFDSSLAGQLWHE

FIPLALQQITWNGYAGEKNDNRVEEI

>contig50246 Frame-0R

MVSLPREKRLPLTERDSCVGELCVALDECLILGLKSRSNSEQPCWWHVLSASTLILDEPT

LVQSVLSAAFLSETDVEKARCWLKIALNNHTIESSIMMIFSMTCEKLIRSHYEEWSLVCC

SEGLGLFLELVIALRDVHFAIEVNGESFRVSEQAKVLEPKLISENVNGDIVASITDADIA

AAVGSSKSFLDSEFVQIENIVDEERPSTEISAIEEKDDEFVHMSSGLFAYRLQGIKPWQY

VFGVSLASLSNNSLHSRYALIDPLLALPNILNDCIAIIEEHPHTPRLFRATVLSGRLNQL

REMVETEGSVPRDLDPRCA

>contig50651 Frame-1R

MSLLGSSRVNPVDFFCHDTSTLQNPCLSGFLADIVSNRRCVNCRYGNRTVSRLVIEILSF

NNS

>contig51065 Frame-1R

MLTSRRLPNSLQLAIADAARRRHPSALSLCPCVTHEHLLCSICFEILSFPVTLPCGHNFD

RGCIMTAWAHDASYTHVHSARRVAVTDNDLEIFRAAARPRSHLCPLCRRKTDIQELQVNL

LLKELITALFPLEMQGAATLAKQQCPHLTMPSPPHTALSTNTAASAFRRRPSLRTFSSFL

YVCAASVTDPPGFVLAVLLLLVLLATACNPPAPPAASAMYMFDTMDRVCNGLSFMIHRIS

MQLEQMDQMFSWVRLVSFLL

>contig51436 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57901.1|) 4e-18

MIPIKEPLSIGKIGTSTSSSSGGLFPLQISMAPSRLDKDIDRSLIMKQQRLMGAPAAGEQ

MEILLMRLLTQNTETQEQLALQQILISKILGEHTIQLNKLMTAFARMEAKVKARSERQEQ

>contig51573 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53041.1|) 0.0

MSCISSNAVKDPKRRFRLRGIERFGIAEQDVSIKCCHAIAISGDMDQLLKYLPTAVMGTF

NRHPRLRALVVQDKEYTAEVQPPITLDDVDAKKLLRVREFFDSSEDVAEWSNWNQFVQTE

TEIPFDRFTQFMFYLTVWVNREENKARFFVFSDHVMSDGDSGQIVVNDTLEHVALLSIEA

AKPVNELPLLPSLYDMWFKSTPWWLKPFAKTMLALVGGSAFIKVMKAFRPVLTPREDQVD

FGVPLKSNSTTLLSLAGSPTNMQNTLRRCKEEDVTLGSALVSIVVLAFYHASKVDRKLND

TEEPQGPFKLVFDLCYNMRQRMPKPAKERQVGLYVTNSPLQWLATEGVDMKTVKFWDLAR

TAKQQVAIQGNNLLNMAMPCFLMDRKLVKPKVKKLLGDFRIPSSCTGDAILSSIGRYLYK

TKHILASNGVLVVEDMFAFCAIPFVAASSTIWLSTVNAFNYSLAHKVDSQVGNALFHAYV

HICENASSIHRDDTMEIVLKRLGIDIEV

>contig51942 Frame-2R|Blast-WD domain-containing protein [Phytophthora infestans T30-4](gb|EEY57502.1|) 7e-73

MVRVWDVASRQCLRTILSEPAAPVGSATFTPNGRYVLSSTLDGTLRLWDYMRDLCVRTYS

GHVNRKFSMQCAFLKHPKTSQPLVVCGSEDHRIYMWDISTQEVASVLTGHNHPVLALATH

STRNFMASGSFRDIKLWSLRGKTNQGQSTTADN

>contig52785 Frame-1R

MPHRYLHGRRVNLQRLLIAFINRVLHATPGRIAAHFPPQTLQHLCVTFDPFPRFP

>contig53081 Frame-1F

MGFRLEENIVAVCAPSASRQAELLLCQAFFESCRFLMYASKSLLVILAEMPPVPMSSASI

QSNCNTKFVLWQVWDAQHAIQCVRFNSSKIAARGALALLIDKGGGVILIPASATSNRAAA

VASRALDKGTRSHPSSGFLKDDFLYSYDYEKTHLHLHLPKWAESARWQCDDRHLNHLKWV

ESGDDLFLLGAGEKLYIWKVVDDSVQIYLQRAVVLSGGGGSDMDTSLPIFHVCHFDVTPS

GRYVATAGIHDRIVKVWDLGALSPHESSPESIFLAHTRALVSLVWSKDINVYDARSNDAT

TMGAYDMLFALDRAGNVY

>contig53496 Frame-1F

MTAIAASINHVTPPLTQKTALLLKKMRVNRCFKNSQLGLREQDVGAPKANAMSHTVNVAS

AAAKCSVSSNYASNVTTAAVKCTESSYSASIESRSAVHRKIATKFSHSQNATKAVRRVFC

RNIPAIIQLFTSVGQIIAAAS

>contig53513 Frame-2F

MNVPEMTMELLQMQHGYHPSNYGDLDMNEKGKSNVGSICILTLTMLSGRADYNLTSGKVI

AIADLEGVRIRD

>contig54013 Frame-2F

MIGGWQLPMAFIRQNICEHCRITILLAFNNFWSQYDLFSDLTVMQRISEALTGHVYERAF

DPSDSNNSIFSG

>contig54475 Frame-1R|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72292.1|) 6e-28 NOT\_ORF

MKELGQAKFILGVEIDHNRNCGTLMI\*QTRYIHDVVSRFNQQDAKAVFDPCASGMKLSKM

QSPTTDSEQAAMHS

>contig54581 Frame-0R

MAESSGPRFLLHACVFLLALISSLLQLAFFALLPQINLHTDYCNATLASRSLLETTSAEL

AAPMKLLFQSLFLSPHDLEQEELRRNEMIQEPKLTIRGKQSHAPDTQSEKFRDPMWGEGE

TFTTEAMAV

>contig55292 Frame-2R

MLDNLETFEDSCAATTAVAYAGLMEYEKLISLLSVMSKSLIVSDRLGRQAMRGIKLREDY

DNPNIHRYRIVCRNVNYNDEEYSNEDGNIDD

>contig55366 Frame-0R

MQHVPCHEGTQCRSPAAFKFEYLEWMMDPRMDDMILSIRAQGERCDLPSMVRPSEISSRS

HHGDELHENCDLALPASVTATEFLQLDGEYDVVLMQILLIDQVVRA

>contig55388 Frame-0R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY58105.1|) 4e-29

MSSFSALRIRKNQRLEIVRIVAALLHLGNVDFIPDPEGGKSIPGS

>contig56284 Frame-2R

MWTHAILPFGQIFNSVIDSLIGNV

>contig56815 Frame-1R

MPHSVGLNDGIDGLDEDLLAALDDVLSFSEHNSVADAFAPTPNVPLEDDLDAVLSIESPP

LFGSTAPFETCKPPESITQPPNRLPCSSNWQPHTPSSKGKDVRTTPYTTNANKARRRKRP

KDELDYLRAKVTDMENKLAVLKQTDQASCTTSSVDMLCIPPGSSQDMLLRWKHIAERQKQ

EVNRSVVENIRLRSLLEGQLSIAKSLEAAIDQHQQATAKSLSSSDEFNQNDPVKTSDELL

FAYVNSTLQAQYAELDTVFERSGIAQMNHDMDNGTKAHQDANGIYVRHEVVRVLPFSMDA

VQRTIWGIFRHSAAKEMMLGPFQAEVIDENRMNITMMEKVTLNKRETTILRRISVMRVFE

KHRTVLVWSSFGEITGSMFVRLHEKGYWTSSPFHFGTNELSGGVQGSVTRIVLLVSPEIT

AGPSLVQPNAHVGEMTELVVGTSRMTMNLIYQITDTLLLLEAMGGQITGEEDASQLVTTS

SN

>contig57333 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63149.1|) 8e-06

MNNNPASPLANSDADDGFQDCVSEDEENETMLYQESIALVRRMQT

>contig57834 Frame-2F|Blast-alkylated DNA repair protein alkB-like protein [Phytophthora infestans T30-4](gb|EEY68761.1|) 8e-54

MKLAPEAIIINFYKTKSAMGGHLDDAEFTMDHPVISLSLGSSCIFLIGGQS

>contig57841 Frame-0F

MSAKRQRANGISFTGLVYCPLRSHQSQ

>contig58228 Frame-1F|Blast-metalloprotease family M48X, putative [Phytophthora infestans T30-4](gb|EEY59998.1|) 4e-10 NOT\_ORF

MYVVSHVESMPLFNRLRIMLLFRKYEE\*LSEQSYREILSNGRLTPKSHP

>contig58457 Frame-1F

MYFSWQCLALDLFVWYATRSYLFGNSVAQSLCVVVAVFDRACARERVTTHLFITCLCSKT

LFLAVGSSFCSCVVA

>contig58615 Frame-0F

MRSACQRISHSASLSRITLHLELKAPSHPLREVRRLIRVMTHDIYRSNKWHRSNQKHRI

>contig59340 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61418.1|) 4e-09

MTEDETSTIAMRRLAEVVLYAEFDLTKGSTLRGSYPTSFAHYS

>contig00316 Frame-2R

MLRYRFSNKISTSSYVFKYFKFNIFKKIKNINDTHYLSHKYCPVFRYMEV

>contig02044 Frame-1F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY64568.1|) 2e-36

MTAAPLKKPVELAETGWSSQGVDARASVSNPANQAKFLADLFYVFSNIGFPFSWYLALDS

PWRTRE

>contig05625 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61446.1|) 9e-24

MHAQKMDALNGDLREPSSIKDKNVQTVEKLYAEA

>contig06611 Frame-1F

MFKVVLDAQKAIQTKLLGGLFVRVSNLLG

>contig11383 Frame-0F

MQVQARSLADRLSFSWSCNIPTKAESQYKATNADTCFQREKFYA

>contig14212 Frame-2F

MFGEYSAFEDSYNMVQFVTGNYSGTTHDSDDDMLCDEPNVVLTRSSPSPNLVVVPVARVA

EVKQEAMPFESAMGRIDYPIKAKTVMVSATPKTAASGFLSISDRFPLSKVGKVSFKMSKQ

GYCTS

>contig15444 Frame-1R

MVVTAPGHIRNRVVVCDVKCTILIGKKKPIAPTLDWQVIKNAKRKSSKSSMRGELSKEIS

DKGRRLLRRH

>contig16997 Frame-2F

MPGTELAQSACLSSHACSPWYY

>contig17121 Frame-1F|Blast-N-acetyltransferase 5 [Phytophthora infestans T30-4](gb|EEY66623.1|) 6e-07

MTSTRKLCCDDLFRFNNVNLDVLTETVRRSDQSLTSLFSHYAVNTTFCCL

>contig17323 Frame-2R

MGSELGSPMHHPMLQPLRSITVNDLSTTFMGL

>contig17569 Frame-0F

MGFFTELNATGTAVAWRKTDSVSLDINLETGAMGLDFEGILAMSWREKKRWFLKQVTRIA

VPYTDSMLKLDVRRSDILCDSLPQLVGPNVTQMMMREHLNISFIGEPALDAGGVLREWFQ

LVCQELFSAERGLFLTTHAEDSSYWINSESAKTVPDHLLYYKFAGRLVGKAILDGLVLDV

SMSLPLLKHLLGIPITFSDLEFLDEELFKHLCWVRDNDHVDALCVTFSIQTPSGEMVELK

PGGNDLDVTDVNKMEYLSLVLRYRMLDSVADPLTALLKGLYEVIPKSLLTIFDYQELDFF

LSGLPTLNVTDWQTNCQVRHGAHYKDTKGFLKELEVIQWFWDVVGSFTDDQRARLLQFST

GSSRVPVEGFRALTSASGIVHPFTLQMVPVGTPPLGMCPRAHTCFNRIDLPVYETKEDLM

SYLSLVRLKN

>contig18928 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54997.1|) 1e-112

MSTPDSSMGFLTQMFIVSPAISWILKPGRYSKRRGFIYSVAFLVAITAITIGSDLYSQEG

NFYHVIGVDRDASYADIKRAFRQRSVELHPDKNPSPSATEDFNRLRMAFDVLGDGHKRSL

YDLFGEEAVTKELWTLQIETIAGSITFYVCWAVITFVLTLSDKSREVRAWSFAAGVLSFV

VELNLIYGRGRLPPYFFPRMTVHDFIIILHTIFPPFLNGCRAIGVYFHHDFARENFALSV

ELLKSNQ

>contig19413 Frame-0R

MHVHRWRWRLHGNKGIGTRLFLSVCDFFVFDKNELPKPHRGLIKRRIQMHVSKMVCGQFA

LPSMVIALPNYRCSNSCCEYLRSKLSERESGLRTYSTLRAGLDHSKCNLKEAGVPSPEKL

PHRDRRRDDTNDSTTLALDVRSFDDHEFAQQCVAKYLRVMKFKRFLRSESISYPISLQYA

QGADNVMRNFNKAQQIKFMKVPVTPAKEYKQYRWQQNSQWMSPNPSACLIRGSLLNRLPS

RQFFISRKLNKTLKNTEFQSTYVCNQSSALKDDALLENLRMVTEQTWFKAEQLIDVMQGK

FLSFLVQTTRAVRVLEIGCFTGYSALCLANGLAPGGSLTTCDIDKNALEFAQKYFDQSSH

ANQITTVAQDGVVYLNSIPQHQHFDFIFIDANKRQYRTYYDTIMQRSLLHPSGLLVFDNT

LFRGRVAAYASGLAVNKERIARRMAEFNAHVCEDPRTIQVLTPLWDGLTLILRSQSHR

>contig19484 Frame-2F

MTTTFGDRMALEEAIQSCSISVRTLQKKMHNKNEDMDVVAKEVSRLVRLRKELHDWTEKE

DKLQKEMTPETINGDKLQKEMTREIIDEDEPVKLADELEQRSTMLESRVALMNDGLTTIE

MDVMRMERTKRALRYLEEHKTTGEGSKDAVFKSEDEPKTVMNAKKSRRRNKKVKEEVKTK

GAIVDSEADSNAVDKLIVQLEAERRKVVEANEKTESFKNSLTRLSNENSVVVAKLTAELN

VERVKADQALQKSLEVQKVEEEFRQVQAKLEQEVAKIQQEKADIVAKLTMELEAVQQTIQ

QGRQSRSIATSELEKAVGLLTEKNAELMRKLATAEETARTVCDEFQDKLQAAEDATKAAS

IKAEDFQKELLEIQNVRG

>contig19651 Frame-2F|Blast-phospholipase, putative [Phytophthora infestans T30-4](gb|EEY61139.1|) 1e-136 NOT\_ORF

MRRSFFLRNVVLPPLVAAESVVRYVVIFPSHIVFPSRAEIEDRTDLFFEGSTTRVQMLVE

HLYSATEVLDQHLSMVQWNILGRGPYESLSSSRRSEVIRSVYQRMRLLVSYYKRFEFLAT

IKVQNEMLYMDLHRAFPDVNGFPLFSHEIALNQELTKDLADQNLTTFPIWFYKKLHYTKG

HGQGAFSTGLLHGQKKGNLKDYSLNNGATKASGDSSRGWIEFPPNETRRLERKY\*WYHQK

KKKSLGPIGPNSVVLVDEGRHEVDLESMRMTPVYWPPLEEIVVCRSQWVYAQRHYGLAPY

RAETANILESAFVYYLGFYSREKERLMDIEAQKPRGFLSSRARLSDAVLASRVEKDCT

>contig19888 Frame-0F

MRIACSSIADPLAPFICFEIGEVASKIFGPSGKYLLYLITFNWRFSSVSDLLNNHGFT

>contig20857 Frame-0R|Blast-ribonuclease H2 subunit A, putative [Phytophthora infestans T30-4](gb|EEY61842.1|) 5e-66

MQRQTRNLNEMSRDAAIQLINEIQKKGVLVKKVFVDTVGDPRWYQNFLTKHFNGIIEFCV

EKKADSLFKVVSAASIAAKVTRDRVISDWKWESPTLSLPTDFGSGYPSDPKTKMWLTNHL

DPVFVFPNIIRFSWGTVEPFLEKAVKVDWIYEKELTKANTPSGTQSITSFLAKPVSEVKP

IVRAAFFTQRNMQDVIDF

>contig21362-1 Frame-1F1

MIYFYFYFQLFLYFYFFFFCPGVLLLLYSKVYYCVPATRDRHVLPANWHLVAAVNGIGFQ

LLGSNRVICNARILRKQFCYQILCF

>contig21803 Frame-0F|Blast-calcium/calmodulin-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY62621.1|) 5e-78

MLQAHEAERISANDLVTHPWFGDETATSDSSSEALEFVRMKECEALGFAELLSRGFQVVK

YSSKGSTQPYLTTLTLNFLEESVTWTARKNLGMPALQSQKRKRAIRLCEINEIRRGYTTK

AFQAQKHLTS

>contig22033 Frame-2R|Blast-ADP-ribosylation factor family [Phytophthora infestans T30-4](gb|EEY59698.1|) 7e-19

MGMAFSRVFERLFGKKEMRILMVGLDAAGKTTILYKLKLGEVVTTIPTIG

>contig22297 Frame-1F|Blast-serine/threonine-protein phosphatase 4 catalytic subunit [Phytophthora infestans T30-4](gb|EEY66035.1|) 1e-179

MVASQSELDLQIEQLKRCEYLKESEVKALCQKAREILVDESNVQRIDAPVTICGDIHGQF

YDLKELFNVGGECPETNYLFMGDFVDRGFYSVETFLLLLALKVRYPDRITLIRGNHESRQ

ITQVYGFYDECLRKYGSVNVWRYCTEIFDYLSLSAIIEDKIFCVHGGLSPSINTLDQIRI

IDRKQEVPHDGAMCDLMWSDPEDIDGWGLSPRGAGYLFGGDVVEKFNQTNDIQLICRAHQ

LVMEGHKSMFNNALVTVWSAPNYCYRCGNVAAILELDENLEQRFKIFEAAPQDARGVPAK

KPAPDYFL

>contig22561 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69290.1|) 3e-76 NOT\_ORF

MHWTRVAEYSVCALDIHSLDIVIFALIADSVYGWNTEVQVESFTQRFDDTELGNWVYVSC

NNEKAGHLLWAER

>contig23944 Frame-1F

MVTKMTAARPSLATLSARVTGHDFRTFYVYTTVVTLEGASWSLAIRYSKFLSFYDALRSA

ERTFKFDFPPRGGIFSKPKPDERQVRLDAFLQAVTKFYRLKKQPPSVTRLLCDFLLVERN

FSRANKFQTTKEKPVETPVLKDMGTAKTAPLSLKAEEGTKALVNATDGIAVLSGIKETAI

ELTKENCEATKEETKGAATTDQQDLADFEVTQTKQTREEGKDAETEATVEKVVEKEDAVM

AKEWNETKDALKEVNVKAKEPAVSVNEVKENEVKTVTYVEVKESEIQATQSKENEVEVKE

NEVEVREDEVESIEQTVEVKENEVIATVSTENDTEELEVVVKEGVVQAIESSEKDTEVVQ

TFVEEVKDSKVMTIETKEVQVNTTETERAENEGLETMIEATRNEEEKDDAKKEEVKNAKI

AATVIETREQDIQSEPEMSPITSRTSGPIVVETNVTSQPSPHKTIVGKTVTITSQLDDSH

SFTVEMTETKASVVTLAGKSKKKKRNHRRKSMSNAPGSSSSTGSDGFESPVGVDQLGRVS

DVTLTEAQKKARNQRRKEKRKKNQKKFLSTM

>contig25779 Frame-0R

MTTQTFTPMMVKTILGIETTAGDIETNSVWIIWIEYLIARFLKKKDCPSGPIADTLRVLS

SPDNNNFRTEYAKRLASGLTRVQSGDAKVKVFLEKYSSQRPPQNIKVSLDQTRSRWGLRN

>contig25797 Frame-2R

MFAQWPQQLEERRKVWYTPQIYVNKTNGVEKKPQPVVYWMHNTFRVMHGNFGLEAAILLS

KRLNEPLVVVSLITSSIIYPICHSSTASDAYARFSLVELHQHFSHAGVPFFGLTAMKPKA

VKVANGQKYLPLESSPIYDLLDALKPVVVVTDAMFDFSSRSDLVHLARFLDIHRLSCSWP

LLSMDSVTCYPVYQLSETLRGSFEGGADFTSEEQFGIEYASFAIPHNETYNFSPLAFDSK

QYRGLKQQCYELLSPIMQRLDLEEVNWRLVKAENSQSSCQVRQFCESEGLQKLSTLLSNS

NGLPTIKAELRGGGVLSLLPFIRHGTIFAGYVLQRISEAIELTTPPVNSKERKALAMRKV

MRSRAANHLGRERDYALYLALWCAVNGERSEHNGNAHIDPALLLTSKIIASLDIYAPRMT

SL

>contig25890 Frame-2F

MFENSMATKIQRLCRYSGALVNNSTENISPELRSLMALKIQRRWRLLAARHDFVQHRQAR

QKVAVKAHSAVLIQAAWRGRSAWKKSAICRSLNDALIQEATQNCGQPTLAELQLLSQSGR

FSNQSSDSEISEDESEFEDAPSSVDNLLDSVSCHLKESDTTEKHISSPPSRTPSFSDPSD

ASSQASSLSVELGYEFSNPEDHWTLNDDKSDASSDCFVDAMEEHKPTDFTRVENETSNND

NPILNTSPCMTNRDFLSDTASTTLLKNAINEEAEEKLSSMISVFNRPSSVRSDSSVQQAS

VVANSPRGSNCSSSLCSVSVTIPYATRKDSYADSYTDSPRTRGISYADSYADSPRLRGVS

FADSNVDSHRSRGDSFADSYVASPRSRNSSSTDVFRSRNNSCDEALRSRQDSYADVPFKL

DFDENNLSDEDSHNSPGSIDADSPRESLSVSDSPLPNHDTIEIEKDEEPEAEREPRNKSS

SRWRAASVLNALSSRRSSKQSSSTTSSLEDEEKDIDQKKARSGTLPSVAANGLSSVAGLI

NRKLSVQTNSNTSSSKSSEYDIEESTVISPPASKSRTRFGRFTAPTVSKQTFTGRFGWKS

QKTRQGMSDEGGEER

>contig25915 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69870.1|) 6e-52

MSQVDVLCESTIGSPLSPTTMASPWTKDGTYIIEATRKAHACCKTCDAIIEADRLRVGVV

YQHRNGFVCINWHHVECYKSVREIPLQCLEGFQELNSQQQKVVARYHIAESELHYLPTSH

TCSA

>contig26059 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64462.1|) 3e-74

MSGCQTFGNTTKLNSSRHRMVEMFSRAFIEMDGDVSVNLAAAAYAEKLMALASNMECANG

HKLTWMMRKADRQVRLGTNSVLGRMTSNSHCANCKRSLRKFSTLIMHRGGTCQICYRVLC

SKCCVAKKICVGLGCEVLQKSMLFCLSCLLEAKSLSA

>contig26136 Frame-2F|Blast-tRNA pseudouridine synthase B, putative [Phytophthora infestans T30-4](gb|EEY68894.1|) 6e-31

MYKLAREKRDFELKARRVQIKNIQLIKFVPGEYP

>contig26341 Frame-1F

MDRFALDKLKNVMDDAKSAVKAKMGTDVERKMEEALSNKNWGASSTLLNDIAQLTYDFEA

YGLVMRKIWESLDAEGRQWRTVYKALSLLDHLIKNGTERVIENARDHMFKLRHLLGFSYH

DGSIDRGNGVRDKAKQLVDMLNDNEMIRTEREKAGRLRNKYVGIGSGLGGGMGGGYSGSN

NFSGGGYSGGGGYSGGVGYSGNSGGYSGGGTGSYSGTGGGKSGGSGDLKGPQEKEKNYSS

RYADDDREEGSGESELEEETQPKRKPATAKRKAVAKKKEESKSKPVTKAPSVEPSLLDSD

FFTAAPVVAPVANTFDPFAPAPVPAVASQTSSFAAFGDTPPTPQPTFDAFHASHHHQQTS

FNAFGNVAASAQGNAAQFAAFATAPAQQGFNAFGQQGHTGASAAMSGSHNQQQQFGQFDG

LQGGMQQQPVQSGMNMPSQTTSNSVSNASQLKSEQKKTDDAWGAGSSLFNLNNLGSNASN

TGHTGSHQEQQSFAGHNSFRGLDTLAGLPRKPTMGAVGGMNPATGGMVYGGNMAVNPSGM

QHQQQPFGQMPLGGLGHASMGAMHPQSMMRGMNMQPGMGMQQPNYGIMNQGAYGGMQQL

>contig26411 Frame-2F|Blast-fructose-bisphosphate aldolase [Phytophthora infestans T30-4](gb|EEY64241.1|) 0.0

MLDLSEEPMEENVSISKKYFKRMAKINLILEVELGITGGEEDGVDNSEVDNASLYSQPED

ILLACNELGSVSPYYTIAAAFGNVHGVYKPGNVKLHPEILGDFQKYVAKEKSTASEKPVF

FVFHGGSGSTAQEIQTAVSNGVVKMNIDTDTQWAYWNGLRMFYEEKKDYLQCQIGNPEGA

DAPNKKYYDPRVWVRKSEEAMITRLKEAYQDLNCVNVL

>contig26864 Frame-2R

MGIITWISLLRFDWLRRCRTCGVRGSKCLCRRPSLALEHIFFLEERKNKLSGRNFSHVSD

TLISTSNTMFASSTVGTGATCSNSGSTVIMRGAGSSIDGDVQSTDFYDTTGPQPFNSSES

HGELLSTAQNRVHRQYKRTLKASAAADGNLMDLVPMPSGCLMYKARHDKNGQPLIKEIGT

DEFLVCPKENMPMSLPHRQQHKQIVLQNRRQAQVPKQKTITIRSSRPHRKDESGVSFQFH

GRSGALPLNRSLSLSSSCSTNESLLIRSNSISSTRVSQYSDRVSLETNFGSLHLQSNLSN

TGRFIDSRCTPSIQENEEAQALEVLNGWLHASSVSTQDSFMWSR

>contig27052 Frame-2F

MRRLKIFQGGRFQNLHVVYIKYKNHKRLILDTTDYIQHARKSMKEKRDEFRRHINTFRDL

RHA

>contig27777 Frame-1R

MMHPSADQFISAGLDGSVRLWDIRNSDSTAIIRVDHMPVSHICAAYDQEGVVFGVYADDH

LIRMYDARNFQEGPFAKFSLYDASILEALEPFLAHMQAPNIRAKKLHALDLKFSPDGNQL

LVTTDRGVFLHLDAFEGKLLHLFKDHGLARGDLQLGCCYSADGAYVVTGAEDGRVLFYNS

STGQCVHNLPPGHHGPVLDLQWNPKRHLVVSAGGNSTVLWSPTGI

>contig27984 Frame-0R|Blast-methionyl-tRNA formyltransferase, putative [Phytophthora infestans T30-4](gb|EEY54544.1|) 1e-101

MLRNLHYGAINMHPSLLPKYRGPAPIHHALLNGDATTGVSVIEIDPKAFDVGRILLQKPL

TIKPFIHFNGLVKELAAFGADCVVATLKKLPTLKKSAKNQDDTIACKAPKLKYRDSLISF

DVSAGNILHRWQALSDSFGVNVLFRGKVVKFVEVRLPRTEELEF

>contig28417 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58735.1|) 1e-102

MLLVMTYNVLAQCYVRSSSFPYCKSIKLRWKERSKDLEAMFASSLPVSPHIICLQEVDHF

EDFWAAMMKILGYVGIFTKKTGTKADGVAVFWNEEMFEVKTFKQISLDLSHGNEADISHE

LLSRASSRGSVGAIIYLEHRETQSRFVVATTHLFWDPMQEDVKLLQVRRMLRSIDEFLSL

LDASTPTIFAGDFNSLPDSKVYHFITRKHCFKSAYAQYNDNSEPKFTNVNGGARTDDGRM

VPRFVGTLDYIFYRSSR

>contig28462 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61056.1|) 1e-147

MSYSLQRRLPLASLDQQVARASMQIFHKIVMQQLYLSRIDALKQWVVVSNPSDECIDLTG

FSLHCSNTNDIFYFPPKYTLLQGDEVTVWCSPGSLKLDEDYLRQPYLFWTNTTGTLRHLP

FDFSTTQAYEVFLFDPLLVEVASIYVSADGSTEFRVLHCKSTHLRTVRSDIINPRFCAGC

LSPPEFKKQTSWPTFKKGTIFSTSSYPREIYIFSRYWGVVSNKSLLKHFLAILLVPLMES

IRAVLIYFLFIMCQPLRDFY

>contig29784 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62400.1|) 1e-177

MGASFCTSPMLSSLEFANLQLANISYAIAVDQVGILPSSGTLTLHVNPRANDSTSLVNAF

LKAPSASSAVIEGKSGSLPPTPLSSFVNDAEFGQRELVAAVLAGYDESYSSEKTYNSRHD

EFIGLNVDAVVQAAQILAESVLMLASSNATSAQMNAIEVNASLVQSMLSCITLDWNCDLM

KRYSQYMVTTLIEYLSLTDSAMPSYSEPATLYPGAINRDRSMLVLKKSDNTLYSLYNESW

SDDENAVRLFPNAYEVFTRAFLASAMVPYATAEASATCKQTQECIDGGKGMECVYPGICA

KKSAFHHEASSPGIERTATLSQYDIVNSSMPIWAEPQWSTDIGGYSFPDPGAWIGWITLA

IGLIVTGCGVGVSLMMLRSVQKMKLM

>contig30122 Frame-2F|Blast-ribosomal protein S6 kinase, putative [Phytophthora infestans T30-4](gb|EEY53403.1|) 1e-48

MKKSPVAAMTNIREAVRRKSVGLSFTTNFSIFSRGTGSVGEDDRSEHEGEGDDDNDESEG

SHCNRSRQNSTPGEEDADSSPSPAMSSHNSYVEPPEPPLPPPGGLLEAATKNVQGKMQT

>contig30849 Frame-1F|Blast-alpha-1,3-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY57731.1|) 1e-135

MDARSQLAAVGNKAMGKGTEISSNYRGSKLVFMNVDNIHSVRQSLLAIASIFEPKKSVSD

ESSSSFYGRIDASGWLRHVRLILKASIELAHTVHNGMSVLTHCSDGWDRTAQMVALAELF

LDPYYRTVRGFQVLVEKEWCAFGHQFALRSGHARRDVSNDQRSPVFLLWLDCVWQYTRQF

PTECEFNERFLLTLADHVYSCKFGTFMFDCERQRKEFFANHRVFSIWSDINRQSERFTNP

MYASGNRTTVLFPSTLSKNIKYVATLTDALMVFLLTASRDLL

>contig31792 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59616.1|) 5e-24

MRKKKVKASKAEREAAALARLQQTY

>contig31907 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54721.1|) 4e-24

MAIAEKVNTMLPGIYDAAEFQ

>contig32313 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65817.1|) 1e-45

MLGKRTIVHSLAFIATADIADGEELFLNYRYNPDRPLPEW

>contig32843 Frame-1F

MRLDGQDVAMGGESQHVNETNDEGMTITSSLTPRRRQKKASGGFEFSVTPEPSCRRLSAS

RGRQPVGGLEESPARYSPSKVKAAVRSFADFLHFLEEKHQEHALMPVIIKRFADLGAVIE

SQKRHIDRWKGKELDLAIEEAQQNLELIRELGETIQKQELQIAELTVTKQEWEEKYQLAA

LEVESLKKQGTAQIQQLSLEVCSLRQSRVEIEKKLKERDMSCASFETTSKTLLSQLQQTE

RDRSVIMLENATLQREQAKQSDKLRVFEQQIYELCKHSDLEVNKAKDFEQNVAAWQSNYN

EKSRQVEHLEDALSRERQNTRQHEGKMNQLMDSYRKLQEHVENIEHEHEKQLADEHKYRR

E

>contig33035 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY53433.1|) 0.0

MTALSLSNAATYGTAGATNSKSFDVSPRRRLSKWYINMFMINFVEFAAESSRGVVLATLF

LYTKSLGGDLAFMGMLTSLFSVGRLISSTVFGWMCDHFSFRSVYIASSIICLVGNIIYLI

ADQHVASSLVALAVSRFIVGFGAGNRSVCRADVASITTINQRLPYLTLLATVVFLGYALT

PGLGSLVANTDSFVLGIHFNKFTSPGMILIIFNILTIVGMLTVYDESVSVHDGPLESPRT

AATSNTLSDPTTMPDRIVNIGATVFIFLNFNARGILSVFETVNIPLFIEATGRDPESVSA

VVAASNFQFYLGLLGLLSYFSIEYFRHNLKDVTWVQIGFLTLLGGNILLVMAPAQLPFAQ

LALAEFLVWSVGCPITTAVVLAAFSKLLGGRPQGTLMGLLGSAASISRIVLPLLPAALPS

LTPVFWINVVLCASSMVLLWWYSKLVHMTKTAMLADVESAFRIASPANDPRSPLGSDKVD

FPDK

>contig34742 Frame-1R|Blast-nuclear transport factor, putative [Phytophthora infestans T30-4](gb|EEY55858.1|) 6e-30

MIIFVQGKIQIEDNNPIQFTQVFQLVAHQPGQYYIHNDVFRLQYG

>contig34856 Frame-2F

MLTNPPKTIQRTSTRWGPRLNRASSVPVRPSHPAPRTQQRARGQQQRTQGSHRRQHHRQG

TRSNGLTNQAARN

>contig35129 Frame-2R|Blast-putative NADH dehydrogenase (ubiquinone) chain PSST precursor [Oryza sativa Indica Group](gb|ABD91507.1|) 3e-07

MTFGLACCAVEMMHSGISCNLCYPC

>contig36047 Frame-0R|Blast-DNA primase, putative [Phytophthora infestans T30-4](gb|EEY63518.1|) 1e-13

MRIITGDPPKSGEYHGCPFRHFEQEHLRKA

>contig37116 Frame-1R

MEEGVLSKNLGVPLVFVVAKADLCPENSVKMDYVEFTLRQYAIRYGASLVFTSAKTGSNV

DRLRKYILHRAFPSHFKFSESPQLVDRSCIFIPSGYDSISLVNQSLAGAQARWPSDKPFD

KIIPAPTEETEDTASLIAAEICVDSHENWLEKLEMTAGAGLQELQKQSIEASKKAEQAAV

ARRAAADRRKREDVSSKHLQNFFNNLLSRPEKTKTSRSISDKKKEESEQSLEDQEH

>contig37646 Frame-2R

MTQFYEKRGSSGHSLNTTRGLYLFVNVKLSGDTTNSFDCGDVASF

>contig37758 Frame-1F|Blast-putative dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48kD subunit [Phytophthora infestans T30-4](gb|EEY70299.1|) 0.0

MALLSYLVALSLVYTLPAARAVRTAVVLESPKLHETHSKFFKQLEHRGHELVFITGEDSL

SLTLEHYGERTFDNLVLFSPQKALGALRKSDLLHFVDQGGNLLLAASMKITRVQRDFALE

CGVEFEKKGTVVLDHVNAILDDDDIYNSVIAANDFVASERVVGSLASKPKHVAFSGVGMS

LEPNNILAFHALMAPATAYSANPVKPITQKVISTDLLFGTQVGLVTAVQSRNNARLIFSG

SLDLFSNKYFNNKKFANAEFADAITKWGFQESGVLRMTNVKHHRADGSLPAKMLSNANRG

DQPITLYPDAEVARDSLVYRVKDNLTYSMDLHELKSGQWLPFKGNDVQLEFVMLDPHIRT

TLTHDEQGHFSVTFEAPDVYGIFLFRVMYRRLGLSTIYTTTQVSLRPFKHDEYERFIPAA

YPYYASAFSMMTGVFLFSVYFLFYDSKN

>contig38038 Frame-2F

MKHDACPTALESKAIQFTRFSSALI

>contig38166 Frame-1F|Blast-dolichol-phosphate mannosyltransferase [Phytophthora infestans T30-4](gb|EEY56408.1|) 3e-50

MTSKHKYSVLLPTYNERQNLPLIVWLLDRTFVENKLNYEIVIVEDNSPDGTLQAARQLQQ

IYGKRKIVILPRKGKLGLGSAYRDGLKQSTGDFVILMDADLSHHPKFILDFIK

>contig38841 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64237.1|) 0.0

MPKSRRARTLFIEADALSPDAPSCLEGCWGLQRGVLHVKIDGTNIGAVVAVVEYIYRFKV

RVIEESNAREAAKLGQWLGMRHTMLYYSLVLAIRHVTTSTWMDILLDASALPDKLMRRFL

CDDLIGFIKTLKPEQHPDVLKNMRCVYISRVKHHDVLVRAVIGLLNNIRLVEFWRNLLDG

VSKWISYRFQMSQPPSLRAMHRHFAPAWKPYMEREPVELEVKSGEGNLFTLLEFGNFQLQ

IRIDIVDEMPILWRIIRSSSPQLLTSDPDDCTALDTDPQFWIRGQMKVKYWRAQPNHAEV

FHDVVIEYQHCLKQYSQWGDLVPPSPTSLAPAISTVAFQPEHTGKAQFRGKFFIWGDPVC

SMYHFLLQTTLFYSAPHGASTELSDLMVVSEMQRLPLETLELVLRSDRLRIPEGERTLLR

CLNKLVFGNSFTYLGSLSNQLPQKYNGRAKDVIRLYQCIRWCFIPLDDIMVTLRRSPREL

QFYELIEIGLQDTFRRFLRRRPWGWRKYRH

>contig39275 Frame-0R

MQRREHWTGPATLRVSKGVYRRSRRKTIKYIFGWVSQNNIVAFRDTALSDC

>contig39789 Frame-2F

MQQLGETPVASIATKEKTSDATTTGAAAPWLLPVKTPLSTAAQPWMIQQSMGAPGTAVAP

DVQGSGMTVLGSTPATAFPPPVVPPGGYDYQLQSQDWEKQGWNGRYNSYYASWDQSGHNM

DYRGYGLYGIATRDASADGDASGNKEESQYQYGGPL

>contig39925 Frame-2R

MELHIRKVIFDIAKLPFNADEFKTLQAYYLGGQCSIGANGCGNLVSEDVTSELTSCAASH

SSRMARYRRTMALINRLEASKQATDVVLLMLLRQLHYLVGAFKNTKNAAQTIDEILVSVH

EEMDELNIFSNVALLSHKPAT

>contig40129 Frame-2F|Blast-TFIIH basal transcription factor complex helicase subunit [Phytophthora infestans T30-4](gb|EEY64472.1|) 0.0

MDAIETCSFYEKYDTRRSDDTVLPPGVYSVEDLKALGTKKGWCPYFLTRYVVTFADVVVY

NYQYMLDPKVSQLVSRSFEKESIVVFDEAHNIDNVCIEALSVDLDRRSLDRASRNLSTLS

SQVNKLKQADKSRLDAEYRRLVEGLRSSNAVVAPSYLNPANNRPIDTSNDILIANPVLPD

DVLDEAIPGNIRRAEHFVAFLRRLIEYLRKRIRVRQVESETPQAFLHHLHQAINMEVKPM

KFCYTRLNSLLRTLEVTNLEEFNSLTKVADFATLIATYAEGFMLIIEPFDGASGVHDPVL

QLSCLDASLAIRPVFERFSSVIITSGTLSPIDLYPRLLNFNPVIRESLPMSVYRSSICPL

VITRGSDQMPVSTKFDLRDDLSVVRNYGTLLLELAACTPDGMVCFFPSYLYMEKIIGQWD

SLGVLKRVLSSKLLFIETKDIVETTLALDNYKKACDCGRGALFFSVARGKVAEGIDFDRH

YGRAVILFGIPFQYTLSNTLRARLEYLRYTHQIREGDFLTFDALRQAAQCAGRVLRSKTD

YGLVIFADSRYNRADKRTKLPPWITQFLVDSHLNLSVDMAVFMAKKYLSLMAQPVNESVN

VNSILLDADGVAK

>contig40451 Frame-1F

MDALNSLCFTASSFSLCSYRSEEPHLLSVPVSKPKPNSSVTILPAPGSSTSVYVPSASAR

DSVLTHKSNEALAKTNSKQT

>contig40802 Frame-0F

MAKDRQHIFSRSATEASAAAASTASMIRSNFATVSSALKNNYATNGSAAMSLPSLSRPSS

AESLRDKETAKAVPHHNKTFSIPSLMHIRTGFLDKNHSRSMASDSSTGSPEPLSQRSNIS

VDDAEHEFTTPRHAASAMKTASRFVMGMPTLLKRAVSNNHTLSNADAITTTPKKSPNAPA

LSTPREDFFEDNLEDNDRHSLLLMMQVPEGRNSWIPLMAVGEAW

>contig40877 Frame-1R

MLFYLTLRLKSFRYIIGRSASEWSFACLIRQINYCCRACKIFWAFSFGSNLTTIHCRLIT

RRFTASFIIRKLATKRINIAGHWQLPSKFGKIV

>contig40899-1 Frame-0R1

MYKFAIKMGGSESAVYFFKCVCVKVIMVRSDYSRWNVVLVFIFIRCVSRCIMSL

>contig41153 Frame-1R

MMIVLFLLLLPLVEAKCVMTQTCVNPTNEPDYDTCIPEAHKEPVEPQPMTGDRWPSVVGG

GKCTTATDCNGKGQCLNGSCVCRRDGMAAGPHCDQFIIQCPAYTKSACCTWQQNQAMAEN

FKLLASVFAKNSRGGCDACAANLMALWCGLVCSPDQADFMQMTHEWPSINYRPDPMTGKD

KVKVVEVTVALAKDMTCALFDSCKNTAMASLAAAMKSSLGFLNYQMQVGAVGHGEFITLS

FDATQDKAFDHDVLKCSNYSKVLPIRETLPAQAQLLDSIASDSIHDKQCPCGSCRASCDT

HTSGKSHFHVVDNPISVFTGFNPKLVAIVYGMLLLLVFSWNKWKHT

>contig41355 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66530.1|) 2e-55

MSVSLDQSADAEFLRFVARFCGVSLGSAASGRLRVRLGKTNELYEPSTIAKYLARSADRE

NELLGQTPLERARVAMWITFARNIQRCPPSSVSAHLQMLEEYLQQKTYVAANRITLADAS

LFYTLYATVRDFSPAQRE

>contig41405 Frame-1R|Blast-elongator complex protein, putative [Phytophthora infestans T30-4](gb|EEY68724.1|) 1e-39

MVLAALAHVAAGCNPNANAISIVPLDQQQYSSCSTYCGAFVSKNVVCIMCRNVNDNPHSS

PLKVVETLKHGEVTAETTILTCVKMMREDQFCDVCILAGDSEGRIFVWTRNTDGDWKVQS

PQSDNQAVSAAAVSALAASEMLTRKIYAAAYSDGTLAVFERREGRGICCGPPLEYFGLE

>contig41737 Frame-1R

MTTSQSSFAEIVAMSQPFTVPTFAVPQSQRHLSDNPLRSQFTAVEQALQHKLQQQLMKQA

DVAQPRSPIQQDIVMPSLTFNNNPKLPSLVGLLKKMQTISSFAPVESSPRQSQLSPVLRS

LSSTPFQQNMISPSMRKHAEYATSRHQATLPGWEPISLQRENLSMSRSFPVKKLSWSNAS

SAQIVSSLRPYDGHATLRSRASKYCKIEGCERVSQRNNLCHSHGGKRLCKENSCSSKDRG

NGFCIKHGGGKMCSMSCCEKKARRKGLCTQHYRMFNEHHFQGFVSTPYTSIVQSV

>contig41742 Frame-1F|Blast-GA23283 [Drosophila pseudoobscura pseudoobscura]gb|EDY71480.1| GA23283 [Drosophila pseudoobscura pseudoobscura](ref|XP\_002136386.1|) 6e-08

MANVCQFQSLTSVRKYDYRLPDAQPLFSVLSLEIQ

>contig41856 Frame-1R|Blast-UDP-N-acetylhexosamine pyrophosphorylase, putative [Phytophthora infestans T30-4](gb|EEY65532.1|) 1e-168

MKHHVAYKKIPFADDSGATIMPTGITGLKLETFIFDVFPLSTRMAVLSVPRETEFSPLKN

PPGTFTDSPDTARLMMHSEAKAWILDAASSLLKCSRDFDSFVQEKLNKAQFIEISPLVSY

SGEGLATRVESMMQSLPRKTIRWESSEAMANANSVPRSIRIAFAEADQSHVFRFIDAGKV

TTQDACELVETLRQYDPQQINALFARSIDADSIADVSADELTPLEDKMVHQLSETSPELK

AKWLDLGLDAVARGMIGALVLSGGQGTRLGFAGPKGMYNIGLPSGKSLFEIFALRISKVQ

DLAKTRNHLQDAPIIPLFVMTSEMNHETTVSFFRAHDNFGLLTDQIHFFCQGTLPCFTND

GKFILETARQLARASDGNGGIYPALSRSGMLDLLSNRNVQYLHVFSVDNVLCKVADPVFI

GFSIAQDADCANKVVWKTSPDENVGVVAKRNGVLCVVEYSELDRAAAERVDLKTGKLTFG

AANICNHLFHLDYLKRCCSQNDAEYHVAKKKIPYLNNEGTATIT

>contig42039 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53416.1|) 3e-79

MIDFFVGLTLQRENSWPSRAVAKDYFCNLKNFAKWDRETLAGYLQGGFYDEEDGTVTLAC

HPHVEASLYCQPPLWLKDHELQQPKCSITFHWGSRSKLWFRDRFQELERKLPLIYTVREP

MKGNSHLLMLENPALAAEKIAQDLELLEPYAASTLF

>contig42220 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60996.1|) 5e-67

MNKNVSPLYLACQMGYVSIVSLLLDRGADPTFHRPQGGVTCLYIAAQEGHDQIVRMLIRA

GAPVSTKMEDKSTALHIAARMGRKEVTRVLLRAGAYLNDQTRSGLTALYIASEEGHLELV

RYLLEIGAARDIQAASGATALFAAVFRGHRLVVQALLMNGASATISKHHGASPLDAAILL

GHDKIARLLQRFGARAKEHAMQFAERRREAAVWQSRPRLSYCTQHTMPKVDASETTGLPT

SSVTSVATRALGLT

>contig42646 Frame-1F

MDFKVAGTTSGVTALQLDVKLPEGVPLSILKEGLREAQLARLHILRCMSNRFAKPRDILN

SCGSALPNVSMECVIPTNLIGALIGVGGTKIRNLESQFNVSISIVDRREGIVRVVGTAEN

ADKARLWLQTDFVRSGQCESYPNSKGNDTRRDDDRQTLRNDRSLYFRQGQRYTMRVTQIM

DFGAILESSAGLRGFVHISELAREKVSNIYDIVKEGQEMEFECLQDGASGKMSRRVLLSE

NDCDSSPDVTDSAEEKVYVKPRASHHHNRRASTSPNGVKSHPRHART

>contig43032 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64445.1|) 2e-16

MCSKCSVAKNLTMDVSETGAYQQCSLRFCIRCLLAAKQQSSVELAISCLKATSGSSTFVA

PRKNN

>contig43047 Frame-2F

MLYCNKLVLLQFSYKSRQVKAKKKMLSNCLKLDIVNSERMKCWST

>contig43281 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56344.1|) 2e-71

MGKKKSGSGKTDKAAVKVHRLEVKKAKQTAKSAKKDRKALGTDEEDIELILQEFRKKDAE

RTQVLVEAVPQPSPRANFTLSALPSGEMLLFGGEYFDGDVNECYNDVFKWNLEAKQQKNA

DEGQQSIEAVSIEADVLREATWKSISSPNSPPPRCSHQSAVYR

>contig43490 Frame-1R

MEVQKLLKTLPSHAFSHLVAASKRITDFTPESSEKKTGDDEREGETEMEGEEQVDKEMGV

AVVFDDDEDDDESDLDEIREEEDDEDGTAAGREAMKLKAGHDSEDDQDVKYQLDVHAIDA

FWLQRELSKFYKDAEVSAK

>contig43704 Frame-0R

MRQEQRDLEEALRLSIDEARRQPSMPSAPPSSDTMLETLGYSETLIGSDGVEIVQLLRDD

DVANFSSCADLFRSSAVRMSNSQRLDECVVCFDGPQEAVCVPCGHNAVCMNCAQELADTS

RLCPVCRQNVREVVRLYRV

>contig44006 Frame-2F

MLAEHQTKVVLVTKLELSNDDVEAALDMLPTLSQLRHPQLLSINGLVWDERHAMTAVCEY

MTLGTLEAYLRTSGANLNWMNFKMKAAAEIARGLAYLHSQHMVTYDGLNGQSVYVDPIKG

CKLNPIQAALTTNGSSPYSSQSYLMRCDSTLKAFMAPEILKGEISRSSSDMYAYGVLLAH

LDTCQTANELTKILWRIRSQFGDLKADNATPFSCDGTVSSKDSNFTQSRNNHYKDSSSSS

RTLQSSRVLSLEESRLQMTFVLGPCKSDDRSFTGTFTFTPDCPNIIRDLAGACLQFDPSL

RPSASYIAAMLRI

>contig44231 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64246.1|) 2e-70

MLNSTINELKDFLAEQKDDEGQAVALDEVEQDNEFGFESSLTEDERALFESGLKLLSMCA

TIMKRGVLTIKNVTISNSQDVFLKWTARLDVSYTAAQDVIVDFGAALYPPIGTEELTEAV

NELSGSAVAILTCLKEMPELSSAEENALSIGEAAFVKQVATVKSQIEAS

>contig44709 Frame-1F|Blast-scavenger mRNA-decapping enzyme DcpS, putative [Phytophthora infestans T30-4](gb|EEY57723.1|) 1e-139

MGMTNLFAQVEILSSCIALLVVVLGALFIRQKAGGDVGSTKMLRNFNFVRVLKRNDTELA

LLGNFLNDNHKKAAVLIIQTAAMNSRALNQLLTQMSLHETLVNDIYTTFEGDVSRDVKPY

KVNLIYPATERHVRKHTDQNFHMVVETKETYRMITKPFIDSIPAENIEWVYNILDHKSEA

GRIIYEDKHPTNGFVLLPDFKWSDQSKLEAFYCLAIVHDRSLRSLRDLTGSHLELLRNIR

NASLQAFNDKFGLTFSCIRMYLHYQPTYYHLHVHFSHVKMSQGTSSGKAVLLEDVIYNLS

CDGDHYKKATLSFVVGELQHSQLFKLFREKHII

>contig45096 Frame-0F|Blast-nucleolar complex protein 4 [Phytophthora infestans T30-4](gb|EEY57287.1|) 0.0

MQSMRRVLFFFLEKGDLRPKQTEQHTTKKAKSANSEAIDTFQRWLWDIYVSYIQEMLHWL

GNAEADSNLRVGALRSLMEFVPREGDIRGCSGPTFGNETFHRVVHELANTERLTGELTSV

LKGEYIGAYMDVQYFMLKNLAQILDSQNDKETELVLVANALRMLDMVNMPYDPEDISSFL

VVPKDSNLLEQDQVSSDEESDDEILETTAASGEKRKAGPDLDAKKASKAKGLYNIKQHRN

AFSLAWIAVLRHKLPEKLYKKVLAKLPDEVIPHLVNPLLLADFLTDSYSIGGVTSLLALN

SLFILIQDYNFDSPDFYNRLYALLDNRFLYSAKQRNRFFELLNLFLSSTHLPAYTIAAFA

KRLSRGALTAEPGVILFIIPMVYNLILRHKECLQLIHRTGAFTAAEKAAKRRQELSSNSA

VDAAANKLIDNKTELAHKDGHDPFNNDATDPVNSNALQSSLW

>contig46466 Frame-0F|Blast-hypothetical protein PITG\_05628 [Phytophthora infestans T30-4](gb|EEY69396.1|) 2e-27

MVDYKGQERAETLLVLCFVVICTPAWIYGFIYQDFSYAFQAWVLATVTSALLILPNWPFY

NRNPIKWLSSVMYVKRETQKGSIKTE

>contig46664 Frame-0F|Blast-pre-mRNA-processing factor, putative [Phytophthora infestans T30-4](gb|EEY56427.1|) 4e-68

MRRALEFIPNSVKLWKALIELEDVDGARILLGRAVECVPQAVDLWLALARLETYENAKK

>contig46800 Frame-0R

MVIHYLQLWRNGYECFEAASVYASGSLPKGPTKTHVIKTGRLRIDASDASKLCNKSNPVG

SKAQRSSPIDVGPVKKVVSPPSQTSTYAAVVANRQAVDGSRCSALSEPRLSYAAVAAGTA

K

>contig47151 Frame-2R|Blast-small cysteine rich protein SCR76 [Phytophthora infestans](gb|AAN31495.1|) 3e-12

MEVPEPLMNGSITYLVLTLLTCFAGIGMGITGKMSRENSS

>contig47384 Frame-1F|Blast-26S proteasome non-ATPase regulatory subunit 13, putative [Phytophthora infestans T30-4](gb|EEY57465.1|) 0.0

MEQLLGQLSTKTAQEAVLLCKMHIAQLKFRRGAAFLPEVKATVDDDKQIIEALVGAEPVV

HAAYYRVACDYYTAVGPAHKFYKNALMFLAYTQYDEMRPDERFDLAVNISIAALTGDGVF

NFGEVLATPILRALEGTDKQWLSDLLHAFNKGNIDRFNEIVGQNSTEFEAQPALVSKQAY

MKEKVALLALMVLVFQRPSHERNIPFYEIAETTRLPLEQVEWLVMRALSCKLIKGSIDEV

DGIVRVTWVQPRVLDNSQLQKLVTRLDGWEKKVNSTLLYVEEQTPELFQ

>contig47429 Frame-2F

MEQSKAVPRLAATYAAYAAQVSHALQTLLDTMRVNVEPAVDFVSCGAGLHEHFVPKASLE

KHLWKCHGERKPLL

>contig47726 Frame-0F|Blast-inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY59677.1|) 0.0

MGNVKNAELSVQTVMMPGETSNRDDASSHKNIGNIIRFFQYDTEDGGGGLVVEDLQESIY

SNAIPRQLMELIAAERQEQADRAREDLHSFLNQKKGKQNLGFYGTLIGQIQDDTDSSLAR

EWLEDRVRRRKEYVAMLRRNIQYLVNRDKHKNYFKASVEKKSADLRFVPINMHIQDLLIG

PTHAFINDERRRSSKEVSAYDFTTVGAPAAHVYKFNKGGILSYQNRRKKMEAKIADADLD

LSKWPEEIREYDDLKWDLQLRMDCAFAQALAALTCSFVRKVEVAIQNPDVFRGEDMLRQF

SSLGFLFQVESLLSTHGKEIGMLEDMAGSVEHLSCVAFVIQDVRDKPSNRFSFRMSRRKD

VADEAGVVKVTVSNKTGAKRSHIKYIVTVQVATSDVELPERLASGGEINVTPALFSQGIN

EMQTIANNTERAKTELQDIINFRSLKPLKAFCEKYRRLIVAMPNSGTSGISSSLNRVGSH

RYKAMSTDSTFASPLHLTQDEVTQELRALETCINEAAQSLVKTKRTEILKRSSDLCRELG

GGRVTVCKSAKDRTAMSVTLEQVRILQRHHDLPAHRVPATVSVMRSHGVRIENALKNTGK

RQFAFNKLQRSLLPEDYRCPDQVGGTGNVS

>contig48060 Frame-1R

MASLQQRNTALKKAVSSTLDSASSNDRETSPMLAKTIETINNEANDWPSILLLLLLYTLQ

GIPMGLTSSIPFILQEKVGYGDQATFSLVSWPFSLKLLWAPIVDSLYSERFGRRKSWLIP

VQFICAAFMVVGSWFMNDLLGEGEDQEPHVIYLTAFFFILYFIMATQDIVVDGWAITMLS

EKNVGHASTCNTVGQTIGYFAAYVGFLALNDPSTCNTYLRSEPKNEGMVSLPGFMSFWGW

VMFFTTLGVWLFKHEKPEHDSSERLSISQTYSQMYSVLRLPSVMSLSVMLLTSKIGFAAA

ESVASLKLVEYGMKKEKLALLTPILIPLGIVIPVLIGRWIKPLQPLNLFLVGYPVRLFVG

LLYAGLVYVTPMAMAQDEDSHYVFYGVILAIGALHEVAANMMFVPQMAFYARISDPSIGG

TYMTFLNTVTNLGSKWPNSLSLAVVDRLTTRDCFGGRDLDIGMVTCSDAEARRACADAGG

ECVIVRDGFFVETGICLGIGIVWLLFFYRR

>contig48183 Frame-1F|Blast-DNA polymerase epsilon subunit, putative [Phytophthora infestans T30-4](gb|EEY69170.1|) 1e-140

MLRGSAGALLLRRSTRYMSLLGSIFGIGEFEVARNSSLTRSTRKEQAYKLALLDYVSMNS

HPKFMLQQILEDETPFLMGHVLVGASQCLAPLMHQDTLDAASRLHTANEIAQKAKQTTAS

ERMHVLALNAMIFGRQSEAATIYETILQNDYTDLLALRCCYDIYRLIGDSKNMLATIRRR

LPFWSPSDTGYSFLIGMQAYGLKAVGQLDAAEALAEKALSLNGNDRWALHTVLHVLEARG

NANHGASYANQYKARFDNGGPLESHLYYQWALYMLDLGHYERIEKMLEVYIFPSQPITSP

HAVPTLCDATQLYWRLRFAGQDTIELGKQLLQNWSAILSINATPKYSSPLAKILQYSILT

CVNRVAAPPMNLLTAEPAVDIDSLKAKLDVTPFQFSYSPLSGDLERVYTSICRSFQAFSE

ERYEEASLFLLPVRGNLSCLGGTDVDLDLIEQLLIECASKCDDLRLAKLLLNE

>contig48428 Frame-1F|Blast-PREDICTED: hypothetical protein [Monodelphis domestica](ref|XP\_001373977.1|) 4e-19

MDSSLELNGSMDIISNSVEFDLSSKSSAFENITELVDSSLPSKGPAFVITSKNDVRDDGI

AHPGPIGPATSDETPSNQLSDDKLIHHLDTNNGSATESGWPRARLKAMLSIVGGFAIIAS

LAVVIAMHRKDKTTSDELGTPSDDISCFATPTTDRVDEKISHRKLYDRNEFADSIDNTPL

TSIVVMGVNDDVTSVLRPQSQLYFETGGRIMSGMYARSGSAVVSNGEVLQNSYYNAIPAS

QLQFNISHGPSASQGLPSFQFESIFDTSNTQPSFSSNMSSDYVRPTSERLYESIESSTES

FQNSSETSSMGSMPNSEDLTDSKFFEQHVDTINSIDDSTSFALSLLSSDQGTSLSSSLSI

SDYTSRDTEASEHLHSPEMSTNSSRIAMSFDMGSSSL

>contig48855 Frame-2R|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY62028.1|) 1e-22

MLEMKLIIASLLSKYHVELESPETVTYAVSVTLPVKGQLNAKIVAI

>contig49669 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59939.1|) 1e-24

MMGYFPLSILFIFPPPSTSTPFDLTRLHSSFISLVEQDYPILIGELYTEPKSGVISVMQT

AKHRDNGAYQIKFETNPRYSMTTRQAIQSRSWELMPSSKSKLEL

>contig49687 Frame-1F

MWYLRTKWVSRALRSSFWTPQSQRWCSVYWGSTFSTHNRNFHACGAINSRASLDDSESAL

AQQMLDFMKLAEDE

>contig50102 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61370.1|) 1e-59

MIPWEPHDVNLEHLKRRAKVSAYMPLLNYQGLVGILSESLERQTSHRTLYRTRLRVGRIH

DRLSIACYSVVFEVIKRSLSVVSLDTYIPVMNFSVSDMKMQCVTRTEFLTDYAVDASVEI

SARYYNTSLADWEPFIEPWRAYAK

>contig50245 Frame-2R

MCPLRYILLLLSLLVAMIGLSQAMTDQEISALTEDEDEVGSKNKKQRSKARVLVDMLNGK

YLFDTYMARRSLTTMKID

>contig50388 Frame-0F

MPCQAVSSSQGSETSAPTAHELAKTILKQSPSKETLDAVVALYVNFLDDSSNDDRTLHSL

QELDTLQYLDHALWPLVDVVATAHHPVKKAWLVSVLLLAGFRAREKNAESNVWSLFGKKV

EAWKTCMTTLWSTLAEAANGAMWTYKEQTALTQFLILGFQRLDVPFVAASLLQ

>contig50443 Frame-0F|Blast-exosome complex exonuclease RRP43, putative [Phytophthora infestans T30-4](gb|EEY54228.1|) 3e-26

MESLSIVKGQSAWKLMVDVYSVSHDGNVLDAALISIVAALKTLKLPATSINDVDNVVSIV

P

>contig50829 Frame-0R

MRQKLWGKVVLLSALRGTSSSDVLASSPTIQAVGLRLDEAVHPCKDIISCSFCCCNGHWS

TNPLREHHGIKQICDESGA

>contig51570 Frame-2F

MEARIMARGGSVAQMMKVPIDSLENEVRHHSPIGAKNKLKIETVKDARTRDFFSKRENED

AERETARRAVPFKSSLREHVSGKSQTASINSTPQAILKPASNDTRQMQTLSAKLTSSQKS

VSRARKLQYSVTELRRLMIFAAPKPPDLINMKIVEVIQVRDAIFAAKRS

>contig51668 Frame-1F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY69816.1|) 9e-84

MKQKRTDALLVVDDNGGLNGILTDTDICRRVLARNLSPEEVPVRTVMTRDIKYVSPNDSA

IDALLSMQEGHFRHLPVVDRGAIAGVLNIGKCIYDVSKRLEHAIQSTDQLKASLLKSGKS

STLQQLLAPMLEKLSAPTLGSILESEAL

>contig52698 Frame-1R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY58649.1|) 1e-31

MVMCALVEATVITTNTIRAKWYFAILTGLKAWPMAWLSFLTVLSATEIAHVGCEGITMGL

VLSGQGL

>contig52786 Frame-0F|Blast-insulin-degrading-like enzyme, metalloprotease family M16A, putative [Phytophthora infestans T30-4](gb|EEY56192.1|) 1e-23

MASILTINGMDVSSLDERKYETFTLSNSLQVLAISDPKAEKSAAAMDVHVGHQSDPEELP

GLA

>contig52878 Frame-2R

MHAMPALWVSGRRRHGRVRPRRRTASENYLHDHRHSIDYYHRNSPLLSSTPPGEY

>contig53082 Frame-0F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY56470.1|) 5e-50

MRYICVVQLFQLPMMFCYSLGYGAVSHVTYEVANCLVFSVPLINAVVFGWWHLGEAKFPQ

DDLRDNGTMLQSSCYN

>contig53301 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56011.1|) 3e-33

MNSTVRLLRREIELLEQVQEDLFCAICGVVIANTREMIRMTTHDALMETFVNPMGHVYQV

LTVRDVTRSHVFTSTARSIQDTWFPGYAWSSIHCNSCDQHLGWRFDHVTS

>contig54010 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69019.1|) 2e-45

MPPERQLSTELERAQRLCASFQEQCLWRSVKNIELEGHLGAIQIEAASWREKYAQQSAKL

TELEKQNSTLRAHKTMLVQEVKRLQPYSQVNLAALVQEAQEARMMQRSLQAKVATYKQLH

PAIGKTTAETSASGFVLVEASDEEA

>contig54519 Frame-0F|Blast-leucine carboxyl methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY66691.1|) 3e-23

MQQNMAHDAEHDDAVRETASDASQCKFSAVQMGYYEDPFAQYFVRSPSRCMPIINRGYYA

RVAAVESLVRKFLV

>contig54601 Frame-0R

MPNQNIKRSYCEGNKKMMFRNLCTHVMQSHAHVITTVTQNTETERAAWSMLKVHKRNSNA

C

>contig54973 Frame-1F

MSKYGSSSCAGCSCNKGAPLDGNDFESEPEPGSTNCYKQLRCLRLQRFDSADWVLQTQCT

QQSLLKGHLTTNMAQKLIDRHALKRCAFVGPVAVRNTGHSAIL

>contig55291 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67791.1|) 2e-29

MKIHGGWLFLRGKVHWRKRWGVVMACNKQRT

>contig55772 Frame-1F

MQEYINSKRQLGPSKQAARHSSVIVSLMKSNLMATTQGFKNILEVRQENMKLQQSRRARY

GKTASSALGKPLVFKPPRSNHSQNGSLDDVNLSTSLPRPGKNPSLSTERIEIQPLITTRT

QEQMVAEQQNYTASRAEAVSQIESHIVDIGQLFGRLSNLIHEQGDLVRRIDDNVEESLGN

VSSGEHELLKYFSNLSNNRLLALKISAILLVFLIFFMFVLA

>contig55844 Frame-1R

MRKLVDLRNRCNSPMCRMGITQGIIHRIQTAFHLARKVRYAATWFCYYFKLHHLAT

>contig55909 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60983.1|) 1e-41

MSDNGDIPSEYRISEKWDKCLENFTLYFGAGLVAGGLTSLVLARTGTGRGLITGVGAGAG

AGSSWKTCQMAFAGDANAQASLDKADKIVEDFMEKSSGSK

>contig56287 Frame-1R

MASTPAISMKVLKSWKLRGESPLRFKLPLGYDDEGKVFTEWFKYLSQYQFEHSLDVRTIY

NKLRDWMPGSS

>contig56423 Frame-1F

MAESRQLALERLLKEKRRQKHHKSRKATTTSHSTCHAVSMKDPTISLCEKTIILDSPILL

VGPHK

>contig56816 Frame-2R

MHDAIATKQTFLDTVPDQVAGIQAATTGLQALMGKPIVATRTRHSRAEMELPTPLYVLYC

ELEAYQEASEDAGKQLHLAIVNATNLQQSTKEYRKRQFPSALNVDSIKKRKPSSSSLTSQ

DIVSRSPSLQRENSISHERESGEILAINPLEKHQKEEQKNGTFWHHEYEKESPLYKVWTP

HVKALELKLSLTLPMDEPQEPFQTGIFTLVFQYYPIAKIVTVEVTKTVPNILNAITTSQR

ILMNLFPGDDGNQVPQGFINYAFQEENNPYVEMTFPTTASCRPYYWTQYICGLTPLQRPH

ESNLSAKKTRQLLSRRIE

>contig58616 Frame-2F

MTTRLRSSESSNALPAKAPKASVACKYCKKIFTSRGISRHQKKCIMSFVGN

>contig59343 Frame-2R

MVRGWIRKSSVDGLIAITLVVSLF

>contig59488 Frame-1F

MHAEDTTMENEYFYLYAISGFCVISLLLL

>contig02193 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59871.1|) 3e-17

MPLTIDHLKKTGIARAVSKLRQHGNDKVSSKAHELRQKWIEQRSDQSVDNDSASNPLETL

KTLIRLLDQSNDDVSDHQVQSKQLAALEQLHSMVLDTKDIIDSKVGISVSKLRKS

>contig04270 Frame-2R

MDTRIHSLEFPKLRYVIIDFGLVPSFDATALLNFRKTSILADLYLFDIYFCGLNTAIEQA

LRQNAYSQRIHLLQSDVDIALEMCENALLPEKLWATPDTPRCVKRMSQLELWEHFMTASR

EQDGTASYKKLLPLAAYLDIVVVPNNSQLVPDRLRDDTYFICSGYINFIMDSEFSTFPKI

PGIRSERKPPFHENRTLEEKPGADSSRKLSFVIPEESQWTPFTTAKSRLLKIGPGSVITP

NVAGMDPDYKYLASSDCVMLRLRAVAMETLETNAPHTAVAVLKLINVRLATRFCHSSKRV

SQMSSLLYK

>contig06401 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60767.1|) 1e-06

MDTKVVHKERKKTNRVPDDKNAQEAQPSEYLNKVFCKRLVP

>contig09804 Frame-0F

MEYKIMPKLTNANPVYTKLTWPLWNNNFLRFTSGRKTLALLHRKASQYFSHQGIRRLTTF

SICYDRVPDTDLLRSALLDSSIQSTRSLIR

>contig11157 Frame-0F|Blast-tRNA (cytosine-5-)-methyltransferase NSUN2, putative [Phytophthora infestans T30-4](gb|EEY57861.1|) 1e-148

MNSELREYLSYEQYVQENIKDKSQDKLRATMFPPTDMERVDFHLERCMRCLPQDENTGGF

FICLLQKVGRTPHDKEIKLDEATDGATKANEAVNAVEGMQEATKADDEIASTKARVEIMK

TRQSRREDRNKKNGEVYVSFRPEKWAEIRESYAIAPSFSGDQLLTRSDDAKSVTFVTKSI

TMTLVEEMKRKNIHVVYAGLKMFERNETVEGGKIYRVCQAGVPHILPFMNKRTTKVAAKD

FQMMLERLGDLFDFDEFEASTRDYFEKTSIGSVVCMLDYPGLSNVALKVMNLVVWRGRNS

VNVMAAKADVAVLVGTMKELKMYDEAVQETIVNAKRIKDAERATRNELKEVETAQGKKEN

DRMEDAITTTAT

>contig11382 Frame-2F

MQETHQLNPLTVRPQVITGLLDLFLKLCHNYNLVVLHQIFRGVTLQHFQPKFMSDFVANL

TMQITSFESIFLPFLLIKLPSYTKARLIFFFRCFESPDVSLVVKGMSNELNQYIWAWPFI

LECCGSDTHFAFDHFQIKRHAEKEIPELVYVGKLQLSMASFNSYLEKYLSNVPGKDIVVL

EDHATKKTFTIVASENIIALNNLVLAKYCAQLYNDLIKGFQWDVFAGGIHCLLQYLPQSS

WHEKFASPCLHFNFPGARGSLTDPGNGTTDTAYQVLVGSLELIIFERFEPQFKADFSLIL

QRAGYDASRKTMLMDAHLHALRSAGFAFSTVLLQDGEFVHVNKGRQHFWRVVEKDGTSRS

INAPCVFLSWEWVYQGVSQLGISTECWFAMKNASLCSDGWVFDLRRAIVEAAKCGVAIVR

TGQFLRSAIASGRPRTTQLLSFTAAPAPIDRSVVAQRQAQMILFLESILPCLDAIVEEAY

ELGTSSTDDSEEFRKVFDDEGMWSTVDADLRDPPADTATNYICGICEREITNLYKQCLGC

TVYSRRCRPNMAYQIFRICLRCHSQPERHHFKPRAITSYYDKMLSSEGHTGILPATRRYQ

SVRSYFKCRCVPSLRCAHCGGCESCSCLCHTLFQTRFRFTAP

>contig12628 Frame-1R

MLETVRLYGAVLSLQRGILHAQSSADEQYLLHIARASNNAIAASPTRRIWIADCRPELNA

RVNNFTGGGTESGNLAHARVTFLNIGNIHAMRESLEAVRGLGGFLASTLHTQAMDFAWSS

RVDDTKWLSHVRRVLSGALEVARAVEAKATTVVVHCSDGWDRTAQLCGLAQLLIDAHYRT

RRGFLEVVEKEWVRAGHKFQERVAPGIDEDDDDQQAPIFLQFLDCVWQLLRVYPTYFEFN

ARMLETMADALFSGQYGTFLGNCERERAAWSVRERTPSLYTCLLQDDRFVNPFFRASSTQ

ALVPYAPAILRQVTLWISYYFRGAPFSAIPTGNPTPPLYADVYEDGGSRDGQEDMENAMT

AALRRIQELEDALRAATSSPSSPRLAPMSYPPLYAKGQMLSGSMNDSNRSNTFQDDSATS

NTMHAACMPLAASIQALAPAATWTCSVCTKTNVAEVLQCIVCGRAPR

>contig12826 Frame-2R

MASIWRRDANCSFLQRYTKPGIDATTPPRPRRPRELLIFLVVLVIVGIGVAARMTGHLVF

DVSSSQRFENGLSSSQRAFQLSKYAYAANGSRQHPQSPYYKRSHHFDSSVSRDRGIVLCL

ADKIVAMGLSLIREMRCLGNQELVQVYHCGANELSAKSQELLLSVDNRLEIVDACSDLVY

RNLLPENMVENFQNWFTKLLAMYHTDVGHVILMDADDIFLTDPAQLRELDGYKQTGTVFF

YDRVVPRPKFLSIQDHNESYLNRLVRTFPYDEFNITEGEHVSDQMKESFAYNGKTCHEMD

SSLVLIDKTHVPPRVFDVMFWFFTKERFRIRYSLGDKETFWLPFEIAHEPYFFSPWGVSV

VSSTPNEDMAKHPDSLCGSMLQYMPVESGEAEVLYVNGKALLAPYPQGMTYFTKVGLNNR

YNPFPTHMTPRQRRTGIRNTNQKLQMECLAGLGSTPLPQKFLESLLRRRLHYFGIMTGVL

GPLKLCEL

>contig13469 Frame-1R

MDVQDANDEGILCAECQASSDRRHRDEIENFFNRVVTIQQLNENQEVPATENLTTDANHS

GRRRSRRIRPGSVCTWPVVANATDTVYTLKANIYAEIGALPMHQRLYYKGQLLENNYTLK

HSGIKAGDAVYMRLLEDSADDHVLDEEQEREVGFADSVLLSRPSTKYEKGKQDGVENTSS

CTMMDQATLDSHESFVWVCPDCTFVNDDTDDICEMCCATKCSA

>contig13858 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61882.1|) 1e-114

MVTATPAQVLQDLRFEERLADVKARIPTTLELAKEGSLAKRNQAKRKLYHDSELIRIELE

ERMNELGIESEWLTDPQVIVANTKLDSVRNQLKLDVLQGNFSPLEKIYMLVRMLTMVLVL

VGWLSCVTVLIPLKWLTPLLVKLGVKKNYLPMDILSWGTAAMVCVTACTDVKAEGVENLL

NLKDSVVCMFSHSSNLDGFIVNGSSPIAFKFAAKKSIFLVPFLGWTSRWGFDFVAIDRSH

R

>contig14774 Frame-0R

MKHGQVVHLSNEEIRRWRRLAQHDWAVEDVTTVAAARALGVCGKDVEAPNSRSSSIETDS

TDSDSDGHSLHESAVEDEPEEEHEDEVLEVPLGIAFDRLCAVVNVCVNFGDVLFTPEDIC

HLVHLQFLVEEDG

>contig15207 Frame-0R|Blast-FACT complex subunit SSRP1, putative [Phytophthora infestans T30-4](gb|EEY62317.1|) 0.0

MSDTMLSNVFWGHSAGVLVLSASGLLWRSRTTESQKKLLKDDIVTLLWTPVGPKSHHLKV

YQKGGKYVRFTGLKAQDVSQLKTHVESYFDRELEQEKVAAGGGNWGDMKFEGPNLNFRTA

NASVMELPLEQISQCALPGKHEVELQFHEDDTVAGDEETLVEMRLYLPPGDGDEEVVTAE

EFRQQVLEKANIRSVMGKSIVDLDETIGTFLTPRGRYGVEIYGSFLRMHGKTFDYKIMYS

NINRCFLLELPNGLNTAFVISLEEPIRQGKQGYPHLVLQLSKNDVHIDVNLSADEIKKYN

GNIHERMSGALPQIVATLFKFIIGKKVYTSGKFKTHSGDRAVKCAVKAQSGVLFPLEKSF

MFIHKPTTFIRYEEIDYIEFQRYAGQSGSSASRNFDLLVSCKSMGGEAAREYIFSAIDRR

EFPELSQFLTSKKLRIRNLKESHAAVAQTGSKKRDFNEYLEELGPEEGEIEDEEDEEDSD

FGPGDASGSEPSDLSDDELSEKGSDDDDAG

>contig17322 Frame-2F

MLAAGASQHLLQPCFTLLFHLMPWPLEGQGQGQPQETNYQICQERNRDQSPPSGL

>contig17847 Frame-1R

MVVASDVFPLMHALLIGVGFKRSANALAKEAKLQPKAFESEHDLLDVYQFYLTHNVNTIQ

TAKGQAEKLKDAAKKSKKKMAERSSSSDRVKSIKEEKTIAKKGKVVAKQAEKKVKSALPE

SKSKSETKTLAAKTDSKKKKKTSHPVNKIAVVKKASSDDSSSSDDSSDSSDSSDDEEKIK

TKKAASINKNSTQRKESDSSSSDDSDSSDDQKKKPTSIKRKAEAHSTPINSKKFKENAES

TSEDTSSSDSDSSDSSDSSSDSSDDEEAQKKEAARRELATKAALEWQPKKIEQVGSKEKM

TGTPFQRVDGEFWSQKIVDDTLRDNSYEGTFGVDGVGVKANNKLLKTRG

>contig18929 Frame-2R

MKDESVPAAVKKRLKVDSRPSLTRIADPLADDVAVTEALRDIVAPKSEVQEGGVGIPRWV

WGIGLFLAFNYFTG

>contig20148-0 Frame-0R0

MAEDKNVVLLSSNIKKKHSNATNRDKTLGLSADTPTFFPRQSTEMNEILQLVSIDYLSLF

WYT

>contig20148-1 Frame-2R1

MRFGLQGDWKCINCGNHVLLQDYRLLSLLSLRLIICFLGLRTFLTETRASDAELADKKML

VLCTHQTQSAR

>contig20997 Frame-1F|Blast-ribose-5-phosphate isomerase [Phytophthora infestans T30-4](gb|EEY68245.1|) 1e-105 NOT\_ORF

MYAAERLGELVKDHKLTDIKCLPTSFQSRQLIAQHNLTLTSLDENPLIDVAIDGADEVDL

QLNCIKGGGGCQLQEKIVAFAAKQFVVIADYRKESKQLGEKWTKGVPIEVIPMAYVPLMG

TIKQNFGGMPALRMADKKAGPVVTDNGNFVLDVNFGILNDPKTLCNHLKLLPGVVEVGLF

CGMAKKVYFGQLDGSFTMRTAE\*SAVILYLAMIFIDRTKKLCDLSTASSSSRAKFCCAGY

C

>contig21316 Frame-2F|Blast-histone-lysine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69457.1|) 1e-57

MILCDGGCLKSYHFSCLGIDSAPGGEEWLCEQCRTNEQLCFACGRNGSINEKGGVFRCGV

ASCGKFFHQTCIDANRLSRRAGGKSKPSLSTLEGLLESEAFFRCPRHICFVCEQKRKSSD

LMYCLKCPEAYHPQCVPPSARYNSVGLLCWKHVGEQLPKIPPYYLSDRSIDTVTVDSSMH

LPWIFLPKVDPDASNSEDCHHFRLLKKYH

>contig22278 Frame-2F

MYSSQSNESDATPRTLSVSEKYLTEYAKAETVIFSRPLARIYTLILCRNTLQAFKVVYVD

GVTRQYYSSFREKIVCELLASCHALGNYQVGVESSEVPETARMIPRKFIHQEAKQFADTV

TNVTAMDRELRVVQGIILHLLMAHGHRKTARIQRQLPQGLDEDMHSLTLEFNANTPTSGA

TPQPNKLFDKVTYMLARELHDIVARHGATHEFISTYLQSLYRLMLAPPAINEFMKVLTER

EEEYINTITRVLESQNSVAIYWMFMVLSRLMESKLHQFPCRQLLLSNTLFMKTLLSLLDK

DIQTDAFLSELPTMKLCQFLVLLVKTNAEKQLELSEALYQNLATKYRMLLRILFSFPALY

TVEACVSILNRMTKTPVFLNYGNSDSPLRYNDEKVPRRSLSFGETLNFRPESYRGAPLAP

RSRPFLYSSRRASSRNNTILSSGSSASGSA

>contig22946 Frame-1R

MMTETSEVPNRQADILPSAVDSIQMYWIDAVEVRERPGKIYLIGKMILPTSKDASPLFQS

CCVVVNNLQRYMYLLPKKPRLIDLSLTEQQNAWMAMHEEIYSILIPSCITLKRDQENFQT

KLVKRDYAFEDANMPRGTNAYVKVKYLAKYASPPSDFCSHGGKTFDRICGAFTRPLENFL

LTRRLLGPGWIEIKGIQKCSESVSYCKVEYETFDPKHVSSLASGMAPPPLTVMSLSLKSV

CNLTTGKHEIVA

>contig23549 Frame-2R

MTVLVEGGTNDMTIKAEPESATSTTVVAESSALPQQVMNDVYNYRATEVEEIEMEQLRWN

IQEQVFQRYFHQAQKYDEWGRLEEQG

>contig23673 Frame-2R

MDYQQTAQTFSLSTQWFNTLKNAEHTVNSF

>contig25262 Frame-1R

MLDVSLSSNKETYAKQQRRRKCVKEGTETTTEASKANIKKCESGSDDEVNRSTDSIEVDL

SEKATPPSKKYQPAL

>contig27053 Frame-1R|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY53511.1|) 1e-133

MSMTMVTNGVLKRIPHDASPEQIAAMVSASLALLMLACVSFIKYLYGFIVSFIVTLMLAI

WSLRWVYQYGAGAFGWNYSWLRSSNRILNSLYSNPKDKETLRVVCISDTHAKHRHLRNLP

DGDLLLHCGDFTNRGTHDEISDFNEWLGTLPYRYKVVIAGNHDVCMDAVEYDQHWDKAFR

HTKYNDPSLSKSLLTNCTYLENRSIIIEKVKIYGSPMTPPISGRAGAFNVARGFGGQQHW

AKVPADVDVLITHGPPHGILDLTFTGLHVGSETLLKETMSRIRPRFHVFGHIHESYGATR

VGKTVFINAASSTLLAKPVHAPIVVDIP

>contig28041 Frame-1F

MMIAKLWELVFPGEPFKSNNDPKWLEIGFQRGGPASDLRSSGLLGLYCLIYFASYPSSEF

QRILKRTRHGVSEGNMKNYPLAIACINVASLLTETLGLGDAGTHSEGCSPSAMMTYSLLI

AQSVTTSQSIKPTKTLPFLSDYKCWDDVINEPGNYVYETIFCLLFPVLDSLFVEMDAGYM

EFGQVIVAFRRRVNEIFNMQPKSLTELQELTKKPSIASLVLPTTLAKQHKIGKISKGKKV

IMGGM

>contig28579 Frame-0R

MKIRSHIHDNGARGPAFEDYQDLPSVIACVGAGTPLLMDYRVWHRGLGNLSKSTIRPLLY

FKYVKASAVTQVLKERKRITPTII

>contig28874 Frame-2R|Blast-phospholipid-transporting ATPase, putative [Phytophthora infestans T30-4](gb|EEY63415.1|) 6e-44

MVCILQSIPSISNTYGYPTNAPVLFFVISIDAVFAIMEDLRRHQSDL

>contig29976 Frame-0F|Blast-sodium/glucose cotransporter, putative [Phytophthora infestans T30-4](gb|EEY64122.1|) 0.0

MVELHMQSVPDLSAGARVNWADILIIVSVLCSTLTVAVIASIQAGESRLAKYLPCIQRAN

QSEAPVVEAPGDVYLVSDATPGKKLSAGDENGSTTSHRRPSASLIARDGPENQHNEVSNF

FLADRGMQWYFVGGALFASNIGAEHFIGMAGDGARRGMAVAMYEWYAAILILCLGWIFSP

IYRRSGVYTTPEFLEYRYGAPCRHYLSLITVIMYVMTKMSASIYGGAIVFQATLGWNLYF

GAGICIALSATYSMAGGLRAVMYTDLFQMCVFTIGGLVVFSYSMSQIGGFDGIRANLAYQ

NRSEWFRLFKPTSDPDYPWTGMLFGQPMGSIWYWCMDQDLVQRVLSAKDTAHAKAGCSFA

SLLKVLPPFLIVIPAIIASIYFDFSQIKDGTDAAYPTMLMTMMPHGIIGLMISSIITAMM

ASLASVFSAGSSVVTNDIYLKFRPNASHKQLVWVGRVSIFSFAVLSFCWIPIMRNGTGLY

EQIVEIQSYLTPPIGIVLVLGVIWKPANVYGAFSAMVVGGLLGFTRLIFVTINDDSEDGD

LPGVINTFFYMNFQHFALLLWLTALTVCVVVSLLTQHKKPPAPDVRKYMIHWDKVFKLDA

TELAKPRWVNALVAGSGLSALAATFSMWVYFS

>contig30097 Frame-0F

MRLELSFLCTRLIRWFPDEFGSIRSVFMTPLHSHFILALKAFVKEAARIINVEDPSMNST

LVPSAVRIEMALHLYLSAAGL

>contig30372 Frame-2R|Blast-ser/thr kinase [Phytophthora infestans T30-4](gb|EEY57890.1|) 8e-09

MMLEIATGIDLPKAGSKWHDLRSEILPSFSSEYSKEICEIIR

>contig31119 Frame-1R|Blast-homeodomain transcription factor, putative [Phytophthora infestans T30-4](gb|EEY61507.1|) 4e-09

MNVYLRLLAKPHKKDKLLVSNNVLKLACKLLKVRKSDFYQWEY

>contig31793 Frame-2F

MAGRDGRGSLQVSDGDWSCPNPGCSNVNFARRSSCNRCQTPRPEGLSGDKSKVKGENDFR

GPPGLFQPGDWTCNTCGNVNWERRSECNMCKSAKPGMTGL

>contig32312 Frame-1F

MHNTSAARATAACESSTCRRSLMYRFM

>contig32428 Frame-1F

MAEFRFRPTTLLFLIVALIFRCAIDPVSANADLTPSPRLLRDLVQFDATQTVAHTLSNSP

SASSSSAEATVHPAASAEASAISNHTTDNAASAESSAESKHELPSIMSFIGPAAAGVLAI

VLIGAVIAFKYRSSK

>contig33034 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65556.1|) 2e-91

MPLWRVFVIHHVVAVLPYLIYTMHAGCGMDLYLLQLFLMVEFAVIPLNITTVLEQLGYGQ

SKTHEFFFYTTYLFWFVARVLLPIYNVYVLWTKVIPDAAVAPICTVPAAFCGHIIAAFCV

GVFVFVWTPDVLAKWRVPVLQMEEYPDYMLTMRQSMTPRSNPILSPMNSIDKWGTSYGTA

SDDSRESQWSVKLIA

>contig33171 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66617.1|) 1e-65

MDAELDVPRSYYLLRAEPVAENGLEVRESKIPGAGKGLFATRLHERSSTICEYSGVVLPN

EVAWKLHDKSYLMKIGDNVYVDALKCPDVLARYINDCRGRRGGFNVHFVKRPEDGRADVV

AMRDIQPGEELYVNYGRLYWLAYNMMHPSNPVR

>contig33539 Frame-0R|Blast-hypothetical protein [Plasmodium vivax SaI-1]gb|EDL47246.1| hypothetical protein, conserved [Plasmodium vivax](ref|XP\_001616973.1|) 6e-22 NOT\_ORF

MKTILAIIAVLCFVAAVALSEEPTVKVGVPTEADHVKSDAGVEAGDVVPDLQENHRGGHH

GGHHGGHHGGHHGGHHGGHHGGHHGGHHGGHHGGHHGGHHRGHHGS\*LGCHGYNRGGGGV

CGGMW

>contig33665 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57395.1|) 6e-21

MNVERSKLSPTAAVRRFLSEEDEKKVVLILNEQLHRHRRITSDDVRLTVRDVASQGGTVR

LPPDFPQSRWVLDFKRVYGFMQYHSFVYNGATSFCRDKVAVVLDRQDTVPLRSAIVATDN

QGATARICTSSGYNDTNGEQNNTFGANTVPTRDSSPSSGNASDDEKERGPSDDGVRSIPS

DLTRKVVYHMTPSGRRAPSGIGPKRHGQMRHSVNQRDQRHHHQHQRRAMLVNDRRRSAAW

SSSDAAAIYEER

>contig34743 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY54397.1|) 0.0

MVKKQVKQHVKQQQKDVDLLMTIASDEDPTNTEESTDLEVSDDETSARQQDLQFNESFEF

DDGTTFRSAGGSSWDFTAAISRIEKMQSGTPTATKCTSIQSKIDKRRMEMELIKKEKQDQ

KKKKSVEEKASKDLNGNNRSESNDEMKKVRKGTSKDDKEQFEEADSVEEEDRLQSALVGS

KNDLKARDELVDEMEKKKAAEFFESDPFAAQEFAKTKFETFADLKLSRPIMRAISRIGFE

KPTPIQQRAIPIALTGKDICASAQTGSGKTAAFLLPILERLQFRSRRVQSTRVMIICPVR

ELATQCQSMFEQLARFTDITCSLAVGGLPLKAQEAELRNRPDVVVCTPGRMIDHLRNSKS

VHMDDLEILVLDEADRLLELGFTEEVLELVRMCPVQRQTMLFSATLTSKVDQLINLSMKR

PVRISTDPLFDMAKHLVQEFVRIRPNREDDREAILLALCTRTFRSNTIVFMETKAHAHRM

MIIFGLAGIKAAELHGNLQQIERLEALQKFRDGTVDILLCTDIAARGIDVRGVHAVINYE

MPKDITTYVHRVGRTARAGRNGRAVTLTSESRRMVMKQVSRHCQGFVKSRAVPDPVITQW

KARIESMQEDVKEVMHEETLEKRMREAEKEAMRATNLLKHRL

>contig35450 Frame-1R

MKGYEKAGLETADASVIVVGILTKEIGHWGASKFLSDLAKVNAELSRRTRSSLYRYWDQL

QLSLSEFEAGKITSSLKRGVNVRAVKQIIDCFSEYFKYADQVVGREENSAYKALKELLEN

LNHGDAVDYVVQFFSKRKKYKLFNEDQWIALEYLERQYAKYNTPALIIESAQFAKDGLYL

LGRPYSRLNFLCDIFVKVDDRAEYIVEKQAKWLIDQLTHWIFDKKLFLIMYPMQDKDELA

ASVLKQLRVLWKNDKASSIGLALDFIKSMLQYKEPTPGAAPYQRLEFQKLKGFIDLVFEK

PIPNEIAQAFSGQNRAAHTIALLNE

>contig35803 Frame-0R|Blast-elongator complex protein, putative [Phytophthora infestans T30-4](gb|EEY68724.1|) 9e-08

MRGRDEHAAVICTSVGNVEWKLSPSSAVLRLAWRPTICIDELLLAAASSDSSVRVFAVDI

>contig35876 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY61544.1|) 7e-24

MSPRRKLKAFRLTQQVLWRRRYFEGILGWEAALRVVFVSFPNLALLRVESSRPVVSFFFV

YVMLQALAILWG

>contig36033 Frame-0F|Blast-snurportin-like protein [Phytophthora infestans T30-4](gb|EEY67592.1|) 1e-129

MLFATMKRIAIKQQPWTKDSTARRQATLALQKKARRDLTMHARHLALHAEYLYLDGRDED

TQLVNNVTSAASKRQNRENRVKQRREHFSKQLMTPEWLVDIPSDINGSGSTYGEGWYVLP

RPEGKRCLVVANGGKTTARTPSGCILKKFPSTLPCGSYKTNKSTEGYCILDCIYQEQDET

FYVLDVMCWKGYLLYNCTSEFRQYWMRDKLSEESTASVSSANPFLILPLPYYECDQAGIM

TAYSTNYRFVKDGLLFYMKAGHYETGLSPLALAWKDARTSRFFIISSKPSIVLRLERGNE

FVTLECIVLFACDQDFIQQQELSDGDLACFNFERHNVDG

>contig36280 Frame-2F

MKFAYQFQHLCGSVYTQGNVIFTPDGNSVLSPVGNRITQFDLINNTSRTFAFEARKNVEQ

VAISHDSRLLLAVDEDGRCLLVNLKRGVVLYRFHFQHPVKALNFSPKDEFIAVAIGNKVQ

LWRTPGLVREFAPFVLHRTYTGHYANVTCVSWSHDGKFFVTGAEDLSARVFSVNPYENFK

PLTLSGHRDVVVGAFFAQDDQSIFTVGRDGGAFQWKYKLLENEIYSLNESKDQVGDQSDA

SDKTDGNENRKEEAVGQNRKRKLSQALDPIPDIARATKWYTCQKHVFKMDYAKVLCCTFH

ASTGLLVVGFGNGTFGLYELPAFVNIHTLSVTQNELETVAVNATGEWLAFASRKLGQLLV

WEWRSETYVLKQQGHYFDLNAASYSPDGRLLATGA

>contig37759 Frame-1F|Blast-phosphatidylinositol kinase (PIK-L4) [Phytophthora infestans T30-4](gb|EEY63983.1|) 4e-76

MQCAVMAYTQICRITAHHQVSWRQLCVDFSEELYFPLVDELLETKTLQLFLKTFMGGKVS

VRVFLTASASYVLPKYVVKQNERMLHAYVDAYNETKDNIGIAGLNADEEFSMNITTFLCN

HLEFVLKELLIHQVQAVANNNRLAEWEFLLKFLPENSTVRDVITHSPLRLINLLA

>contig38039 Frame-2F

MLVLIGIAAGALVFIGSLLAVFMLLRQGGSFERMAQEAVGLPVSLEEQKLLLYDELLDKA

NSFEQRPAPIGINKLLEGNIVSVKDLVTVGDVVKLHDISCGKPCGGIFQNLAFDANEMIW

RYLPQGPFNSFTELKNFYLKEEKDSRHFVLLRSNSRLPIGMVTLGNHSPRDLRIELMNLW

LSPAFQGTAALTEVVLLLLTHLFEKGYRRVEWQCDGHNVRARRAAHSLGFIFEGVMRKHR

ILKNCNVDTVVFAAINSEWGLMKEHLQNRLQQKKVSSSVAH

>contig38167 Frame-0R

MLIMVQFALHRLKSVLREQIHTPTRFLMLPRVLSR

>contig39199 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61844.1|) 2e-89 NOT\_ORF

MKATNIVSRS\*NGSISAVVSRRYIQKDFSAFDKCFREASASFSAAMESGFSSALLETRYY

QYILQMEALDSPDKTSLSSALASRARRSSGAAALRSINNHKLKSWLLSISDTNRKEDLAN

HSVKHMAAAENARRKCQQTWQGVEMSRIRMYRAVQAVLADYQHLAEARIDTIAISLRKHV

VFASSALANEQYDWQALAQKLEDIDVQGDIVNFIQTTRGDIGHFPNLASLTVSDLCNNTN

QPLMVSPSMRPCQPLRKSCLKIQDISTKKVPIDYDGNQKLLGETLSANFDTSSEVQTLYK

EDVCSRSGSDFYSLGDSSCTDAEALMVHATNDDEKRVSMEQDKQELDNDDLENKSEAI

>contig39274 Frame-0R

MPCCWIVFNLSLCRLCGVYRLFVRVPSENIQPISSLRGSRICRHQRRCSRSKRSIMTCER

SRARLITRRLTGKRTASGLHSYSEERSQCSFVNIGLDQ

>contig39502 Frame-1R

MIPRSSPSVYVELDDSDQETSCTPDGQHSVNIVTQLRSVREDLIRETDTWELVLLLDHRE

VIERRNPRILERKLLEQNVNCEVRALGVGDVQWIARRTRINEDTEEFMLNVIVERKEVHD

LSGSIIDRRFYEQKIRLATVRESCGDVRVIYLIEGSLTQITTVRSSGLQTAMGRTQMQNN

FFVQHCQNTDETVSFLARVYARLLAVFPRHSCSVKPSTSHVLPVHSFDTNAFAQVFCWPP

QTFDPFNSQFRKKTQFTVREIYQRMLLQIPGLSAAKTVGLSAQYKNFSELEAALRKRGRD

SEVEHVRCGKSQRRLGGKVREALEHLLTSLEYSENT

>contig39595 Frame-1F

MRRHDSPYQNICVAIAAREVTGRITAQPNLPHRTISLHKVLRHDEGGVLLGFSSDGNFLC

SIPQCSDPINEMD

>contig39924 Frame-0R

MRGYKPSDLLALEKNGSRLQRWLYSTYASHFERVSKMSKKAANQ

>contig40128 Frame-1F

MTVIFFTWFATSGLLSWSKAAISASISAMYSETCWSTKMKFSLSITNVIGLRSSVMSFIK

>contig40450 Frame-2F|Blast-14 kDa zinc-binding protein [Phytophthora infestans T30-4](gb|EEY59043.1|) 3e-56

MRLALHSNTLITKSLLLRCSLFRLTNRTMSTNERAKADAATAHKPTNAVGGTIFDKIINR

QIPAEIVYDDEQCLAFHDVNPQAPVHILVIPKWRDSLSQLAYAEERHKPILGHLLYTAKL

VAEQQNLDKGFRVVINDGLDGCQSVFHLHLHLLGGRKLGWPPG

>contig40803 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63014.1|) 1e-104

MGELEHFKKRNAEIKTEWQRRLQGERQLRRKWKQREEEFLDQLNESLTKLDAAEMEVDQL

RVLMRDAEKRFAFEKARSEQENSVKSRYERLCLQLNDKMTLLSDQKRLLEQTTCSLLAEV

DRNVHALKNAVCLEKSECVVCKDRQAVTAVVPCGHMCFCEQDAETYRRNCTTEYPTCPIC

QQEIVSLLRVYS

>contig40876-1 Frame-2R1

MSRQYNRKVVSKVYRSGSEIVVEDDARRFCQCRSYCKKIVS

>contig41354 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66530.1|) 8e-54

MSVSLDQSADAEFLRFVARFCGVSLGSAASGRLRVRLGKMNELYEPSTIAKYLARSADRE

NELLGQTPLERARVAMWITFARNIQRCPPSSVSAHLQMLEEYLQQKTYVAANRITLADAS

LFYTLYATVRDFLLAQRNQ

>contig41743 Frame-1R

MSAPWRSVIVNLSFIFRLPPSKENIHINVTPAFTSEMTVIQHRLLIQEKLPELWYKDEGG

RDKCMTLPIFLVNAKNERVGNRPVPLRVTLLYENEHPVLKQDILKMSPDCQRIVDSTGKA

VLKLRIEDVSKNHQGQAFRLKVEADTAQSPLNFDVAYDLSSSISVRSKRNKRRPGKSTPA

QITHHIIAGASTPLSSSSSPGSSAEHEIILARAFGTAAFSAEDRRKRMRIGESLSPGTPR

INGSPQAANSLTGAMESILTWTGGVVNGLHQLEWQTVGYESKTDGMADPERPIYRCPACW

RYKDVMTYETAQHDTKCLIANLLLTYATDTMGHLDFVLKGIERFPAMIASAQAAAQKAAV

KPIGQLHGQMPSLVSPQNAGMMGVNPLADDSSSNQQMMSMMNSNMGSNATTNQFTMTKSS

SAMLTTTSGAMNGLAGMDGPPGLFRNNSGGLTEFMRSLDEHDSSESIFYQNLTGNGNHHN

DSGNSQLADAIEMQIFYVVARMVTLNASNAIGFPAFDVSMNLLGFYQEGRENATTEVVFV

PASDIPAISQGEVLETQRLLQAEMKGNSSAVHTLARCNNDLVKLKEDVILFHWNAKDRIT

PKW

>contig41857 Frame-1F

MFFPTNSNREAQYFFFLTTPSAAAVEPRNSSVSANGPSGQTLFFTRYTLTYSIQIAHTGF

FST

>contig42038 Frame-0F|Blast-exportin-T, putative [Phytophthora infestans T30-4](gb|EEY56559.1|) 0.0

MLVAASSGAVLHPSVILTYYDLAVRYSKVLQHESALIPAVLEMMFGPYGLANSAAHVRSR

VCYLCLRLVKAIGASVNPHASGILSALQPRLAIANERQELASKRNPTHLAYDDQLYLFEL

AGQIIASLVVLPEETGMHARQLRSRYTIAVLNPLLETLNTILNELASGALTDEEYATESC

ASHLNAIAHVLKAFKGTDCMENQQETFAQVLTAAACVLRALPHTPRVRSKIIFMLHRLTT

VLDPTRFLYNVQETLETLMLGCEQIEVVEIVQLLDQLIIKYKHALGGFLDKTTLPFVQHL

CALMPERSAVTNTETKDDSQLEREAIQKYLYTFLLHLVTHGLDAVLISMQNVPQLENILR

LVLEGCAEVLDANINRACFSIGSMLVERWIGNGVALSPATKASGSATVATSTESAALRAE

LHAELSIEGKKRFIQIAVQDFTRAMFTVTNLRHFNINDMQVVVAIKEVVNMQVILVASVG

RKYVTFLRDVFLPSLGCPHELACSYTEQVATGDRKKILGAYRALISKMKLTSCST

>contig42355 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70300.1|) 6e-30

MKLGTESLAGQKIPRKVGGSVFVAADPLPSEDERREIESELAKLREANFSSGVLESRDYN

EEGG

>contig42759 Frame-0F

MRRLIVPLLKNRYDLKVQSYVRARYVRVSDLKITLDHMHKDEVRLEITDSDSDGNAEDLL

YKSPLKWATGHLFYGPKTDASSPSVLHASRVLLPTKGRFASEPVDLGASITESKSMMEAP

RTMLKLNRNPSLPFDSYHCLESRQSTGGVFSRLRSKAAVGSMLDGVKTRVNFRYHKNYVH

ENAFCDGCGMSPIIGGKWKCNTCDSFELCDGCYAAGIHGFEVSNELCRHVEQLAVQKYRL

LGEYSELFELVRCHICHDNVIQFRRVVEWLCAIVSGARSQKIYHKMIVKSGLQPDIRARL

VAQLGALASERADISLKIEWFVELTPEEEAAGSAPPDPMEPASALQIEYKQSLSNARHET

LRMYIMDTSITNQGTEAAGTGALSDLLDPLDKSDLADVKSLRPTTEKS

>contig43033 Frame-1R|Blast-cytochrome c oxidase subunit VIa [Ectocarpus siliculosus](emb|CBJ28645.1|) 2e-06

MSLLNKGIRLTSQSIRAGARGMSSATEQEAKEQMQRWTTISKGMIGLVAVFTVYAIGDHL

NHEHHDEEEIAYPYLKMRTKPYPWPESNCDLMDFECRRLAREAKKALE

>contig43280 Frame-2F|Blast-BCCIP family protein [Phytophthora infestans T30-4](gb|EEY56480.1|) 1e-111

MVCAEGEDDIYGFVTTLNMKRYVTETSFQQILQYVTKKCPITELPKLQHILSTKNVGLLI

NERMINLPYQLIPPLHSALHEDIEWAFENEDTEELRDSFKLDYFLLLATCTEESRSNIGS

KKGKKSKTAYEQTMKFFHNFEDEFFEQEAELSFSFNASLAVHESVNKSSKTSVVMLIERE

KHKAALATISAMINV

>contig43491 Frame-1F

MRANADEVGAITRDQLLMLAQLHGSAPKAMPYLLTQALAILCKNTAGSSSSTVLSLLSAA

VELRLPEWTQSLTQKQEYKRQRVSSSNKKDVVFAAKMAQSLVKTYATTSGVAVKDEELAN

LVAAMDLACVALYVVCALEHTVRLGELVVDNLLYQVAKKYAEMPDKLESASCVAACVHVR

LWN

>contig43792 Frame-2R

MSRAGRAAVFNTGTTETDRSPSESTANTPTTTNQTSSSESRPSTPNSFSRTDSPSLPLTA

VSTTTTVSLTPDTPNPATVAGVNVSYSQTTGSSSRDRFDVVAPTSSTANANATATIVISV

QSQSSDSDASSGIILVATNDEGFSIGAVVGIVASAIVLVVLIAGLAFWLYRRKRRNRTTR

SSSFDASYSIASVTRPRVNSFQLDNHILPPAIAVDQFNNFDRTVDLASSGPLDSTLRLES

SAMSMPSSKVFSRTGSELWEDEAILAARIPMEKLVVKELINEGGHGAVYHGQYHGKSVAI

KMLLPDKKKDLRQINYFLAEIKMMATVEHPRIVLFIGVAWDALSDLCAVSEFLPSGDLFS

LLQRFDRVDHRPQGFDGDKAKIAQHVAQALTYLHSLDPIVLHRDLKSMNIMLSESWDAKL

TDFGVSRKWTVDTMTAGVGTKRWMAPEVMMGKRYDTSADIFSLGVVLSELDSHQPPYASA

IECKTSELGEKVSETALIEMVAAGRIRIKFSPNAPSSLVSLGHACVNLDPRERPSANEVH

YLLEKISRKYLEYTL

>contig43932 Frame-0F

MLGPSARRESPLRRRESLGTLGSADSRSAIKHFQKNQHFNITLTNSIDRFYEYINHEVQ

>contig44007 Frame-1F

MRNLSALYLQGNIIVDAHVTQSQLQHLQKLSVFEANLTVGGSCFSGYEFITWDDKSVCFT

SGDGLGSIYGSGYDEESSTSIASESKSSLILLCIVLALFSFIALAVVGGVVLLRRWKQKV

ARGQHDQLASADSKLKFQLKHLRARMGVNTTIHTTDLETSLNEYNFEGGLRK

>contig44119 Frame-2F

MAHIFVKHSMASDVSIGYHHLAPLN

>contig44384 Frame-0R

MTQNQETAPTWALLRLAQHIVDQNDEAAVGKLHLVLRNDPLNARHWVIMAHVYHHFSKHV

SAQRSYVKAIELGENSWSVRCELARIEGSMFLFDDALKRIKPVVVGESSDDEPDVTVAAM

IYCDLLFQQAKYLCVEGLYGRAAENLKEASATIKSLPSTSSFAHSVEACKLMGDIHCFAF

YLTPNSFLSEGSTWVEFISAGRKAYEAGVLLAAKRENETTDGSDAVTAELYYDIGLGFWY

ESQALSNIRGIFRSAFSGETELDTETAIAKLTMKASTNFKLALKKDPSCALAWNGLALVS

KNVLVKQFCWARAIQSGNSDASWANLG

>contig44708 Frame-2F

MLADEMGLGKTVQTVMYINHLAVVEHTPQPFIIVAPLSTLGHWQREFDSWTNLNAVVYHG

SAAAREILQKYEFFMSEDELVRADELIGNSSSSRLATSRQKRSCYRFDVLITTFEMASAT

DLYKLAQIDWQLMVVDEAHRLKNRNSKLSNILHTRYTYENMLLLTGTPL

>contig44793 Frame-2F

MENDFHLAAMLPTAGYLFAEELDAHFLAVDDFHSMLLQDDYAKVSVVDTSFSLTGLSPSI

APNSPSSVINLPPYYPSPDNCFIESEA

>contig44973 Frame-2R

MCRPVLGESILGLSAKKLLSNRQFFMLYRNVNYCLLVTSSRLIS

>contig45570 Frame-0R|Blast-plasma membrane H+-ATPase, putative [Phytophthora infestans T30-4](gb|EEY58081.1|) 0.0

MTEHSPLLANSDEHSYSGASNDDRFYMGVDKRSLLDTGEAGLSTVEASRRLKVFGPNELE

SKEKSPWLKLAEQFWGPMPIMIWLAILVEAITKDVPDFFVLLFLQLLNGTVGWYEELKAG

NAVAALKASLKPEAQVIRDGVHQTINAVLLVPGDRITLSAGSAVPADCDLCEGNPVQIDQ

AALTGESFPVTMASGDNAKMGSTVVRGEVEAVVSATGGQTFFGKTANLISSVDEVSHFQK

ILIRITMFLMAISIVLVGFCLGYLLYNGEDFLEAIAFCVVLLVASIPIAMQVVCTSTMAL

GSRKLAEEKVIVTQLQSIETLSGMNMLCSDKTGTLTRNK

>contig45848 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57413.1|) 1e-61

MPQLAIPASLDLAMPQLDLIPRLARKESHRETAAAMKAPPLTPVPVEPLRWSTASSSLSF

LSNIDRIEINATVERSGVTYYVVEVYQFQHNSRLPTNVNNPRMAASSVPEASEQRAPAFR

VERRYSDFFKLRRQIKLWTCPNAQFMCQYCYEYGRYM

>contig46467 Frame-2R

MTTEKSSSICSQAERSSANGAYLYPSANENCVYSLRLQNRYVVSQI

>contig47312 Frame-1R

MEISSIRVILMLSMIWGVRARHGDVPAAYVKAITEDEYDI

>contig47727 Frame-2R

MGRVSSKRKLKQCDPFFNGKRDNGKKAKAFDLPPIKSKRSKKRRRKMLSDESVDRFVTRT

SAVIGDGMASKKKLQIGSIQEGESMRDFNKRISTEVKRVIYDAAKQGRRTSEKRKIYLAK

KKAKVCDQKMTEQERYERDYQMTGNTKKDYFEDTAPVRFGERVDAPPIMPKLSGIFKKRA

EQLKQKQQVKNALATR

>contig47842 Frame-1F

MAQSNGGDDFNRLYERLVLQCTSKKKTAHNSADVHQYIEPVQQTHEVTIKLEDSRRQEKQ

EHDTKVASMVRCLRLARNLRRFALGIQ

>contig48061 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58888.1|) 1e-146

MVAVRVRRWSDVEARRRPIHRAAYDNSTPSAAPAAPMRAGPMPSAKNVPLAVMEDASECV

ICLDELALGRALFTAECGHRYHFSCLLENVNHDEANSDKCPICRKTQTQWPEQTEGLVKA

HPYCTNCGKRGSGGQFCDGCGQSLAHTPTAQERARAAAAASAARSNVVVECPTCRIRCLV

STTARGTLQCPNGHLFQLRMPPSMGNSHGIRQSFNGAGPALMTLGPRPIMRQCPTCYTRV

QMPPGSQAGQYMCPHGHTFFFSPF

>contig48182-0 Frame-0F0

MSEQMNDLDWREPLNSACNGTGSRAICDAQICQLMCSDALIIPHLDKSCCATSATIDCAA

ASSLSVCCENSTMALNVGN

>contig49220 Frame-1R

MRHEALIQRYEVVTRNQRVQLLFELLELLVATARQRHFNGKRQPDYQLNIRN

>contig49668 Frame-2F

MLYRFFRLGAQPIYGTFRDVNLKAMITTAIWRVYFRASHCPPALAVSSIACDQLVFDGRV

YSANAKNSPFPTLRLACGRRSLHALDLTETATSQPSPSRTMPDVRSSQLSDNSVVSSGAR

ETSLRRSLRAGSSTKPVMI

>contig50103 Frame-0R

MTNTSNATCCFTQPIKSRQRSSSARLQAGAEQQTCVCRILGCGLNDHERRYKRRFGRGKK

RHFTMEGSAISRKFEDNLQTFPADGLEDYGVCGTWDGMEPGDTTYTNVSNRIDEDAGVDL

DSSESSDIF

>contig50198 Frame-0F

MEETQRTFTSVEQQLVAAQETAELYVVEDTQLQLFILETRTKILIAQEEVENEIMTAHQE

VDRVRQLALENVATWKKTLQGLRDATQKMEEALQNAKAIKECQANVEAQNKLKEKVTAEL

EILQELEKRRAIEKHLENEEIKRLQEEKLQELENSDKLPEMQRLHQEVQNLEKEQESTLK

KINSALATNGEKVKNLEDVTPVKRLLDWFGLAENVLLHAVALLYRQLMLPVVVILGFFLL

LTVLIAKFHAMMQARRNQRVLYSGYPKSHHVDDQRQ

>contig50244 Frame-2R

MLASLSGKKHGNASLEVLFGTHELGQIFKLPGGNLRVKVKSQEASLQLERTKVIILGSGY

MFKEFDILGSKYFFDISNVDSETDTVLILRRLFLLGCKPVHDTFREVNLATGITSATWPV

YFLSSYSPSALLVHEVSVTKCCLRTSLIRTRKEYSVRVGATTIRLSLASWHMYGHDCQRP

STA

>contig50442 Frame-2R|Blast-exosome complex exonuclease RRP43, putative [Phytophthora infestans T30-4](gb|EEY54228.1|) 1e-47

MSEVTLSFGPDEYKKLFPAAYMHKCLANKVRTDSRGIEDARKVQLQTRVIQTAASSCLVK

LGKTSVLSAVKLAVGAPAVATPDQGEIAIQVHLSPLCSNRFTLGRPSEEAQSIGSQLTRI

IV

>contig50626 Frame-1F

MIWRVLAAVAVTLTTVDAALQSAGICYSAWHHPSVTPENVHNDLIIVGKYFSSIRTFQTL

FSSVNIITAAAKANIQVAVGVQLTDP

>contig50653 Frame-1R|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY66016.1|) 4e-16

MKFTLLMQAAMGVASTASAVMEDITMSLAGSGFEQGTVQAFNDRSTLNSNDYMAPFSTED

ISNLFQRNGNLTKLAPIVNVASNLLDKPLPTNKWWGNL

>contig51067 Frame-0F|Blast-cleavage induced hypothetical protein [Phytophthora infestans T30-4](gb|EEY66778.1|) 2e-16

MQAQREHLRQLEHALDEKHVLSASH

>contig51139 Frame-2F

MLCHAFRKGVAFNACSPTSCSSFLNSQGGMRLPRYVPRRWALSATSYVFPQAYVTFDFDC

IAQLSSSTCWPELPIIILAWQRFIGVQNADFILLLRHVSHC

>contig51434 Frame-2R

MHYFIMTISHYTTHLSLDIYSRCKEFVNLFSSNGTAQIS

>contig51571 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66749.1|) 5e-43

MDDIGYYVDTQEGSSGAPIISTVDNNVIALHHCGGCLNGGIPAQSIVNDLLQKGVLPDCT

VAMT

>contig51669 Frame-2R|Blast-translation initiation factor IF-2, putative [Phytophthora infestans T30-4](gb|EEY60007.1|) 1e-159

MTPGHAVRVIGLKGLPGGGVALLSVSTEDRAKEVVEARKAMMRWDQMAQAEEEEADNFGG

DSPGPRRRRQFAGARRKWQQVEVRRQEAAEEIKRVAALKPGDEGYIANVVPIIVKTDSVG

VISAIEELIASLPSNEASIKCIMSAVGPVTSSDLVMAEATGATIFSFNIKHPSSIDQEAL

QKQVSLRQHRVVYSLLDDIKELLQENLKGVVVFDVTGSAEVQQSFPISTVGTRTTNIAGC

KVTSGSLNMQAKYRLVRNGKIIVENADMASMRHFQQKVSEVNKGQECGLQLAGTDEFQPG

D

>contig51940 Frame-0F|Blast-40S ribosomal protein S3-3 [Phytophthora infestans T30-4](gb|EEY56169.1|) 1e-29

MAANISKKRKFVADGVFYAELNELLQRELYGDGYSGVEVRVTPMRTEIIIRATRTQEVLG

EKGQRIR

>contig52013 Frame-1F

MGPDPDADALADPVALVIVFRPHRCSRGLIISPYRRRGPMVHSFGATPLSSFTAWVQALL

LHTAAICASVTAVVEAGLYPV

>contig52066 Frame-2R

MSNIHSFPPIHSSNEHCVDIHRVIKLIHLSNFHLQISNCVSTSVH

>contig52088 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69120.1|) 4e-44

MPYNVWIWRADTQMLHSVVSLLECVRNMRWDPVSSRLAITSGNGRVYFWANETVSWVDIT

IDSFQALGIQWAPSGDALVAVGRQQCCRISLPSVRNDI

>contig52879 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61931.1|) 5e-46

MYDFSPSWSWKQRSTYQLHQSEVTSAILTHENSYLFTTSKDQSLKLSSVENVTQKRIVSS

KFALSCCDVSFDERVVFVGSWDNSVSMYSTSSGLVLDTIVAHSDGISAIRVLPGRILTSS

WDSSIKLWRFTPFCIVKTPL

>contig52916 Frame-2F

MLPSRMPDETQRKRSMSFSPSVIAQTDLDSPQWKRNKGWARLLLRELYDLGFSDAAAALE

RE

>contig53177 Frame-0F|Blast-calmodulin-binding transcription activator, putative [Phytophthora infestans T30-4](gb|EEY57653.1|) 1e-21

MSSVNDAQTRAAFLRHEATRRWLVKGELKFLLLQQNLVGVAVLHSRQMRPPSGTLLFYNT

LKVLDYKKDGW

>contig53494 Frame-2F

MNHPDIIYSKLCPSQQETTL

>contig54011 Frame-0F|Blast-protoheme IX farnesyltransferase, putative [Phytophthora infestans T30-4](gb|EEY59675.1|) 7e-57

MFTSATLHAHAVLLAASYGQHSGARISRCAIRLYSTRLTGEVAAAATGAKATAITTIHAV

DAAPLSETMSLKDRLSIYSQLSKARLSALVVMTTSAGFFMAGGPITWSTFAAAAVGTSLA

AASANTFNQCWEVELDAKMQRTHRRPLPSGRISQPHALTFGAVTATASTV

>contig54583 Frame-2R

MYPPHNRMSPVMAPTSRYCSSPSSADAPLTAERAMMDQIRSKLERAQRRLARTSSGSSGS

HVRAGYDSAIRAPPVKSVLLEDMPATTSRQYTPPSTLSHPAILPPSSRHSLPCTRREHKK

QQAFQYASQQYKSRSKYSLSDTDPLNGGPPPLSTPYLVYAKPRPTVTRPKSSV

>contig54600 Frame-1F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY66249.1|) 6e-39

MTAMQHVGIKRKQIELVIQTLAAVLHIGNVNFQP

>contig55135 Frame-0F

MQSSFLAHKPTEQSAFKTRSDRRSEAMTCTESHQQDEDWHHQEKVVENLSEEGKVNEAAS

SGLIMSDTATMTVQTDALMAPPVELTSPAGDFWNEEDALFDHDDHAKDDWNETVEDSSYR

TFAAESHGNTAYPDFSSHDNSFALPTKQEVTKSAAVFDHSGSQYQEKKEIGRQDDVTGQD

TIAMSPSQTHQQSAQLHYSERKPELKPATYMDTGSPP

>contig55364 Frame-1F

MENAMEVATDILNGLVQRLDVHATDNMVNLDDIATRERNEAAEADIVVDNQVIEM

>contig55908 Frame-2R|Blast-Rab1 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY58069.1|) 5e-18

MSRDYDHLFKLVLIGDSGVGKSCLLLRFADDAFTESYITTIGVDFVSESGTTD

>contig56422-0 Frame-0F0

MQCNVYYGPIINPLCAGFTINLSGVHGRY

>contig56422-1 Frame-1F1

MSTMVPSSTHCVPDSPSILVACTVAI

>contig56817 Frame-2R

MESFFYGGVLINSIDSPNLYFQFPYEYQLWPSVATPILKDIPPLPSRRTRFVQQITLYCF

SSCTDHIE

>contig56938 Frame-2F

MSAIGALREMEKKKKPNNIGLKELFLNIPTRIRQSGPIKRGIKFAT

>contig57029 Frame-1F|Blast-coatomer subunit gamma, putative [Phytophthora infestans T30-4](gb|EEY66011.1|) 0.0

MKLGASQDTYGSGGDSSRSGSSMTISSVMADIKEKFKNDEEEQISPFQGLDKATVLQETK

IFSDANTVTRHPKKCCQLITKLLHILTQGEPFTSAETTAVFFGVTKLFQSKDANLRRMMY

LFIKEVAEATAADEVIIVTQSLTKDMSSDVDLYRANAIRVLCRIIDGSMLNAIERYIKQA

IVDRNALVASSALVSGIHLMKSNPEIVRRWVNEVQEAANSTNDMVQYHGVLLLYQIRQHD

KLAVSKFITQLQKTNLRSNLATCLLIRYTAALLRETATGQDTAPLYAFLQKMLRQKNEII

IYEAARALCALPVDSRDLTQAIVVLQLFLSSSKPILRFAAVRTLNQLALSQPMLVTRCNE

DMEALITDNNRSIATLAITTLLKTGAESSVDRLMKQISTFMGDIADEFKIVVVEAIKNLC

VKYPQKHRVLLNFLANFLREEGGFEFKKTITDAILFLIERIQECKEAALLHLCEFIEDCE

FTQLSTKILRVLGQKGPTTSAPALYIRFHTQPHYSRKRPCARFSRVSSCSICHSRCFAPN

>contig57836 Frame-2F

MGTIRPCMRFRYNQQAFFSIYLNLVCALNTSVAFIKNKAFSILHFDILFPRSLIYTRKNR

RACARVFEAIYCVERP

>contig58521 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY66867.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58787.1|) 9e-18

MASASAAQAEMVASLIGEKVLKALDQKEQKLDETIKKLEEADEDELERLRERR

>contig58617 Frame-0F|Blast-alkylated DNA repair protein alkB-like protein [Phytophthora infestans T30-4](gb|EEY68761.1|) 4e-11

MGGHLDDAEYTMDYPVISLSLGSSCIFVIGGQY

>contig59126 Frame-2R|Blast-dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichyl-alpha-1, 6-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58713.1|) 1e-36

MQLVTRWVLGFMTFCGLFFFSDSVGMRFGRDVSRFFLLICACQFHLLFYMSRTLPNVYAL

V

>contig59153 Frame-2R

MTVKTGLSSSKSASAEHLVILNSNGLTPTTASFGASIANIEVNGVVFNVFKRVNEGVAQY

VYVPT

>contig00026 Frame-0F

MVHERVNPIPSRGLKTSVPLSCRDTCVVFACRMKRPDC

>contig01735 Frame-0F|Blast-anoctamin-like protein [Phytophthora infestans T30-4](gb|EEY66036.1|) 0.0

MSDAVIKGAVGGAGFLASAYALTKFIAVTPVKIAPRGNGDFELDVVLCFDTKTFSLDALN

CFVQMVEKQSQLILVSKAKTVMEKHDKVQLSKENAKNDETCYLLGATHDTLINIKKQKEQ

VLHGFVSDEPVPDHFCSGDRIDLLLFELGRIKVHPAHYEPPKNYMKTADGQSIKPEPFQD

EEHGLLLQQAMNSKFLKDHFPLHDDKERSDLVETWVKQWKRNQSLDHIRSYFGDEVGFYF

GFLGMYTQWLAPLAAVGLCTFVIDFFPNWAAYGRGAYSLLVTSWATAFLKFWKRRESTLR

NEWNISATDLMVLEPPRTDFSGEQRFDPVEGCYYTFFSSKSRAKRYAMTISVTMAAMAVV

TLLIIIYCWMEEWFAIAFIPSTGWDGFWEYVYLVPSICYSVVVLYVDAKYSELASLLTQY

ENHRTESDFANARVLKLALFYFVNNFGFLLYVAFISRDMDLLEHTLSSLLITRQLLGNLQ

EQLVPFMSKKSSYKAEIGKPAKEVQKTDAMLEKVAVELLFPTYDGTFDDYLELFVQFGQV

TLFAAAYPLASLWSLLNNVMEIRSDGFKLCVSFRRSHRTSTQGIGTWYYAFSALGYLSVV

TNCAIFGMHSGFFTGLFPKMSFAGSLIAIALMEHAMVAVKVCVEMLVPDTTAAVLEAHRM

KRAWLRKKASLQRELSSRQLKQSHEFDSQTDQEKSSEPQSPNAIVAADMHEWLSSEKERR

NKLERELKSLNDLYMGWIREEQTKRKKAELKLATLLDHVKAPLHA

>contig01818 Frame-1F|Blast-asparaginyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY60437.1|) 1e-178

MVPSSPSTAISTLFRRNRLRVKELLASGLELEGKTVTVKGWAKTLREAGAGAFAFLELND

GSCFHGVQCVITKDETHGFADAMASGGVGASFRVEGVVVKSPAKGQEVELKAANIFVYGT

VPDSASYPMSKKRHTLEHLRAHAHLRPRSNIHGAAMRVRNAMAFATHEFFHQQGFLYIHT

PIITESDCEGAGEMFSVTTLLSQHSNGHLPVTKANEIDYSNDFFNRPSYLSVSGQLNVET

HCCALSDVYTFGPTFRAENSNTSRHLAEFWMIEPEIAFADLQDDMDLAEDYLKYCVQYAL

ENCRDELAFFHKNVEKGLLDRLRGTVESPFQRMTYTEAVALLLEPEHLQAGQFAVKPVWG

TDLGRNMNGI

>contig02042 Frame-2R

MIIENTATKLVLSVFDTRVYIESKSTNALQMEEQMWSYNATSQQFRSQDGRALDAYEPED

GGDVHTFRSLSTEGNQKWKFEKETGLIKHQTHVGFCLEADQSRGNRVQLFTCSTSRKGQL

WSIV

>contig02194 Frame-0F

MQLSFFRLEQQRATSVSTKKYSIHSHDRGSRLGFCFRLPLLSYLFG

>contig03777 Frame-0F|Blast-ADP-ribosylation factor GTPase-activating protein, putative [Phytophthora infestans T30-4](gb|EEY61406.1|) 2e-45

MSSAGTKAVFVPTEVRDAWFHKLRLSVANKGCFDCNKRHPTWATVTYGVFICLDCSGYHR

RLGVHISFVRSIDMDEWTEDQLKSMSEGGNAEARKFF

>contig05861 Frame-0F

MLFASFCWHVEDNYMSSINYQHLGANKRWYGIPSSDANKFEAVMRTQLPERFEENPDLLL

HLTTMVPPSILQDRGVKVFTLVQEPGDIILTFPKAYHSGFSEGFNCNEAVNFALPNWIDY

GRECVEMYRLYGRLSIFSHDRFVFHFGSTQNLGEYSFEDCEILCKELRRLFHEEREYKKL

FLLKGLESVDELSGDVMLDEQSMKVDDVRQCFYCKHNVFFSGIICACNPTRLSCLRHTNE

LCTCAMRKRTLLQWVSTAELRYAIRRVQTKMRALKEPSRKASRHDMHHNSHAITQKESEA

SGANTVVMKKHIDTFG

>contig06406 Frame-2R

MANNSMKVSGNHSASVSLDGSMDADGSENDEEEEDEEEEEKEKGEGKDHAKHDTENQVKK

KNETKEDEKKDSNTVTDGSESHSESCSDDADPGDKKDDTEGTKGTEGKKTDDKKEEGTQG

>contig07258 Frame-0F|Blast-cytochrome oxidase assembly protein, putative [Phytophthora infestans T30-4](gb|EEY64598.1|) 3e-73

MRESPLAWWLFGTAGLVACTLSVGAAARLTRAGASTLYWKPRFMYSPKTSSEWHEEFEVY

RDFCARYQRTPMTLENFKQNYRWESAHRELGQLTALAFVGPLTYFATKRMIPIPAQAPLA

LVAGLGATQLYIGRELVQRNVYGSKRGKTEQEEEFEGASFFLPF

>contig08145 Frame-0R

MGVISVHGDLDWNSQMQSAGGKLVVVDFSAVWCGPCQHIKPVYHQLSDQYHDVVFLEVDE

AQNRSLIGALGVRGFPTFHFYVSQNKVDELVGADSNQLRAKIEQWRQSAFNPFASPGVTL

NPSGGNSAKPMSAAEAREARLKRFVNVNLVPNVPASAPSTVPDSTAVCDPVSEICCPPLE

NEEMKDEGGEIGLPIVNADFLKQLKEMGFNDLYSRKALLATDNQGLEVAINWLGAHQEDA

DIDKPIQFVDLSKGAHVVTPEEKAAKLEEMKALMAKKRAEREAQEKEEQRVNELKRRTEG

QGLLEAREEIEAIQRKIAAEKMKKDKEDAKRERERLRKQLEMDKRERQARGGRLGGPPID

IPRIVESLTKEEEKKTPSLVLTPKEQMLKNVGILKKYRVGNDGLTALKTLDVYVKNLIEK

PEEEKFRTINLENPAFRKRVGTLLGGVAFLKSLGYAKDESDGILKLSLDNRDVELLQYAR

TQLQGA

>contig08857 Frame-1F

MSYAYLFKYIIIGDTGTECLLVVLIPTLIKSRCHWNCPL

>contig09685 Frame-1R|Blast-serine/threonine-protein phosphatase, putative [Phytophthora infestans T30-4](gb|EEY61625.1|) 0.0

MQILHHKYVLEILHKGVKSLAPLPTLQEISLNEDETITVVGDLHGQLQDLFSIFSIHGVP

TRTKKYLFNGDFVDRGMHGVEVVMTILLFRLLDPTSVFMNRGNHESRNQNSWMGFEDEVW

TKYGGADEDDVERPARLFESFQTFFGSLPLCAVLQQKVFVVHGGLFSRDNVTLAHLRKIA

RKREPPLHEMTLEDKLFEDLLWSDPRPIASRQPSERGAGIEFGINITNEFCRLNKIALII

RSHECVVEGFEILHGGRLITLFSASRYCGTQMNKGAFLTLGPDLPS

>contig10852 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69837.1|) 1e-110

MESSTDASATDNLQEQPFLHHKSMYPHHQFTASKEFSSITSFCNNNFTKGIKVSPDGLCL

LTNSDDNVVRLFEVSNETDSTSLLQYHESGTVYDYAWYPFMSSVDPISCIFVSTSRDQPV

HLWDAYTGELRASYRAFDHMDELTSAQSLAFNTTGTKLFAGFDRMIRVFDLSQPSRDFKA

RPLSKTRRSRDGQRGLISTLHFNPDHSKIYAAGSYAGTTCVYTEDEGEEVLALRDHDGRG

ISQVQFSPCGRFLFTAARRDARIHCWDIRATNEILHTFHRVADTNLRVEFDLHCGGKYLA

AGSQTGQVLLYDVLTGHLLDNSIQLPDCANGVSFFPNPSKAMLAVSSGQRHYALPEDMQD

ENETSKTKGLERNVVQAYCFQLPLNSVAQSIERHVSTS

>contig12520 Frame-1F

MQSSSNEKASAASSTSCLRVQEDALFPCNAIKPESVQGIRRISTKVVFLTVNDVYELFPC

SNGVGGLAELATMLRITRKRIPRDTHVIVTLNGDFLWRSERDRKDKGALMVELLNEIGIE

YVVVGNHEFDFGAKDLQDLLQGAHFTSFGSNVRSSSSKEIFAPLVDTCIIPLRFGLQLGL

FGVVTTATGKDEFAGPSVVFENEHLHARRCVEILQKQGANVIVALTHLKLVDDIRLATLV

PSIHLILGGHDHYPVTSVAGVSTLLHKSGRDACWLGAIEMTISSLIDTDFESNGHVSFQW

KMLQNRGFQADQNCRAIIHQYICTVEQEELREGQLEPLGVVQTALDGRRVTCRTQESNLG

NLVADSVRYGLQVDVGLVNAGFLKEDRLHHPGLVITRKWLLKYLPLNTPTVVMRLSLQEL

QNALTYWLRRAPEMTASFPHVSGLRIVYEMSSTGTPTISSIQLTSEKYEDPIKPIGTTKE

LDLKDEEKIEWTRLVTVGMPMVCHLDGWHFFESTC

>contig12821 Frame-0F

MTRRDKKLIGSSSFEAFVQDTEQRTPTTLGIGQEYS

>contig13138 Frame-0F|Blast-heat shock protein 70 [Phytophthora nicotianae](gb|AAR21578.1|) 0.0

MTQASSGYSVGIDLGTTYSCVGVWQNDRVEIIANDQGNRTTPSYVAFTDSERLIGDAAKN

QVAMNASNTVFDAKRLIGRKYSDPVVQADIKHWPFKVTSGAGDKPQISVEFKGETKTFQP

EEISSMVLIKMREVAEAFIGKEVKNAVITVPAYFNDSQRQATKDAGAIAGLNVLRIINEP

TAAAIAYGLDKKGGERNVLIFDLGGGTFDVSLLSIEEGIFEVKATAGDTHLGGEDFDNRL

VEHFVQEFRRKHRKDLTSNQRALRRLRTACERAKRTLSSSAQAYIEIDSLHDGVDFNSTI

TRARFEDLCGDYFRKTMEPVEKVLRDAKLSKGQVHEVVLVGGSTRIPKVQQLLSDFFNGK

EPNKSINPDEAVAYGATVQAAILGGNNSSEKLQDLLLLDVTPLSLGLETAGGVMTTLIGR

NSTVPTKKTQTFSTYADNQPGVLIQVFEGERSMTRDNNLLGKFNLDSIPPMPRGVPQIDV

TFDIDANGILNVSAVEKSTGKENKITITNDKGRLSQAEIDRMVNEAEKYKTEDEANKVRV

EAKNALENYTYSLRNSLNEKKMKEAIPEAEKKRVDEKVTEVIQWLDAHQSAEKEEYEAKQ

KELETVANPILQKMYASASGAAGGMPGGMPGGMPGGNTTFNPSGETNQGPKIEEVD

>contig13260 Frame-0R

MLRCCLLFSLALGLSSAAVVRIPIIKRNDDEFVSSLLHDLRAAHRPTIWGPAANLPIETQ

TITVKDTASVVIRDFQNAQYYGSISIGTPPQPFSVVFDTGSSNLWVPNRKFGSHRVYDHD

HSSSYKPNGTTFDITYGSGPVSGYLSQDALQLGKLTVPDQFFAEVNVTKGLGPAYYLGKF

DGLFGLAFDTICVDHLKTPFHRMIQQGLLDEPIFAFYLGDKKDGELTFGGVDKAHYQGEI

EYVNVTSATYWSVQLDALVIKGQKFTDVNKAIIDSGTSLLAGPKDQVAKLAKLVGAHKFI

LGEYIISCSGEAPDITFVLSGKTFTLTKADYTLKSGPICLFAFMGIDIPAPAGPLWILGD

VFMRKHYTVFDWGTNSRKPRIGFALAT

>contig13633 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60245.1|) 2e-11

MKTWTPAQYEQKTLKKMPSAD

>contig14092 Frame-1F

MQLRWLLASTAALLSPRASVLDAAVDPKAKGEPLFPEDHPNITFLTDKNWDEKTNKTDKP

WMIDFYHPFCPHCKHFAPAFIELAAYYKEQDNLYIGAVSCMDHVKCRRVGITGFPTLMTL

NFNPRMPMVENKRIIGTHTVQEVKDYVNSVFAEVAFNETGTWPPGYNSPEDKAKEEEELK

KLQGSTNASKDSAEAPDTPEPVIWEESTLPMNQTTRIQDAASAFVFGLKQGVFMGGDVMD

DEEFDALKGWLKMVSETFPGSVNRKVIRPLYEQVKEKELLDFNTWDALVKQWQENSVAAF

KAEEARFNYTGVSLSEWQQVNNLFLGQGATYQACASYTCGQWNMFHMLTLNPPETGSRSP

ELMVSVVASIRRFMKHFFGCVDCRDHFLKENTVETVKNVQNAEDKPLVLRRWLWKMHNSV

NKRIHHPIWPKPDVCPTCGTEAAWDEIEVDKWLSRTFAYRDVVVPLVENAVDTPAVALRS

ETVAERAALTAEAPAGIAVATAGPIIAVEPKGGDEYVPKDAERGIKNAANTLELVANTKT

EPKNTLQGTSAPPVTLFAWYILPVVAVGGYLIFVRSRSKQKPYFQLSRQ

>contig14261 Frame-1R

MTDEARCDLALLRMRNYLDPKKFYKSSDHARTLPKQFQRGQVIEGAQEFYSARLAKRQRR

QTFTDEVMADDAVVQYTQRVARNLHNARSHHGSKKSRHK

>contig15200 Frame-2F|Blast-regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4](gb|EEY67562.1|) 5e-51

MQELVTYLTQQYTDGKHHDTRSSAGHDMQVFTDFVLHHENRPPRPVNNNALPTWAQPPLD

TTTTTWADNESLSESDEVLEQHI

>contig15756 Frame-0R|Blast-tubulin-specific chaperone B, putative [Phytophthora infestans T30-4](gb|EEY56721.1|) 1e-116

MAQNMRVLRDYVTAMDGHQYDNVPDAVVCLLITHSNLKLQMVDIRLELHSTIGELRHKLY

LHTGTKPDAMELLVLHGDGSVYACLDNDERRLGFYSVQNGMRLHIVDNDPFSLSRSGGLE

DVSRVKKYEISEDDYDKRKRCKWPNAMILLLTHITQDNLIIYLLIQQAKRRCAHTRGSSL

LRIQTGSL

>contig16241 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57419.1|) 1e-66

MAGMSLFQVGEDVEFWRVLVQLSILAFCLVLVESAVHQLEHAFPPSEKYQHMLKKAYREL

MVLGLISLGLKILKETPAVDSYSKTMLAFQVADLTIFLLALALILQSTAVFLLLRNQNDR

AECAELIKTQDLVDVVTKADDPNNVITFMFQSLFYWFGTAKEMAKTRELIELRLLRRLL

>contig16595 Frame-2R

MRPLFRLGLPLALLVPGVKASNGSLPTWLAYVTGGLLIIIIVYYCCRRARFDENLQQPLL

GGQYTEDGQPMTRQDVQESNDEVSTQWQCEVCDFHNKSSSKGCVLCGTERGFTLGLNSPV

RPAGTGPVAVEPDLLRDKSFNRTRSFAIRRLNMLNSRQRGARNRQDWVRKVGLDGKRYWA

KRELPFPLGNAKLQH

>contig16713 Frame-1R

MEATDRAMFVEKISESRIKQLKTPAVDADATVSANTAIIKRATPEYTIKVAAEARSSPSK

AVAAKIGASSKALNGGTEADTLNSEHSLESMSFVGHISSYSSCSTVMSLLNSSPPDEKPI

MDLSPVLTSMSALAPVKNRNDIPASSVPAL

>contig17325 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53794.1|) 8e-08

MPTQHWLFRMVWKLWILGSGSSCHVVGDESWLDDSEDTDGMCVQPDGQPLRKKGNLKSSF

PFQKNRS

>contig17581 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57332.1|) 1e-138

MRKKKKKSDKWKTKKTNTWVYVNGLPLDVSIEEVHDHFAKCGVIQPDITTGKPRIKLYED

KERGVLNGDGSVCYMKEASVELAVQLLDKSQIRPDWPIDVQPAVFQQKEGKNVKRKKVKI

DARAKIRMFEKEKALSWNEGEVNEPAGYRIVVLKHMFTPAEIEDEAFEKELQEDIHAECS

KIGEVSKITLFSKHVDGVVVVKFASSGSAARCIEIMNGRFFAGRKLECGFWDGADYTHRE

SQNEELQRAEKFQEWLDDASSSSSDDEVEETNMEHIGNDTKAEEGHPERKLHPLSGDSDD

RE

>contig18131 Frame-0R

MLLPVLERFAELGWQPFVEPAETFEFFSVSGVFRRTNVDTTSMHTGQSITHLFVQRSALF

DVCLKSGLASLVVAYIRAEEPRLQPESVFTSVKTYVLKEPIALQQWTHCRLEAMEQSVNE

IVRDQQFSRDSDTLRTATIETVASKLRQFNGLHVIIIALIERLQEGSREAAMSSNGVDFH

GNIKNDTELLRLTTAGVHNLLQLLARTQSGACICNCLLWLYEKEVAAETELYTAFYTQAR

SLRVTYREQFEAIYGKNRLYKEDSKAPLLLIEHVMESASISIQDLGGSCPPTQLNHLLEI

LRMPRIQEEMIQFYGDEVDQEPIEGYFRVQVALVLYFCLDRAYLSVWKQHTQNGARIASN

MRLFADSFAAQLNVRDEMKMTLLALWLMENAVVVKTSGDDQVAAIYDHAIGLLQQSSVLH

IHQQYDLEAQLIFRVLETLVHRGESLVAWKVWNLFVVDLEQCSRATTDLIAIISLELDLW

ERVLTLIRRQKRLDLLSILFEWLMRSNRLKELVQGATLLPDEEKRFHAYMMVDNHQKEED

ILRDDNIKRVDFLVMYYLLRHKYEQAWEVHHEHLAMIRATSRGDSEIAMAVLNQPSLRIR

ASLLSNMCPEPPTKSFTHQSRHVRREGWDRHPLNKALLVDQDMEHEDEDTSASPKASSTS

TKKTSASAFSSNQIEQSTHLQEMAASGTFHYLPGIFSSRQGLSLTSQSIPSSSLSHNDTQ

KLSSPRTFNESSFNVASIVSSPESVLHTLTCSKPFESISTVSSDTNRLQTPSVPTPFRQT

TSSLQSLVSPFGDRRPLGAPPQSRSKIQPSFASSSLISSPLHTGISSEELSLRPHCNDKT

LDPTFANELQDCKASFPANGTLQDTTSNNVDMSGPKKYRFVDEMETTDRLEGTFSDTDPI

RSPVTEELEGMELERIDEDFSTPISR

>contig19020 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62003.1|) 8e-06

MFASKFSYKSAQTRFNLLLLEDGEFFLD

>contig19415 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY64137.1|) 1e-57

MTERPQQLALARVAELELLKTNSSRRPSAASSTSSSELERLHEELQLEIKPQRLQRQYTL

HVPPCSATMDFMSHSGLLNATPDVLEDVLVRWEKNQIKWRRGACNDENQDTLTDDDGLDD

QEDSLNNVQPLYVFDVTFGEGFLGLEFAVDAQKNNKIVIKRVHNETWANKVVAIPNHETL

VKGLSIEAVNQRNVCDMTAEDVLYTLQSSPRPMTVTFRKGHKAMVVC

>contig20770 Frame-0F|Blast-ATP-dependent DNA helicase 2 subunit, putative [Phytophthora infestans T30-4](gb|EEY59535.1|) 0.0

MDAWGSQNGAVNEKLVEEEENWEIADSGKDALIVLVDVRKNMFSPYPHAAADAPCTWFHA

VVELAIKYLKSKVVANDNSLLGVVFFGTKKLGEAGTLEQVYEFHSLGYPSARRIKDLQSL

LATDVQSDFESMQNSEKLSFSNALWHCGISFSNANLKKKDSQRIWIFTNDDSPEGSDADE

CGRIQKQVQNHTELKRTLNLFYIPPLGKESFDLANFYGCCFKNFAVEDDEDMSDKKESFQ

PAFPVSSLNDLMDGSLRKRFRKRRLTTFSMHITKGVSIGVELYAMVVIQRKNVPVALDAS

TNIPLKTETKWLCEDTGAYLTPDQIKKYIDYGGRRVYFTRDDVVEIKHYDAPGLQLICFK

PLHSLKWDENIRSPYFVYPCDGYIEGSSTAFMAILTSMNRKQKFALARLIARKTSEPRLV

ALVPQEEVYDEMGQVQPSGFNIIFLPYLDDIRDISFETLTEVDQEKLDAAKHLILSLKLT

EAPSFENPELQKHYAAIQALALDEEVLEFDEKKDSTLPDVKGFEQDEINDAITKFRDKCG

GELIDASTSAKRKSSAVTGRKSTTKKLAKSKAGDSNEADALETFDKEEWAALATSNAIQK

KTVVQLKAFLRAHSLTAVGRKAELIDAVKRFTEV

>contig21078 Frame-1F

MCSMPLPFESTPHLESIHDRAIEPMKRHGLSHGFQGTLSQARHLEKQELQKTSLLPPSAE

TTSSLVKLTALNDATLPCREKQHREAWCSTRARVPCSPPVPIPQHHCHDGRKHDACKRES

QRESPCWDDVSWRSKFAPGSKKHSFLLECRTKSVADTRKEVFDSPRNSEDQSNEPHDGGV

FQMDDL

>contig21364 Frame-1R

MHLNHVVAIFLVGAVTCFTETIEGSKRRGEIIRERLSYPVDVAIASRALRHTVASQVEDK

GKEERALWEEIAECFLQAQLGRGNIYRSLHIAEKMQNLKEQLLEAFQNLKPSRMKYVKQQ

LLEIEANPALHNSRYEAWLNYDINPQEIFEARPGHDFESWLGYIKFYRLKGRDFSEDDMV

VLLKKHNLIEEAAETFILMDREFFLRSVVRPMLAYMVTQTDVSDIVLTTWLGNGVHPNVV

IKILFPGRFMNFDSDKLVYGLKYIQMFRKFFRKFSDDELSIMLVRAESNSKLLEKLEMLH

DPSGNQYDINEVIEKGLVYVRMSVELDKFLLKGQLPDISALSQVELDAKDNFFRHWLRCV

SIKFPSKPSSVEDLYALLMTHGEATNEKLTDIFDTLQDEHSMDEIS

>contig21746 Frame-2F

MGWLAPEDEEYAQKFVDELVAMADNPTQLADAVVATTTLDKRIEDDINTMLAQDEELKAT

APTFIPRKLLSPEVAEFVPTRSPETPCRGNLNHFQSASTSCV

>contig21805 Frame-1F

MYAASIVHHFPAGVTRENLENNLTSTLTSGMFQDEHVLEFREYLHQLLFCLQFFANNGIS

EDKIKDEELETFEID

>contig21892 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67188.1|) 1e-71

MVPRMSYLVTQTRDVVEYFRDAAPPVPAMQGSSIWFEAKGVPLQWHLPFGLLRDVLCGIG

ATEDSTDLPWALTVHFLNYPKEHLLPCDNEQSIEMHFMHTLKQATFLRMGTTKAVMALPE

AQQTCIWSSVFN

>contig22659 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63744.1|) 4e-60

MRKCQQCQKSLENELLSTPVLGESYVLLPTASASQSMLLLQKLPTNAITPLEMDESGVFG

DDLYASARYNLSLQQHYDQEQKRQQVQRRQELQHRQRRQQQRFKNSFAGSGKYFEDRASY

PSRDEENLGTENSMVAVPTYADLSHHVQLLTTQLAHW

>contig23032 Frame-1R

MTELSPAVNCGEDNYRKPGSVGRLLPNTELRVHCIDSNRDVPHNHKGELLYRGPQVMLGY

DNNIEANQHIFTEDGFLRTGDIGYIDDEGFVFVIDRVKELIKYKGHQVAPGELEDVLNHH

PAIAESCCIRGKNAQGEEIPKAFVVLQYPDSLDCPTQEDIINYVAKHVAPFKRVREVKFV

ESIPKNASGKMLRRRLQEQENLFRNDYKI

>contig23263 Frame-0F

MADKDNLIMSDNSGSSIGPGFELKTGFRRRSHQSWRKQHEILVKEASCICIEKSYSQGKD

SSVKLSLAETLLQKGYGLNPGQATADSVGTSSDVKKTSESHASALLPQKANAKFKDRLVK

FYTTYNPSKLCVVDSTLATYNGREDELFQKLHERYVSKTSLQELKKKYITKASDPTVFMD

LSIAGASVGRITMRLLKKDAPLASENFRCLCTGEKGDTLKYKGSKFHRIIKNFVVQGGDF

TMGDGTGGQSISRGTSHGDLWGNFIDEKFLPHNDVGLLSMANAGKNTNGS

>contig23601 Frame-0F|Blast-phosphoglycerate kinase [Phytophthora infestans T30-4](gb|EEY55430.1|) 4e-52

MGLDIGPKSQEAFNKAVTKAKTVVWNGPMGVFEFDAFAKGTKSVMDAVVNATKSGATTII

GGGDTATCCVKYKTEDKVSRVSTGGGASLELLEGKILPGVDALSSA

>contig23708 Frame-1F

MPRQSTRLKAITEKTVAASLKSSKRKFFASSATTSEEVSTKSQTGLKKLKLSTSDSESAW

GILFSEFKKDKRPHPLAAAPITPEFQQSIDSFPLFENVSKRLPNIDTKIIAWNVNGLRAI

LKRDKSLHIRAYVAQEDPDIFCLSETKICRDELQKIENFLPQYEYQYWSCAIKKGYASTA

IFSKTKPLSVKDEIVVGSHEAKGVSNSSNGGKDQEGRFLALEFANFWLVHTYVPNAGGKL

ERLNYRTNQWDKAMLRELSEMEKTKPVIWCGDLNVAYQEIDIHNPKGNHKSAGFTDEERE

SFGKILENGFVDTFRNLHPDKVEYSYFGYRNNMRAKNKGWRLDYFLVSEALLANVRSSFI

RQSVVGSDHLPIGLELEGIS

>contig25067 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68459.1|) 7e-73

MQTDRQHLIAHLKAAFVEIKRLRVLYSHAVEQLRSSALPNLTIQSASKWFEMYLRAMDLG

VQIRRGEIRHRTAQHFTYACMHETGIKGAVHSGLSIDDGNSILQLLEKRKLVKESLLDNW

FREMDILDGDIVGLIDKDFTRCLGDFKKLSSIFYDRVEVTGDNLHQKMLVLDARNGVAAS

ILATITRKCFNPETCTCEEDAKPWENLSLESADSHDQNHGLIDGDNNTKIPHLGDVGITE

IKRQLGFQQHFFEEKIDSAMEISSNKDELVRRTVRLGKIITAADGQSTHSSAISIYEKM

>contig25359 Frame-2F

MTAVDMPPAEYMGRTVEDIINSWSEQLERNADTFTTEAVKVSQWDSDVLDSQRKLGDLAG

DVRRIQVAQNELDSNLDTIFAYQMELKSTLEQLEKSVDKMYESQDQMPVAADIEREQTLQ

LSVDLDDQLNSMTTTLKETVETLNQAHNDVADESNPMVQIMKVLNVHHHSLQWIEGSADR

ITSEIGQLSRKLHESVL

>contig25535 Frame-0R

MFHIWTSQNPLDTILNCSIKQNQNLFDQ

>contig25791 Frame-0R

MGLGHDIAQFESCFAPSRSNSNGTTSSSGLVTASKSVKAIPGDETTLLLWLIPELSSLID

RVRRKSWSESAVKLASILASLVSEPLRSSDQLAQVLAREEFITNNQEVRRRDRFYHEQMA

HARDIRALRRVGMFTEEANEKIRAKHELARISQFTRSSASLGTLSSEGQDHVWLERVKAK

DIDDWMKLRVLAKWGVRHVWGVKEEAMGNSVGEDGTIIGLWGDNEFWRVDIYTSSNWIRC

RLLPDTDDTITYRYGTTLSSSSTRHEMLSDDLTMPSVDAIVVDDATTLVDSGELIEHVFE

EEEDDDESHTMSSGGDGDDSEVLETDEMGYVGLSQRISDVGYLDDYATVALLHDRRSAND

RVARTKLHNRIHSSELSSDVVGFTSRVDAAGRSSEFVSTAPLAPPPLEGSTNGPLEPSYV

RDRRAVSVDVATTVKSAKGRMNTISTRFSTSIKRLASARST

>contig25809 Frame-0F|Blast-THO complex subunit, putative [Phytophthora infestans T30-4](gb|EEY53395.1|) 0.0

MALKLFKTAEKSIGDFIARDDALSCLGRLHRHTLETVEHVLNTSRPQEFTHNVLEMAVQK

VVEKLSWKLMTEARATASSVGVPALLDLCIAGVTSGYLINSTPYKVLEDLMEGQTISTCE

KVWDLLEARKVKLTAPAFIAEKGRTTKASLCLLRMCNALLRRLSKTHDSVFCGKILLFLS

FTFALSERSAVNLTGKANVTNVTAFEDEEAFDLAEASDGAKTADVVPKLEIDSDSSTDVG

PIDYNLYRTFWDLQTFCRDHELATRSMENWEKFFTELDMVLAAFEGNAFSQDDLERSRNL

SSGPIQSADGTMQTSDGNNGNFRAELSSQEHFFQPKYLTNSRLFRLQLRDPILRQCMLTQ

FLILFNDLARAKPPADSITSKAKLTDLTKRVVALLKQTPFDGEGFNEMVSYVLERERNWV

KWKLEKCPGYERFPVGTENDVSSTPVPAVNRTRRQLSSPLLEQILSESSKPSQILAKIKG

KDR

>contig26938 Frame-2F|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY64792.1|) 1e-29

MRSPVSTGISLTAYDILKEVLGVEKIV

>contig27054 Frame-1R

MGYGKRIAWLSNGQPGRVESREVTECRKDDIGYYVDTQEGSSGSPVIATIDNHVVALHHC

GGCLNGGVPAQVIIEDLIKKSLLPNCTVAGGGNATSTL

>contig27339 Frame-2F

MSRSMVYLPAFTLAIAAVIVPQIQHATAGSLYYGPYTVSGTDDKISKSAPFYGAEIPDED

CAIEVQEDPTLPDVRTIATVPVIYAELLSNKSRAPIEPVYTKVGKKIMAEESECNDAYTD

ETTQWMENDERSMKQSERTSKGCVSGCDAFGAQQDEYDDTRRLQSEKVVKYMTKLGIKRR

LESEANRDIEKLENFYGVKMQVKLEYLPTVCVHSMAPWAGPFWPTFEDSINVIWRKSDPS

PAEK

>contig27898 Frame-0F

MTRFAFVLTTFSILCGHVFAQGRQGPIPMGPRARNREQFGNGVGMGGGGMNGLGGAGGGA

GGIGQFNGGGAGMNQFNTNAGNGLGQFNGGFGAGGNGAAMNQFGSTLNGQMGGGALGAGA

VGQGIGTNGARNNGFGNNNGPATPAPTMPNGEPGPGNDNGAMQGGAGAGPRGAGGFAGAN

GFGRGAGGGIGAGGQLGGGMGGMNGRFGGNNGVGGLGGFGGGFGGGAGGMNGGAFGAGGL

GGIGAQGQGGGLNN

>contig27982 Frame-1R

MLPKLYEFLQPQASHVALAAEAAWVISNLAATDTCIVDRLIHAQLLPLLTHHLHHGTYLV

RREVAFALTNVALTSVDHMNQIVELHVVTEFLQLLSVSDVALVGNSLRFLEQLMRGGTPG

VALVEAHGGIDALEKVQFENEAEYLSTWAAALVNEFYGENYGVQSPPLCGGDSLTEESTE

MEIGTSNAVVSGGRGRGVHMTMPAWKEGTNWS

>contig28046 Frame-1F

MLILERKCKSVSDNDINALNQKTSVASDVMTEVFRQAAQKVVDELNASGIDSSVSGTTAL

AMLVHEKDIIIANLGDSRAVVAKFSEELQRYELHCETKDHNPDVPEECARIEISNGRVFE

WGTPRVWLQDTDMPGLAMSRSFGDLVAKTIGVIAEPDVLRIEIEEFCTCGKKQRPSHFAI

LASDGIWEFISTDECVQFVAACIFESEMSPQETCIALVDEACSRWDVEEDVIDDITAVIV

YF

>contig29557 Frame-0R|Blast-synaptobrevin-like protein [Phytophthora infestans T30-4](gb|EEY54303.1|) 1e-93

MINFFSRTFIKRTKAGQRQSVQHEEYNCHVYVRQDKLAGIVVCDQEYPPRVAFALLNKLL

DEYDKSTSGGWKTQSGSPKEFPPLTAALAEYQDPSKADKISAIQKELNETTAVLSKTIDN

VLERGEKLDDLVSKSQDLSSQSKVFYKQAKKTNSCCVVM

>contig29715 Frame-1F

MDPKQTALKIDYKGELHRLRVDLTAFSLDVLTALFVETFNLAPGSFMVQYTDAEGDCINV

TSEAEFEEACRVFLNVLEGPKSIRFAAVSRSTVAFQENVADPILKAIEKLVETLNVAMEH

VKHEQWAEKAHQTAQTGLNQTNEALKIVAHDARESLNAARQSIQDIPLDQLLKETTEGIK

CAAEGITEFAKEVVGEIKNIRVPLAKTEVAPASEGQQETVVDDVEIPSVTPVAPPCDSEW

EQVTEQENIHAIGNESVVVVENPLTPAVTEEELKWSTELMMVRDIFPGVEAADVIERLEQ

CNGNVQVVLNALMEKM

>contig30469 Frame-0R

MSHDLVRIRYGIVVRQLLDVAMIALDHSLICAFVKAQIICTVCYVQH

>contig31000 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61361.1|) 2e-14

MAISNGSAITTASKACIGSPNAIALNIPPFCQCCHVACHRFRLAKPCSFCHALVCPFCSC

GQEPQVLCKNCQPKVRGAQPIFSFRQLLWRIKMLPFGCQGEKWLFLVRKRQSTIQLSDIP

GSEYKWLTQQLPKLRSLQGPYLEQKQTLDK

>contig31383 Frame-0F

MSVISEKIEGTETSQEIEFSVVSDKITDISETTELIDVGDGKAEAIEIVKKAENAPAESE

KVESIEKSKETEVVVISERDTEISKEIDNFDLSDVKVETSERPKATQKLNEEAGTVVTTV

LASEKITNDSVTE

>contig31556 Frame-2F

MGKRRGRRRYSSRTPPASKKKSKLPGTLLANNHASEVKGNEGETTLPSLKVDGKSVKGAN

DTVVNANADDCCFANETSACQKSDVMKTVLPVSESEEHPNDFCVPALLKLSNCYPPKQPG

TVNGAYEYQEAFKKSMPYFSINQRLNEP

>contig31901 Frame-0F

MKAYCSPGTESVEPVSSNETDEVLISKMLDFSDIS

>contig32382 Frame-1R

MASFALERKRNAIVIASLACVRNARVVLREHLATLASETLAEYGPNQTQAFSAAILGKGV

TRCMNHLITLLRRSCTRVLKSRYNAMCCTSFLPTYSCFANQIKN

>contig32720 Frame-2R

MGSNPAGEACFIILQQSCYHLQTSPQKLAKTRNNILKHYALRK

>contig32939 Frame-2F

MSSIPLQNTALPISPRSGSKMVWVACLTH

>contig33176 Frame-0R

MSGRPGVVQLKLLGQRYAQTGEAVIYVLCSRSLGSWSPPSSRHLRRIFSFGPQLEVSLTP

LILSTKNKAMQSGLPLFQQAIGHDDVHGEVPRLRQDHSRSDEEAT

>contig33662 Frame-0R|Blast-transcription factor, putative [Phytophthora infestans T30-4](gb|EEY61664.1|) 0.0

MLQAMRATRKNSRPLKGIQLLKEYLPEAMHPPIRPYWINTFQKSKDRDCGSAQGDEIRKD

ALVNGDSDADELEEEADDDEDLENQTRMEIAHDPSLSVNAMENGIRLKLLIEYGQLKKLS

GEPEVLCQVGIPIILTSLGQTSFRLSGRVRKTLAEAQDVITECDAQSMGFQLLKFEYLVD

ITDAKQRESFIGIVIRVAQQIVISRVLGEQHYYNLVVDVAQTLTELGKYVAAIELLTDVN

TSNKISKPALRFELRFLALVIALEFKESRMAYECARLNIMEDPHNLGYWNLFSRVIAITG

VFSWHQKFLAKLLRDDPESYPAILLAGHQSSAWDIASLTVGELTLAHQKHTNDPLTLFCI

GLAFLSASMQRTINDRQHTVAKAFAFLQQYEQTRITAPSDINSKFRQIEAWYNIGRAL

>contig33899 Frame-1F|Blast-cell division protein kinase, putative [Phytophthora infestans T30-4](gb|EEY67760.1|) 1e-63

MERYQKLEKIGEGTYGVVYKAKDRVTGEVIALKKIRLEAEDEGIPSTAIREISLLKELQH

RNIVRLYNIVHTERKLTLVFEYLDQDLKKYLDVCEKGLEKPILKSFLYQLLRGIAYCHQH

RVLH

>contig34058 Frame-2F

MNSAMAVCCSSLFRVNSMATTAGSAYDRTHAVDRSPIQRHSND

>contig34155 Frame-1R|Blast-exonuclease, putative [Phytophthora infestans T30-4](gb|EEY57481.1|) 1e-171

MRHNGVDNHATSRHSRKVLGTCTSGAILVGHSIENDLQALQVLHRRVIDTVCMYPHPKGP

PFRSALRFLASQFLNRSIQTGTDGHCSVEDAVATLQLAQLKIKHGPTFPNIEHEYKQKKV

VQEMARIKKSVLVVDSLRACRSISGGVACIIPQEDSDEVVRTVVHQLTTGFPPHLTWARA

RGSKRAEIVEYVRKVKANLPQCSCLLTVLCGDTSELRALYKRRTARTDPRSSLLWDETQK

EALKQTALIAQMGLAHICLS

>contig34249 Frame-2R

MHTTPSVSIQLTQRESSERRSYTLVVTSTKTAILAKKHSRRTLRLFCCVLKLRTRSNKYL

KI

>contig34744 Frame-1F

MAPIESLDMITNEGLHQRKPTSAVNTKSATYTWQDVAQHNTATSAWVIIRGVVYDVTDWA

DRHPGGRELVLLHAGRECTYTFDSYHPFSNRADKILSKYVVGTLVGESEFPMYKPDTGFY

KECCERVQEYFTANHLDPRSPYSGLWRMLLVAIVGSVAYCGMNQVFSDSMYAQYAWGALF

GVCQALPLLHVMHDASHAAITSSPMGWKLIGRIVMDWIAGANMISWLNQHVVGHHVYTNV

AGADPDLPVDFQSDVRRIVSRQVLLPMYKFQHLYLPPLYGILGLKFRVQDIVETFGALTN

GPLRVNPHTTGDWVELIVSKAFWAFYRLYIPLMVLQVHPTRFWGVFLLAEFITGWYLAFN

FQVSHVSTTCDYPAADGNMKSLEDEWAISQIKSSVDYSHGSFLTAFLSGALNYQVTHHLF

PGISQYHYPAIAPIIMDVCEKYKVKYTVLPTFQKALAAHFDHLVIMGKMGKRVDFHMG

>contig35804 Frame-0F|Blast-elongator complex protein, putative [Phytophthora infestans T30-4](gb|EEY68724.1|) 3e-19

MFALGSRDQSISLWWLAQGIWCRACAPVCFEAAVTA

>contig36496 Frame-1F|Blast-rRNA biogenesis protein rrp5 [Phytophthora infestans T30-4](gb|EEY64678.1|) 2e-38

MNVGIRGMLAFVPRKDLTTPVHKGQNLLVNVQSINTHTNT

>contig36935 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64071.1|) 1e-107 NOT\_ORF

MARPQLVKALWAYIREHDLQDPSNRKNIILDDALRRVFQRDAFTMFTMNKFVKRHVRKPD

DLPPGGWSQISRDGLSSEEDTEAKVVKKEAIKRKKRKSSANDPDNDSKSERKNPFNIELA

VSPELASLIGSDRMARPQIVKALWAYIHEHQLQDPNDKRTILLDDRMKAVFQRDSFTMFS

MNKYIKRHARKVDDVPSGGWSEIPRDGFSSDEDKTKKEK\*TRVALIEVGVET

>contig38533 Frame-0R|Blast-glyoxylate reductase/hydroxypyruvate reductase, putative [Phytophthora infestans T30-4](gb|EEY67099.1|) 2e-98

MSSAAPLKVFFSRNIPCAIEQLRKVLAEAGANSFKIDYFSHEERCITREELQRRVKGCTG

LFCLLTDRVDAEILDAAGPSLRVVSTMSVGFDNIDVEACKTRNVRVGYTPGVLDVSTAEM

AVALTFAVKRRIVECATSAKNGDWGVWRPFQYCGSDISGSTIGVVGLGRIGSTYARMLKH

GFNCNILYTGPRAKLDVAESLGGGPGSVEYVDMETLLRRSDVVSLHQP

>contig38847 Frame-2R|Blast-glycyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY54238.1|) 1e-138

MLARCIRGVATKPTTNLQERVVALCRHRGFVFPGSELYGGLANSFDYGPLGVLMKKNVID

RWWFEFVQKRPDCVGLDSAVLLNSAVWKASGHVDNFTDPMTVCSNCNTRVRVDQLLESKL

NSDDNTDALALPSLAQLDELLKTHDVACPKCNKTQSFLPAKHFNLLFRTNMGATDETCEW

IYLRPETAQGAYINFSIVQSTMRKKLPFGIGQVGKSFRNEISPGHFLFRTREFEQLELQY

FTHPRESDDWYQYWINQCYKFLITYGIRPDSLRKHEHSPEELA

>contig39592 Frame-1F

MPLAPPTEASFVSLEKLLEELTSHAKFEKYAIKIGCSRTVGNKKGNTFNCIGPRSPNIKT

P

>contig39761 Frame-0F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 1e-157

MAQEKETNRLIHSANAPIFGVDQDGCVNIWNLKVAEITQFSANEVMGKNLVKKFVAEDHR

ESVGTLLRKALHGEHTGNFDFPLITKSGRQVDILLNATPRYDELGQIFGVTGIGQDITER

IAQEQEYIRLIDTANAPIFGVDSEGRVNIWNKKAAEIMQYTTDAVMGEKLVEKYITEDYQ

EAVSNVLFEALSGVETANFEFPLITKAGRRVEISC

>contig39923 Frame-0R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY67925.1|) 3e-64

MVKVSRTPLAMIALAWSCLQFASSAEDLCSITPSSYTMAKTTHPHLASALTTIEQYAIVA

WYTDRTSEADRSAMLSSITTDCSEDSRMTIAVYGIPNKDCNAGLSTSGSVQSTTDYESFL

STLSTAVKDRKVLYIIEPDAVGLLAENGCGQSSGYLDNLKIA

>contig40220 Frame-2F|Blast-eukaryotic translation initiation factor 3 subunit, putative [Phytophthora infestans T30-4](gb|EEY59042.1|) 2e-77

MGMMCQDVGQITLALMCHRESLRRGEFDRNQAANVLHQMALACSIAGGFREALAYEKKVY

SLIKEAFGSEDSRVIESAKFMAKFTEKAVEGAKGRREVDAAEAAEAIANELLGELELKTK

AGQSSAGSPTTAKKKNRKSKSGGRKH

>contig40804 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66034.1|) 3e-07

MVARLLISLSPAMCHHSALRGYRSTYLPVLILVHNHSAHCRSVLRYSILINSIPQVTFCI

TFTGRILPRISSPMKAWCDEWRCARLHIALRDDELFLGEKITVRVDADVMTTTSKYDCQS

A

>contig41155 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68232.1|) 1e-104

MRSLIFSRLKTRPRPTGRCFKSRKLVDVLSSSEMMLFKYCSMETLQTEYAKLKDQRAVVR

VGVGVLLLSKKYPNCVLIGQRKGSHGEGKVALPGGHLEMFETWEQCALREVKEETDLDLQ

EAKFATVTNDPMENEGKHYITIFMQAVVDDKQIVRNMEPHKCVGWSWVPWVDLRSRSDMF

TPLYHATHSTFSPTFIEH

>contig41353 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64348.1|) 4e-10

MYSCFLAYRERVNDQETQTWLDDWKERTSRNLEWSVIAEDLNSDQSSVLDRFRANGLDVR

IAPH

>contig42110 Frame-0F

MKRALVIRNVSSYDVPLDSLDNACVQACCREGFVTELAVNDDQKVIEQLLKAHARSNDRN

FSYLQAAPVPDSFDVVLFRASGLSERRLYPLLHKIRSISKKIFLCVFSPHLAEHPMARYQ

CFQEGASMVTHSLEAVRDVLSFITSCGKENGCKALSGRKWRGRSGGRDGFACPFCGMNDM

NEDQLWRHCPLYHINENNTDGINCPICRETPRGPFQVHMYNAHGPPGRHEMTSEFHMADS

MLYSFALVVCHNKKYNRFLLVQEFANSGFWLPGGRIDSGENPAEAAIRETKEEAGIDIRL

TGVLKLEYHPKQDRNGSEYVRMRFIFYAEPLDCDQPPKSIPDYESAGATWCCADQVASLP

LRGSEPVTYFEHIVSGKPIYPLDLIHMTSSSS

>contig42226 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61370.1|) 1e-115

MVLFCSLWVYNQSHVPMLLFRCAENLEASVLVVPQLVSQRPVPRLLDCPSQAFEIGTIID

TEVSRWSEKIHATIVGVQEPITLKFGSTLGPRTRIELGISIQRPLGQFHRTTQVIVSSHF

VFVNKTFATFKVSQYMRSSNRVVELLAMSKNGMPFSHPFDFDATTSVTNRRVYLRMDHYG

AEWSGPFTVDEENEFSLKLKGHVIDSWNHASGGTVYTHEGLQPSDVEMHRIKVRISNVGP

TIVITLLRDDPPMYMIR

>contig42352 Frame-2R

MLQPTQRNYNVNSNNEKIVVKLLSKSKSMMIFKQKHLGQN

>contig43034 Frame-0F

MSLTDTKIRAKYSSRNLNAVYKAPLGTKPLSENATGPLQRHSSRMIILRRATVAPPAPIN

TPSLERQGRLQNTRVSLVPAASYWAEGGAKMQKASKLELPTASADGIRPTEAFKKVRAPE

SEAKRIHTESSLTHTKLIAETSGRWGDDAVEHDIAHQNICYQARKETEFPDLNGSVKGVI

FVDESIKCAAASNDSPLQQPEQQQHGRATGRWARINAELPSSRSWCAGYDDHSEDFFWRK

NCASHSGKNRNLSSCSPNCRDASDQVDQSYKSA

>contig43148 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53133.1|) 5e-26

MRHEVADTIVQRYEDLRANIQDQQRLNRFKVV

>contig43513-0 Frame-2R0

MMSKALNQLELKKVYLSRQYDLIHFLDEVDPTRSFTVSQLLV

>contig43618 Frame-0R|Blast-arginyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY68517.1|) 0.0

MSLSRSALSCAWHLQQSLRCSLQSLQPLIDVSNLPDTSLGVRRSAQKNADYQTSIALQLG

SREKKSKAAADTLTPEALAQIISDSFIMKKSQRDTLFKDVFVTKGGFVNLVLHDEWVARQ

AVRLATEGVCPALLPPSEQKHILVDFAAPNMGKKLHVGHLRSSVLGDSICNLLEFRGHRV

ARISHTGDVGSALATLIVALQAQQIPLETLTDAQMGKYYELGKMQSEVDAEFKHKVKDVV

LQLQRLGSDTGVDPDIRRTWERACQVSRVAYQRIFKRLGVHVQERGESTYMPFVPVIVQK

MKDNGLAVESRGALGIFLDGPDKPPMLLRKSDGGYLYATIDLTCLYYRIHGFPGVDPILY

DEIVYVTDQSQHLHFKHLFAAVRQAKWDKRLKKENVKLTHAPFGLVLGNNGTKLSSRNGA

FDYLEDLLDGAVAECSKQSLASATTSTVATELLLTKEQIDAQNRVIGDAAVRYFELAQQR

ERNYKFVMSNVLNLKGNTGVYLMYASARLQGILRKASGLENAQTSWESIVGLSSDTLAAQ

ELLAQASLDWHPSERALALLLSQFHDEVEAATIHLYPHILCDYLFRVAGHFHSFYEKCRV

LQDPRQDSRLLLCAATDAVLRRGLQLVGIKPTDRM

>contig43702 Frame-0F

MSNKRGTSRASALPMEFATANHADLVAWKTFLTTLR

>contig43795 Frame-1F

MVEWKLQQKYANEDEGAATSHGRVDSENRWIVYERYCHVYRNGELEDIVAQVPGFKIVSV

ENTRSNWCLCLKRI

>contig44237 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66692.1|) 3e-26

MSSTNPSDGIPGSFSHRPSTSACQ

>contig44556 Frame-2R

MGGKRHLSIEKDAGALKPAGQSQLTKKSRVSEIVAVDTTVLTTKRVGDRTSGLMAPTMLL

SGHNAAVYSLKFSPSGQHVASCSFDRSILLWDVYGECRNFNVLSGHKNAVLEVHWTYDNS

QVLSASADKMLGLWDVESGSRIKKFVGHSLAVNSCCPVTSGPTLIVSGSDDCTTKIWDVR

SKRAVKSFENKFQVTAVCFSGDNSHVIAGGLDGDVKMWDMRKDEISTVLQGHANIVTGVS

LSPDGSYLLSNAMDSTVKKWDIRPFVKGDRLKTTFLGAKHSFDRTLIRCGWSADMRFVAS

GSADRYVYIWDAETGNLRYHLPGHTGSVNEACFHPTEPIVGSCSSDKTIYLGELADV

>contig44642 Frame-1F

MARDAGTNLDENLRVVRLDPCPVMFWIRSP

>contig44794 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70534.1|) 2e-19

MCSDSYYGLMSIFHVPSILVAKLINHKSKENDGLVEYESCLGGISADKFKDHYRNQFYRP

R

>contig44808 Frame-1F|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY57226.1|) 7e-63

MYNDHHFHYGYWVHTAAIINRLDPSWTDLPKLNTMVDLLIRDVANYDLNDKFFARFRSFD

WFRGHSYSHGVTPFADGKDQESTSEDVNFAFGMYMYGK

>contig46176 Frame-1R

MANILFHYINTTLHVRHNRLLRLDRLIASLFF

>contig46662 Frame-0F

MVAHSLYYYRAPLWTGADIAH

>contig46806 Frame-2F

MVRVYVTALTAFLAFSASVSSTSKLARANPRPVNTDHSDAPAQLRLRGYTATNVETDERV

VLTEIYAFVRKFMNPLSLPTEEMVAIVNRMKDLNTPVKEVLRSAELQQLSDLVKS

>contig46899 Frame-0R

MLVWGCGTERSCFTASCSEICLYERFDIRLHYHYAGP

>contig47298 Frame-2F

MLTGFLKRHKGFSCLLRFARVDTVSNEMIKAVFSYPVLICLIVLSVHCQRRVSIRWC

>contig47720 Frame-2R|Blast-L-gulonolactone oxidase, putative [Phytophthora infestans T30-4](gb|EEY69252.1|) 1e-136

MLLDSRHIQISKMLRRSTLARRALSIHATRLPCSVQAARIFETNTWQYRVTSSPKWQTWA

IALAAAGAALTAAGSADTALNEDHNEFVNWSATHVCVPYQFHVPETVDEVQTLLQTYQAK

KQKLRCMGAGVSPNGLGFSSKAVGKGNVNEALMTLALFDKILDVDRTKLQVTVETGIIVG

DLLDKLRAYGMTMQNVASIRDQQVGGICQAGCHGTGAGIPPIDDQIVEMEIVTPAKGKMT

LSATQDPELFLLAKCGLGALGVVTKVTLQCVPMHKLIEKTFVMTLDEIRKNHNRWLVEFQ

HLRYMWIPYTDAVVVVQCRRAQEEDLLDETQFSSQENSDKVRMKAPRKLYLELTNGKPEP

DFLDWGFTKMRDKLLEIDPLDKQHVIRVNEVEKQFWMLSKGSRIA

>contig47845 Frame-0R

MYLHAKRMRFPHPFASGQIIDVSCKI

>contig47939 Frame-1F|Blast-ribose-phosphate pyrophosphokinase [Phytophthora infestans T30-4](gb|EEY56308.1|) 1e-42

MVHENVRGKDVYIVQPTCVPVNENLMELLLMVSTMRRSSARRITAVIPYYG

>contig48066 Frame-2R

MIKFVSLLSLFNCHPQRSKSLDLKYGVLHKIMVAKRRRRRSKEYVVLQRCDVTCNFVKRL

IIPL

>contig48112 Frame-1F

MMKSIRRSTVTRLNRRRSMLEKERRDFTTDQFSAHYIIDRHSYMDKLEANSINRPVAHKD

CHGGLSYQLASFLGLVAGNGADRKSMKSAIGLWTSLFAASILLVIALADDFSLYQRLFCC

VATYGVFLMLHPWIHRELPDK

>contig48228 Frame-2F|Blast-zinc transporter, putative [Phytophthora infestans T30-4](gb|EEY61698.1|) 6e-26

MDEKLPLKSSRTRLDRKQSRRIPLTDGAKNAQRKLQLACVCSLLFMCAEIVGGFLAGSLA

IMTDAA

>contig49025 Frame-2R

MYPSSASLVGNFMFFIFVAIVDEVLQQTRQDKTRTIRF

>contig49681 Frame-0F

MMSSKRVLEEHTHRHVSIVRNLTTWLTMSQCRAFESGSVTHYIYNRSLYPTNIMFGSDLR

KMTR

>contig50171 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53759.1|) 1e-112 NOT\_ORF

MIHTASLMHDDVIDEADTRRGRPSVNKVFGGKMAVLAGDFLLARSSVSLARLRNFEAVEL

MSTSIEHLVKGEVMQMKHATARNDISPFEYYLRKNYYKTGSLMSHSCMAALVLGKHEPQI

CNLGFAYGRHIGLAFQLIDDVLDYDGLNTGKPLLNDLKSGLSTAPLLLAQEEFPVLQKLS

KRNFSHIGDIEMVPFSLVTHRDKHCR\*VFMVVL\*ARELVEKSTGIARSKAMAIGQAELAA

QAAMQFAPSIERDAMVRLAQKVVYRSK

>contig50243 Frame-2R

MSSLSSDMAQNLPELSTERTEALVKFIDRSVDDAYNLSLGFGRVRWTPSRTREGVTIYRA

RTGPDDTLLDAAVRGSCNVSATSREISDLLITETSSDFTDHESAVNPSEFLDGKLLYTLV

PRTSKERFVCVKYHCVRSLAPSVTKHRDYVYVELVDSFEDGDGRRIGYRLCKSVDLDIIP

RRNTKHLLVRAKTLTLQTWSERAPGSLEFVTMVINDLGDRLPSWLVHKMVDTAALRSACI

RDYINQCRLDMLVHAGPREMVPLSRRVCCIVCTRSFSLVRKKYNCAGCGDVICSQCSVQE

LVTAHQRLSDLSAPGGKRKTRICAKCSSKMQSRELPRRASSARQSDASRVSSEGSIRSSA

SNRSFLARSHVSVGKPSDEMRRSFLSDSTTGTSSQDSA

>contig50654 Frame-2R|Blast-tryptophan synthase [Phytophthora infestans T30-4](gb|EEY70396.1|) 1e-119

MATTSPSSPRHRKYLDVSNAPPVYTSSDELHAYFGQYGGCFVAETLIQAHRNLIDAYVEA

TQDPTFREELEHLGRDYIGRPTPLYHAKRLTAHANGAQIWLKREDLAHTGAHKINNALGQ

AVLAKRLGKSRIIAETGAGQHGVATATACALLGLDCVVYMGYVDTQRQSLNVFRMKMLGA

KVIAVKSGSQTLKDAVNEAIRDWVTNVETTHYIIGSAIGPHPFPTIVRDFQAV

>contig51262 Frame-2R

MHRWFNFTISRRRIIFQDSSLCEIIVGACSARYKWARYFFEPERCLRSTLDAHHYAANN

>contig51338 Frame-2F

MRVFSLGNAICLAFAIIKTSVTARRAICATELNAAALKSSYNFQSLSPATPPSDSGAPDV

NGE

>contig51947 Frame-2R

MLRQKFLDGHRRHNLGFTAHRDASQERKPVTASVLTASLISVTPPRLNLMRALSAYRSTT

ALLMISFQIAQRARICHDNAKKSVELW

>contig52014 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64386.1|) 2e-36

MTQSAKVLTLYRRILTLHRKKLKPHMRVLGDQYVRDEFKRHKSSDPKYVALFIREWEQYA

AVMATKQNRFGEMLSSEDNELLDGEQKKKLRSLQEAARKLGKNIGSS

>contig52061 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57515.1|) 1e-28

MGRNLFDYNIVNSSTKFLSGNSAAFSDDRNTSLSSTRSTVSSSTDSFRIQSLGLQSQTST

VKDMEALNLSQMHRNRTADHSSRGVRKPLAFNASSST

>contig52379 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69970.1|) 4e-50

MLHVLNAAYRAPWFVVYLAAGIGVMVNLIDEACSTALAVCKLYPHFSFAETLGEEISMHT

TLVPLVRVRMPTLQFLGVYIALYAAKHWGLLDRGWLLLLDSFSCRWLKHQLFEVLPTYLP

FMLSEPDLPELLSEDETQYENCDNIDNMSVFPPVDNDACIKAMAKLVQVKMQYANRTIRR

PDDWLVFDPIQNKLVFQKDVISNEIHALNGPSSGYKKSLSQDSVGEKQASPKCDSDVYGR

DIVQEVARRSKT

>contig52429 Frame-2F|Blast-trafficking protein particle complex subunit 6B [Phytophthora infestans T30-4](gb|EEY58304.1|) 3e-81

MGYDVGCRYAERAARERPRMIEPLDVIKFVCKDFWIAIFKKQIDKLQTNHRGVFVVQDFS

FRWLAGISAATDQETREMALLFLVFPCGMIRGALANLGLSAIVNADVPDVRALPGCLFNI

KIKQS

>contig52911-0 Frame-0F0

MQDVDASSLSENRGYKLSHTVPTETWEKAIAAVELQGLSLRAAAKLYGVHFAALHRRVKK

RAQNVQEKGIIEYFHPSDEAGIMRVVVARAELGVL

>contig52911-1 Frame-0R1

MQCCKMHAVELGRGSQTQTLQLDGCNSFFPRLGRHCVAQLVATIFAQRRSIHVLHCVHTT

LVIAHSALSRARVRRAKVGRFTKSTVRLICGCSVLTTATH

>contig53084 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67166.1|) 6e-09

MTTSADNETWDEWEVDGTVSSATLPLRSLNDATEAKIQLPTDSFNISPFDTEKWRFDLSE

LEQEMSSLTPAAYVTPLSRSCFSTNSE

>contig53307 Frame-1F

MFGQQGKHSHKFCNSTQIIVNEQPYY

>contig53493 Frame-2F

MQQLIAGTLPGRGSNGKISVDEAETIDDFVRKLGRLRWKVTGSREPLLPGAQLAAVPKEK

PAIEVTTVLRIMEELIPSLTVEMEKIVTSLRKQQLADAEFRLQLSQQYIEVSSKKTEEIC

KEYKVNVQAFQDALMYYHDDEIVEKTLAKLAEQQQKRFQKLGL

>contig53516-0 Frame-1F0

MQDLVWRRLHLLLVKTSIQLRCESSRRLRRSVCTIRIIPFNMLISI

>contig53516-1 Frame-2R1

MLINILKGIIRMVQTLRRKRLELSHRNCIEVFTSNKCSLLHTRSCIEPLISRPVPCVPQY

DCVLQSRKSQLFRI

>contig53589 Frame-0F

MSFIAARGDFGDDVSRDVSFLSDYCDDTDCSRLSSLVTASASSSNSSSLSCSFIP

>contig54016-0 Frame-2F0

MGDFEIRLRSKKRSVTYKACRIGSCSPSNNCELQLISTSSTGAETGALFTLIKSFDSNTF

RSVLLSIFNGP

>contig54016-1 Frame-2R1

MDSKTLRNVLLSNDLISVKSAPVSAPVDDVDMSWSSQLLLGLHEPIRHALYVTDRFLERS

RISKSPMNWKVREFFSW

>contig54089 Frame-1R|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY60597.1|) 2e-38

MLHYAQVHHVDTMDRRFATEAPGVAAHSTTRGLMQGIVTKTLPAEWRMVEPVDFPVDFYP

L

>contig54470 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61888.1|) 1e-20

MSGAALEPEELQEEPRWRSIRYSPHARPLHWSRLIDEKLVLLVIESTASGERFPVGVNWL

EVSRVV

>contig54975 Frame-0R

MILLNSSPKSCNQVNRSHETARAIMFHIALITIPETKASGSEKLNPPAL

>contig55019 Frame-0F|Blast-U3 small nucleolar RNA-associated protein 6 [Phytophthora infestans T30-4](gb|EEY57485.1|) 3e-62

MRKIDAMRYIEYELKLDALRAARKKRLGIVKVSVGDTACLKRVHNIFDRVLFKHRGSIEL

WLQYVAFCKREGSSRVLSAVFSRALQSHPRSAELWIEAASYEFSVNL

>contig55363 Frame-1R

MPMQVTVQSIVSTTLAAGVLVIGPALHGELHQILLT

>contig55774 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66835.1|) 1e-10

MDGVVVLETQFSKSFMLHIMNSIDYPALCHTTKEARCNILGRRRYYV

>contig56425 Frame-1R

MIVLAQDGHMAAGTSSNGAMHKIAG

>contig56627 Frame-2R|Blast-U3 small nucleolar ribonucleoprotein protein IMP3 [Phytophthora infestans T30-4](gb|EEY69772.1|) 2e-84

MGRQLKFHEQKLLKKVDLLEWKKENNLHEIKVIRRYRIPDREQYHKYNRLVGHISKVVAR

LKKRPANDPYRVKTTTALLDKLYAMGLIQTKKVCLRLRKSTFLLSVVVAYPLVMVRVKMA

ESIKEATTFIEQGHVRVGPTVVTDSAFLVTRSMEDFVTWVDSSKIKRTIMKYNDKLDDYD

LLGN

>contig57336 Frame-2F|Blast-predicted protein [Physcomitrella patens subsp. patens]gb|EDQ80476.1| predicted protein [Physcomitrella patens subsp. patens](ref|XP\_001754506.1|) 8e-20 NOT\_ORF

MTMVVRLTGGPGATICSPFIIF\*NKDCSYPSRGVPDDVPGVSYRSAKKCFMTKKVWLSG

>contig57831 Frame-1F

MALYAFRAATLNNAFISKIRSPILLDKIWAIWPLNVHIDNM

>contig57844-0 Frame-1F0

MCLLLLRKICSCKQRSLKKNSLASKITLKYLLQNVVVHHRVRP

>contig59345 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65987.1|) 3e-30

MIFYLVFNGGLYLAQLVLYASLF

>contig01064 Frame-1F

MAPSIYGHNHVKTALALALFGGQAKVIKNSRVRGDLNVLLVGDPGTAKSQFLKFIQHTAP

RAVYTTGKGASAVGLTAGVTRDPLTKEWVLQGGALVLADQGVCLIDEFDKMNEIDRTSIH

EAMEQQSISISKAGIVTSLQARCSVIAAANPIQGRYQAARTFAENVELTDPILQRFDLLC

VLQDCVDPINDERLAEFVVSSHMKSGAMEEKTAQSMKEIKGLAPEVLRKYLVYARTYIHP

VLGSNVDTTKVEAFYAQLRQASQHTGAVPVAVRHLESLFRMAEAYARMHLRATVVDSDVA

FAIHVLTESLCRAQKYTFQRQWRRLFRPYLIHQDDPPVVLLLHVLEELFQSAHAYAQLRR

DSLRGATHASPTVVVLREDLVAKAKEMGIDDVEAFCTSTAFQRAGFRIDATGTAIEKDVS

>contig02043 Frame-1F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY64568.1|) 2e-36

MTAAPLKKPVELAETGWSSQGVDARASVSTPANQAKFLADLFYVFSNIGFPFSWYLALDS

PWRTRE

>contig05110 Frame-1F

MRGESDLDDLTLTNKLTICVEITQLEKLRSRALNKLCPVVCRVFTEYWLIDRTSLSLAFY

TADNFLIPSNHPSRLYDKDNDKAESSSVSLSVFSCESKQIVSKMKIGIQGGIGKREVQSE

PFDISAVGVRGQIFVPTTRSRDARSLLSTIAEFGAPSDGLEATFKQYEFGVMIEQGPEKF

SRSRVVTLVPRYYFVNSSNNYEIRIRQECSTDLNAEIRLCPQETKFFHWTDSRLPLRVQI

RFVLAEKGHNKRDIASCAISSQWSAPFELSSVGNFVLRVKAKVRPAPPC

>contig05622 Frame-0F|Blast-2-oxoglutarate dehydrogenase E1 component, putative [Phytophthora infestans T30-4](gb|EEY57954.1|) 1e-166

MGYEYGYSFESPTTLVIWEAQFGDFFNGAQIVIDQFLSSAESKWMRQSGLVLLLPHGIDG

AGPDHSSGRLERFLQLVDTPGLTPRVLEKRNDLERVWKQYEHDPNMIVVNVTTPANYFHL

LRRQQQRSYRKPVIVMGPKMLLRLAEATSLLSEMGPGTHFQPLLSDPMITDASQVKKVYF

CSGKFYYELAKERLVRCKNPQSIALIRLEELAPFPFEQVAQELLNFSKAKTFVWVQEEPL

NQGAWTYAQAHIEKLLQKNQRLDYIGRESLAAPAVGLSKRSQAQLEVVLNKAFGKHKK

>contig05860 Frame-1F

MANHSHFLHAHTHPISPSSVLYKRDSITPLLHPQRASRTSPSGTSRRSGRYKKRRVTPAS

DVDSRKSQKLLKLALAKSMVETTMRQVVPLPQGAVFYPTREQFADPIKYITSIEQEASRT

GICKIVPPQGWKPPFAIDFEDERLRFSTRTQRIHKLQEGHAYGDGRTHTFKSFRANAHAF

RDKWFQTRGLNRNNMTSEEIEKEYWHIIQTGGPSVEVEYANDLDIAQVGSGFPRSQKRFM

TPRL

>contig07354 Frame-2R

MSHLKQVDESSANLAMATFLEAKYGLSHLAGRLEYVLPKAIGKHHVLFQAVENGLVSLLK

SKHLPLSDVIDRVTSRAKQPIGQPFSLSAYPMRLLDKYEDDAFELMKALIDKFGYQVLLL

YTRNSNLLPKKVAREIDSIIKLDNTALVEKFKLKPLNDDLFTRSEMRVFLFIVKHRGTDR

EKETKSSAIISALIQNNLHDMSPSAALRKLYEIAKGTEQKKGSTPLDENVKHLMSEVINL

WKKMNS

>contig08742 Frame-2F

MLVKSEADVEVAAALASLTIAFEKHEHRELPTTEDVIAELSYLPGLSTKNLVFKDKKEGL

FLVTVAPTTVVDTKKLGAHLHAAGIGGQKWNLRFASEDVLASTLKVTKGSVSPLCVMHDV

KCEVRLVLDKALLDSTQINCHPLRNDQTYSIKADDLLSFVKHYNHEPIVVDFAAHLDEPV

ASSAKTPKEKHEEKKKTVDQKANEGMSATKEENFADWYTEAITKSGMIDYYDVSGCYILR

PYSYEIWERVQQFLDRNLKAIGVKNCYFPMFVTKEKLEREKDHLEGFAPEVAWVTKSGNS

DLKDPIAIRPTSETIMYPAFKNWIRSHRDLPLKLNQWNNVVRWEFKNPTPFLRTREFLWQ

EGHTAHASKEEADEEVRTVLNFYAACYEELLAVPMIKGVKTEKEKFAGADYTTTIEGFIP

STGRGIQAATSHMLGQNFGKMFGISAEYEDGKKLIPWQNSWGFTTRSLGVMIMVHGDDKG

LVLPPRVAPTQVIVVPIPYQNQHEAEEMFARADEIVAKLSEAGVRIEADKRRVYTPGWKY

NYWELKGVPLRFELGPKDIAKKQVRVVRRDNGSKEDIPEAELTTRIPALLEEIQKEMLKR

AAALRDSHIREVTEWKDFVPCLQEGCMALTPFCNETEWEETVKTKSREESLDLMGLEEEA

ENTATSAAAKTLCIPFKKNEENPVTADTKCFISGKPAKVWVLWGRSY

>contig11384 Frame-0R|Blast-reverse transcriptase [Phytophthora ramorum](gb|ABG66534.1|) 5e-34 NOT\_ORF

MSMQITVQAVGCGVHNFLAAMLVDQARCKRHELHVVWYDFANAFGSVPHDMLWEALE\*LG

VPPEFVACCRGLYAGASFTLGNAADGTMAPIALRVVHNSYG

>contig11854 Frame-2R

MTEPQHALTMTSIASIAISKNQN

>contig12099 Frame-1F

MNLSGKRDSSRDAVDARSSIECNLILLYCDAVVDCFDGMDERMDEVKASDKRLRSAIPVM

RGLLKDLGEKSRNTLDSLKDKGPPMTRRVKTRSEILKEAKEKNKSAAPVESEAVKEASPS

RAPHPLMAARGRGRGGRGGGRNDLFSAIKGRGDGDDAAPPVDFLASIRGRGRGKPGGPGR

GNLFSAIKARGGDDGCSGGRGGDLMSAIRGRGGGG

>contig12820 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55515.1|) 3e-52

MFASRVLRMAVTKTSTGLVGLKVNPNARQDLIKIYRRTLEEVKVLPPEAKNYRDVVEQIT

NFRLNVAESNEDEEVIERQINCGQLEELIEQAEDELSIIPVYIEHELWKSPLESDK

>contig13632 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60245.1|) 6e-12

MEISPEQLESKIRREIGAKLVEAVDLSDGCGMKFSLVVVHEGFEG

>contig13931 Frame-0F

MQPSCAAKNKHGSLAVAWNFALIGLVLIGFLQLQYIKEPLGGESQIGSEVSRRLREMNED

IKKEPKNHHFFPYRSASRAWGKLHSKNLPR

>contig16240 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69156.1|) 1e-86

MIPDVSVLQQLIPIPKLCTAQSLNCEEEPHITINNAILRKHFRKLTIAFLEPFEQYFGVW

KANGGTTKLYINVEDSMKPFTLLDLLSTIKPQKLSLQIKQTKWKALYTAFVKGPHFEPWF

NNRRKRCIHEFTETLRFLRNGVEAQYLLCSPFGTNLSREQYLSLKKEMKLALAQENARGE

VDKQQVKTIKRHLQVVKNKICSVRKEN

>contig16503 Frame-2F

MEKKYGEPAVAKFVNKALSLDPKSTEANRIQSAMLDRWKKEGLSVQEVAEKMTPKKFKLT

KETLEDFPREMLMRYAVKIGSAEEDADFVTSAVLVVQFINKINTEEKLSALLPNLKAIQD

LSSSDLTRILHVEKDATADIFNRQVGF

>contig17324 Frame-0R

MSHFSTDITSPCIGDLTVLNSTDDFFSYALFTAP

>contig18659 Frame-1F

MGKWAITRASNPYERCDSVARPLDRGLQNLKKDGEKRQTACSAWTRSMSRLCPSPSSAAH

QAFLGDFLAYCSPLASDLPREVFVSPLRDSDEGKSEDDAELHGSRHSSLTLLKGHSR

>contig19021 Frame-2F

MGTRGFFFEPQDSNLPILRFFFRDMKEMPMAELHNHPEAGECAILLAFTVSSIIEMKERG

VDHPYVSKDTRGNATVPEKYLFSLLHSKMDEFLKIVRPIWTLAHQDSVMNKVDEEALLAP

VLSPRQTDQFDSSLLVDFRERPLLLKGKFVDRIVPLLKYPGCLMLTNQRLYFQPAQVNNV

GDPVLNWAYHTIEYVYKRRHMLKQSGLECFLKNGESFFFSFRNHTDRDEVYARMVTQPDL

KHLQETEMIELMLRRWQQREVSNFEYLVYLNNAAGRTKNDLTQYPVFPWILSDYDSPSID

LRSSAVYRDLSKPIGALNQERLEFYKARYDAMPRDMEDEGLPPPFLYGTHYSTPGYVLYY

FVRMAPEYMLCLQNGKFDAPDRLFQSISSTWSSCNTNHADLKELVPAFFDESVPPDEWLC

NGKNLDLGTTQKLTRVGNVELPAWASSPSDFVRINREALESEYVSEHLHEWIDLIFGFKQ

RGPAAIDANNLFYYLSYEGSVDLETITDPVEKCSLEAQIQEFGQTPTLLFAGAHPSRNDR

GNSIVLATPDVVRP

>contig19414 Frame-1F

MIISQEVSNQLINLIHIEEMVPVFWRLDSRILATYQYLEAKIILCKACHKNFLNFTRRHG

TAHVHLDLIADHIEHASHSILKGLYKSFL

>contig20317 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY65567.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63458.1|) 2e-31

MDMRDVVAQVQTLEALRLFVAAFDAGQVAPKPARFRITPDAVLDENTPKKIFYIQQKQFS

LHRQRTLLDVRNELPVATLRLSMFNRTPTYSAYRNTEHE

>contig20825 Frame-1F

MVESKVARPNPTVLVVSLISGPLNGPSTTERLVKRNVEFNSEFQLGTFEQKDTCVVLLND

GEELYISQRVLGSDRRSLLKSSKQIEITTPARSQPLQPQVVSIKKLFVSFRCVLARSSKA

SRRDTCPQPVISSLPSTFTVAFPGILGGLFLISCLVSLYCATSFVGLMKITIILGLIFSM

SQISQFVICISEKQSQKLLSTVLSPIGAAKLTATAVENEFIFYLTIDKLELIEADQDTEP

ILSDTTSSVSDESADRVADIERNGISGGPIDFLPRFIAGEKGDEEKGRARYLATLEWRKE

HKIDDILVMPHPNFKIIKQYYPQYFHGRTRDGLPVYYERPGKIDLPALKREGLSIDDLLR

HYVYITEYLWRVVEPNDSSRSITVLDVSGIGMYDLGGEVLDFIKRASAFTGAHYPERSAH

IFIINIPGWFNMIWRMVKPMIDPVTREKVHMLKGNAILDELEALIDRRNIPSDFGGEGVA

LGDSDEERALAAHVEKYLGNSH

>contig20850 Frame-2F

MQLRSRVVSTPRQENKKFAIRRTATLSLNNTRSHTLTIVEAPKTRHSASRRDHNPLHTRC

NAVDRKKRRLARGEDDPEEVTKRRLRLLQSAIGPEDCVDESNWITGTLIDLVLWKFAKSY

AAVYFLPTAFYHLHLEMAQEIAVRPSWPQRSRGLRSKRDFIVRDVLGRVVDYNSKKPVVF

VVNVDQIHWNLFRVQLSPTPKLQLFEPMGKLASRSGISYRSVPRAVIEWLNVCYPQHKCW

LQRTMSAIENKQQVSGFDCGVACLLYADKCGRGQSGEEINDSIDQNAITSFRKQLRLQFG

KHGFGQR

>contig21747 Frame-2R

MTKCVRWSTVTVYEFDVGLGGSSVPKHGGPSIGLARKPRCVWSTPLDELEGNELLSSSPR

TTKGDGKKTKTATKMRTHRNRKVRWLKPLERVTMLTKAGCSEKRIYRMMMESSEIAMSRR

LTLRVLDM

>contig22034 Frame-1R|Blast-ADP-ribosylation factor family [Phytophthora infestans T30-4](gb|EEY59698.1|) 1e-71

MLNEDELRDSVLLVFANKQDLPNAMSAAEMTDKLGLHGLRHRQWYIQACCATTGDGLYEG

LDWLSASLQKQK

>contig22764 Frame-0F

MTDASAIDSEIAAVCDGFKANPDAVLAVLVGNENLKNGDFGTYTAEELVSYMNKVKACVG

DTPVGSVQRINEWLDADGAATLEEASDVIAVNIYPFFTVSDQTPIQKLETQWKQMTDKYD

MNKLQLTETGWPSSGEVYQSNAPSLDVMAQYLNDFFTWSTTVSQAYWFMMYDSTISYTGA

EYEKHFGVFTSNGTKKVTIESNGVTAQTTPTQTELSVAFPTSAPPVTNAPTLNSTVQSEA

MPAAVTTPRSGACKRAAVRKR

>contig22849 Frame-0R

MVRSFTLNLTTAPRQDLSFSAGVYRMRFIPIFIVATFGLAISSDSLTAASSIQLRVLQTN

PPSELIISRARRMRLVATQINLSVLSDVFTRDN

>contig23187 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57690.1|) 4e-33

MSTVEGNLDTNEGFEEEHVLPDLEAELQQVQTIKLQIRQRLNDLLHEQKVLKQQQQRRQR

RSDRLDSGAPTARMRHLQEKQQARHAEEEAKRKRYEIEKKAKAEEAQRKRKFIIETQDKD

LDDLDAFLVQDAVQF

>contig23262 Frame-2F

MRHCCNSLIAFSRCSTTKNSTLALRRKQADLGKERSSQNFYCRRAAIASISEKRDRPLLS

VSNVAKHLIEFCKKNSAANDHTNDSMLQVEVIGKAYSVHFANCRQYRHDYPLQALSFVT

>contig23675 Frame-2F

MALSWLFPPSFVVQTPFTRFKSSSPSLSQSTYQHSNQHTQ

>contig24241 Frame-1R

MRGKLSQSTRQSLEVSFLDTAHIVFTTLSSAGVAALDASARYDVLVVDEAAQAVELSTII

PMKFGSKQCVLVGDPQQLSATVFSRNSSQSLYERSLFERLESCKHPVHMLRTQYRSHPII

SDFPRNYFYDGKLQDGDNVNGGDYVKPYHSLGEAFMPLVFWNLLSSREKASKSVSRMNVG

EAELAVNLYLTLKNSCSPDAITGKVGMITPYSQQMEELKKRFYCALGERYEQEVEINTVD

GFQGREKDIIILSTVRADPKAGVGFLNDIRRMNVALTRAKFACYVIGKENALRSSKPWSA

LLDHAYKHHCIVHVENPLCNLITLKPMEQPSEASRKLSGVSINSHRQNSLQKYEQSIGNS

RSKVIGDGNGGGRRDGQRRERGRGIRGRGRGTPAQHFSPLHQYAQNIEPHYSNKTPLGAY

AQPLSTNMSTQRTPSALGAPLSQPASEFYSSNRPPSIHSHAIQESYVENSSKPGNGTNGR

GPRHSRDPRQRSG

>contig24627 Frame-0R|Blast-histone H2A type 1 [Phytophthora infestans T30-4](gb|EEY66322.1|) 2e-71

MSGKGKAATGGRGKKTGKSSTRSSKAGLQFPVGRVARYLRKGRYAQRTGSGAPVYMAAVL

EYLCAEILELAGNAARDHKKTRIIPRHIQMAVRNDEELNKLLGDVTIASGGVMPNIHSVL

LPKKSASTGKKGKSSASQDY

>contig25264 Frame-1F|Blast-60S ribosomal protein L23a [Phytophthora infestans T30-4](gb|EEY64162.1|) 3e-57

MAKATNNPKTAAGKSAAKLSKKVMKGSHGKVLKIRTKVHFYKPKTLRLARAPRYARKAVP

SRNKLDKYRIIKSPLTTESAMKKIEDTNTLVFLVDLLANKRQIKDAVKQLYDIKVAKVNT

LI

>contig25534 Frame-0F

MPQQLSGQLQVSQVMATPSNPHQLPHRMKKGPPSTSNNKNSSSASYFHHVLDRTNNYSIS

TNPSLYTQTSNLSADTVPVSTGKRQRPNTSNNISNCSCLAPFGFLSPLLETEHPLPELST

NWGYNNRNMSKYPSATIRMGNYSSNNTSSLVNTSGIGQEIASSSAMTMFTGVDSFLPEYD

PTLYSLWNPTGGNNGMMYAPEDDLVQGDQQQARPPLYMASDEELKMEYPQLSEFTQDFES

YLNDTIKANASPSNPLTMSTMKSGMKRDFFMARDSGDLGLGAKTELDIANCGTREVRDRG

CSARCLQLQHRIYHCYQSTV

>contig25808 Frame-2F|Blast-ribosomal RNA methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65142.1|) 1e-107

MGRTSKDKRDIYYRKAKQQGYRARSAFKLIQLDDKFGLLRDTTRVVDLCAAPGGWSQVLA

ERLPKESVIVAVDLMEMAPLDGVVQLQGDITLKATADRIVAQFDGQKAQVVVSDGAPDVL

GLHDLDEYLQAQLVLAGLNISLHILEAGGSFVAKLFRGKEVSLLFAQLRRFFSEVLCAKP

KTSRNSSFEAFVVCKDFRLPKTFVPDMERNLLDLRYTEDSEADNFDDW

>contig26863 Frame-0F

MADVEMKTMEDPMFEGISSRNRSTESWPWVEKYRPSSLSDLIAHQAIISTLNRLIDAQKL

PHLLFYGPPGTGKTSMIIAAARKMYGKNYSSMVLELNASDDRGIDVVRNQIKEFAGTKKL

FSQGVKLVILDEADSMTNDAQFSLRRVIEKYTKNARFCLICNYVSKIIPALQSRCTRFRF

APLNDSQVSDRVKHIVQLEKLNMTEDGFKAILRLGQGDMRRILNILQATSMAHEIVNETN

VYMCTGNPLPKDIELITQWLFNESFPTAVRKCLEVQKIKGYATSDILQDVYRYTMELELP

PRCRMYLYDELAKLEHRLSNGTTEELQLASLVAIFAITRKQMSNAVAAASIS

>contig26939 Frame-1F|Blast-formyl-coenzyme A transferase, putative [Phytophthora infestans T30-4](gb|EEY57719.1|) 0.0

MRLRVTSPLPRASQLTTGRNKLVRRPAHRSVTTINCGLSTKKDRPLPLEGIRVVECGQLI

AGPFAGTILSYFGADVIKVEPPGGDQVRNYRELDRNKTSLWWYSLGRNKRSMAVDMNKND

GRKLIEELIEQSDVLIENFRPGRMEKWGLGPDHFEKTNPKLVYARVSGFGQYGPYSSRPG

FASVCEAMGGFRYVNGFPDRPPVRPNLSIGDTIAGIHAALGIVIALLGRERGISSGHLSK

GQVVDVAIYESMFNLMEAVVPEYDYSGSIRECSGSTITGIVPSNTYVTKDKKNVVLAANV

DSLFVRLMKAIGREDMAVDSKYSTNADRVKFQAEIDATLAAWTATQALNTVVSVMEKAAI

PVGVVYSVEDMMEDPHYQQRNMFEEVEIPDGDNFRKLKVPAILPKLQATPGVSRFAGRKL

GQDTRQILQDVLCRSQQEIKRLLHEKVVFES

>contig27770 Frame-1R|Blast-Resistance-Nodulation-Cell Division (RND) Superfamily [Phytophthora infestans T30-4](gb|EEY58756.1|) 4e-55

MGLSCLIFQMKMTMIAFEVVPFLILAIGVDNIFIITNEFDRVGAERGLLIRNNIPQRREY

LENEKVVVHQVMNETMRNVGPSILVAAIAETLAFLVGAFTRIPALRNFCIVAALAVTINW

ILQFTWFTAALTLDTRRIRARRYDWCPWIKEKGTRKPFEST

>contig28173 Frame-2F

MSNEFHECLASCGYGRKVSVDMSDVVTSFNVSYCRNSFKPLGSRHQYKVLVTPAFVKVCE

FLKPAVPERQDPVKTVESRRIRT

>contig28322 Frame-1R|Blast-peroxiredoxin-like protein [Phytophthora infestans T30-4](gb|EEY57987.1|) 5e-17

MVSTRSRKTPGSLPAIEQPQKRVAASDASTRPVKKATTPSAIASHLVVGESVTKGVTLSN

QDEKKVVVADTYREQ

>contig28465 Frame-0F

MCAKHQKENQNLPQVQDCYDDSFLSGERSGHFSNAVESVTKPEFVAMSEKTQVSGPSLSN

GLTSMA

>contig29783 Frame-0R

MLDSPIEPLVASKSSKTAGEPYLVDNVYDDDSVGTTGNEMSTEEMLLSLKDLDSILKKNS

EPFKQVSSN

>contig30150 Frame-0F

MLTRNARLKASAVATFVGEYLHGKAKRRRIQINAIAEESHAAVHSLSYVVGMFCKNSKNW

RRVGDCRHPDHSEFDPRALVRKVPIQFAL

>contig31557 Frame-1F|Blast-copper-transporting ATPase, putative [Phytophthora infestans T30-4](gb|EEY66507.1|) 0.0

MSIVPVDWKLDLGGSTSNGHADDFFLSILFAISVVVIACPCALGLATPTAVMVGCGIGAK

HGVLIKGGRALETARYIDTIVFDKTGTLTVGHPSVRDVIVADRLYTPRELLYYGASLECV

SEHVLGKAIVMTATEHEKLELKDPTNVCVIPGRGIEGVVAASSVTSRSTPSNVLVGNLEY

CEEKGIEISEKMRTHVHELEMEGKTVVVVCVKNKLVGVIALADAPRPGAAAVVNHLKSMG

LDVWLITGDNLRTASAITRQMGINHVKAVALPGEKASQIKALQSQVNPVTLKPRIVCMVG

DGINDAPALAQSDIGMAIGAGTQIAKAEADMILVKSALTDVVVALDLARVVFSRIKVNFF

FSIVYNIVGIPLAAGVFFPLIHRMMPPACAGLAMAFSSVSVVISSLLLKSYQPPVINKTD

RKIRFNEDVKVKELKDIMRQKLGPSQTTYEPLAISDEWEE

>contig31643 Frame-2R

MNVSGPTAMCLGMGAAMLASVTLFRHNKCAWQFIRHASASCHSKRGLCSSADRLSSQRLL

PCAEELSQLEPRRLSKQNITVVQLNILASNLATRNHFPYVLDSNLNWDYRRTVLLRQLDK

LDADVLCLEELSDYWTFFKNELQERGYDSVYVKRPSIHISNWSGEKKHDGCGIFYKKDKF

ELKEFEAINFHDPHDRVAVLAMLKMRHFAQFVLIGCTHLWWNAKKVDHQMTELYELEEEM

IRMSSDVRDKYERDLVDTVTGQDCVPIVLCGDFNNSPESPIYEYMENSFMQKPNLEGLSE

VFRSAYAFYKPNAIASALHHSEEALQSFKVEDSKTAEPPHTTVNFRRCWTIDYIWYSKNS

LVPSRILEIPTESELRAEDGPGNWYNRLAMSDSLTQLGRLPSGLHGNYNGIPNSIYGSDH

VPIMAEFEFLCASEKGTTFFNG

>contig31975 Frame-0F

MIASLVELSLSLKQQCAACTTNRYDQSNVVTHVLPPVMPQDLACLSSDEFDEMLELHANM

ACADTDVNTIRKEHELLQHTFANNTNLKTMQGLCTKNTPFHVAWSLMDGRFKFLEALAGG

LATVFSSHVVPIADKYKSDLVLCPKELDEARLMLADFELESALHGKQFPALAQLQEEMLE

RDIDQRVRKHQKTTISS

>contig33032 Frame-1F|Blast-lysyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY69737.1|) 4e-83

MSPLAKAHRNHEGVTERFELFVAGKELCNAYTELNDPFDQRQRFVAQQADQQRGDKEAHT

KDEEFCTALEYGLPPTGGFGLGIDRLVMLLSGKSHIREVILFPLLKPKDSPF

>contig33177 Frame-1F|Blast-Der1-like family, putative [Phytophthora infestans T30-4](gb|EEY68036.1|) 3e-86

MLFFGAVVLWVIAFFMTIPFLGTSLIFMIVYVWSRRNPTAPVSIWGFRLDGLYLPWALIA

FTVLVGGNPMMDVFGVVAGHLYYFLLEVLPATKGWNLMQTPAVFTNLFPPPQVALNRAPI

IGARGAANGGATPRAGGYAWGAGRSLGSE

>contig33663 Frame-2F

MPPSSLSHLAIFSRPPSSFLPTKVMKILVPFVAASMAIAGVASDAQHTSRQLIVGGEETF

EGNHPFVVSLRLKKPDETLCHGALISPNVVLTTIFCGLTEPEHYRLNYATIGAYYSRGML

NAEGDRDGEHLKILKTINHPDFEHPTNSVDIAVLILEKESTFKPIGLPTSSEIDLKTPLR

TFGWGSTYYATESEADQSFRMKTILLNPMTQNECSKAYENITNSFFCASGENQGGLCIGD

NGNPAIDEKKEVVVGISSHGKGCNNNVLSNVGAVTEWLQEIIKQYAPKQSQVK

>contig33739 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56450.1|) 1e-144

MDIDLRDANKHLSDSLRKIVEENAVSRSFLESFTAGKAVQHTDVRTWLSSDTSLRTYQQH

GVDWLCFMAKNQLHGILADDMGLGKTLQTLSAMAATIGSTPNALMPCIVVCPPIIVHHWI

QEVEKHIPGVFAAIIDYSVPISDRRNLQCRSGTWLVRNGLTLIITTYSILRTDIEFLKTI

DFAYSVLDEAHLIRNPNTGIFRAVLEIRASRRIALSGTPLQNNVTDLWALFEFLMPGYLG

DFTKFRREFVLPITKSKERNATTKQKENAAIAITKLHQKMLPFILRRTKDQVLKELPPKI

ISNVLLPLSSLQKKLYSLASSPQNESKGS

>contig33898 Frame-2R|Blast-cell division protein kinase, putative [Phytophthora infestans T30-4](gb|EEY67760.1|) 8e-86

MGSRKYSTPVDIWSVGCIFAEMANGGPLFAGTSEADQLDRIFRLLGTATADNYAAIVDLP

DYSRDFPLYPMPETLAHLVPTLDTDGVALLEQMLHYDPAKRITAADAMVHPYFSDLSPAL

IDSR

>contig34059 Frame-0F

MSRFAAFLTTTAPSTHCFHLGLIYVIVCYVACSDGVNSG

>contig34154 Frame-2R|Blast-histone-binding protein RBBP4 [Phytophthora infestans T30-4](gb|EEY57324.1|) 0.0

MVAEVRLPLEDTEIDARKYDEESQELGGFGGVSGKVDIKIRVNHDGEVNRARFMPSDELV

VATKTPHAEVHVFDISKRPSQPEPNSSCDPDFRLLGHTKEGYGLCWDPHQPFHLISGSDD

AIICEWDLGNTSKTVQPLRKYSGHSDVIEDVAWHMHNSKIFGSVGDDKKLLIWDMRSESY

DKPATTVYAHTAEVNCLAFSPFSEYLVATGSADKHVNLWDMRNMKAKLHSFEGHNDEVYQ

IQWSPHNETILGSCSADRRMHVWDLSKIGDEQSPEDAEDGPPELLFIHGGHTSKISDFSW

NLNDPWVVASVAEDNVLQIWQMAENIYNEEGDETEQADIA

>contig34352 Frame-0F|Blast-phosphatidic acid phosphatase [Phytophthora infestans T30-4](gb|EEY59651.1|) 1e-116

MCKLPETHYATQHFYFVAHSGNMVNNNKGLLENGEAPSTYHYLAPYPSQPTGMQITRNGG

QHSEPLTDTSDDIPIHIAEADAKRPLKSPLQQFVQNYRLLEFSSALLLYLLGLVFARIAV

HERPIPGIKVRLSATALTWSLDPSIDEKKMPEEVPMWLLLSLGTVLPIGANLIVNYVLPR

FSQVRVIAHDTRDFLLSLFLSTALATFLTQFIKNITGRFRPSFYDMCKWNDAIDWDGVTN

LCMDAAGEKEGRKSFPSGHASFAWSSLLVLSLYLLGRSSLNSKSRSISTLQVGKKSLMLS

VCCAPILLASWISITRCIDNWH

>contig34402 Frame-1R

MAREGSDKRRKQWMGGRDGNQKRYKGALSAATNAKGHGAVLVTCEKIKERQSVSDALNIL

NEAADRYFPADEETKDQEETSAADESNSMQKQLQEEIKGLQEKAKTRQTGRFTALDTGVK

GAVLIQFKDDSISPMALISKIFEDAETTKSIASRFIQKMIPLEKVGYSSVEGIKELAAPM

IHAHLEAFRKEQKDADKDDVFEFAVEFKRRNCTNLNSMDVINALVELVGEEKTKVNLTTP

RSVLIVEVFRNSCGFSISNDFYRFKKYNVRSFIECIAPGQETAKVGENDKKVEKED

>contig34745 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63778.1|) 7e-45

MRMDPLNSALQPALIQTLGQSHEAKALFQMINATLWYLQSAVWPLRPVFWAWSELRVVVE

SPKVDKLSFTFA

>contig35221 Frame-0R

MAPRCLKMSLHACFFFMAACVRHALSTAIQSASV

>contig35456 Frame-2R

MDKTQLLRATHLVVLQHGLLGSSNDFARFIEIFRTHFQIDELFLHAAECNATSFFRTYDG

VDQGGQRLADEIQEVADKMPLLKKLSMVGHSLGGLYNRFCIAVLFHRGFFDKIEPMNFIT

FASPHLGIRRPRRGATNVMFNALMPKIFSQTGVQLSLMDQASEETLELSKVSTVHCDKNF

YSAFYEVQGLLLCSLPVEEGQQGNAMKAFELFYCSLSDRKLRVFANEEEKDKRELKLELE

LSCAHVNISLPGGNATIFTNFISSTVDNIDDLPDSSGHYDIQIRWSTDSCNADVQTKLFG

LRIAKEDVEHDWKWLAALSNASFGARCSTFQDAIEPKSTAPPLLSCLTRGQFMQALQMFQ

ARTLYSSIFSDMQVPYSCAAVRAFNPYRLGPKKLL

>contig35870 Frame-0F

MACCAETQEPQKSNGFLPNSNGNRRSTIDDDATSEGTRPSDSSDFFNEKSFTDNSRGPSS

SEYPKNHAYHAHQVSGPSKYYFGLVDILQEWTVEKQIERAYKVRVLQKASEGVSAIPPKP

YARRFQRKMKQLFITMRSYPLEDDALGENPVHQV

>contig36149 Frame-2R

MKSNVVSRPSRGRTSGASSSTPEIETLVLRATPSIKRYNIARFDVPNPPTFSKCAQPVMM

YREPERVDDEEEKEDDAPVGFNPALRKRRRRRRKNTRTAGWIIEDSEGKNKFIGTFEGGQ

SSTYMLLVKNRHNEEFSLMPVEQWFRFKKPLNYRTLTLDEAEEMNNEKKRAVERWLMKHK

LAGDEKNEA

>contig36497 Frame-1R

MAGAALWFQQYTGSDGRCNFVVPIGGYGDIRRSRNVDQTSQRVGFWIRIILNKKTE

>contig36619 Frame-2F|Blast-carbamoyl-phosphate synthase [ammonia], putative [Phytophthora infestans T30-4](gb|EEY56914.1|) 0.0

MSSVTFSESAVPIKQAPVLSPVATDGDNASCGTLVMADGMTYVGYSFGAEKSISGEVVFN

TGMVGYPEALSDPSYRGQILVLTYPLIGNYGVPDMNAKDEFNLPKFFESDTIQISGLIVS

EYSFQHSHWNAVKSLGDWLKEHNVPALFGIDTRMITKRIRSLGAVLGKIEFEGQPTEIVD

PNKMNLVAEVTIKEVTVYNKGASPKIVAFHCGMKHNIVRYLVAKGVELTVVPYNYNLSKS

DLQYDGIFISNGPGDPTMASTTIESIRWAIKQENPKPIFGICLGNQILALAAGAKTYKMK

YGNRGMNQPCIDMRTTRCYITPQNHGYAVDSNSLPEGWKTFFMNANDKSNEGIIHEHKPF

FSVQFHPEACGGPTDTAFLFDMFLEKVNSAPPKLTVMDTSLYDRPTFSKVLLLGSGGLSI

GQAGEFDYSGSQAIKALREEGVHVILVNPNIATVQTSKGLADKVYFVPVRAETVLEIIKK

EKPDGILVSMGGQTALSVGIELYQNGDLERHNVRVMGTQIESIIDTEDREKFSAKLAEID

ETIALSQPATTIEGALKAAHEIGYPVLVRSAFALGGLGSGFAANDEELRVLATKALHGSA

SKGQIKQILIDQDLRGWKEVEYEVVRDSKDNCITVCNMENFDPLGIHTGDSIVVAPSQTL

SNSEYFKLRSTAQKVVRHLGIVGECNIQYALDPRSERYCIIEVNARLSRSSALASKATGY

PLAYVATKISLGIDLVSIKNSVTKTTTACFEPSLDYCVVKMPRWDLKKFSRVSNDLGSYM

LSVGEVMSIGRNFEECIQKAVRMVNPNLDGLDGCAVDNETDPAILDAQLSHPTDERLFYV

ISALDAGYTVDRVHELTKIDKWFLS

>contig37227 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53566.1|) 5e-58

MHSQLEHLEIVDCFDAVEGDTARALLQQLAKSRAIKSLHISWCCWLTTEVLVAFAYQLLE

PPVSTLQELHVANCFDVLGDYVQSVYTELLPHVTVSM

>contig37641 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65536.1|) 7e-56

MTDRAIIERACKEDLQAVLMVFHEALMEADKADIFGNPVTNDVAPQYSEIILHPMDFGTI

RDKLCKYRSFRDYFAHVKIVFQNAITYNGWDSFIGGLVQDLQKYCVKFLLDAAGVHLQNH

KNHAKKKKLQSTTGPGNQQARSQPAA

>contig39272 Frame-2R|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY69887.1|) 1e-105

MFLKSYDGDVEDLGLTHTIVHQVFGEQKEIEIIPGGGNIPVTNRNKTRYIHLVANYYLNT

QIHDQSTAFRMGVCDLIDPRWLQMFNEPELQVLISGKSGKIDIEDLKANTRYTNGYHAFD

KRVAWLWQALVSFTPSEQAAFLRFTTSCQRAPLLGFASLTPPFGVQKIPIRHDEELLPSS

STCFNTLKLPTYSSYKVLRAKLLTSISANAGF

>contig39478 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53295.1|) 1e-105

MRTRAQKRDHMEELAEQLQLRIHALEAKSFLRPVNNTLSSQKKRKIDVVSTSSFPLSPPL

HEPPTPMLTAFNSTTIGTTIKISPNDRTAMRRTLNCTKQISSNLIDAPQGILQRICSGQL

LHNRLPIVERFKEQKIIRDVLKSHIAQCTSVFLVGPPGTGKSSSVEEVLTEQGFISIELA

KPMKQNRASECVKIAVKINCSTFTDPAVLYAKVAQGLNATTCWQVPSHLDPLEIDNFLAG

PCHGGKSTSHVIAVVLDEVDHLLHLPKRMQSSIQAMIHFFVRWAAIDPHTLKFVSIMNGI

DLYEQVARMHASGTTTAHVPVPRVVFSSYTHQELQHILQRYVQHACTKEAIVFECMEPRA

IECIARKVAARDGDARLAISLLQQSARHALQRCSRVETNANTYLKDAKILMRDVLHCATP

CSRLPLFYKL

>contig39715 Frame-2R

MKRSGIRHHEATDAQGRRRFHGAFTGGFSAGHYNSVGSVEGWTPRTFSSSRAHRSSRIIQ

HPEDFMDDEDDPLLGKRLETTACYDTLQTGVKHQLQHPSPLNNESIIPGFTLPIDWIVPL

NDSIGATLLQQMGWKQGHGIGPRVRKQKFSKHTCHNLHRHNNEASWDDRMPLNDDNVMYG

PPRN

>contig39922 Frame-1R

MRRFDADKENRVAVASSYSHRAALTSRQFNPSDSILASCGAGKRPHNQMDVSNYLRKAGG

DRPAASRRPHGAVPSSHTSSYMRGIGSGLHKVATHTTISSQSSSRLTSSSATTSAKPSTK

TDETSKKTWKLSDFEIGKPLGKGKFGNVYLAREKQSKYVVALKVLNKQQLMKSNMEHQP

>contig40456 Frame-0R

MAVSFRSILHEFAVVAVKEVKALDFPWDIRQHKWNVPVLPSLIRLSEIATATLQRDLLSR

KGIWRGRKCWKFVYGTQIFPALKTFNREIGHRNVTDRFTVPNKSPWPKATQGIRLGSIVA

SIRSRGTYDRMTLRDKA

>contig40614 Frame-1F

MLQSVESKCFTSEQCHEVIELDVISLSDPQQPSLASNSSTVEILESMDSIVISPIATKKA

ISSKPTKILFLDGARGLAAMLVVIQHSQEFVPTLHLGSVGVDIFFVLSSFLLTMICMKLC

LKLLSQSARRRTWAYTFADYFQKRFLRVYPLF

>contig41059 Frame-2F

MAQTAAEWKAKGNAALSAGNSKEAVECYTQAIALDPNDHVFYSNRSAAFLSLDDATSALE

DAELCIRTKPDWPKAYSRKGAALHALKRYDEATSAYNDGLKVDATNAACLSGLDEVKKAQ

TASTQSFNPLANAFGPDMFGKIATNPRLMPLLSDPAFVKVLQEIQSDPAKINQHIQDPRV

MTVLGELMGLNLNMNGAEDEEMPEPKKSEPAPIPEPTPMEEDLTEEEKAERAAKTAAEDA

KDRGNSFYKQKQFTQAVECYQEAIAKDGGNMSYYSNLAAAKLEMGELDACIEDCRNAIEI

GRSHRADYALIAKAYVRIGNAHLKKGETEANLAAAIEAYEGAQMENRTKDVERKIKTLQV

KLRKAKELAYVDPEKALAAKNEGNEFFKNGEFPQAVERYTEAIKRDPSCAVYYANRAAAY

TKLTSFNEAKKDCEKAIELDPKYVKAYSRMGAIQCFMKEFHKARESYEKGMSLDPNNQEC

IEGLRTVMYKIQSGETDEERARHGMADPDIQAILRDPVMQNVLNDFQTDPSSAQRHLQNP

GIMAKIEKLIAAGVLQTK

>contig41154 Frame-0R

MQKMRNGYEAKLHEITMQCEGMRQHMNKELSALQQRDSLYQEIRGKLVIVDDENVKLKRK

VELLEPRIQEISQTYTAALEEIGLRKKDLSELREKIVTISGNFTAQREELVTAYDESRRL

EVELNDQKVTNETTYKELVLLSKAYKALADEKQTIESEVDLLRLETANLESRNNSIHLLL

LEKEQLADRFERKISLLNDAAAISKNALDSERESFRAISLDLDDTKKYCRKLESNLSTIE

IQLAE

>contig41248 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55822.1|) 1e-130

MKCIVRNSIIQWNSVVESLSILTNAFLCDTSHVERHGVVTSSVIGPNTLIAEGEVTSSFV

GPFVGFHHQALLIASIWPNGKGNVGYGANVGSNHTLKVPDQEFYHGEGVFFGLGCNVKFP

SNFVKAPYLVIATAVTTLPQLVTMPFALIRSPAHVILTLSPAINEIIPGWVLSKSVYSIL

RNENKYLSRNKSKRTHIETRIFRPEIIDYMKDARAELEAAAGMATHHLPNGEAVYTDEQV

RGLGKNYMVESSRQEGIHAYTFFIKLYALEAVLKLVESGRVS

>contig41402 Frame-2R|Blast-ATP-binding cassette sub-family E member 1 [Phytophthora infestans T30-4](gb|EEY69572.1|) 1e-158

MSDKLTRIAIVSSDKCKPKKCRQECKKSCPVVRMGKLCIEVSPKSKVAFISEQLCIGCGI

CVKKCPFEAINIINLPKDLESNTTHRYGANTFKLHRLPMPRPGQVLGLVGTNGIGKSTAL

RILAGKLKPNLGKFDAPPEWQEILTHFRGSELQNYFTRILEDNLKAITKPQYVDKIPQAV

KGTVRDILSARCEKQEMLDHFLSELDLSHVQDREIENLSGGELQRFAIAVVAVQKADIYM

FDEPSSYLDVRQRLKAALVIRSMVDDNGRSYVICVEHDLSVLDYLSDF

>contig41730 Frame-2R

MLSHAPGLGIRIGASTQAHLSHGLEGRCVAKKKFSIIYKFAIFEKSQK

>contig41745 Frame-1F

MASFSMQFQHIHILAIRTLNSADVSVPLGSGLEALIANWLYNPVSISVRRLHRPSRKFCK

NNCTATSPSASRLYLSNRMNSGCLLIK

>contig41851 Frame-2R

MDWDTGRVTAVGMESEQASDVRQSASPAALQRRFRAFLRGFRVGPLFYYREQLLANARRN

LWVVTVNVSHVAAFDQELQDLLLKNPKDQLPLLENAAKEMLMQLLVSSHESGAFESSTSE

LSSNLPDIQAILTSDQALVALRHVHSQEMNQLVKVPGIVISATRVRTKCVSAILKCRNCG

HTKRVAVAGMG

>contig42111 Frame-1F

MKTRVGGNGIVGYAIRFESRCSTETKLKFLTDGVLVRECLSDPLLQNYSVVMLDEAHERS

IHTDILLGLLKQVIERRPEFRVLITSATLDADKFAIFFKNPTSIDAKMAKKTQKIKAISC

PVIRIPGRVYHVDIFHSKQRQIMGHKGPLSNYVRSAVETTIQVHRGESPGHILVFLTGRR

EIEEACAEIRALNREQETQTHELELRVLPLYGALSERLQRAIFDPVPINQVRLVIVATNI

>contig42227 Frame-0F

MDEPTFLAIQTFVNGFDTKTSDFDGSRKNRVQSFSLFFKGNLLWTTMDIATMQLLYDFCR

IREERGMTVMRVDESLMGDNRKVDPAIATGFDPEIWTPRAYEHTFLPIWSSKQSYVEYDI

VSQTDEGPLHQRKTARSLHKQHPVSISTYLSETLALSEVGDLLSSSNSPIVAGKFSLGSP

SQFFATSTRIDGRQSNDPSPQTIKNAINARIQSTSFRNAGWLLKNGYFSKLLHA

>contig42641 Frame-0R

MRLGDVSKLEKYLLCQMKREKLTQKLSLGYSIVWGDAVNFKENLNFQDVTQLPSIRPLSK

CTAYIGLKANIRVEDDPILRYKPYFGEDDDGADIDEAWYDAVVPEASSLSTGIDGEMNEC

MLHLVIREYGSSDQVFTALKKVSGFAQASSNYTEMKELNDSTTLAARRVEEAKNVIARRT

IDIPLKRMTALGSVLQATKVSRNTLEERLAPPISHFDSNLAKNYAIRAFGLGLRLSKDYS

QLLITYRDMFCRRCYDYHCLEHGIEHPLPSHRMDPMNPPLHLSAVALAARKKIEQNNSTY

TFIPSPDSCTSSARL

>contig43035 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY60975.1|) 2e-84

MMRAASLLHRLEAISPLQARSFAHRVNMVLKEDVPKLGIRGDEVFVKAGYARNFLYPEKL

AVYATNSNREKYKVDKESVDEAVLEKKNEVETITHILSNIDLVFKRHTSSKADVKLHSEV

NAQNISDMLEKQHGVIIGVARIDLSTPIKTLGEHTVKIRVDDAIEEELVAGAVKTLAEDG

VEMDPQSDEKKQKIGPSKKKWVSLSINIERR

>contig43040 Frame-0R|Blast-ubiquitin, putative [Phytophthora infestans T30-4](gb|EEY67771.1|) 1e-26

MQIFVKTLTGKTITLDVEPSDTIDNVKQKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYN

I

>contig43286 Frame-2F

MYNNDAGSPQASASTHIWIVIADSHSKDVLMDSSEAFGLHDTILAIRLEVLQNRSFHLSV

FLTQNFSVSLQRRCSRLLSVTVTSLAHIL

>contig44001 Frame-2F

MRIPVLVEPMEMSPPSEDEKLKLTSKVAEAAVGMSRLMTPQHRTIVYESGAILEYLEKKY

PERPSMPASPARYAVAQSRLHEANEILSVVGDLVVYLRRFPIDKRNPSIVTAKWASVETE

LSLWEAYLDGHEFLLDVKVPYLCDFTLFTNIAYAVR

>contig44643 Frame-1F

MFQPPAAAIPTNWLGWTWLGVLIGRGLTTCRPRRPYYEAVRTCAKIGLMRLKSRHIL

>contig44975 Frame-1F

MSGLGSAKSRTPFFKQRPLAALDSSDEARTDTDTATSPSMHLASSPATDATSRNNSGAAA

GTIKATARTSSSHKRRNADAVESCKPPP

>contig45374 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68841.1|) 1e-128

MARLLHRVYRSGTLSIASASSNISGLNLVYNTRSQRHYQLPVKISRVFSTSSSSISDLAK

VLKANNSTTGERVKAINALGLSSTLDETLKEQHALEILYSDALGVLLGFLNDSDTIASSD

LLIPAFLAIIRLSTKTQLTQHLIKLGALKTITPFLTQTDTRLQAAACLVLGNLALEPLAA

EAVSSPAVVGAALNVITTTHEPIKRAACSCIANIASGTQGRREVINQDGVLRMGELLKDE

HSDPLRSIAAFALGNILSGGDIDAQDLLRQSGALPDLVLLLSEVYAEDVNSSAAWALHHG

VHLNTANQSLLAEAGGLAMLAQHIAKAALESLQTNSLLALESAVILNDKNLNWCRANNAF

AVLRRVQEAEGNTLNASAKLALFTLLEQLK

>contig45468 Frame-0R

MRRMASEMDLTHQRYTYLNILVKHKYNFPHNEAVIAAYANCPVDSGCEFEV

>contig46032 Frame-0F

MIRRYVIKKSSAALIRCIQTPPNFRATFVQWRSNSTSIKRKSTVKVLHNKPQTSYVQVEQ

DIAAMQREIRDAY

>contig46177 Frame-0F

MAGAEALRTLETRAIRDAQLTTYTSNLGSLALVVSVSLWLTLPSLWGVVSGDWNDKILLS

LLAATGHGVFVLSVLLVLRVAQVQGEELLIQLNAKYFSHAAKSEDVDAPRNRADQLNEII

KLKSLRGHLSDTSHLSNAIAQTPEKRSFFDSAPVKTVEDGKAYLRRLQKLQKDNKIIEST

ESAVYDMGNSYQSDAFGIFGNASMAPRVYQASGFDPRLQDLNNGEGQEDPLRTSSLPHIA

WQQLEEWGLAMFMHLYCRNIRRLLAYHVKDVVEAFLVNASALNERGVMADVLLRRVPSQA

LLCPPGQTNQMTNVSLSDMLQNLATSPLFYSQERGVYLFKEHQSFEKYLNVGNSSSTDYS

SLERQQYVLERLMMLSKDRSLDRFRWNKGSAWKGKDWTDTLPTDADILMNTFCCMMDNML

PAENERDRPFWRSYFYSQGPSRPFTPRVRSRLFLVQTVIRPPHFKALVKGAVREIVPGEE

NIFHVIVVYLHAVKKLKAGYLESINLHRIIEQVFDVSK

>contig46461 Frame-0R|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY64990.1|) 3e-57

MLAQSDFSVAWLAPELLRGERRSEQADVYSLGVLFTELDTCELPFAAGVEMVDRLDEQSH

LAMLVSSGCIRPALSMDCPAPIQELVLRCLSFSPLQRPPAIEVQHTLRKLINGTSFCDAS

LTSLPSNSSSLQSTPRTASNATLSTITP

>contig46739 Frame-2F

MLERLNTRVAHAKERYDEKQRLLREEKEEEERVRREMEAEQNCKLQLQTEEEVRRQEKLE

AEERRNAEEKEQEEKMVRECEVAKTRVEQRSQGQEEKMARECEEAKTRVEQRSQGQWGSA

GLRGLSNHRRSEETDDREWTRVNRSGLSSRLQTVASESLRDRRGPPTRDIYGERDRRDRA

IGAVSDGRDRAIGSDRDGAFHRSDREEIGQRLGFNSDRDGSALRRGLNEGRDGGSGFRRP

FNGDRAGSVLRRGIGEESGSGGWIGRDSLRRGSDRDGGRDTYRRNSDRDDRGHPRREDGD

RDSIRRTGERDGDDRFFNRSQREGSYRAPHAGNREGSFRAPHAGNREGPRETNRNTTGAP

ESGNWR

>contig46898 Frame-1R|Blast-eukaryotic translation initiation factor 3 subunit, putative [Phytophthora infestans T30-4](gb|EEY59042.1|) 1e-136

MKSGKKSKRNQQKVKQQQHIETNEQKKKEQQPEAKLPVCIKSVTYSGYNPPPGPRKLVGD

LLYLEVNVNGDNTLYHITAHVDGFFVNSSTITHFDPRPNETTPSPSHLLVDLLSNVSPTF

HESYAALLTKAASLAKEGPSSIEWMVAAGSNLGGKLPWNTPITTAIKEHKYDLNRAEDEL

CNTYGMDERGVLRDWNEEIQCCRELSKETLKDEIVRARVMFKIVTEFVEAATQGAVAIVE

GNIPAINPMDDKSAHVYVFNNIFFSVAIDGKSMKDFAGGEENAYSAANRDLQGVKA

>contig47299 Frame-1F

MEPIGFYTLKNSASELLQNLCKSVADIQRNDVDSFKLMYLGDSRREFQIEPQANPVENKG

IRLHDWIIGSNKTHITPIDTLAKLGEAAKLTPPEMVFGKNQLLMFHEPSGVCYNFLAVEA

LKGAHFSPMSDAGKRNEAKQQLKVSIAKQNTIKDNVKELDISYDWTYTTDYKGSLQHLIK

SKDPSYMFLRNDEDVLVEVTHDRINIEKLKEREPILWFDEVTLYEDELHDHGASAMTVKV

>contig47314 Frame-1F

MLNNFILPLQELADSNSRVHCSLNLNTDTGRLSSRKPNLQNQPAMGKDRYKIRDAFTAPP

GKKLIVADYSQLELRLMAHITQCKAMIEAFKAGGDFHSRTAMGMYSYVAKAVEMGEALLE

>contig47844 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61833.1|) 1e-102

MTALPNSFNLVPLCTTSESFNGRRIHIHDEGVKFLHGPKLIVRKVALVGIIYATENVKID

PSAERGLFLGSSGASLSKHDAQMLLVVLRGVSLENEPFWGSLLYVLSSHVVVARAGPIAS

SSFQAALPFLTNFSKLQVSAEVKDEEKNSELLHELTPRFTWGAVDLKIQDMNGCDSATTY

FELQLASGMSDAQLLLSALIPTRDCVVLKSNSFSGSEDLHTSSKLLTHVSDRLKCKSFFG

RFLNGALLVKLIRSLTCIMATPDETPVVLQHVVTNVFTTYW

>contig48184 Frame-0F

MKVAIIIAHIAATIASLSVLPINALNEVENYSQQLGAGSFRGTDSSQQQTAQESITQMDF

TQIQTGSRSSEQTNKKEDDGNDKKDGVEDSDDDSRKKTEKSEDGDKDEKKKDGNEDVTQE

DIKRDDKKEDKEDDDKNEEEDKKDKDENKKNKAEDKKDGNGDDKKDDNNDDKKDGNNDDK

NDGNDDDK

>contig48229 Frame-0F

MHNKTPTSQPPTISDTSTNDNGMVFLRKVGHLYKKTGLRRSWRLRYFSLEGTVLFDYKRK

GDSTFKAIVVLTGCHIQVRQDKIFYSFRISHPKTSKTYDLAAKQSGTTDGWINALSLAAV

IANPGRQLVSRASTSNKVSRFCRSKHVNSFVTEPLEISGVDAPNELNDMMEQYLGELLAI

ARDDGWQLRAEERDVKMYMCHTSKVVA

>contig48351 Frame-0F

MPTLLEAATQQAEFEVDPSRLASDDEDEELTDSEDTQLAHVNGKCLSIRTSILEDKATAC

QLLAGMVTDLEDAFFPYAEQATQLLAPLLTESVHSDIRAAAIYAMPALVKCVAISTATCL

NKGSVAMRQMLDFVLGRLVNALKSEPDVELVIRIMQSMIQCLNDTQDLHPLLLLNEAQLQ

EVVHGILVILGDSFQRRAMRRSLHSSDLNDDEDTNVQVDAMQDMETELHFVLAECIGTLA

KTHRSAFFPVFQSLLWDKVAALAARDCLREDRQLALFVIDDVLEYCGKPAWRLLDVFVPV

LQSALQEIMEP

>contig48737 Frame-2F|Blast-translational activator GCN1, putative [Phytophthora infestans T30-4](gb|EEY69168.1|) 0.0

MLSEAASARGGVLSALLRVTESEEGGEEFRTAKSSSLFNCRLHCCLFDMDDNNRILAKKL

WDATGASITASFAEPLIGLLHHKHESVRASAALAFADGIRHFPNTVTQLLNDLTMEFLKC

QPTPKERKDKFGIPSVRRAGVQTEKVDKDIQMMNTRLGIALCFEKVADVAGPTAMSSADT

MALLTFVMEHGFKDPNIKVRAQMRKTGVQAVASLGGGTNTAPLLEMFERFLENTAPPAPV

ANTSMRTINAKDAIKFAAKQKDFSEQSKYALSIYDHQREGVVVCLGSLAKHMSATDPKVS

YIVESLIEALNIPSESVQRSVASCLSPLMGTVKDRSAVILDNLLSRVAESETFGERMGAA

FGVSAVVKGLGISALKMYNIIPRLETSMKTGGANARQGAMLVFECLSQRLGLLFEPYIIL

ILPIMLKCSADVSLQVREAASHTAKGIMANLSAHGVKLVLPSLLGA

>contig49789 Frame-0R

MTQIHVLLGRQEQLIHWTNEEYRSLFKIVEDLSIELALDTRVSTSLVRLPSRGL

>contig50444 Frame-2F

MGITKNTKKFESVSQRHGRRRRFSSSSYATTCQAHLGQERVSVASKNRTR

>contig50655 Frame-1R

MESIESSLHLLKSASCENLASETPEDVVEAMSCVLAWLYRHDVASVLQAIAAQLQQVVEH

LHGLFQTTDTPINGRLWMLWVELCCKLSMLRYCEIEKHLEIEVDFFINIQPPRDLPILQT

QYDKKNQAAFSCRFWDAAVVRPLLGASVDHATKAMPKLVDFFLHWMANAMLGYEMIFIAN

VAAPIRKHVNKQFINNSPLVDAWLDFVSVELKAEDVTNNAPKTSVIALILSSTNSTKKAR

DAAQFLSLLGAATVKELVRDPFPQPHHPIAAVAMAQGLIYLDDAKDSDSLAVLVESGNVA

VLCQFAALRVVNLKLLSSRLIP

>contig51061 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57761.1|) 6e-14

MDVAMTKAQQHAEAEEKNQFGILLHVGDASTGTVHIVPLTSTHVLVEEIRKDLERLSGVP

TMDQ

>contig51263 Frame-0F

MYPCVVYALGFIPQNLGAGHKKLSTLQIKSFIQAVAEASWTVVKDKKWLSQIEFQALCET

LQNGKRKQLTDDIFGAEDSLYVLKHFFTRTLKTNDSFADKLAAVRDAVLDGEKHRRSGCY

QFALAAYSKAFEYLPLYHLDLENTIVARAKCFFEMHELSRAKTEALIALKLNPYSVGAYE

CLGSVEDKSEHPDEALQNHVASFILDGSRSAQHAESIDRASRLVGRRVAKALFVKMEKKH

ELP

>contig51577 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64425.1|) 2e-11

MGTVVRPGIGTMIGGTLGDSIAYVLL

>contig51946 Frame-1F

MSAPGVHDMYHCMNLTRMAGQSNAQVSVVHELNGCVKNKGS

>contig52060 Frame-2F

MASTDNDESYDAKIFSLGLLLSSFFVFNTIGVIDEGAIDRLYLVSELTKYVCVSAHHSSA

LALDEVVGASPEESLLSDDIEESHELAPHFPPFAWLLRDFLLDMKNDGNSLTANQYLEKA

LDARKVSVTASNSRRARQIERNRIRASIRSLFRRRLCFTLVRPVNDESNLRRAAELPDTE

LRPEFVEQMADIRRRLLSSVTAKEILGTTLRWPANR

>contig52428 Frame-2R

MTYFLNTGNLRSSSGLDLLQVAGYTIVAEKLNFYRYFSHFRSVHRGQFFTEMKTTAVRKL

LPDSWGFLCPVHTPDGSPCGLLNHLAVECQLVAYPAFTAEDYLQQELKFCRFLASLGMVP

SSGYADGALIVPFSYLPVLMNGKVLGGAPADVCNQIAKVLRTLKSEVGSDQRNTCGLVPN

LEVCLILPTRGGPFPGLYLSADAARMTRPVYQLSTKRIEYIGPMEQVFLDIACTNADIRP

ATTHLEIRPTNMLSLVASLTPFSDYNQSPRNMYQCQMAKQTMGTPAHSIVHRVDNKMYRI

QSPQIPLVQNERLREYQLDEYPLGTNAVVAVISYTGYDMEDAMILNKCSYDRGFGHASVY

KQVAIDISTSGKQGATNAKKYFANLQPNGDVCTTKLDRDGFPYIGQKVQQGDPLACWIDE

TTGLPSFQKHKETEPAMIEQINVLGHASSASEFTKASVKLRFCRNPTIGDKFSSRHGQKG

VLSILWPQADMPFSESGMSPDIIINPHAFPSRMTIGMLIESMAAKTGALKGKYMDATPFQ

FNENDRVIDYFGAQLKEHGYNYMGSEPLYSGISGTIMHADIYMGVVYYQRLRHMVSDKSQ

VRATGPMNALTRQPVKGRKKGGGIRLGEMERDSLLAHGCAFLLQDRLMNCSDKHIATVCT

LCGSILSNATQRASVETAGQGDLAVAMKAKTQWFCIVCQTGESCYPVAMPYVFRYLANEL

AAMNIKMSLTLSFL

>contig53171 Frame-0F

MVNGPATLAIDMPLARASICGGFPRPVVTMVTNASHCSPSSTDDRRRSRSHTASDEMSSS

AIALIACSDVKLRTISKAIYDIRGAMAEKSKPLAKCRDPQMSHWLTRSRYFGPTESLRQK

RWQEEQKKHQAAQGHTHHHHTSATRRQSGALKSLHVPSEPQRLTLSARRNSLHLSSISIA

AYEASLMPLVDSGNTQPQHPLEASFALETQKCLARKRALRQQQRAASNDMFERSTMSSVA

YLNCYDEMDMPPQLRPISPSLRQCFPRLKLSPSSPMKSPSSRFRINIEP

>contig53306 Frame-0F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY61593.1|) 2e-07 NOT\_ORF

MIFVICRPLASFKCKVAKLFAKHMKADEQAKQLARNFLPI

>contig54017 Frame-2R

MQHGFRMCSLSASATALRTANSGPPTWTTLQTPTWTSRRKSLRTSRSKFNIFRNPMSIDF

LLNNLDEEQVSYTPTEAET

>contig54974 Frame-0R

MSRTMSKLKCASSPRDADCLTRMPLSSALSYASAHTPIDARLRIDDMEYRSSHRDRFLNS

AEHLVVMDPRKTRDSFAKVNVWAWHEQSVTTILDTLQVNATHGLDADMASKRLAQNGLNA

LEADRKTPLLLIFAMQFTTVIIALLMAAAMASIALHEYVEGIAIIAI

>contig55018 Frame-0F|Blast-putative endo-1,3;1,4-beta-glucanase [Phytophthora infestans](gb|AAM18486.1|AF494017\_1) 2e-22

MSCCPVTAEPAREQADHIGAMKKAGTTIIYVTGPVVSSAGVIVYPDVFGLDSGRTKADAD

ALG

>contig55087 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64569.1|) 5e-17

MMRRPWTLLHLDWLGTLDALLQLVIIWPLETYEAVAILPVSFLRRHVPVLGGA

>contig55362 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59083.1|) 6e-17

MCDTSMPPLPPASRRTSGTTAASSTVAAQWSHVGHHRTSISPEMTFDEHDSQIKHELLAL

I

>contig56280 Frame-0F

MFGGGFESFFGGGFEGGSSGPSKPVDNNKFYEALGVSKKATAAEIKKAYRKLALKNHPDK

GGDPELFKSITVAYEILSDPEKRELYDQYGEEGIQNGAAGADASDLFSQFFRGQGGRRPR

GPQKGEDLTHPLKVSLEDLFNGKTVKLAVNRDVLCSRCEGRGGAEGAEKSCDTCQGRGMR

VQLRHIAPGMVQQMQSVCPDCRGQGKSIRESDRCKGCKGKKVTKERKVLEVHIEKGMRNG

QRITFAGEADQAPGTMPGDIIFVVQEKEHATFQRKGSNLIMEKKVSLVEALCGFEMIVEH

LDGRNLHIKTRPGEIIKPNQFKSVHGEGMPTHGNPFVKGQLVILFKVQFPESGSLSEKQL

SLLKSTLPAPSPLVPVADTEECFLSEFDAEAAKAEQQQGEAYESDEERGGQRVQCQQQ

>contig56626 Frame-1F

MSFRGGRGGARGGRGGRGMGRGGGRGGGRGGFREVEGP

>contig57830 Frame-2R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY57525.1|) 4e-48

MGHQDSHSQVYDLYAVANHVGGLAQGHYTAYCRYDRDFPESSALFRANDENLDVQCHELW

FRFDDDKVSEIAVGDVVTDAAYVLFYKRRTLSSTNVLRYAL

>contig58611-1 Frame-1F1

MRRSELFSPLPLSSHYPATQLSSQAVLKFPQL

>contig03775 Frame-0F

MVCASYKSLFATVALMAMDSTDGVGTCFAPWRNELVNFNTLKADVLLIGQTFSSFRTFEV

RMGGVNIISVAAAANVKVSVGVQMNDLAAVDLEIEAVCKGYAENPQAVEAIYVGNECLKN

KDFGTVSAEQLVKYINQVKACTGGAVPVGTVQRINEWMTASDIDLVASACDLRGSNIYPF

FTPGTQTPIEKFKIQFDQLASKYDVNTIRVTETGWPSSGEVAFGNTPSLEVMQQYLNDFT

EWSKGKSESFWFMMFDSTVSYTGAEYEKHFGVFTVDGKPKVVLPPMTPSGKTFDKLPLLN

NSSLTTGDSTSTPVQQPIGLTPDVGGTGAGSPVQNTPVVETPVQNTPGVGTPVQNTSVVD

TPVQNTPVAETPVQKTPVVDTPVQDTSSPNNPVQNSPGQDTPVQQDHPFRSESPCSERLR

SEHSGGQPWC

>contig06862 Frame-0F

MDELAITRGDSLGRLAEESLDSLKEMCFSPALELQLTHNIIQNALKDYDKEEWVIDVNKE

LTVRDVLVECFPLHDRAFNKQFFDEYRKRTFEWNVRKAAAGNSDRWAVEELRLHFGERVA

FLFAFMHIYTKHLLPLTVACLFYYLCFRFTSAPQWRQYMEGLAVVGVCVVCFWGPSFLVC

WARETRLLVEKWNLAKYQNTVYERNDDNPGFQYMWVKNXLTHEMEKIPKQRKNHWIQLTM

LSFVLVCALIQCMCLVPFIQWYVYAKNAPTCDACNGDSEESYPCIWFVTCFNATTSALGT

DRWVYILIQGIILGLLIDIIFFEMFNWISEKFVQWENYAKKSDHEDRLIHRTFVFVWSNW

FFWFLFLSFVYMPFGDKILKLFHQMGFGALAPYEWNPNLLTLDTLFVTPLVVTQFLNMVL

ETIAPYLLRKLRGRPSIGCRQASPFTWCFRHLSRRFRFVKAPQSTEPGYKPQDTGYTSTS

HNSPAMTDHSDSIGTNLTATRLAQCVEKDTGFHVKVLPMSDDSNNYSAYEILAEVKLPIF

DPMTDYLDACIQFSYVMMFTVVWPLLPLPAFINNILEVRGDAFRLLFANRRPMPRRDTSI

GEWATVLAYANIVGVTVVSGFVVIYHYGFFVTNCNFTFSAAYVVPFDTIMPDETVDPSVC

VNDSGTSRWRMFQIVLFVVLEHVSFCMRYLVMQMEKTPSSIRSSGYRRLKQIQHLTARIS

APPLQLEYVQRFRVLFETYDVDGDGHVAEQELISLLAAWLCKHPSELLPYSSLIFRYMDK

NKLGRVPFSTCCLMMQHVNHDRFFSCLLGLYDPLNGAYNDDIRRTCDPMELRRVLSEVSE

VQQRRSAMSRASEATDTSRPRDSTFFYVDN

>contig06989 Frame-0F

MNFFFSGESYPSILYPSMIMNTKNLIGFRPNFTFFFFGLVSYPHSLCTIN

>contig07151 Frame-0R

MVCKFIIALLIVAFQKPLVTFAGFLFQPLYKNPDIELAIVMIACPCLMNALQFWIQDNFL

KKDVRDESFIVAQAPLSPTQLFKNNGTLPTLNTPTDEESTELSLEIIASSTLQNDTLGNK

NVQTDLHSV

>contig08855 Frame-0F|Blast-Rab2 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY57357.1|) 5e-78

MCIMLIGNKSDLEHRRAVSFKEGEQFAKENGLIFLETSAKTAANVEDAFVKTASKIHSNI

QSGVCDVTNEAHGIKVGMTGSPGPGGFGNSSPPAGRGCC

>contig10083 Frame-0R|Blast-CSH [Phytophthora infestans T30-4](gb|EEY60301.1|) 1e-52

MLPSLVPRLQQKIMEHQIVANSPKLTAMLAHPAGPFTVHFWAPTFKWAISIANVADMRRS

PEHISVAQQAAVTATGLIWTRYSLVISPKNWNLFAVNVFMAGTGLVQFYRKFT

>contig10425 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56098.1|) 1e-105

MGLGDMLSSQAEADLASHERSREVWEFENYPEGEIEEMVELYVKKGVSTEDAMLVVHTLA

KYKEAFIDIMMVEELKIMPVEDDHTPLTGGGITFLSFMFFGVIPLLSYLVNLFPGIDMSP

KTALYLSCFLTVITLFLLGAVKGKFVGQKMWKAGGSMAINGTIAAACGWVIGYLLQLTGI

QNIG

>contig11152 Frame-1R

MSVLSFSSNSTNEDAWSHARLAEEGVAYRVVNVLGSGFVKEPIDIKKLALLVRNADYAPR

GFGALVMRFQTPRATVLLYRSGKFVVIGATSVVNAKLAAEKLISILK

>contig11310 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61417.1|) 1e-48

MQHLNPFLLMSYQRIYDIVNPETRD

>contig11857 Frame-2F

MYKNWQSSFKRSLKISNPAMRNNKVLEALSHEVQATFSDFQRAVIIAACPPKSDSKFQRH

INHERKLLFEEWKAKSPEQVFNMLGLDATDFNFLTHPLLKLFVRFLEIYNKTYD

>contig12856 Frame-0F

MSSTPPLISEWSLGSSLGALNALRGQEELSQEPFRPRMSFLRRLTSAPTASRDDRAQRKE

LERKELLEMILESIANVPTAVERIQTNEKLRQALHEEMGDENLLLHRFFDARQEHDVTLR

DTLSRDNLHQWDLTQHSVNATGQSTRPLCTTMSLSSCDNDEPSQEGNESGSAYGSEYEND

LAEAVNQLCMTDDTLSALNNAVSSSIGIVQTTRNNARISSSPQSSLGLGTSPGNTSMDGE

PVSALWPRQPNQFAFTQEEDHTMRAEDEVYSEMVSSVCEDETFQDEMDEIREDDDNEAFD

DESEKKLFEMDDDEDGKVASTEEVIDQNGEELTRKSNEETSVLLNQERVFQQNVDTPLKR

KADKVHTVDIKGGGDECDEGESSDGSHDDDDNDDESKEYEVIQLRIIREKNRTGFEPNQD

WRPRPGAVIGGQYKVATAIGEAVFSRTYKCLDATTNKFVCLKIIKNNKEFFDQGVDEIRV

LEYLNRNCKVDEKHLVRFLDAFYFREHLIIVTELLRDNLYEFSRLLSQRGVINYFSIPRL

KKITIQVLEALDTLHTLGLVHCDLKPENILIENFSSCTIKVIDFGSACFTTDELASYVQS

RSYRAP

>contig13262 Frame-2F

MRAFVPNSVHLGGESGTCWLLTGPNMGGKSTFLRQNAQCVVLAQMGSFVPATFARIGVVD

KLFCRVGSADDLAADKSTFFMEMQETAMILTHATTRSLVVLDEVGRGTAVSDGLAIAGAV

VETLCATPTRTLFATHYTALRAVIGETCDEALRCYRMEVLRQSGSEERLVFSHRVVQGLA

TQSYGIHTAALAGCPAAVVARARELLEQLQREDPARRQLRRALAHLDAWTLRGEWNHEEG

KERQEFVRALRLVLSESQD

>contig13389 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64269.1|) 6e-09

MEQRKWHVQLNDGRESDLPHKLEPVGYVKIISAS

>contig13631-0 Frame-0R0

MRTCYYLTLAAACLLSVSDVGAAVLRQTSTPVDKLGVLIESNDYDDANNNLRASKSDEID

QPQTNTIDFQALRRPKQRLR

>contig13631-1 Frame-1R1

MTPEDVRREQRRPGFLRLPRNARRRYWGYSEYYYNHCQRFVNRSKAFCRAQNY

>contig15088 Frame-0R

MKLILPSLSSVPSQNGTGWSVMLALALAIQVILYRKTLQGVLRDGRKRLLVFKTIHRRFA

NQRLKRLNSLGDDRKSHWMWNYSQQDAGTAEDSDQSSADGTGSTDGLISSQKKLVLVMVG

LPARGKSFVVHKTLRYIEWLGYPTRVFNVGNLRRKLGKAGEDANFFNANNADATLLREEM

AMRTLDELFEWIENQGHVAVFDATNTTKLRRQQILQKASSRRNVRVMFIESICDKQDLLE

ANYLRKLTNADYQDKAPEVALADFRKRVHEYEKVYETVEDTEDSGRACYVKVFNAGEKIQ

ARYCQGFLQSQIVSLLQNIHLCPRRIWLVRPGRSITSRKGILGLDTELAPEGHRVARAIA

RFVDTLQLERSIEIWTSPVKRARETVKYILPHNLKRYVTTTLLNEIGGGDFEGLTYDEIK

QLYPKHYAARLEDKLRYRYPGVGGESYVDVISRLRFLIVEFERKKRDVLIICSESILRCL

MGYFAGYEAAKVPYMQSHDNMIIELSPHRDGCDIKLIPLEFVEDSSEDASTAH

>contig16243 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56419.1|) 1e-113

MADVSPRDSSYSYKNTPREREVLLNEDHQFDAWENCVEIGRVVIYFLGSVLFLIGSIYFY

PEYSTMWDGDAGIFASWCYVVGCIMFFAGANLDFIQTIRHNHGTQLRQVLRAYNAMMNCV

ASSIFILGALYFLPGWYPKAPEVGCWSFIIGCILYCVAAIVELIFICSTHEDPRVNGFKI

KNIACWGSIAALSTFNGAIFFILGSWYYLPQYINLIEEGTHYMNKAITFYVIGSVLFLIC

SLAMISGVHGSVKFTFSASEKWVLN

>contig16694 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58245.1|) 1e-47

MAARVGASSRHGAKKWLASLFGEAESVSSSKSIAKERLQIILAHQRGSQILAGVDLAVLQ

KELLECVQRHITVATGTNINISVKNEGQLDIFEMQVPVDGDKVVEGRIARENPRR

>contig18757 Frame-1F

MYFCSGPPRTYAASATHERIEDVALSMHPSQRVFARVSASSVALWSALPELPGTGRRQLA

HCHRSGQWIDQQLKLTLQKNDPNDGVYLYESETRQLWAAWVSGNRLAVVEKHSQFVEFYT

FEGLAQLLQRAEAPSIHLPGDDVVDANIILDQPIFTDPEQEEGDGQMATSEVFQLQAKFV

ENYPLNQGSSQNDYDDVAASMSGVCGSKFVFVGMASGLICVVEVAEGGDTRDGQKSWFST

AEQSTKLWKIDVRTHLKVPHDPKKLLSCIGLTCATSDSYSTITSLNLVATFAGGNCFMVV

LSPCTKKINQLLSLVNATRKNANGKSDTGCTTTKLNPMGSKLALGWSDGRVSLFRVSFQR

EPRPAPTKSP

>contig18858 Frame-2F

MNWLSKIGTSFKKFHRINGNAHYKAIIGKSSRTICAQLYFNANAKPIFKRSAVTVLQAPS

DFVLLAISAPCVAPQFCKGIGLHQDHMLHLSEEFEAAMKAQVFSRRPGAAALLS

>contig19149 Frame-2F

MSRAFLDVMKSFNRQRHYAILNLTEVHRAFVI

>contig19417 Frame-1F

MEPHRGLLLLTDKRLICLSGKNGQKLWEVALDSTLEIVVDGATLKVGQTTSPSRSYEIEC

DNGVAATNLRVAVESARVDVSATRYLLLNLEKSQEEVRITRNGRCGSGAGDITMNGEDRT

DLYVLMESVHDRTVCGLSNEDLQSQPLRSVRVEVCHLQNKDAHANVPGRAIDKVLSFSVF

QIQVYGGPYQWTVFRRFSEFRALCSQLEVAGYMLDGLPPLPARTFLLSTREPVAKYRQEA

LNIFLQEAIMHSSISRSAPMLNFLTREAREVRVSLPPLSPTGERSSQRAGDSP

>contig20291 Frame-2R

MAQQAQLKKSQEAQRLAQLQEQQQQLHEQQKADAQRQVFEEQQKKLQQEAAAVALKKQEM

LEQQRQQQQKQLQAQQALLQQQRQQVLTQQQAQVKPRRQINATSDAAGTALTTSVSATGM

SALSNSVPLSNDLSTLSSPRTANTVASLTPAQYRTFKLPEARKQQLTIQHAKLREQQQEL

IMAQSRAKTPSHQAKLAHQAQRLAQMINKISQQLVQCKLAEEYEQSKNMTMPSSTESTGT

LESDVGTLGGNGVAAVSTAKAPELIVPETEAKVMKEDPFAVEKLNDVDEKFKSVVPDMTG

LGASEKLLTAVAAYEKHKPEVLKRSAVRFSRIAITIGAKLNTSFVVS

>contig20992 Frame-2R

MRPLYVFNSKVSTRGDQSSVLPRLLCQTTTKVMYQTHTKSLFEPNVVT

>contig21313 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66962.1|) 4e-31

MGIAFENYVHTLARDGKKIELQVREYNRVKKSQHTYIALEIEAKSCCNDGATAAECDTAM

QRFATSNDDYWYPSCRCLKSIDSVAKLKRDGQPCTTILIQVTKSIRHSFDSSAINKYAGF

FPGGCQYIALVPNKEVSDNFQLVPPNFAASVRLHVAYITTGVFDTTPVGT

>contig21366 Frame-1R

MASTPSISMKVLKSWKLRGESPLRFKLPLGYDDEGKVFTEWFKYLSQYQFEHSLDVRTIY

NKLLDWMPGSSEVDKTNEKALKQDQLRSKLQLVENIPETKDLVGKLLSQDPSVADHTVAA

>contig22037 Frame-1R|Blast-ADP-ribosylation factor family [Phytophthora infestans T30-4](gb|EEY59697.1|) 2e-71

MLNEDELRDSVLLVFANKQDLPNAMSAAEMTDKLGLHGLRHRQWYIQACCATTGDGLYEG

LDWLSATLQKTK

>contig22293 Frame-0R

MDLFRMLLIAVISLFAIACALSRFEMRLDNVHFTPTNLDQFHHGRFLRSFVPAISPESNL

DNYADEKRLLSQPRLRDAAKTALSSLKKKIFSWIKLFLSWLSAKVDEYTPMGIKTTYWLD

NNKNPGYVEAAMGLDTVPLGEREKHPLTPVFEKYTKAYEKKFVKRVIRENISTYSFWRWL

KLDQIVNTTDDMPEAELIAALQKIQETKGFKLYEKYALEYDKLKSMSDCFDKKATRLEKF

ARALIWATSYQRRSNVRTFLNLRA

>contig23030 Frame-0R|Blast-4-coumarate-CoA ligase, putative [Phytophthora infestans T30-4](gb|EEY60207.1|) 2e-83

MAMQTEHEFIYQQIDPTMKIMLPFSSGTTGNPKGVMLSATNLLINALQTSQVEPSGDKFL

GLVPFFHIYGMMLIHLSILQSKSIVVLPRFVPETFLTTLATY

>contig23395 Frame-0R

MMRFYELAIFVSVVLLCQVGVYYIQAWRCNKKLSPKNGNDLTILIVTDVHLLGKRRRSVV

ERMWVDWQMHAAARAAVDVHAPEIALVLGDQFDEGGPWTSSFVWDEYARRFFRVFAHFLP

LKTLYVVGNHDTSFGRDMRLQDLQRFEIAFGPSNYVKNIEGHTFVTLNTMALDSDVASQD

VRIEARSFLESINFSQLRTNKSSKVILLTHLPLFRVDDLQCGDARLREVGHVTYEAPNFR

YKTHHHVLSKELSRELLAKVQPDLVLSGHTHAWCAYNHTNALEYTIPTFSWGQRPDPSYA

LLRFSHTHEPIITACDLPHETFVFVVYGVTASIILQAHVIRLVLRLRARKVKKTKGV

>contig23676-0 Frame-0F0

MLDKTTDLMNFDTLFTLNNDEEMD

>contig23940 Frame-2F

MSPENLSEYFNQTIAPGKPRSKQDETSAHAQTATDLCREGRGFDFTFQIHVITARNEMVK

PINLLHTVGKKAFISMILSVRMWCNNAGTSSFRK

>contig24512 Frame-2R

MDSNVSHSFAKASVVIIRSECALSLVKRADLQYSGLFLALTKHFLARD

>contig25065 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68459.1|) 3e-28

MLAPKAGSHYLDLSDMGFHSAHDLQALIYTFSSSSLPPVKLLDLSCGYFNTAAFQVLCEL

LEVPLIRQTIERLSLRGIAVPTHADFAILMRILTNGLSSSTTSLPAL

>contig25119 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57050.1|) 3e-39

MLIGADVVCWPMLVKPILQTVKYLL

>contig25793 Frame-0R

MRLLEDCNCLIHHSRKIRDVGKETSQ

>contig25894 Frame-1F

MRRSAPPTLLVNFQLNFSLALDLLLFHFSL

>contig26604 Frame-1F

MEGWLTKRRDHMNLIWLDRYFLLDGNQLRYYRKRGDPAPRGTYILTDACVVSPVFNSEEK

HKHHGPVWMFRITFTVGDVISGEKSYKKDRFLDLGAKSEENAKEWKRAIENAVRSLRELV

AHQKKLKTDAEIFPTPTHVPRMLKADEDTMSLFNLDADNVMAEQAWWLARVEGGLRIMQE

CPLGPNVAANLYAQHAATTNGLFISACVSAALSFACMFSYANNMLLSFGSALVAMTVCCV

AVTPTQAPEIPSLRVSQVVHGSPTEVFRLVMNSKRFQRWDAATATMRVIQQLDDHADIVY

VTQRPTQLWPWWQKARDLVLMRYWRREEDGSYFVMYQSIVHPECRVRHNYVRANFLGGGF

VIAPQRVPSGSIRTLVTYVVRYDPGGWSYIYHQLGMAVDLVMPMLRSVVGIRDEMSATDF

ITPNVSMAPAGDGDKTDVDTAIIADSIDPFGVVTGVQKLETSLPEKMWAEPDSSLFCVRG

HNYLTDKKKLPSAPAMFHTMGVDLLSFESPAERYNISSRSDSIGSTSSRFTFVVNMIIPS

PENVCMVFYFQPVRDNVFEDGSGFSELLNDFIDGDDQFRNSRFKLIPTVVEGSFIIKQSV

GSKPTLLGNKLKCLYHRGENYFEVDIDISSNSVANTVVGMVQGVTKSLVVDLAFLLEAQS

DEELPEVILGAVRMQHISLDSPRRMVSPPI

>contig27056 Frame-2F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY70000.1|) 2e-55

MKSVSDLISNPTHVAISASTAVAVSLLLSLLLNHSKSTKTLQSRKVPPMPSTTLPILKNL

LDIHHSVDRFHDWVYEQAKAFDFRPWMYHIPGRPETIVLTSPDSIEDVLSTEGAIFLRGP

MGQYLSYDLFGKGLIIADGEQWHYHRKIASHLFTML

>contig27539 Frame-0R|Blast-guanine nucleotide-binding protein subunit beta-2-like protein [Phytophthora infestans T30-4](gb|EEY55613.1|) 0.0

MAEISIYPRAELDGHNGKAVTAIATTRENPNLLLTASRDKSLLVWQLSNDGEEYGFARRR

LQGHAHYVEDVVISSDGQFALSGSWDGTLRLWDLNTGITTRRFVGHSKDVLSVAFSADNR

QIVSSSRDKTVKLWNTLGECKYTITEDGHTEWVSCVRFSPSTANPLIVSCGWDKVVKIWN

LSNCKLRTNLFGHEGYLNTVTVSPDGSICASGGKDGTANLWDLNEGKRLYSLVAGDVIHA

LIFSPNRYWLCAATTSGIKIWDLETKNVVHDLQPDLEEPKGKYAQPPHCISLAWSADGSV

LFSGYTDGIVRVWAVGN

>contig27980 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53301.1|) 3e-88

MTRSDPDYVPPHLRRYVFHSQDDFYVSRHFDPMLLSDLMYEGFLPIASKYMGSSILIPKL

HRQRCVLIFQPSAPEHVPKIVRKRAKNYQLVLNRDFDGVVAGCHEKHGIPWLYPPIVQGF

KALFQTRENGKTLNGMSKIHFYTVELYDVATNTLVAGELGYTVGSVYTSLTGFSRASGAG

TVQLHALSKLLYLAGFRMWDLGMSMDYKMSLGAKDLDRDSFLTQLYKWRPEHIFMKLDET

NHEGNVRTGVLVKALLDNTRGPFQVPAVITRSIRLADNANQDASGEEKHQDDSIRREATL

F

>contig28044 Frame-0R

MYPSYDGGATRNRGNSLSRSDPHVKSLLTEQRLRERENDLISIATVDDPIPLGLYDPSKG

QPALTVMPNFQPIDEDKSNHGNGSVTSRGLGGGGARSKTAFPPRWKQSRMCHVCACGFSL

VKRRHHCRNCGQSVCNQHATNRVALPKFALSEPQRVCDQCFLSGHHIMVPGGTTPSIASS

YKSLPAHSQPFQTPQLNRLQFQHSR

>contig28268 Frame-1F

MDGREFLGGRIRVELARGGSRRDGGGRRGDDERFGRGGSGGDRVERGRNPPQRTDFRVRV

TDLPRDVDWRNVKDFLRTGGEVTYCNIEADGS

>contig28321 Frame-0F|Blast-peroxiredoxin-like protein [Phytophthora infestans T30-4](gb|EEY57987.1|) 9e-18

MVSTRSRTTPGSLPAVEQPQKRVAVLDASTRPVKKATTPSAIASHLVVGESVTKVVTLSN

QDEKEVVVADTYREQ

>contig28871 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67774.1|) 1e-101

MACFSCCRGVNARMLFLTACAMVDYIAHTVVMVLGPMLTLHFYPETSFLRLGFYTAIISG

SGYLGHALSCGVWISLARSLKSSKGVIFWGLAVTGVGFFCLLLCKSLLAMSIVRFATGLS

SGVLPVALFEIDNICGSRQTDLACMTKTLGVGLGACGTFAFIMLDAKAPQEFNADSTTKD

SSMIFYPFCFVAVLAWSAALAMLTGLSLRSRPSYSQLAKEEEDCLNSMPQFQNDTHCSPC

T

>contig30092 Frame-1F

MSPNREISSLRKHQGQVDNASEDYGVERYAAAALRCLSACSDDNRNRDKIEPFTEAKRAV

KRARKRKYKKRKATHTVRKEEIQALEQEMQLLQKELEKLKVKTRAENDMVSRSPRRCKAI

TTLLTEAVKEQHLVV

>contig30126 Frame-0F

MNFRSVITAATVAVVSLLQLSTTEGQVHLRVSVHSSKNICYIKCEPGQFCPLG

>contig30153 Frame-0F|Blast-26S proteasome non-ATPase regulatory subunit 14, putative [Phytophthora infestans T30-4](gb|EEY55930.1|) 1e-173

MDRLQRLFGNLPGLPGQGGPGADGPLVDTAEKVHISSLALLKMLKHGRAGVPMEVMGLML

GEFVDDYTVNCIDVFAMPQSGTGVSVEAVDPVFQMKMLEMLKQTGRAEMVVGWYHSHPGF

GCWLSGVDINTQQSFEALNPRAVAVVVDPIQSVKGKVVIDAFRLINPQLMMMGQEPRQTT

SNIGHLNKPSIQALIHGLNRHYYSIAIDYRKNELEEQMLMNLHKNTWSDGLVLKKFEDHS

EENEKTVESMLALTEQYNKRVQEEEEKTPEELEVLNVGKLDPKKHLESDVYDLMALNTVQ

CLGAMLDTIVF

>contig30377-0 Frame-0R0

MEAVRDVNIPGLVGAFVARKGAVFVAPTAVANAVSFLAVRVDNNAKDAVMSMVGFGNASM

GRVRKRIEAMAFASHTAVGNGASTLVVPVPFGEGSCARSTKQITRVARVLCCSWTFDDVH

GVILRNERLIANGF

>contig30377-1 Frame-2R1

MTEEKVSQHVNLKLSKGKKCVEANCTRRAQSNSRCKAHGGGARCQYSGPGGCIRSSQGGG

FCRAHGGGKRCEFPGCPRGQQRKGRCYVHGGIRKCQYGTCEKKDRGNGFCISHGGGKRCE

HFGCSRAVRRGLLCQIHEADHESGASFML

>contig30669 Frame-1F

MHLDDLDTTIPTIKQQIEDPFPDQCSWNDAETSSLIVSTDDHKSIIVTDVNELKAIVPVT

TTLDGEPFTEILSLNAINITTH

>contig31002 Frame-0F

MASILEQIVDAGNDTHLISSLKTGQTTCRTGDRGQEPDASYTPVNLGVGGGVMRATGNFP

FPNFILEVAYKNESLRALRAKLLRWVN

>contig31640 Frame-0F|Blast-histone acetyltransferase ESA1 [Phytophthora infestans T30-4](gb|EEY61204.1|) 1e-26

MAFFRYKRELRVHQERRLCNRHPPGNEIYRNENLSVFEVDGATSKVYCQNLCYLA

>contig31976 Frame-0R

MRTTSFSLSTAMRPWHSRHTFLVPLLLLCAFITAQDIPLPKSPRPPISLASRVTGEANNI

VISRGVGRRRSEGFSISHDIADNTGITTNVANVLKFTPKYVNLGRAETCVPQRYDVYVEN

TGSLPVRLERVECTHDAFFLLTDLNG

>contig32847 Frame-1F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY64280.1|) 4e-89

MSDVSQVLSTLLEDRKLVKYSEGSGQFNLRIHSCMPKKFRTVSLRSICDQTYTVVVTNKN

MVKQGADLEVLDEIPDDKAFFQVYPTAVYLHQAQEYLITRLDHDQRTAYAEKCPEPLAYF

TTCRDFTDLEVVRIHTVNQLQGSNEDSKEDSVLVYVGTVSIVTRVFGSTMLEKRTTRIIG

MNEFNLPPLQSFGEAVWLELPRLLRDKVEETSGRSWTAALHGVGHLFVALIRLFVLCDAE

DVGTEHVNDFEQR

>contig33031 Frame-1F

MPGDKDLYALARDQELSQQKRFDFCAEGKTATVAFTGFLAGKNRPYCKNIFIDEFVKAVS

LSPSFRRHENIRKSFDIVVAKYFDSDSAIDSCTSSSALTLLMQYDATLRKNAVESSHSLL

REHLVDIQFRASMLEAYLRSYASMTNMFLRGLGNSSDSIFDFAVQFLTVPHLIQKYTKKE

SLMHPG

>contig33462 Frame-2F

MVASLLECAKQPEQELHPQLMGDFTKGVKVGVGPEHEMSEFKRKEMNGEIAPEPFLVENP

NRFVLFPIQEPEVWSMYKKAEASFWTAEEIDLVHDIKDWASLANNERYFIKHVLAFFAAS

DGIVNENLAMNFSNEVQLPEARCFYGFQIAIENIHSEVYSLLIDTYIKDAVEKDHLLRAI

ETIPCVTKKAHWALKWCNPRVSSYPERLLAFAAVEGIFFSGSFCSVFWLKKRGLMPGLSF

SNELISRDEGMHTEFACLLYSKLVTKLPQSRVHEIIREAVAIEHEFVRDSLPVELIGMNS

GLMCQYIEFVADRLLYSLGVAKIYYTKNPFDWMDMISLQGKTNFFEKRVGEYSKAGVGVA

AEDQVFTLDADF

>contig33589 Frame-0F

MQPSYYNDEHDLWACSRAPEKLPALAHLLRDTVPPNDRNDFGETALHIAAAHGNDEAVTI

LLSYGADLLTKDWESGWTPLHRSLYHRHLSTTLLLLRHAETRFGKQFSLKYLYKTLDHSQ

QSPMQLLSASLRYQHDLSKASGDGGLVYTFGKRDYQLGYHLPNADVQTTPRLVELSANSP

ILYLSANKYHTVALNAMGECFVWGFGKGGRLGTGNEF

>contig33804 Frame-0R

MIYAPIAISNFSPSSVAASTDVLSRYTRCKVLRTTLYGETALYRDNTMKKLVVLKRLSIS

LLQREDKSSSKVVQENPLSERAVIQLLEDPLTDRAPGREYVVKYKRESFFTAGDSVFIAM

DFCAGGDLCDYIMRKPERRLPETEALLLLAEIAKGVSFLHAIGVAHRDLSLENILLKNGH

ARICDFGLSADANQYSTDVVGKFYYMAPEVTQGGLYDPKSADIWSLGVVLFIMLTGLPLF

ADEDARGPTFRVIHKYGLGKILELWGLKKQLSVATVHLLVSMLQVQPSRRLTAKEVAHHP

TLHCTQSRVASP

>contig34508 Frame-2F|Blast-putative chitin synthase (Chitin-UDP-GlcNac-transferase) [Phytophthora infestans T30-4](gb|EEY61714.1|) 1e-123

MLNKSAIYQMLLAFERNPQIGGACGQIAVEKPLENLSNWIISAQNFEYKISSILDSSMES

CFGFITVLPGAFSVYRFEAIRGAPLEAYFKTLQTELGVYGPFVGNMYLAEDRILSFEVVA

RKNCNWTLHYVKDAVARTDVPQDLIALILQRKRWLNGTLCNTLFNLSNWGRIFSESNHSS

MRKLAFSFFFLYYLLSTAFT

>contig34733 Frame-1R

MPAIKEEGNNNPLTMNNSTLNAMMSEHRRMDASTSLQLPAGAVRTPKALITSNGGDSNSS

AAVAVTPAPPASSEVPMSVLSELSNGDLASHVDSLINFYNATVSSANLKKKLEAMLKGMM

EHKFGWVFNTPVDPVALNIPNYFKIIRKPMDLGTVKKKLEVGAYKHLEEFAYDVRTTFQN

AMQYNSEDQDVYSLAKDMLADFNNEVRKVSAEIDVVEKAARSKESSCRLCGVERMVFEPA

VLYCNGECNSRIRRNCYYFTSPDNKYHCCHQCHGNLPDIIMHNEGRQYQKGQLARKKNDE

VHEEPWVQCDKCERWVHQICALFNGKVDSEKKPQLVKSESGQIADSGNASSSPPLSDAKP

TTVTTTVVKSSSSSGSKGTV

>contig34746 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63778.1|) 0.0

MACEDCVGGCPIKCSEVEAKNSCMLKLSPYHAPCITVAGPLQPFLMTPTPQFDFQFTFYT

YLSWVYTQNFILGLLLFYLSEWLSRSRSFHYFLGATGGIFCSALLALYLFQRQARNTTKM

IPGAQLVSTLLSMATVALPVTGFVIMPSLYRLGSWAISYLVFLWNREVLFGVPHLGKFYF

VFFAIFGCGLVWWYQWGASAQTEIQAQDEDEIEEIGHLNDELPPLTNLQLIVSRSLKLAG

LTLLLYSTSSTETSMLLILLVSLTRMFEIIATIAYFWYHFEKPGRHSNLISKSEYKKQGQ

TETEKALAQLQNYLKKNPDKLDLVREDNEIRLRRFARGRGHLDVATQESILSRQRNQNRS

FWSYCSIQ

>contig34852 Frame-2R

MAYAGSIVTPQVQMINGQMVVVETTLKLRDEPLQEDSGLPPRHMNSRLNSSHMNGPGRRW

GKEETKQFYYCLSQVGPNFSMMATLFTSRKRKELKSKFKYEEKHHGRLIEIALRASTA

>contig35222 Frame-0R

MSRSLPGGWLESGHGSVMIFVKDFRDPLERRKKLLLRPWASIKDIKDQLQVVFNVPSNAQ

KLFFQGRELKNTHSLQQCGIYQDNAVVDFVARRPQNISMVYTRECDEQNSAAVKRRNCGE

KSKLKNSASAYLHSKTSQNLRPEQVPVVNIQPYGTHLLPVALLKIMHQACKGITRSCIGS

CTSLGNGWHRWHVFF

>contig35349 Frame-2F

MTDLVTSPPMETVDVPPNHTLYLNNLNDKIKSDRMKATIYAMLSQHGKILEIVMGHSRRL

RGQAWVTFDDVPCASNALRATNGSTLFEKPVAIQFAKEKADIITRREGTFVPREKRKREP

KPVAPQQQSTKKKTNANESASAVGMAQMRAPAHNLPNKILFLEDLPESCNQDMLGVLFKQ

YQGFKEVRMVPGKKGLAFVEFGDEAQAAIALQGLSGFKLTPADALKVSFAKK

>contig35455 Frame-1F|Blast-Resistance-Nodulation-Cell Division (RND) Superfamily [Phytophthora infestans T30-4](gb|EEY58756.1|) 1e-56

MDQNGIPVMRNVVFGGLQRDLCHTNPDPCGDTTSQAIALLVTFLLNHHPENQTYTKYVKQ

WEKEIFVTLAEQAAESLKPSKRNWSNDSVWDGM

>contig35806 Frame-2F

MSRNHDKVSTSLTLGLGLLAATMTLVTASSMGLVGFLLGREYPQRKVRSLSLEKRSKTSM

EQEHRRRLRIPSGTASEDVKISDKKAIMDVRIAGIRPLIPPAILIEKIPLTTKIVQTINR

GRQGLANCLRRLDDRLVVVVGPCSIHDPDAAIDYAERLLKLKKELNKDLLIVMRVYFEKP

RTTVGWKGLINDPDLNGSFNINKGLHIARQLLAAINELGLPAGCEFLDTMSPQFISDLVS

WGAIGARTTECQLHRELCSGLSMPIGFKNGTGGDLQLAVDAVVAAKHSHCFLSVSSQGLA

AIVETSGNDMCHLILRGGKSGPNFEKEHVDDASARMLKANLVDNIMIDCSHGNSLKKHKN

QITVAANIADQLRCGDYRIVGVMLESNIEEGNQSLTPDEPLVYGKSVTDACMGWETTVMV

LHDLAAAVRERRAIKHQ

>contig36043 Frame-0F

MHDPSDDDKIVRSQHLAIPSGAENSLPKQITSNLKKNAFLESLGNNSSWRSWYGDVDVHN

ILDPPLSHIPEKLRVHDALLVNPIEPTINTKVTAPLNETSNLDSLEAAIRQEKQRGITFS

LQLLMMLQGKTVSGKSLEEEYELPSTE

>contig36511 Frame-0R|Blast-ubiquinone biosynthesis protein COQ4 [Phytophthora infestans T30-4](gb|EEY60676.1|) 1e-108

MLRSRLVSVATRTSHRIPTAMASYSVIPVAGFPQRRVMYDTHVPTTPLQKIVLSVSSALT

VFANPKRGDMLAILGEVTGNDALCGIHARMCADPVGAQILAEKPVIRNTTIDMELLRSLP

KTSFGYHYATFMDSHGFNADGRSVVRFVDDPELAYVMQRHRELHDFWHTLFNLPPTVLGE

IALKYVELMHSRLPVSALSAFVGPLRLSNEERCILMKIYVPWAKRASKKAHSLHCVMYEN

EFKTPIDDLRQRLNIEVAPSINTAV

>contig36937 Frame-2F

MQPLLVRTSTSCSSPPIMSKYVVGVCAMEKKTRSKPMREILYRLEKKRQFDVLVFDDDTI

INHPVERWPECDALISFYSTGFPLKKAEEYVNRVRPVLVNELSMQHVLFDRRKVYALLTR

HGIQVPRHVVVNRDLPDGNQDKLIEHDNYVEINGVRINKPFVEKPADAEDHNIYIYYPTS

AGGGSKRLFRKIGDRSSEFYPDVNHVRRDGSYIYEEFLNTQGTDVKVYTVGSSYGHAEAR

KSPVLDGRVLRDSVGKEVRYPVILNSTEKEMARKVCIAFQQTVCGLDLLRVRGNSYVCDV

NGWSFVKNSKKYYDDCGLILHNYLVSALRSRYFRQRRANSLGTQMCPQYATEPSVGSNEW

RDHTHPRPRSGSDVSELSVASASSTSNLPDDESSETLRCVIAVVRHGDRTPKQKLKTVVW

EQDLVDFYEKRRSDDKYDEVKVKAVADLQELLDLVRSLIKAYAPGVGLKDAVWEVEGGDS

FEKLLQMKRVLERWKFAGINRKVQFKPHKSYAAAAAANTDVREGTDKPRVLMILKWG

>contig37350 Frame-1R

MQRYADAIRAEQGSLDLEMQKKKERIASTKSAASHEDLLAEQTALFKQASVQAKKEGW

>contig37448 Frame-0F

MCQTLCPAEEAAERGRNQELSQFECPVPGFEDLVAVKKYRRSAAGRNVLNTSDLRPVSVL

LQTLRHLFTRVLLWPQSGFNGTNESVRAPNFVALYHFVDDRIRSVRQDITVQRIQDASVV

IAFQQITR

>contig38360 Frame-0R|Blast-CTD small phosphatase-like protein, putative [Phytophthora infestans T30-4]gb|EEY66367.1| CTD small phosphatase-like protein, putative [Phytophthora infestans T30-4](gb|EEY59479.1|) 1e-114

MSATVVQYPVEPRISRSRLSNQVSAAKQCCGVHVRVPSERIALVLDMDECLVHSKFQNEV

EHRQNEFRPEHLKDYTDSFEIVMNDGESVVVNKRPGLDQFLKEAAKHYDLYVFTAGLEAY

GKPVLDAIDPKGNLFAGRFFRESCKQRKGMFLKDLSVIRGGELSRIILVDNNPVSFLMQP

SNGIPVPSFYDDSNDRTLKSLTKVLASLQDVDDVRPRLHQLFHLADLLAEHKRLILG

>contig38474 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67103.1|) 1e-22

MTLLLAPILVLELNGVFHERNTSEAFLSGTPGMPQYTDLLLSGVISSALIAVRFASANIF

ASLARVVLSPKKRLVKDRIDRFASVLFKL

>contig39129 Frame-2F

MLSRNRCASILSSSAVAMRRTSNTAYG

>contig39590 Frame-2R|Blast-hypothetical protein PITG\_06730 [Phytophthora infestans T30-4](gb|EEY53107.1|) 3e-07

MALTPSLLSIAHPSGPNTRYLRVALFLSLELFTGTYHIIRVLKVPEE

>contig40349 Frame-0F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 7e-07 NOT\_ORF

MRDGMTGYCSRANIPLPRWRIFSLALREDYIVTSSYAIAVPVEHQPSRLEP

>contig40680 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59477.1|) 8e-88

MKATIAVAVRHRVVAFEAPLHEHKALRAVYRAFKISFSVPGQATSTSFGSVAITDAEVFR

YVTFFLSPNGSKEDPQTARHLLTLLAMYSTKEVLYLSATTTLLRWQDAETSYTVSKDPTL

ATSTNRVFVLVTYRPRELLPLYMASARRAVRFVNAVVALVTANAYVSTLGGGHFLCRHLN

ESTQLANVQIGISMSLHDPVLESKCRVNLLYNALQFGRFKRARRMLKREQAVAEQLESRE

LRSVCHAASVYLEKMATLHQEQLLTCRKRGLPGMLYDNFYRQRILRLAPC

>contig41733 Frame-2F

MLSWESTVSFNYLRRTNDEYSHIEDSINELPIHGQDQLQFSIDLENINATSRLSEESVWA

AEQSTDAAS

>contig41746 Frame-2F

MSSHRRNPAFDVSQLSVDRFKFSSSIAILETPGGSPELVTMMERPSLQSSLGDSLLKEDL

LDQSSSGLKEHINSIRARGAFKIPDEELSSIGRVATEAG

>contig43043 Frame-1R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY65645.1|) 6e-95

MASHIKDVDVPARIATKYRVVTLAEQWKLKPEVCAALDKLQIRSFFPVQAVAIPKILANN

NERVTDICISAPTGSGKTLTYVIPIVQRLLPRVVCRIRALIVLPSRDLAVQVHEIVQQFI

QNTPLKCGLAIGQRNFAAEQSALVGTASKEKVSSTINGGNSIVDILVATPGRLVDHLEQT

PGFTLQHLQLMIVDEADRLLNQSYQDWIQKAYASVFYGQILDDEG

>contig44235 Frame-2F

MQRKAKTDAFKRTHTDVEDVNVASPLSGVSFQMRANFEKLRQDIADRKAGKIAPSTDTST

PTTLAESKVAEECDTSCVGVWRHFCALDTSIKQEFYVNSVTHEIRTELPSPLVQEQSPAN

RYDDLNGVARAVVDIDSAIKDQDDTVTPLKSKARTKRAIALAFASPDATSEFQSAIEEIV

VPEHKEKTEEEKQDTLGKHTRSDASSDLTADVSAEEIEDASETPKKWQCSRCTLINEATC

QQCEACGYETPSAPAPKRLRKKLHFQSKISL

>contig44288 Frame-2R

MSNPFGDSNVMGSDVAEDLSDFAAPVDHCGDFFEAAANEASHDVYENQMDPNYAQHMKDS

YPPQSYGSGPLEQSTGSFHAETPTHIPAVDEDNELTKFMEEYERKISLKAQEQEKVAIEC

KAKAEEDMAQFLAERQRIKESKLQANRVFEQATLEKMVADLQNENPWERVVTLVDLETSR

KKRLDLPNSNESDGKKQQPMPVAVPAKKTPEDEEDVSRMRQLFVQLKASPLEHTRVDAVA

TN

>contig44554 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61848.1|) 2e-38

MLFDKSIMCTGIHDAASLNVIDLHQLRTIRASFPAQIYEPCKEHEAKPNEFELQAVERLD

RFQISTNNIITAVTAHPNQCAVICGGENMTLQIMGVIGRNNE

>contig45126 Frame-1F

MLWSSSPDRNSYLMKMQRKIMSLKKKTGPGDMQQQATMTSNPMNAAASTMNNTLNMNMNA

VNMNAAMNAQQFQQGAPMNTFQQQAQVQAHAQAQAQALQQQNAAAMAAVSNGLSNNSTAA

VNSSVTDGLNAPSTASTTAGTTTATSIPTPPQQQAQQWLQRIQVQFQAQQRQLLHTQNQE

TQQLR

>contig46031 Frame-2F

MTSSCKNVSIGEYDPRTGLTHITQQRGRLLFNMGPSVKKRQHHDLLVEAVDLTMSSGNYT

GLSLYPEEARYLSQQEALIIYLMPRKGEDAPPLSAATFDVMVLNDAHVSLACMQVYAFLK

DHRLHPRRCRRPLMQSSFICDSIPCIMANSECRDVAFDVWKTMTCESAESAQRAKKRKML

MRVFKVIVCRFGDALPSMRSLRNAANSTISHNDLANNHVPL

>contig46174-0 Frame-2F0

MAYLQGPCTSFHLTSAVASMPTVRRQPGIRKKLMSKAAPGRGCRRADLVEWLYA

>contig46462 Frame-2R

MEDPTAEQPLLDEDGSIPKNQTIKGRNWHRLLAFIGVLLVLCGASYMIVSSQITRIATNA

IKDTAMQIERMDLSQPHSSSVTLNISLRFVAASPFPAQVESAMCTIMYEGHKIGTFQIPS

MTIRHGPTSQIFPNSILQIEDAKAWDRFAGDIMRLDTVQYEISSKLNIHVRLLQGLIKFS

A

>contig46804 Frame-0F

MIPGSCYLSRTEWDVLFAACALRN

>contig47380 Frame-2R

MEPRAAIRRAFAGDYEHLRKFLEAGRGKTIALTGAGISTDSGIPDYRGSNGVYMRNKDFR

PIQFREFIGTHTYRQRYWARSFLGWPKILSSQPNGSHHALTDLQQAGVVSSILTQNVDRL

HTKSGSSKVLEMHGSLHEVECQSCRCVTSRQSYQSSLAELNPNIAKWQMEHPDEKTGDVA

SSDEVNPDGDIDISWNYDEFQYRACIRCEGILKPRVVFFGESIPVATRKATFDRVSEANA

LLVVGSSLKVLSAMRLVNHAHASKIPIAIINLGPTRADALCSLRIDKPSTSVLTEVADLF

R

>contig47847 Frame-2R

MSNKLSSSVQAAFGLFDDDSSDEEKNVSLVTLQNAKCDTEADVSRTAALEKPGDLTEGPR

SLYKFWDDVKPLVVGPIDLVTSINSVGGLRGYVALRDLEPGTRVLIEHVYVPWPSDMETS

DPELFLATMVSVLARPDYADIMEHLSHLYPENISEMPEDLLTASRNRYGHQVDEL

>contig48110 Frame-0R

MAQWTLKRLERAVENFTAQLQCSICLCSYENPVSLPCNHCFCEECIHRALEVKVQCPICK

MPTSKRCLRYDTTVQELLRATEILCAAPVSFLAAVDHQVPIKVEKQSNKDSKQPSGETKL

LKTGLEKTEEKRV

>contig48187 Frame-2F|Blast-DNA polymerase epsilon subunit, putative [Phytophthora infestans T30-4](gb|EEY69170.1|) 4e-11

MGDTSAVRDAQGMSYVLGLGQGGNRTY

>contig48352 Frame-2R

MIVEAMSAARQFVVELVVVFMLQKSVSLPALMRSIVSTLILSCYALPFAWLITIYGQSTY

TLKNQWMMAAVRLLFYSVYMYIIVRPPARATRRTLREYCAFGIVYQLLELAYRFIFIYGY

IRPAFALTYIQLAWGALCPIFVYRLLKADTEHWRGLGQRAVGLQAVFRKGNIHERVSSEG

LHVLIEMHRKYIIDFSFLDIKQRIGIGSTAVVYNGLLNSKTPVAIKVYTPTSVTEDTVAA

FSHEAALCGVLNHPNIVKFYGMCVSPPTICLVSELCVGSLDVVTQALGRRQNQHARRQQF

LINIGYMIDAARAVAYLHSFSPAFVHRDIKPSNFLVDAEGNVKLTDFGESRSLPKADIPW

EISGLNDPKINAVVSAAASVLHPVTVSSSLSPDAEHYHEYPNSMTNASTNFHSNGGIPTD

TADEELRLKPNLGKSAPEMTVKGTVDYMAPEINQWTSRRRCL

>contig48734 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64506.1|) 1e-125

MNGVLPGQIYLQNLPCAVVAHVLDPQPGDVILDMCAAPGGKMSHIATLMKNQGLLVACDR

SKRKVLELRTLCTELQLKCVEPLKMDSIHALLPKDIVDLAARNKENTSVSQILEVAKLDG

FNQAGLLPVQGFYPETFDRILLDPPCSALGLRPRLLHTDDIDNLNEFCNMQRNFLWVAAF

LLKPGGILVYSTCTINPKENEQMVHHALQKYPLKLLSQGNAHLGDRGLSRQGLSDEEASL

VQRFDPANLNLDTMGFFCAKFIKTGSIRLDLANEALI

>contig48851 Frame-1F

MMCDFSTLTKQASSVEFKKSTVLIAEHSKRYAWHHKPACSLGFSSKGFESSRSSKICPMR

QNLKN

>contig49298 Frame-0F

MYEENSPKSSPAEVPAAVPSANGTNTVIVFVCDSGGTAQPVKIPSGTMLMDVVRAAFQSS

TFKKGDFFGLEDASLTLDQEVTTADAPLWTAKNPLKIKFK

>contig49948 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68767.1|) 1e-108

MMPSIGVGRFVVPEDYFNPFHIMHLSHDYDAHVVPELHGKLKDMLAQALSTGGFEPHVGG

VYVQTAGPRFETKSEVRFFAQLGHFIGMTGANEAELLNELRMPCAMFSIVDNMANGLGDP

LTLEAFKKTQKANADLMERAFLHVLDELASSNLLSSLASTD

>contig50241 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55174.1|) 4e-63

MAPFPLDSISNAMWKCAKKHSVLNMKGDYAIESKNCDMLYLKRECMLQGESNNIPVLLRS

VCRRFVEPDRVVVVWDGVGDWPKSYLRTHPGSVPIRERGYCVFQSPSHGVSKGGQALSLS

QLQSCICMKPGLSAEMDMNSPECLQMLQDVVIPSYRKILDEREQMLENAILDEIINSNMR

SSSSRR

>contig50656 Frame-1R

MTNPLYAYPAKHVDGVLAETDVEIEQRMTRLRSRDGNRDSVNDTEKIMDAFFYPVYTNDH

RTALHSAYENVLELLCRKIDAPIAQVLPILTKLDKRMKSLIYHFERTTTHTDFLRAGHAK

WKAAKDPLTPTIVDASSRQRHSKRKRDEKI

>contig51189 Frame-0R

MEPIAKRLKQSAEYAVPREKNFIEKEDIAARIEQLEAELHESDNDSSDSRSESEFENGKT

KAVVNLSAYASERIKALPQNMLPAVSLSSSLTPCKQMRLKMEQKNQTAEKNLEELRDAIS

FPSKVPFACKACKYIGQDLTTFQAHRASKEHLERLQIGDKALHCSRCKKSFTSLTQLDEH

RAGKWHKQRAHQKKERHTLKVCYDFIRGECKWGDRCNFEHTT

>contig51718 Frame-2R

MTVCISRHIYIYSICLIDDVNDGIEEATAPRTAYVSEFAVYVGTL

>contig52290 Frame-1R

MHRARCGTSRAENGCYSTTRSQFSSEIMISNFCHISPVPRDMIKN

>contig52913 Frame-1F|Blast-delta-aminolevulinic acid dehydratase, putative [Phytophthora infestans T30-4](gb|EEY61872.1|) 1e-170

MNFLHSSLHHPAQRSWSEPHLHPSQLMYPLFVTLRSEDKIICGLEPEMQWGQGLEGDYFS

LVTHVRALIEKGLTNVMLFGVIEEKDACGCMADDWASPVIACTKVLREALPDLMVACDVC

MCEYTDNGHCGILRDVDGEQIIDNARTLDRLCSIAIAYAKAGAHMLCPSDMMDNRIGAIR

KTLNENSFEHVSIMAYTSKKASVMYAPFRDAVESTFQGDRKRYQHPVGSTSHAALAFERD

VQQGADSIIVKPSLFYSDIVASFAAKKTVPVVCYLVSGEYKMIKDYGESTNSLDAVVREA

HLSLLRAGASVLITYFTPYILDHCAKW

>contig53086 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58151.1|) 2e-65

MAASAMSFEESVTAFFEGFAEQQLDQVCQALCDMRVSVTIVTEGDPAIFAVRNEMLRNCE

VKAQSLREKAISQLTHACSGASVDVDAILCAFSQCTTLGVALEAVPTFSSCLSRIFATQA

RASLIRVRSHKHAAKVNEHGYIDRAFYVEALSELLTGATDIMNAVADLSADTSVLQPVLE

PIHASCAEIVLQVVQMYADDARMGA

>contig53172 Frame-2F

MGTGVFFKETLMQTGMWMQSMIELLSEWAPLKFTGSHA

>contig54586 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66080.1|) 7e-29

MLESIRATVVAHSDPKQGIDLAMNAIHLAQVNLHTYAQYSAIRLMLIAILFDMSYLYCEL

LCLQCRYADMGASIMQIVTLFAT

>contig54605 Frame-0R|Blast-serine protease family S54, putative [Phytophthora infestans T30-4](gb|EEY61351.1|) 4e-72

MSGDVVVLGLISINVAVTIGWMRARAPPPLHPAAQLRSFRPSMETMLTHFTTSTQHLLDG

RYYTLLTAMFSQATLSHLGANMLGLYFFGRHICDVLGPKKFIGLYLASGVLSSAAAVYEQ

QLSRQLNYNLGASGAVNAITAMSILLFPHGTLLIFGLVP

>contig55084 Frame-1F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY59230.1|) 4e-47

MMDHLDHSRQDSRFDILLAECWVPLPPSSLSNTANPMLIDGNPMAEPSALTFNERICALY

SPK

>contig55130 Frame-2R

MSRAPALQCFVQELQPNPVDAQSGNAQSIKEGADTDWTQSPDAIVRCGCLLPRQGHDHLI

TFNSCPNSYANAFEMQLRIKCVGGVQELLMFFCPSSRIKQATAQGAEYELARKKRAPRPR

RKELQELVIKISVIHPRRATNPL

>contig55228 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57749.1|) 7e-50

MCKAHGGGVRCRVEDCTKSSQGDGFCRSHGGGRRCGHASG

>contig56698 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68119.1|) 1e-24

MEATEDNVVGTLFLQNGEDNGYDPEDFVLEIDVGNFAPHFHISVADDDGGIPGSLFACAV

WHGA

>contig56759 Frame-1R

MADAQDVQTLKMQVVRKHENDPDRRRSTHLRLEPPQSDVRLASSFQRARTSGVHRLLRSN

TSSIGSYVPPTKENHSTPTGNNASSSNAIVENDKLYDSKEMPSVPESVKIDVTRHDHLAT

DQVEDDDPVPLYLEHTWTHVVLKMTAFTEEDTVTSFTFDEKGGGIGQTCENIASIPADTL

LAETDHARVLYNGGRFYLVNGDQANGDTFVRLSPVETQANDDNMGDRMQWPLEPHVA

>contig57158 Frame-2F|Blast-RecName: Full=GMP reductase; AltName: Full=Guanosine 5'-monophosphate oxidoreductase; Short=Guanosine monophosphate reductasegb|AAN31473.1| GMP reductase [Phytophthora infestans](sp|P59075.1|GMPR\_PHYIN) 6e-09

MPRIEYEVRLDFKDVLIRPKRSKLQSRLQVDVEREFCFR

>contig57464 Frame-1R|Blast-conserved hypothetical protein [Lodderomyces elongisporus NRRL YB-4239]gb|EDK44744.1| conserved hypothetical protein [Lodderomyces elongisporus NRRL YB-4239](ref|XP\_001526365.1|) 2e-09

MHWCAALRVLHYLMGTQSHGIVYTRSDGNKPMLCAYCDANWGGDKSTRRSTSGVLIFAR

>contig57846 Frame-0F|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY53269.1|) 2e-27

MLDPRETFSGVMGAFCCVYAGLPFEVVKVRLQTQGSKDAYSGVTDAFRRIATEEGLFALW

RERCRLCPALSSKIRCFSALMGLPNALYWRFTQRSVLRTSRSTS

>contig58348 Frame-0F|Blast-3-phosphoinositide-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66101.1|) 1e-131

MEKDVLNRLHHQNIIRLYQTFQDDKNLYFLMELLTGGELLSHLLHEGRQLGLDEDLARFY

LADIVNAVEYMHMNQVLHRDLKPENMVVCEELCGHLKIIDFGTAKNLDDSKLNGPNFVGT

PEYMPPETIANEESTYASDMWAFGCIVYQLLTGETPFGGGSAYLTFLRVQDGSYYMPDYL

SDESRDLIIKLLQKNPHARLGGSKASAMKAVK

>contig58524 Frame-0R|Blast-RNA polymerase I-specific transcription initiation factor rrn3, putative [Phytophthora infestans T30-4](gb|EEY64787.1|) 1e-52

MLARNMGIPQEKELPPDLRAL

>contig59347 Frame-2F

MHLLMTCNCYKMADRWFARELFKFHAKWQSSRQRSA

>contig00025 Frame-2F|Blast-hypothetical protein PITG\_04488 [Phytophthora infestans T30-4](gb|EEY67450.1|) 5e-34

MSKPTDTKKNKPAASKATPVAGEKIPMLVVVTDEDDEFEEFEDADWDGQAEEKDAHIKQQ

WQDDWDVDEADDDFCNQLRKELQKNKS

>contig01592 Frame-0R|Blast-T-complex protein 1 subunit zeta [Phytophthora infestans T30-4](gb|EEY63990.1|) 3e-81 NOT\_ORF

MATCNRSCTYTTTRTASKDSASVGSIVLGIRYAK\*TRPFLFILAHLVISDKPVTLILVSH

NLHIWCAKHQFTFVMSFGKTNYRVGGTRGGADQFKWDDVKNDKYRENYLGHSVQAPVGRW

QKNKDLTWYAKATQSQRADALESERAIAKQRDEDLMNEALYCTKEIPRTY

>contig02355 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69109.1|) 1e-154

MADMQSKINAHQHELDRAREQIDDTTQKADNYLTDLTKRVEEYEKKHADFEPAGHYLKSM

LDASRSATQKLKTQSQKLSERSVPTAMDGMQAVQKSLDELQQQAIQYDDKFAGSRGQQAA

DTLHQLVNAGRQRVTDAAETTTEGLTKLRDIIGNMADQATHGAQVVMGEAARAAEAGDKK

LGVTSTTSGVVQKVIDLDARLGVTSTAAKVDSKITGGLGRKVAETTVEIVNESVNYISET

LHNAKLAAQHSETAQSVEGKASAVTDAAAAKTDDMKQTVAGAFEKGKEKVGMATQKTEEV

ASAAKDTTLNKAEQVKETASEAKDSTLNKAEHVKEVASDKAGQAMDKASEFSEKTKDQVG

HSKEMVNDKVGQVKDKVGDMAENAKDKMSETKEMTKERAGEATEAAKDKGNMVKDKSVES

VESSKDSAQNTAGQVAEKVGEKKDEMESGTDEAKDKSKTVFDRVAEKAGEVKENVKDKIS

TVSGIGNQKPKEPSLTQGENATEIALESSKQRVAKNSEAAQTASGSAVKGEYSGNKQKSG

KKSK

>contig03468 Frame-2F

MKSLISVLLLATSTYAATCETEGQVVLMASGDDNVALVADSSCEQQGVDVSKNALTATSF

GIEKVLSAPDVRTI

>contig04476 Frame-1F

MEMDEEEEEDDDVQMERHRVERHDPGPNDLVFIRNLRQQYAGKPRAKVALKDLCLSIQSG

ECFGYLGINGAGKSTTMAVVTGQLAPTQGFVTLCGFDLSTSTAATRKMIGYCPQFDALHD

LLTVQEQLQLYARIKGIPEAFVNIAIDEQIQELGLSQYRHTYTQGLSGGNKRKVSTAISL

LGHPRVVFLDEPSTGVDPSSRRKMWDVIAKVCSSDRKDGACVILTTHSMKECEALCSRVG

ILVSGRLKCLGSVEHLKQKFGRGYTVEISIRSALRSLGTDHDEGRRVMDEIELFFSAETQ

KDSYSIQRRSSKSYDIKSMDIITSRNVHDLCAALGAPERGRCITDNLGTGWLLGGQLSAQ

GAISTETFCSWWVLETYGERLKAFFDEMFPGTVLSEQQGEHFRFQVPKVRPGASENEVKL

LRPAEIFRALEQARTELFVDEYSVSETALEHIFNNLAAQQDEEKGIAHGMITD

>contig07356 Frame-0R

MLSFEDFAKKFEGQVGKSGDMGGSEMDNLFSGMSGLGDLKSLEGLEGLGSLGGLEGLGGL

EGMLGGMGGMGGMGGMFGGMFGGMDPSIPQNKTISDDDVLLGEIFGGLDHGDPFSDMKNI

KHGQMILNVTLSGAERVDKLTVMAMTQETVATFGHGGDGGVMGFVEPPMGGGIDKVEVHW

DKNKGKTCIFYMKIFVAGKKYISTGTKTRSRGVIAAPTGYKISGFHGRSNRHGIFAIGGI

FTKTTAMDLEVIDRMVLPETASPEIYNYKTTIRNWVGVADVAIDNACYQRRFDASSANEC

PSGYNKDDDTCVAQCPLDYPVKCFRECIPQNSDCAQLIISKVTAVVGVILSAATMGVFGA

LLVAFKTTRKVVLCALNIINALKSLLFYLRMKQTIVPTTDMEKMMDLAFQLQIVILDLPM

AVCGCMAYEIPPKFMWSVMILSVVSAIVMIAVSIGESIFGKKENVLLMLREVGAMNTTDP

QRDVIELETFLNNQSTTCSAEIRMLTNRVMGKVYEIRNNTPDAEEKDVRVAVSKASIITE

DVPIVTNHCMGEIWPNMTGEAAFKTRLQLRKTLRVIVDQLIDDGVTDMGKHITKKEKALE

YGNMALFFLSMLDPTGIAYLASEFIQPICGPSEYIGEIDDGTVRDALGLTVVGDAFVGSY

GTWHKVGDGSVTIYFESADTSEVSVVVRNGGETVREVMLPAKGKVVWKTTVKKLENKTLY

FDRWRPGLFGIPGTGGGSLLLWIPKSPKGGNLILHARLNVS

>contig08740 Frame-1R

MSVTAFVAGVAIGGLRYGAFKFQLFKRENFVLDLLNQFKEDLHGVR

>contig09686 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61626.1|) 1e-94

MDVQQLRQLYHALLPDDIIATDYERWRELKRLVIVHGLPQDEGFELDVEGARTSRNSLRG

RVWKAFLGVENDVDMTKYSALVGKGASHYDGEIRNDTFRTFRGDSEFAQRVPEEKLVRLL

NVFINELGSTPLGETNEEEGELARCGNLPSIRYVQGMNVLCAPLLYVLPEPEAYHMFCQL

IVRHCPHYMAPQLKGVEKGCALVDKCLQT

>contig11153 Frame-1F|Blast-Cullin family protein, putative [Phytophthora infestans T30-4](gb|EEY69720.1|) 0.0

MASTGFMSATNGRTDCSRKQERSSIGPGQTLCAKKKKLTIKPFKNTPKLPERFEDDTWTK

LVAAVHAVYAKEMSSLSREELYRSVEDMCTWKMASRLYKRLEDTCASHIQKRVEALVPYT

GGDMDLFLEAVHQFWEDHCEDMLVIRTIFLYLDRTYVMQTPHIASIWDMGLNLMRDHLVQ

HRSLEMKLIEALLNLVEHERKGEAINRSYLYNLLRMLLSLHLYHADFEAPFLMASERFYQ

QEGAVTVEAVSVPQFLRHAERRLAEETERVNHYLDVSTKKQLISVVENKLLKPHVGTVVE

RGFETLMAEGRIEDLQRLYALFARVDAIPDLKTAFSTYIQKNVSKLVLDDKQEKTFVEKI

LKLKADLNAVLSDSFQSNTDFAFAMKSAMEHAINIRANRPAELVAKFIDSKLRTGNKGGS

EAEVESLLDRVMIIFRYIQGKDVFEAFYKKDLAKRLLVGKSASFDLEKLMLSKLKSECGS

SFTNKLEGMFKDIDLSQNVMTQFQQHAASRHAVEALQRSNRGIPDMQVQVLTTGFWPPYA

AVEINLPASLVPLKEIFDKFYSSKYQGRQLQWQHSLAQCVLKGTFPSGKKELVVSLYQTV

VLLCFNNADSLGFKEIQEQTRLEDGELRRTLQSLACGKTRVLQKTPKGRDVNDDDAFVFN

WDFKNQLIRIKINSIQMKETKKENEDTHERVFRDRQYQVDAAIVRIMKARKKLSHALLMT

EIFSQVRFPAKGADIKRRIESLIDREYLERDPSNAQMYNYLA

>contig11311 Frame-0F

MMLPEGVHNREEDFTIFFLNRQDALQPRNNDNNLYETQEKILDKTLDPLQRFMYCLSVVR

TTHDATARRGAKVTAVALCSSHKSCLALKEVLNMAVLKIVESESDEASEKVLQDLFAVVN

AVDITGVRGLSNIERRLLKCTISSTERAVLSSKDTKNVEKELFFRTQAKWEDRSIPLQVK

LCSTKDQHDNGMLIHLLRTFGEQTMVLFNAVLTGQRVILLGYNRPAGEVCNLVLATSSLV

CPPLFGLLCRQFPYAHLTDLGFLLTPGFIAGVTNPMFKTKREWWDVLCDISTGDVIVSTP

TDKEDYDSVDRTFVLEVLDGVAAGYDEEWVRCMFEEFTLNNIVNIALGNVSNLNSDALAK

RSAINSNRITKWSRTDNYKLFMNSPHLKLFYSPAF

>contig11856 Frame-2F

MVKACWGSVILMCTLALHPYNEIAQAQEESALRAVNASTKGEVLQSHFEERAPSYMDLAR

KAAGFAEKIHYYISSVPNFANSNEKVQNMYRNWHISQKESLQKINPAMRNNKVLEALSDE

FQLKFSNSQRAVIISACQGMASIQIKR

>contig12448 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58055.1|) 7e-93

MELWIYYASVFPYFWVLATPVVSFVFGTYLYLSLNLLGCHYNEAFSSLRIASYKNFLRLH

FDKKGRLEIFAFGVDKMPRRWCRDPRWSGGHGPRAALERNLPSFKWTRPSYWKPLMTKVD

NMLRIDLENPSLNGKFNTADRSKVHLIDHVVIHKPLS

>contig13388 Frame-2F

MGVITYSIQGAGGFFTVDGRSMTYESDTDTVIGFCLASSRICCDSGETCPDTVQKCTNTS

SFLNAQKWPWILIYSFVLLVLFVSVCVLTLAWHRLYLRGVPKTYNIRLRVLNYISFFTGA

YVFYWLLLLLLYMCAYFLSTKSDSSNSRAVAQVLRQLVIFLISSKGYLDYVIWFAVNNIE

RKGGNQRNESADVDVDLSPQVNTALRSEILYYTTSGIKESVRATSDEQIMIPISGESEAG

KSIKFWSFCPASFRHIRRTFGINDAEYTHMFGATTKERFSEGRSGAFMFYTSDESLIVKT

MSPEECAFLRKIAPNYEAYVTSNPDTLLTRFYGCHSVSLYGKMYYFVVMGNLFAETDVVH

HRYDIKGSWIDRNAKVPSFGDKTACRYCNASYTFGSTKNQECGDGMNFHEPDIVLKDNDL

MTKIRIDPSTAHRIYDQIHKDSDFLCSQGIMDYSLLMGIQSSEYFVDTSQLPQARRDLLF

TQPATSVAGPSLYHFGIIDFLQQWTLEKKMERFYKTFVKRKDPEGVSALPPKPYKFRFQQ

KMSRIFALSTHMRAENDRAFNNNYPALIDVLDQGNYDTQRPNTYVNTSVVDQRPVFNPDL

QQDIRAV

>contig13933 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70293.1|) 5e-97

MEIALTKARLAAQADETDEQRRAREKASIEDADFEMAIDAFGGAPSKQAVDAGRDSNAVG

STEDAILGMRLLSLADHEQLGNFVASRLATSNSKYALECIKVIMTKASVNLTVDDIKEIT

TIINIIKNEKIAAAKPKGKKKKQLGKQGYAKVERTVGNGGAGGKAYTGYEDTYDDYDDFM

>contig14091 Frame-2R|Blast-1-acyl-sn-glycerol-3-phosphate acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY63610.1|) 1e-149

MAVFHLYSALHLFWILCNSSCINFLQFCLWCLVRPFNRILYRHLMCFVAQSLWVDVASTS

FPQTKLAVSGELPSNPSKPVILIANHQVDADWWYIWQAARHQKAAGNIKIVLKDPLKYVP

IIGWGMRLFDFLFLRRRIDEDAEHIKQYMQTLVSDAFPFWLAVFPEGTTIHKEYVAKSHA

FAAQENRPKLERVLLPRTTGMQIILDAVAEAKPDIYDLTLAFPSYSGEVPTYQMGYTRQF

DTEVPSMKSLLAGKQPLGRVALHSQRYSYEDVAKDLQGFLDARWKEKEARLTYFMKHQAF

PEATPPVEVDLS

>contig15597 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60533.1|) 9e-37

MNSPEEDKNVKVLHMAHSSDSDGHPSFLIKIQHEGESVVTLNVGEVRVFKELLSYSLPRL

LGFHSTLAGP

>contig16242 Frame-2F

MIAPLQFQGDCRPYYTLYEADFDTLARSQNNGSSSPDHMAVIGSTNPFLLKSLSLWPNAL

IFPFHPHET

>contig16501 Frame-0F

MVFPALFLLIAFALGDAAATSMSNSLQTIPFSGTSVVSRRLNLDPVTVEKAAQAINVEHL

LDIFGKEKEVVGDIPSEFYKIADHTKHQELFKRLGSHLKTLPFDDAHKDHAVISLMEKKY

GEPAVAKFVNKALSLDPKSTEAIRFQSAMLDRWDKEGLNIQEVAKKMTPKDFKLSKETLE

DFPREMLMRYAVKVGGSEADADFVASAVLVVQFINKINTEEKLSALLPNLKAIQDLSSSD

IARCFHVKKDATADILDQPMGFVFLLFNRLRTSQDPFEKLGRVRSLYGKDGGLQPSAKNF

WPTTKDVDFPSKMDIFVENVLPTTFAGKIRYFFRRMWFKLVSIFKKKSTPAVVSNHEIPK

SEIPETTVTDVVDDTSNILKTPVNDDIAATSERPSSVGRSTVINAADNTGGDASAISKSP

AAASAKDLRDVSKKADDVKPKTGAEATNDVKLETVRAPSNTKPENSEGATPVVNTDATST

RKLRH

>contig18756 Frame-0F

MLTNGRQLSGDVAIARYLARLKPELGLYGIVSTDTSMIESAFSSSEIDAWLDFALTRLSV

HARDDSGLQLLNQVLQTKTFLVQHALSLADIGVWAQMTLLQNQVDVTPFTHVTRWMAHLD

SHQTLFASVERTLTSIKPLCEPGDGQNPVLKNKETGTCPPLKDAVDGHVVTRFPPEPSGF

LHIGHLKACMLNNYYARQYHGKLILRFDDTNPSKEKNEYEQSIVADLKRVQIEPDVVTYT

SNYFDAIADFARQMITEGHAYMDNTSQEQMREERMEGIESTCRNQTPAANLVLFEQMLQN

ASEAQGYCLRGKIDMQAKNKTMRDPVFFRRNATPHHRTGTKYHAYPTYDLACPIVDSLEG

VTHALRTTEYNDRDFQYQWVLDTLRLRKVIIQAFARMNFVYSVLSKRKLQWFVDNHHVEG

WADPRFPTIQGVLRRGVQVEALRDFILSQGASRRITDMEWDKFWTLNKRVLDPIAPRYFA

IATETSVPLTLINVSSHVVGIPVARHPKDPFMGEKMVRFCNKLLVERDDVMQFVEGEEVT

LMRHGNMIVKKVHKAVDGTITRVEAENYPQGDFKKTKLKVTWLSDVSDLVPLTLVEFDHL

LNKPKLEEGDNFQDFLTETTRAEMHAMGDHELRNVKQGQVVQLERRGYFRVDVPYISDDK

PVVLFMVPDGKVKAMSTLSTKLAHR

>contig19940 Frame-0F

MKLKDDMKTALELAESSEWSALDRLITAQCECADDMDDFGMMPLHWACTDTHVPLRVIKK

LVDIAPSALLHKNKGGLLPLHIAVKAATKLEVLYALVHASPDVAKCVFEETPTGETPIEL

ARTYQLTHDKITFFLDMEHQLRLAGKAPDRPSARFQAFATPFPTGTSYETSSSPCQESLQ

STYIDQDSRTNTPRNVMNAVRLPDGLATVPLPPRWRLDKRCNICQLKFTYFKTRHHCRSC

GESVCSTHSNKRF

>contig20315 Frame-0F

MNRKLELMDLDEGMDRSDGSSSPTLDMLHRGSNNQEVEMALLEVAHNPDLNYLRASGALD

ETSSKCDSAVESFGEEDEDNNAIEKTVRRKTDSNSKRPWTREENDKLMQLVKQYGAKRWS

LIAMHLPGRVGKQCRERWHNHLNPLVRKDAWTAEEDYVIFECHKNVGNQWAEISKMLPGR

TDNAIKNRYYSTMRRMQRQSIRKKGPLREGKSIRVASVSSPIVPSHNNQVGPSPLQRPLG

SMQSQLSPQQQQYSQRGMGFQSSFQKLFSEIPGNCSRTDPNSLMDFERSNMMASSLRQPT

MVYPLNGGGYSNGMNVDYSRSMSMSSPCSGSPDHDLNQNNQEETFDYVPMQATIQRLRSS

SSGMGTPPSSSSMNMMNSSYSSPANNIQQQQTGNYLMSGNSYTNNMRGAMYPAPTGFGHN

QQYRSADAAFINPSHKRLLDVQGSQRDMWKSDSPVSVTAPIFRGTPTSQVHQSQVTEPMV

LQQSKPVAMPTYRQSSHMVHFNSMEQVWTEDAYL

>contig20993 Frame-2R

MRASSLLQCLPKVLSVSIPSRRASLLSTLKLSCTEALTKTRKKHSRLSTLPVFWPIAGVD

EPPHLPPHEINLVNRLFHVQSTLITSTSDPTDLPEWNIPEIAFAGRSNVGKSSLINALTG

QKSLVRTSKTPGRTQKLHFLSVGGKSGSLPAVALVDMPGFGFAAAPKKVVDEWHRLVGGY

IDRRRGENLKTIMLLIDARRGLGKTDLDFMDFLHELGALYQIVFTKADAMKRSELEKEIV

KAQNVALNGARM

>contig21121 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70382.1|) 5e-32

MSCGSREALVFSMGLLTGTCTTLTGKILYGVDSIGLDGEVKKFEKPIFQTWLMFLAMVFA

LPIHWAYHYYVDHQWRRNPRGA

>contig21745 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61143.1|) 3e-27

MDPHRLCDLLRLVGLDVDKAHAVIKTTLERESIGTGQVCRHYLQGECRRADC

>contig21806 Frame-0F

MLDYLDPMLPECDGGNGFFHIGDDDEVDGLGPDNSISIMSAQSLSDLEGLESPHGHLVSP

SSTSSCSQDEGVETSSQSSFGSPISRTSPLRLTGNHRQSRDLILQPSQLSRSTSSHVPLQ

THQFANERELRSMVSTTSATMTNVMTTDDTAKRGFSRHSSLPVTLKPDILNPSSLLEVDK

DHDEVEIESSRDSSSTMGGLTTYQRGQLFQGQETLPLTRYSVSRDGSQMSSPLVSTRLPR

RASLEAPVFGSIDPPPEWKHDGECSICRATFGMFKHRHHCRNCGKSICSQHSADKKIAIE

AKGFTTPQRVCVTCYAMITHTRALRHDFEVEEMSRQDSTLNVNEFPPFGASQTHLNDRHL

SVVAAFPSAIVSGLSRSNTGFTSTRGPMDAAESPTRSPRYHRKASSIKSSVVSAGEATSG

VRERATSKVGSGPTSPVHELRCLLASQQKQIEQLAQSNMQMQQQLLEQEELKAETMLIIT

QLMTRVSVLELQKDRHFQNKRRSAETGESDDDDEDYPQDDRRPFEH

>contig21891 Frame-1R

MYVCPCLLQCPKEKDPGVSNLRLELRSCH

>contig22292 Frame-0F

MLIKKQHICHVNLDLFFASRCNGP

>contig23185 Frame-1R

MALLFSDSTARSLPSVFKVAAATASANLCLVFVSSEATSKLPTEGSSPATQIVSFNGKTL

LLVPSSVSSPFLSTMLFFSSIEFIYSALTSVFRVSVEDIQLS

>contig23394 Frame-1F|Blast-N-terminal kinase-like protein [Phytophthora infestans T30-4](gb|EEY59536.1|) 0.0

MNFLKTLGGLVGPSATGGLPYTIDTPCIDGNVSAGGAMGESVLFEGLPDFVLHSGKSKQD

PSHLVSIFKSRHPAGQQTQNSLRRIKTLRHPNILAYLDGIEVPNNGPVIIVTEHVMPLSE

YLTAIRMEYGKNSAEFTMCVSWGLRSVLMALQFINVDCKLLHGRLTPQSIFVTKGGDWKL

GGFELTAEITCDGPSSIYTSFQQYADANYKSPECQRSDWKSVALGPSYGVDVWAFACLMF

FVFNDGQFRLGDVSTAANIPSALRNHFRKATDDNAARRPSPQQVLKGSYFITPFIKQMDF

LENLAVKASDEKVAFYKELCASLGTLPRCFGVHKILPVLKQVVEFGAATGGRNGPIKLDP

SASHMLPAMVQIGSSLSAEEFKAEILPIIVKLFSCSDRAVRVQLLQMMETFAVHFEAKLV

NSSVVFDNLCSGFSDTTPVLRELTVKSMLHIADKLSDSNLNNRVVKYFAKLQVRRKLVPT

FYFL

>contig23602 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69160.1|) 7e-72

MKTISGSEIGQRSGLASGSSAISKFSLCYITKRPSYMERKCNAILAPRKSYRKRTRRTLE

LDGEIDRFEESEASRRKPKLADRVTFLLETHRSDRTQITRPFEELETQSKPSEKSIETKK

NQENINLSTPKLLRHLRRSAYYVNNLVTEEESLQSEPASLQSSITSAGNVMANYQEAYDL

VSQIAVQLQIAAETSSTRCKKLLDKQKEEFRG

>contig24049 Frame-0F

MLAAMSSSQIDSETLETMPMKEESFVFVEQSRTRLLEDQTFRNNESFQKMLKLANNAETE

SKSSEVDPLASIVDRMPSYQNLNEIGESFSESETDRMQS

>contig25064 Frame-0R

MKFGSYVVFILLWTSIVYDPLARWMWSLKLDNNWGITAMGWEGKMGTLDFAGGTVIHVSS

GFGALVAAIVVGKRYNHNEATKPHNIPLVMIGATLLWFGWFGFNAGSQGAADGIAAIAAI

NTHLSACAGFLTWSALEFAFLRKFDPCGSISGAVAGLVAITPGCAYVYPWAAVVFGILGA

ATGFGAVHLKNVLRYDDTLDSFGIHGCSGFMGGLLTGLFATSDINPAIEGGAFYGNGMQF

VHQLVSQCVAAAYSAVVTFLILMALKYTVGLRVSEEKEMNGMDVSYHGGQAYGYTAHEEP

NSSPTVKVANPPVGDFMSTMMPSETGNTNVARQL

>contig26133 Frame-1F

MAVAPPLSQNPVENPWQSSYSKEDRAFELVWVEKFVNDAANALEEIGMFPRIRQSVIPIA

LRGKKAPTRIDFFYVAKTFDSFNTKFKMASKAKTDTNVALIDWITGRAKKLKYEPAKAYV

VIGIVLSDKLGYSRVATFLNAIQKDYRKMYFYLKHAVFRYWDFNGLNLYA

>contig26605 Frame-0F

MALSPKAESGSSSNSEDEFDLGGSSVPYNNEETNKETNRSTCMDAKNGGRTKSIDKGDLF

DGQNEKKIGMTTTFLPKNE

>contig27538 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65790.1|) 4e-07

MAFNFPVAHETKKKLQVFECPVETWKERKPRIS

>contig27707 Frame-0F

MHSVALPRQVNMTTTTTTGHPQMELSSSSVPRRRHPLYRGDMRTRDTQDPRFPARTHMQQ

GYTGYDGQYLQQCQGIIKPGQFHGMLKPSKANVPQRNEPPTRQHRAATSEIVRKRSDYVV

RDEDLVGRPAMIALHQDDLQFDDVTELPRADRIDYGHKSRGSNQSDTLHGNSKSGTFHGN

SKSGGFRGNCKSGGFRGNCKSSIPATKATTRQSRPRSGTTDNQVSREPQMVVAPIQGSSR

SVQNDVSSLASGPAPLTSEPVAWRVALDPKSKKPYYYHRITRETTWKKPAELIAAETHEK

RQFFNVMENNIRLKLRDGFYLRESDKTFVAGLHSPNTGFHLAEMSSNLSTRSCTSTVSCN

SSRSSLNSFSNDSTRSLPGSSCHFLTTSTRSLPTTPDRHGNSRMSNELPLQHNVEATDVD

KRPSLFRTLSSYETPVMTLSRKERDSNACVLPSPIQERVRLAALMPRTADLQAYARAVRS

DRGHSRPSLPLSTLMVPLASDKLPCVLKKPVVEHPTSRLRRSNSTNSIYLRMGTMDTPDQ

GATIQCVATVLRAHMMEALDDPIRSNACFDVFVTNRDRQYLPFAKKEAFNDASTSLEKEE

DKEVMVDVVPTLSDIGTFIQTVLSRAQMESECIIMTLVYVERLLKMTNGTLQLRGENWRK

VVFCAMVMASKVWDDLSMSNADFSTLWPEISLKQMNELEWVYLHAVEYNVRVSAASYAKY

YFHLRSMCATMGLLKAFDESAPLNVDGARKMEVLSKEYQERAKVMPVPRRRSVTITSVLS

MENRLMVENNGLQATKASPSASLEQLVQMQVYVAGGASLRA

>contig28171 Frame-0F

MHSGSAEPTGDAAQEDHRYSFAGAANPTRRLGVIYLGHTEHDIRSLQHNAQNRGIPTPIW

MDFSDQEPDFYISRVYWLPDQTLGVQKLNRLQTEITFLRFDVQTGRSRTLIRESNPVWIN

ATYLYRNIETESKTSFRFLWGSERCGFMHLYLYEYTSGECAARLLGAVTSGEWSVESVEG

IDLAQELVFFCGTMDSPLERHLYVTSLVPTSDPPRLPTRLTHAEGMHTIVMDSNCRMYVD

AYSNTTLSPRVIVCTVPSKAQLAVVDHIKLVETADTGALASAKQVSVSEYIQNLAYLLTM

EQEDMRVTFLQAQRKLCIPRIIFRFRHEMAKRCFMELSICPIQSFTVMARIQQW

>contig29248 Frame-0F|Blast-ER lumen protein retaining receptor [Phytophthora infestans T30-4](gb|EEY69550.1|) 7e-07

MDLATRHKQAVTEARKLWWPCNSSTLSAMNLFRLVGDLAHLASFLVLLLKMLASRSAN

>contig29716 Frame-1F

MKTISAHVTGFYHSSFHAYTTEVNVDGHRWRLGLRYSKFHDFYVQLEAIESDFAADFPPK

GTLFFKPKPEERQEQLEVFLQQVLAYYAFKGYPSELEELLCDLLKVPRHLRFLDREDDDA

STSTESGPDEIIPDPPSSSDSASSLNEADLIEEDKPPIAELEKLHKVEEKQISSGIKNEE

TVLSTQVASGATKEILIAEKRDEAVSQDEAETVAKRLTEVEDIEEAKQILIAEKQDDAMS

QDEAETIAERTIVAENVSETKEVCMAEELDHEVAQDEAETTVERIVEAETIVETENVDET

VKTRLAEEQDDASAEEEVEAIVETILEANIMKEVEKMAENDIAAIDIVEMTMESVIATVE

KQQETFETDIAVKAAAPEEDIEPILAVPLINEPLVETTIETAVAAADELIEEHVAEAVID

TSEVDEDPEASRMEEQDAEPIAVKSIESQDAKERTASETSPSNDQVEPIKLATSCFCLNS

YLPEPWVEFLQRRCMNKTNIVILCVALILPLVFARRLVGRVDPRVQDQMS

>contig29781 Frame-0F

MWFDQNALLQFPMVPLETIGELERSGSMTLYDAVADPDAYTLSLKCRKWVQNVPFIDFDT

IRTQPFGSHMLKLTFNMYPLFHEWKEAMFQGKTLTSWLWIEDAVSGFIYHFEYFVLHQHR

FLAWKAKTQTLEMECYLPVFLSSPQTEVQYVLRILSDRFVGIESFYHITYTPPLEQTTTE

ERFTKRLQLHPQPLTSLENAT

>contig29907 Frame-2F|Blast-estradiol 17-beta-dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY57568.1|) 1e-152

MANQLARMHAALEPIPLYVKVFAAVGCIVLSRLALQLLNLVYKFFLRPAKSLKGFGKWGV

VTGATDGIGKALAMELARKGMDVVLLSRTQSRLETVRNEILEKYPLVQVEILSVDFNRVD

EPGVREALQKKIDEVKDIGVLFNNVGVSYDFPEFFDELPGDRVDSLIKLNVTSTTIMTKL

VLPGMAQRKRGVIVNLSSGSGRMVVPLLSVYSATKKYVEQLSLCLAAEYAAKNVHIQCHV

PMFVSTKLAKIRNSSFMVPSPVTYARASVAQLGFDTLLSPYWPHALQICLYESVPSWLLA

KGAMMTHLSLRKRALKKLNAKKKQ

>contig31289 Frame-0R|Blast-Annexin (Annexin) Family [Phytophthora infestans T30-4](gb|EEY59586.1|) 5e-40

MLKSTYYYIFNKDLTWLMRSELSGDYREIILLALERLQVTYDPAIHTYEKAKADAIKLYN

AGEGRWGTDETTF

>contig31380 Frame-0R

MTLRSSVDYTPTYQRFVLKQKSYALQFSHIYVSRLQQLRDVVHQQVQKRTDGRIAVLSKV

IDLKADDQECVVIGTLLKTLDAKPDLFQALMSESGVSLIESMTQPLATDEDKLLFEDESG

RVQLVGEIDVARYVTGVVLGVRGRVARDGTDGCFFVDEIYLPSFPPQRPLPKRIESQYVA

LVSGLNIGRNTDSQPLRNHILVDYLAGRLGDAQEQSFVSKIVRTIIVGNVLEAVDKRD

>contig31555 Frame-1F

MDTCGDDDIYESLDLDTLGAAAQVALPTEQDVGIEDVSVVSVVSSSAATAVATPGRKTPR

KSVTSSVITGIGRAGAVKPIDLKNSTPSRSTSVTKSDMSPLDSNKSEDSKSGKLRTTPQR

ANSGFSPSEKESNEPPTSVPFSPAAGTPTAKVSPPTPHRTPTSSISLEHHVGTSSSSSMS

PAITTPVSAPSLVVSSAPLPPPVPVPSPIAPTTTSKPLAASMPAATASGVESTAPTPPVA

VAKPRYGICLS

>contig31641 Frame-2F

MRSFVGAEDDEPKEYVANEPSDGPGYLVGSTLVARWLGKMERTCVVIDRTALSNNRFKYY

VHWHDFNRRMDEWINEHEIVRRGTDEETLKLQEKDAKEKEKEQRAKNRSKIKSVGSGDRK

DGVAATRTDASARTRGQKRKTPDDQDFAPQDEDHDEHEGMDAASIREHEEVTKVKNVRFV

EMGRYRMAAWYFSPFPKEYYLDGSVDC

>contig31902-0 Frame-1F0

MQVVFKLLFVRSLFFFATKRLLKLSGANDLTLNLFLFLFNNGIIPLFTHPKLILSSAKRW

LPVTQRNNLQYIVSMGEDNMFAGLIICSTGLELDVK

>contig31902-1 Frame-2R1

MLSSPILTMYCKLLRCVTGSHLFALERISLGCVKSGMMPLLKRNRKRFKVRSFAPDSLSK

RFVAKKNKLRTKRSLKTTCIGILDS

>contig31977 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65856.1|) 1e-102 NOT\_ORF

MVLRLRQLQVIHRHGDRAPLMNIFRGSVNAIDEASESRLWMHYLPTSSQLVQIRSKYSVN

FNGQTHTLSQQRPYGYLTTRGIEQMTKRGNQLHAICLNEDLRLDKVTSEQVQVFSNAYTR

TQISAQALLLGMLEAEPHISPQVSVLPPEQDIINTYAIYPEIMRIKVDLERDNADFVAHE

HEMIPIKKELSRLIPAFDSGQIPFSWLTAADYFVCRRAHQVPYIPGTKVHGEATERHLGY

RFRQERKKIVYCGFAKSVSFCFLISSL\*FYSNKKFLKLVAGRLMHNVLL

>contig32846 Frame-2R|Blast-chitobiosyldiphosphodolichol beta-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY59176.1|) 1e-22

MKVLDMFGCELPVCAIGFNCLDELVQHG

>contig33175 Frame-2F

MWLGVINRQVFALRERDTMVQFRCLHPSDLSHQKGLNTLSHYFRLDVSLDPLYERWTEPM

DRMTKIIEKFRGLRIVRQDPVECLFSFICSSNNNIARIQGMVDTLKMTYGDCLYESDSSS

FSNKAQRLFYAFPSLYTLATKCDEAKLRALGFGYRAPFIVQSAKQLQELGGASYLYTLRD

EKLNLQREAETIENSEYSYQEKLMVFRGVGRKVADCVALFSLEKMEAIPVDTHVWQIACR

ELDPTLSDRKSITPKVYRLVGDLFRLRFAPQAGWAHSILFAGDLQIKGVGGENKNTSEAK

KKGQSVS

>contig35454 Frame-0F

MEHQHTEYEAELRAEIDAQRISLQELKQTALDQKTVLEDKERTIARFRDLAHSHRDEIAQ

LKAKLRAEAGTVESLKDTAHVALNQTMGLRALVAAAREHETEAARQKINAEQAWLENSFL

RAVVPSSIFSETDQKILRVRLTLGRIAGKSDILVQHLKKGLEAIAHLPRSNGHRDEEKED

GAVFTATSVEHLVLGGKLAAVACQAKEDLFMLECHLTTEEAFAEGCSALDTSQTAALESV

LDLALSAFSEGALLRHETRGGGDGASLYDRLVQASEEWHSSRSTQVSCASNAASFGARSA

VLKLRTRKSVAKLAFSISSIVTFLRTTKRLLASSEMPDNEQTTALRTELIPVLDQSLGEL

LSVFNLALSFYRRAEIDLAASDDDLDGLVAAGGEVVTCIQSYESEAQLLLTAVQTQLAPD

CFVEHGRSARDLVEFTKQSVYDRAVAFKEKVALLYKLVCRGAFTDAVAPRTRNDHPDGAN

GRPQWRIRAQAIHQELVDASALRSNLTEMTDLCNALHKRIREFERADSQHRVVAQKLESH

VLELTEKVAALTSKKAQLETQLAKEREQFDVALDESNKEKTLLSSLNRDLRKQLKRTSDA

SSSGKTGSSSNGSGNLKSSVLSAADAEAFYLAFHQLHKELHTLRSTLAKERLLQLFGPTS

NRNAVSTPSNRLTNAIKEVATFSREVKAHLSMPRLVDLRRVGTSSTESSPYAQLMAEKLQ

QSRAQKDLVALRERVGAAMREDGWGHDIINAITKGECVFGWQPPEIERPPVLLGRVKFGN

ASTSTSQAVQLVLNRSEVKHLSQALI

>contig35681 Frame-0F|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY63175.1|) 1e-93 NOT\_ORF

MKPSSYLQDQRYIDGHFLNIRGQQLFYCAAFPPQSQPLRGVVLFLHGIGEHCLRFAHVYK

HLCLHGFGVVAYDMLGHGQSECERPGLRAHGSEFKYFVDDTNQFITTAKSDIYL\*MLPEG

SCDPPLVIMGISIGALVALNTIVSEKHHFRGCVVASPAIAVEYTLTLRIMETLSKPLVWL

FPTARLVPGVNFAGLTRNPDFLKDYMADL

>contig35872 Frame-0F

MRDATECAMDAKLERAAAVNSAVAAMDEALILSELSKTQIKKAISILGAKYSLHVIHTYH

TPIVVGAQTCSHQPRKKKTAKKPASGNGTTPALWKQDPEYVKLQRQLEELIVLLKQTPDE

ASQQPLLKKKDELYIALKEAKIAARERVNHI

>contig36495 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65049.1|) 0.0

MQELPEEGESVIQTQMGKLLSSVFQSQEIDNFLALGLMLSMKQEAAFHAFRRQISRENVA

KDFNRFQHLAFIGADAARAWQQIAFLHQCNELEGNARWWHYLQLLGIECDHKLFQSERRD

LEYIRGFVPRLITQSNYDFYTVMEFTRHYHIDDSFPALVYAEALLLNESATTKLEYQDKI

IGVIDEIHEQHLIKMLLKVIGKVSGHDYDRLLFILRLLLDNTSYRDRIEVERRIEILRHL

QRTLLCINGIV

>contig37351 Frame-1F|Blast-hypothetical protein PITG\_06663 [Phytophthora infestans T30-4](gb|EEY70094.1|) 8e-06

MALPKRSIEQLLREVVGDETPISKQTIDWINECAV

>contig37449-0 Frame-0F0

MARERNCYLSGRGGNKRSTQPIRQVPASVYPSLQ

>contig37908 Frame-2F|Blast-GAF domain-containing protein [Phytophthora infestans T30-4](gb|EEY55354.1|) 1e-104

MYEIAAAAASSIHWDDLDLELAAISRDTKYKSAWKRKKLSRTYQNSNALTIFTRNTIRDH

RHQTRWGPKGFAVLAEGTLPCTVQELRLVFRTTSTDTFRNIMHCVYRHEFQDGEQLQTSK

MEHETGTLTRAFDDQDLSIKTAVFRNRRCFSKKQPWCYLELLQPQDRRNNLQSITQTTSS

IESANSAFLVPAFTRTLVSIPRSKVDQTTSTSIRLSASQHVPNVVINYSFEEDPSGRSTR

VIIHGEYLPPGLHNVHKRTNHERRIARLWMLRLAANCHRFLLIARRRRLGMQVVLRN

>contig38163 Frame-2F

MRFAQAENINLCPTRKRSSTCTKMLTLFTVVAIISAFGGISGSHLATHSALTASELQKPR

QLLRRAESTDGERIATEALLNQSKKKFDAALRVAGPRIGKEKIARDYVLPPHKVAKVKSS

GKNLVKQEQKRISIGAQADKAAVNLLKQGKNTILIGAKAEKAARDGTLMKNLIQYLKSTL

EDNSHKKLVDSMTSMVIK

>contig38619 Frame-0R

MVLIVGGTFGTMLSKIATDARIIELSQREPLVKRGTLQINYLLFRTGTEWIGLWVTALLV

QFDDLFHNYNLRIDPFWVYAMLALLSLLPVPFIMRNCSERIVQTEAFEAGTDENTTATAS

NRARAQIRAFFRMCQQRAMWQLVLFQCLLLATTRFYFGSANDVFL

>contig39506 Frame-2F

MGKVVAEGCGDALSAYLQILSATVTLKNAPVRRDATSTSKDQQLMLHKPSTTATDISFEL

TALGSEIGGAFSKIFGTNDLTQSVVVKETDNDAMNPFADSYRPLADPFAANIITHSRVQK

LPDGIREISGAMPDLPLLNKHLSEDIGSPLDIGDYECLEMDSIPKYAAFRSTAQLAARRE

HAPCHRSNSLRADTANDEDQSTNNGLNKDRELFPLAETVSRKQKVMDMTTVAKSSIKPMI

DMNYSYDFECEVTNNPFISERTPTSVGVLSLSTLDASEHLQSSYGYTKLPSAPSEAFGAT

STPTDPASLANNKLVQDAPLAPLQIPYGIEERYSMEQNPRDCDAEFDLFGCNNPDTSAKS

>contig39717 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61021.1|) 2e-09 NOT\_ORF

MNQHVRLCAN\*YGQETYCCFNVGL\*RHVGSHAAHVRPKVQ\*KDDNIIGF\*YSRHCDYILS

PLGPDHDPINAKNIMTRCGLLQVANVLQYIILTVLEYYCDFSL

>contig39920 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68217.1|) 2e-18

MNTCEVQDVASLRLADHICIWDASRWPFRYTHHGIVFATGASTDDISVA

>contig40454 Frame-1F

MKISSLEDNMEALVANSHNQEQGMFQLTDQVQLMHRQMENLIDIKTVEDLVSIRLTRGFR

EMEDRLAQNVMLMADKLEQKVQILEKQSTSQRQESLAALKSDLTDEMQRLQGLAVRKSDL

LPLQNAQVQSKEEVAQLSAAIDRQDKELQVTKSVSATLRDELGDARAELNKALQSQQHSV

AALMEKKLMRMVNESKEKSIKFDDKLSELAKKQNSLEDATKVLQETMDQLKEEASQRLRS

SSIDREEENEKLRQRLARSVAELETMASTKDHLDHRFASEELQLQSRLKELRTALLNTEK

QKETQCLELVQKLQEESKLMGIAQGKNILLESLLAREKNDNYEKNESMRFLKEEATEVRE

KIRKLESDNEKLVHQLTLELHAKQVQVSALSKTLNCIETASAKGKATAWRREKATTEHKL

VLAQLKLEEMERVALILPSGDEEQANITAASIDERKELEELLLQSQLEKDELEEELEMLT

YESNAARERLKDIVKDTNKLSSAYDKKICELEQQINDREQAMRQLSDTLGGKCNLDVLED

ELG

>contig40872 Frame-0F

MHRTVMNMTRCKIFPTGCRFFWDDAVQYALYILIRSPTNSNCGRASPLKLLTKQTPQLGE

IVMGHTLIEEP

>contig41156 Frame-2F

MMDAEKTNVMVSSGTESTKGKPTMVSMFSGLDLALDANGAVISNVFSAAKDLLVTKNAEK

ELEAQLAASYACKKELQQKERKNPPITALTQALELFDQEMDERNAFMSRHTKRRLKGGKK

SRGGILTPSRGRRLRYEKYKRV

>contig41350 Frame-1F

MSSLVSRHYVSEKVKSLCFVKDVRYASETMQDEALPLIASGGWDNETNYVTLHLPVRTTG

DENELRKEFELGEMDPRPCELNTLIKTQHDGDVNALQFVAVKGEKLLLSASSTGGLFAFR

ISSDDAAMSDEDSTKLLDAYAIPQWEQVFAGNAATCVEVSENRTSLVSASTDGALAWFKL

DEVATVEILENKNTSKLPINAVKFLGRDSVVASVGSTPGGQLRIWDVSVNSHFPIATCTD

SSNRSLTTLETHPTRPELLITGSNDGCVSCWDRRKLNVPFRSETHHQRTVRALTIHSASP

RFLYSGGDDAVVHCWDFTSRRNSLDPVAYDYYDQSTAIDRSNVSGFTEERGIQVQRLALG

SQPCNALAVHAESDTLIAGSDAQSIMIVQNVSKSTQK

>contig42351 Frame-2F

MRTVAAISTDDLVNSLLDSVTSGSSSKHSSDATLSTSTMPSVASAWNTESPIHSSSSSTQ

NDVEVPDSVDAIRPAFSPAPTGADSSSKNSTNIVLDQSDGGDLSAGLYVVIVLGILALVL

AAVLFYRSRQRHARKDIELADSPTVGAAHLTVPSDRGFKRERELGMPEMSIELTPGDLGR

SKGFDTSYVSSTRSSNTAQQYNLSLASNGDGSVFNTKGGVSPTGSHRKVTSYSYQYSESE

DSGNPHVASAGSTTFHLTGLIGSGAAVSGRGRNNISRSRKLSAPDEY

>contig42908 Frame-0R

MTDWRVNPFWLPWLLLLWWTQSKSWLRRWIKYWLLRPLMRLGIQLVDESDEKDATIFLES

DGQQSSDSALPGGLVNSGNLCFVNAVLQSLAAIPGFLNGLDRAVRTRSQLIRAPQTDDSQ

THKVLVVETLISIMRDLSINSHKEECKANTEAKEDYGQRLTREDKQQKSRRFRAALSRCT

SLVSSAASRQEQQDAEEFLTFLLELLHEVLRVPAQSIRSNEDEHSRFLELEKNLSLRLKC

FNPNDPRSYVQAV

>contig43037 Frame-0F|Blast-plectin-like protein [Phytophthora infestans T30-4](gb|EEY55919.1|) 1e-52

MELDDQEGVLKTRNQIICSLEKELVQKQRILEEELAKNKKNVEDVEERLKKESQEMLQMQ

EETWRCRERMLQKDVEDYKQKHERLRAFHIELAELLKSKDSIESSSNERMESVEPAMLKA

LIVQNINKCDVFATTLTQMKRKIGLTKRRLSSQKHLEVENTKLRAEYEKAKLAMERMATR

KSKTSVNLPVQVQSYYVSSGGQTDRRAKETDTPLIKRQLE

>contig43284 Frame-2F

MDRNGVAEAARKRKRGALQDISNNTRKKQHNRPSPRRSVSVVKNETDDGDIKPLAPRASA

RRKATTTTVNTALKSSMASTTASKAKKRAPVSKKTEPTRAKKRKLEGVENQPPALHQKIQ

TSMLSFQAPVKLYDKQEKRSADKENINEAESAVVVYQKVVESTVTGEAIQIKSEESREDA

PEIQTPERSVEQEAVAAAALRDEYVPYPYRSIFDHRDSCFDKETYTESVRDVDAPSKIVS

SHHAKLLRELDAFYRKHEIKYLSEADYIGTVQLDINEKMRTILVDWLVEVGEEYELDSQT

FHKAVNLVDRCLKKIKINRKQFQLLGCACMMIAAKFEEVYGPNVEEFVYISDQTYTATEM

LNMEAQVLKALQYRVASTTCYGFMHRYTKAGCSTEKQQSLVLYLCDFAQLFYHMVRYKPS

MLVASAVYLARITTAEPEPWTPTLHHVSKYNPLDFQDCVEELHRLYVIENEVVSTQRDKA

KAISEKYLADKFFKASTIPACSKKQLADSLEQYTPSLISRL

>contig43701 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57198.1|) 1e-22

MVLRTAAPDVVEIDLFPMKPGERRPPIPRYIAWSIILKSQLLPKFYV

>contig43796 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63999.1|) 5e-78

MLKKLEAMGIQLKWERVLEIAGEAAPGRPHVAEALVEAGHVTTFRQAFARYLHNDGPAYV

EGEDFPPEEAIKLIASAGGVSVLAHPWCCKDPMTLVPKLATLGIQGIEVYHDRNKIDMYG

ALAKESGLLMLGGSDFHGIDPNRECAPGAIPFPRLHVDRFLAHALLVWERPLIERLRIIV

DAIKRNISTSEEVLIWKEQEPVVSRTLAELQMGFEVVKPNDILVGNNSLTSVANSHYRTI

RIITLS

>contig43936 Frame-1F

MVPMGRVRFFEIKHRKLNLNFRVRMFRSRIVVLVLLLLYGVRGQSNSTQSGCDVCASTGD

CSKAYSGEPGRFCGNWLDQKRSRHPCCCPNDAICKVAKYDCNCGYVEEDGYGLVWLWYLL

GSLALLLCCCSCSFVAFKRASDHGADSFIPVATPVDGEYYGRRSARGGGMSAATGAALGG

TAGFVGGYMIGNSLATSGDSRVDGGGCTGGYGGNNGGGDFAGDF

>contig44289 Frame-0F|Blast-choline-phosphate cytidylyltransferase B [Phytophthora infestans T30-4](gb|EEY62969.1|) 1e-161

MARKRRATEMNNAEEAEADHRALTAEDLEREAEYVKNDNDDSSSSVSSQESSAEPLPEPY

RKKLKEGEPGTPTGRPLRLYADGIFDLFHFGHAKALQQCKEAYPNTYLIVGCCSDEITHK

LKGRTVMTDKERYESLRHCRWVDEVVEDAPWVLSDEFLEKHDIDYVCHDALPYSDTSGEA

TEGDVYARIKAMGKFLETRRTDGISTSDLIIRIIAEYDTFIRRNLQRGYTGKDMNVPFIK

EKSIKFDMAVDKVRNDVDGFVHKWMSKADDMQHSFLELFSKEGRLRTSFRKRRKIIKERL

SERMSEMAREGLC

>contig44641 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57329.1|) 4e-37

MAKSLRSKIKRKFRTELRKRVGVPHQAIQEEKIQQNLKKAIETQGSGKSVANVKKLIGAS

VHLARSDITGIVEEHTPAETEAALLNQEADVAMEDVKKVKKQKKVSMKRKPKFVHFHQLR

KKGV

>contig44797 Frame-2R

MAGLQTGEEIVMASAAIERPTAGTSQVAVAYATEEKLYLQVLAIPDRALGSEETTKLIDC

EKFELDLAPTCMFSVQATGPNGDVFYGVMMCCTDALMAFGYIENEEETESLAECFRLSND

QFAVYFPELATFSHTVLAVDVFTSPEKDQGWVAFGCADG

>contig44977 Frame-0R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY58620.1|) 1e-115

MQQKAVWSILTFLCFFTLFGGIAFGGPSMVISVWSGTSGDNVFQQQVLQYGAMLVAIVAW

RYYFMNQSWRTFYGMAIVLLVIPRTIVAIFVTQGLIRDRYFFHLMTIFTSVAEGMGWLAS

MVPLTEIIQEGSEGAMVGLMLSLSFSVKAFVQTNAVGLLNGTNFYNIAQVALDTSKARMD

VLLALLFNYGINALALFGLYFLPRQKLYTQQLRSFGGYTKCASSAIVTFAAALFLYSVII

TVLALHPSTSCLTVAGGDGC

>contig45127 Frame-0F

MWCSGSAECIRSKKRLLCPLFPSIGVATRLRNACTDTYNLDRYHELAR

>contig45376 Frame-2R

MMFATLPTSELSNMPRNAKTSPT

>contig45574 Frame-2R

MEQNLSAGRGRGRSRGRGRGRGRGKRFQEPSDTDGMAAFIESKRRKMDGIDKITS

>contig45668 Frame-0R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY66994.1|) 1e-131

MPLPAIYGAVYATATRPKPAEAIDSGKKAMHHLEDLPLLLTSDSFESISTKGKWLPRPIR

RAILRSIASRIAGLILVGTAAFLNSCNATLAKDGPIKLSAVETLFWRSLVAWLITVAAIS

STGTKTRVGKNNNGPLLLRCVMGCISMTLSKLVLEALNFSNAIAVTYFSPLLVFVMATFF

YKTKAEGFTLACSALCVAGAVLTKQPTFLFSTRKSTDVKWYHRSTTSLVTLYLLGEPAAI

FFAIVTAFMQAGTYLSLCRLQKVPYLVVMHYFLLTMTLVALLILLLVQHGKFRAEISLQI

CGYVTGTGVLFFAEQLFLTRGFQFDNPEVLAATWLLHVGSEYAWSVILLGAALNAWSVGG

ASVIAGGVLLLAFRRVRLHWAMR

>contig46030 Frame-0R|Blast-riboflavin synthase subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY64605.1|) 1e-102

MFTGIIEEIGLVVSIQERHDLLLWNGERGKGVELVVHVQVALEGAYVGCSIAVNGTCLTA

TSISDEHVAFGVSPETLRRTNLSALQPGNKVNIERSMGTGSRNSGHFVQGHVDGTGAILS

FTRENDSLWVKIAATPELFRGIVPKGYIAIDGTSLTVCEVNRVHGYFSIMLVAYTQNHIT

LPLKKVGERVNLEPDVLGKYAARSMSGLTTRVDALESQLQRTNWSLKGFAVLTTLLLVAW

LRK

>contig46661 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53680.1|) 1e-158

MYVIGLYLSTESSRWRWHDAQEFENRFWTGTAFLFSAAMLYIKDSPLAVGQWNSALGLVL

VFCFTMSVHYFDRFLHRQEISRRPKLKEASRQLSHKLFKYKATAKEKTFLVTECVSRIDR

HYLPSTINNMINFAEVKRRELKIYRILAGAGKDELNYILNHIQLALLFYKVKDHSSVRED

QRRTLILDLLCTTRLAELSVMSRAVLLDALMVMKISAHPMAEKWVRNIILRTQGDDLSNL

KTYTDAKGDFHSMHKLVFNDVRDSVVRADILGHIHREASVQIAHMRLGTKRGRNRKHQ

>contig47154 Frame-1R|Blast-small cysteine rich protein SCR76 [Phytophthora infestans T30-4](gb|EEY61402.1|) 2e-15

MTGICLWMFWACCWLHQWHILVVPIYGAE

>contig47316 Frame-0F

MHDVVAVVLYAFLNFKQEEQIKDDQVKKLPKHTEADTFLVFEAIMLFLKPFYEIVKTRQD

SVSNNDSSRLFTSFTLKENDSGKIQSGQEAEEKQPALQQLCQHVQYELLQEKDPQLFYHL

QNLEIVPETYCLRWIRLLFAREYALKELLWIWDAMILDTGRATIKFPAINMTDKSDSELL

QQPMLVSRSDDTVWTGFPLLRYICVARLLLLSSQLRQSDNTDCLRLLMRAYQKDERDGIA

LEQQNHPKKLLEFARILRDPMIEELQQSKIRVVPFREGSLGIILTAAGAPFENRLAVKSF

VRDTTTSDGVGQAEASGKVRLGYLLQSINGVPIESVTTEEVKRWLQLVGRPVYIGFCPCN

NVYDAAASKEIEAAKPFVASESKPTSDMALSELVQSVFLPGESCYANVETSMQRVMLSND

GSCVTHYISGKLFITNYRCLFARLLGCKEIDWQTPVLSIASIDRIEPRATSTIVNPTTLL

EKTQSSLDFAPDDSFKVVIHCKDTQVARLSIRDYSEYSKLIKCLSFLAFPKTLLDAFCFA

YCPIVAPSEEVQFDLRREYTRIGLLSYPDHLRCIDQSSEYTLCETYPRHLVVPADISDV

>contig47723 Frame-0R

MQIWPLLRRVLCARSFSSIADDTWQFTHVNRKTALPRMVNVSTKKVTHRSATARATIRMP

PAVLAELQQVGHDELFGSKGPITSTAVIAGVFGAKQTSMLLPFCHPLPLEDCQVRVKVVA

PHTIEIECCVQVTHKTGVEMEALTGASIAALCVYDMCKALSHDIVIENTRLIAKTGGKED

VVVEE

>contig47846 Frame-0F

MQSCTVRDSEAIRLAQASDWKALQRLLERHPHVAQEPGDHGMLPLHWACTVSRVPLSLIA

KLLQAYPDSVRAKNSGALLPLHIAIRARVQASCLRKLVRAYPEAISERTPDNVSALELAE

SIGLDNDRMKVLYRVYDRRRTLELQQHPMLNTSEAADESDSKHMQEEGEASGINNLLEKE

MLG

>contig48186 Frame-1R

MQEVKIHYQLQKPASRAIILPFVKEKLSKSQIVAFTSTARYKK

>contig48850 Frame-2F

MEKKEHLDFSASSSSVKSMDMSAITQKYLKPNPAAAMPTNNLQLTIEEGSDEEATKRELS

RRKAAPQAYSQEKGRNAPSLSPDNKGRCEPSKGLSPSHHNISDSFQDSSKIGPEQNVSNA

SSPSTQNSVMSISEYNGFQDTQTFLNSDNSFSGDNDGIEDSTLLHAAANREKEKRRAKIR

AKKEAIAGIDAASLEAVSKARTAATYSLTVRDKAMMRQISDLEAIVLQHQK

>contig49026 Frame-0F

MMAAPGTTSTVPSQRHLQGLVTRRLATVEPKSAAQYFGHVADVVCINEELTKLRTYNLMR

RAKVAYKGYESVLSRKKRPNIASNGKPLTAGGFYTSRPAQSTATFNPAAVLQLQAMLPRA

QPVAVKPAPKLAAAVPMSSVVPSTSAETSSSPGHMTAAQLQLHQQQMKKAQLQQQPPKRS

DYVVGTTVLIRSTADLVACGARNLAGKTGRIVAAPQIYGQELYSVYIDEHEALFQVPFNA

LTLIARPTPTQQHQKHTTQTIEAQQAASRGRLASNQMQRPQNASGQAQSGAKSAEQIKME

HSFQLHRLMQKQYREIQ

>contig49299 Frame-2F

MFNCYKRHLVQQFYRKFFCLCALHIMGVNSTIACLQRLET

>contig50107 Frame-2F

MSMLFNRQNNSGCHRRAFPLDALHFKILLHLFLEQSERLLQLSTVTKRLNHVKSEVLKRA

ILRIISCCCALDRSEAVAGTVRSSQEVRVRVGCWTNKCYQMYCPSW

>contig51063 Frame-1F

MQQKRRLIRQQMVERKKRFMDAAQAPMEYNAATNMMEPKEPICNLSHEEVMMLEVMLFDD

EESDLDGDCEGFAYPTGYSTEMPIGTYPSHMPSGNMSL

>contig51430 Frame-2F

MDGAVGAKSGVTLSIMKVLFTAASHVTFVSFLEFGDSAQLMYMMMDNQAAIRQLESEDSM

TSAKHLDIRSSYSRLCNKR

>contig51719 Frame-0F

MSVVFAIIGAAIGVIAVAVIFLTLVRRSKAAHDEDEDEITTTSAAYKKSQGSTNTTAAAA

AYASYNGGNQTGNGSDVGADTARGISMNAMNYYNQQPSANSSVPSPRVAGRAIPSQPVGV

SQSCSTSRPFGNNSSYAASGHDAMG

>contig52570 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69061.1|) 1e-21

MAPSFHRRIAEVSESGVMTSAGNTSLSGNNASGIACTKSSRSTGQKRRSAVALGVNA

>contig52628 Frame-0R|Blast-importin subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY62298.1|) 1e-32

MEGRIAVEESGCLAKIEELSYDHNDDVSSIASQLLDTWFDNEGSEVSEALAPAIVRSENA

GQALRFQPVQSDVQFHFDRK

>contig52783 Frame-0F|Blast-iron-sulfur cluster assembly protein, putative [Phytophthora infestans T30-4](gb|EEY66911.1|) 1e-26

MSGIRKANFETRHQMSMLSRPLHRILRAPQLRWASNVQVVRDTGLPDLIITPLAAQKIIE

AAERQKNNNLMLRVAVEGGGCSGFQYV

>contig52912 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY54200.1|) 2e-08

MVMHGSSASLISSAAADKRKHPWNSSDDSATFQKLTDDPSSFGSMLDQLHAEQKGTIEAL

TSQ

>contig52967 Frame-1R

MFNKTSTSDSDTCHPNAEAKEKEKDDIAGGEVPHDIAAYKAIVLGNEEEALLALMRMGRP

LWWSTYHDESVG

>contig53087 Frame-1R|Blast-translational activator GCN1, putative [Phytophthora infestans T30-4](gb|EEY69168.1|) 8e-67

MAEQEDVLRSLLDTAVLHPTEVTSVHSFQLEVIETCKTGKLSLMRLASQIIAEVFRLQYR

IAEQHLHALLAEATRNFPSFPEAFSHALCAKLPILFASFAGARVIVLRLSCVVLDEVLSI

NVNLDDLWLGNLLVAQSQLLESTIRESERNQQLARKALLKNLKKHCQILPQHYMVKIVAA

KPEEQYYQLWLTLSMSGLLSKESEEFMWQKYVFWA

>contig53173 Frame-1R|Blast-guanine deaminase, putative [Phytophthora infestans T30-4](gb|EEY69083.1|) 2e-94

MRVIAYKANVVHSLRLGELQVLQPGLVGVNGHGMIEFVVDLTTSPVDMGHYDELVDLGEQ

LLLPGFIDGHAHAPQHAFLGVGMHLPLLKWLETYTFPCESKFQNLDYAETIYEKAVRCHL

KNGTTTCSYFGTVHLKACKVLVDIIEQVGQRAYVGKVNMDRNASPALQEDTQTSIDETRA

FVRYVQSKKSTLLTPVITPRFVPSCSSKLMQALAE

>contig53304 Frame-0F

MTIETRRRVLCHVLPLLTRRYSHTTQSTALATPLSSSSSLNSRGFSNVLEFETLQPLHSP

LTPRDFGGKAALIVNT

>contig53515 Frame-1F

MLDEVQVEGTFVDGTKLVTIHTPIAKVDGDLTLALYGSFLPVPQLEVFGPLSPTSIEPGA

IITPDTTIVLNAGRKTRVLQ

>contig54015 Frame-1F|Blast-nuclear mitotic apparatus protein, putative [Phytophthora infestans T30-4](gb|EEY54191.1|) 2e-76

MQALERAAKQEALVAPLEHALARAKKETEVAQQHSQWVETQLSEKTKTVQELRLDLAKRT

HDLEEFKIRSTEELTSTKRQLESARLANRKIENALIKSKESLKELQASKMHDEELLQAEL

SAQRRIATLYEESAADASARVAELQKLCDSLRKSLTDSE

>contig54587 Frame-0F

MTIVEPVHLPPKWHKRVSKLFYCSPVKIYMN

>contig54604 Frame-2F|Blast-Phosphatidylinositol-3-phosphate5- kinase (Fab-like; PIPK-A1) [Phytophthora infestans T30-4](gb|EEY53276.1|) 2e-06

MQKSDCNFPCSNFGRQCAFNDIKGVYSAMATICGTFRKLTCVCAPSAESPIAAKTSQIPS

SSSGREIALFSAPKGA

>contig54976 Frame-0F

MNKWHDVVLSLTLLERMFMACDAALLIRVPSLMLFLQDDLCRALLRYCRLGACVELEILI

VSLHLVRLVWTKLRSKLKMQIEAL

>contig55131 Frame-2R

MSVNETAISVIIEVQLKSPDSSAWNGSLMLKRTTSVR

>contig55997 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY60170.1|) 1e-159 NOT\_ORF

MLRSDLERLGKWKLSYPDFITLCIERGIPKKQAPEVLQAFHQSGIVFYFGKSDDEDLRHS

VFLQPRSILDVYLKSIGLVPLSSQLFQHQREALLAKIQALEPEHVALVNLSRELEATAKQ

QANRIAYGLSTSLVGAFGLYFWLSFIHFSWDIMEPVTYFTGFGVSILGYAWWSITNQEYE

YENIYHYVYTRRLRKQMSKAKFNHERFKALTEELYKAKAQVAQTEVVLGKYTPLQSTYLH

LLDSSPSLTVSRHEASRPVSD

>contig56282 Frame-0R|Blast-hypothetical protein PITG\_10650 [Phytophthora infestans T30-4](gb|EEY58560.1|) 5e-11

MKRTKFTVSGHDQLRVVYQFLRKQLRLRDSDSL

>contig56813 Frame-0F

MQHFSPSLAGYTSFRDILKRMKLPCHT

>contig57098 Frame-2F|Blast-cleavage induced conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60142.1|) 4e-17

MHPGPANHNEHVAYQVVDDVAQALVFMKNDFAKMQANETR

>contig57159 Frame-2F|Blast-5-formyltetrahydrofolate cyclo-ligase, putative [Phytophthora infestans T30-4](gb|EEY63484.1|) 2e-66

MTATLKSSMRRSMGATIMALPHAEVLKQSQLLTEKVLKLPEFAHARGISVYLEMPKEAAT

FELLEAAFALNKKVYVPKITGQSPEDLKMLQVSSMDDIRSFPKDKWQIPDPPLHLNGGIP

RDDVECVNDIDLVLLPGVAFDRLGGRLGHGKGYYDSFLHRLMKHYSAIGLPPPTTI

>contig57832 Frame-0F

MACIHTHFAFCTTGLRSTKS

>contig58525 Frame-1R

MILSLRSFTNRYYYELGLLRYQFSGYTYTSAHRKRNSVPNPSKTDAMNANTNSTSAFFLG

ATARVKKSAIITSPVRRSATVRKP

>contig59122 Frame-1F

MVGSKNHMISQTFGMMLTWTIKWIFFIAVFWRPIFKSLRSHLSLLKFTAV

>contig59346 Frame-1R

MKFKTTRVQTNGPPSCSSYTSSADACGSHICAIDK

>contig59540 Frame-2R

MDSIWWITIIITSVLVGICIA

>contig00017 Frame-2R|Blast-PREDICTED: hypothetical protein [Monodelphis domestica](ref|XP\_001362167.1|) 6e-20 NOT\_ORF

MEKKTS\*KIKIKN\*KKKERKKERKEKRKKKKEKERKEKKRKKRKKRRKKRKKKERKEKRK

KERKKKKKKKKRAKKKGLP

>contig02367 Frame-2F

MESSKNLKRDPYGFIDLFLSSQILLGRYDPLATHKRIGIHGSQ

>contig07346 Frame-0F

MSTTIDYNSRVSDRALIRIKFAFSSTSTQQKQQ

>contig10636 Frame-1F

MRKGKWTAEESAYCDRLIEEFKKGNLPLSEGTTLRTFLSKLLNCDPMRISKKYTGDQCIG

KIIFRRREDTVNKDDRTSIRKELAELEKTYLEREQYNQRRREKRLESELSRDKNRFVPPR

SIQYAGTGNVTPTTSSQTPAEPSQGFPSTCGSSLTTHEPKSHDTSTNYRTRATPMLVQPP

LHPAPQPNTAINASSHVLYTDHNIVSLHGIAGALSQGPSLMHQDEKLANNGTLETHSDDS

FPRVSSIDSFSCLFPRVVSIENFQHTTSSGLGPMHSSLSYALPESFNSMSSSGFDAPFSG

LPKMGSTTEGLNAYFPRIQSLEHLSSLLQGHGSNTGALPLRDSLEISTSKQFKKEPATTS

GGLSIRHEETIMKEEPRQTETKARISSYSSSSTNDSVVLTIKTSSLTSDINKRLSPSHSA

CSSVGNQIQAPKPVNKMLRSSSGIFPRVPSMDTMPSGTLMDKIPRVASLDKLPRIPSMDK

LHSLNCSEQRIPRVPSTDKLARVPSSDMLSRFNASDFSSFPSFTNLTSLSASTSYDKLSS

LGGFKSGFPRNSSIEDILSLVASSESGLPSNGSALQLNALAAVAGEESSHYERNGGWTTR

SRNRR

>contig11051 Frame-2F

MLRLIYSTTVTVLLLLQCSNAATIFKDEPFGGSETNCQTAKDPSRTVTGLMVCSGDRVDK

IGVFYQGVDEPETLGGP

>contig11763 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57383.1|) 4e-88

MNSVFATCTTIEEKRRITSLEPFDEYADWVLCNAHYALILADNRKCDDKGEQEWTNAFVP

STHQHRYLLTGTCIRLSKASDNVIIRAFQPEDLAAVRAVFENTHLEFGKDSRAVRQFVAN

RLRGPCGDMFDVTQAFQTPTSAGIQISGFWVAEWNQKVVGCVGVKPLNRSSITQDDERSA

ELCRLSVTQAVRRRGVATALIKVAETFAVSCGAFDKICLETIGTMKGSQQLYCSLGYVEQ

LDRQKQHSSFNLVCFHKTL

>contig13394 Frame-1F

MVQRCHQRKEYVELLRQLRRVYVIRDQRKLYFKASTEKKNPQLRFLPINLHLQEMWVGKA

DNVTQASLGSSGTSDSNASAAVYDIVTVGAMAAHVYKFKNGGIFGLEEQYAKLKPRVREP

QGLIGASHQAPLWTEDEQKADDTEWVLGKRMDVCFPQAVAALVTAFTRKVDLALQHARPE

QGLAMLEQLSKLGFLFDVESLVSTHGNEAGMLEDMAGAVNELRNVRFVLVDEQEELSGLD

EESSGNKSPRCLSYRLDEELKHAMSEASDSSNSEANRSNDDHAKRRDMEVKQRQSVHQMS

SGSASSSISSTNLTGIGGVIDVDVFTCMDDALSESSANAGDSEFANATPKSRDHFRSQSS

SLSGVGQRLLSTFIKARNHRLLGGPGNNWVNVQSLAPASVDKLFRYTHLVIRVKLRSGKV

KLNRALRHGGPIKVCPVLFTQGINEKQTLANNTGSSVTRLQDVINANSLKNVRSYCDRYC

NFLSMRQGKTMHRRGNSTDTPLSHLTQGAVSSESSREEVYRFLGELEKLIGTAGRQARKK

RPEILQLSSDLCRSIAGGRVTVCKSAKDRTGMSVTLEQGRILVQHHALREQKKAGIVSVM

RSEGVRIENALKNTGRRVFAFNALQRSLLPEEYRCPPQTSGRNVS

>contig13523 Frame-2R

MGDLSALQVEELLCPRAKVIRMMPQGDLEKAGVPKGILPLHSWATVYGSHVNDQDVEKVM

RIAGIDKSVKVDENATSWAFPSPTKQGPSLIYRFSSHKSDSVAETALEIDNFHTKSNTIV

ANFNDLYELGSQLGGGKFSTVFKGFCRLTGELVAVKVAKGTAQSHEGEDELVAEMGALNR

LKNPNIISQNGFFNEKGKLLLVLEYCDRGSVRHMMDTEKVVSEKLAKEILKQVLSALQYC

HFQGHVHRDIKADNVLLKTNNDGLLVAKVADFGLSEELQLANRRRENMCGTPQYLSPEVV

AGRLYGTPADIWSTGILAYMMLTGLVPFGEAKHEIELLKLISLGAVWYDQPQWNNVSPAA

KRFVQSMLDISPDSRPTAAELLKHEWLHDA

>contig14162 Frame-2R|Blast-30S ribosomal protein S9 [Phytophthora infestans T30-4](gb|EEY60312.1|) 4e-95

MVSVEQERAVRAKEARVAFHNAKNKIVRVRTVDEQGRAYGTGRRKTSSARVWIKPALVPF

MGRIQVNKKDLVDYFVRDFHREEVLKPFSVVDKIGGFDVYCTVKGGGLTGQSGAVRHGIA

RALQAFDPDLRPAMKKAGLMTRDPRMVERKKAGQPKARKKFQWVKR

>contig15279 Frame-0F

MEVLLDELLKDWMARYDLTSASVLFTELYNGVDFKDVLSTPTTCVWFEFDLKLRKRENPG

LKAISLVNLEA

>contig15943 Frame-2F

MGANSFVLFESASGYAIFEVVENEEIGSLLAEVQAAVADVSSFGRTVKLKAFQPFTSAEN

ALENINNISEGLLSDDLKNFLEMNLPKVKTAKKGKYTLGVQDKGLAQAISDDLNVLCNTS

ETTLEIVRGVRMHFATFVKELAKGNLAKAQLGLGHSYSRAKVKFNVNRADNMIIQAIALL

DQMDKDINTFAMRVREWYSWHFPELVKIVNDNYVYARCASFIKNRSSLSEDSLEGLSKIV

LDEDKAQQILHASRSSMGMDMSEIDMINVDNFTTRLVKLAEYRCQLHEYLVSKMSSVAPN

LASLIGESVGARLISHAGSLTNLAKCPASTVQILGAEKALFRALKTRGNTPKYGLLFHST

FIGRAASRNKGRISRYLANKCAIASRIDSFIDEPTTKYGDKMREQVEERLAFYESGAAPR

KNADVMQEVSDELKKAATNSEKKKNKKSKKRPVEDADDRVEEGEQEVPVKKLKKENKNKK

QKTVEKVEETIVATVADAGKKKRKKQKKKSKTSE

>contig16003 Frame-1F|Blast-Arsenite-Antimonite (ArsAB) Efflux Family [Phytophthora infestans T30-4](gb|EEY66916.1|) 1e-122

MAEQEVDVPEASLRNLVAQKSLQWIFVGGKGGVGKTTTSCCLAIQLAAQREKVLIVSTDP

AHNLSDAFGQKFTREPTPVKGFSNLAVMEIDPNVDLEEMNADGVQDNSGMASFMKDLTNS

IPGIDEAMSFAELMKQVQNMDYSVIVFDTAPTGHTLRLLSFPTALDKAFDKILSLKNQFS

GMFSQVSALLGGALPSQEMLLGKLEQTREVIQKVNAQFKDPGRTTFVCVCIPNSYHSMRP

SDLYRSSRSMKSTCII

>contig16331 Frame-0F

MKGYRPVTPSCTRKPSMANCRNFVSSPA

>contig17570 Frame-0R

MESGDSNAVGATPMKTRRGSGGAVYEKYLNIKSNVLPDDDNTASMDKNKDIPNSTDKQEL

EAGEVLLALFVCLNVLVLLNQILRRHRMYRNVQYTAMQVGATTNNGHDMILSKNGESRSP

KRGLPESPLRGRSRSHGRNGIPDHWNEIGRPRSSSRNQPGNGRFNEFNRNNGPYNGPRSP

RDGFGGRPESFGGRPSSPPRSGGNFNRRPGSPPRGGSPRGGFGGRPGSPPRDNFPGRLCS

PPRGRFNGRPGSPPHNSFIGGCRSPRRDYPGNNFRGRSPPRDDFQRGLPRDGPGEVRGSP

RMSGRGPVRSRSRSPPRNGNGFG

>contig17714 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69403.1|) 0.0

MWHSYSISNDVPRVDQCLIKFATCNIYRELDRSTAYLRKYVLRWQKSHQGRLGLREVLWM

AVVFRYCNRLETFYKLKGIPSSDDFFQFKKRLQTLAKRGGDCDLLAGDRELTVDTYLETL

ENFLQNIDEITVAVKRCNTSENTFEALRKFNNNVLGSFTSWQVVCDLMELHMVADDFTTD

KFVWLSLDARKSLIQIFGKNRARPSEFVALTKLLQQRQLQGFQALQVEFPFFMNQKINLK

NIGHALHSFQVYRNMKLLEAKRIDKQEIGTSQPVLYSSRTYMMDSENCEVCMQPENEDEL

VLCDMCQRMFHKNCVNMKELPPASWVCTACKKLQNYPHEGLVMEQEIISIE

>contig19406 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62498.1|) 9e-46

MSSVQEGDVSFAACAACVAAIVLFQYLVSTSRLDVVQKEALNRREDVHPRRKVQHLVTGL

MIYGASGIFGQLAGAAVLLCFAVLFYGINEYRGHNEAFNTLYTKTFRSILRQHEVSRASL

PGSFYFLLGSGISLAVFPPRVARLAILH

>contig19648 Frame-0F

MNTFVSSAIQLTGGARNRQKIARELFPHLFINCFEDDSVSMIGHGAEVDSCDESYQTKRQ

FKRHQELLEAEKLLLHDVVEGEALWFVDKDGNSVRSLDCLGVIDSNAAEVRCTSCTALRS

NAALRTAAAAQYKMATRSGRPRNPINRKFCSGRVCSLLETEFDMQEPYAKVLRDLALAEI

PSALNTWMEMASMGLSGEFETHAVLLGLIEAMVRLKDKEQRGVGLQNMMYSDHLDAFMQS

LDALSSEAYELFQRHLGGRKQKQLVAATLKRSKRKIQSVTMKASQDQLPRGSDDDG

>contig20709 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67655.1|) 1e-06 NOT\_ORF

MLIMLEVTRINP\*MEMQRETSRSGVF\*PAYNDAGRVRG

>contig21001 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68244.1|) 3e-09

MKPCSFFAAGKCRNGKNCKYVHASYENLTESPRPSNLFPNGACINGRVSTRVVEAGTSLL

SDITG

>contig21553 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60283.1|) 8e-09

MRNTVELKQKSSGRSQLGKLWQCVKAGDKSRRL

>contig21962 Frame-1R

MWGLRDTDHEPGGPSHVCGRKRDGFIPILLQECSSLISVRYCI

>contig22181 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70228.1|) 6e-12

MESKDNKGMTWSSVITRCFEGEDHAKMKTCFDVKSHDLLQK

>contig22215 Frame-0F

MEEPSRMRGRIWSRRHHKHRRSTANSHYEEEPHSALSMEGMLKKRLAKMPVMHDRYCVAT

WELDDRDRKCIMLRSYKSRKAYNEQPEKPTSVHQVKCISDWDGKTGFHRYQHAFTVETRD

RKLFQCIAPSAAEKGKWIEFIAIPSAVQSGERMGAGCLVPLRRSQSAESVVDSGKAQSNT

NKLIFKKGHDGIADATHSSDSEDQLDSNRHDKLHRSASGASSNTWELLTADKNEPADWGL

YGEDEGAGEGKSKYEVPDNAKPVLLENDLLDTRREPKTLASDLFLFDDAGSSRFGAVVVK

EAVENNDNEDDEFIDEKFAALEAQKENEKKLKRRAQKLETNRDRYAEMAAVRLANMRKDA

RTPAKYNSHSRLSAESVKSDAELVTNDQALFDDGHEIGALNDMGGRRSTQSRRSYASHVS

SSTSHRRGNIEDESGFTKESDDIEDAVNAHASDTEILAVDELNLRRKKSRAEWRAKKRLL

KEQEDEDRTAFAAAELARAHREEQRNREEAKSREEQKKRDKKHRREVKEKLKHEKAKQRQ

AEAEFQKLMELKQAEEERREQKKRERKEMKKKKRKEKYTSPAERIQKKDQRVAEQAAELG

NEVSRALVVVEKPTEAKLDHEKLAAPKSVLTSNSTVVHTEASGMQHAATTQVANPIAASI

SAPALSSTTQSAGQGMPTHEMIPSAFVNTNSTGPQSLPAYGFAATFGAYHPIYSFPYSYG

GPMGLQPLFTRPPSLSFVNGLGAVGMYEKAVDPELAPKNLHSAQTMIGPQLPPMQERAFA

SSSGNSVNSSLRPP

>contig22578 Frame-1R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY54022.1|) 4e-68

MAFGNKFVMMMDEISTGLDSAATFDIITTQRSIAKKFRKTIVISLLQPSPEVFQLFDDIV

ILNEGHIMYHGPQDEALAYFESLGFKCPPRRDVADFLLDLGTDKQSQYEVSTMPSSSIPR

SASQYAEVFTRSQIYGQMMDELHSPV

>contig22776 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68738.1|) 0.0

MRRSSLRPRQIDIHARMKIIREEEDLEVEDDPATGASQPQTSFQQLVANLKARQQAVGQS

KRKKKDIPIPVILLVPTYDISVPADFDVPTSYVRFQALPRDENVVGFEVMGPETQKVEVD

LDLEDMKWLRHHSKYGLDGDPRYQLSQEQFAQMLDALEKASALLNPNVMTLAEAEDVFAK

RLGMHKTPLNRVTCDVYAYWATKRQKLRRPLLRRFWRQTPLNDTNPHAVFRPREKERYKL

RKHRKNDLEGFRKLQQLRVDFERVRRLLDLVHRRERAKRLQLDFLDEIRRQAEHELTSRG

PDAAVRKLVIPVDEERERHKKKKKKKKKHRDTENGIDYYAGSSALGDAKVGVNEELGAAV

VEGPQIAPSFMEYDTSANFVMEDITDTDGSPRRLRGPVYPSYPLSPPRLMAAIFHQPPKY

RCRGRIGRGGRLIIDRIPVPSSRYYSITETNAPTLKITTSMPGSTVSGITAPQTGVAGVI

SSDSELGLATTNGAILVQDLSEHPPNEKIKSVTSTRLDQIYDLSDSEDETIESLSLSVKE

ATTSITASGGKSLPTALTGPGRGVKFTLDI

>contig22831 Frame-1R|Blast-peroxisomal 2,4-dienoyl-CoA reductase, putative [Phytophthora infestans T30-4](gb|EEY64424.1|) 3e-47

MPIMPRKTLESWSKEMEKKSRFVSDSKL

>contig23685 Frame-2F

MPLLGRSAHALVRASCSHIAKAIATSCPSSSPSLSSVAVRSVATLKTDTLELCSNLHNHV

KARLDYKKLV

>contig23810 Frame-2F

MENAASRFGQHLAHTEKKYRDRAFKKLSVYLTKKINWTPIEWDKLWKALFYCMWMSDKRQ

IQDELSTKLAALVHNLPSPELVLQFVHSFFRTMQREWHGIDGLRLDKFYTLVRKFIRETV

VFLRHQQWNQTYVQTFTTILSTEILSQLPNGLRMHVADVYLIEIHTAAGKDVTTAAFLSL

LEPFVTLLRSEYNVTVCKRICDVVFAALAQSFKFQGPDLESQDETDGEEETTRVFACVDL

AAVQHRLFALASADDVAERNRGALYALYQKLRAITHVDSLQAVQIHEKPANEALLSTTKD

TVKTFQEDDKATESGVTTSGQLFPRCSSCGGFGRGVLSKHKALCGHCTRQEKARKKEATR

SRRKRKAETRTVNQNLVKARKVTFGRSKALRHGVSVKRLKASATRSVVSKDKDELKSVLK

GARIRTNA

>contig23865 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY64219.1|) 1e-17 NOT\_ORF

MLNYEKLHSKTKMRILRDVHHPFVAPLRFSLKSQSRVYL\*HAILL\*DSLYTHMNR

>contig24420 Frame-0R

MMRKSAPPTDVAYFQLIYSLVLDLLPFRFTVFMTCQSSAGALGFFPPV

>contig24569 Frame-1R

MTEFIRTIWQHSAHPRKPTSTTARPVDQLRLPPSAVDTTVSGSCCMETQQMIKLEPPASP

SSSVTESESGKAQRMARVNARRDKRKPLDVADMEHSSMSKKLKTETTLDPSGEERLRAME

AQLEHLDPDSKEAKKKRRLIRNRMSAQLHRERKKAYVGQLEDQLHAKERELKVLQEQLAA

MAVESQQLKQQLGRKGSVEQEPLIKVEPTLIEKVREAALAPSEATVDWAACLDDMDDAMV

GEDLLCDLDESPLTAYGLCSISDDPMAAALAEEEQRQKLQMQTQSHHEIHAAKKNLAMMM

AMMFSVTFCGQSESVANVTSGARFSSMFNAVPVKELSQMSIASRIVACLEKTSWKDFQDV

SSWTASAASAAAAAAMAVSEKKSRARSVANSPSAASDVTDSGSCDSPKELEDLGKSFDTD

LIEEFVYPVDQPFAPALADTNWFGTGVDDFGHSDVENDDEHLKTTVKPIPVTSQLYAKLT

ALWKEKNQVLLTIRNGKNEVTRRSVADMSTIRKGLATGALFSSASNVAVSLKDKLVETQD

RSIMFLYPLSAFSEDQSSDALPPSAFSDHVFLEVSCQLNGVANLVF

>contig24936 Frame-2F

MSSVSIVTMPYELTEECATETLEIIQWALLKEKHYSAVRNPHYLSEVQRHGMTSTWRLRV

CRWMFETAKEFELQMDTVFGALHFLDQYLSVHSVDRVTLQLLGMICMWTASKMHEGKPIL

LEEMALMCERKFSRVQMIDAEAQLVRLIDFRFNPPNVFTMARDFIHELPFNDASRRANCV

ASVFNLLERLVEDTSSIDCSASSLAKAAAQLVAKSEFNLSITQVLKALKTVKIKESSYRA

AFKLVRSAYFGPSSSLPRIQNPHAATVEIQKPIKSPSKSPTAIEQETLSYDNNKRDDTFH

FQYASYLVCPETLTISPCQASPAPSRAAACTTVSIGVAQTASSSTQFESKTERLIKRRRS

LTMQ

>contig25078 Frame-2F

MLKKLSERFPAAAMRLEAYTSTSNLASTENSPSLESISSPNPSNTHSSSPVQNPDVNTAS

CPSPPTLFGEECVSSQSDDLQSSTFKTSLTDRFNSESVSAAASTMLSLMQKAKVVAATAA

KDGADKARKVLDAADMDALQRRLSYALDRSTGEANLDLLNFSYIQDNIVAMGFPNMNLGT

NRTLLRDNPIDLVAMYLNTKHSGHYMIWNLSEETYDYTYFDNQVLEFNFPGHPAPPLGLL

FKICSSIENWLQADDKNLAAVHCLTGKGRTGTVIACYLAWVGLFPNAMESLEFVAEKRQT

SVEKLTIPSQRRYIQYFNHVMDGVKPRSSPLLLRRVIINTIPVFEERRVLEPVLKDSVAE

DGSETIGIEGEALSAKSAKEVTEEDFVETLEEGCCPYLQVFKGGKLVFTTTWQDMEDGNG

VQWANTGDGSISFNVNCMLQGDILIRCRHLTNSGQRVSMFRGAFHTGYIPQGILRLTKAQ

LDGACSDSRFDQDFFVDLIFADVETGDNASSVDASDEAVKTPKSEGVSLNEEDRLAYEDM

LHRDEVFWQDIEDRKRRLQKQREEQLEKKQKEAIAVAEAIARAEAEAAAAEKVQTIREQT

SFSISGLDEDTVVVQKSNRKGSWNEEKDKELMSELESFTSRTQAKNVDVQGDEKTRDATA

SSSKTDSVIDLSEDVEEMKHLEKELELQSLSNDLASLSDNKIDPELELLDAELKGLEDIS

TTGDGADDVMNFGADDFEELEEYLSGLSTK

>contig25715 Frame-2R

MDFWVTYFDFYRRHNSVSSNFMIKGFLNPSRLSTAISDSEINRINELHVSAK

>contig25812 Frame-2R

MVCWRTMRAAMKTSVKHLDLAITGTDSLVKGILGFQATDVNKDTPISTLKEDNLEKLDRD

AHTRNLTGAKRDRSGSPKHD

>contig26358 Frame-2F

MTQGRRHSSADSVGSFHKNRRMRGSMDSTASTNSVSGSACSSVLRVSKEIENIGERVPVS

KKRVTWRFVLAGSEQVHTVMLEHSRLSSKKRLKLDGRRLFSSDQYATNWHYDFHVGDDTL

TSFQVSIRDATLSVVDSTRLEAVYDLVADGVQWDQLAERFLPVAHRHQAASVWSSDMYVR

RVAETQGVLLSDGDDRPPGTLFTWTFAFGVAGRIHKLELRDLEKGEFVVVLDCRELERVR

FEDIHADRWEFDYDLEDHHELDVVVTLVDSDKTYELFIDGSAWRDIGETNFVLEPGWYPV

YSRSRSAVYFRHEQTGNTQWEKPLIDRESGHGTRSEHTFAQVSPESQGCTALLHDRTGGA

RKKSSSPEPESEVGQTASLLGKEPLPSVDEGPEKNEIDLMDFTDVVVQSKPRAFDPFDPT

THLTSAGKEESEHETLPRVDLLSI

>contig26493 Frame-2F

MENPELRRCAKCDKRADSGKELRRCTRCQCTFYCDAQCQRDHWKDHKVSCTPPGNASNGP

GEHKIVWGAKEMSILYGPHTSVPFDDLDIITKHALPIAKVKGETLYPSAVVFRKGDPSGP

DVSELAWLIRALNAQIELVGKQPLFMQNTMEELVGLGDPNREPRKLELKCQTLGFDDHLV

IRNSTVLTMQDVERLRKVITTQQLQVEEKAKELNEERKEGRSESDVDGKDLQENEKGCIA

M

>contig27256 Frame-2F

MVPQQLPSTLSGFQMGHGNNLYNYAQAAPLQTPPGSIQRQHMQHPPQPDFINQFSSNPMA

GLAMNTAQDFLQKQSEMYLPGAYGVWGSLKYYFLVNNSYVKSRLMILLLPFRHKNWRRLN

NRGQDETKPV

>contig27322 Frame-2R

MRFNLQLSVYKDGRQTFAGRQLVRLGAEAGAGRGLELYGT

>contig27906 Frame-0F|Blast-enolase [Phytophthora infestans T30-4](gb|EEY66152.1|) 0.0

MDVAASEFYTGAKDARYDLDFKNENGADSEKISADKLQEIYEGFIAKCANSSKLVSIEDP

FDQDDWDSWVKFTSKVGKDVQIVGDDLTVTNPTRVQKAIELKACNALLLKVNQIGSITES

IEAVTMAKKAGWAIMASHRSGETEDTFIADLAVGLSAGQIKTGAPCRSERLAKYNQLLRI

EEELSAEARYAGDDFRNVDKLGKYSTF

>contig28701 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57234.1|) 1e-06

MTTADSMVGSWKNNFNAVITGNFTFIGVGHVINPDSEFVDYWVVTFATIQNEACNK

>contig29030 Frame-1F

MGCAQSKTEDNVIDASSPEIEVVPAETKPVVAEDSVAEVEQPTTEKIDLPTEPEAETAEE

PTTEQFKIKGHEIDEAGVVFYIVEGKSSSKKRFSDFKALVKALNNPKTLPALPFSGLGSK

LRGKHNPDLIQEREMQLIIVLNAIANDAELANKEAFQKFVQC

>contig30850 Frame-0R|Blast-Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4]gb|EEY68576.1| Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4](gb|EEY61751.1|) 1e-116

MLLAHSFKQFYTAFSCIENDCKFGFKDDNQGTAWLATTGCFIGGIGISYVVDIIIRKLTP

GENMNGTARTQPEPLSFEEGTYELKPPVELAQSHGHDVFIKMDEAAKEKLKRMGILSAIA

VGIHNIPEGMATFVASSEHGWNGLSLAIGVALHNIAEGVAVATPIYFATGSTCRGLLWCF

LSAFAQQLGGLISFAFLGMNAAEGTRGILYGLCAGMMSGISIKEIIPTAFMYANGQLHLV

SSGILGGMILMSICLIFFKYIGV

>contig31710 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68284.1|) 2e-89

MGRKLLALVPSTLPLTVNFGRFHSDAIDNPLTSLYVWTSRPSTESTRSRQLALDRSRHQL

LELQRLQSIGGSRSWFVGNSVVQDGALIVFTPIDSLFLLLDAASGQRTRFLSVYDLLARD

NNTWLLQLQTFRLETINVLCDVQLDGVERGIDDLYIKINESKVISWLKAKVEKVALVLAT

HKLDASKHASAIDESVYLPGYPKKELKTVVTQEDIASYYREAIDVIGDYLSNEWVEALCN

TYK

>contig32654 Frame-0R

MPRKNQMLRVVRPWLLWRLINEAMKSSSLRLPFTKQDYAVNSKMSTLCQSLLR

>contig32759 Frame-0R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY63349.1|) 2e-38

MLYPYRNEQLSRGERTLIVVCSLYITFYVVFLIVMLRDSWGEDMTIFKSVVVYTILAGVL

PSGGKAI

>contig32856 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65502.1|) 5e-30

MEKNCHWKRGRALTSLSHLLFTARFSFFPFADIIRWVAPFLPEFAVFYDLGSGTGKAVLA

ASLVHPFDQAIGIELL

>contig32922 Frame-0R|Blast-cytochrome oxidase assembly protein, putative [Phytophthora infestans T30-4](gb|EEY58076.1|) 1e-96

MTRDIISPDVLKKVTRIRKNLGYVSTALGYTIISGAFVAGIDAGMAFNTFPKMGEHWIPE

NLFALEPVYRNFFENVPLVQLDHRILALSTLTGFAGVYGMARRPHIWSQLPQQSRNALNM

ALAAAGGQVLLGITTLIHCVPFPLAISHQCGAIVLMLTTLWSQHTLNFAKPVKQIAQSAR

NVLPKTL

>contig32997 Frame-1F

MQEEQVETLVEETFGQIEAIMQEMMRGLQNHHAASHTQFENTDNKLTRSLRAHNRV

>contig33323 Frame-1F

MPEAQRNKIIGRRRKKLEKLKNKECGKKVEKRIGLGSQAFLQHLASLGDWQIGVQKSAFD

LRSASLSHFLNELFVRLNSGGVRRKPKIAKGSQDFLPHQMALREKIFNKIRMVFKRHAGV

EIETPAFELKETLTGKYGEDSKLIYDLADQGGELLALRYDLTVPFARFMAMHNCGNIKRY

HIARVYRRDNPQMARGRFREFYQCDFDIAGTYAPMLPDAEVLSIGIEVLQQFPELGPVKV

KLSHRLLLDAIFALCGVPAEKFRTTCSAIDKLDKEPWSEVRRELVEEKGIAAEVADRIEP

FVCKVGSPHELHMELMNENMFGDNMNARRAMDDLKLLFDYLEAMGVLDIITFDLSLARGL

DYYTGLIYEFVLTSPEHLVGSIAAGGRYDNLVGIFSASEQQIPCVGVSIGIERIFGILQA

HAEKQSANTTTPSQVLVASTSDDLIFQRLELCKQLWLANISAEVMQLKNPKFIKQLHYAL

ERGTPYMVVIGEDEVSKGVVKVKEMATKDEVTVPRSDLVAELLRRGCPTTNTLRI

>contig33882 Frame-1F

MTSTPGVDISNHPYSFWTSCRHLVVKRLDRQLRNRNSGLLSDRSTQILCTVDLMSSSYT

>contig34252 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61303.1|) 1e-30

MAVRKDSDDEMILNDLHIETGDQVAVKNLLDDTIIEFFKEKKAYKLHYGWDNAKMILMGL

AVVIAAASHFYKHPTVSEEVFVYSCVIGYFIIQGLLLGYVTFIEKDILVRMTRS

>contig34829 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66779.1|) 4e-55

MIDPFKDKFAYFKDNIQTAEDKEEFDASQYYYHRDEFSSSKGPMSSSSGLSSSGGPPINL

SSFHSLSGELNMGAMDLDTSDAATAQAHGLYSGYTSGLISSGSNSFLGGSGIGRIQASGS

AIPPTQDLQRIYSGLSFQLSTEKKAPDISEFPVLGS

>contig34951 Frame-2R|Blast-26S protease regulatory subunit 4 [Phytophthora infestans T30-4](gb|EEY59610.1|) 0.0

MGQGQSGLPRQTREEAAKKKEDAAKQKKKKFEPRGGAMTRRRRKKKGPSSAVRIPSVYPT

AKCKLRLLKMERIKDFLLMEQEFIQNQEVMKPKQEKDEEERSKVDDLRGTPMGVGTLEEM

IDDNHAIVSSSVGPEYYVGVMSFVNQDMLQPGCSVLLHNKVMSVVGILADDTDPMVSVMK

VDKAPLESYADIGGLESQIQEIKEAVELPLTHPELYEGIGIRPPKGVILYGEPGTGKTLL

AKAVANQTSATFLRIVGSELIQKYLGDGPKLVREMFRVADDHAPSIVFIDEIDAVGSKRY

DSSSGGTREIQRTMLELLNQLDGFDERGDVKVIMATNAIESLDPALIRPGRIDRKIEFPL

PDIKTKRRIFGIHTGRMSLAKDVDLEEFVMSKDELSGADIKAVCTEAGLLALRERRMRVT

QSDFRKAKEKALYKKKANIPEGLYL

>contig35145 Frame-0F|Blast-glycosyltransferase [Phytophthora infestans T30-4](gb|EEY68934.1|) 1e-135

MSNYTEWCQFLAVPSTTYVGQTQGDLKSPLHMDIMLFLLLWGEAGNLRHMPECLCYLYHQ

SLTMLNQDFLGEQKVSEGWYLRQVVRPIWKEASNMQRKNQLGKNLEHTQVRNYDDINEYF

WKKHCLNIDVTQIGDELTKKHTKTYYEHRSIFTLVLNYYRIFQFNMMFMMVLMAIGFISA

ISPSGGQQWFAQFGSMGQVVQPYQPQSVKLTYVGIVFALSSMGFCKTVLEACHGWHLL

>contig35880 Frame-1R

MRASSIKTKSSPLNLCYRKIICLRSYTTLPRSICNGKWHCYISRVTNIHEVPCVSSPCLP

LRLNFA

>contig35989 Frame-1F|Blast-cellulose synthase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY56432.1|) 0.0

MHKQGKRTIKGPMHKSWKRRYFALEKAKIYYFHSHLECRQYFTSRNTDLVVGAIELKDAL

QLRPCARLDLPHRGFEVMTKRRVWVLCPETDEEYRLWFEGVEEAIVACGSGNIIERKLPN

VRKYYMKGITTYRVLYTLFLIFSVIEIFGLVFWFVVGLQPCDASIRTLACADVYDSTPDV

LNCLADPMSGWFTPPDWYMQLAGVDDVACFHHPPIAQWVAWCALVVAEIVSIVLGALYYL

GMWKPVRRGAHYFDEFDPKVPDDLWPKIDVLLCHYSESAEETIDSLLACMNLQYPPHLLQ

IYVLDDGYCITKWTKGSPIPSIELNKEILEKCGDLRQEVAQFMYDRVCDPNEDIEVYAWR

KLHSSANLPSASRPRVVKRADCAVGSFRDDYRYPGLPHVTFIGRVKPQSHCSKAGNINNC

LYNEGADGRYMLLLDSDMQPHPKFVLATLPFFFDDEDRQFKNKYSCSCMGCQNVAKMCCA

SCKIAGVPEERISYCSKECFENAMHVQSDLHRRQVNGTLSDVRATKKELRCMNCNSKLGK

SAVCRKCNTKNNNGDADMTILHTYSDDVRDNAVGFVQTPQYFRDCVQLQIGDPLGHRNST

FYDAVQTGQDGYDCASFTGTNALVRREALDSIGGIQYGTLTEDCYTGERLVSMGWKALYF

RKDFEGEAQERVRLAEGTIPDSVAGAMAQRKRHAKGNFQTLLMKKNKNVADPEWKRPHVD

IPKYRKPNTFMRLVFYLNSTLYPIDSIAVILVYYITLYFLYTGYAPIYVNGLRILIALVP

KLIIQGLLSAMSTRGVENNDVVRSQETRFVYAFTNFTAMLGAIVWKFTGRKSKWVNKQDA

SRGSLAELPNVLLFSGAVFGVIWATVRYIVSYYNRVFSHGDSMLCAAILMGLHIAYNLGP

SVRMSIQEYFGWSYQSLMDQGNFMGSISIAVGLMFIALWVQVEKPASG

>contig36203 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59024.1|) 1e-117

MASASPKTTKGSAPQTPKRSPPRSSPSPSPSCGLDVVNADELTALITAVKFAHPDFGVKR

VHDQVLSHGGKFASVPMKRVRRYMHKLGMNSPLGDDDKTPVKLMTIGGDSISKREEGPES

SGTTDDMVWLPVKLDEPASKLQDFPYQAVIRMTTSEEGDAEGSLGEIYKIQVAVDVNGAL

STIHPMLVYNKARSRKTFLHPDSPAYLPVQRLVAEQGQKGAVGGSKAYFWGRYFKIEDML

YINTVKVAPAQQW

>contig36298 Frame-2F

MRSLYTRRNLERDLRAQCFFKAQYKSYCGIQLNCKLFKLLIDCCKSAMWHF

>contig36412 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63195.1|) 8e-17

MEPYIRVKRRNQTVFLDVQLSDSFLSVKEKLGVLFHLPPTSIRLWQGPS

>contig36881 Frame-1R|Blast-cleavage and polyadenylation specificity factor subunit, putative [Phytophthora infestans T30-4](gb|EEY70241.1|) 1e-130

MMEILKTIRNGGNVLIPTDSSGRVLELMRVLDQYWIQNKLRDPIALLHDMSYYTPKAAQA

MLEWCNDRIAKNFDVGRQNPFQFTHVHLVHTLEELDALPNPKVVLATSPSLECGFAKDIF

IRWAPDYRNSIIFTSTTPDMSFASRVQKLTKDSSEKATISCSVTKSIFLEGAELALYDVK

ERKRLRTEAEIKAKEMEEAAMEDMMMGIEDFESESEEEDTTQHEVQLRGTFKVGLGQFAS

IQHPMFFAVERKIEWDEYGD

>contig36926 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57380.1|) 3e-15

MPEADAKVVNVESAGELPMPRYSYLEIKEAQRVCGEKMNAAALKECGSVSVAQQQIFRAH

VNDLCATVFAAALRKYNPKDK

>contig37217 Frame-2F

MATMVLSHLLIRHDYLCGRRDAAPCSVSTEHQIGIQARIQAQFQIGTVSERKKVVNEETA

MWSALFVRGVWGTGLLKWYTTVAYTALSGEERVTEEVILAHWEANNLEVALPLLLMCPFD

GLREKYVDRTLPVVRQLPQGSHSWSTAMELALLRFDMAMLLQHNLYSSIVAFLKQNSSTA

PALWTSSGAYVVSALVNQCEFAAAGRLTCALRHTHPLLWDLENARLVLGSYLRELATSPV

PNSHESSQYLEFAHLQHEVYNQTYRRFANALLQEEHA

>contig37899 Frame-1F|Blast-guanylate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY53008.1|) 4e-19

MTAADMPAMRPLPFVLVDDDGSFRVNLEACSLLQKVKSPLVIVAVAGLYRTGKSFLLNLL

VQGISRS

>contig37914 Frame-0R

MRGQVCGVVGVEELKNCADFVKAYDWYLEKYPDRSKAYAEFVATDLPSIKLMAYSPKDNC

AFHALKMAFELMGGLDEAVATLGFLHDAAET

>contig38119 Frame-1R

MSPESSINFWIQVDLANAMVPAIYNTFCLQFILLINSCRIYRFCKGRFVL

>contig38447 Frame-1R

MLRSHILMFITALVTRAVSADVKTTSELRRLVTLSRHGSRAPNDVVKIICPRNKANMDAY

EVPPTQLTEIGMNQLLSVGEHVRIMYMVDELHHKEAFLSRSLNGVNNSHFETYFRADAAT

RCSQSAAALGYGLYPDGTGPRGFSHEPVPITMQLVENEHAFAAPKGPCKNVLNDDLAVYA

RKRAPELFDKYRNVLDKVSEVCGVAIEDIPSLVDSEDVVLGVKDLADMFVFDRDEGLPLP

EGMTVEAREQLEQLAFTNLMERYFSTDRQVTYWVGGFSDLLLTTFQDGAVPTAPSPTDYR

YFSFHGHRELLHGLGMMLGWDFHLKGMPTALNVSAIHPGTTMIFELRARPLDKVVAKKLV

PKEMYFVRTFIWSPFTEREQIKLTKCSALDCALEEFSSIITKHIAKTGTWKTICDYNEPS

VGQGQVAPAQKASLDSQYKFSFYFFLCAIGIGIVLVFTLISYKVYIARHNGYAVV

>contig38623 Frame-0R

MFTGSNRASVSHDIGAFAARATSMSGNRHAVTRFRDIPYLIDLYTSILVSLKLNTNDALH

SPLKKRFHSVSLASHNVWLQTLINKASPW

>contig38964 Frame-1F|Blast-PREDICTED: hypothetical protein [Apis mellifera](ref|XP\_001121792.1|) 9e-13

MIVPIKVDAAAKEWSVLEFQGDLLPSDSANTLSLREIDVGTLRYGDGGEITLRIGNHILS

GKVAKLAKPFAILQKDCGNGDGDVVMTDATIEVATQVKYEVVGIARTRVLFDSRPKPVLD

>contig39790 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55530.1|) 1e-139

MTDPAKWQALMKWTMKQTDGTTPTEVTPISEEKRQFLEKVMNEGVMDENERVKDILRILE

GEDPRLVFATEDGTIADENTDVSPEELAQYKDALLDELLTRIDQIDNAQNFVKMGGLRVM

MNVIHKYRPQSSRALAAEVCAVVVQNNPFCQDAAVDSGLLEVLCSQAREDEDVTCRVKAL

LCISCLVRHHAAAESRLLSSSCNGLEVLQSNLKSATDIRLQRKSLFLLRYLIRNSRSTAD

LVLQKDFYVQSVAALISYKDVDLCESAVEGLVEFAMIGPDFMAACKQSEEVIVAKCNSCI

NHIDALNGESRDVAQETKVQVQNLKKVLML

>contig39853 Frame-2F|Blast-elongation of very long chain fatty acids protein, putative [Phytophthora infestans T30-4](gb|EEY60010.1|) 1e-153

MEMASNLLESYKQWAGGMDVVLMDWVDPTLRYRLSPMRDYFLADFGTVFALCVAYLTFVV

VGTLVMKSGMPAFNMAPLQFIYNPAQVVLCSYMTVEAILQARRNGFSATPCNAFDHEKPV

MGNLMYIFYLSKVLDFCDTFFIVLGKKWKQLSVLHVYHHVTVFFCYWANFRTSYDGDLYM

TIVLNGGVHAIMYMYYFVSSHTRNIWWKPYLTTVQMIQFLLMNAQGYLMVSRSCPGMPYK

ISVMYLIYVQSLFWLFMNFFIMNYCLNTRKPKSVEAVKKTL

>contig40130 Frame-0F

MGGSTTASSGDTSRVLQEVEYQGRVGELVSAVKTMCGHDKGRFTLWFLHKIYDETTFFRF

SDYGSVEHVMRLVCLVLEIVDVLSLLEVLLHFLRRSPCFLVKNVVLAMIERNELAFCATD

QIPFLLQSFVDRFHQIPKHADDKAGNVAQFFCKMYYAHIKNKEIAKLDLPFALLKPIAET

ARKNQDATTANGTVNGTSSSANASGANGSHKRELSLDATNPIVRIPPPREVLPIELKTAL

ARSFKALQARSFDGPNVDGKQTPATPGAGNGAPLESLNNLGQDAQASDFQTVFEPNHASL

SWQEVVGEASATAEAKCRDSAIDFAVNSINMSMTSSSVGSTNANATRERRTPNYVFFFRA

ALSEAMDKWMANISARIKSNCKRPITTPHYVHRCVRLIREVVEQHPDNNEEFRDKFSNTL

VVWLQKEVLPGFAGSDTPKRSRNPFLNADNSKEAFVLNQKGRLDRLQYGLKSFLVSLIVH

QVLDLSQVLRLVLVPLFPRLRRASRDPPPNLPTQLLAMALVFQLFSEPPQNLLLDPQKLV

MFDEPLTKYHLRFLRSQVPACLMFPLCFRLCQISYQMEDNFLLRKREERGVLASATLFNL

TSDGIVRDTIFHDTKEAREKHILPVYHKKQWHTAVLLTHFFRSPSSPAEDS

>contig40145 Frame-1R

MQVLRFDYHYHLLSTTQIQDTKTLCWIPVAKMNESIQNSRLEIVHTCRHGTLGLWTISTD

SLSSLRHELSMSKFLVKTCVGSNEPVRVYSFQDGFPAISKKANEDASVEKKVLFHLIIGR

NDALSSSIYEVTQRARARRERQQRTDAAMTSVENAARGNLTASTRASNVSVLATALTPVR

IKRESSGTDVQSGSVQTEKRNQDCFFETLSYQFLMDIPIVVKGLSNGNVYINLLSHEYSS

NSTKKTGTHFACHSGRITALAHCFWGVNSTASQKLKDKTDNTANGTQFVSSHFFNLISEQ

NRSKQDYSFQNAYNPFNSRLMDTSNLKTPLDSDALMKSQPSIKLFVFSGGTDGVFRVLEL

TIYRSADGRIQYQAAIMQRFRNHRGAIERIEVSPRKKGCNKEVGGLQDPDRLVATIGIDH

KVVIYAPQDSMNRLEWACLLEFAENGDQIGRLEWHFERGLLYIECDDLMVYVWSLDTGIL

ERIIPTALLFDESNASGALKTDTLSCSHVDYSSLIIGGKTVQVMEFAVLSSADRLKQNWT

SYYSSLMSKTGVNSIDVTKETFSEYATGSMELFLLSLVLSWGIDDTIDQSCQSILGVTPI

NALYSCALQEFRSKALTIPVPWATTDLKTCDPTVAPVSPAFARNWQHSTALSASIALGIV

SLCLSCMESNHARTVQGPTFSVSREAFQVLWSQLITLHSIVLPESTPLFQEPAL

>contig40259 Frame-0R|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72331.1|) 8e-08

MFVPPNQAFRVRSRLLASRQPSGLCLGFE

>contig40880 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64438.1|) 1e-26

MVSLCGSLFLLVVGVLFKLQPEYMKISKNVKSAMPIFESAALYAALFVASSFMYLKESKK

TVIESYDARGSTFDERQGLLAQPVVTYS

>contig41146 Frame-1F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY58155.1|) 7e-83

MTLGALTFLTSVCILGNYTLLSYTVPTDLPQDIAAGATGIMHAIGYFSTGLSSAVMGNVI

DEAGYSMWIVSLIIASVLSGVFVKLGSHFSRRKATESQAEPMTIVTMTHASDELSSCSVS

FENDFAMVGETPTHVDPSKSV

>contig41533 Frame-0R

MNHNCSRLYAFLQQTCMILCVVPFGVVHVFMLSFKAINRMRILVAAKLAEHKRTKKLELV

RKIGHD

>contig41951 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62019.1|) 1e-101

MSIRYALAYALSEATIELNERLEIQTRLRFKFHKLMATAITEATTSTSASACASGFTIWS

HPFEFINERMTSCLERLPLLASFLESGNESQNDALDIDDFETQRNLKHLEMLVPRLAAEL

RVLQQSLAYNERALRPLQLRTRQLHGEAQLARFEVEETQLFKDKLADQLLQIMLTSEKLK

NERMQQLFAEVDTNEKIST

>contig42020 Frame-0F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY59855.1|) 1e-125

MNNSIFNNVQDCDARPVVSGTCLMFPGHTKTQWTIAVSSWIVGGMLGSLLIGRVSNKFGR

KRTMMANCLFMIAGGAIQATAHSIAVFTIGRVLAGIAAGGSAAVIPGFIGEICPPHLRIQ

LGVCFQISVTLGHLLVAITFFFASTSMGWRYIAGFPIILGSVFLGLAPVVLVESPAWLLM

VNNSAEAEEALAQLYGEDNVYTAKKWINQQQQDPD

>contig42055 Frame-0R

MSHPSSEEPPAITLETTDVEGMMQSHRRKNFQ

>contig42217 Frame-2F|Blast-hormone-sensitive lipase, putative [Phytophthora infestans T30-4](gb|EEY58722.1|) 1e-124

MNSSGPFRDSVRSQSSVQLMGFIDHCIRVNVQETTEEGELRIRGYETLLGTSTAVLSCIQ

VLRRIIREYAYGRVGRELQHLSLTVASFERVLYTFIKEEIVVASKTYASRPPVDFRTKTA

LKDIIPLIPTDERYTILSGGVASLLRHATKSLEETKHVLEELQSGYNPERENRWSRTSIV

LSLVFVFLCKKFRIRSSFKQFVLQVMPTQQMIKWGLVVLVATDYYKRAMYRFSTLRRIKV

HHARVLMALRLFL

>contig42473 Frame-2F

MVQKMPEPMNVVDNDVALATMERTFTADQVYGSPIGRSQFLPVVSSPLSSTSFVSLEGRM

ATPLSTTSRSTVHSEMPLPMRSLSPADEVEKMRGSSGMKTSKVNMLRGNFHLSPGRGRKC

TTVLPPPYLREPSESLTKRRAHSKTFHAFAQSLSFSFANNSLTDR

>contig42639 Frame-2R

MATDQNKALMRAILAKIVSSAKYKLVLGSSNWKDLLSFLQAIGESSMPSDSSVRFESVTN

EVGKDFAILPPPKKQKVLPT

>contig43786 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61073.1|) 2e-55

MILVDKHQLLTPQSTVGRKRKIVFGDECWEKRARGSWTELEYEIVLEEATMLCEEIELLL

FVAVDLCHDLHCDDRRARSFSIALQEIRVVLTSFEPLTVVRIREMCHQMLNIMQYLCCVH

YNDFALVDMQDQLQKCRNHFMLFICKNAAMIGL

>contig43881 Frame-1R

MERCLVLDLDPRYDLILGIAFEHHEPWIDWRSRTLGATRNVPSKVLESHESTFARQQKRY

QRGSLNESVSVLDIGMSELINSNVNKH

>contig44079 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61355.1|) 2e-56

MAEQLSACARQLFEGVSGSNEQCAANAWLIQFQTRKEAWQAALELLENPVRDPQTQQILA

APELVAMQILRLKTQYEWAHINEAQQQVVLRPC

>contig44228 Frame-0R

MDHYRALCVLAGQNVTWKSDVTLFGGKTLYLERCSICTPLLP

>contig44765 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59495.1|) 6e-89

MGMGYPVDGVQNMAFTVGFLAYLSYPMYIYGNASLLTDVQITMNDGVKVNQDTLYDSAGS

LETQYSAKYETFMDIEAGTGKTMHAMKRLMASYALAPSNSNSSLAMSDVLYPALQTEVII

PVYWVEEGSNITDHLVDNYDSLETLLDSMLPVLIVSLVVGVLLGSAGVFVMRRRRHQNVK

L

>contig44985 Frame-0R

MLSSLPAMTVAAMKSSLTPCETRMVEAAREAQDSAIASLYAATVCSISRRAMGSVIAKIL

QILEDDVKHTLPDKFARQLNTTSILRLVGGIMCTPPGNAFLPRYMMSLASQLEWLFEGCT

RYDKQLKSSCNRDSLFQRRLRVKLAVRLQLVGVIGPGKHAVLTISYRDRIVKTLFACLGT

SIVSTGPGLSLFSWILDLIPIVNASVLHDRQFELVEALQLPNELKRRVWSVLPRPMNMFG

AANVFVARTAKSSAAVSKDAKPEYVPMDPWTLLEHVPNLPSDALVPALIHPVPKRPRRVF

RCV

>contig45850 Frame-1R

MSILVPLPRADTNKPEFLNGVLRLFPYLPCPTSASINLVFDSSSLSRRPVISLISTRSSD

ASSLMVFALSTAWKTSGLLNSSTSSHKRPLRDRWGRCCFRMHAVARAALACRMLWAQNLI

KINT

>contig46147 Frame-0R

MHRTFLNMARCMVFVSNLPLCYWEDDVDYFTYILNRSPTRPNLCRASPIEVLTVQVPD

>contig46419 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60628.1|) 9e-34

MLMTGPHVVLDLYCNTCWSPVGWKYREARNASEKYKEGKFILELARTNQSSEAR

>contig46594 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63474.1|) 6e-45

MFERLSRVYEEVEELQDRVIDEVKKREDLETHLHQLKCDNLSAFTEQLEQMTQIRDSVGS

VVRRSENDAIQHTTECQKLMVHQQELASRIDNSLLLKAEARVHQIYRIGRKFVPHRAFKV

ISVVLFGLRVWDILRRHRFPQFVAQHLIRWLVKFLALDGASVPQLSNSAAV

>contig46837 Frame-2F

MSTCDTFFKHPRCGSSHTIFLQESYDLVKESLSTRTVVDATRATSEIR

>contig47148 Frame-2F|Blast-beta-galactosidase, putative [Phytophthora infestans T30-4](gb|EEY58470.1|) 7e-52

MILTDQDGDYEELLPFDAPSVPLKPRRHLQRKDIALLAVILFVTCFVGIRPPAPRVSNPL

LVSRKSRTYQYLTYDDIDTTKRQVGYSVTYSPRGFTIDGRPTLLLGGSIHYPRSSPGQWK

QLLQEAKRDGLNHIEM

>contig47306 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63969.1|) 1e-101 NOT\_ORF

MEGNPYACEHPTCAKTFCSPKSLKKHIRLWHNPGGKRTSMEQQLRERIIKMATRNKEKTR

RFESTVRTLMDENESLKRRIVELESCRLQQHQ\*QHLGSLQQ

>contig47430 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57113.1|) 2e-29

MVICSTTSNREELEQLLIEDGFPVVRILSEDLERVLVKTETMSSYVGPQSLRDLYKSKLS

SHAGN

>contig47856 Frame-2R

MDTLRNVELHLSRVVVIVQQRLLSRDALDHNRAPSNVESAQVLFNIDRLQETLRVATKML

AARVSQFSALATSNENVQAPDSSSNINLASDTDTEDEVDRQKETVLCVGKKRMRESDTGD

EKEDPCANRSNMQNEREEQLEASIQDYAESVAEAAQIYAMMPPELLQTRLNAFGRTPFIA

MCTLAKFIEDGGIPRLVVAESFRDTTILLPPVVAQNQEFKGTSRRWIFKISKRLRLILDL

AKKSCHLPAPLKDPQLKRARSALIDYEAVSNQLYKMSTFIKKVESQSTELTAGTIETSLE

RLVCAYHGYFKLFGRLQRYGMTQPQSEECWAQFARIGNALAQWIQRAQQMILPPKLRANL

SRFSWELRKFAEKYPNRVPTTLLAVSCAFTELMQPEAELKHEK

>contig47922 Frame-0F

MRRSGDDGVSNGAGRKRVGEHHDGSFNVYMSHKVQKLRGQNESFAAAMSSSPCGNTTAIF

RGVHVYVDGYTVPSKE

>contig48196 Frame-0F|Blast-mevalonate kinase, putative [Phytophthora infestans T30-4](gb|EEY57207.1|) 9e-10

MLRGVSSIVSVGINQHGVPSFSMPAPVAEHPEIVRVSAPGKLLLFGEHAVVYGCPAIAAA

LSDMRIQVTI

>contig48329 Frame-2F

MLAYEKPKFSLAEALNVLRPSYGLKYLETAEDAWLSIETQAQFDAILANDTIASLSPWPV

FVAKEPLSTRRGGKNVFLAVSAADDNSILRAIGVHIRPLADVFEGFVVGVNQLREVNDTS

SFTSVNAHETTPLLENSHHQSPSRRSVCRLSNEGFSIRRKKSSFLAQIDDSFVLSIPLDQ

SPRSMLPSSDRKEIGLSGQERQAYLIELPHVRTSTASSSPSNELSPQLMLAVPDSGALYK

HPTFLRRFMSLPTDICNISVETVELRNNTMALQLLVTRQVPLIGYVLLVAALVSISYMGT

ALNLQQNVNPFIQLFWRTTASLLVLLPLAAIAVYHDGLPHFSTQMLLRFSICALSYAVYV

MTFLWSVSHTSIDHAYIFNNCHALLSE

>contig48563 Frame-1F

MFTTPSTKITLPAPVLPWVEKYRPKNVDEISHQEHVVATLKTSIANGQLPHLLFYGPPGT

GKTSTIVAVGRQLFGSDFRKNGRFLELNASDDRGIKVVREKVKSFAQGAIGSASGLPPFK

IIVLDEADSMTGDAQSALRRMMENYSKVTRFCLICNYVSRIIEPVASRCAKFRFAPLQKI

SMASRVRYIASEEHVNVSDAVLNLLLECSNGDLRKAINYLQSAKQLCGENGVSEDDVIAV

AGLAPPEVLQQFWASLASNSFEKMQTDIEGILLSGYPVLTILRQLADDIHTHDKLDDVQK

AKICLRIAENDKKLVDGASEHFQLLDIASYAMRVYHTPS

>contig48952 Frame-0F|Blast-ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY54768.1|) 4e-25

MVRQRQPGHRQRGAGTVSVSKEDTIRQGVMCKEWQRTPMQLLQEFCHSKKRRNAFYARAR

SK

>contig49414 Frame-0F|Blast-nardilysin, putative [Phytophthora infestans T30-4](gb|EEY61296.1|) 2e-13 NOT\_ORF

MVRSVMRLMCSTLIPRPSFMV

>contig49599 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64642.1|) 6e-49

MDANTTEVAAAEMRIAQHRDNAARAKAELAVTLDELKAAQDQLLVKRLDDAIEEQRKVEQ

EALAYSKNVNSLYQRAVKWKADQKRFQSSLKELDQFAKWAVATEHDLHAIAGNLEYVWAV

LEKEQETMVNSGHAQAQSSST

>contig49605 Frame-0F

MGPFVSVPLSVLPPRSKLHWDLCEFAAQLQADSDARFSAQLGVQRLCTATVQSLWPRAQV

RPYGSHVTRLVLP

>contig49670 Frame-2R|Blast-nucleolar GTP-binding protein 1 [Phytophthora infestans T30-4](gb|EEY57350.1|) 1e-159

MVVYNFKKIQTVPTANDFIDIVLTRTQRKTPTVIHPTYAISRIRAFYMRKVKFTQQTCQE

KLSQIIEDFPRLDDLHPFYADLINILYDRDHYKLALGQVNTARALIDNIAKDYVRMIKYG

DTLYRCKQLKRAALGRMCTLLKKQKASLEYLEEVRKHLSRLPSIDPNTRTLLITGYPNVG

KSSFMNKVTRADVDVQPYAFTTKALYVGHLDYKYLRWQVIDTPGILDHSLEDRNTIEMQA

VTALAHLQASVLFFMDISEQCGFTIEQQLSLFENIRPLFANKPLV

>contig50324 Frame-2F

MDQALVTLQKHKQKQTNASSSFILSFADLHEIAFQLFLDTNVHTKFTCDVDASAKYVALL

TREFVNAASRATANEERLESVCRYTSFRVTPRGERAS

>contig50522 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56218.1|) 4e-16

MRFDGLRTRSASALPKPKPAAANVRPQRGHSVLPPSSMPIPHAMKPTMPVPASPLADPSS

AASTKPP

>contig50711 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57344.1|) 3e-39

MVLDDRLLPFLRVLHAFVTRRRQLGMLDDKEMLQWLPFVLTACCFVSKADLPGADLMQSV

TLADKTLVAAVDLTKAEDLRSLIAKYVAQIVALCSQDVNKQQWVQAASINKKIMLKVVE

>contig51341 Frame-1F

MNHLRQGFGRRNARAVKIRSRCLSH

>contig52090 Frame-1R|Blast-cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|EEY66756.1|) 1e-34

MDWTESGCVVGVKNQGQCGSCWVFAAVAALESAICLAGKPLVSLSEQQLVDCGTSTDACE

GGYPSDALTYIQRSGSVCTDRTYPYTSGESGKSNQC

>contig52432 Frame-2F

MESSEMASPVPPPDAQLLHTSSTSPARDLSLHEVGVTEAVSSSIDFNNADVDTIAAEDDE

SCSEVSMRETNRTTTASLSAPNAPTPLDATTSPSLLSTRSSNDHLITEFPGASTQQQDDS

EGTDVVPQLVRIDSARIAP

>contig52487 Frame-0F|Blast-phosphatidylinositol kinase (PIK-L4) [Phytophthora infestans T30-4](gb|EEY63983.1|) 1e-113

MHAQATNSLYALTEKAKLLVSQDRMYEALQILEPVDIDTSLLDFNVDDRHLCAKNLLLAT

NWMQESSQRQGQKVIERYQAVIRFDPTWEKGYFYLAKYYEYLLSVSHPDALSGSISCDDA

AELLVDSVFHTHLINLMKNYVFALAHGTKFVFQSLPRLLTLWFDYGEILYGSSSGRAGYK

ASKALRQIEIGQSQSTNEQHVLNDIMDVVDEAVESLPAYEWLVCFPQVTSRICHPNPVVV

NGVKRIMIQVIMA

>contig52634 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67851.1|) 3e-13

MSLEIVEQFLALEQSYASVNEAVKRHIRRQVTHFDRAIQNVRKQHQSQLQHVVEESLAEL

KLVRG

>contig52995 Frame-0F

MQTYEHSAAIAKRCITVFRNMAAADDFKSTILQSGGVKQTLLVMHRHQADASIQQNACAT

LAAIALRSPTNSHALIELGAARQISRAIKIHCHNVAVLRQASLAVRNIVARSIELRSRFL

HDEPEIEPLLREAQQYRGCGDEAYAALRDLGCKIQLSSFGAIAGTSRSENAGPCFNPVQ

>contig53000 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59223.1|) 5e-17

MRFLYTIWRKPVLFEITRKSGCLFSHFGSHRITVEKLITSLRAWTCDLETWNTTKDPVAL

FASNSGVSALQNRKTKSRVDDPMLESIGLQLQGLRSMSETLTALFSAAQYELLSTDHA

>contig53075 Frame-0F

MTNLQLPLANIQDTCEHTHGVKTVARKLDGTLVATENAGVASAAAPEPCYRWQPHHRFDA

GARLSRVW

>contig53109 Frame-0F

MSQQLLCALVYHTSIATLHGKQTDVLSEKLRNHVSLLVSATRLTIS

>contig53750 Frame-1F

MNAASGKYMQSGISAPKAGIVPLIVASSCDAFAAREDMAVVHKRISRDCSDRPSLCENSV

VSDTTMSSSEHCSSSDDSSSEEPDDDNGAHVLSDDGERVTDEHTTHQETCKYLDKPRV

>contig53974 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68139.1|) 1e-34

MHAPTESGVLIENEEFQIEGSMSVEEAITHRIKRAQAEGV

>contig54027 Frame-1R|Blast-DNA ligase, putative [Phytophthora infestans T30-4](gb|EEY68207.1|) 6e-31

MMTAWIDCVTLAYAQHPNFCVLAESVHASQHNDNVSRRIEWMHHQALPTTGVPVLTMSAY

PVSSIAAVLDRVIKTKSRTATCEYKYDGV

>contig54225 Frame-0F|Blast-ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY57180.1|) 8e-44

MGIGDSLTGFQIRLESRMTRHTRLLFCTTGILLRKLQDPRTLGEYVSHVIVDEVHERDLQ

SDVLLALLRQFLAENNAARRLKFGGTLPPLKVILMSATLQAASFQEYFGGAAVC

>contig54409 Frame-2R

MRVGAAVAVVLAGSSVYSKPSLKATRLNALDVINRDAQINCTDMKILAAKTKSKPNVRDE

ATE

>contig54500 Frame-2F

MKNGVEAHNLQVAVKVSLGKVQNVTQSDSENDESICGFDESVEAACAPSYVDSNQGAYML

AKSHSVARLSITKDNGR

>contig54575 Frame-0R|Blast-putative CENP-B/ARS binding protein-like protein [Arabidopsis thaliana](gb|AAD14510.1|) 3e-28 NOT\_ORF

MAGILYRRFGESGSVDMVAVKDTLPPLHEVLNQYDWKEIYNMDETGLFYRMQADNSLATR

QLERR\*KTKNG

>contig54683 Frame-0F|Blast-glycerophosphodiesterase, putative [Phytophthora infestans T30-4](gb|EEY60528.1|) 4e-15

MQSSYDSRVRSLQFTVGSGIQDLDEDITTANLLSPVGGRYVRLQYEGVSCALQFAELEVY

TQDPVALIDIKDR

>contig54966 Frame-2F

MSSRRLELPSRSPIRAEECTKKTPPKVEPSIEIVKSNRGERIEQELENPDIGSNRFRQAE

QSEAALRRQLTADKEAKAKELLQSGERVRAVARDRSRPPLPSA

>contig55213 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63617.1|) 8e-17

MADKLDDYVIQRRLAPALFGDVLLCEHKPTGDLVAVKRVLQSAADAQLTL

>contig56638 Frame-0R

MKVVQQVATALLTLSLTAASIINTEQIFSPTIGGNNDSM

>contig56744 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70346.1|) 7e-20

MSSCSGVTMCLAEGATLCNVLAESCPPCLYVLTGGEYSCYSRNPTQKCPYPSTYAECDKL

NPTPLNTTLSNTDNPNDEARSITPSNPSTTAEISTNPLVNTTTPSFESPRIPTN

>contig56869 Frame-1F|Blast-mitochondrial 2-oxoglutarate/malate carrier protein, putative [Phytophthora infestans T30-4](gb|EEY67662.1|) 2e-57

MRFAVYHFLKDEAVRRNDGRPIPTGYNVILGMIGGILGGACGNPADIVNIRMQADSRMPR

ERRRNYKHAVDGLVRIKREEGLDALLLGLKPNMIRAMLLTTGQITAY

>contig56920 Frame-1F

MEAISKLLGVQTDAAVAVTSAVAVT

>contig56955 Frame-1R|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY69285.1|) 1e-07

MIEPYATRVPYMVGIGNRKCPVYSI

>contig57307-0 Frame-0F0

MVKSCLSVVWPFSREYRNASWVKGRNVACTIAPTHFL

>contig57307-1 Frame-1R1

MRGGNCAGNVPSFNPAGVSIFTAERPND

>contig57596 Frame-0F|Blast-mitochondrial carnitine/acylcarnitine carrier protein, putative [Phytophthora infestans T30-4](gb|EEY55598.1|) 4e-59

MARAFPANAACFLGVEFSKKFLNYFGVY

>contig58755-0 Frame-1F0

MERAVGGDLALFNVNTLVHFR

>contig58755-1 Frame-0R1

MHERIHVKQRQVASNCSLHCT

>contig59011 Frame-2R

MKALKHSIKRVEHHWKPPFDTLGEEDVYHAFERNSTGQPSNLF

>contig00672 Frame-1F

MNENVVLQLSYAGETHEMTISLRSSSPKDDLSYELVLAKVQETFPQLAHKCWTLVYRDDE

GDVVTLSHTLEFDEACRVFLAMSPKDKDTPRTLHFCVLQRISLREKVVAPVLQKIVELAR

DAATYMRNSDRTSTGRCPLVRLANVAILQAGVTINNIRNSDVLGRGRASLGISAAHTRTL

LLSARSGMSSQFRRASSVVSAGIERRRSSSGVTSAFDSTPFSKPHSVHQQTSMPSAEVAE

TVDLRQTELPVLVAEMTVNNSDEQPPALILAADVEELQEPAAVYESDTDTLCDDDDREWD

VVNTTGHSENIIAETDEEWSRELQVIREVLTHVDEERCCELLCQYDGDVQTVLMELTDL

>contig04908 Frame-0F

MVFKDQDLVVPDHVTLSKERQKALTVTADRVVAETLHAYEHFIAADRRFDLRLWKHVKSR

EKVHLYRTRRVNSDLMRLAEKEVSRPRFLSSTTIEQHEREAHAAGRPHAFTPDDEDIEPD

HGTDNSGSSASTSQSHHVHSSSSDNGSFSIFPEESVLAKIKPSNCPLVAAIGTIEGAIDD

VAFGCLAPTRETWCERNSYVKNDGFDGRKILASFQFPSPEDPFRYVGIKWATRDIATFVS

RRDILFIESSGIAFDSDGERVYYTLAHSIDLDECPLLPECYHVVRLNLSICYIMRQVTES

QIEVYARGYADMGGNLPKMIGLNVFSQGVVDVVNIVEASYLKKLAWQIARRRASDTHSDP

PKNCGVCGKSTKKFGNFYTSGIFCVICRQGICPKCSVQKKLLLDASKDQQRQLTFCVPCV

IEARQMSAWDVALQQLQLQLHDEATMRSKS

>contig08625 Frame-0R

MLVRRCARPLSKAVQRSTVSTRHWYPSQHLVLSSVASRPTTYRFTCPFKDTNVPLHVPLC

RQFSSTQTIKWPSEIAKRIHRRMRHFPRNSQAKELIMEAGMNAAEWAMASSSFRQSFLKE

PFQYFENQAELEAFGRVLDDKTRHSSFIFYPYFVDYAKAQNYVPTDPEKTKALSLQQLTD

LRLPHQMYPFATAMKRKIIYHAGPTNSGKTYQALARLKQAGPHGGIYCGPLRLLALEIYE

RLNADGLYTSLVTGQEKKIVPYATHISCTVEMAQITKTWDVAVLDEIQLIGDLQRGWAWT

RAFFGLQAHEIHVCGSSEAVELIQKFAATTGDEFEVRTYTRRSPLIVASSHLPSYSSVRR

GDCVVAFSRREIFRIKREIEVQTGQKCCIIYGQLPPETRSHQAQLFNARTNDYNILVASD

AVGMGLNLNIRRVVFSTVQKYSGPHGGMVDIPSALVKQIAGRAGRFTSDYDAGEVTCLSE

TDLRYVQDSYDHVPSNLTSAGLFPTSDQMVEFAKQLPMITDLADLVDKYVMLARLDGAYF

MCNSHDMKDAASVLRDTNLTLSDRFTFCMSPVGLRNPLARRVFLEYARAHSLQQRVKLDI

YLPKVAPRTAEALGEIEIKAKIIDLYLWLSFRFDKTFVENRLALELKARVLELVEEGLVN

TTYDREERKTRWASGVENGRNTRWQQDQKGRWKQQEGRGKQETKKASDEGGAMGKRMKTW

FARVFGKEGQV

>contig10545 Frame-2R

MLKKKMALARSCKDGNGPLSSTVEAPSIADKLNQEKWPVKVCNPRAGTKAQKRLQTGLQC

QGRINASLFDTLEESGEDSETSNSSYSSSNSSEHTEIFCQRFLYISSANSKQLEGFPLLL

PPHSRDFKSDLESGARNSLPTIKTEVFKLVKLANPVIWTYVLEFFPSIVSMTLVGHLKSP

LTKQYLDGVALSTMVLNLTAIGIGFGLATAMDTLCSQAYGAKKAKKLGIYLQSGLIVLGI

TYLPVFLLNWYTEALLVAIGQPAQVAAFAGRFSQILLPGIPALYVYELFKKVLQAQHVVL

PMVYIAVISNLVNVFLGGYLTFYTSCGFDGTAIARLVSDLVLPFSLIPYFYQHPHVLAKW

WPGWHVHEAMQHVSIVLELGLPGAAMLLLEWMSFEIMAALVGLLPHSIMAITVHSVLVNV

STFAFNFFLGISVAANVLVGTYLGSNKPQHARMASMLGMVLAVLFSVVLAVVIVATRYLI

PAIFINDTVSIASSGHAILYLMPYQLCDALNAVMQGVLRGTGRLSLGATINLFSYFVLGL

PLGTYFAFSMGMGVPGFWAGLTIGIVFGCVVSFVKICETDWNGMADDARVRTS

>contig11847 Frame-0R

MYRNWHISQKESLQKINPAMKNDKVLEALSDEFQAKFSNSQRAVIISACKGMASTPITRS

MYVARILLFKEWMAMSPE

>contig15564-0 Frame-0R0

MLVTQAALLQQHVQTHTVATMWPPAKRL

>contig15766 Frame-2F|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY64152.1|) 1e-166

MLRLLNCALFATVSAATSVGQILHFSDVHLNITEPSSNSNASRIAISYFQDAPLSLLKSA

LFYAKRHVVADPELFLYTGDHVVHGHYSDEVIAKTVETNVRTIEDYFPGTAFPGTLSITA

IIGNADENPDYHMEVTDPERELNPSIKLISDTWKDSFSPESMDLLNRRGYLSYSMDNQLE

VITLNTVPYSPSHTPDTSNQSDPFGQFAWLDTTLARLEKAGKFAYITGHIAPIVDSYGGD

PQWHSNYIVKYKKIVGRYGHVLKAQFFGHVHSIEFRVPVASLDEPNENAATLNLPPVFMT

GSISPLFGNNPSFMVWVFNSETYEVLDYAVYGTDIRKSEPQLDWKLLFKASEAYGLMSLS

LTELSSFVYRAEQNVSLLENYYWNMKARSPNAPPCQDAVCHVRTLCSLKWWDSKREYLAC

MEDTGKRKSSAAISNRPIANAETIVSFSLLDSSTTTDDVLVTIGVTTVAIVVTVLCVAVT

VYLLNRVGILLIRRQYASV

>contig16002 Frame-2F

MAMAQLASSASSNHSASSSASTATKTEIQTFLSHFDAQINTMMDYPAKDTINALTIMAER

IEFAPEIVSFLETKIH

>contig16914 Frame-1F

MPANPTKLPTAVTSGLQLLSPTLHHAIQHSTQEAHEGTKTHAFDFDHFTLESVLGDTAVI

EPPIRMSTAYPLVNGSCALSGESSTSCYGSSSVGSIHTITTTEDLEMSRLARPYLSNSHD

SEQTRPTFQVSATAAAAGFPMAKIKESTAVVRQGWLQKRKGRVLRRWKSFYCLLKSDDTL

CLYASEDTVNGKLTQRYQILRVTLTDKKDSFHVIGIDDEGVPRREELRASISLEWTHWFQ

AFRRFFDSASMAQACERKPQLMVSNAWDQTSTSQEDSIDYERHSFGCERKRMPVANSSLS

NDTNERLFASSLGLSHKAAKRCSQHDGDFFIKERRSEGIVSFSEKHAVEPEEDELEAFVP

AELTWPRLSDCDAPIDELTR

>contig17045 Frame-0F

MAANYENMEAPAPKKESFACKVLTSLTFWIVVSMVVGILLGQFAPSFSEKAAPMKNIFLR

TVQFVVFPLVFSSLVVGIADQKDMKQLGRLALKSIIYFEIITFVALLFGLLAVNLVKPGN

VGLPEGDEFESTSDSGMTFEKWINHLTPKTWGEMMGGSGSSELLQVLVAAILTGVATSQL

KDEQKYLIINLARAVLEMMFKFVDIVIWTAPLGVCFAIADAVGKNGLSSLASLGALVATV

YGTILLFIVVVFGSVCLMFKINAVEFLNAMREPLIIAYTTATSEAALPKVFESLERYGVA

PHISGFVVPFGYSFNLDGSTLYLSLAAVFCAQAAGVEKSVGEQIVMVLMLMISSKGVAGV

RSATIIVIASTLDQFDIPSWPVALILGVDWIMDMLRSFTNVMGNCLASVVMAKMENEFRT

EQWEREYRAPAEHGIDDKTSAIDGKVSRISGVSGISVL

>contig18453 Frame-0F

MLFLFLFLFMLGNPWTSMATALLRRPCIRVEPIRKVYPSMKRFVSLSSIAPIPSDGNSQK

HVVVGMSGGVDSSVAAVLLQRQGFRVTGVYMKSWDSSDEKGKVACPVDEDYADVQKVCEQ

LGIEAQMVNLVQSYWNQVFQPCLEGYEEGLTPNPDILCNREIKFKAFTEFATKIGADYVA

TGHYATLQLEKHDHVPQLFAAHDKTKDQSYFLSSVNGNAFANVLFPLGKLTKTTVRELAE

SEGLCTATKKDSVGICFIGKRKFANFIHQYIPRQDGYFYTVDGVRLYTHEGFTAYTVGQG

ARLQGKSAKWFVVAKRKSDHAVIVAKGTRHPALFTDTLFASATAFNWIAGEMPQELYTTG

RLRCLYRVRYRQDLDECTISFVSAFEAQEAASKLHDWQPKRVATDTKRSYLRVDFDHPQR

GVTPEQSLVLYRNDGLCYGGGPIAVAGETYLEQKKMLAEEATDWRR

>contig18747 Frame-0F

MPKYQFEQTERPYQFIRLAPWPQLTHPTAIRLRTVATGELCPRDYFHIQILA

>contig19331 Frame-1F

MLPIEVVQECESLKFLLWRRHIFVATIFLHQLPFKIERNALIKNESEKNSKATEKNSKAT

YQLTPSLRLVTFSL

>contig20090 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53304.1|) 4e-35

MLACSKDGTLKLHSLADSRKPHQTLPTAALALNSKGQVAYSHDFIDRSCVSLRIHRHFSV

NSSLFTVAGVTPSSPTLGQSIQDGGKSSP

>contig20326 Frame-0R

MDTNWGALVASYLDGQNVANFEEYVVDGCSRALGCKRSVIMKATCSQKSMWNLRSRAFRH

AWNTFMRNRCRSFLANLLELLPAAVKGETMELLKGLGLSTNSRQRPSFENIYARSGYIQQ

KINCCINLPNLLFTEELSELRSEIFRGKQSK

>contig21963 Frame-0R

MSPLVLLHTYPRRKRLVGAHHYDDLIVTCRIKPEEVDFCSRNAKFES

>contig22180 Frame-1R

MQTEEYRNVINLNLIPAAGMKELKDGTITCEAGPLECLGHRWEVCAMDKDRHDVVKYLST

VACIEGDESGPMEDWPTKVQNCVTDEERVVIQKCFDEHSEELLRKMIREERSGSVLWMPY

TVVNQNVLGSATEGVSLYMLKKSICSAYTGPKSFYPAECGTLVEKQKVLAPEALNLENAL

LVASGKNSTDAIEAQAPAKSDAHEGTDGKIGVDATQEMSTSASPTPPTMIVVAGKVQLQI

IWRAFCPGCISFITKPLISLTRNRQVSRNHRF

>contig22579 Frame-2R|Blast-inositol 2-dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY55931.1|) 1e-146

MPNSDPIKPLRVGLIGGGRIGKVHAQSLKRVGAVIEIIADPVGDVAETVAGEYGISKWSK

NASDVFCADIDAVIICSPTALHAEHIVEAAKHKKHIFCEKPIDFSVAVVNNAIKAVDDAG

VKLMIGFNRRFDANFARIKQAINRDEIGKVSMLRITSRDPSPPPIEYVKVSGGLFCDMTI

HDFDMARFLIGGEVEEVYAMAQSNDPNIEAVGDIDTAIVLLKFHNGVICYIENSRKAVFG

YDQRVEALGSKGSVNCGNIHPNQVVVSTQESVRRDLPLYFFLERYMDAYVKEMEEFVRVC

TTDAPVPVGGDAGREALLLALAANRSLAENRPVKVEELRKLA

>contig22643 Frame-2F|Blast-ubiquitin activating enzyme, E1 family, putative [Phytophthora infestans T30-4](gb|EEY53384.1|) 0.0

MATSQQLERDAGFMDKYSRQIGAFGLETMAKLVRLKVLIVGLQGVGIECAKNLILAGPGA

ITLCDDGITEIKDLGVNFFLTEQDVGHPRAVAVLHKLAELNKMVSVGVHQGPLTEELVAK

HNAVVFSHTSRQELVRWNHFCRQQSPSIGFIMCDIRGAFGYAFTDFGDEFKGFDATGEAP

ITRIITDITNDEDGTLSILGPDEDGKMHEMPDSDHDGWIEINDVQGMQLKTDPSQSINTM

PPRRIKFVNKKAFRNGKETEVFDAYRLKIGDTSDFMPYVGGGVLVQHKKTFQVNFKSLEE

SLVSPVPEGEFGLMFTDGAKFGRAEQLHVIMWSLMEFEERHGRFPKPHNDKEAAEVGKIA

KQGIQHLSAFTREGAHKQEVMHLEELDEKLVHLAALYSAVELHPLAAFYGGVIAQEVVKF

TGKFTPLTQWLHFDAFEVLPDEQPTDAEPIGSRYDHMITAFGLAFHEKLGNIRTFLVGCG

ALGCEYLKNFAMIGVACGEKGLVTVTDNDRIEVSNLNRQFLFREHNVGQPKSVAATAAVH

QMNADLKVKTFEQLVAPHSEDIFNDGFWTDLDVVTNALDNVKARLYVDSKCVFHKLALLE

SGTLGTKCNVQVVIPYKTQSYADGPKDAEGDGIPMCTLRNFPSLIEHCIEWSRAQFEDLF

VVPSADAKKFVEDREAYLEQVKKATLDNPNSKLVPAAIVQELERLRGLRSTLQMAKGITF

EKCVVLAFDLMTRSFRDRILQLIHNFPEDHLTNSGQKFWSGAKRFPQAIDTFDPESPLHL

NYVRATANILAVCHGIQPPPEQELVAANSKWRDPLTFKNLGNCYAPPSWKPSNEKIAADS

EEIKRLEQEKVENSNESDRNELVEILHELETFDLAGLSFEPADFEKDQDMNFHIDFIYAA

SNLRAFNYRIREASRHKCKMIAGKIIPAIATTTASVTGLAMLEMLKLIQQKELAAFKDSS

NSLGLNMYLMQEPAAPAQAKDEYDVVEMSEVKCKPTGFTKWDSTLIELPADSTLEDFLVQ

FKEKTTLNCDLLFHSVAEIGNTGGAEKDVRYRSVSGLMLYDRNAHGKTLKDLYADQLNKS

LKAFVESRYEGLVDCSRKYIELQTSCSDDDGNVYKVPTVICKFN

>contig23770 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59902.1|) 2e-12

MEYFAVCLLVFLVLQGFAKAQSDTVTCTTPADCAWGETCVAGDSETSVQACVP

>contig24937 Frame-0R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY65715.1|) 3e-81

MTRVESVRLQLKGSLEKLKLSIGSSYPDIDPLRKSIVAGFFLNTAMRSVAEGLGGSKTAY

KTMCGRSEIVKVHPSSSLFMRNPPPKWVVYNELVFTSKHYIRSVLVIEKAWLIEMP

>contig25079 Frame-2R

MSFLNTTLFHPLLTRVPTSVMQVSHLVESIIAAFLNVPQV

>contig25105 Frame-1R|Blast-palmitoyl-protein thioesterase 1, putative [Phytophthora infestans T30-4](gb|EEY53377.1|) 6e-28

MINLTDRERKMLLYVAFATAGLILVQFAFITKASEKYFQDVETLQLKAVEKKTLVFQQMT

DLPVVLMHGMGDAAGNGGMLRIQKAIADYLGVYVASVQLGESVTEDVYNSFFVSMNNQTD

RFANIVRKDPHLANGFNAIGFSQG

>contig25480 Frame-0F|Blast-ribosomal protein L7Ae/L30e/S12e/Gadd4, putative [Phytophthora infestans T30-4](gb|EEY70309.1|) 5e-43

MLLSIGATFMTVGSESLSMASSEKSSCSNYEERIKHVSVIAKPLATKRQTKRAYKVVKRA

TKVKSIKRGVKEVVKGIRKGEKGVCIIAGDISPVDVISHIPVLCEEYDIPYIFTPS

>contig26041 Frame-0R

MNSTKTPEDIDMDNEPDQFLADLPPLAEPIGSVLSSSMQPTPLAMSAAEPQERRAQVGAS

PYVAPFTPSASPPRPKTPSTTRGHSSIGTTRTTMPQIALVSRSGSAEAFEPGPALLQDDV

VKHLPPKLLETLVNIIRTLDQLATGVADFRPEQLNFMSEKAQRYVELLHDADRAAVEYSA

SIPLEVLKMIEEGTNPELYTKARMEKCQDESTRTAAQVETLKVLKSALQTGLDTI

>contig27257 Frame-2R

MGFLTYILIVGYSKGTSNQFSPDVISKDASYCLVMQLIEIGVLAACLYVLKSTISFLDLV

SFSGYKYISLVINAVVFQLLGSVAYYVSLLYTGVAVS

>contig27323 Frame-0F|Blast-DNA polymerase subunit alpha B, putative [Phytophthora infestans T30-4](gb|EEY69357.1|) 7e-21

MSNPTTFSINGVVFGTSALDVVLQMSSNELYRAQARDQHRLLRLSEQVVDQR

>contig27525 Frame-1F

MDLSMILSPVLEEEQLLPPVPPRQYQGPNHKWSADELQCAVAILQDFQQPSVNFSLSSQA

DLRSRIDAKVAPFYLRQEQRSKEEVQDPSNGIMNLSAHEELKNCDQKHLAIEQVQKLNTS

PTVWKEDSMSKLDLLVQADAIIKRRRSNALTSPEGDQTT

>contig27688 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57391.1|) 1e-51

MIQFELYPQRGPNVPLFLSLNKLETPWMYTQSLLKIMYLRKYLAKKLKLAKPEEIEILCK

GTVVGPEYSLEFIRRTRWKEEDSKMMLEYRRQLIAS

>contig27907 Frame-0R|Blast-serine protease family S09A, putative [Phytophthora infestans T30-4](gb|EEY59532.1|) 0.0

MKPILYLEDPYFYVRDDSRKKEEILGYLRKENEYTENRTRHLANLRSILYDELLSHVQET

DEDYPYPHGPNLYYKRTVKGRSYPYHCRKAKTENGPEEILLDENEIAAGHKYCQVASVVQ

SPDHRYLAYMVDFSGCETYAGYIKDTETGELLSDRIENISSLCWGKDASILYYATQDGSL

RQSKLWCHHIGSKVADELLYTEDDEMFNASFQKARSGKYIFLISSSSETSEVSFIDTDHQ

SQVPQLIAKRRKGLIYSVDHFGDSFFIVTNKDNASNFKLMRTPVSMPSSEHWVDVFPYDE

SIKVDDIDCFKDFMVMEGRQGGYSQLWIIVAENDNKLVRRQLNFDESSYTVSGSVNRNFD

TDKFRYVYSSMTTPWTTFDYDINTGESKLLKEKPVPNYDRSLYKTERIEAKASDGSMIPI

SIVYRSDLRSQDRQPLHLYGYGSYDISIDPSFSTSILPLLDRGVIYAIAHVRGGGEMGRT

WYEGAKYTKKMNTFTDFISCAEHLVNTGYSSPNTMTCEGGSAGGLLIGAVLNMRPDLFTA

AIAGVPFVDVMNTMSDATIPLTTEEWEVWGNPNEKAFFEYMLSYSPYENVKQQAYPNILV

TSGLYDPRVAYWEPAKWVAKLRDMKSDRNEVLLKMDLSSGHFSASDRYHYLKEKAFNLAY

LLDHLITIMGNQNDGEDVKNVNVKA

>contig28076 Frame-1F

MRSALAAPSSCHALFYLAQSKLTFTPASSLAPIQPSTTSGKSATVLIKKVSCAQKCNSIA

GFLSLQLAIKMELPLTVQLCTYHHLTP

>contig29031 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55585.1|) 1e-127 NOT\_ORF

MARAGKCFECVLQGEVVRLCAEKYVKRIRRA\*\*LKFFGRANCA\*NFQHFPSFVERLSGLC

DENVVKEDIAYKEYVYNFDDKCPQYINGVPHYEVRARHVFSGSTTFQGKAVEMPLDGGQK

WELRYIGRWERKKMSEHVGSASLGVPFRSQIAVSVGQNVRSFLSTLGFRHSYRYMRLGTR

WQFPNGITIEATRMKALHNEDEKDQYRLVDLENLRVEALLVEIFALTTDEFIDEVSQKIR

RFAVDLDPYLIERPSEGKEILHSTATLAAEVRRKRPRQ

>contig29255 Frame-1R

MKQFRCLVCAIDMASWTLLERELHVNTCLDALEGYKRYVCPTCGQDLSQSDELQRSEHAN

RCIDRAEAVDSDAGSETECVFVKDITKDEEVKMGLDLLPTQIAEEAQTQGHAGLTCESEY

RSECKICGIDMQEIDLMCRVRHVKSCGQKFGVRSEFMGRVEQTETAAPKTKKQRELPKLN

LNAFGIITKPSLQNAKAPVAEFANSNVFDVLMRSSKSAAILNARKRPVPLKFTRKAVQRR

RLSYPDCKCIQGTNPPFIVDGFKYACKENSSIYFLTHFHSDHYGGITKEFNCGIIYCSEI

TAKLVVLQLGVQSKYVFPVGMNSTVLVADVQVSFMDANHCPGSVIILFRLKNGKTYLHTG

DFRFHKTMLERRALQTYIPTGHENIDNSCKIVGLKRLDGVYLDTTYCNPKYTFPSQRVAI

DHAIELVGKHLKQDGILFLFGSYTIGKERLYLEIARKIQQKVCVSRTKQKIIESFGWPAE

TMQLLTTEPAATNFHVVGMQDLQMDSLKLLLAKHRLRFQRIVAFRPTGWTYGSKNSRSIS

TCCTDPSGKIRVYGIPYSEHSSFAELCDFVQVVNPATIIPTV

>contig29888 Frame-2F

MVSSFPTSLPPHVPSTLHVTASDISLFAATVEENDAPEFEQLAVRALASEEQMGGEKNNT

LGLELLEALRLGKSNFLLAYNTRAGIAVLLRLLKFLQRRDWKAAANLPQLLDEKYLNFRV

DAVRLGLFLGWFTGSYKGLKALLPLLLRRIVPIKQLRDEGELKKIAASGSGAIAALALGF

MYPKRRRSFALYALTRALQCGYNTAKRQKRWHFWGSDWQYGDALLFALSCAQVMYAYIMR

PSTLPSDYFDFIQRTGPVEPETLEMVHNVNRGDPVSAATFQKLMDRKPGIPRALPLPTDI

VSCRLVHANADSCLVGALLCFKRAFQKTFPLYLSLFIVPNMVIHFERFLRKPFETLAQST

FGAIRSNCFLASYVTLYLSLVCLHRRVVSADHRFFYYLAGFGASITILLEPKSRRSELAL

YVLPRAIDSLAMILQDRQVCFGFKYAEVVLFSASMSVMMYCYEEEMESMSPLLYNTMKRF

LQTSTDKKINT

>contig30569 Frame-2F|Blast-glutamyl-tRNA(Gln) amidotransferase subunit, putative [Phytophthora infestans T30-4](gb|EEY66350.1|) 8e-86

MMQRDIGVRTELKSSCALRPLQSSNSIRLRSKRSWCILINRSVSDWCTKTLLFTSKSLAS

GDVSAVELAQACIKQVENTRAYNMFVSTDFEKALQLAKASDKRRAAGQTLGLLDGIPIGI

KDNFCMKNMPTTACSKILENFVAPYESTATQRLLKQGAVPLGKLNMDEFGMGSGTLYSIF

GTTINPWSKNLGDDAVVAGGSSGGSAAAVVSGCCFATLGSDTGGSVRQ

>contig30675 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69104.1|) 4e-44

MTTPRKVEGAMAKKVYMHYKEGSEDQALTLKMTLPSRWAGHTSDYLKNFFVEHYNNKKPE

SALDAAELHLEKKNSTALFGDELLHTAVQKYDDLFLKAGASPLKPVSAP

>contig31078 Frame-1F

MIVFVLIQTTARFAVTCTYRHNNNNKQERKTAECEHNLPRAKDSGK

>contig32149 Frame-1F|Blast-ribosome-recycling factor, putative [Phytophthora infestans T30-4](gb|EEY67787.1|) 2e-35

MALRVISCRFIRLTSRSTPRSLVPIAASAWTCPTSQPVSVLPVHTRSFAKTKKRNSSAVL

PPRVEEYDDDNELNDGEEEEPARILAKASKNMKGAVVNFMRALNQMRPSCADGGIFDELH

VQAYGHHVLLAQVAQVAIAGTHALSVTVYDAS

>contig32923 Frame-0F

MVGGMIAVGGATRLTRSGLSMTDWKPQGSLPPVTPDEWEAQFDIYKQFPEYQQRQNMTVE

EFKHIFWWEYGHRTLGRTVGIVYAAPLVYFLLRKRLPRELYTRFGVLLSLGATQGAIGWW

MVRSGLEEHGHEQLENCNEVRVSPYRLATH

>contig33418 Frame-0F

MVALVQQLLTAVVKVPRLLRSKYVAAMFQVSNSTFDDDMGRTSVREGWLKIRFWLKGNRE

NVRINRASFSWDNECCNCMCVVKRLNFRAKRLRWVSLKSSSIAIFDSIEDSIAVQACLFD

NKFSVERGLATTGSNTTLLVSNATYVLQMEAKTKQVLVKWANDIRRVAEASNWSQIHRDG

SYSIPRNPAHMTSFAQWYVDGSDAYKAIFEAIQSARKEIFIAGWWICPTIHLLRPAAHHP

ESRLDLALKKKAEEGVQVYVLMYKEVSMALTLNSMFSKQELSKLHKNVHVLRDPDFLMKQ

LGLWSHHEKIVSIDQRISFVGGLDLCFGRWDTHQHELFDEPEKPTNFLGKDFSNPRVKDF

IEVDHPNEDMIDRNEVPRMPWHDCHSRLEGQPARDVARHFIQRWNYSVSTRKKSKKLRHL

VPMKDFPVTNVTKHGPRKPTKRLQKAVHAVRAMRGLSNGRGNTDNRGFNSDRRMARLLSS

QQESGTMPILQDENNEVMLHDSDGGEDSDNAFEKHQQKMSARGYRVNTQILRSLSLWSGG

VATERSIQNAYIRLIGSAHHFVYIENQFFVSGLEGDRGCSNRIANALVERIRRASDNNET

FRVIVLMPLLPAFPGKPDDNDASSLRGVMHWQYRSICRGEHSIYQRLYEELEDDDPFKYI

AFFGLRNHSVCEDAQAQTEEVYIHSKLMIVDDRACIIGSANINERSMCGDRDSEIAVLIE

DDEIEEGITIADGVYNVGKFAHSFRMKLFEEHFGVQPGTPLYQKYVDPVNKEAWFSMQEQ

AMANYQIYDSVFGCLPSDSVTSFAQIDSHIQSAQDLDTSGRGADEAVAAATGANSTDTSS

NKEDRTSSISDKVMSPGSSSRVSSSKGPKSVFSGAMNVNMKERSQIAQRKHELCNVRGHV

VYFPLKFLVDEQLEPKLFPAELFQ

>contig33595 Frame-0F

MARQVTMSVEIKAAVAAVQSGSMSLRKAARKYDVPHTTLQRRMQQSASVASRSGASEITM

EVKQDVNTAAADVNIQRSTSSEDASELHNIYKMPAITKTKGSASHEFICSQGGLISIKHY

R

>contig33883 Frame-2F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY64041.1|) 0.0

MNSESETVMCTRVSTDGSAITQELYGCQTCNLVHGSRICRTCAKICHEGHELVMLGETTA

ACACHIRGSGLCRCICPIEATEYPLLSRPVNASLWGCNKCTVVNSIDLKQCNVCGNNAPE

QLPDTGPVPLESTSTALALVKQPEPAYDWSCEACTMRNDSTTTKCSICDTPRTKNLVPDD

VGMSQESKTDNALTTLYHAAETAAKKHDLMSILPATSWICSVCTIVNQATNTTCYMCGNA

FEASAATTADTTDVAMMSPNSKVDATSTSPPMNMDIDRNDEAPYVKPNVDVETSQLWNGK

YLDEYKRTVAVTFRQLLEVENMSDSVWETTGGKMHVMLSKSVVGKYVRGTYVENDGIVRG

LARPTEDGFWKFDGRFKRSSHSQYNACTLYWNKPASRFDGKWYRGDGSGDWKCLASPYAS

DFCGLAPIDPVKKPSQLQPY

>contig34147 Frame-2F

MAAQSLNFLPSTTAPIAFGSSGDVVKLVTEVECFHLAPQDDGFQTVKSRRVVLNESKQAR

QHLSSIKATDLAPNDTKYLKKKQQRSGEHMNKHCGLKVKVTDNLQTPSEPQKEKIKFISD

PVQSLAENRSKTKRPKQAKQPKKKIVPAKSSTKGCKRSSEKTMQTVMDLTEHLADMASTD

SPGFKYGTQHVNAISATVASKNSSPSFMNDRKTAREPKIIDQKTIVDNKPSGVVAKRKPK

QVYVVKTNTV

>contig34828 Frame-0R

MGSMSLEASFAGSVVADPIRARHSEFVIQKEDFPALSTFGPVSSGKSTIGSLVESKRHSS

FTSSAADGMLLSRLDQQKGSTLIGSRAGGATHAAAGAGISGSVNLGTQAFNHFRAPRPDD

QNVEKNSTTNSELDPNNQYGLLGLLHTIIRPGNSDLMKNLAMGCDLTSLGLNLNKAEPLY

PTFASPWSEEQLTKESQFSLPTCYYNQPPVLKTTHLSKFHLETLFFIFYSMPKDVLQAYA

AQELYSRDWRYHANLKTWFKRASSSDAALLNGNGSASTGGSTNGSPKAGSGSGSIGSIGS

APSSNAGQLNASTTLQFLYFDIATWERRVFTGNINSLSA

>contig35144 Frame-0F

MSIKFAIPFLLNPQHTVSATTPLLLRIAPIDKTGGRNHTKKQYSVSVRSLSVLCHTNRAS

GNLNKNDNTKKFLTETSPSPATVEPAIQAAMSQTRFIHAMDNIAKKPSSCLHRKRMPPCQ

IKGCSNIAVSRGCCVRHGGGSRCMNVGCPNRAKLFKKCFQHGGF

>contig35258 Frame-1F

MIGFVNDLVTRIRLEEAGPEHSNTMNRMTTYTNFYNFGKRDMKLDH

>contig35607 Frame-2R

MTHVLFPDAQPCASSASITPPSPVFRSTGDLRKLISPNFIYRGAQVRPIPTNEWWGNLLA

WDGKRDSDAVF

>contig35881 Frame-0R

MTYSLQLYCKLVPRSCVSHKQHVKRSCWW

>contig35988 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68017.1|) 1e-49

MSTHIGLGATAVDGELTLRAAVASRRRNQRQRLVEQQLGGRAPLNLSRPSGEHQLNANRS

TQYQKKDGLTFGEGAGRLEGAQRKDDALFETVTHQKKEIVRLLNTVKTLSSENTKLVKKC

EALTNVQAENREIRESMDVFKKDYRQKLIMIKKALEEWRRQRNIGLEVSRQPCAALEDHS

VLEIKLKKQEETITRLMEEARLQDDRIAKY

>contig36202 Frame-1R

MSLRVAGNTDGSKLFHGFIVGVGNADTFEHSHQGANGSEVGLPTNAIELESHPLLSHNTR

SKEVWSSHSMRSPFSARTCMDSKESALSESSPFVLSFPMDTDTVEAVEGANLRHHAYLIE

MTPGDPSGMVPPDAGLSEYLLAVTGKSEVAFEDDEGTSGGSLVTPRAMLTPLHKATILPS

DITKIQVNTRGFEEHLEVTVVVKREAPMIGYILLMVSLFTISSVGVALDEITNVVTPEIR

ILWRNMATSMVTFPFALTIILRGNESEHGGSWKRCLTFVLIAGVAYAYYLGSFVVALSMT

SVGHATLFSNTHSMLLVFWKLLQRKPVAAFEALGAAIGVVGGVITSTDSTPGGPNVVSAS

AIGDLVALSGAAGGALYFTLAKKVRPSMHVMVFLCGLTATSATALLCYMLAAGQDLSLST

DPYNGVFGWLTPSSNRLLAVLYLVFICDCIGTMGYIGVMKYFDPIVVSIVCLVEPIVATA

QGIVMNVDVMPGPITFVGATLVIGGTCLVLSSQSRKTEKVDATEALLASDATPRAVYSSR

ARIRTPHYGSTPH

>contig36787 Frame-0R

MQFMHSQPCFVPDQPRAFSSLRASSLQFDFDQYSCLKCVLRDNFSRCCKRLVMDWICRLS

VS

>contig36927 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57380.1|) 2e-63

MNQTTDTINIVELAIKRPKTEVDIAMENSPVKAKALLDEQEKNSLQKHSPLRSRLAWQSS

ATKNAL

>contig37216 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62434.1|) 2e-18

MDYSVSTQAYVKLTLHAAKHPAYTVCGLLLGRVTENKIEILDAVPLFHHDAPLAPLLEVA

CA

>contig37915 Frame-1R

MQTRCKEKKWNVQFVEADLTQMKGWKSNFVDCVIDKGCLDAMLLKPETVAIETNWKRVAP

DSMDDLSDAKNSMKQLARVLKPGGLLFFITFGSPSNRLCLFDGAISSDMEWEILQCLEMS

PIKSQYPFSTRFYLFIVQKKVKLGTVLTKKQDCH

>contig38118 Frame-1R

MKMMELICLPEHFANERESRAHKEMAAAAVNLHMKDPTHVIALLLRAAKIHLTTNCANSA

CKSSPLASPASRLPKSTLRLFSVPFRHIFVSLTKLFRGG

>contig38622 Frame-0R

MRKNINTEYRLIVKMYAPWLVSSIIVTETSIKIGNMEPSIRWSKFSSEATEIESRSRCST

TKTSLFNCLRRFSLTKVWTVQKLPQPCDIRSCAV

>contig38965 Frame-1F

MVKQLNKSHFWLILRVGYGHVSAPCECEALEVACATSFEARVVRLFSQDSIMLRLTIDVR

DGFARPKLSTLESNYF

>contig39135 Frame-0R

MRARQYIKLRLSDARQRPKSVKAAVLIRTMVLTTDLAVYLSSKTKKKNGTWLL

>contig40131 Frame-0F|Blast-ER degradation-enhancing alpha-mannosidase-like protein [Phytophthora infestans T30-4](gb|EEY55417.1|) 3e-59

MKNDHIMTLVASPAKFGLQLTDLSRVEAPLLLLTSEINEACGLIDSELVRGRIVMVARGS

CSFAEKALRLQQSGAVGAIVINSKAASSRYLNRNYFLADDAQRLGQKVNIPVVFVAREEA

SQLHRYFGHKMFGSADGSNTSVDDAIQLDSADLIGSLSPWLY

>contig40144 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55053.1|) 1e-90

MRLQDIVLLFPFFVIHACGHTRSSDYFPDHLYIEPGVVAEFAIIAGLVICFCGFRLLRVM

TFLSGFLVTGLLFSTALTNIFGLKTWVLAASWISFVILGLAGGCVALAFFSFGVTLVGML

LAYVLTLSLPYRMLPIVSSTVLDGAVVLMGGTLAWLLVRPLAIVASSLVGAIVTVWGVGY

FTGKYPSSEDINLFHSSVIDNRRTWINAVPTAWWAFLAAMLLLFIVGMVKQCHDVAKFRR

SNHIGNYTGLRSNLNLPL

>contig40355 Frame-2F

MLFSVFFFLVATCVKSSYGHSVAVSTRDPENIALQLHEYASIPETIETIRRLRGALAHDA

TAYDERMFFENAANKMYAIAQKTRLSAAAVKKLIPESQEKKLLSYYLTKMKGFIKDREAL

YSITSSYDELALLGVTPDLFRTRLLSVESPEVAAARAIEYEEYIKNICFVSSEKNPCKTV

TELVESNKFDKIKELMEKHSIAELLIGALTNLNKVNHLDKLTTRIQLKYVLENTPELGPL

LSRDVNELLKDPSVSKIFSRFLTFVYGIPS

>contig40607 Frame-1F

MYTLILMVSVLRTLHARATQYLSTYEDLDSLNNAKRNEADIASSLFTPQKLWKVMGEGPL

EGLKRWYALIESHLRCEFDYSVNEVPCLCGLYGLDGAATEEVAAADNSNDVAFETSTTDD

YN

>contig40881 Frame-0F

MLLRLSSVHTVPCSFPARSEMLHAMDENTSGVIWMCESVGRRTLSQFEDASRDVLLVKNF

YNGFEMWWLAGMPITLVIVLALLSFSLDSGIFGLCKSMRWYEVLSTLPILRLVDWLSRPL

CADVAVLENESDELKIPRHIAVIMDGNRRYGKTKYGAGVRGHSDGSRTLVNFTDWCIDAG

IMVLTVFAFSTENWNREQSEVDALMNLFTEFMDEIVPGALKRGVRLRVLISDRRKMPVYI

TEAIQEIEAKTRHCSTFSLNLCVSYGARDEIVGACKKIATDVASGKATIEDINEDLLSQH

MLTA

>contig41020 Frame-2F

MSAQIQRFVTLAICKRCFPISRDLRQVNFTRHADCHGQPRMWRFYYRLNGREPPLISSAL

RVGKMDKILRS

>contig41147 Frame-1F

MLEIVLSGMAVLENIQEKAALETTITEKRSNSLDLNETQDTPTSNSVHDLLLSGNVNPLK

LPFSHYRLNNHRAASALSAPYGREWIEMTPLGYIANAHVTRYLGRVTLHFIKESWTVRES

GGLGAFYHLFLSEAIAIVRAHVRSLGGNAMLTFRLVPIESSQLYRNQVYNMISITGDVVM

IEREKDTHVAYPLPMGGFKSSLAVGVDRKRTSLGESDDSDMFCT

>contig41532 Frame-0R

MIKKTRDEGNYDELHTADIVPFLESCEDNSLDLLISADVWIYVGALEEVFELCARKLRLS

TGWMAFSIELLPIEYASDETTELLAGFRLANSGRFQHSHEYIMNLVCRWGFDVVIQQDVR

VRKESGEPIPGRIYLLQHQEKKV

>contig41828 Frame-2F

MSAIERKAQAFREDSRANQDTVFMSLLLAQSQEDRLASQPKGSARGGKCYEPMPPEKDSA

LQMWEISRRMMSELGFLSVRNWGSVFAMDSTVATDFLCDLESLDKLPERETFDISIAYVF

TGSSRGGYDQIHLATSMDVRAGYVELSKDYRLFLSLIGEHDGRDHAGNSGFDADIINGRM

LYYSHYSHEACIYVPTLLTDGEENNSSDSDSDAEDTEGSSARMQFQRANVLIVWNECQQT

YRPGSVLWDAVFQLPMPTSGVVLIIDPLGNDLYCVHVSHESSPLFNQRDKITNQEDYVDE

ADVFTSRVLGPLLDGMVVNGAWLAPLVRQTAINAAILSRSFHRYQHDIGAASFAPMGAEA

NRSKAISSLVKKHMRPKLPGQFYGDLFSKLTSARSTS

>contig42021 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60907.1|) 7e-48

MDHGRQTLDSLYPQARKLQFELKMQISYLDSRRTGGKTDAEVQAEARGNLNSLEQLLWQL

ESLVQTSAKPAERDTWIKKLQQLRSETCGLRNTLEQHIYSLSRRDVEARERETLMNRRHA

>contig43202 Frame-0R

MLLIASTYKKVQKLRSESLVMFCWHWVTKSRPRSHLTRWQTL

>contig43299 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69506.1|) 9e-52

MGPEFAKHILAFPRNHDDLDLQLRASFVLDRLLHVARRNPAAVARDTYELWMKQICYWTE

TKEPVIKCNSKKVWRQRIFGQCSQNVTDEASVLQQRLLLKLQLTSLRCMRTLTTSPQSRR

YFCESFITRKCLIRLSHQIHERSLYELNFVDEDTARSLVNMQRHISWTFRNLCKGFQSGA

>contig43927 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54599.1|) 8e-72

MAFRREVAPLEKLVLKFISKAPRYLDVIINEDTLERAHRIGKLANARTHKAKQEVIRALL

RGGRVGDDTLPRSFFHSSMTRIEIIGAKISTVFVELLSEMCPKLQIVNFSGCFRLTDDAI

ELLLKSCPEIKDLNIENCRKLTDATLDHLRKLSPKL

>contig44566 Frame-1R

MTCTTLSHKSSILPREMQCAYRSKLCDAPRATKLDGTLHKLCDFHRHKANANQQRLHKRK

KRILEAQVDVSLIPHTPKTEEHTIKRLCSSPDSPQSTTEPIDGLTFRSNFNVLEVRILEV

LLFGADGMTTRRPSQTTFNESDACCSDSTMLASVVTAVPEFHDTWSVTL

>contig44711 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57725.1|) 1e-52

MADEARIAAEVQTRAAQVQGLLTQRKNEEAVRVALQDPPLLSKSDAVKDENAKVVMGALL

ACNKGEMQRTIDSLPTTLEDNLMKYIMRFLGIASQSASMLEWHQKLMAKAGSGCAMRAFT

ERKQV

>contig44870 Frame-0R

MLACVGVKELPEKITFVQDTANDWTRRVSLDTDTCARVVYAIVCFLAFLTASARQGLRHS

ILEMVIWLLVLLLQRDTNFQTLCLLCLQLEFVAKFLDRAHDSAFQHRSIILAGL

>contig44984 Frame-2F

MQDLKCPITSPFTRALTQDPMSPQVPVHRQYHSHSIDGLHPRKNSSMSSVASLAAKETVS

QHIRRLSTGQMADEKLSKERIDIIDEFLQKRVTVRPLIGVVCGSGLGCLSDCLENKEVIL

YEDIPQFPRSTVEGHTGELVFGDLAGNRVVCMRGRFHCYEGYTMQETALPVRVMYLLGIK

YLIITNAAGGLSPELNVGDVMIINDHLNIPGLSGQHPLVGPNDLRFGARFTPLSNCYDKK

LQELAHKVADTLGLSHKVQKGVYCFVSGPTYETPTECRFLRLVGGDAVGMSTVPEVIVAA

HCGLKVIGLSLITNKALFPGEEREAASHNEVLEAVQAMQHDIETFVRDLIIEVGEQHV

>contig45367 Frame-0F|Blast-pre-mRNA-splicing factor syf2 [Phytophthora infestans T30-4](gb|EEY57885.1|) 4e-08

MADLEQDELTTMTPAQRKLFELRMKMNAGRKANKQ

>contig45569 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70345.1|) 2e-20

MWVSGECGISLQNYSKTETKAGAQIAVLQHADGVTTGINKCRLGDHLITINDNRV

>contig45851 Frame-2F

MQQRKDRQQKADERNLLRKRKRMLALEDDGSGQSLLDKAKRRKQLQEELKQLAKTEAQNR

GYQEMLKKGEAGDGVDGDEVDDGTGKNVIRCTQCLQVGHMRTNRSCPLYMADEARSKKLG

PYFETQAGSALAEPLKMNKSSSILSGGDSSTKITVNLAELREGARKHNAEKKRKREMELR

EQAELYKRPYAKGVVKLSRSRMPVEHLNHALDMIVQRLLEMPESEIFRAPVDATAVHNYY

QIVKQPMDLSTIQSKIEAKEYDSMREFVKDLELIVNNSRIFNGEPTKSVITANAQKVLRR

AQDEMAVLNADGGMTPTTPHRSNNSPA

>contig46322 Frame-1R

MNLGQMKNEPANGSAQAIPSLKRTLSGGATCSVGHGGISSHLGVGINSIPSVLHATPNTN

PPQMLRAVTSSGAYNRPSANQNYRGGSNSLSNTGGNGANSNFSATAATRSVSQSSTMQDW

RMYLTIEERQAVRSKIRDAYTSRCVNYEDLLQV

>contig46418 Frame-1R

MLDIIADRGRCDGCRMARVAFVVLK

>contig47149 Frame-0R|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY57664.1|) 1e-109

MQGDLSPGSEMAGIIPRSVRYIFDTLETRGEEFSVRVSFLQLYNEELKDLLDPDTEKKLR

LMEDTKKSGIYCMNLLEVTATTAKHVYELVNTGVKNRITSETLMNENSSRSHSIFTIRIH

SKEHNAAGEDLLRVGQLNLVDLAGSECVGR

>contig47655-0 Frame-2F0

MSNEVTVEIIQPSSGSVSQATASIPTPSAPETDLRSRVFKRRRKESEDEQSAVSNGRRVA

TIEIGPTEYLRRKLNIKAARVE

>contig47655-1 Frame-2R1

MFSLRLKYSVGPISIVATLLPFETALCSSSLSFRRLLKTRERRSVSGAEGVGMLAVACDT

DPEDGCIISTVTSLDMNVGCGSLELVNT

>contig47758 Frame-1F|Blast-lysosomal alpha-glucosidase, putative [Phytophthora infestans T30-4](gb|EEY58718.1|) 4e-50

MRVHADKRGDLYPMFSRAPNTSAPAHFRSGGDNSYGVHPFVLQLEEGESGNAHGIFMLSS

NAMEV

>contig47857 Frame-1R

MPRLARRHLSLQPCFYYHELQFLSALDFCCGLLC

>contig48056 Frame-2R

MNCTSTHSVKTIPYVATEAAEYTHVTLSQQNKKVKARNETTITKKSAYCTRRSCFDHVM

>contig48328 Frame-2F

MAKQPLFTVEDAKCSFSLICCMCGVGTLSMPSNFARTGLIWGIIAFVTMALANIYASVAM

SKVLLLAPSSVSTFGDLGDWCMGKAGRWLCILSQMGSCLLIPCAYLVLGGGLLDGLFPGA

WDSTTWIIFMTIMVLPLALVPTLKEGAGAAFGGFMATLFADTLGVAIVVHGMSGHASVPS

PELSMPQVAGAFGSLAMGFGAGIVLSDVQRQHSDPRRMVRVVIATMIFVTCMLLLLGIVP

YLSVGCQISGNLLYVIYPEASTGLTTLGFAPKWGTVVLAYMAMQLHITIAFAVIINPAFY

IAERLVLGMHKNAAVDIENGAAFRESATPGDQQKVVNDSHVSATSSRRSRTSVFPLTGER

NDHDLEAAEYRGANAIKYVLLRLSIIIALVILSIIFKDHFSDFVDFVGASAITANCIVLP

VIFYLSKSWRTISMYEKFAAATIVVVCSVLGIYSTYAAGKNLFVANESDTIFPFCHAEFR

DNVFFNQTSS

>contig48562 Frame-2F

MGPFAAVAAADLLNMVVMRQSEYLKGVNVYDENGDYVGKSKRCGALAVASCAAGRIFAAA

PILVLPPLVLSRIEMRSNLFATTRWLRVPTLLGFVGCAIQFSVPLTFGLFRQTAQLNSKY

LEPQLQHAIRKQDGQLVRVVTYNKGI

>contig48953 Frame-1R

MNSSILDLMNGLDSAVKIQQIKEIAAKAAKHTVDKHKSKAFSSWRSRARSRSDGSRQRKP

YIYNMQHYGSRQREPYIYNMQQYGS

>contig49239 Frame-2F|Blast-hypothetical protein PITG\_19772 [Phytophthora infestans T30-4](gb|EEY53725.1|) 2e-06

MNIVITQKEREEAAARNGGDHGHSDKH

>contig49345 Frame-1R

MGSYAYYQFLIQSCDGGSLVEATKYINCERSSRQHQLVGAFSDPTDFNSLSLSASDQNRA

RIVPHCSKRQFEEVFASITRLFGILYLQIRRGSAQTSTKQIYDVKNLPNV

>contig49604 Frame-2R

MPISTAIPTSSSSMDTYARLPQSPDALNDVYSLQLKFAETMLKLEKSVQMRNHLLHHRAS

SRKAKSGNKVPLRQKQRHHRQIQAQSDSNSASSVSMYRESCDSESSSSSASSISSLDSTK

HQNQSRRLSISKVSKATLAETLAPSSSDGAGSPEISTTERAVNTLSTAVTRASYHDP

>contig49671 Frame-1F

MGKACRDMAEALRDCMIQQECMSDGTKTLKQCLHDRRYSHECKEYRVAYFECKRGQLDMR

QRIRGPKGGMSKGAEKAD

>contig50181 Frame-1F

MVAKRNDTTFLRFAMVFLGWALLASIHTVAMAADALKESNEVTDTVNGTKDFHARPHLRT

LLVSTAEGTSRDERSDKWHPTSQNVLVRYISPSIIKSTGFRTLVKVLRSDN

>contig50325 Frame-1R

MGHPSASPSAMHSNSPLPWDGKCHKCRKLMSRCICFQEIDIDIDSLRITSEAYLELNKSR

PLWNALRKMHRTSTTSRPHPTNSKEQYDHKRSEALPPKAQSSSSRHPKSRPFDSSTRQEE

PKREPSPERQSISPKDQMQYGNSTSSSSKDAGGMRSVQS

>contig50523 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57021.1|) 4e-35

MTVLILKDMYFSSEIIPLQCRLDGSILKVA

>contig50596 Frame-2F

MREVARFRGQKAVELKNIFVEFAQLQLRHSTELQMMVTQSLGELETPLPEKLLEAAQTPA

SCLKMFEPQDSFRLNKNDVIGACQSTASTGSTSTDVMVKPDQMRDMPDGCIKA

>contig50831 Frame-1F|Blast-APS kinase/ATP sulfurlyase/pyrophosphatase fusion protein [Phytophthora infestans T30-4](gb|EEY66435.1|) 6e-15

MTDVLYAPIRQDDLQSDEDTSDLLSSRGPVFDDRRVVTKKIVLAALVVMPYLVLVALFAG

AGGPVG

>contig50844 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60075.1|) 1e-21

MEHAQRVLRAKLREHQSILQRHKTRMPWTTGETGDNVTIKAV

>contig51018 Frame-2R

MINVASTSAMNASTESDVELMRTILGEHVPQSVILTCLNACAFDVSAALNWYFAEVASSS

AAASSSFASQQPIEAEPFPAVPTIQSGLGLTLHPRSWEGMVSKSDAYYATLTRGDPAYDL

LTPSNDKFLTIRLRKRG

>contig51546 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY57212.1|) 9e-53

MDLLSVMFVTLIYLTYFLCTRTRASDAGGVWSKIDHDIQRFVTLKCFLSLFVALLVTIVY

VWLNVGLAI

>contig52635 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65847.1|) 5e-98

MRPVFAHTQSDVLAYIDTGNCFIIDVLPSDVLATCLECGCEALLKKVAPAQRSEQACYNC

HVKLAVMFKRFVAGKMEGSRAKCRHLSDNTAVKSVKSLKNGVKPVIETFVLGQPLPQNGA

CNHYKHSLRWFRFQCCGKALPCDVCHDSSDCLEANLGKFASRMICGLCSKEQSSSIKMCS

CGNDVSSKKNTSRFWEGGAGCRNLLQMSRSDNHRYRG

>contig52994 Frame-1F

MANFSKNDERMVQFETESSALSKQLQAVTAKAVDLDAKAGDELRALQSEESLLEEHVSSK

ETQQEKLLAKQNEFAEAKRVLLSEVSALKNSQPDAMVNCSEKDERIMQLKIELFSLSELL

QASTAKAEVSYANAGSEMLALQSENPFLEEHFPAKIVQ

>contig53319 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57662.1|) 6e-28

MEILHRRHAENTVLWPYTYNLLLRHLCIQQKTLLNT

>contig53526 Frame-1R

MLGRNCLSRLHRSLNNTTLISYKAQSGLQLFANAVVSPHYQLHLLQAWLPLQLHHHSCSK

QCK

>contig53593 Frame-1F|Blast-insulin-degrading-like enzyme, metalloprotease family M16A, putative [Phytophthora infestans T30-4](gb|EEY56192.1|) 1e-131

MYGNLQQSAAPQVMQQVLQQFNFDSNESKTRGSLPLFSSQITKPRIVQLADACEYRFERR

DWNDANLNSAICTLFQLDCETEGSTVALRARLELFVHIFKEPCFNQLRTQEQLGYLVFSG

AMRTEGVDYFRILIQSDVASPQLLDQRIEHFIAHFRSILAEMPAATWLKQVNAVVKALEE

KPKQEIEEAMRAWREIANETFMFDRRQRVAAIVSTLQPRDLVSFFDSFIALHGKRRSKLT

VSLYGANHPITKLAKNNFASCDLPAVTSTGLTAAMLLQQQLQLESVDHIKVIDNVGAFKL

RMPLFPERATYICRAKR

>contig53975 Frame-2R|Blast-acyl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY63794.1|) 1e-16 NOT\_ORF

MLIPSMLNDRCMRLGGFRIATAPSLLSDVQVLHQTQTRPFMAK\*VYKLANRVMP\*MSNLE

KAVLESGTMGFDHNTFSGSLSLYNLL

>contig54093 Frame-0F|Blast-mitochondrial carnitine/acylcarnitine carrier protein, putative [Phytophthora infestans T30-4](gb|EEY64441.1|) 2e-30

MEWLEIAKDLNAGTIGGVAGIIAGHPLDTVKVQLQTSRETSAGILRTLRKVVGAEGAAGL

YRGLLSPILSNAP

>contig54390 Frame-1F

MKKRAYYRGLAESLFSIHRVCDFMRINKCPVVYSFSLSYVVRLFNNLARIGIKQIGCCYA

YDRMGARDVLV

>contig54501 Frame-2R|Blast-phosphatidylinositol kinase (PIK-L3) [Phytophthora infestans T30-4](gb|EEY66032.1|) 6e-55

MNDDVLIGKGRCSFYQIRPLAYSTLADMIHHVRDMLTLTQVSTIVDFYGKRIHDP

>contig54574-0 Frame-1R0

MAQIIFLEWLRDFDRRMAYRKVLLILDNCSAHVPLADLPQRIAPRNTTIHYLSLNMTSKL

QPCDQVIIRNLKAYYQRSFNCMLLRDLDNGVVQQANISILHAIQMSV

>contig54574-1 Frame-2R1

MVSFSRQILASFMLSRCQSERITSYISDVDDIIEDHLPTQPEDEQDDSQELPKMTVVDAQ

KALEMLETFWLQQDGDALGFLKSIQQMKDRV

>contig54967 Frame-1R

MPSLVVIRSGSKHVDYLENRSTWQPCSSNFLVTLTKIYG

>contig55003 Frame-2R|Blast-pre-rRNA-processing protein TSR1 [Phytophthora infestans T30-4](gb|EEY65644.1|) 1e-44

MAQLVEVQESILAGAASVEEPDHDVTGLKNCTIGVFSQHKQKLCIINCGCNLLVALD

>contig55212 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65879.1|) 9e-32

MYSAERNYSGCTNHAMAARCRHDFCDKFVVGQDSEWCRLHQIS

>contig56204 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56134.1|) 4e-22

MVERKIGSLIVTEPSKGIVGIVTERDILKKVAPRSIMTEEKLVRDVMSSHLICIQPNITV

LD

>contig56271 Frame-2F|Blast-serine/threonine-protein phosphatase 6 regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY61995.1|) 5e-64

MAVAKGFSLGYMGHLHRMCNIILTMLDELRSSTNEEGSLNDMRHADTVLELFEADDVTWK

KWEDMSTNVLAPLYEAERLPLGGVMLPLESDDPYSVMGFNQNDELLNAQFAEMLGASGFD

AENTNGFETEVDGKFTDTPMLP

>contig56921 Frame-0F|Blast-hypothetical protein PITG\_06232 [Phytophthora infestans T30-4](gb|EEY69745.1|) 1e-14

MGHLSLKQFNKGQLLIKPICLTCATVGHTRQ

>contig57085 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54809.1|) 1e-48

MRVDVTTRFRELAPARSVSTSNRCSAFSTEAMDLRSSLIELEKLLRRVKPQYLLPKCFIR

STGSLRMTEEEKDALDADLVELIKSCGSRIEALKVVAEAQPTVSSIEEYQREVVTYLLER

LKSIANGAKQMQNKRYQQPFLLSSRLLPEEDRQELDALE

>contig57162 Frame-1F|Blast-triosephosphate isomerase/glyceraldehyde-3-phosphate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY61612.1|) 0.0

MSEVHIGINGFGRIGRLVCRAAIENPKTKVVAINDPFMDLDYMAYLFQYDSTHGKFDGTV

ETRDGNLVVNGQVIHVYSARDPSEIPWGKAGATYVCESTGVFTTTEKAKAHIDGGCKKVI

ISAPPKDDTPMYVMGVNHKDYDGSVPVVSNASCTTNCLAPLAKVINDNFVIVEGLMTTVH

ATTATQLPVDGPAKGGKDWRGGRGCGQNIIPSSTGAAKAVGKVLPVLNGKLTGMAFRVPT

PNVSVVDLTCRLEKAASMDAIKAAVKAASEGELAGILGYTEDQVVSNDFLHDKHSSTFDA

DACIALNEHFVKLVAWYDNEWGYSNRLVDLMLHMATVDK

>contig58372-0 Frame-1F0

MLRTAFRLSITPRRVTTFVSRSFASYPPHEVVGLP

>contig58372-1 Frame-1R1

MRRVRSKATRYKSGYATRGNRQSKSGTKHDEYVAMRSNDL

>contig58668 Frame-2R

MCVFTIAPALARDTANSKGEVVAASRLYTSVTGIFRARLTTLLRSATVCTSVYVFEDTQY

TKMP

>contig58945 Frame-2R

MTKQTLESEAYDELAVARSTYVLAAATQDAEIIDKTKIDSAAKVPDAGATDVRAKVAQVA

YRKERKEKNTTAIKNIPEEPIVKIEMEATGDNRPIIGEGLAAKLESLDLAAETETETLTI

AEKETATIADEETATIADKG

>contig59223 Frame-1F

MTFILIFTNDVFFCYPMKGYYCINRRHTKRCYYSVSFHSGSGMCSSSRYDRSVSLCRFL

>contig59296 Frame-1F

MRPRCINDVVGQEGSEGCFPRL

>contig59357 Frame-0F

MPPTGLAISWHLALQCSFGTLSSLDNSRCCLGLLQCFHGKD

>contig00015 Frame-1F|Blast-ribosomal protein S2 [Phytophthora infestans]gb|AAF24805.1|U17009\_38 ribosomal protein S2 [Phytophthora infestans]gb|AAW62576.1| ribosomal protein S2 [Phytophthora infestans]gb|AAW67062.1| ribosomal protein S2 [Phytophthora infestans]gb|AAW67108.1| ribosomal protein S2 [Phytophthora infestans](ref|NP\_037632.1|) 1e-78

MYGESLTSINKDILPFVYGSRYKRSIINLNSISFFLKRSFKLIKIILQKDEKILVIGNNP

EVQFLLNTSFIKKNLNIIFFNREWINGLVTNKIRNSIFNKIIHYLIKEEELKLILIIKSS

VKDNFLNKELSVIKIPIISLINTNQTLKNIDYPIVTNSKNIQSIYILMYLLRKMF

>contig03890 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58293.1|) 0.0

MLALTPRASKDCVPAFGHFRDQLYVSGIMSTKAGDGSMSLEDEVTDVFAQLEAILTSCQM

VLTDVCYVHLYVQDMSSFAQLNDQYIRHLGQHLPPSRSCVEVKALADIPARVLLDCFALR

GSGVQKLQALRVRRDVLHVKSISAWAPCCIGPYSQANVLHRALILLAGQIALYPQTMELI

PGDRDVQTLQCFRNVCHVLEALDSNLRHVCSGVIFTTGELEDYEARERLLAASRHHLVTN

AELPDTFENALDSDESDDNIDKEESRLLFVKEVPLLVVQLSRLPRNALVEIELQALTHIA

FKYLVPRSFTRTNRSNNLCFHWQTGMVPRALCQITCTASVERRKDFPETRGLAKAVAEGM

WTCVLDSLVQALMPWDRVIHARTYYVASAFSSEVELAQMYLDTVTARGKVKSMPGMTFVP

VDAIQSNALVAILVTAQDLDKLETELWLHKQI

>contig05203 Frame-2F|Blast-SUMO protease, putative [Phytophthora infestans T30-4](gb|EEY61940.1|) 1e-114

MDKIFVPVNVGNVHWCLAVVYMSEKRIQYYDSMHGSGSICLKVLLRYLNDESLHKKKQKF

DDAGWELVSTTLDTPQQNNGSDCGVFSCIFADYLSLN

>contig09005 Frame-0R

MTDEDGELHNVILFAAEGQTDRYPMWATGTFSSKKKANLNAGLLTPHMVGITDRSDWYAN

NIYTDKSGKDVVIGWITEDNNFLNGQPQGWDGILSLPREVTITILRDIYDIDDHLVGKGD

WIVSDVDNMTCADGSTVESKTIKTLGVKPLSDLHLLRNEKEYEQVAHVSVKASSRVLKST

DLSFELMAEVSRFKRGSKVGFEVRRSLAGDEVTTIVYDDTEKKIIIDRSKSSSGDCAVFA

EHDVEPNAEPIWGHFYLYDLFTNAEQNDECVTSRENLRFHIFVDVSSVEVFVNDRFSLSA

RIYPCATQTESDGIALMASASATFKNVQVWTNPKPAWPETRKVPTY

>contig11844 Frame-2F

MDELNFVKELDAASNQALSNFLDVFLAGLENALYERWNQVEKLTALKVAKVKLQLDLTAA

TDFFQRPLCRIYLSYIKF

>contig12104 Frame-1F|Blast-chromodomain protein, putative [Phytophthora infestans T30-4](gb|EEY56540.1|) 9e-54

MWHLGVRYISPNRWAAELHVDGGGVRRLGLFSTEKEAARAYNQYLLQIYGNGAVQFMNSA

GNWSNNNAPLAISAVQPVPR

>contig13059 Frame-2F|Blast-serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A, putative [Phytophthora infestans T30-4](gb|EEY63669.1|) 0.0

MEDEVYPMTLLREELKSDEVGTRIKAMRRLRTVAQALGPDRTRSDLLPFLREATDDDDEV

LVALADELGGFVDLVGGAEHAAALVKPLEVLAAVEETVVRDRAVASFQKVVAVVPNVGDV

MVPLAKRLAEGDWFTSRVSVCSLFASIYAKVTDAGRKKELRDLYEKMCEDDTPMVRRAAA

SNIGNFAGAMEIEHIASLILPLFRILTTDFTDSVRLLAIENSAAIAELLSQEENLMQVLP

VVRSSVEDRSWRVRFSVAKDFFVLSRAMGIQITESELLGCFTNLLQDTEAEVRAAAAKNL

SGYVSIVKSELFTTEVLPLLSALSQDTAPNVRTAASVACMELAPHLGEATSKSTLAPLLL

LFLRDEVVDVRLNILKRMELLAQWMASFESVLLPAIADLARDLQWRVREAVVLSIPALSG

SLGGQYFQEHLLEIYVSAFTDMVGEVRLSATKILPKLLESLGSDFILQNVMPRLNQIFDK

SVIYQERVNVLHALKQMAVEKSSSDLLAHLMTLAIRGAHDKIPNVRFVASMTLEQLCKLA

DASVVASQVRPCLTEMVNDSDMDVKFYSSIALDAVQG

>contig13521 Frame-0R|Blast-cytosolic endo-beta-N-acetylglucosaminidase, putative [Phytophthora infestans T30-4](gb|EEY53227.1|) 1e-102

MYLVATASAKDSSSTTISVEGITTLVVVGLALLYWCFYRTQPISPPTDLSINSARETRFI

TFIEHEISTNETVLFIASKDHLAHFQDFFNALRAPFHVVNLSRIAGGTRVMELLRERYKE

PTKNEFLFRKGTFVGGSQPLRSLLVEERQTKLNDQFDWSRIRLDTKSNTGVLVLSPMNGF

QCVQDSNQVFDVATLKMKLLHTVLELRAFDIQNLSKCRVPIALKATKQRRRSKLLVCYDM

TREYKEDRFKHKLADLNETQFYQWDLVDVFVSFSHALVSPPPSGWIAAGHRHGAQVLGTL

LTKGPDGINQCNEIFKDTRSAETFASKLAAIARQSGFDGWLIVVQNDVSPELVMNIHVFL

RTLSTMLQLHNPLAHVIWNGSLSRSGKKCAYVRFDDSSAEFVCNVDGFF

>contig13842 Frame-2F

MLVLFETAAGHALFKVQDEAKLSSAEDVYKHFATPEKAANMLKLKGFNAFKDTTEAVAAA

TEMVDGKMGKTLRKFLKKNVVDAGLKDKLAVSDKALGSLIKEKLSIACVNDTAINEVMRG

IRANMETLITGLKDDDLKAMTLGLSHSLSRYKLKFSADKVDTMIVQAIGLLDELDKEINT

YSMRVREWFGWHFPEMGKIVTDNLQYAKCVLKMGMRTQVKTLDFSDILSEDVELSLREVC

EVSMGTDISDEDVTNISALCDQVISLTEYRAQLFDYLKNRMNAIAPNLTVMVGELVGARL

IAHAGSLMNLAKHPASTVQILGAEKALFRALKTKHDTPKYGLIYHASLIGQTAPKHKGKI

SRVLAAKTSLAVRVDALGDSTEATIGFDNRAKVEARVRQLENGFSGVPNSNGKTKNEAKK

YVKSESSKSYNADVDMTVSSKKRKADEADITEEPKLKKEKKGKKEKKHKKKKAVEDAVEE

KEDKKEKKKKHKKKKSAEE

>contig14436 Frame-0R

MRIAAPLSPSRGHRYSEPAIPDLSFQMPSNVHRKSFMPLDKPCLHDAVELRDSYVSEANG

LNGFTFWNHEASSSQLMTPTGFEDPYQGVIIDVNNHSVNNQGVVMYHVDIQSPDGILSTY

TIRRRFRAFKNLYNELCRLLLDYQSSKAPVQTPIASFSMDSLENHIPLSPHSALTFKGSP

VSTSNYRTVTFPTLPSNGVWSYLKRHDVRLVEQRKKRFQEILRLAIRHPATKSSPVLDEF

LSVAPSEISLRGSSYVSLQDYSVPVFDRQRESIERRQRKMRVLEDRRLRAGSDVGTRCGT

PS

>contig14685 Frame-0R

MQVSDFAVNLSSTDLGILLSIVASLNESMKEDIEVIKKRQESEVRINKAQRVVEENRYMN

KLKKEFKLRDTDGGGTLDLSEIKSLIRSAADCDNLTKTEFDAIVADFVSIVDSDGSGDIS

FEEFSSALSRDKILYPRLHCKGVTITGQEYVHPDMQRTKVPFLSGDKANTLANAAALVSF

WECYEEQVGASKSSLMGQRPITVQKKMVRTFKNYEYAQEAWNRIINPSLIKPIEQTPWLL

SKEMNMGGRGDVIDQLLSILKDDDINQASLISAFNPEQQLFVQTVVSTCFGGFYMRMIDD

MLPMGMPAIETSLEELGIYANFSVWEGGSSVSATEFPDQGRSGNNFGVAKISFNVYGNYY

NAKVRQVEPFIEFYQGTLDIKKELESPLMIIYSSDRYFQFNVTSSFMEAVNTNVASFSKA

EHRSEAVRPHVKEIGALFWLLNDSGVNVKYYMVSKQQKKGHVREEVVTAVTAVSTGSTHA

CTLLSTIEEEQYEQQSLKEKQLRQAFRSADQDGSGELDTEEVRAVLRSVYEEEDKQRRPS

GSKNVLMRRRSSSCMLENESEFAKVVEDFIALADTDKSGQVSWEEFKTAIAKSRVMVERY

LSVEIEGYQAIHGVPLMSIGQTQVYELTPFFEDVESEESIAELYDLGVALLTKIERPTRQ

ELQKAYACLHRVKEMDDNYEWIDSYYADCMRQYLPVLAAIHISVDGLYGLQVKISGAEFI

RNGTAKNTELLMYNELGDIACCNPKHNGGDNCYFMMSALGTISIPLNLVGAGTFAIRQTG

ETEWSNQLKLSVSDQRLYKKMTKFEQLEVQKAVRGDGHSSVLSAKRAKEKLGMNAILPDP

NEFVPAGKEVVYPSSSCIDNQPTIVVETISANSPQLGTWSLTIQPQLVLHNVLPCGVEYA

IVQAGDCPLDTLTNKKEFRITDNAGREKNSRSVKILGQIDYFSYVGEVNCRRMWIESGKS

IQVFGLDLSKPALMKIRHCASETSRAATWSAPFLVHLETSRQSFNEDAFKLHFSDGPNFV

FHPQWEENAARSVYFYTPFWIQNRSGLDLRFKLSRGRVCTIEEHRLFFPDAKEIPLMVVA

PPDKALLSVRPYQVTPNTYEGESLMSETTAKCLPNFDKLGWSDPVDLATVSRKGELRPSG

SGDYSFVFAYEIRAAPAQFFRSKIIVISPRFIFLNHSPRLLQMTPIILDKKGNRGRTYFR

EANCTVKEGEAVVIYHLIGPEKYVAGLRIRDMTTDSQEDVGNWSPNLPLFKLASKLSDPN

VAFNIAEETVFWTRGSLGNGPVCSVSTRETAETIFVTVKDVSASPNYRIENRSTRYSFRY

VQRGVKTAEELVLKPLESHSFAWEDPTGDMELRVTASHWKIPTLVDFMRIGEVKHAPEGL

FGEVYIDGSTRVFALGDTKVYSEVRRRAISRDWLSNTVIDVSMHGLGITLVDEQPQEILN

ITMENIRFDSKTGSRRVCLMVHHVQFDDMTPHAVYPVVFAPVDSGFNSDKREGWLPGDGE

RPFFTLSFETLPQSGIVIVNDFDLQVEPMTVKLNLEYLLGTNNLLFQFIPGSDEATILQQ

GLEAKNAMLQLNVPFPDNSISAGMLMYFKRWRMSGYELDLVFDSLQEDKGEGISAILGTT

MGSIVGGIAHVTPEFHFGEIVYYNRFFYEYDLIYDVVLKIVYSVIGQWYKIVGSVEMLGD

PVGLATDIVDGFALAARQLKRDIRGKSRRKGESAITVVQTVFGVPLRSIGKVSNGLGDVV

KKATYFKSQEDTNEPRHIPEGFVQSGKVLGKSIAYGVSGFVKEPVRGAKRGGFKGFAKGV

GRGTLQLVASPVVGTLGVVEKMSQSMSNTTHLMDEKPFNGTRRPARNLQAGSLKQLSDSN

VITEVEVHCLYIEGLPDNVSPKVVVRVYSQTNGYPATELGLYKSSTARHTGTPTYDQSWL

VGVSSIDTFIEVNVYHKRKPLPKKRLGYVRFSMEEIFREFESIPAKLLADTNVKMQLKRR

KRVRGSIICKLASASEHRMEIRDDSWRQRLNRAPKSGSSFLSEDEDEGFEDYDQEVSVLS

GSSICLDSTFPPSPVGFPLQDCETEAKIYLSIRYVNDMRRYA

>contig15479 Frame-2R

MHSQLELISLQQLNGYRGFSFSPCILCLETEPKSRGEKTQNTVKKQFVNVYSIPNIFF

>contig15765 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62020.1|) 5e-37

MSGEDVSVVATEAMDIPDVIERLNKPDKAEHEAKVAALDDAIKKLQARSNVIHTEIDALK

SNRSGYGGQIQEAKVKFAALRAEKDNLIQQRNMITARLRQARDE

>contig16001 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56544.1|) 1e-106

MVNGRGGGRGAVPGGPSAPNLVGNPPPNYVCYRCGTPGHYIQNCPTNGDPEFDQHRVKKK

TGIPKSFMKAVSDPSEIPVGGGKTVVNAPWGGLAVIEPQNKNFSKLMAQSGGSATLDQFI

SNPPEHLACPLCRRLMSDAVLIPCCQESACDECLRSALIDRKLTCPLCSVNNMPP

>contig16258 Frame-0F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY54248.1|) 4e-30

MKRSTRLPHWHFVWGPFFIRGWRLSLLLKLLIGILLVLYFFWNVTTFVLTMQSRPPGLRS

HGDVQDLHGDVLDQRASVLDPHASVQSLDDSYEEFPEITDSEEAWWLQPDMYIEDGGCDF

SAVVALFKPRQLELNCGNINKLDVGDYVGRGYWRKVYKTTW

>contig16539 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54937.1|) 7e-99

MNLFGYKLLRPTMFTCGFLVGGYLVSAIVEYIVEGQSYHRTAFWISFLIGGVVLGSLVVA

IYNFGIFLIGAAAGVFLATIINASFGYRIYPNDPTTGLLIMAIVLGLICGIISYKVERLA

IIAATALVGSVVLVNGVGYFIGNFPKLTGIKDYRHEDDYGDYVYDVPQEWWAYLVAMLVI

FLAGLTIQIKTTSKM

>contig16917 Frame-0F

MKLILGLNLNKDDLNYIQRNGVVLRSASKQLCIWSLVSAI

>contig18744 Frame-2F

MNRIFPPGQRWLKLLLLVLVMLPMVQAMDPSKDYYKVLGVKKDVSDRELKKAYRKLALQY

HPDKSENADDKEAAKEKFVEVSEAYEVLSDAEKRKEYQDARQYQSTTGAGQAGGFGGQKS

TTEDDLASFTKMFEGIFGHGFGTKGGFGGGTQEFQFDGFDGFGSTRRSMPSHLQPRQPKT

LFGPDSIVKTLSKKKFQAKTRDTSGSCGFMNSTCQVRNSVARMKTSLVICSKKCTWGR

>contig19332 Frame-0F

MQLKYFVAIFAVQHGAGSALDSNEEEQLIDPTLRRLEPPSSFSANQQVNNSQGALKPSRR

RVRYDDHDTLDQRSALLFATPLDRFSAAEKLIQDLETIQASGFTSAHTILGNLKLRSASI

PPENLHAVTDSHIAEASRTVEAKRPNTKSKRSKTKSKNRESRAKKLSIQDTKNEKSTYEI

QLDSFLQTYLEGRAKISDPILCIYYDYAYYVALKSNTPGKQFNAFALPRFKNDGFDGFEF

LATIDAYVQQIWKETRSIEGIDAISPKDATFNAETFMKVLRYVSLMKENQNGLLTEYDVV

YLSRFFFFKKVTVRLLDWLGEHSDLKDLVPKIHQIYQTAITNAQTRAAAEVLKAPSDTL

>contig19404 Frame-2F

MTTLRLNYQTQASHNQPSSLFSIEVPHRTPNG

>contig20677 Frame-2F

MTRHNSTAEPEAEDKTEMKLANDPIKTASINTFAKKTSRTKKTQDKTEDLLSPGQKQLLS

RQTTLDADYKSTIKTV

>contig21551 Frame-1F

MVHELSQILGKFCERCLKLLRPSLYMVMRVSVSLYYGTQRA

>contig21649 Frame-2R|Blast-serine/threonine-protein phosphatase PP1-gamma catalytic subunit [Phytophthora infestans T30-4](gb|EEY68260.1|) 0.0

MASSGLDPIDVDGIIEKLLSVRGARPGKQVNLSETEIRGLCLHAREVFLAQPILVELEAP

IKICGDIHGQYYDLLRLFEYGGFPPDANYLFLGDYVDRGKQSLETICLLLAYKIKYPENF

FILRGNHECASINRIYGFYDECKRRYNIKLWKTFTDCFNCLPVSAIVDEKIFCMHGGLSP

ELSQMEQIKRFVRPTDVPDTGLLCDLLWSDPDKDIMGWGENDRGVSFTFGPDIVSQFLKR

HDLDLICRAHQVVEDGYEFFAKRQLVTLFSAPNYCGEFDNAGAMMSVDETLMCSFQILKP

AEKKQRYAYNGLGAQRPATPPRK

>contig22099 Frame-0R

MEVVGRTETAKIMQSLIANNQGLGIVTAMSFLAAIILWVFLLMQLKRIAQNETANESFKR

EDLREEADLDGETSGRRMFRFLFKRLSFQKRPKMVVPRRELKKALDATWGGLFSPDAIMN

TEESFSLEDVNFNPYKLGSFKHNLFDALNFRLKQKSR

>contig22262 Frame-2R

MLTAVLKYLGACIKVVKFSAGLTAHILRISAKLHDLMWWDWFISLASSRKPLVTCPRKDS

GRCTGTREGI

>contig22833 Frame-0F|Blast-vacuolar amino acid transporter, putative [Phytophthora infestans T30-4](gb|EEY70051.1|) 0.0

MEDNTTSKLQPVSGSDGEPLLPADVHDITEEGSDMTRDIFFAILKDTQDGPSRPKSLPDQ

SEILHEDIGKASDIAQPGGFRRDHVITNLGGISPNVPSYVQDSFLESIQPSPSILQSTYG

DFIVANLGLADDGDDIDETVTPLLSRAWKRRPEKQQRGATIGKTVFTILKSFIGSGILFL

PKGFQNGGMLFSLAALSISAALSGFCMLRLTDCSDLLLRKGRTNVSYGLVGEKAFGKLGR

VAVNTSLVLSQTGFCCSYLIFVEKNIGEVILAAFGIERTTASSSLTLILLQILLYTPLSW

VRRIEYFALTNLVADLLILFGIAYIISYTVETLHDAPPNSATWENFNPTSWAMLLGTAVY

CFEGIGLVLPIYDAMDDDIKHKFPRILSFTMLFLVTLFSVFAGLVYAAFGQNTQSVVTLN

LPSAQVSIATMAVQITYSLALVFTYPLMLYPVVKILEGYFFPEFRRKGYWRWEKNGFRFA

LVCLTAVIAYYGKDELDNFVALIGGFCSVPLAFIYPCLFHSKLLSQGRFLNNTVIAIGIF

TMVFATYQAASTWK

>contig23687 Frame-0F

MVEQMRSVGVLEAVRIARHGYSVRLTHAKFIELFSGFQRCLSTRDRATKMSKHDLAKCLA

TALIDKLLMEDGTVRMDEKFSVLTRVTNDGQGTAFENDNRRKDVQIGKTLVFCKSSTYNQ

FSRYRAELRCHCATVIEKHYRGYRRRVWYQKLRGFVVHAQAIVRGFLGRKRTAKLRQLRR

KNAALHIQSDWRRFVTQRKFAMILEHKHHVDAATVVQSHFRRVMAQRVFALLVMNKQRIT

AVIRIQACYRRWLVQQQIADQLQQNLRIAAAISIQAKCRYWLVQLHRARLQRKKIDTTAA

VRIQAKCRQLLAIRKQEKLLRHMVEVFAAIRIQRLCNRWFFLRMQKRRKRELVAAAIIQR

YCRRWLKLNSCVLAKVKHFRLSMAFRKFCRACQASKTTYEIKAKPPSLSVDSLASPVKRN

SFSVPVTQSSSEQEDSSTSDDRMEPPLCISAPSHRRISSKQRSRASNRNRSRVSSSSYRT

DNRNSLLENEIMRLQQMLVEQQNEPQPDKKCQSFSSFLPPRSRTLGLHQSTRSTRSRNGL

RYSMDGASFENEFLDNDDNNSLLPPRRMHSATAAQQTDQVSALSQKIEELDAKCKFLEQL

VSRTVYENAARDSFTYGRASLSAREQILADRSLLYDERPGSDAGSDVDSIIFNMQSQMNM

LRQSIATNEQTLHTSRKSHVMSLSSSTRLTRTSSSASMPSFSSFPLNEACPTFPSLPLSE

SQLSVGSSSNDYGRRVGSNSLKFPSTPTSSNASSSYQGHPPLAPAHFGRSMPRIVKWARS

ANCYECDESFSIFARRHHCRMCGNSFCHEHSSRRLSVFGIGFDDEPVRVCDNCFAEYYAA

SQELPSPLYSTQFGSSADPPLSSSMRLSGL

>contig24071 Frame-2F

MEVVAFETSTRVRVALIQTTSDAELINAAVQNCQTKLQTQSLDFEIFQVGTIEQLPYAAN

KVTKSGAFDGAICFGYLATQDPQFATFSAALTQSFMKISVQNVCPIVQALLMTESRVALV

KVRSGWGTAFADEIMALIHVGGYNKPSMYPASGVLGNKPFEISRGNLLPAKLLRGSTTVQ

QSLEKLRTSLFEHGATGIRTLGRKFRIIDDDGNRLLSLEEFRKALREHAMALRESDQDEL

FHFVDTNHSGSINYDEFLLAVRGELNDRRMQLVLMAFQSLDTDGNHVVDLNDLKGKYNVT

KHPQVLEGRKTEDEVLLEFLDTFDGGAKDNKVHPNEFVRYYANISASIDDDDYFELMIRN

AWHLSGGEGACANTTCRRVLVEHDDGSHTIEEVKNDMGIAAGNVEAIRTNLQAQGIQDIQ

SVSMKDTIQTEANKRASTYPQMARKKLQHGAGASSIIFG

>contig24457 Frame-1F|Blast-GTP binding protein [Phytophthora infestans]gb|EEY57534.1| GTP-binding protein SAR1 [Phytophthora infestans T30-4]gb|EEY63603.1| GTP-binding protein SAR1 [Phytophthora infestans T30-4](gb|AAN31482.1|) 3e-95

MLKDDRVAVHEPTLHPNSEELIIGKLRLRTFDLGGHETARRLWRDYFATVDGVVFVVDAL

DRERFPESKRELDTLLGYDELANVPFLVLGNKIDVARAASEDELRSSLGLYETYGKEARS

DKDSSIRPIELYMCSVVRRMGYADGFRWMAQFL

>contig25106 Frame-2F

MLKQSQKDSDRDYGDLKESNRLLFEEVNERRRSIKHARKQFKKAIQENTELLKAIEMYKD

AIAGRDKDIDKLKSTVMKYAQQLQRRVEFKEVKQTLLEQLEQTQYMITETYKRWENSPIL

VSSQGKDPKYKAAILQLDDYIGRMHLVSGRKVRDLENEIQKAQN

>contig25274 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57771.1|) 0.0

MEEILSFAYQSDVVLVDLPVAISHCLGYEVPTTMVFSGIVMMIVESTVKQAIINGDQIVF

SAKNVYNLVFNSTAFHDPHSSVQELQDFIDTNSSCGYQLKRLTDHVIFYVNTYRMKHPKA

SINDIRVEMSRSPLVLTDVPAATNNCMSELLAYKSIQAAFETRDLLRKTFGVIVDQLVET

ATTDRGHFVAEAQYMLETANYGLTAISGLDPTRIVWLASQFVQPTCGPTAFIGEIDDGSL

YDALALTILDEAFVGSYGFWTRKGDGVVKLIFTSHDTKEVSVVIHSGGVKIDEVRVKAQG

KATWKSTVSKLHDKTLYIDRWRANFFGFPGSGGGSLMLWIPRASQGGHLTMHVRINIS

>contig25810 Frame-2F|Blast-geranylgeranyl transferase type-1 subunit beta, putative [Phytophthora infestans T30-4]gb|EEY70138.1| geranylgeranyl transferase, putative [Phytophthora infestans T30-4](gb|EEY59744.1|) 1e-153

MHLRTLGDDLSRMNKLAIINSLKYYQNKETGCFSSTNSGTEEDMRFVYCACAISHMLDDW

SGIDLEAMTRFINSCLNYDGGIGLSTGAESHGGAVFVALASLNLSKRVSKLECEQAELER

WLVFRQQGGFQGRCNKSADSCYAFWNGAALDLLGKHSLVDIQSCKNFIYTCQFPSGGLCK

YPNTVPDVMHSYLSLAWLSIAARASTHMNDKVDLPDLADSNTKLQVPFFPRSREQNNKAS

>contig26680 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54074.1|) 3e-60

MASVPMCMLAVMRLREDFAFHLSDSGKLVAIEYLTPYVESDVCTDSRTRSLEDMHLSPSG

TVFKVQGGPLPPKNVVGMRDRAPQGVKPVKSEENNDEPEEASQSFLRK

>contig26943 Frame-1F

MAYRLVLEANVLSHLSLNSRKQSNYIEEQRTTWCTTSTQRILDRGSTNPRFHQCAEPKHL

CIVIGSDDDVTFGNFLNQELAALSLKCQNINCNSLMADHAHSFSCRSGTIKISFEELPDI

VKLSSPNSVSQLKGAGLMDKSFGFEQDLNLRAKITPDFLAQTSLRRTETPSSTENEYPQV

LFWRWCRECEKVLTPIIPLEKYIYKYSFARFLEVLFTEAEGNSLPTSPSATCTHTIKSHV

FFFNIGNSVARFEFFHKVSLRLACIDIKCSDSAPSRAKFERAVVESEASARLASLKRQLQ

SLTKSFTEKVQGINGAVKAFEQTNMTHYSPQLILEVMCISKMVRNGDALFRFKLKQLEIE

FAGNLGACDVTQRALYLFACKWITCLLRLRKLIKKHILIQAAPLAPKSASFTLGSSLFHR

MAALSSMQSPRTAGLSPPELGATVRYYGGDEMIDPPYRCRSSVALGSLPKLEASTR

>contig27904 Frame-1F

MASDNGSNPSSTVVLKSIRDKFVEYKESLLRQLVDERNGSRDSQKEEKPERGTQFGDNSL

AEQEMAPRKAAESDEGIVANEETCLGAKQVMLKEVKTEALPLAEVPGDEGIVLNKLETKS

T

>contig28985 Frame-1F

MDTLYHQLLATEATRLVRVPVSKGRVLNLRGSFEKSVCRISFYELCETEKGVTDYKVITE

TFTIIMLDNVPVLSLNEHDAVRRFVLFVDEIYEHRTRLILSSEAVTPREIFCFNEASAGA

TGNVCHLVAFQDLYVATKRAVSRLYEMQSERYRREHELTRSKRREPRV

>contig29256 Frame-2R

MLNNSSKNNKYQQIYYKLNILTRLVTFEL

>contig31712 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY52981.1|) 1e-121

MADVLQEDIEERGSSIVSTRGLKIPMAHRVPSTFLRYISTHAAIKSLELPPLTDYSPLAS

LSSTLHHVRLQQWCTDDLAQIVALGNMPALTRLSMSLPPIAQVMDLAPLEGFQHLTQLEL

LDVLFEDLTPLGTLFNLQKLVLSLLNRNKRQLARRHKQHQTAFTFLMQLTNLKELSLVGR

VDFKDTALLSGLVQLRRLWLNATKIDDVAPLAALTRLEVLDLGLTPLKTIEGISELLSLQ

SIWIPEAIDCKALRDATHFPRLRWIWHPDKCNCLWTNHAF

>contig31987 Frame-0R

MQRFQTSLRPKTVWQRVVLFNAPSTVQREGSAAVIRRCFSALPDHEVVGLPALSPTMEVG

TIAKWNKSEGDFISAGDVVCEVETDKAVVDYEATDDSYLAKILAPAGSSDIAVGKPIFVT

VQEEADVTAFKSFSIDAVPAIDADPTALAIDAPAPGQPASPAPAFAVSAS

>contig32995 Frame-2F|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY60597.1|) 4e-95

MVKAFEIKKNLIADINSEWSIALGQSYYFNGKASQKYASLCLMAGDPAIVGEDDTELLSF

CIKKLEGLVAPFLTNGWTNALDYDLIYRGVLSSQGFTLHDASVDFGNTMYNDHHYHYGYW

IVTVAIINKLDPTWSGIPALNRMAGFLIRDVANPSDADLNFPKFRSLDWYRGHSYSHGIT

ALGDGKDEESTSED

>contig33145 Frame-0F|Blast-ras protein let-60 [Phytophthora infestans T30-4]gb|EEY66370.1| ras protein let-60 [Phytophthora infestans T30-4](gb|EEY53051.1|) 8e-59

MREGKGFLLVYSVTSRSSFDDIAAFKDKILRAKDVDNVPIVLVGNKCDLDNQRQVATSEG

KELARQWGCAFMETSAKERCLNEECFYQVVREIRKSERPVRAERPQLTQKPQKKSGLKCN

IL

>contig33596-2 Frame-1R2

MEAFGCYDFCRLKKRGGGFA

>contig33659 Frame-2F

MKSKIVTKQQKMRLETERSILLESKSPFLCQGIQFLESTDEVCIIQEYVEGRALYECVWK

YSDKGRFPEHVAKFFAAQLVLALRDLHTQGYIHRDFKSGNVIVEKCGFIKLVDFGLSKKA

SVAGNRTQSLCGTHYIMAPEVFNKKTYNLSIDWWSLGVVVYEMVVGHPPWEYLCPTNTTI

DEYFRSIECKAKSLFRATDENITDTLSCFSPELKTLICALLQKNPRERLGKNGAAEVMKH

SWFYDIDWLRLESKEDRITVPYDFYNDYNVLHARTPSRQYKARESISSAESIDSDQNAKY

FADF

>contig33880 Frame-2R|Blast-GPN-loop GTPase, putative [Phytophthora infestans T30-4](gb|EEY65657.1|) 4e-30

MVQLELPHINVITKCDLVDEKELSKYLDPSEGYLLESLANATDPKWR

>contig34144 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62254.1|) 1e-57

MALIDLSDHYPVHSTFEFSVTRGNGKDSDPMTYHLDGCATDADCHFRSFHCYCHGRGCFY

KGKPTDGWHLDANHGVNRNCLYQKTSFRCLCGPL

>contig34531 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54823.1|) 4e-54 NOT\_ORF

MTCRTGMNQSGNTPKKRVFLDQPLLGESFGTRDKIIQAGRVALLSRWEVRVFAI\*ITFCE

ILLTHWLQTESVTEGSTGGQTSYYVWQLHERRILVRSTTHARLFDRSLSKGGLDTGTTNR

SSTPLSVFIKPDYHLLGIEEQLTISERCRFWLHSWLRGGSSILVARVHPDANAITSFKTY

SPASLIYGEHTDQVLPLELFNPSCKFQWLSTLFSTLGELPVGNYLLRPRDGYGSSTFGKK

RGGIEVLMATTEPMKHNESVVDLYSFMPKSVTAGTTMDLKACPTSILPSWNLPDRIPYTF

QTGTYCLSFFLNGECSTLSSGKSCDLVHLRLKEHPASSSKRLVRMKRWNFENYTEVLKTA

TRSNSKALIRPKRVTLPLSFCGEKNRPPTAPSLADVYAPVHCNKRPDACSLPHFTLHQI

>contig35604 Frame-1F

MLAYVTLSKFPLEIVELCEPSDIAVRQKIDEKSQRTESNLEAKLDGLLQRLQEENDSNVQ

HEIEKLAAKVIESVSLKLNAGIGRGKRMLTGGTRSQHQRRYGFQQTTSNSLISSSATREM

KALLPLRAEVQSMALILADLSGFLLAYQPTTPINTIGVKRKDKLLRLATQNVDDFMKTVT

STLQSMELPWGSSCASADTNENCKDFVRTLVFMEGWWGFMATYLAMMEELAELKTPTGVD

DADVVFRVFYEGAAGLLGLLLYDTSNKLGGALAAGALVGQLCDSKYWHKPQIRLMYEETI

NELSRLLALSMEQSRVFTVDSGNAHVSPLGAIIALQLSFGRRKIGANDCNNFLTLLNKIE

KMFVEIYADTSSAFLAAFILLGRSHIAAVYLNGEELETSNNFQQRQQRVKTLAEYFLFTF

LHNNTMQQNQHFFTHGNVLFPLSPATGAITSIDEIAATYKQNLSNGILLRWASMMGLALI

ASAFPNIGRMDWLDNLRKVLVFLWKSEKSTSIVAVALGPVLLQCVNYNMVHSSVLETFVA

TCNQRAANFDSKSLNAGFLTMSAAYILSCLNDFGGDRAFVQDQTNLAVGQIERFIKDSCG

AVRSLMLSAVANFFYLPLGVSSLFVPNDLNMEGMLEMTLDLKSIAVLVKCTQSIHESERG

ISLAVLGAIARATDRIFVSQKNYSLEYEIRTLPSEKLLTKILNWLRNTKASTDNDLSPRK

TSSKRSTAVSLLGCLTLAGSVLPPLDYSSLIHNVMLRFCSVDVSIACIKFAATQENCDDF

VASKILSSKWFGNADAFLQSELILWISRAAFRVSAEILRCLILKTFGILNIIWRQDTCSR

SSILLFNSWTTMFHDILNNEPIHEMPRISIKTVQEIILNRILKELPFGLHASNFVDQFAT

RVLSEVDFGKRGFAAVILTPAVSSPSIWSWWLNGVFFLNVAKGRLSSISKREASLVVQWI

IRHDFTEWTDTVFINAHLQPIIAEIGALIAVSIKPSNAVALLLDVIDAFSRIFECSSQSN

VVKRRVLFDLMAYIISWDVCTIYEQFQMIMPQFTSASVINAVDLLPFGFMKFAYDSETGL

VLGEKLFSLLQRLTHKRTDDLDKFVDSLQTLCHQMHLASDDWYVLSSLAGEIKEMWSLKV

>contig36410 Frame-2F

MRVGFNKRKGHELRKEPRHGERLKTNGLSEHGKPQETAVEKLSGSDLDDVIKASDNGSVT

AETSRAARKTFKFSSIPLKPSNQVSKKKTVRTTPVAFFNLSNGGSDSTLNAEESMRQRDE

KGLLEAEKKKEVAKFLAEDDAVPKQLDVAISEDEDAKKRKSHEMEAAKQNAKVQKVVEEA

DPLDAYMAGLVDESARANSSAYVISQSEIEAKGKINIYGTFLPPDAAEQSVAVASSQEPS

TLNHVPNETLEEREAREERDLREFMQAIKDKRIQEKENEYSAVLTGHKVGSEADEDIILK

QNDTGRIYQGFEEDVIGEDSLLVDHRSALEILQEQQKKREIKPVDHSKVSYMPLQKKFYV

VPKEINEMTEDEIKIQRTESEIKVRGKNCPRPLQKWNQCGFSVRMLQLIKKHGYEEPFAI

QKQALPVIMSGRDVIGIAKTGSGKTLAFLLPMFRHILAQPPLQESEGPIGIVMAPARELA

QQIFVEARRFSKGLGLRATAVYGGSSVSEQIANLKRGSDIVICTPGRMIDILCMSAGKMV

SLQRVTYVVLDEADRMFDMGFEPQITKIMMNIRPDRQTLLFSATFPRSVESMARKILRKP

VEITVGTRSTASGDITQYVEVRDEDDKFMRLLQLLGLWYEKGNILIFVNKQQACDQIFQD

LMKAGYPALSLHGGKDQVDRDYTIDDFKRKVRTVMVATSVAGRGLDVKDLVLVINYHCPN

HMEDYVHRVGRTGRAGRKGTAYTFISPDEEEYSVDLVRALVNAKQTVPSELAVLAENFTA

KVKRGEARYHGSGFKGKGFTFDETERNETQRTADLQRRQYELDQGILVEDSGVADDDDAE

EPFKESVVSTTDKQYAPAGQKTLPVDSEAMSAFIKAQKIIQNLDLKYKISGSGDNHFVEE

LEINDYPQHARWRVTQKEASDSVAELTGAAIITRGSFIPAGRKPNPSERKLYLAIEGPTQ

SSVIEARRELQRILDETTMQVGLGGDKYGKYSL

>contig36663 Frame-1R

MEISIYASCQLDLASTISDDSFTFEFIEARRLDAIHMALHYHDADIRLFCDGKAYCIKRL

SKKHAQVQHVKTGYADTEELMIDGHRRLALEPCDINLLEQQRCTQCSSARCSIFESIRCE

KSYARVIYVSDAFDNVCFASRLTATDLVIARSPLPPKEPNSYMINAPIVTWCSEDDLYRC

FVQFCQSPYALVHSNPRRKSNVLVLFDYDWSLINENSDTFIFQTLYPELLSTLHTRCKTE

PSWTKIMDDM

>contig36739 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65543.1|) 7e-88

MDSLKSMLFSGNVTPRPKAVKWLGMDAHVAGKSDQMFISAEASTQVLQPLGDTPINIISI

FGAARQGKSFLMNLLADQQDLFKISNLREPCTQGVDLSGHFVPLQKFSSFNGCSTITSKS

SQDIHVGFVDAEGQGDRDITYDSRLVSPVLLASKVVLFNWKDSLQADRMLNLLAVLARAA

QG

>contig36784 Frame-0F

MTSKRRGFGRCNNVVFHRCFKNIGRIIHDIGHSSFRNLALGNLMIRHNCKS

>contig36999 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67506.1|) 0.0

MSAPPPNPSAAADTPPLKASFSPRDELNENDLVGRDLIQWLESNGADSKKLALQEYAPEV

RGVHSRKVLVPGERILVIPKKCLITVEMGKQTDIGRQLVARNVDFVAPKHIYLMLFVLTD

MEHLETSFFHNYYSTLPSTLSNMPIFWSEEELSWLKGSYIIQQIQERKAAIRKDYDVICK

VDPSFARFSLDRFSWARMIVCSRNFGLTIDGIKTAALVPFADMLNHFRPRETSWTFDQSI

DAFTITSLGTIGAGAQVYDSYGKKCNHRFLLNYGFAVEDNTEEDGRNPNEVLMDFQLSPA

GGQLFYDKRAYLHESGIYTMDARLSCSHSDTNTREGLSFARLIVATEDEFSIMKMTSPAH

SSPPISFDNEIRALQYLRNLMTYQLSLYSTTIEEDNELLASKQYPLFSNRIQALFFIRGE

KQVCRYFQELADRVTPIFSRPLAQCREELQRHFNGDGDIDRYAQDVIAYLVTQVYRES

>contig38359 Frame-0F

MPPVPPERRVDEGAAPKSFGDVASCSYCVGFSVYTKAMWRERQTPECRGIEITVNSSRER

LQELRERSSHPRKEEFTFIGVGLSAYSSEWMKEGTHLPFVKGVGIIAIHTEVNDELMKHI

EERKRIKRELQKNAGNRGDLQDGGSDDLIDDNDDDDTFGYEDEEAVDDGQALVESEVVHG

LKTPRGPAVVPASITVGEMKDRIVETTSHSVNAMFKFWERRMDGFSDRYLDSCRRLKEQM

EIQVVNTPRNATWLLRRIDEYMFGDEKDNNKAQCTVRPRLVDYR

>contig38445 Frame-2R

MMLSTGKRLLKPNTKNYSKAPRGPRGTMRNAARLSGDQF

>contig39460 Frame-2R

MQLLSAGADGLVKLWTIKSNECIATLDNHEDKIWALAVSKDSSEMVSGGADSKINLWRDF

TEEEEQTRQEDHDTKVLKEQKLSHCLRNNKLLDAVQLAFELNHPSRMLQILRDLLEGPRH

KDQPALLGDDIDTFVPEDIFYPVVQSLTDEQLVTVMEWLRDWNTNARNTCVCQVLVSSIL

HQMPPCRLKSLQGVALTVEALIAYSERHFYRIDRMLQKSYLVD

>contig39514 Frame-2R|Blast-ATPase WRNIP1 [Phytophthora infestans T30-4](gb|EEY53542.1|) 2e-36

MAISSYQAAHFIGMPECDVVLAHVATMLARAPKSIEIYSAYKRAKKSIQEWDKGALPDVP

LHLRNAPTKLMTSLRINRITDGNAWLKLF

>contig39792 Frame-2F|Blast-branchpoint-bridging protein, putative [Phytophthora infestans T30-4](gb|EEY69167.1|) 1e-52

MERETNCKIAIRGKGSVKEGSKGKKMIADENDDLHVLITGDREDEIERAAKEVQSLLVPV

DDTQNSHKQKQLRELALINGTLRDVDYCHICGEKGHRQWECPNRDAQ

>contig40147 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54226.1|) 2e-38

MPARSIRQVVQRSLSPMSRALSTATDNKYYILRYEYVSDILDRRGPFRAEHLERAVIAKK

DGHVIMGGALVNPLDAGVFIFNVPDKKIIEEFAKIDPYVQNHLVTSYSIREWTVVI

>contig40604 Frame-0F

MYVPSDEIIHGLGFKSLVSFASFQHRFPGGVHITFGAHLRCTLIALNLLSEGNKH

>contig41250 Frame-2F

MNAALIHQESGLSSGTLPVGSGVAALKIKGKNAQSVARMKTEKQGEASSTLVHDNVSGKN

QKDPTGINPLINHEAARMRLLFSQHPRGVVSPISYPGEFTLKLLSGLCEVTSELVDFFAP

ALLKLAQRFTREHLIQSAATGGGGHGGSNGAAMGVESGQAVVDSFGRNRVMATPSLAIVN

EWNLMQLGRSNLAVNNVVRRAVKNREAVGDKMSSKKTSNVSDSLGNDATSLKTGGVMNKM

GASLISGHSALTSSSSNGERPIELLVLCYALLAKSTFTTGEHRRLYTNLLVHCLEGSYNI

PLLLQITKIVSKLIASTDARHQVLTTKDKLTLLSKMATFDRLNEISALPLNEEYYRLVLK

LCESARGDLKHQTPQLHLCPTPQNHSLTSHFMAGLLAPDPAIRDRFLQLFFAVTGPGPVA

RLQLVLRQDWQACGTRYWPVIAIESLMAAILSPFVLSTLRRGQETQAVSSAHAMFLKSYG

QVKSSELIMALRDLAHIDLELAKELWVHLFRAAWALLEEEAQTQVSGQLLKILASKYNKR

DLNVPLDMSIPRRTNVVQTLMKGIVNTSPSTPVMTPELVLHIASAYDVWSSAMRLCEFQV

EKPDLCFESRLRWIEALSAIYKQLSEDDLRVGLSLENISQPETRAALTLEALGYVHEAQE

EYFRALSNARSGRVSVDEISFFELRLWEERWVGCAKQLCQWQIMNDFAKSTQNQELLLDC

AWKRGDWASAKQLLLAPSMQSSTELGCPQTRLQRLYISILDADKRSVIDTLASQTADLAL

HQWQGLPRILSCAHLPLMHLFHKFVEVNESIQMMQDLKSASAQHAALPNLKPSINTWRER

LPNKWEPILLWDDILTWRSHMFQVVKTTFAWSDAQVLACMHDSPWSVIKLAHTARKQRLP

DVCLGALSKLYSVPAMDVQDAFSKLREQVNICYESATEYSGGLSILNTTNLDYFSLRQKA

EMFRLKALFLEAQGSFSEANKTFSHCLQICDSYGKGWLSWGHYCYRLFLVRKDLALASQT

IACYLQAIHYRCNSARLMIARVLWLLNMDDQRGVLIQTFETHGKQLPIWIWIIWIPQLLM

ALGRPEAPQIRGLLRGLSAKFPQALYYTMRAFFLENRDNTLMQTNQQLHSGVFHSATSTS

SADSLTYYRTKSGHVVGVPRAMPHAQIQEIPGLVGSARPTPAAFNASPSVVFTLEAWNEK

IRNNCGDGHSLKTEFGPVQYTEDLLNFLRRSHDSLTFEMECMLEEMITRFRPEPEEELLT

AVHALLLKCYQLPKLTKTEPVPKMLGAALARVCRKLFVLLPHQINEKHEAFVNEYKHAFE

RDFTPFREDEVQPQVESATTLYEIMDRLKRWKSLLQMRVKKVGKRNAAKLYLEECSRHLM

ELSSSNIEVPGQYVSDGEPIKDLHARIQYFKSTVDVLLRNGFTQRRVAMG

>contig41531 Frame-0R|Blast-hook domain-containing protein [Phytophthora infestans T30-4](gb|EEY55947.1|) 6e-14

MQRRTMMPQGPAAGTPGGGSWLASKRTEERAKRRQGA

>contig41953 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY69207.1|) 1e-75

MAILRGIQGVGLDRMVDTMQKAFTIDNSERFMRAEWLVVETEEQKLQQLQEVVFKLQKAF

QFSNRLRTLVKLANSTLAKCQELVERSQTHLEQCNMMFAQCTNEISTLTDYLSKLKEAII

PPLQAKDHNEEKRNARRAEWALARMAQSAQSMVLEMRESLDELD

>contig43058 Frame-1F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY64041.1|) 0.0

MPQETQLYAITGTIGDGKGKPIAIRGFQISRKVQIKWPISSIVVLRGDECVPEDVQVLRE

TCSGRSGNVLAQTTSPHTLFLGVKREEQPTDGYITDICVIYGEIDAVPEQFTCIKTTPAG

HSANLNDGTPGVPVFICFRRSGYGDNAFAKSLLDLALVWTTGVQPDTLPTGFTKIQHTPL

GMEANLNQGTNGVAIYLCYSRCESEDIYKPVENLLNGEYEITSSPLPAFGRYLTLSVVEE

LDEIRAVEGNFGIVLHTHLFGLMNGILYTSKRQQTENTKAHTIVGAWGINSPAAGNISVG

MHQFLPSSFPFELTLNNTITEMDGWWSGAESLPSNIVQPTDSVVTSSVVDLANASESGLN

RAGSGGKWKLIKDSYVHVAFKRDYSTEWKNNQLLFSERVWQHDIKSMLSRFVATRTLGGD

NALSCSVCQTKTESRTHTVIIEPPEHLIITLKRMYYDWTQQKARKCLHDVRFPSLLTLPS

LTKEEELAVYGPTINDDVNRKIGQNVSRNYGLYGVLVHSGLTADSGHYFSFCRESDESTR

QLHLEDSPLSPWIKFNDTKVERSSWMEINTLVSNTVSDTVYLLLYKKLSYDPRPCVNNDS

GVIGSADDEEAMLLAKAMVLSMSAAKHHRPSNEIESKGETVNSDIDLSMLSTSNEVKTLL

RKVEAENAAYLHDSVARTSSALHADDIHTLLSLRHSIPLQLRAILDDIC

>contig43201 Frame-2F

MLTKFESKSNRVKGLAFHVSRPWILTSLHNGVIQLWDYRMGTLLDRFDEHDGPVRGVDFH

RSQPLFVSGGDDYKLKVWDYKLRRCLFTLLGHLDYIRTVQFHQEYPWILSCSDDQTIRIW

NWQSRSCVSILTGHNHYVMCAQFHPKDDLIVSASLDQTVRVWDTTGLRKKTVRGAPSAMD

DMVGPPSSRSNNHDIFGASDAIVKYVLEGHDRGVNWASFHPTLPLIVSGADDRQVKLWRM

NETKAWEVDTMRGHTNNISCVLFHPRHELIISNSEDRSIRVWDISKRMGLQTFRRENDRF

WMLLAHPTQNLLAAGHDSGMIVFKLERERPAMDIHDSRAYYVKERYIRMYSFVDGSDVPV

AAVRRTGTAGTGMGNCPRHMNYNPYDQNSGTSSVLLTSDTDGGSYELVTFTHGSNGDTSE

SSRGPGLYAVFVARNRFAVLDKSRHIVIKNFQNEVTKKITPPNGTADGLFFGGIVGRVLL

HIDDKMVLYETQSRRVLADVQASRVKYVVWSPNYEYVALISKHSIVLADKQLTLLSTITE

SVRIKSGIWANAPAEIFVYTTLNHIKYSLANGDGGIIRTLDVPVYLTHLDDSKLHCLDRE

AKMRTMAVDLTECEFKIALNKKNYTEVMRMVRHSRLCGQAIISYLTKKGYPEVALHFVND

EKTRFKLAISCGNLEVALNSAYELDDNKCWYQLGVEALRQGNIQVVEMAYQRTKNFERLS

SLYLVTGDRDKLQKMLKIAEVRNDVMARFHNALYLGDVEVRVVTLEAAGQFGLALLTAAT

HGLSDHVERLRAQLQVTNPDFDVDEFLAREMLSNPTLLSPPPCLSRLENENWALVEINEP

TIQDHAIAAEKREAERSLQPLQQETNHRSVEDRSTPKSSIDLTLDAAGDAWDIEMDGDLD

LDDSLTIDDQSLGLDTAALENDLAGLSTDGFVAAPTAGSSLAVQWVRNSSLAADHVVAGS

FQTAMQLLHRQIGVINFEPLKPTFFQVFSGGAASLPTQSNYPPLHTWLQRNDASQPSVAV

SFTALVEMLKHAYRSFTGAKFDDVKTHCQSILYAIPFLAVDSKEEAEKVKGLLAVCREYL

VACRIRSEVAAVPLDSDPKRNIELTAYFTHCELQLPHSVLTLKIAMTNAFKSSNFITAAS

FCRRLLEIPEVSQHPRHEKLRLTARRVLQKAEKEARNEHAVDYHDLKPFVLDVRHLTPIY

VGQPDVRCPYCAAAYNRQCKGTLCDICGLSKIGEETIGLVVTTAQ

>contig43410 Frame-1F

MTRTLRGICSSPLSSDDEDKAFPEINSSPAVLRKKIRLARVKRKPRAKRSIVQQKKLKTT

PRKSTTELISEAPQDFVEYLSEQLSPLQQAKHGIEFNYAQGYIIKLPQFKSKQGDLEKWI

QALGFFSSSSKQPNIMCLSSLKVDIIVNEIKQRVPLPAAAMDSTMIRMNNYYKHLDSKEI

EVVSPSRNQR

>contig43739 Frame-2R

MATEIQQVRAFINARKRSIEAAEKRYDIRTAVNELCELAAPLHSPERFSSLWKNLYLGPC

YRDVVAFLVTYVAVHVEPCFTPQDRGLALEVFFDSANVPSSKAIGALVSTLTAVSRKTEA

KDSTTEEDREASIAMCVQLLEKVIHDGGIQNIVTELVLQEHESKMNENHNVIGLQVLISQ

LASLPDLVYNQRQRATPTVFHRKRYFSMLCDSLFRGLIHQEPLVKPSRTFRMFADKLTRI

GHSEDIVKSWLSFIGPKLTSFMNSMLFQSLPESCYEQLLLQIASINTPSSLNVHDTLRFP

KYKLLAQIPPELCESKQFQYIVVHKLLLRKPIDDFLFWRVLVDVMAEGSSTSRQSPLIEV

FQGILTRWSQSDFALATEYTINASVCFFIRYSLLQFAKNQKEAS

>contig43999 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53323.1|) 1e-32

MSSPVLVSHDYVQTHTMHQRATRQIIDVLGVCLNSTRPKNQWTCVRRDKHQELYAKRSLT

KFGISCTFTRRVNFDK

>contig44565 Frame-0F

MAVLDDQDCGISMDDILMAPDSEPMNDSIISDGGYIENGAADYFRRHDQCSQTMFSTIDE

LNDWIWTNEKKQLGLSSSAASRQASASGRSEMASEVEDDHEKEYLEEFLKEIPSRSLSNA

AYQIKAFARAIQYFEVHLRQEEFKETEPKNFDIEVAGPVRLSLVSKNAIYLQQLYKSVDE

PDMLVGLASLRRLHDAYQHSGIGNDEQAEGLNLTDLMHQIVDYEQLAQWEDALACYELAI

QVVQSALSSKSLPANTP

>contig44712 Frame-2F|Blast-hypothetical protein PITG\_00292 [Phytophthora infestans T30-4](gb|EEY57724.1|) 2e-21

MARELQAQYDRENEAIAVAQPVMQDELLIQCGECGLTHVVRNATHGSTFLCTTCGAETQI

LLVHHIPYV

>contig44767 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64393.1|) 0.0

MESWTDYFTSHFYAMKARPVSAFDPSGFIIVVSFFLLLVGVTAATARKLVSSSVGLLLRS

RVEKNLQDMSIYVLDQRSRVGVNLLYIKGCAIDHSGRQGFIAEMLSYAYLSRLAFSLCIF

AIASYLNTLAAVIAGWRTPNVVILDLAKNSTSLKTLPDLGHDLFRFVMTKIYGHTTYMEW

FDLPDEFLAAVGMLTSLIIILHPRRLLIIRRFCFIFAVINLMRACCVAVTSLPDASPMCI

SQFDSFERGNYKALPIFPKAFFRAWKVLIRPSQHITCGDMIFSGHAVFLALCCMFAKTYC

VRSELNTPFTRRFPYVLWLIRYYNYIGSACGIFAIVGTRLHYTLDVLIAIYITIQVWLTY

HWLMNHPESSFALLNWLEHAEVHLVDHNAYRKARQSNILGGCIDKIE

>contig45364 Frame-2R|Blast-pre-mRNA-splicing factor syf2 [Phytophthora infestans T30-4](gb|EEY57885.1|) 5e-67

MKASKMSKKEKRKAAFGWDVFNQDSLYKGYKKRLANLPVSEESVVAVITTHGNPLGDELT

YGKNDKVEEANLERMAQELEQCIKSRKKFSRRRQHYEGEDVDYINGQNRIFNRKASQAFD

KYTVEIRQNLERGTAL

>contig45470 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54033.1|) 3e-86

MGISNARDTNRLLTVFKTSKGDYSSHYHFEIHSVQAKPPRIIAMGFPSDRFNLEKQVAFY

LSYHSNKINQGIHFVCIWPVFVSGLVLLAHTKPLIETPVFLTSLPYGQYMVFNYSAVVVS

IYMLWYIALDVFAGTLGAAIVFQCFVLANYLVIEGAKTMDIDILHAVLVIQALAWTLQFI

GHGVFERRKPALFDRPDQAFITAPLFVLLEILFPLGYRPELYQRVMKQARINVKNFQVEK

TVLSS

>contig45827 Frame-0F|Blast-bifunctional aspartokinase/homoserine dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY61951.1|) 2e-14

MDCTSPSLLIGSNWPQEILPAPLSLYGTSLSSPSCNCLVLKRCNSPGSPQWHTQCL

>contig45993 Frame-0F

MMLTVMVVATTSFLAAFCVSILSTATRLYSIIAVKIQAPVDGFNSRMRFARNVGVHDQNN

QK

>contig46145 Frame-2F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68035.1|) 3e-44

MSTQWVWLLGRSVGTIKQSCVEDEANISIQSFRMYEVEKGTMGYSIVDHLSQHDEHDGPL

SNVAPIIRILCIIPAYQSRLVGHQATLNFQSG

>contig46321 Frame-0R

MRTAASLAPTAPELLLSLSNTKERYIKTGVIDATALTPSVPSYKARFLLANEPNKRLPPL

SFLLRKPQVQSRYRSINYKSTYYSASFHPTAPKFPTKPQHRLLPLVDDCASNL

>contig46743 Frame-1R|Blast-importin alpha-2 subunit [Phytophthora infestans T30-4](gb|EEY66875.1|) 2e-11

MFDLVAPALPTLGQLIYTHDAWSGVGLYLFCLYHQG

>contig46835 Frame-0F

MSRLVHLQMSRRWYLLLVFLFILISATYANSFIDIFSNFIENFRAEDPTPTPEEAPFASI

PLVSHDESSCAAPPIPSSPPSPVILENRHILFVTIAMKSHAQPLLRVASAMKEQGYRVSF

ATHDSGREWVEAYKLPFISAGSFPISSDNLREKLQAISRDTSRLNGLVTMFKDIYVEAAS

PMYDALLLKLKNTEFVPDLLVLDIATIGAQFLAQKLQIPYVLNSPSLLFDSGSVPNYVPA

YGTGFRQDMSLWDRCVNLLYPTLLSMALTSPFMVLNQIRDDVGLPLFRSQNDLFNGARII

LNTAFGLEYPQPLSP

>contig46880 Frame-2R

MMGRKLYGPYLPSDQLLNVVRGRTSRGFVRPFELLSRPGRENHANST

>contig47432 Frame-2F

MNFLAVQPPSMESGTTTKLAIVLKREKGTMPNCLSESFVWQNPKSIQMDSE

>contig47854 Frame-2R

MTCAGYLVVCNSHPAFVEISTGVLVCSLFTDSCADPADQATPPLEPWHTAKVEVCTSSRS

IKDLIKQPESEIELQKWKQQQRLLQLSGCMIEVLDQDAELDVPSLPNSFQVNTYKVHLRP

DGSCVRTPSDSLILSAIDQEAKKIWVKSVKFWNRYGWKETQPVGATPSVLVQLQRKLQRF

TDPAFVEVCPRYSSDEMFCCSRDRAMLLCGGRRSFSASHPPRRRFYRATIPNALAPPL

>contig47920 Frame-0F

MLLSLQSVGWRRIDVLFGGIMSHEHIIAKRADLKKPLDSGIDVVHHVMDTFLM

>contig48486 Frame-1R|Blast-hydroxymethylglutaryl-CoA synthase [Phytophthora infestans T30-4](gb|EEY60264.1|) 0.0

MDETTQLAVAAGLEAVRDAGLVDGIRGNWRLPESMRDSTGVIYASSFPTMNAAVSETKRY

YESKETNHQSTYEMDPKILFRLLVLANAQVAQLTGARGPNTQINAACAGATQAIGMAQDW

INTGKCQRVIVVSSDIASAESMMPLIGGGFLTLGAACIAPTVTAAARPFDVKRKGMIVGG

GAIGVVLESPMVFAARPTTLNTKQKTVRLLATQFSNSAYHGASLEPSHVGQELVRFLQRV

EDDFGITRETIARNGVYYSHETGTNASPKASCAYTEVTALRTAFGSKLLAELMITNTKGF

TGHPMAVSFEDVAAIEGLRRGSVPPVVHFETLDPNLNESQLRLASGGPYAHTFALRFAAG

FGSQLAFSLYTMST

>contig48705 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61712.1|) 6e-62

MSQSIERCLEEISLQVKDAGEPISYRTLSIHSQAPSKLCIEALTSYYTDDDSVEALILLI

KRVAVSKNGDKTETAAAKHDPRARILSLAVGVEENEKDVLCHHIYALFDKPSDTSKDADK

VATMATACWAQERQARNKVLSSVVKQEPLPSAAKVLYASSVVCEEATARQAFGDDHGEET

ISAFDAISASITQKTSSSSFFKSTGKKGH

>contig48950 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68144.1|) 1e-108

MCILCSGDPVEDDVRKNNPGSFQVGMMHAPGADPLCCMSACLCPCCAQIVIRRKALNYDM

SNYTCCQGYMDGLVPCARSGQCGESSCPNFCLCLESFCCNGCAVSATRMLVMDRYRLQPD

KWDNRIIRCNNCIQLVSCVCSLLSICISELGDLADLMYCIAQCTYATTQGCMTAQVNVEL

REREKGFEVQDETMDRV

>contig49034 Frame-2R

MAEVIGQMTQLDVGIVLNTNEYTLNETLVRLYAQQYVGSYLNTAWDQPMGNKYGWNASEF

RAIVNRIQEISMEENGGHPIIYGLDSVHGANYVDNAVLFPQQINGGASFNPDLVFKVGQI

TARDTLAAGIPWVFGPILEISQSPLWPRTYETFGEDPYLASVMADAIVRGLQSHNQTAAC

MKHFIGYSKAPNGHDRENGMLSDFDLLNYFLPP

>contig49672 Frame-0R

MAYSHITRRIYRLYNSLPREQYLNF

>contig49698 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66395.1|) 3e-53

MAPHQATDSLYKCTISAIPTRRRFLVTGAAGFIGFHTAKALLARGDDIVIVDEMNDYYDV

KLKQSNLDWLTTMYGDRVDVHIGDLCDKQLVHRVIKETKPDAIVHLAARAGVRPSIENPL

MYIQA

>contig50168 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53794.1|) 4e-26 NOT\_ORF

MCADVCVQLNGEPLLITKDGTLTLHVTARGVEKTIEITDVYFAKDVKHNLISYGVFDIRY

TNSMKRGPACNCAGRRRCYCF

>contig50182 Frame-1F

MIKTCRLTTLVSTDWSRIAAFLCALNLRDSMVDYIRITALPYGELELVLRAG

>contig50326 Frame-0R

MLVAFKLAVARLHKKALALVLAMIVDCADSKLSF

>contig50520 Frame-0F

MTNLSVYSSYMLWKRYKWTLYLCRPGPSTGGGKLFIETMMTTVKADFSTLYEKKLRHNLN

DCFFPSRHALLRFNSPNTLEALQFSVGLASVRPLYPTIAYINELRKT

>contig50638 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65182.1|) 1e-103

MTYGRKVNCSARNMTLNDDQRSTNEYFSKTPAPAWVDERRDQVECFLDHHRVVGKCAAIV

TSGGTTVPLERNTVRFLDNFSTGSRGAASVEYLLDLGYAVIYMYRPGSVAPFARHLQKAT

CKSLDLDFLNHVEVLKSNDTVDEQQIRLLIEDPVAKKKAVEAVNKLHHVRTNNLLLALSY

TTVDDYFYLLRIVATCVAPYKERALFLLAAAVSDFYITQEKLALHKIPSQHIPLMLTLQQ

VPKMLGVLRHAWAPQSFVVSFKLETDW

>contig50832 Frame-0R

MTIIYQQISTKRLREPLHIGTSYLSHGGKYELNLLDGEFVSRVEVHAIVMKKRKRISFIQ

ITTSKGRSIWGGTETNDKVTYENGKKLAGFHGTAGAEIDSIGPIWMR

>contig51196 Frame-2F

MAEFIDSVFGVYSSKHSLSTAKSDQSGLPVVVNLTAKTKCDEPVAEMTVKADTKFAEKNV

HCGALIAAFEAEEQVFENQRSKEQWIKSRHQVLEEEEASAVMNDSGSGILEIGTATAGET

NIKQGSKGIALANQLRAHKHVAAFLKASNESAKAHGPMPPSNVMFSSQYAVPAATPCLSI

PAPISHVSPVMTLCMRTDQQFIRPAAVKTNTSKIALPSTHSMPNMVLAFPGLMCTPHTVG

RLIPMPQWQAHLQTPLPARSVLAARPTAKSHPFKRMCELCRKRHLSYRHCRIVLQHTEAE

WQPAQPPSSGRRRRRKQFAS

>contig51721 Frame-1F

MDNSSITAYSMIKVDQSGKLVSFKGYPQGAKMIGDHEYWQIA

>contig52430 Frame-1R

MPLLKQWQLRREQIKNDFGKADSLLALEEVLVQIIKPSDSDEMITSIYLDLASLSRKAGR

PAVAYRAL

>contig52636 Frame-2R

MPGDNLRRKIKSQSACLLLERTSVNILVGICPFKTFDVLANKFYLDISNDGFDADMNLML

YRRHVPRYKFSNRSHVCDLACLL

>contig53590 Frame-1R

MMLSLDVRDMFIGKRSSEAAHIQLEQQLDGGESASDASLTEQQSGRVSDDDMDVSTKATA

RPMKKLLIPKVRTYSMLDHETASKLGSYLKDEEALHPPLVSLGSGSSLRASLLSSSGSTV

PLPPHSKNFILDPESNGSVLQAAVSSGAEAVEVVAEQSWLITK

>contig53693 Frame-2F

MVVTSFFKLTRLALLMSRVWHHTLTYVYW

>contig54577 Frame-0F|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY54703.1|) 1e-43

MHVHVVIVLSTVLHPPFYMAERFLLGMHKEPVDATVNLQAEIDSNDGYEDMRVKLSTSVL

VTSIHEQAAKHLKSNDDSDIESRTTFA

>contig54964 Frame-2R

MIHKISTQYCDKITRGVPSILIAQ

>contig56746 Frame-1F

MVKARWGSVILMCSLALHACNEAAQVRGESVSHAVNESIKRQESRSHFEERATDDMSFVG

PISELAQKAIAEIQSGLNGQIIKNARGNVESIRNSVMKWVRWTKKSASISKSATENDQSK

QLFNVFKAHFSEVDRARVIIASLNSGANNSRFQRHMRHMRDFMMEEWNAKPREQVYNMLR

LDATHSDFLTSSMLQLFVKFLDKYHHKNYNILRDKLMKAYVDHRQILRDRLTNDTGIGKT

LLGIIPPNYWNSPTFYPAILLLEENELAHLSVTELVRSPKLDSWCSFVRDKNGEDPYRIL

IKKLLDEKFELELATELEAALKQEPPGDFYWKLEQLEN

>contig57086 Frame-2F

MESNRRIALKQKTIAGRNDIQVVCSTCTFSNAPSVSSCGMCK

>contig57594 Frame-0F

MAINPSDTDDNQMYACSLTIEKCLLPCCYYILLTLAVNC

>contig58371 Frame-2F|Blast-catalase [Phytophthora infestans T30-4](gb|EEY62821.1|) 2e-09

MNGNMHGTSNYFPHSKKGPQENRTLRFRTYEGDHATVDKY

>contig58515 Frame-1R

MLHLIIKAAIHFIAHLSKVERKQVLLYQYAISRVANDLHLRNSMSRKARA

>contig58722-1 Frame-0R1

MFVLKLEDDHDDVSSGFTNGQKGGLSSSGIGITS

>contig59354 Frame-1F

MILFASMRRLNVRSNQTESETMPLLTVEDLYLCYCDVSKDVGV

>contig00223 Frame-2F

MLPSVNLVWTLASRDEARKHRKYPRLRYLGQYHTISAIVNSKQIVTMLIASREMINQRPK

FRIPTDAMLKSQLGSKH

>contig03824 Frame-2F

MDAKKWLLETGMLDLYMKGKAAKEVRAHVDHVCPHYKVLEPAFQSIPVTPKHAETIELDE

DSAGEMETDENQEEESEEEDVEAYEKTAKGIKKGDTFRDRLFGAVTSGSTKSKFFRSTET

LEPILNDRIASKKPKASVKQGKKKTSRLAKQIAPSPGYAAARKSVTTPELQDTAIASNVP

SSATLSSAKPMIVSSEKSLPDTRVAPAIEIALEEAFPATLNHAPKKKRTGRYLKSSVGVA

SSPLNEGGRRQGDMDVLEATEVMPREPEISKIAGKRVQRQESIDLTTNDVGMIERDALLK

RVKDEENQRYEVFTLERAKLKCELESKRVQLLFEKAAARKKLDLLGVSQAEIDGILPL

>contig03891 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58293.1|) 5e-92

MQVVALISGGKDSCYAMMECVRFGHEIVCLAHLHPPSELSADDAEIDSFMFQSVGHQSVE

LIAESMDLPLVSETIIGTALTTDMNYHESMAGDEVEDLFRLLQKVLLQCPNVQGVCTGAI

FSSYQRNRVENVCSRLGLTSLGYLWRRDQTELLQEMIDSKVEAILIKVASIGLQPHLHLG

KTIAELQPQLMTL

>contig04803 Frame-0F

MNASRPIYRCPHCRRLNDVDMLATGPLFSHNPHCVFYPTQHPAMFRTPFDTSSLPDVPLR

RYSTTYSPVVDPSTDISPSYPLTTTHESDAGVFHNQQNTVHIISKPDEMSSTTLASLIAS

HRSSVSSSIHMSKDKVENGNLFESHGFQDSLERIEKGAIHSRALVEDDPALELPVPSLLG

NSHSDDEKTTAFHGVVPLFQDMSSKMNGRDLDTLDNGTDGEDEVYYILARMYTSAQDHKL

GLPAFDQFQRMLGFYSENQDALQTRVLFHPLIESGLTDEEQGHITSQFVDELRQDSLAVH

SLPKYQHNLIMLREDALMFYWSQSLV

>contig05202 Frame-2R

MYTCSKNYARRSRSGIVRHYLIVNPSLRRQALCASIISLQCSSPLLTIQRSRACLVVGHE

QQIRLPDLPTTALSVALVFSAIFYFGSLSCVAATKSSYVPYFVPLLAKLSRFLA

>contig05750 Frame-1R

MRFGVDEEIVTTRALEKAPKALLRRESCAINTQRFRAPSSDSLQTSSDEEDSSRSLLSMS

YNPRHLTRKSRRELLKQVERACEHKAVIAVTSSKAYKVLCETLQRARQDAEAQLCWNPDN

SVWKENTLVSTNTTGKNWQAIRLKERKK

>contig07529 Frame-1F

MVDSWWDDYGYRDRRLFLSHRVRCSNENTKENRVDATILRHNTPSSSPASVCSTTTEEDK

SRTPPYAIPSTFVEKKLRKRNWYKKFIAGDHLPEMRAHQSFICGGKCDWTFDMNTKTPLS

LPGRWQGADCFIVKRSHVEQMATSAKPTRMRLIPQRPGLAQARARGIQELVAFAQCSSKW

NKRILSSVSIDSDRIQRLIDRVNGNHIFTNTDQ

>contig08155 Frame-2R

MRPPLVLGMFLTGVCVRFVLSVIVIDVPPSTAQEEYIFPRVPKESTTKIKAVGDRRLQVL

ERLLVKKTLLNVADDIADKKATWEQVHLDLKDVGWSDTNIVHGLRVQLEEKNPATLDRAV

KMGAHILFSKSTSEDVKTEVFKGWKALGLTPTKVCDNLVMSDVDADLKTLMVLRYHALFR

EKQEASQIYDIVTAYDRLALAERLLKDDQLEKWILHPKPQYEEMAKSLHDIYKRRISFIR

GDPKFMIVLHFNEKSPVPELFRMLYYFRAISDPDTLKRILARLQTSKVLTAESRDELLLA

MKESISMEKIGTQLNELAKDS

>contig09754 Frame-0R|Blast-NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit, putative [Phytophthora infestans T30-4](gb|EEY57213.1|) 1e-157

MNGNGYVLPYRGDDAEVSHLRVSADLGNVAALPFHPRDRDSIFAAVEGSDIVINLIGKHY

QTKHLLPWWINYTYDDVHVDVARTIAEVAMEAKVPRMVHVSSLLAQPNSPSVWAASKFRG

EVAVRKAFPEATIVRPANMFGPEDRLLVWMGNRLTYGGLPVVDNGEAVIQPVFVNDVAKA

IYHITQDETIRGATFELVGDEEFSYKELVDYVFDITKTNPRLINLPLPIAQAIGYFCEQF

PDPKFTRDWATRLSLTEVKTSDLPGLRELDVEPSKLEKEAANFMIKFNPGGHFQEVSGYH

>contig11395 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY66131.1|) 0.0

MRFHDFKPALCPEILAETDALGFEHMTPVQAATLPLFLSNKDVCVDACTGSGKTLSFVLP

TVQMLKTKLEDGSITTARHSEFTRLVAMIISPTRELARQIFECAEKFFASALANVQLLLF

VGGTSVEEDLSLIRSAVGKCLVVIGTPGRTEDLLNRCVGCSVDTREFEMLILDEADTLLD

MGFEISLNKILEHLPKQRRTGLFSATQTQEVKALARAGLRNPATISVQVANNTQVTPATL

RNYYCLVNHDQRLSALYHFVQSKQGMKLIVFFSTCGSVEFFSRVLEELLKGEVDCSVVAL

HGKMPQKKRTSNYDHFSSLKSGLLVCTDVVARGIDLPDVGWIVQYDPPQDPNFFVHRVGR

TARAGRSGCALSFLSSNEDAYVNFLKIRKVPCEEMSLPLDTMEDVLPKVKSYILEDRDLL

EKGTKAFMAFVRSYKEHQCQFIFRFKELDLSAAARGFCLLQLPKINELRNVCIDFEKAGI

NTTDIKFKDKAREKERQKKLVAIAKENEARERQNAEMRERKRKWPLEEEDHKHPRRREKK

KGLHQQIVEEWDELAEEEKLFKRMKKGKITTEEYEKAFFGKAESSDKEEEDETKDSGMKN

MSKWQRSEEKLKDRFKKKEQTVQKTAVQKREAAKREERIRKRKKSQHVQRAMKRAQHRAR

R

>contig13058 Frame-0F

MSSLTKTVLITGSTRSIGLALAEYYTQSKWHVIGTARASSNTDELKALSPSRVVTLDTSD

ESSVLDAARQLEGVPIDLLINNAGIWLPDKLQAAKKEDLMRQFEINTIGPFLTTRAFLPN

LELAAKTQGAAYVAQLSTILGSIHTNTPKMEAYFAEAFGYSASKTALNMINRSMAVSLRK

HNIGLVTLNPGYVKTDMTKHKGFLKPSNAAKAMANALEKLTLKDSGKFINADTKFPSAEI

PW

>contig13397 Frame-0F

MHQNHHHHMISRSNLSTHLCVNYSSHSFSTIQNLSFRNYNRTSFLILLYCAVCGGES

>contig14293 Frame-1F

MDIRSFFQKEPSSRNIKGNSKNKKVATPAKSKRVEPEPTPPTRPATRRTPKKNKAVFVES

DEDENDIKLIASAKKNTRHVDSDSEFEMLSSDNEKLSVKLKKEPMKHQRRAINKDCGKTP

ERESKEKKVLETESRTTPVLLVDHAASGDMKIAICKQESALKKIPAPCPGSLVGKVFAFS

GVLENLSREDAVHFVKCCGGSIANNISRSTKYLIVGKTLEQGGKVTDSSKYKDALAKNVR

ILTQNDFYNLITEAAASQQAQDLVAEKAKIKSEAAIAKIASTKGKQMLNASTNNDLWTDK

YKPQSLKDMIGNVELGKKLKTWLIDWEAVHVKGTKKVPMTTKLSENRGAKSVLLSGPPGI

GKTTIVNLVARECGFECTELNASDTRSKKLLQTGLKDVLGTQALQFGGRSGKAQEKMHLA

RRVIIMDEVDGMSGGDRGGTAELIQLIKKSKTPIICICNDRQSQKVRSLANHSFDLRMRR

PTKVQIAKRLMDIGLNEGLHLEKNAIEEAADRCGNDIRQLLTQMQRWRLTNTKVTYADMV

DPSSQHNKDESLRLNPFSATQQIFQRDLSFDARNEAYFVDYDLMPLMVQENYIQSIMNNR

RSADENLRAAMYASEFISESDLLSSYIRVDQRWDLLTKQAAMNVGACVYSAGFVGHPEFS

KWLGKNSSASKSKRLLSELSVRMRSHASGSREVIRLDYVPYMKEILLSKLLVGVDNVQEV

IILLDECEISREDLTESMESFKFPGIERHSYSELDTKAKTTFTRVYNKASHRSQAVVESV

LGSTTVKKGRGKAVVAGDDESGITPLSDAESEPEEEDVDVSKFQTKTRSAKRKAPVAARE

KVPRKAPKKKRRT

>contig16000 Frame-2F

MRNAAIRVLQGIDAFGQTCMEPRRPIDLKVSTTKALEHQDVALRTLLTKLQNDMGIHPTE

HMSLEEVRLKNPDYYHQLLAFQQTLQGDESFQKNDRKSNRLQSRTLPVLPTQPLDTRTKS

SRLSPVQSSNVAHLMQLLKRKQRPKASLCSEATHVVSQTPDAAAVMSILQKLKTLSKPSN

ALETSCRNDSFPRIESSSRNQETGSRMWFSDKIVDCKDRVESNVQKLYAALPLVCRASGL

RFREQAQLDAHLDFLFQYNRARKERGKGGISRSWYLDETHWVVDFSGATAPRESTSSSFF

DQPPVERTTELPTWEKACVPVDETITRCRICGESFSTRWDEDEEEWMYTNAIVGAIHDTM

EDGIKRIHETIFHKYCYDTVRTNSTNISSAHLIPLEVDGIEEGNDGKSKDLRDKSRGGVK

RTLNEVDCESDGDDDLKRVKGVCTTKEGGNNHDKA

>contig16332 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67872.1|) 6e-55

MIQSPPAVAGKVINDSFCGMTMVQHDAEGGVLFLHRNSHKLMGTVRRGPTVYKAAAIRRA

RKKRLRKELAEKDRLTLDDSKANEDELENSVSSDLNALGPDGYPDMAIWTHLITFKNTSR

RSNYRIQ

>contig16989 Frame-1F|Blast-phosphoethanolamine N-methyltransferase [Phytophthora infestans T30-4](gb|EEY63549.1|) 0.0

MAINSSRETTRKEMKSYWVEHSSSADIKTMMLDSNAQILHELEMPEIMAHAPSMDHKDVL

ELAAGIGRFTSIIGAKAKTVTAVEFIEDFHKANLATNSHMANVTFLHKDVVTLEAESNSL

DVIFSNWLFMYLSDDEVHQFAQKAIKWLRPGGQLFFRESCFRQSGDVERSTNPTQYRHPS

FYIGAFGSVISNEANGTMEYFNLESSGSVAVYRKIKKNNGQVFFRYSKAIKEKVAKHNKQ

VTTFQKFLDEQQYSNESITRYEKIFGHGYISTGGQTTTTEFVQKLHLQPGERVLDVGCGI

GGGDFYMAREFSVSVVGIDLSTNMVHRALETSMSESNIDVEFEICDATKKEFPAESFDVI

YSRDTLLHIKEKQTLFAKFFRWLKPRGRVLISDYCRGEQEPTDRFTAYVQSRGYHLLSPS

QYGKTLEAVGFKSVVAEDRTEQFVAILKDELARTLAQKDQFVAETSVSDFEYIVDGWEAK

IVRCGEGDQKWGLFYGKKE

>contig17335 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70538.1|) 1e-57

MLLAVALTTLVLLTSSSLSSNVGSIIELQPDHALQSQRGLYGIPQFFHVVGLQPASVYDI

KVSYLATQPSLIVVHVERVLLPSLLINIDELNAIDRAQKKDLMAPTRRKLLTAPKFRLHP

IKLKEHKSVQYRLESIDNAIEVEFSLLAEVEGVRHPDSVSETNEYLFDIVVEEVLLGVFP

KHTLVLIGWLMILLYISKKWVLPFLEKKIALGFLKDRVEVEVT

>contig18330 Frame-0F

MELQMNLQACIVLDPDNVNNRKKRKQQSSNGDTDDLEIEDLIQSDGSSLLEEEEIEEDME

ERDRIETSSVAESVEKEAVSTQLTKTERLIARFIGADVDIEESTKFKIRPILKVLSWLSA

QSKLCGTQEASPRLLKTTEIVKNRFCNSIETKDVRVWVFLERRCHCRVVAEYITAALFDF

DLPPSCCMLGSSNARISGSLRFSSFLKIMQMFTNYETKILVTTSVVISSHKVRLAPPPCD

LVVVMNELLEPNKLYDYGKRADLSKGFIKYITEDSVAARKKFEVLIRQMQEHIRLEIESS

QSHAPAIQPASSLASESSRLLMPFPATSNPIDSSVASLQVESHVLTNLRRLQPIVTSYEL

IDHDTGAILNVKNSVLCLSKFCDTLPGLDTYDRRPQYVVKRISTAKHMAP

>contig18451 Frame-0F

MSTTLSYGPRTVPEEAPYMTPPSGDTIFHDNLNTPPGSQGKTSSVHFADMEEPSYSSQSS

HI

>contig18745 Frame-2R|Blast-homoserine dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY63706.1|) 0.0

MAKPLIVGLFGCGTVGAGVFDLLHSPVRRQKFAAMGVNVLISKICVQNVSKDRALKHFSA

SETIITSRFSDILEDKSINCIIELMGGTNEAKDVVFGAIKAGKHVITANKALVANFMSEI

LQLLQEHPNVHFGYEAAVAGGIPIIHTLQNAYNADHITEIAGIMNGTTNYMLSKMEAEGV

AYDVVLKEAQELGFAEANPSADVDGFDVQSKIAILAKLGFGGSIRPTDVPTVGISRVSAA

DFEYARMMESTIKLLGVAKLLQPANDVTGQPQEVTVYVSPVLIKRTHVIASISGATNLVN

IRSTNLDSTAYVGPGAGRYPTANSVLNDIVQLARGDAPLDPFKASVPLTLQPDYEARFYV

RITVADGLGIIRHVGQLAEETEVSIYSILQAPIVDRSNVQFVVTTESSLLSKVRTMCQKI

AALPFVRDEPLYLPIM

>contig18860 Frame-1F

MFRQPIQKTGSLAKFWQQEATALNVASPKGISIKSHGKLPVAQIGGDLVLGLQRRRLFVD

NNRVDVMGAASIGNTDSSVQALGDGTCAVVALAGLSKKGYAPYNPRKKNQDALVIQFDQK

TQSLLLCVFDGHGEAGDSVSGAIRDAFATTLFAHAHFKRSGEISKDAKWLQTAISDTLRL

VEQMILNDLNIETEFSGTTAVVTVIRENLVVVGNVGDSRITRGFLKGLDMSGSLPALACQ

ELSIDHKPDRPDERTRILASGGRVFAVEYDDGIDGPPRVWLDQMDVPGLAMSRSLGDAVA

HTAGVLSDPEFTTHWLDEHDRCLIIATDGLWEFMSNEECIKMAMEQQNPKVAVDRLVVEA

TRRWMKEEQVIDDSTIIVAYIDTTRMIKTHTNKTL

>contig19157 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67559.1|) 1e-07

MSTADRAENLKLQGNLCFQKGKFFAAIDMYTEAIV

>contig20126 Frame-2F

MFGQLTATPGPYNLLTATADAKYAAPISIDSKMLEIVRVQRDRFRKRMKELQSEKNRVEE

LAKSPNSSVARLEXDNMQLYYKIRYLQNYGGNTKSGGSCSNPIFKSLEGGNRGAYDFKAR

YRGTNRR

>contig20603 Frame-1F

MLLLLTQYFSLNFHKFLLQGEKSFDALGFKAACQFD

>contig20676 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55953.1|) 5e-37

MSINVELHEGAVPYLVSPCESFFFLIHEVKLTVESGNGYPGQGGCFYGGKGRCYVSQYRL

VFVSDANQDNTAHKSFSLPFHGICDWKFEKSIF

>contig21118 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57144.1|) 1e-67

MLSASQKHKSSMKSLDDHTPDEIYCDSQAFDIDFHPKANIVAVGCIDGVVQIYKYSDEMN

TKLIDIKNHQEAVRALLFSPDGQTLYTASTDKSIRAFDIQGKPVWAEMRAHDHPVNRLHE

LSDNVFVSGDDQGCIKIWDTRQHRCLSEFKEHT

>contig21961 Frame-1F

MRLDIYFNRTIALINSVMASTF

>contig22098 Frame-1R|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY63539.1|) 3e-21

MCTKDPGVIRRENIHKFEQYVNHPVLFPEGKFCRTCKT

>contig22407 Frame-0F|Blast-mitoferrin-like protein [Phytophthora infestans T30-4](gb|EEY57472.1|) 2e-82

MQCQQCPVNGHPRRLSAIQTARHLVAEKGPLRLFRGVSTMLGASLPAHAVYFSVFEAAKK

SLGADTSTLTPMASGSAGVLATVCHDFIMTPMDVVKQRLQLGYYNGVSDCLKTVMKQEGL

RALYLSFPTTLLMNLPYSMIMVSANESFKKILNPSGEMNISAYIASGAAAGA

>contig22641 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY56109.1|) 1e-175

MLTVLQEIKTQRGRQLDEARSTSKVITSTPSVGKMKIIYVAPMKALAQEIVTKFGQRLHA

LGLQVRELTGDMQLTKKEIEATHVIVTTPEKWDVITRKSSTQQSLLSQVKLLIIDEVHLL

ADERGPVIETIVARTLRRVESTQSMIRIVGLSATLPNYVDVASFLRVYVPVGTPQQQNAA

TNGGKGGLFYFDATYRPVPLDQTFIGVSTNASLKEALGLSTAAISTVITDKGDCMKDKKK

TASAAMSRQRQVQMMMNKLTLAHCLKQVQQKEQVMVFVHSRKETAATMHAIMDLARANEE

EPGLLEAFLPPLELQLPLPLQDRVQKSRNKELKELLGYGLGIHHAGMLRSDRNLTEQLFE

LGYIRVLCCTATLAWGVNLPA

>contig22832 Frame-0R

MKIFSTAVFLSLVSTCVDAIYGGVSIQSGNGEVMVTMRGQGNENLCGGTIIGSSHVITTT

SCAKKQIKDVVVNGTSSVDVSPGASVYKIKSISIHPDYSPGSGKFDLAILQLDGQSQVSV

ARLPTTDALSQFGSVYGWDSSESPSSVNLLTVSLPIVPIAQCKLDTGKNDLDETFICAGG

EAGKGVALLDAGGPLTTIGPQGIRVNVLLGVLSEPRGLGKVSIFVRVNTAMKFIEDVFKQ

HGDTFQTCC

>contig23686 Frame-0F

MPLLGRSAQALVRASCSHIAKAIAISCPSFAPSLSSVAVRSVATLKTDTPELCSNLHNHV

KARLDFKKLV

>contig23772 Frame-1F|Blast-SNARE associated Golgi protein, putative [Phytophthora infestans T30-4](gb|EEY61510.1|) 1e-118

MSDWRRDLQLVGVVFIVTTALLGVTLHSLVISTLTDAEWLALRLPTTLEAAQELGKTLQS

FSERQRGSLLLAHMGCYLYLQTFAIPGTVFFNLLGGALFGMTLGFPLCLAYNTLGSVFMF

LLSRRFGYRVVTHFFPQKLDRLSSILDAHRDEMALYMIFLRVFPFTPNWFINMASPHLAI

PLGQFTLGPLFGLVPYNFLSCKAGLILRELRSRGDIIDSATTMQLIVVAIVGGLVLPRLK

RRFTTTTGTKHD

>contig23813 Frame-1F|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBN75315.1|) 4e-92

MSAGIEQRNQDATVYVGNLDDRVTEELLWELMLQAGSVCNVHMPRDKVSGAHQNYGFVEF

RAEECAEYAVKVLNMIQLYGRVIRVKKASNDRKSLDVGANLFIGNLDPEVDEKLLYDTFS

AFGGIVETPKIMRDPDSKASKGFGFISFDSFEAADLAIECMHGQYLCNRQVVVQYAFKKD

SHNERHGSEAERLLAQTNPNKLKPHTMFAFTTGAPPGMEVPPPPPLHFNQGLGGYMGMGM

VPPPPPPAIIYAPPPPPSMGILPTAT

>contig23866 Frame-1F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72292.1|) 1e-44

MVETQTDCKIKCIRSDNGGKFTSYRFNKYCVNHGIIRQTSVPYTSQQNGLAERMNRTLAE

MARSMLSHMEMDRMWWGEAVMTAAHILNRLPNTARPNKSSFEVMNGSKPDLSYFRVFGST

GYTREADCKRPNTTTRLISAFFWFT

>contig23978 Frame-1F

MPFFVDNGFAHLYSCTDGSVTRQESSECSNSTWSVMFAFYFTVVTLGTVGYGDNAPQTVP

SRLLAIMFIAMGIILFSLEIENIIGLYKLRQIGNSPFTPKPESEFVLIIGNPSFAQLSAI

LRELFHADHLSNINTQQLEAVILGELKANFTKSLIFKLKADPIFASRVTYIAGDATRAED

LDRSLAQHARAVFVFPNKLTGDAGAEDAMNIMRVLAVKRFVGSSVRFLVMVLRAESARHM

LAAGVHADDIICENVIKMGALAQNAVSNGISTMLSNLASSLSVDSSKFINDLATALPAAI

DKNELTGLDTSTAADNSSHSTRNWIKEYYAGAAKEIYLFNLSKRFSGFSFSEAATRIFQE

TSGSVLLIGVEIMYFDDKPNSYTVESRVLLNPGKSLLMTEWIKCYCIADDYDQVFNCNIC

QETVSVEESFRISSFMFQKKDVLKPIFSVDHDGNDSSSNEFHGLTPFIAQMTPNSDMTKY

RYPLASPGAVSLYL

>contig24070 Frame-2F|Blast-anaphase-promoting complex subunit, putative [Phytophthora infestans T30-4](gb|EEY69744.1|) 3e-61

MISKKRYLLLSVACVGRWSVETLAAKLDVSNDALLKHVSVWLNHGLVAFATERTELIAST

SFQGTGRDDNTIVEELETAVSSDAQAQEDLQLLESYLVGMLSNFGSLTIQQIHNMLATFA

RSGAQPYTKTISGLSVVLEKLVNRGKLEIVGGQYQLIQ

>contig24423 Frame-2F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY63451.1|) 0.0

MMSPLKFLTHPVVIGLIVAAAGATLVALSNRYAVDFDDDKEDKVRPVPYLPGGHPILGHT

LLMARNLDRFQDWLVETSVARNGKPFVLRQPGKNDWFFSARPEDFEQILKVHFDTFIKGP

QVRELLDDFMGENIVIINGHRWKFQRKALVNLFTAKAMRDHMIPIVKKCAMVLQQVFAKA

ARKGEVLDIHRIMGRFTLETFAEIEFGAQLGLLKSGQGHSFEMAIDDANHISLERFAVPM

WVWKLKRWLNLGSERRLRQDMKVISTFVTNCIAGAIQRRQERLLATARGEPVKPVAKDIV

SILLDNFDTKGEPVLPQDVFNISLAGVLAGKDTTGDAISWLMHLLHENPRVENKLRNELL

AKIPKLATDESYVPSMVELDGVTYLEATIRESLRLKPPAPCVTQHCTQDTVFPDGTFIAK

GTDTTLLYHASALLPSVWGPDALAFHPERFLDEHHKLVVLPPLKFIAFSAGPRICIGRQL

ALIEMKVVAACLLSRFHLTQLPGQDIRGSLGISFGMKNGMMVTVEPTPGVAARA

>contig24988 Frame-1F

MHLRLVVAVATFFPCVTSASPMASELNAPHLVTNDEAALRLRGRTTNEDTENRSFFWMTT

TEKLRRTLEDRMAIVGKLNKEPDQFSKYSKALKGGDSKIEKLYQKHKRELDKLQKIIQDK

RTMKDNLSVTLRDPKIDRVLRLKTAAAEDKLTEEISRLMNRKADMEAGLA

>contig26942 Frame-1R

MGMYNANFDGVHPWFASCLGYEGTVFITEAQMGGQGIDVGVTLECGALQKLERMVAKVCE

ELEKKQ

>contig27255 Frame-0R

MERPSHARPVAMRLLTTSNLSEMQQAARKASKLCLSPTDPSENLTESISMASPVLTGKSA

PVTSPNPAKNPLPGLQFAISAQRLPNRELRLPSFSCPSYELESPPFTASSADEEECEHVV

EKTTIVQRRKKGTRRGTLHPEAKNVLKAWMFSPEHFAHPYPSEEEKEELASEAGIEVKQL

SNWFTNARKRLWQPVLRQSGVEVKNFLSTGRGGPRGNKLDVPLNLHQLVSSSPVPSPASS

PRKRSREHLSPCTTSFMCSDDRKHSKDYTVQKRMKAESTPRDDATNPSLQDLELLAATSL

LGLQHLTQSVH

>contig27321 Frame-0R

MGDPVYGDTVSYASNGVTAVVKAGTYIAFTWADAVNVTYISLKTGQKKTVTPTVTDSAAT

KKAQTFLICAKSAGLITFRGWGSDTCREASPEHSVTVEPSDSSSTTCGDSDVSVSTEDAE

ESASKAQRSSAVGVPADDTVATCNAQRASVQVIDGTQTCVCVSDWTNPPVCDQWPVWKWI

VTVGGGVAALFSIIISVRALLAGLEKKKHDEEVRINMIRITPKSDVATLEGNSSVYRGHS

MMVPIAYDPQNDRTSGIPRKPVDNEFTL

>contig27769 Frame-1R

MGPFKTTIVKGDAYTLDIFSSMRLNPTFDVVV

>contig29257 Frame-2R|Blast-RNA-binding protein NOB1 [Phytophthora infestans T30-4](gb|EEY60575.1|) 1e-176

MKAVVDFSRKTGDFSYLSLTDLRVMALSYQLEVESNGSDHLRSSPSLSQTVTRAANGKII

GGSQPTIPCKYYGTTMGCKYGNECRFTHVDTENANVENGAEIPMKKIAIPCRFLNTPEGC

KYGNDCSFFHEILEATEGTTSEASKVTDDEGTDAGAIPVINENIRNADVKSRIMGGLGAS

SNAGAADDDGKNWITEDNMNKFTTSPFGDCHNFEEIATRLTVACITTDYSMQNVMLQIGL

RLLSLEGMLIKRVKQWILRCVACFTTSTEMDRLFCPKCGNSTLERVSYSLDRDGHMTFYT

RASRPTKLLGTKFSLPKPKGGRHGDLLLREDQLLVGIWGQRQRRH

>contig29705 Frame-0F

MPNFENLATQYNATDVSNETQKDDFRPLRTTLPSCPDGFAALADVTWEADSVESLSCPST

VQQYECPGQRTNQDWVTSPENQETKGGAGTRDNGGGNPSSSSAMVPLSIGLSAILITMAS

ILIEKA

>contig30992 Frame-0F|Blast-nucleolar protein, putative [Phytophthora infestans T30-4](gb|EEY63085.1|) 0.0

MKRFFAVLMRYFLTIANHYAEYMHDLDTLAVTLFTLAQQMGDTSALIVREFLSQLYTRLH

KRESTSAWPTLPELLLLKSLTAIFPTSDLRHNVVSPMETLLSESLARGTINSPQEATQAL

FAVSLSLEITQSKARFMPEVITFLTRMLRAFVTIQDEKTTSTHWLRSTLWAYVTTHANEK

ELTLPRLSLAENTSCTGAEVLSSLLVLIDVASAQYAFLPSFDELFYPLYLLLHALLKQLD

NVELDAANAVVSTLHTRLKTCWNTRRPLRLQSFAPTMLPTLDPLYDANYTVRKDKMAPKD

TAQLKQLKRQVKRARKGAARELRRDAEFIHREKQKEEETRLAVKEEKQK

>contig31564 Frame-0F

MSEGLVAIGESYVGCLWATNASRTLDDVVARLLTIPMEGRQEMYRSWSARFVALAARMFK

YSPSSMGLVVGAVSEQFDLCPEFRRAYMDRYLHQGFGVWTPGTTTIDVAQANKLAELDHQ

LAIQSGHTILDISIGSWGGVGCHLAQKHSNVVIVSILSSIQELARAKKFAHELKVVNRIE

FVLAETPQKLLTLLSGFCASRFNRITLCGVLETTPESQQSRLLRTLKRIQKPNGLTLLEF

SACTATHMATHAWTNKYVHGAYPCYAITLPMLRQLARATGFTLRHTLGYSDNYERTFLEW

NRRFQAQYATVEAVDHATIKNSPMPSLPESFKRTWEFYLLHSAACYRSGALQVFQIRMN

>contig31713 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54431.1|) 0.0

MLLARAVSVFLTHSWKGGIVLALLLMSVGILGSMITMNYTLESLARAEGACAASAGGGPR

HQITHRKFDFATIAEMFVGRLGKIVVQLVMGLYCIGSLWSYASVFSSSTASIFFSFVLGE

SCDVYGANPSSGCLNGYYVFMAIFSVIVLSMVVMDISDQAIAQKFLSVYRIVAFALMLLT

MAIKVTSDGGTLVASRYDTIGSVNWGNFRKAFGPTLLALNCQYNMPDALQPLSPKSKARL

VAFSALLIAGTCYLLVGLLGALSFDTINPLATLMWSSYTGCGNGWQQCEFTNPVGICVQL

IVLLFPVINVVSAYPMVGVTVGDNMLMSFPKHLTERFGRNVTRRMCRLSVAAPPILFAVV

FKRLDFIFAIAGLFGFLLGLTIPCWFQIIGSRYCQRVWGNPGAAITEFTQPFVSSIPFAT

VLLVLTFVITAVAIATLNT

>contig31766 Frame-1F

MADEKLQQEQALLRAAIDTVSSENLRTYMLTALSEFGTSSLTQSTSTASSSQSENDKNDA

IIVELEENPIMLQKPQDALFVAIHALLLETGFKLLADANLAFTLPTNWDAESSNGLFNAT

YIHLNDDSIRFIFQGLFVNGRFEVYISDNTDHTHSIELL

>contig31872 Frame-2R|Blast-GPI-anchor transamidase, putative [Phytophthora infestans T30-4](gb|EEY65990.1|) 7e-72

MSSQDLADSIEEMHVKKRYNEIFFMVDTCQAGTLSNALKSPQVVTIGSSKKGENSYAHHS

DSELGLSVIDRFTFSTLDYLQRMKVGDSIRNGTLLDLFNFYDRKMLQSTPDYRTDNLGRS

IDQVLITDFLGSILDVHLHYDSEAYPIEATVMETPIENAETITEHDVVVKQPLESTKPQS

FNFSRQFLVSVAAALVGAILVTFKAV

>contig31986 Frame-1R|Blast-hypothetical protein OsI\_18788 [Oryza sativa Indica Group](gb|EEC78667.1|) 2e-34

MGQLTRGLKHSWHDGLHYDGKTIVCHASILHKDFWLEALDKHHRYGFHLRAFHKAWKHEM

ATYEDHGHNNCKNASFFDWLDHGNGQYVELPECTQHGLRSTRVEYCNAEERQVYKLEFVA

LKESKAVRVQYAMSQRVIHTDERSKWIFVIDLSGFMYLGRKRKGRFHHSSFVSGAPIVAA

GKIIIKNGIILAVEPHSGHFKPRLENLQALCSILATHGVDIDRIAFIKPKKWSCVWPFPP

QMDLELEDFASASDTDYSLDRFEEDGAMLECT

>contig32446 Frame-2R

MSNSLSCGFSDENPKPMEKNVGAQIDTNLDQVVELSQICSFCTTFRQPLRLPSFSRTELQ

EAILGASNGDATHVELLAELHFKLAREHSTAKMEKMMQDWKKTLARKLQDNWRKVFSANP

MGGGVTYAELTVLERVKILHALCHWKLDTCAEIHKHIAMLQKDNDNDAIEHLRAGEIGID

DEGVSYWYFNDGCWIYAEDKPQWQLKERKSSYSVEFASGKRIRLSIDFDTEHNSLAPPLP

ISVKSVFFADKVNEGKTTKDAPIASYLESTRENGVLLREKSKTETDSAAADSVKVQYKEP

IDGYICSRKSVVFIREDLSHDAPSRSTSQVETKKIVLSGIPLKEEKKSAQVGQPHAGETQ

FDEFGQALDIKHKNELKGQVSKFATAIASPRSLSTLKEGLSLCAEGGKVYMGLNKNFSAL

KSSETDSPVKVSKVNVSEQNHPNEVAVVGSKKRTIVDDDRSDSSSSDVDTLEESLRTMVG

NQAIISPPRPKRRKAILQTTNIGNAKSTEAIDGNLSLQVNKAAISQISYFGAEANFYLAS

TEKDGVTTLNTEKRKSTENLEELPGPSSSSSTELAVPLDSFDITCESCKKCYDMRYVDPP

LMERPTEEWRCFECLVNDARGWPRRRKSTHRMPLSPHGDNFLSQSRSFSSKHQSESLQTS

SKYFRNSCPSSSFKKNSSHTSTYRRIDSKSKNNYSKKSSSAKKQKKRKSSSSSHNHHKSH

GRRRRHHSHYCQAEFAKLLALFRERQHQRINIEEARVNKNYREASDEAPQGWRVASSTLD

NLRALIKALFGGSLEQDRLRGRLILILKDQEKTDELRRKQQELAWNILPRRQSSRIAIGK

MKSQSAQESETEERYSDEDVEARRPGLRSRRPRLATSDFIGNKRRAWRAQRRHNHSENEA

SVEIEVDMAGNWIDWSFVKSNARSLSMVCLAIVDRLLKEEAA

>contig32657 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY56233.1|) 0.0

MQEEKNQLVIKNEEEVAQYYYLSRSLVRLKEEFLAIRNKPDVVVRFLNGGRLVKLYCPQS

DDGSRNVQWDWGVIVNFTTKNATNSTSATPDTIVHVLLNCVKTNGTAKSNEATNNSTTSE

LPTPAPEGMMGLSASLECEMKICPVPLEMLDLISSLRVYIPTDLRTLDSRQAVGKSVREV

LRRFPQGVPLLDPREDMDIKDEQFMRVIKRSIEAEEKLKNSPFHNAKDKDARFALYNLKM

ESEAKMRELERKIQESKSLVLRDDLRHRRRVLRRLEFVDKEGVIQRKGRTACEVSTTDEL

LVTEMIFNGQFNDLSVNDTVALLSCLINTEKRKDSDKPPQAKGLEVPVRQLRETAQRIAK

VMQEAKITIDVDEYAGVFNTSLVDVVIAWCQGAKFSQICKMSDAFEGTIIRCLRRLEELL

RQLTLAAHSIGDVELEKKFDEGGKKLKRD

>contig32855 Frame-2F

MQLFYQAAYSYFREWNKIIVAAERLKQGAFFNPQLM

>contig35146 Frame-2F|Blast-mRNA turnover protein 4 [Phytophthora infestans T30-4](gb|EEY57065.1|) 1e-103

MPKSKRQRTKPLTKANKKGNELKKSVVDAIRNAVNTYDSIFVFSFQNMRSNHFKDVRMEF

KDSRFFLGKNKVMKLALGRSKEEEYAQNLHCLSNDVSGNTGLLFTSKPHDEVTTYFAKLS

IRDFPRSGFVATETVSIPEGPLSQFTGSMLESLRGLGLPVDLRKGTIVLSQNYTICKAGQ

SLTPEQAKLLVHFDRKMADFKLVLLSGWSNDKYRRIAVESADLSGEG

>contig35883-1 Frame-2R1

MTQSLKQLQSDRFHQHRYFVSFRFPSQSIKRQYLSSPTQKGRLHW

>contig36059 Frame-2R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY58698.1|) 1e-44 NOT\_ORF

MKEFCQFEINGNDDQCSSSKSEWAFKQQSQASMFLSFGETLKQHSLLYVLTAVILHHGNE

RSGHFTAYRRVSNLQWSFVSDDTVREVPVAEVLKSCAYMLFYERKSRTQQIARSSETEEM

TDDDDDDHLLDFPFGPDFML\*NDRSCKQHSHYETAEIRSVECIDNYCCN

>contig36662 Frame-1F

MIDADGHVALVDFGLAKLHVSEYKGAKTMAGSPQYTAPELLLPKAKRSYGKAADWWSLGI

LLYEMSVGNSPFYDNNIEKMYHKIQNDPLVFPTKPQLSDELKSILRSFLQKDPTKRLGTR

ISDILEHPFFRGIDWDLLLKKQITPPWKPKLSSPLDVEYVDAEFTDLDVHREVQSPTDKT

AAKSKGFLSLVSSRGSRDKAAPPVQDPTFKDFTYFCEDPDSLVEVTNLVSELRPAPASNS

LTPNRYSNEEDSDEAYRPSELEKSIPAECEGTPLSSFVENGHLNSIPISTQQFHEGLLKL

EATMTEQFERVEVTISRERAPMKKPSGSSNSSSEEREQDLVRVEKMVISRAPSLRNAAVI

PNSPSANMRDPSGTSDVAKHENLSQSSSRGAVAFAADKRQPIMEAEF

>contig36738 Frame-0R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY58105.1|) 1e-157

MLRGGFRRKSAHLLYVMRGLRDAMVERDPNDIIQHLADCKQIIGKRASADIRVLNEGRQL

IAHLDEEEYVHSIIADAKIIGHPNLIEFAVRVAEKSSPWLAVDPLRRKSRSIVALQKQKM

EQLTAMNMKLRASMIANDPEALMGSLATLEEPSVESLERKLATMLIIRALEEKSAVESVS

HVLSKIGKGDDGATIFNKLLGPATKAISLGVEAKLPMLVDAVSSISCNVNAVTDEEENEE

IEEVVEKEVEKEGGTLSAVSPASASIGTLTIDTTNLFLALQKALDDENYFAVEKVLARLK

AHGVPDDDSRTVDAERVLATQSIPSTTHAERKQIVKLLAVAKISQDVELLSEAIEAALSV

GLAKWDFNLKNAEREREKLLMASESGELHRVTPVSAEQPALLKPQMIVEKVRTILKDKTT

T

>contig36882 Frame-2F|Blast-cleavage and polyadenylation specificity factor subunit, putative [Phytophthora infestans T30-4](gb|EEY70242.1|) 1e-104

MAVITFTPLYGVHSSVPCCAYLLEVDDVCILLDCGWTDTYDVELLKPLQRVVDRIDLVLV

SHLDMEHMGALPYAMGKLGLNAPIYGTLPVHRMGQIALYDAFQAKTKHDRDFSLFSLDDV

DLVFERFKQLKYSEKLTLTSSGEGIVITPHVAGHLIGGALWKIMKETDDIIYAVDYNHRS

EHVLQKTILDSFT

>contig37214 Frame-2R

MQRSAISIVEELEFVAIWSIIGPCRRPSEKSASSIESCDEDNDVHHPRITSALYREQLGH

CHPLVLRSRILGDKAQIDV

>contig37368 Frame-2R

MISLPLSVRSALIRQSNLFSRNTRKCSNFFLDFKFSCNKYAHVICSVFNKVHHTPIAVLI

VAS

>contig37470 Frame-0F

MAKTDDDEALRRRGRARPRPPSSEVDASVFASIESTNQPLPRSSKMKMASLMAVVDDESK

SKRAKSADILSNSHVVRNASISISSLTSSTEAPAASLFQNEMPTIIPSFSRDAPVGNGES

KRVANGSASAFGTRSMLEYCFPSGRYEGNGSSNTRSLKRKRRSGRRDESSIDVDMLPFGI

DAAKLVPQGLVDRVDVHMSHVVLLAVVSNHVTNWCNRSGFASSFLQEISTLLAAYYPCNY

STLLDEVLARFLFKRPEFIGLLLPAMLEKMSKAGDSVTTTKYPVADALVRSCGVSCTLFG

PLQARHDLACLTLLQCLVEHNRGKFPLTSWIVSCAFASSDRVLLLLWKALLLCIEDDDKW

HIEEPMQQIVELLAEEDKRRDCRISCGFVKLVLSNDFVRKELVESRSYLIVDCLLRAFEY

ASPSWSASLMAEWMERRRKQQSDVTGSLKELLDFLVCSNWKLSLKKPEWFVNHLLRFLLS

PQCHEAEHEETLGAILHDHMRLVFGFVDATENRQNSGSDSLGAAARITW

>contig37917 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61937.1|) 1e-47

MRLVRALYRDLLAAAKVLDSHASLRALVTTHLRESALSPVAKKRLPHVEAFNRSLVSYLG

GRHMYLPDARRPELSQLVREAFHDAQTLASDADGIDTAFVALRALNQILADAKALELPPS

NAPEPRKPYDVQLTENVASGVFLLAHPLL

>contig38620 Frame-2F

MVNTLRVFCANGVQLQQIKHDTNILITHLSCCFALIVERIHDENYIPSLMSLLSSQDRLK

LNYRRLVCLLAYSLKQHGGMMRIKYKHSKTYAPPLP

>contig39137 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53245.1|) 3e-07

MTKGSFDSIVELYLVLSNTTGRQNLGTYLRTASAFGAAQVLI

>contig40133 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67001.1|) 6e-41

MPRMARGDFVKAIDLVQCSRNGGQRWELVLTRWSNGMETWLPHEVVQLLAPDLLQEFYVN

SINSWAFHARLQQGSLSAYRTEVELWLFHT

>contig40357 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53546.1|) 1e-105

MREACLVGPYEQEVVKYSAVSYKVARHGLVKQQKQSRRLGMFFGMMFKCRAFHFMIWNSL

KLLSAQCTNDASLSAIKSGASSGSFEDITFALKDVLDLLTVKEYVQLVGVPELLTDQEEA

AVRSAASKGVSWNALPGNFVDKLRSCEADRFSKIVRVLLDLGLLCVVQDTSSMALFNVFQ

TCGDFDSIVSRVAFAALSGGLFTITRHVRISIKQGARVLHRLPSKFTYAYAPGFSCKSKS

DHFTG

>contig40883 Frame-0F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68035.1|) 2e-52

MLSFDSASADRFLREADRQALTVNHTLSVWLNGNRWVSANPVIVDMVGHVAVPLRESLVP

>contig41145 Frame-2F

MPPMRVWVPKSEGGIRGAPEFNHAPLTTHGNDHAGLTLENQIKTCGLHLQHVYVFHWNAH

LRHSIGFALAYPTSPCPSWNLHGRRLTSSTVTVLTPKQAAYP

>contig41530 Frame-2R

MPQMQSQWQAAPDGPEPMQVSNDSRARDGVVSAEMACLVTPAALESGHVVRPGGTMQAPV

LASGSVLVTSSNNALSTAQIAEYQDKLDKLEVEAEAVDSLRATVSELTKRLKEKESSINE

LSEQRAKLENYTKKTLHAVQTKYMVAMSSHRNQINEKQERVDFLEKKMKEVRASYSREQA

LMMSSFYE

>contig41729 Frame-2R

MNDFKAHKRYQKQERLREEAHRVAILNRITKGATIAISPTTRDPTAFFKSDGSSTFECDD

NDFLDEALYAQYTERRVKQMQEAARIRKVYGELEYVSPTRFLELT

>contig41952 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62019.1|) 1e-34

MDGWKAVYQVALAIIAELRPTLLTM

>contig42917 Frame-2R

MPLKWFRGHCNSEIEESRSTTHIPTSKSTTSATKHRFRRSRSHGHGLHSVISSSTQEVHS

TETQRRLLYQSKTSRRFTIHGISYHSKHTPEAGWSCTSETSQSTASSPPGLTRMIKSHFG

KNSSRTAPCQSPPRTQMTLDSNPSIIFIDCPP

>contig43059 Frame-2R

MRIQELRCFSDLIVENAHQLLLLLSTSAQKVHTEVTKILQRIYAFLFATAPSRIYQATVD

SSRWLAGLLKDVRYESIRSEPFASGNSSLATDMPSLEGVRLSEAFTAEDISSSHSLETAC

KNYMDRCKSLEHANVSLAKQVEELREQLKVARVDVFQTQQTPEQDVTMLQARNDDHLGR

>contig43411 Frame-1F

MTSCVVQVQDLSRRLLKRIRPSLPGSTSASVEGCSPTANAATSEALRKVCKHQIESSPRT

SAPAKELPNETIEHQSLSITNATEWPRVTGCEGVRKALTFLQTSRQHALMLMLQNHWERA

VSVLQKVEKATESVSRQRRQVVIQLANAGRNRLVDTMQELGLSTPRRTVRFSDIVSVTIA

DDMDRMCDEVPEPVREEMLVLRASRKIPQENLSEFWNE

>contig43662 Frame-2F|Blast-phospholipase D, Pi-sPLD-like-1 [Phytophthora infestans T30-4](gb|EEY67671.1|) 2e-10

MSRRARRGDVAVVFGLFWAVSCIFLVWIRIKPRTIKVADTSSASKPRVFEPTWPSDSDSS

SLFTN

>contig43925 Frame-2F

MWDRALRILDKALRKSNISSAVFLQHQSSESKSAHVASFRDGDTQVLILNSLRSASGINL

QVASHIIFLDPVGYNPM

>contig44564 Frame-0F

MHGLFIFIFQVATPFEQGINTIRTMFA

>contig44766 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62725.1|) 4e-11

MKFLLPPDTFSPVTLSPDHQQQILHEANTIVKETIHANDAFTSNNATLSRQDWRLLRVKE

GVHVYRQRKQATLQCTSPIFYPMVQSPSNQHVFSKYCTTSSSFSSINAKVNTKTS

>contig44872 Frame-1F

MEPFFAGFNAEELAMMQELLRLLLEDDDVLNQQPSPGTNARQDGNGLLNELAGGIATNDN

SDYQWRASVPNGVAWNAPPAMMFPTPQYATHASRARTSSHFGSEDEPMLKRGRVDVSSTM

RTPVNCNPFFQDAGFAFY

>contig45149 Frame-2F

MLPVNKSTLRRGLAPYRRQRLHAAVASGAALILLFFLLMLLSWEKPRSVTVRPIDVVVSQ

SEEAPVPAAEDGGGMMDDESQVDGGIELEKKLKDQKSATHAPFVLRLLLPLIAGYCFGFL

GSMPIAGPTSAMVLRLGIQGKYNAGLTIAVGGAISEATYAGIAFWGFGSFLAGAKFLLPV

SKVLGAIMFTLIGLIFLKADMKPSLDPDAEASHEKGSRRPQGVILKNILVGLTMSGINPA

LLASYTGAIASVYGTGMLEFTLFLAVVFAVGVCCGVSTWFYLLLFILKKYKERLKNHTID

LIMRGLGCFLLTLGLLCAKSSLDYFLMA

>contig45853 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56330.1|) 2e-17

MNSRRFTIFVAVTLVAFCSAAMDPVRRDGMLRVVGEVHSNRYVVVNSWEKRAKKHPHCVD

TGAVDKNPVCASTGVLYMNKDVFEFHKCLIEAQYGDVITVAEIDLCKKAKREDDEHTNVY

YDVS

>contig45992 Frame-2F

MMLTVMVVAATSFLAAFRGIRTSILSTATRLYSIIAVKI

>contig46597 Frame-1R

MTLDATGGVSCTIELLVPSYTELPKQEGAEANYSVALHRTTDNWLQLVFAGPDVRKNVTC

INGPSCRCFYASFLKKLLMLDEQHVLAVDVAYVVIIGVATLQVRVRVHEDAKHSTSLKDF

DLVLCHLRSPALEILQCNEQARKKARNAALEDAKNSSCHVVGCRLHSLDKADQPKRSFNL

PDVFRNLVSQNAVDQMEIRDDATYVGRMTCCTKKFVMTDLPTNVLQHIVCLMSARDFASL

SGVCSLFQHLAYEVVPGLNLVLYA

>contig46658 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58303.1|) 6e-70

MGLDISSQALERSKEVWKRFSEHLPKNRAKPLRLYHHSCERMKSLLPESVDVAVAVQSIQ

EMPNLETAATEILRVLKPGGLLFIADYIPPNVAADHLIQSFVSPNSSTRTNELPYEVLQE

QRVTNQAVKSSELSSSALRDLIYKFTPPIRHSELETLFFIQ

>contig47657 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61439.1|) 2e-22

MSPKRTRTSYQSALSDNVRPGGSTTMDVLIRWMRTSGNVKRWRTEPRAPLIREVVDMMQA

EGLAHRQPPF

>contig47921 Frame-1F

MYTVPMLHHHSQTVRASCATCVAAIFSGQIFSLQSSLSTFVQHFLLQILFEKDKSVQQSL

LSTWKQIIFSLLKEDLFMHVVGNYLPRWTSMLWSFDE

>contig48054 Frame-2R

MEAQRNALNAACISLRSLSVANRWVVRKLHSEEILATADNSANPILNIVTLEDMRREVAI

LDGKLRLLALGHSDCMLLSTIDGDEVVALLIDAVYSSCHNIRSSTLAERRQLGLQLIEIA

ADIANRGSSACVSGLTKSLARYCVASEHSVVSSPSISRANRDLLWDFLEMLLKNMGSLAQ

YEIAADTVLEYWQQQGRKLALPLWLQERLMDATDGNPAKLLRLYLKHGLLIEGLQLVDHL

LSVSMASTKSENAFQNQVENAKLQNLPYIPHNLVDEVLDSTAAVLKEDVKGQVSPAAMKR

LRKLDHHLRQQLMRYFCMVNALQQAQEASHLARSR

>contig48195 Frame-1F

MAQEQTPTSILHPHQTLGMPPYMVSGPMMGAPGMTHPGVAAPGIAPIEMGAMPLGMAPPG

MGIPGVSTSGIGPLGVVPSQMLASGAFPPLIGSGPPGIGGGPPGVSGPPGEDFEPSAKRH

CSSGSMLLPEKEFASRHPRNGAINCQSSE

>contig48252 Frame-1F|Blast-RNA polymerase II-associated factor 1 [Phytophthora infestans T30-4](gb|EEY65838.1|) 1e-116

MAEATETKGATYSTNSSSNGRNRNDENNDLRNRRAPPGANATSEDRARYELERKKVAKYK

EDKLKARRDHTRMILESHAQAKRRALLGKQSEFLATLEFRNTLPDIPFDTKFVKYPHEPE

RLIKYKPNSLEMDYTYEIHEEPNLGLSIDLIDPAKYDAPTNPEPLEIGDEQTLMMKEDHA

GSKGRSKVRPTVSWLRRTEYMGNDLYDSVHKFKSEAEIQSTLREGTENALAEVVSV

>contig48560 Frame-1F

MLDSVIWKDGPCGLDQWMYFPEFNHVLANCYGRPVHVFSAEQMITFPSHRIGLTTAKPVN

SLCIC

>contig48951 Frame-0F

MSAGAAEVGGATIKTQPEENTVGTVVGFIESSPRRIFLDLIYSTSLRTV

>contig49673 Frame-1F

MLRVLELLNSVLLALTSIAVPAVASGLLYVVFLIQLIRYTVFVRRMTMEELLARESGVKR

SSSFLG

>contig50594 Frame-0R|Blast-translation elongation factor 1-alpha, putative [Phytophthora infestans T30-4](gb|EEY69116.1|) 1e-79

MPQLGRLTLRDEGKTIAIGKVMALEK

>contig50833 Frame-2F

MASVRRILPDSKGVRVLPPGVYLVCGSKRNMRAHCFAMEFTPEEDVLVLEDGVNSGIGHQ

IWARTIMFICTLKVHICGSSNRKVSMFWT

>contig50846 Frame-0F

MLRGGGKVRQHSLHELRCQVSRKRPTCTHLADGNCVIHGPKITMSPDMVVLVATVKAVVV

VFSHLLLGYGNTSV

>contig51197 Frame-1F

MSPLRHEFRITATSMAEDDEVTEFYPLDDETPQPPQSTEPISSVHSEPVENTPWMTSRDQ

IALQLFWQGYDAYVMCKEKESVAPCFYNAQCFGQTADNEFVQIVPVDEAPERHILDEMRV

QLISSSCSGKYLRATHVSKYLKWSRSRDEQTVFVIQISDRKPLSPNSKFTLTSSFW

>contig51720 Frame-0F|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69651.1|) 1e-119

MRGEFETVQFLVETLDADVNALDAKKRTPRDLAQLKRFHHVARYLKQREIRLAAWNFAVL

TWWCNSDSRTPYRFTVLNAILFALVYVLKILPMMPDRRNVIVPHLAWNALTWYFFYRVGA

TKPGSVTDDSRKYGVEYEKVTEALIRGDDTEDDDLLGETVSARAQQECMDRPLCHTCHIQ

RPPRSKHCRICKTCVPLFDHHCPFIDNCVGRDNYALFLLFVVFLTLDMIGMEYVLYMLWR

YHHAVRLYAV

>contig52431-0 Frame-0F0

MYHGDRNIIIDVAYSHRVRSKFLSCNNAFKQTKRSSALLFAMRWSRENDLFNCMD

>contig52431-1 Frame-1R1

MQLNKSFSRDHRIAKSKALLRFVCLNALLHDKNFDLTRCEYATSIIMLRSPWYINLPVVC

AASSSTSPL

>contig52484 Frame-2R

MSRIRSVLMRWSDENGISKKRATAPSICNRCYRIMLRTKILSIATQLMLEHFTLLLFCNI

RMCSFRVNAELSSTYMRNHKQINSHDYLAHMSAAPLLSKGLRRK

>contig52909 Frame-0R|Blast-N(2),N(2)-dimethylguanosine tRNA methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56619.1|) 4e-50

MQSSTAASLAQKLQNKVAPPGHKIIREGNGVLVFPEQNQVFYNPVQELNRDLSIAIISEY

ARMRAREQLIKEARKAAIAEGQGAATFEPKDFSDQEIESQLYETSKDKGIRILEALAASG

LRSIRYFQQIPGVKSI

>contig52996 Frame-2R|Blast-AP-4 complex subunit sigma, putative [Phytophthora infestans T30-4](gb|EEY53525.1|) 1e-06

MFNLEKAHFILDEMVMNGYIVETNK

>contig53003 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53261.1|) 9e-31

MTLLLPFIFHPSASIRALMYYIILLLTCSADNFIPNRVPVDLTNNALATTNEDAKVPDLL

KSSFGLYSSRWTRCC

>contig53380 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53356.1|) 1e-15

MFGGSSNDWRPLVANFQRQVKDKSTSLVTEDIDHVIRVCLQHDRVREASDAICQGEKHGL

MATSESHFQVCYSWA

>contig53591 Frame-1R

MVLPDRISFFEIGYGQTTVMKSRVICSEINIRCFIG

>contig54024 Frame-0R

MNFFVIRRSHGFKQFWKNSRGDVISSFTSKRAKRDPSSVFFFLTLLVFVTRLIIMIRKLI

FVILAVFVQERIIFITLFRIRIFFTIGRAHVP

>contig54091 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57198.1|) 6e-25

MGNATGWIAQSLYPVEQALWVAAKSSDLATLREGLVRLTPQTRYYSEWRDPTYGYTPLAI

ACSQGHL

>contig54226 Frame-2R

MQPQEITTQLKRKRKTRICKFEGCEKYVVDRGLCIRHGGGKRCSVAGCDCRAQNRGLCWK

HGGYTRCTVKGCTKRAKSRGICWSHGGGTRCKHGECAKIAVSHGLCWAHGGDKRCLIDLC

RKPAYERNGNLCAEHCAQQQASTRDLTAIQWFCLKYT

>contig54392 Frame-2R

MMGVKIIAFARIAVHISLAITLTSVASKRNSPRRQSFFIKNHSLHIRLAFGSIGSRSNRP

SMLIRPFFLRQKVPMQIRLFRSQ

>contig54503 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61885.1|) 1e-26

MAMAMLPLRKSAEIIGRSADVTTEKPNTLMVDEAAEEQTDRVLAKVEAAMVRLREMA

>contig54680 Frame-0F

MDQSPTSTRSERSLQGHEIPSRSNKSTGNVSSLRS

>contig54965 Frame-0F|Blast-exportin-4, putative [Phytophthora infestans T30-4](gb|EEY53544.1|) 7e-29

MQFLLEHSTTLPRFVEAAALQTVVLLVKRGWLDRRESERVTVLQQMGIMLQPGKAPFHRL

LAARWLLAFVTEFSTASRAS

>contig55001 Frame-0R

MEEKNTWIGSYERNLHRYLRVHQSPRANMTMVGSSPNLRTRSQTLSPPTSRAALRSRSPR

DLSRVRYPEHSTEAAR

>contig55786 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66087.1|) 1e-15

MYRARNPLLFSPKLEASRDICQIKTDPRKHLELGNDSKPRSRLSTKFRKKTVYANSRFSS

NNVQ

>contig55878 Frame-1R

MQNDNGLFDSLILLHISVFARLRIVICYSTRLCVLLGTS

>contig55913 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64601.1|) 1e-158

MLPLERLLPLFHARNIPVLVDGASAPGQLPLNLNALGADFYVGTAYKWLFSCKSCSFLHV

SKTYQNTVRPVVTSLAYGQGFVEEFAIQGTRDEANFLTIVSSLDFYESVGVSRVYMHNKA

LIDWAGEYLATTWKTNVLLPAWQRAPFVSNVRIPVDWPTNEDTTPLSHEEALLLCDAIMN

FLDDQYRLVVRVVPFQNQLFVRISAQMYNERKDYEQLGQAMLEVTNTPTLDDYLTRMRI

>contig56206 Frame-1R|Blast-GTP-dependent nucleic acid-binding protein engD, putative [Phytophthora infestans T30-4](gb|EEY55155.1|) 8e-38 NOT\_ORF

MMLLAHRYVMMTCTPVGYRGFQRSVGIVGMPNVGKSTLFNALTKTEVAQAANYPFCTIDP

NVARVAVPDQRLQHLAKVEKSKRVIETQVRATFLMDKCKNVLLMIPR\*LEFVDIAGLVRG

ASRGEGLGTLAQKPFY

>contig56747 Frame-0F

MIEYLEALSVEPPNKRLRTSAHNP

>contig57454-0 Frame-2F0

MTEGTNEVKENGVRTRRNLGGGGGLRGPYDEDPNTTSQPEIAPYGPNTNTPDQTNDVDEK

VEDTKNEKDEEEKKEKEEKEKEEEEEEKEKKEKEEEKKEKDEKEKDEKEKEKKEKDEKEK

DEKDEKEKDEKEKDEKKKDEGFENKDPAGETPVTMGGDHVQQLDPNQSSYPPVTGSQPGM

GDDHVQQHEKEVENESEKNEEEMKKNEEKKKM

>contig57454-1 Frame-1R1

MVITHTWLRTSNRRVRGLVGVELLHMVTTHSNRSFSSRVFVFKAFILFLLVLLLLVLLLL

VLLVLLLLVLLFLLLLLLVLLLLVLLLLLLLLLFLLLLLLLLLLLFLFLLLLFLLILLVL

RVLYFFIDIIGLVRSVGVRAVRSDFRLASSVGIFIVRSTEATATTQITSGSHSILFHLVG

TFGHQSLRGD

>contig57528 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57929.1|) 5e-18

MSVGVYTSADEEEAEEPMENFEKLRIWISDKKTRTTSPFA

>contig58370 Frame-1R

MFCDVALNAYIIKFYMAAGDPVTCWSARDLCQS

>contig58514 Frame-0R

MLARKNRFNNSANLGNFFQTQNVAAIFLELRVSSYHGRFSVSSTDHLQQKQLYRQQSQVP

RNGAGT

>contig59012 Frame-0F|Blast-coatomer subunit gamma, putative [Phytophthora infestans T30-4](gb|EEY66011.1|) 5e-37

MQPCENTSVPQPKAKAHILLLSGMFVGGIKALVKSRISLDEQSGSMILQMAVRSEAEDTS

QTIMDCIR

>contig59355 Frame-1R

MQYINMYMYYSISCLCISFIIPMSLFN

>contig00677 Frame-0F|Blast-predicted protein [Populus trichocarpa]gb|EEF02533.1| predicted protein [Populus trichocarpa](ref|XP\_002316362.1|) 2e-25

MLKQKNVESILFGGKRIGNQSNFEKLDWFAEQLVLEHQRRSCRIAPTVAFKQAAPNST

>contig02363 Frame-0F

MPATKTVNVVLARGINAISRNSLAKKNGRGKIFKKGGEKKVTASVKKISKKWFPAEYIPK

PLESAKTKRNSVKTAKLRKSITPGTILILLSGRFRGKRVVFLKQLASGLLLVT

>contig04376 Frame-2R|Blast-metalloprotease family M76, putative [Phytophthora infestans T30-4](gb|EEY54858.1|) 1e-23 NOT\_ORF

MLPNVEFFQKSARWLNARCVHEHAVRSTSVLLLYTYDVFLFYV\*YLRRI\*\*HLVL\*SIFP

IEARAEVDKMFERCYNDKSPF

>contig05191 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55956.1|) 8e-43

MLSLVKKVTPSAGRSTLAQTRLMGHGPAAPEGSLEAKVRHYLPKDYQIVLATLGAYTSLF

MLFKLKPTKKKEEEIAIPSSSSSGLTSIPSLFDEEFDEWSKLPG

>contig05894 Frame-2F

MFTAALRSSLRIQRCNTCKLVPSFPIALSCSSKRTFASATSLGIDKYGVTNATTQIYHNL

SFDEIAAHEEANQEGVFTKNGTFAIDTGTFTGRSPKDKYIVDQSPSNQHIWWGDINHPVS

PQVFHELYDTVAKHYSTAEKVYVFDGYAGAHAASRKKVRFITELAWQHHFVTNMFLRPLS

KDEIVNFQPDFTIINACKVTNTKYKKHKLHSDVFVAFNIENNLAVIGGTWYGGEMKKGIF

SMM

>contig07342 Frame-2R

MADVRRRLPAPPFSASDGHATPEILDETKRLRRFHPSLPRSSIVMLIFLT

>contig07953 Frame-2F

MIIGLIVEVFTMADQHPSVNLISIAKIQQRLCRYHVLYPTTTTISSLFGWSLERETS

>contig09753 Frame-0R|Blast-NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit, putative [Phytophthora infestans T30-4](gb|EEY57213.1|) 8e-14

MSVLSPVAKAALRHPVGRVRGNGITATVFGSTGFLGRYVCAHL

>contig10001 Frame-2F

MKFLLPQNVASNVTLSDERASALIEEADTIINETLVANESFIRNGSTLEPPEWKLVRVRD

GVQVYRQRQNWAQRLGTPPPSYPVIESPNAREFKRYGSTASVDQVHDNQTSWSSWSSLGM

NGDTIMEKLRPHGVTLMALHGTLDGTLDDCMFGCVAPTDDAWMLRSSHLKDGVDDSRIIA

ALRRPTSTDPCCFLGVKWFLKAHPALITGFVQKRDFLLLEATGYTQDTSGEKVGYVLLHS

ITLRDLPELAHLGIVRGLIRFCYIFRQNGSGKIDIFCRGYFDSRGDMPRRLSVSIAAEAT

IAVVGVVDYAHVKKLIWLIRHSRKQVAVDATNASCCGVCAKNFSKLFFHSSAPCQICHRV

ICFKCTVLKKMTVHVATSGKVLQRSFRFCLQCLLQATQMSGWDMAISNVEASSTSSS

>contig11055 Frame-1F

MGKSTDRNIPTDDEFYKLEQLLNQTADDASTCLKLLKKELSEYDRRNGNHFVNTATTYMR

RDMRHAKDTAMDMKHVSHNLNKEHKSSKTDVSSAQNVTHTTAKAFEALEITARNYDKENG

QRMGVKGRISAAMGGHHHKDETHAKDEKHPKHGESNEGLLGKHDKESEGGMFGMKKSDEK

SEGLVGEVKERSKDVFNTKDENGSGIVGSSETVETIVKRILHDHFNLKALDHQIKAAEKS

LSPSIMERAKEKMHDVKEKLVGNKSDSAHDGHGDPHESHPVHERVVSP

>contig13390 Frame-1F

MVELIEKTGDLLHEMFYRIIRWLGWYVSFNDAVRGHDSTRIWPNGGNSK

>contig14683 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66291.1|) 4e-66

MIEGRRRMKQMQGLLLLARLDEFPARRHHVEKIKLQRVTVMLQPQMLQLTYSSLADQNML

CPLGRMDLHGARLEQVLDGFVIYEAGNTLCKKIKLTDKEKATTDAWFLAIYTAITEHERI

PISKSEYTGHKFSAMLTSSLRDGHTKEMEFEISAQLLLHARPVDKPSISWKVWKTWSELQ

SFN

>contig15763 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62020.1|) 2e-36

MSGEDVSVVATEAMDIPDVIERLNKPDKAEHEEKVAALDSAIKKLQARSNVIHTEIDALK

SNRSGYGGQIQEAKAKFAALRAEKDNLIQQRNMITARLRQARD

>contig18980 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58121.1|) 0.0

MALSSDVFPPKTSRHKFTESLPPISIPLSVLRQPSLPIDEITKHAMSTMSREKTLTVPTL

ERKSSLQQVSILLICGAQNLAASVARSLFRGRMRLVDRIRDSTRLDLIRRPSFDPKDFFN

AIRENDVTSSFCVQKGATLEDVLSDRQEQRQKFFLTRMSDPTSYFYKYHFDTRPERRPKK

LDVHLALLCWLKPHEHVVSWDRVENLRRATVHWSAYLEPLLVDRVTGAILDGHHRYHVGI

QLDLKCVPVVLVNYLEDVTISVDVWPKCGRDSLTKQEVITMAISDDLFPPKTSRHSFSDD

LPPISVPLERLRQPLAFSFVPL

>contig19150 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66191.1|) 1e-112

MDTEIRKKCSDVVEHFFKLESCEPFRERVNWEEWGLYDYLQVVKEPMDLGSIRNKLSKNE

YKRPADFARDMRLVWSNCKLYNQDGSDLYLLAEELAKKFEDRVKAVKLDVGPVPKADKSV

PAPSLEEKIFFSQNIYKVKPKDLGAIVQLLEEQCPKSLDKSSPDELEIVVDNIDNKTFRD

LEKFVLENVPEGSREPIETPKSSKKNRRPPSKKIKTDA

>contig19334 Frame-0R

MFQLSAALTSRGQTERQGALFSPFLIGGFFVP

>contig19341 Frame-1F

MTEEAAKKKLIVGSKSKAKKDKGDYNVGDLAFFASKMARLYANESSRNNDELVGMMQELF

KEALMYRSDVERSGLAAIIARLRKSLSPTVGHTASALRKHMINILKNDTDIARSGKRGFH

KMTAHGTKKRKTEASNLIQSQADQVKEELLSGTSDNKEVKPATSTALSPSKVESPVEQAK

DLNGPEIKVKDENASIELPEKVVDNAAPVDDQFVKMEAMANSSIEPTENRLASPTKIEVP

EEGGLMNDKAELIEKPGNVENNRKVCVDMLSKILDHDGSNRADLAAEIEAALFERFKETN

EDYLTQARIIIFGLKENDSMRKRLVSGALHCLELAYADHAFFKETE

>contig20288 Frame-2R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY59592.1|) 1e-146

MPAGLELCQYEVTDFTRDSFLYYFLTQYPGRTIIFLNAIHQVRKLTSLLTLLSLPVFALH

AEMQQRQRLKKLDGFRSHANGILVATDVAARGLDIPSVDHVVHYHIARSTEVFVHRSGRT

ARANKDGLSISLVSPADVKNHLQICKMLQRPTGLSDFPFDHRYLKAIDERVRLAKSINEQ

DNAAGKLKAEATWFKQMAAAADLEMDEDLMFELGAKKRIQENMKRMTVNQSVQSLRSQLN

RLLATPLRPVGSARKFRQLHKEMGSQISNDGEYCARNASEDLASKGKQSYKRFRRRKIGH

L

>contig20323 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68003.1|) 5e-95

MAKSYLEKFSWDLMRAVDEFYANGGENLVRKSSTVSMSAVNAWFDNYVDPDEEYDIINEE

GILKFCEDLGVDPQDLVVLVIAWKMEATYMCAFTRKEWQKGMQKMDCDSALKLKAMIPKL

REAITSEADFKKFYCFCFGFSKEPGQKSLSIDIAVAMWDLLLSTRFQDLTASWLTFLAER

KPVKGVTRDTWDLLLDFFLKVRESYDNYDENEAWPVLIDDFMTWVVRPN

>contig20569 Frame-0R

MKWMMDKVPLDKVWSYVCKDREDAPTDDEVKMFSRLIGYVFLLSSNDKIAEGSTDIVESK

LAQAYHVNLNELAHDMLVSIRLARQYPMSIEYFKLPNPLSFPIQKALFEFMKHCDDYNLH

SHGSDKKDSSKLIAQIYRDEIKMDDFLKKSIQHARYSQNKKGFEAT

>contig20671 Frame-2R

MSNSTTSSKALRESFAHHSSSRGPRSSSLSVRGVKRPKVADDY

>contig21557 Frame-0R

MKLYARKYLNCRGKSSRFYASNLCILAVLNDLPIEADALFEIFLESRFEWIKPFFQREEN

EKMFQENSKKTNCTLMIMLKSIGMTMTQTEDIFGNGSESGLLSSIVQLSPDFKKNLAQFI

SSGKLLQRFSSWFQQNRHQILRIALPIILRINSISQLSRLQFKLNAVDHENSGYHNSKLW

GQILSTNCGCLEKHIHASAKSVFSILFADAFRKQTRNFVQQSFIEALDEIVRQIHASLND

AAANALRSEYRLQNVKFYNYFGNIYAKTADLDASDLQSVLIEEFLRTIVKLVVFFEQEYP

LSGGKVNAASDSIQVSIFFFGISNILAGIVTEFHCHMDKLFPGSSSDVSIHEDVPHESKI

SPIFDKNSLNGLIMKAQLSKTLEEILGSEDKDVVCFIDEELERMKAVGFYSLYLISEIKL

KASYPQLFVSVLHRLSTKYCEAWAAIVVEQKIEPLRELMAIEQYGMTNEEWIASHEGWTR

QVIAHEDLDGDLEDSASECEMTLGEEKVWLPWCETPAVSSFLFSCCFSLDDANRMIQHSI

GAKARQVIMMQRTIREALLEQVTIASVAVYDAAVSLLVNASANKKESVLNFGECCIQQFL

FDMYFIRAALGIFDFVRFGWGDELKSEEISPSLLKLLKLFARMREFIDPVDWEIYGPQLI

ENVVLQFRRSRLLFSSLSASNDINKINGKELVLGAQDKRSLARIAEPVSRFSLLPVPSNR

RKFQRATSRSKKY

>contig23106 Frame-1R|Blast-ATP-binding cassette protein, putative [Phytophthora infestans T30-4](gb|EEY66578.1|) 0.0

MVEQVVASIFTTAFRGLDDTILAYIIGTVTDELLENVYSEAAALKELVNASVAPFLIDTR

FCKDAAAAAKICDSLSLKLLDSSELQDHNKHHNEVHMLENTQSIEEQARTDEGAADAEQL

MARIWGFDKIRKTTNDELEAQQSACSARQVRKQVKLELLTAENDEEQAELDREWEDARFL

PDLTQDNGERDVHVPRLTIHFKGKTLLADTALKIVAGRRYGLVGKNGAGKTTLLRYISHY

ELEGFPRHIRIQLVEQESASKLSKDDRSVLEVVLAADYERTMLLQEEKELVAMESNKGVD

HSVRLKEIYDRLINIDSDTAESRARTILCGLQFPDDVVSGPAKALSGGWRMRTALAGALF

MAPDLLLLDEPTNHLDLEAVMWLEHYLEKYDKQMIVVSHDRNFLNAVTTDIVYLTHQKLV

YYKGDYNTFERTMKENLRQQRKAYDAQQMKIQHMQEFIERFRANAKKAPLVQSRVKALDK

ILRNQLIEEPEDDHAFRMHFPPPEPIGRPIIAVEDVGFRYSPKSPLLFKEVHMGVDMSSR

IGILGVNGSGKSTLINIMIGKLRANEGSVTMNPRLRVATFSQHHVDSLDLAKSAVQNMSE

AFPGHEPEEFRSHLGRFNLSGELAIKPTRTLSGGQKSRVGFALMTWRLPHVVVLDEPTNH

LDMETIDALIHALHEYKGGVVIVSHDQHFVQ

>contig23278 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65735.1|) 1e-08

MSHVFDVNDSKKIRKEARRRKEKLKRSNMIGKNTSREEGEDTEAKKRVAFYGLK

>contig23861 Frame-0F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72292.1|) 5e-26 NOT\_ORF

MQYVIRQFDVETAF\*METWKKTFSMEPPPGIKFTPGSVCKLRRSLYGLPLQFGTRRYALY

L

>contig24099 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60067.1|) 1e-117

MAKFTSLPQQAINGTSIGAVAIAASVGAYNYLESGACNVPLALTTTIPAIIATKYGVRTA

HRLSSKTLSFVVGSAMLLCSPLIFLKNSSYLPKWSDRHDPLDLQFYVLQQKDLEAIPQSN

HDKLKHATIAAKSAAVSNSYIEQIKSNYAQFAIVNVKYVAAGIAAGYISGLCGLGGGILI

TSYLTAASDMPQSTIIGTSLLSIVPTAASSTVFNLRAKSIHLPTAIRIGSSLAAGVYITS

KYITHEMPEDLLRGILSSTLGAAALVMICRAL

>contig24451 Frame-1F

MFQIARLLRSASQASPNTTIRLNRGICASAVVSARHNRRGSPSRLCSGPPIHGEGDENSD

KEIAKWFKDMQKQFPSSVPSQDEELPDLMELIDDEDDENDDDENPDKETEMFLDEAEELF

SLSPTEFQKQMESYDQRYARESDDEDDDSEVEIDRATERIPKKKLIKVLGELNASHFPTR

KNAERLPNAILNKNSAPLEKKVKLQKAERVTYRQESVGIAVLEFVQNLLIEDADLSGADI

VPRFVEANVSPDLRRIVLFWEPMRVNSENQKISKKKGEAVRNRLQRQERWVRRNVTQHLN

LKYSPIVQFKQQVEAKAEAARTLFEDEMKWLDTV

>contig25100 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54182.1|) 1e-116

MQYIVFYEITIVQPTKSIKYYRNHNPFEYGPFTAMDGGKCTNSGSDIKTSCKAYYGLDGV

ENIGTNVGCDSKSSDPRAPYPGNYWYSFPNSCAHHLRADKTSACRGQFSGGLCPLGDQPN

GLTCTYSYTILGYLNIDDLVGITKMGFYNYHDFCQSGGVEFKARNTGNGFQVEQSLEFWR

NPGDPNANSNRAVQMVAMYNQMIRSGQRTNMTLLPTVETLAAANPECYKNSGICARAKFG

CKRQMLSQLCTVCSSEGSDCVVAPPNYLFPDF

>contig25485 Frame-2F

MDELSDFEQELPQQQQEPSRDMEENALDVEMDEERTDTACEVCKKSDREDEIILCEDCNA

EIHIGCLQPPLLKVPDEAWYCPNCIVKYPATSVVKIKQENEKVGTEEIIAVNDNLAKESI

ATNDKTAQESIAINDNSAAAPKPILNAPIAHNPPKSPTSRIDPTSIPIAEALEADPEKSN

LLLIHASNCDDIKCTDPELQFFCPHMKRFLRSICWASHSDKWRSYRLARITADLFAYHAM

NCSVPQCNVPLCVKIRQEEIV

>contig25522 Frame-2F|Blast-N-carbamoylputrescine amidase [Phytophthora infestans T30-4](gb|EEY60418.1|) 1e-159

MHASVRIGNTTSVMGLNSTNVIAPGLKAPSPMIERVVTVAATQMSCSNTEENIKKAESLV

RIASSRGAQVILLQELFQFSYFPIELNASNFQLATTLEDSALVQGMALLAKELHVVIPIS

FFERYRSSYYNSCAVIDADGSVLGVVRKMHIGDRLGYNEKYYFTPSDDSFKVWTTRFGKI

GVAIGSDQWYPEVARSLVVHGAELLLYPSAMGSNHYDPNFDARDQWQRVMQGHAAASMVP

VICSNRVGTEVVDGIQVTFVGSSFIAGQTGELLKIADRESEGVLVESFDLEKFHVRRASW

GLVRDRRPNLYGVIMTRDGLQ

>contig25908 Frame-2R

MHPNKRFDSLVVRSNKNQFASPFAHQAWLYLVLGLSLIIVILITITLGAKY

>contig26044 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58223.1|) 4e-83

MSTNIIDPMNMRGLVATVTSCIGGKHEKFAVRVRTKGPTNVYFVYKTMSEFIGLWGSLET

LACGVQHRTHSHVITKMARKQNEEPSRLAHWIASVVDCYAFRQIIRDLQLQDKETMSTLN

ILLQFLVARVSSTSMDHNMLLASSVGRQLVTLVRNFLQQPVAAIYKTEAVVKTSFTTYEG

RKRSFEEMRPEDSQRQQRSSLFPAHSGSERALKTQKQCGLREWVIPPAGKLRLVGGVTSR

RRVFAEVDF

>contig26260 Frame-2F

MARLMQQVAQLRADRRENGQLVAYEEEAMRQRRKRKQTELTNEQLKQALFQQMAFVGGMR

ALMGSHHLSSSKTLEFHDWVHSYTKFAFRDPLARRKEYVSHFSKSKTELSTNIVLKNTEI

ETQKLLATGQLYMGKVSMLHDGTRQGQELTDGLTDVIMRNLLDKTQADVNGDGRVIKEFT

SVFLFPETAQCSLEKLLDLVFASMRTVGVYYPNSVYQSRAVDEVTKVEADGVTQS

>contig26497 Frame-1F|Blast-NADPH-cytochrome P450 reductase, putative [Phytophthora infestans T30-4](gb|EEY56613.1|) 0.0

MLTRLGSNDGKLEYQKWIIDDERSFVDVLAHFGSVKVSLQDLLHLVPSLLPRYYTISSSS

LVSPQRIHATVSLIESQKDDNRVFRGVCSNYLGSLLPLDVHMDERKKRESRPGEQGSKKP

REWPMARIFIRASSFRLPTNPLTPVILIGPGTGIAPMRAFLQERAKQQEDGIEVGKSIMY

FGCRRRKEDFLYQDELELYKTSGVLSQLHVAFSREQQKKVYVQHLLLQHGQETWQLLHDQ

DAHIYICGATAMGNEVHRALLEIIVNCGHQTAEEALTTLKRLQDDHRYVQELWA

>contig27393 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61490.1|) 3e-92

MEQVMIQYETRDEMPTYQLERVVKSALDDQWKRLDFGKMIDQVIPFLPFEHQHIVEIIAL

KLRQLDQNYRGKYWHRLWIENNIADYMSRLDSVHYKVRSAIVNGKIKSSKVFAKYGARDV

ETGPIQLLKSKLLRYLRPFNPDAEIRVTQDVDTKEISIVSCGLEIASKKVKKRRQVPVED

KFVHVGCVTKWSGRFE

>contig27784 Frame-1R

MAAAATSVERSVKQFLNMMDTPNTTECVLLDKFQFLKLYWRAFQRLFIVFNNVVKDELNN

CVLVCVNMTASFVYFQWHKHFSSQAKQELRELIDQTLAFCEKLADKQVVNDHLQNRIRTF

LWYSSEDMKCAVRQRQGSLDSTRNDVENAIQWGHLLVLTTFAGASVPNSFHSDATNPVET

NDLIRSVEISHLFARYRDCALFDDVASSNKVVQVFTDVILQYFEHFEQIKDLQLVLWQQT

MYPDWMQRTVCWEIWRELLCFCWKEALAASMLQLVLDTILYNENDSMVVLASEVEDELFQ

LLCYVYRDLPVVLKDMCIHQVTRIINVISTEGPSHPFSLCVASQLQLLEHLVAVEFLKNY

NGLLKEEWIAQYLPLCLECCGTVLELLSTETLTFSTPWENWLGIARVGCEFTRVERSV

>contig28073 Frame-2F

MLDLSSNRLSSWSQVLRVVGGMFVNLDQLLLNNNCIGTLVSEDGKSNCTFQELTTLSVSD

NLIDSWTSIHALNAFPRLSTLRFLKNPLTKQMSPGEARIFIVARTDHIAMLNGSPVRMKE

RMEAEQLYLKRILHELAVLIDSTTERERVLAAHPRFARLCELYPEIRIDDRGNNGNGGSS

SGPLKMNLFQVALIPTSIKANSYEPLIKKIPFQMTILQLKLLVEAKFGIEVSAQILSFRV

DSKSIAILLDDDNAEVGYYGMQNQCEVLINSKE

>contig28868-1 Frame-0R1

MDCQCQGVGRFCRVNKCIIT

>contig28936 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56863.1|) 6e-33

MGVSVQENHLTCHDHRHLRDTKTPGRISKRASIRRLRHPVVIELPEAARRLKQKIIASHR

VKLTRFSLSHMRHVTVPPVQIPDLLNDYRAVNTLVSGKKVPLTMRMWMNCKSKMKPLDMI

HEHVSYR

>contig30362 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65759.1|) 1e-121

MIVCAHNVLLPAVQCVGRNRRAIISGEMYREIVAYAPELRGFTLGSCRDCPKCVLEQDTR

ELEAEEKKRTRFENEIAGSEEMLELLERKNGFPKTLFSPVENGSRRQQQLAPHLSVGGKS

KYATYFLVPKKWLNKWRKFVRSQGKDAPGPVLNAELVCLSHQRTIVPPYISMFLSGFSLE

QSLKATQAHGSIPARQYEIVTFSEWEALYNRYCAEFAVGFDVINGAYYWRTQECQICNYG

IGGGSSSSQRNSRR

>contig30854 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56026.1|) 1e-159

MLSVQFAICAHVQWETAARHKHQKQLDVVLQHQMTEYRVALQCVAGTSVVKFGRKGKPHG

TNLCVENGDTLRWTSKLLAHATHMAVDGVTATTTMGKKRVKVKNAIPLATIIRITSGPST

SVLARALHKGTLILPDAGCTLSVVTHTRTLDLKAKTTEEREWLQRSLEFLVALARDHERR

VAQQVELTIMKRMETLPVWKYGRKGKPHKTRVCVDRYGEVSWLGRSGDSIQLDEIVSVCP

GHTTPVFARARTAGYVTSTKATASFSLITSCRTLDIEAINEYQRDWFIVAFRYLLDKVHE

KTAAMQRERAERQLRMMQDLCRDNTTEKFFPNTRHENYDDDDGLVRHI

>contig31398 Frame-1F

MEKVKDAKITSKESEISEASDGKVQIPEISKKVEDTDDGDGNAEIVAIVKDAENSTGSEK

VESIDTSLEADVVVVSDEVTALSGKAELTDVGDGKVENIEIVKELKFPVVSEKVESVETV

QETKVAVKSDEDFEISKKSELTDIGDGM

>contig31563 Frame-2F|Blast-copper-transporting ATPase, putative [Phytophthora infestans T30-4](gb|EEY66505.1|) 0.0

MKLQPKTALLVVENRTRDREIPIELVQRGDLLRIQPGANIPTDGVVKSGSSTTDESMLTG

ESMPVRKTEGDYVFGSTVNQQGTLVIESSCMGGENSALSQICALIEDAQLHKAPIQAYAD

WLASIFAPCVLGLSVMTFIVWITFLSVDLVPMEWKMELGIDVETDHSDDMYLAVLFAISV

VVIACPCALGLATPTAVMVGCGVGAKQGILIKGGRALETARYIDTVVFDKTGTLTVGRPS

VRDVVVADRAFTPRELLYYGASLECVSEHVLGKAIVVTATEHENLELQAPTKVCVIPGRG

IEGVVAASTVTSRSTSSNVLVGNMEYCEERGIEITEKMRTHVHELEMEGKTVVVVCVENK

LVGVIALADAPRPEAADAVKHLKNMGLDVWLITGDNLRTASAIARQMGINHVKAVALPGE

KASQIKALQSQSKPSDVKATCRLHGWRWDK

>contig31714 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53587.1|) 1e-120

MQTHLPTSSSSCDATPSSPKLCDASMEVQNLITMMGADSMSAPKDIAKFLHRRPHSDLKL

VGQLLGEPDAKSRSVLHEYTNGFQLKGVTFEVALRVYLSRFELPREAQKIDRILQAFAKA

YYKCNPDSTECPSEDAVYTLAFSVLLLNTDAHNPRLARKFKMTRNDFICNYHRLGGKGGS

AKAEVPDFYLGQCYDRFLADAIKRLERKPTESLRDEVELEFSDLALGLDIETSFDGRTAI

VKKFISDRSRSLNGQRSQSNTSTDSAITGSFFTPNASFFKTGTMLANIFSIINPEPEFSI

KGYVIVAVGDDSTRQIGYALTLYLLKTAPRPVLIRFCEPSVYYASLV

>contig31875-0 Frame-2F0

MKPTANEVVIFCTLVYRRVRGSCGTSQPWSVYHLSCF

>contig31981 Frame-2R

MQRARLDCQNHKKMVIYSGHDVSLLSVLRTMDADLANDISFWPEYSSALALGLLEDENGN

FFVRAQLNDKALAMGNAPDGILSADRFCELVISNVEDHA

>contig32926-1 Frame-0R1

MLAQAARRGATNCFYRAVRALLTHPFVSVVFHYFDVQ

>contig32993 Frame-2F

MTPEDVRNFHTKVPEMALTYDFELDTFQKECILHLERHECVFVAAHTSAGKTVIAEYAIA

MSQKHMTRSIYTSPIKALSNQKYRDFRKTFGPTNVGLITGDVSLNPDASCLVMTTEILRS

MLYRGADVIRDIEWVIFDEIHYINDSERGVVWEEVIIMLPEHIGLIFLSATTPNHLEFSD

WIGRTKQKKIHVISTYKRPVPLQHFLYAGKELFKLYDATSGYVATAHSAAKTKLLPEKAK

ASTRGGKTVARGGGGTANARTLRTSGGNQGDWTKLITTLKDRSLLPVVVFAFSKRLCEAS

ASKLAKVDLSTPSERSEIHLFLETCVQRLQGSDRELPQVLVMKEMLKRGIGVHHGGLLPI

LKEMVEILFGRGLVKVLFSTETFAMGVNMPARTVVFNGIRKHDGNNFRDLLPGEYTQMAG

RAGRRGLDSVGTVIIACWNDVPEPTSLRTMLAGKATSLSSQFRLTYTMILNLLRVEVLTI

EDMMKRSFSEFHTQKALALKNIPTLIQKGKALLQQLKQSLVEEYPQMDASGELAQMHEYY

QLKRDKRELEKKLIKWLLANNISAAKNAIAPGRVVVLSIKGLSSDQVALVVRTTAAVMGE

GGTARSKLSFETELQGTVATDTSHRGVFKSIMVITLCPDNYEPPRIETVSDKSKSLNTLL

GGGRMLRSKRYDDRLIEQTSSKGQVNCLDLTAPFTATLVGRRYAVLEVPESCVESVTSIQ

ASNVNMKQLVASSSKTDIASCIDFLAQLEKELKTQKLAMPFVDIIRDLKVNDLEVATGYT

QWQQLYSMVLSHPCANNVTAESRVMSKVEKTFKLEAYLTRMSRELSTDALTLFPDFQQRL

RVLKRLGYISEEDVVQVKGRVACEINTCDELVLTEMIFENVLANLEPEEIVAVLSALVFH

EKVESEPMLTPTLEATRDVVKRIAESLGLLQLEQHLAIDPVGYSKGALNFGLME

>contig33028 Frame-1F

MVSSTSLTVKASTTTHVQPLDKTFTAVVQFTVEKPTFVATIDVDMFACAPGISAVDCSDL

TVKEIQTKLHQATTVQHFASLLKAILMRFQSAKV

>contig33886 Frame-1F|Blast-26S proteasome non-ATPase regulatory subunit 12, putative [Phytophthora infestans T30-4](gb|EEY63841.1|) 0.0

MSAEEIGKKADLGPEFQRVLPEAQSLASSGNLERACDMLMALEKQARLANDVATLKEVVS

SILTLCAQHKRWDMLQAHVALLPKRRAQKSSAITVVVQRAMGFLSEAPSGAIKMELIYAL

RTVSEGKIFLEKERATLTQMLSRMKEAQGEIDEAASILQEVHVETYGAMTKLEKTKYILE

QVRLTLATRDYVRANILAKKILRRTLEEKEFQECKLKFYHLMIEYDTHENHPLELCRHWM

AILNTEMVKEKEELWKKALEHATIFVVLSAFSTLQSDLLHTLAREKLMEKVPEFAAVLKN

FTTREIIAFPMKEDALLKRHSIFHNVERGTEWWNTLHTRVVEHNIRVVAEHYERIRLPHL

ANMIGLSEDVTESNISTLVSEGAIYAKIDRPAKLVSFHRPLLPEEQLSNWSGYFPIASTR

GDDVPLSQQGKHDS

>contig34348 Frame-0F

MHIGTFKKYFDLSQNTVSLNVLRCQLMNLQVDRNIALECFSSFCLLNLEHFNLEDESRIW

LN

>contig34537 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69135.1|) 1e-94

MSSKATDDWVTWQMVDSLFPTGGFAHSMGLEVAMQEGLVVATTLRQFLSASLHQSANFAL

PIVFSAHQITTIPDANPGALIEAVLKLNSCAVALYSNHVARKASFAQGAALLRLALHIYG

SSNPRVQTLLTIRKEAKTQEHGGVHHAVIFGVVCALLSLDVEQTQRMYLFVTTRDVLSAA

TRLNLVGPLEAAKLQFETTLLLEKVFQAKKNRSVEDSYSSAPMLDLVQALHDQLYTRIFN

S

>contig35134 Frame-0F|Blast-3-ketodihydrosphingosine reductase, putative [Phytophthora infestans T30-4](gb|EEY63971.1|) 1e-151

MDVNYFGTLHAIKAALPAMAQRSEEGGEGGQIVLISSGLGLISWIGYAQYAATKYALRGL

AESLRNELKLYGIRVSIFYPGNIDTPGYVEENRTKPSETKTIEGVSELVHPDKVAQSLIN

GVRDGLFSITNDPMVFILRVLANGVAPRYNTMLETVLLPLVVPIQVGFGFFMDYIVTQTK

RARETKPNGETKPNGEHAMYQEIRDA

>contig35439 Frame-1R

MYAWRYLSNLERKDNETWSIFLKALARLKAFFCSVVIIEDIRASNS

>contig36135 Frame-0R

MGNKSSVESGDRPQVPDQWSPSQIASQEGKTVIITGANSGIGYETALELARKGATVVLAC

RNEQRGKEAEAKLREALATTKDAGTVSFQQLDVSDLSSVNAFANDFKASHDRLDVLINNA

GVMAVPYATTVDGLERQFATNHLGHFALTAQLFPLLKNSLPSRVVNVSSLAHQSCKLQHF

ISDSEIMRTSEKDYHRAEVYGESKLCNLLFTFELARRLEAQNVTGVTSVACHPGLTATNL

MTAPKEEGGKLGRILWNLVGYLPILQDAPTGALPTLYAATGPDVMNHDYYGPSKCFEIWG

PPKRVQAKEQAYDTTAALNLWNESERLAKIAFDVKA

>contig37499 Frame-1F

MTNDPIPPKTPLSAVSQQQQTAYLVSSPTRGPGRQSWSRRLIKLPNPTSDFQISSTIIAI

AGNPCLRVMMTVWLTTICLQSSRTFSFVFNP

>contig38245 Frame-2R

MISTARECLRLWNGDEDKAFNLFVSLHDEICKCDIFSLDTVCTRCDRMVPSLITGGALC

>contig38528 Frame-2F|Blast-lactation elevated protein 1 [Phytophthora infestans T30-4](gb|EEY56948.1|) 5e-58

MLVRRNNLRGIRSHARWLHSLPLSCPKPSETYDALVQSHKVTFDAKQAAIVRHYLDPLHV

RLDGYKLPSFDPLSNPTDANPSLKTYSIPKGLYIYGDVGTGKSMLLDLFYRGAHVQCKRR

VHFNQFMLEVHMRLQQAKTMQIEQFGRQRHILLDQSRDVVLQVAHAMAHESHLLCFDEFQ

VTDVADAFIIRKLFHVLFRRGVVIVATSNTPPKELYQKWHELGLFRSLFGPIDAAYSNCV

DCVLKGLS

>contig38960 Frame-0R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY66920.1|) 5e-80

MRTWQYLTLDATGTLVRPAEAIGATYLRFWEAESGNSFSSSRRTVLTKALTAHFPSEFRM

LSQRRPNFGSDGTDPSAFTWWRDLVIRVMNRAEVFICTSINTEQSERFTSQLYAHFGRPE

AWSVFDDVRPTLELLQKSGVPMGVISNFDERLEPLLVGLGLRDFFYVVTKSYDQPHMKPH

ASIFNSTFKNLQGNGERVVPSNFLHVGDHLTKDYK

>contig39130 Frame-2R

MVQKRSTALKVLVQFVFLVTGVVSTCVAQYVFYQGAGDQKAMLLPLCNYLGMMLVGLLPT

AADGQKAVNATRLKKIKIQSLTCEADQKLEISMSPEVDVEQPELTPTQTDRRLSPKFLNS

DLEAVDMELTRRPVVSEDHYHAEEALSSEDETKPPLGLLVTPSLVSLSLSTEQLCIIVSV

VLDFAGCMFSNIGLAMAGSGLYQVVYSSVICWSALMSRFLLKKVVSKEEWFGIALVTFGL

AFSALGESRNERDNTIVLMGCLNTLVGAAFYGANYVTGEFTLKLAERPHPKELCLKIGSA

CVTIIAIYQSLFVLPEWNALVTQPIMEAKGNTTHIVAALVAYTLSQLAHGLTYFVMLGTS

GAVTTGIIQSLRAVCVFVISSMLYCSQQESQCFDTKRGVAALIVVSGVMYYSWAKNQQGR

ANAPAPSVLSRPSQITANTKIVAGKNYVN

>contig39268 Frame-0R|Blast-NADH-ubiquinone oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY62419.1|) 0.0

MWTRQLINVTKTARSTSTSWWKRAPSSMEYHQDESKQTENFQLVIVGTGWAGYQLFTQCR

KHLVDIEESVGRRVDLVVVSKRNHFLYTPLLASTTVGTLGFRSIIEPLRDSWLSHESDFH

FANVQDIDPEKKILKVTSAINAASRSSTYDIRYDTLVLGCGSRPLTFGLPGVEEHAFFLK

EIQDSQKIRNRILENFEAATQPGITPEEKQRLLHFVVVGGGPTGIEFCAELYDLVQQDLV

HKYPETSKHLQVTLVDSGEILNGFDKHLRAVALRKIQKRSTMKLIKKKLH

>contig39857 Frame-1R|Blast-DNA polymerase epsilon catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY63268.1|) 2e-73

MHSSPLARYSQKLVASYFSDKLLRLLPEILRHQMNQDSFPIFVGSHLAMESPALELVKFV

TAVFELEPSVEAQVGKMRRMMLKVLHTSEFSDAAQFRNPSLSFTVQDVICLNCNLCHAVD

LCRDP

>contig40141 Frame-1R|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ28385.1|) 8e-14

MKTMDLSAVAVDEAQLFKGLVDLQGAVREATCVAIATMFGDVEDEKAEENSRRKLQRMVD

AGLLKKLIPRVVDPLPMVRQFALGALRNISVTGGLELCELMTMQNVVTPLIRVITENSTD

VALSSNDNLRA

>contig40439 Frame-1F

MKLFGFGAIALAVSASLLHAEETCDNKSFYLGSYLVINDLANIKGSMCISADLKSNSLSW

LTKANASPIEYGSPTGYDHAPCYPRVQRNLGYSPLSSVSSLHTSMWYEYTGSANDASLVT

LNLLIGSKPALVPALDILKTPSIQIMVILSVHGNESPTWLNTKIVSIEIGIYAFDLFVGE

IGGVTIYTYLARSVIVKLDVDVTEFYKKLPKEYIIDDSQCLIALQAGTQINGIVNAELKV

LDFSVDLMLK

>contig41955 Frame-1F

MYLKLADIKSLEDTATLESTGVEGEIDRDIERTFPANAFYTKHGDGKRQLGNVLKAITSY

AHDVGYCQG

>contig42051 Frame-1F

MASPLRRNCLVWTLLVLVSTLLNNTSASECAACGYLARNCSHTKASDSVNVCTALGHIQI

DDVFCDDDECQCADRHACVSTVVGCSNLFQSRNRRRCVSNATLARRFTQCAFDQGLTTLE

HSNVASDWIYYRQSRKCQSIDCLAVQMFHHSRLSQCGHLLAVWKTNASTNTVDEDVVMYH

FIADGSRGSDLKAGTFLYSVPWVSDSLVLQSKGATTRQIETCYVLQTRNEPNGTCEGVYV

QFDARVQFAHSDTYVISKLSWPVWCVVVGSVVAAMASVASVGLVIYRSQQQRSTLTPSVD

ANLSLRKLIYPQQSVAMESVALGPPTTASERRLVTDLRQRGAPLPDVEVGK

>contig42213 Frame-0F

MILDTGNSPFRCLWYYLIYFNCYYYGFCLHTAILATVSCNSKISDEIIRSDKQNIVAQLL

CSCATRR

>contig42910-0 Frame-0F0

MRKGAPAFSSSRLILQKGEFSASIV

>contig42910-1 Frame-0R1

MDAENSPFCKISRELLNAGAPLRIGGYRNLRGDLKWEMWG

>contig43135 Frame-1F

MTLKAEFIQYETEYLALKQVTDHEKLRLQKDIERQKARILDLETQTGRARASAVEGGSTP

FSPTNSSGMTVRERQHMRSIQQKLEQLVAVHRLLLRKYASLELELSEAKKKLVLRDERIK

QVEANNRIIAGNMRAQAEKHVEELTHLRDQIADFRDAQRSHLETQLNHTNAALVASMGNP

DIGVIKTLRGGSIYNGDGIIRPIRGGGRRKTRDSEAAFGTAGVLEEFGDSADSNVSTSGF

LNRLFGKSN

>contig43416 Frame-0F

MEPIAPLSDTDVVRTKAERRERYMQKTRAEAGYLFKYLILTQIIVYLEAGSIPCLLDQLS

VSLNLNASQQGALGGVVYLALSAASPLCAFFLHRFPPRIVLGLSLVCNNVAVLMLALTPT

GFAYSGTMLILARAAVGFTQAFPCIYTPLWVDEYAPRAKVAGWMSYLQGSVPMGVMLGYF

AGTVTNWVVPETFSIIQTWRWPFLLQFLALLPLNVAIFFVPPKHLLIRRDTEVTHVTGSG

STSSSDDSLTTAAPILQDYQLKQDDRGSADHEPCGSSRGGVRSAPSRHGFGLHSFFDEAI

ASTP

>contig43782 Frame-2R|Blast-cellulose synthase 2 [Phytophthora infestans]gb|EEY56433.1| cellulose synthase 2 [Phytophthora infestans T30-4](gb|ABP96903.1|) 1e-124

MWFQGVEHAIVANGAGNIIERKLPNVRKYLMKGNQTYRLFYFLFIITGIVELLALVFWFV

IGLEPCDAARLEVDCATIFNTSLETLRCSSQPFSGYFTPPDWYREIADVSNVICFRDPPI

PQWASYFAMLFAELLTFALGVLYYLGMWKPVRRGAHYFDEFEPPVPDELWPKVDVLLCHY

SEPA

>contig43885 Frame-1R

MHVDVCSRSAVVAWHVISIVCCFASKQHRQCDELKTSIGSRLVRDNARELRNAVNIGDKG

DEELGSGDEDALTSLNASNRACRLYHREKRAHAYTRSRLVATLRSEADLTQRILLVGGSV

QDNERGRMKTEDLEATVRRLEEKVDSVSSSQTTGEVDIVLKAFRSKSQTDNDEANATVLY

W

>contig44259 Frame-0F|Blast-ribose-phosphate pyrophosphokinase, putative [Phytophthora infestans T30-4](gb|EEY62052.1|) 1e-144

MSRFYIQAKSLVTRNMVALMAVGTVGMLNGGRSSRAEHSTTLAEANKVATNSEWYPNTTT

KHWHFYKGKMTKASAKSVKLFKVADTPIADEIASYLGVELNDMEVKKFNDGETSIIVNEN

VRGKRVYIVSSTTTVDRLMELLLAISAMRRASAKSITAVIPFYGYARMDLMHKGREPIAA

ADVARMLETMGVDHVVSVDLHSAQIEGFFKPQIPVDNLQAFPVGAVYFSEQTLGDPIVVA

PHSAAVNRAAMFRDTLSRAIDESVPLAFVIRKHQLDEDQPGELVGDVNGKDCIIVDNLVD

TGSTLVKTAKVLKANGAKTVSAFAVHARYSAHAMQTLESCEELDKLVTTNTIPARYKLDK

IPS

>contig44398 Frame-2F|Blast-T-complex protein 1 subunit epsilon [Phytophthora infestans T30-4](gb|EEY69814.1|) 0.0

MRIADGFEEACEIACKHLEAIGDVIHFTKEDATPLVETAMTTLSSKIVNKYKLQMAQIAV

NAVLKVANFDTRDVNFDLIKVEGKCGGTLSETALINGIVIDKDFSHPQMPKEVNDAKMCI

LTCPFEPPKPKTKHKLDITSVEAYEQLYEQEQAYFTTMIQQVKDSGANLVICQWGFDDEA

NHLLLQNQLPAVRWVGGVELELIAIATGGRIVPRFSELTPEKLGRAGTVREVAFGTTKER

MLVIEDCASSDAITVLVRGGNKMIVEEAKRSLHDAMCVTRNLIKNNRIVYGGGAAEIACG

IAVREYADKIAGIEQYAIRGFADALEDVPMALAENSGLSPIDSLSAVRAQQIAEQNPRLG

IDCNSSGTNDMKDQQVFETLIGKQQQLQLATQVVRMILKIDDVIIEGSYA

>contig44563 Frame-1F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY61609.1|) 2e-57

MLLAKVAHPPVWVLDSERLTCMECDKQFNLLRSRRHHCRMCGRVLCLECSAFKVRVNLLP

FSLPRRGKKTTKVEKANTKTRVCKLCHDICVQDKVQPLNAHA

>contig45519 Frame-0F

MIKALESLVMPCVRASLRSTEENTRQGFVTLLGYLADHHQVFQSFAFVPTDLALVRNQKD

PEVDFFYNINHIQAHRKRRALQRLSGSMVSMALKAKTDVDDKEKEQSQCFSIGTVNTIIL

PLVLHFVYETHAKSQVSLRAEAAACVGSAAGLLSWSHYLSLLRRLLMSIDRHAEMEGGII

MSICAVVDHFHYETPGAATQWKVSTSDCTKQTSDKPDTAEDETEEVERSSKMQDNMETQV

LPMLYSHLFRSVASKKRTKSQNDFESVSLSEAAVAVRVPLALAVVKVLRRLRAAVFQREL

PKLLIKFANLLKSKEEAVRVSARTTLVRVGVELGAKFLLPIVNELHHTLRDGYMVHVLSF

TVHALLEKLPEIVQADGETKSLVK

>contig45821 Frame-0R

MRDGSLSYEAFCAEAELLQQRSHELASRQRVGRDKCVATWDWKHGNRQHLDGNSYLISTE

NVRQLPFDIDLNTLTAPDIVEAQHDGSHVEEVQKTVHQSGKGRLVLFEFHIVYHTIYQTP

VLYFRALAEDGTPLSFNCVTNDVLFPGSDEQSTFVAMDMHPVLDEPFAFLHPCETAPVMQ

LLQAQFKDLSSLRNCNVPHYLASWLSLVHPLTGISPLDYYFRQ

>contig45995 Frame-2F

MMKRSYRVGEYPDIQITQQDIVDPVMALCEISVETSGLVFSALFSSITGNYQFEKIGIAK

R

>contig47302 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69840.1|) 1e-44

MERGSVKEAIGHGEGMLEFYRRVYNLNHPMTGLHLFTLGDLYRQQAQVGITLEQSRMKSW

EYFAEAQRILRITHGEQHRLVALLADRLTSEVV

>contig47852-0 Frame-0F0

MVECKTCHKIDQFQDDTDSMSRNLHLSDTSIYSLC

>contig48567 Frame-0F

MKAKQCNKFVCILTLHLSADVWIQPQHARHRYQEEDLHSHSKELHSSKEL

>contig48589 Frame-0R

MLKSRESSNNTESQSCLCTNMKYIAPLNYLHSLIRCILHSS

>contig48848 Frame-0F|Blast-Voltage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4](gb|EEY66467.1|) 1e-10

MFQKQEQKNELAIEESIRLSMTRGLRSLSSSNLAFAG

>contig49032 Frame-2R

MHLRRKPVWPRSGRTPCSCRLKKRALNIPFPYPPQPLAFSMQREASTWALAADGLQQKFK

GLKQRTVWRYKTLKNNNTAIVFSDDKEEVFLKPRNRRQCDPLACHNVLATASAPILNGIL

GATSPEESNQFCRTMVGFMLHSCSPSERAKVLNVITITRLEEITIANRALIVRAIQQCIQ

SPC

>contig49674 Frame-2R

MVVANRCTRRANLIKIHVFYGSKSMFQVLEIIRYNVNHVEGIYAADSAKVSASTCACFL

>contig50452 Frame-2F

MFRVHYFANSELLIYPEIDRAVEKGDAVLYWRS

>contig50593 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53669.1|) 2e-35

MQFEDLESDVAALSIGLAKTSMDGEEDMRATTSVRSPTAALAASAFAVAMKQARLNAQKA

IDDRASRVIAA

>contig50715 Frame-1R

MFSLTVTVISVSSGPFFRSGPSSSVKFKKECRFRQHAGGYIPLSHKTEFTTHEVEEVRRS

EAAIMEISTSEDMIKFDFTNYSCSDTKETSTKYVKPSALLRKRSSSPYLSSSSICSSSLS

SSTSSTSVSHKGVTYDQDGEMVHCRFCMILQSNTETFLHEDDDVVVFRPLNPQTMRR

>contig50834 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54868.1|) 6e-31

MENSVPASRSQRFNIIEHLEKRYGGGIVRTNSINADVGGGGGFNRRVDDDLYDSEDSFID

DAELQQNIEDVQAQTRVKTKHSGFFVNAGDTIEMVAKDDDDECVD

>contig50841 Frame-2R

MCGTIMLFGLGTTSLFHFLFQPYVMRMWLVGPATDYHGATSAESTMTVETVTLFAQLQQH

SFRLSDVSPPTQAMHPMVSFQACGRHYFIHPESFEDRKLLSHLVGSKA

>contig51727 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59159.1|) 6e-11

MPSSASSHAPWRRHEAGSRPFYRPPNYPLRRSIDASTSYDTFRSEASSFSSRSAFSPVLG

>contig52094 Frame-2R

MPLTCPLSICKLYQIEFISHATLVPRVEWKTHVLTPLPTATRHLTRASRYVLPAASNEPS

GKKATGHFVAVARSASGFTSNMSISSHNPEITGISASSC

>contig52436 Frame-0R|Blast-myb-like DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY59971.1|) 3e-20

MILSAQSRLGNRWSAIAAMLPGRTEDAVKIRWKSLCRVRKGYVVNGRGYMRIRD

>contig52483 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67783.1|) 2e-65

MATDPRPKVRKAGQKWTVDILELHAAKGCEALSTHIASFAENVFASSKKGGKDDQRLVLL

VAFLKLALPLLHRKVVASLVAALAKFLDAGSKTLRLVTYEALDALSAAPESQLTADALIK

LILAVLDAQSSNCMLAQGGPMAIYAVRIPSAALLRLA

>contig52568 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53199.1|) 1e-34

MVQTLALRAAQNGVIWPRRPLVSSKGLLSCVRNIPINSYDKRPTTFRTVAFNSSGELLAA

ADERGRIFVFFVTMNRYSLVQHLGAP

>contig52630 Frame-2R|Blast-myb-like DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY56006.1|) 1e-50

MQELETPISSYKSVISPISIPETPLSGHASEKTKVQQLQDRLAAQELLVQELMTREHQHI

AERECMKKSVLALQQDMLRLVNIIDLQLPISSMQLQLAPLVSSVDTAAFRGALSPQFAAT

KSINASPLEHNVFNTKRRHQSPDDRDVNVSSAHDLTILMSDTSPHRKRHKTVLRSRKKLS

KRQWSLTEDKALETTVQMTGANEWSAIAELLPGRSGKQCRERWVNHLSPAVNKEAWTEAE

DNLLFATRDRMGNCWAKIARLLPGRTDNAIKNRYYSTMRRCGRQRRGTVRNQRHLDDSLL

KTS

>contig53071 Frame-0F

MLLRSCSTNSRVLRAPISLSDLSATLMPRGTCTYISKSSSLSALTKAFELSPYFAGSIHV

AASANIIFIVDMFMWAAKVRPLSIPRTITFPNATNRDLSLSIPPFATVLVLKPI

>contig53369 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53974.1|) 6e-54

MMATAAAPIRSSKATITFHNELWTAEGARLLLEVDEGWIGFLGDFAWSWHDETFTVYLAI

CRERNWPCNSHAATEAMLRALREGGISMKLSNATRSSDNCAQWSLIEMRELGAQMRRVVD

GRSPAMPWAAQLEDFVENMKAMDAKYNIDDRTVEEFALRAGKYVPEHIVMLIELQKVNRK

MQPEINSPHQKAVMEPERRRSISIQSPDD

>contig53523 Frame-0R

MTLFKALKESILYAPILAKPGSDRPMTHLILATTRLYYRQMLKDSVRH

>contig53596 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59159.1|) 5e-34

MNMLLNMTQKRRNHAEMAERVRFAVHQMLQNNVTKKSEDVENVDPPVCLDSKP

>contig53721 Frame-2F

MSIALMLHETYSLQFLLSRSFDKNDACLVRHHIAYEGITWSMNPTQSHSGFPLRSDFFRS

LPLAKFN

>contig53970 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70365.1|) 8e-22

MKELAFAKMQNIPVVAIQCEDMDISEELQVYLWTRQVIDFRPAVKHMEKCARKSCGGDEG

EHDRAKELMMDRNSSHTVEDTESYEDGASGKHDF

>contig54023 Frame-2F|Blast-hypothetical protein DDB\_G0271670 [Dictyostelium discoideum AX4]sp|Q75JC9.1|Y8484\_DICDI RecName: Full=Uncharacterized protein DDB\_G0271670; Flags: Precursorgb|EAL71525.1| hypothetical protein DDB\_G0271670 [Dictyostelium discoideum AX4](ref|XP\_645495.1|) 2e-15

MYQTTTVVLANTSQAFGTASATVAAATALSAKASGSSLLTPMIETPSKTNSSMTTLSDTI

VLQSVIATTELPDTSASSVLSGINATSDPSFTSMAQQSNLSTETSNLRSAFEETNGPSSQ

LANYTFNTSQLTAPSSTLDNAFLETGCRNSSVTGYETAESRYRSNDSATKAGISSLSSAS

KLLSSSSIPGSGRSGPADSNERVNSGDSFRGRVVASDSKAPARISMPSMRFPPSSSSSSW

LSTPPESSVIESLTPPNFISSSGKLQLSPINDDSEDVLYTGGSMLAADNGCTVGSSALGS

NMIAFIIVGSLAAVAIFFGALYLRPKRVNPLQQLTHLEYSHPMLHSSDYWHDQSIESEPS

ESYNVSRTPRAIPPSF

>contig54571 Frame-0R

MRGMGRYSTQAFLIIKPSPTSAFFRYEGNASI

>contig54669 Frame-0F

MNSLPTASPIHGSTTSLQNLLAKKQYDSSSAGSIIDAFMVRLQQLQCRDSHSGVTGFKRE

YKELCHSIDKAPGYDAALTPQTTARKAKNRYQDVVP

>contig57303-1 Frame-2F1

MLSATAKRMHARSMHALKAYDKREHCLLVIGGNGF

>contig57453 Frame-2R|Blast-peroxisome assembly protein, putative [Phytophthora infestans T30-4](gb|EEY69439.1|) 3e-24

MKKFELLALTCQLANLLIFVRYGKFRSLPERLLGLKLESIMPSITPRAINFEYMTRQFIW

TGL

>contig58751-0 Frame-2F0

MHNGVVMKFSEPIEARQPTKRYRLYVFKNDKII

>contig58751-1 Frame-1R1

MHIARRLVFRQCSRESKIGFFDLSRLVFFLFMLRLAPF

>contig59293 Frame-2F

MYLGQFPATATMPFGYYRAEVIGALLSVLSIWVLAIGLLGTAIKRLVDQGRPDAEPTVDG

KAMFLVALSGLGMNLVLMKILGHGHHHHHHHGHCHEKPDNEELHTSIRQTPVSSMALMPT

VDGPSNKEIQPSSRPTSVFENMNVRAAYIHALGDFVQSLGVCLAGALIWYKPSWQLADPI

TTIVFSCLVLGTTQGMLTKSIHILMEGAPRHLPLGVVETQLRALASVYDVHDLHIWMLTE

DKYAASVHIVPNGESQVAQRETQRLFVSLGVFNVTIQVDDTITKDWNEELPCCGTSYATD

GANQMSVPRASTKKAMEIV

>contig59558 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65133.1|) 9e-10

MLCAFTWIYCGLPGGKRYERWHKRWHYVSG

>contig00012 Frame-1R|Blast-NADH dehydrogenase subunit 5 [Phytophthora infestans]sp|P50366.1|NU5M\_PHYIN RecName: Full=NADH-ubiquinone oxidoreductase chain 5; AltName: Full=NADH dehydrogenase subunit 5gb|AAA99061.1| NADH dehydrogenase subunit 5 [Phytophthora infestans]gb|AAW62559.1| NADH dehydrogenase subunit 5 [Phytophthora infestans]gb|AAW67045.1| NADH dehydrogenase subunit 5 [Phytophthora infestans]gb|AAW67091.1| NADH dehydrogenase subunit 5 [Phytophthora infestans](ref|NP\_037615.1|) 0.0

MGKSAQIFFHLWLPDAMEGPTPVSALIHAATMVTAGVYLVSRCSPVFEYSIFSLKVITII

GASTAFFASTVGLVQNDFKKIVAYSTCSQLGYMFFACGLSNYPLAIFHLSNHAYFKALLF

LCSGAVIHAMGDEQDIRKMGGLRRILPFTYVMFLIGSLSLMGFPFLTGFYSKDLILEVAF

ASFSDTGHFSYWLGTIGAFFTAFYSTRLLFFAFLSETNAYKNIIKNAHDVPFEMGIALGL

LAFGSIFIGYITKDMFVGLGSNFWNNSIYINPINNQMIDAEFLPTFFKLLPVMLSFCGLF

GALYIYFFKFKFLYNFKISKYGLYFYNFLNRKWYFDKIYYEFINQYILKIGYNVTYKMVD

KGLIEICGPYGLTTIFTVLSQKIVLLQTGYIFHYSLLMLISTIFLINIIFFSIIYYFNMI

TVLLFLFIFLLIK

>contig05756 Frame-2F|Blast-methylmalonate-semialdehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY64588.1|) 4e-70

MRQATAAAARAYKTWKEVGVQHRQRVMLKLQHLIREHTEELALAITTEQGKTLADARGDV

YRGLEVVEYTCGAATLMMGETVANLATSLDTYSFKEPLGVCAGICPFNFPAMIPLWMFPT

GTVTGNTYILKPSEKAPGAAM

>contig06432 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67169.1|) 1e-169

MQILTLGYIAVLLCLLKCKGHDVETNNCRFKTAPIYKRLKWITVAYAVFAFHYEVTSLFA

YVYTPRDNTTLSYIGLSQVMYNATGFALALCTGCSQSCTLRFCGCCLSDEKLAQLVVDSN

LDVLPYFHDQHITIEPPVFNPVFVVTDIESSCALWGINDGKVMQRAIQVHDDTMRALLAP

HRGYEITTAGDSFQLAFHTIREAVSYCINAQLQLLAADWPKELHGLIPATKKRRSGYRVI

FQGLRVRMGIHDAMGSDGYLHTSLHAVTGKRVYTGASEVIATEVSNVAAGGQILVTSRIA

DWLLTNKDALPMAYSVEYLSGYLVPKVNFPVGVYEVLPKDLVKRKKVFAIDQNSRIPHVT

KRFVSGSTVLDSELETPLGSVMQQLHLLQTIG

>contig07343 Frame-2F

MDFGYRPVGTEANEILVPNYLLEEIDKIQRTKPAGVTVDVDVQKPSGAFGMDFIAQFQNI

YANVTNILVKVSPANATVEALNNSLMISSHYDAAIGAAAASDDGVNIAIMVELLRLFVLN

PPTHATLVFNFNGAEETIMQAAHGFITQHPWTETIRAFINLEAAGAGGRELLFQTGSDEL

ALAYAQGAKYPHASIIAQELFQSGIIPADTDYRIYRDFGFVAGMDFAYIANGYVYHTSLD

DLSRIQFGAIQRLGDNIIGTVYKLGNESGRLKKVTTNQNSQTFFTDVLGLTMVTASKKTT

FFLCGSVFFLALVYLLRSHVSLLEHLMAGKLLLRCFGAALTSSLSVAILLSLYAPLSWYS

QPYLAGVVFLAPAVAGMLHQLAIFFDTKVKRISANFMASRRELV

>contig07619 Frame-0F

MARHNVAKRYSPSLIDLNVDNETNKKLMAAADGMKMLNPTVRSGPFMANENALDAVEAGD

DAPTSIIEANVDVNHKSNDGEQDLKMATFEVTAALNTRTNNKKRTSLDNSILKKPGKKRA

KPTGKVLINGQSEVRVYKTKTKAKSRTQAVSKPKKQSQKAPPGVPFFVETGVEWNNTNID

FNELSVLRSLWELPAACHLLWLLQSPLTLRFSNTLLEYEAALLKPEESPVLEDVFTKLLL

KKSERTCLSAGIGLKYEWWNKQLRIYYLDMYDKWYALLRKAGERLPETFSEDEDDENSSI

SGSETDEQVDVELTDDEWLTLDILKARLETLGLVCPLKYQSYADLSIELRCKILLNLCEA

VVDDPANTEYMRQMEEDDLRVEPLGNDRAGNRYYFFPQFYEERRLYQLDSKTQHWALWAK

GDDAFHAMLHAMKQTRGRP

>contig07736 Frame-2F|Blast-eukaryotic initiation factor 4A-III, putative [Phytophthora infestans T30-4](gb|EEY70599.1|) 0.0

MPREDTKRRTRLVDEDDEETVEFTTSKDISVFPTFEAMGLKEDLLRGIYSYGFEKPSAIQ

QRAIKPAVQGRDLIAQSQSGTGKTAVFSISILQSLDTSSNETQALVISPTRELAEQTQKV

VLALGDFMNVQCHACIGGKSVGEDIRRLDFGVQVVSGTPGRIFDMIRRRNLRTRNIKMLV

IDEADEMLNKGFKEQIYDIYRYLPPATQVLLVSATMPQEVLDLTRKFMNEPVKVLVKRDE

LTLEGIKQFFVAVEKEEWKFDTLCDLYDTLTITQAVIFCNTKRKVDWLTAKMREANFTVS

AMHGDMPQKERDAIMQEFRSGGSRVLITTDVWGRGLDVQQVSLVICYDLPNNRELYIHRI

GRSGRFGRKGVAINFVKDDDIRILRDIEQYYSTQIDEMPMNVADLI

>contig07952 Frame-0R

MPSLASMPQAQLFQRIFILLYIYALLACSNSITVVAVAVRAVAIKARPHIGKHHDPNRVS

ALVKNEERFLDLPHISDSFYEAKLTQKAKALLKNSEFVKMYDELRKEAGFSVHTSNIAIP

LPQHPISNQELAEMLYAAKERVQDVLKVPLFKKWSLHFGAEDMFFELRLDVDKFHYEFVH

NPKFTIWVEYAQYLNLSVKEILDVIGKHFNLEYFLLRILEDYPVPKAKTVLTTLAEEMLS

KRVVEPLSPQKTHMDVYDYLISVKEERVENHFLRPGAPWFVEYARMHELTNWPHEVIKTH

SIRL

>contig08485 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55205.1|) 2e-36

MEFTTIIAGFSILLSAAIYAVYQVALQLAMGDDNITDTSTLLTLAGLTGLFAFPPWIIGT

LLLNASPLEWLHESFAFP

>contig10912 Frame-2R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY61023.1|) 5e-81

MRTNAPCQKKFIRDMRVFLGSCNNFRAVPVGVVLADPDTPSNNREVNAKYYNCRTDATDT

YENAEWYGLNTYQYCDATITELASSGGFQKLLTDFTSYDLTIPVLLSEFGCVNPSFPTID

GFEAQRTWLQAKWMFDSTFRDIFAGGLVFEYSTERANAQDESPYP

>contig11788 Frame-1F

MPVNYWSLNWINFTLTFNKMPDDIERIVDRKLIKQRVHYLVVWKGFEQENNTWESRIDLM

ADGYSDVIKDYEDQRKQELQNSTPRGRSPSRLRSKSPRRSKSPGRTRGRRSRSRSVSVNR

KVRANDDEKENKASEREENSSKITDTRQRTSPRNIDKSDGLDGKSSLRHRSSRIQASTET

SSSTQFVSRLDDEDDSVITRSTMVALTPQVRELAYSSMEINNKKPMTLMYEEDEDSDVSY

KQQDAKKNAKRENSNASSYHYKHENSEPSGLVARVVNSGHLASFLSTAAVVGSLMASQLL

PHEAEEEMDIWRSWLSFVIPVVALLLFFHQKDARSSAKWIATGLAWRAAAELLLLIGVTP

RQFEMMIAISVILANVSLLNALVSILRNGKHEHNNSALALVTVGITSLFISD

>contig13391 Frame-0R

MLQNDYGYTHYQPHHQHSGERPKLFNTSLDNVGGFHHAPGMHDFHQLVHSNNMTPLHHMQ

HASQHPTPQHQQNDFDNEPIMMNMQHPGQYYAPPPMTAQMLHVSTDYNSGGSADGNTPSH

LNSKRSREDLNMKEKKRMFKLNDRINQLKSLLDEAGVQSKKNKQSILDNTYHYVGMLRSN

LLIAKQKAERAEKQAESFRLRAQTGSPMDAVFKRCFNQSSTPRLIVDLNMQLVAVNSAFL

VQTGLPEDSLLDMNTMRACLCLDDSKLDAIVQSVSTNLKPISAIVQVQGAGNSIATLTLL

ASVLMDDDNVVTSIEFSLVPFEISPDFASPSSTSYSDAIKQDMIKEASPSGVNDLCL

>contig13526 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53273.1|) 2e-10

MKLSIIERKREKAVRYFSQSQLAFS

>contig13830 Frame-1F

MEDDAVMGLPISTGNYVAYLVGQQVSGIQQAGHRNRGYSTLAHEKELHIDDSCGSSSRCG

TSSPNSTPLNGNKRNDSCTSCFDTRRASNAAYVPYSSWVYIQHGAFKSWKRFYAVLSGLE

FKFSKGAGHSLKGFGQLAAVRRMDALRYGLLLELGDGTTIQIRCPGEKEFEQWLDATEKA

IERHQHQTSQSKTSYTLTATEQHDGYLFKQEKNKAWKRFFFIVRTDGYIECRDHEQGAAD

RKHSGYIKAVSFADCHSNGLAIQLSTDVSMVCYADSYDEQMLWYGAISAAAAANGKTAEA

KTTVKSCYVEMAILNHAGWLFKQAGLFKGWKRLYFTLHGIELAYAKDTNSEILVCDKVQS

VDEWEGHANGLLIRLISGRVWKIHADSYETAKRWRSVIRSACRHAETFSLKKYLTGRRRK

KLRPVFGGWLTEVRKDFSLRRFFVVDGVILGVANDVDNQLCRLGNVVEVGSTRDLERGIV

FTFSNGTTLKVNCDSLADSRYWYECLSFSIK

>contig13845 Frame-2R

MASTKNAGSKTFKRNKPLVPICVKKTKKTKASEENTKDVAGKVKQGRKRKRVMDTNEHCE

LIVAPSLTKEQQTERQLAVATKKLVQLDEQVAKLAKKRKTFVKSIERLEKMKIKLQKSQI

LPPATVRKLLNLQVAFKVLFPRNCEANPIDFREKNKRVQYASLVAKRYAPSRWKDREKCH

EKEQKEIAAIATISMWARASQQRFACDAVLLYCNTIFRRYVDRNPVTNAEVLIQGKDVGA

SNSFNETVPDVVKRVFLNWQHDIALIQELQVEELERGIAAIETKNLLADAALSGNLISNL

WSGSCTEENEASNEIKSTVDIFTTAKSTEEDMRLAWEYMATVIKQLIDRKRVCVDSVDVP

EKEAVS

>contig14167 Frame-0R|Blast-protein phosphatase 1E, putative [Phytophthora infestans T30-4](gb|EEY59029.1|) 1e-141

MRLLNHMHLYDRAAFMEGYLEKQSLEDPERWKKRWFVMQDSKLFYYKTQDDVKEQKPTDD

SCCGVISMENIDSVTTAKDFGIAAFQIRMESRRYVLRAECKDMMHEWLFNFQKSIANIVS

ALSRSQAEQRPSRLSNNFSRRQSMPRVNRSVSFDHQDFMDQQSGVPVADETYRGRASIGF

FASSHLSDDSEGEDEVLSSRKSPCRPTSPLTFGSFGPRSPLMFAFDPMDDVPEHQIHPRR

QNSIVQTGEESKDHNEQLHLNVAWGVGATTGDNSDTTTEPPVVIPTGTSPHSTGKYIPRY

LRNRSAAVSTSPPPLSVDLSSPPEPSPAPTAGRWVPRHQREGFAEMQPIESFSIDTRNSF

HETITEDSSSYSTGDDVHGVTSLLGVRAAMEDVCCCIPDLNAHFSDDQFHHQRQSFYALF

DGHSGVRAATFSNQRLVSYLTSHEAFLSDTRLAFEECFARIDREFLQKAEEESLGDGTTA

AVVLIRGNRLITANIGD

>contig14769 Frame-0F

MDAATNKRRVLFDAKSTESEYNQTHSRPRSRIDDRFIIKGSWFGAPLVYAVIIFFCIMIS

VHVWQFSSSQMHPVLSLPFFNKTMVQFFTKFGTFTVDLYPEHAPKTVEAFTRLVNTGFYV

KDAGFYYNEPKFVLQGGGFLYDKKSPVGNLPVEYSVPSSERMVVIARNHKSDSGSTEFAI

MLHDNIERNKPSEDGPGYTTFGRVVEGWHTIELIS

>contig15762 Frame-2R

MSLTEEKRIIKEIEQLQTQRLQISEISGNQAIMDKQNESMKETRSLQEKKNEEIDVLQEK

LNEQKKVLDELYRLNEEENKKDRFPALAKERKEIKEQLDEKFTAIKSLRKEFKEANDKYY

NNIRLVRRKKEMERQKEEEARKMEYETKLADYEKEMAKIHPYQNEMDLCDALVSFLEKTY

GKELKEEQAEQVNETIATPLVLDGMKPLQRKEEDFMIISNGKKSKKMRNSKKTKKVSKLV

LPLAQLEAFSTIGLLPPRAVDVIAESLAAVKAKKDYFRVQDMRVTTEKTSSATMEVVSLD

DVVSLHKSKKKNKFNASDKDAFPALGGIAADLPSWGPGMAPSVTCEVTIADEFADADVVT

EDE

>contig16965 Frame-2F|Blast-DNA-directed RNA polymerase III largest subunit [Phytophthora infestans T30-4](gb|EEY54825.1|) 0.0 NOT\_ORF

MLRERVGHRVERRNPLVKQFVLENDRPSKISHLNFGLLSDVDMMRMSELRVQSKDLFKVQ

TREPQVGGVLDKRLGVSNKKDTCTTCQLNLADCVGHFGYIPLELPVFHIGYFKAITEILQ

TICKTCSRVLLPPTERELFLKRMRDPKADVLRLVGLRKKIMTLCKKTVKCPHCSGINGTV

RKVTSTTLKLVHEKFRAKATHDLRNVFVAQFAEAQATNAELSTHLGKAQEDLSPLTVQQL

FQAIPDQDCELLWVDADGGRPEKLILNAVLVPPVCIRPSVAMDGGSGSNEDDITIKLQEI

VQVNFALQAALQKGASLKMVMEDWDFLQIQVAQLINGDTPGLVKPLGVKTSTRGLCQRLK

GKQGRFRGNLSGKRVDFSGRTVISPDPNLRIDQVGVPEHVAKTMTYPEKVTRYNREKLRQ

CIINGPNIHPGANVIRIEGHQFTKNLLYGDRALLAEEIKIGDVVERHMEDGDIVLFNRQP

SLHKMSIMSHRVKVMPWRTFRFNECVCSPYNADFDGDEMNMHLPQTEEARTEAITLMGVE

ENLITPRNGEPLVAATQDFLTASYLLTQKNIFFNREQFCQVLSIMSDANEHIELPRPAIV

CPVRLWTGKQVISLLVKPNQDTTVLVNLELKERNYTDRKYLCWKDGYVCFRNSELICGNL

GKKTLGDGSKQGLFYVLIRDHGSHEAARCMNRLAKLCARWLGNFKGFSIGIDDVTPSTEL

AAEKEKLLQAGYAAANKSIEAYRRGKIVA\*SRLQCNSIT

>contig18336 Frame-1R|Blast-26S protease regulatory subunit 8 [Phytophthora infestans T30-4](gb|EEY62105.1|) 1e-105

MTANVAMAAVDDSAGLTSYYEQKIEHLEMNTRDETQNLRRLQAQRNELNSKVRLLREELQ

LLQEPGSYVGEVVKQMGKSKVLVKVNPEGKYVVDVDKAIDISKCTPNTRVALRNDSYVLH

KILPTKVDPLVSLMKVEKVPDSTYDMIGGLDKQIREIKEVIELPIKHPELFEALGVAQPK

GVLLYGPPGTGKTLLARAVAHHTD

>contig18866 Frame-2R

MQATFGQSRHVSILHSLKLSPSNCLFYSLKQLKKIRYLTILLERKYRSKNEGIRRPFHPT

D

>contig19151 Frame-0F

MHRNVSPTCDTREFNYTIFFLREQAYSAPLQITFSVPLLTKALLQNW

>contig19335 Frame-2R|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY60551.1|) 1e-111

MRKDGWEKPFHVLQLATWVVFPAAVALFFAFYTPILEKAPAIVLSIVYAAVCLFTVVSVA

YCTGTDPSDDCIMRPSTFIGNRDSRPDNRVYCNVCMKYVNDQSRHCRLCDKCVDVFDHHC

KWLNNCVGKKNYRYFLGSVVGASLFLAVQIAVGVYIVIDLYTGENDMKRHSATSYGCTTA

KNNFTGLCENEQYRISLQTLRILHIVLLAFLSPWLFMMVQLTLFHFHL

>contig19403 Frame-2R

MTTLRRNYQTQASHKQPTSLFSIEVPHRTPNG

>contig19959 Frame-2F|Blast-ATP synthase subunit delta', putative [Phytophthora infestans T30-4](gb|EEY54196.1|) 5e-74

MLSATNRVAARALHTSSSLLSAAADQVATTATKVTLNLSTPYQAFYKGAEVDLVQIPGVI

GEYGVTAGHAPVLSQLKPGIIKVHLEREKEVQSFFTAGGFALTHANSVTDIACVELVKVE

DIDPEKAQSGLIKYQAQLAAASDGSEEKLNAQIGVDTHAAMVAAAATN

>contig21556 Frame-1F

MLGAPALGRLLARQSVSVLGLTALGVMATITGRDTEMHSLGEKGLVAAVNSRDSDDKSTR

LGAGRRLILKQRSKHQAH

>contig22210 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56112.1|) 1e-147

MAKLDHPCIVRFLGIAWNSLSSVSCVTEYVVGGDLRAVLNQWLDSRARPKGFDYDKIQIA

LDVANGLSYLHSCEPNILHRDLKSRNVLLTSELHAKLTDFGVSRERSDDRMTNAVGTSLW

MAPEVMMGAHYGNKADVFSFGVLLSELDTHEMPYANFNTPGVRKPAEPDMLQMVAAGRLR

VNFSSDCPEELLKLAQECIAVDPTDRPTAAEALYRLQCALKAFEVAEVAL

>contig22773 Frame-2F

MAQVLPRTSHEKAASMAAGAIPPHTHERSADANALKNVLTMLSGIDKRMKKMILSQARIT

KDERRRGFADSDMFNLMLGTACAGKLHQEALGCSDLRNYQAPCPVMERLDKFRSRDHQDL

QQPAQSPLTRPPHCYRTSSCRSRKSRARSKDDSRYKAGQACDTQIR

>contig23107 Frame-1R

MDSKVWQRAAADLNPPGVPNSFRHAKIQHNVASMLLRREFGGSRRHQTVRAIGDDREENF

WAESESASKHQSRYFELPQTTKSTISIAISPDGKMFASTHGDHTVKIICIETGNVIQTLV

GHPRTPWSVKFHPINPRYVASGCLGFQVRFWDIETGRCLYVSTLRHAIISISFHPSGDIL

AIASGTCVYTWDYQHTCPRIAMFSYQTLRSVTFLPDLSKIMVGEANERYVRPQGQAPPSD

LTVTLTMWDFDPSWALSTEPLLTKKAMNNSRVILSHALIYNDGGFDISRCGRYLAICADF

SLRQAEKEVELEAENEAATDLESILSSVPATHETGGVTSPNDDVNDVSVPNPQATTSNES

SSSSPAAAVRMTAGDSVAPQMMPTAMPLSLPIYPQPPRLVPVSGMHTGAPNMLAALQSAA

ADLSLTMDQYMNQQIRRVRPRLHPPHSIQRYTAAMEPARSTVVPAVVPQQRYSQIRPNIA

LSRTRFTRNQRNRRGRLSSENQSTWLALISLDPEQLGRVVQTCHLAETAAGGVTSVKISP

TSAYVLLGYGVRDRIQRETEFPIHRVTRIYRWEDMELLSHVESALDDVNIALFSPICGGG

FLYGTKQGKLRVCSTFRGGFYDEENCNVLDGPRRCHYDQNIYGDDENDDLGEEGDDDDED

DEEGVDDDEEDMEGDDDDDDVEGEVEGNDDEDADMGE

>contig24612 Frame-0F|Blast-histidinol-phosphate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY66078.1|) 1e-151

MDKQSAIALGVTAGLGVGYLLGKVQHSALRLELENDTAENLDEIERLIRPNILALTPYRC

ARDDYDQGILLDANENSLGPPLEGHEQLEAMNLERYPCPRQLELKSLITDLRNQNTTEKI

SQENTFLGVGSDEAIDLIIRVACTPRVDKILITPPTYGMYSVCANIHDVGIVSVPLQVES

LSENMQGLKPDLPLASFQIDPNKILSAADANTKVIFLCSPGNPTANLLRLKDVLMILNSK

KYKGFVVVDEAYIDFAENASLCTLVNKHKRLIVLQTLSKSFGLAGIRLGIAFGDAKLIRV

LNNVKAPYNISKLTSDVARKAFLNLNKLRRNVDLIK

>contig25008 Frame-0R

MRVIFKRCTRSASTLVHKNKVVLNDHDLSIDHSKNVHANAILSSILVGWHHKYYPTCVRM

TSSGVTFRNRHQSTLRIVLRRKLADCTPCREIPVLCIQRPLLLGGDFEIDLDNDIYPVRM

LPVSGNYVRNLRFGLVHGPKRKRVRFRARDLATYEKWTTVLEAAVEKAATKRSMVATWLD

TVPILSAPEDSYISDDFGFSDGDESCKAVPLETKLDSGSTPVDLLHLKKPLNDDDDTEEE

YERDCSTESDDEATILPLAREFEVTRPMVPFYGTYQSIGRTHDHEIDWKSHLKPLSTTHA

MGPEVAKLAIRDSFSWT

>contig25347 Frame-2F

MRSEGHASKRSPRTRLNLLQRLSKNDVDISPSVTCFPAVQDIKWHRNKTLLQEFDSALQP

HSSSIVRRPVQYHVGIEMKQILAPTMARARKTKIICAIGPASWSVDMLGQLLDEGMNVAR

FNFSHGDHQLHQKSLSNLRKAMAARPGCHCAVLVDTKGPEIRTGLLKEHKPVQLK

>contig25484 Frame-2F|Blast-RMD5 family protein [Phytophthora infestans T30-4](gb|EEY65014.1|) 1e-47

MRKLASVMDSKLADWNNLEELPVEIPIAKEFRFHSVFSCPVSKEESTPENPPVLLKCGHV

ICHSCVKRISYNLSRQFKCPTCPVEQTESDTCKLIF

>contig25523 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65234.1|) 1e-143

MQLREQRVAEREVELQALKEENSVHETEELEQYTKLSQDENDTEEEQEVQAEIMELQEAV

ALRAEEKRDIKAAIDSLQRKRLRRQAVIAEHTKQREAENMVIEADAAVAARKQVLRELRD

EKDVLQRDIIAAEEMEEKLEENMQDLPAMKEELAEVKTTRLKVQTRVDSLRLELARRKRK

MRHMVDILLLTARDTNPPTLREEAVLLHLLYQNEGEMGMNELKQEASLVLKDHDKPNGLG

VVTRALYSLLANGVVQIDWSYGNGLVTSLLV

>contig25710 Frame-2R

MIKILNLHFRKILLILNKSA

>contig25817 Frame-2F|Blast-hypothetical protein PITG\_01582 [Phytophthora infestans T30-4](gb|EEY61305.1|) 7e-07

MPMQRREKEEKEEGLNLSDVEVDDAELVFMSVLFDRGEFGVAIYNAQTASLKTLQHQITD

TSELEEIIERLHTQFEVNHVIFSSRNASTNGLLRIIKKLDDMHQTKTAISIRKHSDFKYL

KACQAIEHVQIGAVSNEYRARTS

>contig25909 Frame-2R|Blast-dolichyl-P-Man:Man(5)GlcNAc(2)-PP-dolichyl mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY63923.1|) 0.0

MAHSKTTTSKTKRATRIDKDVKTTLLHSRVLSFLYDLMWSYRYFPQLACCLLLVEACVGY

IIIQKVPYTEIDWSSYMQQVELFKAGERDYLKIRGDTGPLVYPAGFLYVFSFLHSMTDEG

QNIRRAQYIFLGFYLITIATVLAIYYRARVLPPWATVFLCISKRLHSIFLLRMFNDGVAM

MLLFLAVYLFARQRWRWGCVCFSLAVSIKMNVLLFAPALFFLLLQSCGPLRTAWYIFICA

AIQVVLAYPFLKNSWWNYCTKAFELSRVFTYHWTVNWKFLDEETFVSGGFAILLLLSHLL

FMMLFLDKHFNIIGTIRAVMMKPFAIYEPFPIQSEIIVTSLFIMNFTGIVFSRTLHYQFY

SWYYPTLPYLLWCSDVPLLLKMAALLNNEYAFNTFPATTMSSLMLQLTNSFLLVTIFLNQ

KNNSFVPYLDAEARTNLIAFVNEECFDGARQLALYYGSVNEELAEGAVVSSIDEREIVLS

LPKMKLTLAVGFGSSGPVTGEGYGRQVLKEMMKEAG

>contig26030 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69184.1|) 2e-11

MGLHEKINANPTVYAVTVAAHKKFDMAEALDEDVTDPFEPDEIF

>contig26045 Frame-1F

MISHLLKVISQQNTKNIMVQVLLRMISIADAKDHAIIVIIENLDAFLRTLHQIDLALPVR

SNLLIHLLPSVTKRMPAHFQPLPSDFFETAVLEYNILYYVKQYIMTEDELNQWFIDAYNI

VAIQDTVKKLQAAYARDDRNSFLLLERMHSTTYLTLLSNGNVNSLDPPSLLQWLRYCNIY

LPSLSSSKRGLEVEANVLTKVETVVNEISLNVPANLYSSLERIIDMKSFISKTTDLAYRK

RRFIVE

>contig26261 Frame-1F

MICAGGENGKGACVGDVGGPLVQKTQSGDVLMGLSSMSDCNPDGTPDIFSRVSSAMDWLS

ECI

>contig26328 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64206.1|) 3e-44

MHNMHVLGLMIIVGSKLKVVIGQLLERSTRKKLHNVRDLTPHGRLASANTFPGVIASASS

LGSTSVIVRFCGQDAEAAMNYVKTTLKPLSEIIGVSPFQDNR

>contig26478 Frame-0F

MVGGLDKYFQFARCYRDEGGRADRQPEFTQVDIELSFVTQNDVMALVERLIQKVWKAAGK

ELPDSPFQRIPFKEVMHRYGVDKPDTRYKMELQDVDSLLQKCEFPPFQTALVHANEKPFR

PCRVVRAINAKSLACGGFSRKDMEELRQMSQSLSKTTSVFVVTIEADKHWKSSLASKLSK

VEIELLNTRLNAEKDDVLIFATGSYHHVNEVLGRLRIYAAQLLYAKGFLQKELDPFNFHH

LWVVDFPLFESNDDNSDGMSLSATHHPFTAPNSDDIVTLKEILASADSDNKSLLKDPVIV

QKLLKMTAQHYDIVCNGWELGGGSIRIHQAKLQQAVFKHVLELSSIQQKSFQHLLDALSH

GAPPHGGIALGVDRLVAILCGERSIRDVIAFPKSSTGNELMTNAPGPVHPELLQEYHIHV

QKKE

>contig26632 Frame-2R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY61201.1|) 2e-39

MERAPGLVKDNQKRRKKSQESTTGHSGDMEEEELELFHVVQEDLRLKSTVGWQNAVKVLN

LAYQHIERHESQSFLDDAFQKVISIMLDQHASKIGSFEKS

>contig27392 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61490.1|) 1e-62

MANLIAEAVFKRKKKLFPNSEKRVPTGLLFLRGEDFSDNFTNPITEYHTQIKTRLAEHLH

YCSGNAVVVIDEVQKVIPHTLDVLMEAVSERSQLSYYKHGVTKNIDTANV

>contig27521 Frame-1R

MATTCNEKLPFFIIELSTMPLAALKASMYNSSWLQKITMGVRYRGQIFTLHALT

>contig28072 Frame-0F

MPRPPVKAGATAVHDPQVTSSQAMQPPSATRFLQLKEEVEMQQLQLQQFQHQQQHHHQQQ

QFQLHQHAQMQQLQHQVQMQQQQQQQSLQITQSVGTPSNTLGRSSTANTLVQAATNAGNA

NPNAGGGYAFPRNSPEFACENVGERVKGKRRKYCPHEVTALVLGVQRYADDSCPWSSILR

DPHLGHLFHGRSGVDLKDKWRTLIKTRPELAAYTENRKNHRKYRPFSATEERALLEGVKK

YNGQRNVWSLILIDKELGPQFNDRSNVQLKDKFRTMRRAGTTSSLLVSGNATSHRPTAAT

TTSPVEHTTSIAMTVPTSQVAASKSLSSSSSAMNTAVVPTNRISSTLSAASQQAATLLVQ

NSHAAMFADPTLYLGGSFSLPLHYSQGMNMHSMNRQQSAQVQAQVQAQAHAQAQAIANAQ

ARAAQVQLEAQMQHMRAQSGQNAKQQYQALHALNGVFNTGLPGYQLVGNQLLPQQALYYP

MTPTIPTQQQLQQQLQQQLHHTQQLQQHQQQQQLAAAIAAASNQSHHHPSQQQNKTQVTN

SAQSGETSRV

>contig28869 Frame-0F

MVAVIIAVATTILGYVDMSRVYHAIRGQAMIKLYVLFTMIEIFDRLFSSLGQDVLDSLYY

TAKYHPRRITRMFLDFAVATTYVVLHALLLFAQVVTLNVAVNSSNSSLLTLLISNNFAEL

KSSVFKKFEEQNLFQISCSDIVERFKLLTIIGLILLQSSSGDVAWGTAMVLVAEMVIDWL

KHAFITKFNQLSPTMYSKFITILCRDLTGWQSEDTILDHTHHVSKRLGLMSLPLACVVLR

MVSKALADVPINLMSPSGGLVLVAFFLCLAAFKALLSLSLMVYACQSGRLDDTRPKSPRS

VRHLESIHQYKY

>contig28937 Frame-2F|Blast-ubiquitin family protein, putative [Phytophthora infestans T30-4](gb|EEY64133.1|) 1e-133

MMEPERTESITENKPLLSEGVVEIAINETLRDKIVLKVKTLSEKPLRVEIVSLASVAELK

ELVKKKANAEGKFLRLIHQGKMLSDDKATLESCKIKDEDFIHCAISSAPPKAVVNQMSAV

DVEFDERDDASTRRGFDRLRDRLSREEIQALRLYFYPQLSIYISQAEHVHGENSEDRIYR

LEEEWMAVQGPQSEFALNVVPTARIAMDTQIDMNGVSNSILAADNEGTGTEFLWGFLMGL

LLGVFMLLMLLDRSVPRKQKVGLLLGVSMNFFLSVVPRAVSNQ

>contig29703 Frame-0F

MLLYMASTSKVSTKVLRCLVESGQNPFSFILPLGYCEAVTFTKWFKYLTEYTIAQGRIDL

KGILAIYNRLNSRMPGIHGP

>contig30477 Frame-1R|Blast-delta-1-pyrroline-5-carboxylate reductase, putative [Phytophthora infestans T30-4](gb|EEY57032.1|) 4e-19

MATALSGSGPAYFFLVAEAMIDTGVHMGFSRPVATV

>contig30994 Frame-2R

MMNTTATPISTKWMRISILSRLTVKTSHLEHQIRSQNVVLLIVNGATLYTWPRVRLATNP

FDKSQQQKIFADEQARRDWPMAPARSR

>contig31980 Frame-1F

MVITKLSKKQRGKLKSSETKSKAHIKFDENGEKVIPKIRARVSKKNNGEKAKEGGGKSDR

SPEMIQQAKYYLEQWRKRNEPKADDELPWKFKKIKQQWILRWMYEADVIPKTMFAIVLEY

LNDIQGAAR

>contig32435 Frame-0F

MNVYTTRDLVAALQVSEQEVLAMLKELHAFEDAGVWRLLESTYQSQVFTDMLDLVVQNDW

NVFIEPGVLVKQFVNHLDEPSLVIRQCCQLYGSINTILGQEYCLFDRTKVATFRAKSLFD

DQVAEAHFQAQLQHATFPLLDAGWELNEFVQKWKLRVPDSVPVALEMLRGLALIKHFKAG

KPSRIVYFPEDLLSPEPKKRFEQLFQTQEKWTIEQLEPYIKSLVTPTTTQASLLLKHTRS

TRQSNSTEKLYSRR

>contig32440 Frame-1F

MCNAAEKEGVDFMKDRPIGDESDSDDRLSDVSKVESRGSINKGWSESSASENSESSDSNL

SSVGDSECDTLSCEQQSVRATSKNSRYRSLTNEQISCSRLSGQLPASTPSSKNECLALEN

EKVHSDEPKSRQLPQISTMSLKGECDPTTEIEKFGGGTNSNEYAAQPQNDIPSLYRQLPA

KHMSQRRLKPRLVISDTSSSEESSDSGNYSSSSSSADPNGSESDRCMSKHLLPPPPSATE

AAIPPPPLPPPPYRSPGKNKSAALSLSRTRTGASHEMETTLLISAKPGESSSVTHFPPLL

NSYLSPSSSSSSEVSSGESDSSEGDSCSD

>contig32853 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65502.1|) 2e-18

MIFEGPFRFSRASSADLALR

>contig32927 Frame-1R

MKDLRQRSDIMEKRLRELEIDNAIVRSDNIKLWKHLEQSKDKQMIMQVKMKKIMWILFQI

YRGKQQTLPKLSGNDGTGAVITEDYANSSMLGPKEFRDVLRFLAIDEPPLLPGSNANVSN

AASASRKRKFVEVSSDRDGFPFKFDAEPYSLFQMPNALEESNPFAMTVQQSSSPSLAADG

EQTNVLSIFSPITNVVNNCLPNIDASLGNFLSNNEETSRVSSPPVSSPVTSASTTPVSTA

PTQAVSTPIKSSPPTNNEIHTQDGIEVVLNNIASSGQPDANNQLAFLDEDLPLLPDTGHY

SFTDGE

>contig33029 Frame-0R

MVRLYFPTVFNAMIANTYEPMFGATCLLEN

>contig33591 Frame-1F

MVPYRHKTVNFVQFFVPLRLEAGRCSERFCSPPRMRFTSFELWSCVTKDADEDQSAGQEL

HVGNIIVHKFYLLAYRRYIAGAAFSRLLRSCWRSL

>contig34024 Frame-1R

MSKNYSLALYSYICSKRLAKKQFKA

>contig34536 Frame-0R

MAYNYVATAQKPTSVTHSLTAAFTGPNDTNLLLAKSTRFEVHLLTPEGLQPQHDINLYGR

IAIFEVFRATNESQDWLFIVTQRFQFCVVSYDATTQQVVTKAHGSIRDAIGRSSEIVTSG

NIDPEGRLIGMNLYEGYFKVIPIDTTKGMLKDTFNIRLDELRVIDIKFLYGYVKPTICVL

YEDYQAARHVKTYHILLKEKDFAEGPWNQSNVEAGASLLIPVPPPIGGVLIVSNQTIVYH

NGTTFHAIPMQNTVIQVYGVVDADGSRFLLADQYGTLYVVALDVTGKEVEGVHLQVLGET

TIASCLSYLDHGVVFIGSTFGDSQLIKLNPNRNDQGSYLDVLDTYVNIGPIIDFCVMDLD

RQGQGQIVTCSGADKDGTLRVIRNGIGINEQARADLPGIKGMWALRESFAAEHDTYLLQS

YVREVRILGIGPHDEMQEYEIPAFLNVKTLLCRNMLGDVWLQVTELEVRLIHCTSFAVES

TWTPPVDSRITIAAANPTQLVVAISGGVLVYLVIDNARIIEQTNVTMAYEIACIDVTPLQ

DQDVSMTSLKTPSDTTGLRTSLCVVGLWTTFSVSVLQLPTLETVTTEVLGTDLFHAPYSV

TRLKANITYLLDLEMEVLFITN

>contig35603 Frame-1F

MDEKEAAKAKLFIATLQKYGYDLTDPSLATSSNSSLDSSSTEWSPDDDVEPVVVSRLSST

SSSSILALRDRKNQQSALHIAAKKGHFDVLRALAKLPGLSEHLNAGDRHANTALHFAASS

TRSNAPDLVELLLNLGANPSALNVRGQTPLAIHIITAKPETPTTITKLFIDKFRHLKHIP

SSPSSPSSPTGFRFTTPCAALNELVNGTTYLHMAVERQLGEIGGALVQGGASINVPDHNG

VMVSDTIPKKLLVKLITFMTEGSQVAPADIVRGSCKICRNPKSLLDPLRDCALCSRAVCK

NCSQKASEIRKSTSDGTYVSLKDKDEGRFCAVCCTVKILRSKKHNQRENFNKKLMGCGMK

>contig35885 Frame-0F

MGMDNFEGLQAFLQNIGMSMELHNMLTQASDDYVLLLMQNPKVGVRTSVRRFRIDPRVYV

KSLVLRDVFSWFARLEIFRSDFSEAHTIAQIHAFLSRCCKQRKLRLLVAHRGEIAPTFAL

DRPRAHSHEASTSGIHLMMRSRFSSANGSESFIPDSFTKLLSEAFYLQSLMFVDPWEVEA

EWNVRRFMHDNQSSLHVELGWDRLSPICSETCDAIVASVFEDPDLVAMWKATGGEGWLVT

AITQYRIDGLHSYRTLHQHIQRGLAEKEEPRIPFLVAIYSRSQRNAMFKVAGLPHRFVGA

VTVELVEAKDLIACHWLQHWSDAYVFVELCHAKDKCRETAEEWSLQTYRSSVGEGGVNPH

WESPKNRFVFRFAIPTHNKHTCGSRRDVQYSNREGIAREINAHSSLIASQIWNADINDLN

RDAVDALDKLLSSVYKGPPSVLQCTVYQKNKVLSHQFMGRATISLDQLTPGNPMDCWLPL

QDTSSGLLRLKISLSFQLMCSTMAGKSELNDLR

>contig36134 Frame-0R

MSATRVLRGGLTWPAVRGARLLRALTAVHDELGKEQEDEVFPYDLELCVPTAGHVALVLV

QKPSENQVLATNTQQSVTGPRVVYVLDALPPTRQKPRNEKAPIRKKRAPRVQFPPCQIDD

LELLEELFAPQTRAAGGNDGSVILKPP

>contig36206 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64078.1|) 4e-20

MSTGEEHYGNTRHAMGVSMPGMTGSAIPMPGLAKGGFRLPSMATPGEDPTSETTFDD

>contig36417 Frame-0R

MASMLIKNALKVGLRARKGNSSMHGLYKFPNTSFSIAFNGESPSSPVLSMPTNHMS

>contig36509 Frame-2R

MMGRTVLHASQQDSSILNLLICIAGIYICYLSYGIFQEKIFTYRSPSGEKFTSTLFMLFV

QCVTNSLVAYAATFVWKPKRARMPLSPFAMTAGAYLGAMLCSNEALKHVSFPTQALGKSC

KMIPVMLMGVLIRRKKYTLCDYICVVVITTGIAVFQLGKGSAKHPERENSTYGLLLLFLS

LALDGISGPKQEEIAHQLRPSVHQQMLNTNIWAVVYTGIGALLTGQALEGFFFCMANPAI

LHSVFYFSLCSALGQNFIYFTIQQFSALTCTTITTTRKFFTILFSVVWYGHELSVMSWLG

VTIVFIGLGSELSSKYQKYQSQSAKLT

>contig36783 Frame-1F

MNTGTKGNSTVAAVLKGLKQASASSSGPIFFDEAFRLLVDTTSLVETQKIVFGLQQCAKN

SPLLTLDQTRSLYDGLQQAAAICTEPPRKAEFLGFVLFRQSINQLETQELTTLCRTVLQV

LNANKRVLSGYMAALASADGAIFGMKLDFCRVQRVLELISTVFMAILTNPSETVERRVSV

LNTVTSIAWHFDDSSSVRISVALLLVDALGLVTRSQFAETTYVAHVALAVNLLSSIRTRN

DEVIELASRAALLVLDSMEYLICKDVGILPLLQSLTQLARCLPEAFWCSVFLTSAAYFLM

DKFKAPLEEGLMLSVLRYALDFGLNVALDQKDKRSVYVEILLLPLSSMLTEHCFTSMELL

QQVDAIKLKCDFVWKEGIVAPMTENSTHARSAILLVSNIETCQRWLSSLFQPKRSATLAT

SNDSTDKWLALLLMALLSDARSCVRACAGECLERQVNKNPNFWGATTTKAVVASLLYLTT

QHSPSHDSSESMHRSGRWMTLCLYSLAGLAALTTETMRIIFRLIDNMKIMAKVRSMAIKL

MYQVWLNEPRVFPKLEAMLLDSTTYDNDVELHVIKTATIKLLCEKNPELGVLFISCIQDF

LENSLESVVSMAIDAITALCCGDCLDFYVAFKIIAQKMRKNKILCADKPLVQECLCHFYS

LGGA

>contig36923 Frame-1F

MVRLKTPHFSSAIIRNDSAQEGNEAERQYKEAWVPCRSLRNEILLEPHQGPFISDGMKEL

TCRYFRCVVEGCKVRGQANLSMQEIGYVLYGDVIEVVESTVVEGGIVFLRLHERYFDGMA

WVVERSLDNESVLSEVEGPWTSLPTHPRKELYRCVQDTGAPIRMEPELTAPPVGRIPCGT

VMTIVERTLTKQRQIFLRIMEVNTVHPNEKDTQGDKWVIETSSCCASVMVKVT

>contig37025 Frame-1F

MLNRFSSAVQTAVSGAASAAVSGAQNLQGILSEEYLKHYETPRDCTASGGHELSWKIFPA

VHRKTNNEFSVFLFDKDDLKRIRNKEAQDRVLEILRQEMKTLRVLRHPHVLKVEEVFEET

RRSLCFVTERVTCSLANACKNFTNAVNVTPEVLEIGLTEFELACGLMHVGEALSFLHREG

RRVHLNLSPSSIFITPKGEWKLGGMGFCRVVEPGQSSRSEYYSFDVSTGVRNPVTGAIEG

SWEPLLEYCAPELVTEPRQFDSKADMFSLGLLVYELFVQPRADGSRNPVLDVHDGNKMTH

GYKVQSLHPISFPDSVPTTLQNTIRSLLSLEPAKRPEARAFLASPFFDSGPIKTLRTLQS

LVEQEPAAQAKFLTTLPDAIDGFSPRVLRDMVLPGLQSVVINKAVAPFVITPLLKIVAKV

DKQTFSYSIAAMMVPLLAITEPVQCMLMFVSELQTLIPKAEDGYIRDHVVPMLCRALDST

VPEILDTVLNKIVDQASLFEYRILKQVILPRVNKLILSPPQPSVRINALVWLAKSFHVFD

KDLLIESVLPALHQTLQVDKTPAACMCILGCYDNLGKHLGPEFTAKLIIPAVAPLLWEQT

LNNSQFDIICGKIQDMLKAVISERDRSFTSQSSMGSVRTGITAASGMSNAIRAAEASKER

ESGVAAANKLLSEEYIPKTKSEPEASSNKRPDRYSDDPFYIGNSSGSTTHNTRGERLGSD

GRRESATERAESFSARRRAGKKGNARASRRTSKSDTGNADLLGINASTSKSSPMSTDLLD

TGSLQNVFPPAGSVSSSSGASNSLFNDMSAGVQAGVSPYTSQSIVAVHASQQQRPVAYSH

NMGNEVLHQQQQYPSSMTQMTPYGMQLEAPVNNNVYAQPSMGFAGPGPMLQIQAPYAPQQ

PGDKFSAFDGL

>contig37050-0 Frame-0F0

MCVRWLEYACINLRYRRKECVVETMSSRWYMDLRSIEASYLIRDRSRGLKGAANRCILKI

LVESWFIFYIVALC

>contig37050-1 Frame-2F1

MVAAYQSFHQQTDRLCDRPGTSYRRMSSSPAPCICCTERQNFLRVISVVKFTGRFRWLRS

VPDDPIPSLLCSIAGAVAKSALYDELWIVLPPSVVVFPKSGR

>contig37498 Frame-0F

MILARRSLAMSSRMRATHSLGVLQQQQKSMKHTHTLVLIRHGESEWNKQNLFTGWYDVQL

SAKGNEEAAAAGQLLKKEGYAFDVAYTSYLKRAIRTLWHVLEQSDQMWIPVFKTWRLNER

HYGALTGLDKQATVDKHGAEKVLEWRRSYNIPPPDLDTASEYYPGNDVRYKDVSKNDLPL

AESLELTAARVLPEWARTIVPNIRSGKNVLIAAHGNSLRALVKHLDNISEDEITGLNIPT

GVPLVYHLDENLKPIPHKDAIAPLKAFYLGNQDEIRARILGVKNQTK

>contig38529 Frame-0F

MTKYKCSSLICSLLLLSCYHVVTSIENVALIEAPVLGKSRQLRSSVELVEGLLLTSDKLA

KVIGTLPKNLAKEWLATFKWGINHFKILLAEDKVAAAGKIFPDDSANPIMTKLFESDAFL

WWEKLIRRTVDDTQEEVDTIITSALVTRLGKGRAIKLFTEAGFEADAINAKWLALLYHAL

DDEDMPKLFKEIVSSGGFDKNSVEFFIKLCARENNKDAAYEIINSLLQDKKEYREVYQKF

DGVVETYRTKWDSLKSVYFKAVSDPKLDKSVSPMQRLRNLYQTEELDPVSVASKIAD

>contig38626 Frame-1F|Blast-lipase, putative [Phytophthora infestans T30-4](gb|EEY57047.1|) 1e-55

MRLLRPLVLILQSLVVSSATPVWQHSFPLDQAPSPIIVSSLSSDGAGFLYNETTALYLAH

VTSISYCQSRHIIEWNCQPCAFVRPLVGVTVFEDTKDNFQGLVGYSELYDAIVIAFRGSM

DVTNWLDNLTFIKTRAYVHFPSVMVHEGFYWAYRSVALQVTKALRKLQKEHPFASLMVTG

HSLGGAVATICAFELEYIEKISVKALYTFGNPRVGNIHFSLKMKNTSMDSVRVTHFRDIV

PHLPPTWTGFKHT

>contig39337 Frame-2F|Blast-phosphatidylinositol-4-phosphate-5-kinase (PIPK-D1/GPCR-PIPK) [Phytophthora infestans T30-4](gb|EEY69098.1|) 0.0

MYDDRVRPYDPASSARSRGVSSPTVSDPDVNLLQGEDNATPAVMRTCLQSTTRWFQFVMF

NAFVAALALAMTSSYENLSPGLIWGGVLSIFSVFFVILSYASVPSYRQHPNPLVFWRTIA

DAVFVLQLMAQQFVRCLFFDCVPLCSSTNLQCGCSMNSGASSTCGIFAGLFQFTLLASEC

WFFCMTANLLMSLTNPFTDFKRNTRMFHLGSWFVPLILGLLLMTTDDWAGYSDLGVCWTN

ALKNLAADNMTDCTPGYEVTDNFTSDYKAVNANIISWMFFYVWMGLFIVCGIAVWVWAWK

RLSEGMPETYAVRVQSINRARFNVFAVTFYWIIVGIVYIKFLSRDRSMPDKSSELLNFFI

AGKGYLDLVIWFALNDFHVVHFTRCLGENTGEIDVDLNPQVNAALRREVLFYTTSGIIQA

VQAA

>contig39856 Frame-0R

MVSFAALKIALEEYKLRLGTSLETNESNDVKMSGMLTSTIGIPCRHKFRQVAAETAAAIL

SRPPRI

>contig39939 Frame-1F|Blast-methylosome protein 50, putative [Phytophthora infestans T30-4](gb|EEY63004.1|) 4e-55

MDQTIATFDGHTDLIWGVAMNPTHAPVLCSASQDSTVQVWDARHPQSAALMVSTLLPALS

VDWHPKQATIFSVGLEDGGVYIFDVRSPRMPLVRRKPHRAAVHVVKYSPYHNDLLATGGD

DGKAFVIFNSCAIDHKEGFGVRELRGKDDDSFAHRDYVRALEWFQNESLSPNSDEAILFT

GAWYKTIRELNIDSLATLH

>contig40135 Frame-0R

MGFALDKSEAAVDLVSIVFESFKESSSSGLALISLLYVTSDILHNSSAAVKNASLFRTTF

QERLPEIMDILRVAHKNIAGRMSANAMKEKVTNVLTAWENWSLFPPAVLVGLHATFLRKL

EENEYIVMHDLNFTGIGESDLERLRKTCRQAGIVATGDAKSLVARLQWLKEFTSPTAQIA

SGPVLATNSSLPYASTNKIAPQAVSETHSKRAEVNDFQEKRTIKGSLVDEDLDGEPVDEK

NSMEESNALDEELGGEAIDGDLLKRNDSLKNDFNGELLDGEDLDGVPMDEKDLDGVPMDG

ENLDGEDLDGVPMDEEDLDGAPLDGEPI

>contig40351 Frame-1R|Blast-inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase, putative [Phytophthora infestans T30-4](gb|EEY66971.1|) 1e-141

MTSCTNDTYGAPVARYTLGICVMERKARSPPMLEILGRLPSDLIRVEFFGDNTILHEPVA

AWPQCDALIAFFSKGFPLDKVQEYVALRHPIVVNDLSAQYLLQDRREVYRILQEHDVPTP

RYVFVSRDGYGGETKPPDVVEGEDFIQVDGVRINKPFVEKPVDGEDHNINIYYPMSAGGG

CKRLFRKIGNRSSEYDPQVNTVRAKGGSYIYEEFLSTQGTDVKVYTVGPHYAHAEARKSP

VLDGRVVRDADGKEIRFPVILSTEEKHIAYRICRAFKQTICGFDILRVRDASYVCD

>contig40438 Frame-1F

MNLNLEDTSKLMDLLHEMDFSEEHRDDIRRAFCQIQEDGEVISERLNRFRQLTIELAPRK

HHSDVIDRLLHLLQTCHAKVFKFYELACRGYSKYLSLRFSDASPNFPRQEIAVVMLRLLG

LLTTYGSEKEVSSALEDVISTGPVAPWSYIIPQIIARAHHPSLKVSSLIYRILKRLAHQS

PHELVYPAVVASMESEATFASIHKDNDASHDTFAAVLHELHHASPGQAEGVHIFISELRR

ISILWDEAWISTLVKLSADVFRRKSTLEKEAIRVEKNTSLSTKEKKQLANRVLGAIMKPI

YVSLEKLWNDTCGCIRDQHLVTPHERKFLKDYGRIIGKALEKFHSCCIAEFSTVSLKDPQ

EIWQPFEDILKALLNSAGRREQLLLSDLSPAMASSPHLLALTNIPGAAASTVSGQIQP

>contig41143 Frame-1F

MITSARLLVACGAVLMSLSVDAALDVAMKLVTSRVPLTADSQELAIVVTPKQPDLKYLMV

ESLVDTSGTAVLSDLTLNGDGSTFMTKLEGDQKLQAGMYKLKVSAVNEKTKKTANAVLQL

KVTTPVEVASVKINDKKLKSGDKLTGKKFNAAAADALKIEVKLQQLHENNPISAHQAFLR

FTHVSEKTETYFVLTTNADLVHSTTLQFVALSKKFGYNSGKHHVQLILGAAIFEKAIVWD

LGEIDLQLGAAPPKQVSPLYKKPLLHESDTTLKALPEIQHVMRTQDPRPPVAVSVASTGA

VLAPLVFFVVFVSRLGLNVKRLFESSVLVLGCVFLTSLAGIFTLFGLYWLKLTMFRTLGY

LSILGTVNLWSGLLTLKRLAKAPVKKTTKIE

>contig41257 Frame-0F

MSSQLDSDAIMTTGGTLKSDQVEELLAETKRFRHVQISALAGAAGTYYQVVQQSDGVYEA

QLFVDNKMQRLWPNRVQSEDGDILEMDELDTVIGGAITSVDVGDDETDFLDAVTITDGAV

VATGILKLTVGDLKVLNGSFLLDALRVIPHQLSGSTSFQSTSAPPVVQICAQDIVVSSES

RLMMPTCALQLSARSVSMDATAALDFSWTAQIVTSQNIHLNANVSSNLDPIIFAPETTTF

TVLNSTEKFNNKMLVLASEGDIFLGGFITVGALSVASKISVTITGHVEVLNIPSIKSAFH

SCKEQALQPIVYLKADLEKNSSSSSPKKEASIPIIPTMLPSPSNFTLIVHARDSILLGES

KEKAQEIENQLQQKDNHLPQPVGLVHGGAILLCATNLIEISSGSVISTDGMGERANQGPG

MGSCASSIGGGAGYGGHGADSSVITGIGNYASGGLPYGTRSGTGMLGSGGGCVDGGSGGG

IVILGASGLVLSGEVKCNGLGGANGAGGGSGGFLGLSVAQFLRGHGHISAVGGGSECIDV

STNFLGTAMRQKRSLSFLKAKVKTNAANEDAEAELPSTDIVPRFCGGGGGGGRLQLTGCE

LSTFDRCTREFDGNYTVAGGATSYLLNSGDLPESPASTPASSDVQASVLSGASGSFFGFP

CPPGSGGLFCRLCSVGKYKSESNSAECVVCSNAPSNAHYVGVGEISARCDWACDPGYSGY

YCVSPIQQLLDACGGEFGFALVLMSIVTFFILLGYACRNRKEPSYTRTYNSRSAKGERQH

LLSSAVANSQRSLFTSLFRCFYWRRVDYPKLMERDLPEHMARLYFAGYNDPDSPLKLRST

VPPTLKKVLYDVEFNNLANRINRVLAWHRGPCSSWGKIVYFLVAVLCYPFASEVKQFRRH

VRVNELKRIVGKYNHACMKGPRARGLLNAVKLGYCADYSLVYLELLYKESSQSVCVPTTK

IGKPSLPLVLLFAGCGTYFSPFYLDPNDLLIRSIPQCPELTAFIDEPWIEFVAELNKLLR

VVQQNKDALVESLLPVAVYLEKQRAMSAMGSNSSKLGGLRIYLGRFYVQDELDMGEEFKL

GIFLTAANESSDSSSNSANLVPSHIQPSCSKRYNKYPKDSHRFNTNDVYGYERGDSLDYL

VSRRDDGNFDNDAMLNDMEGWETAPKDRDSSSLNRSSESSHVLPLNPVSSIREEALRIRS

NSLHGDASNINGQPGRSGTADDVLVVMGAAGSTKAKQPSTAVHHTIYEGWLGPVDASLPI

PGVLICADELRERLADQSFRQMLHVFLRFHLLPRNLPRSTSLSLSWMLSISLLTLLMVDL

AITFAILVNLKCVTEGEVDHDCSASIMVPVLLVPPLALVMSPIMGIISLALSSSTFTRRF

SVWNALSMISVGIAILACIAQSSRLVAPWFAGPLPLLPVIGMGVKAGQAYLVERYIAFQE

TQRRRRGWRGIMKRRLSDASIPAESP

>contig41536 Frame-0F

MIPHGQPRSQGNATSSADFASLH

>contig41954 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57346.1|) 1e-154

MELTPSLKDVLKALASSLYVAATSSDHGARMASLSCMSGLLNIQETIPAILDWMVHTSDP

DEVVRVAHVSIACGTWLLRRRSFVEELLLMASRPDDSTRTLLRLEAMSLLSKIAKNYSLA

LNVFWHGLAEFMLAAFQDMDPNVRLQAVKILENYIKGGNCSVEGVVATCPTGEHTSRVDC

LEFMATHLVRAFFDTSHHVRASVCACFTLLTSQDWVYLGEKKSSRRIPVLAAKSGGCTED

DSGRSCLDSYTRIFLQIPKDSSPVVRAAGYRLLGSLCLAPTFKTRAFASSVVTLTLEALS

DPTLNVRVRAAWALGNVCTTAGPV

>contig42025 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60907.1|) 4e-15

MYAAQESESLQRSSQMVADLKSLSQSILGDLGAQRNRMKVGTSLDHNNRQH

>contig42212 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62796.1|) 4e-61

MGVTSTASRKLSNNLSRHNRRRAMSIELPEATAWLENLHLRMETAVKNRRVHYEVHATYA

QPCFQSGDVAWVVSYPFDAYRRFRKQLLRKLQPGHTCLAECKWLHSVVKKHFPKHQFLAA

NASRIVEARRESLSRILKILQNALINRGNQSCNVLVNDVCYDFAAFIFGNHSRLPDFSLH

QHRHHNATLSIAYATQ

>contig42498 Frame-0F

MTRLTLEEEAFKGTRVDDDISNEMYKRAKQGYSIGLQTNLKLFSEHSPRSRQLRHLWVWV

DQVEMLRTIQASRMEQSRASSVGNSTTNAGMIGPLRGWPVDPNALVYAGVKNLLKVSGDP

LTTSKANWSSSVTDQEDSREEELIVTIVSVMKTDQILGCLYFEGLGRRLALLACYWDPDS

GQGGARTTIVGGGPGLESAAGGRNMHRSSSSTWNSQKLFDENARLGNRPGFENGHHELSS

ILNRCEVEGNYARAAALAVFHGDLNTAVTLLQKGASWVTQMQHLNIGVVSPYSPDLLQLV

AMSVAGYSTSIASAGGISLWSTMTQQLLKRSEIVSQANPRYFHAMLSFLCVISSTFSSTT

TVNSIRA

>contig42911 Frame-1F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72305.1|) 1e-07

MYGLPADAQGRTVNLVVLDRFSKKVDLLPVAASIT

>contig43134 Frame-2F

MLTRCTMFCSVTAIYATSLVRKTPAFELLLKFGPALSQEPVIEKTHFDMSFQ

>contig43206 Frame-1F

MADAELVALVNQLFECQDQFLIADGEIPAVQLKGVSIAYEYSRLLLHKVDFVRQTHEHWV

LLGPNGSGKSSVMRVLMQTPGHGLSKGEVSVIGEQIRAIGSVSSKKDIYMGKKPRLEAIS

TDQHIQILNNQVEDQTAFRLVEKNAASLKAAKLSQRLLALPDAVQTHAFSQLSQGEQKLV

LIARALAACPRLLILDEITHGLDPFNRAHVLRVIEAIGQHATPRTHLILITHHEEEITPC

FSGIFEIRNQQLVERSRQVDIKP

>contig43417 Frame-2F

MSPTSSRLAPSYSCMFEGSGGDDVEKLNHAALLKCLDDRKEASKEEQNLLLPQDSKAQGQ

GGRSKVKHKTFTFEYWRLRYVMEVLVVVLVVAGCLRLLSINASNRALNRAPSFSLHRSGG

KLMSGGHRLRSFLHHMKSHPPVHSKITSDVSIPLGIDVDLERAMDIYCRGPLLHAVQMTN

VFSDSKHFVDMPIKATSSAFDILVDFQRRELSMTDYRPIENATHKEELRRFINDHFDPPG

TDLLPITPFDFQGLTYPPMVSDIQDEELRDWAFEMHHIWQSLGRIRNPKVKGSLLGSRNV

EDDSLNNVLIVPGGRFRESYYWDTYWIVQGLLVSDMPVTARGIVNHLLEYVSDYGFVPNG

GRIYYLTRSQPPMLSDMVKLVARLPVNGNESDYDTEYLQAALPILEREYDFWMQQGPCGH

TVELPRRNSSADATGKTTYVLNRYTSNANHPRPESYREDVFVASEIFDRTMAMEDGNAAA

TERYKDRYYNNVIAAAESGWDFTSRWQRDPLDMKSMVTSAVVPVDLNSIMYRVERNLMEF

NRHLGKDKRAEFFEQAAAQRLEAIDAILWSDKYKCWKDYDTETNSHSAIASVSDYTPLWA

NAFNASDFDRLKQVVASLKSSGLVQVGGVQTTTIFSGQQWDSPNAWPPMQDIVVEGLLAV

NSVESYKLACDLLQVWTKTSLAAWKQTGLMFEKYNASAIGGLGAGGEYFPQFGFGWTNGV

MLKFLTIHQDLLLPA

>contig43509 Frame-1F

MRPCSIRFRSLNCFELLWQAYASVASPYLLSDSGRVVKM

>contig43783 Frame-2F

MTDWRVNPFWLPWLLLLWWTQSKTWLRRWIKYWLLRPLMRLGIQLADESDEKDATIFLES

DDQQSSDSALPGGLVNSGNLCFVNAVLQSLAAIPGFLNGLDRALRTRSQLIRAPQTDDTQ

>contig43884 Frame-1F

MIYSFYIYTRNGSCLYQEKWNVHGGKSVTYSDPEEEKRLLFGLLFSLKEFVGKIAPTTAG

ADTIGAMEANVAGFCASSEGMHRYQTDTYTCHQYETPSGLRFVMMTDNQAGDLTPTLNYI

YAQIYMETVVCNPLSDTKNGRPITSQLFRSQLTQYLENQTCFK

>contig45518 Frame-1R

MEAGPVRSSLLPPVVQAASPLSELYAAPHSVAIRLPSLAPRLPTLPSLMSTFRAPGVYTN

LSPTRASPSISNLLVTSNRQPVENYYLLNQQQVYAPGAPSTILYHSYTTPASSMPISMTT

MQPQAIKVQPKKKRKTRICKFDGCEKYVVDRGLCIRHGGGKRCSVEGCSCRAQNRGLCWK

HGGYTHCTVEGCSKRAKSRGICWSHGGGTRCKTGGCIKIAVSNGLCWAHGGGKRCLIDSC

QKPAYERNGNLCAEHCSQRTQPPEAI

>contig46029 Frame-0R

MEMYGIHVKIANATCNVFSGNVEYTSEHLILLLIARQISTLYIARNGMTIGPQLVRIATW

PLCILIPAVEREY

>contig46326 Frame-0F|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY54166.1|) 1e-145

MVVSENHDELLPLVQGVHGGNCVPLAEDVPSVTSSQRRNDEDWVVFLVVPGLARHGLDAA

AKIEKTLKCSALGVRRVQLDRMDNLARIELSCRADEALEAALVDEVRRVTPYQFVAYPVW

QHRDRIVRLQVDGMRCMRNCGWQVIRALEKIPGVLHIHVDSKSMTAEVALAKGCTATEVD

LIKNIRAANSRFNASIVKEKKRRAISLPGAILLNIVGMSSAINCATKVEAALRAAEGVIR

ATVDFENKRATIILEPESNVMEKDLIEVVRRAGPKFDASRYEYFNNDGDSRVVYLTINGM

SCAKNCARKVQDALNSAHGVMNAKVDFKTKRATIFLESSCDVTEKNLIG

>contig46591 Frame-2F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY65715.1|) 1e-135

MTDGMLVREALLSPTLERYSVVVLDEAHERTLQTDILFGIVKRAMRTRKDLKVVVMSATL

DVTLFQTFFEDFRPAIMQIPGRMYQVDVFYTAKTQSDYLDAALVAVLQIHLEEKMNGGSI

LVFLTGQEDIETLETLLEDYARSLPADVLKLMVCSIFAAMPREQQMKVFEPAPDGVRKVI

LATNIAETSIT

>contig47303 Frame-0F

MSHSLERVRALGMRVGESLSCVIASEKPLNFDLTEEDPIKVYGYPAQLEELETEMAELHL

NKHESSEPKPVEETQGRRKKHSQRQVKSYILDPDEFVESNDENDASSESDFESNTSNLEE

SDSDMSLEPYDLEDNEEDLKTKKPLYLKDLIAGLLAADDRETTEGALNEAETLLRRQPRD

LNDKAHDVVRALLRLEDKYTTPHFVQLRLKALIAACALAPTQTVPYLVSQALEREQVLQS

RIDVLQAMTVAAQELSDRGGRSCHSTSPKTLLNEEKDLTTRTMACFKTRRWGYRRDPLVH

PTRNAFAPYAVDFFSPLLFGYIAYMRQHSDNAGKARNEIEETFLAHLLHALANFVECAGH

SPQTLAMAKCLLEFASNERSSSSAEVRRQVLFSLSRVLLVVPPALLRQEVGQAISEVVPW

LHQVQNYDPDAGCREAAQLLSVYAIPKPSFSLM

>contig47435 Frame-2R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY61609.1|) 3e-70

MRMDESYGRAYTTSQRPSALHRSIEGLPPLLQAAQAGDIVLVNALIVQAGTDILRRDPMF

GQTALHFAIRSGHLNVVQALLMPHLRGSIVNVADNRRNTALHLAAAKSRRMTKVLLDCGA

EVNFLNMRNQTPLGVHIL

>contig47440 Frame-1F

MGLVVNCLNIGVKGSLRLVLGRESYAAGEVVKGQLVLRVSRYIECKEFSMHVVGAEIVTW

TDGASNTLTPYRMRDEFFYEDMYNVDPIPRTLEPGEFHFGFSLPLSDSLPPVFRVAEGSA

GAMRNVHATVAYTIRARLKLRGKVAAVIETTHDLAVFRPSLCHPVRSLQRLSADEVRLLS

LIKSKGTCEVMVTLDRDVQISGSTLSLQARISNYSSRDMHSIFVLVHEDLTVELPHRRLN

KGTRTVCTHEYSGVAAGQLTDKVLHLPLIYDESRQPVAPTNSAAFIRWQYRLEVKCRFLL

SKSVKVEMPIIILRNVGAPPASVTV

>contig48052 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54821.1|) 1e-74

MCKLHGGGRRCKIDGCMKSAQTGHLCIAHGGGKPCNVEGCPKTAQSRGLCKQHGGGVRCK

FQGCTKSCQSGGFCRGHGGGKRCEYPNCTKWAQKNGHCAKHAQEIATQQLQQQQAIQAQM

HQQLVRP

>contig48566 Frame-1F

MPPDIRILELERKRAMTTAEHEVVEKKNEATQVVEHGNDEVLKQKKGVKTSKMIKTGREI

VDAFLLHLRKQERIASYKSQHEAP

>contig48588 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60766.1|) 3e-11

MRSRITLTALLTIAFSLRLLQVRAAACAEICYTTELTGFGPGGTAGCTC

>contig49411 Frame-1F

MIAFVDHSKRHRFVTERKTAANCFSNDNDRGISNERDYESTLYCNAGCCMYPSFAIETHH

VIIASFMSCSRHFLNA

>contig49675 Frame-0F|Blast-condensin-2 complex subunit D3, putative [Phytophthora infestans T30-4](gb|EEY58314.1|) 2e-45

MELEEALVRALRPLPLGSVPESAISSLFDTGGTASVREEWSDGVTRRHLRALDKVFGKYL

RCQSTDEHLAHFWRFWPLKKLLTLYTRLKKAVKIKTWSIARSLHYYKPLLMYATSMVP

>contig49998 Frame-1F

MQQYALLKCSVEMEIKQKYKSRRQKESIRLKVATRKAQHQKLPAPTKTDKQDKLCAKSQA

KPKVKLVSPANTMLCILCRTQRPPDGP

>contig50321 Frame-2R

MIEKRRQQALEKRRSLSSLPGTLTKEQQDRIEVRRKEALEKRRRAQQYEKAHAITAPSPN

VIQSDVIDKLQHGMHKTFNQINQEATQVSWKKPSEASVDTTHCIVIPES

>contig50453 Frame-0R|Blast-Glycoside-Pentoside-Hexuronide (GPH):Cation Symporter Family [Phytophthora infestans T30-4](gb|EEY58275.1|) 8e-35

MLPKYAVQITQFIGPVVGVLLGPSIGVLSDRSTSTIGRRRPYLIVAGLLSIVCWIAMSYT

REMGEALGDHGTGIAGEPMSRT

>contig50592 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY57551.1|) 1e-109

MTYLMYLMKMLDPNEEEGEDEQSNRKLSKSHNRQKHRDLEMLLHAATSSSRQLRSMIIFV

STCKMCELVGEISHELGTKCVVLHSMMSQNRRLAALGKFKSGICHILISTDVASRGLDIP

EVDVVLNFDLPRDADNYIHRVGRTARAGRSGRAISLVTQHDIELLQNIEAKVGKKMDDFE

SEAPEKKVLQLLNDVTTASRIAKMKLTERGFDEKVQARKAKRQEQYSTKKVKT

>contig50840 Frame-0F

MEKLRTRCDLRRMRRVSEAASLPHLGHALTETMTCRFSNAVLSIGRRALALTRCRNKEDN

AIQSVDESPKNDPTTTIARPVVVTIQDGDDETGSGDENEQHAMLVAESSFRNESTAFSDE

LLAVIWMLLARLDGYCGQVLLQAAEDGGHDKIRAWIVSLLTWGGHVAPERRHLRSLEPFD

RNGIMILPLSVFDAREMLQRIVEQCPSIKFDYDIGFVVHMMNYLSDTLERRWRQLDSAKI

KDPKAALRDEKLIDQAMSMVIYTGV

>contig51191 Frame-1R

MLEWTRPSNLNATALAGILLCYPCVYTMAAGTKATHISSEQLNCLAMCPLYLLQTSIL

>contig51429 Frame-2F

MCDETCQQQANLPGRYIANSSVVRGLPPRTEIAVSSKTCMLVGYHFHF

>contig51542 Frame-0R

MNDYEKLHELLKHYLENIDIVTTDQAIISSLVEHYGMPAVSRYVDKISFTFPEFVGATNF

KNAMLDSFEQEKALSELGSRENVSQGC

>contig51726 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60668.1|) 3e-47

MNFALVTGLFVACYAAFFLQNALDTWVKHHWTAPVLAGLRQSSCCTTYSDAVVYLHKRSV

AIGA

>contig51861 Frame-2R

MLLLFAIISYLLDELRRRQDIMISGVQVLTVVLQWLISLIFKRSEQINQRAFRRGSVKAS

FGR

>contig51928 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66855.1|) 2e-07

MVDSSDDATRNVLQYVIFALLLVMVLFIFLFTLWKYGSYRERLRDIIW

>contig52213-0 Frame-0F0

MSQNSRFERKFFIPPHTMFQPLTRHFGILRVATKRPCWSCFPFILVMFHQ

>contig52213-1 Frame-0R1

MSCQGLKHCVGRDEELAFEAAVLGHFDGKIHCRDQFAARVIVTLLGKVGMFGSIAITNSR

ELQHL

>contig52367 Frame-1F

METVAKHSGAASCTQTNHAHHQLDSYDLDEVDMAFDPTLASCCERDEQEYKKSMKVKAVL

TANDPTSGAVRMRQQLFTLPPIVTQQPLVLAPQVSQLKQALISDSESDVDDFDESDDDLS

MEVMLAARRQELEKQMQNAKQNIAEGYGVALDAELSQLVQELRNEPEVPRVALVVDNSAA

KTAQYLRAMRNKMTEIAQRFLGTKFYIVILARDDESLRVLRIGSAPALAAFRRGECVNSL

ALDLKALLSDLDVLWEARYLPWLIKSNVLTNERQILKGCQNKASRKEIIKKDESEHKDES

EHEGFDCGVKNCRLRFGYEHEHVGSSQLVKDEIASWRQTLNK

>contig52437 Frame-0F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 9e-10

MTMHYTASPHLTSIEWQDLYHLSAVSEEVDVTSLMRSATPDRQRLAIHELMDRELAD

>contig53005 Frame-1R

MYWSSTKMGDIGQRMIRRTCTSYSRQRKGW

>contig53070 Frame-2R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY57525.1|) 9e-53

MLQPVGNDFLCCPRSSLAKFARTGNWKVLRENTAAKHEAAANLSSALTHSNHGRVLVGLM

KHMETT

>contig53368 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56891.1|) 2e-78

MTRDTTATFTRSRPLLHYKDLEISSQNRKVRFTCVHASENFLACGASNGSVFLYATSALS

RSEGDRGPSKYHLVKTIALFSNDRMAITCLCICPLQKRLMVGTMRGVVYAIQLADYHKIG

EKVEFSHDFHAGFPITCFLWDTRGTRLFSACNAGLVCQTVLRAGVSAIFGSAD

>contig53386 Frame-2R

MRYLLRVYELDDEDITASDKRDTMETKLPMIHPVSNPLQLSPKTVIPDKKNIIAALLQER

PIKNARSSASTLLKEVQLPRQLQSHFQQSKNISTNHDNST

>contig53522 Frame-0R

MTQDGAIKSIQEPAPIPRGRERPPGSRNKENTRTRRELCAFESRVLRAKYN

>contig53597 Frame-2F

MKSSADSKVVTARQARSTSIAEILPNYSYEPVSFTHQMAESSHVFTRQAELGAASQASTD

IPALSQEVYEGESQQLSAITSMSQSSFSETPSQNLLANHGHQQWQTEQTPSARISPSRCC

DNENVQK

>contig53694 Frame-2R

MMLLFNDQEPRFAYWIAKWHLFSKNRSVSGMYQSTPDLQVGLLGIGSAQLLARVAIYIS

>contig53720 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58712.1|) 6e-27

MKQSRKHVEACIQSLHREMMELDAEDVLPEYLASDDMQDLVAQGFVHVTKKAPTSTSIVA

DLTHLKLKL

>contig53971 Frame-2F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY54394.1|) 9e-37

MLGRQSNVLQALGVVKGTPHGAFPSLVRYCTAELGDVTSLSVSAPSLGPLPPPPIATEST

>contig54097 Frame-2F

MLRLHEELFSHCKNENIRILGLRI

>contig54394 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61820.1|) 3e-53

MKVECISFLMHHIVKLSKWQQRGGYEVSTQMEIDSMKKLLAHAFSTFSVTQVQAFLGKVI

HKDDHCYLESTL

>contig54570 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67851.1|) 4e-30

MEAQYSKDKHMLNGAIEKLKTLHRREMQQVEARVRIDTEEQVIRNLFPEMQASLRREHEE

SLQALMLKHKRQLVQMEERL

>contig54963 Frame-2F

MVSDDEFEYSADELDDDDVDWEDVTASQQTANSAALVVHETAIHPDVQSNDAPQIDWDEV

NRAL

>contig55379 Frame-2R

MNAHLDCCSASLMHELSVALPLIVPCNQLTSATVISAT

>contig55915 Frame-2F

MKRPLTCHFRPLTTKLFFYQQISFFLG

>contig56275 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65329.1|) 6e-12

MAVSDYYNDQIREIHANQHDMGELKE

>contig56648 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54790.1|) 0.0

MRSKSNCGYDLRAITDRSWNTVNQLRADFPGISEDELRLKVQNTQLMRSDISIATNNCME

QLIEESDEFTAYMTRERIRTAMSGMINELISTGTSKNGSTEDANQFMYVAFSKVLISLAV

TGLDMIGIMGTIAAYQQKFCGPTNFIGEIDDGTDPKTLGLTTIEKAFKGTSMVWRRKGDG

VVTVTFESSDTKKVFVNIMSGGNKIGELYVDAGKTVRWVSKVSALAGKTLYFDRWRAGIL

GLPGTGGGSLLLWIPHASEGGHLDVRAKLHDSDSSARPK

>contig56741 Frame-0F|Blast-pterin-4-alpha-carbinolamine dehydratase [Phytophthora infestans T30-4](gb|EEY70438.1|) 3e-45

MHRLTTLSSTSLFSRKLSTRAFPTLLTEAERHIIFQKLTNAWKVVPNRDAIRRSFKFQDF

NEAWGFMSRVALLAEQMGHHPEWFNVYNRVDVTLSTHDCGGLSQYDADMAIAMNSYAHAV

RGKETEVKSG

>contig56925 Frame-2R

MDDKSRHVATCIKYECTCRMCPFQAAYTSLLRLLRVRGFQQLYAPPEGANSALYCVLYRL

QQLNDLDKRLYDAFTEFPPPSGGTIEAQVAMQNEAIHRQLATTVELLRQTVANYGLLHVD

TLSRHFHMSIVDLKKRLHEFQSRDEMRVGAVELVILTTMLDLSITLITNDHEETEQQIMP

LEGFRSIRNGGRVAMTFGYILPTLVCLNGYYLLAEPVAYQDQKESSVVTKRQQSRMWLGI

DEMDRCFMAEIELTVATRAETFSPVFDLSMADSLNSAILSAVWDDCSHNPNTFHLFERQA

RQFGKGRTTAHGFMQYLEVAFGFEGATYLVDFLLHVLPEKDLCKKLLHVRWMRVHRQLAK

RVSP

>contig57081 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65370.1|) 2e-57 NOT\_ORF

MIASVSASSVSGSDNHNHSVQASTQPLDLCGLNDRHHYDSEFAALFVSGVRDFYDKLFAL

CVEKNHKAKGSNKTKNSTSSGHSKRQEIKSWFLSSHDFDAFVDHFENSSLFKAFEKDKTK

AHEETKSQARSLHRSERLSSEHEFNSLKSSRSARYSPTPKAVVNLNSSQPLKSFGSFNSL

MAFNRTPRGGER\*RR

>contig57188 Frame-1R

MTKHDWPKNVIILILCHFLNYMATYKFGEPPFLSVRHLWRLQFSMT

>contig57302 Frame-2F

MLSATAKRMHARSMHALKAYDKKEQCLLVIGGNGF

>contig57593 Frame-2R

MSAIISFAGSAELQHKHVDFLPGGAAA

>contig57654 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67962.1|) 7e-13

MTPVNIRGDASAARMWTRFLAPYYVCNTVALLMYIPIRYYYTSEALLKRDNFLNMPL

>contig59227 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62937.1|) 3e-11

MSSHRERLQRFYEKYNPEKLHEIDSVLERFKGREAQLFSSLVKKYGAEPTEGELVSE

>contig59353-0 Frame-1F0

MILFASMRRLKSNQTESETMPLVTVEDLYLCYCDVSKDVGVL

>contig00011 Frame-2R|Blast-NADH dehydrogenase subunit 11 [Phytophthora infestans]gb|AAF24792.1|U17009\_25 NADH dehydrogenase subunit 11 [Phytophthora infestans]gb|AAW62563.1| NADH dehydrogenase subunit 11 [Phytophthora infestans]gb|AAW67049.1| NADH dehydrogenase subunit 11 [Phytophthora infestans](ref|NP\_037619.1|) 0.0

MIDIYINNIKLTVNKNITVLQACNILDIEIPKFCFQENLQIAGNCRMCLVEIENSPKPVA

SCAMPLMQNMKIFTNTPLVQKARESVLEFLLINHPLDCPICDQASECDLQDQTMIFGSDR

SRFFFKKRGVEDKYCGPFIKTIMTRCIHCTRCVRFANEICGVDELGTTGRGGNTEINFYY

PKIFNSEFSGNLVDLCPVGALTSKPYAFKARSWELKKKEGIDVLDSIGSNININIFNNEI

VRILPKTNFNINKEWISNKTRYFFDSLKYQRLKYPLYKDDKNSFHKISWFEVLNIINNKT

ITTDSSNIKGIIGDLTDLESLFLLKKKFQ

>contig04778 Frame-0F|Blast-undecaprenyl pyrophosphate synthetase, putative [Phytophthora infestans T30-4](gb|EEY69127.1|) 8e-28

MAIENISSSCRATVMPEIERGLEVPRHIAVIIDGNRRYGKSKYGSSTRGHLDGTKNVMRF

TEWCIDAGVQALTIFAFST

>contig04806-0 Frame-1F0

MMEPPLCKYGGTPPSSTYTNILPMGSMSWSSHVVQPPHPSLSVATPLRHPASTPSP

>contig04806-1 Frame-2R1

MVWRPKGKGEEAGRRGYSKTWIPLVEYLYTSTRVGFPHIYTKGVPSFQYCPEGVQKGYAV

YPRHFVAKPESCTL

>contig05755 Frame-1F|Blast-methylmalonate-semialdehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY64588.1|) 3e-33

MALSVVLFIGSSKAWIHDLVKIGQSMTVNGGMEPHTDVGPLISQAAKDRANALIQASSDH

GASILLDGRHVVVPKYPHGHFLGPTVLDHVTTDNPAYMNE

>contig06695 Frame-1R|Blast-40S ribosomal protein S6 [Phytophthora infestans T30-4](gb|EEY57856.1|) 1e-129

MKLNIANPLTGAQKVLEVDDEHKLRAFYEKRISQEIEGDVLGDEFKGFIFRVSGGNDKQG

FPMKQGVLSNGRARLLLSKGKSCYRPRRKGERKRKSVRGCIVGPDLSVLNLVVVKAGEAD

IPGLTDVQIPRRLGPKRASNIRKLFNLTKEDDVRKYVIRRKFESKTGKKNDKAPKIQRLV

TPRTLHHKRQIALKKVQQREKVQRDAAEYNRLHAQRVKEQKERRASEFAKRRSSRRASSV

KA

>contig07227 Frame-2F

MSLFTKKDLGLLLPDDTPGDPVSLRLTKTKEETEVFKPLHPKVDLSKKVSRYRAGHEPKF

FSGYQDERGFVTANSQVRAFSKTKAPVRVIPVIGTRRKRVEAQILSSTTSSTHVTDSREE

DQTFEEDKQKSSSDDVAKALQDSSSQEEDDSDIDRRRRMLRMKAMSREAKNDDMAASEEK

VARQPMQPQIVNQSATAAIKTKATDNNLESTTSGSSSSGYDTDTDDSEAADEIMKPVFVP

KVARESVNRQEELAAEEARRERRKQERLEARKLESRRLVAEVVQREQTGADKEITDVEMP

DDTDGLDPVQEYRDWELREMRRIK

>contig07735 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61381.1|) 1e-146

MWIGICYCWLKIQLIAYAFHGTAYYILSLVIIIVYFVYAFLAFGFHSGPLQFLFFDNISR

TKMTQSLIYKMARVCQNVSSRVECYILQQLLCCLPLEMRDCNAMTASSIPATHPLEPFNP

MPRNSNRAMGFSRVTSFFGRQLNVSIELWNHSMCQQWILPLSSKARATASRVKTSCANEN

VRDDAVFECRYMFVMQHDGLLLGFFLTAPSATLMVKFKHGKAMPFELLLRFHCETRSVLA

NVSPVVLYAESPKLVGRANVAQKNAVFRLLLHLNKAHGNSVDVSLRALRAKNFVDAGVGQ

VMKKKTRVTGSFSELSG

>contig08486 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55205.1|) 1e-36

MEFTTIIAGFSILLSAAIYAAYQVALQRAMGDDNITDTSTLLTLAGLTGLFAFPPWIIGT

LLLNASPFEWLHESFAFP

>contig12759 Frame-0F

MRVGAILSYLVGVLVSTTANKTYANCNPVCSKNETCETKSVQCVTYPCNPISTCVTKPMP

EPKCTLKCPEFETCRFDALDNSQICLGPCATVRCGSGYTCVAEKGKCNSPQCPPVARCKL

VN

>contig13147 Frame-2R

MGLTTQGAVQAIKAKGILVQGIQEFVEPSGN

>contig13288 Frame-2R

MTTLVALQESLRLGPYTNSTETKPLLTKSLP

>contig13741 Frame-2F

MNTAILKIPGKSAAASPYAREEQLKTMPRLLVIFLVAHLHISAFYGVDRMPQVEADKPVT

LGLADGTTRELSTAEFE

>contig13833 Frame-0F|Blast-malate synthase [Phytophthora infestans T30-4](gb|EEY65909.1|) 0.0

MSELNINAANVRVLGQVPDAFRRVLTPDALRFLAFLHEKFEPRRQSLLDARVRRQKELDA

GVLPDFQPETAYIRASDWKVASIPNDLSDRRVEITGPVDRKMVINALNSGAKCYMADFED

STAPTWYNQVDGQANLMDAVRKTISYTNPDTGKKYALNENVATLLVRPRGWHLDEAHVLV

NNQFMSGSLFDFGLYFFHNAHELVARGSGPYFYLPKLEHHLEAKLWNDVFVAAQGYLSIA

QGSIRATVLVETILAVFQMDEILYELRNHSSGLNCGRWDYIFSYIKKLRNHSKFVVPDRS

SVGMTTPFMASYVKLLVRTCHRRGAHAMGGMAAQIPVKNDPELNNKFMTAVSEDKSREVA

AGHDGTWVAHPGLVKIAMDAFDKMSGPNQISFVPEASKDITASELVEPPMGAITYKGLVE

NIDVSLVYTEAWLRGSGCIPLHNKMEDAATAEISRAQVWQWIRHGCKTIEGKTVTKQLVL

DILKDCVDKRSQKFMAGNKWTLGGEIMGKVLTDNVMVDFLTLPCYPRIVQLSSSI

>contig13846 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54784.1|) 4e-28

MQRNYLKGIRHCKQALDLDAHDAMIIVHMGQLYHALHKYDNALECFKQAKTLVRAAMADE

GRTEMLVRIEKETDKCEYTRSQYDLEYLLKVQTISNGL

>contig14010 Frame-0F

MMARSESTVVVGESFLKGFVDTSEFPILGDNVSPVNPDEHPSMHTCHPRFSVSKRKLAQS

PLSQTRSSSSSLAAFHASNTLPDRLTMMNYHTQELKGAVFYGWLWKRGHSFKTWKKRFFL

LNGVALTYYAQCCVIASDVLGGGTQCLDLPIRGGLRVAKVELSSLTVYGLQITSSSGRVL

YVQAGDQESREQWRKVLDDAPYVRSEMMGPISLRGTMVSDVSQRSYEGSCIRHSTINELS

ISDDDDSGLNCDMQGYLYMRGGLLYSWRKRFMVYTNGHLSIRRNQTLRSSYPLEAEKTFV

VLSAVRWNGRANGLCIRLENHKALYVFADHEADASMWLEALKSC

>contig14296 Frame-0R

MHSKASETKRLLMPDGLPFLEEATEFAEKFLEHFSTINKADIPASAYAQIERSLRDETPI

PRINEKLIKYLYFPKYPWVERELTLRNKILDPYRSDYFDFYLHYSIDLINPADVCVLAFK

DLKGLPMTFWPLKSFLSILISSEMTEFFKNYGFIISKNILKLRDDIDWVDFLTANQPEYL

TSTVVRLKNSLWMKWINEFKSPADIGELFNVASNAKYQPILDGYKNFIKNGGYTEFPRSE

YLKFVTG

>contig14432 Frame-0R

MASAALFGHTVDASAEVAETLGLLGLGGLYGGVGVGLGYPYGGGYGYGGYNPYYGANVAP

VGPVAPVGPVAPAAPVSNNVNSYATASASTYRNLRA

>contig16467 Frame-1R

MYPTMHNPNHFFVIFLQSSTLKHATRPQQFLLFCFRQSNLSYRNYDRTTNRNASTVRSKT

VRSREIPHKCLSRESVQNSSRYLCVQWPRPPLSSPIKFTCHHLNNVNSPKWPTPLSPRPS

TCTNILSPTIESFLFTHGNSRNRVKMSVYTALGNFQRRPRHTRFVVHGF

>contig17608 Frame-0F

MAGSNSQQQKCSIIKGLLVKCEKEKKDKGALSAEGAKYIIRGLQGKLRIGLAEKSILMGV

AYAFMTDKEYNDKEKQQEALNSVKKAFAECPSYNALVAAFYDVQKTSSSAPFLCVNNFKQ

VAEKCTLTPGTPVSPMLARPTKAYAMVFDRFEGKPFTCEYKYDGERAQIHILSDGKIAIF

SRNFENSTERFPDVKLAISSAAKKTLVSNCIVDAEVVAIDRSTNKRLPFQILSTRSRKNV

KVEDIKVPICIYAFDLLYLNNVSLLGVSLAQRREKLRELFEVHPGTFEFATSLDVKDCVN

VKNNSEAMEEAVDKVRNFLEEAVRENCEGLMVKTLEKEATYEPANRSHKWLKLKKDYLDG

IGDSADLVPIGAFYGRGKRTGVYGAYLLACYDPDTEMYQPITKLGTGLSDDVLKKFYDLL

KEKVVNKPPTDYAIGEGIKPDVWFEAKYVWEILGADLSISPKYTAAMGLVAKDKGISLRF

PRFLRIRDDKNSTHATTSVQIADLYRAQGITSVVNVEEEDDDMLI

>contig18740 Frame-1F|Blast-ribosomal protein S19 [Phytophthora infestans]gb|EEY53144.1| 40S ribosomal protein S24, putative [Phytophthora infestans T30-4](gb|AAY43420.1|) 8e-66

MADKVPVTVRTRKFLRNTLLARRQMVVEVIHPGRPNVPKAELQEKISKMYKVKDPNTVFL

YGFRTQFGGGKSSGFGLVYDTINDAKRFEPKYRLIRQGLG

>contig19259 Frame-0F|Blast-metalloprotease family M48X, putative [Phytophthora infestans T30-4](gb|EEY59998.1|) 4e-47

MIEQKSNAPFMKWTSHVIESEEPNAFCLPGGKVFVHSGLFKILSNEDTLAAVMFHEASHG

LAR

>contig19400 Frame-1R

MVSADLDGSTSSYKYLFQSLARHSHVFPLCSSNVILLATPTNFYQRLLHNIQHAETRISI

ASLYIGTGPFEKALIDAIIARINERPLLRVQVVLDYSRGQRGEPTANSVTVLAPLLKQYP

DNVHLFLFRVPQLTGLKAKLPSPLNETVGVSHAKVYLVDDMLVLSGANLSSDYFTNRQDR

YMELRDCGKLSDFYHRFVTLLTHFSYQVKPSSSKDMDHYTLLPPIQPHDSEDAKLAMRCN

FKKLLKPSSSTTKIDTNSALMDTWAFPTIQFSPIALNHDQCVLNKFVYHLPRDSQLLIAS

GYLNFPPFLSKLLEHCKAHLDIVSAAPRANGFFEARGVKGALPMAYSLLEQAFYERTLGR

GYSTVMREFNRPNWTFHGKGMWWKPPPQKHQSMKQCLPELTIVGSSNFGQRSYGCDLESN

LVLYTRNSDLQRRLQEEYDALIRDAEVVNEALWQRSDRMLHGFLNWKSGHWIRPITRFIA

AYL

>contig20606 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56027.1|) 3e-10

MMACVAKNVVAVQLFIEMGARLDLLNASGLNALMCAARAGKDPRPAAPAVPETMERSAAI

VEILLANGADVNALEKNEGNAALHLAVLSKNFNAVESLIKISLDLDITIRNKAGKTAMDL

GRQIFGESSKQMNDLLSEKWAQNFEESICLSAKVEQQLLALTAQEENIIALDEKPSLKYE

KKKNKKTKKKNMGLVKAPERLPIECGHKDKMKADSFIDSSEDDTLSLKQSKAKADQESAS

LYSELRTIEHEFDDDGGWQSVSTKKNLVLQGARN

>contig20798 Frame-1F|Blast-chromodomain protein, putative [Phytophthora infestans T30-4](gb|EEY56485.1|) 1e-121

MRAYEPAEDQPITSEICMESLKETARSERKERERQLQEEKHALLTSAESDERQKKRQRKK

EKTTKQRKRVHNKEKQKPNTKEKTVDKLSKPPITGLKRHMQLGSDDDVLSIEESSCSSSD

ESSLESTSSRDSVESRSKKPKNVTGNVPPKEVVLSSDEDEEPNDMFDTDDPDVYEVEKII

RKKTGESYGDPDLYEVKWEGYEETTWEPASNISKDLIDEFEGQPVREDVYVVEEILDRRS

KRDPTTRLKTHQYKVKWVGYEDVTWEPADNLPHNLRRKFDQKYESR

>contig21810 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58292.1|) 5e-38

MGLLEYTAIEIAPGTIEKAASGEDMIAALERRSVLLAHEEIREHVKGIIRRLAMMQETQV

DTRTKELVQPRVLMQTLMDKCRTSSYLFKQLFTFQEDDDTKSKRDGSGSMHHEEH

>contig22169 Frame-1R

MQLRLLLPIFLLGTSNCVVFNLNASSLEVTKIASRDSTSKSVAKNTPNFKTLPKSNATST

FDGVPFATKNEEERGWWSQLWYWILHKWAWWRRPTPSNTINAIPAVKIFKKKEWVGKDFE

NWLRRAVKQLRKEPYTKFTADNIHFHL

>contig22338 Frame-2F|Blast-eukaryotic translation initiation factor 1A, putative [Phytophthora infestans T30-4](gb|EEY59158.1|) 1e-54

MLGNGRLEAYCFDGVTRLGHIRGKMRKKVWVGAGDIILVSLREYQDGKVDIIHKYNADEA

RSLKAYGELPDTARINETAVDMAMEGDGEDDIGFDFDDI

>contig23445 Frame-1R|Blast-hypothetical protein PITG\_19063 [Phytophthora infestans T30-4](gb|EEY70155.1|) 2e-31

MFYTLSQKFSKGTTMAITIPTIIGVSYATFAFLRYTGPDLGGSVAGQPKTTSLAWQEASV

EYAKAQKANPIRHFKD

>contig23683 Frame-0F

MMELALVHWTLNTLRARGFNVVFPPDVAHYKFVEGCGFQPRGDATQIYSIAHSDLCLTAT

SEITLAAAKSNEILSTSLLPLKYAGFSHCFRTEIGHGGRQTRGIYRIHQFSKVEMFAFCA

NEIQAQAFLEEMVDIQTTMYAELGLHFQLVDMATEDLGAPAYRKFDLLAYMPGRDEYGEI

SSMSMCTDYQARRLNIRHKDLKAEGSKPSFVHTLNGTACAVPRLLISLWETYQQKDGSIV

IPEVLRPYMGGQEIICRTA

>contig23863 Frame-0R

MYNANATRPLEKPKHMYWCAALRVLHYLMGAQSHGIAYKRSDSNKPMLCAYCDANWEVTK

VLVARPLVF

>contig24075 Frame-1F|Blast-hypothetical protein PITG\_18705 [Phytophthora infestans T30-4](gb|EEY68804.1|) 7e-34 NOT\_ORF

MLYIASIFETPLWARRQRLNLQKQF\*WRHSTDIASGRHKIFSALLCRSKQAGRVGWPQLL

VRAKLKVKTRNALAHPTPRYTLYGLAGLAISWSKTG

>contig24930 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69823.1|) 2e-31 NOT\_ORF

MEVMNNPDRKAEAEQFLRSRVQPRSSDQDQNQ

>contig25102 Frame-0F

MAAFRSSDDIIGFFGVDIPYVYFQPDHEMKRKWVALVGSGATNSDTIQGYALLSLVVLGP

GDQSKLYDSAEDNDPNELLVKTKADINSMVLVPPRVTQEHYYLVVTVYRAEELPDMDYSL

VMHGGIDGYVRAYFSGQDVLETKKVTTKGSNDLAVLFNQELWFPVLLPTMSDNIFISVWD

WDMTADQLVANIVQPFSFKQVHRYPNQFKHIWANLYGPPVGYDTKSIPLQQMQNYPTHAS

SYRGRLLLSLRVEKNLQSINDEAHVKNILNVVVSPKMKRYTLRAALFYGTEIPVFTSKTS

WNRNTRMSLKISVGRHVVESSRVQNVSGICHFNQYIDIINAELPADLDQIPDIFVHLVRK

TMNEARCICFARFKAQDFFSEELKSIKPPQWVVLQKDKVVDELKDHNFTGNVLMNLRIDD

AEQNGYREEEIAQQWRQHASTTVSYTKYVLFVHIFQGRCLPSTDYDGLLDPYVKVACVGS

EGQVSTRMSTRDPSFYETVVLDIELPQNEQFLPKVSLQVYDWDRYDADDYIGGINFSLAD

FPRMSSTEYTKIRANGEYSAPRPKWYPLSCIKVGDTQGELLLSFDLIKKDTPGVILEPPE

SIRPPAEKAFIEIMCLGCRGLQPIGLMPINTPFAKFEVGEVTKTNQPKFTNPSSKPASRN

PNFLQRIVIPVEMPLDSLFAPRLNITLYDQLLGGFYKPVIGVCSVDLNKKMTFSNGISNP

LHIDESSNSSSRGNNPYVDYGDDLSTFPGTVPAAVLKAKSFSNLTDNKSIQVGATEYCSS

NSFGYQDDEEDELPHYMQQRETVSGELENMLKSPFETFALFRAARASRDEQGFCERTAGT

YRSIGKFKGTVRILKFRDDPPLFDLKQFLNPQPYLIRVYVLDALNLHPTDANNKSDPYLR

VSLGDGQHHEQIYNDRDNYQSETLTPKFHKMYEFKTFLPGASELKLEVLDYDSFAIPTLP

NGLIRALSSAIQNTVGGDDFVGATTIDLEDRWFNAKWQELGLLPGSSERRKPVEVRPLFA

PSSTRPQGCLRLWVDILTRAEMNVMRPLNISLPPPHMFEVRV

>contig25487 Frame-0F

MLISPDHVVTLSTKEKKHDPSHPQRVCTICAPLLQCFQNNWNAQYANCHKANPHEAKSRV

HLPYSRSLESACRSAADILGNFFRPEHGAESDRYIPVRFLKRAQGIAFLTVIKAGLLITA

KMGTGIVIVKLENGTWSAPSAIGTAGIGGGLEGGGELIEFMVIMGSKNAVKVFYRTQVNI

GGGLSVAIGPFGRDALAQAAASREGFNANYSYSHSRGLFAGISLQGALLSARTEMNSNFY

GQKVTPQEILTGAIPPPRAAQCLYDAIEQAKKGIARFEASETQRRRSASSHSQGMCSSCR

CQEFVAKAFSKKCKTCAHVHRVT

>contig26262 Frame-1R

MICAGGEVSEGICMGDVGGPLVHKTKSGDVLMGLSSMSDCNLDGTPDIFSRVSSAMDWLR

ECIESYTSYSDKA

>contig26684 Frame-1F

MYGEMLQAKVKENSGATDAWLLLAIHQLELVEGGLSDDFINSSNDDLLQQQLVILCKELN

CTTTRLSVDDANLKRCLHTLSRALEIEANAYCEALWLLYLHLCEQVMDRQTEIDMVEQAV

QFLPNSHALWLRYVSTFNYDSVGMVEGIHRRLLEHLAQTALAANGSKNSKSTLKKVSILL

AAIYLHLCIKLWYAGATSRVLELLTALLQLGNESLEPTWSSMVRSRLRCDELIVLCLVLA

HVLLFNELPSLIEHWVAASNCECIPIKDFIYTADILKNSSQGIKKAVGSQTLASYKLAFH

FFQSGCDAMHDSGNVIFNNWMLLLALQGDDKNNESLNAFFVEHLVTIQRFPGASLTAAKL

MGLTSTEAQQLMITMINQSSSTHFPKALHNYLFACRLQPALVIHLDEMFPDVMERLASLV

DINIDQVQKSVKDIMHDSCQISKSRALKSLLDNLLGAWMDQLALMWREAANHQFADRVTT

SKADIYVALDICHLMGVLLEISVAIDGIQLLLGSSSFNAISYEAKQLAWMQRFILQVDLL

QKETLQGLLWREYQARVSKLFRKYMTEMSVESEMMRQVTRKIKTGIFNNAVEDAVCDCLN

PEGNELLTYGANLEIFRLCSAAIAGPDKAAFHASCTDLFTFSSAFSLSFSDAATHEWELL

AARASLRKCLFGAKSQRSQILQALVAVDLRLKNMKAISSLLESEIQLNPLLLEPWCLAVA

LEILFGKRSDDRSKIIANEIEKRQVVYTCNTFGDDQIPNIEETSHLKLRGLCLDFIPNAV

LLQNKLVSLDISGNELLELPKGLRYLTNLKQLDASENALFEFPTGINRLVKLEELRLAHN

NLISISVPVLPRLNKIDVCWNAATNLSSSDIATLPKLDKSAKKIVSADELSIRSDLLSSR

KKILDAKARMTERDTMLYEDKQSGQLAKQIIRMSSLGESSPAVTPEFETRSASSEMPIAT

GNELITAADIDAGQSTEQECVPTVSSCKEFDGGEVMIVSTMNAVLTSKRLIIISLRAMVA

VISL

>contig27250 Frame-1R

MEMSSQSAIFEFNAECKAWHYGWTAPRGQGFSGCDAHHVLEVIFMKPMGSYMYCLERLHS

DQFTIYSSRRAGHAGTKPVVETFEIEENECNRTLKRKRVLNLESDRPPAASVASSNLTNL

SIHSTSNEVMPDIIGSSASPAMIMTETATMDFVDIINVPPLKMETDFDSMPLSYLATCPQ

LPTSLLNTAAPGYDHNGLDNLVSGSGMLQDQSIQQQNHHQQRHQEEQLSQQQQQLPIDQR

HQQLRNEQQELLRQQQQLIMRLSEQVMISQRQDLQQQMQQLHLNHQQFLGGLQSHVLFQE

DEPARRIVSTDELPWSELYNLFNPTPLSPATTDDDPDHDEDGIMPAIAKVEMSSSIPSMD

QAIMDCL

>contig28255 Frame-0F

MPLKWFRNYYHGSTTDEMTTKTKRRPHHSFRARLRLRTASKGQQPLENAITSCKIKDQRG

LSITIESHCRVTLDTISYPLQHPLKESTLPVSVYASLSPTHRDVRPFRFSSRRVVSQDQ

>contig28493 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56098.1|) 2e-17

MNANGHERATPSTSLSNAANEKTGYGSTNYSGVLVDVKDAYGRGDSKQSRLLHQLKTEMG

SHTHAQENHMMGGE

>contig28707 Frame-1R

MGKIKFVTDGLLLRETMRDPLLSRYSVVILDEAHERNLETDLLLGLMKKIQRKRPNLRVI

IASATLHVDTFVRYFRRKGVEKKLESGVNLSKVEAQRLQDVVAVSVEGRQYPVEIEYLQE

PCSDYLQKAIDTVMAIDDHEGEGDVLVFLPGQEEIDFVVRALNDRAPSHLLPMPLYGTLP

LHMQQKAFLPAPRSVRRKVIVATTIAETSVTIEGVVFVVDGCFTKLAFYNPITGIESLLT

APVSKASAKQRAGRAGRSRPGKCFRLCTQEYFHKQLRKETIPQMQRTNVAPVALYLLSMG

IHDLAHFDFVSPPSPEALIRALELLYSLGAIDTECRLVDPLGTQMAEFPVAPALAKVLLE

SYQFNCTAEML

>contig28934 Frame-1F

MKSSSLPVRLALLFGAVFALEDVKSTIAVFGNLGNYKLDPSVQHIPVDPNDQRLRPPPAM

IPATFLIHIGSSVFRDGVRCGKTIFTAFKRAVKPDRFRFGIVEQLLDTDPKCLDEYCKLA

AIEWPQDTECRYKNFIQVNPRPAAEASGCTTARHLQQKMIQDEEFCLQVDGHSIFTNGWD

EIMLNEWKRIDNEMAILSVYPHDLHDFVKENGDNNAPDWIPHLCTIVKGGNGLARIGSAS

IIHGSKFPQLSALWGGGLSFGKCHAERNVPIDSHTPWLWDGEEFVRAANFWTHGYDIYSP

SRLGTVMYHNYSAKPANFWKSSVDPAVKALNTERSHNRVRLQLGIDFKGQVDASELDKYQ

FGSARSLHEFFQFAKVRLDGFMNETNSCQQLHWVPYSNATVVEAIVANGWKMKTLDLAVY

DHDIAKAPQAQQGSRQKAAVDEVAPSQDMTETGAGEAEVVVTPLDVGMENNDGGGNDRPI

MRHVQPESGRPVETFGLMAWGFLAVVLAVLFVMLSNDRISHAIRQNFVSPQHRSRD

>contig29036 Frame-0F

MQAQNAFLHGYCQFKSLKPVNYFCLSRAPSFNPDSDDALVRLCN

>contig29159 Frame-0R

MWPSHVFSAFPRCVQPHSPFCQATTNTQTFFVPIYASRCLVQATSSKSRCLSNRTMRLIR

EARRFECENQRRESRRSQLKKWLDLSHQDVDECPEDEKQRHHVRRAPFSLPIIRRTTPVS

PLAPSLKRSQTPLAVKWTSCFKAIGRKDMQKTQRRVKFLENEVEEYERPEVTKEEKATYH

YSATELGEMETIAKQFVHRESRFAGQPRDTILEQGFLSLRMQAPFFQSKRYYCLLRGHSL

QLYSSAVHATKKTSTKTEMTILRVQDCQTLTMKKKFALFGAHLPTQICLMFYVIKTNGER

VIFTADTKSSKRNWLHSLTRLTYVGEGDGYTSTSRLRPRASSAPSSCILPSVPENEIEED

ACDDMTTLGPPKLDRRNSCR

>contig29252 Frame-0R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68831.1|) 0.0

MDAIASVKNYFEKIISDPQLEGMKALLLDDETKSIISMVMSQSQILQREVFLVEHLDASH

ESMLHLKAAVFVRPTALNIELLCRELKAPKYGCYHLFFSNILPVEALEKLAEADEREVVI

QIQEYYADYLAVNDSLFDFCLQDYIQMNVKIPAASIGGALLSTATAGVLRTDPVNNGKMK

APQLFQRSVEGLLSVLLSMKKRPIIRYAKGSEVAEKLAREVSARMQLERDGLFDFRRQEI

APLLYILDRKDDPVTPLLTQWCYQAMVHELLGLHENRVNLRDAPNVRKDMTELVLSTISD

TFFARHVHANFGDLGMAVKELVDKYQSQTQTHENIQSIDDMQRFLENYPAFRSQSVTVSK

HVTLMGELARRVEVNNLMDVSQLEQELACGDDHNAHFRDVVAKIKDAQVKPLNKLRLAIL

YALRYEMHNSVQLNTLKELLASSQGGGLSADRVALIDAFLKFGGQKARQGDLYGDRAGLK

KFMRAVTQGVQGVPNVYAQHVPPLAKKLELILKGQLLDQEFSVVNGGAISVRVNDYNGSN

SVKRVREVIVFVCGGVTFEEAMKVAEINDKAASSSSGQRVLLGGSSIQNSTTFMNEIASA

FIIKSFFENGGDNAIRNYDGKEL

>contig29700 Frame-2R

MKRGRVDVGVSKQQYAASLDAPASENDEEGAFPRAPMQVLQGRRILTATPSSRAQETVRQ

LAALNRAFVATLKTQWAHNKHDSWENNMKEYIIYAREIDANFGTHAGQILTFGSGDCGQL

GHGVEEESDLMVKFPRVVRPLATLSIVRIACGGLHSAAITAAGEVYTWGCDDDGALGRVG

DENVPTKVNGFGPQEAIAIRIVGGDCHTAVVSLAGKVFTWGCYRDKEGKQWCDARSAKDS

FLQKQLQPFCIEALENIADVRCGSSFNLARTNDGRVYSWGLGEMGQLGRNVDAEMKDSKG

KYKLDMVYQDHLQPKLVTFGNDSLPVVKAIGCGSYHSLFVLSSSGYLYTCGLNNYGQLGV

GSTENCTELQLVEDLSAKNVAFVDGGAHHSVILTSTGDVYTFGRADSGQLGMLESCSTGD

YKDRPQKVRIPKPRNGKSSEVRMVASGSNHVLALTESNAIFSWGYGDMLALGNGADRDEN

TPHELNWSKVLVSEKGKGQDFGKAKILQVEAGGQHSAVLAQACEDN

>contig29986 Frame-2F|Blast-phospholipase, putative [Phytophthora infestans T30-4](gb|EEY61139.1|) 1e-170

MWASLRQWRCNFESQVLAGAHSVGLVESPASMVPLTDALNVVTRSSQSPQQIDEEPIEQQ

REECEGDDMKENVAVFGRLCQGLPIDYSLQENEIEIANEYLFALTAHVIYWTNRDASLFV

AQKLILEPAIHDWHSICHEQILSGQERNCEINLHDKDEATTTSDVSSGSDGESLAIVDFM

T

>contig30078 Frame-1R

MDTLQKTSMHSPGLTARIKREVTYSAMDLQQDINGWQIFTGMTPSGHNDHVSWLHFPVAQ

PCVENTDLEFTDRQYGSLIKMLLLIHSVI

>contig30360 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65793.1|) 5e-60 NOT\_ORF

MGANANVCNGKGRRSLHVVELSIDMARITTSLIDAEADIDATEKHGFTPSMLMCFKVSLE

SSATLLALGADVYRIAWSSGFSALEFAVKSERSKLCEHCLSKGAN

>contig30474 Frame-0R

MVTQVTLNMNQMTERIDFKHELATNALPRILGVNELAKQKASKTRQASRAGGPTYVSPLG

TQQQSPIGWMTSIKDGGKRNKPEAPKFLLLLYEILDVENSRVIRWSEDGLALQILDPVTV

TEQILPKYFNHTNFHSFQRQLNYFGFRKWTKSKTDICTFSHHFFRENQPELLQLIKRKKA

PRRAHSNGAGSTPHSGNFGSVVVSELNKLSPCGKRKLSLDKESPVGDSIQSTEMLLQMNT

SANMPEPSINEMPLSALTTPHNASSNGPVGFSHDGLMRKYLPELNNVISPVAATECKKKA

KKLDKKDYDASAAIHAPLASPHEVSNSLMHSSSVRFLPSATNLADKNSSANADSKYAVAA

SNSSKGSLPTLDIVRSRLKQQQHIGDPKQQQHRFIHQQQHYEYDGLTGVLRPNEFQRLIA

PAIASGPEFLAQSIGMASVARAELSSVQSPVLSNSFNDPVSILLRIKKSRTPSGEGKDIS

EQQGRGANQNESLASLHNYLLGNSLYTNRLQAQLKFVTEENEALKQSLNSKKREVDSLQV

ERKALVQENAVLLEDKNKLFEINRDLLSKLFPQ

>contig32436 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61805.1|) 1e-80

MKMFRMIMSISRRQGPQTIAGRSQHANFSDSNVHSRTAEEWLENIRNLAKKDVLIKRTKL

ASFLKSVTTTEQLEASKEIMKIYEKKRLDPDSTAIGLFVKKALELDVPEIAFEVLEADYR

IGLFLEATSLNKLLFKFLVDKNFDKVFALHEIGRTKYNVKSTDRTYDILIRAAIEQADFE

KAISILKTAADSMKLQRVTCNNLLYKLKANDMLDE

>contig32652 Frame-1F

MIQAARDCDFVIASIVESTLEEVWKEKTMAYVFENLNLHHVALMECLRSRWFAYWARLAH

KFSKTDEATNFVFPWLSDYMKKNGVELLKSAMLETSSQDVQYLLSNVLSKHIEQLS

>contig32850 Frame-2F

MSSFETPKAAPCVAVKGKRPSLKHRSSDPEFSDAEMDDAVDLGENAVWAHLEEPIYSEKD

VEVFRPTQNGSSLPVYYTKGWLPFSADTLFNTLLDVRYRTLWDKNVHQIHVIEHQHVSDV

MYCALKLPWPLANRDYVYRRRVKFYPIENTFVVLYQAAHHADAPATRNIVRVETCTLRLC

IRNLASSRDTCDFHLEYEDDTNFSIPNYGINLLL

>contig32991 Frame-0R

MVARKESDCDSTIKKTKKRATAAIDNGKSSKTMSVEKPKTSVPGDDNKSESVATRTLLHR

CSREVRALRDKFELGVYDVNLSRIVNIVDSLWSDMGHSEMVSLSTALFTMVEIVDKIVIE

TTRRDRLMCLESVLGVIVNSSKLPLSARRKTMVEEYAMNCRQSIEQLNRQASRSDHGSSN

QPRAQVPAKNDTFWAQSHVRFN

>contig33488 Frame-0R

MKKAQVLLSPSKQMQDKISFFSLAESYKVEIGLAKFYPKKDKRLLDSHALIG

>contig33592 Frame-1R

MKMTKHKIIPYQSPFIPFTANANSFAVALKRSPLLYSAYMLKDRIYGGEQIRSEQRPASR

RSGTKNCTRFTVLWR

>contig33747 Frame-2R|Blast-4-coumarate-CoA ligase, putative [Phytophthora infestans T30-4](gb|EEY60207.1|) 1e-13

MTGQNAQGEEIPKAFVVLQYPDCLDSPTLGDNINYVAKHVAPFKKVLEVNLLSPYQ

>contig33831 Frame-1F|Blast-4-aminobutyrate aminotransferase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY69051.1|) 0.0

MALLRRCFNHRSLQSRRFVAASAHAFPATPTPSFPREYANSEVVTDQVPGPKSLQQLQRL

AEMQNTGAINFFADYAASRGNYLVDVDGNCFLDVYGQIASLPIGYNHPAILKAMRDKANV

AMLAQRPCLGVFPPADWVDSITNTLLRVAPHGLEDVNTLMCGSCSNENAYKAVFMWFQAR

LRDGRPPSEHDLETCMMHRMPGTPKLSILSFYGGFHGRLLGCLSTTHSKAIHKVDVPAFD

WPVASFPKLKYPLDVHMAANEAEEARCLDEVERLLIRSSKGTKFEESRIAGMVVEPIQAE

GGDNHASPLFFRQLRDLAAKYNVAFIVDEVQTGGGSTGKFWAHEHWDLENPPDLVTFSKK

MQTGGYYAKREFRLKESYRIFNTWMGDPSKMITLKAVLDVLESDHLLENVSITGEYLKAG

LFDMAAEFPALVSNVRGQGTYLAMDFPTEAIRNEFVRVIKRKGVASGGCGVKSVRFRPAL

IFQPKHAAEYLTMMHEVCILLSKR

>contig34140 Frame-2F|Blast-PREDICTED: hypothetical protein [Mus musculus](ref|XP\_001478231.1|) 4e-08 NOT\_ORF

MYNK\*SLVTGDLKNVTLSRI\*SCSSSRTCSCVQCSNQLLISIISKVSPTEEASLSFDASK

SNCASWTKPSLFFSSRSKNLYGAGKKTST\*RIVSSRSLDFKYVKHLSGSGMTKYDAIDGS

NSSFQLINRFS\*SFMPTSPPSFRRLLSISVSCE\*VFSSVTLSTL\*LYSGSRSRSFFSNGL

LKNVGSSRIQFASLTVSSGDN\*S\*RVDKIF\*DDSAISFEFRTLLASVVVLAFLLGFALYS

QDSKSAASSYSSFSKLQCGLNRSVTLFSVSATSWAYKFVAAFGTTSTISWANFSTSSMSF

V\*GNILSSTRLCDSSISDGLLIARDAAAPSNDAASKDANWEKAYKSPMECKFVETLRFIL

RPSYFRSCLMGN

>contig35136 Frame-0R

MATPPRDVREALQASLGWNFVFPSSESSAVRCLVAHPQDESQLAEWLVRALPALPPSSES

VSCSQAQATAHNYQPIYPCSDLETLLAHKLSFKGLEQHIETSKSLMFHQSHGSELQTLSS

TDVLKLLYTDIPLYVPTNNAQVTQGLFANHARRENPHLPLLRGVYTDPGQNCSYAIFKYH

PQSFQDVLKYNHSVLDGHPQVDVPSFTTEPQNALGDLKKRLVLYQLTRILAFLHTRGLAC

HGFTPRELFLSDTLWVHLAALPRILDACIHARKRPYPDQIQAPQLFRDIESYTSRSMTDR

WSTGDMSNLAYLLALNTAAGRRMEDGVFHPFVPWVTDFTAGPFNGWRDLSKSKFRLNKGD

AQLDRTFASSAVPHH

>contig36205 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64078.1|) 1e-24

MSTHSTNDLDSSTTSVGSSSHMSKESVASEPIDTSAVAAAQEAAGVRKASSKIQQLQGSL

GINVNPFQRPGKPP

>contig36348 Frame-0F|Blast-pantothenate kinase, putative [Phytophthora infestans T30-4](gb|EEY68288.1|) 4e-14

MQALSFLLFSTAVAMFCLERKRHRYREWCQRLTHKKLSESSDLGTSFGLDI

>contig36667 Frame-0F|Blast-RecName: Full=GMP reductase; AltName: Full=Guanosine 5'-monophosphate oxidoreductase; Short=Guanosine monophosphate reductasegb|AAN31473.1| GMP reductase [Phytophthora infestans](sp|P59075.1|GMPR\_PHYIN) 1e-146

MDTVGTFEMAVELAKLDFFTCIHKHYTLQEWATFAATHPNVLSKVAISAGSSDADLEKIT

AILQRHPAIRFICLDVANGYAEVFVHAVRSVRAAFPAHTIIAGNVVTGEMVEELLLSGAD

IIKVGIGPGSVCTTRKQTGVGYPQLSAILECADAAHGLNGHVISDGGCTCPGDIAKAFGA

GADFVMLGGMFAGHDESGGDSIYANGKLTKQFYGMSSSEAMKKHSGGVADYRASEGKCVT

VPYRGPVVATCKEILGGLRSTCTYVGASKLKELSK

>contig36689 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY59728.1|) 6e-31

MGETSTALAGSPEVAVPLAVVIGYGLARFSASASSELANAVFATVAQKTIRKVAVQVLKH

LHAMDLKFHLDRQTG

>contig36780 Frame-1F|Blast-aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B [Phytophthora infestans T30-4](gb|EEY53410.1|) 0.0

MAQVATKAASQPPLQLLRGSSGKLWEVCIGLEVHAQILVQSKLMSGAAAATLASALPNRN

VSFFDAALPGTLPVLNRECVRQAIRTGLALDATVHPRSLFERKHYFYCDLPLGYQLTQQR

APVASGGILRFELPASAVISEHINAKCDDVTRFDTSKFKSRKEKNEALIRRKANQSAQLQ

EIISRSVRITRIQIEQDSGKSNHDVEEESTVVDLNRAGTALLEIVMEPDLRSSLEAGHVL

RQLQHLLRHLNVCDGNMEEGSMRCDLNVSVRPTAMNAEADVETLHRALALRLTTPFGERV

EVKNMNSIRNMMRAADYEARRQISLIENEGKEVHRETRSFDAVSGETKRMRSKEGAKDYR

FFPEPDLPPLGVPEKLIQEIRDFMPELPDALKHRLCTQYGLTIYESSVLVNESNAALYFE

TIASRPSRPSKMVASWVLNDLFGHLKAINGDIGSSPVEAAELGELIDLIQNDTISGKIAK

DVLEVMFYENEVKKTPLEIVESRGWKQILNQNEIHAICQAVLNDPATKSNLDAYWKGKTQ

LFGYFIGQVMKRCGGRVHPELANTIMQEVLNKSENIR

>contig36887 Frame-1F

MRQRTKSVVTVREYFRMDGSGAPEQEDDDDSDDWMLIAMQGSCVNMIKPGEKGRARSSTC

DSLAETDDDSDSEESDGILRIRACSHDRRISFDDDINVVEIPARSTFDADYKHRVWYSRD

ELRRSQECC

>contig37053 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57730.1|) 1e-105

MSPEVAIKHMFNYATRQWSSTQVCINLDETPFSKGSLRLVYHLQDLSTDSSSSLMYGGSH

TDSHVAKLAIDPDEDPQTYFRDIELQAHCAHYAHVYNSYNPPKRVEFIPAWVLELLERNG

LLCAVEAYIPGEYRKHNNNFGSVSDDERNTPQAFSHFTYEASNHELLAVDIQGVGDLYTD

PQIHTLNGHNFGKGNLGVLGFQKFLSSHRCNSICRYLKLPAVNPKARHADSGTLPVQELM

NRDCVRPTHFDSRHYYENAPMLQKYVS

>contig38188 Frame-1F

MGKKKRRDEGGAGGDALPRRIFCYYCDRNFDDEKVLILHQKARHFKCPTCHKKLSTISGM

IIHTQQVHKETLKSIPNAKPGKESADVEVYGMEGVPDAAGGTSKKLRVDVPLMGAYSSRG

LPFMGGRPPPSMQFPGGVASPGVGMSMRPPPPRGFPGGGIPPPHMLVPPAFSPFAGAPQQ

WPRNLPPPGYASQHVITPPGLNHSNVFDTTVSTTIKNDLGLVYADEYVSMEERRALRPKY

AYKPLGSMTLTSGSAVA

>contig38625 Frame-1F|Blast-5-oxoprolinase [Phytophthora infestans T30-4](gb|EEY63846.1|) 2e-54

MRVFRFAIDRGGTFTDVYAEMDVLNAQGDIVDVIPNVIKLLSEDPANYPDAPREGIRRVL

EAMTGASHPRKKPVDTSMIQSIRMGTTVATNALLERKGERTVLVTTKGFRDLLYIGNQSR

>contig39334 Frame-2R

MIDRRYHRSLQVLSWVACAAMTSKLVLFTEFGNRRGHGKHEHVFSG

>contig39464 Frame-1R|Blast-acylamino-acid-releasing enzyme [Phytophthora infestans T30-4](gb|EEY53660.1|) 1e-110

MVTRNPVTNMASVFYTSDILDWGLACAGIQRFEAIYTSQKLQSCHQNLPPLTPEARLAIL

SKLWQHSPVSNDLSKVTTPSLFGLGGKDKRVPPNQGLEYQATIADYGVPTKVFWYPDDSH

PLSSVEALGDFTVNWALWLLKYNSI

>contig39510 Frame-1F

MRPRCINDVVGQEELLGSGGLLSSL

>contig39855 Frame-0R

MVPRAGSEVSFAIYVYFRQRRSSIHLSSTTVGALLVLLGIICWTPIAKRDLSQFKVMKNS

FFAAFTLEHNIRRCRQPFRTPAVTVLATFTALGADVVAELPRS

>contig40059 Frame-1F|Blast-cysteine protease [Phytophthora infestans]gb|EEY64276.1| vacuolar-processing enzyme, putative [Phytophthora infestans T30-4](gb|AAY43369.1|) 5e-73 NOT\_ORF

MAPLSASRLKGAMQMMDRKKM\*KELLFYMEACESGLMFSDTFLTSINAYVTTAANAFESS

WAAYCPPMDLVNGESIGSCLGDLYSVN\*MDDSDRTDLSG\*TLTTQFHCVKRETIKSHVNS

FGSSKLSHEIVGNYQSTCDQSPNEDSSDKKKN

>contig40143 Frame-0F|Blast-GTPase, putative [Phytophthora infestans T30-4](gb|EEY53631.1|) 1e-139

MNKFRPKFVYPSKVNWFPGHMALARRQMLAQINAVDVLIEVRDARIPWSSANPILEEALS

KSKPRLVVFNKCDLANSNMQQRIEKQCRENELGKATDCLFTSVTKGKRLHAILQWCNKHS

EAQFRSTAGSMVMVVGIPNVGKSSLINEFRRLSNSSKLARGRKRATVGPTPGITVRNDII

KVLL

>contig40352 Frame-2R

MGCSQSTINAHLHRRNENSAIELLIAKRPGGQDVGPIRVTGHMDKRSRDLNSLRLANERE

PIIEEDGVIKSKLPSDVITFDVVKVAADGNGVIFYHFCGTSTNDSTYSVRIVKRYSDFKA

LHAGISQLLVGGESRPALPEMPKANAWTYFCGRSDRIILKERMEQFVRILNALSKNPVAV

KSQIFTKFLLA

>contig40709-0 Frame-1F0

MKKSHSTESSYHRSTSATTRPRQYHGTPVLEEQTFMNNFSPPFNGVYLMDTSTQPDSLAA

SDGHCSQRQLPPVDQNGSFQLRRGTLNTSDGFISMDNNSNISGNYVDAMSLTNPMNATSQ

QPLISTPRAAQKNIVRVIDKDM

>contig40709-1 Frame-0R1

MPVRSCKTVRLSRCVHEVYPIKRRTKVVHKGLLFEHGRTVILPRSSGGGGRAVIRTFSTV

RLFHLSSPGLLLCVEAGTRSLLLTRSKQNEQRVALLAQQATQATKNVLDVCVV

>contig40886 Frame-2R

MRRIQHEAKEAGIENIISIYLISAMKRIGMKEIVEDVAKHRQGRDICVVGAANVGKSTFL

NSFLSHLVDRKWQHNHRKYMKMSEVQISELENEETATMLNIDDNLLNEATKTIEKGEKSV

KTPYGELYVAEGEDPEMIETSAEEDRQMTTSPLPGTTLAVQYLPVMVRNEVFNILDTPGL

ITDAKRQKLVEVLALDGAAKLNNVFPAKQLPVTTYRVRPGRSLFLGALVRFDYETVGDEN

AKNFLLLTWYGVLPGHLTSTERAEDTFVKHAGGILSPPRGLDAMSFTGPLVHSQNVYLKD

YVLDSVMVKSKQKKPKRTTIVELEIPSFGWLSVTAVDLDGTVASQTTLNRGKIAVHTCRG

LSVVPRPPLFPYELSDSKSTTWKR

>contig41027 Frame-1F

MQFISYDPNYNYVNSADEDEDMDAEEEEYSDEEGDYSDDDDTSWKVRRATLRVLTAIIIT

RPELLEQLYIHCAQPLISRFKEREENVRIDVFGVLSELLRATRKTLPSSSGTGTFYSPAS

NACIEQLEKRVIAIIVGANKQFGMKASVPSRCAVVAMLSELAMVEHGKLGPYIGRLMPNI

LHAVEDKHSDLKLDALSFLRLLVDTHTMEPYQPHIDSIVNVVVQCASGDWYKTVAKALGL

IQSLVRIIRTDDIKDSTYKPYAIPLFEAVLPNLIAHDIDQEIKEAAISSIGEIVAVLGDE

LGSRVAEVYPLLMERLNNEITRVQSIKAIGVIARSKLNLDMSPILVECTQTLAQLLRQQS

RTLKQATLTTLNEIVIHNGATMTESLHCKVLLEASLLLVDADLQLCRMSIALVSNSLRVC

PQLALSDTFSKNAQVKMLELCHSSMLQGPTLDALNDFFAQMTIKNYPGSSFSELFKTLMT

TPMEDSKHSVLNIARCVAGICAATTEENRKVAFATFVGDITQTESEKSKVLALYCLGEFG

RNIKLASYTDVKELILQCFDNVSEEVKAAAAYSLGSICVGNMEEYLDTIMLNLELGDNSY

LLLTSLREIISNHAAKPHHDFAMYIDRLLPVLQNMSARQEEGVRNMVGECMGKLAVTNSA

KAMPIITELCGSLEVWSRWTAVASFKYAMTTSAEEPAINMIFAHIDPFLAALKDEDLHVR

RAALLAINTAAHHHAHHLVPFVRERIFPVLLQATEIKLERVVDLGPFKHKVDDGLPLRKA

AYSCVETLLQLLPQQLDINLFFDQLKRGLGDQDDIQMLSHQILIKICYVQPGSIVGALDS

LIDPIEKTINKTVKEDQVGPEVERTRDLIRSALRALNAVSAVRDTDSHPKLNSVMAYAKN

NPMLGPLLETIRNERGKK

>contig41535 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66877.1|) 6e-72

MAGTVMMSSFFKGEERVKLMVKAPNIQELYVESLAAGEVRGKVVFVDNLLAEPQGSKGHM

HISKVLYGATKPYNTSIEASGFPELDWQRYFDVSEQTPTIVRIDSEAEEDHTRVCGLIVQ

SMPSKMTHERHFELEDLAFDKLPFLATELRNNTDMLGYINKLIPRSDITNKTCKRV

>contig42053 Frame-0F

MLAAYTTSASVSSTMIRHISWDAGFRFAGCIQSRGNTPSITAPMNILSVHVV

>contig42211 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62310.1|) 8e-14

MSRLQRSQFVLGNSGKNHHRGDAKTDSAAKSREVINGLKKLYATKLRPLEKRYNFEDFHS

PLL

>contig42912 Frame-1F

MVFRNHGMSATIVSNRVSRSNAAFKPRMFELLGTR

>contig43205 Frame-2F

MCFYGLSGARYAILATNELYTGNTNTGWRYDFAVSGVMSPEIQPITLAKRPLTLTLTKQE

LHDVLHFHLVVMRLACMGVQDAVRDVDIASDDVWDEFSEQNDKGYLIVPSIMKESEKSST

LSLDWDYVREIIGKPLLEPIWPLPTVKDANTVEEWICVPTHRLNVSYVVQALSDRTVDDI

RKEYLADNLVWA

>contig43780 Frame-2F

MVFDTDLLKTINYSVRNLECYPRYPPYGMK

>contig43869 Frame-0F

MTTTSCTELKLSISASVGVVTICGGGNGAHVAAAYLSSKGLRVQVLTRHPERWAQTLQLS

TAGSSWEHKGVMTGSLSLVSKKAKHVIPQSDVVLITAPAHVHPAILEHIAPYLKSGVKLG

ALFAQGGFDWAAKKALGVEKLAKIDMLFGLQNIPWICKTIEY

>contig44877 Frame-2F

MVCRLTRGSSKTINILSYFRSLRKSTFINKSQVVQRIVRAIFCHICAYVTAVLTSEGQEH

EHIYFLQNINICWLARGVHYAASACMCCCAWQTSVD

>contig45078 Frame-0R

MYMRGGVDSAEVLPGMADGASSLRSSAINAANFQTFNKPTTDIRGNTGRRPPPDSYTCNR

CGTKGHWIEDCPTKDLVTPAGQMQRKVPPEGYLCKRCNVPGHYISDCTEPKVPPPSYTCH

KCRQKGHWKQDCPMDGNGTINALLSQIRPPGTLMNSNVPMSTGGVGSGPLLPLSAPNYPP

RGMMAASSIPSGAPGLLVPPPPPPHILAGMKRAREDDVGGGATMLPPQMSGWPPISGGQS

GPPLGLSDPRHLSGQSDLKKVNRDPRRR

>contig45229 Frame-2F

MSLSAPDIGRSTTASGSAVYESERAVQEYLQFHYEEPSTTVPYSFAPLDALQFLPRTVER

CNNISPSTQHDRALDIGCAVGRATFELSKYYDEVMGIDYSYHFVDAANQMKEKGSMEYEA

HIQGDIHELRRVKLPSGVKAHNVKFCQGDACNLSPS

>contig45474 Frame-2R

MVSTIPSAIGMKSSVSIISTLHFVFRRFIYYTLINAFICSVALGSFVTVSSLTGKGLLIV

QIYIATLLRILAPIKWFEWIGTKKSHINGAKRIHLTKIQIQSIYWRILWLVVTTEGISFW

FAKQTAVPMQSRLTWKSFMLEYASFIPKSLVFEIIFDYFHYAMHRMCHYSSWLYVHVHKQ

HHRHIHPCPLSTYEQDGFDLCLTNVLPFCLAWTLCFSFSEIQLHMIFAYKAYVEVAGHSG

LEIKGFSFPQMPLLNYFTSFGLRVHDHDLHHTIQR

>contig45672 Frame-2R

MALHRKQRGITDKAPQFVRIPTSRSSDRSIAFSVHEMHSRSHKRIVGGDQPRKISSLQLR

ACFVLCVLLYFGAIYFADEIAGIGRVVGSHQTGEIVFVQSLRPRGRGSRRERKSFERTDT

DDNNLKGPIASSVAAITLREAESQPVKQDKSLLNEASVIAPPAKNITGETSKSVSAALRH

QSEAQTEVLNSTLKTVNTAAKKSAVEVVSKGEDVDSSAAELGQPMKDPPIKRARPTLEHN

FTLKQERDDRQQRGSLASAAVKLKLNTSRAQPRLTAAVQYPKKMDGANVVFTSSLSHTKE

EQHTRDTKSVEVEHSMPQVNQSYSPTVVKRLGRDHREPGPQRQHAGDSI

>contig45856 Frame-0F

MTSEPLLLAARELARGLVASLPVDYEVVASATAATHLAVLLRSRKGPKCVRLGVLKTDEG

ENSESFELVDIPTNLGISASFTGSNESWTLAWSPDVRFLVVSGRVSYTGDESQSALWIFT

HREWISSAKVSCSSSVLMRFNLSKLLAAKQWNPATNITHVFFPVHNGSKVFVLSEDGV

>contig46325 Frame-1F

MILMKVVTYRAHSTFTSPAPCIPMMMSLLVVLFICRASVKFSRKAKVHVQAPIFDSHGIL

ENSSSFSHTRCSMRLFYGRRVITDFPIVVFT

>contig46488 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65511.1|) 3e-11

MEPIVAAAEAIAFEATEMHRCENVALTRMMEIEGQRQQIMQEFQEYAKRKEQGNRINRK

>contig46592 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56054.1|) 4e-20

MTIQNGRNSCIHVSVVEGSDALVVVYKQGAQASKNTAAIMESVRALRYG

>contig46747 Frame-2R|Blast-CDK5 regulatory subunit-associated protein 1 [Phytophthora infestans T30-4](gb|EEY53383.1|) 1e-72

MKTYGCSHNVSDSEYMQGVLASYGYRFTEDPDTAQLWLLNSCTVKDPSQAAFMHLVVKGR

KQKKAVVVAGCVPQADRYIKGLEDVSIVGIQQVDRVVEVVEETLKGHTVRLLAKNRLPEL

DLPKIRKNPMVEIIPLSTGC

>contig47300 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57134.1|) 9e-43

MGRSRSSRPAARPAPRRAPASAQPRQSAPAPARAHAAPPTHRSSSSSGGMMSGLMSTVAQ

GMAFGTGSAVAHRAVGAVAGSFSGGSDVSHQREAALDSQDHQAVKPPQQDQCGMDQKAFL

ECLNSNSNDISSCQFFLDQFKQCQMQQQSTFL

>contig47436 Frame-2R

MSSDRQSLRKFEQLNEHEGESDSSMLVERLSQLSTKAKSAMSLNEIYRVQICGTYVSHGV

TFYVVNVFLRTTQKGLPMAETLEQRRRRLRQEYQDQTPDYQIDRRYSDFRAMVKSISKVV

NDHDHFRFCAYCSRVGTIQSAARFPSRIPGLFGACGRQLLTRIRKYRLESFMNHLLNTSK

DMSYRTSSYNQCSRFCIVSRILNQFLASGEEIKPSAHAISASELSPAERSR

>contig47991 Frame-2R

MNTKKFNWHMQWSKLSSTTRARCKRYSSYNRICSEIENKSAIFLTSRHLNVWHP

>contig48051 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58047.1|) 7e-96

MIATTVLKLLVLALSVSILKAVQFDIRRQSDKCLSDEVAEGSLVVVHYNVIGGMRGQSGV

ALTITDPLRKYLKEDTNIDTSSDDIHKFSFTADIGGIYAVCFLNSNTRPVRVMLDYKHGV

EAKDYTEVAKREHLMPVEKELRKMEDTVDEIHREMLYMREREAMMRNTNESTNSRVLWFS

FFSIVILLSMGLWQVLYLKKFFKSKKAHLSIA

>contig48257 Frame-0F

MTGMEWMNPLDQLSMPDSAPSFKLVDSNNRVRELTDPLKRQLGTSSIFYLPQESDDGLSA

AELEEQRQLEQQLQMQKDEMCFVSPLPRHDASRMRVPTTTHAFTYGSSCSSNLHVTPPLA

PPVSPFASMALSAPAAPARKTHNPFMTGKLDTSSRLPSLNMMRSSPGPHLKSLGIASRPT

PPSLRSFSDVSTLSSASPSPSPSPSPLQHSQLHQYHPDARLRSPSHSTHTSVVPTSP

>contig48482 Frame-0R

MSAPKRQIQVLLTLHDGERSFGMSLAQKSVALGNPYTVVSSVFANSPADRAGVRKGYVVR

SINDKSVSGLTVAQVAQYFRNVGQARITMEMGELPRMKAAAALLEDATRSKRFKQQDIGP

GTGVTPSGRAIAAPGSALAVPSIAPSKQL

>contig48701 Frame-1F|Blast-Pc21g00130 [Penicillium chrysogenum Wisconsin 54-1255]emb|CAP94910.1| Pc21g00130 [Penicillium chrysogenum Wisconsin 54-1255](ref|XP\_002567088.1|) 2e-13 NOT\_ORF

MQEGEIPAHVVRYCNDTWLVYKERFVSAFLRGKKH\*GHISTSLVESAHAAPKKWIGTSTG

MHIFQFSHMRSMLLRTDKCIFRSP

>contig49342 Frame-0F

MRNAHRMYWWRLNGFESQCLQSFTEKSHPRLLYHYF

>contig49603 Frame-0F

MMVKCETIDESARRPCDSMPRDGTLSLTCTSRITRYSSAHRGQGSLSHSDHLIGTRNSLA

PNVRGITLLFLYCEISSIVDRRKVVVGQP

>contig49676 Frame-0F|Blast-Ufm1-specific protease, putative [Phytophthora infestans T30-4](gb|EEY69016.1|) 3e-11

MQGFFPRPLLRSLQRFAQSNANASSDTCTRNSVVTRGALLGTERDVRTNPDETSITQQVA

IWGLTCLSPED

>contig50018 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56421.1|) 3e-33

MKLRKHLRGKRLSALTQLEGDRVIKFTFGQDALQYHLILELYASGNIILTDGSYKILSLL

RTHRFDENVKMAVRQEYP

>contig50450-0 Frame-2F0

MAASPGDDRRSEFANCLDCIDPAEFFKPKCRRVARY

>contig50524 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68433.1|) 1e-38

MVESIDWVVALSLLRWQRTRRSYDENANLAKAGIILLQPDANANFGPESALRRAELAFNV

SWQRIASEVLQFAVNLSVRVQHSDVKQRSQALRLLQQVLNVFAVKGNVQQTSLPLNSCNL

MLSALAEMLETIQQDTGT

>contig50591 Frame-0R|Blast-carbon catabolite repressor protein, putative [Phytophthora infestans T30-4](gb|EEY61326.1|) 2e-58

MQTSQVCAIDRIYGDLQPQFVAKDVLKALSQLDAVVGDIFNRLVHKVSFEKERVAAVDKR

IQLCQAKVNALTARRSTNKPTTVFSTSRYPAPKHLALPKTLFCDKPYADAPLLVPDADDE

THFLPAEPLPP

>contig50717 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56357.1|) 1e-67

MQDGSTVRNSTALAARRSSLKLSYAHIKSFNESQKAKGEPSYHDIPEDKRMIVLRSWKNR

NSVDLTKSMFDALGRIIAMDDRLTEIRSLRPPVSPKVSNSDKSLNDTSTFKSGVDSKLAL

KTAKWTTEESFDLIKACADVMNAPADNDLSQRDREALIFDAFLARRETAGDTETPFRRDL

R

>contig50959 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60031.1|) 1e-12 NOT\_ORF

MIDGISAALVMPNSLLSSSFIS\*QSALIGDSIEFAFASLFSRKIFRVASSWSSTYNPSLS

RSTRMPKNDQLLLHLGQSPKERRHIRQPRRCHRRLSCGTLVSSICSSLSMVSAARLGYER

VQCAYLSHVFSVYFCFEPSSILARLLATSLWPPLGL

>contig51088 Frame-2R

MPAYAHKSTEELRYEDYLKRTNPAAAQAAAVQNVPVSAPTATGVTGAFGGFGTQTSTPSA

FGSTSNFGSSQPSGFGAPSTGGFGSSGFGSSTIPAASSGFGAFGSQSTAAAPSGSLFGNN

TAAVTGSSTFGAPAS

>contig51541 Frame-2R|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 1e-15 NOT\_ORF

MHFLIASLVGLTKE\*DLARLETDPDCFPSIESPKEDLRLAF\*PLQVKVKYRSACLAMKNG

CMAMRDHIQHARHLASCMLTHPIDVANQAHVSS

>contig51725 Frame-1R

MVAAFAFWMVATIIVQAELTTATLQDHGSMENAATTSWPSLRVHFSVKRSSRKLHGQSEF

MIVADPVVSIDDSTRVLYNTFG

>contig51862 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY54305.1|) 1e-82

MISSSTIEKAKATKAYLEQKYATMKREREESRERRNTLEKQMTEMRLTEHKKEQYRQELR

SKELQSLRHQRKRLAVGDFQPLAVIGRGAFGEVRLVRKRDSGEIFALKSLEKSAMVLKNQ

VGHVKAERDILASADQDNNWLVTLHYSFQDDHRLYMVMEYLPGG

>contig52096 Frame-0F

MLSLSDLRIDKTSHKAAIAVEPKVEEPVVLDRRLTATLRSLRHLDYVLSVDEQDIVDELD

NDLESDELAELESVDDGSEIRSSYASSVAVMDDDSESCLS

>contig52139 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55405.1|) 4e-38

MRIYQSYLGVGLTGTGSFVPCFALRMLTQLAGSDTRCFQVVMHELVLMSTFRPQLPFQAS

QFPQLDQFQVFTTDCILQLMQT

>contig52210 Frame-1F

MGVVLENEDIIATSEWKNEQTANENNENSADDLARSRTSLELAIVKEKERPELFQTTSKH

IDNEGKKDRVRYDRVELGSLANFLAGSTCLDHQAGDQRHNDVITVPTAIAAIEDELVEKV

DSTTKDYDMELHSSNGCIANASVGSSWNFVR

>contig52481 Frame-0F

MGVYVDDLVVTGKRACGVYLYFTGMKVLA

>contig52632 Frame-0R

MASLDGSPVSSTKLTELGKALDQTSISKASGLSSPLQSDIAVENAATSSVSANKLPAKSP

KKRGRTDSLKKMLPAPASQRHKLVTSSYYSDTQDTEE

>contig52768 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68206.1|) 6e-14 NOT\_ORF

MQVNNRALRPLSSLAQRIVPSLIWQRSQTTNSVFRSVSCTHNSGSFEALARTFASIEVSC

WHRRESRRYS\*RTYCVV\*EVKSSRIVSMGRLADEYRRLLALSTPRALASALYLTASQLAS

PYEGVELR

>contig53073 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY56412.1|) 2e-81

MYSSYWKPSDGRESNVATDHEALHRDEATHKAMQSDETELRPLDLETIMSSKAAVKFWYL

HRPKTMAYVHKNATKMQSLGRAFAVRKLRAKHGAEYMAELARKDQVRRDADTLKDLLPEE

RAAKELNDAAYDARVEESRRQRREQIEAERRAEEDLRIKMAAEASERRR

>contig53679 Frame-2R|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY66337.1|) 5e-32

MFGMDPVLSGSLCFLVLAIAMYLKFIREQPWSDEEFLDRKKSSVESDDMMPFLRSSSSVG

RLETQQQKRGPGKGRQQLHQKQQVPRQTQQQRL

>contig54021 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53272.1|) 5e-14

MPSGDIEVLVRALGEFAVLLRKRHSFDKIRNADKQAILKWLRSLRLEELASLCCVEDVGF

VKTLL

>contig54256 Frame-1R

MLFMRHLYPFLCVEIRRDSHFDSTFPLRAPRRFYPR

>contig54379 Frame-1F

MTDTINASTATTYAADIDIVVY

>contig54498 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65718.1|) 5e-17

MLERTNQQLTRLALPDVTLVDAHIALIVRQQKFCVFRAHKMQTKHVFEVIKRCLNFLCGQ

S

>contig54506 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69871.1|) 1e-64 NOT\_ORF

MDVQMEPQGSAPHEEKFRVYNAALVHAATCAETQCDAYSGRCHKVKASIDHFVRCYGSRR

KVSPIERCVAESMRL\*MRDFMHCCRVLRLRSCEMCSKIWGLLCFHAKTCLTPSGQHCTVS

QCNYLRDKIARKRENDRRELQEARVVLQTQLEEWPVERRMAQLEADRQQVLALLAEIRAE

KTPRSRAGTN

>contig54960 Frame-1F|Blast-pre-rRNA-processing protein TSR1 [Phytophthora infestans T30-4](gb|EEY65644.1|) 1e-21

MTSHHHRSGPLKQSNKKHKTGRHESKTLLARRSGGKVEGRRASVRSTGSSIGS

>contig55215 Frame-1F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY57029.1|) 4e-10

MWSCKSCTLQNNAARTTCQVCQAPRVF

>contig55783 Frame-0F

MSFLRYVVRQLNFQFRRAPGDSAFEDLVHVRNTLFNLVLLSSLNAA

>contig55963 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64471.1|) 2e-50 NOT\_ORF

MLKDLESHLKRCVYRQVPDTLDHVVEDTMTDFYSYDLVCPNVLLGCK\*ICVRENSASRLA

TCPVNGISQEKEWDERLEWRRNVIPATKLERARRMDEDREATNGLCRLGICNNCMKRRRQ

GCKWCYIKRLQSFIRIISAWRD

>contig57082 Frame-0R

MSLVEIELDQPLHRAHQDLCPFRLLKSYQRRVCAQQRVYDQLRMYQTEGEINGSFF

>contig57165 Frame-2F

MARQSSCTFKAREAILLGMGLFFLAYCLVVNVYSNASMHEPLLTPLQTTDETLTD

>contig58511 Frame-0R

MDLRQDESASIWTQLHASSPSSSHASLTPAARSGLAMTVLSPTRSVLLFGGADGKTFFED

IFL

>contig59350 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67986.1|) 1e-32

MECFASPLNCRYSRFCSAFLDTDYVFGSVGSFFHFSPRSGCFEANPPFIPKV

>contig03675 Frame-1R|Blast-5-oxoprolinase [Phytophthora infestans T30-4](gb|EEY63846.1|) 0.0

MTRFYSEQDKAWKPIPVYLHEDLMERRGAVYSGPAIIMQGTATVIVESEWDARVMPSGDL

YVVSTRDSADLDQKLMAVKATDFVPLDPIQLSVFSHRFMGIAEQMGRTLARTSVSVNIKE

RLDFSCALFGPDGGLVANAPHLPVHLGAMQQAVRCQLQFWGSDLHDGDVLVSNHPQLAGG

SHLPDITVITPVFDQTSSQIKFFVASRGHHADIGGIAPGSMPPLSKTLSEEGAAIVAFKL

VDGTVGKFREEEMTEILLQKGRLDDHGRPCIGTRNLRDNLSDLRAQIAANQRGVVLTREL

CSEYSLPVVTAYMNYIQQAAEMAVRQMLCEFSLQRQLPPVGIVHAHDFMDDGTKIALQIT

IDRNTKSAIFDFAGTGPEVFGNINTPPAVTYSAIIYCLRCLLSDEDLPLNQGCLTPIEVR

FPTEGSILNPSEKAAVVGGNVLTSQRITDVILKAFGA

>contig04807 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60202.1|) 4e-47

MRPNMTHGRALISFRIDDVSKNHQGQSFRLDIGPEQQDGSFMFKDIAPTRTSVIAIRSKR

NKRKLHA

>contig09691 Frame-0F

MSQSSERNIVRLYDPKIGHSKSGFAGFKCHALYCAFLPVLCSRFNIFNI

>contig10910 Frame-1F|Blast-beta-catenin-like protein [Phytophthora infestans T30-4](gb|EEY69790.1|) 5e-94

MKDRKRLIFGEALRAMDHALMGNKRNCERLIEIGGLRSVFSAFMGRLGKYKTGNSSKASK

ASDKAKEEENAASIVASMCAWVCEKAPADGYDRLHAKFVENEMEKVDRLVDLFVKYHARV

ENSNFDMDIEEMKDKENRYFQRLDAGLFVLERIAFVVAHLCCFSRKVRAYVMVKFHERSV

DSND

>contig11056 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64066.1|) 4e-27

MDLVAKSPTGFEYLTKLYISVNWRAKGNGTLPDTEMFMVKTYCEPNKAATKAASHEVIES

DLASSHEFQILEKTQYD

>contig11250 Frame-2F

MLSSKRIGHEATLVFLKPLYTRRLQMLPQQLGGSLQRNGMHGVFRGMQRDVALARQFLPS

TTRSHTFLRRMNADKSLDWVTWLNDNIPKGFGRFYPKNGSGGKGVGPPKTAPKTGEKGAT

DVKKLSSKTAEKKLGGSGSSSGGSKGPNSKDGMAYFVPLAVAALFLSDMVFSDKPMQEIT

YQEFRNSFLESGRVEKLEVINKKYVKVYLNDLAGATPSNRRGSGLGGGNDFSDWHDPHAK

GQHEYDFGAEPDRQTNSDGRTVSLPELSARGGATGRSNSSPSYYFNIGSVEGFERQIEHA

QHQMGIRPHDYIPVQYSNEISFTAELMKFLPTIMLIGFLLMTMRGVGGGSGGGGGGLGNI

FKVGKSPAKKIVKEDIKISFKDVAGVDEAKKEIMEFVEFLRNQKHFTDLGAKIPKGALLV

GPPGTGKTLLAKATAGEASVPFYSISGSDFIEMFVGVGPSRVRDLFKEARANAPCIVFID

EIDAVARSRSKGNFSGGNDERENTLNQLLVEMDGFNSSEGVVVLAGTNRADILDKAILRP

GRFDRQITVDVPDIKGRREIFKVHLKDLTLDGNVDDFARRMAALTPGFAGAEIANICNEA

AIVAARRKGTSITFKDFEQATDRVIGGLETNRIMSPEEKKTVAFHEAGHAVAGWFLEHAD

PLLKVTIVPRGKGSLGYAQYLPKEVALHSREALTDMMCMALGGRASEFVNFDGRITTGAS

DDLRRVTQIAYSMVQLYGMNDRVGQLSFPKEEGAFPDKLYSDKTSEVIDEEVQKIVHNAY

ERTKQLLKEKRLQLKELAEELLQNETINHGDIVRVLGPRPFGGNKTYTEFVEESWKDADI

YEASKAKKALEDTKGEVKDGDEDQGKFDALDGKK

>contig12101 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67066.1|) 0.0

MENDKNCTESIKNGMSGYCEVRNTHTGELRRVLSMHCNSLRAQVAFTCNMFQSLLRYSIL

STDYEHDKNFSYEKNQVSFQTTNYLDSKVLPVDNNKQTNKSVNQLKTLSFERGIVFVVFE

KILLGAYVSVRTLREFGCNLPIEMWYKTSETDRQHPLLQLMVDQLGVYLRVIEDPLATHF

YTKLYAIFYSAFDNVLLLDADNFAVRDPSYLFDTPEFVETGAIFWPDFWRPANTIFNIHD

QSYVWDFFGLDYVDSFEQESGQVMINRRMHYKALNVLMYYGFSMPRVHQKLRLVWGDKDL

FRFAWMKSQSSFFMTQRPPGSAGTKHPDYNLFCGVTMVQHDPSGNVIFLHRNTEKLTFTN

NRILWTHLQQYKNTSSLSNYVVRGANGGKVFAQFKRCFGKDVHYDKLFTLQPMSAFPFEN

LERNILQFTAAGAEVVRLAGLNLDDDR

>contig13524 Frame-2F

MQDTVKTLPHAAVPIITLLTASPYNVRLDISFEGPGHNGLATNDVVMALLHEFPPLAPMM

LFLKSFAIERGLAVAYSGGLSSYALLLLAARYLQEHSDTMPNGFANASRAVQHSLSTVQA

GVADFGLMLMGFLDFYGNRFDPRTTGISVATRCFLNRESAFMAGAVAGSSSMNDPHQVPH

QYQQQYAADDAAVDDRTSQYGYYAQHWQVSAQPQMQLLPNVDSASAHGSRRYGYRSSLDL

PASRAQDGLGATTGLLDYQQLQQQTYDPHKFDPVFIEDPLCPSNNVGRNCFRIMQIRRAF

SAAHFALLAASRDPTMFADNRVDLVAGVMLHPDNILRAILGQRAPVNTKPDATTSANIGV

TAYIHGMDHPHPYVFHPNNLQQQNQQYAYHHHQYHQPTQQPFYQTGMHPLRSVRACSNEP

SSRRHSESESAKLTTRSTTSAASHNPRTQRRQFGSPRLILQSQDPESRIHSHLSRQKSTD

RLHRQSKLQLVHSPSIAKALSRKNSERSMSFADVVRDGGGSSKPIPKTSPLSLPRPPRFS

RDDMALKENINERWETKDDSDLK

>contig14297 Frame-1F

MDPPSPSSSRAVSATARRDETLLVANASIVASGLDNVSDSDEENPEHKRRRLRRGTTAPP

VTTRPRRASTDDKDAFVMNPYTLNDENDNDINEEIVDELDIQERERQYFSEDELDDDMDG

EDLDEHAERDYRVMETLDQYDPSMLDSREYDPMDMTTRRAVEVELNRRNARLGRIDQAFQ

DDFETEYNDSHRTRPLSHPTTRLVSSLEEDEEELLNLEHFDVPLREWIAMERPRQEIKRR

FRHFLTTFTISPGNVLYLNHIRHVAQTNQQSLIIDIGHIIQSLSLLAAWIVEAPSEMLEI

LDEVALEILLLYFPYYQSIHSHIYVRIRDLPSTERLRDLRTAHLHFLIKVSGVVTRRTSV

FPQLDRIHVTCPHCQARLGPFLQPKHQEFHVHVCSECHYQGTLLVNTQYTTYRNFQKLTL

QEAPNAVPPGRVPRSKDVILVADLIDTARPGDAISVTGIYCNTWDPTVPLRNNFPIFCTI

IEA

>contig14338 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54775.1|) 2e-32 NOT\_ORF

MIYAPPFLDRTMLRIDIRLGQQCLYDAACSLERAQLPQSVLNFICEKCGGLVVPSVSADV

RVLPQSQNSPLN\*LLVKQQRRAQLQKGFIKWTTFGAKDAFDNAEDKLPSVSAYI

>contig14433 Frame-2R

MMYHIQLAVSIVFCVACCGGHAIRTLAE

>contig14569 Frame-1F

MGCGGKGQSRQSILKAPDEELPMAKQTLLLNLVW

>contig14680 Frame-1R

MAHIIFPRNRKRDSLFGDFRKKSLQEIKQQQLALFIEQVFQMPEISTQPLFIEKLKEFLG

FDSFFEIVNNENGQKYSNATASADPLHNSPLSIFAATELYKKPLDNELQGISLAAAESVK

SNSDENFSQYCDNTDLDRTSPSLLRKFSFAASEEEEENFVSVIPETESKAMKKLHKKIVQ

TVRELVSYEEERVQEFQDQTKDFGRNKLSAMEYCAFLHGALGAQESCKLIPEMARLLPGE

LKRKELMEARAVIWRRTCGRQRRRSKQISEGGVFIKHREAQKQFDHVHSRMRPKSDGFST

VTLDSERVEPIKLPERSLMAKTRLIPAIDSENELDRQLNHTLPVIPSYRAQLADPRRHLN

RRASFNSMFGETLRTTSIKEEHPEDSDAVNEDSEESILDQSRNLSKEPLSACRMSVMSEK

ALSGPSVSKHRNSSSHEDEYYDSTEDDDENHLSGHSYSNRNRQGSGSREIQVVKGKSRNF

GNSQSQLVFAESDDSHSDGEQGISHTRFRRSQRRASRKFDVDFKMGPANEEENPVLARLK

KQGAVNFMMQLH

>contig15562 Frame-1F

MKHHALSIIALAIEPKLFNYELGRSILTIVFTLP

>contig16488 Frame-0R|Blast-conserved oligomeric Golgi complex subunit, putative [Phytophthora infestans T30-4](gb|EEY69412.1|) 5e-19

MVSADCKKVLPAIRTVKGQYQMTNKPSPSTRSTYVPNIV

>contig16967 Frame-2F|Blast-DNA topoisomerase, putative [Phytophthora infestans T30-4](gb|EEY63719.1|) 0.0

MNSSDDDDLIPISLLRKKSNPPSTSNQSLPRAMRNAAHATKFCVNKEDSESDSVPLVQLK

KNATVKRKMAAANVDKDIVVGDKKMTRVKRKAFKASTFDLLSKPGMKIADKSVSSHKVKV

RKERGLNVRKLKVHSKSERLDMAIKAFRWWHAEELPEGIQWRMLEHNGVMFPPPYKPHNV

PLLYNGKPIDLSPSQEEIASFYAAIPKDGPQLGNFKTAKIFNHNFFTDFKKALGKQHEVK

TFELCDFSLIAGHLEKLRAEKKNMTKERKLLEKERREMELFCNGFAFVDGHLEKVGNFRI

EPPGLFRGRGEHPKTGTLKERVLPEDVTVNVGISDRVPICNVPGHAWKQVIHRDTVSWLA

YWNENVMGGIKYVFFAASSSFKGKSDLAKYEKARQLKNCIDKIRRDYTKGLRAKDMSTKQ

RSTAMWVIDVLALRVGNEKGEDEADTVGCCSLRVEHMSFSDENCALTLSFLGKDSMPYNN

TVGLAQYGDVGKQVFKNLQTFCANKGKNEEVFHELSVTELNKHLSSLMPGLSAKVFRTFN

ASFTLEKELHQLSKQELDPRGQLELAPKVVLYNDANRKVAILCNHQRTAPKSFDTTLDKM

NTQLDQLKSQLKDLKQMQSMVLEGESSSIKLKKDQAAFNKEEDAIAKKAQAHIFQKTPSA

DQVAKKIENWKKKINALTLRLQDKTDNKEVALGTSKLNYMDPRITVAWCKRNEVPISSVF

SKTLREKFVWAMDVDPMWNF

>contig17502 Frame-1F

MSKAPRTVHAYASFGKHEEMKPWEYTSRPLGDGDVEIKISHCGICGSDVHTVDSGWGPTT

YPCVVGHEIVGHVTILGPNVKDLKIGDRVGVGAQVSACLSKDPAVCKECASGSEAYCPHL

VYTYNDTYKNDGVPTYGGYADYVRVPHEFAFKIPDNIPSDLAAPLLCAGATVYTPLLEAG

VQPGKRVGVVGIGGLGHLGIQFATALGADAVVAFSRSATKEAEVRKLGATEFVVYTDEKQ

AEAAEKSVDVLLICANADNMPYMQFLSFVAVRGSCIMVGLPNDEIKFYAFGVVAKGLKFV

GSSIGSIQNIKDMLQLASEKNVRPVIQKMPMSKVNDGVKLVRDGTVRYRVVLEN

>contig18059 Frame-1R

MRELQLWLLESKALYCFARQKAHTQR

>contig19153 Frame-1R

MGKGKKRHSKKGPKHHAPKQNGESLENISSYNCSILESNEDANPMLHNSNKHLDACKQRK

IIERLFDQANQQGLQVGDKRFVLSAKWWKGWCDFVGYDGKKHAPVAGVDDIAPGRIDNLP

LLFVSSNTPLDELMGGPMLPRLEENHHYVLIPLEVWDALRIWYGGGPTIARFVESVEGPK

LDSFLNFVQLYPEKGKELEKLTNGSINSSNEETKELKEEMADAIGAKQVVLPNVVVTSSS

IPKVCGACRKSSGLFKRCGSCRLVWYCGASCQTSHWKYHKVICCSANSAHEKEGGILRDL

QAERRGKMGLRNLGNTCFMNSALQCLSHVDLLTRYFLSNKYKKDLNRDNPLGTGGNLAEE

YDALLKELWFGSGSNTSPANLKGAISRFAPQFSGFQQHDAQELFAFIIDGLHEDLNRVKH

KPYTEVKESDGSQDDAAVAEEAWKRHLLRNDSIFVDHIQGQFKSTVVCPVCDKVSITFDP

FNCIQLELPRQLYREIEVIFVSSDTAQLMNRYLIEVPKKGSVLLLKRALSKLCGVSPKSI

LAADIYQSMVYRLIGDTERLDRLREDDRILMYQLPHMPAEDAPLYGFLYNRVGPTLTGDP

LLFTYTASTKCSEILEKWSELLSSHISRRSRSVISATMLSQCVYLTDRDGVLLRNEPIPL

AIDSKFIDFASLPDEDAHKKPVFFKFVWSSSMLSSFSLRPEMDRIRNHESMRVKLNGSRL

HESVSLNDCFRNFVKPEVLDHENLWYCSKCQESSTSAQDHGDMATT

>contig19258 Frame-2R

MLPIRTLFRQSGGSPLLAQCLTRRSSSKFPLKASSRFQNVFLKSLQAPSFASVPSRDDNT

RQQLHGNTSKSKNQQIQELIETNMALKKEVETLKAEVAKKPNKFIGTLQQYGLPFLAWWT

SLYVASGVTIYVALDTGLVSGASIIDFIMQIGLDKLIDPARLDPKYGNIAIAVIVNECLE

IIRFPITLATLPFIKRVFSRKKTTEAT

>contig19337 Frame-0F

MQINGVANTVVYTPRSESGDANYLAAPYSPETPSPHSVASSAYFSNALVEEKDNHSARDI

KN

>contig19508 Frame-1F|Blast-threonyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY66527.1|) 3e-54

MYLQDKATVSEADFDDITRRIQKIVKARLPFERLEVTREFAEKMFTYSELKREMLHKIPM

DASLSLYRCGSLIDLCRGPHVPHTG

>contig20607 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58739.1|) 4e-43

MTALLRNTNSAPAKAQAFAHRLVEFADYEMCVRFFSERNINFDRANDMGWNVLMSVCACG

RDDLVGFVIDRTVAVDCATYTNKTTVLHLSAMSTNPCVVEELIATANRKQKLQKIINQSN

AHGDT

>contig20799 Frame-0F

MDMVAKEMSMSPFSLLGNMLLSLDLKMNDCRVLLLPTRAFSKQLFTDFNVETWQSESVVD

CRVDIPVTLHIHLESSKVKELLELNIHSFSIGAQYLEGAQKLETILAPTSIIFQFVLEQD

TNNSSICHQSVMIHMPDVLVAGSDLSLSLLASCGEALGNVQFTTHDQALLRLESRLKQDE

IRRQAEVDAVLDRLHRLFNEIDENKNGSVELAELLLLLRRVKVGDTLLESELEYFVRELF

KEIDRDGNGYLEFQELRVFLRDDLLLDEGATAAVSTARNGSNSLSGFLNLRGNEYHSFEV

ISNMCETKITSSEHLAEWIKRPVFQNRFWGLFESETRVTIRTLGDQNPLDMQKKLVRLLK

NYDAANLIWDALILPAMESNCLDLVAFKWLLQPFTRCGGISEYQSVAKVIAKKKRNGIFS

AAYEESAHLVSKLTENVNSVKKQLVFTTDVKMGNVKFVLTDSSLPARFCRGNFVVLDVKI

SMELSSKEIDEIGPIDWISLATSGNSEWTILFGFKMASSCYSDIANDMENIIEPWEFVAG

ISSDAGANGFSVLVEAAKRFQINVTPSVLKTYRALMDALDGEAHDNALLKRRDGFQSTAV

AKKHKDVNCLVENMTGCSVTLKLSGSDDAIEIEAYSRAETKNGVLIDRKATLEFLSIGEW

GTSTSAVELPSFGDVSVSVSTADTKSPSTLFVTVSSRLENPQRQVIVLRSSTYFCNHSSE

CYEVKYLSLACEDRKSIESPVINVRPNERISLPLSLLMGITEFYARPTNHEHWIVKTSLN

NDVLTSTEAIKNLEAHEAERETKKKYRRGGTIVYGETAETCSNIITALTPNIIVRRWHLL

SYFEWELALLPPFVVRNSLPYEIEFRFIEYKTSSSRDMKAEYAKVEALLRRENTLDPADR

VLSGVIKSGYDAEVSGVSGIYPGYLSVRLVVKKKTSSTDRLLRSSWSMPLLMMIHKGVEQ

FTTSRESIEADPGLKFNIDRITLPGYPRLVRFSSPYWIVDNTSLEFTFASTEPGAKRNSF

KAMELCAPFSYPIMTSIQHDRLSMKPLANLNRRPEAWEALGSMPDAAYKVSAVSEHAIKN

AEWSEPINTTAINTMGEIVCGPSVFSVQMKGLYGIFEPGVSLTLSPRYFVQNRLSQKLYI

QTFASQDSDPRKVHDMFHKRSVEDVKHLHLALEDGQTTPLYHFGSLKQGQSAQHSQRYVS

FSFTDGWGTDADKQNWSFAIPINTAGDLYLQVYSSVRQRHIICQASVQVVDMYVYVILTD

VSCAPPYRIENFTPFLVEYAQLGESSIFSGGQKKETATIKSGAWHAFAWFNPLSKERHVE

LRLSHIDAPKTKSKKYDIDYVGFLSPITMWVSHDGEKQHAVVLTVQVVVEGSTRVMKIAE

KELELSLIERQDPDGEGDLQQRRMLYASSFDVRFDGFGLSVLDGFPQEVFFLSVDVIKAQ

KAPASLEWTLSVLHCQVDNMLATAKFPVIMNPVNTGYSDKSVGTEPEPLLKLVLDADLEA

RSGTYKLLQFSLNDLAVKVDIDYFVNLVKLLEPYLVSQATMAHRSRLTLEGTLKRRAPPM

PKMLVTEDGGIQTDLVYFDLLRISSLSVDLEYSITRKDIVSSTGGGHSIVFGGLSQIIGL

IGSNLSGSPTFSFSEIVIVRCFTTKQRLQSQLVANYVQQGVLQAYRLIGSADIIGNPIGL

VEDLGSGVVEFLKITKGEITGDAQTRGEGVKVLGKTIVKSSASSVAKITGSLDKFVGEFA

DENRQNDDDGSMSTDNAGIKFAKDLGRGFTGIFTKPVEGAMKGGVTGLVQGTVQGITGPG

VVLLKGLTSTSHNLALGVQSTVVDRSPFGGRRRKPKDVKQGKIIAEFDEKHYKPTLLELE

VLGANGLDSDQSCDPLCVVRLDGKDVMKTAVIYNTVNPVWHEKTQVALTGEEEEVVFVVK

DSYGGTIARTVGKCFMSMSKLQEDFKPPEYSSDLAEWVHTQVKPGNTQKNASHAITEKEY

PLVMLKKDHAKKVAMLGDEKHQVLVTILSLQEMVVTSSTGSGMLGLGNLGSRTPNISPYI

SVHVGKNGNRTNTTKMTFTKNANKEQVGYASWNESFTFPLTAKELRRGGADSKLVVSLKD

KSMIVDTRLGTSTLDIDATRINNSTMEKLELKDHAGKSVAYLTVKVEVTGSATSSRSFSK

SSFVSAGDNMANFPPDAVKAGTIRLSCVFK

>contig21554 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61485.1|) 2e-57

MATFQDGCHGELPSLLEPNLVDYEDKTEPQGVLAAMQRASMSAHNFYSHVQAWPRIPRSF

AHMLDNERSLLETSTLRRWLHTELSRPGILPSSDELDEEVVDYVLGLLDHPDFCHPDQLV

KNFMSFLAPTSSTLCSPCGNLWSSRLDCTVSLATKNLQ

>contig22212 Frame-2R

MPFKLMENVSAFLKACRVMGVNEFDLFETVDLFELKDLGNVVRCIFSLGRAVQRDYQEFK

GPSLGVKESSKNQRTFTLDQIAGGKNIPAQQTLGSYRTMQRQTTFHTNKVMLGAAAAQSA

YRAPPPPPPPSAEKIEQLSRFRNVDHLAMKFSHPKGESS

>contig22339 Frame-0F|Blast-eukaryotic translation initiation factor 1A, putative [Phytophthora infestans T30-4](gb|EEY59158.1|) 8e-11

MPKNKGKGGKNRRRGKNDNEENKRDLEFKEEG

>contig22645 Frame-2F

MMASWEFSSPFCVGRSRGCEVSISTSEATRTVSKRHVGIVPLTETLSNPVPAMLGKRRWL

IYDLETMNGTAVNGMDIPKGGNQELRGGDEIVLASAMRQCVRLLVQFPDEIHSRIIVKAL

AESAALSPALSHHRLSIDEAASRRSPRLNHIINASSAATGFRHSSVTILGSPALASAECQ

LLPGTLNGETSIVTPSTSQNHLQKRSRRCLTKSAVLKRSLSKQIQPDVLYCQQRKRLRSS

GASEEEAVVIDGGFNTAAQKRARENEEEEKERLMTCPVCMEYFYGSATLPCSHTFCGLCI

SSWFRTSLSCPECRNVVKTVPVRNRALDELIEKLVGEKETFKSLVRRRAWMQRRLMGPQG

YICDGDEIESGRITRGGSVEPGSGIIQERIIWTNVFIRWSAKEKLAFSAFITEQFGDARV

ASCRIVGLTEPAADRANITELFVAAQNLLLDCNGLRLVDDECCHRLKIFLNFG

>contig22771 Frame-0F|Blast-elongator complex protein 3 [Phytophthora infestans T30-4](gb|EEY58432.1|) 0.0

MCKPHRCPHIAMTGNICVYCPGGPDSDFEYSTQSYTGYEPTSMRAIRARYDPALQTRHRV

AQLKRLGHSVDKVEFIVMGGTFLSLDKRYRDQFIRKLHDALSGHSSTSVEEAVRYSEQSA

MKCTAITIETRPDYCLKPHLHDMLRYGCTRIEIGVQSVYEDVARDTNRGHTVAAVTHCFQ

LAKDCGFKLVAHLMPDLPNMGMERDLAGFQEFVENPCFRSDGIKLYPTLVIRGTGLYELW

KTGTYKNYTPEDLVDLMARLLALVPPWTRVYRVQRDIPMPLVTSGVEHGNLRELALARMR

DLGLVCQDVRTREVGIKTIHDQTVPDQVELVRRDYVANGGWETFLSYEDPEQNILIGLLR

LRQVSKTSFRAELPPGSSIVRELHVYGSSVPLHARDPTKFQHQGFGTLLMEEAERIANEE

HLSKKLVVIAGVGTRHYYRKLGYEIDGPYMSKYL

>contig23105-1 Frame-1F1

MRIPERKKSYLLVIKVSLLVVVVVRPSLSSV

>contig24610 Frame-1R

MWMQNSAGGGNLHDRNRFGSNYAQNSYSGGGSYDAGSGDWKSKILESGQWLGGKVIEYGG

KLARGSSTNSIPDHFGQQMPRNDGRANWMADIRSNTSSFSGGYNASAGGYQNDFASERPK

TYSDYGQGYSSNPPGGYESKSISLIDQRKSRHVNKTKHERKSKNNKIKTKPRSQSECSSL

SESEEKSLSESSESSNDRRRARKKKSKAKKHKFYSESESDDHREATPKMDYAYSFDPAKL

PPPPQDEGKTTTRTSKTKSKKKDKREKTTATTRVKAKKRSGKKSVEATIESVDLLGVDLI

PQATSSEKSVFLDDSGSHTPLEDLAGLSFTASASAFVPTQASTVEKPSIQSDTSSPLPNT

FVSNVLPENNLVDLNCLASEKKKALSAHPIEKRTLNDLKKAQSMEHSTPVLAMPMPPMQP

HLMVNGMVQYSTNFNQLPLAPEGSNLMYSSLQPQVARTVQPQMMILPRVQPLVQGQQSLQ

GQMTTASTYKSLDPFPTS

>contig25103 Frame-0F|Blast-palmitoyl-protein thioesterase 1, putative [Phytophthora infestans T30-4](gb|EEY53377.1|) 8e-95

MYRDGDPYKHVLGFNETRWYQEDLFGLQTLDKDGKVHFLSTDGDHLQFSVEFLLGVVAKY

FRLQVRSYS

>contig26032 Frame-0F|Blast-hypothetical protein PITG\_05455 [Phytophthora infestans T30-4](gb|EEY69244.1|) 1e-16

MVACLENTSLRLNQPCHLLNSIIQ

>contig27390 Frame-0F

MEKAARQSPEFGPRRVSSRVF

>contig27787 Frame-2F|Blast-DNA-directed RNA polymerase II 36 kDa polypeptide A [Phytophthora infestans T30-4](gb|EEY68040.1|) 1e-123

MPHPRFPKIEIQELRDDFIRFELSETDPSVANAIRRVMIAEVPTLAIDLVSIEINTSVMT

DEFLAHRLGMIPLNFDGGLENFRQRFVYSQDCDCDENCPNCSVEFSLDVTADSGVLSVTS

EALKSSDPYIRPVNFSSEEELNNTQDSGVIIAKLGPGQRLRLSAIAKLGIGKEHAKWSPV

AVATYMYDPIITLNQAVLSSYTPEQKAELYKSCPTEVFETDENYEQLTVGDPMRCMYCDE

CVKLADSFKDNPEDDSAVSIKMREDKFIFSVETTGQLKPEEVVICALDLIREKLSSLKHQ

CLELSQDDQGSAAPITPFG

>contig27808 Frame-0R

MFIILSTQWMFIPRCGISLYRQVKV

>contig28070 Frame-2F

MADSTHNVLLHRQNELFADAVPKLAEFDLKAPDLLKNPSLKRFLDDNPSNNYQELSVELE

KAYSHETEELSKLLKNGGDIGRSIQDERLNNWRKEFDVGPLGLDELAKSLLAKSEGDPTV

ISVDANLERKLIDSWVKHCTQEQVRELLQLEKLRGIAFFKSPSTRLYLLYITESSPTMQN

ECLSWLSKYFRRPQKVLQYAASGIVSNQLLLLGLQKKQWIGMNLHSSIVDLGLDHIKYLM

YENQLFQFWANIACERNQEAKAVQILWKRQREFT

>contig28254 Frame-0R

MKCKLSHRDRSVMNSNPGVFAPANQSS

>contig28492 Frame-0F

MYNTWYRPLAHSVIKQSYTLVQLFFIYLEQKGDANTNESHDYERGTDYNGLSYSW

>contig28935 Frame-1R

MHQTKAIKVDLNGASKRQLQQLKGVGPILAQRIIDARPFHRNEDVLAVKGISIKSYLRMQ

GEVFVKDYLNCMRKCDSNDVNSEENFRKKIREAPRGRAIESDVREHLFSTWNHGCVRESA

LLVASWNIRNISRRKEFHLLQRIANILDEFDVVALQEVRDLIVLKKLKTMLPGWDYIVSA

TVGPEILGTKRRVERYAFFYRRCAVKLVKKCSLLESRRDAMMRQPCVATFRATQSLHSQK

LDITLINVHVSFGNKESRHAEIAEINRLAKAFEASDPIKRVIILGDFNLSPQDLLKSLGK

HKKALILAPQSTTVFNKLYDNIWIDRFDITDADGDEEFNYIVDSGVLRIDWRHYPLSKSD

HLFIQNPIDAMLPRLQTYMARVQCSYELSDHCPVWIAIAAASKRYIGDG

>contig29037 Frame-2F

MRACFKCLERYGRAVSFNQSRGETIGIAILNVRRCVVVIFRAANG

>contig29042 Frame-1F|Blast-DNA replication licensing factor MCM5 [Phytophthora infestans T30-4](gb|EEY53798.1|) 1e-115

MARDPNLYEKLARSIAPSIYGDYTVNMKKAIACLLVGGSRKRLPDGMLLRGDINVLLLGD

PSTAKSQFLKFTEKIAPVGVYTSGKGSSAAGLTASVIRDSKGEFYLEGGAMVLADGGVVC

IDEFDKMRESDRVAIHEAMEQQTISIAKAGITTILNSRASVLAAANPVFGRY

>contig29253 Frame-2F

MTLTTFEQKLAHLKKEAERYAEYLSDEEEEDALMTKAHEEADFCNDYSMAIVVGGLPLVD

ESKHDKLLNVVKKIFGQVGTVVDIHMPYGADGKTTSFAFIEYEQEAHANDAVRTINNFAL

DKRHTLNVNKYEDMERYQKTAEFEPSVVDKFVEPKNLKTWLMDPARRDMFVLRHGSETEI

FWSDKGELELDYAGDREKKNGKQWCSQYVLWSPQGTYLTTFHPQGIALWGGEKYEKVGRF

AHKNVKMAVFSPHENYLITVSETEQEAAIIIWDVHTSKMLRAFPAGKATGSKGEVVQGLT

TPFKWSADDKYIARRGKDVISVYELPSMKLLEKKSLRAEEVHDFFWSPTDPILAYWAPEG

NNVPARVSLVELPSRREVRQKNLFNVSDCKLHWHPNGTFLCIKVTRHSKSKKTMYTNFEL

FRVHEPLVPVEMLEIKDNIVAFAWEPKGTRFATVHGEGQQRLNVSFYDMDGGNKSAKEVT

LLYTLKDKACSHLYWSPLGNNIVLAGLGEINGQLEFWDATEQQSLTVQDHFKCTHVEWDP

SGRVVATAVCQPLDNSYYKFTMDNGYILWTFQGMQLLAEKKETFYQFLWRPRPRSLLSDE

EYNNVVKNLKKFEKRFDQMDRFKERERLAAIKAERMQKEQEFQELLETRQTTTAARRLEY

IALLDGYDSEDEREYIFQTHTYDDVLEVNEEVMRK

>contig29608 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67527.1|) 6e-83

MARNALLTIQDLIIALRAEMTDHLHIVVPVLLNRACSEKQFLKDLAREVLDTTLQAEVDE

ALLKPLLAVSATERNAQIISVVRR

>contig29819 Frame-2F

MNIDMEQTSFTSMLDHAQYGGALQEPLMHSSPYELQGMMPQVEVPQYMKHQTVQASSPTQ

DLADQLVPSVLENMMNRSNTLKLMPSPTEASLLSLVDQELRVSSISNLSIFLKLLPRCKT

EPEQTLGLIVLRATSTASNTNLSHACASAFEKNGGLRLARTWVDSAVTWEHNDLLVLLLE

VLQTLPLQLTSITEARINEP

>contig30673 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69104.1|) 1e-101

MKKGWQCCSSKMVYDWDDFEKIEPCVVGCHSEVGSNEQFAASPTVAAADIAAKKSLGTAI

SQVAPLKSIEDFNQKNPDAVTAVSAAKDSQLAPPPKRLDGKAKCVNFGCQQEYVVDENTE

TSCKHHAGPPVFHDAGKYWSCCPKNVKYDFNSFLKVPGCVVSTHTDIKTA

>contig30729 Frame-2F|Blast-transketolase [Phytophthora infestans T30-4](gb|EEY61451.1|) 0.0

MADHVDKKARFGDELCINTIRMLSADQPTAGKSGHPGAPMGCAPMAHVLFGNSMKFNPKN

PKWSNRDRFILSNGHACALQYSMLHLTGYDMPIDELKKFRQWGSKAPGHPENFCTPGVEI

CTGPLGQGISNAVGLAIAEKHLAAEFNKDGLDIVDHYTFVICGDGCLQEGISSEASSLAG

HLGLGKLIVLYDDNKITIDGHTDISFTENVQMRYEAYGWHVQIIEDGNYDHASILKAVET

AKAVADKPSLIKIHTTIGLGSKLENTHTVHGAPLKPEDLAATKEKYGFNGSETFVVPEQV

KKYYDKTIAGAEYEQQWNSLFATYAHKYPKEAAEFTRRMEGKLPVDWKKHLPTYTPQDAA

KATRQYSEIALNAVATALPEIVGGSADLTPSNLTHLSMSGDFQKDTPIGRYIRYGVREHG

MAAISNGLFAHGGVRPFCATFYNFIGYAMGAVRLSALSRFGVIYIATHDSIFLGEDGPTH

QPIEMNAALRAMPNMYVYRPADGNETVGAYIAAVESHDRPSVLALTRQGLPNLANSTAEA

VMKGAYIVANTCKGAEIQELNGEPDVILIASGSEVSLAIEAAKLLNTYQVRIVSAPCLDR

FHEQSIEYKRELLGEGIPVMSVEAAATFGWATYSHSHFGLDRFGASATIAQLKEFFGFNA

NTVADEVRKLVKFYAGRTAPNLFDIPAPRVLNIQEH

>contig31560 Frame-2F|Blast-S-formylglutathione hydrolase, putative [Phytophthora infestans T30-4](gb|EEY53250.1|) 1e-135

MKLEKQVKSFGGVIKQYSHDSTVTKCAMKFSIFLPPNASESNKVPVLFYLPGLTCNDELL

FVKAPAAQKAAASRGIAIVTTDTSPRGISIPGDDDDWDFGTGAGFYVDATEPKWNEHYCM

YSYVSKELPALIIAHFPVLEDKQSIMGHSMGGHGALVLGIRNSTQYKSISALAPICHPIQ

CPWGVKAFTGYLGVDQEAWKHYDATQQILSNGSISPSILIDQGREDLFFHDKQLLPEAFE

AACKLVGQDLMLRMQDGYDHSYYFVATFIDEHVNYHADSLFK

>contig31762 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55555.1|) 2e-93

MYPLQCLRDYPASMTVVNVGAADGMAPRRIAAAQYLRRQLMEYALTHSTKLALFLMQDEV

DVRDRYETFRDTQDEQATTAELYAVASMFNVELVLISNDHNFNIDPVVPIEGLPSVRDGP

RHTVTLGYLIPVNGLAGHYICTREQRGQGRLPTNSFAGGSYRGSIQIGPPKTTSSGVSKY

RRFERIPEQRLE

>contig31898 Frame-2R

MLSKQLENHTTVITQLYYNNILFCQ

>contig32437 Frame-1F

MSTSLPLPKGFFNRNVRVSEDMRRQYIEFAEASIRKVFALSDCHKNSWIPMREKKGVAIY

RNFGQMRGPKAYKSNIAEVGCKGQLSASLDQVGRAYAAHDDALFRRLMKKLNPAVMDAAV

LLTIVPRTPLTPFRYIGIKWYAVKTPTPIVSHRDYCCLEVQDKIMDSFGNEMYIRVLNSI

DVNECPSLENSHGLVRAKILAGYMYRLDRVESNVVRVHHVARFDPGGYFPAQWAFKTAES

QLLNSIVQVRRIIDKQQMNACTFVDKKQWVPNHERLHCAVCSRTFGTFRPRHHCRSCGEV

ICGKCSVFKSVEVPGTTLKNVRICSVCNMGVQKAVGQDEDENMSDISTSSITSGSTIAHN

EMNLMDLYMVNGGGSRTPSAYSDASAQSNLSIRSTTSTRSTYDARAREHSRARVTRGPGA

FFNESNTPRSYIANNLTPRSTLGFEIATSQSGANSSASTPSGGGKLSISAATVVAAAAIT

AERLSSYKQNPVDIGYLRDSAPDISAIIEAREHTKDHTIVWPLAKMQQMAMEEVAGVDLD

LDNQQEIEVKPAVPINCDIKDIQQHSLKQHLPTVDRISESSIEHSIRASTLLRISMETDK

SDTMASSDATSSPTGIKRPFLSGILSRVRGESVDLSVKRAA

>contig32558 Frame-1R|Blast-alpha,alpha-trehalose-phosphate synthase [UDP-forming], putative [Phytophthora infestans T30-4](gb|EEY68908.1|) 6e-15 NOT\_ORF

MGERWPDVPLSALSTLELLC\*RPI\*LSVYCQKLQLWSRQLKNWRSPD\*RFVAEHGYSVRR

SILGNDARTRRP\*ERYGDLLVTEGELQRWHVKAKTITVTDVITQL

>contig32653 Frame-2F

MKLLKVAHCDCLLRNKTTPSTRKCPLSVNRCCND

>contig32851 Frame-1F

MENILNTSRSSLCDLPLREYVSFEVTAAAELSDREWPLKSIRAYAHLIGGLRGVSMIFVM

LFLWQALQVMSDLWVVCLVHSSNPPNFMNG

>contig32925 Frame-1R

MRYAFLHDAREPYNLSEAEQLSEVKTEEEKAGMSHEEHKGILLGSDDEFLVDETSISDFA

TPVASPKLQLLDAFEDFERCEPSSPGSPPPFAVAKSTSVKQSEDCGLGGSPFRWENLVDD

PNYTAPVFNSPPSVRHKHNFKGRFGLEDDEFKVLTSNLPLRQSPRGLMSPPDSQDNRSNF

GAYSTYVATQAFKGLKIRLPPGSPLLDSPLIDSPSLSRKISNSEYPFLKEESICTGQRAV

SSNNNAFYGVGEMDTMPALTSFLGDNPFSGSVTQSALEDAFLDMAGSRLDASNVLLSSRM

TIASAVHSQSRMHYHADDCRDAASNSAD

>contig35058 Frame-0F|Blast-dynein heavy chain [Phytophthora infestans T30-4](gb|EEY64009.1|) 0.0

MRKTLSLLLEVAVRSYPNDDNADNYLKWVSDFPAQVIILATQVQWSNEIENRLKAGSDNL

SLVIKQLDNLLLILSGQVLTDVKNDVRKKYEQLITELVHQKSVSKRLSQAKVSSTDDFRW

LYHMRHYFQANESDPLKQLTIKISNASFSYGFEYFGVGERLVQTPLTERCYLTLTQALDF

GMGGNPFGPAGTGKTESVKALGSHLGRFVLVFNCDEHFDFQAMGRIFVGLCQVGAWGCFD

EFNRLEERVLSAVSQQILAIQSGVSSLKIGKTAVKSQALTSGSSPSITIELLGKNVKLNP

NVGIFVTMNPGYAGRSNLPDNLKQLFRSIAMVAPDRDLIAQVMLFSQGITTAEQISAKVV

LLFNLCEDQLSKQ

>contig35137 Frame-0R

MNTCLPSTLKPGAKSLVTTSDCNRRFNGLWILIKGVRDNTY

>contig35142 Frame-2F

MSTLDAMSRLMSAAATNARIKKLTSNSCLFAGKRGDCCGVCESIKRQFDLRLMLRCSHCD

REMGDCCFQECDACCNVFCIHCSTLNCDEKLDRVFCLSCNDDLHLR

>contig35708 Frame-1F

MWMPYRVEFEAFDDLDKKETVSYHMHVHAKMFLPYLKSD

>contig35919 Frame-1R

MMRVQEFGRDECNTTALARLKRIINGCAFVAIDTEMGGISCQDTPRASVMDTIDERYAQY

RQSAHEFPLVQFGLSIFTWDANARVFRVETFQFPLFPVFHDKGQDHSSASISSMDRRFLI

QAKCLQYIRAHGFDLNVWIDRGIGNLSHFEQQQEPCKSALEQSAKPAILRKFDSTQP

>contig36415 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66416.1|) 3e-31

MEFTLPVPSRSELYPTLTLHSQDVHVFSQMSAPDITKLNLQELDL

>contig36781 Frame-1R

MAFGSKYNLTPRQGTPEYGPTTSNLSPSGGQDRGNNNFSNQESTIKGSRVYGKVKHKNHR

SHESCKSCGSLANKCSCKECECQICAKKGGMAENFEPPIKSATSSTVVCSGSCIAAAQRA

AAGKCPGCACVADNCHCTNCSCRKSEKAKNRNLGGCPACGCSLGKCPCTHCKCPVCKSA

>contig37474 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69019.1|) 2e-07

MKKQGFVYGHFVTRKRGVVTLEWENVDTSSVISKPLQFQVKVLPLCHAAEVLDVASELNR

VNTAEWLHHFVRASDVTSLSEILDWEDDEHEATLNKVNNLSDENLEKTMQVETAALEERT

SQLEAQVMHLEASLTLTKKELKSALDRVQISDEIYKANLEAITQ

>contig38246 Frame-2R|Blast-ornithine decarboxylase 1 [Phytophthora infestans T30-4](gb|EEY63811.1|) 1e-140

MVHDVPDLLNYASSLNLDVVGVSFHVGSGCFDVQAYTDAVARARRVFDIGHSFGYRFDLL

DIGGGFPGSESAPIRFEDCARELKKSLALNFPQGSGVTVISEPGRFFAAATHTLAVNVIG

RKVAPNFEIPGKPPVLASAAAAEVPKYMYFVNDGLYASFNCMVYDHPTIQPVIMSHTASM

DAITMHKASLWGPTCDGMDCIMKEVDLPLMDVGQWILFPSMGAYTCAAGSDFNGFQRPHK

IYFDSNYVADDQQQFVH

>contig38624 Frame-2F|Blast-ferredoxin-dependent glutamate synthase, putative [Phytophthora infestans T30-4](gb|EEY58996.1|) 1e-94

MIASLKKKRSRSTVVQANEMLVRMSHRGGCGCDPASGDGAGMLVALPHEFLQRVTKEGGF

GTEAKRFALEMEKYAVGNVFFNKNAPNDIPLAKQTFNEMAQAMGLRVLGWRAVPTTSKTL

GATSLASEPHVEQILVLNENPKLSGDDFEKELLRLRNVVTSVNEKKYSDFYVNSLSNRTI

TYKGQLTP

>contig39511 Frame-2F|Blast-ATPase WRNIP1 [Phytophthora infestans T30-4](gb|EEY53542.1|) 9e-62

MILWGPPGCGKTTLAHVISKRTKCKFISLSGATSKVGDLKNAIDRARAECKLFHRRTIVF

TDEIHRFNKSQQDIFLPPVEDGTITLIGATTENPSFEVHSALLSRCRVFTLNKHTPESIE

RILRRAVQDADFGGMRSLTTNRNLNAVPYSTANCHRKMMKNHRSKSMMRRISTWLCSVLV

MRELL

>contig39638 Frame-1F

MNFSKNTGMTFSMRLPTGKSKQKPLAAPFASKSKQYGLLIPLKDSVKQESRKSLNVFAAA

AEKSKKEKIADSKENAKCQKEIESTRSVHACRVDKLHALALAEDASVFDYDAVYDDMKSA

RAIEAGKSAAKREDEKKRPKYISTLLQQAKIREVENERIRERRLLNERKADDVLYGDKEK

LVSASYKRKLQEMQRWDAEDARLAEVEEREDVVKQAEHGIAGFYANLNKNIAMGGSTDNA

RSAYTAHGAPKIDRIAAVECKHEREHENAERATIEKFKDT

>contig39854 Frame-2R

MSFESNSLSVADASNHDDIPENRTVFELRMRCRRSQRDPPRIVVASFSLRLRSHFSTRAC

LISLSRRLVMWDHKAALNGLDMTEHDGHLDETRRSSFQLRE

>contig40058 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63745.1|) 0.0

MIYYSDRSLWRLLLHFDGSAIVSASTLIRSFLIAALSFVLSALQHEKPSLVPTGAPGQLL

LSASIFLSILLGLRVFTALRQWQRGVEDVSAIADAARMLTTTACSFVHFSRKGVADRAQI

RNKCQFIRDVKRYILLYVTLVFHDCNEREASLELRALLTQKEADEFLHTEVLKLGEHTWN

RERNVVGSANKMRAAVVELWLRRTINRARRKSYVSVEQAMELNKIVSSLTQMYTRIFNLC

NVRIPFNLAQCLHVCFVGYLLLMGAALAPVIGCFSSLFVGIAAILLFALDSVASSIECPF

GPDANDVDLEARILCIQDELKVILQAHFYSVGHVDSFNEQDRMASLSSLLSAGADTLSLG

HTRRESVSSSYSSTERPPRSLAPSSASTTDRAVLLSIHPDAYGT

>contig40708 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57746.1|) 7e-81

MVLSFALRKLPKCTGAFIVPTQGRSVYTKGLAKDLMGKSCYNGVNFIIPAKATVFEALTR

MAGINLGCLAVSSDDGKFAGVITERDYLKKVELQGLTAKDTLVGQIMTNRARLTVAVASE

TPSQLMTKMLSSDVRHLPIVNDDGDLIGMLSIKDIVREINREHDADMDTLSNFAMGHGGH

FVLD

>contig41026 Frame-0F

MVPFQSDPDELVRITFAECLPQLAETSRRFLEIAHAMKQKTLTSSGSAASLSNRSNESSV

STTIYMASSSFDKELSVLHKMISRFVIQLTTPDQKASSSLVKRALLVDITRLCVFFGQER

TLDVVLPQLITFLNDPDWELRGAFFDYIVGVCSFVGRVVVEHNILPCIEQALFDVQEIVI

TKAVECLTGLCQLGLFQKKNSTLVEKARMTCSLLLHPSWWIRDAVLKLMGEIALKLHSVD

ANVLLSPVIRPFLRKTMVFLPNEDECEVTKRLRDCCRPHVSRETFDRALLASSSLSGLRE

VIAEMEQSFVEAPEESDDEVASTAPISAITTTLRESLDEPIGEMARVRRNRDALLSADSS

DGYGMIRQHSSGEAVASSAMATAQTILNSVADGEACTYDQRKHEIQSLKLIQQYVSIASM

QLRSKLEMAKTEQAARMQGPLKTDRINLAHGPVTSSSVAGAAGTTSNPFARKLSRSHLRV

LFVPDMRFALSTAQPVKASSFGIPSTSSIMPSSSASSASTALVSRSRSHAASNSPSHRIG

SVTSTAFKAGTAPSLESLSLSQVGKMYSLVEPSTPIVASP

>contig41141 Frame-1F|Blast-chromodomain-helicase-DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY57581.1|) 4e-94

MKRFHEKEFHLSQYPHRQANDMKEESLALDDLEYFNPDFLEIHRIIAHRKDRPMPNDVDF

SDAPIDDGMRYFIKWRILSYTDATWERACDIKDDVALAKYKASTLVPDENVWKPRPRPSI

REYRKLDESPRFGEDQSLSLRAYQLEGLNWLLWNWYNERPSILADEMGLGKTIQTL

>contig41255 Frame-2F

MTDSKTFDLFDGLPLDYNFLEGGRDSSSGVSLNAEGSNSSFNEASSTSTAYVMLDDQMLL

DSDVPSSSPTNMMAPKSEGEDLLTPLNFSFNPNVSTAMGTNYRVAPQHKHKRVRSNPDIL

QGLGIATMAPSVITQPALPPHRLEFTQQHNVMSLGLDQIEPLTDPVQLVGIASSHGESFQ

EMDEFLKDLSWTELNNEHKRTPSQLVTVNGNGYPSTGALPVDYRTQRIQEGVNELKMKRK

RPVNHHIRHHSNPVNLLYNLDQFRVLAQQNKEQRLVPLQVHQQAQQNINPNQGYSIPIAN

YLDSTSFLALPQINVQQVQFQVPPEIASGATISLHGRRSSLGSNLPPRAAARSRTHRSSG

LSMDMSQMNLDFLSVLEEPNMTGLASQRSPERNSSSPSASSSGSKKISLDDINKKMYKCG

RCGQPKVGHICTMPDQRNNWTQADLEVTKGTQSHAC

>contig41534 Frame-1F|Blast-Annexin (Annexin) Family [Phytophthora infestans T30-4](gb|EEY65375.1|) 1e-164

MLNLYPPSTHSAWNGQPPSYPAGTDSIVNEIYEATKGTGTKEKQLNKALGGKTATERGYI

ASRYKELHNQQLRDVLDDETSGHYGFLLKLLASPLPEAEAGILRKATKGLGTKEELIYPV

VVGRTNVEISMLKKVYFDLYGDDLGSVLDSDLHGDYQKVILASLQASLVPYDGSIHNAAK

VQADVEKLYAMGRGKMGTDEDGFVGILVASPPEHLRAVSAAYEKKYNEPLAKAAAHEFTG

NAEKAVLFLIRMITEPLDLLAELFEEVMKGFGTDENALSSAVVRYHIVLRDIKPVYKKKY

GKELRERIAEEVSGDYGELLLSVFDARD

>contig42052 Frame-1R

MDLAIKKRIQVGLNVKQFEEWVDDTLEQFAHFSPALMYDPMFQALVKNHKDYLELANILY

DPALRKTEAVLKFQELLVLHLGAIHMETMRSLFDVLGLNALDLQFFQNTSFRIWIAFAKY

WGNASDRWTLFVLRKLRIELSNDVEVALHLVAVKGLSKESYAHEVMTELFADWASDPDKA

KAVRLILLPRVIARNEPCQNVWHAFASFLKEEHRK

>contig42474 Frame-0R

MALPSGMHLVSALDDADLNVLWPLRNDEAIYASNDVRRALLLPLEGDEALDADIDVDVFR

PSAMLDTQLSSAFGNSDTLLYGSIFQPELVNAEEDIEQLLLSGSEEAFASLQSHHQHQSA

PGKSCECRTFAIQASHVQAQQERVATNVIATKDQKRVLRHTFGSGT

>contig42809 Frame-2F

MSLLISNINNSPQLDKNEHQGCEYLDMVLTIFVIGASGDLAKKKTYPSLFALYTMGYLPK

HVIIVGYARSAIGDSDFRSQIAPWIKPKTSEDEARKEAFLNKCIYRNGNYDSAEDVDKVS

KEMESFEEVHGSNEVNRLFYFAIPPTVFVPIGTSIKKAALTTRGWNRLIVEKPFGHDLSS

FDKLSRDMSALYCEDEIYRIDHYLGKEMVQNLLVLRFGNTIFEPIWNRNYISSVTITFKE

DIGTQGRGGYFDSFGIIRDVMQNHLLQVLSLVAI

>contig43349 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66641.1|) 2e-70

METAAKHFEQHVELDDNVLATSAPLEISQIDRVILQVSEGLAGYPDLSQKSINLRAQLVE

EKTINAAGAIQGMLDMLKANCKALEYFKGSIVGVLTGQPLPLNPPFFGGTIPKPAVEAVG

CEVEVPLTDTAPDGKAKTEKDSIAAYEEKETPILSNQPETLRKHSLEKSSTAEESSTSKR

PRVETSSETCIEDIAAPPLRTALSEETIFDSEDAKIQATNPTYTVPTQWENLYYKQVEVI

HV

>contig43415 Frame-1F|Blast-argininosuccinate lyase [Phytophthora infestans](gb|AAN31472.1|) 0.0

MTDAPNGAKKLWGGRFRGNVDPVMNKFNESLTIDKRMWRVDLDGSQAYARALEKSGVLTT

AEANEIVLGLDKVGEEWAAGTFEPKDGDEDIHTANERRLTELIGAVGGKLHTGRSRNDQV

ATDVRLYLKRTIVGLQNGLKELIGTANQLAENNIDLLMPGFTHLQPAQPLRFSHWVLSHC

AALLRDADRLTDLTKRVDYMPLGNGALAGNSFGLDREGLAKSLGFAHVTPNSLDGVCDRD

FVAEFLFWASMVMVHLSQMSEDLIIYNTLKFVTMADAYSTGSSLMPQKKNPDALELLRGK

SGTVMGRLNGFLVTLKGLPRSYNKDLQEDKTALFDVVDTMEDCLQIATGVLATLTPHGGK

MRSFLATEMLATDLAEYLVRKGVPFRETHHVAGAAVRMAEDKNKALSALTFKELATLHPK

FEEDVLDVWDFDLSVERKNVTGGTSKSAVEKQIADLKAWLA

>contig43781 Frame-0R

MKTQSHVQYLNTFFFDRNICK

>contig43868 Frame-0F

MTTFNSPIWLPLWCNVALWSAEHPVDLQNYRIRVNCRLAVAFIDSPILTYIMCT

>contig44717 Frame-2F|Blast-unknown [Phytophthora infestans]gb|EEY62661.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|AAN31499.1|) 3e-37

MISSWLLFSSAIMAVAMAAHIKVNHHHRGHHQKFREVTVIPDNGICPNGGDVLLCQSASF

ACQDDGTGKQKCLNRDDSFLDSIDSKTAAPWMQCSLTNASLPSLCL

>contig44898 Frame-1F|Blast-phosphatidylinositol kinase [Phytophthora infestans T30-4](gb|EEY59985.1|) 3e-24

MEKAAGLYNTNIVSATFWSYEKSKYLQKVGMLDDGRRLLEAQCEACLSFVESNQTNPEQK

V

>contig44982 Frame-2R|Blast-glutathione S-transferase, putative [Phytophthora infestans T30-4](gb|EEY65707.1|) 1e-59

MMLVSFLETDVEKMKASREELAMDLIPRYAKLFESRLAKMQEIPAFQTEKVFIHDVAIYC

WAEPLRSGNTG

>contig45361 Frame-0R

MQKFLEQADGIEEEAKRLAMKDYEDVLPHVFKEKDRPLDAAPSIASIQQESLLLLQRQDF

ESLLRVKDHMIYQL

>contig45822 Frame-0F

MEKTLNEALDIHTGADLFAQRGKLCYLFSDKTASWLLQISLGIQVRREKLERKSFSRERT

FGALNDPIKLEAKCLDICMLLAEDLEKANKAAKHVTFVYKGTDFARYSRSMSLATAIYTA

DDLYSIAVELLRRELPLSLRLMGVRAATLVSRFQSTTSPTTFSLAPASKKRQIVIKKFAE

HVSDSATALPDNLAELNDRENIRCSDKHAPDSDPLLQLERNLMKPSSVLHSADTNVDGIY

RPLAPCFKSMKARKVVIRPCPICGRPLNTLNNIKVNQHIDACVGTKMPSTSLTDGCGSKG

IAVSQFFEYSTKRIKKKQRHVLSAVSC

>contig45857 Frame-2R

MKVPLEWLAAWQVIHWTCLGAGATAALLLLLHSATFRCKRRMTDLLLGGIALADLCFVTL

EALKQALHTSYFARYRRKDEGLEEFHYTTGDFILTLMSRFSFFKSLCWIANLSLLMRLGA

LKALQVKKNLLISSLVSFGYGCMHAT

>contig45996 Frame-0F|Blast-Phosphatidylinositol 4-phosphate 5-kinase (PIPK-D12/GPCR-PIPK) [Phytophthora infestans T30-4](gb|EEY54682.1|) 0.0

MGAYEALAVAQSAQLYLLVGVFGFIVYLVLVLSFFFVPNIKGQHPAADLVVWHAGCGLLM

SAGLIFAFTLQQHDKLPQDDLLIQWQCSLLGPINQFFLMAGACWYLMLSLDLLVALVNPW

MGYSCKSWTYHTIVWSISAVSAVLLYQQDLFGLSPLNICWVKRTKDPMQLNMANWIFLFT

IVAAICVLSFAVLLFASFRFVRRQLDVTYRAKRRNLMQYYRYLLVFASNWTACGALYYAA

YRQKFDGKTAKRFELAFALVYGSYPVLLLIVWVLNTEMYQNLSSENNLPKSVRGAGDVSS

TEHFSAALRKDLMRYTTAGIRCSITGSPLDSLRSPLLGLTRDRCTSVDRTAALSFLQLEE

NDSANLYHEKKRVATTVYNGEYRYYEKLGFTDYAPKVFQNIREICGVDNEMYEQSFADTL

LERASEGKSGMLFYFTSDR

>contig46489-0 Frame-1F0

MNLSINSLTFAAFIRLRISSTIFP

>contig46830 Frame-1F

MKTHSPTPCENLSSLKVALLTHLFADKTRLPRCLNSLDQDNRDVVVLATTVHEVPIKCHE

FAFEKSSRELYSTMKVPHCKI

>contig47208 Frame-1R

MKSHPGTSQIIAKLLTITDVFAAGSKKTRDWRHQSRQAREFPARTSCWISLNSLLWTQCF

SRPFVKIVRLSAQSGLSRGKYG

>contig47301 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69137.1|) 2e-08

MPSAKLQETVSKPRHGSVGRPLKTRKVLRVVDTELNLTTQKDPTETSDAAKSSPSASDDV

MRLDAMQFGHYTHRCALCCEKDTVCKASFLDALFLCPACDQKYPTQQTLKWRACVT

>contig47437 Frame-1F

MLQHFFCALCVLALLACLHFVAAAAVANRPLLKMQQNRSLASSVKGVKGLIDVFGSTLPK

TAVVGNDLLRIEGDVKNSVKNAVESWSTISSNFLKMTLDEEN

>contig47990 Frame-2F|Blast-SUMO ligase, putative [Phytophthora infestans T30-4](gb|EEY57558.1|) 8e-06

MESFADKARGTTSAGFYNERFAAGMRSIDQQTQGRTSCLPFPQATQASYRTVVPQIPGIF

GPLAPTAPPARPIPAPIYAHNSTTQAPVSYGSTGAASLGAGVVSL

>contig48483 Frame-0F

MVLLLIENGADVHAKDGSGIPPLYLACARGQDVVVEALLKKGATCMAVGPNGETPLHIAA

QENQLACIKVLLDVGHVHVDQVTHDRCTALHLASQRGNTAVAACLLDFGADIHALTKENE

SPLLKASRMSQFQTVKLLVSRNASSKPFQTRHKLEEKSVVAKKKTSFASSMGTGVDLEMQ

LPRSRSWSSSGNDSHRKSGKNSSDRICIVKSNTHTSLKHWLRSVLHN

>contig48564 Frame-1F|Blast-calcineurin-like phosphoesterase [Phytophthora infestans T30-4](gb|EEY64315.1|) 5e-36

MGAANQSEGTSYPLTHIAPWNAVTNYKHFEYSMVEANRTALVWTIF

>contig48700 Frame-1R

MSKSHLYAIQGGSAAIVHILRAVKLDAKGGLSQTIMDAIYAISEELVESQFLNECADSIW

LTCTRAGWTLVGSLVSMNDEQWVTANLEKLLNLWLKSSVLHSRE

>contig48955 Frame-2F

MDETAQRSLLLWVQSFQSKLATDEHIRSISDLCDGVFLSKIMHHIDPEYIKLEQICKKPS

DNWALKSQNLKTLLRAVEMFYIDELGQICHANELVDPLLIAKENDFHEVSKLTELLLGCA

VQCPNKSEYIHPIMQMGASEQASLMHAIEKLMHRIQPLSPSRISMARDSSFDGMTSPNLS

APA

>contig49509 Frame-1F|Blast-DNA repair protein RAD50, putative [Phytophthora infestans T30-4](gb|EEY58381.1|) 3e-24

MRRSQGSSGYSLSDVEAEKDAKQSQVQELNRQLQLKQKDLEHINDVLQQLQNDVHRRKEE

KLQLETQR

>contig49718 Frame-2F

MAAGGLECSGSLSISSFVSPMMHVLYLTSRIMTRRSPDCYS

>contig49974 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66024.1|) 1e-110

MWVLDAESSDGDSKTTFYLAAGEWSVGRKNCHFSFYADLSISRVHALIRVGALSSKQLED

PSTRPTLELVDKNSRFGSFVNQQQIIGTRSLQHGDEISFGAKTTVLRLRYQIFILVASRI

RRANRAKLNDACQCLGMHLIAMESKNATHCIMDPGHVVATIKMLWALVYNQPVVCTPWIY

AILNRSNLSEPLPRCEDFLPANSSAPSKESNYLPNPLRKTLFEGYGVVFFTPQLIQEIIA

AMGGVVIAAYEDPREISDFLRQLALLAKHKRLLLVDSSQESGFSGIGGQNKQRSKATVDS

PCFAENADQRAKFLLSIGGIFTSVQELAASVILVKPPSTSNSPSFSSSLASYADSQVQNI

IAWQEGNHKGANVKSKQMKIVEDTVGTCKKSSEQITGPHNDTVKVHMSKDGKGNLCKTRN

PDESQEVALVSRESELVMPIRKRNDELASSWKSSRDLQSRDVKLEADDIRKPIVVSCSLI

VKRSEPDQSNKKDRSGLKNFKRFKKGNGCGSGSSTTS

>contig50187 Frame-1F|Blast-dihydroxyacetone kinase, putative [Phytophthora infestans T30-4](gb|EEY69770.1|) 8e-78

MEDLKIHYPLNDASQTMCALADSVRRSAGGTSGVLYVIFLTAASLFLKSCKEVDTVAWIG

AFRAGICAVQKYGGAKEGSRTMMDALIPSLRALDNTNMNTRFELVEAAAKAAQDGADATA

QISTQQACGRAGYIGEEFGVGIPDPGAKAAALWIQAIADSLKAHN

>contig50716 Frame-2R

MGQVLMVKAFGLTLAACSSGLAGISIYGSDIEIQITYLKNRVLIAVPHVLGTCAVATKAT

EMSDIAIALLTGGEIPNNEERNLNLIFGLSSTTCSCKSVPRPC

>contig50842 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY65878.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62348.1|) 3e-08

MLRTSRRSVRVGETLLSSLLQRSPFSCILIHPASTAALQRLPINVFSSRNAICNEAAMIR

FFCSSRSSDAQRKTEVANVLPHDEKDSSELVYQAPMARAVRLMKAVSVTSCTLTSLGMPI

LCIISPQDTSMLA

>contig50958 Frame-1F|Blast-nucleolar complex protein 3 [Phytophthora infestans T30-4](gb|EEY59642.1|) 6e-83

MIDLLKVLKAVLRKEDLLPLPASLQAVLTGLRALEGPGGQELMIDEKEFVDILYRLLYRF

AEGDVSSDSSCFLTLLQCVEAVFLRRKELVVERVASFVKRLLLVAQHLPPHQALAILSLL

>contig51089 Frame-0F

MQQQRYQEAATFLQSLKNIDQQMPLDAADKLRIDTIENDLKGVIEGEFEDGLKGGHNQQI

QTYAPLFKAVSKEYEEHGLVLLLEHVQKTLAQSLTGKSGTQVGVFSTQKTITCLTEVFNQ

IAQEVQQYEELLSQCFERVHGLNRFVAKLYTMGERSAVAVLNAYMVQRQYYKRITNKDQP

LSSTIIGTMSPSGRNHSIQSALENSTDNDIAFMNEQLNEMALVIQHTQTYERFMRSRVAF

DGEKNANNIEESGMNEQTYDEKDIVVPVLPPVHNSELGKSVQELAGFYCFFENDLLNQAA

RKAFQWDELHFSSGNGNLNGANGSGIDNNLLCCPISSAIDEIFYVARNSGLRALATGHVD

CAAGVLNVINTVLRDIVGDTMRSRIRQMTTGAKME

>contig51346 Frame-1F

MHRHKVFSFFSPWSTGKRKMRFSRPYSFFAICRIQRLYTVDRRTKERDTGISHTVFVPLL

FATQPREESNRLLYLSHDNSCFWFESIFLNCKPRTSATTGCILTVP

>contig52365 Frame-1R

MGASCCHCQRLDDPLLSLPPASSMRPSLEHLYVPAPLTAVSGSVSSSTSSPRSTSSSVRQ

SLANYISFPFT

>contig52435 Frame-0F

MLRQISTTSAGYTSVKLPVGALEGFLTALVPTSVASKLHNLVCLPSIFSSVAHEFQFQFA

SPQLER

>contig53007 Frame-0F|Blast-general transcription factor IIH subunit, putative [Phytophthora infestans T30-4](gb|EEY65991.1|) 6e-89

MIRLRLAHNSTLVLEFVATSTRLEDAFKVREQAKDYIARRLRENGASGTHSNAAALCNPT

EIKQRAALLAASPTLKRQHTEMVNDGLISEEDFWASRRHLIAGEASKRQKTAKTSAILTD

LAADNETGGNVVKYNLNAEVIHQIFIQYPAVYLAYQGQVPDKMT

>contig53384 Frame-1F

MLEQVCALEGHSERAWHVSWRFDGKLIASTSGDRTIRLWSVKSNGSWECVGILEDAQGRT

IRACEWSPDGRYLASVSFDGTTVIWEKQGTSYEVISSLEGHESEVKSVAWSPSGAYLATC

SRDKSVWIWEADADTDFECISVLHGHLQDVKFVAWHPTEELLVSTSYDDTIRIWAENDDD

WYCKETLVGHTSTVWGVALSPLGTQMASASDDTSVIVWQYDPSSKSVNEDGSSRQWKQAF

TLPKCHERTIFSVDWSSEGDYLVTGASDNAIRVFKGKPEGQITSFELVVDQKMAHTSDV

>contig53678 Frame-2F

MSCNSFAQAQAASLGLSLSNSLSTKAFVSYSLEDMQHLLEASDYQVSGVDLQAYYLV

>contig53696 Frame-0R

MASQSFKSLVASYQSRLLSPSGSSFPTACDQSSTASDSSMTTLQELFQCMNVASHQPQRV

RRTTFTLRDLVQSQLRGDPQDKSLISSIL

>contig53722 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53214.1|) 8e-93

MRAQLSSTGMGFRMTMTGSDIPPIVPDSLFESTTDCFVCEKKFHAFRRKHRCRACGNAVC

GSCARTHKILPSSTLVRYNNEPVRVCDTCVRDQNLLLLERRRSEDVERARARQVAAQEEA

ERQREAERVQRERAVTEAQARREMRLRAIEERHLGPRPDFRTLRLRYSRSLDDCARDGHP

RSIYSKELSSFIEDAEKRSVALTVKPYAAADVFEDKM

>contig53757 Frame-2R

MSSVRRSSWQESICLYPPAVPRTDIWCQRRRRRWGGGMPKSFLWMNLICTYTNWPYKIVM

QSGLSIHGPQYVLYTLEPHDGRYPRYYCCQ

>contig53829 Frame-0F

MLRITQALRIEINSVMGSSWHGKDTQHGNTHVSHVISSDLAREEQQQHVDYSLMPPVVLA

HDTSSQIVTPFASSASVKIDDTPASNDNGVFRSDGAWSEDSEKYMLLRRVHNGLDSLKQQ

LEQLQVAGIQFEVDRIKEVRATLSQDRKPAFSSSTRKQGSGAAGRSASGSKGKSGA

>contig54020 Frame-0F|Blast-alpha-1,3-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY57731.1|) 7e-13

MALALATALYVIVASGIILLIVVGWAFLHGLSCVIPRAIRPSKGTELLRVGFLHPDLGIG

GAEN

>contig54222 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55750.1|) 8e-15

MATKKRCGQRYDRIICLTLRSVQLAMCIVALAFVGASFQSHTLSFETDDGETHDVTVYYG

GPA

>contig54257 Frame-0R

MTARAVGELRDHAADSMVSVSAGYVLAALGHESSVSFAHVLQIAIPVLVEQLDNESVKSE

PVPSKCEAALSRILLLVDTIDREVDQSGHAQPMRPHVPVVIDTLVQFLSSHSNNQTMTAR

CVAVQALCHLLTFPPSPIVSPAQVKALINLYTRMLLLDPAAEVRSACLHSLKEISTVSTP

HVASMTATGGDPVTSGYAAFVVEITLARLMAAVNERSDHEEDDDDKSTSKIALLSASNRN

FDSFFEETLLAITEL

>contig54396 Frame-2R

MDLVSIVIRRRTSAINTGVGLIESYYARECTSPTFVS

>contig54499 Frame-0F|Blast-CENP-B protein; Homeodomain-like [Medicago truncatula](gb|ABN09791.1|) 6e-07 NOT\_ORF

MKTMYQPVKDEDAPTLSIGNLKIATASACTFALAKADLS

>contig54684 Frame-2F

MAPMSSDGEGFGCAMRASTYERSTACIAKRLRESMEKTTRLLEAFEHELGESSVPMGTYQ

RCCRQ

>contig54828 Frame-2F

MNVASSYIFRGGIFAILNRCTSAVCVAHSARHNGLTSNVYPL

>contig54961 Frame-0F

MDARAAMDAPAAMDAPAAMEASARSFIGNCTSFLSPKTTLLIPYSTTPHLNTQQSHERRH

KRALSTRSSLWDTVGAN

>contig55005 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY64219.1|) 7e-29

MQRQRVTLFSSEDANAMALRERSRTMLGLSRGSTRYDNRAQSYSLRPSTTVYGHEGDELF

DGSISYSSVTERSCTGSNAPVRTRLSVSP

>contig55782 Frame-1F|Blast-nucleolar protein 10, putative [Phytophthora infestans T30-4](gb|EEY53610.1|) 1e-140

MHGFFMNARLYNKVKAVAEPFAYEEWRKKKIQEKIESKQANRITIPRRLPKINRATAERI

LQNESKRKKGNTQVGDETNSDQNFSNPLRDERFSRMFTSSDFEVDEESEAYRMLHPSAAN

TRQKLKQQEDMDSDAGTDDEAADDEVSDRFCPCDRR

>contig56318 Frame-2R

MKHQNLTSIITTDIAEIPADSDHRSKSRLRAKRLYDKKR

>contig56952 Frame-1F

MLLYGAAGNCRQSFSYFCARR

>contig57164 Frame-0F|Blast-peptidyl-prolyl cis-trans isomerase C [Phytophthora infestans T30-4](gb|EEY61046.1|) 4e-87

MQFPDEPNGLRLHHSKRYLLQMANAGPDTNDSQFCFMLKASPHLNGKHVVFGEVVEGFEV

VDKMEQAGVERDGIPLQHQVRLIDGGELLV

>contig57300 Frame-1R|Blast-dihydrolipoamide succinyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64480.1|) 2e-09

MIDIDRLEILYRDNVDMSVAVSTPKSLI

>contig57656 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63563.1|) 1e-24

MSILLAGLIGFQARRTVARISIVAGGDKLRFTTHKFF

>contig58374-1 Frame-1R1

MYLKQVRKERTDLWKHRTPR

>contig58752 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57929.1|) 2e-72

MDPVVGALWTCSVCSNYNLCSECYDLGTHGMENTEQMQALTEAIVQFKLQKRCKYFTPEF

LLSLRRDICKGRPDKFEYLGEWIANIVVGTSVAKITVRGIEIPTLLPMARQRFVSYLMPL

VSNRTD

>contig04260-1 Frame-2F1

MSKRSHLRKKPPRRTWRVPRQKLSRRTARAPMWKLP

>contig04808 Frame-2R

MMEPPLCKYGEPPTSSTYPNILPMGSMSWSSHVVQPPHPSLTVATPLRHPASTPSP

>contig06811 Frame-2R

MVPAVRPLHGLYLFECFLYGQQACNHFVYPMDDDEMEAGFEITEKITKGTTLNGFLDGNS

TAIGRMFILVGGVIVAVGIRNGRNRVNGYDMVH

>contig07229 Frame-0R

MSVPTIRFLYARKSRLDPSHTHAPALIQDRLYT

>contig10445 Frame-2F

MGYYAKIALNCTLNRNILDRYKDHRRRNPQDGIHANLSPTLPDILGL

>contig11929 Frame-1F|Blast-N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase, putative [Phytophthora infestans T30-4](gb|EEY53387.1|) 9e-76

MHVTEQPRHETHHRWIGGSYAIIVCFIILLSSAYKIPHHKVVVINTWPFVNATRAGFQAI

QGRHGGLRALSAITKGCNRCETDQCDFTVGYGGSPDSNGETTLDAMILDGTTMAMGAVAQ

LRRIKPAIEVARAVMEHSAHSILVGDGALNFAKMMGFEETRLDTPHSRELYQKWLRTKCH

>contig12340 Frame-2F

MRRAMQLQARNGLWRHVQQPKFPYAAAHSQGALARPAQSLRAMSTVAPKALEEDTIVSMP

ILEEATCEVNDMGRKLKPREVVEQLNKYIVGQADAKRAVAIALRNRWRRQKISDALRQEV

SPKNILMIGPTGCGKTEIARRLAKLSEAPFVKVEATKFTEVGFHGRDVDQIIRDLVENAI

NMVKKYRKERLRKQVQHLVESRILDVLTGANVAERSRATFERLLRTGELEDRIIEFDVPA

SRNFSGQPITIVGGEGKGVPMEVFGRAFGEKKLERKRMTIAESRGAFEELEMENAIDMTD

VVREAIQETEENGIVFIDEIDKICSSGDLRRSSDPSSEGVQRDLLPLIEGSVISTKHGNV

NTDHILFICSGAFHSSKPSDLLAELQGRLPIRVELKGLTEEDLHRILTEPVTNLIKQQTE

LILTEGVTLNFTDDAVREIARVAAEINQTVENIGARRLHAVVEKVVEEISFDSSEMAPGS

SVTITKDFVLERVDNLMKTTDLSKFIL

>contig14337 Frame-1F|Blast-putative 3-isopropylmalate dehydratase large subunit [Hyaloperonospora parasitica](gb|AAY58912.1|) 1e-32

MSTEFGGIAGVFQADDITQRVLTQR

>contig16487 Frame-2R|Blast-cysteine synthase, putative [Phytophthora infestans T30-4](gb|EEY69413.1|) 4e-70

METWSVPLWRWSLCAAMATLSLWKMGELVISSGSSWCRLFKKKSQKEMYPTGFSGLIGNT

PLVELTSLSKATGCQILGKAEFLNPGGSSKDRVAKEIVEKAERQGLLKQGGTIIEGTSGS

TGISLSLLARARKYRCIIVMPDDQAKEKSHLLELFGAEVVFVRPASIVSAKHYVNVAKRL

ELKTEG

>contig16533 Frame-2R|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY70000.1|) 3e-97

MQRTKDIMETIVVEKLHVLLDVLATYHARHEPFSLKTEFHHFSMDIITKIGLGVELHTLR

DSPTRDSEHEFLEAFDSAAIGFAVRVQTPTSIWRLQRFLNLGKEKTFRNDIATLHNFINQ

VIRESMEKKAQRAAMNQKLVEKDLISLFLESNLPAPENVKKHDDDLVTTMRDMVTTFVFA

GKDAVAHSMCWFIIMMNRYPKVLRKIRDEMQQNVPGLLTGAIRVAKAEHVRHLVYLEAAI

KENLRLTPSTGF

>contig16836 Frame-0F|Blast-ras family GTPase, putative [Phytophthora infestans T30-4](gb|EEY61618.1|) 5e-29

MTIEVQRKLTVLGYPGVGKSSLTTCFVENRFVENYDPTIENTFHKTIRVRNAHFVTDIVD

TAGM

>contig17578 Frame-0R

MVACDPSNTESRGIISMLLAVHLAKSISPRFRPCSSRKNVILALVSTTYRTFQPPDRSPK

PCLNSKPALITPPRGTVAARTITVSRE

>contig17691 Frame-1F

MSFSPPTTHTMFVGDRDKRENTPGLGAGPPAQSNGCAVCGLDQNGDSILLCDGCDGEYHS

YCLVPPLTEIPAGDFYCKRCTEANVAKQQKVVAEGLVAAPVPVVTISKVETDSSVALHTP

APAPYVPPNPGIHMKDSKYRGVSKVYMKGVKKPFVA

>contig18056 Frame-0F

MSVAVAVMSVAIAAAIRNICLAAINLNGFRCDYCVSLDLVIIRSSSNHMRFFLCTVGTFS

LHVVAKSIPRACFSPTLQELAFCNTSLSIPERVEDLLRRLPLNEKVMLLTARASPKGNLS

SIGLPEYNWGANCVHGVQSTCGTNCATSFPNPVNIGAIFDPRAVFNMAQVIGRELRALWL

EGARENYEAGPHLGLDCWSPNININRDPRWGRNMEAPSEDPLVNSNYGVAYTKGLQEGKD

PRFFQAIVTLKHYVAYSFEHYDGIDRQAFDAVVSPYDFADTYLPAFQASIVHGKAMGVMC

SYNSVNGIPMCANEYLNTHLLRDTLGFQGYVTSDSGAIEGIYRQRHYTKSLCEAGRLAIE

SGTDVNSGEVYSECLAELVTKKQLSEEVVNKAIRRTLKLRFQLGLFDPIEDQPYWHIAPS

EVNTATSKYLSLKLAQKSLVLLQNHGMILPLAKGKRVAVIGPHAMAKRALLGNYLGQMCH

GDYLEVGCVQTPLEAIQRSNGESKTLYAYGSGINDTSTADFDDAEAVARKADTVVLFLGI

DTSIEKESQDRVNIEIPMIQMELLKRVRRAGKPTVVVLLNGGVVGIEELILYADSVIEAF

YPGFHGAQAISDILFGDAVPSGKLPVTMYPSAYIDRLDMKSMSMTQFPGRSYRYYKEVPV

FPFGWGLSYTTFTLALDKGMDSSEIIEITRDQYHTVSVIVSNDGNYVGDEVVFAFFRPLN

VDVTGNASLLNQQLFDYRRVSLRPTQFHKLSFRIQQSTLALVDEAGNHVCIPGFYEVTIT

NGVHERVTFAIQLVGEPEKLHLISKYVDRGSLHEKDVTLSVP

>contig19257 Frame-2R

MGRKALWRLSHRKNPFLHGFASLARSYLGREMSGEKRSEPKYHKSRRTRPRFGDPNGSTL

NY

>contig19507 Frame-2R

MVLAFMVTELHPYVVSLLSIN

>contig20158 Frame-2R

MKEDRGYGFQQPSKPPDLRRESQVQYITNKRHEQQDPERPYKGKRPRSRSPRHGESRSRR

RSYSRSSSCSRSYSSRSQSPSSYSYHRSRVCAARDREKMKVKREYSRRPRYRSCSSSSSR

SRSSSRSFSASPPSKRYHRRSSDISHPRSSYRHSSRSLSRRRSHSRGYSEHPKSYNENYS

KEYVTKENVKNYPKTYVETYSKEYVTTYPQEYVKEYTTASAKGYSKEVVIKKEYLKDHAK

GYRHYPSSPERRYSQPQGPQFRRSPSIDRHQAQLRDYSRGDETWAPESRSRPISVPEKHR

RSTRWQPRP

>contig21113 Frame-2F

MSDRFPGHPDSVEAVLKVDEDTILTGSSDGIVRVVQLHPNKLLGVIGDHEDFPVENLKFT

YDRKIIGSVSHTNKVHFWDVAYLFEDDDEEDEDDNEKVDSTIDTN

>contig21302 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65370.1|) 3e-49

MPIFRDSRSSSSSSNPDHLRDSGFERGDLSKGLGGWSTSSNLFKLLRPSSRSRNLALRFF

YERIAVGKFSLVKAKCALVLGTMHVTSNASHG

>contig21643 Frame-2F

MIFSAKKSGKRQESSPSLKSCRTDDHLRHALCLMSTSPQRGPCTPSCFHTSSTPPIVMAA

SAATASAREYFKTLGLRTDARGSRFLDVPQSSASTHIPMRLGHINSPCVVPGVVAAHYSR

GTPLGQASRPDASTRGHSAACVFHASNHPICGLGLVGNGFMARPIIFAHGDEIPP

>contig22093-0 Frame-0F0

MQKTMLGVVTRVRDYVFYERNPLV

>contig22167 Frame-1F|Blast-serine protease family S54, putative [Phytophthora infestans T30-4](gb|EEY57799.1|) 7e-27

MLMLVQQILQLDHKPPVTLGLIALMCGIHYQNQLQPMHFNKYYLCPDQVLNHGDLKRIVT

SGFIHVDDWHLYHNM

>contig22268 Frame-1F

MDRSGSGAEYRLRSIEEAFARERQQRDVLEKKYSRLKRRYIRLERSHNRLVMELHTKRSS

KERITLLQSETPTRESSVAMIDLTSTQENVDKNASSCLYNSSKGRHFDDICPESPSSSLD

SSTREQSQNGEDQEEKERTLQSLQPSSDRVTSNPVRRRRLHLDFSLPSNVIEPNRAVSSP

RRQMQQSRHSNRSVNSNNSPHTARSKLRHDEESRARTRPRLRLHNFSSERSAARSYGQEI

EQEQEPRANHHDRYHWVSEPSPEPTTPSPLLSSPIQSVDLAPVLPTIRSEASRLRVNSDE

EASLALALYLQHQENIAAHEEYEARLSRHPIAQELNHESLFSSSSLMSSLISRQNNIDPD

NMSYEELLRLGDEVGDVKKERWQEMAVQVLSSLPTHRWRRVHGDDTCIICQYNFVPNDRA

MTLPCAHVFHEDCVGGWIRENNSCPLCKREINSK

>contig22282 Frame-1F

MLFIKLVVRCSRRTEYLKHGPTGCTRWARFGYSQHFKENIFVDVGVKPEAVKIVPEVEDR

SFFNLEKVNQVFDLASNAAFELTNDRVLFHFQVGRTKSMEGVVDGIF

>contig22505 Frame-0R|Blast-alpha-1,3-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY57731.1|) 1e-153

MRILYPPVDVKAYSDTANADVQRDAGLFVSINRFERKKNVALAIEALAELRNKIGMDTFQ

HVKLVVAGGYDPLNAENKEHLVELQEVVGKYGLEAHVDFRTSVSNAMKLELLRKAQAVIY

TPDQEHFGIVPVEAMACGTPVI

>contig23779 Frame-2F|Blast-mRNA decapping enzyme [Phytophthora infestans T30-4](gb|EEY65612.1|) 2e-95

MPQLSATPITMTAKKSKEKPCLAEVMDELQSRFLVNLPESELCSSERLFFQIEQCYWFYE

DFYADQYAHLQHVKLNDFARKLFVHCPLLRPLAHRCDELFQDFKTYQRQVPVVGCILLNL

ARTKVVLVRNWKGTSWTFPRGKVNEGETDIECARREVLEECGYDVEDSLMPQHYLELVAN

DQRMRMYMCTDVPEHYPFA

>contig23797 Frame-1F

MNPNAHHFLLNKDPLGSLHPTIMSQAMVSSFSMDVSAYSSDLYEYPATKRPDTILPNAFV

MCWENVLTPNFWLRQKFGLKSSIESLDAVKQQILRSQHLQMAFATIEQDLIQLLNTVSNY

GPLFIVSDESIHYVEAMCKTLFPRLAYCLNSTTTMTRVHVIGAPTRFQSAAEKADWRVNL

LQSLCRDTLFAARPQNLLDSQAGKFGLVVVSPYQVDVAASRATHKVAPFVVAKSVHVQKA

RHLTLQDFTLHLRVLADYVPSAA

>contig24095 Frame-0F

MGTSEVLAVDMVATEIENAAADMVKTYKKKRSNKLKKVNKHEQDGDLGRLKEANQDQQDD

ETEHAIAKAADLAESIVDKRYFSSEDFSSLPLSEPTRKALTDMGFSKMTKIQSKSIRPLL

AGQDLLGAAKTGSGKTLSFLIPAIELLHKVRFTARKGTGCIVISPTRELALQIYGVVRDI

CKYHSQTHGIVMGGANRRAEAERLVKGVNILISTPGRLLDHLQNTKAFIYHNLQILVIDE

ADRILSIGFEEEMRQIIKCIPKERQTMLFSATQTKKVEDLARLSIKDKPVYVGVEEEDTK

ATVATLEQGYVVTPSDKRFLLLFTFLKKNLKKKVMVFFSSCSAVKFYGELLNYIDIPVLD

IHGKQKQNKRTTTFFQFCNTKTGILLCTDVAARGLDIPAVDWIIQFDPPDDPREYIHRVG

RTARGANGKGKALLMLLPDELGFLKYLKASKVALNEYEFPVSKIANVESQLMKLVEKTYY

LHKSAKDAYRGYLMAYASHSLKGIFDVGCLDLQGVAKSFGLQVPPKVTLPVKTNGKTGKR

KGTSFGNDGSALRGKFQRSGHSFSASNPYGKRASSDTRQFSH

>contig24763-1 Frame-1F1

MYVAAVPLVLGTFAMRRVVTNVRKSFNILVFGNITMFTCIRV

>contig24763-3 Frame-2R3

MQVNIVMLPNTSMLKLLRTFVTTLRMANVPSTSGTAATYIK

>contig25070 Frame-2R

MLAPNGRMYLVGLQPLIDPQTSLGSSDADADASKMIQHVARTRNACLLLAGRRCYREYPM

EWAQRQLVQSGLSVTNTVRYANVYGLSAIIRQLEVGRRHVPMFQDADLAACMQKALDRIE

KLLKDEFGSSSDAKQRKISFGFDYVIAAHKKVTSKCCDVNVREDFDTAPQFLDGGLWCLP

FRLS

>contig25489 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55878.1|) 7e-15

MTTSSPRVRFSWEDAVAQDQDLHRIDAFVKLTIFKFSGQAALRAAAFRGSSYEPVPSTVK

VEQ

>contig25593 Frame-2R

MSCLYSNTLVCSSSCGPTSERMSRLIWLTTLINTLLFESLWFFFLFFTYGIESYPEHYSP

HIKQGTNFKLHKSKLPATRHLRCGFCSRRSYRQKCHRSKMWLPVIFNTPLPSRDKCLVFS

HL

>contig25904 Frame-0F

MKPKNIKKRKAITDEAASAMKMNVHRCRFVDWMPSAIHALCFNAAGDQLAVARATGDVEI

WSVRNKWHLKFVLAGSAQSQVSALCWAPNSDRLFASSLDGTLWELDLQNSCRKNVTDSNG

GSVWCMVLDAKSQQLAVGCEDGRIRLFSFADDQLYFSKGFLPTGGRVVSLAWHAEANKLF

SGSEKGVIYCWNAKTGRNESRITLETLAKQQSIVWSLAVLNDLTLISGDSAGNLSVWNAP

TGTLLQKFSHLTADVLAICVSQCNNKFYSSGVDNQVVEFRRSAIEGGLSTWSYSYSHRGH

SHDVRALAISSTAKPVLVSGGIDTQLVWYRGNSFGASRPVKIASMPYPQTISLANQKRVL

MVQKSTSFEFWHLATQTAVTKDTTHKHKLLLELNVGSDFNTACSALSPNARFMACSNSKE

LKLFKLEIDRQYQPKKVTTLPSHVQGPARVLAFSPDSTRLVIASVAHQICILNLTKMEVM

KSFDVAVPSLSGDETANVPSPLTSLAISSDGQWLATGDALNTIAIFNLDSMQFYCRLPRP

SEMHTSMDFSPTGKILVVTLVSNTFVCYDVETKGLSEWYNENHEHLPKEMVEGRNLKGMA

FNPANPDSLFLYSQTSLYQINLSKQASATTALKKSRRRSVSNSSDTDGKNSALVGESVEL

KDDFCRIIDRYRPVSFVDFVAENEMVVVETPWLKVLSRLPGTLHRHKYGK

>contig26747 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53680.1|) 1e-154

MMGMHTLPTLLAGNLTSGRAFMWQGDLEPMAQKKFENFGEFYQLYPEFKHVFVGDNGQGD

VRAAELIVERFGSDALEAAFFQRVQPMEKMFNYHSREDLTRWRKMNILFFDTYVGAAVEA

FGMKMIRLSGLKKICDDAGHSFANIKSWLTSQSRERARLQLNCDLTAANALISKTLGSSS

LVMKPQVFALNSVVRTSMGRGIVRKYRGIDGIYCVDLTDWPSLTHHKRVQAFLPEDSLTA

YVSSDFSIIPKSSLNYVKFYRSPPVRILAAHTLVKTLFGIGRVLSYRAEDNIYTVSIPGD

QTVLHIVAYLNMDSLQPVD

>contig26949 Frame-2F

MGKLRGYDFYRAIGSPKRIVAPMV

>contig27032 Frame-1R

MDIVQNGRSQSILISGESGAGKTEATKIMMTYFAVTCGTSHTSTASSNPLEVNPALVLPS

RTTIEEQVLQSNPILEAFGNARTVRNDNSSRFGKFIELRFRDQRQRLAGARIRTYLLEKI

RVIKQAPHERNFHIFYELLSADEQCVTKEQRNDLALNGGSEGFRLLNQSSCCKRRDGVKD

AVQFRSTMRAMQQLGMSDQEICGVLKIVAAVLHLGNVEFEQVPYKRENNVFVDLARVKSS

ISGACDHFTKTAELLGVPTEALDHAITKRWLYASNETLVVGVDVAQARNTRNALTMECYR

RLFEWLVARVNAKIQRQATGSWDAERTVEDDENDSNSFIGLLDIFGFEDMAENSFEQLCI

NYANEALQHQFNQYIFEEEQRLYREEGIQWSFVDFPNNRACLELFEHRPIGIFSLTDQEC

VFPQGTDRALVAKYYLEFEKKKPHPHFCSAPVIQRTTQFIVAHYAGSVTYTVEGFLAKNK

DSLCESAAQLLARSSNPLVRALAAGSANAVGANGDSDLDGNSRNRRRAKSTIAAVSVGTQ

FKIQLNELMTAVRATIPRYVRCIKPNDSHKSLVFQSTRVVEQLRSGGVLEAVRVARAGFP

VRLFHKQFLERYRRVLLSLSRLKDENFNEMQKKGTELDLCLLQLTRVLLAGSKSDEELES

VPRDGVLNCQISCGVSIGKTRVFFRRKPFERIEKLRAAVRQEASLSIQRHVRGFMARRDY

RQFRRVTISMQAFVRGRRAYRHVCWIRTMQQARVLQARMRQLCARSKFLRARAGVRAVQC

RFRCRLAIRFVQAIRETLAVTRIAAAWRRSFAQRSYRNLCGATLALQCAFRGRRARKILK

VLRKESRNVAKLKIDNALLKDELAELRRQLQAFVHSVSNEGLSAALVPTIGGISKEAVHP

SPQNVNLLTLQNFPARASCKNQLSENKLEIKLSDDLVILDSGGNPNAANGRDFGFVMDQS

YSCEKPTQRTPELPQRRRCSLPPTLTPANEDAEFEVAAPPISPQPLRPRGRRFSLDLWRH

QEVMAQQEASQLREEIREAAADEPSPERQQQQEAALQKLVASQIKRKMMQLQLQQPEFEL

KVDTIVSEANPASCSNHRRRSRTASYHLPTPAPITSCNGQKSSRWNFAAPHSMTHASSSR

MPANLNFQTYGDGGNKCSIDGEDELYGIDCYSVPRRSASAGIYRARSSSNASSCIISSAV

ARPEVVVPRFTKAPTCLECDCTFDFLLRRHHCRQCGNSFCFEHSTRQLALPHLGYMTAQR

VCDMCFETHIQVLTSHKLSTFMRHPTDELSTSSFASSPRGIESNDSYCGLDSPNLTAARV

GPLHA

>contig27119 Frame-1F

MTTLVALRVLCAAVGVCFGCYVLARGGRFNNDSIVKGLEQEVERQKQLRAQERAGRTKAE

RDAREALQRRQEAVGYNLDAIAYVHSCFSDRRGTPRQGGLVKNSRARITFKRSIPPASFE

SLEQFSHLWVLFIFHENTNLVTKAQKTTFSAKIAPPRLNGKKVGLFSTRTPHRPNSIGLS

VVKIESIQDRYIEISGHDLVSGTPVLDVKPYVPADHVSGYVVPDWVAAETDVTLRTVDFT

LEAMASLTELINAKLSLFYETVTELRTAIEQMLILDIRSVHQGRG

>contig28334 Frame-2F

MSLKPKHPMLFFYLFLLLSDHVVTSLTMADSIMALPSVENHSEKLRRGPDVVENRGIEAD

VARAAGKELAISPECLTHLALLDKKKYKFKLPSFLRTVKITRGKNVKALEPFGLNVRKKL

IKNPSSLEPFANWFNKIEAKYRKNPTDAHLVVITDLSSQFGDGLVVRFLTDVGNKYKEVY

FKLTIALFEFWAREKVDLFELLSRMPLQWEGDASNVAKTLLDPVFSVWFIYSKHIGLDTG

NSAFLALKKMLARHNLDSQMNDIINAGLQIGKQIAERDNNELSGMLNYFKLQLEKDTDPN

VLFESLTLVPSLENLIAAEKVYDRIVSVCHYYGDEMSRAKWLVNSVSTENKLNLFFVMLQ

ANVDKSRKTFSGLVLNKLALFWQNWKSSTNIVALNLFDQLRLRDLPDNSYSPGQLIRLRY

WKEFMYLAYGDNIKQNPSHVLYDVYSARVMKALHDVESLAGVPKLKDLQRAWAIDFRKQ

>contig28613 Frame-2R

MAHNVLDHEKGTTMKRDSFGEDTIPILESRMTYGPIKEMYSRITFPPSLANGDLLVGVGP

IVRRLGWSDERILAVGMYIDPETATKELENPNFQGRDAKSLHGDQQFYNYLLSNTTFRRS

FVVTARKRVSKSVLSALLRDELGPRMGVNATALQTFLGFIEKSLKKAESMVLRIHEDDRF

EYRLRGQLYPPIASHALCQCIQAIFFDSSSIQHDAKRGLVERLPSLWGGEMLDAHDEIFG

HLHDQNQSIDTDDEEDSDSDEDDSGAENLFGDVGEGRERKEQDAERPHDDHERSSDDREE

EQVTIKSRSNSRSKRHSVHDESKPHEEPSTKDEWAEYDDQELERLRRESCSLTVHFGPMI

DRDSKVMFSGDLAADGSALLGTYTHKFIVPSAENLETASCHYSRFTVGLYVDPSAISESL

LKYKGLSIGSIVQDTNFFRQFSQSKFQKHLVFKVDAKLKLRSLLQYIDAQLCSLTSSFAD

LTQPLDSMVELWDHAYPHQQQLELYPKDETHFSISADGKLVLYVRQRGSLKSDKSQTQTS

ALKLATLSLSENVTVASIENSIDSTADLSGDASPSHGSNGRLNTEMELVLPPPPFYLVFE

SLIFGFHAFDPAARTQLMERIPNLLDLARDDLVHTYHDEIQALRENYKRQKPENRVKVGY

LSISFEKRKLQRNADKGGAKEITMVPSRWSKRWCRLDGTLFSYYSHKRSRKYREMMELTR

CEVMEITANSDPDVARFAWEKGEHDSIRMAIIKPNGEILALRTETIYEGEEWMESLTDAT

KVRRHAGSADNWPTWDKSLTKLQRQSSSAHDAEQTRVGSLEHSDRPSTDDPDAKSQGLAA

ASKGQDDNGMGGYDSDEDLVDKDGSLLAWVQEDPRHALIVFLLGFIVYLASFMHCNH

>contig28709 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63888.1|) 1e-15

MRDERRFLRPRVNFLTTRGENVLENVSWILMSEVRFIEKYSGYAAYVAQYRHD

>contig28864 Frame-0R

MCAIMSSILDSIVATIFVCFAEDPAALQRSHPEEHARLVNAWTRLQPDLLTFPTHMV

>contig29988 Frame-2F

MGVIARDPSIKMQKGEKDIQRLAHLQKELLLAAIDAVDAKSKTGGYILYSTCSVMVDENE

AVVDYALHKRCVKLVDTGLDHGKSGFARYQHQRFHPSMQLTRRFYPHVHNMDGFYVAKFK

KYANSMPSEEKEKKKTRDELEDDAEQASVTTKQRIKAEKERKQAAEDVEAVVTQENQSDD

DANEEDKRPIKKHKQGPNREKKHVVKGKKPNRSRKR

>contig30142 Frame-1F

MKENLKIVFVGCLVLARACWSCCLHSKWP

>contig30726 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY69738.1|) 3e-27

MPVVSVGFIGSGRLAERVARDLIKNVAPQRKFNYTKQRLVSTLLASDPSEERRRVFHRLG

FRTTGTSQEV

>contig30977 Frame-2F

MIFEDVEAATDVFVFEPEVTFELTVGGAALVSFRGTAVGESGVTLVTRESFVDGSRGGSV

IKKTSLSCVVLVCRRCGLGGSCSLAISSSGLSTFRLLTLLTTSYKMNPV

>contig30999 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61361.1|) 2e-52

MTHSKRPPFWSKSKSSSSDFIQWKYNTQQLLHVFLILKPQIGYCQGMSSVAAVLVDESKM

NSEIAFRLFLALSEKYRLDNLYRPDMKDMNLRYFQLDEALRLYLPRLHAHLSDLDIHPST

YAS

>contig31071 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57247.1|) 0.0

MESQLCQELQQLSPEQLRKLLSASGHGELLRNDNDTYVVDEKLVTELKSEGNTFFRQGRI

HDAVSAYSRCIDLDPKNAVCHSNRAAAYLKLNYFDHAITDCSKAIAIAPTIKPFMRRATA

HIGLKQFCQAVDDLTAALELEPRNKECLAKLQAIVEIATSVPGSDNNINQELRKASARAL

AIVSLRQGWSIIAVRGNPAPSAVNGHTLFTGSDGRIYLFGGRAVREQKPQVFVLDERDNT

SWSIVPICGLGAPLSCAWHSTSSIGSKARDIFCVYGGVSSRGEDSCVHLLVPSSPRGFQW

RQVHCMQDPTTIPAPRSGHAAVSIGECNDQQAVFIFGGRTKRGVSNQLHVLRLHTGNSES

DASGLEDMTISWTEISTRDQANSVSWPSARDGHSMCLLQSEANTAPRLIVFGGNGQLNDD

KKNDVWVFDVEKQFWRFLQCSGDIPPPRSYHTAHAVGEFLFIVCGRTAAFEDDSIFMLDI

EEALWYKLPVPCDQSFSPRAWHSSVLTKAGKLFVLGGGTYHGPLKKAAELDLSYFCLKAP

MVTCKRRG

>contig31394 Frame-0F

MNQTSVLRSHRHAANVFATRIAATAFIRIGTRFSSSSSLQLNDKKPILELLQCVADGTVS

PHAAADRCDLVSEYMTVGNYAKVDTSREARTGFPEVVYGESKTPAQVAAIMKAMLNEGKD

NVMASRVTSQAAEAICTLISGPELTYYEVPRILASKALQKRNKNGDNEKTACVLCAGTSD

LPVAEEAAITL

>contig31897 Frame-2F

MCDSYTDSLLIKGKPEFHYCITNVRRPCLKGRRPVQKGLHGNFGHKPYPAICSRDNAEQE

IPNQQQAFCFV

>contig31912 Frame-2R

MFRNELLRNFPAEVFLQRPIILQYLLHLIQQPILPERSPPRIIQKGSDDTIEGAMAVAMG

VNYFDEVLNETFAA

>contig32135 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62250.1|) 5e-46

MKMSAFHWIANFLLVNFVELRLHSLVWNKITMLLTDDVQVKDPQVAWDEEYPELGMGILI

PLGMNVDILIDFMYEKIEDLECALQATTTNAGAASGKQSRQSRD

>contig33024 Frame-0F|Blast-Chloride Channel (ClC) Family [Phytophthora infestans T30-4](gb|EEY55986.1|) 6e-28

MPPAVSVSVATEEEDDESDTPSSGPDVVISNAPRRFQALARTASALRSPSSILRSPMPRF

TLDGPHFPSWRVNNRIPSLPL

>contig33486-0 Frame-0F0

MQIGTLRYWLSLPLLVSLRKKRVVVSRCLGRRGYTARLETRASSVLPPFATRLFFVVRSR

KELR

>contig34344 Frame-2F|Blast-histidine biosynthesis trifunctional protein, putative [Phytophthora infestans T30-4](gb|EEY55727.1|) 1e-172

MLIPKVSIPFATTNDAESSLLRRLSIIGIVYAKLPIQKLHELAPLEPAEDTKPCELALKA

SLLDTRTLLGPFSSDMIDVLALWLDQGIAQVLVDLATSEDVELERIATAISELPASRLMV

RISVLSPLADEFAKLQEKLFKLRGLISGVVLVLDSVTLLHERGFKDLCLSLQALRKSLKD

SFRIAIEMATFPASDSDSFIILKQIQELHNQHIDVVTSGYCNDNETQQPCTVLTADNDGV

VDAARSFVQCLRTDRPDGLFTTVVTDEGGVALGLVYSSTESVLAAIESRRGVYFSRSRGG

LWKKGESSGNAQRLIQIDVDCDSDALRFIVNQSGTGFCHLNTRTCWGQDTGLRALESMLY

RRHAHAPAGSYTKRLFDDAELLRNKLVEEAQELAEAKSIPDVAGEAADVMYFAMVRCVAA

GCKLSDVEKMLDKRALKVKRRPGNSKPYRISVANEILSCNSNSAT

>contig35435 Frame-0F

MIAGQWTLMRRSAHLRTRASARLMLCIRSISIPSSPKPHARGHFKGFRQPPRGAQLTETE

ASLNLSHNKNKQRPKRRRPVKSADKEPTVFTNKFQNLLSFVFEDVPLVKPKATKGKASSL

DLVDGIETRRKDSDDSELPLAQLGLDALEEDEAFIKRQPKHLRQKPQKTSLFSGNSDPST

VLAALGLSVNGDSDGTALPSSSRKAIKMNTKRKKNSRNLLKNFQFENSIFDSEVDLFGDI

DWEGHNDSEDRERRRSQRQQRKEAKRMPAQELPAQEVEIPTSLTVKDLADRMSIKTRVVF

RALRDLGENRLQEDSVLTNDIAELVVDSQNMIPVLLPPDFIDLELTSPPKDSSEFPRRPP

VVTVMGHVDHGKTTLLDALRKSKIAATEAGG

>contig35440 Frame-1R

MKLNVSLPLQIIARQTSATWQKYVQT

>contig35707 Frame-0F

MESAAGGKVAEIVPNVGLCRGLMTPAGAFLELESFGDVSRVPADVQMATDALLIDFGFRR

VDFDMRALCEPWVWFDLTVPKAACVYLHFRLPPSCYNEDTRECKTCQLQALVYRLTLPFS

EKLMTHLWNLRVFFHKLGVEVRETKIRQTDTKILSSTNHRFGLPVAYALQCLLSHCSYFM

NGILPSQFFELLTNQDEKVQEKALLYFRPHPSSTSVTDQFSLYLQDEGPTLKSLCGSMFL

NPTNIVYKVIVTPSRIVYCPPDLAPNNRVFRHWGSANFMYVYFRDDNMERLDYTSRNILV

RIRHVLNNGIEIPNVRGGLKFRFLGCSLSQVRNSSAIFTLLDHQEVRSWIGDLSQLTSPA

KYLKRLGQAFSSTRETF

>contig35916 Frame-1F

MALKSDNARSSTAIAEALDANYALIANLQSLENYFAAAEAKLLARIQSIRREVALKRAQQ

AMDSLLPSTSQKETLRQCFERTPRIRAKFSGTTIRSYLRPQVSFFTDEEKRKRKVGRPKK

KQKTLESTNIDTNEHTRLGALIEPSINADTKFLRAHSHEAFVAAPPAIFSARERKVVKDF

AEDFYMTHAPIVEMSLQVWNGIHKWQEMRKSRQLPIERSGFSCKLWYDLHEAPTLRLCAW

TKEEDVALRRLVDDSALVNQWHAIAKRMPFPGRPPAHCLTRYQTALCASNAKSSFTPEED

AIVRQAVPIFGEKWNVIADLLDGRLAEQIRHRWQLTLAPGLRRGKFSVIEDRRLILALCA

YTPRNCDFDLDAVAWNEICHHLQGRTPPAIRDRFLNCLNPE

>contig36290 Frame-1F|Blast-chromodomain-helicase-DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY57581.1|) 1e-138

MLKPYLLRRVKEDVEKSLPPKEETIVEVELTPVQKQWYRAIYERNTAFLNRGGNPRNVPN

LMNVMMELRKCCNHPYLNNGVEEVLNEGLNTDTQRHEMMVKCCGKMVLIDKLLPRLKLGG

HKVLIFSQMVRVLDIIEDYLRYCGHLYERLDGNIRGNDRQAAVDRFVKPEYKRFVMLLST

KAGGLGLNLTAADTVIIFDSDWNPQNDL

>contig36346 Frame-0R|Blast-pantothenate kinase, putative [Phytophthora infestans T30-4](gb|EEY68288.1|) 3e-95

MTRCDTYDEALDLSVHGSNKSVDMSVGDIYGGAYDKFNLPASTVASSFGKLIFVSRGSVS

DADLARSLLVMITQNIGQVAFLNATLYKTKNIFFVGNFLRHNRISSRTLAYAISFWSSGA

MQARFCKHEGYLGALGAFLRHAEATDAHGDKFTSATRRQQQST

>contig36669 Frame-1R|Blast-cytochrome c/c1 heme lyase, putative [Phytophthora infestans T30-4](gb|EEY57855.1|) 5e-95

MGSQVSKDNGSDTATNLHQSESLVQHESKSKQNECPVQHENVEKIQGCPVQHDKKLSIAD

AMGGGCPVVREGKDDNEVFDVYGQRIDPTNMMPYNPNQDPIAEQRYPLPKNRVQSTIPKG

GTESTWLYPSEQMFFNALKRKGKGEDVHEGDVRAIVSIHNNMNERAWAQVEHFEKVCHPE

LESVKLLKFCGRPDKLTPIAWVKSMLGFGKPFDRH

>contig36687 Frame-0F

MERGGNFRNNRGGRGGRGFGRGRSTGRGARGGGRGRFGGRVEQSGGFQPQHRHHNHTGPL

KGYTPHQLGLPLAPQQYPPQHLLPQEMYQPQYQPPCHQPSLPYQQQSCGDDGRGYTIATP

HPSPAQPERYLQPMNKFQHFQQHFQQPQPSTIP

>contig36733 Frame-2F

MSLAKSTKTQPKFCVVGNFQASFIKA

>contig36889 Frame-1F

MADYNALKSPVAHGSRQSPVFQDKLSPTVHVVRFFIVFGIAGFIFGNIATWAPLYELNLV

NTMMEWWNGYPNTPVSNDHGHTSHVVDTGIGRNITESGHTEMIRPTFLFIFCIVPFILSV

LLIEYLRHINTARRLTSTLIWQFAMLMRRKPKFPILGVSRFTVGEWIVGVVYVLGGNALC

WYFQWDRRIDSANAAGTLTTSKYWNIIGISSSYLCIYNMAFLLLPVTRNSPWMEFLNVSY

ANGVKFHRWIGFMTVITGVVHMLGYWVYWVRLGQWQVNQLPCTNCDFTLDYSGGGYYAWF

NVFGFISTLALVLMIPTSFPIIRRKAYEWFYITHWVLFAIAVLFAILHWAQIIWWILPSG

CVWFVSRAAYSWNAMTPVEVKEVTIIGDGQEELIKIVVKRAAPGTSPSSSSHDYKVGNYL

YLNVPQISKLQWHALTIASSPLASPTDLTLLVKPLGGWSKDLVMYAKECHHGNVAPLIYM

DGFYGASLNLYQDYSTLCLVGGGIGVTPVLAVLDDLVARLSTHRAQWSQRVNFVFVFREL

SLLQAVASVIAKLREMDPNEHLFQIHLFATGSYPEEELAKQLESSPTKELMDSAMQKSSS

RAARAFYEPLRSSDTLRFFMYLMLFVVAIGVVFGVRWGNGVIQGDNHWELWPLDRAFQLL

MFCLTILVVYAFVWFEYIMFRRNYATKELTPAVIESPQTNYALYGGDVHSVGDLLNYFNV

VVGERPNMQSLLQRTLEFHKSNDSKASLLPGVGVIVSGPPALKMATNEAVYALGGGNFDV

HEEEFEL

>contig37495 Frame-0F

MYEALTSNGKRIMHIQEEFKRGPHTGSEFSLTIWMCFRHRRSSIHLSSTTAGVLLVLFCI

NCWDTNCKALLSGIQRSLKLEEFLRPVRRCGNCGEAEYTIEGVVGHVFQLPQ

>contig38186 Frame-0F|Blast-hypothetical protein PITG\_06681 [Phytophthora infestans T30-4](gb|EEY70113.1|) 2e-34

MPLRSDSYTLDWACSFTGGLPEEDSPLSELESNWLEQHKSSRSVDGQQLMTTSIAWNSEP

VYCSDLFTPECNKLNTILKVLSQIKNNTQQV

>contig38353 Frame-1R|Blast-importin-like protein [Phytophthora infestans T30-4](gb|EEY65606.1|) 1e-103

MDFRALVAALMSNDNATRKQAEILFESVKVEQPQTLVVNLVHLLRSSPEPEARAFASVLL

RPLVELKGGIYAQLDAPTQLTLKAQLLEALTNEPLPHIRRKLGHPIAELANFSITNEQTW

PELLSVVSALTTHVDALHRVTAFDILAQLAEYASDVLAAHKKSFLTLFTTSLNDENTEVQ

IASLKAVSAFLLTLEDKQELLAFAHLIRPILRIIEMLVNVGDEAAFRNVLSALVQIAEVH

PKFFRNALDDVARAMIFV

>contig39264 Frame-1R

MSYPKLLLPCMVVMTLSYMGFAADTRHLMDLPPSTAKGDAHIVLIAGIAIAAVVAVAILA

LYKARSPSGGVEPKDIELHEVVISPSNPTAQYTSTKKQFVYTAHI

>contig39798 Frame-1R

MPTTLTTPSRKGADNTTGAFKMTTSITADSEDPNLEGVANDSETDTSNADVYTFDTIEKS

ATPILSNNNNVSEIGKDPTSGTTDMPKVSDVDFYGAVNPKVTPAIPSVAPAA

>contig40435 Frame-1R

MTFLRRAGVAQLLNRRVTKLQGADASRFIQAILTNDMKLLTHRGSAIYGGFLNSKGRVVG

DCNVLQLSDDAFLLDYDEELSISLIKHWKRYKLRMKVAIEDVTDAFKVYSTVPALVGEAD

TALVPSLMTLADLQSLNCGPNTLVHADPRGEYFGVRAIVQADCSLNVPEGYEVMNTSAYL

DHHIALGIVNGEEIVDGIPLECNLDLMQGISYRKGCYVGQELTARTQYKGNIRKRLVPLA

LIPSDRPDVIKKISELAFRRFDDPSHGELRAFLADSKGWEHAKAPSVGNKILNLAEAKTV

GTILSVAQNLNCVVAMMRLGTLRPSNLELGEIEFTSKFQTQDGSFHAVPYQPSWWPQVDW

KTGKMVL

>contig40440 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65892.1|) 6e-46

MGRYTTVQTFSDQDAQVATVAYDATVKEKEPSGTTSEIKDGKLHVNRVDNVSGSSAGAGS

GEFHSYRAARRREMERVAVMEKRYNDKKAQQEFEAERKRKAEEFEAKMRKRTEKRKRRRK

RGKA

>contig40862 Frame-1R

METNGDARVASRRVRERKDMVSWCCAGGYGQPRLFVLRDRE

>contig40981 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57783.1|) 1e-33

MIGFPEASNRTNALAVLNTLLLKIAVVDRFRMLRHLIIMCPYGNVAAVLMDVVRRDTVQA

WSSSEINPESPFMSSAMTLLLYETLNQSAERDLILQT

>contig41959 Frame-0F

MLCYGVKHATILRTKAQQLMNNLRMEEPENMVWSCSTCATSGKKLILDENDG

>contig42161 Frame-0F

MKTFYDPKDERQDASLNKEGEGSTTTVLSIGGQEIVAEAASITITPETFTLLYIGAESAH

LDCILMRYSAVDCFSYNPEMNCTRKEGVSVNRLLMRRFYLVQQAKEAQVFGILMGTLGVN

RYLDVVHGLQNLIKKSGRKSYLFVVGKVNVAKLANFAEIDAFVLVACQQNTLMDSKDFYK

PIVTPYEVQIALSPSEEWNGQYKTDFSELIPMLDQGFQCADKEERDKPFFSLVSGTYKTS

SFSNVAERKDTTHALTASEEAAASSALQLKNERAELTTYHNVAAAF

>contig42363 Frame-0F

MGGRAAARVIRREFIRRKKEEEKKAEEAAAPSPSPSVNESSQLPEDGDSLSSSQKAALIV

TELVNNKCSFSQPGSPNPAADGAEANGTDLVTTFPLKAKSMVLMTSSESTGKRYHSGTTL

IGDDCPDVATVVADHDSSQTSATGAAAQGIIAPRAEVFKKPFESVSSGVSSPRKRRKMKI

TFAKLN

>contig42631 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66272.1|) 2e-89

MVMIFLFQKGSIRQKLREVVHLTYEHSKNLAFFVGIYKLVLAMLRLHKEHALKQYVGVGI

GKPSAHWHAAVAGGIGGYMVWGRYSSVNFQIVMYLMSRVIISIMRTLAAKGFQPFAQHQF

KHVYPMLATVMWASVMWLYENEPRTLHPSLLKSMQYLYDESCSWKDGLIELLPSPTTTAV

ILLTWLEF

>contig43052 Frame-2F|Blast-alpha,alpha-trehalose-phosphate synthase [UDP-forming], putative [Phytophthora infestans T30-4](gb|EEY68908.1|) 1e-159

MVFIVSGCHCDLLTQKFGGVPGLGLVAEHGYFIRRAVLGKDARIGRPWERHGDLLVAEGV

HQQWRVKAEKIIQLYVDRTNGSTLECRQSAVLFRYGKSDFDFGALQAAELKDHLEGVFEG

WPLNVVQGKDYIEVRPEGVGKGKVIGHLLNKLRIDGNSADFVLCIGDDVADELMFEQLNT

MVAHQELLEDKVFTCTVGQKPSKANFFVDDYTDVIALLQSLKVVATKSNRNYSLSDLQSF

VKNSRPFLSSWSYGHSADSRHAALDKVIRKSASRRVLHRQLAPVIEDQIVSPEVGRNGVR

QPLSRHHKFTWISRLQQLGAGAILIGILRWRSGIKNPREKRVLMYLVASLGVLYIILRAR

IKSHK

>contig43139 Frame-1F|Blast-cell division cycle protein 48 [Phytophthora infestans T30-4](gb|EEY70132.1|) 3e-55

MEQIGSHGILLSGVSGVGKSIALSALNQELLHQKIKTWRIDGLSLLMGSECSIESSAYEY

MLHSLEQRFKEVEFFGKNVSDQVSSTFLGVVLIDDVDVLFRHEKGQIGDRANFRLPQLGS

ALLRLIGELSLHNLRLVVVGTTLNADTMVPDAAKRADRFGKVLDLVIPSEQPRREILSLH

LNGL

>contig43290 Frame-0F

MKVLRKNICWPEPESRMMNYQIPFSTNIT

>contig43346 Frame-2F|Blast-cystathionine gamma-lyase [Phytophthora infestans T30-4](gb|EEY54883.1|) 0.0

MTSADSNVDEHHGFGTTAIHAGQAPDEHTGAVAVPITLASTFAQASPGVVAGREQVNSFG

KGWEYSRTGNPTRGALERALAACEQGRFAVCYSSGMAATTAVTHLLKHGDHVLCIDDVYG

GTQRYFRQTVSPTYNIEFTFTDMGDLDKVKTLVRPGSTKLIWIETPTNPTLKITDIRAVA

DFAKKHKLLLVVDNTFMSPYFQNPLTLGADIVVHSITKYINGHSDVVGGVVITNSEEIHT

KLRFIQNGIGAVPAPFDCYMALRGLKTLHVRMATHAKNAQAVAEYLEAHSAVEKVSYPGL

ASHPEHEIAKKQTSGFGGMVTFYVRGGLEKARAFLENLQVFTLAESLGAVESLAESPAIM

THASVPAEVRQSLGISDNLIRLSVGIEGLPDILADLECALAAEPKA

>contig43669 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65940.1|) 9e-18

MGNEQSTASTSRGDGVPFVSWQHSCKQQIEEDHDAPLHAVVTASSYHFAEPSSYRYDRVP

RVVSG

>contig43687 Frame-1F

MTFAAVMEMSTVKITLALAVAWGVLAKHGKADKEEHLEIYLCAPIGIEIGEKILRSLRVQ

SPRISFSGCKKHYELEQAGRLWSQLLHFKLT

>contig43733 Frame-0R

MSGLQEATKKMLEPIQTIPCFKKSGTRHSSSLLNHQ

>contig43867 Frame-2F

MGSVMSMGGTPTGDRNTFVSRLSPADIKSLTEGHRRLCRVECAPSSPSSSPSSLLQLASS

SNSSGSSNNSTAAAEVATERINGSLLNKKVFRDKVLGAFTMIPHTLADRLFEVLDTERSG

ELSLANLLSGLSWLKYGTYEEQVNLLFIIYDLDAIGEVSRDVIERFMDVIYGRKRGRHAT

TVTFLDKVFDERDKLDLPKFRKVVHLKDARGDALLVKWLAVLATKIGVEDDPGIIA

>contig44673 Frame-0F|Blast-phosphatidylinositide phosphatase SAC1-like protein [Phytophthora infestans T30-4](gb|EEY54523.1|) 4e-90

MDGYNSCLRYIINNFMDGHRQDVLDLLLGRFTISRSKPSPFRSQRETLESILTKLLGLVA

AFFLVETLRSGRQSHVIERLLRSVFLTLLICAGVLVVLVKKGNMLGEKLVRLPSLRPQDG

CMTSWKC

>contig44879 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55688.1|) 1e-50

MENPLPTSIYPTTSGLRKSSSTRTLASLVDVQALINAQDEEEQTRRRRKSMSKPPRHARM

PMYAKVLLQLWQRKLQCDDVDLSSDFFYDLKGTEEQGTQLVSQMQALGFNITVSQFLAMH

RCSIYSVLMQAL

>contig44912 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59939.1|) 8e-52

MNASYVSTLDAITALFIVLISRARGHDDDVKCSTFVNARRRLEPPMPPNYSGNAVFKALS

NFTNSELQPQTKDNAKVSPETLGMVARRVRGSILQCNDAYLRDGLNFLAEQKDDAVAQIG

THVPFGPDIMFTSWLHIGMYNAEFDGVHPWLASCPQVPG

>contig45227 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69381.1|) 2e-44

MPRTLIRFVLGLICVAFLAPQALQSQELQTLGGVAESHNNHKIEDDGLVVRCRACGAPVA

KKKDYIDFHDTINTVGSRYEAVLGDDTELFTFANPSRTEVELAGFKEVSAIEGDTYTKKS

SFFDNYSWQDLRCNHCKKHV

>contig45726 Frame-2F

MAQCYVTLLMVALLFLYSMHIALKQSVGTVSQKSETISRTTRLLRAHGMSGSVALRTKAL

FSNARLDTSIHEYLAAINSIDKHEAPAFAKKFLHSPEFKEYVHNVRQTNKNDPFKA

>contig45977-1 Frame-2R1

MEYCSLFVQGSILELEVGSLIERPTICSDTQIQGLVFDAHPCCIVPRGRYTGNE

>contig46411 Frame-1F|Blast-cell division protein ftsZ [Phytophthora infestans T30-4](gb|EEY60941.1|) 1e-170

MASHRTLLVLLTRRSIALSTHRPSPLLNSVRWLHDTRATSDTAKLNGNSTSAFNVPTSMP

PRNSKRTSEQRKRSKTAARVAVASKISAGTSLNEEANKVKEQGNIRPLTSALKDGKPWIT

VMGLGGAGSNAVNNMIASQLEGVEFVVANTDCQALGRSLAPRKITLGKNITKGLGAGSKP

ELGKCSAEQQNDEIQQMLHGSNMLFITGGMGGGTCTGAAPVVARIARELGILTVGVVSTP

FRSEGPNRTRLANAGVKELAKYVDTLIIVPNQNLLALADKSTTMLNAFRYADDVLLEGVK

GVTDLIVRPGLINLDFADIKTILSNAGRAIMGSGTSSDNSRARKAAEQAFVNPLLGDLPT

ESAHGLLVTIRGGQDLTLFEVDEIMEIIRSRVHDDANII

>contig46486 Frame-0R

MIKGPFTANGLKEQLDGDLINCHRQINAIYVCCCSKHNYANSNDEHRWSLMVEYPELRWM

ELTDEPIDARCAAFALKSLRNLLVTDQHNNTSKALWPPTLVNSVVANTLPLALLIQLLIV

NESNIRSYVCEMLMSLNEEVLQELYKYGVFYFILSIIATPSVGDQLPVFVPEAVLLKRIH

RIQRSSELLEGQSILTDMLPETLISVLDLDSP

>contig46653 Frame-0F

MVVYAVPAPTNMSQQTHSSRSAMMSYCKSLEARLTTLFRSLRGNTVGMLRTRDALSASNL

NKERRLFHFDSAHCVVVVSRRTTTRREVLLDNLLAAIDSNVSAVDVLNNNSLLQPLMDDN

MGLQCLDQYVQRYLDLLFSYSPSGTKDGGRTELLNPSQWLKAFHGLFSSYSRLDSNRRKY

VVVHETEAKDVTSDHFSSVSQATYPTDLIEPS

>contig46749 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69364.1|) 1e-100

MTTIFDGYDEEYRTLASDISKKLSEIASFDEQKDKKKASIVHVGDLLTQATQLIQQMELE

VRSLDANTRRELSNKIHQYKKSLASLYGELTKIREKEEREGLFGDRDDNAALVEHRDRMA

AATTKMQGTTNRLVAARKEIADTEEVALAIGEELSRNREKIEATHAKVKGVNEMARRGGN

IVGRMSARNKRQRMALSIAAGFIIVAILLLIYFGIFKKK

>contig47135 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65168.1|) 9e-84

MFQFRLRQLEELTAEQSSKHIAMEKTIEREVQTRTQKLMETMEKQISMYKQAKELECDRE

VQRRVSEHFENPRRSHGNSQASSTPRSSAGNSRHSSNPAASFRDSLNKVGVVKDESNSFE

KLLHPRRSRKRLEQLKEREESQKREMEQFREFIRTTEMRVLQPQRVDDGMSAVDAEKAKR

TFLELNDPLLPESMLLSSPSDLIEVICVLRKSGQEQEMQIEEAKRLVLAAIEARESAEAT

AREAIELTLKLDAILDEKKSMGKQCPISTSEEFRHASENEHAADWQSDTPSSSSTL

>contig48123 Frame-2R|Blast-U6 snRNA-associated Sm-like protein LSm3, putative [Phytophthora infestans T30-4](gb|EEY56319.1|) 5e-42

MASIDEPLDLIKLSVAERIYVKCRGERELRGVLQAYDQHLNMVLSDVEETITVQELDPET

YEELIKQSKRTIEMLFIRGDVVILVAPPLLTA

>contig48259 Frame-0R

MFVLDWNEIDPFWKQARERIGFERTKTIYWRRWLNTKDLMGHCLVDGFCANFGHKKMIVH

VTQLMMDICIYSDTWVQEFVAVIQQADEMIQVQRAMKAYLGDVPDRFLDPLLRTLMTDPV

RLPSGNVVARAILALLLAALQQGNEMVRYP

>contig48585 Frame-1R|Blast-tRNA (cytosine-5-)-methyltransferase NSUN2-like protein [Phytophthora infestans T30-4](gb|EEY64040.1|) 9e-32

MNAQQNIAGKRAQAVVQRYAVDQRKKRSREEKAEKIVWRKFDRENRAFEKYYEECLGLEK

HDFARFLACLKKPLPVYLRVNGNYT

>contig49083 Frame-0F|Blast-tRNA-dihydrouridine synthase 3 [Phytophthora infestans T30-4](gb|EEY64037.1|) 7e-43

MRTGGIVHAPGLTVKLRSGWSEKQPTAHKLVPKLQAVRASLAYVNAAVVTADFKLHATQS

IDAITVHGRSRLQRYTKNADWDYIY

>contig49591 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64707.1|) 1e-22

MLNPQNAFELGVLTFELSLAKDDPTGVETKSPQRFTHAGVLEFTAREGTVG

>contig49678-1 Frame-2R1

MQAHYYKFIATRESNRRPVCCQMHIDECVTLFHNSTVDEAIIFLQKEVV

>contig49717 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66214.1|) 0.0

MSSQRKGSAPRGFGSLTAICTLIERSNLDRKSKLDSTGRICYELKNDPLLLDSFPMERLM

KAMRRLVCDSDTSTRAGAHRALRYAISSSCSIKHFVDLNLPLFAVRSLEREQKYLAERIQ

ALKVVRRIIQIDAARMPTGLVASLTAIAGHKDDNMRRVCLETLRELAVLNVEVVAEANGT

KVLVDAILEPSFQDLADSLIMTLLFVLNESSTRKFIQPFVDSQVLIAPFTDTDLPAGNER

RQRWMASRNAIVTMMRSWTGMVVLTSNPQGLQSLIQLLVRPVGEDVQKAVLSTICEIFYK

KTSFYNSASDAVTETSALSVTLSSAEQLPYAANHNLLDTYTAIILVAMIHCGILEALVTL

GTGSSRALAEPAIDLLADILRMASRLLPDQHCASLLALPRLVSATSSTTTTTMTVGDHAK

SLLERLQREKS

>contig49995 Frame-1F|Blast-S-adenosyl-L-methionine-dependent methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65508.1|) 6e-39

MEQATERAPVVSEPIDALPSSFVSSKMQSEDFAQFMSFMDAYLRAVEDVREDRLIHDFFA

EPLTCQVAAQLSPRLHKWKQKHPHPENYVALRGRYLDDALLQRDPSIRQIVLLGA

>contig50016 Frame-1F|Blast-FHA domain containing protein [Acidovorax delafieldii 2AN]gb|EER60354.1| FHA domain containing protein [Acidovorax delafieldii 2AN](ref|ZP\_04762840.1|) 7e-06

MACCFQLQGTRGPHANFILCHCHVAAASPSEILCIGRKKCCWLRLPEDLEVSSVHAEIHV

RKSGTSVSIRDVHSTNGTTLNGKFLRAYDEYQLHNKDIIAVGKTSLRFVHDEHGPSCGKE

IRETNSIQKPRLWTPATSVSTEKLLKQDSIINKRTVSISNEPDRELAPDELVMKPFHEIN

SA

>contig50254 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57849.1|) 4e-17

MDVFLQKLANSILFTSVKSEPVEKTKRQRPVLLASGSSRSPSGCRTTPSPSSSGALLLEQ

PQDLPRRRIANWDKKREKCQ

>contig50632 Frame-2R

MLQRDTGGAIVDIPDWKQINKTSATLPDMKDKLIEGLETVENVSSHSNPTLWSHPPFMGN

KKDAASLSTSSQQPLSPAFSTDAKGFQGEAVMDGDQKEGEPWSLRFGADKCLGGNVIEYP

IAAMLERLNISSPIARNGAMDSPSAKGAIAPTGSNAAMRFTNYLASIVIPEGDPVDYSLG

VQQCGSQEDLFLSLLEKFTLSSEAIMTRILAAYERGDITLTRRESHSLKGSSAYVAAIRV

SKAAFRVQVACEQLQESRAEIEFVQQPSTRADAAVLISLEQSLENSITVLKKEHQHLRGY

LRRNFDFHD

>contig50838 Frame-1F

MLANAIIGFALDCNDLGAVWVMPF

>contig50957 Frame-2F|Blast-peroxisomal targeting signal 2 receptor, putative [Phytophthora infestans T30-4](gb|EEY62520.1|) 1e-129

MTLTEHSRGVYTAVWNTQHDQLLASCSGDKTVKVWDLNTARSVTTIAAHTNEVLTLDWNK

YHEFEIISGSADCTIKIWDLRNPVREVRVLPGHSYAVKRLKCSPFDPDVIASVSYDMSVG

VWNIRSPYPRLQNAQHHSEFVFGFDFSNFVDGLVASCSWDRQVNVWNYFGGPPLC

>contig51349 Frame-1R

MNGEPRIQPPDASSQYRRQMYQCALALR

>contig52902 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69435.1|) 3e-75

MGGMLGQLFMLFLGDHARMNGWDVSKINFVGFGSPRVGDIGFAARLRVLFDPQQLLIVMH

PSDAVHAFPPTAEGYVDACIKIFLRESGKGVGRRAAGPFSLLPVTKSIDRAFEHAHKANT

HNKASNPACSFCKSKAHRTSQHRCRYCIERGSHRG

>contig53008 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59389.1|) 1e-22

MFPTTDYKMGKPSNIRKRKAGHVGFQAGEIAFIEDEMAALAAEYGLEVDGDVASHVKQRQ

QSKKTRRRQRPRSTKLA

>contig53101 Frame-2R|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY53469.1|) 3e-15

MDETQSLSGCDESDSASLPRATSLSLASAALLAVMADKLKNQSPTEALAIVMAAFACMGI

VVASLAWNIATMGNK

>contig53365 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68516.1|) 3e-47

MADSAPASLACPVCFECFSSINTAAFALHVSSCSSSSTSRPDSPSSPSAYCPRCLHVYAA

GTPAHEISFHEHECARVNEQSDDNIDDELSSTACNRTNKRPRYEAVARTSSTPRVTLFPT

VCFLCGNGGRGLFHCAGICARVAHQNCVEHLQAPAVGEPLSVT

>contig53484 Frame-1F

MVSNYTPAYALSVPSLHTICVACVFISIEYIIELYSSHGRICRLK

>contig53699 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65279.1|) 8e-22

MEEPTVSGGIMLIICLGVTIVMQCSFFTVAYICQFDKVTDLAGALNFIVLAVLSLVLQDV

F

>contig53826 Frame-2F

MLKAITQLSRHIAAGQDDINNDFYKDTAALMVLAIVTVRIQILAGEAMPNSF

>contig54184 Frame-1F

MADAAEAVQTGADLQLDERNMYAVKWADGVAFGFTVTPVQSDRGTVLCLARRTSPGVPDV

MPGDMLIAIGDVKVYHLGAQNAAKLLRSIHKPVWLTLQVSPYGPTVKE

>contig54258 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69292.1|) 2e-11

MTASTPTDAIVDTSILRTFAVILCSKCQYLEFPGCDVHGTLYTELLIDGLGKQHAKCPNC

TAATSNARPFRDGCRRCKSPTTVLMWASSLQEIQQAVEAFPNSIEEIEHTVISCECCCTA

IFPKANHILTT

>contig54496 Frame-1R|Blast-phosphatidylinositol kinase (PIK-L1) [Phytophthora infestans T30-4](gb|EEY63188.1|) 1e-80

MEHDVEALPIDIRELGELAQKCHAYAKALHYKELEFHTSPSTCIEALISINNQLGQPEAA

VGILKYAQAHHSRVIQVKETWFEKLQDWRAALALYDRRLQFTQQQSGENEGFDIELCIGK

MRCLEALGKWEELSVLAAKVWAALRSSKHSASQTSALPPRSRQSTATRNLSSSSTGINSG

R

>contig54508 Frame-0R

MVPNFGTGNHGRTSDLEKLLECSREHSSDWRFDFLTTPLVKFLGSRYSFIGTSPVLARPK

EVMNIERLVAPTQVHVKCRSCEMVAVVAEEANLYL

>contig54665 Frame-2R

MILAKMCGRLQLYIDAAQVKHVAISENVYEPRASAQTQNHWVEASKSIRKCNMVILINL

>contig55918 Frame-2F

MRCLPSYAQKTLQEHAEDKRNVIYSRDTLESFQTEDRYWNAAQRELVISGKMHGYMRMYW

GKKLLEWTRTPEEGFNAALTLNNKYAIDAPDANSYAGIAWTFGKHDQGWRERAIFGKVRY

MNEAGLKRKFKMDAYVLKVGRLAAKAKRGAASDNTDNVDGHVESGGKRKADSEQTGAVAK

SKKL

>contig56317 Frame-0R|Blast-mevalonate kinase, putative [Phytophthora infestans T30-4](gb|EEY57207.1|) 7e-16

MSSHNKLPLQRTYSTSTLQKVVDGLEDEIHYVPIPSAMVMTRIES

>contig56645 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69867.1|) 1e-36

MGDLMTDVVANGSAAVASTNGLSGYGSTHSRTCVTFEQFGEWYNTGGYQLISWVELLDVT

KWQQQQDFQDQTIAMTTTDLTSTSQRTRTASV

>contig57721-1 Frame-0R1

MRFKVLWNEKANVKMKKVDWLRKAASSMKIGVWLEKNSDQETGIMNTSILTAGRHK

>contig57956 Frame-2F

MLPFHLPYPVPRCSFKGPRLDTHFPLVIHTKLNEVK

>contig58131 Frame-0F|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ31781.1|) 8e-06

MEECFVNGDSDDEEEVEDDDGTEKDGKDCMNEIVQASSDMRLELVSFEDFGRWYNGGGYK

EMSWLELLDLRKWVFVSASFDLKGLDTRSVDPI

>contig58830 Frame-1R

MMGSDYLDRVKEMIYSGKSKIPDLSSEI

>contig58845 Frame-2F|Blast-atlastin-like protein [Phytophthora infestans T30-4](gb|EEY69647.1|) 2e-40

MNVFDDGARMGRRSEIVRYRQEVADLIERERHRYLEMNAERDPYKNLEFYLIPGCLALAL

LVFRV

>contig59132 Frame-1R

MQHGGYYMFEHICWYRQIINYA

>contig03277 Frame-0F

MFRRLAISSTRASVVRYQSQAASVSMTVPGLSTDVRHDWTTDEIHAIYNQPLLELVFQAA

TVHRMHFDPTEVQQCTLLSIKTGGCTEDCKYCSQSSHHKTFVKPEPTKKIDEVLEMARRA

KAAGSTRFCMGSAWREVGRKNAFKHVLDMVRQVKSLDLEVCCTLGMLTSEQALQLKEAGL

SAYNHNLDTSREHYAKVITTRTYDDRLETIANVRNAGISVCCGGILGLGEDTIDRVGLLH

TLATMEKHPESVPVNALVSVKGTPLYDEEIPPVTASEMARMIATARILMPKTMVRLSAGR

MSFTDAEQGLMFLAGANSIFNGDTLLTTANPAFEHDKKLFQSLGLKGKPAFSAHKASPYL

VKVTHAAATEAVA

>contig04261 Frame-2F|Blast-glutathione peroxidase, putative [Phytophthora infestans T30-4](gb|EEY67905.1|) 4e-51

MIAAQSMTLLAENARNLEHLEREQLEREPSFVTAISPSSSRCCSIEKADCSCMSCSVAVN

GRVFRRLQRYQTLAHELKVQSDMVATYLLTPSVRRIVFQQRKHWWQHPLHLATAGKGTFI

QGRALLRAIRKYLQLSHAAHSSRRDAQQLAITLILSGFL

>contig04777 Frame-1F|Blast-tRNA (guanine-N(7)-)-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69128.1|) 1e-77

MCVQPRWLHLLPPARACKHDQLRRCLSKSLQHFEAGKEVAYILPGDSPSSSKRFRQHVNP

LSKLYLQPIQLPEWTEQFMDASLPIHLDIGCARGKYLMDVAESQARERNFVGVEIRRNVL

QEAEREARRRELQNLAFVHANINIHLPKLLHSFPGPVESVSILHPDPWIKKRHRKRRLVT

EEFVKTMARHLSTGTPIYVQTDVKELFAYMVEIFELSGLYTFDALFENPLRIPTDREKVV

YNGGGKIYRIKFTVNKQEPEEV

>contig08463 Frame-0R

MLMKTLCAVKLALSGRDYGAKERHPFTAK

>contig09815 Frame-0R

MVSPVFGFTFAILAALSTGEMDQCEPTDPTVASGVPGNTMLYHRGPCPALNTLANCGYLN

YSGQSLTRESINRAIVDVFNQDIAIVTALTASLKEPISLSDLSRRALGEHDGSLVHLNSC

LGIDPMFADKDLFTDLINRGQGDKLCAKDLGEAYLNRRTTAQCYGTPPITEQEIAQSYAQ

GSGILTTFGTGECISKAHATAFLLNEVIPSGWTKRSTPVTADAASKVASEIKRAAEMRQ

>contig13849 Frame-1R

MRYFMKITSVLNLPFRASPSVNNRLFTRSKNSFPFSCSESYFMKFK

>contig13940 Frame-2F

MVWNNKTGGITGYIGPRPRGVPGEIFVSFIKVPEGVRVTKSSKKEKGDKADRRMSSSSAL

SISGSSPMSEVSEATTEPICFGDTNVAIEVVESNRHSQMFNKRLSNFKKPTSRIMGGYIC

CDGKGTELRFTIWPMKPTIEQISMLNKLITPYNYGQKIALPLGLLEGIKPNKANVCTDKA

VAEIIFKLSNGAKAVLPGSLLQKKMLDYVKPRSSSNDEPDSLFEVPLQNGPGVLVARLTG

IAPQQMITRLTVKNEKHLPVTKISRGMTIFHLVSGTLRRVPVPVFALFYAMLTHHLWGAL

SIMDDGLRREFVVLVLVIVPTFYVAVKMDHPFSSLFHPPVSELVADSSDYSSSASSGSLK

LIVTEYRFANKFQNGSDATKSVINSSLANAAFSRSITTFEATGIVPARFILAEKGDEAKA

MERYNETTEWRRSEGVDLLLEKPNPHFKIIKNNYPHYYHKRGKEGEPVYYEKPGKINLKA

LKSAGLALDDLMHNYLMITEFLWQVIEQDDNRKGISVLDVDGIGLSDFAGEAVEYVRKAA

LVSGKHYPERCAYIYVINVPSWFSIIWNTVKGMVDDVTREKVIIVRGKKKILEALSEHIP

VENIPAEYGGMSDGKAPEEDLLLQLMAYVNNDENASANNPIEEILKKKPMRH

>contig14273 Frame-0R

MIKEVAMSPIRPKAKELLPLTPIVTEASRIHPSPNRTEAAAAMLHLLTGSKGEISETSLT

FKPSIAKRRYVRKISKKVGTSTKRQIKTALIDSNPAAREKPPVSRATNTEELSDKEAGNQ

NWRINNNDMLIPFREYNRKDKSLGLLCENFLKLYQDDKTLEICLDQ

>contig14299-0 Frame-0F0

MHQLRHLVLIMSVIVMKRIRNTNAVVFDVAPLPRQSLHDH

>contig16486 Frame-1R|Blast-cysteine synthase, putative [Phytophthora infestans T30-4](gb|EEY69413.1|) 2e-42

MSRFLLREEGIFVGSSSALNCVAAVRAARKLGPGHTIVTILCDSGLRHLTKFWNEHFVHE

KWHLTPTASHLEFLDGSTGQP

>contig16532 Frame-0R

MFTRKAHVPMHSMGPFIHRHFGIPTRTKRRNVYDDQSLDAQESATVRDLFKGLNEKFYIK

QLNEEWRSAVAGESFQQDDVIGSSPGVVYPEPTRFTVQMTPEKHVHMSGGLKFVNHSCEP

NTRIDLVETEALVSFIAIKPIHKGEHLSFDYATSEWDMDEKFACQCGSPKCRKDIRGAKF

LTDEQVIACMPYFTSSVLRQLLTRKLLA

>contig16837 Frame-2F|Blast-ras family GTPase, putative [Phytophthora infestans T30-4](gb|EEY61618.1|) 6e-26

MLGSKPPRVLVGSMSDLEKAR

>contig16969 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63718.1|) 3e-45

MRTRIWEDAAAMGVVSVLGFLMNEDGEVVGSERTQVLCKLMPSIHTLPHRAILALFITQL

SEADAQVFYAQGGLKVLSAWLMDGATEKEIGLSKEKKRIEMYSQLRALLR

>contig17131 Frame-0F|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY66304.1|) 3e-47

MDWNVYDDQIEWERQGLFEIGQWRVSSCNENFCAIETYPERLVVPKNVTDEVLLDAINFR

SLGRIPCLTWLNSSNGAALCRSSQPKVGMSKATSPADESLVAGITSPNLLQDHVHIIDCR

PMSSAVG

>contig18057 Frame-1R

MKEEGQVKSDTNENESKKKKKKRKRKRNENLSITMR

>contig19256 Frame-1R|Blast-mitogen-activated protein kinase kinase, putative [Phytophthora infestans T30-4](gb|EEY59831.1|) 0.0

MRQILLPLFLLSISPTSLLSISVVASREICQPSDVLWLWSGALTSRSITFKFGLREGYTC

TDQDFVLYAFPQLLEGEKPHSSIASCSIVDSGEAGDGEVQSPSSFEPPNVKQCTLSELPH

SDRKYRYELSLVPTGTIIKAGTFTTPKQEGTPYNYRVAFASCADESSDPKVFENIKNEKP

LLFLHTGDLHYHNIVINNVSAFRHGYDSIFASPIGQAMEAMDVPFVYMWDDHDFGPDNSD

SKAPGRNASVQAYHEMVPHYPLAGGRSRTSTIHQAFTIGRIRYLLTDLRSARTPNTAPAA

PTKTVLGKQQKLWFKNELREATKDPRIRLILWINTMPWLDDERKWGHFVHEQQEIVNFIK

AHGLNKWVPIVIVSGDAHMLAVDDGRHSPGNLTVLHSAALGRPGSIKGGPYSHGAFPGTG

QYAVLDVTDEGGKNGRVCLYYRGMNIYKGMLLEFNTCSPERTPPVTPYYPPPIPVRVMLR

ILKKIKKYQTSVALVGMVLVILLVYRIKRQHAVHSKKRS

>contig19506 Frame-0F

MITHKMLPRAVRCKVPVLQRLPRKWLTTISYQEERIFLWQQEFQRQQVAQVQATQDILTR

GESLELAVHVPAGQILAFRGVAGASTSIDVLKQLQESGLPKFQALAALNKDTGELIDLRT

PLQHSGTLQLL

>contig19634 Frame-0F|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY60576.1|) 0.0

MAHVFGDNEKESDFGYVYKVSGPLVIAENMYGAAMYELVRVGHDKLVGEIIKLEHTNASI

QVYEDTSGLTVGDPVERRKQPLSVELGPGIVDNIFDGIQRPLHAISDLTKDVYIPRGVDV

ASLDANKLWRYKPVNIREGDPISGGDIFGLVHENDIFHSHKIMCPPNVFGTVVKIYGADT

DNNEEYTLQDTVLEVRDDTSNTTHKLRLSHMWPVRKPRPVAEKLAGNVALTTGQRIIDAL

FPSVLGGTCAVPGAFGCGKTVISQALSKHSNSDAVVYVGCGERGNEMAEVLNDFPELTMT

INDREVPIMKRTTLVANTSNMPVAAREASIYTGITLAEYFRDQGMNVSMMADSTSRWAEA

LREISGRLGEMPADSGYPAYLGARLAAFYERAGRVACLGSPKREGSVTVVGAVSPPGGDF

SDPVTAATLGIVQVFWGLDKKLAQRKHFPSVNWLISYTKYMRVLEPFFNKIDPEYSMLRT

KCQEILQKEDNLTEIVQLVGKESLSEDQKVIMEVAKIIREDFLQQNAFSDYDYTCPLVKS

VGMLRSIILFYNLSQKAIADSPPDAKVTWAQIKTSMNPMIQKIIQTKFQLPKQPEAELKA

FFSGLDEEVEQAFQTISD

>contig19955 Frame-0R|Blast-strumpellin, putative [Phytophthora infestans T30-4](gb|EEY66160.1|) 0.0

MCEALYLYGVILLLLDRKISGPTREKMVIAFYRSKGESALENIDEVCKLCRVTGYLPGQS

KPAQYPERYFRRFQPPEEVVSMVIGKLQSDDVYLQEPCFPHRTHRSTRLAAQASMLYVIL

FFAPDILIHEKASMREIVDRHFNDNFILTTYMGAVADLSLEWAAYPAARLALANTLEPSN

IVQITKTKAQQTQRSIKELNYFLTEGVLTEMYVLENLDPLLNCIRNANVTIRWTMMHSRI

QPVIPMMDNATAQREIFDKGSDPDKLITLLLKVSQLEWKLKQMFGALLASKEDRWQRCMK

ETSERLEELSDYFSGEKPLTRVERNEDLMKWFMDLAEKVKSLDYVDHIKAGRRIKRLIEA

LGHVEQFDQIDTNLQVKAYLEESREFLTEMVRTVRIRDEVMGIIENVSDLSYGWEIITDF

MKILHQRVKNDPSSVILLRAMFLKFASILDVPLTRIHQCGSEDVISVAEYYSGELVDYVR

RVMEVIPQSVFRILAGIIKLQTDHMKPIPVKFENTLLKNHAQLNERYRLARATNEVSKYT

EGILAMKRTLLGIIEVDPRQVLEDGLRKELVFRVSLAFHEVLNFEKNTSKECNEIFVNLA

SNLDAYRLSFEYIQDYIGIYGLRMWHEELSRIINYNVEQECNRYLKKKVYDRASQYQSRA

IPIPRFQPSSEDMSVNFMGRLMHALFTMTDPHLTIYSPQSIGWFSEDGTEVCGIGAFSVL

HKSVGLLGLAGLDRMLSFRIVHTLNNLVKFWSSAVTPYFPLLDQLSAALVPEWKLLEHST

KLYDAALRKVEKIMSKLLKAVLIIGQAALIRRQISSELSFSSRLDANLLATTLDTLNSSL

LNDIRAHYRDPKTKPYPGSDGNPLLVELNKYLENTGANDPFQKIYVTVAEPMEGLAAMFM

LFVVAYMPKLQYNRNFGALNRVGKNPIDGEPLLVGILTILKQFHPSYTEIFLAYLGQFVR

TKVNDIFAEKADKKVKSSSLPIELSADVVNTLIFMLEFARCAKIKRSILDGHVPSYVFDA

IQL

>contig20700 Frame-1F

MFRSFIMICSILRVEATTLGEVITHFSKIVELRSEFATSLLECLKAQDYAIMDLRRELRA

YDSRQTGKIDVDNLRTVLCAFGFRLARFRFNTVAKMLFELNGTKVEYGQLLVLLANAQQD

IAREHLQSSQVRQHPLLQRSQTTLEGVGNATFRANHANASGSERQAPSVPPSMEHSESPR

TSSVNTSRLRRLSLYRVSNTLRPSKTDSRARTSTLESSDTSQRMTQNELRNTRSESAASM

DNLPSHTVYTVL

>contig20843 Frame-2F

MSFDTMKFTIPSPMNRHQTTLVSDNARALECQPQEATNSKNAPSLLFTTAAETSKEHTGM

HLTTLLTSTTSLLSHRPLATTTKDKKIGSYTPTERKLRLEKFHEKRKNRTWKKSIKYDCR

KKLADDRPRIKGRFVRVQENATMCEQGHAMAAGYASPTSLIDSKLSPLMAPVVKTQVPRG

ASVKPVALSISVPPLSSSNTTSTLACARMIASV

>contig20977 Frame-0F

MPTKRVKGKKKLKSVKAKQTDAMGSKRRLAKLGKEQRKGMRGSAANYITRSQALKKLQIS

LKDFRRLCILKGIYPREPKKKPSGTDKTYYYLKDVMFLAHEPVLHHFRAFKTFLKKVTKA

MGKKDYSTAMKKHENRPLYELNHIVKERYPRFVDALQDLDDALCLVHLFALMPTGNGVQA

DVTSTCLQLVREWQNYIVESHALTKVFVSIKGIYYQAIVHGQILTWLVPHQFTPTVDKRV

DVRVMLTFLEFYQVLLKFVNAQLYLHLGIAYPPKINLQLDAAGAQLAALKLERTKDDTTS

NDNLENETNALEKTISHQQKESEKRIKTVPQSLDETMLIDDDPDEFDHTIHALKEPLEAA

FASNELATQVFPNSSKEPTPLHLFTNLTFFLSREVPSACLELVLRSHGATLAWNGVGSPY

PEQSPRITHHVMDRPHQGHRYFNREYVQPQWIFDSVNNGMLLPLTRYVPGADLPPHLSPF

VTDNQEGYTPEYRKELERLKSATQVLREVGTIEADNVSESEEDDAEEMYVTELQAERHGD

DDRDSCDENEARNEVGTLKRNVEEAGFERVSNKKQKEDEANELKELAKTMMSKKAKRLYD

RMQYGLGKKADKIQMLEDKRRKIAMEKATKKASQDGGS

>contig21008 Frame-1F

MEAVATTTAMPAAEEEVVNETVEEVTQSLEDILALGQGLDDEDYKAELEVLQNDPNSNLY

SAVTFEELNLPEQLLKGVYNMKFAKPSKIQSVALPLILANPPENLIGQAQSGSGKTATFA

LGMLYRVDVSLKAPQAVCVGPTRELVRQIMAVVNAMGKFIGVDTFLAIPGNDLARGETLK

AQVIVGTPGKVEGMIKKKQLETRDVKIFVLDEADVMVAEDGMRERSVAIKRFIKNRACQY

LLFSATYADEVRDFAQKMVPDHNIITVKKEKLTLDGIKQFWIDCKSHGNKFQVLSDIFAI

LSIGKCVIFVQQRETAKELTRSMRTNGHSVGILHGADMAKEVRDQVIDEFRAGTTNVLIT

TNVLARGIDVAGVSLVVNFDIPLTRDRRPDPETYLHRIGRTGRFGRKGCAINFVHDDKSK

QDLAEIEEYYARPITQAPSDDIEELEKLLAWE

>contig21642 Frame-0R

MVQDNPVRSKQMELFGKLHVSMDHVLGKLLMAAPPLPDKLKLQTETQSLAATWVQVSEAF

EKRKAMLERRKQKAEGKKESFKEASSTHKNKNPIKKDSSRKQMSKSHGSATSPRTTKSPR

SVKADKKASKKVIGSPSTISDQTKVNLHGELSSYDKFVLQKLHKLPMCQDVKFGTNKYRA

IVKWMELDKG

>contig22166-0 Frame-1R0

MGHTCGILAGEYNTEGSLRKAFHYIELYLLLF

>contig22269 Frame-2F

MFREIPTLKEVRLVVKTRGERMLSRGMAYVQFTNEEGVEAGLRRDGFLLHGHALRVKRSQ

PPVASASKAGKTSNGEGFRWNYDPLTLYIGNLNQEKSTRQVSEQELQEALQQSMQQVGEL

VVVTRVSILQDRHGKWKNYGLVQVAEASQVAVCLANVAALQGMLGNQVTMKASRFSIAHM

LEQQAKQHSQKRARQAECHSTNVPHVQRHKGIDSATSLMPRVLRRKAAVSIDASKASKVA

KSGAPKTN

>contig22838-1 Frame-2R1

MCSVKTNDKVAITFCYKKIF

>contig23275 Frame-1F|Blast-chromatin-remodeling complex ATPase chain, putative [Phytophthora infestans T30-4](gb|EEY63798.1|) 0.0

MRAYQLEGLSWMINLAHQGINGILADEMGLGKTLQTISVLGYFYEFQNVSGPHIVLVPKS

TLSNWLAEFHRWCPSLRAVKFHGNKEERQRCVQEVLCPGLPDDKRKFDVCVTTFEMCLKE

KTALCKFAWRYLVIDEAHRIKNESSQFSTVVRMLDTEHRLLLTGTPLQNNLHELWALLNF

LLPDVFASSQEFDDWFNLDVDDDEAKKQMISQLHKILRPFMLRRLKADVEKSLPPKKETL

LFVGMSEMQKLLYKSLLLRDVNTVMGNSGGVSKSALQNIVMQLRKCCGHPYLFEGQEDRS

LDPLGEHVVDNCGKMVLLDKLLKKLKQRGSRVLIFTQMTRVLDIMEDFCRMRQYQYCRID

GQTSCEDRESSIDEYNKPNSSRFIFLLSTRAGGLGINLYTADVVILYDSDWNPQADLQAQ

DRAHRIGQKKEVNVYRLVTADSVEEKIIERAQQKLKLDAMVVQQGRLQEKQSKLTKNDML

EMIRFGADQVFRATNSTITDEDIDAILAKGEQRTEEMKQKMQAHDKGDLLDFKLDGGGCQ

NHDGIDYSNEKERQEELKRLADAELARQMAEGIGKRERRTVHRHSHVSLESKHRTKQKQL

PKVLRLPRLDEWQFYNRKRLIEIHEIERANYELAKLEMEKPPLPPHAQYLTEEEFKEKKQ

LLSEGFSDWNKPQFFLYVKLLARHGRENIEAVARELMKPVEEIKRYSKVFLARGQEELSD

WPKILKSIEKGESKLLEIERLTEETACKVKRYANPWEDMPINYQGKGGKVFTEEEDRALL

CLVNLFGYGAWDRIKQEICNIERFAFDYYLRSRTAAEIGRRCDSLMRICEKDNADLEHRE

KKENDVRRTLQLQRIKLDQQLAEARTDVKQHQSRVDELIMKEAKRMQRQREAKRAKKRKE

RDENEEMVDQRTEDLVHFLLQATSMDAAKVALDFCAMISHEKREELQPSYVLKKIRQVAE

IDENATKGAVAWTIKPEFVNIANDTLKKETKVPKHELMTHVGGSASPIKFEGTSRLPRSP

WSPTAMKHQLQNAKKEKKLNKGSALSSVRKPRSAYVQFSMANRIVVKQSLRKDAQIIDVM

KELVQMWKAMSTEQKAPWVEAAKLDKMRYDREMNETTD

>contig23778 Frame-1F

MEKFVMLQTSKAKSLGQAVPLLSNDSNPLTLEVLWTTAVELVADRSKAFSLRYEDSEGDE

VTIARNADVEELLNYMTDEKLKLVEVKVVESTTQLSGLTTTMAKGSTCEPQLLPLATIVN

RLEAVNNNKLEAVTLVDLLVALLKSTQVADEFKEVLAMRRQLIDFLLDEEVKKVVKELCA

CDEFQELVDSLRLAISSKNAEGIETIVMTRFSELLVFIQRLIERCPALTRVLLDVLKQFK

TEWIRMHELPTTNDVLELNTDSDKSTLEGKLPEHFGIICNSCRKTPLLGFRYKALDREDF

DLCKGCEASGQWIDYEPFIKITDPSRAPKHRGIQKMAKHSSIKCDGCEMKPIVGHRFLSM

KVHDFDLCEGCEANGKWGESHGPFKKVLETGIRNRMTSIGRFRGNERHLRHCIN

>contig23819 Frame-2R

MNRRVCMPLRQIIELRPMVGASGDIRAFFGVQPLNKKRRTMLDTKILAVNYLHSNVSIQK

DEIQQLQRNKDDGKMLPVTSFKQLQVEGQLRSLMHPSWFDLLQKETARSSFQELMRFLVN

EEGRQKTIFPPPADLFAALRDCAFSDLKVVILGQDPYYGPQQAHGLSFSVRHGIPPPPSL

KNIYKEAMKDIGIERPTHGCLSCWSRQGVLLLNTVLTVRQGEPNSHKKRGWEQFTDAIIS

KINHNASNVVFFLWGKPAQEKSALIDTKRHLILRTSHPSPLGATKTNAPFLGSKCFSRAN

KYLL

>contig24094 Frame-2F|Blast-Amino Acid-Polyamine-Organocation (APC) Family [Phytophthora infestans T30-4](gb|EEY67063.1|) 3e-53

MPGSHSHRQLGIVSVALITYFNVSGGPWGSEPVLAACGPFVGIVAVLLFPWVWCLPLALT

FAELFTAFPTDGSFCKWVGVAFGRPMGFQVGYWSWVS

>contig24230 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65597.1|) 0.0

MFQIRVEATDTVEEEEAKAEELILDVMHDMQDTSFLAGNPQVRVITGKLRFYRADKPYSS

SSPANNYHQLPSERSILVCVVTMPSHMSLVEILGFLASFRDDIAQVRILKDPERSNCMAL

LQFNSQEKADQFFLDHDGKYFNSIEQERSKIVFVRGIEFDPVLCDDASNYEALEEKVADG

VNHVIMSPLNSRSERGEKRAQMKHLFPPPPAGMTEIPTCAVCLDRLDASASGILTTLCNH

SFHCDCLYRWEGSCCPVCRYSHGDIGSSCEVCGTAEHLWICLICGHVGCGRYSGEHAKQH

YQETLHTYSLELETQRVWDYAGDGYVHRLILNKRDGKFVEFPCPNNFSGERSQNPPITSA

EEEEGEHRKLEKLAVEYNFLLKSQLEEQRLYYERILARVKEGESRQLLNAHEHERKQLRK

ANLTLAQKTKKLEEELTFV

>contig24762 Frame-0F

MCLYYNQGDNVTIAGVYVKRLTSLSVQSEVGKSVFGAMVCLSIGDGNVRKFLGTRVSFRD

ENTGMMDKQAKRCLRIMV

>contig25071 Frame-1F

MTKPIPVNPTRHMPINKAADDAAGLQIAGSRPETRFEGSEKEESGKLHPACEAVPHCGNE

NVKP

>contig25466 Frame-2F|Blast-peroxisome biogenesis factor, putative [Phytophthora infestans T30-4](gb|EEY70091.1|) 4e-08

MTTRGAFLAPVLVPVKNCFANLPPDFVNAFLGGPDHV

>contig25905 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY53370.1|) 4e-76

MHYLEKVHIPLNDLTFLQAIGRGSMGDVIKARYFGTIVVCKRMRREHIVASKNGRHRHGS

NTFILP

>contig26140 Frame-0F

MKFDILKNIYQRRTADTKSTGLMSAPEATGGIGLISIPVAVKAQRVKHALLWLTQRADQY

GTA

>contig27033-0 Frame-2F0

MTFQRRKQPQLLPMDPNAPDTSTFFGTVGSPIKMGPLAAVGRRAVKASGRVGDGPVDSEA

ATLDVTQKAAFREELRRQKATPRVDNDDNDTQVATIRQ

>contig27680 Frame-2F

MIQRGTSEHLEDFPETNLKLPRHDTTLIHEAMDQNSRKCASGGFEIGSGRRYSSQQAQTS

N

>contig28403 Frame-1F

MEEFAKELIEVIEREAQIEAWAAKKVHPSKVYDELELGTTNSIDITRFIQWLRYLQKIQV

ENDVFVHFSKTIPKGQEIEYASILKDMTLFPDLETFSKDLRSVLYKNWAADTDMTPLMLM

KRMTSSVATLSSIDPKRVVLLEYTKYFIIRYNAALWPQFQKIVEKNGIVAAVKFASNVNL

>contig28708 Frame-0R

MAYMFMHVHIVIAFSTITMPAFYMAERFLLGMHKNLSMVDQEQGIVVREKASPVVGASPA

PSNTECNFVNSGVSITPLVAAYDESTEYSGKMNVFRYILLRLSILILLVIASIFFRDNFL

DLVDFTGASAVTIGCLVLPLLFYLKVFGKKLPMYERVGCTVIIIVCIALGAYVMIYAGQN

LFSPVSSSTTFPYCTEADQSSPYYVLDSVAFN

>contig28865 Frame-2R

MSNGDESNTHDSETNAMAFEPLSLHQIVRD

>contig29156 Frame-2F|Blast-prefoldin subunit, putative [Phytophthora infestans T30-4](gb|EEY62517.1|) 5e-62

MADSPSEVNLVDLSLEQLSALKDQLEKELQQLTASFGGLREAQSRFTESKEALKSMAGSD

LSKEVLVPLTASMFVQGKLVSKDEVLVDVGTGYFVEQTVDKAEQFMDRKVAFLQSNTEQL

KTIIDGKRTMLEAVLMIMQQKIQEVQRK

>contig29880 Frame-2F

MFLEFKDKIHSEDPILLKWFQHFSTHETVIADKICEKDLYTLLSKSIAEMDLLQLLNSLQ

TKSESQLLAEKMLMFMSNDADISIKVLAAWLKDNNDLTEFWKSFPLDLTQVPLSPAFSVW

LISYQQGMQKMGTTESKIFGHLVEQIHRFPVPEQTYVARLHELVAVLVSRVDTNKKTAVA

ELMLLSDGVNNKDLREFVIRSLAIANFDPLDAINVFGLDKVIAAGTSATVVGELVINWCK

YIEGYNKLAAVQFTVDKAYKALVVLLKLTDNTIINLYTALFNSTNRNSVATGLLNLIIEN

KIYKTKSSDRFAALLNLNAMLHL

>contig30143 Frame-2R

MQTSLRHENSVTLAIETFAVVIGGPVSFESRPFRMQTTRPVSFNQGHIECEQH

>contig30514 Frame-2R

MEASRPLLASDDCEKARVVARSPNCLSRYLKAGDEYINTKKNTATDDFLSIVCDRNSADG

LHQGNKLLCCRQFACWKWLFPDRVCEYEDFATSAQMGEIYALRQAARKEFDLTSSG

>contig30976 Frame-0R

MAMVEMHKTLWDLLRLFYKHCRSCHRPKVAASALRGQLFSCLNRPTLEEQQPIHVPWWTF

RNDQEGVSRL

>contig31672 Frame-1R

MLIASISCCYQSYDINTIRISIFMIKQGNLAICGRSNYCNHDSTTRPYKVSHQSLPLLST

ISTFSITVLSP

>contig31719 Frame-1R

MLGAASHGSEVPITSFAGSCPVVCLTRWLQEFLLLVRRVYFLLLSFITGTFFLMTGESSY

FFNRPHRS

>contig31896 Frame-2R|Blast-endoglucanase, putative [Phytophthora infestans T30-4](gb|EEY56199.1|) 1e-173

MTSRRMPLCFEAARGSIWLNNKPFFLKGASYFGMESDICVPHGLWGGHDSTTLAKVAQLL

RTNGFNLVRVPLAVSAVVNNIKVDRYKIGNEIELLKAFEGRDLRYLDVLDYVVQKLEHHD

LLVLLDAHVMHPAGAITPLWYDDAQGCSEIVVAKMWTSLAFRYAKQWNVIGSDLNNEPHG

KATWGSGDIKTDWNLAAMRLADKVLEMCSHWLIFVEGVQTTSYDADHELPCFWGENLQAA

GHDPVKLCVENRLVYCPHTYGPAVSYQPYFDAADFPSNLPRVWDIHFGYLTRQSEIPLVI

GEWGGRFENQRDWSWQKQFVEYVQQIGVSGLIFWCVNPNGSDTDGLLSADWHTPNVNIIQ

LLSPFVGTPVPPAY

>contig32134 Frame-0R

MQRRWLASIRSPRNLKGLNLTSFVSPLLLRLHPDTLQREAPELAQENEGALKQLNIFLEL

AAFGCNNDAFNARKQLLGHVANRYDILDEPLHFPLTFHVPLDDYKAQVPVGRFVAVKYTI

VVPSRLVQRTLSNVARSISAREDPYSALSAPFAREWQRITKRILQDLFEVAQVPFVVGEG

ETMKTTALAMWLAEDDSAVEQGDRDRICAGQQNRAKKREHEQFNKIFHKMLTHEREIVQE

TTTGLEDVP

>contig32439 Frame-1F

MRRQQQLNEREARYQRQREDKMKSRDACTAAGAVSAATLRGRPSLLEKPPSSAIKVSAYD

EIAQTMPASSVERRSLIMASPPKSDIKVSAFDELVPRERFADAQRETMDQSTKQAFEENR

KKGLNLKRETKVAKQVLLGTEKSSIDSKPVYGDMDRFERDDGDTSTYDTDDSFEFDSDSE

KLTYAEYSILEARVRKVKLDALAADESRNCLDVSSHVDLTEEDIAASGIELSTVKEEDED

ASTVKLTAKDLALYALGRTSSHSLSDLASPVVSASKSHLVVHTQAPVSYTPTPSAFPSSR

ALESSPRRPATTGRTSSNHMAQSPSAYSYVRRSLTRAPMDLKNHLPPSIGVLSGLSSGSS

TFVLDSTLFYDVTWQSGEFAFSVQHIYTENEFEFDDRTQEPQLFLRMLLNTERSTCESFN

RVRAGDVLIRVDDTNVSELGLEGSGSVLTKFFANLMGRTPVKLTFQRMRPSDWEGGVEL

>contig33487 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63198.1|) 1e-29

MELTQSKLSFCVKCLIDANQLDTLEAARCQFVYGRHAYQNAHKSSGTSQMSSISGSIASS

TPSSSGEF

>contig33946 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61074.1|) 2e-84

MTSRTFDNAKPHITAIEDTPIVNVDTAVPSVVEDNNLARYRTMLKVGVPRPAVERQMLKN

GINPAKLNDTVQEGALSAEDTNECVPNKVVVATTMRRRWHWHEAMQADRAKPSSNGSVWT

QCSKEDAHRRITALSQSRIQELFVRGMIDNSIENDDRDSIVSNASDADIPSIRQHSFRPV

KVQKMRVMTGTKGTNLEFVVSRLKIPFAEVAKDVNILTAMYLQETDIKTLLAMWPSIAEQ

VALDEYAGEL

>contig35250 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69277.1|) 1e-157

MARVRSVTYVQLPELDGHSRKVYALGFNCNGTMLASGSNDRSIRIWDPVTERELMDLRGH

SDSVMSLAWDPTTPHHLASTGADKTVRFWDAKSGRIINSVSLPSDAINIAFSHDSKYVVV

GNLDCITLIDTCKARVVRRVVNPFESYEMQFSRNGYLFVAAGHAAGFGTFEIMRVIAEKK

GNANLESAHKVMAHAGSCLCLDLHPSGRYLALGGLDSLASIWDLDELFCVKTFVVTTASI

KSVRFSYEGRFLAIGMDDPLLVVVDVESGETVVKLQLQNSLQYLSWHPRKNLLAYVGDKA

SSEKNSNRGGVIKIIEMKE

>contig35863 Frame-2F|Blast-PREDICTED: similar to retrotransposon protein, putative, unclassified [Nasonia vitripennis](ref|XP\_001599390.1|) 1e-09 NOT\_ORF

MLCEIGVVLKLSMLMHVEKQAATRQLTSEASPLRAKHN\*IRVKFVCNFARLRTVLAQYVQ

SE\*MLAILMTKALEATKPTKLRV

>contig35917 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66494.1|) 1e-129

MARKDETWRRHLLVVQFFIYCFQKDMVACRSRYESFEGKSWMFHTRLFSLLQTDAITSKA

RKTSRINSTKLRNNAHIISAIGWGLQLWKRVYDEEAKETLKKDTTNEECCEMKSFLQQEG

EQACMAVVRLIEMLYMCTDQHVNALQRIQAGLGEFTRPTCIKFAQSLQSPALRTELATTM

IGLSNKARSTEIEWYECNALGRVQLAMKSDTSSDLAHTDGYSWSHFDSLLTMQPQNNFTK

LLQEISRLQHD

>contig36347 Frame-0F|Blast-pantothenate kinase, putative [Phytophthora infestans T30-4](gb|EEY68288.1|) 2e-42

MNEFLREHQSFGSTGVQDIRLRIQFKTLNGIFHFVRFESSKTRDAIDFIVKYGIHQSLRT

LPCTGGGAHK

>contig36505 Frame-0F

MPLDNEFEEPDLELKWLLSDTTPVLFAFQRLNGVRSNDVDALELDTECGSTKARSWQMRS

WEDFYNHMEWIKSFDDFVVVTKGCLHAFQQWMEITASPTSGMVPVFFAKCNAGYHLVRIL

HCAVGL

>contig36686 Frame-0R

MAGGALTLPSSTQRTHYKGYEHVVIPAPAQKALKSNETLVAIASLD

>contig36992 Frame-2F|Blast-kynurenine-oxoglutarate transaminase, putative [Phytophthora infestans T30-4](gb|EEY66134.1|) 0.0

MAHQLSKRLEGFDQSTVWQEFTPLALKYKAINLGQGFPDWPCEDFVKQAAKDALDADYNQ

YARPQGHKKLVQVLAKKYAKEFKRDINWSNEVAVGVGATETMYAAINSFVQPDDEVIVFE

PAFDIYTAQVQMAGGVCRNVPLHIRTCDETGNKAFYIEEVTLAAAFSSKTRAVLLNNPHN

PTGKVFTKQELEIIAKYVCQYPRVIVISDEVYEHILFDGNPHVRVATIDGMWDRTLTVSS

AGKTFSVTGWKVGWAVGPSSLIKGIFLANNWIQFSVASPLQEAVANMLELAEHPYNGFSN

FYAFVANQYKHKRDRLSRALADAGIIPITPSGGIFLYSDISAIKVPKNFIEPGMSYDWAF

CRWLTVTKGVAAIPSSAFFCTKNKAEGSRWVRFAFCKTNQAIDEAIKRLARINES

>contig37029 Frame-2F|Blast-short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY65022.1|) 0.0

MFMKPLQRATAASSSLIKHARRLTRSIGFLSTLPEEHTMLRDMCQQYAAKHLKPIAGELD

KNHSFPAQQVKDLGEMGLMGIAIDEKYGGAGLDYLAYSIALEEISRGCASTGVIMSVNNS

LYCAPLEKFGTPEQKETHLTDYASGAKLGCFGLSEPGNGSDAGAAATTARVTDNGFVLNG

TKAWITNAHDATQAIVFATTDKSLKHKGISAFLVPTDAPGFSLGKKEDKLGIRASSTGNL

ILEDVEIPKANLIGHQGDGFKIAMITLDSGRIGIASQALGIAQASYDCAIAYAQTRKAFG

VPLAKNPIILTKLSTMATEIEAARLLTWKAAVEKDAGRPFTKLAAMAKLKASEAATMCSH

QAIQVLGGMGYVSDMPAERHYRDARITEIYEGTSEIMHLVIAGVLNKEYNELN

>contig37362 Frame-1F

MTGRTREAEEVLSMLALEAGVIARDHYSHPSKNNQLSQIPCHGSYAHKNASGNRRPLTAV

YGSMPSCLIRKPRSVPIAPRPTEADALLGARDQHSSQSETDSDSDGSCTAGSTRLSLQSI

LRIPTANFSCRSVKKQVSVDFTLNTDEDNGSKQSFDGPVAPRCMPRRLTLEEKAALYRVR

PDLELVPTVLLFSEFEEMRRQRQRKLMFSILGASLLLLLMIVFYYLVSQM

>contig37494 Frame-0R

MNPDGIEHVSYTILNLSLSPSGMFLLAATDSDRIFIFSLQHKVALRNFYGHKAGPYSQPR

AVWHPSEKYIISNNEEDGTIFVWSVASEKIVETLYAHNALVRDLVCTGPASSVKLITVSY

DKRIKVWKL

>contig38110 Frame-0F

MALTRSRASTTPTALPAPPLASLSIPIRFQCPLCLDVLRHPIQLPCCHRYLCMECFERAL

ELTSVNCGFCRRRVVGFARTKQYKVDEVMWNAIQSECPFLGDMVDDREPLVDFFDENAPR

LHSSSENRLDTHNESTGALKAFYDQQLREHQYQVHEAEQRALEQTIEFLQNDLEFTASFS

SPPASSAFSPVSSTVSSASSLPEPKMATDSIVTSRARHRPVTRSALNAVNESQPKLDTFF

SSTRATSSHAGQSLHGVHSTSSGLSPPRVRKHLEISQPHRKYFLRGASHSPTPIKVRRRQ

AIKGRKTLRQLTLGTTVSPIALHTRSRDLKQVSARLSEPTKMLTRQRQQRSSWKCAHCTY

TNTCFDSRCSMCRRLTSFTSLSF

>contig38187 Frame-0R

METSSLEKTLSHVKSMLNKLTREKFVKLTNELCAISIDNYVLLSSIVSIIMDKALEEPSF

ADVYADLCKEFYIRTIKQTWNFLSVLNDEKGSFYWTGIDKAKFAEYVGPFDSPRSCFDDA

DASESTATEICEFQYISGVHYRRQGDCLIGVGEKAIGAYFYSKRKINEIGDDEPFGGPFL

SAELARLEAAKQTTFKRLLIIRCQSEFEKTNKHAGFIKAKEEEENDPRRREIRAMRAKAK

MLGNIRFIGELYKVDLIKQAVVQECIFYLLGLDLMTGEDGQEAHAQAVRFPDEQDLEALC

KMLATVGKKFDQPNTKTIMKIIILRMVELSNDTKLPSRARFLMKDILETRDHMW

>contig39265 Frame-0F

MRKTLNNVRLASQKLPFATASLALYLPFEIEVDDTCYENAMVLR

>contig39773 Frame-0F|Blast-glucanase inhibitor protein, putative [Phytophthora infestans T30-4](gb|EEY60885.1|) 4e-08

MMNIIATIIAAATTFAGVTGNTVHTSRQLILGGHPVTDSSHQYVAGLRDSPYENTFCGGV

LITKLHVLTT

>contig39799 Frame-1R

MRTHKRQRYEVSHCNANETIFSPLQKSLTATMDSKIYL

>contig40056 Frame-1R|Blast-dicer-like, putative [Phytophthora infestans T30-4](gb|EEY56422.1|) 0.0

MEQVELRAFQREVLELAREKNVVMVGDTGIGKTFLAIALLSEQDYSGDRRAFFMAPTRQL

VVQITAKIRQTSTLRVNSFYGQSADLWDAMQWEREMQLTRVFVCTPEIVRNVLLKGYVSL

SRMNLLVFDECHHVTKRHPYAQVIKMFNQDNMSSMPRIFGTTACPTRHCAEKLHAEMKKV

DLDRSQIAEFAAAAPIIFETFPVQKPWSIDGEKMEVDATSGAWIYDNIEKELAEVKAVAV

LEKLIRKGKSDASSDQTKLDKAAKKFMQNCVTVYKRLGPWCYYRYVELEIHRLAIAASLL

ITIPGSMFGLDRDAVKTMLLLAAKREKCKFACSSIVEKVEEILRAQLFEVECEVEGASRS

EIDESDDMDSDNELSGETILTESASFEGKEKPVPSSKSSRLDLQGIVFVNTRTECRVLSD

FLNDKFAASAKSIEKSENEELPVEPNALNSDDNSLDEPFASILGRASRSDTASFQLPKME

TILQKFESGSIRVLISTAVSAEGIDFPQCALIVVMDRVETARRLIQLKGRARHEDGVVYI

LAEEEDLSHEVHFKELTLEAKVIDQLEFSREKVETIQQQPRSVAAELMGAGVHRIEIEST

GAVLDLDSSVACINQFCQSLPTQLFTVDNKQMYSITETRFGGKSMFTAELNLPMELELEK

FQSDLMPSKGSARAAAAFGACQKLLEKRLIDDSLNSIYRTRKVKSSSNVRDLTYFLNRLH

T

>contig40250 Frame-2F

MEEALSKRSDTLLASLNLYHGGGVRVINPLSSACPSLNAVSSPCTFKKFASKIVAFRAPM

RFFFKEIFFKTSVTSECE

>contig40434 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66708.1|) 1e-153

MLSRHLGRSILKRNTHAHFSTLRDFSPSSSAPSFGIAFDIDGVLIRGGHELPGAKRVLQS

LRVNKVPHIFLTNGGGCMESLKAEKLSSILNLPINPQHMILSHTPMRELAIAYEYKRVLI

LGSHDVWHVAKCYGFKKVVSVKDLLHHFPTQYPFNHYEQKPAPHYEEPIAAIIVMHDPID

WAPDIQVAVDVLIGGDPPGSGHPLGKQTPLFVSNDDFTFSGAYPFPRFAQGAFTQCLKTM

YENLTGLQLEVTKYGKPHSVTYNYAKRLLHTTSGQSKPLKRIYGIGDNPSSDIQGANNAG

DEWTSVLVRTGIYDGCKRPEHEPDVIVDDVWDAIEYIYKREGIKEIAL

>contig40863-1 Frame-1R1

METNGDARVASRRVRERQDMVSWCCAGGYGQPRLFVLRDREVRF

>contig40917 Frame-1F

MSEQDDSRKRKRQRRKNRKNKQQLPQRGYYADPLSPISSTPMKHQLAKTAEYSVCKTKNA

PSSTSYNASGRQVATEKKLLSPRMLLKVSDQDESRKRARKPRSLSYDSTSSSNSILEEKS

KVDVDTSTDKNAKDELFSPALKPLKSSRSSSASPTKSVAAQSDEIVEQAAKEEDNLSYCC

VDVEDEEGKVVTYSEQEFNPFFFMKTLPKYEDIVDRKRPISLPVRSRHSPKICLVLDLDE

TLVHCSVDEVKDAHTKFPVTFNGVEYIVNVKKRPHMEYFLKRVSKLFEIVVFTASHKAYA

EKLMNLLDPHSNLIKYVRHIVYSNVLTNMLALQQLPTLPR

>contig41345 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66531.1|) 1e-118

MASLFKSKKRNRDADNTKVLNSTDLSSSTTSERICDSDSGDNEVENTMFRPAPEHTELEQ

IESDAEQNEGDKRSLLRKFDEDVASGTQNMETERKELVEDFQEEVDRKTEATVYVEGIPY

QATEGDLVTHLSSCGTVREVRMPRYQDSGKPRGYAHVVFDKEAALEKALNMDGKYLFNRY

LSIRRAEAPRAVELALKEKSQNLLKKAIKGCRTVYIKQLPYEVEEGTIREALASCGTITS

VRLPFWNHTKKLKGFGYVEFSNEAEALTAARRSGMKIGDRMVLISLDVAGSAPKSSFRQR

DGQYWNKGEEAKKSLAKKIVEKQQRQSAKKKRKST

>contig41657 Frame-1R

MLHKNYSRQSKSMLRHVLRVHSQCLRETGCHAFASVPALKRGDRCKSLLVGETYHNFTLK

RMATVPEYGIDALELCHEPTKAKYLHLDAKDANNLFTIMFRTPPTNSTGVSHILEHTTLC

GSKQFP

>contig41958 Frame-2F

MLCNGVKHATILRTKAQQLMNNLRMEEPENKVWSCSTCATGGKKLVLDENDGR

>contig42029 Frame-2F|Blast-acyl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY63794.1|) 3e-14

MFSSLFLDHSTMLFYKNYRYVDEIDVLFYYARRSCVTRLSRVSVASARIYLCMVSALPCV

Y

>contig42160 Frame-2F

MVKAMMHQSGFPRSFWVHALENAVCVKNRVYCKGAGCMPYETIFVSKPDIHHVRSFGSLT

YCHAPVLKKRKLNMHCKTGFLLGYREIFFICHVYFPTEHKKGFVGSMAFSASLRALSWSP

SPYATSSPSSGDSLNVCSHYITFARYELS

>contig42494 Frame-2R

MNEDPSTDSIQAASMAATADGVSVSISESGGSTALDVVESIKGLTTIVDIASPSVNTGAG

STTSTIASHNGEALPVICDFDDRWNSTIQMMCRIVELEKMLLRYKMGLDSDTNPARRPMQ

LRFTCCELSSNEWASLKQLVKLLEPIEGLVHITPLAYPGLSIIYPLVHSLKKHLADAGAW

VTDPLVATIRQTIVETLNMDLCSSGGAPSSPYLSCLLDPRFKSLPFLSALEKQRLVQSLY

VLLRVSDKDDDVRPNDCNMEKKQSSNAKDSMGSNASPSITKKAAALLHEFFPLEEPTTEV

EKVKLQVQQYLDSPCLPATDESEHDPLEWWSRYQR

>contig42630 Frame-0R

MSLSSLSSSDTESFTLARDDICKKRVEANTRVHKGTVVQLRRECNGIRVGSKVRIHQLMG

EKSSTKNKTVSSDQSPEPQSKVLTATRSFSNSELSSPSVVSSDKSLLVNDMFP

>contig42890 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56178.1|) 0.0

MLAGVLHKELVPPNDQFPLVLSPHHTKCAPTDLHLREFAQLEVQVKALQIPAINSRTSAA

RLAECFHYYSRLFTVESFLWPDFLAVVFTKLAEHFAASENIIVQSAILRVFQRAKGHVAQ

VNDPSKLLGHLMGPLLHATACTARTMALQILATMPSLLLENTTVQQQLIKRIKATNWDER

MAAIETVRALLPLQPSFQKDLLTATLEDKTTETCCLAADAVTTSIEAHKVWTYCAEFYER

LASDKSAVACVRAMTKLCAAYPDTLLAMHGQVLHHILMHDPRPLIQNFALLITQQLVFND

GKDRDNEELIAIIEGIFSNFSNHPDKWKLRHQLSALLLLEKWSAGYEVGNNAVMFLEIIK

TVLTTTADERFGRAYTCIISNIAQQTRIQDHSTAFENHIDELLRLLHPRAANIATFTWGH

ALSAISRLCQEFSVRLTPLVTSRLIELFSILADAKVDQYVAMPRRNGIMKVLGAQAQPPP

INLVHKALPMLLQELSTIDQTDANRMQALARTFFLWTHELVRTPLDPDHVTSQTIRAFEE

QLITFESNKSHAERYEMAKIAMLRGRFSLAKQLLSEVAAMVSSECFGGWLHALLTLCEAE

SRIANHQSVD

>contig43138 Frame-1F

MSRWSKKPAGYEYIQPVMDALDRELRERMNEPHEGKRQCEALWPVHQINWQRSRYVYDMF

HKYKKISRQVYDYCVRRKLVDASLIAKWKKPGYERLCSTFAINSKNYNYGTVSICRVPRQ

QLSEGQVVQEKHSGCRGCASGPGGYHNIFGNKYGQYLARIQIMREEAAEKIENKQVWATE

QEGEEIAGGESEKRKRE

>contig43291 Frame-0F

MQRHLVTAIFLVGVTACFVTTLHAINLKNRDDYRRKLNAEPLLR

>contig43347 Frame-0F

MCEVDPNRSSISRQCRVTGIEVYKRSTLPPQDLSLFNIIVIKTLHWARRLSTFCCFTYSQ

TSAGTSRPILVSGSHKSSMSAVHVRKQEHITVWRIVSVVLDLLNPLCPPGFHR

>contig43505 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63802.1|) 1e-11

MEGRVRVGQLYVKVVEAIGLPSTDSITSDPFVRV

>contig43686 Frame-1F

MRALALEVINKWSAESQSDYYRDDRLHEQAVDMDELLEPIATLENIV

>contig43888 Frame-0F

MRALLAEIQGALCFNETKIKRVSAFECAELCSAKAFFQSRPTGVYTCTRLKASVETTSKV

FTILDEWSFHLQRLSNGVTLADNSFNWSSSELEKLKVTTDLLAATAVDQWLVGNTDDGML

SVLWYPRPDIHDYCVAVHVCPLPTPLRFTSTVLVYGEGRTNAHCKHTQWIKDRVIIEQHA

ARIRENRGEPIDEVLLSTTISGGDKLLLEGLTTNLFVVKGDKVYTAENDVLHGSTRMLVL

KACADLSIPVVLEAPKLSERDLWQAAFVTNAVRFIIDVTRILIEGTG

>contig44221 Frame-0F

METVEAISDLAVAAHHADAQMYLRMSQLDSSAMDKNAKVVMTTAATDDSKDGGGSDCDSI

EITVKTKLEDLAFEPHAAELSSGGSCDYDSDEGADDLNELRATIEAAMEKENYKNGPALT

TEHEVVLPPVREPGVDLTNDCPIAHCGSILNISATALMITVQAISNTTLLNEGSVLCLED

RTVLGCIDEVFGPVMMPMYLIRFASTFKIPKNARVNSTVYYATEHTTYIVPEDIKHKGTD

ASNIFDEEADETEFSDDEAEAAAKRGGRKRNRGGAQNHGIKGTNYAPSQANGGGRGGRGG

HGKFERNAVYNYSRHRASPPRIVGCSQHTPTYQMLAMPSMQTRPYGGITNYTQPQSAAYG

SPLYTAFRGNRLLVSSHDISPVSQEHIVSNGYYQPLLPSQDLTSYPPHALYPHSQLQLSP

QAYYCQPQQPRTVPHSEAYPPHRQSKSVAPPIPRPFYGNGQ

>contig44672 Frame-0R

MKLIKSIKKKKRKRKDKDREQRASSPAVTRSASKLNKLRKRCYAGVLEMAGHTPVTRSMA

RMKEKKRSSLEMIEDVEIEPEDEDHVE

>contig44719 Frame-1F|Blast-unknown [Phytophthora infestans]gb|EEY62661.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|AAN31499.1|) 2e-37

MISSWLLFSGAIMAVAMAAHIKVNHHHRGHHQKFREVTVIPDNGICPNGGDVLLCQSASF

ACQDDGTGIQKCLNRDDSFLDSIDSKTAAPWMQCSLTNASLPSSCL

>contig44896 Frame-1R

MCRIWHDVEAHTDRCQNPNCEFKNRILLRETMHKLGIKEQQMTTGMGELEQKRAEYIQAA

GDKKEALQNDVKRLELDLEEGKSELDELEATKKTFWSSLNEIGITERDDVVDKFPDFATH

YEKRTPRKARKAVAASTLIFPTAAERADFYLKKDSPHKVNTVDEDIASNDDRKRLHESSM

RNKPLSEHDVVSLLETINGEVETMEDVKYHDLADLAQSEEPPLPPAGPPPFRQNPELDQD

HTFSSLDFSVQPLVNEF

>contig45143 Frame-2F

MLREIIGDLAESSQETVEGVGGLSSPTVDLEPLTQGILTMRTVMSTAAVEQPVQREQQQD

ERVGENLQAEVEPENPTIIQRGPRRFFVGQWLDIQDTVNQWLESTVMNVADGKILVHYHG

WPTRWDEWIDADSDRIAAFRTRTLHVQNSRQMSPIPSTRVPSAPRVGDNDVRQLVMDVRN

LMHDMMPHIDRLAALCEADYNYHRQSGAGVDNTETG

>contig45226 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69381.1|) 3e-62 NOT\_ORF

MKTISNAFGSKWSISFRRYQRKPTSRYNCTEREN\*FSAK\*AEWSVPFCYSDWWTYEICYE

TEVRQYHKDPGGSRVSEWSMGVYKTFTEENDDASAGTDVVQYYAGGQHCDENGKLRSTSV

VYKCCESRPKQIEVESVDEPELCSYLITVCIPRLCEYEQESMQNPDGNLQLSGSCKDQFD

ATHADETVLPKFAALRWSSVISEDSSELDWTRKMQFAT

>contig45859 Frame-1F

MEEEMQHVLHLLDTSIITPPSGSDLETQHTQLVQPESLESRQPTPENICNSASHRENSGK

PVYNDLGEVIDLLGSLDANESYLVLQHQQEQLEQVDVGNLGSGLPPSAASSIGASQKVQL

PRSTSASTIHSGLDYISPIGLLNGSSMSPATISWLQTLIPSTSTESLTGLISPATLYTAG

SGSSSSVGGIGGITGGAGCSTQVDEFASTKGDELPRISSSDIIDWKAYNESCADKVSKGR

AKWL

>contig45976 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59958.1|) 2e-37

MKIKRGQVEAKWIQLEIQIRTMLAKRTSVVAFDALKKESKLSTVGIRQRYMKLLQEERAL

RESNALDCCFLADSQALTFYGGGAAPSRTIREQLNGLPNLR

>contig46487 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53822.1|) 1e-174

MGMLQLSNHEKDMAVMMSVGTVVGGLEDLMFGIMNTTKDAMRIRAAYVGDVASGAILCPV

VEPSEKEPFRSLTVKWMTTDTVPKSTKYHDFVCVEATDILLLENGVRIGYHVLHSIEFPQ

TKPLSYYVRGNMSCVTFYRQMHSTIIDAFGSCIVDPGQKMKRQVFVPAAAHVILTSTNLV

RCGQLKKIAWMLQRQHAGFKFSQDDNRKKGCVMCGKSKSIAGIRRGTCKLCNGDVCYSCK

VRERMHFVGPDNELIQRKITFCSQCMSKAINCNAQEAAQDQATGYHDSYDSNSTFSESTL

SAFSESSSVYH

>contig47141 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65357.1|) 4e-32

MELSRAESALRTLKNRPKVSQASIDTALSIKTLLFPSKSLNESPTQLPLVLSSDVDETRR

EMLETDLLTLLAYGKERWEPVAVFFVVVRDLLSRYLDIADLDTSPDLNL

>contig47439 Frame-1F|Blast-phosphatidylinositol kinase (PIK-J) [Phytophthora infestans T30-4](gb|EEY61830.1|) 2e-70

MVNFSTGLQLTYILQLNKSRGRLADEKLLRDVTCETPRAMWRSKWNTLGKQFPGRRQTKD

STFEAIVSLYAH

>contig47556 Frame-1R

MLTRALNSTSPLLFSLISRYRQNNLFFAESSTSPLSEINQRLNHTLLTKKLSLSRLSQKV

NVAPTLILGSTAGFLVKQCRIVPK

>contig48845 Frame-2R|Blast-Voltage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4](gb|EEY66467.1|) 1e-07

MKNLREIFALKKEELGVVSYLTVVIVLTSSTT

>contig49082 Frame-2R|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY57756.1|) 1e-72

MLQNQLEFDANQVTLTQVVANIGAICGGTLVGYYSQAFGRRLSILIMTVTGAALLYPYCY

VGDETIMIAAFFEQFCIQGAWGVIPIHLMELSPPSYSAFVVGTAYQLGNLASSASSTIES

SLGENFQLPDGENGESRYEYGKVMFI

>contig49590 Frame-0R

MSVFAAIREQDIPFGDKPSHSALERRALPSLNVGPSQVCTSKRFTPKLLHVTPMSLRPTH

VVQTPKMKSVRATPKASRSITLDMLRPHFEKPLTEVAARFGVCMTL

>contig49994 Frame-0F

MATVDVLSKSYILLTPTAALESNCNARMEPASDLLARKWAAAVKRKASMEVMNAYERE

>contig50017 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56421.1|) 8e-33

MKLRKHLRGKRLSALTQLEGDRVIKFTFGQDVLQYHLILELYASGNIILTDGSYKILSLL

RTHRFDENVKMAVRQEYPV

>contig50080 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54011.1|) 1e-92

MLRPVRKLARERNAIKVCVYLLRYKRSVQNADAIRLLATRALLGLSRDRHISQIIEKMQV

GQLLSDMIRSDPVLEENADIHVRFRESALDLISHVTHRASNVVINEATDPTVRKIEKASI

VANTKISYDENELLRLIHDHLVTKGLHHAASALVNEAKILADNSNKVLSVAAGTLSNDES

MLHDQNMLTHHEKRALGKHEVLSSFVSQREGGYLSGDEIPRPRKLQRISS

>contig50163 Frame-2R

MKEVARLLRSSRPLCLKIEKSP

>contig50255 Frame-1R|Blast-hsp70-like protein [Phytophthora infestans T30-4](gb|EEY65065.1|) 1e-160

MTTNTYDSWGSAAERFADGSICLGIDLGTTNSCVGMWHVDRNHVKILKNRFDRGRTMPSV

VHFDPDSQSVDVGNQAIRLETLDPVGNTIRSIKRLLGHKFKSKATDVARIYASYKVVPTA

QQNIAVQVVRSHQKVHVQPEEVSAYILRELKASAEAYFDGHTSLDNVVITVPAYFSDTQR

KATITSASMAGFKTVRLLNEPTAAAMAYGLFLSGQKLVTVVDFGGGTLDVSILRIHDGKF

EVLGIGGDTHLGGEDINNILLDHVLETLCERYHVTRAQVNEKALVRLKQEVEKAKIMLSD

TESVTILAHEIGNIPKCTYTLTRRTFEQVCDPIWTKYVALWQQEGL

>contig50633 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70087.1|) 3e-60

MGTEPKAPFQRVGIITDEAHRSHSSSTRDAIETVVKAGEGSCARLTFIGFTATPNADALK

LFGFEREDDYRYPFHCYPIAEAIADDRIINVLNDYTCVLCEVETSVIPEPFQEILRTTRG

ARRRLLDHASDDVAVSKAKASIMMTHFQAMKR

>contig50718 Frame-2R|Blast-histone-lysine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62225.1|) 1e-107

MRKIANLKPKEGERSSLAAYELSESERKEHCYGAWLYVTAPEVLLGETKYTWRSDIWSAG

CAVLAILLEKVPFLHGQDVKVQLDLIYRLCGTPSTSWEGALKLPLFNTYRPKNEYKMRLR

KTLLEQRSKYPDFPEDAVEVLEAMLQLDPTRRSTVKKLMEMRYFEDVRNSKQAYDFSNLP

STFSMQKKKLVQHLIKSKAKKQRNGGSSRSASHRHSTLKHGSSEHHRNKRLASSALDGSL

SSTNKFGHHDRHKSKS

>contig50839 Frame-2F

MLANAVIGFALDCNDLGAVWVMPL

>contig51252 Frame-1R

MKCFHTRQKLPSNLFDFLGVKHDADKRSLLQIYADNHQPGIKKSATTTDLSMLEHQCTMK

KSSTTPNLASLAGSSPSKDCPHVDQCMICLDDITHQSCPNGSSSIVLQCKHAFHRECVFE

WLL

>contig51348 Frame-2F

MFLIKVNEIVMITKAEREVSIKPSFGIYSCQRKLQKALFKAIVQAKRSFLSHSTSEN

>contig51924 Frame-1R

MSLANPPRLNYKPAGCGETESDMPITDRQQAADTTQPEQEPESKRVQTPENDDALSVISS

NVSLHDSDFDFSPLDFDKNFTLLTPPPHRRIFANFSKDSSGKLSTPSP

>contig51951-1 Frame-2R1

MLLKCQLEVECSVLICEFNGLD

>contig52099 Frame-0F|Blast-splicing factor 3A subunit, putative [Phytophthora infestans T30-4](gb|EEY68972.1|) 4e-52

MDFQNRVGSKPGSGGVASDSQSNVDRRERMRKLALELVDLSKDPYFMKNHLGTYECKLCL

TLHNDEGNYLAHTQGKRHQTNLARRAAKEAADAANSVATANLQAAQAAAAAA

>contig52767 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61841.1|) 1e-26

MLEIVSRRRSHKYARNRRVLLFLRKDATSECSVTTDPATELNSVYPGSSCPQIRWRTEKM

YVRASDMQRPSALSVIASKPVLA

>contig52903 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62379.1|) 5e-55

MMFNWGDDELQLLLETIKHFLLGINVFLLLTAALVFCAPLVDLNSATLLAAPQLKRALIV

TAHPDDESMFFLPLMHSLQQQSKDPNNKWQTHLLCLSRGNFDGLGHVRVKELEACATYIG

LATDRVSILDDPTLQDGIKNYWNIAHIATIVTEYILKHKIDAVFTFDNYGVSGHANHIAT

HDGVKQAVRELNHTCAKAESETTTVRGWALESTNIVRKYVGLLDTALSYWHSRHQENDEK

ERPFVFIFRPRWNYNAMAMHQSQFVWYRRLFVIFSRYTFINTFRPILSVDTATRRTA

>contig53100 Frame-0R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY57250.1|) 6e-46

MMQSYFFVITHMVHSMSEPFAHPSLLYVGQLYYYVYWYILVGTDTPIDALYWAMLLLNNI

HIAFLNTGIYTDFKRVSSVWLETPLHVDVCTSMSVCLRTTLSAVDGSRCLW

>contig53197 Frame-0F

MTRVADQEKQYSEAMLLLTTTMTRVAEIEIRLPMEQSKSSRGTGGSTTAS

>contig54185 Frame-2F

MGKNKRKQQLKRHVLPTAPASSCDTNAKRMKTNQKHKTQKSTTTTEIQVDLDTLSFDDAF

SAGLAFEQLES

>contig54259 Frame-2F

MTLLCMVEFCAALLLMRRIHMYWILIWMMWKQIACHNISSNVHIHIDYHKVQPQVS

>contig54398 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65357.1|) 6e-47

MGDQGRDYVAKYATEIVDYYVEMASHCVRESACQCIAELGTKVSAQAVRPHVPRLMQALL

ICFYDVSNLVRDAACLASAQLVLGFPDECRVFLPELYQLWIDHLSDE

>contig54400 Frame-1F

MSSIKLLFSPGSKMVGASETL

>contig54509 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56936.1|) 2e-57

MDPMITTGLASSTHEAVTSAAIADLLSLNHTSVVQCPHTDDLARALAVVSQCYSVPVPSS

AASTISKALTDVSDLLQHHRQNSNTNLSPKYTQAQCVIIENGLRLLWAHVTMYQLHAALI

DLVRTIDFMPRALGFWRQLRKHTIREILQRGPLQWLLSRA

>contig54664 Frame-0F

MTSNLVDNASYFDDDTHVIPPHAQELLSSLSSISLQSLADSAVLELTGHHTSEPQPQVDN

EAFAAMCA

>contig54826 Frame-0F

MRMTEPLEKARLPVLFSMFPKVQIVASAQHLAHQPHLHELAKENKQKASLGPGHMPRTYS

ETQILLEGKDAQHASRKLKRLNSQAMLCNPSNHRWSEVEFKRLVAESNAQARLAGTFPTS

SAMSMRSKALSVSFASPQFGNAVSRDPFCSDKQELKDAGIFAMIGLSKNAHNESD

>contig55102 Frame-1F|Blast-nardilysin, putative [Phytophthora infestans T30-4](gb|EEY61296.1|) 5e-09

MSDPVEQSKSPNDQKKYRLLTLPNALQTLLISTADVSHVAEAVAHESESTACDAEEHSHS

EDDSDY

>contig55281 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56178.1|) 3e-30

MAYTNAPGHVAGREGTLSTQFRALAHQYDVLRTMLLGANQSDLDSLQFHVQLCLLLAQAV

EGLMLLQPIDSIDFAV

>contig55375 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62990.1|) 4e-17

MRTCLECEKPQVAVWKCAMCNDALYCDDCNVMVHKARVMRKHERIKLPP

>contig55872-1 Frame-2R1

MVSIKLFATVAAMLAPVLSVRGHGYL

>contig56107 Frame-2R

MTGSGPGCSRCWRTYQQARLALAAQNFFIAT

>contig56190 Frame-2R|Blast-tRNA (guanine-N(7)-)-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61502.1|) 5e-37

MRYLPHYFHKGQITKMFFCFPDPQFKARLHRRRIV

>contig57823 Frame-0F

MEAVRSEPLDTAKLKDKHVFDDDDTELLKVDWMTDGEGLTEQLCSHFGY

>contig58729 Frame-2F|Blast-calcium-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY57833.1|) 1e-65

MPWVLRAKDAATKRRWLVALSDCIDILVWLRHYQVGAVVGVGGNGVVQELEDKRNGTVFA

VKVLDVAKFRHREQAVAEIEIMRSITNNITHPNLVKIHKVYEELQKVYIVQEMCTGGELY

DRIVQRGKLSEQDAANILQQLMSALEAL

>contig04378 Frame-0F

MELYECEDAVEAALQQERPKYIVSIINK

>contig05100 Frame-2F|Blast-electron transfer flavoprotein subunit alpha, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY60455.1|) 1e-134

MKDSKTIVAINKDEDAPIFQVADFGVVGDLFVVIPEFTDKI

>contig06813 Frame-1F|Blast-NPP1-like protein [Phytophthora infestans T30-4](gb|EEY54948.1|) 2e-29

MYVLNHAVHVTEDTGSKQDLVLWENMPDIVRLTLNNTKFGAANVPMNDHNFINKIEEAWP

WKWPPEGSK

>contig07616 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61501.1|) 2e-65

MVSKTSSITVDNLPIGRCDECTDDGLYLDRVLLTHFSLRVCINCKQDRIMRDGAFELLSK

SRARAEYALPDSAFIGLPSLSKPNPRHEAFAPLQLYLRKQLVQEAYRLYEDEDGLQREKQ

KRKKRAFHSAATRTNRLLKKQHVLNQNQGATQEPQATDKPKKAQIVLAVDTDHRHVFGAE

TFNKESNNWTKTCICGLLVNFEK

>contig08460 Frame-2R

MVGNKKNMEQIAHDLVDFIGDESADQFVAWLSQLLPKFEAQAAESINERSAEEVSKPQVE

EATMQEEQASETKEDNQRVISLKVLSSSSSEVSTKKTVSLGGNRGTIRSLYPSKTDADDV

IARRARRFGVVEHSPTSKKSSFVSLKKEDRHQRDEARSTGNKRRGHERDSGKESGGRLSQ

RLGPPVNIDQAELDARDTLGGHKKQRGDHDEEYQHGGGRQNRRKDRFDNVEDVDKKGRQR

NDGFRNDAPPLPLSSDKDSSRGKQGHGQNHSLGPSMGFQNGPMGFGVYPPPYGGPMFYPP

PGYGPMNTFAMGFPPQGMPPYDGRSYPHPMQAGPHGNRPFQNRTWVNPNVVKAEAAKDNE

NQPVLDATEDGAGGSNSVLAPRNPFYSSQMRPRFQNKTWVRQDTAKDEELSSSLPKTPPR

ELLESTD

>contig09287 Frame-2R

MQALFRAGGGWRGPLRRPRPVLLHVSSRTWASMGQPQTWINPPNVPQGESLRKYGRDLTE

IAKAGNLDPVIGREDSIRRATQILSRRTKNNPILIGEPGVGKTAVAEGLAQRIALGEVPE

SLKDKKVVALDLAALVAGAKFRGEFEERLKAVLKDVDESAGNVILFIDELHTLVGAGGTE

GSTDAANMLKPALARGSLHCMGATTLDEYRKYIEKDAALDPT

>contig09423 Frame-2R

MACVLLKRVVPAASRSFSSYTKLWDLFSTTKVPAAKPVAPQYMMNMRDNLEFALERMRLA

RGPFVLQLLDQTARLV

>contig09939 Frame-0F|Blast-cell division control protein 48 [Phytophthora infestans T30-4](gb|EEY53004.1|) 0.0

MSDKKDDFKAGIMDRKRSPNRLIVDEATNDDNSVIALSMAKMEELQLFRGDTVLIKGKKG

HDTVCVVLQDETVDDINVRMNKVVRKNLRVRLGDVVGIHTCGDVPYGKRIHVLPIDDTIE

GVTGNLFDVYLKPYFVEAYRPVKKGDLFLVRQAMHPVEFKVVETEPAPYCIVAPDTIIHC

EGEPVRREDEEKMNEVGYDDIGGCRRQMAQIREMIELPLRHPQLFKTLGVKPPRGVLLYG

PPGSGKTLIARAVANETGAFFFLINGPEIMSKMAGESESNLRKAFEEAEKNAPAIIFIDE

IDSIAPKREKTNGEVERRIVSQLLTLMDGLKQRASVVVIGATNRPNSMDPALRRFGRFDR

EIDIGVPDENGRLEIFRIHTRNMKLDDDVDPELIARDTQGFVGADMAALCTEAALQCIRE

KMDVIDIEDESIDAEILDAMSVTQAHFKYALGVSNPSSLRETTVEVPTVTWKDIGGLESV

KRELLELVQYPVEHPEKFEKYGLSPSKGVLFYGPPGCGKTLLAKAVANECQANFISIKGP

ELLTMWFGESEANVREVFDKARGAAPCVLFFDELDSIAQQRGSSSGDAGGAGDRVMNQLL

TEMDGMGAKKNVFIIGATNRPDIIDPALMRPGRLDQLIFIPMPDFDSRLSILRSVLRKSP

VSKEVDLNFLAQQTDKFSGADLTEICQRAAKLAIRESIARDMERDRLRAEAGDEMEDMEE

EDPVPEITPRHFEEAVRNARRSVSDRDLAQYSTFAQTLQQARSHVTAGGTSLANFSFPGR

NVSAGVAGGVASAAAEEDEEDLYS

>contig11787 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64191.1|) 1e-108

MLNPLVYIATQTPALDGEIAFEINQDGAIACKRANLFSQCVDLCEKYLYFEGMVFLVFVE

DLTNLSNLDCVLGKLPESSASKRLQLFCKKYEGFDNFLFLWYNGEIQNPWARDDLEKSSS

LMMAFLLAHSQTFAPSLHKFMKSRERLNKYRWLTAVSIERYDQVATEALREAKKERRSLL

KRKTMASIAKIAAVASPSVSCPKRDQEIQQVACPR

>contig13284 Frame-0F|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ29892.1|) 6e-49

MSLVTKPKTVEAEETRIHRIRITLTSRNVKNLEKVCTDLKRGAVDKNLKVSGPVRLPTKI

LRLTTRKSPCGEGTNTWDRFEMRIHKRIIDLHAPSDIVKQITSISIEPGVEVEVTIADSA

>contig14168 Frame-0R

MHKIATDGVLMCLHNFVHRDTPLPTNVKRNENLALQASHAHRERAETAPSYQLDDVQNES

DSAIPVPSTISSFSRFFERGGGHSSSSSSSASLDNELDG

>contig15196 Frame-0F

MATLGVQTSASPSERKPLYPNQDAVACNVDNTNNESCPGMKNEGFTVKEQSGATQPEATQ

PEAIETNTASSSPYLPAAITAQNDSETRHNPAVVADSMNAVSDTEASEPEAESITSFVSK

TTSKAPCTDVHDESATSIGVHQDANGGTPVKQVICRFETPTKTDLNELERLKFRTKRDFF

SETQQSISVSAEREKYDASIAPQGFKDTDQHLSPLVTKSVKPSTSVLSRVRNMASRFETK

TEESLDDLSFRTVRSFFPKEKSIHVGTAKEKYEARKPKEIVQNDDVRVFQSTDVENETTW

KDGVDRNTLAKEWENGNRPRRFTGSEDSSKVRGIASRFESKRAYSVVTAPVRTIDSFIVS

DTDASVRVSTEKAKYENKTTTSMPVKRAIDSFLVADKDASVRVSTERAMFENQQKFATHV

TRTIDSFIVPPSEFSVNVSAEKAKFETSANVVKVPKRTIDTFIVPENEASVCVLAEKARF

ENPCNMSIASTTRTIDTFIVAKSDASVCVSEEKEKLESLEKQVRGPVVRTIDTFIVPASE

GSIRVGVEKTKLEALEKQKQKEMEAQAVLAMYKMTRAKEEKSKVEAKKKARMAEEDTERQ

EVAAMAAEEKARLDREDTMKEIEMEEKARLEMEEKARMEEEERAEDEEKAKVKGVEKARL

EEEEKARLEEARGDKMHELNHELPRSSPVRLPSFVEVTVEHQMLADVGSSAQHTHWLSIP

VSVNPALARLHTVLNDQDVLTAYALYPSSPSSPSSPASD

>contig16009 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68431.1|) 1e-160

MATKRVFSGARKRKFGMEHVESNLSKKQRVRMATITAMDVMNKLLAPGGDVAYDVTDAEW

EKLVQLTQAHERFETLYRFPDLLPGWVTTTSKKKKTHYKIVAIDCEMCVTQKAGVSERKS

NALCRVSAIDGENILKNIISDFLVHQPEPGFHMVDPKTDIHGITPIQIADCRITMAQAQK

KMLKYINKDTIVVGHSVSGDLSCMRISHRRVIDTALIFQRKVGNLSSSTPGLKDLTKFLL

GFDMPQGHDSTVDAQASMLAAKYGVRHELGRIIPSSLELHGPRDIEIRRVYPIPRMEYAG

PPILVTTAYQPRQVIDQPQKLMNGGNVNIANNKKGTMCKFKAMTARSCRLRVHRIPKGLT

SKDVEKWFLENACIVPTAVEKISWLPDQNRGSCIVTFSTSAHAALAFESALGPDGKTKIT

EDSIGRPQKTIAIISYMGKTFKNVVLGVS

>contig17132 Frame-1R|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY66304.1|) 2e-52

MPVGYEQEVASSRLIGEADVLAAITSEYLDENASRKDTSAATVCLGRVFMTTFRFQFVPD

EHEYDRVRRHLLDRIDDEIESFFCIPLGCIASLKKKNSIIELFTKDLRQLSFRFDIVEIT

>contig17147 Frame-2R

MSALRTLLEDTNITKIMYDVERVAKSLHSFGLAGVDLSSCMDLQILYQLLVDSKVSKENL

KNIVLAFGGKSTISIQQQVAEFNANLKPNAWKKSPLAPPMQKMLVQSMRLYTRCYSGACG

LSGVNSKFPSVYAATKEKWKNSLFARSSTSIIAGVPVANEATKSHLGKTTSLILKPTRST

PHVAAIEQTVSPSPFIKIEYVSSNVDLQRLLQKNNKLMVGAPSVVGIHFQFTQDNTNSSE

KIDHDQLALISIVSKTNAHDTAVVLQLDSLDLRRVLSALQMLLNDP

>contig17693 Frame-0F|Blast-heat shock cognate 70 kDa protein [Phytophthora infestans T30-4](gb|EEY58912.1|) 0.0

MAPKRRSRKTTKDVYANVSPEERTKLGAEAKERGNAAFAANDHATAIKEFTTAIAYEPTN

VIYFSNRSAAYLSVGQATPAMQDAKSCIELDSKFAKGYARLGAAHFYIKNYAKAITAYTQ

GLTVEKGNKALQAGLTQAQAAQQVQDEEISGVEMDEATRKMKRMEIEEKINKARKEREER

AKRAEKGFSEVIGIDLGTTYSCVGVWKDGQVEIIANSEGNRTTPSWVAFNDSERLIGEAA

KIQAASNATNTVFDAKRIIGRSFSDDVVKKDAAHFPFTIKEGDDDKVLIEVEFKGQKKSF

TPEEISSMVLLRMKETAEAFLGQSISQAVVTVPAYFNDQQRQSTKDAGAIAGLDVKRIIN

EPTAAALAYGLDTNAGTDGKACNVLIFDLGGGTFDVSILSIENGIFEVKSTGGDTHLGGE

DFDNNMVEYLLSEFKRKNRELDPSTSARSMRRLRTACESAKRMLSTTTSASVEVDSLFDG

VDFSSTVTRAKFESLNEELFKRCEETVLKVLDDAKMKPDQVTELVLVGGSTRIPKVQTDA

LVSLWWQGIVQVYQS

>contig18458 Frame-2F

MKRTILFESEVQVQGDDEDTEDEVLYQLPSNSASESDSSDTSSSRQLEEEIKLRKLFQKN

EVLSSSCISSDEVVMKEPRPT

>contig19956 Frame-2F

MCNVLRLQPAGAFLRQNSNVQPLRLQSNPVLIVGNCTDIDEALRLPDNQYAAESLDFACL

CEGAPYRQKDESEDFLTSIRRGIDEFGTAATDDDESDDDSDEEGSYYQASKQNTYYSPAQ

NVSCSFSNDNLLDVSDTSTSSSSLIPWDSQSTDNEQDEVDNLIFQL

>contig20398 Frame-1F

MNRASDDTMEKNVALLRSSSEGEDASTCRDIPDTLRDASARKKCNSISAIDEHESVQGAE

KKLSAVASTESVKSENLTLSEKRSKSNNERTQASTEQQRASLKKQSKKKATAVTQNSLPV

STKIVEYSYLFRLYQILFAESEQDDRDSHREKFKKDRTDKKKLARGKKDKRKSPVDSTAL

NAVNGSTTEAKDKLLKLLALKRKPFLTKVKQGVRKGSTLASASGLLAYHNTRQWIADRLI

LTGFRATTLRSIWSITTVALKMGLLLSLHAASGLIRIHRVAFHATMTHRHIGICFAIVYG

YPLLIQYVFSWAPPWVPVCLWYAFLVQLFCTNGPTAMVTASRVLLPLVFLIKGLAHHSFL

LDLNGSELLLISFIVLALKTRKFCNLIFFLSLATQCLLAVCLGLELLVQWLQLTLALYSL

HAMA

>contig21641 Frame-0R

MLTDSQQEEACRDVETLRFVFSCLLDSEHYEILKTTEMFLLRNFMKFSIPLQVKIVELLG

THVKRLFLHWNRDVRYCYYHILLYLTYPGNRMVLCAKSDEALMGADASWLFEIPGLIRTG

TTESWEAFDVPLHEIVTLYMQRIKRRPQTPSWVSAVPSSVVQRSVTEYKTHMKTYFAFAQ

QLSMHQRVPTPEFSIKAVVENSVLPSTTLA

>contig21968 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61318.1|) 5e-89

MRRVWTKATEGKMTPMIELLRHQDFVDMNREMHEYDEMREKIIKRSREILKASKQAIFAL

HRSDKTEASKLLATAEKVIPELVSLIETNPSLREGALSSSLEEYAEAKCFSYYLDNKCLP

PRDEMPIVMKNEYLGGVIDFTGELMRYAVVKATAREVEEVQRCKDMVEAISGELIQFDFR

NGPLRRKFDAVKYNLRKLENTLYELSLVTNSGLSLQAYSVQETPSAKTRDSDDDL

>contig22165 Frame-0R|Blast-serine protease family S54, putative [Phytophthora infestans T30-4](gb|EEY57799.1|) 1e-32

MSFLWKGYNLEHSLNSVRFLGTVACLLILSHSLIVVVAFVLATSFQNPNILYQCSVGFSA

VIFALKVLLNHNSPTFSSVYGFQVPTKYAAWLELVLIHYMVPRSSLMGHTCGILA

>contig23610 Frame-2R|Blast-2,4-dienoyl-CoA reductase [Phytophthora infestans T30-4](gb|EEY58091.1|) 0.0

MSKYSHLLEPLDLGFTQLKNRVLMGSMHTGLEEGRSLTRLAAFFAERAKNNVGLIVTGGI

APNRAGRVSPLAAKLTTQSEVLAHKEVTQAVHAYDGKIAMQILHSGRYGYHPFIVAPSPI

KAPIGWFTPRELTTTAVEETIQDYANCAARARESGYDGVEIMGSEGYLINQFIVEHTNKR

TDSYGGAYANRIRFPLAIIKAVRAAVGQDFIVIFRLSMLDLIDKGSSWDEIEILAKAVEA

AGATMINTGIGWHEARIPTIATSVPRGGFSWVTHKMKGVVSIPLITTNRINMPEVANQIL

AQGHADMVSMARPFLADPEFVRKTEEDRVDEINTCIGCNQACLDHTFKGMTASCLVNPRS

GYETLLQYSVTNDPQRVAVVGAGPAGLSFATIAARRGHHVTLFDQHDSIGGQFNMAKIIP

GKEEFHETLRYFEKQLKLTGVNVVLNRRVEAREVIAGAFDKVVLASGVLPRTLELEG

>contig24079 Frame-1R|Blast-C2 domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY58868.1|) 1e-82

MDLTRPIFDTLEPEWNEKFYFQNVPRDSKFSLIVMDTDLYNDDKLGVAQFPVRHVMNDID

VAYDLPLTLKDRKAGVLSIKVTCHHVNTDENALIEEVGPVRYSMHTSFSKDLLRAFSSRN

AKLNSFAYTVRLHNIPRFLPSNIEWTKSYKKAQHVFSSKHPESPVFRRAVKTQHAMTYEH

NRKSSKFGALSSPLDFFNLINDGKRDNKPVLFTYVITSKGWYFSETGATFLKDIMSKHML

HSNAAYYVKYAGEFHVQKTSNNTLKLVLDNNSGTYTPPKFLLLEL

>contig25072 Frame-2F

MPSIVRPSPKAIAVAPPPLNTKRIFIEPEQEHDVDLPGTPPIDPLSRRAWGDAHPKLTEA

RRLVELEKLQPLERHKVRHVAAMVLQRLVRCFLSRRRLAKRLSAVGRPVELQITRMRGLQ

MLCDFRNIVSLYCNVRVLKKPFGPFMFHFSSSKTPNRNTPLWTDKFLVPMLSSKCDIIIT

LIGVTSTGKLRFLGQAVVALDYGWESKRTFSVPLGKWKFPVDESIIGLHRFVQGTVELEI

TPLSSQMPCKSGQFLMAPILPTRTRRAYSYWSRSGSSNKLLSSPAPRTPQKPASASPSRK

TMVIRWGMLTDTAFHLFDNTTAKLLTSLDLSTLQFIKSNAKLNSQFFSLKLYAKGKVYVL

YLSSYAQQQSWEYRINLHRRELIKLL

>contig25348 Frame-2R|Blast-pyruvate kinase [Phytophthora infestans T30-4](gb|EEY64214.1|) 3e-60

MMTVLECLSEWIVVRVHNDHILEEKKNMNLPGAAIQIPGITEKDKNDLLHFAIPNGADIV

SGSFVRSASNVRAIRECLGQAGRHIRV

>contig25465 Frame-2F|Blast-peroxisome biogenesis factor, putative [Phytophthora infestans T30-4](gb|EEY70091.1|) 3e-36

MIQLHAGAIEVELLRQMCVVNDKQVSPIWIN

>contig25906 Frame-1R|Blast-phospholipase D, Pi-PLD-like-3 [Phytophthora infestans T30-4](gb|EEY58278.1|) 0.0

MPALLLTKIVECFNNVFEFIIDPFHYKKKKYKVVTAPFSQPYLEPSRWFLSEEEMLRSRN

GSARNNMQLYTTGNVVELYVATAGYFADLADDIMTVSNGDIIYITGWGTSNIPFKPLESG

TKLCDLAEKAVKQGADWRMLVWSNIPERKQNHEVRDLINALPLPKNYGPARFVYDDRLPF

PTSSHHQKSVIIRRGRDLVAYVGGVDLTTDRWDTLEHDQAHLRDRTGIKARWDGWLDAHA

RIKGPATKDVAQNFLDRWNATHKPSQDLIDDLLDFENPKFSNLPSIDERPLNAFEKGTHA

VQLCRTFSPDYKRYEFAPLGEQSIFHARLKAISNARNYIFIQDQYFILVPELLKAILKIM

PNIQRLIVIMQRTVEAEYTGYAKYLYDMVSPIQKRYPHKFK

>contig26352 Frame-1F

MVRMRALFTSSKPYFTAQFHPEHAGGPTDTEFLFDTFLNAVRSKEKGAIKSMDHRPHIER

IKVKKVLVLGSGGLSIGQAGEFDYSGSQAIKALKEENIETILINPNIASVQTNIDRSSEA

QASNVYYLPVNADFVEQVIKRERPDGILISMGGQTALNCGVELDKRGVLEKYNVQVLGTQ

INVINYTEDRELFNVKLMEINEKIAQSEAVESVEDAVQAAYRIGFPVMIRSAFALGGLGS

GICDDEAHMRTMAEQAFSGSPQILVERSMKGWKEVEYEVVRDAADNCLTVCNMENFDPLG

IHTGESIVIAPSQTLSNREYHMLRETAVKVVRHLGIVGECNIQYALNPESEEYCIIEVNA

RLSRSSALASKATGYPLAFVAAKLALGINLPDLQNLVTKSTTACFEPSLDYCVAKMPRWD

LAKFDNVSTEIGSSMKSVGEVMSIARTFEEAIQKALRMVEPSNEGFEPRYELSHDELIEA

LGKPTDRRIYQIAQALKTGQLSIEQVHEITKIDTWFLSRLQAICDCDVNLTGKKLNDVTA

SDIAEAKKLGFSDRQLARMFSCTDDKVRAKRKELGIVPVVKQIDTLAAEYPAQTNYLYMT

YNGTEHDVPAQDPNDGVMVLGSGAYRIGSSVEFDWCAVSCIRTLRKLGYRAVMLNYNPET

VSTDYDECDQLYFEELSKERVMDVNDREGVQGVVVSVGGQIPNNLALPLHKAGVKILGTH

PTMIDSAEDRYKFSKLMDKAGVPQPAWKELTSKAAAREFAERVGYPVLVRPSYVLSGAAM

NVAYTFEELDSVLNQAIAISADHPVVITKFVEGAKELELDAVAKNGKVIAAAISEHVENA

GVHSGDATLVLPPVQASSFYKNQIKRNAEKIAKALNISGPFNAQFLAKGADVSVIECNLR

ASRSFPFVSKTTGADFINAATKVMVGVSTENDNLPPLDGPKRPEGYVGIKSPMFSYTRLG

GADPLLGVEMASTGEVACFGKNLHEAFLKALISSNFKLPEKNILLSMQDKFSEEFVHAAY

KMHELGYNLYTTEKTHAYLMKYGIPSTKVDFPSDGESKNNALNLIKEGKIDLVVNLPNNQ

SLQMKNNYQIRRTAVDFSIPLLTNISLVQLFVEAMAIHKSKPMLGLEPDSLFDYYKREKE

EDAWTDVHEFH

>contig26745 Frame-1F|Blast-cytochrome b-c1 complex subunit Rieske, putative [Phytophthora infestans T30-4](gb|EEY70427.1|) 1e-112

MLKRLNSSVPPRCVQALQGRAAMSSKAVVDTYESPDHYFESDRIDAGDPSKRAFTYFMLG

GARVAYATAARLAVVKFVGSMSASADVLALATAEFDLSNISEGSTVTVKWRGKPIFIKHR

TPKEIDISNQVDVKNLRDPETDAVRVQKPEWLVVLGVCTHLGCVPTSDSGEYGGWFCPCH

GSHYDLSGRIRKGPAPLNLEIPPYQFLEENKILLG

>contig26851 Frame-1R

MILLPIQMPLFNFIRLLLRATFSHALHFACGLDRHFLSLFRDIVPKAHKAVALGEDCMIL

AQTHACTHVVLGTTLANNDVAGHDALASKLFHAQALGLRVAAIFCRPSSFL

>contig27328 Frame-0F

MAILILIALFASSTVSKSTLPSFSSSLDTSYVVQLHGNRDDFSLPGDGSKMRTQLMATES

GQHFECFLPPLHSNTESKEAISLSVPQSPNANEAEKEKSDAFLSFGRAAAEKMKPKCIVY

VGKETNAFYEVCVGLSVQFTDMISFFSPKESLSTVDVEVDAASATSTNKGKDEVLFNKDF

SGFIADSIQPLLRYDYFVLPEVQARVKSHEKPLYTQTFGSDVQIQVQFICNISSQDDGVI

AVQWTGTPREGEARKVAAFLVGSGMFCDPKYSDADPSDVTSVRSLLQPLEIERTCLTRIE

GWWTYEFCFGRSLRQFHRDGDGRIEIEFSLGTFDVAGNLDLERLGSALVSEPIDATHEVS

RPAYLELYDGGTNCKGFESRAPRKAKVFYYCSQGGLSHHILSVKETQTCSYTVKISTPVL

CGHPHFLNDIQKSDQGVEILHCFPVAEDAIVIAE

>contig27456 Frame-2R|Blast-FACT complex subunit SPT16, putative [Phytophthora infestans T30-4](gb|EEY54832.1|) 0.0

MVDMRAETVILPINGVPVPFHISTIKNVSKSEEDKATYLRVNFFVPGTSLGRDVLPAMAN

AILKYPNKMFIKELGFRSSDAHNLNNQFRLIKELQKRVKQREQREQEESDLVVQEDLIIT

RDRRVPRLIDLSARPHLTGRKTHGTLEAHSNGVRFTTNKNQKLDILYANVKHAIFQPCDK

ELVVLIHFHLKNHIMIGKKKQKDVQFYTEVIEGSQTLDNRRRSMYDPDELDEENRERALR

EKLNTTFKEFCHKMETVSERHGKPVVFDIPYRELGFMGTPFKEMVLLQPSVHCLVSLTDM

PFFIISLDEVEHVHFERVMFSSKNFDVVFVFKNFDVMPIRISAVSMSELERIKEWLDDID

ICFTTGTANLNWKSIMSTIKSDNRFYLDTDEDGVPKPAGWEFLKMEGSDDEDEDEEEAGD

STYSGASEEDEEDSDSSDSDGSDWESIVDEDSLSEEVSDEEDAPSWDELEKEAQASDRMR

NEKREHEEEDEDYRRSSKTKKSRHR

>contig28336 Frame-1F|Blast-retinol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY66900.1|) 1e-134

MFNWIWPQKSVKGNVIVITGGAMGIGRLLALRFALLGAVVIIWDLQSELGLTLVQEIEAA

HGKARFYKVDVTNREQVYSTGQEVLKEFEAVDILINNAGIVGGRPLLESSDAMIERTIAV

NVTAHFWTIKIFLPAMSKRNKGHIVSVASAAGIFGSPGMVDYGASKFAAIGLMTSLRQEL

HEAGLFGVHTTIICPGFVSTGMFEGVTPPPYTRWLTPELVADRIVQAVRNNQWRILMPSI

LIIMEFVAGIMPMWFVDWFIGITRTSQAMKQFKQTRTHVLKEE

>contig28866 Frame-1R

MRYISSSGESFASPLEVVGHIALDNELLRTCFPSNVHSAILSLLPHDETNNSTDVNSHFA

SSKRELRKHATSDSPRIKYFDSKRPRRAWEYMGANLSLSGRAGLSTDRPLYRDDVLDYRA

QASSRLAAYRGQVMDGRIRLLGGRFLDDEVTSQVRYEAPPDFREYRHAVNSDVPRENRWA

GANVVPGIDSTEHAHRLVSSPDWCERGTMLESKCLSEAPSDARMRAEGRYMYRVNAPNSI

ESSEGEGVARMQTGCYQDSSGPCCGSPGLIYPQYDTMRARASDGTRLSYNSRTTASFMSP

MDTFGAAISMVDVDRNFTLRPGNVTADQPRGRSPRQSGAQPMYQQQQIHRRSSSSHSYHN

QQETLRHYSSEPIREVRKDSNLTGSVLRSSH

>contig29542 Frame-0R

MAETNDGNAQVSTAAAYKKFLRRLRINV

>contig29605 Frame-0F

MLQMKKQQQQQKKVQSGCNDISVVVVAQPRSKSSLTQAAPSL

>contig30478 Frame-2R

MCFLVARHMATRLSYRSTCKWNRTSFLGAAANLSRCVQSATFSTEGKGPVIYSRTQKSVA

DSERAEVQLSRLAVIGGGNIAEAIVTGVLKTELIPSSKIVVSDPNPTMRDKFAKLSVETH

ARNSTAVTDADVILLAVKPQMIDDVLQAVKVAMDRKALVISVMAGPTIKLLQKHLGQDSR

IVRAMPNTPAMIGEGATVWAMSSEVTSAQHELTKQILGSFGIEVFIDDEKALDMATALSG

SGPAYFFLVAEAMIDTGVHMGFSRPVAT

>contig30517 Frame-0F

MIRENRFPVCLCALNLLEMLLCHLKLKRPLPLVCPCCGTENAELETSQQLSRPHLELLGF

TALMENAFSLASSLFSNRFAYAEGGSAELALAHVFSHSMLVMDAVWKQQLQQDPSTNLMR

FREALVETRKRIVAFLSRQCLPLTLTELDTWGSRQRARCHIFPTTPLR

>contig30562 Frame-2F

MNRMLNVTVSAVSPKYNTTRDRVLGIFTEGHVQLSFYDTPGLIKPKESHEYVQTLVTTAA

ETLQSVDLSLLVVDSVKRLDEPALQALEKVLITSAQVCSPTMLVMNKFDLVGKREQINLE

YKVKEVSQMVKEIYAKHFDSNGSSLRIDPLAYIGENCVKVSATKGYGMDRLKKTLLSLAV

DRQWSYHSSISSDLSDLDLVTEIIREKLFRRFNKELPYAFVQENVGWTKFKDKSIRIDQD

IFVPAARIRKMVVGQNGNTIRSVGMAARDEIELLLKCRVHLYLNIRVR

>contig30724 Frame-2R|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY53155.1|) 2e-99

MRFLSGLATRRIIATSSAVARRGKSTLSYRVFEDTRSGKEPIKTAFVIHGILGNKLNWRT

FSQNLTKNNPEWRSICFDLRGHGDSPSFADPHNLEACANDIFKLADHLKMKPSAILGHSF

GGKVALTYLQQCIEHGHALPSQVWILDSLPGTGATDYASRDVTNSIETILPVLKKIPLPI

CSKAELVIELQRHGVALGEAQWLTTNLRLISKSPESYEWKMDLTVIEQLFHSFLTRDLWP

VVESSAGMKRRDVEIHFVRASANRMWTAEVLARLDAQRKNQVFHHLLERSGHWLHIDNPA

GLMKLIQTYLV

>contig31910 Frame-2R

MLLSRAISVVALLACILCGAHAQDSEADLGTLLTTLDSSMVTSQRLLRTSVDLDNNEERV

KWPFQNLVTDYLNQKAIRKSLVNQAKKTVNAHDENVLEEAVKKEINAGRVKNVKQALSKL

KNGDPAKAKLQRLYNAEILRNLPKTHNSGQVRISRDKVSR

>contig32555 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69925.1|) 8e-28

MLQRVAKKSFKVLVLDVTLPVEGRDTFIKERLNLTTRLQNVQLLTVTTFENERMNEINDL

DLDPMEQSERIAKTIEAELLFGIKSGGFVAFPGAVYQQICVNSTTVTARERVLVHGLARV

>contig32928 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68279.1|) 9e-39

MNLTAKNPLKSSKPDSSDPAAGIMDMMKNMYDEGDDDMKRTIAKAWSESREKQGAASPF

>contig33413 Frame-0F

MLPYVMKAKEDKLGIVVFDDIFKDLVRSGEIDMISALQRFMTGWRNHVLTSRATHVFIVA

YRDGGKLLIEALRTHMLEMQRHISGVVFLQSTHHISSDDSYTLRKMIAQWCLAYMSSPEG

VQVLKRMKARETPLGCVVLSAGRASSDVDLLQAVVSSVYASFKARWSGFRVKNVNSGMEK

GCYLCKGAFNMRRWRRHCRTCQNPCCEKCSTVETTRHEGQVRLCLTCRALPSLIHWSRPR

AVRTGEKESVFSGSAKPGKMSVNDFELVTVIGRGACGKVLLVLKKDGADAGHLYAMKVLK

KEWVMNKDLVTQTMAERRILQEANHPYIVQLKYAFQNQDKLYMVMEYYSGGSLRQVLRRR

GRFSIKRARFYLAEILLAIAHLHASNILYRDLKLENIVITADGNVACTDFGLSKEEMDDN

ERTSSFVGTCEYLAPELIMKEGYGKAVDWWALGILAYEMVQGDSPFRHNVPTILFDKILK

EEPEFSDRFTPEAQDLIMKLLTKNPEHRLGCGPDGVEEIKQHPFFNEIDWDMLLLKEMEV

PRPPHRMEDVTDESHLSRAIAKMREAREEIMPDSPVSLPSSPSEQKHFDRFSYQGLGDWN

PDMADMEFDEETGDFKQGTIHEDEEYVEEDYAELSGDGDGIPLSPGSKDNFSTSKSSPSK

ANGSCTPPASSSAASPRSPQSVGSPDGLPHTPLSPGSAGASAPCTPTEPQSQTI

>contig33484 Frame-2R

MAVPTANVNAASVTKISNFMWKSPALISEGSLIILFETHNSLTYCYAKRDAIYQNRHGAF

YHNDMIGQPFGSKIISRKKNARGYLILLAPTPELWSRALRHRTQIVFTLDASAIQFAAAL

RSGSRVVESGTGSGALTSSFARTVAPHGHVFTYEFNAHRADIARDEFHRNGLESIVTVEC

RDACEQGFSVELEGSIDLVFLDLPCPWKAVDHAAKLLKQGGFFASYSPCIEQVQKTCDAL

RIANFELIRTIETRLVPYNSRRIDLPVPDFGFGQKVNPKKDGESIILDEQTERDTPGIDE

EKKHLKVDERKRKYVPGGVGEHIVAKKDDEIRGHTAYLTFATKFF

>contig33888 Frame-0F

MSPAKNPAAGSLVLSMISCLVYSIMSNVMVLTNRYLLGKKYYGFDEKFFVVAVQAGVAVM

VLELAKMRKFISYDSYDNKVAGKWAPVTFFFVAMLYTSMQATAGLPIHIVTVSKNVTNII

IVFGEWRFFGERVGCLVLMSLGVMLMGAVMSSYSDVGGNATPSTITGYFWMVLNCASTAG

YVLYMRYATSRSSLKISKFGMAFYNNLISLPLLTPALVLNGEAFTVWSNPLLSNINFTIL

LFISGVLGVGLNLASFWCVSVTSATTYATVGGLNKIPTTFIGVLLLGESLKPDTAIYVTF

GMVGGILYGYAKFKESEATKKLKIAQESLPQSAHVRKA

>contig34539 Frame-0F

MSDDRTRAEVAAKLRAAQQQKSGNGRKLLRWDTDCWKRFEREPLYTTRIKSAPILPIRAP

LSSIYEIYFSARKSYTPSGIMEKLIAEARSGSVINVGLVIDVTGSDIFLHDVKEWDDWDV

LYVKLQVDEDTNRSDSNEHDERMVEAFCKAVECHLKNERKDMDVAVFGIKGYNFIGFLIV

SFLVEHVGLNLDAAIEEFAHSTAPGIYSQDYLERLYRKYFGTLPSESIRLAVPSPPRWEL

EETRKRKSATSIGSEVLTELDRANKFVRKNETEFQSTGSSVDNGRARPSDGSHGAPVYKP

PLYTPPVRKEPRQPKRRKIRSWTDEVEPLAYGETLATSSEEHKKLIASLKKLTGAEGFPG

CETIPFTATHVAEGAYKRKGCLTKSYLVTWRARGRRCLLYVTADGTYVVSRNMTFTKIEM

KFPRRRAPEESQVDTLIDGLIVEDQDHDTKVARYLAFDIIFLEGIPIWQKKLDKRLQCLQ

NEIIIPRKNDKSFDYTKEPFRVRMKDHFRLAKTEYMLTKFANSVTHQVDGAIYTPTEASY

NLGGYECDEPVFKFVASEGGGIPGLDGSISERQLLDYINSLPN

>contig34654 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53010.1|) 4e-14

MICVLFFKNHGHQQWQTEQTPSARISPSRCCDNENVQKIKLSITEALVEHSREHLHQQKE

LLTRFDSSINASVVGINARIEKSDALQEQQAVVLTELRRGLSDMAESVAELRK

>contig34823 Frame-0R

MATSKRRSVVLHFDLNRTILMSDAAGGRTMENTVDYLLSECTWGYVNPHRPSEWICVPDV

TNHSRPTLLTYKQFVDEVYPYQSLATAEVQDIDQIKALNQITKKNRLMLQSAFTGGKDAP

GQSVRDSFKEVMQKLHFPLQEQREAANELAATMPTSSLQEAWSKGRYYLLPSFLQFLAFL

ASPDVTEQELDVKLIFRTFGDDIEWVAKELELLVNGQHPVGLPPLPDRFRLQLEPSACRV

ATFYRDGFEANGTALALGTLLKVPFPSNEGADRFYAALSPQIQVIRGFQSIHETLNNMLQ

GATILALRDYYEWWSAHAEEGQYGKLLLIEEMAQKEGDVTIFFDDHIETHRSHIVDVRTV

RSGAPVDFKQSRGTYLERVEPFAAITD

>contig35437 Frame-2F

MLLTPCHWSKDIVQTPSYKSSRTHLYILYRTNAVGQTPLDMPLE

>contig35442 Frame-1F

MTQEERTLKSFTLGKSHALGQLNVL

>contig36209 Frame-2R

MTQRDVFGMNQRYRFSKATSYEFKGTTKQKRRSAAFQVTRVPPESLMALKPAFSPLSKKH

EKRTKPKQQLFHDAAESSRYQIDKIHHQKVVLAPRTGSATSPVSRSMLDKLPTWTAKYNN

QGISKPCVVNQTECLVSDELHEEILAYSTYTKETVNKMSVHIEQMIANVRSSVQSLWPQA

KVETFGSYSTGIWLPSSDVDLVILNVVEVNDSKLTAKHLRQLLNELKKKQWVDSLLCLDT

AKMPVLKLVCAESSVPIDITFESTATHSGLLARDLIKRYADTTPELYP

>contig36344 Frame-0R|Blast-D-Tyr-tRNA(Tyr) deacylase [Phytophthora infestans T30-4](gb|EEY61053.1|) 5e-17

MKVMMQRVISACVRVEGEIVGEITQGLLCFVGIGHDDTEDDAEWCCRRL

>contig36506 Frame-1R

MRQKSVNYDEACSSSRVNIVVTGKMLL

>contig37163 Frame-0F|Blast-folic acid synthesis protein fol1, putative [Phytophthora infestans T30-4](gb|EEY54477.1|) 4e-25

MVSVYAALGTNLGEKVSNLENALTMLLRLVGPIEATSRLYATAPQYVANQPSFLNIVARI

RTDLEPKNLLEAFKAIERHRAHSVHK

>contig37361 Frame-0R|Blast-ubiquitin family protein, putative [Phytophthora infestans T30-4](gb|EEY65648.1|) 1e-176

MKEEDKKVGLNPEPLEDVDPEAIHIRILDLNGKYFDITCRLDSNVAFIKHKVFESTEVAI

ASQRLIYRGRVLEDEATLGSYKVEDGHTIHLFIRSAPTPDPEILSTEFNTNGSSSGSRED

GMTVVNINSDIVSSAVFPSDSARRVDPLMLDSPLGNCARRVKLWSSFLLIIYTMKVMGQF

ALLANDQQQRAAQQEQEATGANITGRPENRYDEYPQYFTPTPLIGGIELVVHCFGVYVGC

VGFKAAHDTDIRPIRFYCRGVVWLAMLTVIEQIYTTVQVSEANIPSDRLQYPYGGQGPTK

DDIVSANIFQTIMLMAMWIFAIRHSYLHQQEVMIYNQSFAIAAMNAAPPVHLPEIV

>contig38113 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62772.1|) 0.0

MTGLFTWEIAPAMMNRNVQSLSEVHSKQPNYELEDKVALNEALTPQAELKPSTSMTLHRP

TGAVQVELKHTDDGSGLCKSCGGEKLFIKAATTDAKTGRSANVKLEARQVSWEHELAVLS

NNLCLGKNSYVFHEDGTSASSNKDNGENKKKDKSRASEIEKMPGGGNKDERFERLERIAK

QNEERNHTGVAAPTAFEPSKAVCQCPLPTESKFKRRTTTTICGLFDMSINEANVGSLDDE

RCLLDLVLDSIPMVFRDCGGDTTDKTVLGGRYSMMRYNLMDLSPATDPLVMDPAEAPGFS

FLQRLIHDEECYAQLKTFLMKNDQQEGKELAEFCDAVKKYERTSVGTDRLGQASIIYWEF

LTPDGGKKLIFPSTVVSDIHDQIHKAQAALRAAAFANVDDLIDSSFCLPGLLFQHAMTFV

ESEVFNKSGLLDKYVAALDQPSTAAATGGTTSNTKNNANTSSIPPQLALFDSFSIMELNA

RVSHLALLKRNADEQLVRMTKPDAIHGGLLPQTSSGSLKDSRVSALDICRL

>contig38184 Frame-0R

MRSNALADCNTIVDMSLRLSRFVLCVVAALLFAFGFALVTSNKKVLTHVYEDKLAGNETL

SATASSVVENYNTLLATSFSRVARSLKFFARRLFFQRWLPTCTTAVCTQETNQRGCTRSL

RHVASFGGLRL

>contig38526 Frame-1R

MHCRSSHNTKDPLQMIKYYLMRNHHYSIVGFQPMMGRL

>contig38629 Frame-2R

MLELVVTRIQMRLDLFDDAETQPLASHTVLALGDLELLDYISTSQIRKIICYWKSAATHP

RESGSSMVRLQLITVRPGPKLCEEHRLKARMLPLRINLDQEVVKFLRQFVPTEDPHRQSN

ALLDETDEDVTMQEDGSEMTQWIQGRAIASTRKSVGAWFFQSIDIKPCKIKIDYRPNHVN

YAALRAGDYIEVINLFVLEGMELVLRRVQMSGIDGWAALGEAALVSWVQDISRRQIHKCV

ASVSMPPLRPFVNIGAGAADLILLPMEHYGRDRRFVRGLKRGASSFLKSVTIETLTTASK

VAQGTQALLEHADDVVSSSSALRRKQLKYRQAGSRIARNSRRMGGGGIRNAQDSGGGIGG

RQYLTQQPASASEGFGQAYDSLARELHVAAKTIVAVPLVEYKKTGSQGYVRSVIRAVPVA

VLRPMIGASEAVAKALIGVRNAVDPELKEDIENKFKDFRAN

>contig39064 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67448.1|) 1e-23

MSVKDEEQVLVAMEESCRIYVGNLVPKAKEVHLTSKFARFGTIHSIWIARKVRL

>contig39338 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57571.1|) 3e-63

MPECTKTALLGGLCIAHGGGKRCQVEGCSKSAVGGTLCVSHGGGKRCQTEGCSKGAVRNG

VCIRHGAKRDSMLH

>contig39859 Frame-1R

MSSTQVAWDTWWRTTKSGSFRTYVSIVLFFLSTVLANPIARCVFWIVRKACPKKWIWPDD

ARRMMMWQTSLVCRVGLLWIAVVVSRLSLLLYELPALLFGACFMIWLDAGGNVLREVIVR

QGVVGYKNDEKAGRMTLLYEGSTLAKMLLLVLIIYTYYVAPRIEDSNELRLLFSVGFFVS

IALGALPLLRNIMGAHYM

>contig39936 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61506.1|) 1e-115

MLPHRVPVTASEGSCTPRLRQVSYCALFFLLATAVLRLVHFLYGKCDTREHMSTLLTKTA

RILKQNDIEYWLDKGTLLGVHRDKGLIPWEYDVDMGVMNATCAKISALKSEFKAVGLTAY

DREDAIPHKVKLTYDTENHEFYWSDPKLHDPCIRVYDTADVGTWVDIYWYVELTRDEVAA

ARDRVLLPPDYDNKDSLICCSEGLQAYTEHMCCGGCVPRKSLFPLQRQFVNVYDGVNAAQ

KQPVPAQVSQFLSIQYGADALLRREI

>contig40055 Frame-0R

MPEPQCGGVIARLLGRSYANAQRPSCLQRFTPRRVIASPALLLWLGHLALNISS

>contig40705 Frame-2R

MQILPKEVRPEQATDKSIRHHHPVLCAKFPLVEYNAQKRSFVRTCLEIQTLSTLERKGTV

RKPT

>contig40914 Frame-2F

MSRPMAIPRSNNKASIAIAANRAILQHAHSYGGEDDTHLLNAAANLNVAAAPYGYGNVAI

GREREHTLSPSLAFQHRQQQLWEGHAAHHDTESRLHSSPSCLDEPPIHLLDSSSHGSTAY

QCLSTPPRHPKTVALLRTTSPAVTHKPFLETHAAAGSFERFALDSVPPSHVQPHRLESRK

GSFSGAFVSECSISTGGNESLVPLNEGTTDMPSTAKTETITTYSGSHVHPSTECLPPFTS

SPPFQANPCELLSKSPGYAYAKSQLCSGSSTVPMFITTDRFQRSSETAKPVKSATMSTGE

HCGYLPDFGHTGVAAWGISPDSPDSLSLALGSTGNSRDEEAAVESRDNFMDDLDALILPF

AIHDGQLSAATTAGDSVSSGAGSSFSRLSGASVGNFLQQLKNAPRLSKSLSTLGPSMSPD

EADNCIDTRQEMKASFSMFDEELAGFRNLREELTQML

>contig41539 Frame-1F

MARLLPRNFRSPPIVAAFAAATGLSTVTSNSSTRLESIPASKPTFTERTIGNYENRLRKF

SSPERVFEYFSSV

>contig41720 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70414.1|) 4e-12

MTKKLSSSDHRWVRHIVRAEDCEQRLDRWLRNLYPGLTQSFLQALLRKRKIRLEHTTESS

SQATPA

>contig42497 Frame-1F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY54199.1|) 3e-96

MHDSQTVIHTAISSVRLHIAGALVRAGAKMDVEDAEGKSVFEKLPRKDLRFLISHIYFPP

TYITKKERSECMLCHQKFKFGFREHNCTHCGRLCCAECSALHVEMYRFPLGFPGRTRRGA

ANREQKRVCKTCYNVFKERNEEPEKSDVSKFINRVINIEWDEVNPEKLQTVQEAGRRGFF

RFTRPCR

>contig42804 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60635.1|) 1e-08

MLDDNEATNSSISPPKGWKSNEEEHVVAAFVDAKPTEQLLDLPA

>contig42893 Frame-2R

MVELHWRNAVRAELDSMQLREVFKPQSSPLDNTLSEPRGFKIKRKADGSIEKHKLLLHQR

VSAKIWNRNFFPIEEINIEVQYYYHK

>contig43209 Frame-0F|Blast-inactive ubiquitin carboxyl-terminal hydrolase, putative [Phytophthora infestans T30-4](gb|EEY64894.1|) 3e-66

MRSSICQRDYLVKYTEDRNTDVNPNRIFEDESSERRNFKGDYRFDSVASIGERTLAIPET

PLMMFDVCLNASDGGIGLLLEEAAKTDTFVSSRFTGKSFVVSGFEVNGLGAKLPAEASGV

IRKGDVLVGINGHLLDTETYVQMLEMLLMSPNPVQLTFCRFQPWACPQCTLLNTKNDSFC

AACGHAPSVPSVAGLRTH

>contig43506 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63802.1|) 5e-33

MHCNTSFTIITRKHHCRRCGNVVCHNCSPHKRRISSTDPFPMRVCNACYAAVDEHFALLE

WSGHSSS

>contig43731 Frame-1F|Blast-unknown [Hyaloperonospora parasitica](gb|ABG23233.1|) 3e-31

MSTTSSDESDAKKRSECLELFRALKNKDELSRSCKEIMNMITANDKGVMENEPLNTYGGS

RLRGGISHAALQRRFTGKMSGVRLSG

>contig44222 Frame-0F

MELNVSCVNHAALVNSYYLRILFLRVSSFRLPLKALSKSSAAAVRRQRKTVARRRAEQLK

ELIAQGKFVPLSFKVRTALRNAYDRFSGERFESENFLPSYQDGCCGTDALLDVLNTLREF

PRAENLNDGNVHRNLMNCLQVAEVNGNKYILPAGSVFARRDVRAIHEVALGKHKLIVIDP

PWHNKSVSRGNQYVTFDHTDLLRINVP

>contig44257 Frame-2R

MLKSFDQMVCSGRFLRMQWENSQDCLEDGNTGESIEYGVERVLTVDVNVPHQENSYDCGV

FVLKFAEVILLNCLKLNLLAKNDGVIGKDITDGNLIALITASAFCAQDITDTRKQIQQYI

ETDASDFQVRRNVERKRFKGVE

>contig44396 Frame-2F

MEAAELKQTFGKGMAGLCLMKPLPIVSRHFVKAQEPVACSYRRLITA

>contig44895 Frame-0R|Blast-threonine protease family T01A, putative [Phytophthora infestans T30-4](gb|EEY63538.1|) 1e-108

MQEFTQSGGVRPFGVSILYAGYDDDGPQLYQIDPSGAYFGWKATAMGKDSVSAKTFLERR

YHDDLEIEDAIHTALLTLREGFEGEMDETNIEVGIIKSDKKFHVLTPAEVKDYLEQAE

>contig45140 Frame-1F

MILYEVLASIRSMPDLITKIPVPPPLNSKTLHSKWNNTSTKTWMALGNELHWIARHRTII

RHYLSIAKPSSSPDNSWWLFFSVFQYVVRRSNETVHQLLRKQSTVADQSQAMNDLLMACM

KAFHALGPFINPNASP

>contig45517 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57191.1|) 8e-63

MIPVPMQSSQPLPQTAIDIPQQSYVPLKNPMTGIETHKAECARCRKGLYEKDIVKQLQCG

HLFHGHCIDNHLRVDIYCPVCRMQVLFPTAVPATIVHEGRAARSVYPSAKLPPRTEYVAT

AFVPSDGTNRSNYAPCRECGQMFYRDLTKVRPETNAWYRCEQCAPTDIIDFIRGSCAVQ

>contig45724 Frame-0F

MVSRIDNNPCLLRMSYLATSTHFNNWIFSAEELKQVRSLQHVKTKRALRTDIEKSQKLDK

TATNGRKARSFAALVPRSSSAVHDASASDWNDDVDEDMLLIKESEEKFNLKLTPLLDFLD

AEQEAVLRQFYEVKLQESCSARFLRTSDKVKCCAMLLFKRFYLSNSVMEFHPKYLLPTAI

YVAGKVEEQYISVDTVADQLQVDHKEIIGHEMILLEGVRFQLIMYYPFRALLGFLDDFRA

FAKKVLKIDLPATVLQKLHSNSTAILNDMLLTDLPLLHYPSYLALAALWSVTDEVAACSA

EKACGLASADILSYIKRSKISKQQPGDEVSDRIAQITEAFLRARTKNEKCSEEAMQHHRK

QVKQIYKKLKQFFEDNDVKDKKKKKKNNKKRKSEFKDDKNLKK

>contig45975 Frame-0R

MDEVLQFERSIDEEIGYESWATADRQAYPRCIDVFTSENDVLFAWTSVDVEYAHHILTSK

LHDKPEIEWYVEDGDGTEHSRQDSIPPLALRLVTLVDFLSQRFLLIETDEMRYLYVMQVH

LPLLSQFMRLCEARGRRLIASLTETMTTADILSRCRNLFLVGNALQHVAQALAAWEQSSV

FLELSRKVTGSRATQAHVLQMHMAYSKQVLARASAAVLATEEATAVRQALAGPGAMIGPA

AALTAAYSAGSKTMKSLFRRNETKQETPSVAPTCASTATTATNDKSVDDQDDAEALLFTP

TIFERPTAELKMLASTLLEEGKNTLMHVFARDMETYRSSPFWTETSQNDIDENQLCGVSA

ELGICYEIVSIVLSCAQKVLLPECWLAFWKPFASGLDDALFDAFYNPAMTEGSSQLGEFG

KRRFIRDIKTMVAIFTAVSSKALPSSSFRRTREVCLLLEIPTPRLREIYKALKVDETRAP

LTVAADPMEQLTTILEACRVFCLTPAQVVRICTTRLNITE

>contig46484 Frame-0F

MEWQEKKCLEQLLGRPLAFQPVVKQVTTKEREEDLIRIQSAWLCHVKARNRRRRRRIVTP

RGVPRVVESTVVLPMSGHFRQKKCTHGGDSRLIRTWYRKDRRFKCFDVSHSQEMTITSVY

CLGSSRLLPRRKCTC

>contig46888 Frame-0F

MITPRPDSEPSPARGPRIRVTRAFTQVDEPASLQEMLTPTSNALDAWRLSPPHDCDVVTM

QTPLVPPTSPA

>contig48121 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54204.1|) 6e-55

MSFYRAGSWLISITCLEDPSRDSLSTSMPPLVVPSVASLMPLNQSTQSFLKVGVILDKFL

LHFCDEHDTVRDATGMMFYPDILQFSCDDVSIIFNTAPDPPEASRHNSRLGYLSHIRSYT

SLYISIEHIEVGHFVQACNFPLL

>contig48323 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54280.1|) 2e-23

MILISRSLAHSITMLSALVRPTVSSALRQRHIFGEHGFLSRRSLSSLNKWGKTNEYIDAR

IVNIVEDGGNVRTNIPIHQAIEIAQSQGLDLVQVSPVGKQPAICKLFDTKKRLYELRKAN

KNATKQQKPKPDKEVLIGAKI

>contig48587 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60766.1|) 4e-10

MRSRITLTVLLTIAFSLRLLQVRAAACDEICYTTELTGFGPGGTAGCTC

>contig48846 Frame-2F

MAISLGFSWASDSLRSAAMVCN

>contig49081 Frame-1F

MKQDFEQAKVVETRRSGKGVAEVHDVTKDLSLAQTSQIEEEPVYDLSTERLVAVAEIQLL

DSDTNMSSSTAAEETDACESEDLAADVVDESICEITTNPVVSWFRRIGAFGQYAAEMTEN

VLCPEEEVDNEAKVREKAKANEARAKRDLKFETAAGEAMAKMDLEAKAFAAEEKAKRDLK

AKAAAAEAQAKLDCEAKAVAAAELLRAEQEHYRRTEQYRYPIFFQPFNCDENTLRFSMSQ

RSCDCIAF

>contig49504 Frame-0R|Blast-SCP-like extracellular protein [Phytophthora infestans T30-4](gb|EEY65662.1|) 3e-52

MLRKLNKTNAAPRHLQAALPSNRHQLEMLNAVNRERAIVGLYPLCMNTKLQNVALGHSID

MAVKNYMSHIGSDGSTVQQRIQTARYDSIAAGENVAAGNLTVAQVMKAWMNSTNHRANIL

RQKITMFGCGYAYNQKSTYKYYWTQNFGASRMEKCS

>contig49690 Frame-2R

MRPRCLKWPVEVCGSLKVKILPEVNGRLLSRGWRWQWRGLCEWAFVEMYCIAVTFIMILR

R

>contig49715 Frame-2F

MLLKKTNTSQQHHEPASGRVVATSSIALAVAVQPRIVSKFTSASMHRQCDYVDKWSTEMD

WTRLQVEEFDTISDIDSDAIATHQHIFVNVMESSWLLSSIEQRCAENTTSTYKTPRTKRS

RPSLVRQFID

>contig50014 Frame-0F

MSRRQALHMSSERRHTHTGVNVSAMATVPLNCARRLSLDQTAIASTIYCEGYVHLKRRNM

L

>contig50955 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53165.1|) 7e-58

MREGIGIFEGIVRALTYLHAQNVAHLDLDVYNVAVDVRASPRIIDLGSSQIMDNRGLVGT

GNVSIKCKPVFVSPEVRSHQRMVPPRPGFDGAAADMWAAGVI

>contig51426 Frame-0F

MLEQPVVVGIIIYWTYIVPASLHCVPVIKAANSGFIFET

>contig51927 Frame-1R

MVNFGLRLRDNAVAEWHGDYLDYDRLKLLLEQQQIDRALISSSTTLERRAPPPDAEGNVF

GGHKWRLTDTAHFGKKVSCKLAFLRWPESPPISAELEQLQPLLSSPIAFEETLEHEYMKV

EHAYVRHAAQLLEQLDHLRAQHRSDAPATAQESLKNALVDLHRLLHLLHNFALLNYTGFV

KILKRYDKTASPPSDKYEAKKA

>contig51952 Frame-2F|Blast-alcohol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY68781.1|) 1e-10

MTTVNKMMSSLHAHGQDTCCNDPAGCMRAVVWTGKAV

>contig52135 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57344.1|) 2e-62

MVSSPGDYQYYDRFTLRLLNDASLCSDVKVRMIYVRHVQTLVIRQGAPHSLNAIRYLQPL

LKVLIAGFESVNAKFLIASLEALKTTVLATWPRIASHTEQILVGVLRAVAFCEMFDDCTE

LIPSSEDRRQILALCEDVLDLLHNANTNKSAVSD

>contig52566 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66749.1|) 2e-20

MQLRFALVLNALFTLGVVAESKGKVVKLSVGVGCEFSSYSALPVATASKPSYRLQLDPGL

GRGIYVLLFTQFSLPDDDLVIVR

>contig53389 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58441.1|) 8e-22

MAEELLKCARFGDIDELKALLESVKSSNLDALVNYVQPETLNTPLHMACANGHITCVHEL

LHHGAKHVP

>contig53675 Frame-1R|Blast-tyrosyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY64400.1|) 2e-80

MSRALATLRQRGMLAALTHKDAGASIDKMIQGSHIPAIYCGFDPTSDSLHLGNLLQGIAL

RHFQRAGVRPILLVGGATGMIGDPSGKSEERVLMSDDKVIRNVQQIMKGLSAVVDFDDPK

TGAIVCNNADWHTKMSAVTWMRDIGRHFRVNAMLQRDSVKKRLQTDQG

>contig54098 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64982.1|) 2e-14

MLRVLRLRRASSTALSYCGISALISSSSSRPTRMLPPVRWTSLQTLRRNRSYSSSAEHRV

ATAADGLTDANRENVVLLLKDRCNALYQNNEAYVPPTEALSLWLRDLQMLHRQYEPS

>contig54186 Frame-0R

MHFCVRTLKTQCNIAIYNRFLCQTCDLKSLSRRSHPLP

>contig54375 Frame-2F

MLCFSKLAIHGFATSNISFDNLHIFPSLKQETLAT

>contig54494 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67728.1|) 6e-27

MFFWRNMKTLLIMAVILSGVLHMLLLPVEWICTLFLRPETVDASVRAFRYAAASTIPFFL

ISV

>contig54612 Frame-2R

MRARLFEPSGISVVKELDSLGSQASVVMTRDMMIILVCPRETTIPRHSQRVVNTMMNLEC

DDENPSSFVCAKISPGRNTSVFVSD

>contig54689 Frame-0F

MLPMLGHGYKLDNRVRSPQKWLQSDR

>contig54825 Frame-0F

MKAVNAIEVIEKLENQICTLEAQLHDCVKLQSETSATEIAALTDQIGLMFESSRSALAEV

ALLRNELAVKEKSH

>contig55101 Frame-0F

MRFDVVHHGDSFNARERPRQPIIMCASLVDKIP

>contig55710 Frame-1F|Blast-Putative beta-1,4-galactosyltransferase [Phytophthora infestans T30-4](gb|EEY53624.1|) 2e-34

MHIARLWERYSDSSTYFGGIVAFTSKHFIKVNGFPNNFWGWGGEDNELYSRVMRKKLVIQ

APT

>contig56863 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54043.1|) 4e-16

MTAADDAEELAMRCCVCGTSAEDDSNYLNTKMKMLISKCGHR

>contig57820 Frame-2F|Blast-calcium/calmodulin-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY68479.1|) 4e-06 NOT\_ORF

MRHMAKFVQYLH\*CVTNFLRVCRYGIVH

>contig58397 Frame-2F

MQSYQPHHLQACGLSDATPMPRIDMQLVPNRIYLLCDTRDTHLVKIHVLAPLPTARDISH

PHFTLRITGSKQRAVRKESHGPLCCRWLDRQEDSHLRFRPAVTNCKITGRAASSYQIAST

GWDDCLRFA

>contig58461 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY69268.1|) 8e-33

MVAGKPYEHQTDSWSLVVLTYELLIGSTPFHCINQMEMYKRIELADYHFPPIPLVFKNAK

LFISGLLKRNPSDRMSLEDASNTLRL

>contig58832 Frame-1R|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ25475.1|) 7e-07

MGRRKKSTKKIQTRKKQVVSTVFKCPFCSHDDAVECK

>contig59228 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62937.1|) 1e-10

MSSHRERLQRFYEKHNPEKLHEIDSVLERFKGREAQLFSSLVKKYGAEPTEGENFDLVSE

>contig04025 Frame-1F

MKTVASLKVATSDDVRDSLLDKTSHLTQELMILQHQTAQLMTVKAKIIARLLAGKQSGSV

ATTVCLKSTDLKVQGHVEAKHSALALSKGALTVGELQTIKKSATRVNFVLQRDAKEDKNG

GTFQAATAPVPTLDDPFVLESAPRAQTELLDATHTTESEKRFDWGAFN

>contig05310 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53445.1|) 3e-91

MGSEVTSKSGLVLQDRRIGHGKLPVAGDMLTVKYRGRLGCDGLIFGKGMLTMTYGAGSVI

AGWEEGLGTMRPGGFRLLTIPSELGYGESGKGDKIPPNSTLFFEVELVRIGKRKREIVGD

DDVPLPNSFQRKRIKQKPGKKHGDDEKYTEIKLSKSQIKRRRRKRNEGRNDAAVELD

>contig05758 Frame-0F

MASSYNLRPQSGSNCVTRQQMKLFMKCLRLRKM

>contig07617 Frame-2F

MFMKNTVLTVFLSLVSAGTAFYALAYPAWFQQHYRRDGKDVYQGYGLFAFYSTNSLESPF

YASATVLQYADFCVQNYTTPNYMLGDGADFHHALCSKRMRSAQATTATGAAISVVGLLTA

IGAVYSPSAGYMERIVSFCTLVGSLLLAVSLVIWGALLQQTLYQIDTINSAYSSCKADDT

KWQCWFYGYSFWVCLASVIALSITGYLSSAGRAEKIRYFRKTYERDLAIALQQSAEVTRT

QFVRTESSGGFGVNATQQTYGQAPTPSQSFTGHAYTTPQNLQQSHYGNTSHSGPKPVGYQ

RQVGNVPLTAPFTNNLSRSNSNESDAVYPSYSDQRKNHSLLGGRPSGGVV

>contig09422 Frame-1R

MCKLKKRKRWKWHFARIAKNIESARLWLIRYTSFTDQYMTLLVLFPAEL

>contig12336 Frame-2F

MRYHLMSAPLKPTVVLFHLVMLLSSHWIACLGLVAFDDSSVSSDDSHDNLRQGSHLVVSR

LDEDSDNSMQQVSSVDEDRMDPNSEMIAVLAKKTLSGKSFWKVPYRTVRSGLKRMVMPQR

YIDNPYKAKSAFKSIQYSKGDFVSKFARFDQVVMEGYSKAGLKETEASEVVVKVLNDEIG

PWRAAKLLKNLESVNPELFGRTRLALYRYWNVKQLSFVDFEGGKISSMLGKGETEKAKER

IFNCFSEYFKYAGQAAGREENSAYKSLMEIIENLGYGHVLDGILRSFSQPEINELLDNGR

RIALDYLKKQHEKYNTPSAIIKAVPYWDKGLILMGQPFFRLRALCKTHVKVEDGAVSEVE

LQSKWLIDQLDDWVFDKKLFFVMYPMRRDILAATVLKQLSHRWKGEVASSIAMAQDYIKS

MLEIVELKGTWPMYSIEYHAFQDFIDLAFDKPIPVQIKEAFNGQEGVDELIYKLNNAF

>contig13050-0 Frame-0F0

MLGIKEVFSMLPCVQYRKMLCVCDPEVAFSFPSSEFMSVK

>contig13528 Frame-1R

MSDPLIAPFAGLCGALRGLHEQVERLACVHDAIEDFNAAFGSFQGAMALHASCLTYPKNV

PAPEAHLLPKDKNLMASGIGNSLQNISQASLNRNFIQNKQNLSLGSTKSEEMDGKPKQLK

KKPSIKLKSHAKVDSNNHYLKRRKAIPKTAPPAWTWDRHIREKIPRKYQSPAELKKLENI

VLYLKNRHCAISISDLVKHSGLPVIRCKEILQTLMKLSIIERKREKA

>contig13942 Frame-0F

MVGTMVEISSCTAVNSDSSSGGYNLSASHRATSLKRVGSKSIPEAVTWLDHLTMELKTAT

AGGKTQYQLTMKYTPCQQKLASCTTWTINHSFDEYRALRKRLLKRMQHGHLCGAECKWLY

KVVKHYFPRKSLFGNYWPKVVALRQQTLIRCLTTMQASLVNRGNQCCHVLVHDVAAELKR

FVLKDMKNPDFNASPSISHLSLLSAATLHSTREADCELEGE

>contig14565 Frame-1F

MVDRDFFVDVAVTDFVASAATNKLHYLPDFWTATYSKRLALHSISIPSAPLFRRESTRSS

WPLSGI

>contig15272 Frame-2F

MHRIFMCTCYCIGVSWVKGHDRELKDLSAIAIRNRAKFDHFSIGISIGDISIDI

>contig16093 Frame-0F

MKDFKAQAIDTPGVILRVSTLFRGYPNLILGFNTFLPPGYRIRPDTSIEVIPSQMAGRGG

GQQSMYSSVGAPQSNGSNMGHRPPPVTIPPPPYSPPELHKSTPLSCQPVAPPSQIKTSGK

PKKTQQTLSTSSGNAAATRSSTNPVEFDHAIHYVTTIKQRFADEPETYKEFLAILHTYQK

EQRSIRQVLDQVSHLFRDHPDLLREFTFFLPDAVQEQAKERLNRAAEKAQLRKDQMALKA

KKYSTAVPSYQPDRLDDRGGDSPSSAAMKGERSMVNDEDAYMKYGKKGVGRSFKDDDLHL

TGKALERREKERERERNRSQFNHKRIKRRPYDGKERRAYLAISDVLLDKEEWHIFEKIKK

ILPSRDNWREFLKCLELYSQEVLDREEMLSLIRNLFGRHTDLVDEFDHLLCSHGVQKTPK

EIWPFIPLAETDLSQCRRATPSYRSLPASYPIPPCSQRSVLEKEVCNDLWVSVPTGSEDF

SFKSMRKNQYEEALFKCEDERFEIDMVIEANASTISILEPLAQEIDVLKENEKSNRDNDK

LWNYVLDKGTFRVTHLNAIARIYGEAGSQILELLRKYPAGAIPIILKRLKQKDEEWRRAR

EDLNRQWKEVNEKNYHKSLDHTSFYFKQKDKKQTGMKMMMLEAKKRLEGDEKRAEEARSG

LSASPSTVSATFAVVSAKAPPKAADIANALKKEQLLGSAKPLAAADSKAPSTVSQTSLLP

TWKPHFVYKFASVKIHKEAFGLLSYAADKNLSVVDKEKLCKVWQTFFFPFFYLEEEWLVR

KPQYATVTPEKAKTLRVGTDVSTEFGEGTVQHFNRENGYLTISITISGCQAYLQPSAVTV

QEAADFPPGLPELDSKQDAIKVQMNHKSLFYGNQHAYAFVRLYQILHNRLERAFDLCEKA

KRNRNRRTINPAARALAHAHHSLSASTKEKTGDYQAFLAELYSLIDGSVDNFKYEDSCRS

LMGSTSYFLFTMDKLVAQILKHMQHLASDETCQELIKAFTDEKRDESASVDLTSAEAKAV

AYLNRTKTIFEGEGAFRMEFKPGVLRKTPLETRGGSTPLGVPEPFKIWAPSPRVKAPEYT

KWLIEPELAIMYLGSMDDDGEEDDDDEDSPSATPVDTPSATPVYGSPMHDSQDEEEDLME

ESKGGGLKKENLASTLARDIEQSDSASSDDTASAAKMLECATLLKKRARDSSEENRAMVE

VSLSTLVAADTVVASKRVKAATSDERSDDTATRTSATKEEKIRIKDEFESKTTEVGLAIK

IETPDRAQERQYSTAAQRIGDMY

>contig17605 Frame-2F

MFKDPFACIPILEPPRKRVKAGGEMQTSACTTSDTSNTASAMAGNDGVVDDHDDSSNTSS

STHTDALSSLANGEWAGSISFIEWRGQVALHVVGDAPLVMVGQQARKLALVALHKYTDMA

GVASSDNHEDEKIFNEFVSWTTPDGKKPILPRLHFARDHSICTVFPPRSSLAMRQEYTLT

TKEISRGLMLHSFPIPLTNASIETLTNVLQVCGRSLFFHATLLSAFCSKSNTFGQRIHAD

NDDAVNARIKVDVAAPERITMNTGDLLGTSRQVLIEVLTKPDYSLELSVKYQLKTSPSLP

LESAITLEKLSSSCHSIPLLTYYALKHTVQAKNGPSTHGVVGVNGEDCNGIAALDGELSV

SIKMEGEGMLLDEMDMF

>contig18121 Frame-1F

MSVHEASDVIEYIHEFRRYEDVEELRDQLNGCKAMILRSACVQLDLRPNQRDFVKPNYVD

LLVEYWKDTQEVGFKPPVTPEVSVLSVKESDFAPDISKDEVESQLKRIRDKAPLDEETMI

DLEKRRDNKKTSGNLTALLEKAKVVKEWASAIEVLSRVDGSQASIASIRALIHGVVKSAA

TDAIESSIRAGKS

>contig18459 Frame-2F

MLLKENVNSVVKIGERNEKDAVIRKAKERESDLHCLNQMKFSDRNCDENITQIIEVDGYD

EEKEAEVGFSKERAFDLDTYDEDWIQDEELQMATQKRNEIVNDSNDEWFEEKVDKNILGE

DENDEVVCDSDVTQAKFLLRNITSRVPLIEETAICRGVKLSGPPHEFATTHLDEYAR

>contig20588 Frame-2R

MQREKECALKRCRFLLVVMRSPIDVLKNPVSMVLSINQPIKSCLKFSRTGIVQPSRLERE

GVNKQN

>contig20702 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67655.1|) 1e-29

MKTITTELEREHLLAFIQLAVVKSMEEQASIHQEKNMLESMLKLNAASDQQDLFSEAHRP

TPPLQSQGI

>contig21558 Frame-1R

MDIVADAAFSSLAASASLDSSESSIKVPDDPENEEDSGPTGNSGGAIAPRQGPMLPGSSD

AVLPIMTMMNAIAIVGTVVISYLL

>contig22164 Frame-1R

MRGMMNFSFHPSAFLLSSHVWHLRSGHQMDSSLLLWNKIRQPRATTILASFISLNGLPKV

PSYGDKELYWLACELAETAYAFSDYGTGTIGWEIQENSRHEDNVLCGDALQYFPEPIYFT

SHVEEKEGTLLYMNSDNIVEWGRPLLDACTATGLSRRLVFRLIYGARS

>contig22506 Frame-0F

MPSAADDLRARVEPFTKAQLALLSIRMTDFEAAIPKVQPSSKREGFATIPDITWDDIGAL

KEVRDELSLAVLQPIAHPERFAALGLSMPTGVLLYGPPGCGKTLLAKAIAHESGANFISI

KGPELLDKYVGESERSVRQVFQRARASSPCVIFFDELDALAPRRSGGGNGETSGNGVSER

VVNQLLTEMDGLESRRNVFVMAATNRPDIIDSAMLRPGRFDKLLYVPLPQAFERYQILKT

ISAKCAIAASVQLETIAADPRCEGFSGADLSALIREAGMTALRETDFSTIETQTTRFEIQ

HHHFLSAFDRVFPSVSRADQRLFDRMKKNLRKSRLAIPKVANGAIEAVSEANNAISN

>contig23000 Frame-2F

MQQHVAQSLASLAVNVKADNSQVEPEPPLDQAAEISKNDASKNKKKKKKKKNRRKSVEQA

EEEELQRDSASNEEEEGTGSCVEETSVVPIYPLGGESTVSETMKTAIMMAERTLDQESVV

QNAVAEKACAKDKTVVEHLHHSDSSGESDDELAAPSLERTSSLGVFKASGTKAMGSLFSR

FKVGLKKPPSSRNESPVQTGVAKLDDRSLEVKADVSGSDKHRSDEKKQSDLLKIEQQPNA

AAGKVQDLSISNLNVIATVHTEYEEAKEHTNKENEDEVPQAYKEKSVESTVANDNLSEEP

LISISKGTDETTKVVSTVNSLITTIEDVALDESVKPSLDTMTSTLVQDEKIKADFQIEGE

SEAVTLESSEGNEEVLTSQVSKDAVEAPANALPPSEPERLSPVKSLASRFEGKRQQSLDD

LKFRTVHEFFPTERSIRVAAEKEKYEAHAQQQLTKARAEEEAIAKYKPSSKSFDDVREVK

SSVSETVFATANATNARVSQTPDAAYSSQKSSSFDDSFIVSQSSCKHSDDALTPVKSIAS

RFEGTHDQSLDNLKFRTVRGFFSDETERSVHVGAEKAKFEALTKQQEEAAKAAKQGRLKR

LTPSPSTDSLLSIGALNVSTENDSEKVVTSADAVASNLIDEVDSNLTETLAKSEDEGQCS

ADDSGEVAVAVEENSLAVFGKTVIDSQNIEVNVTTGHVDTEMRSEIINSVGFGETLESKA

IEDQLCDIREKSRFDEAVDSTQIIAGHNVTSIVNDLADADTGEESAAKLDSDVVNSDFGG

SSNEELSVASLVFATQENVNLNAEMNKVEEKMSTESRETAQIEEEMNESDCGSGLSQLTL

FKTASTIFSNGTNQSDIPMLTTERSFVMETDHTIKMEDTVVVETRPHSTARGAVIPLSVG

SSQQTVASFESKRGNGKETTLRKATKKLTTTPSASLVTKKATESARKKQGSTLQQ

>contig23277 Frame-1F|Blast-mannose-P-dolichol utilization defect 1 protein [Phytophthora infestans T30-4](gb|EEY55637.1|) 1e-110

MTLETMATKFTLITATLVTSAIAMSKDKDELIMGLFTPECFEVFAVDHDFANIACIKAVV

SKALSYAIITGSLILKLPQILKIVGAKDVTGLTPSAFYMEVVLYLSSTIYNVLRGYPLTT

WGENLVILAQNMLLVLLLWTYSTPKILFTTRIGLVATLCAMAAGMLVIPDEYQWLLASAG

IPVSIVARIPQILSNFKQGHTGQLALITLVLNLGGSIARLFTTMQETGDPIQVAGFCVGI

LLNGTLVLQVLLFWGATNKVLAHAIQKKKK

>contig23318 Frame-0R

MKPAPDVIIVALEGCHGCGKTTLCNAFAAQGYDILDEGFLDMASYSLHPQSLLMETSWVC

SWFTRVLRIAEHATPGRKRIYIADRSPFSSVLYSAHGHLLEPVIREQMREVQDFTNVQIY

TVLVQVEPERLWRRICTRLKQEPKRLHLKERNRDWMEETIAFYDNFKWDLTVTTNEDSVD

TIVTRISRLISAPCERTLPCRKIRHSPSVSSTLSTDSECDSAEEEHHVPVASR

>contig23611 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57113.1|) 1e-114

MIETKATTEDHLEETIEKYLVCNQIGGGKARDMACAAENESLKLIPWVGIASRIDGGPTE

GRAFCFLPLPVRVGLPVHVNGYFELSSNRRDIWIGDDMSGDGKLRSEWNANLLVDAVAPA

YLNFLLKLKAMNQIKTSQYLSYFPVNLPSSPWNSIVLELFRIMKSQPMFLASASQHMKNE

ILEGLIKFVKPSSCVLIDDDLSDWKILEDALGTVSLTTVHVPVALRKMLLQLDGVYGALT

PAFFRQLTRQGDFLPVLERGCLKRVIRF

>contig23970 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58059.1|) 2e-23

MQYDDFMQKCMTNVAPGNALARTFALTSPSIERVVPIQCLPPPPRVRQLFE

>contig24562-1 Frame-0R1

MRPIATLRRQTSKPSSRFFSSNNSSTFNNL

>contig24562-2 Frame-2R2

MEDTTSSSSDTKLVFTDSDTNAANSDASQADLQAQLALFQQQQQQYIQQLM

>contig24760 Frame-1F

MDSGSQDEMVDVEYPVTSSNDQWRVFLGLALLVAAYVLRVEVVRFSLRVARRIVPALFVW

LREFEKMLLRPLSWVVFVLLAWFSAFVMDLKHLLNMETGSLESIVTLLLGPPLVWVVICL

CNYVTWGIVRVQGWSRAVSKDDDDYSRVMIITEGIGVIKVLLVAAVVSTCIIDEVGRYTD

FESGQVSTVAVVMVEFVFVFGAHSWLKNIMGGLMSLKDEQIKSGIHVSFQGHEGVVERLF

LQGFSLRQYDKGLAYIPNSIILENSVTVQSKSLDRRIVIPLHLSHSTPTTAIRIFIQELD

NFLTQHMTDIRINKKNHVLGLEKPRGGWNMMHLYERSKELATEESQSPGGRFWISIEAPY

LVHVVYYSQERHLKGILAEKTQIVLQITETLLKLQMSLYGEEPSSTELRASATSSEIGME

EQASCEQFSTLNSAPLPELSRNHRWHESAIIGPPDQNDANLLRHRRPHDNRSDLI

>contig25907 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67982.1|) 2e-32 NOT\_ORF

MLRYYTAATFCSIFSTKVIAQDVYTLNFKDNPVQAFRYFLGLFPVFTVKLTL\*TSHGNDR

FISASFPLICITLRENIQYLVLNMSESVPFSAAIAPSSWMCGFLKPNIFALLALLPPLLV

AFFTEDVSMLVSFTGAYAGLCI

>contig26498 Frame-0F

MIEHGEEESSHSNPLNSDTTTVGHQINFDSRTSTWTDDRSPTDVKDVDETNCSNATTEQI

KDSHWSVVSTQAQCLQEVLTITHQLLVDALECNLVRLEREGQLRSVTVEEIWRSCSSVLS

FEFFTAQIGLFEMNNISMEVDHPFRALIDILDLDVQNDVVASDSDHSEGHILSPRLQPQL

TAENHCVLSSVRRVLEWEKERLQQIGTESNKLNQLVASLGFPSVEGTALFPIICTMNHSC

DPNCTVMYTQNGNGHVVAIRDIQQGEELCICYIDIDMDVQMREANLREYKFKCFCSRCVQ

ERQQLEQQPPHQIM

>contig26689 Frame-1R|Blast-SEC1 family transporter SLY1 [Phytophthora infestans T30-4](gb|EEY53279.1|) 4e-97

MDRTEDIAASLYHPSTYQALVDDVLSIEMNRVKVRVKAADGNEDGMDGRTVERTYDLDVT

TDNFFKMHAGSLFPDAIDANEEEMKQVSRKEEQIRAQAGGNDALMNGTKDLVAAVDTLPA

LVEKKMMLEVHTNIFHAAFECVTKRQIPSYSMVEQKLIDGLHVDKAEVLQLLSNTEMGTL

SDKMRLLMIYFLSSGASEAEIAEFETAYQQCAATLEQPEAHMQAWKFLRKHSAFQRRTSV

GATLQTESGAGPDSGVNMNKFKGLAQGFLAQAAASFKNFLPENKKLHVTRVTDAICEMKP

NTEDESFLYLDPKIKANGDVPRQRSPFREVIVFMIGSGNYNEYHNLMAYAKGQQPPRQIW

YGCTELLNPEAFLHQLGSIGT

>contig26744 Frame-1F|Blast-transcription initiation factor TFIID subunit 1, putative [Phytophthora infestans T30-4](gb|EEY64028.1|) 0.0 NOT\_ORF

MNLSGRTCRFIFYGCLRKRATGSD\*RLRILHVRFRISQGTAIRKRMKEVATFERGGNDSG

WWKKKPTSQLQSEEEIRASIPPESVCLYESMMSGHRRLLDIGLTKLFTPSGVNGAINHLI

RRLELRKNALSTRLVALNLERRAREKAQAELWKMDPVVRKLEKDIQVARYINEQLQLTPW

NLTNNYVECHLQGKGSGMLQLGGIGDPTGRGEGFSFVRVPQSRAKKKDGEEDVAPTAESK

ISAETAAVQKAVAAVTGTTADLRKLKMKEAGDVLRNLGLADADIKKLRRWDRIHMVRELS

SRATAHGVAGSLSKFARGARKSLSAQQQEYRKKCDVIYERQMDVLSSTKTTFSSDEESDG

DDELDELGADVEADILGGTDTKRGPKNLFRSGGGGLNRSKEVLAEREDAVELRRLMEEMN

EDTGLNANGKPTSAVRRPDVDTNGLRNQLRASG

>contig27329 Frame-2F

MTPISDDACRVCGKEDDEEFLVLCDGCDRAFHTACIQGCTCCNTKPRNNFARKPPVPDGD

WYCKFCAGRIPALEEGKMSVSSVFVWGDNEDGQLGLPDSDVKVIWKPSKVRELEGIGVLA

IACGETCTYVLCNDANIYSVGTGLSGQLGHQDIVHEKLVHFRKLESVTEDKRSKGEGRFS

QIHAGSNFGIAITTEGHAYTWGNGELGQLGHQDNKNKKVPKKISALRELEVPVELATCGG

DFVIMTSKDSGDDDQFNTKKPGVFMSMGSNIQGQLGDASNKNQWVPQLLNNNASDFTNPE

DQDINDPAEFLLGRDITQLAAGKSHAAAVVAGTKSLWTWGYGDRGQVGHLKPSPIEGQSK

FFRSQFRVSRPRFVQAFKSDTVKLVACGAQHTLVLLTDGRLFAMGDNEYGQLGVKRGMTL

ESNCVDTPILVASFGVDKCIKQIGCGDDFSAALLTTKDVYTWGRNQLGQLGLGESQIALQ

DMPTKIVDLPPIQKLAIGFNQVFAIEFTDETQPPPVVRATASKRGRANGPDASSKKAKR

>contig27804 Frame-2F

MKVFVMGRWVIALCDVRVLFRFKRRRLKILQPFVLAEWRRNTVKNLATMQSVFFYLVVAI

GRNRHNVVFGNASTQRNFL

>contig28258-0 Frame-0F0

MYTSSAPGPTRGRGGNPNAGVPPQQQPQQLRGPSAGNPGAPPQLATAATSR

>contig28258-1 Frame-1F1

MRVCRPSSSPSSSVAHPRAIRAHHRNSQQPQRAA

>contig28258-3 Frame-0R3

MGHGAAGAAAGAAHPHWGCRRGHGSGRGQTTCTWQKE

>contig28401 Frame-1F

MPPEHVRKIIKDHGDMSSKKFRHDKRVYLGALKYVPHAIFKLLENMPMPWEQVKDVKVLY

HVTGAITFVNEIPWVIEPVYIAQWGTMWIMMRREKRDRRHFKRMRFPPFDDEEPPLDYGD

NILDIEPSESITMELDEEDDEAVIEWLYDSKPLIESKYLNGPSYRSWRLPVPIMANLHRL

AGQLLSDLIDPNYEYLFDKKSFFTAKALNVAIPGGPKFEPLYRDVDEDDEDWNEFNDVNK

IIIRHQIRTEYKVAFPFLYNNRPRSVHMQPYHTPVLCYIKAEDPDLPAFYFDPIINPISH

FRVNRIAKDQSKTVEVDEDDEFQLPMGFDPLLTDEPLYTPETANGIALYWAPRPFNLRTG

RTRRAIDVPLVNKWFQEHCPQGQPVKVRVSYQKLLKCWVLNSLHHRPPKALNKRCLFKSL

KSTKFFQSTELDWVEAGLQVCRQGYNMLNLLIHRKNLNYLHLDYNFNLKPIKTLTTKERK

KSRFGNAFHLTREILRLTKLIVDAHVQYRLGNVDAFQLADGLQYIFAHVGQLTG

>contig29543 Frame-0R

MWYIQVIHLFTGWHLSHRMAIWLCFFPLTPFTALKIYKASRMCVPTRSHDGSSINDHM

>contig29961 Frame-2F

MHESYSSPHETRTDLTQSSSSSNELDISMGPDDDNHSFLGPLPTHGPPAIAIKHANLRAS

DESMGPDSPITKRGKHPNLMYDTVPFSTGNPLATSQSSMENFHDRSSTSVLSASSVSSIS

NRDSMATAVSRSAYVASVPLLQHPSTYYGEDLSTERASTESTDSANTTRSGSLIALDLKA

KGSCSEIAI

>contig30075 Frame-0R|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4]gb|EEY67457.1| HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY61445.1|) 1e-90

MRSIANQLYVFLKGIYEVLPQHLLMLFDHEELEYLICGSPEIDVDDWKGNTLVAESVARS

PTLGWFWDIVREMPNEYRRRLLQFTTGCSRVPLVGFKGLTSYDGKVCLFTIRGIVGAPNE

FVRSYACFNRLDLPLGISQCELKSMLYAVLDTEQYGFTTD

>contig30141 Frame-1R

MASQCCKNGSLNTFQFDDFLHYALLEICALQKTPSG

>contig30479 Frame-1R|Blast-delta-1-pyrroline-5-carboxylate reductase [Phytophthora nicotianae](gb|AAM10930.1|AF466195\_1) 6e-34

MLGSALYMQSENVHPVELRNKITSPGGTTAAGLYRAEKNGFRAVIADSIWAAYERCHELG

LPEPVQRQRPRS

>contig30516 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69609.1|) 1e-10

MLQHLWDGLFSTLPYEGRVNERWRDVGFQVRVSVVLFL

>contig30563 Frame-2F|Blast-nipped-B-like protein [Phytophthora infestans T30-4](gb|EEY66198.1|) 2e-67

MQDHARTIILEQEFRRKSACMLCLVERVGNAAEDQALKKFIMDIFQEVWFGANRYSSENL

NLLDAPRNHSNLPGSGTAPLPVKSGKYDMTTSSDKNTKFVSEDGSFACAIEEGWVSSQVP

TVMPSCILKSYDYKLDNSAEVIATIIEVTHGTPNREWFTKLLKSLLVKSREKNIS

>contig31256 Frame-2F|Blast-inorganic pyrophosphatase [Phytophthora infestans T30-4](gb|EEY54450.1|) 1e-120

MEIAGTEEFNPIKQDERKSAPRLYHSASLVNYGCLPQTWEDPNYVDPSTEYGGDNDPIDV

CEIGSCVARIGEIYPVKVLGVLGMIDSGETDWKVIAINLNDPLAAKINDLKDLQNTPLYD

VVHHVHRWFRDYKMPDGKPPSDFAFDGKAQPRDFAIEVIQQTHQSWKQLVEDKMTSKTKL

WTGNTTNNLN

>contig31397 Frame-0F

MMMGSNDKVTSLELAQVFFERLAASDKEFKIFEDYFHALFDDPEHDAVFDHLDNWLKTRF

PFPESVLKDTIEEGEKDAEAKPIIAEVGLDSMEKVKDAKITSKESEISEASDKKVQIPEI

SKKVEVTDDGDGNAEIVAIVKDAEISAGSEKVESIDTSLEADVVVVSDEVTERSGKAELT

DVGDEKVENIEIVKELKFPVVSEKVESVKTVQETEVAVKSDEDFKIFKKSELTDIGDGK

>contig32554 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69925.1|) 1e-71

MIRSYIDALINAGAEKKKLVVCHADRWCYRESNGKVSSFLLEVFDRGVSVLFDTIGLIAV

SDVMLINSYSPSSAELPGTNSQEPPTHRCIARTIANIIKINPQYCHQLLLSTNVHQRIQY

RRYGGGGYTYLFKYFKTYVLGQGVSAAQWDQIVRGNVVKLWAWYVPPEVPPIPKNYLQCS

ICDKHFEPIEGEYFTKFTFIYCGTKCLRRHSRQNFVSLH

>contig32929 Frame-2F|Blast-developmentally-regulated GTP-binding protein 1 [Phytophthora infestans T30-4](gb|EEY66827.1|) 1e-175

MSSAMTKIAELEAEYARTQKNKATMKHLCLLKAKIAKLRREVTDAGTKSSGGGTGEGFDV

NKAGDTRVGLVGFPSVGKSTLLTKLTGTFSEAASYEFTTLTAIPGTLNYRGARIQILDLP

GIIEGAKDGKGRGRQVIGTARTCNVILIVLDAMKPATHKKLIEFELEGFGIRLNKKPANM

VFRRKERGGIHFQTTVPQSELDADTVYQILHEYKIHNADVTLRADVTADEFIDQIEGNRV

YIPCLYVLNKIDQLTIEELTIIDQIPHNVVISAHHGWNLDELLETIWDYCHMIRIYTKPR

GRLPDYNAPVILHEESPT

>contig33027 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56110.1|) 6e-77

MERLERSARAIEGRTMSDEPRQFGTQDRPQTSVSVRPDSCRDYMPMVSSILRVSWLGVAL

VLSQVASRRMSVFAIYTTVEIYSDANCESTPLVVTLERMNTTCTPSGTCHAIEISNSSYY

YAQRCATNRFQYTSELFRGAKYLMIDGFQDANCSSYARSNVFLAAGTCQLASYIGQRSEI

ATLFNDGSAYMTIYKDSACAKKAQVLNLNTSIIQTHECYKGYNKFYTSEYTGISTNQGSA

FNDSANPTTLSLQDTAMSPSAVLGIILMCSAIIVLPIWLSIGNSV

>contig33944 Frame-2F|Blast-DNA repair protein RAD50, putative [Phytophthora infestans T30-4](gb|EEY58381.1|) 1e-107

MSSIEKLSIRGIRSFSPNREEIIEFYHPLTILLGDNGCGKTTVIECLKLACTGGLPPGAR

SGQSLVHDPKIAGTNEVKASIRLRFRNRASKVMLVHRTFQVRQTKKTITFKALDGVIRVV

NELGEKVSLNHKCGELDQHIPDMLGVSKAILESVIFCHQEESNWPLREGAELKKRFDYIF

ESARYTKALEAIRKLKKARLDDVKD

>contig34347 Frame-1F|Blast-peptidyl-prolyl isomerase FKBP12 [Phytophthora infestans T30-4](gb|EEY61067.1|) 3e-47

MGVTKDILAEGNGATPTKGASVTVHCTGYGKERDLQQKFWSTKDPGQTPFKFKVGLGQVI

KGWDEGVLGMKLGERARLTCTPDYAYGAGGFPAWG

>contig34721 Frame-2R

MLDIGPKSSSHGAGKAISSLLSTSKDGSDRIPTSSGPSTQKKRIRIGYVASVRKAMKEAR

DAGKNEEETKVLRTAAMDRARERLHVPYKNARTGPSKPLGKDEISHIKMKMLKLLEEDAP

AEELTDIIELLLTLIIPRAVLIDSGMQRQLELVLIAHKDNKELVRQTKKLQEEFQSIVEN

GDSPSVMAAMSGEATSSKNRKEQSRSLLLSVDTEHLPGTPGSSPNSGPTPSPESRRPRVK

FSLAQLVKLEKYFHKEDTPSKKKLDKIAARLNGIACMDPSSDAAQRSIDYKQIRCWFYKR

RSANQPPQALSGTDLHIDKAASSSSSSSDTESDNDSKSDRIFMTSTSSKAKG

>contig35252 Frame-0F|Blast-iron sulfur cluster assembly protein 1, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63986.1|) 8e-68

MDKTAKDVGTGLVGAPACGDVMKLQIQVDENGTIVDSKFKTFGCGSAIASSSVATEWLKG

KSVEECLNIKNTDIASHLKLPPVKLHCSMLAEDAIKAAISDYKRKQSDSG

>contig35704 Frame-0F

MPVSKGTEAANYNSDSDGAPEVLTKESATEHAIAQQHQVKVARAQAQSLKNARRKRKTKP

EAELKDKT

>contig35861 Frame-1F

MISRILLLTAVALLSSTNFVVAAPNEKSLAALEREKSDSIRTMRNFDTISTAGSTNTSRG

QGSPDGKIVSSNVNLEERGPGVLRTIWLAITEPINSYFRLRGYKPSDLLALEKNGSRLQR

WLYSTYASHFERVSKMSKKAANQ

>contig36051 Frame-1R|Blast-DNA primase, putative [Phytophthora infestans T30-4](gb|EEY63518.1|) 0.0

MQNVGNSRRRAHVPRHGISMLSMYNEAPLIEVSLEQFEEFAIDRLHVLKAVENYRLRSMQ

MKDREIRLEKTLAKHMPLRFTISKRKGQAEDDTAKDVLSHFFLRMAFCQTEELRRWFLIQ

ESTLFRYRLDKLTRDEKIQFMKENGLSYEEATKKEIEARQSKLKAVRDANDLKIRGQPLP

AFFKVPFTEALDLLATRRVYIETGTAYVPFEHVVSILFAAFRANLSKELSGAFRKYNRSL

ISKDDRLAPVLSNLAIHHIDADYSSAPVCSGENAIRPDRIDSLAAISMPLCMRSLHKGLK

LTHHLKFAGRQQYGLFLKGIGLHLDDAIAYWKQEFCKTMSVDDFNKKYAYNIRHNYGKEG

KRKDYA

>contig36208 Frame-1F|Blast-26S proteasome non-ATPase regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY68827.1|) 0.0

MAVATGSSAAGVLALLEEEDDVLKTHALQRLNQVVDHYWAEIADAIPLIEELSEEKSFPD

RELAAYIASKCFFHLEEYEDALRLALGAGKHFDLNTRSQYTDTIIASCIDSYVAVRAKED

LEAEKALDPRLTQVVERMFERCYAAGEFRQAMGIALETRRLDQVRECLVRSTDVSAALSY

CFEICQTVVINRHFRLKVFEIMLEVYCSRPTLEHASVCQILQMLDNHVEVSKILDQLMRG

SDNDCLIALQVAFDLNENENQKFLMNVYHALPSIPTPIAETTTADSTNTAEEGKIEVSTP

AAITSIIPTTPPPAPADASADYWGKLAKLKQVLSGEFLVDLKLDFLHSHSDSDPLVMKTI

KSAVENRNSVLHHAAVIAHAYMNCGTTSDSFLRENLEWLGKATNWAKFTATASLGVVHKG

HIRESMNLLAPYLPQGGMATSPYSGGGALYAMGLIHANKGYAGSDSKATMEYLRSALKNA

GSDETIQHGACLGIGLCGLASHDYELYEELKAVLFTDSAVAGEGAGIAIGLILLGAGGEG

RNGDIVKDLLAYAHDTKHEKIIRGCVMGIALMMYEREEQADTLIEQLTRDKDPLIRYGGM

YTAAVAYAGTANNTAIRRLLHVAVSDVSDDVRRAAVTCLGFILFRTPVQVPKLVSLLAES

FNPHVRYGACVAVGIACAGTAKNEAIQLLEPLLDDAVDYVRQGALLALAMVVMQESEGRN

PKVASIRAKILKLVTDKHVTTMTKMGAILAQGILDAGGRNVVISLQSHTGFTKMAAVVGL

AIWAQHWFWYPLFNFLELSFQTTMVVGLNKDLKLPRSFELTCNAKKSAFANPKRLEEKKK

RRKS

>contig36419 Frame-2R

MMCGLCFEDGSLHVYSLPDFQKRGVFPYLTFAPQSLVNTWTGTLAHESMESTAPVLGLHA

STSLANDMRIQKAHAMNSPVADIVIHRVGPSEGQMNASYLARMVLLVFLANGDLLLYAAT

PTHDRLQSRSSSPI

>contig36730 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54546.1|) 1e-150

MATTMAPAPPYMLGERPTPAHGGSGAPSFRQVPFVRASERVESGVKVRKQLCKYLKAASA

TQHMVAQAHLSDACLPALQPQEVAQSCFQDFFTQMRAYSQALGTKHLAASKAYMDMTKPL

ENSGKSKRWARDTYNLVQRCVSDVQVATKKMDKARQRVARAADELANWKTVLAANEATFQ

VQPNNPEVKRAFQTAQSRFTSAFGEDEAAGAEYDDVRTLLISSIARRDEVVEEATVLSQS

VEEDRLDTLLIVLEQFVETKVAILQAEIEAMVDLRRSLKAVDRDSVVQQYIVDSMTPELT

>contig37360 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61205.1|) 0.0

MDLSLFASQEKMGVLHGKMNLAPGMNTLDMNGYLQPNRNTAGEVSTAVAEFFSHYLGGYS

SRVIVTIKGTQYHNCIWMQEALVGLTIGTSFPGVGKGFKMIQNINLNRLDVILNQKPLDK

RASMTNTRMLVRTDMRGQVKMPPSINIPLKIVNLSVALTLENEHGAPLGVLVSGRESCDF

NQTDAGAFRFKMKNFYTIGFENDENVREMSRFIQDLLTSNSSIIMRLASDDAANRGAFPD

VETRIGMLALSNIPVVGAPLIPPMDSFRHPPVKVLHVDIQRGSPSSMMMRMMFSLFNPSI

VQTKLGSLVLHVFFEGARMGLAKISDFNLNCCGKQTVLSGNFVYQPQVSDLATANRFLSN

FVCGYYTHGAAQEIIIKGSASSTSLDLLQPAMKILTIPSKLPTMGDLFPAAPTLVSKSLL

YIPSPFHLTQIPTSLQLRNPFSENITVTRVDVELYPCEDQVAENDGKLTCNKYFAKSLAR

FAPAIFEPIYIPAKKNSCYSCCQGYRCSDYVHLCPRASVSHCMNADIQSFFTPEAIAVII

HSLTGGLLMRINGTISALIGDYAAHLLYKQDGLLVTIAK

>contig37478 Frame-0F

MSRGVWFQLVKREGNTIGSVSFVECAENAMVARLRNTIKK

>contig37632 Frame-2R

MMLFPVRMKDLINSKIMLLCVASIREQINGAYDSS

>contig37805 Frame-1R|Blast-protein phosphatase 1 regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY62012.1|) 1e-30

MDLGGNCIANIPIIMAPLTELEDLWLNNNQIAEFMDIEHLRPLKGLRTLYLEHNPVAQDF

EYRKKIEELLPALDQIDATQTTKARRRLIN

>contig38112 Frame-2F

MALGKKKVSSMVYYDLMGVSADATPEQIKKAYRKKALQLHPDKRGNTPESQEEFTRMKQA

YDVLSDPQKREVYDQVGEDGIKLMEDYGNMSPEEMSMLLFRSMGAVGAKGKCILILLVSA

LFAFFLLIPIFWCLRADATISWNWAVVCIPLWIADAIYYCCLGCVLASSDSHVDAEEEVK

RKPPLYKLYSFFKALLLLVLQIFIALKLNNDINWTVIEVLVPYFIYDGLNQLQALAGGIL

GYNMLTKTSEGAGVSQTETITKQRSALVAAVLKKVLLNAARITQAVLLSLKIDGDLKDTS

WWLVFIPVWLYIGFFLSFPVRKYVRGKTRTPKPEPETSPQQHDAYTRESVAKDEDEAVAK

FPLLDALCTISVILALMSPFLILSARLQNGSFSTIFVLLPWLILVGLVFCFICCAISCIS

LNDSDDGNTRDQATAPNARGSPSTEEGAGARADYVSVDMD

>contig38527 Frame-1F|Blast-retrovirus polyprotein, putative [Perkinsus marinus ATCC 50983]gb|EER15822.1| retrovirus polyprotein, putative [Perkinsus marinus ATCC 50983](ref|XP\_002784026.1|) 1e-08 NOT\_ORF

MGISSAPDKY\*ACMEQICGDLSFVVGYLDEILVFSLNIDEHLEHLRIIFER\*TKYEVLLK

VSYPPQGR

>contig39267 Frame-1R

MLCSLMFLLASSIDLKGLNVVSLKKEECHNIHFLICSDLITPKATSTKQLTSMLDQLKIV

LSRPMNSTTTRVEKHYDDLPQSSLKMADPSTAFERSGWSYI

>contig39858 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66390.1|) 2e-85

MPAYLQQTIVNLVTVKDASTTQQALQNMHSGVGLCKQDCIEVLETYLAEQVENKTVDIDA

NLALLKLYQMYPSVASAKNVALVLIKGIMALPSTFFTGASTMVPENIREDANVSAALRAG

FMLQSCLFEEFWKERGTLADEVPDFLESVRAYILTAVSHSHSVISTQVMKAKLSVPDKEV

ADIVAAMQWTAVDDLITIDSNENNQMQAKKVQEKIDFEDVLKVIRVLSR

>contig40443 Frame-2F

MNLKIIETAEDLAKYKLLLLFAQSTSTSFAAFEKNVSILAPETLVQLYSRSTKDDPYCAA

LEAVIHENWYRMQASTEELFNLFQYDKFEETVLKNPLLIIVMKFAL

>contig40861 Frame-0F

MLFQKRSTRTRISSEVGMHHLGGKALFLSSDDIQLNVNETLRDTALVLSRFNSLLLARVY

GHQDILDLSHFATVPVINALSDKYHPLQMLADYMTVKEHFGYWSGLTFAWVGDGNNVLHD

YMLAAPKVGAHIQIATPVGFEPDEDVVKETKRLAALAGTRFVMTNDPLEAVKNANVIATD

TWISMGQEEEAQKRIKAFAGYQVTSKMLENAAADHVFLHCLPRHQDEVVDEVFYGKRSLV

FDEAENRMWTVMAVFAALLGKF

>contig40982 Frame-0F

MADTKKQFTSKSKDNLTIKAIDLGLQFLKPLIHSTVLLADALDDKQEAAGQRGVLVAALL

YLFTKAPKETAIQLSLVTNMLECGVEMHVLVATFRFREEVEECSRVLLPSIDSDLELDLA

NLDNDMIEQETEWSHEDTQWITERLAKTYGFTAYQYFLSTSGQEHAFAAWSTSGIAQFLH

VMLTNEQLGAKALSAVVSPYSWLYFIASYAHCMIVSKDDQQKSP

>contig41259 Frame-0R

MSSLEAQIKKQVEFYFSDSNFRRDRFLLEETKTHDGGFVPFSVLFTFKKLAALTVEDSVL

QAAIADSDVVELNDVKNALRRKNPLPEQDDASERTIVLAGLGKVLPTIDEIKEGLKPLDV

ELLFIDRKSFRRNFSGVAYVELMEKEAVKRAVETAASLSINGYVPNIISMVDYEKLPIDE

RIEFDKATNAMLVAKNVPKRPLTFFLDELLPIWTDNAKLQARVRYFESTKELYLLFSQIA

FAEIVQKRLSDDLPISLDDQKLVFELITDREAVKARPRRPQRDMDERNSNIKRKRDDEKV

IHISNIGPRTRLDDIKQLLATVSDQSPYVEYDGLDTASFKVSVTAATSLFEKLVALPVPE

LGGKKVSFHLLDVDEDLKVDVQYKEGLIVHFDDVKGEISRDDIKDAINEKLGDKANDGAG

VAFIQYQINDKGGYLRVTSAELAKDVVNMFAEGGLDINGVKIPKAAIIEGEEEKKFWEDA

RSARHKRFKQSRSNRSQLRGGRGGR

>contig42162 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61350.1|) 7e-10 NOT\_ORF

MGSNV\*SSDGPAAEWELPSRRRLLIANSRYKYESCQILDLGGRYMLLIIAFFLVLW

>contig42632-0 Frame-2F0

MQDALLTILRGARNGLLYGTKVRAPH

>contig43051 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65717.1|) 0.0

MVNLSMDSSVIDSSSDSFDQPHPSIGLINSGGSRPSDSKFFALTVSNTNISGKSSQYATP

FVYGTPVRKNYKTWPFVTVGLCATIVLFAVVYHELPEYRLGFRYRLYVVFGSTIDNAEWV

GGHREVVEFFVNYMLIGVPFMIGGMALALGDALPPAPTGGHRTIFRFLKRKMFVGAINIS

YAESLCTLVFLGLNAIWFSATFSRNYEGLVKAESTDFASVFRLIGQVFGSNAVLCFSLLI

LPATRNSFWMISVGIDYSHAIKYHRWIGFFTVTMVALHAIPYYYGWYKSGTIIESAFPCM

DCDYGTVGKARLQNFCGQLALLCCLIIGVTSLGPIRRKYYDVFYYSHHLFLFVLFLSAMH

FSQFVIWMYPAICLYVMHRILARSQSRMPCEVVDLEAIPGEITRLVFRRSPGKSGHYHAG

QFVYLRIPLLSHTQWHPFSISSSPIEYEDTFTVHVKCIGNWTQSLYGVAIQAREERKMPL

IYVDGFYGKMSDDFQHYPALVFVAGGIGATPVISIVGKILDCMRNNDPNVEFTEVYFHWT

SREIGIFHE

>contig43293 Frame-2F

MVGYEVYDLDGKTLSDLIPRMSCATKREMFTNNETYTASFFGVSRTAPTAESNGIDKCKS

QTPNCYEELNFERLEDRNCYQRRMYGTVFIPQKVRGRITLKVQNARFERKSTGIRFNQDR

DRESFAATLSQRYTMNKSVPRCEINRDNWQRLMKNGLGTVNLHYYNREDAEQASQVFTDD

LGEPLQIQWNLKAGARIQACSTLLNKSRAQSTPLRSCSSERIAPAPSSHSSQIDSNTSPR

RQDFEPTAGGTHRNSRFDRREHPTRHFREQSRYAPTLSKRSHVLSERKSRSRSRSKSVHM

QHYDFFGPANRDEYRIKNQHDGPATDNHARIDGGSIHARNDVCDDISRRRARNMPGSYPY

NGHHRGMCEDSDRSVWRGEVLSETRSRFKSEPNDAADSFDNGFSSREEQRAYFSTDLWEK

KPQFAKARERRDRFTDNFRDIRPQHYSGQQQLSRNMGNTRSRSRSRSRPRTVWPARGGLS

DQNMRNDRRTCGRGGYDNRCGRRSNYGS

>contig44223 Frame-2F

MDRFNLSPSKQQSICGWGRSRQMEEKTPESSSEPSLNFSTYHSTSLQNAAQSLECPKMLF

DPVTGVMVNAHDELKRRTDGRNAKDRTFLEPTVASRRCKG

>contig44397-0 Frame-2F0

MTRPRATLQEDSSAVLYWIEKSMEGG

>contig44397-1 Frame-1R1

MDFSIQYKTAELSSCSVARGLVISLQKCKRHSF

>contig44670 Frame-2R

MIIRRKTSSMLQIVGTVVKKNCFCFPFCLHLLSSRNPFCPRIRKSLVRIRTCNDTCLFNI

SPRRYLSAYLAKSHEWHNAASFSKTSTFVNRFATCSFERTYWAASTPRLA

>contig44894 Frame-0R|Blast-glutaredoxin, putative [Phytophthora infestans T30-4](gb|EEY55291.1|) 2e-67

MSGLAKLVATFTAGSAVGVAATVMMFRQPKHTKRLPILYVYDHCPFCVRARMIFGFKKVP

HELVFLANHDEATPIGLVGSKQVPILQLSDDHAFPESMEIVKYVDERFGGPAVLAPSANR

PELARWIEESAGVFRLLYHPRFHAAPFPEFARLESREYYRKKKEKSIGPFQDALDKTAEL

VEQANGFLEQLAPLLRSTHSFNETLSYDDIDLFGRLRGLTLVRDLDWPSKLRNYIEHMSE

KADIPLLDNMAMH

>contig44911 Frame-1F

MGLGKTLQVITTMQAFLTKKTLDENGALTNRHRHVLILAPTICVRNWEAEVVKWLGKKEA

RRLGLFTLESSREKKMSDRVHVVKKWYKCGGVLITGYELYRLLVLQSSGAEKIAAGNQKY

AHLIKQAYKCLCDPGPDLIVLD

>contig45075 Frame-2F|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY63900.1|) 2e-44

MYVTCFMRSNTNEDSIEQKEGIPSRSIHAIVTILLLIAQVLGALQAPGLQVVFSFVGASI

LWILCYLFPLLFYVRLTSWRSSRKSIARMVLLSIVAVTASVFCIAATLQLVQD

>contig45224 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58346.1|) 3e-23

MNTYFNKSPFIMLEVFNDSDCKHLSYVQGYYVSGECEGTRNVDSRQVNHVVAKLNAHGCS

LEFLQRFLVHRIGAVSYVYSRHQDS

>contig45563 Frame-2R

MLKILLLLEFKCFNDKRLIFYYRFVCVATV

>contig45725 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59543.1|) 1e-15

MALLQHELVVDGDIMQALDMCRRLLRTENSYQRIETAHLVLERLRSNSTNDSVDDVNALL

RL

>contig46328 Frame-1R

MVPLRCIVARVDGMAFLWEWQADLCQWVFLNRVCFLENPNLKWTKPVASFTTTDMPFDSR

LSDHSGSSGATEFVWWSTATKNEPRLKLRQLRFERATDALRATDVIVGSAFTFKPVCDDL

VALLSSKLGLFAISRTQGLFFRSSTAS

>contig46412 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70271.1|) 2e-12 NOT\_ORF

MVTFKHESITIAGSAQEFWETGVRQLRCVENREF\*RSETKIIGARLLLCQSKLKRNPESR

HLRC

>contig46485 Frame-0R

MSRLDVTIPAPSPNSELLARAMISS

>contig46944 Frame-2F

MNDPDFTRNHNAFRPRSIGNMLSGSAGESESLHNGNRMGGGGVGRYGVCDYRNQQFDRSF

DRSYDRPFGYQPNGGALPAPSPPMFMGSGRGHDHIGAPDFINRLDTHQYQRSPNQQYYPQ

QQFQHHQLNMPAPTLVGRGGYGHSSLQGRASARQVNWVPPHANIRAMGNGNSGFIDDDFP

PLGK

>contig47136 Frame-0R

MCSVLQRARGHNSLRCESAATRTAGPGGYSL

>contig47204 Frame-2R|Blast-vacuolar protein sorting-associated protein 35, putative [Phytophthora infestans T30-4](gb|EEY60193.1|) 7e-64

MGHTSFVLDDEGEEALLREALQTVSDQGFRLQRAVDSNDQSAVLKHTSEVLRELRTSLLS

PKNYYQLYMQVMDELRHFENYVSDQLQAGTSMKMLYERVQSSGKVLPRLYLLVTVGAVYI

KSQEAPVRDILKDLVEMTKGVQYPLRGLFLRH

>contig49233 Frame-2R|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY56511.1|) 2e-57

MVTDAAAVKIGEGSSAEVYKAQWLGITIALKCLRIRATDSSDAALYMTHLAELRTEFLDE

AVLAVRLRHPNITLFMRIGTFKESLCLVTEYCA

>contig49246 Frame-0F|Blast-hypothetical protein PITG\_09210 [Phytophthora infestans T30-4](gb|EEY55283.1|) 1e-15

MEVMDDKENQPPEAAVESLQEELPLPTVRYAGAQDQPTQILHFGESARSLFMLDKPSEKR

LRLVIALKDAPRSVAKWLELLRCPLTGNPT

>contig49505 Frame-2R

MERQDWNSIGGHAKPKLALQQALEWPLKYPQTFTRLGVSPLSGLLLYGPPGCSKSSLVRA

AAHSSGATFLSLSAAQVFSPFFGDAEAAVRQVFRDARAALPAIVFFDEIDAMVAKREFDE

SNDRGTSCAMRVLSTLLNEMDGVDSTPGLVVIGATNRPACIDAALMRPGRFDRIIFVDLP

TEADRVEILR

>contig49592 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70150.1|) 3e-20

MEFDEHEVQSLGTSDRTKVALKLLKSLYGLKQAGRLWAQLLHDTLVKLGFTQCYTDSCLY

TKGDVSTITLVGVYVDDLLVTAK

>contig49978 Frame-1R

MSERLSSIYGGRCYIDGTYDSILLRRKRGILSHRSKLKYRSHFPSTESSHLDVFRKRIFL

ELDSWVGVAMYGSIPKSKSLRNFLASLVVDWTYMMYKRTIK

>contig50257 Frame-1R|Blast-hsp70-like protein [Phytophthora infestans T30-4](gb|EEY65065.1|) 1e-82

MSVHADEVVCEGAAIQAAILSGMDPKVFRDVLMMDVLPLPIGLEKADGTMEILLPQNARI

PTSVTKYFETHDDGQRGLTIEVYEGHEAMAKDNDHICYFNFALPRNKIGKAGEFTHPVTF

TMNASGILQVQAGVHHDAEESPMSKTAIYLMGAYIFALFGLYVFFRIYFVDKRDITA

>contig50631 Frame-2F

MSASISSSHSGLWNTAIHDHLNLSAEESCSLVNLANQAVTDTVEGYEKFRFTDDRVVNLR

TWKDVGHRDNVVVYRERSGRRPTYPSIRAMDGSMQLIPCKSAPSVKIVGVLQGTLDDEMY

GCFVDSDDTVKMRSAVLGDMVENFHWLATIARPSPEDPFRFCGVARCTLGASVPLAKTRG

ACLVISMGMTTTQHGERMGYYVAHSVELSEPINDDSYIRAKCSLCWIKTELTNGKVELYM

KGFAAPMGIVPEFAAFPVLVRCVLGIGMTSDAAYSKKLAWMIHDTEKAGERSPLLLMNDC

VGRCKKSFRGLKSKAMVRRCHVCRKNVCSTCQVVRKIPIGVTNGTGGINKCSICILCIHR

AKTMSAVLFVRRDLHSKRWKSIDAPRTSITTSTEREIMLTERRFYDTR

>contig50954 Frame-0R

MFGHLDATCSPKSCHLCINFISIPPLIGAIIKRLLHVNPKQRPSAYEVAMALQENRQAQL

FSVYSRKKM

>contig51012 Frame-2F|Blast-DIS3-like exonuclease 1, putative [Phytophthora infestans T30-4](gb|EEY59681.1|) 5e-38

MNRGVHGDRVAVEAFHSSMWRTPQSDHMLVHYTQDEHEHELESGSIEFRENKHKLRTIPT

GHVVSILSRSPKQHVATIIASTVNAGDDYALVVPMDWRLPKIRIRSQRLDVLIDKRLRV

>contig51250 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64262.1|) 6e-06

MDWRAQYTQAVTLEEEEKVSKPTPVVMQQEKKRPMGKTLAFIDLLLNYEGGKWWIDHHAK

YSIQ

>contig51953 Frame-1R

MAAVTVLLLIFKFPHGIKLRV

>contig52071 Frame-2F

MAKLIRALDHSSLALCQYRNAFVRIHKDWDLALTLVRKVARYFHEMMLHLYEVIMGCATS

DVDDEVLLERAMSGDFKDEKEFRSELQLHCDVAASEDHLVRESYVFTPGLLVFLQKWRSS

RDQEVFDFHFAYNKRYARFLPRHASKHEVRDFKR

>contig52134 Frame-2F|Blast-SDA1 family protein [Phytophthora infestans T30-4](gb|EEY68850.1|) 1e-90

MALSFFLGIDEDILDEEEKQKKEKKKNVAVDFHAHSKKTKKRQRDTFAALSKNKRARKRE

INFRATFPAIELLNDPQGVVERQLKLLKSCTERFDVKLLMMNFIGRVSGFHKLVLLPFYP

LLQRYLQSHQLSVTAILAYLVQSCHNEVPPEELLPIVKSIAHNFITERCSSEVIAVV

>contig52765 Frame-2F

MSADCVILISKTWKSSVGMQMGTIARSLVINLGHQHSRVRTCALQALEAAVPCCSEALLE

LLTELLMPAVRKVVFDHAPSVRKQLVVTLAAWLSQINQVQQFDKLIFPAFLAGITDESPE

VRELSIAKMNEISTIWETRDGSEAVDENDMIVDEKAVRSTPP

>contig52901 Frame-0R|Blast-CENP-B protein; Homeodomain-like [Medicago truncatula](gb|ABN09791.1|) 8e-34 NOT\_ORF

MA\*IIFVE\*LRDFDRRMASRKVLRILNNCSARPAC

>contig53195 Frame-1F

MTHIPGKLTLNTHVAVLFKRYRCVLCLDASPSIISIDPSSGRLFLDLLYESVELFVWSLL

RPMEVGGIAFMPEIHMSVLVQGALVESLCVLMQGYIITPSNAAGFLQL

>contig53366 Frame-2F

MSLSPFDRCLRVLFNEFQAQNLDEITLLSFGYRFGASSIAASSTVSAHADLLEDSAWVLH

GGLESSRIRATVEHFSLDRQISTAGDALMLIQDAASITSDCTLNLNEAYDPAFLIPMLAH

FISSSVLSTAGIVQQGLLGLAIRATSSDCETMRQYAFGILAHVHELLQATIETTSSFAAG

RQVHLLLDVFRRGVRHPLDQVPSIVTVFLNDALAVLLRPTHVLYAPVNHFLLARTAIDLA

DVPMFYTLFNSQAPLTFRQERSWLLHTLRRGIRNDADVQLLERRHVLPMLLSFYSSELM

>contig53388 Frame-1R

MSYRSSRVLAIAARASAARAVLPACTSRLQTASLSTIYDRRTPFEDINRHRSDAEQRIAQ

VPIVEVAGSIAVCDGGGGALGHPVEYIQLDTRKQNTPQTCKYCGIRYMMKVGYHGGH

>contig53487 Frame-0F

MCESSLCYMQTRFAMGEWPIDEINTFALQGVNCYRQALLSLICSQDERLASTVVMLLVAI

VNSKAVDPSLLRELDLLPIRYRTGNAIFCQENLADHGESEENWQGDDQGQSDPSAALATA

SLSSSCDSADFQAIEEEGLNTNVANSSGPDCTLSCSEAYPSWLIELIIKLLARNQNMRLF

SVQLCIRLLIDVNFDTRRSFHAGLSEAHTLALRNIHSSSAHCVMESMRGGMAEVDLFIYV

VENEVAKFQRNVF

>contig53599 Frame-2F

MSAKISIISLNLGANLHLHMQGPRCYR

>contig53674 Frame-1F|Blast-replication protein A 32 kDa subunit, putative [Phytophthora infestans T30-4](gb|EEY53901.1|) 3e-12

MSSQPSGSQQTPTKRSSVTQSIFPVTIKQLQSLHASDDDVLRLDGQ

>contig54374 Frame-1F

MKLKTARCFARHCAVAKLLCLAALASFPYLRVTIRLQKNTITSLLGLVLLVVCSPIG

>contig54495 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58146.1|) 2e-35

MRRVQHPNVLQIDRLVSDHKGSNDYVAMVTEYAPHGDLFDLLEIAGALPEPLVKVYACQV

>contig54666 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68121.1|) 5e-26

MSWLRSKLRQVAARASDALAQAADMVAPTINESRVDEFHNRWISVARFLESVLSRDLEPA

DQRRLLLES

>contig54688 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69840.1|) 5e-54

MDDQELLLLAVLAQKIKLVDG

>contig54824 Frame-2F

MLGSLLSLARTSFAVQSNSRCYKNIGSSS

>contig55009 Frame-0R

MGRRGQTLYSITDQYRPQSLSKVRNINPDMIAYNYTLLARWYVEVR

>contig55100 Frame-2F

MWSFQSLVGSLLWVARCTQQDIASAVHKATRQTHQQ

>contig55283 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65049.1|) 4e-11

MIPKPLARFNALIEIIQTGA

>contig56105 Frame-1F

MRAAGIATRAAGIAKRATSSLLRHELEFMVMLIPGL

>contig56291 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70228.1|) 1e-35

MTAVVLPGVCFVALVCIALRLTRDHKKDA

>contig56646 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69867.1|) 2e-37

MGDLMTDVVANGSAVVASTNGLSGYGSAHSRTCVTFEQFGEWYNTGGYQLISWVELLDVT

KWQQQQDFQDQTIAMTTTDLTSTSQRTRTASV

>contig56862 Frame-0F|Blast-trifunctional enzyme subunit beta, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY60967.1|) 0.0

MLAPKSRRGLYIMGTSPLRPLSTAAAKRVVVVDGVRLPFAKSGTVYKDVIAYDMMRDAFK

GLINKTALDPKSIDYVLAGTVIQEVGTSNIAREAALGAGIPKHVPAHTVTQACISSSQAI

CSGAEKILSGHADIVVAGGVETFSDVPIRFSKPIRERLINAPKALKKGPMSVLKLLKGLK

LSDFAPVAPAIQNFHTREIMGSSSDRLATRFGVTRQEMDQYTIDAHQKAYRAHVEGKYKG

EILPYNGSTEENGVNPNSTLEKISTLKPAFIKPHGTHTAANSSFLTDGAAATLIMSEKKA

LELGYTPKSVLKDWLFVVSTPLKRYYSALRTALSRYWTRTS

>contig57520 Frame-0R

MCILTIKIQLCVEKKSTWCVARIKRLFIRTQAPSHLCFRTC

>contig58132 Frame-0F|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ31781.1|) 3e-06

MEECFVNGDLDDKEEVEDDDGTEKDGKDCMNEIVQASSDMRLELVSFEDFGRWYNGGGYK

EMSWLELLDLRKWVFVSASFDLEGLDTRSVDPM

>contig58396 Frame-0R

MSAETMFWQLRALAQILSRLFHHRLTFVQLALTLRGSQMETL

>contig59229 Frame-2F

MALAVDASTSRLPYVIYENDTVICQTSDGRMFFQAIGRGETIRVGKKLSSLTPVIGSFYG

>contig04211 Frame-2R|Blast-dihydrolipoyl dehydrogenase 1, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63148.1|) 0.0

MLRNVATLSRRSVASRSIVLARAFSSTSDYDVVVIGGGPGGYVAAIKAAQLGMKTACIES

RGKLGGTCLNVGCIPSKALLHSTHLLHTAQHDFKSYGIDAPEVTANFPQMMKAKDKAVKT

LTSGIESLFKKNKVTYIKGYGKITAQGEVSVALSENKGNETVKAKNIIIATGSEVSPLPP

VPVNNAAGKIVDSTGALALKRVPEHLVVVGAGVIGLELGSVYKRLGSKVTVVEYLDTACT

GMDRGAVKEFIKLLKKQGLDFRFGTKVTASEITGETVKLQTEPAKGGDGATIECDTVLVA

TGRRAFTAGLGLESMGIQMDKLGRIEVDEAYRTQVPGIFAVGDVIKGAMLAHKAEEEGIA

CVETIAGKHGHVNYHAIPGVIYTFPEFASVGKTEEELQAEGVAYNVGQFPMMANSRARTV

AEADGMVKVLAHKETDKLLGVHIIASNAGEMISEGVIGIEYGAASEDLARTCHAHPTLSE

AFKEACLAAHDKPINF

>contig06543 Frame-0F|Blast-eukaryotic peptide chain release factor subunit 1 [Phytophthora infestans T30-4](gb|EEY60208.1|) 7e-26

MATPTAADDQVELFKVKKLIKSLQAARGNGTSMISLIIPPKQQIPLVAKMLSDEMGTASN

IKSRV

>contig07140 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69815.1|) 1e-47

MSGKEDDNAPECKLLSGNFAIALQILLGLIAISVLVFKRVHEVPQRPLMIWAFDAAKQMV

GATCAHVANLLIAILLYSFQGQMQSNDEAVDQCALYFVNFTLDTTFGIFLNYVLLSAVIQ

LAYRFQWSS

>contig07827 Frame-2F

MWRKRRGSLGGGNGARDSPNIMNSHSMLHTPSSMSITSTSPFLGSDPNANDRALVFRVEV

PTPGPLGLDLRARHIERDKPQRGAVVKGFRPLQGGQPGYVESTGRVKIGDILQILHQTPL

DDMPFEQIVKHAMQLQQDSTAWPLAMEFRREPEKHETNTSSSSSKPRRNSFFRSSISMSN

PVQDGNFNEKLQYFRDFFATRIPTGGAVSKEKEKPPRPPKWDTVDEMYRELMAKRGVPED

VMDELIRIESLETKWHVVWYAQQNENEGNTKSNATEAEKFAENLVTLKWDNKGLKDLEAL

RAKISIASTDWLEAFLAHFGLDYLTMKLPDPSPFPIEISKYEKATRVCEVILRILRSLTH

FTAGVEAITNTPGLVKRVALCFHTENGDVKKYTLQLLGIVCYNSAAGHTAVIEAFDHYKE

TKGESIRFSCLRDALKSTRYSLVFKEDVLSFVNIIVNKAIRLEDRLAIRSDFMALKMAGY

FEEIRAKSLAVQRTKYPLASSAAAKIPEIGSYGVPSPVHDAPATPSPILHKHIARNSPSP

VFNRSTNSPIIGRGKDPGTPISRLDTLNTLSGRRSSISKCSDGRNGRLSASKSAPPSPID

RESVALSPDGASARSSLPLEIKNGIRYGSGGNSIISSSVTQLRNQLDNMEKQIDVFEQFM

EDDRKDTIYEQTDLASVDSVYRSLFGSVTNDPELQACFLSILQQLLFIPGDRVIGKEMWA

LSEKVMKQITLLAPVEEVRKFELGYDDRKTLLKMRDRYAQFLQKCADQDPTFHFRMGPII

LIDNNDRDHDDLSLSDVAAEETDEEETASSVAARDHPDLMKYFKLLKMGMPLSHVQLKMS

SEVQSFDPSVLETPDKMLHILNAGSEAIEKKGIRAEEHDKFAKYFKLKKMGMPMPHIQLK

MSADGLDSSMLETPDLLLDKDGNEVKQPLTSARFAGTPVKDHEKYAKFFKLLKMGMSLEH

IQLKASSEGLDGSLLSTPDQLVDADGKLFVDEVSKQSFQGIPVKEHEKYVKFFKLMKMGM

PLEHIKVKAMAEGLDTDLLLEPDTLLNEDGSKLRTEKVLVKVKDHAKFTKFFKLMKMGMS

MEQVHLKACAEGLDGNLLSTPDVLVDGDGNVLDLPHAKHVRGTQVKDHKKFAKFFKLLTM

GMPMEHVKLKVLSEGLDAILLETPDKLVDENGKEMKHEALESKPIPVKEHEKFAKMFKLI

KMGMPLAQVKLKAASEGLDGNLLDTPDQLVDKEGKAVKLRGKERIKASEHTSYAKYFKLL

KMGMPRQQLELRMNAEALDPNLLDTPEEMISVDLTGAADLKAPENSVKMPPPKPKLRNLY

WEAVKTEETSGTIWESFIKEKEKQMKGPLSAANVSVKSNLETSTRDAVLDKFLDQLSEIF

VNKPPKTKESELIVPTKRRAPTRVALIDAKRANNIGIMLARFRLPYYKLRNAVLLVDKEL

LSVERVSLLLQFAPEDEELDAVRGYTGDTKLLGDAEQYFREMECVPRLTSRLQAIHATWQ

FDAYVDEQRKLMEAVSNACRELQKCDLLKEIFRVVLSLGNALNDGTARGDAKGFRLNILL

KLNQVKAADNSMNLLNYVAKVLRAKNPAIVAFDNSLPSIESASRVTTQMLKAGESAVRKA

ANLILNELEVHAKLPEKSYSQPDDADIAEAISDRFQDVVKPFADRAKKASEQITEDLDAM

MKRFEETASYYGEDPLSPDCGPDAFFSIFYSFAKVLQSADRDNERKRIAEERKIRREEET

KKRLEQLKLKKKRSGFATLKTGDVDDIVSKIRAKRVEEKRRELLQANGSAPSSTGSNRGL

ATAPHSSSNTANAIVLTPAMKAV

>contig08628 Frame-2F

MASTTSASSASALLAGGDPELSLVCCNEQQSRNLFGTANGECSGLPCCDYNGRKAQNHQA

WFPCVGFPTCQSDTNNQAFCNGEDLWSFTGGFNWSCTDECCNGPVLDSNIWRGRSDSYPG

QKNATFGVTVTPLDFLDVFYPNGMNGQRYTVHQIMLASPPGYSFTEDCSCYLEMTESVAA

NAPADETNCEVSTFFGENRTFLTVDITEKYQKNDTFVFIFDGVVTPSGINDTSSTPNVTY

STVSNLTPIYFIFNDSENTVFNTYVRVMDLTTATLSSGSFLPQNIFPGNSGNASLTFFTD

ANIPAGSFIKARFGSRWGFTDDAVWSWDFLPLVDTNTDNSIAMTTSTLTETDAVHNFSQA

AYSASDNSWMLVVEEPINIGWVRLGVDSVKNPSKAYSGLGATTIEIRSPEDLFIIGGTFS

AISVYLASGVSASPYNYVTMVVLVGSLAFCSVAIRKNGLSFSLGSIWTDITAICTVLSLA

TAIVNNFIWFFIRGSTYFYILYVYLCFTFTMLTAVCFHWGTVLSLRLRKLPKRTATVTFV

VLNFLFYAYQVSYLLNYHSLIARVYESENDVTTLAYQQCNKDADISATVFSEIQGYLWAC

YAENDDNFFLVSTSVTYGIFLILTFVVMALGVMVMRRGKLLLGNASGPHQVVIIKALRLY

YALIGIVTIVYLLSWIVQIISRTTRGIAYPWFYIFTVWLPCSIPPCCLIFLQWNATAQTL

GNASREMASDCSPMSESGYGEIRTPSFTFSTTDLWTEASMERIEEIMVEGEATAEAVTSR

NVVKKSTILPNNDYVGLSMALEMNEELEHGCFIAIQRLEAEDGRDSMSTVWRQISNTDTV

MATVKDGASGVFPYQQRYLYTFLSVPRISVGSSAEKLRMVVYSFNSATALGNNEDHSGMT

AAEVLAAMERTRSSRAFDDEDSQHTLDSSLVELEAFGGFLSSQLIDDLFEMESPASTDDG

HESETSRFMNTGSSMAPLSLSVVAEFTVSTSTLVTAGAR

>contig08844 Frame-2R|Blast-dimeric dihydrodiol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY62590.1|) 1e-159

MTPSSPLRWGILGCGRISTDFVSAIKSLESVELRACAARSMDSAQAFAKEHGIHQAYDSY

EALVSDTTVDVVYVGTLHPWHYEHTVLALRHGKHVLVEKPMAMNAKQASAAIALAREKQL

FLMEGMWTRFFPAIRHVRQLLAEKAIGEVHHVHAAFGVPFGADNARMWSNHLGGGGLLDV

GIYPLAFATMVFGSTPEKITSAGKLNESGVDIYNTVTLEFSDSRFATVEYTVLSLMDETV

TISGSKGRIYLPSPAHTATEVRVVKYLEDGSHKESRSLFPWPTPPAGTTFNYLGSEGLRY

EAEAVTQAVQNKQIECKEYSLDESLQIMTIMDKIRKDVGVVYPADSE

>contig09425 Frame-0R

MQRRKSNCAYCFTSCVRDLSCRQGGKIRMKATRSRDWQRDSPSATVSAKISIYVGETEPS

AMTGEECCSCG

>contig10867 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59243.1|) 9e-42

MASRVLQAGTTFALSDVKAHGKERLKEINQQARTKKKSRVAQKLAALERSIKEQEEGCTK

RKRPSVV

>contig14276 Frame-0F

MICPQDDEELHDAHVVTNYDDLLDDVVTKGSLNDDRLTISVDWSDDSIELRRNQAERVSS

RHTEGRMATGASTMIADGTCVPILLRASSQGAYFDFRSLDPDHTVGRTRVPWHSKSISDI

RDLSPPRVVAFDVSGKLFRCKESLIAKYPLKRLNQIITCKCGKITCLDDAFYIDRNPQHF

EMILDWYRTGKLVRQRNVNEEAFKNDAIYFDLYDEMFPCTPTSDAIQTFTTTEAVFPLLS

VRRRSVNDVELARTTPKRVSMFATMASVPQQPSQRKQSEQESEKMINAPDVQLPSTTTDG

PERFIRRERRILTPSSLPLIFLMRSCEHLLVEKVTGRGKLLVRVCDATGLRQVHVAQAIL

FDSQSRCDRFGNGTQIQPYALLPGDHVYTFWMAEHTRGTAAGHPVLSPMLDIEFKLVYTF

DSGDKMSFTLEKAFAHTLKTSMDTIPSLAIGEKVLSETDSSVACLFMPPSKISSENSALL

EVAGKSPSHATKKVTPFATANGEKRAPQIHKNKASIRHAGALIMRSGHVPLPSSSQGKKN

TVYEPKYLVPHLNDQCPATLRGLHHLEAKNQVVEATYHEMPPRLFG

>contig14760 Frame-2R|Blast-eukaryotic translation initiation factor 5A-1 [Arabidopsis lyrata subsp. lyrata]gb|EFH66290.1| eukaryotic translation initiation factor 5A-1 [Arabidopsis lyrata subsp. lyrata](ref|XP\_002890031.1|) 2e-47

MAEEEHDFEFHSTDAGASETYPCEAGQIRKGGFIMIKGHPCKVVNVSTSKTGKHGHAKCN

FTALDIFTNKKYEDIVPSTHTTSVPFVSRAEYTLLDITDDDFCSLMADTGDTREDIKLPT

FPETFGDEIRADFDAGKQLVVTVLKACGTEQIIAKKEDLS

>contig15275 Frame-2R

MSLQPPVSLARIMYSSLDDMQKALNVFAAEKGYGIVTNFSYRQLNGKQKCILIGIAEECT

GKS

>contig16537 Frame-1R|Blast-tRNA (guanine-N(1)-)-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY60440.1|) 0.0

MPMSLLDKSLFKKTLQVVGVRVEAKKIGYVVKRLHGHLLNLPRLRNVVPDPTNPEPFKNS

SSKLILLSSKVKDSETLQPLTNDLVTFLKQESLAFVSHAIELDYSYFAVDQVLKELLPKD

IDIPSAFETIGHIAHLNLRHNQLPYKMVIGQVILDKNAQIRTVVNKMDNIETQFRTFPME

ILAGEDTLEVEVRESQATFRFNYAEVYWNSRLQQEHLRILRRFQPHDIVCDMMCGIGPFA

IPMALKGCRVFANDLNPRSYHYLKENIALNKVTHLVTPYNLDGREFVAKLLKDKVPFTQV

VMNLPASALEFLDVFPGQFDHWEGELPYIHCYCFSNAKDVSNDVKERAEVILKGKLDPER

TSCHLVRDVAPKKVMVCLSFQLPETIAFTLERQALQHEDFKRRKTEMETIT

>contig16832 Frame-0R

MTRAYRAPEIFFGEERYGVEVDMWSIGCIFAEMVLRKPLADGASDIDQLSKIFAILGSPS

ENQWDEASALPFYLRFKDTSPAPLAEHFSMLSSAGVDLLSQMLQLNPKKRISVSLALQHE

FLKESPVLSSMTELVIVEAPFSGISPIVEHTDVGLPEASRTFAIKGRRLL

>contig17596 Frame-2R|Blast-histone H2B [Phytophthora infestans T30-4](gb|EEY66069.1|) 9e-26

MLPGELAKHAVSEGTKAVTKFTSA

>contig17835 Frame-2F|Blast-tRNA uridine 5-carboxymethylaminomethyl modification enzyme gidA [Phytophthora infestans T30-4](gb|EEY67105.1|) 0.0

MSCNPSIGGVGKGTLVREVDAMGGLMGQVADSAGIHFRMLNSSKGPAVRGPRAQMDRTLY

QQGMQQALQTLPNLWLLEDGVNDLIVSLKRPCEDNSNEWVNGVTTLSGREIQASQVVITT

GTFLRGMIYQGPDIRIPAGRYMRDSNGIERPAIGLAQTLERCDFALGRLKTGTPPRLDGR

TIDFTDLEVQPSDALLKPFSFMNENHFLDLAPHQVVCHATYTNEETHRIVRENLHLLPQY

DGGKDGEGIGPRYCPSIDTKVLRFPDRLRHQIWLEPEGLETSLVYPNGISTALPEPLQLA

LLRTIKGLENVEIVRGGYSVEYDYVDPRSLLPTLETKKLRGLYFAGQINGTTGYEEAAAQ

GLVAGLNAGLRAMGRKPLILDRADAFTGVLIDDLTSLGTTEPYRMFTSRSEYRLLLRPDN

ADLRLTRKVFEHGGGISKDRMEVLERKEKATDYARKALMEFVRDPYEWNRYGIKIGLDGV

KRSAAQMLALSTVTSADIERIWRQVAYKDAEALPDEIKEIMKTECLYATQLRTQLQEIHI

FRNKQHVVIPEWVDYANMPMISIEEREKLQRTQPTTIYAASRIAGVRSSTLLLLYQYAMR

QSIDGL

>contig19055 Frame-2R

MKSDRSETFCAKLCDLIHAKMSKVRASHKVMFQQARVEVEHVPLKRTKSLMTMESTDNYR

TSRRSSLKTPSCRVTIRDFQIVKPISKGAFGKVYLARKKTTGDQYAIKVLAKQHLVRKKQ

IQQIETERNILASVVSPFVVKLFWTFQTKRNLFLVMEYLPGGDFMSLLECIVQLEEQVAC

VYIAEIAIALNHLHAKGCIHRDLKPDNILLSSTGHVK

>contig19158 Frame-1R

MAPGRSTYYSNRAMCHSKLKKWEMCRDDSKLALKFDALNTKASYMLGTSLMHLLAFDDAV

EALQRACSSAEKTQKPKPFQDDIKMELLRTKKHQWLHVQNERLTRHKQATDRLQVLFRAE

HTAKVLATTEQGKPQTGFEADELMAYVEHMAETYANDMYPGQVPDYFMCPISMVIMHDPV

TTPNGISYERGCLEEHLRRNGAIDPLTRKELTLEMLRPNTSLKEAIQDFLDKNAWAYEL

>contig20846 Frame-2F

MQISKLSYTSLTSRAQERTKKIVSRVPCSQAHIECVFITINLLDNSLRTNAVHARVVKTD

ANLCGNSRRPTPQSPRRLVHSIDKLVSQRASDACQSSRRAFAVASQSRRKRLRHGNLTTF

YDWRKSVHRYLSTKNDASCRKISGSKSRRPSLYLTLIKLYFHKNPPPLASVSNFRAPPQA

TFVVFFSLFFSPPWTATPSSSPL

>contig21306 Frame-2F

MPLAPPPEHIYETREEAEEAIKTFAWQEGYSTKKLRTKSDKYRKTRKVWLACAHGGGHRS

KTRQTSTRLLMCSWAVTIQRQRNQNAAQKWRVTVVVATHNHEANVHLAAIPEVRALQQKL

SFSDIIAKLQKHHSGLPPHRQRLLEQDLNNLVSMSSTSINESALVAPRERPKGSKNIKRD

PSAYEYIERTGQGPRKRRCGVCDQEGHNKRTCRQT

>contig22332 Frame-2R

MKCVVSCSMSRICAFDKDLAFALVIFFNLLYRKLNNSIKLRKTNLTQE

>contig22408 Frame-2F|Blast-mitoferrin-like protein [Phytophthora infestans T30-4](gb|EEY57472.1|) 9e-16

MTLLDEDWEEWTPDKGSFVNHMLAGSVAGVVEHVSIFPIDTIK

>contig23270 Frame-1F

MLLSSMDHLSYYPMPKDPSFLKVDGSAGPDGYALPPEDMGIVSFMNEENSPKNGTKSSLY

KTELCKRFSEFGNCRYGAKCQFAHGITELRHVVRHPKYKTTKCKSYWGSGHCPYGSRCRF

IHEETEGYSQPQFSPPSNLGAGMFLREKDFLSGLGTSVMAPPPPSVDLSYGGGIYCEHSS

PQHLQQHIKHHRHHQAMSSFSKDNYSLLPSLEDGSSWGAPTMNASSPLHPNYAGNNYDLK

QQRSLGSIGISQAKLRAISIDTSKRALSPGYPDLQDAIDALVKFSLTPEENTIPDTEAAS

KASSKQAGGDRELSDASSPDLDSASTALTKIIKADFSMQSSELWKDFSAVSPASFVGDDV

QEQPWSSRMQSRSLDRKAFDSVVAASSEARDASGSSSNDEESPRLSVFERFH

>contig23616 Frame-0F

MIDTMGQIAVPNGRQNMVQPQHSRDLRHGPAAIVGMEHSETIHDIQLDYYGKRLITCSSE

RTFRVYDVSKAAATASNSTEMLSAKKEVETSQANQHHVLQHVVPLIDDSAAPIYRAAWAH

PKFGAVIALAAQDGKVYIYREELVQQGLGGVDNVTEWRLKHTHEFHSLAVLSLAWAPYEY

GLCLANASADGQVSFLTRMREGWLVSSSFCNSEEGMGCTSVSWAPYNSLGSQGAQGPIQR

VVTGSCNNAIIIRQLVPTAQETGNSYWEIVTTLNGHRDWIRDVSWAPNVGIPANMIASGS

DDHTVRVWTQDEADGKWTSHVLHTFRAPVYRISWSLTGFVLSIAAGDDEVTFWKQRRNQK

WTCMSSVTDQGVSRIVNNEMHEY

>contig24565 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70571.1|) 2e-68

MPYESFLPQEHVRITKVVQDASTNAWMYVLHVQRGNTSTHSSPRGPVVVGFSHEYIISRR

FSEFKQLHAALVPVMGSALTSLPADGLLTLIMADNQELLNERRHVLTQIVKDILNHPVAR

DLPDVLKFLGHESISAKVMAPLRASARVLFTRRSVLRGQRRTERRFCLLRRSHH

>contig24987 Frame-1F

MSFSFRFEFDGKLPQEAVSTAVCDAIKPLRQGERFECSPFSSNASFTTVEIDKMTFEIVN

TTDSDFLKRTGAISSILTTSDVRKGVYEGGFKLWECALDLVRFLEKQLRQKAIKIPLTVL

ELGCGHGLPGIYALQRGAERVVFSDYNKEVLELTTCPNVFKNAQEIYSKAAFYAGSWSSM

SQYMDHVEHQTEEQMQFDLILTAETIYTEAVAVELYQTIKKHMRPTRDARALVAAKKYYF

GTNGSVQHFVSLVKADGMLQAETVWEERNGRSNIREIVQLTYIF

>contig25074 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY69564.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53749.1|) 1e-100

MQPPHQQEFYLLPTEQMIRREALEGVNTRKPGKLLIRFNGYGVQSSYTAVTDGRASSMIN

TFVTHEDEFGRSSKSLIKHNIRAEVRSLQTFHQTKPRPGETWFAIDADWIRAWLLFVSTH

KGKEVYNPGNVDNMPLISDNLMNGTFQIKSGLVIKNDFRMINKKSWDFYQKIYGGGPAIE

VMIPTDCAKPGEWLACLHLDQVGRVNSNYVDTG

>contig25463 Frame-1F

MALPPAALRDPLTTSTAYSFAEIAVNYPFVMAYLNGMYKQEPFPMLHAIIATPSVLAAQN

TFLQDESQLPRLKSYVSFRILDSLSVYLGESFRQWRQDFRGPFQGAKALVSREEFCTRVT

STFLGDAIGTYYMDAVFGPNARASAQALVTEIEASLKALLLTELWLDKLTYEAAENKLSK

VKNYIGGPDTVPRSVPFELHVDDFFTNIKHFLELSAFESIHLINKPVDPQKWDMFPSTVN

AYYDPSANKMVFPAAILQPPFYSAQHYPAAANFARIGMVMSHELTHGFDDQGREYDGTGT

LRSWWTPSVAAQFNVKAQCLATQYATFPVVSSQDGQVLGKIDGNLTLGENIADNGGVRLA

YEAYQLWKATFASPCSAPSASKPTEPLASQSPPTSPVAPPSPALSHPNPVMPSPASSTAP

HVEPLLKQETPHDTISPSSTSPSLPDQKRAPSETASPVPSPVEPLVSPSVMTPPELPLLP

PTVPALPVPPSLPDVLKATPSPLIVPQAKPKDFHPHEPKATHSKKPKDEMQDPRIETHHG

NKKQGASKVHESSQGDKRQEKDKKDTSTGRQETEKDKTVVRHDAEVDDSDSETDEKTHEK

RKKKSHLTQRSIVTKKRNVTTSVI

>contig26145 Frame-1R

MARNLNYNANKNGKHLQIKVHRKTVHLTVIELGQRMPAPASTLRKYSCN

>contig26321 Frame-1F

MWATFRLKLNIYVTLVKSFIKA

>contig27036 Frame-2F

MLKNTYQSIVKVMLLRPLLFRAQRPVSASFARRFSASVFEVPRRHICVVGSGPGGFYATK

YLLKEYAGAQVDMLEELPTPFGLVRSGVAPDHPEVKLVMNDYTKLAADKRFRFVGNVRVG

EDVTLSELKRHYHAVVLAYGAADDSVLGIPGENLRGVMSARSFVYWYNGHPAFRDVNIDL

TQTETVVIFGQGNVALDCARILTKNVEELAITDIATHAVKALRTSRIKNVYIIGRRGSAQ

AAFTIKEVRELTNLNGVACVVDPKDIINSMTVASKVELQEHRARKRMSELLEKAAERFNS

AIESKRTVQIKFLSAPVKIFADEKDPTRVGAIVTEKNKLTGEPNNQCAVGTGEFETIPCG

LVLRSIGYKSLPIETNIPFDKSRSVIMNDQGRIVTRTGDGNQQPVLGFYCTGWVKRGPSG

IIGTNTMDARETVRCIVDDFASGNYIKNIDESICGLDAVEIIIKKRKPDKQLVRWVGYER

INAEEIRRGKLKGKPREKITSVDEMLEIANHAG

>contig27528 Frame-2R|Blast-Ca2 :Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4](gb|EEY64015.1|) 3e-39

MKRVDESTRNEVQNARLDALEADNFGEDVDDGDGGLDGDEAYVEEHGGEAIVALGGREPL

RKKRKSVVLGKKTWKVKSLAQVVFEEVGACENVIGPNYVTIAAGPPIHPARKFCCGCGYF

ATYNCQRCGSKYCSVRCGDQHKESGCLKFGL

>contig27685 Frame-1F

MSLWLSAMASSCCLTQSNSSRIPQLASFLACAMLAWLLDTNDPLKKFGLLMIGIIIGTAV

ASQCLPSDPIDKKLLKERLYVPPGAHGPRRVPFLPSAIPVVGHAVFMAYHAHRFLDWISE

TFVSRHGTPFTLRLPFQRNMIFTATPEHYEHVMKIQYDNFLKGDHIYDLLVDLLGDSILI

VEGNEWKFHRRVFVNLFSSRALREHMAPIIQKHVRVLMRVLTATSQTHKAIDMFSTSGRF

TFDAFGEIAFGFDMSTLTLQHEHPFERAFVDAQHIVAARILVPTWYWKLKRWLHIGTEKQ

LRRALATVDKFVMDIIAKTMEMRCELKDQAVRRQDIVSLILANETVDGKPVDPILVRNVV

LMAMIAGRDTAADALAWLFHLLTLHPRVEGKLRVEVLKKIPKLKTDADYVPDMQEVQDLP

YLEATINEALRLYSPVGLAQKLCVRDTVFPDGTFIPKGSNIALAYHAMARMPQVWGDNAA

TFLPERFIDCQTGDILKVPSSKFSVFNTGPRVCVGRHLAMLEMKMVVACVVSRLHLKELP

GQHVACSVGLTIGMKNPLMMHGEKCRQQRPLQ

>contig27766 Frame-1F|Blast-60S ribosomal export protein NMD3, putative [Phytophthora infestans T30-4](gb|EEY57484.1|) 0.0

MRWSRPPWVAAELESRELLAMCLKKINNLNRVKLIDANWVWTEPHSRRLKLKLTVQKEVL

SKMIMQQSFVVTFVVRNQQCDACQASFANQSWRAVVQVRQRVDHKRTFFYLEQLILKHRA

HEKTTTIESHPDGVDFFFSERNHALRFIDFLQESVPMKLKTAKKLISADNHSNTHNYKFT

YAVEIAPVCKDDLVVLPLKLARMLGNISCLCLVASVTSSIHVVDPFSTQVAEVDSEKYWR

YPFRALRSIKTMSDFTILDSNPMAIPSGGGRAIHVTRKTRLADMEIVRDSDFGVNDTRFR

TVSHLGMILHVGDFARGYDLTSAVFNDADLIPLVQSGTALPDVVLVKKVFPRRIQKRARN

WKLKKMEGVEHAGPIRKTTDLSKEDRDYEQFLDELEEDKELRSKINLYKIETTVSKHVKD

DDDAMVEDDMGAPSVELHELLDDLAVKETESTLQILSEVEAKQASVWELEEL

>contig28406 Frame-0F|Blast-cell 5A endo-1,4-betaglucanase [Phytophthora infestans]gb|EEY56353.1| cell 5A endo-1,4-betaglucanase [Phytophthora infestans T30-4](gb|ABG91066.1|) 0.0

MYAGNSPIGENAGERTNSNVWRDTSEEEMYGSYLAPGVSEAVSEVPMMRPTMAARHSTST

HQEIAVGQLDDTAGSGGAVAKTYSGRKVVWPGAVFLLLLSAVALSLIAYFGAEAYRRAQL

QQSLTEAVTVVDRERKVMSVKTCLLPDYATVDGNIYAINTNSGAKEKLVFTGINWSGMEN

AEGVPHGLATKQSYLDDIAANLSENGFNAVRLPLNAQMILDNSPPNTRLFVNRLETDLNV

ESYIDMIKKVVQGLGKQQIGVLLDIHKIDPNFTDDTSEHLWFTEDYPIATIYKMFETLAT

ELCSDLEYNIVGIDLKNEPVGGCWPADDTESYCDPDLNWPRAVETIGNKILSICPNWLIV

VEGNYAVNTVAEINGANVTYNDWYGASLQNASVNPIKLQMDGKLVFAPHFYSPSVYPSSY

FFGKQSSKGDTVSVTEYPNTTEGNALLKAAVTSVLDNAFGNAVTDVGVPTFYGEFGGIYG

AAELLPGLTSTRVIEILIQYANDMNMTGGFAWAINPDGSYDFNDEYRPDEPWQYGLYKTS

AWDSYNMDFAIGLQNLRGSGKFPCFSKYTRVTASFSGSGSGAFVTTESITERPQSANSTA

PASASPGAAGVLTPAAPAAVTPATVERPATPATPVRAAITAPSSETATAL

>contig28499 Frame-2R

MNVQHICRRCQNRQQFAQYKTISRKLYASRLFLKESSFNVIRCSSLLVCEAAKGCTSIYI

RASLLSFDVNYFLLNLQSFRPFCVGSTIKVQSSFIIQKNL

>contig28860 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70065.1|) 1e-155

MELDHENEEVLLKKVPHQVPGAQRRDRNDFFFAMAFAANCAIIVFLALGVGLPNVSSLYF

TAHNTNKSSHGIMIFLIFFSTSCIGSVVSALWLRILQYHAERVISWTLQTSIGISILVSF

VAFYNSNTAGKAIGFLNVFVAFYIVLYYASIRQSIAFAASNLTAASRILRVFPGVITSAY

VALLAQIAWVFLWGVAVVGILAIAANPLHDSTSYGNVCVFFMLLSFYWFVQVTKTVIHCI

TAGAVGDWWFQAHDGNTIQRAQTRALTTSLGSICLGSLLVATLNALHTLLLSTPRRKAKI

SGNAFLEFLVKFVTRHMMYFNKYAFCQVALYGKDFYSAGTDTMHLFQNRGWTALLKDTLI

SSVLSVGCLAV

>contig29258 Frame-0F

MYQMFKKINAKERIVGFYSSGPKIRKSDLDIDDLFRRYCSHPVLIICDVRPHLEGLPTTA

YGSIEEVEEDGKAIKRVFKHVKSSVGAYEAEEVGVEHLLRDINDPSVSSLAGQVKHKMTA

LNGLKERLLEMKTYLENVVAGRLPLNHQIIYNMQTIFNLLPNLNVDELVRSMFMKTNDMH

FVIYLSALIRCTTALHNLVNNKIKYKQSEEIAFTEKKEEKKDVLKDKESETTP

>contig29355 Frame-0F|Blast-coatomer subunit gamma, putative [Phytophthora infestans T30-4](gb|EEY66011.1|) 5e-37

MQPCENTSVPQPKAKAHILLLSGMFVGGIKALVKSRISLDEQSGSMILQMAVRSEAEDTS

QTIMDCIR

>contig29603 Frame-1R

MVSIQKPPEFFIRQRGSPISLQRDKDPLMARTIVDRELLLVAFRYLCDQLGWESVLSFPI

ALATRLV

>contig31390 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57845.1|) 7e-21

MLNACSPGVGVVNIDNGFGAAVLA

>contig31989 Frame-1R

MANTSDAQQLLILERQRTAALELEVKSLRASLVALGESTEFEEERMTNRLIKRLNDVKSE

KEKLALEVEREEELLTNNLQKKLNQLRKEKIDLENKLENEQEYIVNRLSKQLETARADKE

RLLQELQNEDNGVRKALESQVVKILHEKVHLENELEQEQEYLVNRLQKQLSGLNSERRRM

ERKLAKENVALFDQMLLKIDVLKLECGDNANAFADGVSKIFGKAKEQQLKKAADVVKSTK

DDINFQDWMATSGLKSSLTPEGLVHHHIRRGTM

>contig32131 Frame-0R

MALEYSKSSDQRLPDGHLQNI

>contig32203 Frame-1R

MAKITVAGKHGTVVEADQQDGRGLEGINEQVEKLEVGDDHATNDVEDDLANLPKNVLMRL

DALRKLREAQALVEEKFEKERKALELKYEKLYQPFYKQRADIVSGAREVEAVTAATAESS

EADIIPEEIVKGVPGFWLRAFMNHSVLSELIQERDLPVFEFLNDVHSISHEDDNGFKLTF

EFSENPYFFNKTLTKEYDIGDASELGEAVLRNVAGTVIDWKEGKNLCEVTKKVKQRSKGG

KGESRVVSRTEPCESFFQLFTPVEMPSEEDDEDSEMIMRQLSGDFEIGFTIHETIIPQAL

LWFTGEAVEDDDSDYEPEEDDDYVDSDEDSQSGDEAPKPSRGTKKFPAIDGGVNSSEKPP

ECKNQ

>contig32553 Frame-0F

MWRPCRIAALHYHRNEASCLLTSRTIPMHSRLRNVNYYFTSIAGVERDVLLNRSARDLRT

ELGESTIGMVAKSLRSEMNEAIARDDVTSDEITDLFTVAQKTHVIPVMLDAFAFLEAEFP

SQINFAVYGEVFRILQRKNNCERLIEIYLTAKTRFHLVPEMIYRFGIVGYLQNNDMDSAI

RTWQELIDAGHETTNEIASQLMLAYARKGNVEKVKELYEAVDPQIGYWHESCVDRVILSM

GIIEEPAKAFEFYGNSSMKLSGGTLIALLSVCTNNNCKQQATDILANRKKFDLHLNARGY

NRIMVTLEFLGRNNEIKDVLNEMIDNNVRFDTKTNAIIERNAEFLEETNFVADFSKSRAA

GYTLSPRIRELLAQGKNSDAAEMVDSAVTLLKNSDKFDNKISECAAMIVNPSVAKDAVQA

YIRTNQHDKVAALVQGFSVVPGKYAYALAEVITHYAKQSNKVADEICYAASKAMLFQRAQ

IFRVDDTLKRFCRFRDTEAALKLFHQVLESYIDKDALDEVEDDIKQSKRHYVNFNVGKVI

TLILQALVENDRLADAFDSMNKLESCGLKVTQGNYVTLLSSIRKHLRVPNNDRKDQKVLY

DINSAQTVLKDLKARSLQVNRAIVGYLCPAYVEATKQQRLELLEAFAEARNDPTDNYILP

HSCYETLLNFMAQEGSIEELTDIYEEAVASLTNEENRGVPRGWVTIFVIKLVREGHIDEA

DQLTRRMPEKCGNYSYKAVMSVLRGALEARKLNVVDGMIALMEERAFVVKLSDAYDLVHL

ARKTDLSSKVLNIIRLFESSNLKVVAVEENGKGNLEEAFYRRQRHDAHALRKVKTMYTVA

LKMCEKDGLWKQALVLRDQMASLLGQEAVDVITTSSPGRLKIRKEKESDYE

>contig33657 Frame-2R

MTVLFIIQECHCLAICASPNRSFLKKERADNVMRWHARIHFYGQDVSGTTSSRSWTEIKP

FSVGHVEILTFSLRQIEPASDSYKYDGFFLHEN

>contig34652 Frame-1R

MRESALVSIRPGSGQHELRGPEVQEGRFSHRYLPEASMFEFSNGWLDRLKARSGIKSYRR

FGESGSADMTLIADARPGLREILDTFEWEDIYNMDETGLLKARELH

>contig34825-1 Frame-2R1

MTMEPDLKLPRTCDKDETPGDVDQQERENSLQTEDIEMERTKVQEE

>contig35431 Frame-1F

MSKDRPLRTTSVSSDVSPVSRPSFTLDCINVLRRRSPIPQIWSPWRRADIVMQRIMNPFL

DRESPAQYKPVIAPPELQLAPNTPFPDAAVKNTQPSFEKAVAFHKRLHSTYVADYPKGLF

GLFVLVQSPLLLIAIGIFAGSLGLVIDMWAIEIARYHQWVGGQGFKLFLASALVAGGFSV

VLTHCVCPQAAGSGLPFMRVAISGIDMSKYLSFRCVATKIVGLMAALGAGLSIGKEGPFI

MISCGFASILMNWRPFHRVRDDETKRLEMLACACAAGVAATFGSPFGGVLFGVEVTSHFY

LVRTLPRSFFAAIVGALVADFGTKNTRYGLFGNRSMGISFKKDIGNVSRGITLVDLCVFL

IIGIVCGLGGALFNRSLSILVRARDNFFESSPSSSPRHNWWNALGRRSGLVLVVIFFSCW

LEFYGDSAWFLRHGSPRRILGLLFSKDRQFFAADGTNGIDNTNNESAFLSSSLLIFLPLK

FILTLISIILPVPAGLFTPTFVIGGIFGRLVGESVRAFGLWHTHYEPFEFAIIGAGAFSS

GVTHAVSTAAIIMEISHTDGLNLPVSVAILAAYFTAKRLSENVYDVLIVTSNLPRLKKLP

KAAYDIPAWEVMKDVAKMSVLTADSTYNDALSLLNRDSESVIPIVDSYDNQFLLATVTRS

RLAYAVSRCQRKGVEPALLSPANSRQHTDREFFPLLKVTNPRSVASMTLETLSISSNTRH

STRAVFARYGAINSSLCDDNGASDDDVAIDDLNELREQLLSSPIRFAFKRGGRIMDWGTN

KVCEPCKVTVLINPSPFQLMEMTPMRRVDMLFRMLKLNNVFIAR

>contig35444 Frame-0F|Blast-cytochrome c [Phytophthora infestans T30-4](gb|EEY60299.1|) 5e-54

MIEVAGGKGDATKGAKIFKTKCAQCHTTHAGGAHKQGPNLSGLINRQSGQADSYSYSAAN

KNSGVIWTDETLFEYLLAPKKYIKGTKMVFAGLKKPQERRDLIAYLIESTKE

>contig35912 Frame-1F

MMLACVLYTLSTRVYHERRPEGWLILSIFMGYWTNFGWALYGELVMRSDTSICGDVNWAQ

IQARADSINYFQHFDFVFTLVIVLLGACSSYMCGVHSGDDAVEAEKRWQKRCLCCFHALT

CHHTVEHDGESDVFETLGRVLSKFFVVRYQTNRYEGLSFTDLKFSLDLVAHAQKHERDAA

RVHSMVAPRHFACDIEAQRLNDLAFYARMAIGIYGWPIYIWYTPCRFFRVFGCFRPLQPD

QVFEHDNFVHGNRASFIHYTGVQDADLVYLNCYNFVFQAPYGIVKDQARKELILCVRGSM

SFYDFVTDGMAQIVRMDPDELPDDVPYAFDTRTHDGMLRTARQIFTHLQEGTRKTVFWDF

ALRHCALAHPTECQDKAARAWKVVVCGHSMGAGVGCLLAILLRKVLVDTRAFLYAVPPLL

DPETAAWTKTFATT

>contig35985 Frame-1R

MTWQGKRYQRREKARVEVVAPLSLPVSRAECIAQPSKQPSSLRINQRVIIPSSALTV

>contig37165 Frame-1R|Blast-folic acid synthesis protein fol1, putative [Phytophthora infestans T30-4](gb|EEY54477.1|) 6e-18

MDTEEGPLIIPHERIAERDFVLAPLCDLAPG

>contig37367 Frame-0F

MTSPASRPTSIDIDDGNETIHNTLTSPVAAMINLSLSPTMLCDDDLGYNLASASKLIPLS

LTDSASDERPLPSLHSPLIFRDTSYAGIFILHFLLALVATGSVRMNGDHVEERRDILGDL

RDSQDEDSAEQDDADVIMALRSLCVVNLLFALGWLLLFVFSSKLLFVRGSCIFSMAGLLT

LIVTLFLLGSNLGIIWGIICTGIVMLELVWYIRSSQKLDFVGVFFELVVDFLLTRPALGY

ATCAALIVYTIWAFWLCTTIGFVGREVSPWNISVIYLIFHLYWMSNVFKNIITLVTSGTT

LFWYCRNESTEVSPDNREHIADHDSPKGGGFRQTQQDVIM

>contig37635 Frame-1R

MPDKLSRGDLLACTDSTGVQYVETQPYTLCIRFKSTPRPPHAL

>contig37802 Frame-0R

MKRSHAVQGIPILVIVELIIHDFCLRKKIL

>contig38357 Frame-1R|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY66197.1|) 0.0

MFKDNILTTSCKFTGVVQAAFMSTNALQSSVPQDEHKILQLYHASAGVYPKSVSVQILSS

ETFAFHWQLVRAVGSNPGARFLHFALTHLQQMLDLATIEEKHELLLHSHTHGPLFANLST

SPIDSQVTWLCRVSPAESQGVERCTVFYPPRARCLTRDVVDKLNLCRVVTDEIYGDWSLP

HEGSYYFKGKALQKFGTMCLVAKQLADTTHPEMQDVAQHGIAKLVQLMSAFANNQSAFPL

VYDTVYKGIISSEALTRNDMNVDFGNGVYNDHHYHYGYIVTAAAIALYLDSSWCHSADAI

KLRHFVDTLIRDVATSSPVGADPYFPRFRYFNWWLGHSYSHGVTPMADGKDEESTSEEVN

FLYGFALYGQVTRNTEQQVLAKLMLKVYVLAVNTYFLLRKDGPAIHPAGYARNKVTGVFF

DNKCDYTTWFSPEKECIHGIQMIPVSPILEVSRLPSFVREEWDEVLKKMPIVHDWEANQS

SWTSLLFANYSILNRKKALKRLATCPMDDGLSRAWALYYAATRPSPPWQNKFA

>contig38821 Frame-0F|Blast-RIO kinase [Phytophthora infestans T30-4](gb|EEY66128.1|) 5e-79

MKLDVTAMRYLTKEHFRVLTAIEMGMKDHEVVPVELITCIAKLRHGGLQKNLSHLLRNKL

IAHDGNAYDGYRLTYSGYDFLALRVFLQRGHITGLGRQIGVGKESDIYLATQEDGTEVAM

KFHRLGRTSFRAVKSKRDYLKNRKSVSWFLYVAPFGNERIRLS

>contig39062 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56893.1|) 8e-64

MPASVDTHTAKIFTKLMPIQPAPSLAFQLWHPWRFIVMNPLPVLFAFVLANFVIVAVGGL

FRVLLNVLTLPGLLLVLFIGVFLLIRRIVSLMAYPGQLSLVIREAEANFARLTKRRLQIF

TEAAVELVAILDPTTSVQPMRLHFLQVYQNFTFAQETLLVPVMRSLEVLEQDGHIGSNGA

KLLQSLRAISTIHAQLLATP

>contig39930-0 Frame-0R0

MVSFPQLLDAAGLTITREFHELFLDKWLGLAAHSTRCREV

>contig40053 Frame-2R

MRTVVVGAGWLVTACMAQIAVFHKSVGLHCTRNTDCGYVPALSCISGKCEYCRLNSNDCS

IDGFKRCKAVKTWNGSTNKTQTQQAPNSAGESVPVAYCIEKNLFEPFTWKDVMATYIALL

STALGSGCGVGGGGLLVPMFIFFYGLSPKHAIPLSKATIFGNALSAYLFNIARKHPSNKK

FPLINYQVAGLMEPATLIGSIFGVMMNHVFPDWLILLLLVSLLSYTTFKTAVKGN

>contig40149 Frame-1R

MERELTRRCGRSVRVAEFVAADATSTIWTDEDVTERPFCKMPLFEGYVEVKYARQAWLSA

RVDIWSLGDACFR

>contig40255 Frame-2F

MPTMESRNKLLVGVKCATFEKPNSIANESFL

>contig40431 Frame-1F

MNQRQQHLAEEKFSLCFDNVLLQRHFFRSWPVSIQISSLRKVYPAYPYTIDSRPTYTA

>contig40444 Frame-1F

MNVQDLLTNDATPFAPAMSVAAASSGSLDTVKRGWVAPFLLHLHQMLRRESPRIIRWAED

GLAFQILDKEAMTTQILPKYFKNKNFASFQRQLNYFGFRKWSKVRAEFPTYGREHFTRDN

FSEMSLVKRQTKKPRKRKVNNEEQQAKRVFVVSSKYGKCKPILPRLPNPSTFQTRFIFIP

VQSSPMIDLPALSPPRNLNSGYKLPSIHELSMFSAAIGSIRPRLMA

>contig40866 Frame-0F

MLQLALTWSVCPQNGDIGFSWRYTDVYHNSRTKPDNRDDVVQKDQAACYLKVTFQVRVAC

FLVLRLERREDIRLKYTTSLPISLKRVEL

>contig41410 Frame-0R

MQSIPLSPRKVSFKLRKRLRRFLAPFSFRSLSVHQQSVVQVPLFHFLKLPFKQSILLDLW

LKIDNPVAPKIDEAP

>contig41652 Frame-0R

MVSIQKILTSIQISIDRFDVTHDSTNTPT

>contig41726 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60672.1|) 4e-59

MKQGALLLLLLTVLGRTLAVQDAPMPQPARAHCRVFVVLARTRTRVLVLQNAYEQDGINV

YDHFPLLPSIIEDVFDATLKDKYRSDEIYQILRPAFDQAVKWLLNRVDPSLCFAHFVMAE

SETTPDSTSQDKTVATRVIERLDWLRVRAKRDKHFPFALNVPSIKPQDDHESVISSGDLR

VVPSTWRLYFYVVGTNYFSGKVAPSLSPV

>contig41825 Frame-1R|Blast-spindle assembly protein, putative [Phytophthora infestans T30-4](gb|EEY70519.1|) 8e-97

MEEYSRETPLFDRRFHVLVQYPDRDEKLQQLTIRLLTGARQNNDKNQRERVIRVEITDDD

GIDPFFLYLWSVSEEEFHELKAQQRLLVDFATFPANLIELLQCCVKDTTKIVRKLDTTET

DEHDLFEDKGAVCVNRGSVDAQHSRSAGPVPLSYLAVLNTSDGKGMSLFSIVETNPFKQL

THLSLKFFPGDDTAIKSYLAARLAQVGASRRSLASALKQTSEELQTLQSREKKLQQQLST

V

>contig42802 Frame-0F

MQDKYARVVRLMVEVEREVADVDRATVLSRDPMQETAQAHKRNLPMPTDDQLQVIVKLTE

EIALYRSLAHQTTVEGGSFAGMHSYTFLSPAMVRKGQDRNGSLDDADSRFRDFSRFQQHL

LTPKENLNSMLLTHPTGDEFELDERLSILEEEDSHNLPTSIFSESMRRSSRTDKSLLANH

FADECAFVEQITDIAEALRFVPSIQDRKAQLPSYLEKLRLPPMAYVPLVKATDPFERIVR

IPTKEGTAFSTKARVPILLIFEVIRGNPFDDDQQRVIESPRSPSRQSRIGTNTLDTSEVN

YIEDDEIGQLIGRQSFAGEIDDADETHAEPTIPSLELTVSCHSPVAMPRRVLAPETPTDV

PDIVSTPCSTPFQVQFSDNTA

>contig42895 Frame-1F|Blast-ethanolamine-phosphate cytidylyltransferase, putative [Phytophthora infestans T30-4](gb|EEY66711.1|) 1e-173

MNEEYLQRMIKKHRIDYVVHGDDPCIVDGKDVYESAQKLGKYRTIPRTEGVSTSDILGRM

LVMHKTHHKHDHFAANGQLSSRMLQDKKAKDRPSKFLTTNRMLRLFSVGNHEPQKTDKIV

YIDGAFDMFHAGHVDILRLAKQQGSYLIVGVHNDSVVNARRGLNYPIMNLHERVLSVLGC

KYVDDVLIDAPWQVTPEMIASLNLSVVVHGTHRDQHHLPEFTLEEHYEHARKAGILQLIQ

SPNTLDVNDIVARINDNRERFEHKFASKMKSEEEYYADRYSKSK

>contig43342 Frame-2F

MEDYSACKKIIVFSTVFFECSVSCGRIAIFNESHCLLSHDVVRRKAVKAHATARGLDGSQ

LECFIKA

>contig43997 Frame-2F|Blast-methylenetetrahydrofolate reductase, putative [Phytophthora infestans T30-4](gb|EEY57109.1|) 1e-92

MGKIIESIRCAYAAREDDTTARPTVSFEFFPAKTNAGVFNLLSRVEEMGLALLPTFVTLT

WRSAFKDEALWLRIGAHIQNDFQIDVLLHLTCHLPTEQIKGILKNARAAGIRNILALRGD

PPIGAECWAPVEGGLSNAVDLIKLIRKEHGDYFCIACAGYAEVHTESWNHPDLPPSNEA

>contig44075 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56920.1|) 1e-115

MNVLLSRAKHGLILVGNGELLCAKSPLWQKVIIQLQSDGCYGNGLPLYCQQHPEYECVAP

NPASFALLAPDGGCRRPCQTRLPRCGHVCPKLCHIDEPSHNDVVCTEPCPRLQDDCAHIC

SGMCGEPCGRCEVSVGSGQTPESWQLKLHFSAHTAHDGWD

>contig44224 Frame-2R

MSLQLDLGVPTNLVRAPHHRLRFLRCNWTMCFELARLYSPIAILPEPPIFFDSH

>contig44390 Frame-2F

MTTVCKELASLKNTEECDTSSIRDQLAMTTTMVKNSRVNHIASQLSELIEILQNQYIMLG

STRSRNWKRAFVSSLSYLERFESSLFDIRGISRQLLIDFLVAHKSVMKLDFVLVRVFRNL

FQHGFCQTDAKNDLEGEGGDGKMQFQDDVDGTGMGEGEGKKDVSNEIEDEEQLLGLQGDQ

QEEPERPVDEKPDDTGLEMQNDFEGTMQDVPDDEKEDQDENEDNEEELDREMGEFDQDDE

N

>contig44989 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55001.1|) 8e-98

MAGQRKLLSEIDRTLKKVSEGVEVFDEIWDKVYAATAQNQKEKHEADLKKEIKKLQRFRD

QIKTWIGNSDVKDKRPLVDARKLIEHKMEEFKVCEKETKTKAYSKEGLAQVERLDPEQQA

RQQSHAWIQDCLTQFNVQIEALESDIERLHSAKGRGRHKGDIEEKEKLLSRHKWHILKLE

QINRLLDNAA

>contig45146 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66817.1|) 1e-127

MSEFEHKLATSKRDDRCDEYIGLLHFIRKEKLRVPHVVASMGKKLVTEHSWGLGDELWSL

YEHTFVAALDLHDNDLAETCLQALKNKFPGSSRVSRLEGMRLEQRGEFSQALMLYDELLE

ANPANALVLKRKIAILKAQKKSTDVVVALNDFLRSFGTDQAAWTELGETYLSLGTYRYAA

YCYEELVLLNPMDAITHSRLADIYSTIGGLDNLLIARKHYAHSIELNKKKNLRAYFALVA

CTKAITTQRNYRAEQDDGGINERLQKFALDYIQDLYTAHSSSGLAEIVNVALTSL

>contig45564 Frame-0F|Blast-phospholipase D, Pi-PLD-like-3 [Phytophthora infestans T30-4](gb|EEY58278.1|) 3e-61 NOT\_ORF

MTSDSEIGINIVDAEVVQSPDHITVNKLARDYRIQKFMEATKLTYTELDAMTFLKACDAL

EAAAQGGGTSLIEPYAVYFKPQFAFASNGLRQFIDPDVVPDNERLIKIMQHFG\*RFSKI

>contig45678 Frame-2F

MNRRVTHALETRVGVKTSFSVAKLITY

>contig45722 Frame-0F

MSNNLADGATPRDKRLKLLREAKAQKLRDEKIEKADLLVAATLQPAEVDEGTQQTKLATY

PRNESGGFDEKLAQKHQGDAKFGNESDDDHLELATQRANCDLERDIAPMLRKLERRTQHA

IVEVLR

>contig45829 Frame-1F

MITRSNQIEKQLNEAQILCRKSRAQRPWGMMMDEEVTHSLEQEAIALVNLSNPINSNTMQ

PQHVDSFATSKTEIDASLKQVELLDSTISMKSLLVTLKTRQLPRDDVSIKHEQSVGSHDV

AETVDVSDSGKLPSFRTVFEPPTAPHQEETVEPVPSEIKCKYRTGKCHHMRALKSCGDYH

NLCNYHRLRANANQRKLDRKKKERRLQQQQLTALPCALTQPPMYTSSQAAAAALASLVVA

YPSQPLDLLPQQRPLFTAGATVQEVDKANRNRNP

>contig45973 Frame-2R

MHADETGWICIEPTVDENVTLVRVCVRQVPVRFGISTFQVEDFHEILQSSVHEDMNEITS

ALDKLLLQDTLADIEI

>contig46020 Frame-1F

MTSHTHRVAMCSLGVGRCAFTEHGSVFFQKNDGPKLYCTTNHKPRPRLVDPCRRHVAVWR

N

>contig46415 Frame-1R

MWEFAVPIILMEIFVDTLLPSACFSLVMYASCLIAMPSVGRRLDVSDRWKAMRLAIILEN

ASIVACTVFMGAMVLSTNAIGLDKPEWAWSFKLLFVGTLLCGGIGQVLSEVQTLGIERDW

VVVIAQSSGEDHSRALTSHNTILRRIDLACKVLSPLVFGLIIEFAGRDSTTRAMMGTMTV

AIWNGLSTPLEYFTTQDVYKLVPELALNGKGLKASGKQGSYQAPSSGRSMLSNYAQTWMN

YARHPIFLLSFSYCTLYMTILDNGSLYTAYLKWRGVSYSLLGLSRGGGALFGLLGTVLFP

YLRSLIIRLERVAVVSIWLFWLCLLPVLVGFLLFGESCVSDYIMLFCVSGARMWLWSADL

AETQLMQEWIEPSHRGAINAMQTASLHFFYVLIQVLGIMFHDPKQFKALVLFSIAAVLAA

AVGFTCWNIRYGSHRSLCVLPLLNV

>contig47131 Frame-1R|Blast-DNA mismatch repair protein Msh2, putative [Phytophthora infestans T30-4](gb|EEY64261.1|) 0.0

MGGKSTYIRQLGTIAVMAQIGSFVPAGIARLPVFDKLLVRVGAGDLQQRGVSTFMLEMLE

ASAILQKATKKSLVIIDELGRGTSTYDGFGLAWAISEYILTKACSFSIFATHFHELTALE

QEHPHGFANKHVTAVASDCEITMVYQVQDGPCMESFGVHVASMAGFPQSVIECAKRKSQK

LEGFKNLVGNDTLSG

>contig47449 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54568.1|) 5e-08

MKEMGQVKKISATSRFDSGEEARTMSRKVDLPEGALPSIDEQIEC

>contig47553 Frame-2R

MEDQIKPSFASVLEPAQLQRPHCDQCRVAIADYECQRCIQRFCRQCELVIHHRLAELAVK

NEESKSDGRPHQEFLKWIS

>contig47658 Frame-0F

MERLLCRRQRRLAKWVGHSE

>contig48127 Frame-1R

MASVDTIALYERILWLVDPSELDRTSNAVLQEEFTNLANSVRTVAATFAKVEEVRDAVNQ

LEQGKASVSRSESLIELMDSLIQLQHELQCKIDHVANGMKIVDGNDEKQNEKRKRHEKMD

VDAKASWKDSVSSSKSSKDGNLKKQKRVAEQPHESKMATPRDKKNDSKGSLAHGALRTLS

TIPTINERISHETKNKWEKSLTDLKRVIDHQLVRDTHSNDTSATDIAVRALDAVVAILQK

LEVMPQYAKEVRALIAALSDACPDTKVLRTCLHRT

>contig48325 Frame-0R

MPWRGSSCTIESHTPAICTVLAIFSIASALALGEIKKGPALSLADYSWKMRYIFKYFLKR

LIFVVPFSDSGQIGKR

>contig49241 Frame-0F

MLHGPRKQRSSSSPQSKQHPSCDEHDPFSAAVTEVRQMSNVNNAAMVEAFRRCMVGCHLI

SNYRQMIRRN

>contig49595 Frame-0R

MRKFFIWFGDIVYGESKFRCNYELLLS

>contig49991 Frame-0F

MRLLTNVAVGRREAASSTTRLIQRTLLVLDSVVSNIAAYTRCNDFQHVMHYGHSDVFGIL

LSRMAACQ

>contig50012 Frame-2F

MRGLRTSLSSSRDLIDDALLPIIDQVTTNSSSPTIENADIYNEIAPHVLQELNEQEMLKG

IEKQAITNEDNISLALSKAPRRIVYTIFQ

>contig50328 Frame-0F

MEIDKDTNDAKEKRGLQGMKFMQRAAAKQRAKARREAEKLLHEIRLSEGDGNYADPSEKK

STEAKKSVGTRTDKAAVTSGALPKTSVSLCSGLSARASGVIAIDLGDGGTGFALATDTSR

QSKELELGTKESEALMDDTTPVKTEDVAMELARVDEA

>contig50636 Frame-0R|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY63946.1|) 1e-155

MPSVWILQLLPMLMVQRSVSQEAVLRAIGYSGAVCIALVLCNMTLYKVARTIADAIEMVI

YVLLLVFYFWAKFVFHARATFDFFFVVAVITSMANILSVMVGIAHIDATTTPPVVHCIAM

VFEALLVVAIMLSLRADTRYWLAIDDNAGSGATKSSSAMRRYLNLLSERGMITNFSTRTS

VYDVHHMIEEHRHNVVDFAVLALDCIIAQGATSVVMRGTLRRSTPVPIALKIYTDVQVTS

EEVQRFSRETALNVQLSHPNVVHFYGLCVVPPSISLIFEFCEYGALDGTLRTSPEIWTLA

AKLKAWLD

>contig50849 Frame-0F

MHDRKRVDSKRWKTVRTQDGISIYREREFNGEPQDSSPA

>contig51015 Frame-2F

MTETEIIELLRIEKHIVLVL

>contig51198-0 Frame-0R0

MQDEQQRLSLEGNVCCHGGRGQRPSIVNNRYFCRYAYRQRGLDRCGGREPSGRKHRRANR

>contig51198-1 Frame-1R1

MSNRDYRWKAMSAATADEDNGRASSITDIFADMLTVNEDLIVAVAESQADGNIEGLIA

>contig51257 Frame-2F

MIFKIRLDLMKYVVKSWQQQGRSRINSHAQVPTAAI

>contig51954 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57862.1|) 8e-33

MVVADGVSGTMKASGVLARILVAETLSSLAKLRKRSREKSPCAEDFRQSLQTAIKNARKL

VKRKGRL

>contig53079 Frame-0R

MQRCSFVNSSAFICKQTRYNFPIASDPLAFWKRCRLDGNVELFSQLHITAISRNWLIANL

KNSIA

>contig53105 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65649.1|) 3e-37

MEAYVAHENAPLLTVFFITLYAVIMAENALMRMPREQLRHSMAVTLLNSLLHGEVTKSAN

FVQDVRQLLECTPPSICTKLRNFAMKSSEAVDYKSVGVQAVSTSFGTSSRCGMRNLHTAS

TRSIHNDASSMTFNMPINLLTNVP

>contig53673 Frame-0F|Blast-Voltage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4](gb|EEY65674.1|) 2e-50

MLVHRQSNGLVLLIAVESDGEIAFNPGRWYRIVPSTKAYLIAESVKSLKPFAGTPTMSSV

A

>contig53822 Frame-2F

MGAVLFACIELLERAPEGSSGLSGRSQGLPPETPDLNSWLRIY

>contig54229 Frame-2F

MEFICLACEQVMRIHCSADPAGGLVLQSARTISSNSPAGSFEMSSSTANLSDTVAQKSRS

TRKSTQVARCKVCDGIFHLSCLVEPQATPEHAHSFTCTSCHHKPHDLSTKEQATLSVLIP

ALAFSYFIESQLETMDESMTVESDGSSGFTSSIEVGATCRQVQVEANNQISCGKSNTTRP

YRRCVALAHGQNTRRRQ

>contig54405 Frame-2R|Blast-exonuclease 1, putative [Phytophthora infestans T30-4](gb|EEY69991.1|) 7e-39

MATTAIETGQLWLARRTLEEGLKVDATYWPLVETLAQVLSQIGDEEEYKRVIHYLRQNDP

HCP

>contig54492 Frame-2R|Blast-SDA1 family protein [Phytophthora infestans T30-4](gb|EEY68850.1|) 1e-86

MISLKLVEVQLMRMLLAHSTILAGGSMESAYVSRPNVIGKLPQLQNMVKRDPLGYKAEFL

MQLRHFESEFQLFLLRPTKESAHFGALISFLSHVAKCYPTEMVAFPQQIIGLLRENYQVL

EPELRKTLVQSLILLRNRGLVDAITLLKLFFELFRCPDKRLRELLYKHIVSDIRQLNATS

RNVKVNKAMQNFMFEMLQDESEHAA

>contig54614 Frame-2R

MAARLMRRSATGISFQLAFRPTLRSSIANAAILPSFALHPFSCRLSLRSCFSTAPQPHSK

DYKHPKEDAFSIEKHTWAERHAPEWMLPYIQLARMNRPAPTFMLLWPCFWSIAMATPVGH

MPDLKLLSLFATGAFIMRGAGCTINDMW

>contig55107 Frame-1F|Blast-D-3-phosphoglycerate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY59999.1|) 2e-79

MRRFLFTRRPIALQSPRNRMLTTKRSKRILLIDIPEHVSEVSCAQVLVQRGHTVDQVRAV

SDEYLTSVVKNYDALIAAPGTKLSSNLLSVGTKHKLQLVAVPAASIPSEDIDLMEATNQG

IMLLQLDSKQVGDRSSVEAEYGLSLLIELARHLPRSMAYMRSSEPLDRQHLVGTELAGKI

LGVVGIGQAGRRVVDIARTLG

>contig56102 Frame-2F

MCFSIYACVLSLPQGGGLCVTFEAVINLLTLLVNMSCNGLVRGYTDLESWMVFLWAILPH

>contig56634 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY67308.1|) 2e-47

MALQAEASRFFLFWLTLVLFNIAAGSICGLVGVLSRQVGSANLAATVLLLLMLLFGGFLL

NSATMPDSVAWLQHLS

>contig56748 Frame-2F

MRDTGKPGAKPGAAGNKSRK

>contig56865 Frame-1F

MYELEPSRNSHELRVCKNSTRHGILDLKPNHGHEHFSANSPLVTTRMTEEREKRRRSTVV

VKENNHHTKRHKDRSYSMSETNLNMKEGKEKAPISNQRDKLILPEAVDSSHGLQMLVQKV

AECMASKEPLHSLDWVSSLSTSLQVPALLDLAMPLNVTVDALAAWARNVDSCSAQEIQTQ

KAALILEVVANLPPGTSELNVSFTSLPEDEVLSKSEFEVKAVIQAENEALEHSAYARANA

AKRVIECLSSACKAYMDLLAGFAQADDQSSKVAFDVTNNLEAMSQRVTGLLESCTRDVKK

AEALLCEAKQTKEARSLQIVEFVNARRNELLEQGETEACATLESVVGIWKKDDANIQALW

TACSDGERQVKESKQALTVAEKALAFYQNLCTLFQSVLERREAALTSSLRGLDNARTNSA

ARATAALEMAIPMLTRAVYRYFDFHAVQQAKATEELLEQEAALAAHKEFFGDSAPIKKGD

IEQRIREFMNVRQNSLHVVAEIAEKQQYLWKDKQAVLPQVVRDLLVHEYRALWVQLSGPM

QDVMKQVVTTIEQTGGGAVAIQLQQHQQPSSKLIVAKIDVKDLNEQIVPAFIEPVFLDRC

DETRTPYRTAISAIMAPKENLNSMDVMITNDTKSSGMTCGSTEEGSVPTHLTLSKPPEFD

VGSILYSKITTGTNCTQFVRGVVLERLDNGLYVMQYDNGDKFSVKSSFLFTKEL

>contig56959 Frame-2R

MTRRHTVVYTNVETKLSSARRLSGRLRALHAET

>contig57527 Frame-2F

MATLPSDDVQILAVKVHNFFSRLSRHWAQSSVSCHAFIHAPCHHCRLLCFRCNECQGLDF

>contig57826 Frame-2F|Blast-ser/thr kinase [Phytophthora infestans T30-4](gb|EEY57890.1|) 6e-15

MARKLATPSPMRARSLHAAMEEASSAHVEKAIIFTSSDEEDQSIEKKEPKSRCMQYDKSK

ESPRQGSKCTEAAAFSGKSRFRKGVMKKMGLRDTKQLSLRRLVLPRSTMPKQRRSNSEQR

TPTSHR

>contig58135 Frame-1R|Blast-beta-catenin-like protein [Phytophthora infestans T30-4](gb|EEY69790.1|) 1e-07

MAQLRKLVEMLEAKDILLTNENDDAIKPSETPTLDEQSTLLKEDEMSDSYKPTPLSSRSE

EMF

>contig58467 Frame-2R

MFALLYNTDCFDVGTNCRVLWFYPFLVNYL

>contig58834 Frame-2R

MITMWMIIKWPCWGFAFMMECAEIIISNLVLPSRCHRGDV

>contig03710 Frame-0R|Blast-phosphoglucomutase, putative [Phytophthora infestans T30-4](gb|EEY69540.1|) 1e-140

METAEANGASLILANDPDADRLAVAEMDSNSQSGWHIFTGNEIGILLGFWELEQHLRLHP

DCDRTQLFFIASTVSSKMLQAIAKAEGLNFIETLTGFKWIGNKAIELRDSGKKVLFAYEE

AIGFCVGDLVKEKDGVVAAAVFTEMAIYLKTIKKVTVKEHLNALYERYGHFVTQNHYVKC

DNPRTIRAIFERLRNDGNYWDKCGEFVITGVRDLTTGYDSSQLDKCAVLPVSSSTEMITY

TFANGCVATLRTSGTEPKLKYYVELAGRVGQTREAVTMELKNLVMQLLELMLQPEVNGLE

LPLVNK

>contig05631-0 Frame-2F0

MSKKQVVVGSAGARAGGSISNLNSLINLREMH

>contig05631-1 Frame-1R1

MLPPARAPALPTTTCFLDIS

>contig07826 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63828.1|) 3e-62

MLLDSGPLIKAAERVGFKMLELSEEAWGIPMEIAPPALGTIDDLESNSSSEIYQLHKCDM

RTCPQNGCSRYMTTVAHAAALAVGWAVPGCGMSFGGECTCGDNCKCAGCPEHNPAPLNI

>contig08584 Frame-1F

MLDIASERDSSGDVFLQDMGGGLPFRPGVFDGCISISAIQWLCYSDKKEHTARKRLTRFF

TSLYTCLKAGSRAVLQLYPETPEQMEEISGTAMRCGFSGGLVIDFPNSTKAKKFYLCLFA

GYMEPQKVPQGLGTATNEVSYEGRGKNQRQRRGKGRDSIKGKDWVLAKKERYRKQGKKVK

ADSKFTGRKRPGKF

>contig08845 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57001.1|) 2e-37

MSRQFSFNGAVFAFHCLPQSECCNLKNLLQHNHGVIYDATKKETLKVVFVITSYWVDCEP

PASLTQAPYQLVTCFWIKEILRLGRWLKLDSHLFFTPPPRPRTLWLQYPPHYQEVAHEQN

VELYQNYHLENPYATALKRHKMRLPCAPSYLYRNQVPLWPYIAALLARPIQNVHDLTTRI

QSLSLSSLRRPLNCLNYAVTELLTQNEQKALFTWGLPQMVQLILTMPQLFKTPPPLLTPP

EVSTTLQDHATNTCAGTNKTRIVTQTHQFTKLGVLTLLCGCFFGIVPDQDIVQNTSLKKT

FQTFKNHYPN

>contig09280 Frame-1F

MGKASLLCDLKHEPTLCIAVETSIETSVHDSHVHSGHTASSSTHLSNADSAMRKLQLACC

GSFLFMCLQ

>contig09389 Frame-2F

MRLLNIALATVAVATAGPRFSVSADSQTLSSFQTGVATVDRARRILLSSRSEEGTHLVSQ

PSTIPDEERFWGSKKKKRKKKKHKKHKHKHHEESGSQSLSDVPDSSDSSDPRVKKKRRFF

SFRGR

>contig10008 Frame-0R|Blast-glutathione S-transferase, putative [Phytophthora infestans T30-4](gb|EEY65707.1|) 1e-174

MCAFPSIKLTYFNIAGAAEASRLAFYIGNVPFEDKRLSKAEFASVKETLPLGQVPILEID

EEVFTQSHAILRYAGRLGGLYPVSAPYFALKIDELLHAMGEIEAMMVVSYHETNVEKKKA

LREELATDIIPRYAKIFEARLSKMQQIPAFQTEKVFIHDVAIYSWIKPIRAGNIDNIPCT

VFDGYKLLNEAFNKVANHPKVTEWYTIQHCTPKLKLTYMPKPGRAEPIRLAFFIGGVEFE

DERITREEMLARKPSLPFNQLPVLEVDGEVIAQSLAILRYAGTLTGLYPVTQSLMAYRVD

ELLAILDELCNCPLWGACFREKDAKKQLSMRATLVSGALAKALSGFDKIIERNKGPYAAG

AKLTVADLAIYGLLLTFKNGMAGVETNVADNFENLQRVFKLVAEHPKVVEWNASHG

>contig10112 Frame-2R|Blast-hypothetical protein PITG\_01286 [Phytophthora infestans T30-4](gb|EEY61042.1|) 2e-08

MIGTIVWLARKSILSLFLPQVNLEVGGNRELFLRGACLALAVCGLSILHFQDHISLNILQ

TLALMV

>contig10549 Frame-0F

MVQHRNKVALNPGYSQLHWMQLSQSGQDLSGLRGGTPHRDISMEDVSRHCTESDCWSVLD

GKVYNMTPYFKYHPGGVAELLRAAGGDCTDLFNEKHPWVNGHGMLDKCYVGQLDSNLKES

SSHVSRFALDKIQWRAFSLVSKQTVCQQTVKFTFKLPGTKVLGLEIPGQHLKLRANINGQ

IIERAFTPTTNLLQLSSFDLVVKVYPDGVMSSYLNTLTVGDSVEMQGPQGTLGYPNAGIV

TVGGQPKMTKVRHVVMVAAGTGITPMLQLIRAIVENSTDKAKITLVYCNHSVEHIIALSQ

LEPLANMFVDRIKVHHILHEVCETDLGSVKSGKRLDATILAKLLPIPAHDVAVFHCGPPS

FDDAIQEMLEIIGL

>contig12459 Frame-1R|Blast-Equilibrative Nucleoside Transporter (ENT) Family [Phytophthora infestans T30-4](gb|EEY55327.1|) 0.0

MESPTKSEKLVHDDQVALGRDGMPEDIWNDMIKNERTIFFSLMFLNASVLWAYFSCLSAQ

DFYTVEFADSGLDFSFLTTLCTSWPMVIGQAVQMIWSLDKKWTHDVRVHAGYGVFIIMAI

LIMVFSAINFSNQKMGAILVLFCFGCIGFGNTLSESTYYTIAALFPVPKFSQAVQIGNGV

AGILNISLATLLRLAVGGVHQTSNATKLAFYLFFGLLIIVLIVALIVYRRLVNLSSVKFL

LERNAASATTENLTNQPICKTLGNLRRIFIVIAIPAVAQFLIFFVSLSVFPGFGCAASRN

LAPPYSDVTHIVAQNWYCAPGIVGSYNYGDFFGRILTSAAVYKLLSCEWCLFLSIARLIF

IPLLLLGVAGTSLYAFGHDDMTAIVYNIILNLFIGLTNGFLSTVTMGAGPRLLRPEDRES

GGAVMVLCLFMGIASGSTLGFFFSDRGWLGL

>contig12648 Frame-2R

MLSKPKTVPLLYLYLLLSHAVVTPTKTTASSNGPQASKESLQNLRQVAHVTTRTLSKESP

ENLRQVSNVTVPAPNHDFLEYLQTRLPVVASPPMNVIPKIHTQDSHGIEDRLLDIGEFRD

AVNTLAKSLQTDQFRPTGIYKYVPKLFQKPQIISSDDSRLLNSLIREFKSEIRRDVIPFP

HNNVRLIKWIKKIKKSFPVRRSAAYSVIAVILSENLGNFKASEVIAGLMQHHSHDFQLIQ

TALFQHWRNKNMGLKNLLEEEEWTLSEDVIKTLRNPGFSVINNFASILEKEDKQIAFVSF

MEKLHDSKLEDKVEEIISLGQRAFPEYVRTPDGYVMFHNDVLAQWIMKLGHEYVRSNI

>contig12837 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62607.1|) 5e-62

MFLVASQAIRYRHAIPIFHAYEVKTQMIFWEGPWIYFLHQFQDPSTGKQFAEGLCRVMVW

QKGEAVSLDKMISEIYVGSIPPKPAQAPDIVTSFLEWDAASRSSMETAHEVEQQNIGMNP

LSSTPETLWGRIWKEMQRSMNRP

>contig13838 Frame-1R

MKNLHWLIVLLALGLLTYIETKSVEIPISNTNVHAHGRLRLLTSSTSSQAQTFNEERAFE

ILEKVRQVFHRVLEKIKDSRFWRFVSRKRKNIPHPVDSDPAEKLRAATDRVAPASSSTIV

RFSKSINKYRGDQSINPLKTTAFTVLLATTRTKHADDIYTFLIQE

>contig13944 Frame-0R

MVFSYALIGMAAVASTFVTASPKSLVPLPWDGTGTDLTVETLTKKYQDHILIQRNGGNNG

KPSDYVTINDSGRLPAYTDDQSVINIGVDAKAQFLTQTQLIRTELVRNVTANTKGTTFFR

MSLMKKDPFIHPFPWQLLFTETHIFEIRVDATKSPPMLIYLNNATWDAKHEVEFVYGTWY

NFGIGIKAAASGKGSVLDFYMSEGHADLVLITSHEVSMQFPDFHEFHVGCLAYFDKVVPP

MVPGQDIFSYNGVRILDEVSTSSDGSNLNVPTQMDPTGGSSEKLPAKQSPINPPKCA

>contig14332 Frame-1F

MAIPGSILDNAQTKELKTYLAGQVARAAVIFQVDEIIVFDDQLGASASTGGVPKKRAHDC

HVFMARILQYLETPQYLRRALFPMHSDLSCAGLLNPLDCPHHLRAHEWSVYREGVVTDRP

LKEKEGSHVYVGLSREVVVDKRIQPGIRVTVKIDEASKEFKKKMVGTLVSLAEPREQLGV

YWGYTTRFAPLLSNVWTDCPFSGGYDLKIGTSERGTLSVDDPGFSLPTFRHALIVFGGVA

GLEECVDADETVVVSGEDSSTLFDMWVNTCPEQGSRTIRSEEALLISLAALRPHVKRSGR

AL

>contig14439 Frame-2R

MATSLWPQETWGLDLGNRLRLFTRGRCSPYKCALLQTIGFPFNDWKSYVWEMQIIPSLRV

FQEQEGHLFVRQSFQVPVGDTKWPRAAWGVKLGSQCQLLRRDADDGLTAQRKQELDAMGF

IWSDAQWKWKMQFLKAMKHYRQLYGHSEVHHSFRVPLSDPEWPSGSWGYRLGQNVAKIKA

SLEEQNITPRAMADLRQVGFFHERQSLQVWQQTLLPSFTLYPQVYHQACIPRDFIVPSET

PWPESAWGMRLGYIVATINSHRMFYTEMQHDKPHLQALGYTWEVLFGKWAKEFVPALRYY

KAQYGHCDVPSWYVVPSSDTLWPTDLRGYALGKHVVHVRRKGRTHSDVADVVTDLDTLGF

HFHAFESYYVDRVLPALEVYARLYSDLHVPPGFIVPCNQSWPQPSWGIKLGHTVRHLQTG

HQYINQVEKYRPRLEALGFVGHFNHSTATVQREIVTPSVRVFHSVNGSNTPVPRDFIVPS

TDARYPSVAQNFELGAWLEHRRTRTGLTCPRVQGSKKALKPRIAQALSPHADEYWNDIVL

ASFRAYARAEGSCDNMDGSFRVPEAPEYPFAAWGLNLGLRLRHIRHGVRYARERAKYKDE

LVQLGVLRDGDSVLVDDERQV

>contig14761 Frame-0R|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBN75017.1|) 1e-29

MTEPHMKTAGVAQYIRHQDDVPANAIAPTDAVVAEFKQLKMRRKYRYALFRIEADKIVVD

ITAPPSASFADFCAALPDSDCRYAVYDHDYQVSDGRKTSKLFFVTWIPHNSHPGFKMAYT

HAKSAFQGVCEGCYEVSAVTKKDVAIGMNISAGDASDSDSEFEDD

>contig16257 Frame-0F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY54248.1|) 1e-113

MSDFPQQMQDLIVRGWDTDPTKRPTSEEMADEIDRILMSYESKQ

>contig16701 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56410.1|) 6e-67

MADPDAKLNSLFGKKKKKKSTTVNANVIVKTSALNIERATAERMAAAASAKPAPKVVAPA

TVASGKILSDLLLNKEEEQTKMSFQWAKQPKKYKKPSEKESVATTWAEQEQRNRVNRRIQ

LDNERAFPSLGSGASKVQLQSMKAPITKAVETKNAWASLHDDEDEE

>contig16918 Frame-2R

MRTTKNEEDGDDASSLLTDEQLKVISTVRQQVEKVLKNFGGKFFPKTNWSAPRDASWLLG

TLKCTSFEDVFLLLQASDFVVHDLTQPYTGCCGELVDKRPTNSYLVLKKWCNFLDSMLFR

CFVIDHRLVAVCQRNCGEFYKFLLDLQDELCELLFEFYHGNFRSADGKLKFPDPNYSFDV

YVDKRRRVYLIDINVFGAVTDTLLFSSEELLGLQNTTLTPEEATAEHNVIDFRVVESEKG

ICANPLGGYRAPTDLVDHLAGGNDFKAF

>contig16987 Frame-1F|Blast-malate dehydrogenase [Phytophthora infestans T30-4](gb|EEY63243.1|) 1e-157

MATLKIVVSGAAGQIAYSLLPLLCIGHVFGPNQRIDLRLLDIPPAQEALKGVTMELQDSA

YNLLNSIVPTSDLELAFTDVNVAILVGGFPRKEGMQRKDLIEKNVAIFQAQGVAINKYAS

RDVKVLVVANPANTNCLIAMEHAPSIPRRNFSALTRLDHERLRSFVVEKVNATRGTKVTS

KDVTKVVIWGNHSSTQVPDVTHAEVNGAPLTKLVVDKEWVETKLVKDVQERGAAIIKARK

LSSAMSAAAAIGAHLRDWFTGSKDGEYVSMAICSDQNTYGVPQGLIYSFPVKCTGNGAYE

VVDGLPVSSRIEAMMKATAQELAEEKVEAEEILSR

>contig18053 Frame-1R

MPGGTHDTAGRYVEPLLAEVRAHLLEKEPGRARSAFLRLPDLDSRRKTYFEATLRDFYAA

GLFDVPVLLTFLEVLPSWHWTLDGCAVLHSVNAALRAPSSGAKGGGNALRALETRQCKFP

QLPLAFFLLKLMSHLEGSARVRAESYWYAWVSPTLRAVASGQPLELKILARTGRSEYEQG

DASKEEVLYAPGHTGIYDNDRRNAFCWVDDGHDSAVAAWPDEKDRTKVQWRLIPSDVHSD

TFLVQNVHFEEYLYAADYAKFKKDARGKSRSRVFLWRRPAETPGPAGKWQLLALSRDERD

VFALYNPYQREFLYVPTAEKWDNNRRHVLTRVAPDGAREASSTEGGNMWCAWRITPAEQS

LMELGLEAFFAKHYPVAVEYLTQALDELPDNTEHVKCFAYRMTANLRLRQFDLVAPDFQA

IQALGGDKAAIFHGLAHLWEENATYLAAMATLSPELQIQVMELASARENPFFMRHQLSKG

DDYFVRREFQAAIACYQDAATCNLTIPTSSTFEYQNIEDPETIGQRVRAYVSCAKCFFAI

DESDNAWQYLSIAHDIAGVSVEGEATILLWKGKCRRAQKLYDESIELLEKAFDRASAAST

ASVSLPSTVPMSATVLKRSILMEMKVAGILRQGLYNTTLLSTKGIGETIESKIVEFKYGQ

ESLAGTKKSLTQMMDIFHCPLSLELMDDPVTTPDGNTYDRIMIEQHLEINGCFDPLTRAP

LMKSQLHPNRALKQLMELLLGDHCLGLLLASCST

>contig19252 Frame-1F

MQVKSSRQFKRASYLFWCLCYFTCLVDKKANGIHGLG

>contig20072 Frame-2F

MTKGKTGITEYTFAKTPGVKKCNILAWLAFTNTTIPSRFSARRAHTDILALKQYKYFKYK

FAVGIKRLRRNMGLCSMAAA

>contig20678 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55953.1|) 4e-06

MEFLSFGFDEFRNHVLPLAGELKTFV

>contig20847 Frame-0R

MRDYLKKNSAVNVESIQLELLDINKPKNIMLNAAANLFTRLRLHKASTLRNEIWLCWINF

TEGSIARASQVIGILKFST

>contig21116 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60904.1|) 0.0

MREAPIDRELNTVVRVGHRLRKCELRLDPDTIAWSRGEKMLGILATDDVVGAEVVGKQKA

ATFRVHYFQKGNGTGAKALLRTPKFIDFHCLETEVMESWVGAIQELVRWQARSPPIGEKR

LLKVVVNPHSGKRQARQIWQEKVRPILDLGNFKYVVEETTHSGHGTEMGKSYSSDDGFEA

LVFIGGDGTLCEFMNGLLTRPEHEWREIVASTPISLISAGTQNAFGTGAGIPTVNSALYC

IMKRKMRPLDVVTAISVANPEVVHYSYCGLGWGVAGDIAAESERYRWMGTLRYAFLKAKR

TVVLPKQHTGHIRYVLTEPQPPLIRYDDYPDMGALDQFDVEEGTVYDMDRFSQQRKSWGG

IAGGISSPASRKRFPDILWKEDRNSYIVVGVVNITPDGAYSHPSDGNMDLIITRKGGFLA

TAKLIGLYIMGKELKSELISYLKIKAVEVTPDQADDCMNIDGEVLQNGPWRMEVVPSLFK

VLSEK

>contig22287 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61896.1|) 5e-08

MKSTFEVTVLLAVTGVTNLCMLPAICSLCRRQLVFEAFI

>contig22333 Frame-1F|Blast-hypothetical protein PITG\_05488 [Phytophthora infestans T30-4](gb|EEY69273.1|) 1e-110

MGTADEPSTASMEKAATDAVAAPIDSSQACDTRPRAKSSATWPKTFNHEEYLALNRGKER

KDYLMRFGVRHGLSLPVPEINRPTPLQQKNSVKRLHSIVGWPKGLTQKEYFATKPGLERK

NIMTQYRKAQTEKSSKHNVPPTFVWPKGMNQEEFLSKKPGRERMTYLAKYITTNNLNLKK

LDVRSHVPIGYQSEPQRSPQCACYSSEACASCSRCIELHCSCGLTGRQRRAICHESRACS

CQLVDPSTRCKLCYGCRRPHALSHCRCVLHQRLLWHKRHPDFPNELTEDEEQVVCSCFML

AHRHGGAAATRKRKAKALRNIERVRRIKRAAGFPSSDNLYRDQKVRRFIEDEGLESAYDD

GVDDGEGSEVYSPRAETVIPRAMTRRMLDPEYNPASYHPLFRSEGSSLLEAIEPRNGRIS

RRGNAAFKSDAIQREICRGLTNYLFEIDRNETMPADDLVDYVVYMASIKSANVGELIGIF

EDSAAVAASIVIEEYVKQLVEEAIVAEQSSNSLTKASVKAYTLLLLKGFNWHLLKQQDIV

SSSRVTNSWLSKDQASLKDKVAAFILHELISTYPQCSFNNENLLEWIRNAIVIPSSVMTD

CMSSKDMTMISKGSQRLNEEPLSATDVSKHSSPEVRLSVQTNAVHGNPSYKLKFAAALED

GHHIEASIGGLDSRATAKATILKLAHVLENQARRSKGAFQNSPKAPGPPPIPRSLPLPNA

NDPYSSMYEHVWGHFNAYKLQKWEASRDKYVSAPVSGMDT

>contig22409 Frame-0R

MEQEGGTVMDTPRVWSCAQWGRDGHCE

>contig22500 Frame-0F

MMLSQDQVIKNILPALSARPIHDEKIKQILISSQNRLKSLWTYNRISPRDALAFVVDLRR

>contig22575 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68153.1|) 0.0

MTLEELNKVDDRAFKEWMEYLDREMAEKEDEAQLNLFERNLEVWRQLWRVVERSSVLVHL

ADARCPLLHISDQLMTYIRKKLPWKHVVLVLTKTDLVAVERVKEWTSYLQKRYGQDIPVL

AYSRENVDESNQSLMRTIGNFRVDSDHHSQNDDFIKEDPSEKVLTIGFVGEPNVGKSSLL

NSLFGRKLVSVSATPGHTKHMQTHYFDHVEMLERCDSVFSRILVCDCPGVVFPRFKVPVL

LQILFGSFPIAQTREPFSAVRFIAENCVPHLHEVYKLKPVDEDDEEWCPYTLCESFAQLR

GFRVKGGKLDVHRAANLLLRQTLNGNKVVLSFPPPIAHEGYLPKKD

>contig22957 Frame-1R

MCILGSVIAPLAFDSFGTFFGYF

>contig23271 Frame-0F|Blast-phosphatidylinositol kinase (PIK-I) [Phytophthora infestans T30-4](gb|EEY57127.1|) 1e-149

MQDRIRERSTFSRFDGWALAPVIAKSFDDMRQEVFVLQGLKLFQLIFRKHKIDLWLRYYS

IVCAGKDCGLLEVITDAQSLDSLKKIGTKVTGIGTSLLRIFERACGRDPIKSEHDLNRLE

EARTNYISSMAAYSLFSYIFLVKDRHNGNIMLDTDGHVVHIDFGFILGIAPGNTFSLETA

PFKLTPEMVAVMGDEGFDRYRQLVFHGLLALHLEAHQLMSLVYLSSKDSCFPCFKGQSRA

RIVRRLGRRLCIGLNAQDVERTAARIVDQSYGHRGTRQYDWFQKISNGILP

>contig23617 Frame-2F

MFAVNGPSGPITRHERRAASDQQREKKEVINRRLAEKKRELFFLERQLLPDGLKH

>contig23792 Frame-2F

MAPQTQLRTTPTTQTATFQKFEWKAKGLGEVQQVQQQEKKIKTEKN

>contig23976 Frame-2F

MSGNPYESSQVQAKMLSGRSEKAWDSLQPPPLNVLLHPNHILVCSFLGELSLESLQWLIL

PLRSPYAAVHPPITILDSAEPSDIIIRCISAFDSVYYVRGSPLVYTDLQRAGAKAAFAVV

VLGKRVETSELSELASNAELESGVADAEAIFSTMLVELKMNLKKTFTVTELADEANSKFM

GTPFQSNKHQTALNGSGYANVGTCTDITSMDMLTLWDSILQHDAPEQKYEKCIFDLPLYM

SGRILHPQLCENMVVQTYFNPSIYKIVRQLVGGPRCTGVIHMLSIPYALR

>contig24766 Frame-0R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY62470.1|) 0.0

MATSKEPLGASSGDAEQRAKLVRRSSRVAVDELLREAFARVDTDMDGKVNAIDIQRGLRV

AGVNLSIEDVGRVMKRLDPTNQGQLTYDDFHALHDAIIVETFRSFDTTKKGYLVDVDLQH

GLQTLGISVTLNEAVNMIGQLHPKDAHCVDEADFKHLYLLLRSKMLSPTALEQFLWDPDV

RELSRNWWKASVEVGEDGLRVPLPVDNDGKFKKVAPSIKFLGGALSGVIEALILTPLDVT

KTRMQLDKSGQYRGMVDCGKKLLAAEGPKGLYKGFAPWTTHVVLKNGTRFYFNAIFRRML

SDKNGQVSGANEFIAGALAGATEAVLIVTPFEVIKTRLQGQDIVKGEVPKYRGPVHTAAT

IMKNEGLLALWKGLAPTIGRQGLNQACSFWSNNFIKKHVWKLQDGDALPAWKSGLTGMIG

AIPGPCINCPMDVVKTRLMAQEAAAGAGGKYKGMLDAMAVITKEEGFKALYKGLVPRLSR

LCPSYGIQWLVMDQVTAYFSRN

>contig24986 Frame-1F

MSPNSSRDVGRNDYRGSKGGKKNHSKKS

>contig25000 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58246.1|) 2e-17

MALLSPSRLEAIGLIREQLRCTLCDRMFQDPQCLDCKHNFCHACILWHLRHKNSSCPTCQ

LPTRPSEV

>contig26144 Frame-1F

MGGPNASSTTLVRIDQLSQEPGLKRGTIKNRSKKPLLARHSDIFRQSGIFAGQSNSNIAV

VSFGDGQTSSTVSNKLIEKQNHPERAEAFLESRVDFCAEEEAKPANDDFPVCEVFSVIPN

TLKPLGFESKEQLQSGEKSTTYQMMLQASKRGQENAVRNQIDGGMFMARSFRCSWGPNGE

LVNLGKLTTRFENTTNVASQRCRVCVEFPLRLYEKVKSDLHDGLKLHYEFTSRERNSDDF

IDRDGLEIPAQFSLPGRDPLLNYINLYVAYAENLSRERPSEKRILVLWKLVQALWGQEHV

IKMEGHPDTAFSLLASRDHPIALENFNTFQIIDIRREAISQWFEAAIQLTENVVISGDTP

SLQGVLCLLCQHRVVEASEMAIECGDVRLATLIAQAASYESDGFRSLMETQMAQWSENGS

LEYMDKTFVLIYSVLAGSVEVLTAHKGSSMSWIACLALFMWYKRGPAMPLKTAITLYEDA

VGKQQATSSRSLCQTAATDKNDLLMELLKLNCEDVASLCQVLSPSGLMSQNSNYLDYEMS

WHLQSVLLALGYKLDREWESHIHQNFIRQLEGAGLWEDAVYVALNIADVIERENTCRELL

LRNADVLKSDSSNQKKFCKRLSLPPEWISEALAVRAVTKQEHHEEIAYWVAAHRYEEAHA

SLISHVAMSYLFSNEKHSLMQLLVELEPMAMYIPQWKSCESVDTIGGGLLLEYIRLDLQK

GLEVGLEERFSQRVMLILQQLSSARDASAHNISSKVEKNVVLAQTCVSSMIVSLATKAIQ

LRSLLSYGQESDTTSDIFSTSKPLELEPEFLNVLSHLVTGRETSFVESFRTTQLMHLCST

FIDWRV

>contig26405 Frame-2R

MALRAKLLRCMVVCSSSERYKNFLETSQFASICHLAPTWTTVKRSRVWTRPNCSKLSTAF

PVGVINLGAALPPSIAWCDDHRIVMICLA

>contig27037 Frame-0F

MICGQAVPTKFIRGARAANIVSSSKAKSSIASAAESGAQAFDPRDFVESVDLLSKLAKSD

FKTKLALPKWSKKVEALKIVLDLIGPVPKLVNGDYYELVSTLKTLTSDSNVNIVAKAIEV

FGALADGLRKSFTQFARMIFPELLRKFSDKKSVILNATNKTLDLFLQHAMTIEMMMDDLK

LACDASKNKAPPARVQVMAFVARAVENRYVDLKDKALILSFGGMFMKGIEDTDPKVREAG

QNDFVFLLQASDQAANWLLNMTNEIASKNPRAHKAIQRGLGGNAVSTPSRPVSSQLSKSD

GAPSRSPSHLSSAESAASRSSFKALETDVDMDVDSSSTIAECRGPSLKKRGPPTRFGLKL

GNNAVPKANLSKKALVSGSNTDSPKTTSTEFINTAISVTAEEADVIVADLRLENWSSIQE

GFASTKWMERKEAIEGLEEFARTNANMMSVQVIEAITVYLSKQVKGFKDSNINVLKSAFQ

AVGTFAEIASCKFPRGVVCVVTPRACDKIGDKKANEAVRA

>contig27529 Frame-1R

MSAAVAFDFFNQKQYFQSLDALFCKCL

>contig28498 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65853.1|) 2e-10

MLSRQDFQLIGMFPFMTSTREGWGLTTDGEFLI

>contig28616 Frame-2F

MCLAAAKVACVVPRNLIQRMWGQAIVLSGAGVEPLELDALTLSNLVHVFRVLMDPKLAHS

AKRLALTFSSPDAIEAAVNTFYSQLPLTRMTCDLDPARIANVYDSLHNLKLSYAAQLVVR

QITKNAGNANGLKYKPLKYSQHHLPQPSLREVELLHSTSSKNSSQQPKTKVLYTYDRANE

EHAASTDIKSDLFASGCGIRKNRTQLCRAQSLALNAVEVLLS

>contig29259 Frame-1F

MLMKNAERHAFDVLKAPESTDTLARRMQKLQVVSDSTHEKNVIPTIVDSLVEYHANIGCY

QCYLFLDCHEQAGTRKEMLDVTHFRIVAKFPRINLAYMPQKHGAHAVDQQEDVKVVWWTD

IERNVDIAQSFLEDKNDHWYMRLAVRPSDMQLLGGFSSFTQVSYKELRPKYYASVRCRGC

NTQLLQGQEGNSIVKVLPLPSANWMDMFDFWGVGIGAFEHIPRDTIQAQQHRVLVGESYV

LLHASDFVAKATVRGCDNEVAFAFEDDAVEEHDWVPLMCAACSKRVGSYNIEQPDTIRLD

KHLISACNILDISTEQEDAENIYANYTNDSILSAKLLELADSDGKFRFVLTSSCADRGCP

DSLTNDTSKPRLQLQLLGWETMIKRQHATKYSRVLKVLYGPRQPMHELLSSHQLILPPAF

FTAIIERLRISSTMLPLSLRTFNRLNIGYLYA

>contig29530 Frame-1F

MVTLFCAIADAAGGAFPVDIDAGATVGHLKKEIKKEKPNKITCDADELQLFMGKKDEGRG

PWVTEAEVLSSVVDTTGLNKLSFSHLKLQNIGLACGQLGQVSAEEEAAGKGPVHVMVVPS

EPVPPQVVLWLLTGRVDDALATKGIRSKLYWMASSRTGYYDPARRIGDKNVAFWYEDKNL

CFHVLFKIESDALKFETGLLNGPHTLGSPLTGHHIETHLAQARAVSVDLKRIIYHDYTPN

DSESPENTISSLTTSVSILDLSTDEFRYQRIEHEKFFKPYGKAESCHLVSRKDNRDYKRE

YGKYDRDPNNRLALSREMHGWFDGLSIEFPIVNMLPGT

>contig29545 Frame-0F|Blast-Sulfate Permease (SulP) Family [Phytophthora infestans T30-4](gb|EEY65009.1|) 1e-175

MRTLCDLGPLVVCIFGGIVGYTLGPSHLRLTGEIPSGFPAPKVPWYGLTSHLIETHRFGT

ILYHSLTVAIVVFLSSIAMAKRLAIQRGEDIRTEQELTGIGLASIVCGFFQAVPPTGGMS

RTAVNMQNAHTQLSSMITCCLVVLALYTLTNTLYYLPSATLAAIIIVAGSTLIEFQEAKW

LYRIKRDEFLVWAASFVLTLGLGVLNGLFASILCCLLALMWKSKAQKVTILGQLDHGTFV

DREKVSDIVFQSDVIAIQVESSLYFGNCDRVVQSIEREMVRLSTLGVATRGVVLDARYMN

DMDATTIQVLSEIQEKLAVRGVRLAIANAKSRIYDLLAATNLLKRIVASDSTISVEQAVE

MMRELPRIGVTRG

>contig29602 Frame-0F

MKLPDSEPQNDAQIDAEATALPMIPVTILSGFLGAGKTTLLKLILSTFHGKRIAVIENEF

GEEIGVESLVAKDGVSGDVMDDFYELNNGCVCCTVRDDLVNTLERLLERRNRFDYIIVET

TGMADPGKVASIFWVDDELEGRIYLDGIVTLVDSPRLDFHLKHVDTQRETAAQLAYADRI

LLNKVDLVPDDEQRAVIVRKVTEINGMATIKWTEKSKVDLADILDIKSFTTSRAEQVEKE

LRAFMNNNIENESLKVYNNNQLIHTSGMQTICVRIRVGSLDQDFLESWLGELLWEQEYED

VGTETTLGTTAISRQKLFRIKGVVAIVGKANKFILQAVHELFEVYASDECWTENSLMSDT

NRVTQVVFIGLHLRKDELESGLRRCVVADATNL

>contig30073 Frame-0F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 1e-139

MAPFKRKRGRRALTDAIDSSTSNSAKKEVPLNMHENVDFACPCVKELFRMLNDANAPALG

VRCDGRVALWNPRMEDITGFKASLVIGRPISDFVYGKQCKQDISETIELCLTERQSVLKL

RIPLRNVKGRSAQVLTNMTPLMGEDGSCVGVYGVGQDVTEWAIQEKQYATVMMQANAPII

ELDKEGNITVWNSKTESMTGYASVDMVGEPLLPVVDKCFRKIVSQKIDQALTGIAGADFE

LPLMTARGSRVEIVLCLTPRFDTMGSVMGVVAIGQDVTERNTKEMEYRKLIETANAPIFG

VDTQGRVVIFNTKASHISEYSPDEVMGVDLVDTLISEEFRPAVAAVFQSAFQGIETANFE

FPLITKTGRKVEILLNATPRYDHTGQLVGVVGIGQDITDRTIQEKEYNRL

>contig30510 Frame-1F

MAPVTNRKHTRVNDPAPSSTSSKRLKTTIENSIKSIDQSVLDAELSSINALLQEEETSQK

>contig30972 Frame-2R|Blast-glycerophosphodiesterase, putative [Phytophthora infestans T30-4](gb|EEY60528.1|) 4e-60

MEMVKRQEFESKWNVNVAFAPSTSTIDYKYIVKHSLTHELVSWEGLPGNRTLTIARGTNI

ALGASSTQMSTYTTSRAPVPGPRVAKLGNNGNTNGYQEWRCCRTMKETNPWWEVDLGQYY

NISSIHLWNAMTYHEQA

>contig31676 Frame-1F

MDESKPGAMRNSNHRGGLWKMGSLLLLRFSLTMRGLLSAHSKVLLSAPLQHRRGDDVIVP

LAPHAKALARAAAQIIKGHLYYITSATRATQIDTFVRQYYLTFVLETISSVLFEGKKKQA

NTLLLLELMKPISEICDVQVCTRAHPIFGNDIAIVDDDVSDAVMTAKTIANGAVAQISVS

NLMEVVMNIIQQLLCACLAEEISLSSVSTEIKASQMALTSFHIAASALRKLSNLELLSTS

PLTAALLRGDEAIESGTEPFEPEKLKLQLHAMCVRALLSIWKSPTFASLSADLCLFEIMP

IAVTILKNRVNSVTEVVESEGVARNEHKDELRRGSRERNFSTDFHDESLSLQRSLMDGNN

NGELLGTGGNICRQPLISDPEIIDNLISMGFLRSRVERALQEIQANNVVLAMEWILSHPV

DESRGEDVTLQPDKTSKVDNADALCHEMKAAEKNKMDDQLQALYALLRNSFEAVCFQILR

VQSRREVNLCLNRNVESVGSETVLFNQNLVKTIAEYFNFLCSQSESDCELVMRHLNRTIL

HYFDGAKEEGGDNYLAVLTHLLALVLRLHPNSWDVMQRQSPLCIDKLVDFISSMENGNLM

PSFTPVVLVLDAVVAGKAAMQNSIMRSPSYLCNKASDGNKEINSTSNFEKNHDEGTVFER

HLVNICLNMLRQRSFASSANESNATAHAVWQLLSRLTLKYDLASYFSAHGGLDAILDIPD

DWFFVGYQELTCALLSQALESPEVLEHSMEDKIRRAVAKLSTRFGSPNQMRITPRALLTE

VAPFAARNETVFLRALRNAVRVKKTESSRAYIVPRPADRTDTIPEQLEEQPFLNRESAAR

GTKALHKLPKDHKQQAHVIVNKIVGRIRRLWAVEKHTKKQFDVQDTVGSASARMCVGVYM

QLLVHLITHFPACATVLAKAKDETDSRDSFIYLVLREFLPSSGLCQFAKTRKKLKEEGYY

GIGRFDSSDTDLLVADIKSYIDNCTRMRVHNAHRLLVSVGGHSGEGSKCIISELVHLLQD

WPQSCVADSSIQNVDLSVRDEIALSSLHAWSGLIMSVLWPKGSSKGFAWDKVVLERGIKG

KNLFVTLLAEALRKIDLTHPLAHATCTMLLRPLSTLTRSFVTHRMKRMLKKRNDSAISGN

AGVVEVHSASNAGEGLLTVTGAPTILREPSTSTAGNSMAVNIETSEADNSAESNFYPLRD

DEDDDVSMRSPLSADSDHDMQDDDEEHSEDDGSDRSSVSGQSTDEGEGEDEGDDDNDDDD

EEDEDDDGGDEGEFEAHNHLHLSRRASLHGRRATSNRLWGSIESELSILDALDEVDEEEF

SYPFILDDEAYFAEEQQRRLSLAAARNPRPGDEARFTRNNEDRLVESMRDALGSLNTSGD

IESRNFSNQHTLLLTFGDFQESEEREGESLSDFATIENSMGREGLSVSEVQTPLTAGRMA

NSLLQYIEELPEMLDDDFLFESFDTSGRNDRSHRERQLVRPDPYAVNTTMHPMLRVNGRA

DAFLLESNGQLRNASRLPVSRHSSLLRELQDLTDQVQIQPTVVGSRSRLALGRDMLQRSS

GRSRGRTPSRVNRLSAVSNLLSDFSLDIPSSTLPSRNQRYNLRRGEQDMFRDAFVGVDLT

RSHTSRSGIVIGGNGSSPAIWGPSALGQDVDVRSVASRLEQQLMRICADDEPTVTPASGQ

GQTEASFQDIDDIMEECSTTRTLQSEQVVLSNTEAANVVEESHLQLNIPTSTNRTDSIEA

TADAASVLELTSSLGETSLLRSPPASDVEVDLADVGFVSIGNEVSLASPQAITSEQGSNI

ESTASSAPSSFVSAVTTATPSDAMLNFTLDLSAFRASATAISPAGGMPPSVEVPLTDTHS

SPA

>contig31917 Frame-2F

MLIIQKSVEWRENVHATHKFQPLRAKLTNKAKDRHQTLNAKSIGGTLLNTLLSQRHFFLQ

CC

>contig32552 Frame-0F

MHRSSLAKEGEILPTELPLMFNSTLE

>contig33021 Frame-0F

MTDAAAEEFKSQGNELYKRGDYQRAVEKYTQAIDAAPTVVAYYGNRAAANFMLGKHKDVV

TDCNRAIVFDPLYIKGYVRKAKAQLALGENDAAIKTYQTGLVRDPNNSTLLNEKRTLEMA

LDKFQRGKEYVAAGRFSQAVNVLDGAAQVCLGSNQIKLLRGEALIGCERFDEAFALLTQL

MRTNPSNPELLFLRARCLYYQGEFSTAIKHLQQALRSDPDNSKCMKEIKRIRQLESSKED

ANNAFKAGKMSEAVDLYTACLSIDPKNKSFNSKIHCNRANALSRLNRHEEAIKDCDKAVY

YDHGYAKAYLRKAACLKALGGLENLEQALRVYDQASKLVGGDAQRDIQSHIRQTKLDIKK

AKRKDYYKILNVTQSATEADIKKAYKRLALKYHPDRHAGKSDEQKAEAEASFKDIGEAYA

VLSDAQKRQRYDSGVDLEDLDSEFSGGGMGGGMNGVDPSQIFQMFFGGGGGMGSMGGMGG

QRYHFG

>contig33483 Frame-0F

MTRLENDFVDLLWSVLNEVYDAIEKFHRFSPNPVSTSFLKN

>contig33599 Frame-1R

MQLARRSFAIATVTRSRMQGLQTLSKIRMWDRVQPSLWHPLASLEQSLMELEMMASREVS

PRFSPFAPLTLDMLPKLNHDDDDFFKDLPLKRVGEMTKETLKAAEPKYSASRLPDDEETK

GSPDAKDPSASAAGTKPYPAYTSYSYTYSTVLDQNGHRIATTRRRYEDSTGCLKATHERE

IGDKKLNFMWQRSSKEDEGGLETICSSGSPDEFEKEWVDTPFGRAEGEKLTKWMEDRERS

VYDAFGIKHSKTTDERKICDGSNQEREDVIQKMSKRQEEETTPPQFTS

>contig34653 Frame-1F|Blast-hypothetical protein PITG\_19880 [Phytophthora infestans T30-4](gb|EEY53011.1|) 1e-30

MYVAQLRSKDEILAIRTAEREYAKRVQLAQENVKIVREELATCYRENGVNHKIACKALRE

EYGKLIQDPTHGAGYPTRPNL

>contig35052 Frame-2F

MMNAPQQPMQSLGLPLSHPKSVTSVSRNSSKSLPRPPLSNRMPSFKASILQQQPPRSNNE

TNRNYLENRATSEVAPHMTPEEAAVARQERSNSLAGMESLRSHVPGNGHTMNGKVIAKLK

KEMDHATQVVKTFLSPKLLQDQSIPRELLAEAYGLMFITIYKIGFLFLQKSVPDL

>contig35254 Frame-0F

MLALPIVDFSSSNASEQLRAACTDVGFFYLINHGISSVLISQVYTEMATFFNQPLVDKRK

VLANKYMRGYTQMNEETLNPKVQTRGDTKEGYYICRHVPMDSDEMGLPLHGPNIFPDKAQ

FPTFQVTMATYYVAMCELGYKVAQLFAKAAGEAEIFDQPGMFDKPMAALRLLHYAPEKSD

VANGVFGAGAHTDYGLLTLLSTDLSEGLQIFYKNQWIKVPPRQDAFVVNLGDMAERFTNG

IFKSTLHRVVNQSGKERYSVPFFYEPNLRVKSSVFRAVSRRQIRPNTCPPRVASTF

>contig35359 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56927.1|) 3e-43

MDDGCDVLECCLCGALCGACCASATDSGKNRRRNGRYTDNYHNQQQPVYVQPVVVQQYPE

YGLPPGHPGYAPPSQAYGPPIGEYYQYPPQQYAPGQFAPQQYLNAPKH

>contig36057 Frame-1F

MSNAISKASSSDTIDPLAGLFRRFPRLREVVDLEFRAAPPAFDFVPLELFTVTSSSAEAE

ATTFSKAAYCLSTGCLESLITGTSSDAISCCLRCFVDQFCAS

>contig36295 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54261.1|) 3e-55

MGSSMVHCNEQPTKRLGNGEHSWTTARAETFSVRSSDYKKSRKKEASKAALFEFVGADLV

RTESKVDLISQRVEFPAEYANSRLFIINAQLPSYGPSVWGDSSYDGPGYSLALYWKIPDE

VV

>contig37164 Frame-0R

MDMLKIEIKSNGIINSFLQYPVRALEVGFYRNHLLYLFLPEMAVIGALDGVLRSKGNERY

VMLKTIEISKVKEQARKIWCFLRHICRHRMIDIDEYVNTFLAQSAECDTDNLLHTVTVHV

KQWQSAKVVSFVLSLHWSFMDTLWLTTQGLWSLFDLKDKRRSQHEVVRQVQNLAKELVLR

QQLFHTESLCSESMIQSLDFLIESEVLQQEPSKDGKSRVLHILIDECGLENLTHEINARR

KPHTFLWRQDDLPMNLTRKEAVNLMQKAHDSCSFYAKWMAPPATA

>contig37490 Frame-1F|Blast-RecName: Full=Heat shock 70 kDa proteingb|AAA33009.1| heat shock protein 70 [Bremia lactucae](sp|P16394.1|HSP70\_BRELC) 0.0

MAQSVSGYSVGIDLGTTYSCVGVWQNDRVEIIANDQGNRTTPSYVAFTDTERLIGDAAKN

QVAMNAHNTVFDAKRLIGRKFSDPIVQADIKHWPFKLTSGAGDKPQIVVQFKGESKTFQP

EEISSMVLIKMREVAEAFIGKEVKNAVITVPAYFNDSQRQATKDAGAIAGLNVLRIINEP

TAAAIAYGLDKKGGERNVLIFDLGGGTFDVSLLSIEEGIFEVKSTAGDTHLGGEDFDNRL

VDHFTQEFKRKHRKDITENQRALRRLRTACERAKRTLSSSAQAYIEIDSLFDGIDFNSTI

TRARFEDMCGDYFRKTMEPVEKVLRDAKLSKSQVHEVVLVGGSTRIPKVQQLLSDFFNGK

EPNKSINPDEAVAYGATVQAAILSGNDSSEKLQDLLLLDVTPLSLGLETAGGVMTTLIAR

NTTVPTKKSQTFSTYADNQPGVLIQVFEGERSMTRDNNLLGKFNLDGIPPMPRGVPQIDV

TFDIDANGILNVSAVEKSTGKENKITITNDKGRLSQADIDRMVSEAEKYKSEDEANKIRI

EAKNGLENYSYNLRNTLNDEKLKDQIPEDDKKAIEDKVTETINWLDANQSAEKEEYEGKQ

KELEGIANPILQKMYAAAGAAGGMPGGMPGMPGGMPGMPGGMPGMPGGMPGGMPGGMPGG

GPPAGAPDQGPKIEEVD

>contig37803 Frame-1F

MGFTLLKGCHNTRMTNRIGKLITTVVLRTTLRAAKSVVKQSHPRRAHHELLVDSTLHPRG

RALTEEQR

>contig38099 Frame-1R

MKLFKQTPSDITGAPQKNVPNDIGSMEEWLS

>contig38114 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54116.1|) 1e-69

MHRTDVLQDADVKKLIFSAIEAALVGTLPDGEWQREVERARILERRMSMPLLFLGLQMRS

SLDNEPGHAWLKWFEEVAVAAEGLLMHLLHHINGFPSPAGVDQMISDCSEIYELDEARAN

GGKEAPPAALSFVFM

>contig38183 Frame-0F|Blast-60S ribosomal protein L44 [Phytophthora infestans T30-4](gb|EEY69005.1|) 7e-48

MVNMPKERRTYCKGKKCQKHTVHKITQYKAGKASKYAQGARRYNEKQKGFGGQTKPVFHK

KAKTTKKITLRMECKECKSKKQLPMKRTKHFE

>contig38820 Frame-2F|Blast-RIO kinase [Phytophthora infestans T30-4](gb|EEY66128.1|) 4e-60

MSLVDGCPLNQVRRLANSKDAYETSMSIVVRLAEYGLVHCDFNEFNIMIGHDGKITMIDF

PQMISTSHPNAADLFDRDVHGLVKFFSRLQGGAYTPD

>contig38969 Frame-2R|Blast-exopolysaccharide phosphotransferase, putative [Phytophthora infestans T30-4](gb|EEY53592.1|) 0.0

MKKISTGVRLRMALSHQQNLRYVLLAACGTLLLVMYLLTKTPTPYTYDKLSDEEDKRYNT

QTIMDQWPGKCQIKNFEQLRRISIVYTWVNGSQPCYRDIREKAGGKKAVGGSRDREIGEL

KFSIRSLEKYLPWHMGQIYVVTPGHIPDWIDLNNPRIKVINQDDIFPDYAQKFLPTFNTH

VVEQFLYLIPGLSDIFMQINDDYMFTKPVAPHEFFTCDGGIRLLHEAGLISHTPPTPKKG

IWIASVLNTQQEMDLRWGKADRHFIKHAPFVYSRRAFERVHQIFDRPLYMTLKSKFRNKP

DMNNPLLHHYYMVSQGSEELGIPVYSPPAEEMTGYKLILMKNDNIDKLKQIFGQILDGST

PFRIIALNDEYTDMRVAQTALDFLNKFLPEPSRFERKPDSKPHPLTVRKPGTCEVDLTIL

SPFPRRVESAPKYQVIAYRELRWVAFVNSLLRGIGFGLGLIMMYILYLLFLRRNKAPTGL

HSSFDKV

>contig39632 Frame-2R

MLIHLVRLGFQENLARTALEAGVRQIAHYDADCELAYVDIFMSLVKTVCDAHVDVATDSL

WRNKEEETYEEECQLLLPFKWPVFDMAQFEINNARPGTCFNSVCVLTNLPKVALDRTDEL

VEVLSCQLFCMVGDPIQVVVPSARTSGRTKGHAFLEFDDPKLAKKCAEAIDGLTWGRGPF

GQIRGNLFRQYQAKSFGEYAQQNFLCEARIDQACASSSIVEISRSEDEDFSLLRNRLERY

RPHLIENDCAVDQNVFCDSDDDSNASGDYVDSRPHECVQFSMSPLLDQSSGSVEQEQVLL

DEVDNWP

>contig40359 Frame-0F

MAETGILAGFLPALAKQVSESVVEVRGEVENVLHKRLESTGSKIKQAKQLNAVAKGSEKY

MTKVHRAFEKNFDKFELYVRRNIVSVPDALANEVAQIRAEKQINDKETTRTQEDKDAVLL

TQEESEERQVDTQLEALRLRLRALTSSNQRLCLEKKALEHRIQQFQALASQVAFLEDVPE

RTTLPLKRTAEHISALHEAFVQIDSIQAELVEDSRQFQKSKKATRGSFRNLRKRFTARTA

DLVYRTTEDLEELHSRLLTM

>contig40867 Frame-0F

MLGQLKTITYNQTTRSITRYTAQRYQEVRVPFKGTVYRLHNA

>contig40913 Frame-0R

MASTSTSPAVSAMAQQASQQYLQCRRSVTEKADEIKMLDKQIASVFQQISALSEVSEGHD

DMSEAKKAAAKSVGRLEVSLLGVEGDEPIRGATITVTLDPEYEDDEYDTVEEVVEKQDVV

VTDEHGNVVTDGHVPEEDGESTPRKLKKTTKITRTVIKKRIKKEPVLRSIAWTASDQSDE

MTARTFPISFVFDPVQSREAVLIITVAAAIYNNDDEEPEIVKEIEVPISSLFQDKVLDQW

YIIVDEDEVPTSITELKEESVSETVTEEALETSQETEAFEQVTKDSEVKKAIKDGQDTED

KAAPIEEIADKAKTELPEETAKAEDTMEKTEENALEKSEEREKTNGMEDENEKTTAEEKR

IDEPKATGSRIHVKASFELSEAETLSLSVVALSKEKQEAEATLQELEREVSVLRTKYERV

ATSQRRVNVSKPKSNLLSTRFSASSVPMQRKTWYQSSYERVTGFATKHQQLLVSTAMFTG

SVCLFHFNGENLLA

>contig41411 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67960.1|) 3e-66

MSSCSQTLAGVGLFIFNGVDLVAGMVLCAYSLYLGINHFAPLWLYIPLLSIGSVLVVASL

MSSFGLVFRSCSGCMALSSSVLIWISLAELGLAVVILTQGENIGNFLRKHGHELKLSDAQ

IATFKCHEGYPAYALLALCLMEALRQRYSTTLHHMRVRRQYQYEMLA

>contig41653 Frame-0R

MVSIQKILTSIQFSIDRFDVTHDSTNTP

>contig42366 Frame-2F|Blast-MAP kinase [Phytophthora sojae](gb|ACJ09359.1|) 0.0

MKTLSTILDVILIPPNVIDFHDIYIVTDLMESDLERIISSSQPLSDAHFQYFLYQILRGM

KFVHSGNVLHRDLKPSNLLVNSNCDLSICDFGLARGVEMTYNEDLTEYVVTRWYRAPELL

TDCQNYNDAVDVWAIGCIFAEMLRRRPFFTGRDPSDQLHMIIRVLGSPSEEEMAFVPHEA

ARRAILQHGFYPKRPLIEFFPDANPLAVDLLAQMLKFNPAERISVIQALAHPYLAQLQNA

ADEPVCAAPFNFDFERESLDLGIEMPKTELQRLVFQECMSIHQVEPHHMQ

>contig43501 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56544.1|) 2e-61

MSIHFKFKSAKEFDTVTFPGAVIRVLDLKKAIVDKKKLAKGLDFDLVITDAQNGKVYDDE

NMQLPRNTSVTVKRIPSQQPGSGLLARMKQEAAVAAAAAAAAAMHASPPVTSIAGPSPVL

PVGSSPVQP

>contig43682 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66787.1|) 0.0

MPSTPREEHRQYYQTVASATASILSIIGSCYIIGRYWYARRLKAKSLSVYAASAHHLDVT

KELIHIIAYLDLFGATGRAFGVLPTETFDQDAGEPVTPICKLQAFVITFGDGAPIVWNFI

IALNLYRWVCMGEDQQMLMKKIKWYIVSTLAFTTSIPFICLVFNKFGDAGLWCWVVVDDN

STEELLWMYGALYFWVIVGGTAMTVFLVLVKINMKKRLKSNQNDDANDAYYVVVHNLTFY

ISGFIFCWLPAVVDRAYTTITGKTSFTLDLLHATIVPLQGFVNAVIYGKFHIWVVRHVRG

PWVSGCEIPMKPTKAPSEMLQQSMRWREQERHQMGTATIFVTTFDMNWSSCPTNLKDWIP

SGKDLYVFSLQHCVDVQAIEQAIRGYLIQVNFPTAYRSITSIAGTAQRGHHQDASVCQIV

FVNNADDASGNVKFQAADGRIWAQRKTFNEVVGIPIRYFDASIAFVSCNLSTSLSNSSQR

LYRPVDRILAKHAVASSLIHSFEMDADRAAVDFPNLYHHT

>contig44391 Frame-2R

MADTATDNQPEPAPENIDNFGDLLAQLLQSLPSEASRLFLMALSGLSPSESAELCRYVDR

LRDEKQFRVIKAVAESTVDGKKKFIVNLRNKFIVQQAKLAEVHALETQNMESLMKRKQAI

TASCRVKMLNGNANKFHSFNAVVGPDGPETDGHKLMAQHLAGMPNADGVVAGRSLSSSSV

VISKEDINLMGSLLSNSHIADSEMNLRELEINKKGFSLDNKDSATFELDQEVLASKRDRP

QSSRALIEGEQKPTQRTRPDSAAYAASAYAASTSEIADNFSQMDDADENVDAPTTKRWTK

NQDAALRESVRIHGEKNWKAIAELVPGRNHAQCLQRWRKVLKPGLVKGHWSFEEDQVLEY

LVTQGCNNWGQIAERIPGRTPKQCRERWKNHLDPAINKGPYTEEEDSVILTAQARLGNKW

SQIAQLLKGRTEDSVKIRWKSLKQNPSKAAASHAQHKKNQQQAQAVAAQHAAMGYHNSAI

MRQRQLQLLQQQQHLQAHNNAEAVQQLDQQQQMQQMRLHEKMMQQQIQQGQHVSHVAMLT

EDLKTEPYQSNRAMLMGHSPVGDSNLYADAAYAQQPYDAPQQFDSQGYVANNCYDPRYYE

RETTTSSQGASPAHPTDQQEQNSHNTWLHTSTPDANGEIDQDGMSRVGNNPQQQSQQLQQ

PGADGAGMWDPYPRQETSQLSPISLQVSEFLF

>contig44892 Frame-0F

MASDSPYSPASSAEDSLFTNDSESSDGSASSEHSERHVSPVRSSTMPSGLTSTTSFEPLV

DDDFDDEVQILTAVEAAAEVAAAAKKALTEPTRKRKRLLIETRPEPTECSICCEDCTLIG

RHRLVALKCGHLFGK

>contig44917 Frame-1R

MAGRSSSSGDGARRNAAVQRLIDGADQSLRLLASIGEAPELEQSRSSGFGVGSTIDKGAD

SLHFSSISGSPDKFGLEQNFKINNENLSNDNDEETRLLEPVVTTSVRQGRLHVKGVFPDQ

STEFVDIEPRFTTIKDLKKALCEKRDSVQALG

>contig45073 Frame-2F|Blast-caltractin [Phytophthora infestans T30-4](gb|EEY60867.1|) 2e-16

MARRLSQKRNVKTYERPGLSEEELEEIRKANNLFDTDGCGTIDPKMLRAAYSQL

>contig45510 Frame-0R|Blast-unnamed protein product [Vitis vinifera](emb|CBI19201.1|) 2e-10

MGLLDGLILGLARKSKFGRSHSLRPLTSKRANRRFYKGNGCRNEGTHAKRGRYVVDKDKL

LQLEVPDLTDFK

>contig45679 Frame-0F|Blast-putative P-type ATPase [Phytophthora infestans T30-4](gb|EEY60521.1|) 0.0

MTCSINVDVVITPSLSLNNGQVLSISSISEDGGVLSQASSRAHEDVTCALRVDANYGLGQ

LAVRERQRECGLNELAMDEDESIVAKFANQFKDPLIMLLMGSGLVSVAMGHTDDAISIAV

AITIVVTVAFVQEYRSEKTLEALKKLVPPHCKALREGNVVDMLAKELVPGDIVVVDVGDR

VPADARLIEAVDLEVDESNLTGENAPVSKITSTIADSHLNPVAERKNVIYMGTLVRAGRG

RAVVIGTGSRTEFGQVFDVVNNVEEQKTPLQHSMDTLGKHLSMFSLAVIAVIVFIGAMQQ

KGVLTMLQIGVSLAVAAIPEGLPICVTVTLAFGVMKMAKRQAIVKKLPAVEALGCVNVVC

VDKTGTITTNQMEVIEIFVPFESVYAIVNGIGERRQLCGSGFESEMERAMPTVTMRSDPV

TEASHPHIYHCLLSGALCNNATIVGLDVLGQATDGAILLCAQKVGIVPAVIQQFRRVSEV

PFSSEKKWMAVCCKSSSESFPRWHLKGMTEAILSRCDKIEDNCGREKEMTPGDREHIYMA

SQQMAERGLRVLALSFGEHSDRGMVFAGLVGISDPPRPEVEKSVQELSLIGVKTIMLTGD

SKETAIAIATKVGIVSKTNFGGVDSDEETSKLLDEFVISGQELDIMDMIQLEQRILKTCV

FYRTSPHHKLKIVRALQAAGLMVAMTGDGVNDAPALKAADIGIAMGTSGTDVSKEAADMI

LLDDKFDTILCAMEEGKSIYHNIKHFLRFQLSTSISALCLIAFSTLFNLPSPLNAMQILW

INIIMDGPPAQSLGVEPVDHDVMKEGPRSKDANIITRIMIRRVLTSACFIVCGTLYVFWV

ELSADGTISKRDRTMSFTTFVMFDMFNALSCRSDNKSIFEIGLFSNTCFVYAVGASLLGQ

IMVIYFPPLQVTFQTEALSLSDLAYVTCIASSVLVFDELRKLWQVRKGRGALRSASIAAG

FKPKKRKLSWGHDNKAYDTV

>contig45828 Frame-1F

MNASRSSQRSLKIRDKTEPPYNRKLLVSIIQMWHNNRNDSSKVKLVAHRYCFPLLWWLAL

VLCINTTTAMNAAPNAIENQGAC

>contig46414 Frame-0R|Blast-Ferroportin (FP) Family [Phytophthora infestans T30-4](gb|EEY68156.1|) 1e-07

MLVIGALMLIPITGCLYAARLDSCDLLEVLKKPLLENQEQHDLKPFRQPRRVKMYLYARH

LLSAWG

>contig46483 Frame-0F

MAVKKTAKRVRWSTVTVYEFGVALGGSAVPRRGGPAVGLANTPQHVWSTTLEKVRRCGDL

ALTRPGSAVSAHDAEQKEIVCVSSHLKKRKRQVRWFKPLERITMLTNAGCNEEIIYRMML

ESSDIAMSRRLCVSLQRQVAS

>contig47552 Frame-1R

MLQDLRGSRPNYSESAYECYLAPVRLVMPIDG

>contig47659 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69296.1|) 3e-66

MTIAQLILTVIEDDICSIQYVFDVEANLERLVPIVTGIVQYIADVTTIVQSAEDDETFSN

SDAYLHSVEVFHLLTKLCKCSKVRSLCAQTISLNQSATLIQAEAALIGCVDPQHLICFQP

QLSIHLVSLLSNIVHDESMGNKNNSALVHFLQTDEVSTVISAALCNGVNKTTVKQALILL

VQTLVRSSSNQINVIQFAESVFRYNQRVGE

>contig47754 Frame-2F

MCLNALQIDPGRLWKGPWRWFSEELFECCTSLSVAKEKGISLSEFLYLARCNGVITEDYR

ATKDFTLEHFRDIVKRSCATSSEIVVLNYSRKVLGQTGDGHFSPIGGYHAQEDMVLLMDV

ARFKYPPHWVKLSRMFESMQLVDPAMNLPRGLVVLKEGAEVTCTKNNVRQLMQCNDNTAP

IFSQPCCSSSPSSVTDGRRMPNLAAPAKLKNWRCIC

>contig48126 Frame-1F

MKKKPKKEKPKSIMKALEVLQKVMANDLNCTQHVHVRHAVEKIKNWICDFSAQDKIMNGY

KKFAHHFVTYSNKIDDPHMQNDSQKLATGLLRLISTRKRKVSTDLSHSTSAKTSKNMRNR

LVDVLTQAEQFKSGNFSLKQLNQVVKSYGDIMSYQSSEWNPLKD

>contig48489 Frame-1R

MTHNRRLVLAFRSCNTNATGLLEFSKQDTLAGACSTHHRFAGT

>contig48580 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66320.1|) 1e-30

MTATQGGVPVSQESLDAFVTTQILDNGMDMVANRINLLHDKLLQSGSGEGDEQNKKRWAR

RLQHWLAVACRLLAKQRRQLTKCIDHIEYDYSRGVVG

>contig48841 Frame-1R

MATLLRLAGEDTDAAEKDSLHDHHSLWRARVHALNILKLICQDGVLADDVAQYVVAMFEL

AVQGFECGSWAVRNSSMMLFAAATQRAIGDKRIADGNSHQLVASTDVFSRFQKLRSVLGR

ELTRMLANESKSTSALGGASPPGLYPLLLFLSRLRPGDEEDQRKTDAGASFKSNGTGLAT

FVPLVLQCASQPTMAIQFMASKALASIVKDTDAASVVLLLLAKLPRGNGRAKDSVAISHN

TVHGILTQIRHLATKHLARNSPSTVRPTSVQVDFFQVIAS

>contig49235 Frame-0F|Blast-calcium/calmodulin-dependent protein kinase kinase, putative [Phytophthora infestans T30-4](gb|EEY66793.1|) 0.0

MTGSTRSIKGPTQERMITHLRAGHYFGELALIYDDPRTATVRAVGDVELLYLTQEDFQHI

GQVHLSLMLQQVPLLARLNARDQDIVLKCLRPANFSDGEYIVHQGDEGTRFYMITRGEAI

VLEKSKGPDNKPYEKELTRLYEGHVFGEMSLIYSEPRTASVRAAGPVKCLYLSKEDFDKC

LLSDHFQRFIQEAYVEKATRRAMRLRLQQRANSAASVAYARQAVSGTNSSSGSIVAPPAA

PLPSPVKATETKKLVKQRLKNGEVVVNKYVIKGDLGRGTFGRVKLCESQEDGRMYAVKIM

HKTFVQRMAGKEDQLYDVLRREVAIMKKLNHHNVVRLVEVIDDPNSQKMYLVQEYVQHSL

MEEVTQARRLNELVARKYMRDLLSGLQYLHFHKVIHRDIKPENILVSSDGVAKIADFGTA

RMIMNETETISGAKGTPAFMAPEMFDIDATYQGPAVDVWS

>contig49419 Frame-2F|Blast-reverse transcriptase [Phytophthora sojae](gb|ABG66531.1|) 2e-29

MARPLSNLLKKDTEWCWTSTENNAFRAVKDSLIHAPILALPNPNWPFSVSCDASDFAFDS

ALL

>contig49503 Frame-0R|Blast-aurora-like protein kinase [Phytophthora infestans T30-4](gb|EEY65332.1|) 1e-119

MKSNMEHQLRREIEIQSHLRHKSILRLYGYFFDSKRVYLIIEYAPQGELYKKLMRAGRFS

ETQAALYIQEMARALQYMHSKHVIHRDIKPENLLLGFHGELKIADFGWSVHAPSSRRTTL

CGTLDYLPPEMIENKPHDENVDVWTLGILMFEFLTGAPPFETENTKETYRRIAHVDVKFP

SHVSPEARDLLLKILRHDPQQRLSLERVLEHPWITQ

>contig49697 Frame-0F|Blast-5'-3' exoribonuclease 1, putative [Phytophthora infestans T30-4](gb|EEY67074.1|) 3e-27

MGIPRFYRYMSERYPLLNQPISNVSLLPEFDAFYLDMNGIIHNCTHSDAADDALNSLSLE

>contig49990 Frame-2F

MTIVGTSCFMTRCGLQIYLSTEKRQLHDRSTWFVVVVYYAVLEIVPALSVLYFNRRLPPR

QKLASPIRGPIRGGRLFFGQGMCVISAYDEEDSLRKSLLR

>contig50013 Frame-0F|Blast-farnesyl pyrophosphate synthetase [Phytophthora infestans T30-4](gb|EEY57170.1|) 1e-160

MLDLLRSKHQLPQDALDWIEEVVEYNCIGGKLNRGISVVHCTQAMAPGKILTSELKGKAI

VLGWCIEWLQAFFLIADDIMDDSMTRRSRPCWYRKPNVKMIAINDAFLLESFVFQILKKH

FRTEPFYLDLVESFHEVVLHTEIGQLLDLTSQPLDGKVDLGRFSIERYRQIVINKTAHYT

FYLPAVCALYLNGVVDEASHNLTKKICLQIGEYFQIQDDFLDCFGDESVTGKVGTDIQDN

KCSWLVVQALNRATVEQREALKKNYGSNDVECVAAVKQLYCELDLVGVYRRYEDDTYKSL

TDEISKVKMMPSEVFTLLVNMIFKRNK

>contig50084 Frame-0R

MAASSFTRSLFIARCTSYWRATCSAKTRELPEDLLTFLPGEELLNLRNIDTEVKETGLAM

KGARLRDWNYSDLLSILSEIIRLKLLMYKEYIR

>contig50251 Frame-2R

MTVELEKQPLTPMNFLEGSQGSCSADDATNCHDLQSPAAASSAPPSTRAADAEHAQSMCP

LMSESAALSSSELLGPLGVECDGLGIKGYLSMRDEGVTYHRMKRFYCRCVGISFLRFYSR

DAATAMIAALYSAEVQKVETWDGKGLWHTYRYSFKLSLTSGVVFNVDADSEEDKRQWIEY

IKMAIKGTEAAVQIWRAHTSDDTDLMELTPG

>contig50637 Frame-0R

MVAQCVPCLALSNEEGAQSPFSQVLCCVVSAPQPEYSLFCLANCSGYLVSISNSRHTNFA

PLSVKAIGFLLHHCAVQSYSHDGEFNKIAIVLSNACKLARENFSDLVNPLSLQGAATSLL

DEDISFLTVNKDGQPKRLKIFECLFHFDYANTILYTTQLCLQLARLGGAAALKVLGTQAL

ERLNFHSDERSNPYFVFTATCFILLSRDLADLKLADDDDTLHLIKILDLITSALDKRNQR

QSEFNLRQLCLVMKMACGLIEAVLQRVNDHSDAAETLKRASLRILELATWLLPTKAMVLQ

DYQLSTETL

>contig50952 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53165.1|) 2e-48

MDVWFVTTQYPKYGVYPPYEILSHPAVSIHSRPFFMHVPSVYLAWDSNFGVIALRRRERQ

LAVSRCGVVLAGTYFKIDQATDLQIPVALKIMDRAQVLLQHDDVESEIRVMGQLQVGGLD

APLANAYMIRWEYASDAYNQYVAT

>contig51014 Frame-2F|Blast-oligopeptidase A, putative [Phytophthora infestans T30-4](gb|EEY64174.1|) 7e-44

MLRLLPTLKRACNRRTVFQRSVFSTSTNLLEACVRARKLPPFERLQLIEIEPAVTNAAAK

FRRDLHELETKLREIGNDVQFNDIVEPLETQSDALDRMWGIVGHLMSVRNSEELRAIHEN

LQQLVIKTMTRAS

>contig51083 Frame-0F|Blast-diphthamide biosynthesis protein, putative [Phytophthora infestans T30-4](gb|EEY63922.1|) 1e-26

MTVALAFESDDGSRAIAAQVHVEVSDGVRQDQCDICIYYDIARTVDQIRWGGYTKIALQF

PDSLLPDAPEVQQELKNELQG

>contig51199-0 Frame-0F0

MSLSPCRGTSESFEEFNAGVSQEHSASRVTSWSFGAGSQQPPLAPKGLKRSVGSSANLTV

ASGMSSLTSSLLPSGGSSNLNAVNEAGAGGIARGTGPAPLNHFNVLSQGNSGHTAGENAD

RKFL

>contig51256 Frame-2F|Blast-exopolysaccharide phosphotransferase, putative [Phytophthora infestans T30-4](gb|EEY53591.1|) 0.0

MKSFLALLGFALTVATFLLMRQEPNPPARLADLISGIPLINGSRCDVANLEKLRHSSIVY

TWVNGSENCYNKRRERAGMLHGGTSRDKEMGELKYSLRSLLKYAPWLEGPIFIVTPGQIP

NWLDMSNPRIRIVDQDDLLPKQKNQLLNCDTNVIEQYLHKIPGLTDIFIYMNDDYLFIKP

VTPDRLFSCDGGIRVLTEINHIRHVPSQKSNAWLASVRNTVMLTDQTYGGQHVYNFLKHA

PFVYSRLAFEEIHKKFSKELDKMLVHTVRHPDDLNIPLLHHIYMQEEGSKLLGIPMELNP

LTECDEWLLVRIKDNIDDSLNEQFKMALENKGSEVMLALNDEFSSPKTAELVNRFYAKLL

PDPVFFELPEGQHLSVV

>contig51920 Frame-1R

MVAERSQHEMEQIRAQLISVQQEKYVLESKIGQLNDLLDEKVQLLQEVDEHKRVNQLLQE

TNRELEGLLQKSKAYCDELFRESEDKVSRTQEFARHVEQEARGEIDRIVNENNELRVELE

QLAQTHFEETAVHDELRVKLAELQAENNVLSARAHRLTQQLSQYTELPEDELAAAAQGQT

PDLWELLSSGMEQLKTDLELASKYAASIDAGSVDGGVGDELFSAAN

>contig52077 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY53787.1|) 1e-99

MFAADFIISNGAGMTINFFPLFFKEEYKLTPIHVCALFMSQPLVVMVLSFVAQRMSKTCG

RMPIIVCTRAFSVACLFLMAYAQPIAVQIALFLMRGGMMRCSQPLRRSILMDFVPQNMRA

RWNALEGLSVFSWSGSAVFGGYLIDAYGYRACFVLTSVVYCAGLSIEVLLLPLTKNAIEK

>contig52132 Frame-2F

MSDLHVEITPVHYSDTEESKTEESTPPHVLKNVGGNTFAENHGISAEAGGQAGQIMHGLH

VSSKSPLNPSMKKVASLDKTKIDKTKIDDAATEMLSWVSGYRDPDVIRRKENMRQKRKQP

LRYGVSSEEEQLQIMLQVKKITRES

>contig53078 Frame-0R

MYLELPTDASDGSRRAGLMLDCGEGSVGQLYRYAQGNKQRFQQLIDRLQCVWISHNHADH

HLGLLRLLDCRTPLVEPLLVLGPSPLR

>contig53193 Frame-2F|Blast-DIS3-like exonuclease 1, putative [Phytophthora infestans T30-4](gb|EEY59681.1|) 1e-107

MSIRCLPNGNLELGVHIADVSYFVKHGSALDLEGRRRGTTVYLVAQRLDMLPSVLSADLC

SLHENRDRFAVSVMWELDGTTYDVVEHSTWFGRTVIRNCASMTYEQA

>contig53315 Frame-2F|Blast-hypothetical protein PITG\_03168 [Phytophthora infestans T30-4](gb|EEY65656.1|) 1e-09 NOT\_ORF

MEVLSTTSISDKVAARLIKKFISSKEEEDNTDLMVRS\*IAGRRNSS\*L\*FVVMKMNDEVK

FQLAQVLA

>contig53360 Frame-1F

MICAGGEVSEGICMGDVGGP

>contig54578 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60517.1|) 8e-20

MQLRSNAKQLQVDFFRAASSRSGREVALNSVATAAKMAQALNTPETKATTQ

>contig54615 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61888.1|) 2e-20

MSSAALEPEELQEEPRWRSIRYSPHARPLHWSRLIDEKLVLLVIESTTSGERFPVGVNWL

EVSRVV

>contig54822 Frame-0R

MYTAHPIALRYGTFAIPSSWLHPVGHTAKRCRKSKELMQFR

>contig55788 Frame-0F

MFTRSLLAIPVRRACSLHIAADMTELIGNTPLVYLNQVTKGCHAKIAAKCEFMEPCASVK

DRIGLSMILDAEKSGRLRRDSHIIEPTSGNTGIGLAFASAVRGYKLTLVLPDTMSMERRI

LLKAFGCNVVLTPGEKGMTGAVAKAEELAAREPQKAVILGQFDNLANPQIHYDTTGPEIW

RDTDGQVDIFVTGVGTGGTLTGTARYLKPHKPSIQIVAVEPEESPVLSGGNPAPHKIQGI

GAGFVPSVLKRDLIDEVITVSSPEAFAMAKRLALEEGILVGPSSGAAVVASLQVAMRAEN

TGKLIVTILPSFGERYLSSALFDQEREFAASLPTSALP

>contig55968 Frame-2F

MLYCPTTATKTRPATPSSSGGPASLIHIAATIRSPQVADSATARLRVDNFTAVVHAVWR

>contig56312 Frame-1F|Blast-DNA damage-inducible protein 1, putative [Phytophthora infestans T30-4](gb|EEY58045.1|) 1e-19

MKLHEIPANPTPETLLDIMEKNPQLLVE

>contig56635 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY67308.1|) 2e-47

MALQAEASRFFLFWLTLVLFNIAAGSICGLMGVLSRQVGSANLAATVLLLLMLLFGGFLL

NSATMPDSVAWLQHLS

>contig56864 Frame-1R|Blast-UDP-glucose 6-dehydrogenase [Phytophthora infestans T30-4](gb|EEY67959.1|) 0.0

MSEFKMTICCMGAGYVGGPTMAVIAYNCPDIKVVVVDVSEMQIAKWNTPDDIPIYEPKLK

DLVDARRNKNLFFSTDIDKYINEADIIFVCVNTPTKTGGIGAGSAADTKNCEACARKIAD

VAITGKVVVEKSTVPVRTSESIKAVLQANSKGLHFEVLSNPEFLAEGTAIDDLQQPSRIL

IGGAETLEGHAAVEKLVSIYAHWVPRERIISTNVWSSELSKLVANALLAQRISSINSISA

VCEATGANVHEVARAVGADDRIGSKFLNASVGFGGSCFQKDILNLVYLAESFHLPEVAEY

WRQVVQINEYQKMRFATTMVRRMFNTVTNKKICIFGFAFKKDTGDVRETPAATIIKCLLE

EKAHVAVYDPQVKIDDLMHELEYQGVNKTTFPNVDTLLTVYSDPYEAAKDSHAVAALTEW

DEFQTLDYGRIYNHMVKPAFFFDGRNILPHEEISNLGAKVYVIGHAEVISGNLAF

>contig56958 Frame-2R

MTRRHIFLDTNVETKLSSARRLSGRLRA

>contig57526 Frame-2F

MIKGTPQHARHPGGKKRLSGRNSDPPEVRLSKKLAY

>contig57724 Frame-2F|Blast-nucleoside diphosphate kinase, putative [Phytophthora infestans T30-4](gb|EEY55197.1|) 1e-101

MPAAKVRAYYESKHGGSHRLGADFAFAQALFICRHQDDALEKLYAEELLELYRETDCFDS

RVDQIAHAPVIAIELLQIDCIKNLQEIVTTLSTQFNAQAHEFECAESILEAQVLRRFYLE

LPHASTATFANCTCCVVLPHVIKEDALGNVVAAIQCDTHVRITAMEMFYLDRTAACEFLE

IYEGIVPHFYDIVDQFISGPCLALEVVGHDTSDVVKHFRAAAGPWDVAMAQTL

>contig57827 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58142.1|) 5e-54

MLAQQQEVEADVRKEDQLRINEFGRHNAALHEIRAQKNALKDKLDTLDDANADLMMGEGD

NTRLFIGESFVEASEEFAEEYLLERIEEANDKLEKLQVEETKLEARQAVLKKMLYSRFGQ

SINLEDS

>contig58134 Frame-1R|Blast-beta-catenin-like protein [Phytophthora infestans T30-4](gb|EEY69790.1|) 7e-08

MAQLRKLVEMLEAKESLLTNENDDAIKPSETPTLDEQTTLLKEDEMSDSYKPTPLSSRSE

>contig07142 Frame-0R

MRNSILAFNELVDLLVQFMENVYTKKHEDVRKQVLQLAHPDDGKGWPKGVCGHTGSLKLL

SFSSFLLTFPIPTTLFKYTSTPQNAP

>contig08334 Frame-2F|Blast-proteasome subunit alpha type-6, putative [Phytophthora infestans T30-4](gb|EEY56965.1|) 9e-84

MRAFGVITMLISVDEEKGPQLFKIDPAGHFWGYKATSAGVKEQEAQNYLEKKIKANPSMD

YETTLHTAITCLQSVLSADFRPNEIEVGVVVKGERFRKLTEDEIEVHLTAISERD

>contig08464 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59994.1|) 8e-12

MTSYSKSYVFPLALRDAWKKEIGIRTREKLTDMLGVEVDNVMA

>contig10300 Frame-0R

MKPFLHKYLRKWRPPPELHRQNAMPHMKSYARFNPHDSEAGELDWAIVTSSNLSKAAWGT

YQKNKTQFMIRSYELGVMFLPPLLKCQSDGSAPRLVTIGSKSASHFNAAISDTRPMELLP

LPYDFPLTTYDPQKDEPWVWDLVRESPDVFGNAYIP

>contig10443 Frame-1R

MSHYGPPSNGTAFPRGLTPPLQNPPSIVPRGMVPLFQSPSFPARGVPPSFPFHGPPAAFR

GPPRPPLGINLSPLMATTPYPVPPGRPLNWNDTRVPPNSSYYYHSTPGVLPYDLPPHESS

GFTWVEYHDNATGASYYFNQATKETVWEEPEELRMQKAREQVAKMTTAVLEANAPSSSLH

ASLKPPVSSIESNAISSPVHTHQDDKTTTPPQPLQEAPKQAPIHQTNLLEHAEYTT

>contig10638 Frame-0R

MRPPGNPASFSELRKFGQSGTRTLNT

>contig11848 Frame-1R

MLCRNTTLEYVDLHGNFIGDRGAKALAQALYGHDSLRHLCLSNNIVTDCGASALAEAIRC

NCTLTSLNLTNNQIKKVGSEALLHALDVNMHLEGLYLEANDVPAFVVSQLAAALARNRAE

SLILESHAAEKEAEKMRLKACGLDTEMIDIEMEKNEVETWDDDDSDSASSGFLSCSGLTD

VPLSSSGSWI

>contig13749 Frame-0F|Blast-putative chitin synthase (Chitin-UDP-GlcNac-transferase) [Phytophthora infestans T30-4](gb|EEY61714.1|) 3e-39 NOT\_ORF

MESCFSFISELPDIFSVYRFETIRGTRLKAYFKTLHTKPDFYGPIVGNMYLAEDRIWTFE

VVARKKC\*\*TLHYVKDTAVCNGFRYISIMSYTRNNYYFFLLK

>contig13947 Frame-0F

MKYPYKDYKNLGEFFSRPLKDGARPIDPNTDHIVSPVDGKVLSTGFVNDSTVPMLRQIKG

SSYQLDELLGSIPSFFTEQTTGKNIYYCVMYLAPGDYHRVHSPVDWQIETRRHFPGNLHP

VNARAVASVPNLYLVNERVVLSGEWEHGYFSLTAVGALNVGSILITKEPEFRTNVAAQDE

LIGQCLTKNYSDTMETTRGEELAQFNWVPRSCWYLRLPIHFSLRSHRTRN

>contig14331 Frame-1F

MKLDGCFIGACTTTQEDLILGALVLQQAMLEGKRASMKGKRRVTPGSLAIIDRLKQLGLI

RIYEEAGFTVGVPGCSYCVGIGADVAGEGEVWLSSQNRNFRNRMGKGSIGHLSSAAVVAA

SSFDMEVVDPLPYLNKISKDVFDRYRNWVEPDASTPSRAKTPKTYTITEPKPVLALPNDD

ERQQQAKEQAAVAELEAVLPPKFCGKVQQFGDNIDTDAIIPAQFMGLNKSSPLWPADCAT

ELDVLAAKSFAYVRPEFPQKVKEGFSIIVAGAAFGSGSSREEAAICLKAVGVQAVIAKSF

AYIYARNQPNNALLGIVVTDERFHELAVEGEEVAIDLQNRVVSVKGHQVAFSLTQLEEAF

LNGGGLESLFKRHKADLFRAAMRGKAPKVVASGGVGCGDSCDDDFAVSSW

>contig15475 Frame-1R|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY60658.1|) 4e-36

MFMNEDEAGYIVQGYVESELPNGDINTYSGTLYLEENPLGGAAEGVPLSLKNMLMRGSKL

RNTSFAYGLVVNTGVDTKIMMSS

>contig16096 Frame-1F|Blast-geranylgeranyl transferase type-2 subunit beta [Phytophthora infestans T30-4](gb|EEY65700.1|) 0.0

MNRSLAQPPAFDLALHVKYVVGLKNKNEDFESCMMEHMRMSGLYWGVGAMALLNREADME

PAEIVGWVLQCEHPDGGFSGNVGHDRHLLYTLHALLVLAMLDALDRIKRDECANFVASLQ

QPDGSFAGDKWKEIDTKFTYCSLSALKILDKLELINVESAMAYIDTCRNFDGGYGNIPGC

ESHGGHIFTAVGALSLGFALDQYVDDELLGWWLCERQCDSGGLNGRPEKQADVCYSWWNI

SSLIMIGKLDWISKEKLIEFILACQDPEDGGIADRPGNVADVFHTFFGIAGLCLLGYFDR

EQKNHPEYRGIRQIHPSFAIPTDVVEKLQLSADMIMPEVHK

>contig16535 Frame-2R|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY70003.1|) 7e-07

MFPVKGPLNVTLTPVAGLTTTSGKENDL

>contig16702 Frame-0F

MAVLTSEDLKISFNFFCTVYGIGTLGVPSNFARSGLPMATFALIFMAFANICSCVAISRV

MLAAPPSVKTYGDVGEWCIGIWGRYLVVFVQFGVCCLVPCAFLVLGGILLDGISPGAFDQ

EYWSMIMATMLLPVILTPTLKEGASAAFAGCIGTLFADAISLGVLTNGIGANHRAIVNPN

YDLSQVVSSFGNLALAYSAAVLVPALQREHSQPERMPRVVAFTMFVAACLFLIIGTTSYV

SVGCQIPGNLLFAIGGSALDLHADRGLVVLAYMFMQLHITIAFSVILNPVLYIAERGILG

MHRPPHGATLDEESPAFAGSDTPHRATTSSIAEAKYDQSPQALVDEYRTCGTVMIAKYVA

LRIGIVVVLLIIAILFKDHFVDFTDFVGAWAVSMACIILPIVFYLKVFWHVLPWYEKATG

VVLIVVSVALGSYVTYTTGKKLFLDVKSDKVFQYCP

>contig16830 Frame-2F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 1e-160

MSEHHYELDSKAAANTAHRGPSGHGETDRRRRASSNYFELDADRRRNKSERSERFSKRLD

TMDVSTSSFKGAPQDDEAAVDYCCEFLKAKFGFQEGSVSNQREHVLLLLANGKARCSASD

PTDHHLVQLANKLFTNYRSWCKFIHTPAVSYTGNNIPHATPSGNLHMDVMLYFLIWGEAA

NVRLIPECVCYLYHQMLTMVNADSHGQEQQPEGWYLNQVIRPIWREASNMKRRNALGKPL

EHVKIRNYDDINEYFWKPHCLTIAVTKVGQELTDNHGKTFYEHRSLFTMILNYYRIFQFN

MMYLVLLTVLAFAVTISPGGGQGGLSQFE

>contig16984 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63371.1|) 9e-08 NOT\_ORF

MDRLR\*SYKRVSDWEHDQHVTKIWHIRGLAFGQQKTIAAKLALEGASKMGRSRREVTVED

INSEFTRFLKIPSDRRLSGIGIAALMA\*FTEAEVLQAVKVLNRHLAAGSDGFNDDFYKST

>contig17837 Frame-2R|Blast-N(6)-adenine-specific DNA methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY53907.1|) 1e-104

MEAFLSSELSADTFAALQAHLNTTETQQKATISEDFRLSQFWYDDRTGRALAQEAIDQSK

EKRIAFVSTPAAFRDFLKIQNESESPINSDNVFLFEYDRRFDEKYHGHFVFYDYNEPTNL

PEKFHHYFDYVLVDPPYLNVNCMRNFAITMRWLAKDVKLVSNDTEKILNPCTFITARTLR

KDIYADLGFKPSGFTPTFESKLSNQFLTYTNYHSERFGECMEDFGDLEKE

>contig20071 Frame-2F

MLKRASIEASSDSPTAKTISGTPSQSLNGPKFRRHKSLTSRIRSESLKNPSGNVAGQLMK

GAYDRGISESMQVGSTTLPNPVLEQEGHQRLTSPSRRNELKSDLRHLESQLSMLNHQVAI

KEGLANQTMRKFRCYNYNLPQTALFTDNDALSPSSCKKIRLGGLNKSKPQPSPKTTSSPS

SSSSPNSGSSSDSARVSNDLGDSSSMEGDTHNFTPGSSPLLGTDKVISRGNYLSSQPIWE

RNEDAPCCKRCKKKFKALLRNRHHCRCCGYVFCSRCTSHRMSLPDFGYYDVVRVCKVCYN

SGEDG

>contig20563 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55284.1|) 8e-22

MQDFGSLQTFNGIEVYEATQ

>contig20844 Frame-0F

MKKVKDQVFRLKQDKKAFKKAKKAAKKEQKHALRLEKRGCKQPKHGLKSVDTSRCEDNIV

MTNDRESDDKRRSSRYRSRVNSKSSFRGR

>contig20970 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62329.1|) 1e-117

MAGTSKGHCAELTPCASQIINDTKSDASVNESISGISGIGGFLVCLNVPPETELGVDYEV

FRTGAKFQGVKFIPLGIHFVLFRSREQEHGIRQGFFVHVKRHSQVIVREWSLEKEELGPP

KQGLNVENLERAVLSFQLDGGLGPYSKQHLKTWQRLSCYISSSVLQRCGVDFGAILLPGC

ADEDVGTSSRTQDDVIPYFPDLPRTVRFTTLPRARTDLSAEARTAYHFDKSEMLEELIKS

EFGSDWKELIGELQLSFLIFLQLSSLAALNQWKQLVALMCSCERALSKYVPLFLAFTKLL

ITQLK

>contig21115 Frame-1F

MTYQTYRTMPSLDPVRIVSSSTLRTASTESGWPGKRSDMSPQIP

>contig21818 Frame-0F

MNICEINASAHSNIETTLMLKKRVIYLNKLRSTDLQHTTMKFAYAASSTNHEFQCVAYFA

AQFHALRALTAPGNVAFLNSIIESKRWDTTGGKSGAFFSMTHDKRYVLKGISVTEFNMFV

HMAPQYFNFIAQVVEVPTSTVITKIVGLFKISHSRRLLKHTEYVVIMENFSYGFPPGQIY

DLKGILRRRYNASSTHEEGRYESYNSVSNVQVSMDLPVLLDGNFSERMPVPASQQDLDII

ESAIENDTGFLYRAGVIDYSLLLRFDEEKRQVIVGLIDYLHQFDFLKKMESTSKASLTFR

HPTVISPISYRRRFMNATNRYFVGIEKELEIRMRKRCGLKLKPELRRIGAPKSGPTIALN

ARADEDVHAEVAARLADNMSLISDSSFIVECPSLQIDYALPRLESNWTDSKPRGYSMSQI

TQSKGECFGSPCNSLHESIQSFPATPIKSNAVMLEAHCS

>contig22028 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66543.1|) 4e-47

MHGSSFVGSSILTTFLAIFCRAFTPFQARVPGSEHVVYLNVNGCYEFWKDIDIPLLHLFD

QQHPALYLPFLAIAGNLVANGVPHILVLGVSLGLQFSPLLDGVTH

>contig22284 Frame-2F|Blast-phosphatidic acid phosphatase [Phytophthora infestans T30-4](gb|EEY61895.1|) 9e-93

MGLLWAVGLIGPFEPATTLLLSALSSVITVDIIAIMLLKLIFRRQRPPFHQVDVRFVGPD

QHSFPSGHSTRVWAIVAMLVYLAQNHPWILRQFFYGLSPSLLVTIVIIWGLVINFSRVAL

GRHYPTDVLAGTCIGYFVFWPISLLCINYFHLLKEPRLAF

>contig22576 Frame-2F

MLTSVEAASIVLPAVCRKLNMADGLEVDEISKPPTVYDLKEEVTRLQHLLGDDSCISGND

DASSFVENTVSQFRQNSYTNCGVSEKLSRRGICSGHKNSTNICKISPNKIIGAIARGKIN

NSVLKTPSPKRRETLTPAEFRKVPRPTRVAALTRANISLLPTPRAPNITGSVCGSQKSRT

SIRTDGGAVFSRLYQPDFYKNREEKLRDMRAGRNNFDCTFTPLINRRGSISSRDSIGSGS

QASMASAKTDVVNVSSRLYDPDYLRKRNARLQRMRYEREMRECTFVPAINANASTILRKK

LQ

>contig23272 Frame-1F|Blast-CXIP4 [Zea mays]gb|ACG35006.1| CXIP4 [Zea mays](ref|NP\_001149317.1|) 3e-13

MPATAGRVRMPHNNRMHSSAALKMTGMWKNTIGYDPYAAENEKQEKTGDTSFEQAKGLMA

LAKLSNKS

>contig23386 Frame-0F

MKRWNQAVAMDVVGRPRVQSPRKKMKKLFETSSVSLAGKSTVPTAWNTRRLRPSTRRRPK

TGSEWALHGLLTTDGVPNRLEARDTRGLLGGANIGVPAGNPRAIDVGRRLARRRRALILG

QDLQADDIVDTRLCQENAILHV

>contig23614 Frame-1R|Blast-2,4-dienoyl-CoA reductase [Phytophthora infestans T30-4](gb|EEY58091.1|) 1e-25 NOT\_ORF

MAKIIPGKEVFHETLRHFEKQLKLTGVTVVLNRCVEAREVILIRSW

>contig24093 Frame-0F|Blast-Amino Acid-Polyamine-Organocation (APC) Family [Phytophthora infestans T30-4](gb|EEY67063.1|) 0.0

MLPTLKSIKLVGHTLLVLGVMIFLPFAVLIVLATPLIKPTNWFIVRKDRDWGRLLSSLYW

NYSGFDAAGAYAGEIESPKTTYPKAMILTVVMIAFTYIVPFIAIAGADTPHYTTWDDGSY

TIIAQQIGGTWLCIWVLISSVFGNLGLYVAEMAKDGFQLAGMADSGLAPPYFAQRHPDTG

VPRRAILLAFVIIVFMGMFDFDTILGIDNFLSALSSLVEMSAAVRMRFSHPDIERPYRVN

LSDRSLMVAMMLPFTLGVFIMINELTKSWTSLSLNAIALICGYLLQKYIGGHPYHKYAEI

FDESLRVLDSSEES

>contig24237 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56146.1|) 6e-51

MAQQYTYSRSPDHPYALEMLPLPTEEQVHLLNDAKGAYESLFPAIKAAVRLGSDGEVFNI

THRNESKNKSLAMWTRSILNGTLEEVAALYLDQSDHVTILLDSTRSHRLYELQAPSIDKP

LHSAAMRWSLWRPPSKLL

>contig24567 Frame-0F

MLGFFLKTLKLPKKSPPRYASTPFAALHAPILYYLSACGAMCVITYHAMP

>contig24985 Frame-0F

MELRQFKQATIVFERAVNCPIAGSNAALWLQYADFCVQRKKFSNARKIFVRALQTIPAHE

HSSIWAQFYGFVCTHVDDKLSLAMLQHQVMPDQFPQPGSQGLASTRISGGSSVSSSSPIK

LSTTDQTSLQPPQTLSTKAVALIDPTVVFIDKTGQVPPRAVESKDLGKRVAANVQTSSSE

KRAKLTDTETATAFFLHVPVTLPWIPSCPHLLFDSVVEKETPKEIENELLERLSDVLGDS

AVFEKVRDLCNQQRKRDREMLNRWQELIGTQMKEGSELFARHVALEMQHGFSDPRGLIAL

KTQHLDQRREFTHRCQLSQQHFIEISAVDRASALKAQQFSLETMKIPEMVVTTHTDAIEL

QRAIVGLILEAETLWREEQQSSAEGTTGKKTQPSSSSASLNRRQRRDSQDSTTSSHSTAR

SSSGVRGTNGPASSRQDSRGGVRGHNSTRRRDRDARGGRGRSNKWDIQPLQSNRRIAAVS

ASQRSRFEYPEQQMPSYEQPLPALSQPRHFQHQPYGLPPYHDYSGRPSSMPERQAYGPDS

SSGAYFSGPIDGPQSRGETDRFVGQGGPSRGGGAWPHAAFHPQPLPIRQRTGPLGSEDDF

RPPYDPSLSRYGAGTGPGVAPRDGPMYGESHRVPTEALYYQEVPNPQQGPPYRQHHQFVP

PSQQAPLRHESYAAAYPTYDPYGPPQGDFQQRGRPREHEGPVHPQDLVPRHHQPPPRFQQ

EQLPAGMNNLNRRTRRGGDGRFRR

>contig25630 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68131.1|) 1e-149

MPLMPGSPRPCLPASQDDADGVYRSLFQQPIMDIPPAAPSYAWFEFLLHPDALRNHLNIL

YQQRKSGVHSATSAIELVREFLDQAQLVANEGNVRNKRYTALLLVAAQVALQMQLSLDDI

EKGLPLHFQRLLLDGIVDFADQPCNDRNECTNDITMQPHEAHMLHNRWTLRALVSQSLNG

FLTCNTRSESEEILFTYQMALGDLMKGHLQIAQNIETTLINEESLTLSVESHIATYNDLG

RYFFSFNGFKKAYNCFARAIELLEDVENDNRDMKIGTSSKWPAEIRTNLEGYIAACEAVI

ERHSLNDGLAALNTPMVQIKMAWDDRDWDTVIELLEIDIVASELTRLPRGFRAALEQQAF

HLLRSSVNDLVEDDLQITGVNIRFFYKRLVLENAVMNLLVEVSQEEETALSACVCTCIRL

LQDEMIYSKEESRNSNGPFKNCFAALARFVLRLSEFAMSKSYDDSVKTQVIQFVYQVLCH

FPCIKELVDVLELLRRCGVDYVTHTKVVPFEESLDRLIIVEDRLRVTATKQREQFHSMAH

MGGMIGICSAVVIRDSDVVGLQNELRDMAISGRKSDFVSRNLITFCAENKYWDILSQCTT

AAPVSSYWLSEIHFVASCGALCQYLSTLSASFISANSKAGSVASLATNAGEIAEFSIAKS

NKFMADILLKWRVLLNEVRADSNEEPSNETQTDEKMLMGLPVWIVETLICISAGLLHRAY

MRNACDYRVSFDLYPYGEIAFLEAFVPDKPPSGAATIENSDAQFATVPFLKNYLEDLVAL

HSQALENLVSRCSREPRWHCAKADLHLNPLSKQRLASVSDPRAALESYLVAALLATNFFS

DMYSVKDIIDQGSLVRLSQCLVKVGAHVAAAVLYQCFMPEEFKYGLRILRLAPESHDEAF

FQYFWELSFLELLVDLHTSPRYYNDRHVTLLTSLIQSPEVNSSNPTPVVNDAEQRILRCY

FRDLCKIFLCD

>contig25784 Frame-0R

MLLEKSSGTDENTPQYVLNSPKVNLYKGVSVCTTMNATDELETFLNESDSDLENTRLIGN

TKTFTRRDHGKLKVESSEDDEEVSSRFQSYRISKKKRFERKRQQKEDLRQLHDALDIKKD

TSGHGIAIPDSLLRTSHVIEA

>contig26406 Frame-1F

MKASSLELETTNRIVKVESIAVDITKSERVFSMKTENTNEIMTGHERPASSEMSTALPGS

KAIVEAAIESQDYAKIKAELTNYDGKEEGEVETPTLSVPFKMEDREEASNKISQLDTMPI

PRKVSREGDSYSTASFMIPKRTAIKTGIPSCKSSGSMEQAGTVRTPASDAPRSSQKSLPV

ATMSMTTTQSSSDVSKNGLTRLQRKQTKKTVPIKKSSFSVQDQALMRLSRKRNSIV

>contig26741 Frame-2R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65627.1|) 1e-10

MLLWFGALSSAAALFSGVIADAPFEARARAIVDTFTPAQLLGQMCQLTLGTVMNSTTREL

NETLVRQYAKQYVGSYFNT

>contig27258 Frame-2F|Blast-mRNA decapping enzyme [Phytophthora infestans T30-4](gb|EEY65612.1|) 3e-76

MPFMSRLKRWVKGHKSMKKKSSSVAFSSTTDRASSAPRNRPLTINTRVVTQLKAETSREK

SRLDDRSISTPHNNRPASTGLKKANRGHFGTEFNAATSYDGLNCETFGTVQKGFSVEEMF

SVNKRLTGQKFEYDGNPHDFGKPILPSVSTRVVSTLIHSKGPMPVQILIRPTSVPFQRED

KKLGQIMSPPRQAPHSTPFGSFQFNAVDIMAVVN

>contig27908 Frame-1F

MFDIMHKLPGYHIFTCACFTLRGRCTSFSLLFFISSFTEQSAKKGLCVESNNSLLILISD

ISPSLKPNFWEIKLFGWNFDTKVALSTRRAYNALTGAHILRSVPLPNTYVETPQSVLYKY

TVTLAVVKLQNGEQHD

>contig28989 Frame-2F

MRNEAIIRALLETRMRVGHILIHDIDDLEPTQSISKKLSPKQHEKVITTAWNIVSVLDDR

KYHMFFTRFLKYKLAWRPNRATFGETFLLDVRKTLGPRDAEVIMPTFEEVYQQLSVETLT

ICRVKLRHSRKLLHGRGALEILNESGRKRLETAWQPSHCVFYRNLPHGVTKKHLKNALAH

VGVVKRFFLFANPINGPPESPNEETDDEGDQNDEEEEEPEDDKIIHPNDVDSAKKKKKLK

NKKADISLPKGKDLKPLQMSKYKEKIIASDKKTPYQAVVEFESEGACRKATMRALQIFGV

MMAGWNEYRPVFSSPADKRSGVTLMNIPYGDTVGHIVDEVNSILVKAGLNMKVSGLVPRG

VMLTNGRLDLQFPSFVEAAQVIELLDEHVRKLKCRQILSNRDAVRLNEYMKLKKNLEIKA

KSEEKTRKKEEEEQLAREEEGDVQYDNDSMFFGVDEEEDEDDEDTAEDDDSKKSKKRYVL

EVSETREEYFSEWLEVEANMEAEELALGKMPRPF

>contig29533 Frame-2F

MYSTRKAAPEPLGVLRGHGAPINSVTFLSATKILSGAGDGAVKIWDLSSRRELATNSTAH

SKAGVLHAVALKGATLSDQKFVTQGRDGFVKVWDMQSFGDAAKPLANFYCGSYSFTKFSV

SRWSDHGDSESGSLIVCPSSVNNS

>contig29964 Frame-1R

MAAKHRVDVETANTNGIGKDGPPCAACCAVQ

>contig30221 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68691.1|) 7e-68

MAALALARSLRVCTGQPAPLLMRTFASATEPNIHPRFSVVDHPVTADSIKPEDYFAIIKL

AGTQYKVVQGDIVIAEKIKNAKVGEIMDINEVLLLGNVNQTIVGRPLVEGAKVRARVEEQ

TVDAKIDIFKKKRRKNYRRWNGFRRQITVLRVTDIVPINAEIA

>contig30566 Frame-2F|Blast-glutamyl-tRNA(Gln) amidotransferase subunit, putative [Phytophthora infestans T30-4](gb|EEY66350.1|) 1e-131

MDSTCITDAVPKNWCLDTVETAQRSQQVDLSGFRVGVPMEYFVEELPEDILRVWDEGISW

LREAGAQVVSVSLPTTKACISAYYILACAEASSNLSRYDGVRYGYRAKRITLGHQTNQSD

ALHDLYSRTRAEGFGEEVQRRILSGTFVLSAGGISDYYERSVILRQRIRLDFRRVFQEQG

VDVLLAPTTPSGPFPVQNKLAKIDPVSMYLNDVMTVPSSMAGVPSISVPAALTSNGDYPL

GLQLMSGRNGEERLLMVAQALEQRANFSRQVPARVYTIDR

>contig30971 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60063.1|) 1e-100

MTCSQMQAIVASTTATVCLALYVLKLRAEMTTLGNRKEKTAVGSNKIVYNADGDRLWTAE

ALIAERRSIFPTDYDSDKKVPRDVLKKMLTAANWAPTHGRTEPWRFVVFEALEKRLELGQ

LMATWYQTNVPANKFLQSKYNKMISNCSVSSYVIAICLKRQKSGKIPEWEELCAVACAVQ

NMHLVATTHGVAAYWSSGPPITLAQEMKDYLQLEAKDKCIGLFYVGMPKEDAKVPKGTRK

PIEDKVTWV

>contig31077 Frame-1F

MQLRPTIAALVANVAVSTHSVMVGAVACAEICYGTELTGFGPGGIPGCSCSGLQQGARTG

DGSCTCGQCYEKAQGKVFGFAINADGMCTYGTDCGTCDFSLSWTAGTDKPANVTSTPEVP

FVPATPAPALTTEVTPFVPATVAPSDTVRQ

>contig31392 Frame-2R

MVSTIQSSLLIILLSATYVAWCPSFASAEESVMTTLTNIRRSDYGGRRLDPSKVVTQGID

KLLNVKSVEGAVLSGAAKDAHEAALAAAKAMVKANPKVTSKSKKLALYSGGTILLLLSIY

GIYAHHMQKKEKEKITAIKE

>contig31914 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57936.1|) 2e-92

MTSSTVVTALLNWFEAHGGKNPKLEIRYLGELEGHGVYTKQALTRTETTIQVPFQLTMSI

KSAAQSDLGPVFEKYHQIPDDEILALHLMHERTKGKNSFFAPFIASLPTTFDLPVFWTAT

ELHELQGTNVVLLTQLMQKQLQHDFKSIHQAVIADFPAIFKAFPTLTLHDYTWAMSVIWS

RAFGITRKATYIRVLCPILDMFNHDSRVSDPLDDFVSYDPKKDILRHHVPHDVVANSALT

ISYG

>contig32133 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66240.1|) 5e-76

MSSNPQHVVDTEDAAELNLGDDFRNETCLSNAEVAVILEKQKSDYETQEKQLTNVFQKTY

SYAQRFSGTKDPVANQASVTELREALMSLVFQREEDSGMVEYRLEEFEIACLSNLNPEEV

EEAVALIPSLQKRFAEDEIEEILGIVSRTAARMFG

>contig32146 Frame-2R|Blast-ribosome-recycling factor, putative [Phytophthora infestans T30-4](gb|EEY67787.1|) 1e-22

MNHVKMLKDKVSEDEVEVQKDSIQKMTDDAIAEIGKLLAVKE

>contig32551 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62310.1|) 2e-32

MAENFRDIQQKYHLPPGDFPPIDAFVLQCSDRKFTKFPFLKARELQIIDDLLTKDIPTLM

CSLPMHTRGNSDGKENTAS

>contig32858 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59600.1|) 5e-66

MHHYRAEIAWTDWKLYPQTYRPYVYLSTCNHMIGEKDNNPKLSKHDWIDYPFQQGNEEDA

FRYVVTHVPTKCNLYSYCCFWRALNGGGWCDRNYERKIIAQERKLSYLEYPFTVV

>contig33417 Frame-0R|Blast-NPP1-like protein [Phytophthora infestans T30-4](gb|EEY65232.1|) 3e-15

MITYRKYEPVDDDNLDGDSIKLEYTYLLASNHYLKATSDKGEKQNLISWTNLTGPALEAL

QSKDSFGGYTPLCDHEFAQNMELSFPFSIFED

>contig33941 Frame-0F

MRCEKKRFGGLNGMSGTDVVQEIKSLFQQTPLPLEDKSLYMQTLQGNVGDSISIQHSCLW

CPHFSVFDDRLSFDVITLKQKNCVFGLPDSPLIQHDSIYELTTPVSLKRHYCGQTVDTRC

KGPTRQNKWSSIKENSSLEFGCSLNFGETWIVQSYAWEG

>contig35608 Frame-2F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY56109.1|) 6e-36

MGRVASHFYIQHTSIETFNELLDRKSGSIDEEEDTLTWDKALLVLCSSHEFEQLQSREDE

MPELEKLKHRCCRIDILGGGMDTYTG

>contig35701 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58871.1|) 3e-55

MSKNPESSVFLKAVKTQHAVVYEHDRITSKFGALSSANE

>contig35864 Frame-0R

MTGQAQTEEVMNANQNPRVSNHLHVSIIGYTLHAARNVQILSTYTSV

>contig35987 Frame-1F

MVLRSDVDTSGSTDAHAADSDASMAPFESSFDPRSSCFVMGAPTPSFSINNALSRPHGRV

QRSTSDTEMERRMPYDIAHQTIKARGHSTSLDAERMREEPHCPVLMHSSAPDSENAVSSR

PLHVEPQLTNNQSLVNAYNRTLSNHPSRLDLNENEAIHVETERPLQLHEDTSPRQRRNSY

SSINVPLNEENLTS

>contig36296 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54261.1|) 3e-67

MAKKLLTSHNATPVLTRPQHRIYHFENGTTEIVVDIHAFSYIARRGIHAILDKTSRLVID

VAFVLQGETEDELPEQVLGCCRLDHVNVQKAMDLPS

>contig36788 Frame-1F

MAMTSQKGLVPLSVLEELPETLYDIYAEIFEDKFGQVRTHIWTKAKQLLQLIVGAAAGPY

SLVSEEQAKEQLNFTTEDLKMLRRSMVDLVTIKHGCYRMESSALCDWLSDSCRSEEQFYV

SIEDALFALRKMRRVNSGGSIIVHSSFSSDHCSSYHASTLTRAGSREESSRKSRRFKPRE

NIDFKPVGILKHGRLW

>contig36995 Frame-0R

MLHIQTSCSSMEFVVSQPFLVVVQHSHKYPTQGLSLGSVAVDVFFVLSSFLLTWLFIKKS

MMLLAKKKDLAGAITLVDYQKRFFSRLSAFCIDGNRAFIMPFAMKKRYYFVKKPEYYELR

KVLLFYPGFNQRILDVA

>contig37219 Frame-2F

MNANVHVLLDQSVKMGVKRKRQHRSGLLANTLTGREFLVRLRELELTSKIVDFAFLHGYL

EPTLMVLHEENEKNATSGRMAAGYDTFCLTVLSINLHTHLHPKIWTVKNLPSDSFRIIPC

RAPLGGVVVLAANAILYFNQTQFYGLATNAFALKTVNLSVFPLSEAVYETLEHAIEPLDV

VLYDCQYEYVGEKELVLTVPSGAVYMLSLPSEDVSRRGFYGAGGVGGSRPGVLSLRLLHA

RVLAQCVSVHSETQTLFLGSRSGDSILFAMEKKQVKDYGDSECTNEKELNVEKGLELEAR

MDGKIEGNIEDEEDEEDLFLYGTTRVKEEEDCTNARDTIHDVGRKKEERKDTILLGVGYT

YDLRPIDLLPGIGPITSIDLGMENNADSSDKREELVISGGYDVSGAISILHNGLRPLVGT

EAELSGCRAMWTVSSSLALEPTSNDGRRYNAYLILSVAHRTMVLRTGEGMEPLEDNSGFY

TSGPTLAAANLFQHQRIVQIFKQGARVMMEVLDDDVLNNGDKTELDDNVRVKLVCTQEIT

LEGDVESGGMNVDTSKVGIVSVDVVDPYILLLLTDGSIRLLMGDEADLELTVIDPVIDFT

TTCIDSNGNGDVSMHKSSAACLFYDWTGMFQEKTGEHECKEQVESTR

>contig37493 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53171.1|) 1e-106

MELKAENTKLSEALRALQERYDRLDEYTAKKIQDLTDENEILAEANRLLLEKAEQRVSPS

INEELALHQVPDELLLPGQALKICELAALDNVHTFGNLFSVSIHVARPEIIITGGADKYV

CVHNWKTGKKLCVAETSAPVLALAFNPKSKFADYFVAAGMDAKHAVYKLKQEGEFWSVHT

VCEFQDHSRQGSFNLAWSTSGLLFATGASDKSLNIYQCFHLGRSDEQVEKVKSFYFNGSV

EAIVFASTSTFREADASDDELLVVAVRDDCYVHYVDCSTFEKKR

>contig37637 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55942.1|) 1e-57

MKTRSSSNISNSVAAKTVVPPRGRPVSGRVWKRVQKTRFSSQKLKGTKVLSTTWEEKLQK

RSKLKELKELQKEIKSRRQSEKDAVRQAREEKEKRRKENELKSASVQVISRTHRLKTMSK

KQLRNIKKTIVNKNGVVEYVPVYSN

>contig38180 Frame-0R

MSQIDSEVYHALPYQIRKEIDRYAKKRTSTSRVAMIPKPILGIDEAVPKTSAPSVVLPTI

KMLFENLLHSLQMATSADDKHMTSSIQAPFNAFDALYSRILVEVENRSLDEVLRMLRFVR

RKSNAAISTELDDKLKRGFNHILGLVNQDIQRCFNGVLPPRLVAPL

>contig38522 Frame-1R

MTHNATTNSLTEETLQKRDEINLSASLPVTELNGSNANIIDLDLSKSYTRNTKLMPNREK

STTENKLPPLSSLLSPKSWSETERTFVSPTLALKPGSNPESIERPNNIASELNLSTIASP

TKSLPSKLEATSVASKTDLPTNSATLPSSMLRPGNMTSQEARAERAENVFQKSSFSTSVL

FGVVGLAGCAAIVAIVAYAKHHAPEATSLDDDTRSSTTRAQDSMDSVYTDPLNTRYSSIV

MISPNGNGVCIL

>contig38856 Frame-1F

MTMRNLLPVVLFATILHQVTAFDSIPDIGGILQSTLSNVTDKLIGTTKEASFQSFFDYNG

EYFAPFGTDEPSKELYVQNDSLKDIVPIINVAPEALKVAIPTNDWWTNLIHVTDSMDVSN

YAAWANPYAVKLPREAPYGLQTFYSFSYREFGDEVNGTVRYYNHSFHNDLTLSSKEFFSC

QPVYEIFEWDEGGAKVRTCDEGSGK

>contig39060 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61662.1|) 3e-20

MGLYASITGILWEFDGSQIAGSIHVPAKQQIVRFEIGPSTNRFTTANTLWDKIDEAFESI

EDDF

>contig39518 Frame-0F

MAAANGRKRKASLGGTSGNKSKQSRNLPYKRGKSIDAKTRHKAPTLPEDEDVEIDEEDIA

FYENNEQFTSFLANMNTGALKKPYHSKADKKPVSKLVKKQKDGEKNEMPFEKLEARPRKA

AWISEEQERLNDKLP

>contig40051 Frame-0F

MPTTLAKGISLEQPIDHVRNRSLCTNVCEFKWTYVDTLEKMEEVIRSLKMLEARISDVKV

ATGNQSIVCNMLVAIDCEWRPQYLTKAQTSYTRDEPRNQFDDDQDDQGCVSIYQLAVGDI

VYVVDVQVLGAAAAAPLSYIWRPSSLLMLIGFCVSSDLRRIKNSFPELLQVLIKNENIDL

NPRSPLLALELKHLALSRHIPAQYWGLSKLYSECLGLQLDKEQQCSDWGTRPLSTCQLEY

AARDAYAVQRLFKHLIADMSFVGGDNFIGKIVQDLLKRYDVDRNFSCPKTVATTLQPLGK

EHVQMALVAHGLEARFFKYERGEQTRVVVKSIAMLVRRGTSMHNFKDITYAVVVLALDRY

IDMQALAHLLAVDTKDISLADQETLIRVFGYPRGCLGPIGLREQQTTQVIVDSCLEAENC

LLCGAGLADEVYAIAPTELIRTVDAVIAPISTEKYLIRDKIN

>contig40433 Frame-1F|Blast-RecName: Full=Calmodulin; Short=CaMsp|Q71UH5.1|CALM\_PYTSP RecName: Full=Calmodulin; Short=CaMgb|AAG01043.1|AF085344\_1 calmodulin [Pythium splendens]gb|AAA21424.1| calmodulin [Phytophthora infestans]gb|ACG60663.1| calmodulin [Phytophthora sojae]gb|EEY69969.1| calmodulin [Phytophthora infestans T30-4](sp|P27165.2|CALM\_PHYIN) 2e-78

MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG

NGTIDFPEFLTMMARKMKDTDSEEEILEAFKVFDKDGNGFISAAELRHIMTNLGEKLTDE

EVDEMIREADIDGDGQINYEEFVKMMMSK

>contig40446 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY56714.1|) 0.0

MRKDLEEKGVNQKKVQQDAEEVNMLKEASYVQKVALVSAHERAEGIHYKKVMKSTWKPPR

YISDMTQEECDAVRKKWHILVEGEDVPPPIKSFAYMRFPSAILDALKAKNIMRPTPIQVQ

ALPCILAGRDMIGIAFTGSGKTVTFTLPLVMLALEEEKKMAIIGREGPFGLIVGPSRELM

RQTFDVVKHFTDHLFQAGYPELRSLLCIGGEEKRQQSDFIAHRGVHIVVATPGRLNHFLK

LREMNLQLCKYICLDEGDRMLDLGFDEEVATTFNYFTSQRQTLLFSATMPQKFQDFAKDV

LVKPVLVNVGRAGAANLDVIQEVEYVKHDAKIVYLLECLQKTSPPAVIFCERKGDVDDIY

EYLILKGVEAASIHGGKDQEERNEAIDLFKSGRKDVLVATDVAAKGLDFPDIKHVINFDM

PAEIENYVHRIGRTGRCGKTGVATSFINKSVSESTLLDLKHLLVEAKQTVPPVLKALEDP

YEELKHCNDRHSNATGTKGCAFCGGLGHRITDCPKVDAQVRKIGAGKRDFLAGKSEGYGG

DSLG

>contig40608 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54563.1|) 1e-110

MLSRVVIAAVLAGVLGYRGLKKQSLSLSGAIAAFFVGFLTLASGTRFGLLLLGFYYSGSK

LTKIQARVKLQLDANYKPGGQRSARQVLACSLLGTLIAVYYVAQYGDDASALDFKQAPMR

SFLVASYIGHYACCAADTWAAELGVLSSKAPRLITTLRRVPSGTNGGVSMLGLFASLLGG

TFIGALYYVWSLFSGTAQKEVLLLGAVMGLFGSVLDSVLGATLQTTYFDRSLQRICDACA

RNSDVEHICGANVLSNEQVNVASVWVTTALSGIVATILFP

>contig40864 Frame-0F|Blast-regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4](gb|EEY56341.1|) 6e-65

MALYIWGRNNSQQLGLSLSDKEVFEMRQVEGLRSEVIVDFSAGERHSLALNEFGQVFSWG

RGREGQLGLGDVAGVTKAVPTPRRIGGTLASELVTKISCGESHSLALTLSGNVFMWGLLP

VAKVLHDENGMAVDASDRATFELAGLSNE

>contig40910 Frame-1F|Blast-peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase, putative [Phytophthora infestans T30-4](gb|EEY63832.1|) 9e-18

MSAGETIDVVVVYQLQEFYMSTQASSDRKLIAVDLLQCQLLSLLGVMPDEQLLVSSFGEI

IYSRTKNDVHT

>contig40987 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY66396.1|) 0.0 NOT\_ORF

MSNATSSPSTTTYGTKTDVDPVSAPEARQLASALVGPVPTGTAAITVAKKAGRDGKNIWD

EYYPLVQPAHQYHHRNGRGSSNYFFHGMFSADVMWAYRDAVIAYLVSLYSMVILSLTGLV

FCKQWGISPNTPIVFAFRCLWLISPAIASFALRRIARLRLQACNTPPHWNIPPLYHLFRS

SHSSRSTLRLALLSYTIPVLCELAAYSFTAATRMVNPFNRIFVRKLEMVFSFNNVEALDS

GLVFYVFYITLLGIFWDPVPPQRYDIGLSIGRRPLGTSWFFFAMIQEIGWSGSLFPALEI

VFSHSTILASAITGIIWALWYWPMIVADALDVVPKGAGYSVAETSNFHLLYVLAIFTLLL

VGSRIIMCWIQGNSSYVIWSSVVYHSSHNLFITSVFGQLTAPLYEKAQLFSFFSSEASIC

LLVTVWFSTCILSQMFRWKKLMPMLRRANLSATRALAA

>contig41342 Frame-1R|Blast-importin-like protein [Phytophthora infestans T30-4](gb|EEY63321.1|) 0.0

MAESSWEALLWSFLAVDNVTRNAAEAHFAILKQASCSDELLLGLVHVIHSTSPDDIRALA

AVLLRRVLLRDTVSLWPRATEQTRHIIKKELVAILAAGEKNRSIRRKVCDTVGELASSIL

EDGQWDSLFPTLLQWSKASIVFLREAALRILEMIAVVLASQISQSTLETIGTSSLHSIVL

DILSKGLQDREGRVALNSLRALSMVLLHLDALEQSFRPEILTAIVPLILALLHSLLDLRQ

MDDVMEALEVCIEIAEPHAMFFSPCFQELVDLLVRVAEPSLNDVGERKLPDGCRQLAMEF

LVSLAEHAPSLCRRLSKNSFVHRVYPLVFKMLLDLHGLDAWDVAVCDDDDTSSRNGMEHE

VLNFEVGAEALERLVKALGPKRSLPTCFALIQEYAARIDHWVYRHAALVALSQILDVLDA

DNLDAIANYLFAQAMDPHPRVCCTAVDVIGQLSVDQAPKFQESHHAEALKTLARFLDDCT

KPRLQAHAATALRQFIDMCPPSLLPPYLDQLLHQLFALLQHAKFVAAQEKPKSTSAYITA

RVVQEQAITAISSIATVAGTSFT

>contig41412 Frame-2F|Blast-Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily [Phytophthora infestans T30-4](gb|EEY59454.1|) 7e-48 NOT\_ORF

MRTFALLSAGMTLNLALDEWVYNVISALAGALGAWNLAATSIL\*NLWGLIFSIYCGFGLP

TQVRVAT

>contig41827 Frame-0R

MPHSLSLMLDVPNGVLRHRTRTNVLTIMLLVVNTCSR

>contig42167 Frame-2F

MKTSEPRECPLPPRRCAVPGVSYVHTPKNGPLKVQNKRQLCIHSFRRTYHRDALI

>contig42365 Frame-0F

MHVEGFHDMVERKSLCRNSDVRETGETMWVFDTPAQRLERRQEEKWQRKRAFRILKDVEM

ESSKDLSVEAASSPSSFDQKTQWMSLETAPNRLENRQEEKKMIVTPHSTCSNTKREQDSL

DRDGYNSDKSVDDLERGEAHSTLSARTDVHTVTERRTSRVRRFLAFAEAFTACLSAYNPK

AQS

>contig42493 Frame-1R|Blast-hypothetical protein PITG\_19150 [Phytophthora infestans T30-4](gb|EEY68769.1|) 1e-119

MLLARSKEKQRASRVLLGVGISIFFTLRETLLEAKDAGEVLLAINEYFAREMKKTTDEMD

NFLHFCMIITDQLEPDIVEGFRLVHKDEVMERFAAFEAKKIEMRHQLEEAKAKQRKVTSA

PPSPSKMDRLSTLSASSILAGKPYSSNRIAGLSAYISKPLRGSGSNRSVVADRGGDKKCH

QRYQRIDALHAHHNFGEDLVKMEGQLLDLADLYVRGKIDEKEHSCIRAQIVRKWCKGMNS

PQSAMERVQSVKHSYGERSGGEDFTNNAPDLQHIDVLERS

>contig43340 Frame-1F

MDNRMANGVKKHLKRSLKEAICGASRQTAKRRQLATITNTVDSESAAKIRFSGDNATHAD

NSVVIPSKQSAITSIALCNRMLLPQGEELPTQALSHWKSATSLTNESNLPSQISLTPIVV

STDPCEVSLLSQLVTPRGSQLSGIDQTESMHQKKTDWKDKIAQLQKKNALLARQVKAKTH

ELEKFHEKFEIISEQNKLFTSRQNDGVAVDICGHPLDAKMQSKNQSKAAEQFIKSQIKFV

QLRNRLSPISSPMQLSSSAIQYDTPTDRDLPIFSKQQKSDSVTTANVKASEEAGALRSEE

SVLKEHMSVTKAQLVTFQAQQNAVELHKHMSSREAYAPESGQFEAKAQSSEKSGL

>contig43681 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55865.1|) 1e-46

MTSQFTLVVQQTTSSAMRAITDSTCDYGLAFTDDGCVRTLSSYDLDAYFHVQIVYFVLGS

ITMMASAIMYFRSVKYEASKLQQYNFLFCCYASLTILSSGFDPKSYGHVIPRPITSFLSD

SLTAALYSVYI

>contig43788 Frame-1R

MGQLLSESSFLALKVPFFDDDDSTVVKKFYDPASSDNRKNHMVIRVLNKAIGKDWRLIQA

VIRTHTSVQLIEEREQAKEYLQTFVEDPSCYKSSQASVDIKTPMESEEDKLDGSATVLTY

PLPPCTSDIVTIIRRDVARLK

>contig43861 Frame-0R

MVDFKGLGVEALKRYAKFYHLKFNDSMAKEDLAALVARHFDITLEVEEDDSIVAFMQRLR

NGERAAVKRSTARDKDRKALAAAEKAKRKSNSRKRQRGHSVSVSSGRNFTTSSSYSLSNG

NSGMNVASFGHGNTHANGISNGQSSRGHGNEGRKIPPSSSKSLNSSSGKNKKTKKDADTG

EDNELYCICNLPSYGNMIACDGKTCPNPSQWYHLECVGLADGRHPDTWLCPECDPKGFSG

SGHRKKKNKRSKSPGIK

>contig43928 Frame-2F|Blast-ferrochelatase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY62377.1|) 0.0

MSSARAAAKKAPTAIAMLNMGGPSTLPEVQSFLTNLFTDPELIPMGPVQKYVGPWVAQRR

TPKITSQYAQIGGGSPILKWTNIQGENMCKILDAIRPKSAPHKHYVFFRYADPLTEQSLM

QMKEDGVARAIAFSQYPQWSCTTSGSSMNHLWRELDRLNMKNDFQWSLVDRWNTHSGYIS

ALVNRVKLGLEQYAPEDRDKVIIMFSAHSVPMKTVYKGDAYVNEIAATADRVMKQLAGKN

PHILCWQSKVGYLPWMGPSTSDVIARYGKQGHKYVMAVPIAFTSDHIETLYEIDIEYGEE

AEAAGITAI

>contig43995 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68484.1|) 4e-82

MKIPLAKFKKGSGSPSEWIVEIQPQWKGDWDAAKGDEGLVEIYKTLKVSNGVSDIRTMID

GDASSYGADCGKTDPNAAPETPPTMDNATFSRGIVHAGPCEIWLDDKLVLTNDDCQSAYG

DGTQETISVFKPIDYSSCSSSGCMFRFYWLAFQRRDSKTIWQVYKNCVPLSGPVNGGDAS

TSKTSS

>contig44077 Frame-2F

MPENRYCLSSVSGVGRADPCGHMGLCAG

>contig44392 Frame-1F

MAYICYSKPCTAAFVVKSFREESCQGNADLERSESMTLSFAHVIDDLHIRQRRKVLPVKK

ELDCLSNASFSSSLANSAAPSAMLSNENGRLWVLLLYDRFLATHMLSSVVSSFQGMEFVD

IKVIKSSGEAQGVAFVKFNSEANAENAAIQLHHMELPLGSGKFMQAIVVLAPSQFSTTHG

NISSSSDESMRIDFPTDKCIVTGSSEDLDLRAVEAQFAHLMRSSKHTQAREGHYSRYCTS

TPFQKRKTPSLPIMVRPAHPSGYHAPMSMEYHTMSSTAYPPPYPPLPPPFLTNANYWP

>contig44569 Frame-0R

MLQQIRLLSGGELLAVKQMEEIALVSRELTPGNERILFNPAVVDAGTSALAVLAEHHHTE

LVEQGIAPLVALLSATRVATPALHTQCARVFANLIATFCFHVNLKSSAPFLDQQKGIILN

DHVNIAELFQQTATEKQFFDKVRRWHNCEDPMQRSSYFRVVQNLCAYEEAITTGRLLQDV

YCEGVHPIMPKSTVEFLEQSRNSKAFNAEVDVVFVHGLRGHPFG

>contig44675 Frame-0R

MVSLEELNGLSNVSFIAEGAAGSVYKAQWLGTEVAMKVIKLPNGGVGLVDAELYRTIIQN

SEKDFLEEAKLCSRLRHPNITLFMRAGYYEGKLGILTEYCSRGSLKDVLKSRCPLGWRRK

VALALHISKGLTYLHACNPTYIHRDLKASNILVTDTWQAKLADFGISKVSNFVNRARCSE

RSLEEQNPSLLNELTSFAGTWRWNAPEILQDPHNCRYSRATDMYSFGMVLWEIASDGAVP

FGDTKFDFEVRDKVLMEQRPPIGLRCPQRFTQLIEDCWAQKSVLRPSAPQAAEILNTILD

NMSKDVKDHATMASVSGSEYTNSIFSSLRNGDGSLDLDHRSSSLFGQRFTNFFRGRFSAR

SSSSSAVSEDYHNHRDSEHFHKFTSPYAGPEGISMLSAQGNAAVERNTGNYEALGFPIVG

LPSESRRGEFRVGGRLSSLDEYDIDTPTDASTSYSRSSSERSFSEFRLTGGGHEALRPSE

DQRPSDDSAEFILGASGRIRFHCI

>contig44891 Frame-0F

MSQQLIDAGVPGLHFYTLNLERSVLRIINGLSSLSSRVSRRELPWQASTKRASEGVRPIY

WSNRPTSYVYRTAMWDEYPNGRWGNSESPAFGELTESHFAPSNPSSSSERRALWGENPLT

KEDIHQTFVQYVRGEISSLPWCDAALHAETSTIQQELADANAAGFMTINSQPRVNGVMSG

DPMFGWGGPGGRVYQKAYVECFVSPENMKIIIDSAAKKTSVQYHAVNLQGHSYSNARKSA

VAVTWGVFPNKEILQPTIVDCNSFLVWKDEAFALWMKMWASLYTKDSQSAMLLHEIYTTY

FLVSIVDNDFVNGNIWDLFTAVACPAEE

>contig44914 Frame-2F

MLSMLEATICQKRNSTFLSALTRGRRDSALLRKSESPIQFAGPVCRRSMDCKGVTANDAS

FAVGDITPQSISIETPSIGRGNYVGIEDTPKVLALKNDLNSGPPGQIMFNDIKEDDLDST

GPQDSAGNRVDGQPNFQDSTMSAVTELNLTAVSVRIKQHRDNAVQDSSAKVKQDVLTADD

LRDSVAKGPMALSDLLSSRIR

>contig45144 Frame-2F

MGVRWYDVPTWAAPPTRTKLETPTPYTSSFFFNTMTWCRSDPHELTNASTRPCQCVVT

>contig45720 Frame-1F|Blast-unknown [Picea sitchensis](gb|ABR16307.1|) 2e-08 NOT\_ORF

MEKA\*VMLHYNAVKSKWWAGAISCSTYLVNQFFFIRIQQYSLRELDRLAPKFQLLASNWE

KALRKSRKKNALSSTLKHSNAYCWVLVDVEGIPCSRFMTRPSRDISLNIVQ

>contig45971 Frame-2F|Blast-exosome complex exonuclease RRP42-like protein [Phytophthora infestans T30-4](gb|EEY64708.1|) 1e-141

MLKVSASEKKYIVEGIAADVRADGRRRLSYRSVALETSLLFQSNGSARASLEASGTDVLA

SVKLEVTSPQPEAPNAGIVQVNVSCCPSISTKLHGRAVEELNVELSQLMTRLICSCPTVE

LEKYCLIPGESVWAIHIDVMIFESSGNLPDVISIAIYAALNDTVFPSVRLVGVEGEDKTI

EVETDPAAGKLMMAEHWPICVTLSKIGDYFITDPMEEEELCTSARMSVAVDPNGSVCGVQ

KSGAGAIELEEMQQMIDEACARSKELFQMLQKALGEQRAHDLQAGHRVERVGFLH

>contig46417 Frame-1F

MPSDLKAEEAAKQQQKLLCSLNLMKYAVRGDDAEWVSPLAQTGSEGACFQVKSQSKIQKE

LKEPKVQKVSEKKHRHKKRSADGS

>contig46480 Frame-2F

MFSRPLRDLPLTAVKAGNWTHLGDALMRGVRVFIAYMLMLVIMTYDLTLITSIVMGFVAS

FVLCGKDMTKVPVSADPCCCS

>contig46655 Frame-1F

MLYRSQMAWLTIRLMFDRILCHTLANGRTHGLKRSLTPLTGAVDVCSKERYIRYVNQTLQ

KSSFDKKLRQLSLVTVVGMNCVLYNTCIIGA

>contig47999 Frame-2F

MTTWSGPPPDPYDNQHYHEQQEQPFENVMTDPSTSSGYLYDDGTSSNNAMATGLHEYAPP

>contig48059-0 Frame-0F0

MSDNKVLSVATLHCPSGFKSSLRRLMCHLVSIYD

>contig48059-1 Frame-1R1

MCDEALLHIRLESRRRISCGSNRF

>contig48198 Frame-0F

MIQFGESAFEIDQEKKRVSDPIHDAFEGMDANDGTQALQAFDAYKPSSYASHGRCEDDGA

QAIQSTEPLREVILEIEVPPGPMGVMLDRTIPDMTVIERFVPLPLGGRGYLELHPAICPG

CALISINSIYVEKKGLAEVGPILGSLVDAPKLLRFKKLMTQGRTANPSTLEVPYIPPPLE

DEEVTAVNKANESTKLESEEDTYAAEVVSGEKFMTQLNRYNCGLAEVEAKLNQFIGCEHS

GQLIGDRRNQLAQLHGTVEKIQTQGIDSVIFGERRPSNYEEVKQFRLTLVRKADELARLI

QSIASTEVDSPYESVTALDEEKHPASAFAFVKEDVSHQANVPPFSISQQHNESGFRFLNA

NANPQVADVYGEKIMVPPPISVQADSSYGFSFLRDSPKQQPAISKDTTNILPNFDRLLTD

NANLAENVTNVFAGLNLKESTQHQQPIFAGLSLKNNIQQESTRLAPTLHDSMTKSSHGRP

MGLRDLEASLRSTASIQPTTGAPFTDRGPIGSERTDPSFAFISAARYDSSLTSTQPTSPT

AFGFMRGSNTSSTTPTEASSTISHSHSVLQEPEPSMFSFIS

>contig48583 Frame-2F

MMLSINFILLGFGTRAVVSKATEPCSTLTFDIEYIGGDVGSVLSASITGCCNLCSQHESC

KAFTWNGVNGGTCWFKSSSEHSKASIGSISAAIQQLTSELWHMSPVKVIQAR

>contig48709 Frame-0R|Blast-hypothetical protein PITG\_07649 [Phytophthora infestans T30-4](gb|EEY53969.1|) 4e-21

MRWKLFLRLGKIVLLTDLVKVRSRECEMVLLQTSHQNPSKPGTEGLNTLVLIWDEVSSAE

TDVLQCIYGSVSMYSNTFAFNCMGKLLNFKGQVCRLLWDECVELIGLNRIRVIVCLFHFP

YTNELVRL

>contig48842 Frame-0R|Blast-Voltage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4](gb|EEY66467.1|) 9e-16 NOT\_ORF

MFRPMSLIDLIVLIPFYLEISMENRFVGLLK\*SIDVADEVVMLVISCRVSVSSRGVLTLR

GFRLLRIMSFLHLERSYR

>contig49236 Frame-1R

MLPESSLVIQKLLEIAQWGATADTQTSPRQFQTVYFQAAHSAAKALASIVNKMSDGDDFD

ALMELLLSQKLAVVISNPIESLNVRVAALQVYAWIAKALVIRSHKVYAPLCLRFLCSFLT

PKREDVTGDECSKQAAELRMEVAKTFNLIVSEYPDVLNRKCGAIITLLYQQRMFHLVFPI

FLDYIQDQTSEETREAAMIAFAQVVAHAPRAVFLPHLTQIFPVMVRAINTDDRELGSAAI

QTFRPLLLESVESAKPFLKDVFPGLLKQAQS

>contig49243 Frame-2R

MYSSYTVIFFYYATRLVALGYLKLRHLKA

>contig49500 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57262.1|) 0.0

MQFTELSELNHMVGLMRMAACNSPTFHDRQDSEVDRIYNSSPKMELQLRNSWIDKMTAFK

PQQSSIVSPSSGKKSPKILRNNISASITAVAGGKASEDGAMKTREGREKSVVSSNASRRR

TFTQTGRADKKGSAAASVKTGEQEDQVEGADKKPIDDRFVFEKEEVLPISFHESSMLDKA

LKGPTASGMGPRPPMIGADGGSVLHLTIYLPTRDEMKIDLYDVSTVDEAIQELLRVHQLD

ARQPALYYGHPECYELRLHDSDGIPDEDFPALDRSRKIKNFGDAGGHEYCLCERPDACPP

SGDDSADVATPATVAKPTAAVAKPPLLNDKAFLKIFMPKSDDYTVVAIDGTTVGQDLLPT

LNKKHRLQLFQELYVLKISEAERERLDLASDEIDMHTKLRPLNLHEVTLATKIFADAPQI

SAPAPSAVEETRNLDSRSRPPPETFMFNDVTAAMFKEWHVIKKNKYGKKQQRMLGIDLNK

IYNRKVGERVITSSKSTKI

>contig49993 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56396.1|) 1e-23

MADTVQVFPEKNVDRVEETICVRVNGQDLHLTLLMQEDELAPLFSGAAWAGTLLWDAAVH

LTKRFLVDYHH

>contig50010 Frame-1F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY54025.1|) 2e-62

MSSYAMEIFVPTLISLTGYNVFTSWITIGALKVAQVAGSVAAAISLDAYGSHRSFAVFAP

LASSLSILLSYATWSRAIVVFVLFMVTALLSACWSCVYTYTPQDYNICYRGRGIGYAVGS

SRLAAVVGCYLYPHMFNVWKLSVPVLCWIFGGVLAIAALLIAIVPHFGYQPLAQGDDINL

>contig50087 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53975.1|) 1e-34

MSSTDSSFIFCHRMLSRLLVTHDTLLLDGLDQELGSFDGHEASLSLE

>contig50164 Frame-1F

MQELRFYQLVRHVVLCYRIRKTLARRLEKGGLTRLHETEAPFECVTAEALSNDAVTEYKD

VMNEKVRDGLSAKEGEEYACDKLPNADVTDASNASEKFNGSWNQDKTPGMPLKLENESNV

LSTHVLPVINPCSEPRRALYSDRPLVTVSDLKKKKRAELKRGIKPRPMCYRIGALTLHSL

GHIFVGNASFHTRTALYPLGFRSTRIFWSTRDLATRCLYECVITSTARESQHAELLERRG

TGDRAATQERRRPRVVFQITASDDQARPIVACTPDDALIELRSRVVSLYEEQRGFGAASP

VVEKNPFLKRSSWSSFALSGA

>contig50252 Frame-0R

MYFPVCRLRPFLVSVCTAVQMNKQSPPLLPKAFKISSASIARRRFKSTAAESAATIARAE

ATRGPRCNPSLVVFDKDGTLIDFTLMWGGWVESQAWKVEMTTNLPVREKLFAAMGYDWIT

RSIKSKGALCCTPMGELYKLAVRVLVAEGMHQSKANEIIQQCWSMPDAVLTSRPLANIPA

>contig51080 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65128.1|) 4e-23

MSTRVFVRLYDGTMQNETGDEVLELPPPPLKWKCAITAMVAALSKQTEYEDGVTTPKARL

FLLP

>contig51255 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60396.1|) 3e-18

MQSRALASMVSSPDFYVFNHRGAALHKRLMS

>contig51549 Frame-1F|Blast-IMP-specific 5'-nucleotidase, putative [Phytophthora infestans T30-4](gb|EEY60618.1|) 2e-89

MLKEQDPMIELLRKWIMSPAENQQELRVSVLQVFQYMSELIAEHTKNPEHSRLRSFLPNL

KTFFLPLDLTRAALEYDARTHYLARKHVPPSFKEVRHILNLATTNAIASKLKLVTFDADD

TIYEDGGSISQSSRMVQVIVELLRRGIVVSLVTAAGYPGNPERYEQRLCGILEALENVTI

EERARFLVMGGECNY

>contig51923 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69263.1|) 3e-49 NOT\_ORF

MKRRCTELFSSTRQILESHRNLVYGYDDDLYQELIGRLENRVKMYQQGVNAKYVDNDLEV

SAAQLAFDEEVLPSIPICQLHPASLGI\*KLSNNEKSDLSIVHPASMNRAQVPNRCKEEIK

QHHQRHLGLQREQLDHLAVPSDKYGEDVGGAMYDRHNFTIMNSEMTDRLPSFGGVLEVDE

ISKELDASVRKLVSLSMYNWQIAQLVFERAMCS

>contig52489 Frame-2F|Blast-ras family GTPase, putative [Phytophthora infestans T30-4](gb|EEY58454.1|) 2e-38

MLRSLLQRSSRASLRLMRPNRCVSTISNELDNRVFLDDHPRLRIALVGRTNVGKSTLFNR

LTKTRSAIVHNVPGTTRDRRYKAANIEGMDFDVVDTGGLEDAP

>contig52562 Frame-1R|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 2e-13

MLDYIQRARYLESSIITNSIETVTQNHVIVTVMNAGGHGFNLTWKPPSSLEEAFAIALRE

NFSVADSRMEYFPPSPTEQDSQPWKWTRSSKPPILGVLQVMLFEDL

>contig52904 Frame-2F

MEAPSEFTESPLDFVDWYTDTACTARYAVPCDRIESARQRQKLLRRKEPKRLEDLISLED

QWRTSRASSRLNFDTGDFDDTHSPRTYQHDAIKKV

>contig53107 Frame-1R

MNAIMNECRQLLHLSNTTQDPMLKTQYETQVQDKRVMLKQLDVKFKQCRSQRNIVKHVIS

ERNATSAVVTLSTFNQVSSDMQPIPMPAQIQQQTSIQCQMPAAPATSTKLSPDDLLGEDD

DVFSKSKSSLSGAGKPLEMPIDLQVSETPVSVAAPLDMITAPQQSIRTQNITAMNGSRSV

VPTNLMQEQGG

>contig53316 Frame-1F

MSENLLMKVDEELLQKYSAAPRCHRSLGTLLQVSSTELNRSASGRNLRSKHLPSSAYPLT

PSALTPRAPPLDSKQRPCIADSTKNGPVSENNCTFQRRSSFSISAHVLKDLKRVRSSTDP

KIKVKEICEQPER

>contig53363 Frame-1F|Blast-UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase, putative [Phytophthora infestans T30-4](gb|EEY58960.1|) 3e-18

MPWQRTLKRPLRFAGVGLHSGKDVAIKVLPAPQDAGIVFCTGAPRSHVPAQIANVEARQH

QFCTQLA

>contig53671 Frame-1R

MSLTVEEFATLAGRAFISVHAESQGFLGRRNYLEW

>contig54182 Frame-0F|Blast-tetratricopeptide repeat protein, putative [Phytophthora infestans T30-4](gb|EEY57886.1|) 3e-30

MLPYVTRVLENPNNWMVYSTALLERAWLECESSKRRERAVLQMQALVDQHTTRLTITQNT

LESIADAA

>contig54616 Frame-1F

MTPIRIAVGTMRVVIIVGWLDDRYPSS

>contig54663 Frame-1F

MLRRAFQLTASWQSRPLLLRSYSSRHLRKAPQLRYKDERIGILLSYQTISECFVLACRD

>contig54821 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61474.1|) 1e-35

MTMAVSVAYQKAEEERLDQLSTSLHRFVHVEKERLQRSQQRLTTLETHVQSLSRADDIQL

LIHNQRDPDNLHFQGKALALLDW

>contig55105 Frame-0R

MLSRVDSLLGAQPRSPSPSPS

>contig55286 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62848.1|) 2e-21

MRAKRHEDSRRFRQSSVSKLDQAARRRHEQLAQLQLQCQQRAHLIVAKVELVRAIQD

>contig56294 Frame-0F

MLLPSIIYLCLIFVKYERSPNPGRTTWPYYHSFATIALLCMLRHYLIVHYTKLLMPTS

>contig56636 Frame-2F

MASSVKWTSIASTRPVGTTTFEHWTVRSAEWAGEFDPVTNSYKSINYEHLNHSLRTVAAI

VDRYAHHPAIIGLEPVNEPWELTPIDLLKEYYWKSYKRVKARAPHWKFVLHDSFRFGVAY

WSQFMRGCPDIALDTHIYQAWNSPGTSTDYFSNACQQKYTIAEMENAMMPVIVGEWSLGT

DNCAMWLNGFNDNLPGFPTVQCQTTKCPIQSTYLGNNFPGTPLDTTRPIQGPYGTGQSGP

SFGDCPITSNTSFNQQTADDELVFTRNLNLKKLNAFAVGHGWYFWNFKTEFGSRWNFLDL

VRKGAFPKNVSSYHADDNVLTACVDEDDGAFLCSAKRGVRPLELENGLDFACGGDDGKVD

CTDLLSRFRTIEERCDWAFNEYWHAHREGGATCDFGGAAHLVAIPIPLNVEHQVSFASVY

NEKILIWTLLGVVLGFSGLAFVMAMARHRRREEYSPLIGHIIVAGVDD

>contig56867 Frame-0R

MVVGLIKDRKRVGFYTNTLRW

>contig57183 Frame-0F

MECSKVVYWPRHLWASPSVITSGLSVRCVRLSKTALCVVSLGADPPFDFELLPAKCKESC

RIVLFDAHVAALGNFEKFHSPKLLLQIGDFFRHNEEQRTMASIASDGMDTKLLEAVGYYS

LYLPMTALGSATTAFQNILSEFWILSWLCASGETL

>contig57309 Frame-0R

MAKKSKGCKPLASSLTPNGEKPVDGRSDQEPAATDEQAMASKDDVIKTIDHLLEARPDAE

VLEQRNVLPTASLNVSSTLQGVQRKLQQKMSADELAHRLESRPDVRELRDQAIVHGGDGV

APSLQATQEKLQRQLYSDKVNQRLTKRPSIEKLRTSGVLEATADLAPNLTATAKKLERNM

VQDQVSHLLESRPEKNDLVSHNILEDQDATVAPILQGTKHQLERQLKVDQIARQLRMRPS

VAELEEKGIVGEGELEENKMQKLSQRARYALALKAASRIAADNLISAEEKSRLKDLILSD

DKQVLAALECYEQDKDIEVMLDTLYRVAKVST

>contig57525 Frame-0R

MWLGFEHKTMGSWLELVLGMSTSNDTDFTKLGILTDLHIQNKFDFFQTAVSPMLSTFNPN

PMFIKSQRII

>contig57727 Frame-2R

MVSLESEDATTFIKVLKKHMTQDQLKIFLDKTVQDDYYFEDLAEGLAKTSTWWYQPLLDY

FEKAYLYTTSKI

>contig57824 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58589.1|) 4e-42

MNSYMLSSVGGYYMDRFHYCASNDTTCSSCQATWVRDYHAGVQVEANALCVGESGCICIA

ACALPDRDDSIVENWCSPALDGAQFRLVTGLVIGIVALFVLAMVLAKRQLARRQQQGLEN

REAQNAARAAAREAQRPAALARLPQLTLSGWTGMREKLVSSEHIQLGRGSTVTRPT

>contig57950 Frame-1R

MFSGGGRSRRCRRARDIVSSTAVDNSRNANEFRVRITRSGVISNAVVKIPNYFCRVIS

>contig58137 Frame-1F

MDELNFVKELDAASNQALSNFLDMFLAELENALYERWNQVEKLTAPKVAKVKLQLDLSAA

TDFFQRPLCRIYLSYIKYCKSSVHQSILRNL

>contig58519 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55822.1|) 3e-20

MAIHHLPNGEAVYTDEQVRGLGKNYMVESSRQEGIHAYTFFIKLYALEAVLQLVESGRVF

>contig59134 Frame-0R

MQVSHLVESIIAAFLNVPQV

>contig59358 Frame-1R|Blast-dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichyl-alpha-1, 6-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58713.1|) 5e-22

MAQLMRGRRAELVVASLMTVYLFFCPYNKVEESFNMQATHDLLVFGVHNVDKFDHLEFPG

VVPR

>contig00366 Frame-2F|Blast-PREDICTED: similar to Syne-1B [Strongylocentrotus purpuratus](ref|XP\_001185218.1|) 2e-17

MDDKKEDAEGMEETKKEGTEGLEEKTKEGTEEKKEEGTEEKKEEGTGEKKEEGTGEKKKV

EGIDEDKEEGSEGLEDEEKEEESDVKKTQDVKD

>contig05633 Frame-2F|Blast-mitochondrial inner membrane protein OXA1 [Phytophthora infestans T30-4](gb|EEY61447.1|) 6e-86

MRNAANMKRIQPEMDKLRELMNANPTRDPETTKEFQRKCTALMKKHDVRPLKSVLMPLAQ

IPVFLGYFWGLQNISKYFPEYAHEGVGWIPDLSAADPTMALPVISSALIVATVELGGEAM

AGDMKNMMKIGMLCFALVMIPLTMNFQS

>contig05930 Frame-1F

MAFVAVPKWFDIYRAEFFENGARKEDSESCGRLELSISFVSYKEKENLLDNDFDVNVCED

EEESKKSIDERYSIRKGGQLSQRKSSFDRLQELHNETIQNRQMAELRPPARKIKLVKAKS

LDKKVLGKEEEMHTFTVASTKFCVYRRYQLIRAIGHGAYGVVIAASDQITGNSVAIKNIP

RTFDDLVDAKRIVREIRLMRHLLHPHVVSVLDVIRPPLLATFDDTYIVTDLMETDLHRVI

NSPEALSSDHIAYITYQLLCGLRYIHSAHIIHRDVKPSNLLINR

>contig06157 Frame-2R

MNCTLPIELWYRRDEMIPTTLFKPFKLLAKTTQRLLRFQAIHDPQAFRFGAKIHAICHSS

FDRLLFLDADNVPVRDPRYLFESMEFQTTGAIFWPDFWHPDHSIFNVQRTSLLWELLDMP

FVDMFEQESGQLVIDRLRHAQALQLVQFYAQSQPNYFTTMRLVYGDKDLFRLAWIQLNRP

FTMIQTPPGMAGIFTSSFFNTTFCGLTMVQHDMHQNVLFLHRNQQKLTGKRLPHTNTSAD

PIIWTHILRIRDGLPRSKFVVELFRRDLSFRAQQSCFGRRDVSYNPDFYVQNIRTFPFAT

LESQLRQFALEWTQLYENSSMDSLEK

>contig07525 Frame-1F

MPPEPTGWRGPARKRKREAIVHKCNLQKISRNSNRPAKKKEPKIVSNLELIIETEPQNLL

ETETTVFLQLLENDVSRLPPPLPLHDKYQETALTFQSGKASRSFDCRLRKQSFKVSNNVN

GYADHHHLERSVGVSMCLVRCPLQTFLSTNARVAKGSINSQPSAQP

>contig08335 Frame-0R|Blast-proteasome subunit alpha type-6, putative [Phytophthora infestans T30-4](gb|EEY56965.1|) 5e-37

MPGDGYDRHITIFSPEGRLYQIEYAFRAAKESTLTSVAVRGNDSVVFVTQKKVQDKLIEP

DSVTNLFFITPEIGCLMTGLY

>contig08465 Frame-1F

MANLPSLPKDHVPSLCCNHSVEKRRPWTPEADAEIVRFVQEYGTKRWAKIATRLPGRTPK

QCRTRWLNYLDSKINKSPWHSDETQLILQAQARLGNRWAEIAKLLPGRTDNAIKNHWYST

YRRRCRQAAKMDENHNHDDRMAANRWTHTNGCELGQLSGESACATPVAMRLPSPLSVSSP

IHACGVGFPIVLSPLRLSHRSLALSLPTIPRSSPPSVFRSSLLDVGPSPRRKRVHLEATL

PHPGPSLQNHLSAWKGLVGLRIPDRAWPSPIRSNESPSTAPAYKDHARWSGKSRVAILRQ

QTSLGRERSNSADLFLDCVEQMNVKTSGQDVAKTVKSIATNETDDEGSDPQSLPSPMDGE

TQTQCNVLNAQTWWGDHFDADVAMKQTGDMCFHAPVLSAPLMLQFHER

>contig08586 Frame-1R|Blast-methyltransferase WBSCR22 [Phytophthora infestans T30-4](gb|EEY54369.1|) 8e-27

MSRPEHISPPEIYYDEKEAAKYNSSSRIVKVQQELSNRAIELLNLPEGKEAFILDVGCGS

GLSG

>contig09624 Frame-2F|Blast-GTP-dependent nucleic acid-binding protein engD, putative [Phytophthora infestans T30-4](gb|EEY55155.1|) 2e-62

MGNKLTEIVRECVEAEGNVCLTVSGSLEEAAASFEDDASQLEYLNEGGLRETGLTRVIRA

SQELLQLQTYYTVGEKEARAWNVLSGIHCRCGS

>contig10110 Frame-2R

MGDRLADGSDDTLDEARATEGLPTWNWREYVPPTWPPPDRVVPPLPTVDAKSFTAEDREA

YHAVMCKLHQWRRNFLRAERERGPPLKPDAVETKAAYIKRAKKGKDRLGLRKISRKKKHK

KMFRQKRSGCFISLAEIAKSGSAGKKLTEGPAADRREDQEDRDFWDDLDYCVNEGNNNDD

EEVMVETIDLTQADSDEE

>contig10442 Frame-0F|Blast-hypothetical protein PITG\_09602 [Phytophthora infestans T30-4](gb|EEY55650.1|) 2e-24

MSLKSIVMAVPQLLTATLLLYYACTFSRQSSAFVHPMVADSCLHQCVTSFMLASLIFSAF

HLSQSLCCTSPVF

>contig11126 Frame-1R

MTQQKSSSKFSANVSYGAVPTDLAPKNFVPSPRRRLTQWYINMALVNFVEFAAESSRGVV

LATLFLYNESLGGDLAFMGLLTSLFSVGRLISSTIFGWMCDRYSFRSVYVVSSGICLLGN

LIYLLADIHVADSLGALALSRFIVGFGAGNRSVCRADVAAMTTINQRLRYLTILATVVFL

GYALTPGLGSLVADVDVLFCGVHFNKFTSPGMILMVFNLLTIFGMLTSYDSTVSIHDGPP

DSPNSATSRNTLSDLTSLPGNVVTIGAIVFIFLNFTARGILSVFETVNIPLFLRVTGSDP

NSVAAVVDASNFQFYLGLLGLVSYFSIEYFRKSMTDVSWVQIGFLVLLTGNVLLVAMPVD

LTFGRLALAELLVWSIGCPITTAVVVAAFSKILGGRPQGTLMGVLGSAGSVSRIIMPLLP

AACPSLSPVFMINMALCTVSVALLWWYSKLVHRTRHADIESAYLVALPPKNNLRSPVRSE

KVNL

>contig13216 Frame-1F

MASRLPLWRVGDVLFTTSVRDAVNLYPFEFIYAHELAKSPGIVIVSEFSGSSRVLTGSIG

VNPWKRDEIIRAMEMALTMSDDERMARHQKDLEYITTNSRTKWAERILVDLKRTKKQTTE

GEYMGYGLGLGFRMLEFNAGFKMLDTDVVAKAYRETFRRVIFFDYGNTLTLEEPAGVDNF

SKYISGTEQNAFVSKAETLKASSDLLASLTLLCADPRNTVFVLSGKERLDLEKTLGSVRG

LGLAAEHGYLYKWGTNGGSMSDNRLPVSSASSSTSMASEGEEGVWLCTKDNFDDSWKDVT

HAVMDIYTQRTHGTYIELKGSALLWQYRDADPEFGQLQAKELHDQLLQVLEHFQVEVVTG

TDYLEVRPEGVDKGVIVDRVMSTIESTSGQYVDFILCIGDDLSDELMFQYLEDVRSRSNI

FTVTVGKKPSAAKYFVNDVDQVMEIVHAMTKVSTAAKRNFSMNDLRLFDRNVTTSGGLPS

FQREETGLNRLSSDVEDMSDMSFKDINSFEVETESDESTAATMPSKTRNALLGRGIAGRR

LSGVSSISSGAVRNSMSMSSLSTAGMPSLHPTSSTYEQYLSNVDEAAEEEEGG

>contig13748 Frame-0F

MYASKASVNVVMLLLTVSSFVHQDVLAIVYLVIVYSIMDASPTTVCRRWWALAWLLSCVI

LVMYLMMLWLPPFLNCKREETFPWRVVPDEYEKWLIMSHQHKWALLTDFVALLSVYLLRI

TNQNDQKVETIAAVDDSAAAFSLTFHNENSEDKSEQSLPTSHTEVLYALLMQQNVWYYLE

FFVLAYWLPLLLLLVFVCGANQGGVFSMVYLFASLFMLYRLDEARRPSNLWIHYLRTWTW

AHLFIITIINAPYVYAALSNCLVGDKAANDEHCMSLANFLGVEARKVPYGLIALFVLISI

QCEIVVAPIYATVYATIINEHKRAVKRRGEIMREFYRQRTEQWYAMKKDKNAAIQRLKMI

VSRLVHKVEELMDIARGLHHNLPPMAPSKPIIVETSQNAVLISWEKPSNSYHKIRQYRIS

RQQFPSLTLLGDFSDIVEISGERLEARIEGLRPGTSYQFKVCAVSRMGEGPFSAASDPIA

TYSLNLDGITTAGWMKYYREKLPVSRWGFLVSWMNAKYLHRYVVIDSSHLVFYQDEERAL

KHRSRKQKKRLKTSFKWSDVLSLQLSTSKVQYDDVSLSLYCFELIVRHSSNRGDVKYVFQ

SEHSKEFNLFLSALAFAVPREALGDNIIECLKERQLPSPLDITPLRRNTVEDSTFDEIKS

EWSSVTGDESTLGDPEDDDFDAKNGFAWRIPLYRLLYCYQNAGFKLETVQFEEDDMNEPS

CFELMQLFIHVIRSKSASICCLVLILCFTEQADLLNMVYVLATFTFLLVENPRPIPTIWT

RLLAYTCGIIALRYVFQLSIFCTGMTDHGSFYPSFEPYCMDPLNAAMNAKSIQFMVLFGV

YKFDGTAIDHVNSVFDGLQWNFYVMIVLLWHQRELRLQGFWIEEAIDDSNQASSQYKADV

MRGLRSSLSSSHDSIDDALLSDGRRQAPIIDQIATNSSSRKIETANLCNEIAAQVLQELN

EQERFEEIKKEALGVTTNKDNLAHSVSSRQSLENERSRESVLSEFPQAARNDVVAKLVDM

SGDMSEYGYYTGAKTSWLETTFPRAYSYFQTVICDPPAQWDKDIYVAITGAKPGRDFYTA

SLSVLLFSAIYAVVLYEQLGEADASSTSVADANSRISSSSLLSGYLVLLVFVELVFIIWD

RVAYVTSSLRSKVLLQYSYTIGLHLTVWILLPSNTNIYFQQRPALVVFYLFQCVYLWLGA

LQIRYGYLAYLGSRYNYTKENKVTALGATLFGIMMKAPFYLKCVLYSTTFVRRRLLVGSI

GCF

>contig14688 Frame-1F

MAMTSSIMTLDGYVSRGKSPPSSVPRDHAMLQDFAAYLELRLMCVNMSMLRRIFADFLND

HENTLVPMMQLGSTIITLYPILRTSAKRRHQAKCLLKKRKYNLDTRGCVFLYLQCRTATR

NMALFKQIFLEFVNHQEDALLAFVERGNQVISVIPFELPQRITPECKPLLLEKSNNSSLS

IEKATTEKKNVAEEIRENHVTKRKRDISKTQETSSCLTNQIITREESATNSDERRLLNKR

KRDVERDDVMKSHLQELQKKSMSVKGVKSPQTDASVLQREKVMATALLVSNSPLTSSRDL

NTSRELLHVFPMEAIEPLETEFIIEEQETEPLSTTVPIRDTPSFMPNDIEEEQGASTFIL

NHIDKVTAECVALQEDATLTTPTDVLQETSHVVTAVLQKDSIDSPDLVPNKARTTRQEEK

PIVSDLLPQDPIETVNSDDEVEIEATDFTRSSNESIFSLNYDAVSTSQLASSAVLNNLST

RGTSNVTNSTSHTFLQQVDSSEALASTASLSTLSTHAIIGFTDTVQDVVSAATMTVIEAV

LSEVVSRIIRESLEFKRGQKHK

>contig16097 Frame-0F|Blast-proteasome subunit beta type-7, putative [Phytophthora infestans T30-4](gb|EEY65701.1|) 1e-139

MTDFRRTHNTFGDAFPVAEELYGGFNFDNCRRNELLLSQSGGKQKLKATKTGTTIVGVVY

KDGVVLGADTRSTGGSIVMDKNCEKIHYVAPNIYCCGAGTAADTENTTALISSQLELHRL

NTNTQSRVITAMTLLKRMLFQYQGHVSAALVLGGVDITGPHLYTIYPHGSTDKLPFVTMG

SGSLAAMSVFEHGYYDEMTEDEAKKLVQEAILAGIFNDLGSGSNVDVTTIKKVSGNVEVV

KEFNCIKPNEVSELRSRINRDIVTHVPRGAT

>contig16703 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62169.1|) 5e-45

MVFGADEYIKSMEIHWAKKAKHTRVFFIRFTSNTGNTLEGGDQTKDRIVLEAPPHFQLGG

WTGKCGMEIDMVGAIWTSLPESLDKPELPEPETPSKSSDVEEPTPPTKSEDLPINQVSKT

YGGPHGTGFTDEKDALPGQVVGSISIRCGRRVDGVVMDIVAPIKTTFRHGGEKGGELKTL

TLSPGEYVVAMEIHWAKHDGHTRIFFLRFSTNKGNSIEGGEQKKDNAIERAPEGFQLGGW

FGRQGAGLDQLAAFGRPFRRSRIQSCRHLYRLCLVVGGLMRLLCRKNDSSLKQICAFFFF

>contig17696 Frame-2R

MIWVGKGSLTCKDSNHVPVSTRTVRLENGKRCFVFTIPLDAVGRQFYTELKNQVEGVKVR

KKKRKLHEDLSLGKVFTPVNTPLSPTKEPLPLLTLPVTETVTLKSSPLADLGIPPMRHPS

PLSVSIKQSTPYLHSPSDSPFRSPLRKKSP

>contig19647 Frame-0F

MVVNYSDTRSLKSETANRRAIFTKHHSRMYVSRAFDLSKSNRVGRIPLYSTSLTKAEFAQ

EFLSVAALSNTERSMANALAYSQLGLDYLVLVMVFQTLEVCLSSGKKATPERVARDLLRA

MRVEEFSRHHALFLFNRSLSFSITKCSSILVKVHILEQPTELVELIQDFARKHGALVWQL

YLATYSLDKAQRRISCQLVALLTHENPRSSYVIRNIFPHSLLNDLKASLLEYDEYGRHLP

TANPEYFAKNNGNSHKNGGRRDIVSGRSTLSNGINTRARLARNVKYTVLLPEFFERVGKT

YATKELVWGPKAVEELAHKLQTEMSMLDLYRLKYLAYLYTDPLATDHTETEWDAFHANRL

RHDLKHANFAPFLFDFLHHGSDSRLAFEILKGNLSSSNRFARFMPLSFLLHLDTSDDFES

DVGQDDDNYDSDENTLDENGFVSRADSVPCPGDSLEPKQGDRDSSHDKLRNAALTKKKKK

SAKHLPRWFIAWNCNEFRIDYECFENEVKVGPYYLANMLDDRGVLVEDIEGANKFMTLLY

YRLLAEDRGSSNKNIRSGGRSSAESLDDVDQSDIRLLVLKVMIQIYERHFNELGSLVFLN

HFLRVSMIVSRDGEDRRWPLIVRGNIMLFLDRVLSSAVNVSRFLREDENVTMVLDLLREV

KPLVVKQGPYDSEKEYIVEPAADVQAELDASEEETGDVGEDDESIDDSGNFDEEEEDYEA

ETDIAKLTIDALEESGAESSIVSSHSVSQTYAHRDDESVHEEEPRRVTVVAEHCGAMSGS

MIVQTCLSVLSRLIDCHTAEDEAQMHQDIYFPKYGRLTHFEGSGVSPISRIKRRLCKDRT

LRFLVGLLDCPNRIVFKKCLGLIRLLVRHNEAVIPNLHASGIFYYLLRFSQDVEEMSVAA

RLISHIHLRQSGLEFTNFNDDKQKKLNKKGVISPDPLTRICLRSWLVRLLPVSMVAQLLR

HGSRRFATALFSDANNPEVVWNANMHKQMVSYIEKFMEHHTDDNGVFYISENEGTEHKAC

VPRIQYPKEVHALQCYQYYLHNLLDEKNFPGWPINNEAAFLHSLVDSIRRWVHPELQLTT

CGAMATEDQSTKLLSVSDAVELLDATAL

>contig20070 Frame-2R|Blast-hypothetical protein PITG\_16835 [Phytophthora infestans T30-4](gb|EEY65214.1|) 5e-14

MAVLAQNEMKAIAYVQKGSHMHLHKRLEHLHYNNIMKMAANPASGIHLTDKVRDKCLACV

KRKQTKKRQSSKDFGANRK

>contig20971 Frame-0R

MQERPVSDAALSASASLPKSLLKLQLQQEEERTNAAIAAAFIGSNIPGL

>contig22029 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66543.1|) 7e-70

MSPVPVHVSQKDLPRVVAVVVLGYCIVMFLVLQMDNFFAADDHVKNFSFPKVGAFVALYT

AMMVLSRFYEHGTYVLYEMLWGCNISLVLVVMALYFSKPFLVGVAMVTVSGDQLLWYLDF

FSYIFCGKFIMGVMTYLTYPENRSISKTVFATHHLWFLPLCLY

>contig22285 Frame-0R

MSFVVWSIHLMDLQSPLKERYVQYFFFGMVLVFQEKNPWDEWNSVTPVASSFLLLLATFA

IRRRMPSYNYQQFRRGLLLMALAVMCFVRGLNDDTDPFRVYHGCWHGFVGAAAYFNLKVL

PERSGMQMSHLPIKRHN

>contig23273 Frame-1R|Blast-UDP-glucuronic acid decarboxylase 1 [Phytophthora infestans T30-4](gb|EEY57129.1|) 0.0

MQRILVTGGAGFIGVHLCRRLLELGHEIICLDNLFTSHRANVLDLQTRFPNFEFIRHDVT

EPYACEVDQIFNLACPASPVHYQHNPIKTTKVSFLGAINVLGLAKRVNARVFQASTSEVY

GDPEVSPQIESYLGNVDCTGVRSCYDEGKRVAETLFFEYHRTHGVDIRVARIFNTYGPGM

HPYDGRVVSNFIMQALQGEDITIYGSGSQTRSFCYVDDLVEAIVRFMDCKSCVGPMNLGN

PHEMTIRELAEMVIRLTESPSRLVFRDLPNNDPKLRKPDIALAKSHLDWTPHVSIEDGLM

RTIAYFRDLDLSKFKRPTNNTAHRKSEIANQANSVACK

>contig23387 Frame-1R

MSLESTISPLVASSDTELQCYLSDACAIEHLSILLDDFFTRGIALQTNLVGSQDVDVNAT

ALSISGRAVFSLFSRLLDAPQLLQQAYESSLLHVTRLIPFCQLYGSKNQETIAELLEAVC

DNVAEFPATLTVLQQLYIRQLNDLFKAVRQADVMDLIHRYYELSLSVGGMTTAESVLKIL

LLGKKELSKELREQSHSLLYRLVQFYEVVLPTLQRQLSSLDKKTASRVVLVIAEIRYILL

LVLGRCVDFELDKPLQSGVCEGKVLAGFHTLISGCVDEDAEHGSYFSDLWFLCEYKDKVS

AFFHRHELDQENLSYLALMIEQLPRRRFLPSVIKESLAIEEVKSNSGFEEIERQAMDLTA

LVHQVKDLFPDLGEGYIELCLLSADSQVETVINFLLESNPPPVLIDVSHDVKPSDIEFKR

VEALLKGNLLPAYENKKLDPNRVWVGKKAMETSYDPQIEVKDQQVANKTKELVAMYEEED

DYAYSSGTDRDGGFDSRGDGVAVLDEYDDDYNDEFDDFVPFSIRDGGLGDSQDVVREQNR

RIRAKEEKDAFWEGMKNRNRESVSLKAEEMDYDEEKKESDNFRDRILRSPAAAESTQSSS

NSKISNPRQKDKTHGEKKSNELLTPQQMQRQRAKKDKNKAKIANHNRKDRALKKMG

>contig23974 Frame-2F

MRSELTQDKQATTSVINDLIEMCQPSKHNDPATKCFQYLKLNKMTTGLIDSPQYIVWTEF

MKTARIQFNIISKLMPNSTWTTLCLAFQSIRKIL

>contig24764 Frame-0F|Blast-small mechanosensitive channel family protein, putative [Phytophthora infestans T30-4](gb|EEY57764.1|) 2e-13

MVMRSVLVVGLLSLELVAILSGFTV

>contig24984 Frame-2R

MTNPPSPKRQRTDEKLHDEKVQNILESVKDVEKEIEKIDVEQAKEILVIETKYNAKKRPT

YIKRNKLLADIPHFWKQVFMNHPLVGNYINEDDEILMSLLQTFDVNFINKDGSFKMEMTF

QDNPFFSPPTLWKQVKFSEDGEEVEVTASEIFWKDKANMTEESEKYPFFQWFISTDGDQD

VAEIIKEEVWKNPVSFYMLDEGEDDEDEEDEEDEDVGDGEDAD

>contig25594 Frame-0F

MTPLLCAACGHDATRQVFSLLTAAGGDINAALPLTGDTALHLAVREGHEQSALAILATGG

NLLKMNVEGLRPLDCTTSTRLLFEIKRAAGQRDVMISYTHSHAEFAQKVRNALEEANVTT

WLDQMDPSGIGGGSVWREEIARGITNAAVVLCLLTEDYAQSEWCMKELALAKQVGTPIVA

VSAENVAIGEELQVYLYTRQLIPFECAITQIRRNVVNVRQIEYEYDETKFQTQFRFLLDG

VRDEIEKNREAIQRQNIAMHLPRNGRKQATTSTMVASTRSSGLFLQYDPNAMDAHRPFVF

LSHGEKHLGFVQQLFRELTNAGIVCYGDRSIDGQDFESRIQAAQYAILQCSCFIVILSNQ

TMANELVRDQLAFAEDKKRPIFPIAINDLDLGLDKRYSLARNELFHFMGNGMSFKPSVQR

LVQGLRHFYTERDELFDSARSGNLSSRIASVNTSFVSFTFEKNDDEEQILADGANAMETH

CITGDELLLSSVTRNFESLSDIEEARLDLPSTHIRM

>contig25785 Frame-1F

MALLRRCFILEYPLHAFAQSRLIESTSN

>contig26322 Frame-2R

MNIIHTLGAFTITLAAVEAGYSKESDNNTPVPLVVIPETEVDASLKTLQFSIPSTKHPDN

LSPTIPFDKICPFEMAQPSDARITEKAAIKFRPQVTISQGCYPHAAVNEAGQISKGLQAP

DPTYAKCGDPVQGTQVYGRSAWFGRVWAIMYAWYFPDSPIDWQHAIVWTNNPNVSSPVIL

AVTVTDSKGEYSSKVSPDIDGKTTKLIYKNRGLDLTDKDGECQNLVLWHQLTVDAQEKLN

DDKSFGDTRVPFNDDYFLLSLGKAWPFP

>contig26472 Frame-1F|Blast-endomembrane protein 70-like protein, putative [Phytophthora infestans T30-4](gb|EEY55025.1|) 0.0

MGKWKQYMAIAAAMTAKLACADVETHKYTVGEEVVVWENKIGPFNNPQETYTYNSLPFCR

AHSIETPEAHALGIGEILEGNELLNSGQQLKFGVNTPKMTLCEQTLTDSDAVKFGAAVDE

HYWYQMNVDDLPVWGLVGKVMKHTDDLEQLKQYPVGTRVLYTHKKFLISHNGPHIIHVNL

TYSDVLTSIASNKKVEFTYEATWYETTIPFEDRFDRYLEDEFFEHQIHWFSIFNSFMMVI

FLCGLVALILLRTLKNDYARFAEDDAEELMMDGKSSLLRDDANSGWKLLHGDVFRAPPYL

LLFTALIGTGVQLLVLSLCLILLAIGLSLYIEPGGIVSVGLTIYAFSSLANGYASGAFYH

QFFYPRVSKDWIRAMCLSSALLPTVMFGSVFFINMLAVGYGTTYAIPFLTIVQVVLIWFF

VSCPLAVLGTILGRHGAAKAGFPCRVNKFPREVPEARWYLRPPVLIALTGVLPFGSIFIE

MYFIFASFWNYKFYYVYGFMLLVSIILTIVTLCVTIVCTYFLLNAENYRWHWTSFAAAGS

TALYVFAYSIYFYFFKTDMSGFLQTCFYFGYMGLFCFAFFILCGTIGYVGSSIFTKRIYR

NIKCE

>contig27398 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63966.1|) 2e-69

MASDPLIAVQQLQDVVTTLAPSLRPQILPKGVKYGLDVILSLCKTEKQRMELMALVRSYK

PPSKPVESTKSEDENTDREDQESDYLEPQVIGIFDIKNRVFSVEKVQWMHEREAVVHEFA

RFIELQLENPSVASQIVQDFLNTNGHKKDEIMKAQQCFSAAFALQTLLRAFPKLPIAING

KIIEITSNSDVTTVFAPLFPISTKAKPVKKNCSQNTPA

>contig27611 Frame-0F|Blast-integrator complex subunit, putative [Phytophthora infestans T30-4](gb|EEY65797.1|) 6e-95

MMDPAIDPSVVVKGMSSAGRTSIETARDIPLRIHKSMFNNPSDIQGMLIAEPKRKLMLVS

SGNGARRLKKKKHALFFSFSWKKPFEPSARGKRKSPRPASALSFLLSAAAESADEEDESE

QQPHADVDKILKALENSLKKWLFDFTIEKIDRWLKLRTVGVSVSAEWEVHMEWSFDDEAL

AGRVLGIAKHIVNAEYQKQLAT

>contig28144 Frame-0F|Blast-hypothetical protein OsJ\_20379 [Oryza sativa Japonica Group](gb|EEE65226.1|) 1e-12

MTMLRLLDLGGNNLQGNISASFAGNDALEQINLSSNNLTASTLTFFDAFHQLQHLDISNN

KFKQRLSKSLFASKFLQSINVSYNAFHGDLSILPVFQFLES

>contig29356 Frame-0R

MSPSDHNRRTIPRTAVSSPATSASLLIDTQGAAPDDAYNFISAGARSPGKTTLFGCGGIC

LIAFVTSSSTSYPSSMPA

>contig29532-0 Frame-1F0

MLTVPDALTKRSMCMSLSLFKSSGTRSEGYSSGNTEAYIAAGFEGGQLAVLDLRSGGKVT

CESTITDGSNA

>contig29532-1 Frame-1R1

MVLSHVTFPPDLKSRTASCPPSKPAAIYASVLPLEYPSDRVPLLLNSESDIHILLLVKAS

GTVSIKAGDELRMSKTSN

>contig29811 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57991.1|) 4e-24

MTIIPSAGRLAARLAASYTLLTSHRRLSTALRFQPNAKLSDESILKHLVCPISKCPLRYD

AKRGSLVCDEIHVEYPIWKGIPMLVPSEGRIINPSEPNSSAKQSATS

>contig30220 Frame-1F|Blast-HSF-type DNA-binding, putative [Phytophthora infestans T30-4](gb|EEY54539.1|) 1e-116

MSDTKMRKRPTSSGLDSHANASAAPVFLQKTYDMIESSPMAVACWSESGTSFIIKLPREF

AKTMLPRYFKHNNFSSFVRQLNFYGFRKHKKDEIVISTEEDKSKNWWEFYHDKFLRGRQE

LMAQIRRKTYSEPASPDHEEVEILKQSVQSLQGQVSELMGQLSDLTGLVKSLLQEKQAPI

PVPAQRAPKRLKLNEGPVPVPRMAGPPSANSLTKSYVPQLEQMPVLPPQPCLTQANIVMD

PVSKIQNQRTREMSLMEWTESYGMDYLINDTGRSMPLFTDDMMNYE

>contig31076 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56579.1|) 2e-13

MTEHIPPFPHIELTPEEQARYNRNVTSFLSDAVAEYSAQDSQT

>contig31890 Frame-0R

MSASWDSDLPSIIEKTNNNLKLLRKTGEKPHVAVTAVSHRPRAFVGVHDDTGSTSSRGSA

RPVAFVRNEDDTSSMGSHGSARPRAYIRRDEDSFSSNLSARVRAFVPTDDDSVLNSSRGL

NRPKAYFQPDDD

>contig32132 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66241.1|) 4e-88

MAYSVAHEWDSQIYDIRPATMPIMALVSTALDLEYTSDSQETVDEIMHYLHTDTICYQVT

ADQQKKLLTQQTKKWRPIRKWFSDNFGGETDVSHGSIDRLAHDHDLVANVRAYLVKLNNF

ELTAMRSLTKECK

>contig32200 Frame-2R

MFEFGDELIIDSYRIPWLIWIQLLAMFLLVILLYIFTTTPSDLPLHFSTATTSASASQSS

PALSRSFITPVAANTYQNYKVTENEIIRETGASTSEIAKRAKKPNVGEGPTAVDEENNMI

LEHSYHPCHLFGLAKQAFLKCLGIDSGPDNST

>contig33838 Frame-2F

METASHKDMIDAAKRKRKMTATTPPSSLKRGNKLSRPATSNSSSIFNGVTPPAITTQESV

CTPEQFADNQRAMFSAAAAPTPHGPVEHMPPTPAFFNRNGFSHTPEGFNSTPSDGFPSNT

TTAHHATSSASTPADDGQTNGHSSHAATPSPVPRAAPLNLRDFANWDVGSRYTLLRMLGK

GSYGQVAEAFDTERKQKVAIKKIINVFDQEIDCKRLYREIYILRRLSHSQVINLIDVIPP

ENYDTFTDLYLVFDFVDTDLHKLIMSPQYLTIRHIQVFLYQLLCGLKYIHSANVIHRDMK

PANILLNEDCTLMICDFGLSRVMESNMSLDELSKHLYSPKDSKSPTTSDGGTTSAPSPGS

ASSTPSSSGEFPRMRRQLTKHVVTRWYRAPELILLQDYDFSVDMWSIGCIFAELLSMQVE

SCPRYQERVPLFPGRSCFPLSADRPTTYSDKLDQLNVIFNVIGTPGESDIGSLGEVKQYL

RKLPKKEPRDLR

>contig34826 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64374.1|) 4e-95

MFTTIPVPEPSLPKFSTREIRFRKARDANILIFSIPTRSSVLLPLLNPKSYAFKKQDTRC

LHLLQAVALIPSCKFEKLLATVDEALKMPLSAATRRKLELKLHPLTKKLHDENDESGNRP

LISLQLKETVAKCLRDWIADPVEGYVLRKEYVVSGMRLDDLVATPAGAGVLRAYRGSDRF

CTVVYPWGYGYVHIKDVKKVLNTAKKQQTKKRSYNERVALEHKQLSEQIEGLLGDSSPPA

HDDCDVVKKEETKQEIEDTEEFDDLFDSLKE

>contig35432 Frame-1F

MVNLRDLSALHKRVIRALYFWRDKIARQEDESVAYVMPNHVLLKLTKHLPVRSDELLRVC

NPVPILVRKHALEITKLIIAEKIKFTDDEVPLRVETVNVKSVQRKTWELDGRETTVMNSK

QVGRGVYPLWKRGLRQARVAIPKGTLNSGNRSIFAHENSVLETKQEVAMKLLDKVNAMVA

STRFTITESAPVLRPVFPPTSLIANASSKETHVEEEKPMPLSISETYNISNRTKRRKITA

VDKTRVAHVKDRAQACIEKFESDDSKIETTTEASVFQGFDYASASTQVTGAKLQLQTEET

ENRQGRGGRGRQGTRNVGYDPFVAMKSTELKEPKAAQVKKKHHMPRSATFR

>contig35700 Frame-2F

MFSYTPIFGTYEDTLFNIDLVVVSATGIVNAGEYLNFGTGRLGNFSSSASISIDGHPMDL

TRPIFDTLEPEWNEKFYFHNVPRDSKFSLIVMGSDLDKEDTLGVAHFPAQHAVDDTNVAH

DLPLTLKDRKAGVLSIKV

>contig35911 Frame-0F

MIKRQLTPGTMTYISLPFYDRIWWS

>contig36055 Frame-1F

MSIKRRGFQRTLDGKWVHVVCALWCPKVWIGNLFELSEISLVGSLTEARFFNPVEEIEGR

VAQALGGQHVASKHDEIRVIELGSLC

>contig36297 Frame-1F

MFRSKVAHRRRRHSTLLFYCVCPHEKEII

>contig36789 Frame-2F

MFYARSTTSHIPQTRTTQIRGNIALSALNEDIETSSVSNVSSIFSQFSAATPTTSSEACH

YNSNNYVLPSAQRLAASSPASSENFRLESLRSEVLEIKEEVKSFRREVLNELHLTRYDVL

KELTLLKGVISQLCATQLPNLASPVSPTESSSSDTLSTEVRAILTRQTSAKTSDATRDRL

AASRAVLKRSPSLAARASVRLTQLVPVEDNALSTPLDSHQINELFPLIDCTSDFAAHARC

LTPGSRVWALNRVQQWLDARFHSGSDNFLAVVGEGGSGKSAFCGTVAQQFCGNILAAHCC

QFDRKSESHPRNVLLSMVHQLVYNLPSFKSHLARLNLKYVLNEKDSVLLALKVLVDPLNA

IEEPVQSTFILIDGIDQCSAGTARRNELMEFFTQIIPQLPPWLGLLVSSKPSIEFAKRVP

VSSVLDFSANNTAYMADVSSLVNEIAQ

>contig37166 Frame-1F|Blast-folic acid synthesis protein fol1, putative [Phytophthora infestans T30-4](gb|EEY54477.1|) 1e-101

MERAGVDIIDIGGESSRPGAESVTEEEELSRVLPVIIKIREKSKIAISIDTTKAEVARQA

VLAGANIINDISAGRRDPRMLKLAANFRVPIVLMHMRGTPQTMAGLKEYQDVVIEVSEAI

NERIAAAEAAGIFRWNIIVDPGIGFAKARDLNLKLLRKLSVVKKSCHDLPLL

>contig37218 Frame-1F|Blast-DNA polymerase zeta catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY64210.1|) 1e-120

MFSPDPPTYSQILSSSRDLGITPMKYQPVCYSNAAEIPEKAMVFGGKKYDFTPQNIKKLP

EFDTAFARQLLYRHRSGEGSSKLDNARWCKLSRIKKPSIVRGSGEKMRCLRMPARMPPDA

STVEAWVSIDAEAFQKTTESRRKRAYSSLVPTASLSSTLSSLTIASNITILSIEVFAGSR

ASLLPNPLYDPVQVICYAVDAQEGPSDTKTKDYGILMVKLDGMEQAAPESVILGVGSKNS

SVSFASDEREL

>contig38181 Frame-2F|Blast-catalase [Phytophthora infestans T30-4](gb|EEY62861.1|) 2e-44

MLANFKDVDEHYAQRVKEKMEQMVSAKESVSKSKKLVTAPLTKPRKAFTPVAP

>contig38354 Frame-1R

MSIQSLAFASATTGSFGAAIPLNDNSRRLPLLASIYNALTTMPAKTDSYSHQDGLEGLES

DGNSTFDGQIQENEAINASLATTKAGPVHNKWQELRTRVETVDPRVFAYQNDPKYLQQCE

QAKQRRALAAGTPVWH

>contig38523 Frame-1F

MISNVIQAANLASNSTAMTGSTSQKAAPITLSGTTTLTTNEATQTASSLTHVVEHSSQLK

G

>contig39061 Frame-2F

MRIVIKGGVWKNTEDEILKAAVMKYGMNQWARVASLLSRKSGKQCKARWYEWLDPSIKKT

EWSRDEEEKLLHLAKLMPSQWRTIAPIVGRTAAQCMEHYERLLDTAQQKEGIELSDDPRR

LRPGEIDPNPENKPARPDPVDMDEDEKEMLSEARARLANTKGKKAKRKAREKQLEEARRL

ATLQKKRELKAAGIMSQNPKVNTKKRKFIDYAQEIPFEKKAPAGFYNVTEEKQISRIKID

PKRAALQLDKLEGVRRDALEKRERKQDVKRQNSLMKSNLPHIIAAVNEKNDPINVIKRMP

LNLPAPVISNDELSDLAKLGMHASHAAALALESGSSNETRALMGDYSITPLRSITGVTSA

TPSNRNVHENIIQETANLLAMRNSATPLLGGENVELYEGTGYVGATPSRTPSSALPKAAS

DKTPMSATRTPLRDELGINPEQLFGTETEDAKAEKARAKRLATSLRKGFESLPAPQNEYE

INVPEYREDSGVKVRFEEDAGEREIRQQQHLELQQMHEFKRRSTVLQLGLPRPSKVKKAL

IHSELDEVADEMYRMLEYDLAKYPIENRKSKKSKSKRKKTTSSVAVPHLYEFSDSEMERA

RQLVQIEGSLSGINDDWKSQNIFALNAKWTEVQNRFLSKAEGGGKTDGVYFQFASSKEDK

IRAVQACFANLKEAEQFLAKRALKLEERANIVNGGLKWRSQQGVELLRDQMRELRNSAIE

QACFENILQLESQALQRRMTRLANEVNLQQLVEVKLQKQYAALVQEQK

>contig39519 Frame-0F|Blast-hypothetical protein PITG\_15836 [Phytophthora infestans T30-4](gb|EEY63489.1|) 1e-111

MSVCRDNRERNEKWRYFLQDSQLQIGDCPLEEVVAEARDLELLCRRRLLPGANALGDRIV

SEANSILGGKRGIWLLSITQCRRLLHRVDLFRLLRSQILILPPSQLVELVSRVVKARATS

TTFPAWWSSPRHDILLLQGVECYGLDELLSSVWKLPLFSSANTTKNYPSSSWVENYVTVL

ALTCHNVIVKARTYQKRQVIDLSKDDASSGVATEYDRRSEMNQKVENMRRVREIQSMREE

DPTYAASVRLRQQSESSARQEIKQREEVALNAITPIQTPLKSGDEVEQMKREDPYSSPCV

RDLWADDQIKRDEIKKSRSCLSGEGAASCHDIKGAATAAVETKDVHLWDVIVIDSSDSDS

K

>contig39775 Frame-2F

MEEDKRQYPLSTRPNVVCNSLNLSARSRQLTQFVSNASNNASSRFPSTERSRQMNLSQVS

TISNFMGSEDASCSSMSSVSSAYSVMSSASSSYGGGDRWALQHASNSCNLCREKFSLLRR

SHRCRRCGYLFCAKCSRFKAALTGHTHKSRLCETCFPKVLSGSKPPMNAFVHSKAWVPRG

VFTHMLSYLNHVDLCLASMTCRFWYKRALLDITWRPLYVNEFGDDEMSPQRESLVAFQRE

VHGIGFKNLSWYNKFAIRWTARKAAEKKKSFLVMSSLLASLKLSKYAALFEAEEIDIESL

CLMNAGHLRDLGIPFGPRMKLLNAAACLADFNEDDDDERQSMESMSITPVARFKQKRAEM

KHFRAGLVRRVQQSAVRIAILTNEGELCNVGSGIIIHENGLIATARHCLQGEQFDCIYSD

EYMILVAPTESTSLPPLWKYHARVIPECCNEDLDYALLCLSCEVISDPPSGLYIGDVTDR

MIARNWTVTKLQGTSRETIGKLPAVRIGNSNNVEPGDEMWMFGYPSSGHNTITVHHAICS

GTDSQVYEGVEVGKAMLRTAAQLDNGFSGGAAVDKKGQLVGLISFSVLRQDRVRAINMVK

GAIEYAKNAYDFL

>contig39933 Frame-0F

MISNTTEQSIVVRPFSTLPLAVEWKGEVVEAISEKSDLVARSILVTSPKRSRTSFSPLCL

QYYYGKPYVLRAKSSYLLSFGFADFATTPLLTDTVGNGKLCPFQGIIAIQSLESAKDTDF

DEVCTLAAVNILGSYCEPLFDIEEKLFSLGKIGYGIGWKSSTFQICVKNMSDVSVPIVMS

NIPPCLHVLDARGGNRLQLLDDAALDPMLHVPSLRLLALRAGKSTERRNTSGWAAWNIQP

RDSCLLEMELVRTKESLTAGTHEFSLNFYNLSNPCNHENVLVRAQVISRYAELVIDPESL

QDGREMTTIKEKHVAFLPPVTVPTPQESPRHRSSFWFSLRNVYDDELSVKILSQAHNSFD

RTLELLVMLRSANTPLNSLVIAPGESVDIRVVCLVLPSARFLADTWPTGSNDTSLNMFDL

GRIQLHINIHNVEDAAQREEIHVKGQLLPGKTLVLSADSLHFFATAIEIPPDLQIDQLPP

PLRLKAGTMRESSSNTPPIASPRKIASVVHHLRNSNE

>contig40447 Frame-1R

MRFRAFSMQKEYNTTERTVDDRRGGNAETHSIKESESEICQSFLSSLKKTSFSSEDHVIH

AGAVSIYGGWRQLTHVKVALTLSLLCVCPTYAVDGEYVPDSVLIFGIESVPGKLRVWKGV

RDRSIHSFVLLPVQIQGAAFQTRDNITTIAGERDYRQRAFSSKRADGHESLNSLLFIGDA

VGNIEHWRCQIVESTMHFTVMSTSLIRYTNTPTSINQVCESTSSFYRRGYVWNDQKPYFR

RKDNAGFRKICHIEVDDPNRLAVLYADRPGELQIFEAESGLGMLRPEESIPSNGRGNIIG

FTWCNAHVEFNIDALAVRYESTIVIYQYDTTLHRYGQIGDDIKTLLPLFDCTRDSSALLI

CGGHISKRGTDRLSLQSISNEMPVVIGKWDEPGSLLQRSMDWKATETPQKLPVWHPYVLL

TTMFGMHARVGEKDTYLAGDREAYEFSRAFKDATQMLKLLAKVLEHEPSAQASALHGVLL

YTGPVRLNRRAHKENSEHARKLESIGRYSTSIHRSDQIDRA

>contig40609 Frame-0F

MLLLLLLLLPLARACTMIAVGSNATIDGSTLVAHTDDAGFGAADLRMVRVPAQDYEDGAM

RHVYRLQPGYPRLVTLERGPEYEPKSDEEKLMIPLGKIRQVPHTYGYFDQDYGFMNEVQL

SIGESTSGARTVGWSIDAGPHGYNMFGIGELSKIALERCDSARCAIQTMGDLAVEYGFYS

EDSGDPSNPAYACGAETLGIADRNGEVWIFHVLTGPQNTSAVWAAQRVLDTHVVVVANGF

IIREVDLKDPDRFMASKNVLSFAREMEWWTPEQGNFDFTAAYAIPTPDPVRALYMGRRIW

RVFDLVAPSLQLDSRLGHYSEVPTYPFSVKPDQNLDVAAVTRLLRDYYQDTPYDLTKGLA

AGPFGNPMRWDGDEKGVTGGWERPISMYRTVFSFVLQARSFLPDAVGGVAWYGQSSPHAS

IYVPFSCAQEQVPLSYVLGKESEFTQESAWWAFSFVNNWSILRFNVISKDIRDRIADLQE

ICFDKRKAMEQHVNHTNSLSASDVRAYLQQESNQLASRVIEKWWAFAWKLVGKYTDGYIT

TGEASNEMEMLGYPKWWLKLSDFSKWPGSTLVPPHIPKLEKQLQLFTSRQNASANVEIVP

SLFNLKASISSTISIAQLGIGAIVGAIVGAFAMRLAVRRQGQYQSIA

>contig40700 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57235.1|) 2e-15

MKFILALTAAAVFSLTNGQIDDYNSEVLDFVNKIRTASGKKNLCFNTKVAAAAQVVAKDL

AYYQIPQEFTTEVHSVKSVLTANKVQVKGSKEAYGVGIDSSEAMVNQWNITHRDVLLSDF

SFFGAGFVENKILEFNQYWVIGVVDIMDGACE

>contig40865 Frame-2F

MRILSMRDLLNGDNTFTKLDSSRNRAKEGKQKQVHSNWKAPSKEKAVKHRRLLEQLYKRK

HKSLSMSRVVGDVLLRQHTISQLESTNLSKSKFLSLKKPRSARSVEQTAGHAEKSPISLK

AQPMERQKWTTAIKSMGPMNRQAVASSAERFKQLTRKKMIAPKLASSSGRQQAKGTGASA

QAALATTHTEEMSGCSQLKANMCINNDRKCAGDASDPPTKSALRCHEQKFSKKLLCIAEG

GLVEQVHISKKRRRLKLTAAHMESLASRDTKKPHEEANHILSSQFESRLQAETAVRSSSK

RALTASNISSVENRTIVIFCKRDFMRYQAVKIWRKYQDQFEA

>contig40911 Frame-0F

MADSRDGDRRDRNNEAGRWSHDNRTYGTGRGRGRGRGRGSDRGRGRGFQGSSSESRGPSL

PLNPSNLQFVRSVLKTCPNHKLQTVIEQMDKAWLSSWQGIDALPLDGLKVLLSALSRLPY

SVSIAPPPLSAICKAVSALLGQTAHLQRREEALDGNDETLEIVELVERVVQRLLKFTWDL

GKDV

>contig41651 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65384.1|) 2e-34

MMIKIEGEHLRAELASHSSAFQPVIEASSCKRE

>contig41725 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66709.1|) 2e-78

MKGCSCKKSNCLKLYCECFAAQRMCDHRCTCERCKNQFETSIERERAVALILERNPLAFQ

PKIASGSSQHLRGCNCRKSGCMKNYCECHQAGVACTSRCTCHQCRNTETFVSAKKMLDFA

GVQTDKSNRRDHPERP

>contig41826 Frame-2F

MVIQVSEQLGALQRIIYSPLE

>contig42896 Frame-0F|Blast-phosphate acetyltransferase [Phytophthora infestans T30-4](gb|EEY62816.1|) 3e-41

MSWRVNVDIARAIGAPVLTLSDFNASASTNITDLMTEILSRTALNKEHVEGAGLSFIGNI

ANRVNTKDPTALRKALRAKLHEKNLPFLGFLPNDEFIASKR

>contig43297 Frame-0F

MELVTTQPLSLGDLNGLLLSDDELSELILDQIDFDSNDIMVAIGANDTVMDTMLPETCAA

SEQNEMVSDFRLSSSSPLNLGLEKSGVDNGLTKSDLLEITPDGRISFIMSPIKDTNALVK

TPLRLDKELVPPLTPDHTRRVRKLRGKTISECESQIKVKERLRSYERRSRHKREHTMKTM

RATLAAMETRLFEFVKA

>contig43503 Frame-0F

MSDYAHKHMANGPSSAMNDGYNPSFQLRPPQMQPHRFQELPRLHVPPFALTYQTPAWKLP

PPEQSAPRMSVSNLLSGTFRSRHPTPLLTPPAPAPAPPPVLRRLPSFADILARTNFLHLM

GRSTEPT

>contig43789 Frame-0R|Blast-nuclear pore complex protein Nup155 [Phytophthora infestans T30-4](gb|EEY53449.1|) 1e-170

MLPPPSKQNRNSRPLVAMELSAQAERTFKGLSDVKTRVDQATQEDASFPDLADQLNAQSE

PQNYFLEPYASQWTPQVAKKGSIIPLPSVVAAALDEVKTLTLSGLLPEIRSAWTSVDARL

FLWSYAQRGRFATKEFDQAIVAVGLVIRPATGVFTSKVQHVLVVATTVEVILLAVVIDEG

QSEPLNFKLQPTKLSVSTDKCVVRKIVTTRCGRIFFGGSDGALYEILYAPDQKAAADRKS

ILGAALKNVPGVGISEGCRKVAHTFSYAQYLPRFLAGLASAPGKVVDICVDHTRNILYIL

HDDAQLSVFDLGTNGEESKAICTSHLLTDGAKYARENRRTRVSCPDERLFQPAVVGTSNS

LKVVALATVAPDESKIVTLVAITSNGMRFYLTV

>contig44076 Frame-0F

MIVATGGWTGMSRSLRLASVAYATEEVSLNLGQQLGLLRNLINASSFQIATVHIAGDCGS

LIRRQLGRQPPRASTLASNSGTPDALWTRLTFKELDSGARRGNLAVRTRSGARHATRMKH

>contig44227 Frame-0R

MMMALMQRSEPPVMLNHRGERMMPLPSSCHPKMKVKTRKLSVMEGDCEHGQLTKKPRNDY

ALEPELESSPLGLPRPSTERITPFDLHLQAVYDGHAEDGMHFFESHGYYDITDANTVEMF

RQNCGLSQAFWLDKDENALESNRHALVPAVYPFGSQQQIMSAKNCLQRQRSNSGRFTLLD

IDGNEVDDDTLRDMEREDRLKAKSLELDDEDLAELAHDEIVMSQAITCIRSEKSQLQQFF

LQAFQHEHPIPLPVVRQSLRMEVPSTLPPAELNLPPYCGYVNLLKDTIPFLMRSWHKRWF

YLDFQAGLVLMYKRSYWKSPRGMIDLRNVASVEKMSQGDFRLEFRTTDSSAPTMMLLRSK

TPEESELWVHLLRFAKQASCNAPCLPSSILDTSKVLMKRINKKTQADVLAQLLQTSANNA

SSSHLRAIAQASAVAACAVSRRNCKSVKPKHYPQALMA

>contig44393 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60457.1|) 1e-12

MARGNTMRGARMLLRFFNFAFSVVALATLSRAFVGSSYYGYSSMLG

>contig44568 Frame-0F

MEELQRTERELDGLWRYVLTYVSRTKDNGPEQQRFTFSILEEQTLEEKVSEAIAANKRAV

VEAQDVAHEVQDRNEAQEATQKLEHYKKQLQRNIASCRKALVMYRERAKIERLEQQRRSL

LPLSSRRVQNSVRGSSSGSAVDVTAALKRTKQVMSQEIERVSSVTEVLDDGRQSLRNSYE

EYGSVNAEIREVRKRLKRLEWQAKQDKMWIGAGMLVLLSTVLFIVHERTGFVLI

>contig44674 Frame-2F|Blast-phosphatidylinositide phosphatase SAC1-like protein [Phytophthora infestans T30-4](gb|EEY54523.1|) 1e-116

MMQAHIELTEKLQVNDKTFRMLYISRRSCKRQGMRFTMRGIDDDGNVANFVETEQICLFP

DGKQTSFVQIRGSIPVYWSSPATMKYAPLVYRAGDVERDVAAFQKHAYELISLYGRVLLI

NLIDKKKDQLKLGEAVTKTVAGAATMDSHILAAVRLVWFDFHHECRNMKWNNLEKLIKQV

DTDFLDHGYFCESADGRVVSRQSGVVRTNCMDNLDRTNVV

>contig44915 Frame-1F|Blast-Di-N-acetylchitobiase, putative [Phytophthora infestans T30-4](gb|EEY65484.1|) 1e-114 NOT\_ORF

MHGITSQFLALLMLELRQELKQHALTRHAQVTFGVPWAPRGVDGRFYPWRELAAAADFLF

VMSYDIRSQVYDVCVAGANSPLALIK\*GL\*EFLLGYDIPPSKLVLGVPWYGYRYPCLQGQ

LSAATIDDASWCQIQPAPFFGAPCSDAAGTQVNYGNVRRLMKSQGLIEQWDPTTLSPFVW

YSSPEGGRSQIWFDNLRSLEAKHALMRELGLRGVGMWHADALDYSLANDSQVMWRWLADA

FRS

>contig45220 Frame-2F|Blast-cysteine synthase, putative [Phytophthora infestans T30-4](gb|EEY69777.1|) 6e-23

MRSSFFVHYHHEPSKILSRYCSGLCSKNIAKSFCKSLFASGSVDLFSSIDNTPLLELTTL

SRLTGCRLLAKAEYTNPSGSIKDRVAKSLILDAEERGLLGPGG

>contig46023 Frame-0R|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61857.1|) 1e-126

MGGVETPNFEFPLMTKSGRQLDILLNATPRFDHGGVITGVVGIGQDFTDQRAQEEEYIRL

IDTANAPIFGIDMDGRVDIWNRKAVAITEYTVLEARGTRLVESFIPQDYRAGVSDVMHKA

MEGEGTANFEFPLITKTGRRVDILLNATPRYNQHGDIVGVVGIGQDITERIVQEQEYSRL

IDTANAPIFGVDMTGLVNIWNDKSAEITQFAADEVMGKDLVQEFISEGYRS

>contig46481 Frame-2R

MKSSDSQNAFRCFSSSRLTYQSRTFPSAFLSKMGMAHFCRILNSGANIKICFELRAGRLK

G

>contig46838 Frame-2F

MLSSFRIKSKRRSEQQHEKSQKRKSIRYIADQESLAHDKVGELQNKLNVLTTSQDADTEQ

KDFHVLPLISTHAEFAAESVEQYSELLNKLIKNVMGRHQAD

>contig47132 Frame-2R

MRATTARRAESARSALRYRVQYIYRRNRLTLKTKGLVTYTISSKRPSTDGTTLLSTASFT

TRRNVGLAVKRRAIERTLHISSLFTIQQASSL

>contig47147 Frame-2F

MLSSAKSMDDEAARLTVLRDPKRMAALLIRAFSTSMMEHSMCGSSARRDGNRLVIEDEDD

AGEEDEDDDDEEKPLEEEELEAAATALQIATRIVEELRFKLVLKASKPMNRQQ

>contig47309 Frame-2R

MSSPQVSTKRTIFVSSRKSQLAMAQTNTVIAMLQDRFPDLHFVVGQEDTIGDQVLDRHLS

DLGTSTASGLFTKSLEEALLVKSASFAVHSLKDMPTTLPEGLVLAAITKRESPEDAAIIH

PKHKAKGVKSLMELPQGSIIGTSSLRREALLRSQFPTFQIKTLRGNIQTRLAKLDEHDEY

DAIIVAACGFRRGNLGHRIDEILPTDTFGYGVGQGSIGVECRGDDAEVKDGAILDRKCIA

>contig47859 Frame-2R

MTSYSPSEELSNDEERDNTRVEVSFLNESDSFINTKARDLYYRQINNLIRRTSLSAVSIA

QYSLPLSDGQSSFDGTLDHVHFDHG

>contig48326 Frame-2R

MNYQNKIKGSKQPAFQIASHLRVLRGQKAPEYKPKVAIATNVLATETTSESDLQMTATIA

SNSTEGNFETDFKNVVLEATPSAEMDFDSDSGSIVKLRARLSRFGDDGGDKDADDNDVDG

DVGEGDENLGREGVDEDALMARAIALSLSPEVNLRDRNVSNNASAPLKLTVENDESSVLR

SRPPKFSAEELLELGPFVLPNDLMASVDGVTVAIALIAQMCKLCMEYLKSC

>contig48843 Frame-2R

MYVSASPPGSAPVTTSDWYEIFLYVSTALFTIEYILRLWACVEDDRYTHPIRGR

>contig49039 Frame-2R

MSTKTTKAFVDLKRRDDLAVKSKLHSVFAKVAEGIGLHRQRRALGRIRLHRRPLQVSVAI

SAKNIYLFSNRSQRMS

>contig49084 Frame-2F|Blast-ribosomal large subunit pseudouridine synthase A, putative [Phytophthora infestans T30-4](gb|EEY63303.1|) 9e-44

MARLQHQGSIYSSDLALRLFYGCRKVGVVTVPMKSSGSAEDILTIDSPVKLAEWCVDTLQ

LELSKQLYRHVVRVWLPTREDIALGSPRHQLLVQICEMAECSTIDTVDKVLAAPLAFKTV

FHDNAVIVIDKHANVLTVDGSAPNAPPSIYRYITRAYPEARMVHRLD

>contig49501 Frame-2F

MSTPGLRRKRLLHPDYSDTLLHAPILTPHY

>contig49992 Frame-2F

MQLPWVPLLQDNGAGSGSAEWSVSAAFLVDSILYALVGGAAGVQLVRNCCHHRPWTVQKM

IHLLMFVATLVRAIFLAMVASDWCDVLSGKVSTAICSTGERDLFYISDQVPILAFFAIYA

LLVQFWAEVYYNAVDKLSTLANVIKPSIRCFIAIVLIVQGLYWVFYASVWRNERAFFTRS

QSILNMELYLIIASGFIYFGRKA

>contig50011 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56421.1|) 2e-39

MKKMRMSIDDIHAMVGSIRVNVVNMRVTNIYDVQGQGESGAAKTYILKLHQPPFPKVFLL

LESGVRFHTSKYARDAKTGSALPSQF

>contig50086 Frame-0R|Blast-pre-mRNA-splicing factor cwc2, putative [Phytophthora infestans T30-4](gb|EEY63602.1|) 2e-92

MSNLDEMPRQVTAAGTLGDVGAAYAVYEKNWICSDCSHDNYARRKRCFRCRAPKVERFDA

LVVDSQADAHTWREALDPMSNKIYYYNTQTNATQWERPAEMGAAPHGTGWFGRGKAGASE

GDRYEQLNAKFMSRPARKQLDALPTANSQLEGAYEYNIWYDKYIGDHWDDARG

>contig50253 Frame-1R

MYLTCLNIKKKKRKVSFLDEDSFLMWTNSRGKPLPNGGVAVLSSRAQSPQAAIMSALRHH

GRNIVLLVALAALLGMTMYHFSLSDRNKFQLRTPENWRNVQPLLLPSDSAKNNMRQQPTL

VPPPKPDSLGIVIVADLDKNSKQESSKKPEFMSFIMHATLTVASSSSNAAQKHETYSVTF

GEETKF

>contig50635 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68868.1|) 3e-74

MSSLAAAQADGYYYPVQWRPEYGSINKYQGSHPLGKRAKKLISDGVLVVRFEMPYGVWCT

HCDAHIGRGVRFNARKKQAGRYFTSTIWEFCMKCPNCSGEMVIRTDPKARGYN

>contig51081 Frame-0F

MDKNRSQFIQQLVSALQARDDISSSSSASANCVDGELISDNNQEIDKLLREDERQFLSVS

ISATERIQLAQEAYMQLQFDYPQTQASSIEALAELYRRISTEKLTAIAAQIPITTSLLDG

VAYLNNQISSSSSSEAPTSRCSESSGLLAASILILLFRLCLEMPGDTRVDKLLSSLVVKQ

PLQSKDHDIRSHEFKLLQEENDPLVEIYASEEDPDDLSDVYEGQLLEPPYHSVAYLHHPV

SSQFSFSHTEKLQLIASCTFSSSFHSISIEKWEQWHLNDALFAILRRLLATSPPQDTDSE

RTGPLIPFYGVQGEWKRYLYVLRDRVLRFSQCSQRTIWQFKDLIDFYQKRESAAFAVDEP

RCSTQWRPQHFVFSVLAELAKSQEFNCKGTQQMQQNLSLVFQALVPNIMQEIHRILSRSS

ANVKAAMVKTIHDDEEDEIRVVYLHLLHFMIVASSNVHKTIELLFASGMLQILLKLLPSF

DIDMTQQCNTKRWFRALLRFVGECALWHASFAVYLSQIPKFFKLLPTLRGQLDAEELLFA

LAFNQHNVNLLQIDVWATFESHCYIPRHCESYFHAMVKLRDVLFVVNCLEKSFTALRPA

>contig51423 Frame-0F

MSFAPFVRLAAPVRNLSQCVIILYDFTLRVMHVQVQSTLLLLAIESYKTTLIHCCIIT

>contig51957 Frame-0R

MAHWWRRDELLALLQAWEQTLDMPRDRDEITEMELHQLCARFDALRPRDGASISVQEVEA

QRQRLVRTFVFLRAFNAESLRARRPTWFQLPTNQQDDLRCMNGRLGELVTVTPDEFELLC

RICEEAPPPPSSPMESFQLHPKSQERSMADEMKAAAEALAGLPMFRSCQTPPPPLSPP

>contig52130 Frame-1F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY54200.1|) 1e-102

MTMQQRLNDLQASSDENAQLRFELKTLLPTAEYVVGDDARSSQLSSEIKSVSEKFSNLEK

AKRRQEEEIQELQRQLAASTAEVLATKREVGRKNSEIKEMQLKLDTSTSIFTMRDQLLAT

DDTLKKEFEAQRQRLSSLVSTLEREKSDLQNEISDLQREQKATTIELQAAKSRLITKDRS

VLVSTLRNEVSSLKEQLRNEFMLEKECLTTETQSLKHEITLLRGRLADKDLATRNLEKEL

VRSEEKQQQKDYDFRQQEEQISRLKIDLEQSRTKYQQLQQCRTALAEQLDFGFKELMNDE

ESA

>contig52563 Frame-1F

MAGCMSTLEAVASTLRMLESDTTGGQVHDALLHAFQGMVSIQQQFQARGEKAKLKLYNGI

SKAKAIEATRCKQQQHQTSVDTKAVKDDVARVHRDYVFYTSYMDYRQQQQLTRYVSSSVP

FNCF

>contig52761 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53480.1|) 2e-47

MNDLIARAATLRSYLRSAAQNCAAYGDDTLMENLTQLLNEDVAFVLDHTFLIQPSIKTEE

AFPRSPWSSKACISNTELVHHAIRQLLARNHTTHWEDANLLTLGYREVTPGATGHRVTQS

DDVVCYYPNTLVAALKKPLWGAVHKLIGDDLMMHLLLNFTIFVQLKETPDSYMQLAGKSL

RQELHQTMCCSIEKREKVSINFVMYARAHRRNRAFA

>contig52905 Frame-1R

MVTSHPIHSYLQRQKQSVASASESHLLTKVSSQRSM

>contig53317-0 Frame-0F0

MPSRPNMERMNKQERKAEEKRRKRARRDEEMARTEKRRRTAVAATDDALREAEIRSRRKL

QKLEMAESVLLREERERRMAEEKAERARRSQMKLNAAAWTGVL

>contig53821 Frame-1R

MDGSRGYFSAAAGSTPATEAHAENFVSESISTRPASTGSRLRQKPVSAAPHENFFASLGI

TSASRGNSASSVSKNYSQTTKHSVSNTASRSSTSSWTPPPIGGLGSQRSIPPSIG

>contig54183 Frame-2F|Blast-PREDICTED: hypothetical protein [Vitis vinifera](ref|XP\_002263623.1|) 2e-11

MLANVQRKFYWLNMHKTVAKYIQTCELCQLIKASQCKPAGLLHPLVIP

>contig54370 Frame-1F

MDTAVKQFRALLSECVFISAAAAASTDVENADIRVKSVVIPVGLSADQLQYWNCFCGDSA

SSD

>contig54406 Frame-0R|Blast-histidyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY67043.1|) 5e-25

MASTCVMIGASRLSVADVCSVAALGAFVTLDMKSEAFSTSPKFTMQLVSSTSSSSALPTV

RRAVLVLFLHRLLQAKSVENAHYVAMLLNHPGKTPAQVRYVDLPVGLSQEEQQAFTNVPI

ELLAETALAVGGAISLLPLADAVAAITCETMRADSAAFEADFVDVVRPHRGIVTSAHNLR

MMLDGSKYINSLDKDGAESGTVALRYIPQYHGP

>contig54491 Frame-0R|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY54186.1|) 3e-49

MARRTDIKIRFDGYDLDSISEYLQDEEEEIAAYIDANDASISRISPHFQIEELSSSQTHK

IWTRIQDQLQIAFDKEALETSTNKELRKRAQIIQHITSGLVACNCGEMTEEEFMDKNEQN

LMICEDTILQLRDAMRAKQNQL

>contig55104 Frame-1R|Blast-abnormal spindle-like microcephaly-associated protein [Phytophthora infestans T30-4](gb|EEY64421.1|) 2e-08

MQRLKALQRFNEMMREKKHESCRRELQRRVETRAVTCIQKHFRIFCGANAKLLRRKWLVY

SGV

>contig55373 Frame-1F

MPHSSTGIQSMLTFLALATDHQ

>contig55690-0 Frame-1F0

MDDKKEDTEGMDEKKKEGTEGLEEKKKEGTEEKKEEGTGEKKKVEGTDDAKEEGSEGSED

EEKEEESDVKKTQDVEE

>contig56101 Frame-2F|Blast-hypothetical protein PITG\_05396 [Phytophthora infestans T30-4](gb|EEY69195.1|) 6e-14

MTARPTVDVTGVDISPNPAKLTDELNLQVDFHLDVPVHNGFWNIEYLADSVNKRHFI

>contig56637-1 Frame-1F1

MKVVQQVATALLTLSLTAASITP

>contig56866-0 Frame-0F0

MLAMPQALVCRSMRTQLIYTTKCCCFLSR

>contig57182 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61711.1|) 0.0

MAGIVKTQAEVKDITRIERIGAHSHIRGLGLDDSLEPRASSQGMVGQTEARKAAGIVAKM

IEEGNIAGRAILLAGKPGTGKTAIAMGIAQALGKDTPFTTIAGSEVFSLEMSKTEALTQA

FRRSIGVRIMEETEMIEGEVVEIQVDTPTGGVGDKVGRLTLRTTEMETIYDLGAKMIDSL

TKEKVEAGDVISINKELGKIAKLGRSFTRSRDYDAMGADTHFVQCPEGELQKRKEVVHVV

SLHEIDVINSRSQGFLALFSGDTGEIKDEVREQIDTKVAEWREEGKATIVPGVLFIDEVH

MLDIECFSWLNRALESNMAPVLIIATNRGITRIRGTNYKSPHGIPIDLLDRLMIISTKPY

SESEMRKILMIRCEEEDVEMTEEAKDLLTRIAVETSLRYAIQMIITASLVCSKRKGTEVD

IPDINVSTRSLPM

>contig57599 Frame-1R

MLLYKRTNLSILNTQSLQGTVIVHRHFLYFCSVSPKFTISRKHQLLATKKSPLDAKTSFI

ISLKLML

>contig57726 Frame-2F|Blast-predicted protein [Physcomitrella patens subsp. patens]gb|EDQ80476.1| predicted protein [Physcomitrella patens subsp. patens](ref|XP\_001754506.1|) 4e-15

MNNGKTLGFRGDNDIKYADVVSGGMGMTMVVRPRRYNLLPIYDLSEQGLLLSHPWCAR

>contig58842 Frame-0F

MQKTRNAVLITGASQGYGRCLALDFVRLLQDEGLDL

>contig59135-1 Frame-2R1

MVWSKQSSKSWTGDRKVSIRTRICQCEEVILFFCPL

>contig59359-0 Frame-0F0

MHIRYNDRVVLIYSKLSQRKRQVRQVLTTGMIR

>contig00004 Frame-0F|Blast-ribosomal protein S13 [Phytophthora infestans]gb|AAF24795.1|U17009\_28 ribosomal protein S13 [Phytophthora infestans]gb|AAW62566.1| ribosomal protein S13 [Phytophthora infestans](ref|NP\_037622.1|) 4e-62

MLYIFNKTISDSKSILHSLTILYGINEFQSNKICKNIGINPQITLNKLKNNHVNRLITYI

NKNLKVEQVLKKNKNERLNELLEIKSNRGIRQNQGLPVRGQRTHTNAKTIKKLKKIFIQK

RISRNKRPFKFKPKIKKTKK

>contig01285 Frame-0F

MSTSSPNPNGESDTPGTPVPGNNVPIPDAPKSNGPVTEAPELGGPSMEGSKDEEKPVTPT

TDGLATEAPKIEGPVTEAPKIEGPVTDAPKPEGPVTEAPKTDGSATEAPKTEGPTTDAPK

IEGPATEAPKDPFAKPPSDKTPGISHPPTSYHKSGLVSPEGSGNDYVQQQLRFLRA

>contig01788 Frame-1F

MSMLLKMLAKDDEPLPLPSNPPFIDEKTMELNDISEKLQNYSYTDSSSSVATVSQSHFYP

R

>contig04453 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56120.1|) 2e-08

MSVSFLSVATVLTTVHARTDIVAQLYGNTAITAPMPPQSLNSALEELVVSVANFTQYPAA

>contig05564 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61371.1|) 9e-48

MRRAWSVSGDEQYEMVSRRSSMSSLDSDQRTPFSRGVLLFSDRLNTNVDRNDSESHDAVM

SESFGDVDSRQSTETSSVFADLLDAELSFRRQSSRLAAFLRKPFRRTDSFDGRRLEVRMG

IVSPPSPWTEIAVASFS

>contig06011 Frame-2F|Blast-long-chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4](gb|EEY55995.1|) 0.0

MTSKYTTWNIHDEVAIRVAESGVGARPPVTAMEAFRTSLIKYGSANALMFKKDGEWASYT

YQTYYDKCCEFAKSLLHVGLERFQGVSIIGFNSPEWAIADIGAIFAGGVAAGIYTTNNPK

SCEYVAKHSDSAVVVCDGVVQLEKFLSIQQNLPSLKALVLWNDVVPEGIQSAVPVYAFED

FMKLGKAIKDETLAEVMDAQKPGNCCTLIYTSGTTGDPKAVMVSHDNVIWTIRAVLDMLK

RNFAHEISNSDRIVSYLPMSHIAAQLIDIWLPVCGGLQMYFAQPDALKGSLGVTLKEVRP

TLFFGVPRVWEKIAEKMWSIGAQTTGVKKRIATWAKDKGARKTALAQYGNSGGVPCGFGI

ANAVVLTRVKEALGLDQCIGNFSGAAPISKEVVEYFGSLDLPIYEFFGQSEATGPQTCSM

HGIWKISTCGRPIDGAETRVVPETNELIFAGRNIMMGYLKGEQETKDAIDEDGWLHSGDC

GKLDEDGFMTITGRIKELIVTAGGENVPPVLIEDTLKEELALLSNAMVIGDRRKFLSALF

TLRVTVDGEGQPTDILDAKALDVMKEIGSSATTVKEAKADEKVKAYLDAGLKRANARATS

RAQNVGKYVVLDHDFSINGNELTPTLKLKRKIVYEKNEALIESIYA

>contig06222 Frame-2R

MGYLTFGTTVQNYHSLSVSLTSCFQMLLGAFDYEEIYVANPTMAGIFFFSFMITIYLVCV

NMFIAIMSEYYSLAQSEKKTLEEHKRNLIASTPTSDTDSLSSLEVEYDVMKQVQKSINGL

RIRVKMPPKKKDSQSCHQTEQLVLCGFQRVLLVDYDYLMAERKRLRRTFRAIVHIVVTCG

NLLRRIDMDFSFSTDQDIVAERNRSLMCTIDSSTDIVTFPVTYLPISSSLANTVALLQRL

KRGMLLEIDDESLTKDRITLQVLGDQDAYKWILDVDGNDCENDGLQVQIQNDSCRITNIL

PFGLRQNHLKLGDASHIRACRVLYNGTALLDGNEVVNLPKLSWCRYFLEIVLWNFFKHLF

SYYSMKTSPPRLVTDVEITQLVAKHVATRERDSSCRFDELVRTFRLFMAKKIHTRHLRHM

NLDDRVYHEVIALLERFPSVISSVDKRESEGYKYVPHPLDTQHIKLPHSINLLAELLAQN

THEVWAVGRIQQGWRWGTARDNDLKLHPDLVPYEALTEQDKQYDRDTSMSALKVIIALGY

VLEPPTYPSGYEDTFSFGQTVTQPGETYVPKPIPTDDVVLPRPLRSVVELLAENTHEVWA

AMRMQQGWTYGPCRHDGKKEHNGLVPYLYLTQDEKQMDRNTALQTVKLILRFGFELVHKD

HQRTRGMRNNRFNTHGQKDDRHATYHVRETVTIASGTAQAKRAFLNRV

>contig06297 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63083.1|) 1e-103

MEQALQLPRLLHLDTFVAQPKFLDVIAPPTMPFPPPKWCVHEPPRTISLLDVYKEQVLIA

THTVDQKAFYLIGRNAAVCDLVLSHCSISRLHATIVHHEKGTTYVIDLGSAHGTFVDGSK

LLALQPTLVVHGSILTFGGSSRSYTFKSFDSREQIAEMLKTRVGLPPDELHLQENTLLNT

QISHRLELSPTRRKLPPMFPMDPMSQGAELPAVTSDQDAPMLMASECDRPS

>contig08729 Frame-1F

MEAELDLSGPVNIVRKQWVANLQKKRVAAAAGTGAPIGNGNPSCSALPRSRSSSHSRRTL

LQKNSVAVQEAATNRSTTQCAFEKRILSNGLNQYALNPFTTMSSGLIVDSQIVTDIQEED

PSSMLFSGLDCFELESPSFSQLISSSLDSEHPLPSSAMMRESTSNQAIQATLKKRSPQCF

TNEGNTPEPRTPRRKLNCGLASFDDFDLDCSTTSVYSSVEALSQLQVDTSTRHLWEGSDL

DLTSPEVYANTFLEDLQVPCNPDLPLVPPPLPSSVNLNDNTTKALKTDSSVPFDQPRLIR

SNSIEQDGLRQFFEQTNLDGHDEVDPVPLPSALKAPFSDDSFFPSHLSPRSAATTVDDWL

TSKSFTSTSTGPVSSLLPQGQANVSTKWCRDVKSINEFERGTDEKIFSDDFDPELDSFYL

DAIAAIGTDL

>contig09436 Frame-1F

MLELLRAYCIFFFDDIIQYHIFGDNNAIGN

>contig10386 Frame-2R

MATDMEQQCVPESRLGINSTASSSIMASFDDYRPISPAVRRWHDSTLQPLRMKPIRGSCL

QVETSLSSNLNLMGTMVDDSILCNKPSDGLLVPSIMSPLILKDLQLLDSRFISDNWSYEA

PQNMYALVTQSTNAIDSIATPYLPLQPQLEPPVEHLLPYLISPLHVPSFSSMGITGGAMP

LVSTLMTTPDFTPTSSLSFSDMIPLEDPSLYLSDSPTNRQDHLLVSPMLPHSNSVKDLTL

NELRPHFNKPMAVVAKELGVCITLMKKICRRNGLVRWPHRRIRSLVNRITSLQVLLTNAV

STDQTRLQMQIATLRAELSAVIQNPNKKSPKTLKET

>contig10603 Frame-2F

MHSHCTLHFLGYVHEWTRDFALSESYSSTRVGASPISFFTNLYLPEERKTSFFEAAAAGA

TGSVAGAKPKVSCLKVGVRAGHAIQQVRIAPGTLQGA

>contig12807 Frame-0F

MLQLTAPTFSPRSVHRNHYKLRRSSLAHPTTIVFTACVMSRHRHVPHWTGGEDHDLAASD

LVKSLRQNPSRNHAITDRTPLLPHIWGPP

>contig13659 Frame-0R

MRVYAVFEVGTLVCAISSVAVAKSAGFKALVKNFFHGGDATGSDTSDRTNTDDRTCLYDW

ESLTCQPESKCSIQYTFGDVTPSQACRITDSGDHTKTPQQFHLAFAGTEPGTGMAISWTS

FAEEDAPGVWIGTAPDKLVLDVDGAIDIVMYYSDKK

>contig14908 Frame-0F|Blast-ubiquitin-conjugating enzyme [Phytophthora infestans]gb|EEY70048.1| ubiquitin-conjugating enzyme E2, putative [Phytophthora infestans T30-4](gb|AAN31476.1|) 2e-77

MATTLPRRIVKETQRLLAEPVAGISATPYEDNLRYFQVVIAGPQSSPYENGIFKLELFLP

VDYPMAPPKVRFLTRIYHPNIDKLGRICLDILKDKWSPALQIRTVLLSIQALLSAPNPDD

PLANDVADHWKTDEVGAVHTAAEWTRRYA

>contig15468 Frame-1F|Blast-mitochondrial intermediate peptidase, putative [Phytophthora infestans T30-4](gb|EEY54537.1|) 0.0 NOT\_ORF

MSRS\*LAVSTTGLQTLRTLDDISNAICSVIDAAELCRNVHPIEGFRRAASKCFTELSDFI

QNLNADKNLYEFIKSVTENKEEMKSFSAEQRRMAILLRSEFERDGIHLSQRDRQRVIAVQ

NEITQLGMEFQSSISCAREFVEVPAKLLRGLPYSIASVCERKWMNPSVLRVPTDVYVTNT

ILKWVGDPKVRQNMYIAANTCTKDNLSVLDNLRAKRHELATLLDFPTYAHLATSDRMIGS

PEAVQNFIENIAAQLMSKAKSERQLLLSAKRKHEGSSVDQIFMWDLPYYMGMLKAQTHRI

DSHVLSTYFPLENCLKGLHLLCSSLFGLELKEIPMLNTSETWHKDVVKLALIRKNKTMGY

IYFDLYPRPNKYAHAAHFTIRCGKRLSESSYQKPIVALVCNFAKPAPDSPSLLAHAEVET

LFHEFGHAMHSLLSRTEFQHLSGTRATLDFVETPSHLLEYFVWDYRVVKEFAHHYKTGEP

LPPSMMQGLRASKTMFAAMDTQTQCLYSMLDLRLFGEYPLPCNPPTTTQLLHELQNSSTL

VPHLRDTYWHTRFGHLIGYGAGYYSYLYARVFAADIWYSIFAASNGPLNREAGENLYQKL

MIHGGAKDPNELLTDMLGRQPSPANYIRELRID

>contig15891 Frame-0F|Blast-alpha-1,2 glucosyltransferase alg-10 [Phytophthora infestans T30-4](gb|EEY68864.1|) 6e-90

METKSVRSSSLSVLLRPSARILPVVAVLALSFSWLFAIVNKTVPDPYMDEIFHIPQAQKY

CKGLYAEWDPKITTFPGLYIVSTLFAKAVLTFRIGNSCSVAVLRSINVFFAWGNIVLCVL

LRRHVAPQDSNALLHALRITMFPPLFFFTFLYYTDGGSTFFVLLMLFLAERVDLLQYPPA

RGSFILSAMSGGVAVLFRQTNIVWVGFVAGTVVVRCVELAHSKFIYGSFKQDTDPFSVT

>contig16528 Frame-0R

MVQFAAEMTPESVAAAVLAAVPRLATVDRHEFHDRVAKMYNWNSVAIRTEKIYEKVHDLP

DCSLLHRLQLYYGIGPVSGMLACFIAAVLHLYVVFLEWWQPAAEIELALDWVPFSKQEHG

EKIKPE

>contig16779 Frame-1F

MSAVFPAPVRSYTTFSDASPLSMPPPSPSVSIPLYPYRTKHPFVPRRLEDFGDGGAYPEL

QMAQFPLEMGKTTRNGSFASSQNTLALQVRGDNGTVRYDAIVTQQHRDKTNVFTTFDALV

EKTGHAAVVALPTKDEEIETTTRTREALQVLVQGKVTSALPTNISGRVQNVKDTAKYIRY

TPNDQQQQRIIRMVDVAKDPMEPPKFQHTKAVRGPPSPPVPVLHSPPRKLTLADQQSWKI

PPCISNWKNSKGFTIALDKRLAADGRGLQQVTVNDNFASLSEALAIAERNAREEVNLRAQ

VHKKVMQKQKEQHEAALRELASKARMERAGIRACSDDDDTLHDDDDGQHERDAIRRERKK

ARERDLRLTKLGKQGKAIRDKTRDISEKIALGQLQATHPSDGLFDARLFNQSQGLNSGFG

HEDEYTVYSKPMVDRGPASVYRPTIDTSAMDAAQDYEELKQGPTKRFQADTEFRGTVAGT

RDGPVQFSKEFKRNDDKRQFQDKNVSVVSSTTEQKPRSRSKSNSSRSKHLRSRSHGRSTT

RNEFKRSVSRSYRERSASRRHARSYGRERRRERRRSYSSSSSRERTRRRSYSSSSSRGRT

PRRRSLSSSRSRSRSRRCRRSLSTDSDVDPFGLDQFLTDARKGVERKRRRH

>contig17398 Frame-1R

MDANPQLNDMSRRPRGRPPSRSWAFFTPLGEPQKLISAECRHCNQLVLYHKKWAQARAHL

MKCPQFLQLVDTLPPNDVPQWYLAEIFRRQQSLAQNRSANYYQTNQMLTQRSATANPYSI

IQPVSMAMTSDIPMQNGIENVSLKDEINANGDFVVENVAMHLFTTMQVEKLLDEGFELPY

LVQAFEACGLDVAMFCKEEIMTTLLDQCFNRIQTQVFGFLKNGLVPVTLSLLPAASREGD

KLVTYMVTLASSNKYPMVLESVQIPSIGDPNAIHDLTRIVENLSCPVAGCVVPCSTTESR

QTCEMLQSQFPAMYFHGCMRDALQSLVRQLFGATEDVKAESKHTIPISFTQDLQQFALQC

NDLIFFLPRSKKLDLDWTTSETNTTVHVTARRRLRVKEAFGAVLQAEAFLDVEHVFARLV

SSVGGTSSPHDGAHYQTQLLKIVRSPQFVEKLRKYLALFQPIHTLLSSISEPSTTATLLV

SEVYSSLSKLTHQFDSIGLFSPEDKISLQALTQQLKDKVLGSAHLLAYLLDPVLLAEDLP

TDTKTEVEQKLMDSLRKDDTGLVENEKKALHTQYMDFKKFAWNQKTTKADTLAFRALKER

KKLPLQFWFAEGSKWPVLQAIACRVFVMPVCAANPARLILESGLASSTRHNKTDQSSFDK

LSFIRVNSRQLQLAEAEGSSLAA

>contig17761 Frame-2R|Blast-hypothetical protein PITG\_06324 [Phytophthora infestans T30-4](gb|EEY69818.1|) 9e-48

MRCIEHDFLVIRVMNDNTMI

>contig17826 Frame-0R

MSYTLPHSQETYVRLSKEKGWVALDLPHATYSKPRSKYHSLFPTHQDETLVPTLVRLSEV

LYHLYTLPPSWVSLGYPTRTWFKVPDESCRTILAEETSLQMAVFESRQILASSSQGREGV

PLSREGTVSLQDGKMVWKCTLEEIKHSASALLTTFPWKQVWWILELQDRHERHCVELQHG

LRGGFRRILLDGEPLLQHRTVVDMLWDAGSESTFAWLGQTFKVVIALEGAFFSPYLQFYS

YTLVVNDTNIKPLDL

>contig17981 Frame-0F

MVEGLGDQLLVLNENSQSQQMSGSKPVRINELLIENYYAKNGIIDSLGDASAGAFLKEPE

PNHNDEQQTADRDNPWFSTDASCSPGVREETTKKPFKEEAVRWLARGGSRTDGGNNETPK

SKVPGHDYSLFEPVEDKMPMVEGGTSATPSSGRGSGHCSNNAYEGEEKNETDHFDANHLP

MGAFPAASKNWWGMHTRPFEVELSDIQTEETTSSFSHGMDSMDERSGRDVGSDNGVDVND

AKENGVYPSTMSMSICDVGEDEGKEVKLEFDLDSDLQSRLNQMLDFGSNDGHDGDEDRHE

FLPDHKQGAISSPRAIPTRQTSFCSTRSQSGAPSSLHATTTMSPPDQPTARWFYDGISLN

DGSTPMTGPPSRIYPHHVEIPVGGSATSLSFGKSECEDAIRSIARESAVRKVEATSPVVV

QHVLLRNLNICMRFFGGCDWTRDGSEEVRQITLKASNGIVKTSVQELKRAIGTKEKLLDA

LLDNYVPSNGSDLFGDDSNSTLFRASKSAPSRSFLKHDPTSWTRAASGDKTRSRKRTLKK

SGRKTEEM

>contig18773 Frame-1F

MDLPSTKLRELSPAEKTCPHS

>contig20590 Frame-0R

MAPASSTALFTSEDAKAALNIFCCVCGIGSLGMPASYARAGWTFATSALVFMACANIYSS

MVLSKVLLVAPSTVKTYSDLGEWVAGTWGRLVVLVSQMGVCLLLPCAFLVLGGTILDVLF

PDCFSQSEWIIFMALTVIPMALIPTMKESTGMALAGCLGTIVADVLGISILTYEMRGHPS

PPPTNVTAHQVINTFGNLSLAYAAATVIPDLQRQHSQPERMPRVIIISLTMASAFFVAVA

LSGYSASGCQMSGNLLFSIVNTSDPSAVTSLGFTADRGAIVMTFLFMQMHLSVAFSTLLH

PAFYMFERMILKMHQVEPVMGMEGEDKHSYLDAPTPGDLENTRPRESRRPMSSRHGSSRS

RVSGYNRMVAEEDMSDYAGRKNVLRYVGLRLVLITTLVVLSIVLRDHFLDLVDFTGASFI

TLSSLILPLFFYMKVYYHKLPVWEKFVCVVIAGSCTICGVYVVISSGQNLFHPSRNDGAP

TFPYCTEAFQSEPYYVRDEVM

>contig21382 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64313.1|) 2e-44

MIARHLMRQMRCRDGSIAALFSTTTQQSLTGTMKFPPIVHKTRSQQDMEKLGEWLARNRR

AGDVLFLYGDLGCGKTCLARGFLRAYTQQQNLIVTSPTYLLVNTYDETSKLPIVYHVDLY

RLEVVTGQDVIALGLKEAFEQGITLVEWPERFEKHSVPTERLDVRISYDEEDSEIRHVEL

QPIGGRWTNFLTYM

>contig21764 Frame-2F

METSRRMAPPSWLHRYKVEKTSDNIQWVSTGQSASKQYLRLREQAYDMACARNKCFMGAT

QAFRNGNKALAKKLSTEGHEYNMKMKTFHFLAASEIFESRNPPNQLYMDRMMDLHGLHVA

EAVELLAKMLPKFADEGVDSIYLVTGSGHHSKGPTGNSRLLPAVEHFLAGEGYHYTPVAD

GAGFVGMLLVELLW

>contig22471 Frame-2R

MIGKIGLASLPRLGPIIKEPSLGRTRPVLSTRPSRTQRVTATSEHGKWVYNQFSTVALNR

IRSFSTAVT

>contig22967 Frame-2R

MAPPVVIALFRSLLRSTQTLQRDILAGRLLYNAVRSGAIASYAGIKTDWQREQLFLHCFD

DVKVLKRRTQDDRTYAAIVRAGFVSPVNDKAALNARIDAAFITLKRVDDHNALLQKLIGQ

GCFQPKDRTSAIKFRIGDIIQVKNEKRGVIFAWHMTLKNAAIGPEVVYDVLPHSPGHSFA

SKLYNVPQDEIRLDETPKAIIHSALLLYFDGFDSTRHIPSEALLARYPSDFSKNIQVADR

IVATPSIMHVQSADENELLKYLRCDDSTIVQFAMASLEGKWIGEGGQNAQDHVQRAIRLW

MRRNGVKLVKCFNKSCTMYPCMHTRGTNLPWSSIRAVILAKHSKITKLP

>contig23209 Frame-1F

MEGGLLAILINVSFVAFLATAFFFMRHKLIYKHTQRLRDLAEPLLGIPLSQNDHRLDTIT

REAEKGFDTCIVCEFENFKNALFCSLCGECFEKNQAPYHDLKLKKRCRKGQQESKRNVTS

ALSRCFTARQLRVKKRKEWTRKLDVEGHMFWFRKKETSDLITPASAGKVLYFVKLNANRK

MPEQVKGPEAFESKVAIVEPPTLKVFEDLVSMDIVLASKADAAVRATGEVLESDTQNGVE

CRREILEWAAKDFPSKYAYFVRTTAALLVPPEVEFLKLSIHRDYIFEESMEHLGCIEERN

IRSAMRIHFLKESGVDAGGLQREWLTMLTERLMDPKAGLFKMTHGDDRAFYLNVNSRYDN

GMEHLIYF

>contig23375 Frame-0R

MPSIKVSYAAQTPYLTHASVQENILFGAKLNTPRLHRVIQSCELEHELIQLPNGVHTEIG

ENGVTLSGGQKQRLSIARAVYRNNQNLYVLDDVFSALDAQVA

>contig23627 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69665.1|) 3e-06

MALTSAALTVLPRHSMRRLERAISMRQTAHMETQVLNKLRCISDGLGLGDIVSLGHV

>contig23692 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65739.1|) 3e-49

MALDKKEEDGMVSFVGVLRHGEVKNRFTPANDPENRQFSYLDHGELADAMGVTAADLPVM

VDAL

>contig23872 Frame-2R|Blast-Heterogeneous nuclear ribonucleoprotein A1, putative [Ricinus communis]gb|EEF41060.1| Heterogeneous nuclear ribonucleoprotein A1, putative [Ricinus communis](ref|XP\_002521392.1|) 2e-25

MEGLGVVYEQEEQVADVQQTLAGDVQAAEVSALHHETEDDEDIRALAGNPDDLDTHHESQ

TPHQQQSQQQLHQQHHQHYQHDISGGYGDYSQSSGQHPQQQMEQQLFGYDKTGGGTQPGK

LFIGGVSWETTEDTLRQHFGKYGVLTDAALMKDKYTGQPRGFGFVTFADALGTMKYCCGI

>contig24015 Frame-0F|Blast-hsp70-like protein [Phytophthora infestans T30-4](gb|EEY66008.1|) 0.0

MVVAGIDIGTTHGCVGVWHNGKVNIIANDQGFRTTPTYVCFEGEEVIVGDTALNKLPSHA

DNTIYHLKRLLGKTHEEIKERDFVIEWPFNVTHSTDGVAVETQRNGEKHVVTIVDFMTLL

LQNLKELAEDFTGEKLEHVVISKPAHASDKYTELLDAAAKQAGVDVLTYLSEPLAAAIAY

GLDEFIDNDKMEYVLVFDIGGATHDVTLLNVDKGLFQVVAGKGNDTLGGENFTAAVFDHC

ANFFLRKTKLDVKTNKKASSRLRIACETAKRSLSTQTQVNIEVDSLMEGEDFALKLSRPR

FEELISDCVYETITEIDAILEENDLEKEDIDHIVLVGGSSRIPLVQNLVQKHFEGKHVRT

QMSPDEAVAYGATIEASCLAELVGAPEPKEALNLVNVVPLNLSVALANGSVSELIHRNTI

LPASATEIFTTSHDNQEAVYLQIYEGQRLMAKDNTLVAQLSVSGITPLPKGDAEIEVTFA

VSSKGALTVTASERKAGQKSLEVTQEATRLTPSDVAAIVKKAEDAADEDEELLGELEDAE

EAAEAEELAANAPDCENVSAPVVSVVSAQDLD

>contig24060 Frame-1R

MLAATLLRAARHSRPHLGPMVIARINSPMLQNNTLRQLHNSRPALVQSFDDSGMPHLQAT

PVNIGILIVPQQRAWVVERFGKFHDVLTPGLHFLIPMVDRIAYVHSLKEEAIKIPGQTAI

TRDNVTISIDGVLYVKIIDPYNASYGVEDPLYAVTQLAQTTMRSELGKITLDKTFEERES

LNQSIVESINQASKAWGIKCLRYEIRDIAPPRSVKAAMDMQAEAERRKRAEILDSEGERQ

AYINVAEGKKRAAVLEAEGAAAAILVKANASAQAIQRLSGAIQETGGRDAVALQVAEKYV

DAFGNIAKEGTTVLLPANTNDPSSMIASALAIFGNIQKQNKQGGHIIDKPGKSKDTEGEL

GEYTLDNVDSDATK

>contig24226 Frame-0F|Blast-glucosamine-fructose-6-phosphate aminotransferase [isomerizing], putative [Phytophthora infestans T30-4](gb|EEY63656.1|) 0.0

MLRRSLASVRRISNSSPVYRSIRSSAILSTSLSSDSSGSSWIKALAVGALGVVGVSQYHD

NSSDSCGIVCVVSKSQDATDFLLEGLTILQNRGYDSAGMSTQPTTEKGATAPITTTKFAS

VAGTADSIHLLRETKEKHKGNTTGIAHTRWATHGAKTDKNSHPHMDMHGRVSLVHNGTFT

NYYEVKQELLDEGVVFSSQTDTEVAAQLIGHFMGEGADLLTAVRLALNKLEGTWGLCVMA

RDDPGKIVIARNGSPLCIGYGSNEMFVASETTAFSRYAKQFISLKDGEVAVIKGDSAELN

PNDDGKEEGFLQRFPTSRLALAPDVKVRLSPAPYPHWTLREIMEQPKAVAAALGYGGRVS

DDHVYLGGLEAEKDRMLRIQHLLIAACGTSLYASIYGAKLMRALNSFDSVSSEDASECTS

DRFPNKGGGLLVVSQSGETKDVHRVLKTAEELQLEVPTFSVVNSVGSLIARTTKCGVYLN

AGRENAVASTKAFVTQVTVMGLIASWFAQYRTEGNRSKMNELIQSMHRLPIAIGMALRSR

DQCAKIADTLLTAEHLFVLGRGYGEPIAYEGALKIKEITYLHAEGFPGGALKHGPFALIE

GDKNGKFGATPIILIVLDDEHATFMKTAAESVRARGAHTIVITDNPAMCKNIADEIIPIP

TNGPMTALLATIPLQLIAYELAVRKGINPDVPRNLAKAVTVD

>contig25085 Frame-0R|Blast-26S protease regulatory subunit 8 [Phytophthora infestans T30-4](gb|EEY58006.1|) 2e-78

MESGGGDSEVQRTMLELLNQLDGFEPAQNIKVIMATNRIDILDAALLRPGRIDRKIEFPN

PTEGSRIDIMRIHSRKMNLLRGINLKTIAEKMPTSSGAECKAVCTEAGMFALRERRIHVT

QEDFEMAVSKVMKKDSEQNMSINKLWK

>contig25702 Frame-2F

MGSMMSAIKQGGNVRKTPSTGSSPSGAGGFAEIMRKNREAAARKAGGNMAPCVHHSSSEP

STPRQIGTKSNNFETGSNSTFETRLVAMEDKLDKIMAHFGIN

>contig26097 Frame-2F|Blast-vacuolar protein sorting-associated protein 29 [Phytophthora infestans T30-4](gb|EEY62539.1|) 4e-09

MQHVLCTGNLVTSEQYDELQSLARNVHVVAGDC

>contig26156 Frame-1R

MRNGSAAIARVVPRVKQLFQRVDMDHLGHLSPNDDVECRFAYFQKHVFARLLDHPRKHVL

VFIPSYFDYVRLRNLFHDSMHEKLLRSVQCCEYTTNTQVSRARTTFFHGHCHVMLYTERF

HFYHQYQIRGVHQIIWYGLPVMAEFYPEMLNLLPMQDERDNDGLVDSMDTNASIALFSRL

DQLRLQRIVGNKRAERMCHAKALKSTFLFC

>contig26480 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63014.1|) 1e-163

MSGGNTAMMAAFLSSSKSSGVLAIAVACRDKNLRVWPMQYTKASLNSRKGMNDDSATETE

DKRILGGFHAVSNHFSIQNTTDVVAIHGQYVYGISLMGEAYRFCLPELSSLSSTSCERLA

RQMFGLEKIGGGGGSSKSRRSNVMLESLAASDDGKALVAVSSDGIFYYSNKLPVVDSKEA

AVLRIIGKNASENTMFKAPMKVYTPKIVKKDIKMESEAMMAVVTNSSGEDSESASGYINV

DPTEAFAARWLVPSRSQDCWVCGVRNVKHWVG

>contig26848 Frame-2R

MTWVVPNEDAVTLGELNGELYSVSKRDDAHAGDAYIRFGGCVFPPAQVSCPKPRQSSKRE

SLSDKEDEELHPGALGLLKRAFEFTKILLTQDELSIFNSVLSAAGRVVHKLKAAMEEEDL

VLQPSDASTKNSECIVDLSWHPARNVLAVAQRDGVVAMYHVESATWDTRVLEHPKQMNIT

SIEWGKFTSNTLAVACSSGIFLWKVPQKDKEPALQEILLHSGKEVFSYLCWNADGSLLAA

LTTGSKTVTIFDTIFSRMTELQSPYVLTSLHWSPTGEYLFVLTEAGVSLMWETLTWKREI

WEVAAGSCGWSNDGRCLLVGLRNNHLLYPYIFQDFPPS

>contig27429 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58746.1|) 1e-18

MVVTGMLGSLGGFLWAYQISSFRLQGYKANSGEVQRYITSKPE

>contig27696 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70205.1|) 0.0

MSDPFYLADILLGRVGVLRSTAESIILELSHARSKIESKQPNDDALRLSIKNKLERVQTN

LKLLRKLVPEFDGKTKPIESVNQTHRNLMLEYNWKNQVQDMGIKAQIVFLEQLSGAFPRL

EMLGDVRCPPTPNSLFVPKSHKRGRVFDPYGEKQPATLNEMMDYMMAKNRKLKFYKHAET

TRGGRRVIKSIKCEINKELTVHLSFCPPVPESGPTGESGVAASPMTPSTPTSPAFSSGRL

RSTRSKQKKTQQQLFKKKKGDMLTKAKLAAEEATKMELEELKQRIADAREAIKEQEQARA

AGLQVTRYIQRLSIFPFNEAAPLGAWSESSHNFFRLITLHGREALNQFRKQQPETCFYYL

FTWLGYYDKIYQTPCSVCKKLLTKENEDWAYVPPSFRDYANGQAFHFKCLPIE

>contig28235 Frame-1F

MFRVSLLFSKLKNFYRISIRRCWSSGQQSGGKTDSWRSYTNIERYVLRTARQEPDLIGGC

DVVKIRTLKNRLSPVLTTRTESRNHFYATIECHIY

>contig28819 Frame-0R

MEHLATGKRRRPASASLSPPPPPPHPMREEEKSVVSWKRQRLEHTPTQATELQELRRAKR

SEHKCVKNGKRRRSIPPEKEIKRESCNRNEEKHKTKRCRVKDDASVSSPPPVLPASPLAN

LSDRTIQSFEHTKQRVVIIEEKHETTRFPAVSISIPSQWRQDEVLTKENPENVAMCTNRD

DCIGSSQGSDTDDLVATSANVDKDLRTDSHDIQGSIDVERVPQGMPLRTVQVTPPPSTRM

LDRKNPPPPPKRPKRRRNYGIVFARAYPRLALSPLVDHSPPSSPRVFRSLENEFAVAMQE

TPEIRPRVRPAPRMARGTRRSTRAISSGARRSLETPTSTMVLRSRQLNPSLSASTGKPEN

QREREQRDAQRRQE

>contig28994 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63059.1|) 2e-08

MPSTKAANVSPATSVATNHHETSASSATSRKRVFTFQKRWLHSLPIVERALFESELTGRV

PKALHTP

>contig29052 Frame-1R

MRSSDVPILADRFNRAPSFASDQYSEDRGSLFEYDRDSMADDDVEVKEKKTLNPFSSRST

SRATLQQLEKGKMGSNVYPSDGPAAEWELTSRRRLLVASSRYNPYAHPFPWRVSCLLLAY

VEEESAFWIIN

>contig29896 Frame-1F|Blast-hypothetical protein PITG\_07227 [Phytophthora infestans T30-4](gb|EEY53547.1|) 2e-48

MARGEIDELIQREVDELVSKGSVFEVNGYDNCRYVLRKFSDLWALHPYRITSDSTAKKVH

FLFDSTTTIVARPWLHLDGSLNTKMALKLKRKAVNIVMCCPGIQDFAIYKKMRSIVSLQD

MRSLLEELIISRIVYARVVRGRRSPFASVFGLANSRRSCDQNIMAFSPG

>contig29957 Frame-1F

MDPGVQVSYGIELEELRWHLSLHNLRSILLLDSQRLKPLATVFTAGDITHAQTFEPFSHV

YSFDVGFPPDVMDKMADMFNRSSAKYYTSFHAPRKVVEMYGFSVENIGRVATSMAGSSEG

HQCYFYRRLTSTILKEELISEKLKVEELPVDNTSLAVDPLFTMGLELLKGGREGMIAWLT

DFFGHANEGRTRRQKRELRERRIDTYYPSVKAHVLVPSKGLAQKSNKKTPKITRRKICLR

V

>contig30177 Frame-2F

MISNIVAFNMHVVSFAKWFVIACSRYLFRTLQCLRVLSSLAFTRLHVNVSSSSSVLKHL

>contig30353 Frame-1R

MCDFSAPRTCWMMLATSINNSLNPGLINS

>contig31066 Frame-1F

MQWMEVLCTKPPLMILVGWVSQVARTLFQRYERYGHLSSEYPAEFHSLAAEYEGEASRFD

VVRTSESEFEVIDQQTSAGRIVNFAKQTCTCGEYDVSQFPCLHVFLAVTHAGMLRTDVIP

HIFLMTTLKTLYAGRITPIDISTVPSDEITIPHPLPKTRGRPRKVQQIQQFGDPKQEKLA

CSVCGIKGHNKRTCKQVTSIPTPICEDQTDDIATDTNDTFLVSPYGDALSFENSTLEGTD

SESHVSDGQPLCMSSSKRRRLAQNDSAEDKSSDQDEEDTTGIVLV

>contig31668 Frame-1R|Blast-glucosylceramidase, putative [Phytophthora infestans T30-4](gb|EEY54376.1|) 0.0

MTTEPTAYGTSSLASDERLSARATRRRAIIKWSLVGLGVFGVCVVVAIFSLFALPEDAAT

APAVTTKSPSDSKAAAPVVGSNVACVQSSYVDNQTNMMEPIAGLKWIHGAQADAKSFIRV

DFKTKYQEIMGFGGAFTEAAALQFSKLPKIKQDEVLTLYFDQHNGSGYTFGRVPMGSSDF

SVSSYTFDDVVNDTDLVHFDQNVIHDQAAMIPFIKRALERLPELKLFLAPWSPPTWMKRA

APNHMSSMLDSVKPIGLKDDVRATWALYFSKFITAYKKHGIRFWGLTPQNEPQAEVPWES

CMYTAEYQAEFIGSYLGPTLQRDHPDLVLMIYDHNRGSVREWAETIYNHPTASQYVHGMA

FHWYDNERYMDGVEYHERLNDTYFIDPSRFMLATESCNCPDVGHGDLAWFRAQRYGHDIM

TDLNNHVAGWVDWNLLLDHRGGPNHLENYCDAPIILTEDGTDFYIQPMFYFIQHFSKYIP

RGSRRVKTEVAARFAMLGDPQLFVDYPSMLAACDGSSRQKWRPTDDGKLEVTGTGFCIDL

KEIPWQGHQGLLVDCRYTQQHWTYEIGTNRIRMGDYCISLNHGSTENGARISTDLCEDTV

LPHQQWRFDSKDGTMRSLASTTDQCVTAGYAFVQASAFVTPDNRKVLVAINENTEPVEFQ

LQVGNVAVETMVPPGAIRTFTWE

>contig31927 Frame-2F

MSFQRDLKREKCDKFLSLGFEPCVSHEWHHHVIWPRRDTLPLCPAERQPLPLDPTVLSPV

LSCYA

>contig32333 Frame-0F|Blast-RNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY59589.1|) 7e-31

MDGLSMAMTTTTVTTPHDVEQKSATRLYIQNLPTYVDSTRLREHFSVKGEVTDACVIRTK

DDSKSRRFGFVGFKSAAQARSALTYFHQSFFDTCKINVHVAMA

>contig32746 Frame-2R

MHDNQVYSAGKSPTRTAVRNAGQVKRKFAPTGTFVCKTPPFFWPLLASRPSGPQSHFLNL

PWQIIASPVTSFHRLTHQVFYLSVMASPVLPTQDILNLLFAVMASFRLPTQNTFCASITC

VVGEAPPQQLPYSIYKKTFRVNPFIY

>contig32863 Frame-2F

MQPTSLEPTLLSSENDPLKSAFGEIVHRGWLNLKTRSMVNVRPRHVRYCILTRDTLLLST

FKFQPSTGDLQSGLVKPLRSYRVLGVAPWDGRRYSFLVSVKQADDHVDKVLEIDGLAATS

ASNWIHHLRVLTSREEENWPPSTNAIVPLSNQSSDVLSDAQATTLFGNSKKEANLWVKGA

SVHRGLLNASGENNCFLNVVIQSFWHLTSMRHFLLHVEVKEESRSVESNVLRALKSMLME

YDDTSSGALHSRSIRKGLSVLYSADKNFQEGAMYDAEETLLALLNLMHQQTEATEIEETQ

KTTMMVKSLVRVVSAEAYEEKPQAVFDDNSIPHLVFSHQIYDRYVCDGCNHSSPWNLYSN

LVYSTYASDLYACKYESSEQMYRRLTAQELDVASKCEQTGCSGKPRKERVIHRFPMVFAV

SILWTTQSATKEQVQGVLENIDDRLDLAKCFEAAGPVIRFKNGGLRTTYRLRGFVCYYGR

HYVALFYSTAHKMWLLIDDSRVLEMGPWSNVVSECLKGRFQPVLLFYELPDQRKDSSVGI

FSHVDIRHLERRKSLSIGSQHGELLPPSIQEESFDFERPAVQRQDEAELHTVDTELATQN

TNLVTELEICPDIELKELSRRNSVTQNITPVSAAIAMCPRSISMYAALGEGEYDVRFGEA

LLLGLYLQKIGNELCVTSFPRGANGGMFSAEKCGQIGLFDTVLHANGHPLQHYQVDRALK

MIKAQTRPLIIRFRKSIRVQQLLDMGFSRESAIEALQRTRGDVQAAANYCFESTSSGVD

>contig33059 Frame-2F

MQFKAPYNYRLPFTIMQATIRYIHTRKYSFCKHAFFRQSFHQC

>contig33330 Frame-1R|Blast-tyrosyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY65134.1|) 0.0

MEVAPAIAAPAALSIDEKLCKLAAITGGTLSTEIEAQLRALFADKAHPIAYDGLEPSGRM

TLASGLLRTLNAMRLIDAGCHVRLLVADIHALLNNKIGGDLKKLQNVSTYMVEVWKSLGL

DADKLPNLEIVLASTITADHAGAYWSQVLDAAGSFTVERVQQCATIMGRKTDDAVHNTNR

ILYPLMQLADGFMLQADIYQLGADQEAGNNLVRDYISCKGLPNKPVFLTHPLLLGLKQEQ

FKMSCTDAESAIYVDDTAAEVKTKIKKAYCVPGEVNGNPVLDYMKHLIFPFQANGITLER

SEKNGGNLIFASYNDLEVAFSEEKVHPADLKPCLTKYINALLEPVRQHFASGPLKTMLSS

IKKLNLSPVLDSDKLVNLSLPGFPEATKEWKPSSLSLIERYTVARSVGEECIQENELQAL

LEKKAHPICYDGFEPSGRMHIAQGVLRTVNVNKLTSTGSVFRFWVADWFAMLNNKMGGDL

DKICIVGQYMVEIWKSVGMDMTNVEFLWASKEIISHSSSYWLRVMDIARRTTIARTLKCC

TIMGRKEKEGMQAAQILYPLMQCADIFNLNADICQLGIDQRKINMLARDYCDQAKIRFKP

VILSHHMLMGLKEGQEKMSKSDPESAIFMEDSADDVSRKIEKAFCPEGFVDANPILDYMM

HIIFPCFASQGVTVKLMDGSKKSFVTYKELEDAFVARELSGVEVKAALAKYLN

>contig33345 Frame-2F|Blast-hypothetical protein [Vitis vinifera](emb|CAN79309.1|) 1e-09 NOT\_ORF

MDREIDA\*KAKEVLRQISWSEMPTDHQTINPMWIFDVQTDRLGYVAKFKARVVARGDKQR

PGINFKDTFSLWHACHVSDVIAVCIIR

>contig34173 Frame-1R

MRHIVKYGFRLSRTPVALNLRIPLKVLPSEECLNTKKVLCAAPHKQLGSSVTAEDASILY

RLVRVCDLRRLRGH

>contig34555 Frame-2F|Blast-hypothetical protein PITG\_18705 [Phytophthora infestans T30-4](gb|EEY68804.1|) 3e-11 NOT\_ORF

MCTAQKSSYIPLPTARPPASIRGYLVLQPATTIRFLGI\*VGTDDVREDNWNDRVNRIKGR

LSIAPAVANSVSARIVILNAIMLL\*VLFTAAY\*PPTPEVLIKLERLQAQYL\*RGRASHNS

SRHKINKGLLHTPIMAGSLGLISISVAIKRQAAKQATLWTHTPV

>contig34717 Frame-1R

MQSLASAGDVHAKLQTISDAKFALPTGKSTSEWMASTQENEGAIKSIGHDAAAVEAAFFT

TPSARLSNSRSPGPYRGKCLYQSRKCENERAVKRNGSPHNLCDAHRTKQNKHQRKFDAKK

CYRKRHRDIAPDDDENADKYARREQELSAMHHRPIIKLDAEVNHSSEAAHRTPVYTRTAS

HPATACTPVLTPFMRLPPISSRVLAPSPAGWDTSSDLLKKGMRSEDFEAGPADLSLSRQQ

PMIMNSGPYLPRQVTQPSSDYTYSELVAACTLVRPQHFLDSGVASHSMSHRDEILPSGED

RSHATTTPYLLPSLVGSPTFAPSRNSYTQVGGVGLPLPQRFELSVPSARSIGRLRSYTKA

PVSQLSFPMGSQE

>contig34836 Frame-2R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65627.1|) 1e-162

MFPNGISLRHGFENLAGNDSFTYFNGMLVDGTITDEDLAIAVKYARQHEYTIVAIGEPNY

TEKPGDIDNLELPEGQIKYVEALRATNTKMIVVLFEGRPRLLGSIPSNSMAIINGLLPCE

LGGQAMSEIIYGDVNPSGKLPLTYPKDPANINIHYNHLVSTRCAYDNCWHEWDFGSGLSY

TRFEYSSMTLDTTLLSSAYDSVTASVTVTNKGNRAGKETVMLFLTQPFRLISVPEVKQLK

KFKKIKLQAGESIEVSFTLTTDDISVYDPQIGHGLKRIVEDSDYVVAFKPETWCNVYVSI

THPLCAVFSVKTNSGAGKIDAGGRFDN

>contig36067 Frame-0F|Blast-acyl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY63794.1|) 0.0

MLSPSLLKASTRLGGLRIATAPSLLPAVQVLHHTQTRTFMAKQVYKLAKRVMPRMSNTEK

AALESGTVGFDRDIFSGSPSLATLDKYSAQLNAEEQSFMDNEVQQLCEMIDDYDVTLNQD

LPLDVWQYIKNKGFLGMIIPKEYGGKQFSAHGHSVVITKIATRSAAAAVTVCVPNSLGPA

ELLLRYGTEEQKSYFLPDLANGKQLPCFGLTGPSSGSDAANMRDSGVVCEQNGVLGIRAT

FNKRYITLAPVASCVGLAVDVKDPQGLLKGKGNPGITVALLERNHPGLQMGKRHDTISIP

FMNGPVTGQDVFIPMSKIIGGQERVGFGWNMLMDCLAEGRSISLPASAVAGAKLSVNAVG

AYARIRQQFKVPIASLEGIQEQLAIMGGNAFIMTSGQHLVNAMINQHEQPAVISGVCKQQ

ITDRGRDTVIRAMDVLGGAGICKGPNNFLANIFTSLPVIITVEGANILTRSLIIFGQGLT

RAHPHLYELIKTIQHGDDLEGFKKELAKLVKHGATNMAGSLKTAVTRSRFKKSNGLLAHY

ESQMDKLAKNFAL

>contig36265 Frame-1R

MFARYRAMFSLRNRNTDDAALALAKAFDDPNVLFKHEVAYVMGQMENPVLVPALKRVMLD

QTQHRMVRHEAAEALGAIGTRECEDILRMYLKDEALVVRESCKVALDIMDYWAPTKP

>contig36913 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65847.1|) 1e-133

MTNLSWQEALAHKSDAATKEWMALERRYHLKQRNEDSATHEKHISLFLSLSDPELPTRFR

GQVELEMTLPKLYPMEAAGIDFTQWNSRLSYEQVQVLSSAVNARALELCGSFAMRKLLTW

IDNNFWPVIAPFETGTEATKELEAGRTLQSHPTVIEAIKASPSSVQTKRTRRRGPPPCHF

FKRGKCRDENSCKFLHTTEGKPKTRSGGNALDVDCCEADQAQPIKEVRPVAVSVLTTKDK

KNKDANLMRLTIAAVPTSVNLRMSERVREQIMSVSCRY

>contig36988 Frame-0R|Blast-adenylosuccinate lyase [Phytophthora infestans T30-4](gb|EEY67752.1|) 0.0

MAKHERYEHPLVNRYATVEMSKIWSPDRKFSTWRQLWLALAASEKELGLDITQEQLDAMA

AHLTDIDYEYADDMEKVFRHDVMAHVHAFGKKAPMAMPIIHLGATSCYVGDNADIIQIKQ

GLQLLQRKMIKAIHVLAKFAVKYKDLPTLGFTHFQPAQLVTVGKRACLWLQDFWLDFMHL

SEQIENLPLRGVKGTTGTQASFLDLFEGDHEKVKKLNKLVAKKLGFKKVIPMSGQTYTRK

IDFFVLSILSGISQSAYKMAGDIRLLANMKEIEEPFEKDQIGSSAMAYKRNPMRSERICS

LARYVISLTDNGAQTHAAQWFERTLDDSANRRMVLPESFLATDVILNLIINVADGLQVWP

NVIKAHIRAELPFMATENILMACVKAGGDRQELHEAIRTHSMEAGKRVKVDGAANDLLVR

IAADPLFTAVHGHIDTLLDPMLFVGRCPQQVTEFISEEITPILEKHAKLLEIENVDDISI

>contig37042 Frame-2F

MMSSGDEFPVKASSIAEMTNRQIIIVVVILMIMSLIGAIGDRIWMGSLVIPQYLELEDYD

DSVIEVFIYFITTLASMVPITLYVAITLVKALQGYFMESDLDMYDEESSTPMKVRNMQLN

EQLGEISHIFSDKTGTLTCNKMEFRKCSIGGRSYGKGTTAIGLAARMRNDFKGYMALEDD

LGDETADIPLMGEVSVPNVNFKDPSMWCDLKNQSHPQSGKIEEFMTLLALCHGVLIERHD

PTEEDASPAIEYSASSPDELALVCGAKFFGYEFIEREPGSVSIRKPDGVVDQYDILEVFE

FDSNRKR

>contig37204 Frame-2F|Blast-phosphatidylinositol kinase (PIK-5) [Phytophthora infestans T30-4](gb|EEY58194.1|) 1e-46

MRDQSATLNAKRKSPRAAIFLSQVLYVLLLAGLVYEGRHREHGEQIPVILTECARRHLNS

MSDF

>contig37415 Frame-2F|Blast-DNA-directed RNA polymerase I subunit RPA2, putative [Phytophthora infestans T30-4](gb|EEY63911.1|) 7e-29

MAGEKSFKKKASKSKNHVTKWPSTNPSSSSRSIPAKTNAKLQNLVFPHLDSFNFFLTEGL

DLAVANLCKVPVELPN

>contig37460 Frame-2R

MYSEQERIERARAKNLAYIQSLDDREASQAASGCSLKHPAHGSSKGNNSVYITGLTTYMA

CRQLEGVCHRLGKVRRIKFYEDEKGGLKGDAVVTFSSRVTMLKAVER

>contig37961 Frame-0F

MPRKYRRVSLVNEEEEKGDGINQPSHQYRELPDTLDDRQRRDSNLRTSRKVSAGKQRQSS

TQMPQRHSYGEHAAGGSKHLRRARRSHSEERTTGHGRTKQLNLAKPVPKENTRCEGPRTV

SRRGPSKTPARQSLPPSHGIQDDTDQRSDSMGRLLVQNSSSYVHAASAWATNKTEALAMT

GAFQELMTKLGDDVHFIVVGFSTGFSTEVIVNLLRQLAPGVPYIGGTIARGMCDENAWVS

VNRHINEGLVTLWGVNDPHGIYSVVHAEYTQSDAHKKVFTAAKTALSRVAGDVDAGENPA

FIAAYACPLFVEHAIDGIREAIHCPIIGGCSSDATRHGEGDVSVCWTQISSSCSSDYTKS

VSDGRGDWTEMGIAFALCFPSVETYVSWFSGYSPVGVNSEYCMGTVTKASNKTIYEIDSK

PAAEVYQE

>contig38106 Frame-2R|Blast-COP9 signalosome complex subunit 3, putative [Phytophthora infestans T30-4](gb|EEY57575.1|) 0.0

MEWGPLYPILSLLTPQQGVNDSERTRQTADSMLAQALSGEELTMAVRASSIAQLDQVLDH

KPLADLSLSFLLLLSAKAYKLEHARPQQNLAVARAKLLQQTGQLLYQISATVASKELKKL

SVLCEEYARQAMDMQQSIKAIFPLRSFLLRYHEQEKAVLTPLHAQFLYLCLHSKCYFAAM

EILDQTIVEIHSQLQLVTSVDFLGYAYYGGLLFLGEKRYQDALNFFQLAVTAPAVTLSAF

VIEAYKKLLLVTLISKGERAMLPKYTPFVVVRHIENHCPVYTELVNAFVIDKDLTALQKV

VTKKNELFVQENNLGLVKQVVQAFKQQKLLQLKRTYATIELTQIAMVAGIVNSDAHAAEK

LLLHLISTGQMDAIIDKQKAMARFVLEDEDSENCCEDVRGEATLKLQKEMEKLVMVASQL

RYMDVELVTSAKFQSRMQKDKDRRSRSNMHNQQSEEHTLLDGACGMDTVE

>contig38348 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65814.1|) 1e-104

MWVFGYGSIVWKTEFPAEDTVFGYVEGWHRRFWQGSPDHRGSPEAKGRVVTLISREQMKK

FKDEFAHLADNHITWGRLYKVPDEDVEGTLTKLDNREQAGYDRQLVDVHCVDGAMRKALV

YIATPSNSDFLGPSPVDVMAREIATRRGNSGPNFEYLFKLCDCMRALQIRDPHLIALEKA

TRKYTSALSYGISDTGCGIQ

>contig38454 Frame-2R

MSSGLASPTLAWSFSQNQQPTVRFELLRLNETCCKTRLFSLYLNVFHHYFLSFNLGIQSI

RCKLLAIRPRSITLLQRTARLSTTLGPMPSSSKLCAPCY

>contig38630 Frame-0F

MLSPPSSSCTSTSAFQSPALSPSANPNHTKRTCLERELVGPVKEHQRLIGTAWRLSRSQR

HCMHPRLETDSTCPLRSVPREAQSLELAD

>contig39141 Frame-0R

MSVAKALGVPEGSVLAECLPHQKVDKVRLLQSLGLRVAFVGDGVNDAPALATSDIGVALG

AGTDVALDAADVVLVKDDLRDLLNARALSSATNRRIKHNFAWGFMYNLLMMPIACGALYV

PFGIWIPPALAGLSELLSSVPVILFSLLLNFWRPPFGGDWGLQQYYVAIDVTESTPLLQK

QL

>contig39219 Frame-2F|Blast-RNA (guanine-9-)-methyltransferase domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY66037.1|) 1e-35

MGLVKSCILMLTEHPKTEHLMTAANENTNNFSKRSMRKEKRRLQIEERKAAKKLKLQERQ

RAKKVNRLTSPPAEINMSDDAVLRRKERIIAKREACLMAAEEGLSVVIDCEFEEKMTEKE

KKSLSQQIMFSYGVNRKNCMPM

>contig39394 Frame-0F

MKLCEDGSHIWAGAICGFLRTDGHTKSYAIGSAAFGGRRAIVAWS

>contig39949 Frame-0F|Blast-Ca2 :Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4](gb|EEY69209.1|) 2e-79

MPKQLQMLAWMTLLLTLVVTCFAAAIGGEDPTVVDAPLYDCSGPSRTSDSFIDYDHLVHC

STLLERSPVLARVTLVICLIILLYLLSSTADEFFCPVLQAIVEKYRIPPHVAGVTFLSFG

NGSPDVFSNIAAFATPMPSIAVTAILGGGLLVTTVITACVGLASNGQEQLIPRTFLRDVV

FYLIAVCYLG

>contig40246 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56723.1|) 1e-61

MSEDHFVSYLHVLSVNAHQMKLETPWGSIHINKGFMEQIAITSAVIVLTVMLWRCTARFN

ATLKKKLRVGDESENAIDGDNETEDVNSSQDGNLILKGENSYHYTHQNPVAMTEGVVRTT

VSSYGWSDSKKSVSIYLTDAAIKEMEINQLILKWTSMSLSLNLLDAPGGHTIKNLIISSL

FHEITDATWTVSKDTLTITLIKALELPWNSLNGAAKKMEDHIEYDGAFYE

>contig40857 Frame-2F|Blast-DNA binding protein, putative [Phytophthora infestans T30-4](gb|EEY60352.1|) 1e-25 NOT\_ORF

M\*KLTERNYSLKILLLEAGIQTKSSKQSVSDNAFHHIEMLQSLLVMHGPPKGRAHGN

>contig40996 Frame-0F

MQIDQSNFQQLPKIESRGAISHNEAQATPSTTASIASAAAREALVGCGMIEQSWEVQDDY

EDRDKPWRRYCEDVIARNRVLYDQMTFTRRRIVQLSRLNQNLNLLVDSVERDRDGLLMEN

ELLQTQLHGYADHDQHHDSLMQELMTLRKCLDKEPATTVVKKSRAGANDMHASLYGIQSS

LSLVTGTALNRCTMEELKDWEQVLETTLSYVRSVKEDKALEMQKRLDRQVEEQNELKLCV

ICLADEKTILCLPCRHLCLCKGCSRHQEVVTCPICRLEIQEMLAVYS

>contig41173 Frame-0F

MLRVGKPRGLRQFPAEELLTNCEQQDRETLRRRRQKLRLQYSMMKEDTNDARIRQSLVPK

APDIAQDCAFQTQETDERARLEEEEAETDEESTESKIHRLSTAMHLKWRQCWRWFVSGAF

LLCVVVMTAPLIEQILAPPLPFCDSDWIEAFDESFGVVASPDDFDRSKALAPFLQTTLTR

KCQPCPVYGNCLNGSVISCGHPYLLKYQTCLENPVAQHALNELAQAMQAFIAKKATEIVC

NTSSFSNSLYERDLFNSRRHESVTVPVLLSDVQKFVSSTISYAKAVSMLPSTYVFHRALD

LALRDLEHVSVTEDQTQLLVSEHVVPWSCRATRRLYAHIKSAK

>contig41469 Frame-2F

MNRHRRRNQLNFVYKMYLFTF

>contig41555 Frame-0F|Blast-leucyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY66974.1|) 1e-170

MLRCQLYRALALRRCCSTTSSRTWKDIESKWQKKWTQPDLQPQLSDTKEPFYCLAMFPYP

SGQLHMGHVCVYTISDCMARFKRMQGFDVLHPMGWDAFGLPAENAAIERGISPSEWTVAN

IAQAKKQLQALGIRFDWDREITTCLPAYYKWTQWLFLQMFDKGLAYRKEAFVNWDPVDKT

VLANEQVDAEGKSWRSGAIVEQRSLKQWFLRITEYGDRLVDDLDKLKKWPDAVKRMQEAW

IGRSKGSQVKFLVIVDASAKPISLAVFTTRVDTIFGVTFISIAPDSAKVEELRPYIPAAQ

RAAVDAYIAKVHAMSNNNYSTRGNNDSTNGVFSGLYVRHPLTSRQVPLYLAEYVLAHYGT

GIVMGVPAHDSRDLAFARHHKLEVRSVI

>contig41836 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY58876.1|) 2e-13

MHFESLNKSADMAYSIADGDKSVQGVDSNGILTGRWKTGLFGFTESIVPNG

>contig42378 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53265.1|) 0.0

MDQMGSCSIRVIDLDDGSVRIIAWDQNVPDQDFESFVESQLRAQFGVSDEAWVDLIDTAN

SSLVHITKDVLSNIKESLCLCLSPKTEALAPMKKTEVFEVKFQDRSLGMTIREHNESVIV

NHFKRQSNGSPCEAEASGLIQPNDVIYKVNGARTVGRTYDNVVQMLQTQTRPMNIQFFRP

FRREGLFAVEFRGASLNMTITTDDVNVIVKDLPMAHPNIVGYAEAHGVRIYDIVHAVDGK

VINGLEYNRAISLLSQNTRPMVVVFARSKVMPSTPGRYTASMTNRFSFASTVAPSPRPST

VDSFGSRRGSGSSMLSAVDGENMLVEEMVEFCDGLGTDGILNLKEVEVLKEMVLAMRPDV

CCAVKQKNNNALVALVRSPLMRLWDNLLKTRERILLAGPVSLKRKKRYHLLLTDHERLLF

VNKDTNLLEDEIMGSQIVTVSSRSKYQELTISTSKTDYVLIDNFIGPVIWVRAILPFTCT

QGILKVASSRRFLVSKKRYFVLRGNCLTGYKKESMVHQVGAKSSTISLADAKIDLSDPRN

LSFVITTPEFSQAGKKLILTATSTREFNKWTTALQALQSSTPAA

>contig42460 Frame-0R|Blast-cell 5A endo-1,4-betaglucanase, putative [Phytophthora infestans T30-4](gb|EEY55029.1|) 7e-65

MDKMFGYLIRDDPNSAMVMGEFAGLYGKDAHPMKTTKRTSDFTIEVMLQEGYAGGYMWSL

NPESAYQFNPADTFGHFTEGLLEDDWLTPNKVFVEGMAPLDNVKDAKMFPCFEMEKGS

>contig42886 Frame-2R

MDSFAGELGVDFAIHLEANHVVNMRKQVLIGTIMHGPGNVDLQSTYDNQQDPRYQDSMGQ

LLLQYSQAIPGGILMFFPSYSLLNKVTVRWKKTNVWSDIEQWKEIYAEPRNAGKDFDSIL

LQYRDAVTCSATQDDDGKKASNTGAIFLAVYRGKVSEGIDFSNENARAVLCVGIPFPNVK

ELQVSLKRKYQDERSRFDMKIVNGSKWYNLQAFRALNQALGRCIRHRKDYGAILLLDSRH

RMNKHSQFLSKWMRPHIKEYEHSQMCVPMFIDFFRRNRMELPHLMSLSSPELASFEEKPQ

RSSRVLKYELEVETIEKAVSTKELAVFNQGSSLSSTVKGCLAKQNQGLDPHDSFFSIFRT

LKNPPK

>contig43913-0 Frame-2F0

MLTDSSSSTTPHECNVRRVKA

>contig44066 Frame-1R

MFKVYTERAELLLEDCRAGAGPWLRLAANPSNGGVDIEQQVDRKLQLSDDAAAVSIHAVY

GVYTLLSGPYLAVVTDSRVVGSGPNSEKIYCILELKLLPVSAAVHQSFFKHASTREKQDE

REYCRMLQSALASRTFYFSYDLDLTLSAQKRASASSAVQRPSALYARGEEDFIRNKAVMA

KFIELGIVPVISGFVKVIKNVCQVKRF

>contig44668 Frame-2R|Blast-endoplasmic oxidoreductin, putative [Phytophthora infestans T30-4](gb|EEY65937.1|) 1e-163

MTYINLLENPERYTGYSGVQAERIWKAIYEENCFVPLEDSVLDDLCLEERVYYRLISGLQ

ASINTHIALTYKFGDKWGVNPSLFVHRVGKHRERLQNLYFAYLFVMRAISKYRHELLAYD

YDTGNAADDIRVKEILHQLLLEGSDDTRASGISCPAYAECSSVLSGFDESALFRVQADGL

STDQLEHAKHEKEQLEVQFRKKFQNVSRIMDCVTCEMCRLWGKLQIMGLGTAIKILLAED

VSTIPKLHRNELIALINVANNLSRSVDGVRLMRELEFIEAVKLFSLVSGGAIFVVLVLIV

VIRKRIIRTRKHDKQA

>contig44772 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66726.1|) 5e-27

MGDARIVLKTLISERLLAPGPKKLYVSYYRKRVYADLLPDGSIRFNDQIYTSPVPCALHM

KRTL

>contig45177 Frame-1R|Blast-maltose O-acetyltransferase [Phytophthora infestans T30-4](gb|EEY67669.1|) 1e-64 NOT\_ORF

MLKGELFLAMDADLLQTRHEARKLVKIYNDLDGAETEEAQEILNKLLGTKGQKCLIEMPF

RCDYGSNIRLGDDVCMNYNCVLLDVYAITIGN\*VMLAPNVELYTATHPLGPKARNSGYEL

GKAITIEDDVWIGGML

>contig45601 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58056.1|) 2e-09

MKLEDTHRIVAETEEVGIAVLDTLASQRERLLESHDKV

>contig45832 Frame-2F|Blast-choline/Carnitine O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY67688.1|) 8e-14

MVHDASCALSAAWRLPTDAESNTFFGQATLPKLPIPDLKSTCQRFLKSVQALQTFEEQQQ

TKQS

>contig45887 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY63967.1|) 5e-56

MGFEKQITQIVTILNSQKVPQKRQNILVSATVNSGVQQLAKMSLCNPVLIDADAVTSTDE

SPVTLIKPEKPDTFSIPHQLMQHFMLVPAKTR

>contig46059 Frame-0R|Blast-Annexin (Annexin) Family [Phytophthora infestans T30-4](gb|EEY60274.1|) 1e-124

MRLHKRLASSLCNTLQRSALLSIFAMLNLYPPANHFVYSGSKLNFSSEIDHACQAINDAC

KGFGTDEKALIAALGTQSADNRYLISMRYKELFKKKLETVLESETSGDYGYLLQLIAQPL

PEAEATILHEATKGLGTKEKLIYPIVMGRTNVEMAILKKTYYDEFGNDLGATMSSELSGD

CKKSVLASLQAPLVQFNPALHTPQKAEIDADALYKSGEGRMGTREEEFINILVMSPPQHL

RAVNFVYEKKHKRSIAHAVKKEFGGDAKDALLFLVRMVLEPLVLLSELFESTMKGFGTDE

KALSAAIVRYHLVLDDVRPVYRQLYGKDLRERIQGEVSGDYGNLVLAVFDAPKH

>contig46648 Frame-0R

MSGSSWNSDESWQDSSASAGFDSSATRGLDFPVLPSIPSGSIDISAIAPVFGVAAYDDDA

DYLDYDKTGRPFMEQMSGSCGTAYFSGILGGGAYGAMKGFTRSPSTKFKIRMNSLMNGAA

TRGSKAGNALGCLAMIYKAFEYVADTVEIENIVKFDQVTPILASAATGVFYKSTSGPKAM

VLAGALGAGLMTVLQFGVKPLYPRL

>contig47333 Frame-0F

MQAQVKHHKWVARQGTNSSYLYSFHTNACERVNRSLDLFDYAIQQPLNASHYSYKKGILL

KRWTTTTRPYPATRPFFRSRCYASQNCINGRTAKVDGILRKSFGFI

>contig47452 Frame-0R

MEHCIRLAALHSEQRSIKLEKQKDYEVAQVKIELSRVREQLEFERLWSAFLQGGPTSCRS

STSSDPFVDEYQENGVIEQLRSSLNMVHRGRNREDCRLNGSLNHGSFVRRTSYTHGSPQQ

KAATIVAQSHDVNEDDVEEDGGV

>contig47746 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62662.1|) 5e-71

MHFLACVVGTASLVAAVSAVQPSIKYYVHVVADGEDCDYLDNVLPMCASKNFVCRMGPGH

EMFAEAPSCIAYDPNNMADNPFLIEESASAPWGVCNPVAELKRRIGDPPVCKRDFTCQCL

QGASSSCICAPPDAVDDVNGAARCENESLACAEDKYCHYLKEGGMECGQKPFNS

>contig48138-0 Frame-1F0

MGSAMSKRDQEDCMIELKAKLWEWGFDNNDLSTIERNKKNVAAAMDAIMHYLSVWPECRL

IGRW

>contig48505 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67672.1|) 1e-20

MGTFYIETDCASSRNSLLGLVNQHRVPSQRIVKLEVAHQEIDDADVDFGSPFKYMR

>contig48699 Frame-0F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY54564.1|) 2e-53

MAKAIISSILEAQLGKYVDGLRSDSLVVGLWSGELELRNLRLKPHALAELQLPVTVASGT

VARVVVRVPWNQLGSASVAISLEGISALVVPNTERPSPIELLQAKQNQLERRELIRQHRR

FTAR

>contig48839 Frame-2R

MIRNVTSAASKLSLLPQQRAANRSLKQREREVPEIDWERSLQHYAAAVCDDLDKLVARFL

EEVCLAVLILLLIFYVFKFMQSDITFAAWKRLWIDSRMSAAFHVEFWESSPTSTHKIILQ

QTLDALVNCVEEHNAAYGNLADIMPLIGRIFALYSAYSVQLGVPKHKIEVDPQKWLALVT

INYIICGSEAALFLTAVREVKAIMHHLVVKEKAFLSCLQGFWPSVRVQTAKSCCGRRGLP

LVVGNVTEEDHVASKVIV

>contig49461 Frame-0F

MIDNVQPGDALIFSDLNTLATEKRIKVNEILELENVEKALLHEDTDRTWVERELRKIAEV

EMIWMKSSETSDDIQTAQQNALVEQCSTTSNSAAAADAIKSENILIHAFPRSDLTQISLL

SLVFLGLVAVVMYYLFRHRKLRRVARQQNRPKRWQRRVDINESEEVVLLSSDSSDEENNS

NADTSMETEAENSKSTQSVELNRKMAIEMLQHNEDEMDGAYEYEESPKMVAVSDNVSIGN

NVPSKTYMADNTATPSSDALSDTTIGSLVFTPASSDVAQRTRLRRRPILM

>contig49960-0 Frame-1F0

MAGQDDPRVKRFTVAVPSRGRRKSTVSSNASIEVEVERPSLLLRQPTSTDVEDEAFYAES

TKALQLERQACGNA

>contig49960-1 Frame-2F1

MLQLKLRWNARRYCCDNPRAPTWKMKLFMPNLRKPCSSSDRLVEMR

>contig50229 Frame-0R|Blast-axon-associated SH3 binding-like protein 168 [Procambarus clarkii](gb|AAD23372.1|AF091267\_1) 3e-16

MMLNKLIFALYLASVALYGITVEASTEVAETVHYNARSAYDRKARYSDDSSSDDINRYAG

RDYSRGYKYGSDRYVSRSRDSKYGASRYGADRYARHSHYRDSKYDDGRYVDDRDASRSRN

GNYGAGSVVGRNAGANAGNQNTGAGLQPIAALNTATGVSASAGTMVTAPVGDKSKDINGN

NVVNGPATTSLTTDQKTSDSVTQNSSDPAVKMTTNPATQNTLDPATQNASDAETQKTTDP

VTQKPADPATQKPTDPVTQNAADPVVQKTSDPVTQKTGDQVTQMSAPGPINTLEYHNLRS

>contig50351 Frame-0F|Blast-mediator of RNA polymerase II transcription subunit, putative [Phytophthora infestans T30-4](gb|EEY61185.1|) 3e-29

MSVEEDVPEIVSEFPAPPKFFELYAEGVESGPLPPEPMDPTYHMFGSPCSTMDAVPDLLL

QQGRKLYMPPGENGKSDGNPVDYKAEMKK

>contig50463 Frame-1F

MPAPFLEGVESRIYIVDDLGKDNALASIAKVSEPILHGSAADEKTVITAC

>contig50607 Frame-0F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY54564.1|) 3e-94

MPSKWLELAPQGTANGAVLSIQLLRVVDKRPFKLLVRVIGGTECMARPVRVEILADVWII

NRSGLDLVYGTAADSEAYLPPRAARAQVGNAQICAYSSGNSDKVPVLRIGFRGCNWSTRF

EADPRKLSWQDECISLRSAGGSASSRGVFYELGVSADYATRHFGSVTTLVSVFPRYLVVN

RSLHTLLLLETPSRQLEGIQDSRNENAAD

>contig51248 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56246.1|) 3e-21

MARQVDVAWRSLRRCTPVRKTSISTYNSHRLFYSSFPMNLPKTPPVSPSVVHESLVTTLP

NHKALQRMRSLLQQPHRRVLFLTGSSAVNSSVRKILENESPAFELERHGHGIFGVCEFCQ

LLL

>contig51459 Frame-2R

MIINDDEEPTDTLTESVGSLDATMRIEGLGQGEQWSNGKDCDDKHATVDNSLATIPRSLP

TTFDHEQPQNVGGARDDHRL

>contig51554 Frame-1F|Blast-SCP-like extracellular protein, putative [Phytophthora infestans T30-4](gb|EEY64509.1|) 5e-19

MLAVLVVALLTMNAHVESFSAEDQAIWIDRHNFFRSTGLPWAAGNMRRVGWSADLASSAA

STA

>contig51745 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66692.1|) 9e-79

MFDSSRAMECNSDRVLLDFRASEPVQAESEHSSLCDGALSRSQIQRPSKNTALRWDCDQE

LSRPRSAIRRKLKLPSRSKNKHVTKLPRMDEVIPRVDITDIQKTEMRQQAEGLIASCLLK

SKAAWDGTKQIFDDPKQWKLHSAKPHLAVYKRRDPHRGNSTAQEFVASGRIPGLMLQDVE

YGKYSDTTLDERSICAYLFRDYFLDAAV

>contig51811 Frame-0F

MDPELILEPPDIDTSDHHSKPSDDRRRSCRQDKVEATTIGLPSFIWDYFVKDVSGKFVIC

TLCPAQTTRFAYSGGTSTMNRHLRKKHHKYAPGKCAADYDYPKGVHPRPPHLGSTGAAAS

NGSSLFMPVDTAAILGASLPSEPLGNVHRHQLLELRSARRRAVNANVASKRRK

>contig52494 Frame-1F

MCHEHCEVDVQLLAAAGPVHVQQVQCMSIDGDADESLVGNMTLTSFGINVDHLL

>contig52641 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65331.1|) 2e-36

MGGQTSRMVREIVEDSTYIISQTNRANYERSCMAHAEVQAKLLELRRLKQELLESAESDA

QRSNVFKSFPNTVEQQLEALEEQADGFAKQFELPTGYQKIAESHREAMRQDKRTVE

>contig52982 Frame-2R

MAALHYSSLHYNLHSLYGHAQSVATRSALNSIVKKRTLLLSRSTFSGTGHYAGHWLDNDV

ASWEQLRLSISGT

>contig53732 Frame-0R|Blast-cell division control protein 45 [Phytophthora infestans T30-4](gb|EEY56638.1|) 1e-74

MLWPREEFHAAYAQIKHDALQGGGTCSILLLVALDVDALCAAEILTRLLRADMLSYSLLA

MRGYEDVLEARETRIRSADGRVRGGMELRSVILLNCGAIVDIAKLLALPTHVKCYVIDSH

RPIHLANLYDEHQQIVVFDDEALPLDAYPAFGPDLDVEDW

>contig53901 Frame-2F|Blast-Rab8 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY66513.1|) 1e-109

MVHVLLCNTQFVVDMVHSSKYDLLIKLLLIGDSGVGKSCVLLRYSDDSFTTSFITTIGID

FKVKTIDEDGKRIKLQIWDTAGQERFRTITTAYYRGAMGILLVYDVTDDHSFQNIRNWMT

QIRQNASSNVNKILIGNKCDVDSSERAVTTQQGQDLADEFGVKFFETSAKSNQNIEEAFR

SIAMDIQKRLAESEHDRLDVANGSKFHVDESQDQGKDGCCA

>contig54416 Frame-1R|Blast-adenylate cyclase, putative [Phytophthora infestans T30-4](gb|EEY56781.1|) 6e-43

MDNMHRVQVRDAQRRLSLRADRQCLPASELVESKSFIEARAALLDKCSHLNAFAPGGAFI

LEGDIGVGKTVVLRSAL

>contig55183 Frame-0F

MPQSHKHQTEGRNKRVHENRVHPKHQTPSQQYQSP

>contig55200 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61862.1|) 4e-25

MGSRITKKYLSLNASTRVTLVGEAEQTLLHDYELRVACCLDAGSFSLTDAEDIFQTVERI

QSVIEADLKVNHFV

>contig55525 Frame-0R

MLFQQRNYERKPTNLEHKEIVACAHGGYKERPLKFANL

>contig55727 Frame-0R|Blast-mediator of RNA polymerase II transcription subunit 31 [Phytophthora infestans T30-4](gb|EEY57945.1|) 1e-06

MEVPSNDIRFQMELEFIQCLASPAYL

>contig55868 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70361.1|) 5e-46

MDDAIRTLSIEMANDKDASFIGKTEAELEILAHYAKMGRRRAAVGMICGSSIMAGLWKIS

KNQKRVACIFAMMSGGVFGASYGIISIRQNLFSDLLMLPTDKSPFAARART

>contig56061 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64277.1|) 7e-23

MDTPLHRSETVECATVLLDHGADMNARNLEGQTPYDVAIEDEHEELQALYKSLGADRSNR

ILKSESEIMPDDPYLKDDVFKLDV

>contig56186 Frame-1F

MKRDEVVVVQPGMSTGDERPSCVTPSREGAEKRLKSLRELYGDASSKPKLE

>contig56942 Frame-1F

MRRRLFFWHRTFVCSSIYLSSSIVRKHSDHDSRQPKIILTKLLRIYAVQERKFIRQESCK

GRKSHSSLPGFLHRSRSFSVSTQSC

>contig57299 Frame-0R|Blast-dihydrolipoamide succinyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64480.1|) 1e-08 NOT\_ORF

MGDFISAELS\*NGLKQPGDAVAEDDVVVVLETDKVSVDVRAP

>contig57538 Frame-2R

MSLKSNTTLSPLGEIQVLPKELLKTSTFDHSDDGLFKTSGLPIGSNVPLKIASPDATMPA

GDFSSKGWLYYRTSNEERIRLRYFMQWGYELSIFKHEVLADEAIAIRYGVIDCRALVDVR

FAYINSPENAVELMLGSDTSVIIIPRTDQEAVMWRNSLLDVKRAYGHLESGKNKEDTFGT

GVFISRGSTFSTNKDHEELLRWQIESAVIYSSNLQDWDGRNWISKYVVLTSSRVLMMSLA

LHLYDEEPDILGSFTTKDIMEVRACNEEEEAETGHCKSACVVTLRPSSGLVSAERIIIKC

DSIDHCLEWMRLLCSSNGKLELKKNAATGCWGSVNRIASLSRHQSFLATAPLTAAIAAAK

NSNSGTPARGGERTRRMTRQDAARKRTSELIMNRKSMMKM

>contig58504 Frame-2F

MYRNWRIYRKQSLRKINPATEKDKIREALSDEFQATFSDFQRAVIIAACLSRSDSKFQRH

IKIERKLLFKEWMAMSPE

>contig58742 Frame-2R|Blast-fat-free family protein [Phytophthora infestans T30-4](gb|EEY57907.1|) 4e-13

MNNDHGMNRMQELLSSYYGLEDQESQQEQQRNIDSPGFDSNVYV

>contig59363 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59418.1|) 4e-09

MNGLPTRQLSSVVAAQPPPFRDMRRLP

>contig00005 Frame-0F

MIVPLKLVLAAVVAGYASGEQEPLPVEGRREAINYNDEATTTILPIHHNISTITDPALLT

GLGPVVRGGQGPTLNNPEETEFKTTSLVINHNALKDTDPNIFRGLGPRQRIGLEPSLAPC

QPLPVPAY

>contig03376 Frame-2F

MARGSKKGGRRGVDSGSDDAKTNPSVTSALKEEGDKKAARKEKLKVRKAQRQVIKATEEQ

TSQCTASDAEQEDGDPYAQVARNLSKKKNKKNKKNVAVNIAALEDKSESVEGVQEQIDDE

ESKMICSEMEMKKSKKKAHSVASNDDLVVQEEDEDEGNKPAPMGENMKNKKDKKKSKKKN

ISTNLFFDPVEETEKDKKNKKKKKIKLPFDVCDEDDDVEKNASDNSLKLEKKHKKDKEGK

RLSNKERKRLKEEQERQEREDEYHRAANPMDGAQFSVSQQAITEDSNWENATDIHIENFS

INAHNKLLYDNAALHINAGGKYGLVGPNGQGKTTILKMIALGELRIPPKIDCLYVEQEVV

ADDTRAVDAVLKADAERWALLEEEKKLLAELEIKQDTALDDRLNEVYEQLSRMNASAAEA

RARRILFGLGFDSAMQEKVTKDFSGGWRMRISLAKALYVEPTLLMLDEPTNHLDLNAVIW

LDDYLQKWKKTLLVVSHDADFLNSVCTEVLHLEQRKIAHYKGNYDMFREMEKQKRKQMEK

AWEKQQKQLRNLKASGKSSKKATEIVKKKREPGARATKNKSLMPDDATETGNSLDLLERP

KEYIVQFSFPETTIVSPPILEVREASFRYGNSPYLFKNTDFGIDTTSRVCIVGPNGVGKS

TLLKMMTGEVTVTEGEVRLNPRVRLGIYSQHFVDKLPMGETPVEYLRRLFQDQSYQQVRN

LLGKVGLEGHAHEIKNRLLSGGQKARVVIAELVLMRPHILIMDEPTNNLDIESIDALCDA

IREYEGGVVIVTHDARLIESTECVLWVCGDQDVVVYDGSFADYKQSILDDLHKQAQVEEE

RLVDKAAKKAEARAQKAKGQSV

>contig03794 Frame-0R

MPSILYHVVAKPETPKLRTLLNKLCALISN

>contig05565 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61371.1|) 4e-12

MRKKVSTNKYRYMTIERTSELMHSRYYRPSLSVRYRSSSSSSLSVSACSNSSAVSSYPAP

CSSASHCWYWGPDECHEDYE

>contig06807 Frame-2F|Blast-NPP1-like protein [Phytophthora infestans T30-4](gb|EEY58144.1|) 1e-38

MKLKPFLVSTVFMGVFVDAQDNLQVELPAEPEKPPEEWKPHWIKHKDVKPFPELPPTTVA

EKAALMFKPQLKIITGCHPYPAVNEQGEVSGGLQAKGGQSSGCKGSGHGSQVYGRSTWYR

GIWVIMYSWYFPKDQPAPFLGHRH

>contig07945 Frame-1F

MLISFLARNGSISKDNTGLLHRHKTNFVKNALAYTHLRKHALEKHLHHPNNLCAWSVYRR

VITMLSQLACTPPLMTIRLVR

>contig08085 Frame-2F

MINPAGFNHETLSRTHSFYSEKIDNTTQGAAVREDGMNSRNRQVDNSRSGVPSQVLVLRM

LPPDIEEGELQVAFAEFDGVQDIRLIRDRATNLSRGFGFVEFRDIRAATNALRQCEGLVV

HNTHVEVSFARDTLSTRSQHVTDLHPGPRAGSSLVVTALEQAQWSLSQGRGVDTTIVDQH

DTVVDVVDALLDQAAAAVVPRIEEPKKMWPMPFETAGGRYVFVSEYGLYWDPDSLFYYDA

QTMVYHNSFTGTYYRCIDPESSGAAAFQVLMPPLPVDEEAYTEHVVLKETATIKPALNLS

MKKEKKKAVGISLAIKTTAFSSVSSMEKEGQGKLMESSVSGKSSTAASGTSTGIKRKRAD

DIAKWSQRQRDAKRQEGRNSTPAAAPLSIVSEVQAAGSEHALSSVAAANAVDSVIDALTN

VPQEVPICLLCRRKFGSLEMLRKHEKLSQLHLANVTKANENKQLLAAQYREHENEMKRDE

AKKQRQDDVPMSHEQQWSASHSVSSPRSEEAPLQSIESGIEG

>contig09271 Frame-1F

MSVYVSALVDNPAFDSQTKETLTTRANSFGSTFNLSEKFLKQLEKSGLVEKILSFAAFKQ

TAELRRKGGGGGKRSRLTGIPKLDDANHAGTAKSKDCTLIVTEGDSAKTVAVGGLAVVGR

DYYGVFPLRGKMLNVREASHSQILKNEEIQNVVKILGLKYGQTYESTKGLRYGHLMIMAD

QDHDGSHIKGLVINLIHHFWPSLLHVDGFLQEFITPIVKCTKGRTKKVFYTMPEYNAWRE

RTNQGRGWVIKYYKGLGTSTAAETKEYFSDLQTHQIGFTYDGDGDADVIDMAFSKKRVED

RKDWLRGYEPGTYVDYDVDEMGYTEFVNKELILFSMADNIRSIPSVMDGFKPSQRKVLFS

CFKRNLRSELKVAQLAGYVSEHSAYHHGEQSLQGCIVNMAQDFVGSNNIHLLSPIGQFGT

RLMGGKDAASARYIFTNLEQMTRVLYDPLDNDCLKYLSEDGQSIEPEWYIPIIPMVLVNG

SDGIGTGWSSSVPNYNPLDIIKGLRQRLKGEEMNSLTPWYRGFTGHIVEKANSRGTDSSN

YIVQGLYEVTDDSTLVISELPVKTWTQTYKQFLEGLLDSCTIKDFKENHTDVKVLFTITM

EPKALSDIAKAPGGIVKKFKLESSLSTSNMHLFDASGRIKKYESPNQIMEEFYAIRLEYY

QLRKKAMLYKLQDQIKLLSNKARFVLSVVEGKLVVNNRKKAELLEELAVEGYDPIAPKSK

KKTDNEDSNESNDEESTAVDANRGYDYLLSMRIWSLTKERVDSLRAELEERKQEYSVLEG

RTEQNLWLTDLDALEKMLVETEAERERILSHTPQKRGGRGKKPAVKKRKRKSDDDGDDDD

SDFEVAGSQTSRKKSNTAVKRPAKKEPLARKINGTKENKAAGAKSGTITSFLEKIDEPPT

AKEDNEADMEDLSLAERLARRFKVSNKNVGTSSSLKRPSKPATTKTFVSSPGEQTYDKDD

KDDVFAMESDDIDKKSAFVKSNAATKKAESKKAATLKKAASTKKEVTTKKKAATRKEATT

KKTPSIKKDAPIKKNVKASSLEDDELKYMDENSGGASTPSPVASRPKRELRTHKRIVYDE

GSSDEDNDENNKEESSALEDDADDSDFE

>contig09745 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61720.1|) 6e-07

MVMLPRVLASLALLLGTTRSYDINVYNQCSGDLPLVHVRPGNVNTEWVASGGSTVKTIDP

>contig09954 Frame-0F

MGNSCTRNSESQVLSRDQAAILQRHTGQGRDPERGRWSAPNVECVDLDTLLEAPSPTANK

NAAARRRKKRQSLSDRFHGPRRSAKPPRPPRAPSFEDPNPFTKSRLYRSRTETGRRPVLL

PEEDLIPIYHSYEDPGYLAGDPFELQPFDADCILGSPINSPSVIHARWGEPVDDPDEENL

CLDFSPNPFKVGFCINCMKQHDVKENGEVATRKEYKRIARPTISKTAANALDNPSAIPIA

RSSITMMSDGGRESDIDLAQLLAQRREVLARLNKLNHQKDHLRKQPSGGMMGRRADRHTT

INFGDSSRSNLRKVGSRPPGSGPIVSCGTSLSMAPQPASSHNFGASKSVNIASRLYDDEE

PALNVWL

>contig12420 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69247.1|) 1e-11

MDTEKFDEDAHEVIENSLLTVPVVITAPMPS

>contig13544 Frame-1F|Blast-clathrin heavy chain [Phytophthora infestans T30-4](gb|EEY61684.1|) 0.0

MAQDLPITFGEVFNLSTLGVNLDYVKFGTTTMESEKFVCVCEQVNGQASVVIVDTAAGNT

VQRRPINAEAAIMNPVSKVIALRAENQLQIFNMELRAKMKSHLMNEPVVFWRWVSVNSIA

LVTASAVYHWSIEGDSPPAKIFDRHANLGAGTQIISYEASSDNQWMLLVGISQGEGGRIA

GNMQLYSMEKKVSQVLQGHAGAFAQIKPPGRTDDAQVLVFAGTKGSGEPMQLFIMEVGRD

RDAPGGVFRLPPSPIPFAADAQADFPVSMLVSPNDDIIYMITKMGYLFLFDAHSGKPVYR

ARVSKDTTFVTCLESKSKGMLGITRRGQLLHFAINKTKLVPYVVNTLRDSQLALSLATRL

DLPGAEELYFTEFNRLIGVNDIQGAARLAAASPQGALRTPQTIQRFQNMPSQPGQPQPIL

QYFSVLLEKGTLNKMEAIELARPVLMQGRGQLLQKWLSEDKLECSEELGDLVAQSDTTMA

LSVYLRAEVPEKVINCFVQRGEFDKIVAYAVQTNYRCDYTFMLQNLVRANPQGALDFAQK

LAVAENGPLVDVNAVVDIFMQVNRVQETTAFLLEALKNNRPEEGYLQTRLLEINLLGGSP

QVADAILSNNMFTHYDRPRIAALCEKAGLFQRALEHYTELSDLKRVIVNTQAINHEFIVT

FFGTLTSEVSMELINALMAHNMRQNLQIVVQVATKYAEQLGGKELVDVFEKFKSFDGLYF

FLGSIVNFSQDPDLHFKYIEAATKMGQFKEVERVCRDSSVYDPVRVKEFLKESKLQDPRP

LIHVCDRYDFVEELTQYLYSNNLMKYIDVYVTKVSPQKAPIVIGKLLDLDCNEDYIKNLL

NQVAQCPVDDLCEQVEKRNRLRLLQPWLETRVAQGNTETATHNAIGKIYITLNKDPQQFL

VSNQFYDSEVVGKFCEKLDPALAYLAYRRAGGACDEDLIRVTTENGLFKDLARYLVERQD

LDLWGKVLVRQEEGETESPSRRALIDQVVQTALPETTNPDEVSTTVRAFMNAELPNELIE

LLERIVLQGTDFSTNKNLQNLLILTAIKAGKEKVMDYVNRLDNFDGPEIARIAVGEQYQL

YEEGFVIYKKTNHNVEAIGVLLDFIRDNERAYEFADRCNEPEVWSRLAKAQLEQGEVHDS

LSAFIKANDASSYVDVITAAERIGNYNELIPYLKMARNTVKEQFLDTSLIYAYAKTEKYG

DLEEFISSPNVAQIQNIGERCYDEGMYNAAKLLFQNINNNAKLAICYVRLGKFREAVDAA

TKANSVGTWKEVNYACVDVNEFRLAGLCGLHIVVHPDHLEELILHYEKRGHSSELLKLME

QGLGLEGAHAGIFTELAILYSKYLPSKLMEHIKIFHSRMNVSKILRACEKGLHWDHSVYL

YKEDGQFDNAVRTMVDHPVAFSHDLFLDCIQKVRNQEIHYKAINFYLEQHPLELTRLLQV

LTPNLDHARVVHQLRKSKNLPLVVEYLKDVQKENLSAVNEALNEILVDDEDYQALRDSVD

AYENFDQISLAQKLEKHELLEFRRIAAYLYRKNKRYTQSVKLSKADKMYKDCIDCASDSE

DCELAEDILRFFVSVHDKECFCATLYTCFKLIKPDVALELAWRHGYVDFVMPYMIQFIKN

MNEKVKGLDERTQTQKEAEIDAQTLDPAYGMGGMQPMLAIAPTAYNDPSAQYGMGMPHGM

NIGMGMQPNMTMGGIQQNPYGSSQGSMSNNPYGSSSGYQY

>contig13658 Frame-2F

MVFAVAKDAAELQFFHEDIVALKTFLRQTQLHSVTSWELQGAILEALDLPRRTSSKILLT

QRSTFLRAVQKMCVTLPLMAPRSGSNGLLGFCNDEDTELLHRLLGVFSHECHENDERVVS

DEDTDENDLIDVDAAICGLLVVCEGSMLEKLQCCAALLSDDESTFNGEGEGKEEFDEVMV

QVETIRSSLMCFLMAFYAISSSLSAEVARDSAERGAVAVLESFLEVVSEKSSAGFKISAR

KEKVEEKVSLRVFTDWFSNVGYPTHSWLELVVLHHWPAAMNVCGSNGLPDAL

>contig14909 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55116.1|) 1e-13

MERLQDEFTFLRFQKKTCCRSKLRGLRQEDLEAILSRELYTWPIDFYDHIYRHLRPDSYG

NISFFSLIQFLSIASRGTLEEKACLLFQVPNHRYQEYLNKQGITRLA

>contig14992 Frame-1F

MRLSFNDPQSGEESSLTPKNSFFNFVSRTHMRHHAMSIQLKPSVVLLHLLLLLGSHWIAC

LELVAFDDSLDSNTNSRDNLPQDSHFVAPHLRKDIDNSIHQGPSVVEERVDPLTAAIAVL

AKETHPIRSALKGYYKSSQEAIQRVMMHRNHISNFEQAQSAYKLIQDWNGVPVSKFAEFD

KAVMGGFKKAGMNEAEASEVVVKVLTEEIGNLGAARLLNDLQKGNPELFARTQSSLYQYW

NKIPLSYSSFHDGKISMGMSESPYHIQDVILDTFSEYFKYAKQVPGSEDDSAYKSMMKDL

ESKGYGGFVDNIIRTFSPPSEFKPANDATRIALEYLKKQHVKYNTPSAIIKAVPFEEKSL

NVLGNPFYRLSALCKSKVEVEVGAVDEVKKQAKWLIKELDDWVFDKKFFLIMYPLREKEE

LAASVLEQLSFRWKKDEALSKALESDLKKSIPQIPAGKLRWSMTEPDAPLNYFRDLAFEK

PILASK

>contig15890 Frame-0R

MYHVRLRSDSTHAGTELVTSAVLLEHFGAKLDPREIKKFVLPELKKVQELSILDTAAHLD

LNTEGFNDVSQQQNARAFILLVGLKRNDAGSLQWGGHL

>contig16064 Frame-1R

MMDSTWKATLYNALAFVGKLKNRDGVNTRQVDEALPRLAEAFGLSMHDPELKRQLAINSD

TSFDDIVAAGLKALNLDTGTPSEVPSIAAEDPVVKKHPELWQKWVAKLESKGFFKDALPG

SSEYMTRTNKALSKFKEKFGDVTPELSKEEKEVKAEEVKAQGNAALSSQDYDGAATLYRE

ALQLSPNGPFSHIYHSNLAAAHMYMGKYTEVIDHCEQSIALKPSYMKAYTRLGSAQLQLQ

DFDGAIDTYRRGLEIDSTNDACRSGLAEAENKRQQLQTTSTPSVSSSHATGGMPDLSNLA

SMLGGGDGGLAGLMNNPQMMQMAQSMMQNPQMMQMAQNMMQNPDMMNNFMGGLGGGGGIP

STEANVGNGTPDLSRVMNSPEVLAARSDVDLADFFRDVDTEGPSAAMRHMSNPKVSDLMQ

RVMARIQA

>contig17399 Frame-2R|Blast-ADP-ribosylation factor [Phytophthora cinnamomi](gb|ACL11855.1|) 6e-87

MGNLFSYSLQGLYDNLASYFGNRKSGIMIIGLDAAGKTTLLYRIKSGELIATIPTIGFNV

ETFEYKNIKFTAWDIGGQDKIRSLWKHYLSHNDAVIFVVDAADLERIDEAKQALHLIFEA

DELADTKVLVYANNQDQPCAFSAEEVRERLELSEMTANPVHVQPCVATTGDGIYEGLDWL

CKALTGDLSS

>contig18321 Frame-1R

MSLDGLRQLHNNQVYLHKLQQLGVTIKKGDSGLHIQGLSLQNPGKVDTYKAANTDRHAEL

FTQEGGRYKVQSIPMFLENGNLKVAMVSPSNPIKPMPLFPRGGMLRNEKDDVAAGVLREL

SEEAGVRHWTRGWFFCFFKSSWPN

>contig18772 Frame-1F|Blast-protein phosphatase PP2A regulatory subunit B [Phytophthora infestans T30-4](gb|EEY61246.1|) 2e-12

MTQTNLQGDIGREESRVVTMTRHKHSNAGGLEVEMAEPIEEVDIEWGQVFSAGESSRSFV

>contig19353 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69224.1|) 4e-17

MVDELLFSGQLIAVTMEETDDFRLQINNEAISFLQQLVEPILVVSFHGPKKSGKSALVHS

LLQLEQESMT

>contig20186 Frame-1R|Blast-acetyltransferase (GNAT) family, putative [Phytophthora infestans T30-4](gb|EEY60438.1|) 5e-38

MLRSVVVAWKVMTRPCHLLNWRHRRIAVLDSIHDLIKLRLFNAFVPPELASYGAIVSFAS

HSKRTKAQVEWKVEKNNRKEETRTQDPRKSRTIKDVTFCSVDATNVEQLHELNQELFPVT

YGKGFYDYVIDAPEGYCKLVYTNNGHAIGTTCCEVETIKTSGKHVDCLCILTLGVLETYR

RSKIGTMLLDSVITQARKDNLAFVYLHVQSGNLSALRFYIAHGFQVT

>contig20717 Frame-0F

MASVFFDGRASLLSKTFGLYQTTIVRKDTGQRMVQYICVTENAFYRKQITQRYDLKGSSR

NRFVKPLANLKVQQNVVGPLANLEIQQNVVGDRVLLDGNFLEFTKGFPLGVLAEHHQYIS

KAVENDTTFLCSINIVDYSMILGLSFREGDTDKIQEAPSEMTIGIIDYLRQFDLIKRVES

VSKSVGMIAGQSSPTIIESGLYGKRFKDAMHRYFMPVSSITSGKNEDIL

>contig21534 Frame-0R

MQPHSPRTLQAAPATPVDIHSEPLTWPDVKDLHAAVTVHTRKRQRPFESSPTSFSTPQDL

KLDFTGFEVDVNTAPTDMPLTHLSLDPSGMTYPPTQTAMGYTGYYPTAVSEDIVSFLKTL

QLAHDATTLVAITQRLAQNGFDSTLALAFASVTELQQAGVVEAPLVWQQIHRHFQCLRYP

GPGILSPSSSVSRWLELCGIPKATTYTYAEYLGRLGYACVRDLTFLLHDQRALEMFKTGH

SRLVTHFMTLAATPSEQPPPVQVASYPYTTHSCNVYTAGSSNALLQPLEFQRENDFDVRV

YDSFLEALIEPTDAERFQHFSIPETITTSPENDAPHAPLSDSTDEFEPRLSFHATSSPLA

SNLPLRLLPQEHLQLLYEAVNLPRPNPCRRGKKIYWSVLATGGMKIERFTPLTQFTAPEL

QNAYLRQFELPTPTLVKVDAWSHDNIRQLEQAVKDPRCRHLSKVCWEMLATGRTGVDEYA

PLAKFTASQLRSRFRSLFGDKRPQKLRQKKQLLKLQQHPKVTRDERLI

>contig22742 Frame-1F

MPDSASHCAENDRFAKVPHLWTLGVGAVVSGNFFGWQSGLIAGFDGLLLILAFVTILYVL

LVFSIAELSTTVPVGGGPYVFALYAIGPCAAFFAGLAESLKVIITCAVVVTGISAYINQL

LDLTSGYGPIWWFLFYFIFVTLNIVGVEMTFCVQAFTTVISLLLLLVFYIGAATKVSYTE

WVSNDNYHFPNGWDGVIKGYSFALWFYLGIEELPLAVEVTINPARNMPLGLLTSIVTLVL

LAFCTVVFNSLIFPGAINILNSPSPLLTGYQSVFGDKKGFSWVLILGLIASFHSFVYCMG

QLLYAIARDGYLPQILTWRHPTRGTTYVSLIAGSTIGFAVVIILHYVIGDAHLGSVMINL

ALIGAVISYSLQLLSFIRLRLNEPDRPRPYRSPFGVPGALVSLVLCVAVMISIVYSGTSS

YEFLASIIIAVLYFCIGAAYFWIYVRPRLLAASTPLCATAC

>contig23626 Frame-0F

MEMAQQWKNKAELLVSELEWVKATDFKISKSRPRNARTGRFSSLTHVSDIIAVSSCKGGV

GKSTVAVNLAYSLSKFGARVGILDADIYGPSLPTMVSPANSTIRQSKLAKHLVEPVEYEG

VKCMSFGFVNRRAAPGAGGVGAAVMRGPMVSKLINQLIIGTEWGDLDYLVVDMPPGTGDI

QISLSQQMAISAAVVVTTPQRLSFIDVEKGIAMFNDLKIKTVAVVENMSYFDCLHGQRHQ

PFGPGHTQELVKNYNIKHVFKLPISEHFSSSADSGRPFVLSGISLAEEKTYESLATTIAK

EIVILKHKVRPAPEMNYDRDRGIVLRIFNSTEATEALLHPADLRARCRCAECIDEFTGSQ

ILNLATIPDDIYPTVVEQKGNYAIAVTWSDGHSSSLYTYDELTALIVEFAAKSE

>contig24014 Frame-0F

MIEVAWLLSFLSAREEATLQLLLTHGLIAFFMPSFTTTKEELL

>contig24227 Frame-0F

MVMSEEGDLNGRSSDTEDNETEERDQGIDKSDTTIKDQVFDSHTVLSMKNRNFFEPNERG

VDPGPGLAITLEDHVYARITCRRVVAEGVIVGRLFLCSKHVVFEPLNVQETAHEDTTILP

NTTNFDEPSLPRVFKTNHEETAPGLHRCWRWKYRHLVAVYLRRYRLRDS

>contig24605 Frame-1F|Blast-vacuolar membrane-associated protein, putative [Phytophthora infestans T30-4](gb|EEY67603.1|) 4e-56

MGHRIHEIVYNEETQTIDVKRYLQKVTTRSDVDIMEYKYLLWSPIVDQFVIFSQEFRKYP

QIEYQWNHLDQLICGYIDEMSEGIRYKRSLYCLFPPRFGGSDVGDQ

>contig25084 Frame-0F|Blast-cathepsin, cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|EEY57990.1|) 1e-50

MANGGIETTTTYGPYRNAPDYCHFHADNAIGTMKGFVNVTGIDAFNDALATVGPLAVSID

ATLPSFYFYGGGYYEDAQCKSDFDHLDHSVLAVGVTTHN

>contig25589 Frame-2F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY63452.1|) 2e-14

MLRQWFVKYRKLSPVGPAGLVLLAGAAVVATYVITRSSDDDVNIVTPLSDHDVNPDESKE

KPKEVPYLPSK

>contig25978 Frame-2R

MSGQRLCSPISSYVTSSSYVSPPTPLSPPSVSIVTASQRQTTNGEQITIKSLQVLIYTK

>contig26157 Frame-1R

MYSKNTSSRFSFDGRASGRKRRIRQDCRRSQRILKLSLKCLVQFY

>contig26849 Frame-1F

MINFLLENMALFHKDTSHGNTHTAVTETMSARIGGSISVKRLCVCLFQHFGFKVASPTSN

DMLLETSPGHYYKNQLSSVLLKCGSANTKVGSIVAANSDITSHVIRGID

>contig27550 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70395.1|) 5e-83

MLRRLFTHESVRSHPLRVFFTILGAIVAIETFGFVVFLAKKEDSYWLLIYDDLIVCLLSM

GSLASVLVYSIRMKTVLQAFLEVSLIDTTDRIKAVHSATLSCVFFLVSNTILLLYAIGSL

VWFHRPDAYLPTTKWWLVVVSKHGVEILVLYFLLYTLWGKSADDAESAKDGYEPIPDEAH

LDDEVLAAKKVLSP

>contig28065 Frame-2R

MDPAFFNSPTTRLYLLYITQSSPDMQIACLDWLSRVSGGSQKALQSASKGMKSNQLLLLH

LQKDHWKSLNLRIFFGSLKLGKINFSMYENRIFQFWVEFACVRNEEAVAVQ

>contig28436 Frame-2F

MLLPILVVLILVVPTHVRAAAAHQRDFAACPVRHAPEYYCCEYAEAAKVVYTKYNRPSGG

KYASYYVDGWKEQRQVNFPYTMYHPTTQEFYYNDPTTICRVQAVANSVTGVLTENLQCAD

RNSSLIAASQDSSVFWTYATNFRNNNATFPLGATCYSLLLPDGTVDQDLMDACVITASTV

KPRFTTFTEATLVIIYLLYFAFFIILGAWFVYKKYMQDANRSVHEITKKLINTPQTPSRA

MMGNIQGSHHASVRLSDSRMQFDAEGTLQTGFSKSIFGSFVLGCVVVASLALNVLLILII

CDYYGNFDPPLFDTSEDNALVFIIVWVITATWLVVIVAMQDRLFNFFRLHMPLEKCEFVY

MLKRDETEVLLADRSGVSDFVAKVEGFFASKGKISGYRETVPVVEVENLRFVEFQHLRHV

YDETHQRFVPGVVALGRTYDDMQQEAMGLSSAEAKYRMNTVGLNCVDVAMPSLFVSMAHE

FFTLFYIYQIMCYYVWYYFSYWNMGIVMTIVVLGAAVVNIYTQRQIQSSIVKMTRYRTDV

TVFRSGEWCVLSSSDVVPGDLVKVSENWEVPCDMAIVKGTTVCDESMLTGESMPVQKFPI

PEHSSEVYEPEKAGKKHTLFAGTRVLSSGRNEEISAIVQTTGAHTTKGQLIQSILFPIPM

RFKYNEHLKLLIGLLLLYALIACILVINFLLSNGKLNNRYAAFCYAIFVLSCVISPLLPV

VITVGQVNAAQRLEKLGVFSLNVQRITLCGKVRIFCFDKTGTLTKQGLDFLGIQPVKKRL

FHPIVSVITDASSSEELLYACTTCHSVGSLEDRLVGNEVEVRMFTATGWELIEKEGVQPC

VRSKKDPELQLEFIKRYDFDHHRMSMTVVVRNHKSNKYYVFCKG

>contig28692 Frame-0R

MLAELDELLTLTPEVSLTLAQLPFDAGIDLNAVAFPETKISLGQLNEGLNPPSFEALQPE

PRGKSTKILKTKL

>contig28818 Frame-2F|Blast-glutamate synthase, putative [Phytophthora infestans T30-4](gb|EEY53782.1|) 0.0

MYGIPNMKLDKKTVNRRVELLREEGIDFVTNATIGVTTSVEQLQNENDAVVLALGSTVPR

DMVIPGRHLKGVHFAMEFLTKNQKRLMLTVDGKLQSGWDRNFVTAEGRDVVVIGGGDTGT

DCIATSMRQRCKSVVNLEHNPVPPAQRAPENPWPEYPRIYGVDYGHAEVRSVFGEDPRRY

SRVTKAFMGNAQDEITHVVTILGEKDPKTGLITEVSGTEEEIPCDLVLFAMGFVHPEQNI

AEGLGLEVDQRRNIRAAYGDYQTSVEGVFAAGDCRRGQSLVVWAINEGRGAADAVERYFL

NEGFQPEVSQNQRFG

>contig28995 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68607.1|) 4e-48

MVLVSTDTFLAKVTEIYSKAQDSKGSVAISCKSVPVTKVNGKAQQKILNLTVEDGEHVLL

FRACKYGNNKHKKKYSTVVTAINHASFHSSLSHIINSKEFELTTDAVDKRPKRLVKTVKK

TTE

>contig29220 Frame-2F|Blast-regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4](gb|EEY56311.1|) 0.0

MTVYSWGRGEDGQLGLGDTSDQHHPVTIEALVERRILQIACGSGHTVVLTEDGEVYTWGR

GDDGRLGHGDNGWKFVPRLVEELRGKNIRQVTCGSYHTAAVTVSGDLYTWGGGMYGKLGH

GNETGHSTPFLVETLKGMQVRQVACGSRHTVVLLENKDVYTWGDRENGVSGHGDTEGHQY

LPCPVEELRGKFIVQISACGFHTAALSEFGEVFTFGEGKFGRLGHSSERNQPVARFVEAL

AGKRVKQVACGGFHTAAVTETGEVYTWGGGEHGQLGHGDKVNKTVPTRVESLVDKLIVQI

TCGWSHTAALTDTGEVYTWGNGDHGKLGHNDTTKVTLPKVVDVLEGKRVVSVASYNEHTV

ALVDPVAMLRASMLTSSYVGDMRQLIDSAEFSDVTFLVEGRAIHSHRAILAARSDHFRAM

FSSGMRESHELEIPLMHTRVPVFLALLEYIYVDSINVGAEMALELYAAADLYTLDRLKGL

CEIYVQKSINVENAAALFQSADDLHSYRLREICLSFMVQNFDLVTKSDGFASLSRDLILE

VLQNR

>contig30352 Frame-1F|Blast-aspartyl protease family A01B, putative [Phytophthora infestans T30-4](gb|EEY64098.1|) 1e-51

MRAFQKASGGHEYTEKGVKLTVKELKNLPVLSIILSGMKGDGTDDIQLDVPSSSYMTPSS

DKGYYFGNFHFSERSGGVLGASTMIGFDAIFDTDMKRVGFAMSNCGRTPASSIKFPRIDG

NNTQHQTSKTVTVPLDLNSTNRTATPQPSENLNLFSNTTASNKTMTEYSRTEIITSLNNA

TAVLSIDLTKKQEINTHSAFIGQVVFMSLVGVALAVIVWTKRRKRPWSRIPDVMDKLQLH

AETIDDEIDTLPILREKSLSPRATWKDSTAKFTIGSP

>contig31067 Frame-2F

MLRWVLIYLVLVGGTSSSLEVQVPIQRQNSPTSRFAYVTVHYEGTSRDAEYVLGVQVLMH

SIKLTESPYDLVVLASNSVSEKTKSLFRSMGCRVVDVINIENPFVGGTLRNKGFIYTLNK

LHVWNMLEYERVVYLDADNILIRNSDELFLCGEFCAVFMNPCHFHTGLLVVTPSAAEYQR

LLHALGHLESFDGADQGFLSSMYSEMLRESKLFTPMKSTYAGAKLEIKKPEPKGMRLPVG

YNINHKYFYEQYHWKLFYLRQFASMTSPISPVKVVVESARGIPALTVGYPMASVLKPWNW

WAGFFMDLHSVWHDIRATLPASQEHFGAEEAVKTLLGFFSSLALLTAALYAFKITLPMRL

IQQRFTDLAMRNSKHARHAYMAFRIALVILVFRIAPARVHPLAPVNYGYGLTIFMNVFLH

IYFACVISNFWDPHQEVSMPPVLYVTQFWLYIAITAAFEFFVVWFSTWNVFLNVLWRLFS

IFCSLVLCAYWQVMFYRVVLNAEFNGKKERLRSL

>contig31773 Frame-1R|Blast-proteasome inhibitor PI31 subunit [Culex quinquefasciatus]gb|EDS31702.1| proteasome inhibitor PI31 subunit [Culex quinquefasciatus](ref|XP\_001841849.1|) 8e-08

MLVGPNHPIFGHRVDPSVGPVPGARFDPFGPVIDPLGPSGSFRPPFRGPAPTMPFGGPGP

DHLRMPRDDDMMGPSFGCSGNNRGNGGFHRSDHSFS

>contig31993 Frame-0R

MESRFEVLEEETHYPATESKGVESYHPVALEEKVEESLEEQLERLVLSVKYDDASENAPE

EEKGDSKGKTETVKKASSAKELGNKFFTRGSYLDAIECYTTALKLCPSEEEYAYNRAVYF

SNRAACLLRLGRTEESIDDCTQAVTLSPTYVKALLRRAEAYEKLDKLEEALADFDAVLKI

DPTVPAAVKSHERLQKIVHERQGKNEGRNA

>contig32620 Frame-0F

MKIMQNYGRFAFLALVARRHRKNEPCQAIFLRASVPRSQL

>contig33825 Frame-1F

MSTQSSAVVMYVPVQLFKVEAWVFRGSRGLLLIEC

>contig34554 Frame-2F|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY67697.1|) 4e-61

MTGGARNSFMSLATPNDIKNYTNDVGQIQWAQVPLNAALDKLKTSREGLTSSEAEKRLAE

YGPNKLPEEKVNKLTLFLGFMWNPLSWAMEIAAVLSIVLLDYADFALIMFLLLLNAIIGY

LEEVQAGD

>contig34716 Frame-1F

MALCFLVLQLSYHVVTCLNMAASTGDAPPSDNFLKNLRQGHLIGPPPLRESYLDNLPQSP

HVEEDRYIEVDSPDALVKKVALALKFSLNFPEHEKAGLLDGFRSFLLKKVNNVHKATVSF

RSNVRDSLKMNSPDYTEFLKWCVAIERSLPGRPEKAYAIMSVVLSKELGNWHAARVLVGL

KEINLFRSQKVFQALLHLWQIKELNLAALLSEVELGLLDTPNKVIETFLNPVFAECFEYA

YDMERAGKESVYDSLMVVLKQYNLDSQMDNIIAAGVERLHHAVTSEVEKLRRILHYLVFQ

LNKKTNPIPILESFIIPHGSSNAISRTYDRLAKACHPHGNDEAKSEWLINSLTGSLLEPQ

LLSSCTR

>contig34837 Frame-1F

MAVEEKKQQQMKEQELAKQQVEMEEIVRLLEQEREKMVQIKQSYEESLQRVVSGEHLNNF

SPTNDALDDRTRVLLSVSKERNVVLKRKCEELEKLSCTREEEHQRLKDQLEQEQQDLFAS

KERIRYLESKLKKLSAVAVGASQRPRPSRMPASSCSGTKFAAIPSPANEIDDDEDMGIND

QEDKNNDSDDVLMQSGDDDFSRPRNSRHHLRMKLENVDSSTEHALMNTRKGRGPRQSGKV

DDNNGLYDADSPRVGSDDSSVSKSIFSRLSNPTNFTGIHKNRIRESASKREILQSRTERN

RTRRLKDKGHNRLSRSSNTPSDQHVLTAEAFKNPSIKSNSGLEVLSHLRRENEADYLSSS

SLRQHMSYVTTDRHRDYSSDENEPAGYESNSCGLIPPPPPQGDVYSRLAGQYTASAKSKR

HHAAASARSEKGVEYENSAKAEVQGIKLGDSVHLIHRQGDDHANYDPLLGGESLIKQVHD

DYRERLAQLNTEARK

>contig35153 Frame-0F|Blast-importin subunit beta, putative [Phytophthora infestans T30-4](gb|EEY69227.1|) 0.0

MDISAALLNTQSPDLQLRKQAEEFLNNALQQQMGQFMVTLVQALASEEFAVVGRQAAGLY

LKNVLDAKDDALQQQKVNAWMAMDPNLRNQIKDGSIGVLQSSDSVARHTSAQLVAKIGGI

ELPAKEWPTLLESLLQNVTSGGEGCIHATLECLGYLCDELEEGSIDEQDTNRILTAIVDG

IRADRPPPIRLAAVTALRNSLEFVSENIKRKQERDHLMQKICEATQSQDLRTRVVAYECV

AAIATMYYEYLAEYMDTLCKLTFHAITSDQDEVGLQSLEFWSSMCDVELDLIEEMNYAQL

ENRTDFIPCNFYVQTVLNTLVPLLTETLKKQEDDQDEDSWNLSMAAATCLALVAQVVGDA

CVDITMAFITQNIESTEWRAKEAAIMAFGSILDGPDSAKIAPLVRQALGFLMGCMKFDNI

LVRDTTAWTLGRICELHYGCISGEMLPGLMQLLLEGLDQEPRVSHNVCYAIHNIVKAFEE

SEAAAHMLTPYFTTLFDKLLETSNRPNATESNLRGSAYEALNVLVQAGADEVDEHIMLRL

PVILDRLEQSITILIENPTSFHDDQAGLQALLCGVLIAAIQKLNVGIEPLADRIMQALLQ

VFSTRNAAAAEEAFMAAGALANVVGAKFEVYMQYFGPVVLIGLKNSEEYMVCSVAVGVVG

DLCRALEGKILPLCDAIVAALIEILKNPTLNRSVKPPVLSCFGDIALAIEGEYERYAVSS

LQMILQAAGACGSIASDDEEVVEYMNQLRESVLEALTGIVQGLGAAQKASLLQVCAPQIV

AFLAALANDLSTRSDAVTTGAVGLIGDMGQAMGKSMEMYFHQQFVVQLVTECANNAQNPQ

AQQLAAWTQKIIMDLQAN

>contig35320 Frame-2R

MMEMAMHSFSSDASTVTAYNRDTEADDAVVEVKQLPPVLEEDNDHCFSPIEVLGIGADAE

QRNKEVMVSETVHDAIDDAQQIAEADEEDVSEAETEILDDDEPGADNHEHTCDDEVSGIY

VNSAEKIATHGQNDFADSKEESRNLRGSSLPVKHCDSDAMGTLPSKGKNDCELVASRYGV

QQFFDLTPLQTKPKIKTTSSRVLKPLPVHTNAESPACRDFEISTSEKTSSDPLKQKNGSN

GLRSGKRPVATSTIMKGKYAATRRSTKMLDNGDNLGAKIRPNGLYRSGPPRIIDDDAAKD

LDDIPLSILTKEMAKNVVDVPKVRYLSYAGAKKTESAPILAKEAPRIQVKSRFGGGGHTE

NSLTVLTKQQDKSGLESVFNREPQISIYDALHVETQEKSCDFREESGYKRSSRFKKMQEE

AARKGIPIIKSRPKNTDWDRVPIPRKRKEALPLTSTPFQAIDQPVENAKNKRFTKNTPIS

SARSYYGPQGARLATPDSSSRRTHDKKLSKNGDFTRNEKLTARSEGRKFHDRRSERRRIE

SPRSKTRSSGARAQSYLSSSRHRRRSRERSSEKYLIRNESVSSERYDQDRQNHGSRQYNY

SKFRDSKKKDRLPESSSNNTVEDKDESRKKQKMSHCAQPSSPGALAAVDDVDDSFISNSE

DEIDAPTKEVEDIRFDLNDILVDKTLMARQIYVTGVNPTVFAEQIEEDFARFGIA

>contig35632 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65522.1|) 5e-79

MNDYLDIEAIFAEDERVKCTFETDALDCGYLDPSCHESDLPVKAVVDLPLWLALPLAKRG

DVMVTPPYYLSKRFRRMLKAGPSSVNLREYSSYVLKVGRHLLPYVNSDEQNEIDEILRLC

YGGKRYRELLNNTMNSLNEDTTEFTRKLTQEEQKLVCAGIRDTKDFMEWKGRNAEAITAA

AVVQSSLKKRKFQGVL

>contig36912 Frame-1R

MTSSIQLITTLIGQRRRRAGLTGFKFLKTGHQTFFWSLRLIHLSNQTMVNLRGTANDYVL

RILSGPISQIAYKRT

>contig36989 Frame-0F

MLVVLFAFYMALIEEKRVVLFRNIINGFSLLYLDAENKEFWRMDEAKIEDLDLYRQYFKG

AVLCLDGFREDFIRNHHNVLAKFRLLATSA

>contig37043 Frame-1R|Blast-mitochondrial-processing peptidase subunit beta [Phytophthora infestans T30-4](gb|EEY57641.1|) 0.0

MMSRLFLVRQPLVRAQSSAAAAASAYPSYVLNAPATEVTTLPSGLRVASEGSHGETATVG

VWIGAGSRYENAENNGAAHFLEHMSFKGTSKRTQQQLELEIENMGGHLNAYTSREQTVYY

AKVFKKDVPRAMDILSDILQNSKLDEAAIERERDVILREMEEVNKQQEEVVFDRLHETAF

MENGLGRTILGPMKNIRNLQKSDLQDYIAAHYTAPRIVIAGAGAVDHIQLVELAQKSFGT

LPTTPAVAPTLEPVRFVGSDVRVKDDSIPLAHVAIAFEGFSWTSEHSFPLLIMQTLLGSW

DRTSGAGMNMSSKLGQVVAEKELAHSYMSFNTCYQDTGLFGVYAVADKYKLNDLTWYTME

ALVRLVHKTTDEEVERAKTQLKANMLMQLDGTSPICEDIGRQMLTYGRRMSPAEIFTRID

AVDAAAVRNTADEVVNDKEHALAATGPIHELPDYNFIRRRSYWLRY

>contig37461 Frame-0R|Blast-glycosyltransferase [Phytophthora infestans T30-4](gb|EEY68934.1|) 3e-68

MLWNGAFAGIFGLMIYTPMITNRNTELLDKAASASAAFILPGAIVIIAQAFAPAMVTRSF

AAKFIREGESCYVGRNMAPPLRYQIKYITFWLILWALKAFVSYFILVRPLVLPSLAIYEM

DLEYGSDIVS

>contig38107 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68631.1|) 5e-79

MSKGCSKARFKIGGGRSFMLTETLQSAELAPIFDDAWTASRVWEASRFLAQRLALYASKP

NATFDVSAGQSVLELGSGCGLVGILAASLGADVLLTDQQMVLGLLQRNVEVNAVSEDEQA

RLQVAEFNWGSDQSLPRSKYNYILVSDCINPIYGQDSWRNLARSIHRFSDRTTVTYLAHE

SRGEDEAMVDFLAFSAEMLHSEHIDQQGRISL

>contig38349 Frame-1R

MDQIISVISDAGDKVAGAANDASKTFSNVVGDNKTTTKSGASPSSESDTLTSTCPSLSKK

QRMIGFVSCFVLGFLVTFGSTFALIVGADNGTKFGITYSFGNIISLCGSGFLVGPRQQVK

LMFKPIRRVAAFIYLTMIVVVLTLSIATPQLGLVVLLFVFIQCGAAIWYSASYIPYGRKS

ITT

>contig38644 Frame-1R

MKTLLKIIKALCVIVGVAAQSASGVLFCSSLNGPYCDALDAGFVEAPPHARQNLDVDAE

>contig39140 Frame-2R

MPILNVEFDRLRVLRFYFALNFKRFWQFNVAVDCQKFYSILTGDGERVYLWVMLTVSRTH

NQR

>contig39834 Frame-2F

MELNSFSSAVKRSRLRHSMPSRNLVTPLYSFCSYWEMVLMMAAGEMPNHLLKLTGENIDS

AGKLIKKLVETWKFYCHQLAGFATKHLLCNMAGDFFRSIQSPSSPEISSLVVSPRELASP

SQIRITSSPRAFFVNGIGSSPSSRPKNRRHLLKCDCETCPWLLLVELFTDKHELLLRLNT

LLKYCNDNIEEDIRWGRLPEPASRKVALPRSQKLVLSPVALNSPSFSRAAKFADRSKRRT

MSIPTAAAVHVQCLYRSETTIRAMCFNRAAAKELEVSVCSGKGISRASFIDGADNCHLQF

KGMYAPPKDLFFSSTLLQSSPVKEWQDPSAECSSNASPLRSLAARNIPSPLQNSAQLLAS

PSEASFKPTAMASHPYLPLFV

>contig39948 Frame-0F|Blast-2-oxoglutarate dehydrogenase E1 component, putative [Phytophthora infestans T30-4](gb|EEY57954.1|) 2e-54

MLRAHVFETFLAKKFASFKRYSSEGAESMLPAVETILQACSTANVSDVVLGMPHRGRLAL

LVSSLDYPAHKVFHKVRGNSDFPATFRGIDDVSSHIATSCDKQYGQSNVHVSLIPNPSH

>contig40247 Frame-2F

MNIHMEEGQRRRQVPLNLCTSTCVFCLNPLLGHVNAFSSIPENHVAITCRRCTHFLLAIN

GTIGAIAWIKTSFGTRTKPCIRRLVTEGHEFSTFPESIVFTLALYGTLVVFLTLENPRIH

RIAFACNAKRTDFQVVRGQWGFVPVCVQIPSCWHMFKSNECTTSNGLSHVTHVGSFSFFD

KPETIYVIPCHVRRDRLLSTTRTIRDFMGMKTKTTSIMHKFNGAPTRHVLESMGVLKVCG

RILTTRFFTREFMVITTNFTHATAILALTEAGTSGRNALGTRSVAIWLSYAMGVTIGCGT

PLDTVGRSRVGG

>contig40320 Frame-2F|Blast-glycosyltransferase [Phytophthora infestans T30-4](gb|EEY68934.1|) 0.0

MLRFVVVWNEIVNSFREGDLVDDKEAAILQYDIQGSGDVFEPVFLSAGKLVEALDYTIKL

AKEGKGDSQLQVYMVQKDCLSAVRSFFTASMYVMEALLGSDDADILDALRQMEAIAANGS

FMSTFDAKSLVQLRTVSMEFLEAVMDLPDPDAQSSQLTTSRVHTMGVVRNFVAKMENLLN

TIRIFANRPELAAKFSNSKFCSSANGYVFAARGLVNLFHNDTAMGAATRAYLLMSLEKAD

AMPRVPEAQRRLGFFMKSLLMDIPQLTSVKEMHSFSVVTPFYSESVLISLSELNDPLANH

PVFQKVEEKGKNITILKYLLTIHPEEWENFLERIDVSSAEEAQANYPLEIRLWASYRGQT

LARTVQGMMLYEDAIKILHWLEIGSSPGKSAEQKQAQLEDMVRLKFSYICACQVYGKHRA

EGKAQADDIDYLLKTYPNLRVAYVDTIVTEEGKQFDTVLIKSECNEIAEVYRYELPGDPI

LGEGKPENQNNALPFTRGEFLQTIDMNQQHYFEECLKMPQLLVTADLHPSKKPVSIIGMR

EHIFTGNASSLSKFKSWQELVFVTLSQRVLADPLYVRMHYGHPDIFDKIIALPRGGVSK

>contig40632 Frame-1R

MNLSMQSSPRLFVSMFRERYKANNFEFWDAVAAIKSNCKSRPIVIIRPLTIASSCSHWRR

IETYCARSPKWSIRTTSSSTAAMTASKFLIGRNYDEVLLNTKSCVITCTFFSF

>contig40997 Frame-2R|Blast-tyrosyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY64400.1|) 6e-49

MIHGRAALKSALNATELLYRVKKDTLSAEDMLRMARDTPTITLFRTEVVDHTLVDLAVRI

GAATSKAEFRRLINGGGVYLNSKRVECEKLRVESLHLFDDKLLMLRIGRRKNFIVQVE

>contig41338 Frame-2F

MAHEGESAAYSHYSNGTLTCKRSLVPAKRSVTSTVDLTCHHSQRLPQSRKWNILVSSTFA

SSKIYSILLSSKSADCGVTITDSLHVDVLLSVRTAVLFLTSQQVHALKNTPPNQNEKSGL

LFRLTLAMHKKVIVAVVHTGEKSEIQRILPFPNVTVIVQDCIDALCSQLHQIAHEDLVEG

YEFPSLCLGPLSDQVPRALDENFAPRLEFFRSIPALSLDSALNLSFRFKNFSVTQVPVHK

FNEMHWRRMLPWISEASAVEIQKYVQNIRR

>contig41716 Frame-0F

MSSSFITSATNCFPSNFLFGATVSSLHVPGVSVLETTDFCHAPSKLRLDNELFESMQQMS

DMRLSNFHFSITWSRVMQWDHESERMVSNPSGVAHYHSLLDHLQANKLQALVTLDSFHLP

LKLQTHWDRTGWQNPDIVTHIDDFMTLAFQEYGQKVKYWATFHDPLSFITHDYDSCGAIL

EPNETSAYIIAHNVLRAHARAVALFRDFKHSENSVIDTDARIGIELSAEYGRSPSQLNVS

NLAAIERKMQFDLGWFWMPLVSGDYPEIMRHRVGERLPRFTPEESVLVKGSYDILLLKPQ

PSREVIDCDIKSSEGLCRELPPGHTRDRGIDSRALASELECFTLADDYLASIRWLHTKDV

NAEILLTGNWWEDDRLSNGKQLWCYQAYVKQVHNAVVKEQIPILGFMALPFLKDSDCGTY

SSRVDLHYRNDMDESSFEHACLHLSKYFAKLATAKCMTAELIIEPIQVTLKNQNETGASR

DNAFASDASNDGKMKVPWSLGEVMLLVVVGLIVLSAITCEAIRELHQTSRGSFEELRVLV

TIEE

>contig42177 Frame-1R

MESHRKRRRQMEKKLIIWDDEDRETIILKDIEENDTEDGKEATRLLQELSKTDAIMESNV

LAVINGFLRAHTESNGPEILVEKLSSSYRGHAQMIGLVASWLDSLPGSATALEKKMTFDV

NEGAVVANSGASWDPAEEILYSHLNDIISENYDPKLVSNVLSGSTVEPQWLTQMLHDQKW

RLMLIELAETHKTCTLLQYAIRRISEAG

>contig42414 Frame-0F

MKQLLHGGLDLPALLFVQNKERANELYHELMYDGVNIGAIHADRTKEQRDDAIRRFRIGE

VWILICTDLMSRGMDFKAVNMVINYDFPQSAVSYIHRIGRTGRNGRHGKAITFFTEDDMV

YLRSIANVMKISGCDVPEWMLSLKKASVIKRKELLRAPPLRHRINTVSGYDLQKANRRKQ

MKLVKCKKGSGSQSETRFSGD

>contig42627 Frame-1F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY64164.1|) 2e-10

MRDIKTKRRQWTWDYIKERREDRKRYIKLWHHKSRQLLELLNVDYTFYDSDDNDVDTSEH

GSATNNDVSSFTYSNLSV

>contig42780 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55956.1|) 8e-56

MQNFFIQNFLHESESIKTFRTALRRTSMLRHCLIAMYQSDTSNREKCSIRDGKGIVAQRW

STAVTRVMQQKIQQRRRCSIDGYPEITNPSIVSVVQNEIAIIDSWNFDVFAIAAAVPAES

LCIIGNALLDKYDISCHFQTTKLRVQSFLRQVQRRYHAHPYHNAEHAADVTQTLHHFLSV

GA

>contig43066 Frame-2F

MTSFRIRYKQTNWGDDNSFDELLPRSSCPYSWDYLNGVEGKPSSASSHDPSFPGTSSSCS

RSLQVRFMRVTSSTSHSGEDLDKDAVEVREFNLDEMTSHKRIQLHRSLPSELFLKPEQKG

YLLKKDSMLKWNRKYFRLYEHVLYYFSNESDQELLGVVNLRTGSDVPGVGGVAIFEKTAE

VPLKSGFISLNGFVSSISGSLFGGGSRQLDGGGDDDDEEDDRARELLRLAVSLVDSTLLC

KKSEYFVSTLIKNDAGVKSGNMRPGFYVNSEDLVEYLTTEMCKLTRAQALTTAQEMMQIG

ILKTIQISSGIGARRQAPMRKFQCSKSVWYSVDSINIADESDVDLEDTTSMTTPRDLSEV

SCKSGAKLPIVRSNQFTIITPTKCYDLKAKNSKIAKIWVRRLRLATIDVQNDDSKEALPV

ETPNIGAALSTLRSHRDIAPPIQNAKTFVHVRIRADGPTKVLELSEGGEEDFDEKDNKYE

ASVSASVTSDSPTACEISTTSAFVTLTRGVTLHLCLDGVGVSCVNEFPTELVYIYLGGIN

LHYSRINSNMRMSITLDDLQIDNQSEEATFTKLLCPRGMDIGGVAAATFKRRRQLGDIDE

SLAEMEKSDLEFANERNDDEFKENTGLISNQTVFICADCKYRQANVAAMHFCCTWSIEQG

NTEYFKHCSFWLYPVTTQLDEELLASLRAFMAAVWL

>contig43729 Frame-0F

MTTPGAKSSESEQPATPGNTNARAAAEPGLPQIYPKPVTILVIGMAGSGKTTLMQRLTAY

GVDAGLRNYVINLDPAVRKTGYTANVDIRDTVDYKKVMSEYGLGPNGAIMTSLNLFATRF

DQVVDLLAKRSSNLDYAIVDTPGQIEAFTWSASGQIITESLASTFPSIIVYVVDTPRTAN

PNTFMSNMLYACSILYKLKLPFVVVFNKIDVLRHDFAIEWMTDFEAFQTALDDVQDDNYM

GSLSRSLSLVLEEFYNNLTCVGVSAATGEGIPEFFAAVDQAAIQYEKECLPDLLDRIKRQ

QSKKYAHEEASLSSVMQDMEISSQRDENTPFDRSADSNVAGERTDL

>contig44773 Frame-2F

MVDRMVSEEERALRLELQDLTKKRQALNTSRRQGSAVLGGGLAGRRSVLSRLGGVPTRTG

GGTDRNAVRQKENNSRGNASWRRGKRNHEDNYQITTFKKQKLHSAVAKPEVADDAEERAE

ASRTSTVVVVPAATNTRTQERKQRAVAPYAQKDGIARSKRMFGALMGHLGKAKRQIEKDT

HLFKRQDTKQQEAEQREKLQSLNLEKQARFEAEIGKLKALIARTELDRSEQIARAKLEHL

QTLRKSENQSKFLVTIASPPIYYLPAKHTKETKELVAASMEAYDAKMKASIQAHEEKLRK

LEAEHATKLESLRDQLNNAQQEKKAAGTQVIDGKGEETLSDREEEMEQRSKEPETTKDEM

SDASSQNSRMKAHDENSTPDNDIRDIVADDDLNNLRSDDGKKNDTSESMLEEERNSFSKT

TGKTYSVAQMEGQEQPSSRKQVFSVDTQSDDVAKNATTEDITLETDCEAKAPERILPEMD

AFVAKMKVAELRVELRKRGLDSKGLKVILVQRLQEAMHNE

>contig44926 Frame-1F

MNSCGSVGNPTSVGKTTSTWLSIANCCSNNASRKFTPQRARFSMARSTIQAWSSRGFQWF

RDQLVE

>contig44993 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66398.1|) 2e-21

MAMASLCNYEGSTVIHVGELFGQTICLPNPWGRTSSEEFQIHLATVYHKVLQVPLPSWHS

SIDTLTVWKRTQSSINNGAMYAFIPEDERIDLVAASPSLRHLLLVDKVNVESDMTLESNK

RQRDNSKAKQA

>contig45176 Frame-0F|Blast-phosphatidylinositol kinase (PIK-L3) [Phytophthora infestans T30-4](gb|EEY66032.1|) 2e-60

MNVEVVRQKLADGDPDAVLKELLDLYRRAEILHTPQLSRILEVLFPVWKGLLQSKLPPQL

RATTRNRCRKVLLQILNRLPSNEALRPYVTQLLQLLMEVLQKDNEDNALIALKTLFDLHR

NYRPG

>contig45594 Frame-0R

MSSSHRRRYRSPSRRRSRSRSRNRSRSRPPHRRSRRRLSLSRSQCSPSRSRSPHRGHHEP

SRLHGNREPMGRYGPSIDLSVSRGRSGRFRKSYGYNGQNDDDFFEERKQQREAIDFSIWA

GIPSPPSVKKRMKRIAKVKLTPSVSPSRPNVSDESRADSSSESSITRIGEERRRCKSKSK

KKSKSKSKHQGKHKNRSKSNNKKR

>contig46058 Frame-0F

MRFCTDAFTRGGKRKHRNQNFNQPRLPQKIPTNSQKEDASGKGSHQLPFVGRMSNKLIAM

ADEMIDKILEAERERSWTTYAYQKAKCEVAAIASLTDDEIEQWLQVNRVQQAPTQNGSER

HKTLKRKRPGSLPLSSNGQCSSIRNRKVQGSRAKAPNSKLNLQERTQYVELRCYKMKSLQ

HRLPFGSAQDTTLSSRLQHIMNILLQNELALAFSAPVNVDEVPGYAEVIKHPKDLGTIKF

QLSRGFYNQRFELLVQDIDLVWENCFKFNRIDADISKCANRLRSIFDRLFEQWISEVKPD

TPLSHLASEESCRQCGQMSAQDRMLLCDSCDAAYHAFCLQPPLSTIPPDQFE

>contig46407 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62977.1|) 2e-30

MLKYQKWLAAFAVLLTLWLLLLQYASDQAKDPHMLQVVMALPIYALLSYGAYSLAVIAFS

VMAVQDFPEAAKELENQVVEARADLIKKGF

>contig47332 Frame-2F

MMRQAASEWHRSETIDSQRGQILCRAFANSYGSAHMYVSHEIIAHLLFGKPRSISLLLDE

LCPTLLQTQTDLIRYSHCEV

>contig47453 Frame-1F

MIYFTIITIMTSPSHRDQLRILNNSLVRGSLSRQEFDELLPFVQSPSSIIYATRPQERQT

IVVSSSPGRHYNQQRNVRF

>contig47747 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68606.1|) 4e-06

MPGERVIDREKHCPFLLRAFFSKGAHN

>contig48045 Frame-0R

MLPATRSFMRLPRVVFLSIVYPKGVSSELVLFNRLEFKQSLRRRIEPISSRNNHPVPHSV

IAERFYRVTATLHEAYYPPLPRTLHQRPYIT

>contig48715 Frame-0F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72292.1|) 2e-36

MVRITEAHSNVTLLDAKEMLRREYDTLQKRDKKAAAFKAHAQPNVNRRFQGNRGHQGRQG

DNDRNQAFRRRNDNARFRGKCFACGRHGHKSSQCHNVKQSRSGNEFVFSASSEKLESSAT

WLLDSGASRHMTDDERDFVEYENLTTPISITVANGQHLMAKETGSVRFILENGRTVKLKE

VLHVP

>contig48838 Frame-0R

MYQETEGLTAHLKNGNSNEIYNSMQCLQPSFRQCRMVIEGAQPESGRANSTNADDTENNS

AKLDLLGLSKRLSPSLNSINASYSFLSKKGIKEVYSNQCYQISRATIASSRSYSPRCFLS

TFFHIGDDDFFSESKATSSFSMASRALEVRSRPF

>contig49099 Frame-0F

MEAEGIERVTVCKLSLVKTRDKALGEQLFDQSCPFFLMPLVFTVRSLTFCSGDLGGQERV

VRPPATTASTCLMLKIYVFIESVALYAFACIGEI

>contig49330 Frame-2R

MRLLKVMDNPFNAQLVFASPAQSSQHQALRCKIVLQLR

>contig49460 Frame-0F

MFQFVGRILGKALYEGIVVQPKLAHFFL

>contig49587 Frame-1F

MCRIVGKFGAKIRAPGNPSVGRGQSLYKQETLSVRTHGPRCMQASWHLLFDT

>contig49914 Frame-0R

MAKIFSHKTCLEVAELCASYGLTDR

>contig49961 Frame-2F

MATSKYDTLLVELISTSMDYSTEKEGIKRRKVMSTEVFETPELEATFQPYTLAHGPFLGP

HGSSAAGPEADSGFHDKSSMELDKQELPVAQAFEAFMGKIYKPNLPKQTEYESSSNRSSQ

KSILESPLARFTRLSIEMKELETDLTLLATDAEHKKQRLMVDAGQEAELTEVMQGLHTLQ

LNLSALEQNKAFQPFLGTQTRNADTAVALQKDLTAKFFKQIDVLKRRQEGIKADRLSDNA

SIIYEIYSNGELNAVDQDAKTRVATLEARISTLERAIGSFQGQELRLDGLNALSVASSAN

LTSSVAELEQRVALMSQKNLDAVKTRTTALIHEFTLLSKLKQSPSVQGALNSQADREQIQ

KIYDQLSSLDAVAASVPTIVDRLVTLKTVHDEALDVTTRVDKLEQTQASIHELLSSDNVL

LANMEASLAENVQIFQSNIQQLDERMAKLLFPSS

>contig50462 Frame-2F

MEQTMKRAHSSGHSSGYGKECHRSYSLRSADSASAADLTLLLPEPEGETQIDQLQQA

>contig50585 Frame-1F

MPAVRYIPPELAYIREQSRSTIQRLLSSYVRRKRAYPMYHPRQLLVRCHLGFGSSSALRS

YHRHSPRT

>contig50606 Frame-0F|Blast-pyruvate dehydrogenase kinase-like protein [Phytophthora infestans T30-4](gb|EEY57776.1|) 3e-11

MHRLTSRALLRREALSLHARDACNDNMTQKIHELAQLPQTGVSLQYLLEFGTNISSQKLI

QSAR

>contig51458 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61205.1|) 1e-59

MQHSTQKQVLATIKTCVRNPSVTTIRPIGALCLHAHYPKLGHKTLVAYLTTSAETGLPIA

DGQASHPYCASLARKTNMTTGYNLLELKGEMLGINPNAISGLITKYLSNMSAELIVVTCR

AKATSVDIYNKAMENLTIASLLPP

>contig51555 Frame-2R|Blast-hypothetical protein PITG\_18705 [Phytophthora infestans T30-4](gb|EEY68804.1|) 1e-19 NOT\_ORF

MTEYNGIPALEHGDTVRHLR\*AVGTGPLTDANWAARMLNSSYLLRHNSQPLWRPGYYF

>contig51744 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69842.1|) 1e-65

MCQLCGGDSFKFAPCMLFCSGPCAGRIRRHTHYYSDPRGEHHWCSSCYKQMKDGPID

>contig52518 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63522.1|) 3e-49

MSVRLQVLGGYRRLLRASRQAFRGDTYALQQARKTLRENFLLSSHVSDKDQLFELIKGIE

EAEGMLLHHIVQGRAKHTEANNAQRFEVKLTDPQRQAMRKNEEITPLTESSASEPLVMNS

GNTCQRP

>contig52936 Frame-0R

MEKQTSFLLENDFNFFGINVDHLLEQLATRVGPVIDGNDTPDYDIVGMTNGDLKTMLAAF

DRSEFPQRQCAVAGSGREQSTETR

>contig53117 Frame-2F|Blast-deoxyribodipyrimidine photolyase, putative [Phytophthora infestans T30-4](gb|EEY59021.1|) 2e-24

MASVRRALEKLKLPAGLHCERIQWLCEGAAPQTKDRYLLYWMQTSVRTKHNYALEYAVAA

ANELKLP

>contig53733 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63806.1|) 2e-28

MVQYLVALGGLYNEEDNFFCGVSMMQRDPQGELIFMHRNQAKLTGRRDQKPLISHLQKFT

GGDGTMASLARDLDKYRVHCKMRQLGQYTCFMLDPRAPDGTSTPSLV

>contig54035 Frame-1F|Blast-conserved oligomeric Golgi complex subunit 8, putative [Phytophthora infestans T30-4](gb|EEY57934.1|) 9e-21

MMTSLKTCSLEDLKREPWRLQLQADNTAEQLRSLVVQNYHVFIQSNQCTAIVKNDLVELQ

>contig54233 Frame-1F

MRILKMTHAVGSECYSMFCDNMHIGFLFIRLAKRW

>contig54417 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67218.1|) 1e-133

MDKAATNGHLEMVKWLHFNRFRESWKACTREAMDGAARNGYIRVLQWLHKHRHEGCTVRA

MDDAAAQGYLVIVQWLHENRVEGCSQDAMNLAAANDHLDVLRWLHYNRREGCSMVAMNKA

AQRGHLRIVKWLHLHRNEGCTTNAMDNAAANGYIEIVKWLQQNRTEGCTMKAIDNAAAGG

HLDLIKWLQKHRKESSTSAAMDNAAANGWLQIVQWLHYHHIEGCTARAMDGAAGGGHFEV

ILFLFTKRTEGCTELAAENAARGGYLEILQWLYAHYVDQFDRDRVIAAADRDDFY

>contig54691 Frame-2R

MWLSSFAADASREQITVRARVWSLRSSVSIYPPPNVGKDAFILVITHDLSLLRRLRVVHS

SFVTLHFKERSHVARLCLPPRPVEASNATPKETSCADEKDCVILSPLLAFNLGIDLLTAT

HVELSIRAASLQELGLSVQPSAPFRRKHQEQPSAALYA

>contig55119 Frame-1F|Blast-F-box protein, putative [Phytophthora infestans T30-4](gb|EEY54251.1|) 1e-12

MQHERLRAKREILVLVERLNDCVSASARRMYTQHVLASALLQRPQSEIRRQLPELCTFID

SLTFKAT

>contig55308 Frame-2F

MAQVEVEEIRATVHSNTSQYLDDALRDQKTGHAEASDTASTFAPKTQTLTSSNQADAEID

SISEYSILNETK

>contig56060 Frame-1F|Blast-choline/ethanolamine kinase, putative [Phytophthora infestans T30-4](gb|EEY65348.1|) 1e-136

MSTLSVAPYLAAVTALGKVKLQLHVSVVSALRKCVPSWSDVEPDSVDVEHLGGAMTNLIF

AVHKPEGQHCDVLVRVYGEGTESFFSREEETRLFQLLSDKHIGVELLGQFSNGRVEKLIQ

GTTYTSKRMRLPHESRCIAKQLRIFHELDIDIDRRPTYITGIRKLLDVARVKCTSDAFKG

VVDFDQLAEDVDGLERILAKVPSPLVLSHNDLQYGNIMKNDTGDAVLIDFEYTSYNPRGY

DLGNHFCEWAYDYHKTVNPHLGDFTKYPTHEQQREFCRAYLAGKDGDEKE

>contig56877 Frame-0R

MKSLTFRVRRRPRIRKIMKLVCGGGGNKVSYRHVNEKVTINHVGSASSVSIKSSKGASTY

RNDVYSR

>contig56943-1 Frame-2R1

MSENFFAGFERPQIVVSSSVSSLSFDT

>contig57104 Frame-1R

MPLKPLKSWSLPWSQSSDIIEKATFDTMNVQSSAYRLLYFVVVYAALIMLTWTGASAAQT

SNASVHATPHLDWPSLKLHFTMKRNTMRIHSQSEFDVYANPIVSEDGFKVLYDGYVEFIE

GSTRTRYTLLGGVAYSTTSVQNRTLSAISQCLDPKGLPPFMDLLTATGGL

>contig57171 Frame-1R

MEKVTAVVVDDNLFDVYKSKDDDVTTFTYLSSKPLDHFCGNFMDFFKCLPEGSTSFPLYL

QSMSFGVEVYSGKDYFDATKLEVKIEKH

>contig57737 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63667.1|) 3e-54

MASETHLRSQYEVLLKENKLLKTSVDKLDHENHDLKRSVYELTLKLDSAHAPSSSTRAAA

AKPFAIADLLAAPVVNAESANESSFRRCNGSSGTLLGPKGDLYDGDGDGDTRVLVHKSTL

RAHSGAVYTA

>contig58479 Frame-0R

MENRRRGTVRRTNLHRRCRVVHTKLLACFILGVRNLRLIANIYPGLNTIAT

>contig58677 Frame-0F

MCDNKFHTEALGELMQDQDRFGFLVMDGNGALYGIVSGSNREILHKFSVDLPKKHGRGGQ

SALRFARLRMEKRHNYVRKVAEMATQLFITNDQPNVSNLVLAGSADFKNELNGSDLFDKR

LAAIVVKVVDVSYGGENGFNQAIELATETLTNVKFVQEKKLIVKYMEEIAQDSGKYCFGV

HDTMKALDLGAVETLILWEDLPYHRYTLRHEVSGMELIKILSPMEESIESNFVDPDSGAK

YETIDRVPLVEWFANNYKQFGTTLEFVTARSQEGSQFCQGFGGMGGILRWKVDFMEMDYE

FDEDDEFDEEA

>contig01711 Frame-0R

MSPAEFFDMADDAKDDEPKETEGPLEAERQFWKGLRGTMDPPTYGADIVSSLFGKADALS

WNLNNLNTILRKIDLPGVTQSMLYFGMWRAMFAFHTEDMDLYSINYLHTGKPKFWYGVPP

YAANQLERAAQSMFPEKHHECHQFLRHKTSLISPARLKEFGVPFYRAYQKPGEFVITFPA

TYHQGFNLGFNIAEAVNFATLYWISYGLKAKVCKCHPDSVRIDMDSFLKQLFQEPQCGFE

IMGKDPWVFSCKCNKYCSSNNSFVEVEEQWFECSECKIWAHVRCIHSDLAYTAAENLPLS

LLCHRCIAKTAGVKNRALSGVGVGRRGGTVVKSAICDNLGKRKKDTAIGSAKAVNKSAVE

LSPLKKTRAAIRSRNGGIIMPKSSTKIRAVARKYLTVKGSTIRFENSEAKVAAVEGKYIR

VHYKGESADNDEWLQVNSRKLSRGILSVEPPMSKSKDFSISRT

>contig02664 Frame-0R|Blast-ATP synthase subunit beta, putative [Phytophthora infestans T30-4](gb|EEY70035.1|) 2e-18

MVGGIDEVKTKAAALAAELDE

>contig04451 Frame-2F

MQQGGNDRQQGGYIQQQPQQQYAQQSGYDQQQYAQQAGYDQQNYTQQGGYDQQQYSQQGS

YDQFGQQQGPYDQYGQQGGYQPGMQSQEWDFHAMEAKDGVRFSWNSWPCTKLEQTRCVMP

IGCLYQPLKPIDGMPPAVEYDPIHCKACAAVLNPFCQVDFVSKLWVCPFCVTRNQFPPHY

AENITQENLPAELIPQYTTLEYELQNRQAGPSVFVFCIDTCLHEEELEELKDSIQQTLNQ

LPPDALIGLVTFGTMVHVHELGFPEVPKSHVFRGNKDFTAQQVHDLLGLAVTRRQQ

>contig08305 Frame-0F|Blast-phosphoribosylformylglycinamidine synthase [Phytophthora infestans T30-4](gb|EEY59422.1|) 1e-139

MASSPDKKQKTETTMASSSLLQFYRTPAFTAHGNRTLLAYLRAQVDGDTGVQVEELRTEY

CFYVETKVDTTPLSSSDEETLHWLLSETFEPQQTRANQSFLTVTEPSNEWLVEVGPRLNF

STAWSSNAVAICHACGLVSIKRIERATRYVVRYNATKPEALETLQRALLQRECDRMTQQV

YEKPLTSFWHGKTVKPVRKVPILERGMDALKEINDDIGLGFDDWDLQYYLTLFQEKLRRN

PTDVECFDMGQSNSEHSRHWFFGGKIVVDGNEMPQTLFEMVKGTLTESAQENSIIAF

>contig09016 Frame-0F|Blast-PREDICTED: hypothetical protein [Monodelphis domestica](ref|XP\_001373977.1|) 1e-11

MVRLVEYPESSDDEQSDDSNHNLSFDEIPSSTSAFFSCPMPSPKSDEDDEDYAPSMGDAS

SVTSSVDTDDLDPDNEFDEQQPERTKVDPKLNKLDGAVQDGDIDSNQQPSNGYYYAWKDL

QAAFSENPFKRRSVQKVEEVGTEKEAFKGNEPKAGEAANWLDVEAENQATFAPGVADTKS

RVRKWASTTHCRTNISPRFSTLFSEDKFSRDHRNSSFQTEISSMHPTIPALSATISTNQK

NDSTPFNFTFGAARLDSSRDHASMQSPNFQPCVDVPFVPIEKKSVPDNQDKAPFKPYKFA

EPGVFHAFSSNEQPVLPTDKVEMGTPLNSGNPGMKSANHTPRNGEFLFGQAYKHRNFSST

STFAPEFSIGSNVTIGDPVQGKDNEKKEANQAFAFFATGVAGPQNRSANRRNRKFGPSSA

FMSSSSGGASPLPMDTTSQKFSVSHSIFEKATRTFETPSSSASPSVFLFGGTKATQNVHA

NDSTSARFSNPTVFGPTGGKFEFQSTKASPFHEPDTSSVPTSTFGSNNPFVSSSTDTCGH

FMFGNGSSHRFFQSDKTATETPATNSQFHGLEKAEGSTNNAFQIGSADAKKTSRVRSRNN

GLLSHKRNQRKDGNLDSNEPEPSPVSTSSAFKTPSP

>contig09272 Frame-2R

MNPMTSMLAILVAFRSARAATPLIPTLDVLPRANLSARNDKVTRMNPKAIASTEIGDEER

FKWFKWFNSNNAHGTKIVNDVAKLFKGSSYPSHEVVVQAFKSVNSLEDRRDLMGQLVGKV

TKKIGLENFYLYLKGGEGTEFANELERGLYKSFGKVPVESSAKTFLLGKGTTTEEELFHK

PLLDAYVSYSRATFSKFEFYVAFSLLLEYDNKLAGMVKNAKKSAKSNRATIDIIEKGLNY

PIKEIRNMLEHDYVSKNPSDDAVMRGVIRYAEQYVQRNPSKLNHIEQLKLYYKPERIDEL

LPAVVPASPSKTFFARIRDWIWAKLRWMLRSNKVDSVARDDHKLRRQ

>contig10010 Frame-0F

MSIGSGPPFSCRLFGGLAPKWLETCFRLKPPRNPMWSMIGPNPAHVTNIVVSENIRESDA

LLYADWFHYFKMYWTDLEGVHRHSIFGNEDCIRLLRNTFSDIGVSVLFNSLKYPRIRKFC

RRFIGVFRFRHYDGRSSQHTYIFGQGQRFLQPSTASVASLLRGKRKQEFIQDQTRGIHFR

QFTNASCAVVQKSKPI

>contig10263 Frame-0R

MSTQRSRVQTSLIEKQQIQQTFRYPWDPGHR

>contig10906 Frame-1F

MLPSGHGHRARVAVDTRFVPLHRLQVEVFVIGTVEDEKGNSVMETLDRSGVSNKAAKAHG

VYIRIRIAEDLDPGIYELPLSVFTQDAGFQSEHLTWASTVAIRVVNVRLPTPTSWRFRLD

LWQHWTAVARGHRVPLWSDRHFELIDRYLVPLAEMGQKSLSLVVTEMPWAGQQCYMEKQN

ASALFEHAILNVYDDPTHKTPLTIDFTHFDRLLELGARHRVDQEIEVFGLLSVWQDASAG

FNAPAELTTSHIQAPSTTDPAPLSSERPSTSSSESGLVSPIADALVKTRATHEDHQSLSS

SFESPHPFVIDGWRIRCQDRTNQTVRYLHDVAEVESFIQQFYEHCKALGIAERVRICADE

PRDVAVFHEQLRFLERLAPKFRIKLAVDHAEFFSKSYTPPQVADYVPLLPLACADVEGTR

TLANDARARGGHVCWYVCCGPAFPNQFVSSPLVEGELVGYLTFFFELDGFLRWNYCLWPA

RPWDDLRWRAPMWKVGDMYFVLPGLDGWPVETLRLESLRFAGQAFELLALAKDTLPPAQM

QELQRTVAEQILRSSDLEEFGQCGDRAREDLYSLDPLDYQRARSIILDTLAAAMP

>contig11246 Frame-1R|Blast-Dual specificity protein phosphatase, putative [Ricinus communis]gb|EEF45324.1| Dual specificity protein phosphatase, putative [Ricinus communis](ref|XP\_002517161.1|) 2e-13

MGRSRSATIILAYLMARYNLTLTSALQELRRVRPQAQPNSGFYNELLIFEGKQKRLRE

>contig11516 Frame-1F

MQLTLFVIKDSSSWQGLCPMVLTFITISYARIMSKQSGIISKLRCQHVHKANSWTCDNVS

FSREHHMSQVDFMNVMTWIQLASESCGVQFGARWGVL

>contig12423 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56637.1|) 3e-85

MSLDFSKVENNPLPLIAEKYNENVAFVVYRNKNKNVVVYAANIREDGTLDPEKPLDVYWI

MFEQDGTPREDLNMIERNTAYGASVKPRAGHPGEYEVTLTSLKDRVVYLSLVDGKPVGRG

SINGQEGCTLERVYVLSTSSWGMPKVQHIEIHGKDAAGNAIMEKKLP

>contig12805 Frame-1F

MDYRDRTYKGESTGDIRGFPRNHVEFDQNGHHGLQELDETDVTRTRAYQMGYDVEARYSQ

AQLQRYQQQRQYTNRLLETESSYRRLPSPSHESEFYPPDMRDHEPLDNLTMDLSRRIPRN

FPGVTSPSGSLDLLHSMRTPQARVVPTRRYTNPDELPLEPGILEMYPDNLTSSLFMEGPM

SRRREFVQPSPFVRHRGDESVIRRQPRATQDMMMTNRRLSYDSEVSYDRQSSETHATYDN

LNPSSSHRASLVNYRTRKFGKYSTYHTAASFGCSRPWTIFKATTPRRVVVINIFACQLCA

FSINGER

>contig13204 Frame-0F

MSCNFTSHFHMLRIKRHLRAPPGHSQRWRQSQTANFTLPALNTATSHSSKLKFNTDTGKN

GEETPKYKPGWFSRNPGVTLGGILLGIGLYIYRGSRGKKNFEKLQDKIAEAAVISPYEAW

ELRSSNNITCKNFEDVRDGVKKAFPSSKASMQHFDQYLSYKLTQVCPTGVSKGYHLERVL

LCLEMDGDQKSDVDAQMVAFSMAVKGTVDERLRMLFNLATDAPPGEALSSCEEMEESNTR

EIPSEKLERLLHLLLNTYQIPSEKRVLAKEDVKYPFQEYIVATPTNMLKAAVEAQIKDKK

IAEKEGRNRQSYTFEDFSQIMRGNTVCIWGECFSNSKKKMKN

>contig14443 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61036.1|) 1e-06

MKTLEECSKTKFHDLMSFSSPPQVPCTVARQPHVALMSLNEEGYGSIDMG

>contig15776-0 Frame-1F0

MSSILASLDMSLDDLIARKKTKVSNPASRPARSNKPKDSAGPVRSGNRRNRSRNQPYVRP

>contig16179 Frame-1F

MVTQIQDTFQKNLMELDWLDEPTRKAAIDKLNNITNHIGHSTQDETFPFQLRRNASFVAN

LQLLSNYELEKYMGRIGTSIDRDEWSVSSAVVNAFYLPRANRIVLPDGILQVPFFAHDRH

FASNFGSIGCIIGHELTHGFDSSGRQYAGDGNLRDWWSNVTTNEFLKRSEGFQTQYNRYE

VRSQTGSNKVLGTMNGNLTLRENIADNGGVKIAFAAYQKYRTDNARQDVWSTMNQAERNM

SITVADRLFFISFAQTFCSKRTDTIITNQLASGTHAIEQWRINGVASNMQEFANVFSCPL

DSAMNPKTKHQLW

>contig18115 Frame-0F|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY60824.1|) 0.0

MRRLTSIRPRNCRPKALSKIQLLPILAHDIYSEWILDGASWYFSGKLFQKYASLCLMAAD

NAVVNGDKRLLQYCLDKLEELISPFIFNSFSEPLVYETTYKGIVTNLVFSSKNIQVDFGN

GVYNDHHYHYGYWVTASAILKKLDPLWSGMAQLDTMVWTMLRDVANPSAEDTYFPKFRYF

SWFLGHSYSHGVTAMADGKDQESTSEDVNFYYGMKLWGQVSGNKAVEDLGSLMLRLNARA

VRTYFLMTSGNTIHPRQFVPNHVTGIFFDNKADYATWFSAEKYCIHGIQMIPVSPINGLV

RSTAFIKEEWDDILSKETIVTTGDISNPWLSLLLVNQAVIDKNDALKKLAVAKMDDGLSR

SWALYNAASYLPHTTTSYIEAEIDATGDTQLIDF

>contig19350 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69224.1|) 6e-90

MELMTGFTDQAKGPMQKRELAKFIHDTIRPQLAELSIKLDTIREHENEVLKNMIRDREEQ

FEEFIAKQKLYKKQTADAQDTVNRQLADVAKLQALRKEALVGAINDLTEMHTMATEQKEL

LEEAAFVSVQLPEQKVIEATAQEKKVTELQGYLVKQGGGGNVLNPLGRKNWKQRYFILNG

PNLIYAKSKDDYERGKIIKELCLT

>contig19628 Frame-2R

MFQNEKDQIATAVVLLDRSFISSSENARFPYSLSLGDARLLSSLRPDMKAALDDAIPALT

SMLEKHGKQPAKDFSFTVNEPPKIVPGPIPGVATTG

>contig20714 Frame-0R|Blast-mitochondrial 2-oxoglutarate/malate carrier protein, putative [Phytophthora infestans T30-4](gb|EEY67662.1|) 3e-15

MAVTVPLQWNSTATPRPPLASYTFGGVAAVGAVFFTHPFDLLKVHLQTSKKDNLKLG

>contig21380 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61165.1|) 4e-99

MVSSAAKNINSTYEPTVYTLLLTGMCLLLALFLLTRLVVALNNKNKLLAWSTGFYLLCLL

WTVVRAAYWIIMTTQSSLRYLTLYLLYWSPTPIQFANFSLLILFYIQVLTGPAWRSKWRN

VCLPFYLLLTMTMTTFTVVWAFNSSNDISKAARQGDEYDQEFLKVADISVQLKYSAVSFF

LLSVLFGFFGWKMANVENWKRRRLLISKP

>contig22309 Frame-0F

MALSASLGQARWVVFYFFNFLPSPLSRGQACIEGMETVQPGNGVFFSIRTSRIYESSKYS

GGCRS

>contig23081 Frame-0F|Blast-dimethyladenosine transferase [Phytophthora infestans T30-4](gb|EEY54413.1|) 2e-07

MKKKVEEVLAIEGYGAKRGAKMDQDDFL

>contig23625 Frame-2R

MATGPKKVMESSSEDQINAISSSAQEKASTVFHKPLMSKSKRKRVKKVITADFPPLKTAQ

TLSNVKVASASLTSAKMVVQTPSAASVKPHVVSLTGVKKKKRKLITVVLKEEKVVHRTVT

DDFISNGPILEATESPAVTKKRKKIAVLSHVSASPAAGIKPTTTSAVEPFHLDSKKTERS

LKNTTKKAVTAHETTSPRKSVKKVKIVASSLTTASLNDASQANVKKLKANTQLKQQEMQQ

FQELQTKASDAKAHVPGSDEAETLASDAKESMQNTENLNLELPLRLHTASPMISKPQPIT

FSSTKRDKSKTDHGTSATILTSTTELILPKVSNSTILPNHGSKRRLSIEHAFGTTSDETL

QPSPKRIAISNIRSDGIDDVVPESNTPDMSDVKTNESHVLAKGEAMITTPTKYSSTQISQ

ATTYEFDHALPVNQPFHANPLEDKASMTLTPEKKVNSEESTIANVKELQTAVEFTSASPK

KSSPSFANKDVFEKVEAAKKVGFSLNSQTCVEKMTMDAGDPNILRSCKSSDSIQATTSTP

MCPQESWGASFGMALPSEHSSTGLREVSTTPLSSWFLSKGCA

>contig23690 Frame-2R

MGSAAPEHHVLLPSYSPSVARARLLGHDSAPAWPATFEEGIDVRMASPAAMSLTPSHVSS

FHFSPYAERQRLLQQPREATWSPARSTGAVTPVGTSSFKAAVFNAINVLLGVGVLSSPFS

MRSSGWLMGGSLFLFFTVVTNHTAKLLGQCLRYQEGMTTYPDIGEAAFGTQGRVIIGIIF

FAELFTACAMFYVL

>contig24224 Frame-1F

MERNVDVTKAILQLLWSIQMHCSIANIRLSRSLRDFFQEGLRSEFGDPLRKAFLDECIEG

IKKSCSLSSPAPDSVASQSSTINPAAPCSSSLSTSLTSAALSKKASTASKSLELLKFLID

SYRIDQGVVVESLNLEHGLVSLLFDELATFVGRSNDKQSPSYRTAIGHRLELIHYVHVKS

LKLELSIPQIERLWSVLSSSPAEREFCLIFFNQASMRQGGISPGVSTVGGSISSAFNLDV

CFYVFNELLCKQTDFRTLGCMGYKCFNTFFVGLNTQHKMMRGDSDLSSSSFSQLLGVDAL

WRIAFEAPLEVAEMATGELLRVYEQLSNEQVINNSNSDEGVKDFLARVFKQLSTVEESTQ

DSLKLVQQCSSLLTGLVSSSRKKQDFVSHGLSGRGAYFTIRIVAQKIPLSNASGAGVSAT

VTSSHENAVRTMQASAYSNQTLWHFRKQIESLVGHPMQQTKILSLGSAITGDHKTLAELQ

ITEASELRVLLFKTVVQRCRSSGMDQDQVFISGKESLSTNSSFSTVYHPGPLIARNASYF

EILFRVLDIVEGHSVHEMLWAFLKQIPTSENLLKHVSNIGAIGMTDGDSSMKSVSECSNG

ESSTLDWSSLMKDISSHQAVYTLQIMDALLLPSDVTKIPFAQTYHERFVYGGGFHEVLSY

FINTNFHASSFNEGAAVALRILKFCLFDSGHDSKHNLHSTNVQAPADIYCQSVSEFKFGE

NVKTIKSKIIVEQSCYDQLVLKIAELVVSEYARVQATASANSSTYRILIDAVKTVESIVS

IANDASTKFIKALEPRSIIVDIFTKFESHQVRDQWLSSLESVCKSSDAAAEVVYEECIQS

INRIENVTTSCDQYTRMICSLARLKRGNLSFYCQKLAQAIVAKLRLGFSSKFLACNERSS

EVLVGFLEFLCEVLAVHADVRAEIASDIVDVVYEECLFTLPSEDRRRCPLCVSVDTRRPA

FKLLASAITSDISVLHDLRDRLTKLFTRNDSLRFKWGQENNIDTRGNGEHVGLKNQGCSC

YMNSFLQQLFMHPILRQGLLGAKVAPRPVPQEPSKAEAEKFPERLIGCRVAVECLGGRVY

EANVVGYDVLTGQHTMRYENGGEVTYTLAEGRPGNENGRYVILKPELTGTDATLEVLRQL

QRTFCYLRDTEMRYFNPKAFVDSCTCLNLEFSVYQQNDATEFCDKLLDRLETGLKTTPQG

TRCLQDVLGGKLISQKLPKDCGHRYEREEPFIRLELQIRGKESIEESLSAFVEGELMDGD

NKVECELCATKKAAVRRTCFGSLPSLLILHLKRFDLDYTTFETVKLNNRCSFPMHLSMRP

YSKAGIEEHEARSNLQHEREETPVDEDMASDDSSDSDEFMADVNGDTQAKKSLSSALLEP

IGKVAAPSQSETDRRGVEG

>contig24383 Frame-1F|Blast-Type II (General) Secretory Pathway (IISP) Family [Phytophthora infestans T30-4](gb|EEY67050.1|) 2e-08

MSDINSLVLQPLNHFFKNSLHLIKKCNKPDR

>contig24440 Frame-2F

MSHFTLTPITADDVATEADRDSSDPTDNSESESVHASTLSGKRNSFGGWKLALVVVAAVC

VVLISVYFGHKRYVRNAMANKRDRGSSEQRALDSFFRQNRVTVARDTGVSSNHSVPDPPT

PRSQIVVTMPFNTSHTSDYMVDSSSHVSNRRSRQSIYESTSAPTKTTLNNEYKSYARSSS

PFRLDSSYVYASKPLYSDVGEESILLTDKTKSLLQCPSRDETVAHMHERASVASSIEEPR

DPYRFSSQFSVFDSSSAMSVDSDTYRLSTPVPDAPRATSLPKSESNHSYPSNGRMSDTRS

QISFDERFPSERSRTDSLGTDLSVTDSFVTIDSFLSVNSYASETIQDTDDGRDSDSFVRR

ENEF

>contig24901-0 Frame-1F0

MNILAPLQLFCRQQMRPLVFMQMYMLCKMLR

>contig24901-1 Frame-2R1

MKTNGLICCLQNNCRGARMFMELSAE

>contig25087-0 Frame-1F0

MLCLVVYIELSVTDCPRATKKSAHSVCSS

>contig25173 Frame-1F|Blast-60S ribosomal protein L7a-2 [Phytophthora infestans T30-4](gb|EEY65946.1|) 1e-111

MGLKTQKKLELREKAVAAEAAKKAQY

>contig25241 Frame-0F

MQSTFVGQLSGYGATPSLVSKVLDRLNVKERIDLTTWGEAEVHLLVSAFMEVRFPTILVL

NKADQGDDTDQNIENLVEKYGNDRCFVASAAAECFLKAANKQRYIRYDPGSMFYSTLEDD

KNDQAKADATILKPIPTKIRNRLERISDMVLFRFGSSGVRAAINAAVELADVVVAYPVKS

LKTFATDTTPGIANKGVFADAIIVKRNSTIMELAFRISQFLGSNFAFAEGEDGRRRADND

LIT

>contig25511 Frame-0R

MADEVLHVKVRPKHRPHLYSDTYSDSSVKVSFPSRTIYHGIQTSAPTHFGNDGDCSFKDA

SSSPPPANFIRKDPVSSSLGITHGATAAQRQVHERLHCKSGGVVALLEGSMKRRKGNSGM

NGSSGSSIQLSPVPISTN

>contig26338 Frame-2F

MAFSSCRFSEKFRCLLERSPRTMMAAPSSPLLSSTHRQISSKASVNINSNLRRNSLVSDH

DDMMLLREKLTRIAVGRHYNASNVADGTATNQEKEEKGYGRKSGAGNEHFKVFSLQRSER

PNTPPSSPQPRDVLRKQLYLKQHTRRDETGRRLLVTEDKELVMSVDEVEITAMDVAEEDN

YAVLSPPRVRGYTRAQLSIPGHLRFIPPISGLTKFPEGLRKRKSVTSNGENEQRASLKKT

SSQINILAHLADTLSRPSSATGAQRMFETRLDQDQDMKEASGCTTQPQSPQEAVFKSKHE

QLSAYS

>contig26468 Frame-2F|Blast-voltage-dependent anion-selective channel protein, putative [Phytophthora infestans T30-4](gb|EEY58505.1|) 1e-132

MVALFKDLSKTAENILRDDYDFSRKLKIKSTASNGVSFTTEGALNANKTIMAKFTGGFTH

SASGVVFKKLQVNTQGRIATEADLPNVLTEGLKLTFKLEDGSVAKNTSAKQVGVLGAEYK

HHNVAIDSEVDFVSNTVSAAAVLSQKGFAAGGQAAFNLDKSSVVQHNVGVSYTGADYETT

LVTKKNFAALQASFHHHLSHHTVYAATLDYDLKSASNSLVVGGRYKVDTNTTYCGKINSE

GFLSLASILRVRPHVTLTTCVHVDAKNFEGDSHKFGLGLTLG

>contig26482 Frame-0F|Blast-ribosomal protein L27 [Phytophthora infestans]gb|EEY53168.1| ribosomal protein L27 [Phytophthora infestans T30-4](gb|AAY43423.1|) 1e-81

MPSRFSKNRKKRGHVSAGHGRVGKHRKHPGGRGNAGGQHHHRILMDKFHPGYFGKVGMRH

FHLLRNRTHCPTVNVERLWTLVSEKTKEQAEKAKDGKAPVIDVTKAGFFKVLGKGRLPEL

PIIVKAKYFSAEAEKKIKAAGGACLLTA

>contig26626 Frame-1F

MAEFEKNALQQEQQVVHGRYHMLASELQRRERSVFENAVVEGDSPKMFCSQLVAELYQQV

GLLLPYPSAKSYLPKHFSDGNNYLNLQHGASFLPEISIRKNLQHESEQYAIRRQEALDRG

PQVGNETATIINCLRRHQLFHSLSESELLATASHFRRRVLTPGENVFYQGATGDNFYIIE

SGHCNVYIDYNHPSQICSKPTQWNTNKAPPPATILPNQVQKRTTIALPEFQSSSSLVGQH

EHVHVATNGPGNAFGDSALMYDTPRRATIQASSTDHNIVLWQLEKSLFRKLVAQYPESQH

SLEERRFLLATLSNHPLFTHLDDRAKALAVRQCFPLYVRRGTTILHQGDPGDYFYVIEHG

KCEISRTNPRTLT

>contig28066 Frame-1F

MECKTHNDLALQRFANELVAYNHENPPPN

>contig28480 Frame-1F

MMPSMLYHHHHHRQKASRSMGLQGVLSAGKQRHFDHVNTNGSIESSASSSVDDTGVSDSI

VLDTGGYYFYRAMNKDVAKRGGRKDCIVEIDSTSLDTLCGNESIVETLDDLNKATASGEE

FVFICHGDYHQRFVQKLCAQLCREGGLRCYVDRKPRKETSFGTEDHEEAHERKKSTIPMK

EDLSVRIHQAKEAVLKCSVFVILLSEKTLASELVKDQLAFAEDKGKKILPIVVNRMNLSL

EVKYSLARSEFFHFFTKGDMMGFRQSLRHLLDALREEVSSLRIKARPFKESQVYGRFGEV

RPSAMSARHSFYPLYPTERSVRRHVGHSSSIYASSHSDMANFGVPPLRLSQTFAVTSGRT

RNKALDLSLSHSMIGNFSTFGRITDEFDEDDERLTYGGLEDEDFDTDEEIDVYGTNKVDV

VHEEALRVAQAKHKHLKRGALSSDSTHSTHQGASDSSITILELTGSSDSINISFDVMPNE

NVFIKR

>contig29528 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59785.1|) 1e-111

MVSAVRLLRLFKLFAQPRYLFDNEANHHLVFFLLETFDNIIQYQYEGNQQVVYAMIQNKK

VFYLLNDLQLPPIRAASEGPKIVKKEGEQPKELENGHEIEFVPTVEWLAAWKKKLPLSTS

LRLLQHLIPQLEEACQKVGGTLDEDAMLYFLRTTTMVGLLPVPHPIVIRKYQINQFTHLW

FTTFTWGVIFLRNQALPLFDGGAITLFTISVL

>contig29955 Frame-0F|Blast-structural maintenance of chromosomes protein, putative [Phytophthora infestans T30-4](gb|EEY68020.1|) 0.0

MDKELLATKKEAVVHLAKEVQSLDVDIRNLKTSRQSKIGVLETQFAEAKKETQKIGSRLK

TAQQELSELVLESESADQELAGNKESVAVIQNELAALRKEEKQVEDKLTQTQKTYEKASQ

KLEERKSNLSLSDQQVKELGARLSTLSSKKSDLEIECKKAEHKISRMAKDEKDAKMMVKK

LEKTHLWIDTEKEFFGREHTDYDFQRKNPSTANRRLLELKETQGALSKKINKKVMGMIEK

AEQEYQGLMNKRHIIENDKEKITSVIKELDAKKNEALKTTWVKVNKDFGSIFGTLLPGTH

AKLDPPSKGTILDGLQVRVSFGGVWKESLTELSGGQRSLLALSLILSLLLFKPAPMYILD

EVDAALDLSHTQNIGQMIRSHFSHSQFVVVSLKEGMFNNANVVFRTKFVDGVSTVARTIP

KSRGR

>contig30351 Frame-1F

MELIQLLLRLLLLMVGNVTIYQHLPHNYLSPSTHIPHISVNSMTGSRKVSRTCE

>contig30508 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62264.1|) 3e-34

MKLLSQNDNHEDAVDAALGPVGFSLWGSSLLIVAIETQSQKVLKHAL

>contig30603 Frame-0F|Blast-chromodomain protein, putative [Phytophthora infestans T30-4](gb|EEY63490.1|) 1e-104

MELKPYLLRRMKEDVEKSLAPKEETIIEVELTVLQKQYYRAIYEKNTEFLSRGGKKGDTP

SLMNVLMELRKCCNHPFLVKGVEEREVKRREKQSGVSKEEIERKVSESLVDTSGKLVLLD

KLLPRLKDSGHRVLIFSQFKIMLDILQDYLSLRRYNGERIDGNITGNERQSAI

>contig31064 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61457.1|) 0.0

MYRDKIHNVALCDYLTRVFAANARTCGADAKTLSNSWQGAKGGDISIDLPGQHVIERSSI

NVLPNGDVEARFNINLPARGRSICGDWAHTILVDTLPKLVEQSLVLTSLDANHVWAHLHS

IEDQETLRGMLKDVGLVGFVRDGAILPRQSGASDLPLDQDQAVLFKSPKSLSRSFLLPHC

GNITGMGILQGVTLFVGGGFHGKSTLLKALEVGVYNHVPYDGREFVVMDPNSVKIRSEDS

RSVVCTDISAFIDNLPFKQDTTHFSTADASGSTSQAANIVEALEVGATTLLIDEDTCATN

FMIRDGKMQQLVAKDKEPITPFISKVQALYRQHNVSSVLVIGGAGDYFSVADHVIMMDSY

EPRDVTVEAKRIASEHREVSQIADFGNLQSRIPSRHGFEINGKVVSRGLDKIQYGEV

>contig32128 Frame-0F

MCFEFVHVELFGGDTELMKQLGEVLWTIPGNLETHVLNLLHDHMPQDPAAFDTYRNILRT

SITDLETALLAISFTVCRQNNPLRNFIDELDQVHLRKRRQAILSTGRDLMMQGYQDSIKI

QGALEKGSLRASSGADKKGELAHKQSSGSSTLRASSNSDDVESSCFQVPDYRVSVCAHEV

VEVVHQTLVEACTSSASSAKLLFQTARDLFLLFRSIVPTLYEDDVGNDARTCMLFHNDCL

YIAHHMVIIGHLYKP

>contig32623 Frame-1R

MLMSGMGELHLEILQERLRSEYKLEPSIGAMRVAYLESIVESGVRQYSHDVMLGTNRHFA

QVTVLVEPLLDRERDGLDNSNVIDWLNRGAKKMPQAFVLAIEEGLLAGLSRGVLSLYRVA

FVKVKVDEMECEWDVDSSAASFRAAAALALKEALKAAEPIIVEPVMKLEVRSPDRCVGDV

LADLSSQRRASIQEVGSIGIEKQGIQEYQGRSIVHAHVPLAHMVGYSTILRSKTQGEASF

TLHFLRYVRVDAATSDRLTLRRGLSQHTFGNA

>contig32744 Frame-2R

MTETYDVNCELRGHNGAVRCITSLSNDLVVTGAMDSTVRVWQRDTSSSFVVMESASIYEH

EHWITASVALGSGGFATGSMDKHIRLFDAQFQRYGLLQGHDGGVISLAVSYDQKQLLSGS

WDGTARVWSLETFECLHIFRGHENGVCVLGLPNGSIVTGSTGQQVGNTIVDFKLRFWDAK

TFSLLKTIADHAGPIRQLALVHTIGFLSCSNDGSIKLRTNTGTVLATMVHPRNAEGKPGF

VLGICVLPNGLFVSASEDATARVWAQDGALLQTIEHPGGLWCVTSLPNGDFLTGCDDHVV

RVFTTQAERMNSIAKRSLETAVKEARMVTLRGPNGVEIEALSAYEDRGEKPGTSDGQIQM

FRRGNTAWACQWSQPSSTWIDIGEVTGTRGEGGVVENEAFDMVIPVEIELPGGLQKLEIG

FNQGQNPFTIAQAFIDKHQLSQTYLGEIAEFITQRAKESRPVMLDTEVTDQGPRTLQETN

SFQYFPVSGFNTFETTKITKLMSTLRQFNAAMKETQ

>contig32861 Frame-2F

MKNLKREYVESKKSMLIRQLQLESSNTELVNNVANLEREIAKARKAVATASQIKSTNGSI

TSGSKQSNFASMIEENRRLQRTLVLTKKSLHEESRRNGVQKQEIASLTEEVHRLKQSSNS

AQERFLNQLEITCHANKKLKKQVDELTSPSNRASAINWELRIQRLTNQIIEKQETIDVLR

QSLVTMDLRLQDVILRAQRAEDNLLRLEQNGGVDDMEMATPMGKRGTRLRLNRMAHILSR

VAPVVQRSHRAITVLDGLDRWLLFLGRLFLQAPIVRLGMLCYIALIHLWVFMILSFHTNH

LTEEMQLTEKAVVEPGQSRIHGGLH

>contig32986 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66487.1|) 1e-162

MAWGKSPPPEALVARAPMTANNVIFLILFGMFLMATLLPVLVATLIRVMALTSILFLVAA

VTNPSDQSFAQWVSQQNEPSDLVPDASIGMSKWISAVYKTAKALVQNDSLTWRFYNVLIF

SVVYVPTRERYAFGVFGMWRWADEYGDVVKSLCQMPWVLKVSRGGLLSSMDRYQVIESAS

DSANLHRQRRDATPSGFQDVETASHRRIRAKALQCKVRKDWQQAAMLFADAAKVATALVI

QASYELEAAWCSLEILDTFPSSQNGIFQTIRSVCDALASAGYFDEAARGVSELALRLKRK

FPKDCKTVAKAKDVAELYVLAKDIAEAGGNGYSAAEYGLYAARVYADAGLWSLAETCFEA

VGGIRRENGQNELANEAYGNAVLCHLSRLDFVSAEEKLHRYSKLLGEISCSSDMNLFLSS

VLRACKNWSVQLLDEASERYDSKHRLAPW

>contig33347 Frame-2R

MTLARYLQVVRNLFSTSMWHACHGGLLGLKYLIQAHKKHAQVLIPLVYSDMLSAFTSFDS

EELLVLAADMLGSFVSFVN

>contig33404 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62951.1|) 6e-47

MTFSFIPPSTLNALAPPFYPSMTWYPQSMDDHYMELHHLPGEFGSIFTEYDSPMDEIPDE

ELFDPALYPITATEMNELEQVDEVNEILAELDLLESHQELYYKLNEKTHKLRSSSDVDAE

IYSLMTKTALSKSFFLKPESHSFMKLKIREKGNARTLIK

>contig34557 Frame-2R

MSGTNAASSSHLPSSAQQTEAPTQSSPRSPVATGSIKFFHLFGRDGKMATYNWRQESNQA

TRTFDCYITQSKKVIALVDSASQNTALIRNLQRPRLNNLLAPTL

>contig35323 Frame-2F

MEQHLVKRNKMLNLAVMANPHNIQNWLDLIAFQDDTLRLHIKTKRINSVMKASVMEKQVA

IVARALAKNPGSRVLHRIKLNMALQSQTCNRVAGVESILLQKIEHFLDKDPTNCELWLKL

LQYRLQQFGSFSMQSVRDLYARIFTVLRKECEANATVKISEQTMPDLDKCEKMKTSQHLD

KTLAFLLEFHFLMCRFEKKAGFIERSLSHAQALIDFSFDDCRIIASSSSKDTHLSRLQQF

AKRWNDKDVPRIGEIRRGMTFQSNSLPKDSSNQALVQFQNYIFKIGSVNIDHVNPPEVVR

TDKHQESLLTESAAYKRQTYSSGKKAFDVIGTEQGKLSRLCDESEMEFSKLVYSNLHGYR

IKVDNANDSKEYERILDELRRTSKNGQARQIRLQDKGKKKGAVLAATISQLEDQRANYDS

VDEDDRFLSWLHDEEVQKHLQWIPLRSDNPQNQNLIVQQPDRVTLTEEIQPFLFYVPKVH

RWRLIAEILEIFG

>contig35428 Frame-1R|Blast-pre-mRNA-splicing factor ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY60921.1|) 1e-108

MAQETVPEIQRTNLANTVLYLKLLGIQDVLGFSYLDPPDEDSLLDALKQLYVLGALDAAT

GDVTLLGKLMAAFPLEPKLSRAVAESLRLQCSQEMTQVVAMLSIENVLLEPHDHSGKKRF

REEKECEQNFDWEERLAALKEQRLIHADGDPLSYRLLYKAFQAKSLKVHGNRKELERWCK

DHYLRQRALTLAESIV

>contig35631 Frame-1F

MGKKRVDRSRKDRGRTGGASMCGEEESALSYSRRLFPVTLRMWDFQQCDSKRCTGRKLCR

LGYIKSMKPGAHFRGLVLSPAGKQIVSPADKPIVDGLGISVIDCSWAKVQELPYKQLRSG

VHRLLPFLVAANSVNYGRPHKLSCAEAIAATLYIVGLKQEAVQVVDEFSWGAEFLKINAD

CLNAYSVCKNSDEVVEAQEAYLAACRSEHQERLQKLNLPSLASDDEGEEGEEETLELDRF

GNSVPREKIVLNETESDGVIETADALNSKDQGPLQMLKLPCLESDEDNDEVDDVRVELDL

KGCTLKNSVLRKKSIAGMNDCESEAVEAAVVLTKEQQYFKSMTYGFHGEDAGSDEELANL

AKNLHAAANSVCKTQDLRDVLRKTHASEDKKEMYAYSSMEEFHQRHVATVLLEKTAVAVS

GDAVLQLPESVFYRWAKNSC

>contig37462 Frame-0R

MAHYGRAGGDRMQIAVDVDHTLAKMMECAAEWHEEEHGAKIDVETVESSSWSSIWGENDA

MAKTHQFYESRHFETGLAVVAGANEVLKPLRKYFALVAITDRPRVVEKQTREWLDHHFSG

VFDKLAFVNEESSDRLISRKKLYDDFKVKIAVSSDAAIVEAAANVEYKVFIGSVPWSKKA

VQVSSNVFQVTDWSAAKEVFAQLIEKLELEPIDKIFPGPRLSRYNEDLVTVSTRKPAVFY

ANIINSKFTQKQESIRLQASEAAITTAVQAAEILRSQNNAITTKISTRYALNRPKDRGGY

RVPKLELVLNCVARKA

>contig37839 Frame-2F

MTRTTELITSQSIPEHNENSLTTVAATRKSCVRRFLTLGDGNFSYSLALAKQLKSRECDA

SFQLTATSYDTYDELVEKYPEFPRICAQLEELGVLVLHRVDATNLRESLIAAGGPHLRFD

TIVFNHPHCGEENIQRHQSLLSHFYTSALQVLHGSEDDLESELFLALAEGQSERWQAVER

GSLAGYRLCRKISDVDNNETFGLSYERKRHQNGKSFHQVTLRGETKMQTSTLLIFRRQNC

VQPAMTDVREADVSLPLLLTSMPRKRKAESELPLEFGCTLCTRSFKSAQGLRTHNHMVHE

LDGEMTTVAQLPCNFCERVFKKEEDKRQHQLAKHGKDPLIKPDWYKKQQKIDGAVLITAA

TSELLASAATATSAPVEPHTCSICHFSFASAVEFDAHWYNLQPRAALKRKCLICNREFDE

ERALRQHQNFCEVRS

>contig38104 Frame-2F

MRLSPLEVLTGKISSVSDIIVFGSPCTIYRNSSKKAWASRAEAGMIIGKDDVSSVTNFTY

LATGW

>contig38913 Frame-1R

MWRRAALLHRSVRAYHYQQLVSFQSFLTHKPHQHLTPRVVRLIALISLPVLTVASASCTS

KLAMESADAVKAEELYNDSSFDRFELLNKLKQMHASHPEDIGVIWRLTRAAYDVANLKAT

SADKKKELTYYARDIIQKGLDLTKDVAAIHN

>contig39059 Frame-0F

MSFRTLLEAAMGTEQELSHLEADRIDAQLDLLDDHYRDSGESDDAYVPPSSEDDNDGVGE

EEEMDSDIERQLWGNFRKRKSNGGGKGRRRRRGGPTGKRSVTATKVPPELANVLGEANML

YASHQYDEAIALLKDFIKKAPTIPDPYHTLGMIYEDREDRIKAL

>contig39143 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63356.1|) 2e-46

MQIFVETLSGSPLTLSVAADASVASVKEAVESVEYIHNFRLVCAGKQLNCGSLSDYAVGE

CDTLKMLLSVNGGMRAKWRKKRMRRLRRKRRKMRQRAR

>contig39396 Frame-2F|Blast-ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY54221.1|) 2e-63

MPMLENPFLKCLETKKTGFLRALFEIYRFYGYGASFSRKFPMKIESILPAKKLKLYKKLI

DHYDYPPMAIDILETEACGLSHRFDALASIPGFDEKCLDGMHAPARRLSYLVLGKSVIEE

WTGTNCVQVQVAPLKFLHPFLSIPIQGRSANRVELMFSSLMFVLLYEDPSGGTPK

>contig40244 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66270.1|) 2e-19

MDVPFLMNLVKECKTSAELIALPRYDKSRHNGRGDRAPFSDWDRKQG

>contig40428 Frame-0R

MCQSWWQNTLRLMINVIYRGVARHQKFSSCSTYLTRTPIHGTRRLYMYNSVGRIVRR

>contig40929 Frame-1F|Blast-glycyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY54238.1|) 3e-95

MDASGKSLKYHDAVAKEDFLPHVIEPALGAGRVILSMLLEAYDEEEVNGRQRTVLRLHPE

ISPYRFAVLPLVKKEPLLAIAQQLFENLSASASTDYDLSGSIGRRYRRQDEIGTPMCFTI

DFETLEDKCVTVRDRDSMEQKRVSIEHILQGTAIKQSTFSCF

>contig40994 Frame-1R|Blast-adenosylhomocysteinase [Phytophthora infestans T30-4](gb|EEY56647.1|) 0.0

MASLGDYRVADISLADFGRKEIEIAEIEMPGLMQSRTEFGPQQPLQNARVAGSLHMTIQT

AVLIETLKALGGDIRWCSCNIFSTQDHAAAAIARDGSAAVFAWKGETLEEYWECTLNAIT

WPSDDGKGDGPDLIVDDGGDMTLLIHEGFKAEKAFAANGAIPDPNSTDNAEMKCVLSIIA

RTLKTNPKKWTQIAQRCKGVSEETTTGVHRLYQMEKTGTLLFPAINVNDSVTKSKFDNLY

GCRHSLPDGIMRATDVMLAGKRVVICGFGDVGKGSAQAMKAAGSIVYVTEVDPICALQAC

MEGFQVVRLETVVAQADIFITTTGNKDIIMATDMMKMKNNAIVGNIGHFDNEIDMAGVMK

HAKRQNIKPQVDRFIFDDGHAVIVLAEGRLLNLGCATGHPSFVMSNSFTNQTLAQIELWK

ERETGKYATGKVYVLPKELDEKVARLHLDNLGAQLTVLSNEQAEYIGVNPMGPFKPETYR

Y

>contig41715 Frame-2F

MEKRSTFSNWDYDVGVVGDHFLATCLADDFCQSKFPNVSDLSVFVHELYNTLDAAVANGK

KGSNACADALSTSNQKPSYYLRSTFGEILMSENLRTAIPAILYRAARCTKQDAHALRTFV

ESFTELYESRDTEIEKLLYNSDMLYYLIVFSEMWEFPTPDKATLVQWYENATMASDNYLS

LPYYCVFTGSREHACQELIHLPSALPLIYERDQYWNKTGNLPENVTALLMSGGMDLQTRR

MYGELEYEAMSGDRMLVSFDDAGHCTTFTTPTISGGETCGVRILASYVRENGVLKNVDTS

CMNDLKPMKFSDKTVDVQSLFGTSD

>contig41834 Frame-0F

MQNLILTLPSSTTAAQIIYRERLQVFPYIKVSSVDEDAGRHTAISSHEKVYLYGEGYSFR

RHRSKVTSSQFR

>contig41889 Frame-2F

MSALLGPPSPVPDIASIVSSPKYQAVLTPSCTSAQDGDLLAAEGIGRRHRHSHALSAIRG

ATGRTSTAASTSMDPRSSSHLHVPATTTSIPMDQVPQTDKTELPGTFAKWRHWRRRWKKV

SFFSVAFLLFSGWFAISCLVPVAMAPVLFGTSLSIVSTFTILVSFIRRRACRRQPNELLA

FVAMSECALAMLTLFQVLT

>contig42174 Frame-2F

MLTMASSLLKIGGELRVTTWVNSRRLSMSECEEIRSKMKIRQESGNATSTLEKTRHSQQD

LLLNAPYVGDMQRLFWSLSEDVEVRLQSCSNEIAAAIDGALDSLISSLNWACDIKLRRMT

FRVFRLEEIEKPPEYYGQSAIFHGFDDEEDLKTFQLDDAWHFQKGVRLSIDGNTAQILQT

TWMQKYFTVTGNRSTHYGSFASKALPL

>contig42417 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56616.1|) 7e-17

MVRIFLHKTFKKQNLTKLLPMTGLEHRVVQVLQFANARAPELQALHDLSQHNELYSVTDD

KLEQQKNQRRRRANAFKSHKMP

>contig42963 Frame-1F

MFGKYVNFVVQEISYILSKCKCNSPHQLKERKLSLNADDRTQLEWIIYSVCSSLESGQSK

YALDIDIVPYGVAASLDKLNALLLKLRTNIVSTESLNESDKINKLSHTRETLLTQAERQM

RYFIQREQLRGTKFNSPFFYNEASFLAISTSIKTLRDSSRTAQKLYGSLAHTLLYLSLSG

TREYDSCNRVNGSLKLADALGELGALTPVSMS

>contig44064 Frame-0F|Blast-3-ketoacyl-CoA thiolase A [Phytophthora infestans T30-4](gb|EEY54337.1|) 0.0

MERINRIQSHVATGSLAPIIPEEDVVIVSALRTPITKARRGGFKDTTPDVLLGHVLMAVL

KQAKVDPKTVGDVVVGNVLQPGAGAGMARMAQLAAGIPYTVPLHVVNRQCSSGLQAVANV

TAAIKAGYYDIGIAAGVECMSLSELDSDVPPVNWQLMKKAQDAMDCVLPMGITSENVAEK

FRISRAKQDELAAHSHSKAVVAQMNGWFEDEITPVLTIIKNKEGHEEPVIIAHDDGIRAD

TTISKLSKLPPVFKENGSTTAGNSSQISDGAAAVLLMRRSVAKTMGIPILGRFVSFAVTG

VPPAIMGIGPVFAIPDALQKAGLNLDEIDVFEINEAFASQASYCIEKLGIPIQKVNPEGG

AIALGHPLGCTGARQVATLLHQLKRTQQRYGVISMCIGTGMGAAAVFECEL

>contig44248 Frame-1F

MSSICLSHLWSERNDAVFRGVQSTASHSAARFWELGLRHLTALAKREHRGPDTAVVGALL

HTCLDLFALEPRDGSVSSGDSYDALPYPKLVSWLRMYQTSCT

>contig44925 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61072.1|) 4e-55

MLEKNMFSRRACPFTRHYVNKATIQVPVQRNKVHETPIVRKCGGNLMRWVGIGSRYQMYC

SLLLSGSLVYQAAPSANILELLATNGAICSASVAVFFGAKRMCDTVVTDITSCRKVGDFN

EFVRVTVMGIGVQELLEASPKDFKLLKHDDRDAYSFMLGRRRLQLDISTGKDINRKALNR

LMAGKPLITRKIKQSKKDWRK

>contig44990 Frame-0R

MSRRSGKLNIHKSCEGAFCRYMYSAKQKHASYFDGSQDNAVRTTVCIDQYKYAST

>contig45049-0 Frame-2F0

MKDGERKAARASGDVDIILKESLVY

>contig45175 Frame-1F|Blast-cellulose synthase 4 [Plasmopara viticola](gb|ADD84673.1|) 1e-97

MYDRVCESYELEVDEWRKEHTTVKMPTAANPRLVNRVDCAVGSVRDDYMYHGFPRLTFVG

RIKPRVHHSKAGNINNVLYNEGATGRYAVILDNDMKPHEMFIQATLPFFFDVPQNTKIMR

CCAPGCGDIGKICCALCQAAGVPEAQIMFCSKDCY

>contig45508 Frame-2F

MEAMHRILANFTSRDIELGGQRHVVLAVLNDCSKTIRDLADCCLLQDHKKCPSADDIIKS

ARKLSILRVVRT

>contig46404 Frame-1R

MTTPPDTTRRLPPASMQANCGAKRKYSETWNVPIIDTALPSNDKGYLSDHTRHMLVDSSP

VHRRASIAAGCAGQGLYKG

>contig47128 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57346.1|) 1e-102

MVVLAGKVNVGSPKVRWNACHAIAKVLLCPSLPLASVTWAPSVFQALLIAVAQQENFKVR

ISAATALRVSQTRSAFGPFFETALRATVDALETASDLKDVTEFRYKEQLETQLSFTLVHL

IHIASIEDDSLILEALKAKPRGFLYDWLLHNLHRMVAAIEVEG

>contig47744 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68606.1|) 9e-39

MRNVGYVNSSRRRCVDDSKTLAGVRFYPGDMIDIALVE

>contig47861 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62629.1|) 9e-40

MLRRMKFPRRTLLNYQSKSVCSQRTQRLNTMMDTLLTVLRTKYAMRHFRCYPVSSGTACV

CKVLMTLCQFFELDHADVEKRLLEGDERVAYRMNLHGWQTDRRNLYFHGNDKSEYRTIIK

>contig48389 Frame-0F

MKFITACVVLCSIAVVGHSTSFDFQS

>contig48572 Frame-0F

MLHARGERPVTKELIDGIGMSFLRQRCKSQPAKKASQKQFKQKPIPAEIVATGSLTRTLK

RFQHRRFVFCLEELVLRFAQHDIQ

>contig48716 Frame-1F

MCRCNIGTLFHRRLRWCQRSALKYEIGLKPYVQHRLSSNFRKQHKT

>contig49333 Frame-0F

MSSPSQYMKSSEPTIATSIGKEKQTVKTPQRRSNVPNSKRSFTTMHEKIPSAGQEKEMAA

KRYKAEDKAQSRAVTATIPQQHVSQQLESIHCCKQEVHACQSAHDAIKSVAITSGRVEID

QASLPSGLVRCPSEQDS

>contig49463 Frame-1R|Blast-chitinase, putative [Phytophthora infestans T30-4](gb|EEY67716.1|) 2e-91

MFKVITPMFFLGMILVESNYCSQQSLPDVSSPESSSAPVASVTFRLGLSRFLDQRQFQEL

FPDAIDLYKFDGLVNAAKRYTEFANTSDDTNDRLELAAFLAQTAHESDNFKAAEEYARDT

YTVWQYCDNTTYPCAPGRKYYGRGPIQLSWNYNYFLAGRDLGLDLLNVPELVATDDTITW

MTALWYWMTPQNGRVIHDVVTDVNGFSQSTAIINGGLECGSNAPNTANELQRIQYFMRFC

EVLGVQPRGNTSCNA

>contig49539 Frame-0F|Blast-carbohydrate esterase, putative [Phytophthora infestans T30-4](gb|EEY54423.1|) 3e-60

MSSTTHRVVFAILVLAYFRNFVRTFHQHCTLLLRNEPRLTWSKNILAALKYTSIGQLVAG

CEYLLCFEKHRLAARIGRSLVCRPRNCSVNCRYGPYDRNVLDIYGVQGRKQTIAAKPVLV

FIHGGAWSFGHKWQYALVGEYLALQGILVAVMAYRTYPNGSIVDMVEDVENA

>contig49584 Frame-2R

MLGGTPTTDAERHPPATRPGIDYTPHFWDCVCAAALWDKIVGHWTGERVTRQAVQHFMGA

CASRQVCSIPVNQQNILEDRLKDDVTKPSGFGKLLSTA

>contig49610 Frame-0R

MLESDRKALAEEYSDCKDSDNLRLHGKGSLRRIHVPTRAGACQWIDLDASAEVIIYSGIE

MQTLVPCEIINI

>contig49917 Frame-0R

MPQTDQLEDEAASEPSETEMEEQLCAQAAEAFNHVVRSHHIAASTEVARNRLKSSLYMIE

QQRRRKNYPISADAIALEAMQGCRAQTSEEPVTVNKQDYLTVHFQLSKPSIMIYKRALLL

PNVPPIPIMKTWTALTKNYEVEDEILLETEDVVTAFYENKQQRTSQCEIEFTQQLSERVL

QTLQSTWDLRLVISSVWQMSLRLKKRLSSRYTVGCVKHNKQLKRSGKRWQ

>contig49988 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY67110.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59060.1|) 4e-55

MGKKTFFVKLELFKCQDLIALTNEVQDVSSAYATFTLGGLTKTSTCIKSSLDPRWSPSEK

FEFEVDEWENEFLIAQVFDRSKDGQDNLIGSAVIPLALYAGSRNSEMCSYPLVLPDEVGE

MGLPKSDMFLQIRLLNGDGSLVEELCW

>contig50029 Frame-2F

MLSSQSVGTCSTSASVLSFSFVIERLGSLVLLLSMVGTYFPGGISPTSAREVCDVLVFLL

QAPEQYVASVSA

>contig50353 Frame-1R

MRIQQSATRSSFSAQAPLSSPGGNPDTA

>contig51732 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63168.1|) 1e-110

MVTLLRHNVQALRAIFQGTAVVQLNTVVDCREEDALRLEHTLNVVNLLLRFGAETEARDQ

DGKTALLLATNDELYEVAKLLIDHGAHMDAQDSTGKSSLHLCLRTCPEQSMLVTNLLVSR

GALIDLADKSGETPLTIIVQRGDTTALQLLLNHHSLVATLTRQDFSAAVLLQAAELGIVN

IVCFLLEGMYTSIDVVNARG

>contig52045 Frame-1R|Blast-pentafunctional AROM polypeptide, putative [Phytophthora infestans T30-4](gb|EEY67699.1|) 1e-82

MTLVPSKTNGTVIVTGNNRMKERPIAPLVDALRANGCDISYVEADGCPPLAIRGTGLRGG

TVRLAAKVSSQYVSSVLISAPYALEPLVLELEEDKPTSLPYILMTTQLMQQFGISVETLA

PNRYRVPCGVYENPKEISVEVDASSATYPLAFAAITGGH

>contig52221 Frame-1F

MVERSKCSRNVFGVLTLQLALQGL

>contig52643 Frame-0R|Blast-diphosphomevalonate decarboxylase [Phytophthora infestans T30-4](gb|EEY64532.1|) 1e-29

MKQLAQRVHGKNEEKLNTHLHIVSTNSFPTAAGLASSAAGYACLVATLAEFYGISETDEE

FPGHLSAIARQGSGSACRSLSGG

>contig52759 Frame-2F|Blast-Rab8 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY69822.1|) 6e-07

MSATIATPSNGQHLDAHLAWEREMEVAIEGRGRSRSRSILADDEAEDATSTQENDLGSQN

IDS

>contig52980 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY65780.1|) 1e-106

MLRHPQHPQDKISMLVISPTRELAQQIAVEAVKLTNVHDLRTSCFMGGNSIKKDLKELIQ

SGGIDVLVSTPGRLQAHLEDNSGHIRQKLDCLQVLVLDEADRLLDMGFRRDIIRIISHLP

KQRQTLLFSATLPAATDELKNVALRDDYIFVDTLEGNDQQTNAQAVQEYVVCDLKEVIPV

VEKILEEHMQLPAYKVIVFLPTARSAQFMAHLFQAADFSNVLEMHSRKS

>contig53060 Frame-2F|Blast-diphosphomevalonate decarboxylase [Phytophthora infestans T30-4](gb|EEY64532.1|) 2e-25

MQVATCSAPTNIAVIKYWGKDNVALNTPISSSLSVTLQQDQLRTTTSVVGGSALQTTRLW

LNGQEQ

>contig53114 Frame-1F

MRSHSIRICATDQIFLAKHERRLKRKSSLRQ

>contig53378 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53679.1|) 7e-08

MRRLLYDKQVKSIDAKRRQR

>contig53392 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58053.1|) 4e-56

MAHAEEHCKSESSPCSCEQKTADFREHHDEIVDVSLTYCSTDLMLLQGRKSKSNETISTW

VSLPSNQGMDEDVVRAHLVHYLSLHDNERIERVVQSTAQSRMNPSLGAASTSVSSNQSDE

AEIIYILQTKHHVYECRPQWSRLALFKALCSREIVLRDALS

>contig53536 Frame-0R

MQSHCHKLHRQIIFRIEGLSNT

>contig53730 Frame-2F|Blast-diphthamide biosynthesis protein 1 [Phytophthora infestans T30-4](gb|EEY59612.1|) 8e-76

MTNHHLLMESNELKTPQRFSGRSKATTNSECCQYGELSCLSSECGSQQLIELKPDSKIKR

KASATALRRRTANQIPEEIMIDKELTKAIEQLPWNYNFEIRKTVWRIRQAGSKRVALQFP

EGLLLYSCVISDIIEQFTGADSLILGDVTYGACCVDDLSAIALGADFMVHYGHSCLVPID

VTSIKMLYVFVDIAIDVDHVC

>contig54036 Frame-0F

MATPSSWFSSDALRLLEARNRREVEAFNDVIASYQQLLFRSALGSSSASQRLPSSENQDD

AVAQR

>contig54560 Frame-0R

MDAALRMQRAGQKNHPKYQQIVALLRQYQQQHRERQQQTPVQTQMQQQLPNQTLRNLDVA

ANPFMKQKAMLFSDRQLEYLHNQIRAYKALCRSMDIAIVHAKQLNTVDLNAPVSDPSKVA

KGPSMMSDLLPLLPTAVESSSLELLTP

>contig54951 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66294.1|) 7e-39

MQIEEIPRAVETCHAALLQGEMSVAQELCMPIGIDLVLLLLNLWLLLHYHRRWAKYVMVL

MATMYLADVPCQLYVATFPAPAINHVEPTFALV

>contig55181 Frame-0F|Blast-deoxyhypusine hydroxylase, putative [Phytophthora infestans T30-4](gb|EEY55557.1|) 1e-51

MADVDTTPSFEQLRDALLNLSEPTGKRTRAIFYLRSRGGLEDLHVLLTALLNRKDSELMR

HELAYVIGQFQMEEACETLHEVLTDVLDDAMVRHEAAEALGTIGAAQSLPILVKFSADPA

P

>contig55552 Frame-2F

MQLRLSFVVVGSEMSRRDQEDCLIKLKAKLWEWGFENNDLSKIERDKGFMAAAMDAIMHY

LSVWPECQLIGR

>contig56658 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57486.1|) 1e-174

MFPDDRFHPLGPDADRLHDDLIDSTELDFTPKTFKELGSALVLHQFLPAWDVQAYLRVAG

IRLHVHNSRYPAYEATGELPQLSDGNFLLPKEKIIMHLQTFHKDIDEFLSDAQRSESYAY

RSMLSEKLERVLLYCRWVDSASYREITRPHMKRHIPFPLNHFLPKKMHLDTMENLRLNGI

STKEQAYVIARDCYTALNTKLESVGTTFFFGERPSALDVAVFGHIVDALGNTQLMATVQQ

HAPLLITLSERIRDKFFDALEHHPSSLSDEALYSENQPNFFTTTPLKSAFMKKISPPLQV

AFLQPFRSLDWSRRELAVEIAEKMRVQERMKRGEAKEQRDEEFAKSPRNVIIGALAALVL

YAMAVLPVVVQFDSDDHYEDDKEFDEDE

>contig56733 Frame-1F

MKVGGALGPVVVAVLVALLLHVYNDFVPIDSYYPSATANASIDSYFSDSYYQAQALFRLT

AKSAGATLFSLPLEHLQPLNLSIDIAVMKGSKDRVLLHISGTHGVEGFAGSAIQAALLER

AAGTVRNNENQPTVVFVHALNAYGFAHLRRFNEHNVDLNRNWLTQEEFQERQAKDPNERG

YLDMYDVLNPTQIHGIRNGFWFQCIQTLITKGFDAAKQAVVTGNYHFPQSVYYGGTKLEP

SLLLLQTFLSKHINLKTIQKFGMIDVHTGLGAAGVDTLLLKAGSNISVAQSVFRGPEYQN

QVVFQDDSNHPVTRGYEGTGGFVFDGVAKMLNPEILQNALFVCQEFGTVPGVFILKATIE

ENTMYHYHSSISRLPYAQKLRDVFYLHQSSFWKTEVRRRGIEAFDRLDAYLTAS

>contig57107 Frame-1F|Blast-hypothetical protein PITG\_12566 [Phytophthora infestans T30-4](gb|EEY60231.1|) 1e-137

MAIGGALSALTTWLWTSSNTTPTTNATTLLTSAYDGAMATFNVAKRMRRVQQLQLKLLSG

NAATCTHVVFCINGFMTQSDDPTKNWRVWTQTNEDVAVFAVLWEAGDAAAWNKFCMHATD

NLRQSSIVNVVAHFTENPWHSAQIKAERVGVLLAQMFSQRPALIRNRKISIFGHSLGGAV

IYSAFQELAKLRAERRHRITFDI

>contig57316 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59089.1|) 3e-23

MQLRFPLPAGYFAKFELLSEESQSFQSLATDIIHETRRDLDRYIHDGRNLLEGHTWKLTK

SKDRLHCYR

>contig57446 Frame-0F|Blast-copper-transporting ATPase, putative [Phytophthora infestans T30-4](gb|EEY66507.1|) 4e-27

MKLQPKTALLVVGNGTRDREIPIELVQRGDLLRILPGANIPTDGVVKSGSSTTDESMLTG

ESMPIIKKEGD

>contig57734 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64471.1|) 5e-16

MQQAIAMVSTEIQVVWNQCVQVEGYGSFATRLHGEASDVDLVVFG

>contig57815 Frame-0F|Blast-serine protease family S09A, putative [Phytophthora infestans T30-4](gb|EEY59532.1|) 2e-28

MQYQYYLTLSKKIDNCSVILRETVRMLSLTMNRQIALNLSVGAGACLALYIVRLRRAAYS

KVSMPVSPPLLDKRPKMVPFGAVAGQNRGLNPMKPILYLEDPYFYVRD

>contig57969 Frame-1R|Blast-hypothetical protein PITG\_00592 [Phytophthora infestans T30-4](gb|EEY57994.1|) 7e-10

MDTALMSFVNCLGAIIMVSVVCFHYLTAKPTDADL

>contig58199 Frame-2R

MVHDQPAQTDLFRLLEIIKKRTIGRIMS

>contig58674 Frame-0F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY67821.1|) 1e-177

MKDRCGLRLPKFTEDETKLLKGSSDFFGLNHYGTNYAEPSPEYEAKIPPPNDASGGFGLD

EGTKLTSDEFVEAHRHGLERSRLGFPETAGLDSESLCGAQRHLGDGKWLRVA

>contig01040 Frame-0R

MPNAPTNQARTFYPRQVPTDSLLAASEAELASSNFDTLRNNALKLAPTPAA

>contig01710 Frame-0F

MDSRDPQGSSQSLSPDGSWCPEFYPTRSEFQSFATYIRTVIEPQCVTIGICKV

>contig02665 Frame-2R|Blast-ATP1 [Phytophthora sojae](gb|ACJ09360.1|) 0.0

MTRKSSRWHQHTLLHYCPSCPFLFVVNSVIPIIQKWSHIMKFSRRFFAMYSKRSKLPFVS

IGPLRTNIVPPPSCVVLINLPPVASFHFFSHTLPYATGKENPEIPMLTCVSRGVRSFATT

ATKKPGSVGQITQIIGAVVDVQFKDNLPPILNALEIKTHDKSRIVLEVAQHLGENTVRTI

AMEGTDGLVRGQECEDTGNPIMVPVGPETLGRIMNVIGESVDERGPINAKRYAPIHTSAP

LLTEQGSGAEILVTGMKVVDLLAPYAKGGKIGLFGGAGVGKTVVIMELINNVANNHGGVS

VFAGVGERTREGNDLYYEMIESGVIKINDDGTTTGSKAALVYGQMNEPPGARARVGLTGL

TVAEYFRDVEGQDVLLFVDNIFRFTQACSEVSALLGRIPSAVGYQPTLATDLGALQERIT

STKKGSITSVQAIYVPADDLTDPAPATTFSHLDATTVLSRQISELGIYPAVDPLDSKSRM

LDPRIIGQEHYDVARATQKLLQDYKGLQDIIAILGMDELSEDDKLTVARARKVQKFMSQP

LHVAEVFTG

>contig04209 Frame-2R

MDASFEAAVQLFTATEESTGSTGVAKELTTTKKLVVLSMPLEPDSSQQRI

>contig08829 Frame-1R

MNVQLCAAFRQRFTARHQLRRRRPSFTGKTNASDAKSTRVTAQDTLQDAKMYVAHVLGAT

LQCFPSLASTRQALSSCSLAVERIVFDDIYAMVFSEFQLTFQDADAAFAENLATIRHKPT

TSRSSACFYQPIDKSFQTGQELHLVDELQVAEATLVTMMHETSSPLLKLVLLCDAFRRIC

TFAEKLHQATSNADMLIPILCAFLVECPRICGPGLDFVAAIAFISFFTNGGGKGVEGYVL

TTFQASIQVITAVDMLHGHGQELELILPDEIDTDDDEFVDAVEVSRKFEN

>contig09956 Frame-2R

MPIMKLLITFNYTENENIMTLEAAFDAVALDQRQCYLVVDVKSFTAGLSIAKGGLCRMTF

LRRLVLDHIWFCCERLLKKG

>contig10385-0 Frame-0F0

MHFTLECRLKSTKWIHDGHSDVSSYTVARVSSCYLYLVLVYTVDPSQFVSRGHCD

>contig10385-1 Frame-2R1

MGLVCEKPKSFSNLGTFGSFVNIIILA

>contig12545 Frame-2F

MSPVYNLQRGVTKKKLQMGTLMFNVCVVNSLIVP

>contig13757 Frame-1F

MKVIAAFILLSSASAPAVAFTDTRIMIESTYTDVLGLNDLAKTAYKERGGKYMGTATDLK

QLDDTFYAEKLGNISEFGMITPTHAMTWEATELTQGVFTYENADKIVAFANKAGSGVRCH

TLVSHDQVPEWVQVLEKAELLKAMSNHITQLMTHFGNSCTAWDVVNEAFNEDGSYRESFW

YKKAGKEFISVAFQTANELKVKLKLRARLFYNDFNINVANNKSDAVLAMATDLRSRKNWV

EGVGFQSHYTTDDIVAGAKIFDNFRRFTVNKMDIAVTELDVKTSTATPTVKEQQTQVGII

TNVVSACKKT

>contig15777 Frame-1R

MGEPHTSNAFRASRAVVYNLRFRNLADCTKELPHFFLQYVELQVFDQNFGAMTGRVLPAQ

TRQDGRCALLAFFSYSLDYHRALFASRGVGSVVQIHVHVVVIFIA

>contig15892 Frame-2R|Blast-alpha-1,2-glucosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65562.1|) 2e-66

MSVQRNAGSLKGMIFIFFVTTATILVISRFSPVHKFMLADNRHYTFYIWRRFFRKHKIAK

YLPLPLYLVCGWRCWNEL

>contig17300 Frame-0F

MIVDIQGVADSYTDPQIHSADGRGFGVGNLGTFGMEKFLESHRCNEVCRWLGLRSINEQY

KPGGTAAPGYEMPFGGAIKKSTNRITEERNTFSTSVTVSEAFGDTASADFTEREGFDDDD

DNDEENSDEHSDSTSYATDSSPAMSGLHSRRLKGKSRKRFSPCASRDIRSDQSIDREIGR

RFRHPTQLSKSGGLVTGSPCIGGSGGLWTCVVRNLCCGCA

>contig17762 Frame-1R|Blast-hypothetical protein PITG\_06324 [Phytophthora infestans T30-4](gb|EEY69818.1|) 3e-63

MLIGRQFEDRSYPIETDDTIVGQVRLQLALFNDEIMDEDEIRDCDVDGCSCASTYPVRAT

KVGNVLIDGISPDGVQYLEAGTAVHTGCELAGNYVVDKDVYECDAWGVDELDIRDLDALG

SDEWEGDEL

>contig18806 Frame-2F

MLRCLSCFSRHGTTKDDNEPASSSAQLGFSRNNKKELKFESAYETLRQIGEGKTGQVFVA

KKKRPHYRSRAKTLAEQQQREREERKCDEEVAVKFVRKEYLSTPKRIEALQSELAILKRV

KHPGILRLRKVFEDEDKFVIVTDKATGGEVLNAICRSGTPRICECDVAEIIRQLLSVLAY

LHLNGITHRDVKLENILCKTENFRGGVLLIDFGLAHMGTVGGTEMTGMNGTPHYMAPEMF

HKNGSYGCAIDLWSLGVVTYILLFGQYPFDARFMSQVEDKIIKGEFKYPSELEPLVSPQA

KKFIEYLLVLNPRERPPAAMALQHPWLQKDSSPAIPFRDEHVAALVSFCAGKHSFEPPAP

TEYVPPEPIPKEGVVIYVA

>contig18899 Frame-1R

MAALGVNGASSGTLNARFIRCDGCRVNVPKEDMIALRKCTVCGRSYEPAVGANEIATVAF

DGAGAAVVDKSVKRKRWAMLTSKRGRRYYHNTETGEDRWDKPADVDADAIEDTFVPFKND

AVKKAVLREQMKIEATKLGVPLEVVAALQQHQNETDDPLAQMVGLGSKSKRNSSLADDAS

GSKDEYMPLQEECFEQEAATQQITQEAATQQITQEAANDGGKCVLM

>contig19351 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69224.1|) 1e-15

MFRNLVESEFATFQEKNECMSSELCHSLLATLHTKMTENVNAQSMVGPMDDENGYCVQSA

EF

>contig19430 Frame-1R

MTPKKNEALMKRFQTWIRKCDAELESEDEAALIITKESPPELAAPSDRAAATVTPLSTAF

IIRHDWYQSSAYVTVSILQKHLSREDVEVIFETKRLQVRVKVKDEFVEAYNEALFDEVVP

DESSFKIFNSKIELKLKKKSIGTHWDKLKGVMYQSNDQVVTGTTAVFEAKSEQFSRPYVS

NRDWNRIEKTIDKELEAEKPEGEEAMQKLFRDIYAKADESTRKAMNKSF

>contig20184 Frame-2F|Blast-glycyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY61460.1|) 0.0

MTCKAAVHDGIIANESLAYYLARTYLFCRIIGIDMKRLRFRQHLNTEMAHYATDCWDLEI

KLSAGWIECAGHADRSCYDLTVHATKSRVEMVGTHKFDQPEAREIVEIKPNKGKLGRAFK

ADVATILEALETLKTDVTRAQAFEDALALNGEATLGPMCNGKEFQLQRDMVAIKVVKKMV

SEEKFVPSVIEPSFGIGRLLTAVFEHSFSIREGDEKRGIMSFSPLIAPIKVSVLPLSNNS

AFEPFAMELENIFVEENVECKVDTSSVAIGRKYARADELGIPFNVTIDFDTIQDREVTLR

ERDSTVQVRIAIEKIGAVVETLVNGSATWDQMLERFPKVTAATE

>contig20948 Frame-2R

MIPGLCSACKENLRNIFCQMTCSPNNSLFLDVKEIRIMNGDDEHPDAVFPAIEELTYYVG

NDWIRDIYDFCEDDSSFSLLCNPNQNCRDGYGLMDFMGKYALNSIGSPLQINVTTMDTMP

EEMQAKRFCHCDNANLTNCILPMNEQMTSCVGVCGSLCSVGSDDSRVYSESCYGAVSGIT

SRTSGSRSTISDPTWAELNAYLSSNISVTDWTPLNYFLVIFGALLAFIIISGFVAAAFCE

RRPLAPTPHTGTSRVGPYIPEIYGAAYAVETNTGRLSYVDELMTNKLRVWAVFVSTGNQP

KKVILVVLSVVAVCVLGLYNIEIETDPIKLWVSTSSTSYQKRQHYGKLFNPFYR

>contig21820 Frame-1F

MNQKAKAKRDAAKLEASNVVDSAATAAMAGTCYKRPLQFQGSDSFQKSPISSIQTVTTSV

TSMYRPPSTTTIPPISPQVAQHLYDLDLSPRATSEPDDKMYLPSRIVSKIMYNALPRASD

PRGASQNIQSAQGCNAQEDHDSFQDSITISDDAVTFMQECVTEFLLYFTSEARDVSVLQN

RKTKKGIGLSISGTHIVESMDNLGLTSYAQVLSKYNEKVKEFQEAAARRKIERKKMTQLQ

RATAAVNAMTAERFGVYGHIGANSKPMLLDNTQKGK

>contig22586 Frame-0R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY54022.1|) 7e-32

MVILMGLLYSSVFYQFDETNAQLVLGLIFNAVLFV

>contig23080 Frame-0R|Blast-dimethyladenosine transferase [Phytophthora infestans T30-4](gb|EEY54413.1|) 1e-146

MPKDKKKRARNVGTASAAQNVMGRTLATPNTNLGQHFLKNPMIVTQIVAKAAIRGTDVCL

EIGPGTGNLTIKLLEQAKRVIAVEFDTRMVAELQKRIQHTEHINHLQIIHGDVMRVQLPF

FDVCVANLPYQISSPFVFKLLAHRPMFRCAVVMFQEEFAKRLSAKPGDELYCRLSVNTQL

LAKVDQLLKVGRNNFRPPPKVESRVVRIEPRNPPPPVNFTEWDGMIKIIFNRKNKTLHSC

FVTKSVLKILEENYKTFCSLNDE

>contig23303 Frame-2F

MSFLRNQKPLDIILWLYWGSTQDVRYYVDWQPGSSAYAVSSVKIYPNDVLSAARESCGDS

TWCHESILKVPLLFLSSGSNLIS

>contig23376 Frame-2R|Blast-peroxisomal multifunctional enzyme, putative [Phytophthora infestans T30-4](gb|EEY64084.1|) 3e-81

MRKQKYGRVILITSINGLYGHYGQTNYSSVKAAMTGFGKSLAIEGARLNIKVNIVAPGAG

SKMTKTILPSDIVAKWKPEYVAPTVVYLCHESVPCSGKIFESGGGFVAQVKYVRSAGVYL

DLEKETTPEAVQENFHKVTDFSQATDPEDDEVSPQLVQVLN

>contig23592 Frame-1F

MQLDERPSVSNHPLLENHETEATAVLGAPMSRNELERSAPREFASPHGSFENLDTVKSSH

AYNGTVPVKPKVALFDTSSQVSTEGFRQRAALQTCSLSWQHISYFIQPKDKASHRLRANS

KRRSGGPSGLEAELEPQQPRKIL

>contig23624 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57254.1|) 0.0

MNRALETIFPCYSRHTMTNNYYDYGEGSNKSNFVFLITYKGPKPIEDGRVILFFSPQPEP

EPRFEVYDLEPPSPIFAKDVKNVQPGDVIEFESTEYSVPEALCFVPPSLGAFSNELIVQV

LIHHDVNDPDANTRIGNTYSKPVIVRFDDDKAANVVTIVVDQVVEETMDLTANEWVEHIS

MKSNLLSKYHNQDVFMMASIVLPKQYETIKQAQLLPTVYYIEGFTGTEMYAKRALSFLSS

EMGSKWKAGRWPMPMLRVTLGSRSKFGHTSFADTDANGPWGTALVTEFIPYIESLYPATP

SAAGRFLHGHSSGAWATLWLQLQFPDFFGGSWSSAPDPVDFSRFQVLNIYEAQNAYWDVS

GHPYPTSRKNGVITCSNRDENLVERVLGRGNGGQWDTFFAVFGPRGSDGMPIPLFDKLSG

DINRDVANYWERFDICKLLEKQPKLLTTKLRGKIHVICGVEDTYYLDFACRSLQEIVGSS

NENAQDGSAVPNYVAMIPGDHTSIRSRAHYVQVYSEIAAVFQSNKDV

>contig23691 Frame-0R

MEPEIDDEATTMEDAVLLLLMLFVLVVVSFVLDRYSCNLVSQSGFAMAFGLAVGLLMIMG

GKHAVLHTHLNLDNSLFFNVLLPPIIYEGGFSIKRQAFFRNFPAIMSTAVIGTVVAATIT

GGVLYLAGASRVVTKLSWVEALLFGTLINAVDPVATLTCFNKMHVPPLLFNLVFGESVIN

NAVAIALYQTLHQWNVGTDLSLTQLLQVATHTSGMLVGSLLISATITLSGAFLLKRKVFS

SLHLFPSYEICLCLIFSLLTYYVADSLNLSGIVALFFSGTITAHYHFNALSREARHAFTH

LLHTISFVCENIVYVFMGTSVIMIFSGHPEARIGAALRVDDIDWHFIAMTLAACVVARFF

NIIPLLKLSNWSREPSDRIPLKYMGVMWFVGLRGSIAFALAKNWNYTGRYGPHRRLIEST

TLVVVLFTTIVIGGLTGPLVSKLHLTNHHSALRQLDSNVPEDSNLEEDPARILQRSSRHF

VLRRNSRNLEHHASHRSSKEDETREQETAIDSHPVFTSRPQFRDEDYSENDQSEDIPTLC

NETFTGTFIRNWHTFDVTYMQPAFGGLQSPANHIAVTEEVLPSTEELDKAQLQTII

>contig24016 Frame-0F

MERFDLDGKELTATETEVLVHSGLFHHGEDPNVAGYTMLELLHLARSAVASQRAMALNIA

AKILYHRQLQQQQGSCCVPRVLPSDMALTLRMVLDDQNYTALSAGIAALHAFIVPIPDLS

KDSLPESSFGTILYPRRVHLHPTAGSGYGKLSSSYSDEEVIYIKTPDTDDGNRLSDNELA

AFDPVQALLRMDLGTRLWYILKRIQLPDQNAIEMVLDILCVVARHSPRAAFELSSNTKLV

QLVQQQYIENDQVLAFENENRRALQLSLKALKLVRLLCQGQRSIASGLITSGV

>contig24063 Frame-2F

MTSSSINSFSCKFRLYAIRSMSSQPLTRLSCEESWKPFEVPSPIQTPYHAAAMPYDLPVD

PQQFDRATTIKPTSILRPHMRIFHLSWMSSITGFIGWYAIPPLMPEIKSQLNLTEGDVLN

SDIASTASTIISRILSGPLLDHFGPQIVQSVVLWLGAIPIICAAFVHSATSLILVRFFIG

LVGCVFVSSQYWTTITFARNVAGTANAITGGFGVSGIGFAFLVLPYIYQGMTSGNQVSKN

MGWRITIALPAVLMIIMASVIRIAAPSCPTGDFQELRKKKQQIEQCELSASARGSRSSCS

SVQPRKKAKPRSATNLLQSFRVVLTDRNVLILIAQYAACFGTELQLNNMGALYFHTQFTT

NECQETPENNLCSLLSKTTAATVASSFGLMNLFARALGGFVSDAANRQYKMRGRQHVQMT

LLCVLGTLVILLSQLDALGPCIALYVLVAIAAQATGGSTYGMVPYLNEQHTGTVNGVVGA

GGNLGGVVYGILFRSTEGYSTGLLYTGILVLACALLTPLLRFQHLHQELTASTPLPVEKH

ENSCE

>contig24900 Frame-1F

MLLLVLNVVGNFARYSLPHKTFRIFFTIGF

>contig25019 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58703.1|) 3e-88

MSSDKEQEEQQQRSRKRSADLSECIECGGRGIGLVIHPQKLCVNCARVTKAFFDPDANRF

CRDEGFVDISPKADGGVLKKIIKEGKMSGKLKLEEGCPTFVHYVGRLMDGSIFDTTRDII

DGKHVGGTDDPFEFQLGREKVIKGWDIGIATMNVGEIARFIIAPEYGYGHNGFAPKVEPD

ETLDFEIELLRFK

>contig26094 Frame-2R|Blast-similar to Vacuolar protein sorting 29 (Vesicle protein sorting 29) [Ectocarpus siliculosus](emb|CBJ48594.1|) 4e-17

MLMALQGRKVVAFLYELKGDSVVVSKSEFAKET

>contig27260 Frame-0F

MARSRKSLTTTIDPLFEFDAPQTVVDLSVPFVPYPVGTHDPWFDQVHSQHSKSSAELARE

LAIMVRKLKKKKQQSQRNLMRRERNSSSNKENQQPADEARTTISLPEKRNNFTKLRSMRA

TQEPLKLHKTKIQVKKVSDAPTKSNKRPLADLGNRLESGRKQASSESCEKTLHELLKQHN

RRFKTKHTYEPPQHSVRIVKQWERATKKSFYALSADERVLANKEIAVWKNQREEKTL

>contig27930 Frame-1R

MCVTVFTVSASLVSITAAAKSRERATETAATIVVARDAEAHLVRSFFVPRYEIEMITFLD

MLTSEGIEYGGITTCAKHLKIT

>contig28067 Frame-2R

MYENRLFQFWMEFACVRNEEAEAVQILVKKAMKDYLNYK

>contig28434 Frame-0F|Blast-tubulin gamma chain [Phytophthora infestans T30-4](gb|EEY62376.1|) 0.0

MPREIITLQVGQCGNQIGMEFWKQLCVEHGISADGIVQEFATSGHDRKDVFFYQADDEHY

IPRALLMDLEPRVINSISTSAYRNLYNPENYFVSKEGGGAGNNWASGYHQGEEHHDQLME

MIDREADGSDSLEGFVLCHSIAGGTGSGMGSYLLENLNDHFPKKLIQTYSVFPNQSDFQS

DVVVQPYNSLLTMKRLVLNADSVVVLDNTALNRIAVERLRVENPTVSQLNSLVSTVMAAS

TTTLRYPGYMNNDLIGLVASLIPTPRCHFLMTGYTPLTIDAHVSAVRKTTVLDVMRRLLQ

PKNIMVSTSTKTGCYISILNIIQGDVDPTQVHKSLQRIRERKLVRFIPWGPASIQVALSR

KSPYVETAHKVNGLMMANHTSIGALFHKLLLQYDRLKKHGAFIENYRKEPMFADNLEEFD

SAREVVQNLVDEYKASERADYATWGLPPTSATGDIPMS

>contig28997 Frame-1R

MAILSMHQQKSQKHWVCSALQLVFPVASASASTLGTPMVVAMDIDQ

>contig29345 Frame-1F

MIETNTKDINSLATDVGMKSSSLPRILPWLELFRRAGFACDDELCSRTHKAIDSASRLTA

WEFMDFFSMPFNDPDLPRQREILSIYEVADTKEEFLRNTFRVKKFPIIRNYLNIARRNCL

LTFLLAPVLSSVFAVEKLRNYHSAIFLTDEIITGLFIEWYFSLPLAAVFALPPPTMSSSL

QRWLEPCFDIIDAETEISEEENDNADNAEALFESTETHLRRLHNCPIAMVEIFNSCCKTP

KLFHGFVLSEHCRWGEMESAKHAEEDTLGKYSSAGSGTRWRILQDCIAKTAHLSLRLGKA

GNLAIKTVEHVDDIMRNIAVMQLNDGHDPGEEEAAVCDPNIKANATSGSLDDWVATLENC

QKGAQMKDWRAVLRAYPQFANKDALCCFRVETLCVAWNAKRSAMRQLEDALLELDCLASL

SIKAAMATYIWERYIRIHVMTLVTFWEENAAGKKPQRGLHPKIAHQFFGIIRNLLVTLLD

AVKAVRTAPALSTEHVMDEVESENDCYYGDADAESCDDNNQIEVPFTAEFKMESLTHTTK

WFCQLKNLQNLFQQRWPPSHNNSALMQALQCIKLDMISITQIEDHISLMLLLDSFAATAV

TPISVVKLFSYNGRYLCRPDTFLVSEILVKPIEEEANLILRDRTIFLKELLRHDDALGFA

LADTFGLPLEVIREEHVLFLYQSGRDERADAAIETLQRPERLVLKLGAIARARLALILRR

MKTEAEYAAMMSMLPADLFTWVVSDNKPPLVADPQVEHFDLMPSLTSTHYLLLRCLAMIP

PTGKEFEMVSAMSVLVKDVISQVKLRS

>contig29895 Frame-1F|Blast-nucleolar protein 10, putative [Phytophthora infestans T30-4](gb|EEY53610.1|) 1e-107

MAALAASSLNGVKIYNLSSGKTLPQWLAEKGGNRKALAKDEEYRRRVELLQDFHFRAGSQ

RVRMSPDGNYVVATGLYPPLVKVFDVRDLSLKFERGLDAEIVQLEVLSSDFGKLAFLQAD

RSVAFHAPYGTHYSMRIPRFGRDMTYHRENCELYVAASGSDIYRINLDQGRFVAPLELQT

QFSAANVVDLNPIHQLLGVGCDDGIVEMF

>contig30048 Frame-0F

MENLLAEEVQQAKVTDYNNLRLTLELESAKNTNAHMYLHQRFRLCVDRLRLKYPSNEYVS

>contig30350 Frame-2F

MTIKLSSLYPSHKFIFSSRSVAFLGTPHF

>contig30884 Frame-1F

MKKASKVFAPLTTNCAVLHRPLRRRFFECRVNFFSNGGVQMGTRLTAKEIAKRRAKRLER

RPVSDKDMAKDSLFIEGSMRMYYRHLAIVEPVNVDPKAWPAKLDQTHDHILSSYMAALTA

YYGGDNLKARKSPLLMTAAIPYFKSSLLNFNTNLEKGAHDILVFPDSVRVHNITPSHIQK

LVNKSLEKNPDLIAFLDEQNLRYTRMEHAYHMMVCGHASRDERCGCKGPKLLQWLKELAP

EAKMPLNLWISSHYGGHRYAAACIVYPSGDWFGLLNDKDKAKAMLDAVNNKDPLCVYKLW

RGRIGLSSQEIHHAMKEKIVTIDECAP

>contig31249 Frame-1F

MTLNMNGMISDHEWHLLILKAKGIRHALSIRIFREESKPARNSGHMEYIVRVVDVESGVV

WFTRKRFREFHKLHRKLSRLSNQVNDCVFPARRGHGRNSPNQLAYDRAPVLENFLRTTAA

LVAPSPLSFLHGVALKQLQHFLDVPHVGILERNRTQPISRELRVFVYHTVNDYTSPEGKA

CEKFLMKMRRSNSEPGKNVLDEIGEILDGVQEYMLEHRFAEMELIVQRLMKQILNNNSGN

LAANRHSSFVNLMTTDALSNQDKLQQLLSDAIRHELEDCICVPLMWDLTQHLRRHVQHEE

RQFRDRVFHLKGKPQSYFGVPIDKISLSSWRSVVDIIKEIDEAFLPLDKMRKLVATAHQI

HALYKIERTMYLKSPPHHRRRNSTPMAGSVLQVQTSPISANRTLSPTSSGSNRSLRGLTV

GDESEAPSEVNLIARDQKHGEMEATTSMQDNDVLSGDDFLPIFIYVIVHSNLEAPILTQV

LLNRLCDPEKRRSESGYYLATFEAALHHILSLKLPGATGDNGSSRIN

>contig31924 Frame-2F

MRLLSVTLLTIAALLSGVEASRTLVQTTTAVPTKPNVPATRPAKIDYSRLRRPDKHNVYK

GKPLKRTVNRGS

>contig32745 Frame-1F

MSTLRQFNAAMKETQVATIRCNTCMH

>contig34170 Frame-0R

MQTMRFHLNKRVGRSTPFNATTASDPSLWNDGEPPAPPLSLSIALRDLMADAEAQHDGVD

FANFINFAELPQLPFFRPNHMNWKRVERSSAFTLLKRKDEVLAQARLDATIEEVASVLGA

TTDQLHAATMEGLYDNSFIAGSVAYVERPHEYENDRALQHVAVKTSNFVHSNILGKNEQW

CFGEVLRSKPEGDSFTITQISLDAHQSQSLPARLALKDSKRRVAQLRNVSTAYLVERTAG

SRKLRITFHALHKPDDSLNIDDDNAPVMARRAVRTRLVRLARGTSELSPVVRRRRFGVQV

FADHSAFHVRNPRCICCTRKFQHIINLIPRSRCYLCGYYVCTSCTSTEKMETYTGQVASI

LVCVRCVKSVIACNYDHMLSVRPGPERVLPDELSSPHSVSTADTSSTAASDFSGYSESPS

SEKLGDLLTQVVSDDSDQVTQGQRRAAFMVLEQLLLIDQEEAQSQADKNAQLLHSTNDQY

QSTEAAKRALSVNNCPKDLDACQFASANARPYPMMAAVVPNENEPAQEGSVVYPIPANEN

ERLAAIEHFHLHDIANVPELNVICSLAAAEMGCPHSVVTLVEQEVVTLLATNAPHYWDIG

SGNPREQTFCQHFVMDDKPLLVRHAEADMRFYHIAPVTMRSLRFYSGFPLSVPCVSKKSG

KAEKVVVGALCCLDEKPHEMTRAQYWRLMKLADAASSILEKTAREYMADPENHFLRQRMA

EIQSYKGARPPTVTC

>contig35151 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56519.1|) 1e-40

MEIVSSRYKHSSYIVEAQLDEVRALEIYQDEIRRAEQVASDEAVALSVYAEEEEKLLRDI

LSKPSPSCTCCVSPLKYESSRRMLSCGHLYCKDCIATRCRMAVRDRSMVPAHCCKREYPS

DYVEEALNTAEFNTYKQFLNEKPWRSLDLQSDRDYANVVQQNNGVQCPGCGMGVQRIAGC

NHMTCLNGHEFCYTCGRQWKTCLH

>contig35322 Frame-1F

MADFSLSDSSATWPSSGTNDGKRPPLPTSFRPEKRGRSSDDGPQDGSTPMEVSGTESPRG

QPEQRSIDDLPHLSSWKSNAFYTDGASGDVNTGTYTRVYLKVKAQSRLGETVHCSGSSFV

MGHFNPNESMTLVTTPDNYPYWTTVKPMILPRGVPHQYMYALFSGGVFSSWEQIEHERVL

IPEGREMLVVEEYGKYNQDMDLVPTGERIERSLIYERRKHEVATTIPTNLSADTLSTGDV

ESKETEAQLMNRIVDENFLSDTKSPLSSATGSPGQRFRQTNKLQSRYKRYISSNYHPSPD

AMLFLVCYHLPVKLKKSTDDGSWSATWNRDSLISRSKNSIAESMNTTWVGCVTYHARSDM

EDLSDNDKKEITTILAEMNCIAVFIDRQLAANHHGGYCKSKLWPMFHNVDILDIYYSIWD

RAEVIEWKEERNNGEWWDAYQTVNRVLANRVGKLCKDNDTVWVHDYHLLLFPSYLANMCR

NEKRKRPKMVFFLHVPFPTSEVFRELSHGTQLLEGVLDVDVVGFHSFDHARHFLNACKRF

LGLTYQSRRGGNLGVDYRGRNVVITISHVGIETTLIREVLNDPNVQEAAQNLRRKHEGKV

LIAGIDVCQRLSGIPLKMLAFEQFFSNCPSWKDKLVFVERATLTQTRLGDQKYSSNEISK

LVERITKAHGPECIDYEESSSPLTIEERVALWLASDILMVTSIREGLNLKPLEFVYAKGV

NPIDRPGVVILSEFSACCCVLNGAVRVNPWNITGLVNSLDHALTMVDGERLGRRARDLPY

ITNQPAANWTKQVLSVLQEATENPEGDEEYTNMEYMDMEIGRSHVMRVGDRLDFKQLNID

KVMEAYMQSKRRVFLLDYGGTIIAREHIAMYVKKDFTAVAGKRPSSRMMEALTNLTSDPR

NTVFVVSGVSKANLSASLGHIRGLGLVSDNGALYSWARSIDVENIEDTSMHDDNNFSDRF

WHQHNFKFDWRPVRSIVDPILKVYCTRTNGSVLRYAQQGIAWNFRSTDPEWGLLQANSLQ

NDLEEVIRDLPVCIIRKKGLLEIVPEGLNKGVVARQILTQDATISHGHPDFLFCIGDDTT

DESMFKAIYDYYAERTEENVLGRGPGSYEDFLASSDEGPLYHVFTCTVGKKPSNAHLYVN

NVDEVELLLQALGKASGE

>contig36378 Frame-2F

MHILNEWFSSLKQGVTSLTRLHTDFFVIRLGLFRLVAFAWINGVNCWVHNLLVRWELLVE

RRSEL

>contig37175 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57715.1|) 4e-61

METMTSASNTRAATLIAWLKRLLEEHSNETCVSLNKSLTLHLLGVDHREGNSGADTFSIF

QNFIRHVAIDTHLSSLTLVLVGPNLERKLNLTRFTQQYRDSISHNKCNVEITYFVGVFDA

FFENKKHYIEPDLVACFNAGIWGYEEWLPAIRFVLNEVRVPLLVTSYNKHEAGDDEDVLD

KLKPNKWLWRPV

>contig37207 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66463.1|) 1e-69

MNRLVMDYLVGKGYRDVAEAFWRDSGTKPHIELQLVQERMSIQQLLLKGQIQEARSKLTS

MDPEFFKKNCSMDFLLAKQELIELIRVHNIEEALQFAMKYLAPFGYKSPQFLNEIERTMS

MVAFKNPSDSPLRHMFEQCQRRRVANDLNSAILRSQNQKL

>contig37416 Frame-0R

MEKAPPGSGPPSPTASEISFQIERKTETEQVRANIEKFVDGLISEQYTMAELLNESFSLE

MLELLFKRMTGRLRVILFSKDKTLEFLRLTLDARYPRHTRAVASQFIVVGGAMNAIAACE

PGQPHQCSDFWDSIFDMLQREADGVSSKCDTPLRRKERQASVAELEELIQVAVEVFEKDG

AQTLKESFAEHKDEIEDEADAIRRRKSSARSSLGDDAARKIMVSPLPSPRTCASGTDSLF

EKITDEEVRLHRDSAEMSGMTENDEEFDSDEPDDTGIPAPLTTEVNETAMYGIFSHDSAN

FASQVLRYFAIRGQKGACILHFLAEHPATVDMLLANVGHDDIRTLLLHLIYAEHSEAAIT

SLFETHMMQKLIQKQVTFSPPRNTFERDCIENTFLLLREIVHAPYLTGRGVAISAKTIPL

DKVTGQDEYVSICGASRETANSALRKYTSRKVRR

>contig37625 Frame-2F|Blast-amidophosphoribosyltransferase [Phytophthora infestans T30-4](gb|EEY65962.1|) 1e-142

MALSATFLSKITCLICVETWELATADTRPLVPAQVLRHSRFIPTPRTASHSPHNGNLTNS

HELVDQLANTNFRHVNTDSDSELLLNILASELLKRVDQILDTEMVLDAVTGVFQRCRGGY

SAVVLINGFGIIAFRDPNGIRPLVYGTRQTQYGSDYVVASESVAIATLEFKLERDFAPGE

AMVIKQTGEMTTRKCVANAKLSPCIFEHVYFARPDSFIDGVSVYQ

>contig37698 Frame-0R

MARKYSETLSLLLPSKHLICGILLQEVLNALVHSKLDFAKSCSLFGNVVILHLRKCFEGN

ADVSLKQCSVEKCSVEYDHAQVASTTTTTDLLTMLQSLVLKEDDVGDLTRHVLSSGPVMR

VLVRLLNLSRQRRRQEMLLDVMNVVVRSANGNQEWSRQYVVLELVHCAYTGPLISAKKAV

ALLESIFRHSSNDICALMWMILKQCTKRCCGCEVQDNVVKPALLHSNYQIRADTFAELVK

AMMLSIPANAVCEVRSFVEQKLSSCFIGKTRINLFLLLLLRKLVVCEHHCGVFLPVVQLA

ICPLASSNFEQIRLIQLQLLKVLCTRLVTINCRSVALHKAEVWKRYEILVCNERLQTDLR

QIINASSGVYSNVERISRASIVLAQNILTLTDQLRNNQCPSRRRPWELNGPEAKMK

>contig37782 Frame-0R

MKVEREKAFYEGYQNAQTKVESENTLRKAEPGMFRAFHESAVESAEHLGADTNGNVRNDS

LEDGQVLCSPTSCVSVFTDNGVNDLHVKPTDDWGEW

>contig38457 Frame-0F

MDFDATIERLNALKLQERGSNLNRNQHSAQLQHEVRRLQEESERRVQNQERQLQRWQQEM

RQLQTRLEATEHQNKLLKAALGEVDTYRHQTETQQVVIEQLQTQVKQLRITNYRLQCVVQ

QNEPRGGQGFFLPPPPPD

>contig38633 Frame-0R

MPNSLIKVLLCYSTMPSQIALYERPT

>contig39520 Frame-2R

MRRKGGRDHLSDVFMNDLVLLSPDQDYFSKALITSRGSHGKTKEANEKEMHETKRVGYLA

IVATQRASKEGLTMTILRPGLAKLEKMDNIYLFKLNNLVTSVREFRALCDCSHYKLLPLL

LSGEHKQGTMQLDSLGLKYVQWLHKAFNDSQREAITAAATSEGFTLIKG

>contig39744 Frame-2R|Blast-peroxisomal hydratase-dehydrogenase-epimerase, putative [Phytophthora infestans T30-4](gb|EEY60538.1|) 1e-139

MTFDIKKILSSPEATFTASYNQRDLLLYAVGIGESALQFTYEFDENFAAFPLYPVCLPSK

GQLQDVVPFPPETTSFIPDGMPTVNPAMILHGEQSIKIIRPLDPAGGLLTGKTKVISFYD

KGKGALMETYTQFEDAIGPVATLISGSFIRGLTGFESQGRKLPPRVQIPKRQPDIFDEFQ

TSPHQAQIYRLSGDYNSLHIDPNIASSVGYKQPILHGLCSMGVASRALYKHFCRGVVARF

KSIRVRFSSPCYPGETIQIRIWNEGNGKVLFQALAKERSIVILDSGEFLYDVNASSRL

>contig39836 Frame-0F

MDSFGFDFAGGDLLDLGSLGSWTNSAPMGNSPNGANGGSLPFSVGTPTGVQSLGDDPFAS

MPSGGDNDFSFGDSPKPSPCVQTHKLGDSAALSSAAASASTPSARPSSSSGDMAANYFST

DVEASSLTNHGTSTSTLTTDTSSTSDEKAKMNVKHATEIKKDAGSAPPSSTQSMSNATPS

NLSTAPSPAPLKSENSGSSTDKSTSTATPSRSTLGSDVAGMSNSHASSSNVTTSAPSTTS

SARPHIGNQQQQQQQ

>contig39843 Frame-2F|Blast-vacuolar membrane-associated protein, putative [Phytophthora infestans T30-4](gb|EEY67603.1|) 1e-100

MRQMTVHSAAQIKLHVHGHEFQNGEEIILNPESFLQLKELVWNDYVVEVFHPDCASEQQL

QHLMASDGTATALGDGSPKNHLLLEIQQSSSAPLKGKMQVSVLKDTAAIFQLAPFKDVTV

RFLPKTKVHVDFVEVALKDQFLSRRDLMYLKQSMVGSALYVGKVIRVQGTRWQVLDVRSG

GEKVRSGVISEHTKFTFRSRSSRIMWLVQICPEMWDVTNSGMLYLEIFLLVVQN

>contig40151 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70038.1|) 5e-10

MEKELTALQKVANISVTNGANQGELPALTSDELTQVLEELVQQLVDAFREQQVQVLHAAT

SQRVKFEYEMLHDYPGLDILVLACASFGRFVSFAIPLLDQKRQWDPKRVFKTENADLIFV

PDGFETPN

>contig40322 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53677.1|) 2e-61

MDTNKLFLQKLEASVYGSGIYSFATPGSVDMEMLKLSGLGQLRAGSIVARRSDVKVWGDG

ELFVHVMDKLTYCLRRFGPG

>contig40429 Frame-2F|Blast-RecName: Full=HAM34 proteinemb|CAA34853.1| ham34 [Bremia lactucae](sp|Q99074.1|HA34\_BRELC) 1e-89

MKFSQILVLAAIAVAAISAQDAAPATTPDTATATTPAAATTTTTTTTPAADAGTASTEQT

TTAGPEAAGATNGTTTTPPADGTQTATAPLDATATEESSASGEMTPTVGTDTSDQVSDST

AAGPSTPEGSMTGTSTPKASDSSSSATDTTSGASHTTMAVACATVMTVGAYFL

>contig40928 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60285.1|) 2e-50

MFGKWAPNHLLPTDRPRFSNRDGDKAMSFEQVSLLPHWSWTTPWRIDKSYTDCDDEGWSY

ATDFPRFKFHLARGKSSMKRLGASVRRRRWIRMMAYVPPETGTDPMSSLHSSVRSNRSRA

SQNSSSSSIGS

>contig41170 Frame-0R|Blast-beta-catenin-like protein [Phytophthora infestans T30-4](gb|EEY69790.1|) 1e-93

MVNSLDKHVRRNALAREKYADDPSKFLESEMALDSELSRWKKVAAKPELFAEMTKLQVPR

VLLGLFSHENIDVRLSVLSLLADFTDVDAAASSLEPARMLARNLVDEKLLPLLVTNLNQL

AKAVGSENSEQAEEEKMGIYNSLQILENMADLEPQVCGQVAETPIYSFLLDQVAPKKVFS

ENKLYASEILSIMLQSGAKSREKFVSWIGKIKQTDEQREARNTKVYLMDDLLQALAPYRK

KDPSSEEEK

>contig41523 Frame-1R|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 4e-28

MCINIFNRKAQQITNFSFDEVVGKKYVETFVSPQHQGLVHEIMSRALDGNETASFEISLI

TKTNRAVNILL

>contig41668 Frame-2F

MCMYAARIIPTRTSCGMAFPLIDAHCHLHDKQFRPSGTLSNHQVLTDVLLRAQNARVSHV

VSCATHEEDWRVLEQLMEQQGHRKYLTILTAFGIHPWWAQKCTSSSLQLLRNILMRYPAA

SV

>contig41714 Frame-0F|Blast-serine protease family S09X, putative [Phytophthora infestans T30-4](gb|EEY70528.1|) 1e-153

MGANVSSDMEIFADGEMETELKRLGGAGDASVKEILGKGYHDVVQAVIRPTRVRYDVQQL

GPESFPIAELSVAPTHDTATHTKRKDFDVYNDRGLRVCCSHWQLFTASSNTPVVTPCLIY

LHSNLGSRLDALRVRDAALQHGFSVLAFDFCGSGISDGVYVTMGWNETLDLYAVLQTLEE

DMSVSDICLYAHSMGAFPAITNLAVRAAGAADKKMKAKLQTLPHALRSGHSLKQLKPIRA

IVLDSAYASLKEVNTGLLSEIQQEGFVVPKAVIKVALAAINKSIKKRTEVDIDLLCPTDF

VELCYAPALFVAANHDRYVSKLQSDELAAKYAGPSKVLCVEGQHFDPRDAITYAQAINFL

YRALH

>contig41835 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY58876.1|) 5e-51

MSCCCPGLVVAQMVTRLGLMPFYHVLIIFCALYVVALTAVMTRIDFFNFLFWLCAMISVL

CMTRLRWRIRTLFSLPGSHAEDFAFSLFCGCCSIAQMATHVESYQPGMFAFAPRSTLPGY

SAC

>contig42041 Frame-0R|Blast-polycomb protein, putative [Phytophthora infestans T30-4](gb|EEY69291.1|) 5e-42

MKKWNRHVKEFKILADFMVASSCRMFARKYGKWLLDHGLRHNFLLHLLNLWDNSLLNSRA

IIDCMLIVDQNQ

>contig42175 Frame-2R

MNSSELTPAPLRRQSVTTTAVPTSAKMLFHNTALTSVSSRKLSSRRVKRNLSP

>contig42625 Frame-2R|Blast-hypothetical protein PITG\_14592 [Phytophthora infestans T30-4](gb|EEY62972.1|) 8e-32

MTNTDKGLVEGIEALEKYLEQHEVANLKLKQGLLMLTKAKLRLPEHTLTEISYRENFHAS

RVVTLDSEGTWRLQDTPKLDYNGVDNSTLRNRKASNNINVSASTPSTCMESLLWFSSLPP

TDLRQTQKQFLDGESSLELNFAY

>contig42782 Frame-2F

MHCALAFQLMKDPQCNILQGLTKIEQHEVRHLITDMVLATDNNVHSTYLCKLENLVSRAT

EEGWKVADPDDSRLLLQMTLHAADVSNPAKSLHTYLNWTERIMQEFYQQGDKERELLLPV

SIGYDRKQPIRLEKMQAGFIIGIVRPLVFTLGQLPNARLDHCMVQLDANLTHWQDKMRRN

QQPLSSRKPLVSPKEGLDAGFPFLVAVDIT

>contig42838 Frame-0F|Blast-translation initiation factor eIF-2B subunit epsilon, putative [Phytophthora infestans T30-4](gb|EEY56405.1|) 0.0

MGDNTREVPLQAVLFADSFTETFRPITLELPKVLLPLANVPMLEYSLEFLAASGVQEVLL

FCTSHIETIEHFINCESQVAKRLYVTCISSPSCLTAGDALRELDRTQLVQSNPFILMSGD

VVANIDLQEAVAEHKSRKKLDPNCIMTSIFKELRPNFVTSVRPLDVELIVGIDAATSQLV

LYEDKPEECSTRLATLFLENHAQVALRSDLLDCYLDVCSPEVLLKFAEDFDYQDLRRDFL

HNEVQNYELGKKFFAKVVTDGFAARVMDPRTYAGVSKAILQRWLFPMVPDANYLGAGQVT

HFEYLRGMRYKDANVSLARTCDIQRECILGAGTTVAEHARVLKSAIGKNCVIGKKVTIEG

SYLWSNVIVEDGAVVKKAILCDNVVIKRGAIIGEGCILSFGVVIGDNFTLPPFTKVTKSL

AQVTNDGFFSEEDDEALLERKAHAELGILAQWSAKEVGVGGVGRIWTLDEEDIVVNSESE

DENDDRDNELAEANRQARRLEVLKGHLIGANDIVFKKMQRWEEWDTLSSSEEEDEEADHI

LTGGDATALVVPFHQIIRENVCTGDAAGHNVDDLFMEIKSFKFAQNRSFAEVIEAIVPGL

LDLVPTGNGQSAMTVLANVRDKFQKWSSVIQRCLVEQKDQLAVVYALEGYCAISEEHRAV

WTPLFRFLLQIVYDLDWVSDVIILDWHAVKQANIIEEETLDALAAASKKDVEEFICWLQE

SDGDESEEETD

>contig42962-0 Frame-1F0

MKRRVILTYFMLISVPLSGPSKLV

>contig43064 Frame-2R

MDSIRACALLEILAFMAKITKNSYSLAGMASSWPHAHVFYAFVLVAHISFFFDRSIFFLQ

>contig43910 Frame-2F

MAPLPQGPVRPLPHEYQLISKCGITFSPVKRGSRDILDTIKYQCDCAPRSVSMGEYVASP

RVTSSHVQGFSESDSLLEKSSYAVDVHLPAVARPKEPPRSSLWGSTFTLTNTILGSGTLA

VPFAIASSGWLMGNLVMLGIAMITRYSVHLLLSASDRAGTNCAKTYESLGHYTMGAFGTR

LAEFTFIFGGFGTLVSYLIFVTDLCAAVLRVSSQDKWMITVLLVATTVFPLSLSRRIGKL

WLASVLAILSIGYVVAFVLVAFLTAYNVDNDARRPDVRAIRLESGSVYTVTLLISAFACH

NTALPVYEELKDRTIPRMNRAVIG

>contig44065 Frame-2F|Blast-60S ribosome subunit biogenesis protein NIP7 [Phytophthora infestans T30-4](gb|EEY62450.1|) 5e-90

MRPLTEDEMQSVFEKISKYIGRNVQHLVARPDEKYCFRLHGNTVYYCSEKLMRQSTNIGT

DELMSIGTAVGKLTKTKKFHLRVTFLDYLAQYAKYKVWIKPNSEMSFLYGNNIVKSGLGR

ITEGTPQYAGVVVYSMNDIPLGFGIAAQATELCKDLEPTAYVVLHQADIGV

>contig45048 Frame-1R

MDSSNAFVGDFGVNMYGGDNRFMNQFDSSGGGNVMDLSGGLDFSSGMNLMTDSSMMLDGN

SSASTVGLIDFPDELNSPTTLSSGLSSS

>contig45509 Frame-0F

MITIRIVISTVKLACYALVYWPIQGGG

>contig45596 Frame-1R|Blast-cysteine protease [Phytophthora infestans]gb|EEY64276.1| vacuolar-processing enzyme, putative [Phytophthora infestans T30-4](gb|AAY43369.1|) 5e-30 NOT\_ORF

MPITSY\*\*FPSSLPSIGL\*LWLALADSNYWHQSDVCHAYHVVRHHGIPAEKIVLMMYDDV

AWHKLNPFPGQLSIGSFPQSVTREELSSVNLYKGCNIDLRGAEVTPETYLNVLT

>contig45602 Frame-0R

MCIAYGMFDNSDASIFICLTSLLVRLRAIFLTSIAPFEFNRRMRASIHIYELNDKYNFQK

LVV

>contig45884 Frame-2F

MSKSLGNTIAPNDFIHGCTMSLSVDTPIKSKKSKRGQTSTSSRKDIKVPAYGVDVLRFWV

ATTDYTTDVSIGPAIVQKASDALRKVRNTARFILGNLKDFDPVKHAVPYDKMQISLDRYM

LHELHSLTQTVTTAYDSFAFNRVQHAVSHFLSTDLSAFYMEAAKDRLYCDAADSETRRSA

QTVLWLSLQALTRALAPIIPHTSEDIRLHWVSQLQGDIPLDDVSGSIFLEQGWMPCAKEW

QNQDLAR

>contig46405 Frame-0R

MGIRTLATVIVIACVASCSRFAGAKKAVLDIIDYDKNNRLRRRNSLSLGKTDAYNEERIP

DAPTVIPIIRNVNGSRSSMWSALFLAYLAILAILVAVAGCAAFST

>contig47129 Frame-0F

MQLKSQVQWINRMNLQSFLVRFLSEQDCWYRRHRVHMLDHADAESIVFAF

>contig47622 Frame-0R

MRLARHSFFQLVDTFFSSTCLHKAVN

>contig48388 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69700.1|) 1e-74

MVHPNNTKSRKDFVVLELQQASQYKPVTLDEAQTIVTPGMIGGRIGWNDTLAEAVQSRYL

HSVEVAFISNKRCAAEFPVDESNLCSNGLLPAKSCMGEKGAGIIVKNESHAVLVGLVSYT

EGCGKPGGKNIYARVSAVRPWIDTIRQNT

>contig48506 Frame-0F|Blast-50S ribosomal protein L17, putative [Phytophthora infestans T30-4](gb|EEY70259.1|) 4e-36

MKHRVAFRKLNRTSAHCQAMLRTMVTQLIEHERLRTTLPKAKELRRTAEKVVTMAKQGDI

PARKRAQGIVRTPEAMAKLFDVVGPRYA

>contig48599 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57375.1|) 1e-35

MGLSNATDRDVPTTFLPDGVPELEQLAQQLRPQTTWVQQVDVV

>contig49000 Frame-2F

MHALRIKSSSPMSWPKLSDRSAPTYELGDLLLFALKISPAKPAQRRMKRSQSYGV

>contig49259 Frame-1F

MMSKKKMGKSHDAAKSLRHIDLFSKRNECCLSSGNYACQCCPLQYAEEFSCTASERREAF

>contig49332 Frame-1F

MSAQEIKAPAELKEAIKHQVEFYFSQSNLSNDAYLVSHMNSQMYVPVEVIINFAKIKQLT

DNTALLVESVQDSTVCSLSSSKDAIKPNIKSERTTIILREIPSSTELQKVEAIFEGCGKA

ISARSDVGDTWFVTMKSESEAVSTLLALRSKTFNGAAIKARLKSENVLKSFYPTQPVENV

IAPTVGAPYGGRGYYASTNVGLYDNYSVPYGRVNPRDAHINNGADNGRYASNSQ

>contig49538 Frame-1F

MSTLFLRSRRLLPCLAAPALLLSTSPARLEASDTDSASPPAVDFVGVFVETESARRLSQK

FPSKFGAVSEPLVVVLRFQPSIEEQEAFAPLFGRTAKLQVKGLAEDDHVQTVLVEVTTET

GESLEYEGSAEPAHLTLSTSAAGLSAGYSSVLLERLRASDKLRYLLKDDEEKKHWSGELP

IFESEHLPLFSPFPAVEAKLVKEQDELVLEGTICLSSRFDVASGECLAPKAEFGFCKFMK

AGPCGKEFIAWETCLDQCKKRGDDFLETCGPQTLGLRDCVEANPEYYHVLNEGPGEQDSE

LQKEQDSKNLEFPETDE

>contig49611 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58060.1|) 4e-25

MGFSAALAAHALQQSSNNLSDAVAMLIEGQVEKKDHRMEIDDKTETTTDVGIEHHPSIFP

LQSFLNDKKMDKLRELAATDSFQALLMLEQNFSSEMLHQLNENPVATLRLLSAPAIDSSI

VTADNELKIDDAIDSNDAKYGIVANTVPNDAINRLVAMGFPSDVVEMMYESCGGD

>contig49989 Frame-2F

MAVEWLMGDGALTYQQRQEARRLAQASLAFHELDGEAEQSPCLALEGRATELQNISGLPY

CLTYCALELSNNDSNRAMEWLMEFGNVYAEDPDLLDLLKDPFSAARMDVLDDRAALEEIE

QLDLLVTTHDRHNNSILEDLGPAPSMQNADLTSASNVDGMGVSLAPILASRQAQINLTIA

LPQDASMNAYPPLDPEYLTPNILLVVTSHTGSVQQLRAGVYQRYSSDNGVLLTFLNTETG

AYENEWHSPRDLRRIEKIYDEPLESVASIQRVALKTENALSIFYARRAITALLCAFNSEK

ALKAPAFEFATERDQDIEKKPPRVLFSFSSQIYGVVGSPVQLISLLKLVAASEMNSFQHL

DIEAMDMFAQKVVGGK

>contig50028 Frame-0F|Blast-CASP-like protein [Phytophthora infestans T30-4](gb|EEY57173.1|) 9e-21 NOT\_ORF

MSRKILY\*QVEHRSRTLVSQLESAQLEWAQRRRDYERQLKASRTELREAFAKLDAMQSDL

FAHKQRSGIAVFHLMRRWRL

>contig50154 Frame-2R

MLLAARCASSASPCWLAPMLRMALILMAIKPPSRLTCLARFARPRHHSVTQAPVAAVSQS

PPSSQDRPRRALVRACLYSFRARACA

>contig50587 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57841.1|) 1e-103

MDWLHIWQQEYEAFVQVLDADEESMRHFAPTVAKQYMNEIETEATRLLQGFRTITAVLVQ

QLGISNVDSVIDRHGWTLLMQAANLGLSEMTQELVTSKANVNYCGTSEDDLNPLYLAIES

EHTDVALLLLQRGAIESSTKVVKHSAIEKDDGSEDVCIIEEDCALFQACRFGLVNVVKEM

LALGVDVNFALPSTGDRALHVAVMSDRKDVVELLVNWGKIDVNALNKSGQTCLFGCSDVE

LVKLLVILSSVDPNIKDVDCETALSIAQALGDESVVEYLASVTHL

>contig50851 Frame-2R|Blast-malonyl CoA-acyl carrier protein transacylase, putative [Phytophthora infestans T30-4](gb|EEY62333.1|) 5e-45

MEPAKLELHEHLQQLLYDEKLHEPKVPLVWNVEAKASKKTPVEIARVLEDQVVHAVRWSD

SVDFCVDNGVTHFLELGVGNVLCSLIRQQVGKTDILTSSGGT

>contig51733 Frame-2R

MIRRGEKRISDLTVSDDLDVTGSYESNNTILRRNYVFLANNNKNTDSLVLKSKSFDKRYQ

NLHESSCMVIFIRWLNLQRS

>contig51939 Frame-1F

MAAHACRNGSPLVCSDLNRDVRFAANPWRRDVLQAQFYAGIPLTLSNGHTIGAIEVFSIT

PRFACMDVIAQLQTVVRGLLRKFEEILATKDSAGEKTKKASTGRRSPRENDHSKQRTPRA

PAPCPPSAPAIP

>contig52220 Frame-1F

MILARLGRIYLVSSQYGIETSHVTRRTQWRADTKSATATVEVSQPAIRVENIVLLLNVIM

LPALLFTAASLSHLRRLSKSY

>contig52642 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY65264.1|) 5e-67

MEIAIMRQIDHPNVVKLYEIKKTDKHMYLVLEFCAGGDLQHYMRRQQQQSGSNVLTENVA

QHFLRELAKGMQCLWQHNLIHRDLKPQNLLLVEDSPTSALKIADFGFARHLATASMAETL

CGSPLYMA

>contig52758 Frame-2R|Blast-N-acetyltransferase 10 [Phytophthora infestans T30-4](gb|EEY52909.1|) 2e-96

MALYVSSHYKNQPNDLQLLSDAPAHHIFALLGPGAEAQGNAGQLPDVLCVVQV

>contig53537 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63221.1|) 3e-76

MSASDSSLTHLSSGQRFFAASTEHGGLFTWGDSSGGRLGFVIADGESRRVTIPRRVSALQ

QHTIIQVACGGFHSLVTDLNGHVFAWGSNSRGQLGFSFSKTESGAFATPSVVADLRGVYV

RSVACGEYHSLALSSDGRVFSWGCNRFGKLGRVAKDLLDMA

>contig53818 Frame-2R

MRDHRRPHMEPFTLAFSSSENPEGLQSLR

>contig53902 Frame-2F

MQALLSRIVAPAEYGAMSSPPSISIDPSKSSIIQSPQSNPLQTISTPATITVSPTVKAEI

LQAIERLQFATLLSERKKSIDALQSLAQNLIIRKHPDGRSNSDDDPTMEELEVGKSSIPA

VLAALVSDPRDTELMEAMIEFLHYIVSHTP

>contig54415 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59078.1|) 2e-25

MRLVHLLPVPTISSQDCSMLQALADTLTEHNISQYNNLVVTKDGRANPQRWREVRRQGNV

RIYSERPSTSPQG

>contig54950 Frame-2R

MVTTAQERREVGDDATWSLSSAKPGND

>contig55180 Frame-2F

MDECTDITAMFSEHSARIIQQHRSSNTSIASHAPDLIIVKESKDYSSSLMTTR

>contig56062 Frame-1R|Blast-Monovalent Cation:Proton Antiporter-1 (CPA1) Family [Phytophthora infestans T30-4](gb|EEY53561.1|) 5e-27

MSTTSGNGEQEFSASATGYAAIDAALGLTGSEAAAKHEPGRKDWTRFELCVIASLQLVLV

LVAYRLDRSQHPVLISESAAAIFFGVL

>contig56211-0 Frame-1F0

MDSTSILKHMENPVTKYEISTADNQICPRVRRQSDIFKKKIDKASKKK

>contig56211-1 Frame-1R1

MCFNMEVESIFDEFAFFLVTATAFVHAVVLLTAKSIVLDSVGSVDEGALMMTKQRGALLM

ERLWADFDRFESVQLLAGVSRK

>contig56659 Frame-0F

MDERLQFTATKFCGRRDEKDNIISPLKPADCGSHHRSMGRIPCLHIHSHHMDTLRRRQRR

RQLLHKDP

>contig56732 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69767.1|) 0.0

MKFDLRKYEREEEKWALVNGTLAIFKKILLNLDTTTSEGSLSYQLLARLLSSNPLLNKVL

SILSGDGGVENLESTSTDMHLEHAFFYCLNIVKRETEAKHGSLNFVIDVTKKSSDTYLTK

TTVVAALRERCVQHALELVVLVLEKDVQFVNIDLNRQLSHRLQVEMMHTILCRHRSDFVS

IVKYIKYTKSMHIPHLSAVVLRMVSARMSGTDLVNLLADSGFSADIMIGYMNRLLNIYDD

DDIEQDENKAVSSNANNETESDSGQPKAAESRRCYQDTRTLSSPYELFTSDMPPPSIRVA

ILDLLLENLDKPAPNVAHLLLGYASHSGDLEMAAVPASYMKTGLAAVITLVSNADFGLEK

PELAERCYHVLYSLVTQDFSSSNTIATLESVPNDFFAYQIELFSSIYHVSRRSTAAATIA

ELNMRGWFFKTLAVYLHVQLHKEPPHTKSLNKLIGNLLSESEGHRNNHVISRQDQMLLLR

LLGECSFHISPPPVPTNHQVVAMAEQVTSAVGQECYYKWLKIDIERFCRALQTLDVTANE

NGMSEFYSSSTKRIRVTGDGASSITSQDSAEAAAERFVQWAVQWNIYSERIAAESHALNS

MRELLEVIA

>contig56875 Frame-1F

MEALGGRYSYASRPNVLCLFN

>contig56941 Frame-0F

MLSSGGSRSCSNDIDFCALAATASFQAQLSAMLRFTGSAFDCHL

>contig57106 Frame-0F|Blast-uroporphyrinogen-III synthase, putative [Phytophthora infestans T30-4](gb|EEY56537.1|) 1e-83

MADKVLLLKASDEKYTIAIEQCPGPDSSRRALKAHFKNVLTYEYINSEQLCEVLTHLEQY

SGILVTSPRSAIAVTNLVNALEPMQKLHVLKKLRAKPIFSVGAATSRELLPLKVTCKGDN

AGSASALSDYLHRCRALPADCRDKPMMFLCGDKRREILPESFRLRGLPLKELVVYQSCAV

KNVTFPAECKVPNWIVFFSPSGIKVVKDMNLPWESIRKAAIG

>contig57173-0 Frame-1F0

MVITSSGCRREAQREKRTTNPVRVSASKRGN

>contig57173-2 Frame-2R2

MSQRSPQCVPQQKPRRVLGSR

>contig57814 Frame-1F

MATPAKMRLRSEKHLANITKRGNVAQPP

>contig58932 Frame-0F|Blast-dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichyl-alpha-1, 6-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58713.1|) 5e-54

MISALGFAKLYRNRNKAYLPFLGAVGCLFVSFLGTFVFFTAARSNYPGGDAFRHLHHIAM

NEREVPRSVHIDIPAAMTGVSRFGEEFPAWRYERGGYSRVFHT

>contig59360-1 Frame-0R1

MVPCPSCSADVSHSCSCSQCGTKLVRTSSIQSTYAVRNSSLTRRNTPKDRIKKKKQKDKE

RVTTIASDQAKDKF

>contig59452-1 Frame-1F1

MTVAHNNSGCILQNFLQRCMLSVIFHQVCVQTDPQSLQPD

>contig59452-2 Frame-0R2

MENDGQHTALEKILQNTAGVVVRNCHGALLT

>contig02370 Frame-1R

MPRLRQTSSNRRSRRRSESPTREVIKAVDIMEPRNSLQQQQGFTKLQVQPELESSKNLNE

APMTNAIRASAAANVLASTSGAACRVSVASSDNEFASTIRMPSTRQVSTCSQPMTTHDRV

SKPQQNSLIISTAQFLQQEETIASLIQQQCDLKQIISVLQEQQQQLMIIPSHIQKVNFNI

GEIQDEQMRKLSLKVDALTAANESLHSMINAADREARHRALEIECLSEENDELRHRYGQL

ETRYMEERKQSFVLEEELQRVRSLSVTLQKLQFRQQQQLGQKA

>contig04866 Frame-1R

MSQSKLEILAKMFTDDVNGTTKAPSGRGRDFSTSKRGGHAQTRRTTVGTQFKESLSHLME

KIGRTEVHYVRCLKPNPLKSADCFSHGDIVSQLRCAGVIEAIRVSRSAYPSRMPHLECLT

KFRVLSIRMPHLTQTKMVLSSEQTKTQLEELMHQLLPSRNIQDYQVGLTRVYFREGVLEE

LETKRGWALRKFAIVLQQNVRCWLLRRRYVWQKTQIVVLQTYWRRYVIHKRYVTLRKGVV

LLQAQMRGVAARKMYCVLKFDYCIVRFQAFCRMHTERRQYLKKAAAVRRLQGFFRFSLLR

LVFLRKMENEKAYKELGSKVAQLQMKLDRKQVQTGPKSSPSSKTRSSSPSELPHASVSIN

TSTGNSTRGSMLSSRFSGTSGILDESHEVITALHEENEKLRQQLDMQEAEIQKLKSENRN

LKNWQQSREVGEQVQKLAHRDQESKDLTYLAAIEAEYEKLRGYICELRDLPTDSGTIMQL

STVPPGNTSRSSLTSLSSDKSLVAVTPPIHGVLDPKSAEAHHLLVKSAARIAHAKSKVFS

KGNARRVKDHWEEIRNFPPAMHYSLGSVPWKRLLTDWAQGNPKKLDYMTRWLKNVLDGGP

IVSDTFPMGVELKYVTPMMLDGFMQLVIPKLAERSDIQVHVHTKEFIGTSMRITLSQLEQ

PHNLRSTSVPVRVERSPPMEVEDFQRISILSDSTMRTSNNRMSASTITLSTIDSNSTSSS

GSPGSYRSSIFRSGRGNHSSDHNARNSFFHRNK

>contig06015 Frame-1F

MPRFRGRLGRVGQFDIKSWRFCPRLIMTQLVTELPEELTEIKAIAEAASVKTRVPFEPRH

LLNVGVRKASLYGREVDKWMGETDMEATSGSSDAASQETTDKALAAKHDRVLNALKQEEW

KHRNARRQDLWDESLDMGKVKKVAKRKAFVPNEGRANMFQMTLMRKTKDAKRQRFG

>contig11132 Frame-2R

MLKVVCIVRFTTSPKYPQRHFRHHTHE

>contig14243 Frame-2F

MGAVDWFRSRAKKNLQGKQNVRANSIINGCCGNSSRFSCLRLHDSATLNAKGLLQHTVVT

KLYPIVQLHLLPLLLNYDSEVQEARDNTKPESGLPISTKVERLTTETSERFAEQVKCMVA

DASSSFQMTSEGCGGAYFLTADWSCSCHKKKPLGIFKPRDEEYMAPKNPRGFVKETSVVG

VSEHPVNKGFRVGNGALRERAAYLLDQAYGSFSGVPETTLMVLCLNGEEKEGSMQRFVAS

QCSAEDMGTLKFAIPEVHKIGILDVRLFNTDRHAGNILLSARLNEQTYAMTPIDHGFCLP

AYKHLDSATFDWLHWPQAEFPFTGAELDHIASLDEARDAAVLRTIGIEEECVTTMRLCTA

VLKQGAEAGFSLYEIGSLLQRDDDFASPSQLEVMVAKAVAAVEEILVMSEDKDGIAFFDA

IVAESTRLIGCMLEGQTKKKVRSISCFS

>contig14328 Frame-1F

MCPEFVAIHATFSAVVELAVANVASALDATPHFRVVVEEGAVVMTARNLLEDSVHIDHFH

AYEAPANTPHQKKDSFFDVAELSLELHTDSGLMIAMAAPAYFELSSTGRLVPKATEGRDA

GLYIQTATGEVVRPILESDELLLMLGSGIEDWIETSPPLRSVLHGMQYPRAVSTVGKDGN

QGPPVFRSWFGKMILLPAHQQMKNTGSTFGHYANQTVRYLMQHENQNTVFSVACPPHRHL

EASSVGTCLVKTCSLKSTSSSSDLKASCPITCNHVAPADVALCSKHCDCIDETKPGTTCW

MLCVENLATDVCPGEQKCNTGPSREQLAMTCPGGLISPPSVAPLSPATAP

>contig14997 Frame-2F|Blast-hypothetical protein PITG\_00788 [Phytophthora infestans T30-4](gb|EEY58165.1|) 6e-33

MVRTRGMRRISTADYLRRRNSDTQPQEGLQSCRPSRSPSLERLTDFPPASTHGLEIFEHR

VRDRTHVLNIPEFRGRDGISSSNRSSRSIEDSRWPYLEGNARLQRPSYDSKIRDRRDGQG

DFVVSDQNKAVPWKARSVSPRVKYPLWPQDSSFFKDGSSGNNHSLEMSYSTSPPLVTQTA

YRKDHSREQPKPIRRSESPRHRDFKHSPGKQNDLIDDLWDKDLPTFSYHEAFLPRLLYVF

IHVLPQSLAAIMNVTKKPRKMNWYLKYVERIERLCKSFDLQIKVEGLKAIVNVQGREWFM

LESTSTVILHLEIIKTLRAEALSWRRLYEEMEQSLTHYQEKVGEETNQSFVFVRAWNELK

SKRNYLSVPRQTNFFCGARLHHWNFVVGKVEIGSGSFEEKREAFRLATTSALEFLLNCGR

GLERPSRKVSRNWSHALKEEPMSRKSYQSSSRESSTSAVRATDQENVPLLDSALSAGRPS

TQERTTKTISTRALVPKKKRSDLEEPSAQVPSVSQPHRLVEPSSSPVAIIPVTDCITSQN

NLDLGGKVELDVGNRSTASDLAMLSTRTPSRPSNENLNASELLFKSTPPVLLAVPTLSNV

SAQSVETKKLVTPSLTSTASRGDSVSTPKIVSLTASLSGSRVHNAGQSIEKIDLTSRPKI

VLSPRWCMMCEMIRLRKPDGERCLRCQKNGNSANVMLDAVLGP

>contig15770 Frame-2F

MDTTAWSLSWLIVMLNRNPRVELQLRHELRQKLPRLFSDTDYVPSMVETEGLVYLEAVLR

ENMRLNPVVPLNAKEANRDTTLVDGTFLKKGTRVYIPSYTLGRMKSVWGRDASRFKPERW

LMQDTLTGELTLRPVSAFQFVSFHAGPRTCLGFRFAMLEMKIVAAYMLSKYHFITKENPK

SYTY

>contig15895 Frame-0F

MGLSRRAKLTESPPTTSSRFLAFFSHKKLGSPDEDKRTYNLRLRVKKTRNASKRSRSRSF

SGGEDDNESVVKPASLSPSPNIPVSRNTSPLSQCPGVYPKRSSRSSLLRHSTSDSSLLSK

SSSLNPENQRYFKGQFNHTTRSSSETVRLQLSSSFEAREIWRESSVDEFLSSFPRDLSAD

VRTTCHVVNLKQSKAWMRRWIQSLEFEIRATKWAAY

>contig15921 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64586.1|) 1e-23

MPPQSRRPRGLSANHANENERLETIKSDKSTLSSIRLLGKENWVKIDERPHCFYCARKFR

PFFF

>contig16498 Frame-2F

MVEKRPSPVAESPQRHKKLSTQPSIDAISIDVKTTCNSPQNDTLNEMQMATTVTPTSPTP

NDGQLHMLVFHERFQLLALDNTPVVTQLKHDAQGDSWRVIWHPRSPTDPSFVSVFVELVT

HDENNHSRRAEVSIMLVNHGNHSPIIKHTSVHAFTMEKAEFGMNQFLPRSTLMNPNNGFL

DEQGQVEFKVRLTFVSDMKTLHWHGNNSHEKGLLDTTDHLSSSYDSKKETGMVGLKNQGA

TCYLNSLLQTLFHLRAFRQVVYETPTALEDTNESVSLALQRVFYRLQRQVTAVSTKELTR

SFGWSAIDSFMQHDVQELYRILCDRLEEKMKSTRVDSALQVLFEGKVRSFVQCVHVDFTS

YRDECFYDLQLDVKGCRTLVESFRKYVEVELLQHDNQYDAEGYGKQDARKGLTFLSLPPV

LNIQLKRFEYDAMRDGMVKIHDRFEFPKVLHLEEFLSTDVKTHETRKACYHLHSVLVHSG

DVHGGHYYVFIRPG

>contig17765 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66363.1|) 1e-99

MQRLVDTAAGLCGIPSTVKASRKYLLAEPLVEIPFHHEDFEVEKVYLKPEAAKTSKDYSF

VRCRSQYGIPAYGMTTVRYLETGDVVHLKRVLSARDYSYAVRHRCDPTRHVIKQQRMCFL

YENQSFQIHVYKEPGNLAGLAILHVQASCKNDQDILLPAFLNIKKELPDTDETISAYNVS

KKNLLGDVEVKVAEV

>contig18324 Frame-1R|Blast-Poly(A) polymerase beta [Phytophthora infestans T30-4](gb|EEY66839.1|) 2e-41

MDMQIDHITRSQIPKWVLDSLDDTADDSKHLKKLSPVSNLSKMKKRDCNGVAKGLGEMAA

SAQSSSKKSKGT

>contig19437 Frame-0F

MILLQRVRSSRRVNCRFASVFSGVSEDLLVSSSIGHQVGGSSHAALVGSLIRTNVVVAGS

RLEAVLRRVDRGDFVSSECRVPSERYANKPLKIGTVATISTPQHHAQVLRLLEPHLQPGM

TALDVGCGSGILVAAMTRFVGPK

>contig19518-1 Frame-1R1

MYVLHDHDNLVTLTLRLCSVCFVV

>contig19855 Frame-0F|Blast-GK15001 [Drosophila willistoni]gb|EDW75799.1| GK15001 [Drosophila willistoni](ref|XP\_002064813.1|) 4e-11 NOT\_ORF

MLKIRILILWRIDISNCRKMIALHKRDEAINNELSVLKEKKNLDCGRRTRNKKVIGTKWV

FSIKKNEFGKN\*AI\*SPSRCA\*LSSIYGVNYIDTYLPVVNSNSIRIFMAICCQLDIFIHQ

YNIDTGFLNGS

>contig20712 Frame-1R

MDSQYEKVYSKKTSGRKKQLITDVGFRTEKPERFSRELDSSRGGRGGRGGRGGRGNGRTS

GRGANAPNVTDMSAFPSLG

>contig21531 Frame-2R

MDLSRGMANKDWKPHRLACTSDVLQQFVKDYFDQNPISQLGVIGIKGMTAEKLSDLSGNP

KTHIERIAAALAVDKEPSLQNALEIARNSLKTVPAYGSREIIVIYGNLVTADPGDIFQTL

VSLKRENVRVSFIGIGAEMHLLRRIADGTDGTYYVAMDAAHMKRLMTAFTFPSPTVATAA

SRFATLVEMGFPQRRTGALSLCTCHQAFTTVGYLCPRCKSKSCDLPTTCQVCNLPLVSSP

HLARSYHHLFPVAKFKQLGLRSGMTGEHMDTLVQKKCFGCFLPLRLEGEDIAYECTVCHS

VFCNECDMYVHDSLHNCPGCS

>contig22178 Frame-2F|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY66202.1|) 4e-64

MIREGKCIYKLGLGQSPFPIPQCIVDELRANSHQRDYLPVAGLPELCDDIAAWGRHRLHV

NYSRDDVLVGPGTKELLFVLQTVYYGDLLLPNPSCTSYAPQAAIAG

>contig22581 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62031.1|) 2e-22

MKCLHFSFAVPQPLRMLFSNSILQKYSMLSVFLIQVKAVESAILKFRSTLRHTRSRY

>contig22747 Frame-1R

MAEDIHLDVFCPRKFVCPFCKLYLADKPFFGTENRYPVPGTVLFRQTDVHQASAVLRPEP

FQLAGVLVAEAAALFADDAALVTPRKPWRHVVLWQHLLCFLWCLRRLN

>contig23304 Frame-0F|Blast-hypothetical protein PITG\_12147 [Phytophthora infestans T30-4](gb|EEY59574.1|) 6e-16

MMYEISKTVATMPSDVYVMRYPLEFSHLRALQLLLRSMRQEFFADKQQTSIEFISHGSQT

RTQNTYMSNFRTMQYTTDLQATQLLQTLQKRVNFHMIWFDYKAFGTKTCSNKCDVN

>contig23454 Frame-1F

MRAKINEFMLRAEYLKERMAKKSIKNQPQTGRAKERSNSGRQRAIFTKQHTQHAHAILDE

VLDKSPGVHWTDIAGLKVAKQIL

>contig23595 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56920.1|) 5e-29

MPQQFCFVFQRTGSCRYGDSCRFAHTAGKHASSASGDTSRQQPYANACTNTMPFSLTTLQ

KQLVEKLSSGSLFSSHSDALVVIWPGLEVLWKGFLIPKDPSNVWRVKSQTQALNFINAGL

QALTNENLASQFVRELGKTDGRGIVLIQELLDLPYAIDAGRRRDVVSFQRGFVPFVTL

>contig23696 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65739.1|) 6e-17

MLGRRVLRTVIPFRTQRHAASTAPAAQTKSEADSTFTRYAGIAFFGAVAVTAAYLGTWQI

ERYYWKVDLINQRTKELSQSVADLPEDSTASNKK

>contig23788 Frame-2F

MNEFAPAEEELVHMRRSSLDLLASMRSSTSSVSANATGNVCTLIWEGGLLGLRLRHSQSR

QLPAVSKITGKSAIFGVHLVEVGDLLLRIGNRITREMEFLDAIHYLKEVPKPCQLVFQRL

VADPMAVKPVQPKVKSVIGLKLAAKFDELVAAENEKFPPQAAVKMEAKYELKWIDGPLGI

SLIASKDVPFPLVTRITGKNRSPQVQDVQPGH

>contig24446 Frame-1F

MAASLYRSSDDRRSRRSHRAHSHSPSASRTHPSSYHRSSHRRFSRKRSKSRSRSRDRSRR

SSRHRPNHRSRSGERHKRHRRNSHEKRAKRRSHSKSRIKTASKKEEIKQRDKRSLTRSSA

HSSQDSEAVEEVVDTLTVQVLSNNLSSEEPVCKVQKTEVQQTQTTIKIAAFEQKDEVPAV

DTDKQINNSICAEKITDLSPILPKQVLDVSTIKADVLKALADARSTIAVIKKNGGSTFVA

TTPTISSLVESTEVQTVATLQEKEQDVVIQVPQKTSLSPETIVSGTDELDMFSMAALDDH

NDTMNGSNDVATVTVDKAALQSNCDDAEGYYSTTIGEVLHDKYRVLGAVGKGVFSTVLRC

QCITSSEKASGGVLHSVVAIKVIRNNDVMREAAQNELRILRELSERDSRDKKHCIKLLDS

FTHRNHVAIVFEPMQMNVREAMKKFGGKGGISLQAVRVFSKHLLIALSHLEACCIIHADI

KPDNMVLDEKQTTIKLCDFGSAFKAEAGKQDPTPYLVSRFYRAPEIILGLAYDKA

>contig24709-0 Frame-0R0

MPNKTKGVALKMPRQQIPKAS

>contig25081 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65208.1|) 7e-59

MKTLCDFIILALLAVTTFSVAEANQSPGSNWHYSTPASLTPTVITPKPLSKVVNFVDIQS

FSPNSAFNVKKDTVGYSDDSDDSYDNNGFSSYSNALATVAVPDNINIGSTANTRDKILAT

YRNWIGPSIGKPSDPAFDKACWRKAYIMDTCPDGFNYNTKVCWAQCPMAYPVECGFECIR

QSDVCGAQIYAKFTSVANSFFSFQIMNVFGAFTKLPKTVGIGIKCARAMLGTMRAIVNYV

RALQVSNPQTSKDKILLAVYQTSYITIDLPVSIVMCMGRSYNWEVLDPASVALGTVQ

>contig25175 Frame-1F

MVTWRMLRDGLSTEVAFNAEDTDAWTKFHMKSLGIAVRQELPMSCGLIYNSNEAKEVPAE

RRRHLSLLETYYAVSEGLLLYAKPLRELWDRL

>contig25478 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64453.1|) 3e-72

MKDLRILAHLRGPTRDDPFRFLGLKWSSYAPGQTGGLIAKSRDSVVLEATGMKMDTNGER

VFYFLSHSVEIEEVPEYRKQGLVRLRTSSCRIVRPYTVHGHVEVFFRGYCNVGGHFSVAA

STQLLCIHLLDSAEVIEESYMKKLAWFVHTNARRQQSHKSHDDKRDGCACCHKLPTKGL

>contig25517-0 Frame-2F0

MKIGGIWVNFSIVAFDSVGMAKDVHRVATDSRVGRNLDGSKVALVAATVS

>contig26152 Frame-2F

MAETALSKRERDAVNVDAHLDKTLKKKGGGTVSKRWTPEQDAALKEAVAELGHRNWMAVA

ERVPERDNAQCLQRWNKVLKPGLVKGPWSVEEDAMLMELMLKGYDNWRQISNNIPGRTAK

QCRERWRNRLDPSINKSPFKEDEDQAILQAYEKYGNRWTQIAELLPGRTEDAVKLRWKAL

NPNQKTYTKLGRPRLLNTDDTPRSSTSALQNKVGNENEMPPGRLPNQLVSGDNHATGTNQ

VTLEPILTPLEADPDERMSEEDVMILNEFLRGHSNNSLGNDSFKSMLSATSFRRLSDDID

DAALIKIEPQPGDSTISKLSSLKCPPHRMLNKMLSLGDTKSASLRSITADVEPDESWISG

GLTRRLSSLSVNEDGSFEQQLSEGSQKLLSMDSFEQQLASLNGAGSLLNLSMDTGDGNLS

NASVACENLNGVGSQNSAALCDAPHHSLEPLVLKEEFSTLETIHSTDKNTMTAQDFYSTA

VSIDQISSANSFEI

>contig26484 Frame-1F|Blast-monovalent Cation:Proton Antiporter-2 (CPA2) family [Phytophthora infestans T30-4](gb|EEY57530.1|) 6e-65

MIWTYWHKWPYCLAYQLWGGIIATYFNVPPQAGYVLGGALVGPSCLGVVRLYKEVETISL

FGSIFLLFGHGAAYSPQKPEDVFRKYFVGGMAYILSTVVLVAGVAVYLGWTESFVEGLSI

GLSVCFSTTAPLYEHIRENRIQDSSFG

>contig27003 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60291.1|) 1e-24

MGCCLSQEDDRFKSRHDALLPKSRNENNRVDKSVDADVTKKRNLNGSFQPSSAVVAAADG

NSNVPSKPQPSRKRVENVDLLRLHDKPP

>contig27267 Frame-1R

MRGHNLRFLFLAVIAAAVVLLMAGKQRQCLELISIEYFSKQYIAAVSNVSDPDSRALRYA

SKPGIGTEERGIGSSLKNKLYDSAFKWALKFHMNPKLLLYLLNVPFSHPHAEMDRNFGRW

IHYVIKFESFQDEAHRFSESTFYKLLETKLTTEDMAMLFQSLETWPDGERLAGKMQAYMI

LNAPSRDVMHIAWNRVREPPEHVFRILNLENETIPDRDRLITEWLRYCRSYRETESAVAF

QGLRIPDELFYSELLRLLRKTKADEDIIAFLQSIRNIDGMETFTDHIEAVADRTLLTHEI

LLKRVEHPETFFNRLHLQNAFLAYNSNFLKWLSYIAVYNKQPGIAPFTMEKAFEFIRSSS

EVRRLDLYFGEFLEAKMKDVPELKEELRKMQTEVFKYWRSLNIKPLTLWNTVNVHKRGRL

NTPEMKNSFAYRSIQSYTK

>contig27937 Frame-0F|Blast-vacuolar protein sorting-associating protein, putative [Phytophthora infestans T30-4](gb|EEY66878.1|) 1e-158

MENKFIPQAIEIVTEAINEDNCKNYEDAFRLYKRALEHFMVGVKYEKNPTSKEIIMKRVQ

GYMARAEELRGMLEKEKAPKAVAAAVDVDKGGKEDDDESNAETAKLRGLLASVVISEKPN

VKWDDVAGLDAAKDSLKEAVILPARFPQLFTGKRRPWKGILLYGPPGTGKSYLAQAVATE

ADATFFAVSSSSLVSKWQGWLKICSKWRGRKGLLSFL

>contig28129 Frame-2F

MSAQMQCNTCANGTVAENFGNDECIPVAAPGLGYDTMTNAIKCEPGMFNDGTWRTCQPCP

RGTFAARRGSNI

>contig28231 Frame-2F

MFQNEKDQIATAVVLLDRSFISSSENARFPYSLSLGDARLLSSLRPDMKAALDDAIPALT

SMLEKHGKQPAKEFSFTVNEPPKIVPGPIPGVATTV

>contig28486 Frame-1F

MLSGDCGLRLTRLTNSYDVTTRTPDGPIASSR

>contig29056 Frame-0F

MMPRFRRQVLRLELSDYGNGVKKLIYELQSLFAHLEGSAKPYYNPRPFTRAMKSCDGEKI

SLNVQQDASEFLTSFFQQIESEMNGISAKGEEPYTSDENILDKFFGGEFSNELIAEGDRY

SERFEPFHFISVPIRDRKNLKESLDGWVQGEKVSYMWESCVLNKSVNNIENANETDTKVT

LETHKRISISKLPSYLIIHLKRFEFDFEKMQQIKLHDRFEFPVKLDMYPYTKEGQQESRK

RSAAPVDDEPVGHNVRSSTSADSIEDGRPTAPEYSNYELVGTVVHNGTAHSGHYYSFLRD

QQVPRDNDQWYEFNDTLVTPFDAARIPDECFGGKESPHIPSSESEQIKMKSAPLIRMRSR

SSFMLFYARVSPELQIVSHECTTPRVSFVATVLALAFILRLKRRAAAKLEQLRRVIRIIA

PEPIRKLIAMENRLFWREKYLYDARSLKFTYNLLQFCLERLESANNSGSMSRSEAVEIRF

EALQVATKFVFGTLWQGGYVTKVLEWRHILQSLYNSDVAGSRWLLSIMKANESLLLELLV

YNKHQEIRELMANLLLVAIATISNTTINDNAPKKASNLLVGNNKQVPPSFKFMLFVIQLM

PSLLSVPVHQHHQYFITIYEFVRAGSSEGYFLVTNSVVGAIVSLLTGLGSTQQLFQLQMK

KHKQKQILKRIDLSVTILKLLSVLLRYSLPPAIDIVS

>contig29737 Frame-1F

MSSWSMATLLEAPQSILAPEETVQKTESKDEFFVVVNLVGATLHCVVNPQWPIEALFGVA

AEAYLCNFPNTEVPECNLVYHCNLQQILDPKVPIFKCCAKGDELDLEVSDSGKMSTKVNF

DANRSEFCVIFHKLPLGFTMKRGLQNNTEVGTVFPRSAASRFSRLVPGITIVNIAETPLA

TLGLRQVHELIKSAVLPLSIRFRELECKPTLSSIDKELQLEEAPLLIPASNVALLSPSQH

PDRRRKGSFDRRSAARSNSASGRNRHSRTISGRGKTKGSDSSSTTAQKGSKKDPTH

>contig30173 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56462.1|) 1e-100

MAMRRHANRVSKAATPSESTTYKQPSAGYPLKHLELMCSTIFPNMLVIIVALSAVWFEFT

SINFYMRHPELKVFLKRSFIVWTCLAIRKQLKYFTIPPRLANRRPSLKKKLACHARAIFA

AIAANLLGTFIIRPVFGASPQVEETVRLVVPIYFLVEVVVGYLHFPVPLLKVIVGLCVSW

LKAVMIPKLVMEWHNNTSAHPLGFIAISTANLYASGIVLRYLTKYNRTQRAVPIPWSEFR

YFLQIIGFSAIIGLIAHVANHFVLSEQSMMEARVLYFFVTWFMLDKYWKEALGELLLLTL

PERKK

>contig30591 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55490.1|) 1e-10 NOT\_ORF

MSDATENSFVTRKRLKTITSFFNT\*S\*NVTNQLLHKKVL

>contig30883 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57175.1|) 1e-109

MSLSVNLANASLLLAKASNLLPNSKVCGPPQWRPDAASTSCLCCGNDFSIWLRRRHHCRA

CGELVCGECSPFCVRLPELGFNGRVRVCTDCHAQIDSPFNSSASMLSLSSLETATTSSES

SQNELIGDVEELLVFRSVDVLVHCSREKRLKLRYQYFVQSEAVSWLMDAGIMSSRTGCVS

LFLRLVKCGYVTLKPWSGSARSAFYYISEEITLDNRLSHYETAIHSETSRCYNCTQSFQK

SLAPADGFCSIDCKTNALINQLDSAHIHRFCD

>contig31062 Frame-0F|Blast-lectin, putative [Phytophthora infestans T30-4](gb|EEY59217.1|) 0.0

MEACGLMLMLLCTLLASTVRLATADKIEDVSFKPPFDLMDSHGQRIVNTTWSHGGNADVK

KHFIRLTTDRQSKRGYLWHKHPVNRNELSVILTFRISGQGKRWFGDGIGLWLTDHPTYTA

GSNHGFTDKYTGIAIIIDTFVNSEHKGGHKDISVFVNDGTKEMDQMYTEPRVGCNAAVRH

YEKSAHFDPVHSISRIKVRILNTRLVIEVDDLATGQWVDCHEMTLNLRENWLETSTIGIT

ASTGAVADNHDILRFDAYTDFMDLHIGAVDSETVMNAVSKDYKKWLDSPNCGTECLIAVL

RKEMANFRIDAEHRFLDLKEKTETTVAKLKKQELTNEQRVREIESMVKKGIESSLESSEK

VLGDEVNVKISKQFKENPEIASGGWKMPFALLFLFLAAGAAFVYRKYQALMKSHLL

>contig31619 Frame-0F

MLILCKFRMRCPASKVVLRVRTYGQQGIEFAL

>contig31923 Frame-1R

MHRIHACLVAQFLQNTSGKPSSAVFIDSEGSFIIERVASMAEHCLADFSQLGASRLTRDD

LLRGITYYRVHDFVEQMEVLHSLPSYFKTAIECKLVVIDTIAFHFRHGFEDYNQRTRALD

DVASFLNKLATDFNVAVVLISHVTTKASTTDRQVPALGESWAHSIENRVLFEWKADCRVA

RLMKSATLPHDSAFFEGIRS

>contig32548 Frame-0F|Blast-acyl-CoA synthetase short-chain family member, putative [Phytophthora infestans T30-4](gb|EEY56150.1|) 3e-23

MRATIQAVANLSSFRVPATIESVAVLDDVRVVLENLGCAN

>contig32889 Frame-1R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY55437.1|) 0.0

MQALMLVGEAALPHVLTATKMAANYVSEMDPLHQAFMASSVLFIVIFIRQGYVHKARVQY

VRTRRLLELRYRAFVASLSAKWRVVAILLPHILFFALSYEFLYWLPKISMDILGSEALFG

LFSVGYPLVRSIGVIRRKRLCPQRIEATPRKTSELMKKFEKITIPNYEWRAYEACLKYWV

TWSVAVCVVGMMKLCLPAFIANFFVVPLHFCNVFLIWMHSPFTRGDIALYTLLSPLISPY

ANRLHECEATVNAKAEEKTNFLIRMLVSFRVVPEQYVYLAKDLWSQGPALFGLVFMFTPG

FVASRGCSFMGFGFPAYVTIGVLAEKRTRRYEWWLAYFSVAVTVDYLLTAIGREIGWLPL

FYHMKLLIMMWLQFPYFQGAERIFNACFKSVFIDQNAKTNEKKGI

>contig33150 Frame-1F|Blast-ADP-ribosylation factor family [Phytophthora infestans T30-4](gb|EEY70058.1|) 6e-98

MGGILQKMLQAFYTKKLEVVLVGLENSGKTTLLNVMAMGHPVETCPTIGLNVKLVKKGGV

QMKCWDIGGQAQYRSEWGRYTRGCDVIIYVVDANAFDQISLARKELHRLLEDRELATTPL

LVLANKIDLEPHISEPELIRELNLDYIVDNPWLVIPISALRLVNIDQVIQWLMKQSGKG

>contig33402 Frame-2F

MASFNINTDDTDHKTKLFALLDRLRVNSNLEPRHCNEALESTHATMDTKLSPLKSEPWTM

IKMDNLSALYPHEPLTPDKNSHEVSSVSPTPFNDPPALPPSEQSSHPTFIQENTESFDVI

DVPKTFLLDTESETSICLESDSEEIHPNVRQSSDSNMTRATTDTNQSTATSPCAAETTDD

KLQSSKSLQLPALDDTSNFKPPEKDKKSQNRKQIQSSTASATLLKLKDLTFDEYDDAELH

GDFQHTLHILMPANATSALLECRGEPIQSIGHQSQCSLSIREPSASPFKDDRVLRICGKA

KGICLAQRLVIASIRAYRASKGDANYTDLSNTTRPVTLPTRSHAVLLTKTAKVGNSGPLS

WFLEHQNVGKIMGQRGRILTAIRRDTGAVIHLHDSTPGTSEREIQISGSNAAIAAAVHAI

QSKAGGRPASKRLGQYFAIPEAFAGC

>contig34524 Frame-1F

MISHPSWKPRCKPYRRNTTCHPAGEQHRTEEENA

>contig34551 Frame-1F|Blast-plasma membrane H+-ATPase 1a [Phytophthora nicotianae]gb|ABF85691.1| plasma membrane H+-ATPase 1b [Phytophthora nicotianae](gb|ABF85690.1|) 1e-173

MKEECHDFFKERYQLCVMSNNNTGCGEMTGSIPQSASLSDVGAFRNGVISAYWTKYQQQY

HSRSQLFEDLADVHLNHLPNNAKPSAETSYTQFVYAYTLGIGGQAYEGDYDVFNAAQLGM

GVEFIGDGEVPITNGVGFCNYIWGFSNWNSTWTRNNEMIGPGIQRKEGVLRSLVYLHVSI

SGQALIFVTRTAGSNNWFFAEKPCNLLLIAFVFAQVVASVVGWIGFGGYPTDRIAVIGCG

GGYTAIAWIWAFVWQFPLDVIKFMVNYILTKNTYASKAFTERINAGHPTLTHSVVTSAQR

SIRASRTV

>contig34713 Frame-0R|Blast-zinc finger CDGSH domain-containing protein 1 [Phytophthora infestans T30-4](gb|EEY66694.1|) 1e-63

MDAIRRYLKTSLPRYLKGLPLPRTFSGFLKLKYDDWMYLAPLLITILALGLTLFAGKNST

KPGRLNRKVQLEKEKVVDFISLPDVEEIIKTKGKCTLCRCWKSKNFPYCDGAHLKHNKET

SDNVGPLVLTAKSA

>contig35156 Frame-0F|Blast-general transcription factor IIH subunit, putative [Phytophthora infestans T30-4](gb|EEY65991.1|) 1e-136

MFTKYEEKEKQESKGASIDPRGLVDPLIDLTTTEEDAAVHPIRRHLNEKDNPFSTTIAKF

NRHGAYVLDPAHAGNVQLQTNRKSHAQQSVVLKNQPKGGFHDNLKEATLLDDLQDKVLPT

YNPLTLEDESRYFQHAEKNSVAESKVPGNLSLLDAAEAFRATCKASIDLKMAYPSSKTCF

NVLAEVVACSDSTSDSASTSSAANLASGALGAAYIPNEFKKQVYNQFHDVCELLRHFLSF

KAKLAAGGGPEAKRKLNKIVEKMGSKYDELVKLRESLPPHEKNLLAPLLKPFDDQLNLAF

I

>contig35637 Frame-2F|Blast-glucan 1,3-beta-glucosidase, putative [Phytophthora infestans T30-4](gb|EEY65321.1|) 3e-58

MVGFLEAPTFTNVWVEWHPYFIWGYEQTPAEKVVSIAVKKEYRGRVAKWNAREKHNRLFI

GEWSLATACNMRQNNPNLFYTFAMEQLKVHEDAEGGWTLWTWKVATTGNTNVEDWSLQKL

LTDKRLAEMFHTTSR

>contig35718 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54942.1|) 5e-08

MDLLDAIEALEEPTSADTTPLADFVELQVQFVLQQLRLVWQRKHTIGAEVPQLSYDWVFL

NFLQLIEA

>contig36063 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53636.1|) 1e-126

MLSVPNCDAMSETLPTLSSLVAADGCTADACAVTVYFESALDWAIALQNNGVSNTLSAQL

TAGGSSETVIIATFAPMAAAVILSGNARISVCATELDVTGLRFSTVASCNAALICRGLSS

DTICTTELVNDAHVIDASCSGETCAGKVVLSHSLPCDGSTGDATSLIMGVTVASSFQSNL

ISVGNMIAPNFTIIDASGLDVGSSKVVLTTDTFCADSGIQLNVTVGPDIEDTYNEGVEVS

SINSTPNGTVIVNLIYPLSSNLMGDDIRFSLSQCGVSASDLFVIENDFNDSTSSLTGSTE

ASQRVAESRPYGSISTQEDDSDSGLSGGIIVAIIIAAVALGGFIFEYFYHTRRQPKPLAE

DSTVNNMAAHM

>contig36698 Frame-1R

MRGLALAHTSAITSLPSNTNNVEKRASGSRNWRWRCRSYIMPSAHGCLVDAYLPNVSCSF

ETSAMSHCNRFGH

>contig36917 Frame-0F

MVSIAISVQSTTLVGLRNKAAPSTTKCRYKTGKCLNERSNKRNGQPHQLCLYHRDKANTI

QRKFDRQKRQAARFQKFRDSHGLSSPTSVTMVDTTDLSFLAHAAASPTGSTCSTSPTGST

CSTSSYLSYSSNGAEQSLSPDSPDCYRKERAWLDLPLSKTPLFGDLLVLQGSTQSHQCYL

LSDEVEFLRSA

>contig37046 Frame-1F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY70104.1|) 0.0

MYNMLKRLKQASKPSRMLNVLNTFLYMTNYYIVAPTSGKYAAELGAEASMSGVIVGMTPV

ASLASAVLYSWWANRSYKASLTFATVCLMVGNLLYGMALSYNSVTMALAGRLLNGFGGAR

AINRRYIADNYSREERTQASALFVTASALGMAAGPALAAALHYLPDFEFAGIIITTETSP

GWVMLALWMVYLILLSIWFIEPDRMERERFLESRRSLLESEMGNTSIALVAAQLGEATPL

ITRSQSMSNPPRLSSLWRNVPVVTSLLIYIVLKLVLECLITASSTIAVYHFNWGSTNNGM

YLAALGLLMFPTNMVVGWLSFRYDDREMIMLSEVAMCIGVSVIINYGHYSVAQFVVGGVI

IFISTNVLEGVNMSLLSKTIPKSFAKGTFNSGLLATEAGTFGRAIGDVAITVVGLPGIRY

VLNWTFAPLTAISLLTILYTGRVYNKLTTND

>contig37464 Frame-0F

MESPHFHSMKRFSTDTTVIQQAANVCRLNREIEEKREMQMPKPSKQQCGNSSLQIDATKA

RPRLCRSFSAGSILTQSASFSVVPRAYDDNGLSTMHSFSHSSSDKHMIEGSFDLSRAPNL

SLPGFKSCPSVELAVSVGSKVIQDVPQMLVVLFNIRQGQRPVEISRTEIRSSLSLRPCGG

DFYARDFNALLSVPRTACSMLQLEIFSVVNPSSESLDNQKSLGIVRISALNVIFSRDLSM

LLACHQAGSSKQHYYLVLDRLVPPGHSINVSHAYTYATHHFLVDTQEVEKRTSSDLMSSS

TITLRDGVRYRERLQGQMNSSIASHVLVSEELSASYVSVSMSIAFLKYLQRRNVSRIHEA

KTVISDMRQHIIAATISGNT

>contig37882 Frame-1F

MIPEKESLYQLIHDVVVQLNEKNEVRFNETKKTQYIVL

>contig37965 Frame-0F

MLDPTSSNSLLTAAHARTEVLTRLSQLSDHECKETFATSTATTLVINTTEIGSNGAKQKI

YLAVNDCRRVFVSASGRNPLLSIDTAEVVSIMSTLPASALKKPIFLCTPTSSDYGALRQE

LLDNGNSSLQVLSFMGACMTQQTALLLQDFVSCNELLLEALNNAILLANALKATPSLRDR

VLQSVVSDIDYTKNDASFLMEISVTSWRSIALAMHQATCLEPYLRSAISQEKEDVYMEWP

KMSLVVNKSVTDGYWHLLRHTAQLLVPLNYIAVLTEVQNTTSGQLLALWIWLFGIATHSP

LFQEKTDALATTFLQRLGCYVEEHFIACLILDPRVHGAGLSESGLHRAQGIAVRLATSLM

PEVEKDSFVRSLNDYMKKQGGFADPSVWNATKTSSPIDFWGDLEGNQEHNQLAKVAKIVC

SYMPHTCSFEDFWTRHAHQTEAVAEGSKELEQLAKVRRQAAVYGIKRATDVRQHYLDRLL

ENSPVVVEMLRSHASNLNMEDGHFCNLSVRSVLESVHDGMETDLAKSTIFTELDATWFDI

SETGLEKIRRTMNEYLSSAK

>contig38339 Frame-1F|Blast-Glycogen Synthase Kinase 3 beta [Phytophthora infestans T30-4](gb|EEY57178.1|) 0.0

MRQLHHVNIVQLKHCFYCNGEKPDELYLNLVLEFIPDTVYGVARQLQKAKQYMPVVLVKL

YIYQICRALAYIHTMGICHRDIKPQNLLLDPRSHVVKLCDFGSAKVLQKNEPNVSYICSR

YYRAPELIFGATDYTTAIDIWSLGCVCAELLLGQPLFPGESGVDQLVEIIKVLGTPQREE

IEAMNPNYTEFQFPQIKAHSWSKIFRSRTPPDAIDLLSKMLVYDPKERVKPLEATAHPFF

DELRQKGLKLPDDSPAPPLFDFTMEELSQVNVSTREILVPAHERNSSNWVVLEDGTWPDA

AAHGTF

>contig39390 Frame-0R|Blast-pre-mRNA-splicing factor RSE1 [Phytophthora infestans T30-4](gb|EEY54384.1|) 1e-89

MHLLNLTLQPPTGVHIAVYGNFSAPQAQEFVVVRGDVLQLLRPDEAGRLEVIISTQVFGV

VRALQPFRLTGGERDYLVVGSDSGKITVIEVNPTACRFEARQSETYGKTGCRRITPGQYL

AADPKGRAVLIGAVEKQQLVYVMNRDASSCLTISSPLEAHRANAIHLSVIGLDVGFENP

>contig39527 Frame-1R

MSLRGVRERWFNIEPDGYLRYYKREGDREPRGAILLKQSSLEILHGKEVGKRNEFMICSP

THQTRMLAKTCEEMLVWVKVLELAHAYFMQQVLNEDGHGNSTDHAVSPDAELAYRNKRAT

LGF

>contig40048 Frame-0R

MLDVCRGVSRAANRGFNKLPPAASADNAAVLREVKAALVTNPEALKQLSALLSPSTTRNL

SRALTSMRKSQQTTEFAAPVTLPTTQELKLVALRTGLPFIGFGFVDNFIMIVAGDYIDLT

LGVSLGISSMAAAGIGNTIADIAGLGFGNVIENCCVRLGLPNSSLTSKQMLLKSTRIAKV

SGSIIGVTVGCLLGLAPLMFLQTRPKETSKSVID

>contig40718 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY60165.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60164.1|) 4e-76

MAMEHRPFLAEEELIGRKVVVLCNLKMVKVARMGSTGAILIVSNDKGKIELLEPCPEAEI

GERVYASGEDVHDPVTAIQMKKNKVWETLCKEITTNNKCEVMYLNRYLVRSRAGPVRVES

LTKAVVTK

>contig41199 Frame-2F|Blast-synaptic vesicle glycoprotein, putative [Phytophthora infestans T30-4](gb|EEY59841.1|) 1e-153

MLAGGIVGGVAGDIYGRKPVLLVTLAINAIAAFVSAFSPNIYWLIFFRAVAGLGVGGVVA

ALFALCLEHVPVSARGRYVTILCSFWMIGAVLTAGTAWVMLGTYSTGERIVAISWRWFAG

AVGLPSFTCFLLTMLYVPESPHFLASKGDAKGATIVLQYIHKIHKSGRQIHIKFATEDEN

AELSTIGIQDSVIQKSDYTDARNLNHNAICSRESLRIVARLFERAHLKSTMLLMLCGFSL

SFGSYGLSTWITKLFDSVGMANPFKNAFLFAGANLPGNLISLYLIDIVGYQRLFSGALFL

SALCALMFAFNVEGSKTIIVVVSCLFNACTTAAWNG

>contig42785 Frame-2F

MTCFFQSSWIFLLLLGVLTSVTVWIVDAGVLTVTRLRLSFTELGGDWSFKYLFFVLFRVS

MLLLSVGCTVAICPEAAGSGIPEMRSILGGFSFPKYLTARALIAKCFGLVLALGSGLTIG

KVGPFVHLSSIIAHQLLQLPLFEQIRTSEDLSHDMLAAACAVGVTATFGAPVGGVLFSIE

VTTTYYMTSNYWRAFFSSVVSVVVFRALNSFLAGSYGSLFTTNFDTLPYETFEIALFLLL

AIICGLLAALLVRSYCLTLRLKKKFEDQFLHSCCGQYPRLLPFLYAALVACLFSLVEYPV

GSFMQLTQRQAIDDMLASESLAASSTATHLSLDFGSSWKSPSLALNLLAYAIVRFWALAI

SATVLVPSGIVTPVFAIGAALGRLFGEFIFILSKGELSIGGYAVVGAASFTAGVTGTISI

AVIVFELTGQLSYMIPVLLCVIVGRAVTRFFSLDMYETMSRHKKLPQWPDLTKQLSYTLT

AGDLMREIPTYFLVRRQTLASLKQLLQATSRTQKDKTVRLFPVVDDIKTLILLGVATREE

LDALVVLWELSLHSEKDTHGRVSIAGILLEQAAILSNPATENNEVVDLVDLELLSLEDEH

FHVPRGTCASHIILLISVHKCPQFFVTHRGKLQGIIHAADLLASSRKFTL

>contig43063 Frame-0F|Blast-2-nitropropane dioxygenase NPD [Ralstonia pickettii 12J]ref|YP\_002983676.1| 2-nitropropane dioxygenase NPD [Ralstonia pickettii 12D]gb|ACD29906.1| 2-nitropropane dioxygenase NPD [Ralstonia pickettii 12J]gb|ACS65004.1| 2-nitropropane dioxygenase NPD [Ralstonia pickettii 12D](ref|YP\_001893333.1|) 3e-66

MPFDDKSVQLVRELTPEVISFHFGLPCPRLLNSVKDTGAFIISSATTVREALWLEERGCD

AVIAQGLEAGGHRGVFLSNTKEQNYSSNCQYRNSSMDFPQQTNTLSLVSQLVNAVNVPVI

AAGGIGDARGILAAQRLGAAAVQMGTVFLLADEATTSTLHRNVLKRAANATENEIPETAI

TNIFSGRPARGFMTRVMQDLGPMCAAAPAFPTAGTLLENLRLAAEAKGETAFSPMWSGQS

PNFAFEQSATTILRSIIQDLDERICSRV

>contig43214 Frame-2F

MVAIRGKKAKVTAKLKATKAKITNSKKTKFKHPTPQEDITRSREDTFLAFLRFAIQTNLA

RGVTEASGRSIGSICNALLTVLCGRGKEKSLLPEQILAKLPRTERKRVCGAIFSADEIAY

SCRNCQLDTTCVMCKHCFTHSNHAGHDVYFQRTTAGSS

>contig43261 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66339.1|) 0.0

MFLPWISKCELVPLSADSYVLKKFSDKCQRGMCSMVVGFLTEENVNPQIVLPSGHHIRWA

MEVLGHSFALPIEDSDVIAGSLGIYQRWLGVDDESLASNGTKSIKDHRPSCMQKVEQTFI

HDMLGQMTLLFEERSSNGTPSGSFESNMAKHVALCTKVLDTFDVLVKQRGAQLSHSTWDR

LIRLILGAADGLLHNLRNQLGNQLCGQLVKVLFEIYIRSLSQCGPRGELWSLLQKFCRRW

IHRPLVIEQWNVVSLGLTRSLMKQIHNRSASIEIEIIWAHNRQSSKFELESPMLAYAWYR

LFRVIGHPSAIFDPEVYLAAVKGVSRLADEFARIEKVPRVQWEHVLGALSQAPNRDSPVF

QGIQNGGTNASEALSLTAPPVTTEQPRAPPDVNTILRLLGPWLFDACLTRKPRFAAGRSE

AIRCLGKLMCHYSNGRSKRVNWAYSIRSLMALQSALLDDDERIAASAVYNWSNIFTLYGN

HTLRGAGVVAGSFHKAIERIFRAGDRKDSLLSSNLKADGRRGGD

>contig44923 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65804.1|) 3e-15 NOT\_ORF

MEAIPVVFGPRLDTYAFCRITALSTTNTTAICSCTLLMELHVFLS\*RILIIIDLRVIHSL

CTL\*SYRQLALHTADFLIPMITAVEWTTWKTQLGQVTYDKALYD

>contig45173 Frame-1R

MVECVGVCAEILGADFKVFLLHVLYPLVEQLGSQDVEVERAALAALEKIYFFMGYESLGT

LFEINMDYFVDSLCARLEQLEMYPMTAFVVEALLRHTRLTSLPLFDEVASSLLISVDLYQ

DSTYVDGLLRALKALLSSISRDGKITEAKKNLSAVDAEVEDVAVSHSLLNGFIHEMKVLA

NININVLDNEDNFSEGKNQLGDDSPEQQSVMGALPLEYDAEDGQEENGFRTLVIDIMERC

GYFLVESNPIACCLVLSLIDEGVRFLSKHKKQLLPLVAQMWPELLPRLRVKNRAIVTGTI

RVITTVAEIAKDFVGDRFVETVWPILRSQLQSIESGNDTNLPQLTRSMLLLSKEATSNKE

YVLASENCFAQKMYSAVSGTRISQEIRQLLATLSCLTMVCSQSETVTQLVPEITYVCSKF

LSCAAPQEVVEQTTKLFWALARLNGDEVFCALAALADWMPRVPPCTRFSAYDLDYIRRFY

RSFLSNMKGETKYCRG

>contig45357 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57879.1|) 6e-68

MPVAALYRTVGHPEKARLIFNAQLYQHLKNIAKNREITAVPGVPTISSNSSMRPTQSMVL

NGAGRSTELNGWSLEKKMMALAEVLDLLRCPFFFYLDFGTAAATNASTGASASTSGDRKL

MYHSYFKKMLPLHVGQIVLLDLWVYLMDMVDHVPVR

>contig45591 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66126.1|) 1e-42

MPKFSLPSLHSFGKSSLAKVDTPLRSQLYEDDNHFVSSRHSHQQRRNVSSSVQALSRSPN

SRRIAPAPADEIDPEREAEAESAVAAACGGHANQSIRGGRWTADEHERFLEGFRVHG

>contig45883 Frame-1R

MYPSHRRICMSDSFCGNNWQTLLSIKSNLLVVSELLRRDEQKFWNGVIDEQSRQSLIGAS

KPAFRGRRSIGRIRI

>contig45968-0 Frame-2F0

MCMLNLSHGPYLKMHTIKAIQFNCFYFFSQLDQCL

>contig46334 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60530.1|) 1e-65

MKAQNVRLIDSGTAPYTLAYFTSAWVQSADALVLPRLRLILGGISALCLQQPLIELVEIR

RIGEDEDLGDSNNTKGQKLEPVIFRSLCKHYNVKALPACVLIGAQGQALTLESLALLENE

ICQKYCLSSEDMAESPWNLLCQLLRSHGVSVVACEALRPFWRLRDACENAKTFNFLKVDD

PVLVHMRNEALQLYETGQFYSALSMFVRVLLHCPTCPKANFNLAVILHTIGETYFAVASM

LRVVTLDDSDSVAHTVLRSVYYQEEPDLVVSGYKTIITANRDSHVRAVHALATLNGATSI

KKAAPAYVAKVFDELADCFEEKVIAHLKYRVPWQLVKALTLVSPP

>contig46341 Frame-0F|Blast-putative peroxisomal catalase [Phytophthora nicotianae](gb|ABX61042.1|) 1e-26

MATKSKTATTSAGVPIPRDGLTATATAGPRGPMVFEDYAFIDHMAHFDRERIPERVVHAK

GGGAFG

>contig46402 Frame-2R

MQWGTKWSDAKAQAPTNDSTTDKDQGAQVDDLRRSSKRQEGPIR

>contig47625 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54799.1|) 1e-20 NOT\_ORF

MDRLHHTFKTMIKPAQSMKLMKRKKIRKGHGLNTTSIWL

>contig47889 Frame-2F

MAAQRNAQQQHGNRQTTVTNEVSFQSQHSEIPQQQMQGAHSTTASPLLPQAQSFQSESSN

TDEVCSLCGEKDCDFTCNGGCGLHVHSTCIGEDAIFSFVAGRVCGSCFIVQQNRACSEDL

TKGGPHALSVRRAILCINLETNSNTNFDKFGHLASLRLGEIGS

>contig47980 Frame-0F

MRIEPLNYHGKFSLRPYCVKICDAAGNEELILDAFSPEMQRQWILAITSNVKRLELDPRW

LAFPRKCVHRMTIGEFLRYSMLYHGDASKAHTRKSLCQPGPLRQQFQIEAKRYLFSALLT

CALVRDWKTMEALVQPRSAKSAIISLFQSGTTGKGTATATSVVAASGSIAPSPSRYSVWS

TRPDENHRVSLSATNTISPPPLDGNTAVAGIVDASVIGYGAM

>contig48149 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY53521.1|) 2e-11

MGAAQSWCCSAKGRDELRPGKRRTNGYNHDRNVHASASKPITSAPQ

>contig48501 Frame-0R

MPHGIRRRRDDSLAVEIEELDSRTMRQNSYNYFQHRGSGFGSPLLLSSTFRSSLGRNPAS

KKRQRTLTEQLESLCLHNPSSQIMREDSKRSRCIDSNASRLSMEWARPNENNGARIVKLD

EIGRKTSSFEYRSETDSDEVMEFTEDATELIVYNDINHGKDLCTYLAGRSLDRIYRHSVA

VVGHSNGAAREGNEIVIYKPPRSINVPTTQRLPGYFALTPQEFKKLSMAEKRMWYHENED

IVEDEIEAKAHDYKRCQTSTERSSRLYQQVPRIYGETMSVVDKSRVDVDMVGDDGGLQCP

HAAGVLTHVEWFMDDQL

>contig49007 Frame-2R

MFDEDSISVAITASKEFESSDMIGNFEGGGKGHRYTMYTVFVRNVSTGGKCVVRRRYSDF

FKLRKELMELVSWGHCGFCEQYEQQIAGYPFPRRRLLRSSRAAVVKERMDSLGLFLRHML

LCIMARSFENCSQACENIENCIMKSFLQMEQTEIIFPAMTSKQRPIEIIHAMEEKRHQQI

KAAGFRTTVLANITHLDHSNQTELPRDQRYVSTDTCHLCLRKWTNCYCNSDQDRIYPVNV

GRASNHCDSPTRERPSVSVAESGTSRCSQCDNNWNHCNCCQQVSPTISSACTDR

>contig49335 Frame-1F

MREGFARVACGVALLIRRADTTTAADAAEVAMPEQVQSLEAALNNTSGVQFLRSPLMTAF

NEERDLKALVKKLLHIRTNKVTDVNVLEKKVLNDIIAGDDIEKSMKVAEYAIVYKINLFN

KESTA

>contig49911 Frame-0F

MQMSALITSEGRKNGDNSISGEGDTRRRNLIVHLACPYFKSCSVVDLITQRCQDIANCSS

SEAPQGESLLDDFYTLNIDQQRAVQRVVSSLDYALV

>contig50856 Frame-1R

MLPRQNDCAHCVKKTCLRFRARCPTLPDRGTDFPSRRYLLITRACRTSAVRLLAFGKWIH

PLHYRFAIGLQTFVTLLASASGQRIY

>contig50948 Frame-2R

MVKVYLAAVAAFVAISISASNTSLANIVPVTSEDDDTFAPGRLRANAATNVNSDERGLLR

TLDTAVWSVIPHVPFLVPKEDAVMTVAASLNKNLEQALREDTLQLKVLKKFVKNHNYH

>contig51550 Frame-1F|Blast-U4/U6 small nuclear ribonucleoprotein Prp4, putative [Phytophthora infestans T30-4](gb|EEY66458.1|) 1e-157

MMDGSGSVCLCSGSADGTARLWSAARNEPLAVLQGHKARLGRVAFHPQGNYVGTTSFDHT

WRLWDVATAQELLLQEGHYREVYAIAFQNDGALVATGDLNGNGRVWDLRSGKAILPLQGH

SKQILSMDFAANGVQLASGSDDRSVRIWDLRQQKCSYMLPAHSNLVSDVRFSPGSNELLL

SASYDSSIKLWRTRDWKLMATLRGHDGKVMSADFAPDEKHIVSCGFDRTFKLWA

>contig52128 Frame-1F

MIVQSPGDKARWITNMRVIHAEIQSTIVYVGDSATDLLALLSADVGIWLASNILTPSAKL

LRRLMEVYGIATIELVNCCSFNDCVSKASDSRPVIFLASDWA

>contig52933 Frame-2F

MCVHTHVMAHADAARCRESALERQKLTKQQRMAMCRPSLLLLSAAAALFANTPTTREIRE

QA

>contig52986 Frame-2R

MSWQSRVRSGDTSCALLQPHQALFTYQEAKLHSIKQLDLIRIDFELQQPTHLVLECVVDR

RQTSNASAFLNDRSIQVHSWILEACQKLENSIATLEKVQAVSLACVWMSL

>contig53066 Frame-2R

MRHPAADDISFCHTFNDSPLL

>contig53394 Frame-1R|Blast-nuclear pore complex protein, putative [Phytophthora infestans T30-4](gb|EEY61015.1|) 2e-55

MAELDTEHVRLLDAGRQRLGSSLTLQTTSFSSVASKKTQLLQHGNTYGLTFVASKKGFTL

TKHNDLQASCSNYTTRRQEAMDHNQKLTLEEIHDLPVTREVQLPSIAYWIALSVDELLLA

VAYDDAVALYEVAHILEAATPAPFYTYSKL

>contig53530-0 Frame-0R0

MDTNLSAQLIPACNRTKVTCLGWTHP

>contig53530-1 Frame-1R1

MDYSKRNGIVSQRVLKNYLRIVCKSPQRIRDQADNALTGNDTFFIALLRSLWTRTFRLSL

FLLAIGRR

>contig53736 Frame-0F

MCIKCEEATAIELHSPSWELVLTPNRLTRDRSSPLKLSAMQYWNQCRYFGST

>contig54236 Frame-0R|Blast-autophagy-related protein, putative [Phytophthora infestans T30-4](gb|EEY54259.1|) 5e-74

MQFTDESASDFQSVYGRSSLNEASGVDVSFTNNGQSESMVASRLFGISQKGIKFRGFRMD

LHLSSEEQSHEARGKERRRLSYSDMVLHSFLESSSSKQHYIQVKLSHYEALDAPTIDASV

FFHSIRIVLQPQYLPELGKIVDAFSADCQKSATNQLKERFSSSTLLQSVCDDKPAWLTAR

DEDDNDRDTGALNLSLREFQRIEQ

>contig54412 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65744.1|) 7e-06 NOT\_ORF

MCIVGGNCRLLCIYI\*DKRYADADLPPHFTLRG

>contig54566 Frame-0R

MALNRKDGAYCISCTTKKSKDELRVAPCGHRYCQSCLLCMSKLALRDRALVPLRCCKKEL

PDDYVREAFRRHSDFAKYQQLVVEKDWKVSDLKSDAEYAATVIAVGAKQCPGCGIGVQRD

FGCVHMACPNGHQFCYTCLGVWGTCKCPLIPEAELRAILGE

>contig54957 Frame-2F|Blast-exosome complex exonuclease RRP45-like protein [Phytophthora infestans T30-4](gb|EEY64757.1|) 4e-21

MALRDDHDFLSENERQYLVNCLSQPPHVRADGREMLQQRKIRVQFRRNETESQAEVQLGR

>contig55169-0 Frame-1F0

MVLLPIGSFPHDAAFWSQIHVT

>contig55169-1 Frame-2F1

MVFKRWSCCRLGASLTTPPFGRKFTLQ

>contig55204 Frame-2F

MREGRGNWQRFQLQHHGQIHASESSQRRLTMASSHRSSFSAQVQKDVVAFI

>contig56065-0 Frame-2F0

MEDRILASSPSHRASSAGTANFRTEEIRG

>contig56065-1 Frame-0R1

MRSSIARFANEKNEDLEKKT

>contig56182 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60767.1|) 2e-27

MVINPKSFTQTIENLFDTSFLVRNNSAEIGIDAVSGLPYL

>contig56872 Frame-2R

MKTHQQQNGCGLHKLHVPHAFTGNSEDDESSLRDKLTRLV

>contig57101 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65502.1|) 1e-25

MSWGTATVYIHRRRKIGRWAAQMLRGGRSVRTDLMRQQQKSTGQP

>contig57174 Frame-0F

MRPYPYRTSFISLHPFRHDVLDKIQNELGLHSEFNQHNIHLLL

>contig57310 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53311.1|) 5e-18

MDFETLATGCRSSAFRETLNALHVWTQAADTITTTIKQLQEQIKSVASAKNADAYDHTID

TKDESESGLGYTLRVDGKNITAETIQSDFSPPRLEILDVGQSSAQIEALTMVFRFLRNAC

VACTSNQNMCLDAGLIKL

>contig57549-0 Frame-1F0

MVKRPEVESGQLDRTVSTTDSPRRTDASTLETSVRPLYDEGAQADSLPSPAGVGKKRAKP

PPAAAAT

>contig57732 Frame-2R

METQNSNLTEESTNSIKCKTLSKQLACRSEACLDSSFDPEETPCSSTTKFRLPHNRDPSK

LGSVGQTRQATHLSSRNAFASKLAPPTESAIVRLDFDRNPTSEWKYIPNAVNRS

>contig58085 Frame-0F|Blast-DegT/DnrJ/EryC1/StrS aminotransferase [Sphaerobacter thermophilus DSM 20745]gb|ACZ39322.1| DegT/DnrJ/EryC1/StrS aminotransferase [Sphaerobacter thermophilus DSM 20745](ref|YP\_003320144.1|) 7e-57

MSSTASACLKPFGSLESLSASVPWAIFPRKKLDVTYSDIGAGLAACLQLQESQRFEYEHK

ITTLWDPSGHAMVTLSIRTGFDLLLQTLKLPVGSEVLCSAITIPDMLYVVRYHGLVPVPV

DLDPETLAVDVQMLEQRITEKTKMLLIAHVFGSRCSLNHVLKAAKQKKIIVVEDCAQAYI

GKQYIIGDFQADVSMYSFGTIKTATSFGGALLYVQNTQVLNEMRRRETRYPSHTNVFFFQ

RLVKYGVLHGISTPALYGLFLYACRAIGADHDLVITSAIRGFSGGELV

>contig58500 Frame-0R

MPDCSILFGLEPGLWHLRSTFLLLFDTGQRLKSFVENTPIPTFMNTTTKYGHAQTNLPPQ

RPPSS

>contig58672 Frame-1F|Blast-methylmalonate-semialdehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY64588.1|) 7e-34

MALSVVLFIGSSKAWIHDLVKIGQSMTVNGGMEPHTDVGPLITQAAKDRANALIQASCDH

GASILLDGRHVVVPKYPHGHFLGPTVLDHVTTDNPAYMNE

>contig58746 Frame-1F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 4e-53

MQLDYQNSLVSFHNLGILVALWLPVVCIFNYSTQIFFTILQALLGGFQGILMKTGEIRGA

KEMTKAFRVAPQLFDQKVVTLLARSSDAPTSSMESVRMST

>contig01679 Frame-0R

MVPGNAYTDPGSVVVRHSLQDREVPGSIPGADKSSKYNGRWSCPVHPKRCI

>contig02663 Frame-1R|Blast-ATP synthase subunit beta, putative [Phytophthora infestans T30-4](gb|EEY70035.1|) 2e-18

MVGGIDEVKTKAAALAAELDE

>contig03372-0 Frame-2F0

MSEHEYHMICSWHRSIADFTKITRTNATSDVRVIKREF

>contig03372-1 Frame-1R1

MTRTSDVAFVLVILVKSAIERCQLHIIWYSCSDIVAVFRLANFCVMLSKMSATKTLNRIE

NSKWPN

>contig06014 Frame-1F

MLFYSRVLPLFEQRKAKETMQKTKKGQVGNEEGKAHVPVSEKVVLQPKELDRTQFLASLK

TTLFPNATSIKKTPMTLIVKKSHVTQQASILDGNK

>contig10109 Frame-2R

MATDASASVLGGTVLNAGPLGPDSTYGKLPPLNPDDLKLPSPPPTAAGNVTNLADAISFR

EVWMEIKATTREIIMGSSVSGVLSAMRIANFTVAGCMIALAVGQVIQSNSAFTVMADALS

IIYTVFFALILVGYELRTATIDELLRGSFGFMYSPWGRCLFLSMISIFPFGMCGVYGVLV

SLAGFSNAYFNFFVIMKHPSFTRGVPDYTPPEKTPVTKVVVEMDTTV

>contig13535 Frame-1R

MVGKLNVFNFFYKDSHARVTRVTRPRLSYSMRQCFKIINFTSGCPGLVLHWEFSNLQLVC

NGQIVESVKEKL

>contig13751 Frame-2F

MQSLLALLPCHNFECPNSVLCNVHISNDWPKEVRFGVKHLKARFQSSSTNSFGRPRKHQE

VR

>contig13892 Frame-1F

MATWFQKEIVLTAPSRGFHCMSLLYNCFAQYFFTLCLLISGYTGGREA

>contig14242 Frame-0F

MKRGRVLKRVSTRRGLRRKNIVVDDDDEDDAESMSQEEVEDEDEEKKDTPPPKLTRSQAK

KQEEAKKKKKNHYKNQAKDDEEYADNVEDEEDEEDREEEKEEDEREADLPERRRGSRGRG

SLKKSTQQSKPPPRKKPRRKIVESDDEVVADEEDVEESEEEEEKEDEAEEEEKEEEAEMD

EEEDVEDDGEEEAEEVKPRRRNTLTKGISKTMTRGKTRAKTAAIDIKPLSEKKLKSKEDG

LNNADYSGESEENENDEDYDDTTTNVMKDVKQLSDLPSATVAISSTKKHKRLSIDTLMNA

ENNKDVFEEQIDDMTPSDAGTDADELPDQYLREAFSEATTDLKLMEILTESCGRLIREKK

APSRLFCVALLGAVKENSARFCQPVVFKYLLRLLRSKHYLGMKDVVDYGKKTNSAIALGL

TTSTEFSQIPLPVLVTNVLMLILEAKSDWPKDSVKVFLDDSLFSRVWVDHEYSQLFVQNV

KTVLEMDEIKSTQPFVRRRFQGINLVQELKDLIIGFISSRLVELNKEKSSSSGPSTGTGG

NHALRNMIMTLADFASIPQIRVLGAENMEVWLQNPSVKGPARELLHKIVASCQSTSSQDI

ATVDLLLKLKLKSTMFQLKVEAITHLVCKNLVYLRRALSMFIARERPNNMSRDVDNIKML

QHIFRASRSLSASSILGSPEDIFYRRPIEHQGTLASRELARVFREMASTSDVSPVLKTIV

RKVLKQLTFEQVDIKALCVGFLGNEGHWDAMTGDARVLDYMGLITGVVWLILLMRGAAVK

SLQIQHSSAVNRQSSASSLPSGLKHGGAIVVSRRGANPPLSLSRINRLAPLKGKQSSGKH

PLSSVTGVSGSPAPVSQSITGNNSGNNSSAATEGSRIAKISVWAKEELQQALAFVQREAI

ICCRDVLEHFGLSGDSPFEKKLYENIVKKLLFLEMPSDVQLTEHDRTCFQTTKENIPIHE

DSLNLLTDLFSSCPAIDRMEALRTMESVVFRGADAHLHREALWRYHEDDLASYAQHGGVL

GLTVKNSAIVQQLFKLSLVCA

>contig14444 Frame-0R

MADDMLKLAEVENLVARATNEALDGPEWALNMALCDYANAYQSICDDIVRLLQRQLQSGN

PKVTFLALVLTETVVKNGPALIYSCVASRYFLHQVAILSNGSLGVDVQHQALILIRQWAD

AFQSGAFYDIYQQLQVQGVVFPELENNAPVFTPPSSTTSLKEEMALKPKRHSREQQLQKL

HADLKVVQQKIKILRDLYASTQDEKELDDVVDFLRQCQPRMNTLIEGGIMGKVDEYTLEE

CLN

>contig16558 Frame-2F

MLLHPSNFRSHQASDNILTSSGALRLLRGSAIPQNNNGYQERVCDKIVVNAEGKSAVDFV

SGSDHTPCARQAEPITEVPLELKNCESSDTSDEEKRNLFMQKLDQFVAGQQQPFLVDYTS

VLSDNSYSTGYEVSTLSIEERLKKCPIPSTEGEPATNFTTGSFSSSTLEELSKEKHMFRT

TTNSKDGGFSMTKTELKRQQKLTLQDAVVSVPAATSSLVPAISQSGDFMSGDKNGIYSRK

KSSTGLLTSSASSIKRNSPRILNAGEDKGGQNGKKSGRIVVGNLYSRRNNFQFQTAVSTG

TNKINAVNNPTAQEVASVSISTPALGTVESSGDNSVCLASNKVISPSTTSGVGSSNLNAA

VPSKRVVQKWTEGEKVDFLKYFSQFGKDWATLTEKVPTKTAAQIKNYYQNYKNRLNLQDI

LKRRNENAAASGGGKNAGVMLRVTSGYMTTSPRSAAAGLMDGALRQVGQSADQSSGLSMA

MPCGSMVLNASDPTLSFQAALTAAQPKIHGVNVLSEISVNQFGIQPHHDQSQQSREDMSP

SSSSERYLRLLNMQHQLQILHFQQQQKSQVMTTEANSNNSYQGNQMNPANAQRLYQLSYQ

QQQHQHQVPPQHLSMQALQQVGVQNHIHTSAHNQMAQLSNQHQQARPSYAELRQPTAMYQ

SMPQMPNHHTQAMTQLSPSHAQQYDRQVDSGCNDVADGGAVAARGTTGIVTSQSGCNDIT

QRPIMSMTIMKNIASGSNSSTSQGVSASSPPQPSLPPPRSVAMDASRHAVPHPQPSGWKT

TRALPEKIKTEDSSNKIASQAPQGNELKTRTNLALPSAQLMQPLRSRMSFSSILNESESP

RDDLISQCHSSMVIRQHESPHQFNMSQQMQQRQQQQLHNKHVQGMPPNSIELALPSVAGP

SPTAQVLPRRPSTSHNRMGLMSSLLNVTSPERRISNPSHQSPLMHQSQMQHQMLPTRYYD

SNASNGAESAGTAPLSSLTTMACEISASSAIPSAMAPKESPNASSVSIYNTSSAQLAVAL

SRSGAMTSTLAVSNAGPSGDPRVQQQIWNYEPQVRFEEAELLRRAQRAEEEAARARAVAA

AAAKALQEAQQARKQALDMAANMARYNNAMQQQAQAQQQAQAHQQAQAQQQQAQAQQQHQ

VQQQQQQQAQQYQQLQQYQLQAHHQQQMQQHEYQQQHQAQQLHQQQLQHQALHHHLQLMQ

QQQQRSSVPSNEHVLQQQMHPQQQQPPHEDC

>contig17764 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66363.1|) 1e-108

MSKNKVWSQNCTNLAADSPLPLLSPIQSGQKDIAPIYKFVLTGGPCAGKTTSLDRLSTFF

RERGFRVYVVPEASTLLQTGGAFFLDLQEKDVLNFQWQILSLQISLEDSFYSLAQDSGKP

CVILCDRGVMDGSAYMTPEQWEVLKLEHDLDTVTLRDTRYIAIFHLVTAAHGAEKFYSLE

NNGIRIESIEEARAADERTCRAWIGHPKLYVF

>contig18776 Frame-0F|Blast-protein phosphatase PP2A regulatory subunit B [Phytophthora infestans T30-4](gb|EEY61246.1|) 3e-57

MEELTEVITAADFHPTHCNTIMYSTSRGAIKVGDLRQSALCDAYSQVFEEQENPEARSFF

SEIIASISDIKFSPDGRYIIARDFLTLKVWDINMNSRPVQTIN

>contig19124 Frame-1F

MSSLGTISFLLHLDMLSQGVKNLPVKPNQESSKTITMISREMRDIFFEKVQLTDFGENYL

DMIFLMALPNNAGYTRSQQLVDELIANAVKENIHPADFAIMLQLNSIDPSEANILVLGVF

MRYLKSLNHDTPQLIIDLEENIGQVRLAMLLQAAKTPFDHEQSSIATSFQIDQFKIWQSN

RVNIVLMRNNLNEAEFYGTGSALYNNFLNAFTVYVDAVSQYIEMASVLSPNNLLASKQFQ

DWSENLLAKFPNDQAIVTKVLRHIYTDDELFASLTSQDSALTPTSQYLLEELMGIWAKDI

LASPRTGFFANRENNMYSLNAMAKYIDIMLKKPTITDSDLIDILSLDNLVANKFRLDITG

HIKASEEPINNYELGVFKRWRAGGCTVDRIEKLIEQLSSDGKVDIHKESLADTLVLYKEY

YSSLNYEMNDNDIRKEVSNELIALIAEAKENQENLFETTAYVRWSTVLQLRFPHDKVIKI

QALLGVYGDEELIALLDVPGNTNKIWRQQLLGELVAFWVDENEGTAILKIMREISAKTQS

PSIPLLEIFAKYIALQSREENKMRLVANGDVGGWDLLLAKAIQNAIVVKKSNTMVDLQVA

QFQRWVANNVDYKSVQAQFDEDPRKLLFSETVEPIVRAYELYNIDRNAFLVNVASHMTPE

NVESAINLEQLTMWHDFLAKYFPNHQYMFS

>contig19436 Frame-0F

MSSAYDKTVGGKLQLKSRLPLRAIKLQRKKKKRSAYTKLEHDMDTVEHTSKPFELVKLRG

SGRLLSSGTTLMGLMGSKLLQELHVGDAIVIQHPTSLAEEMRIVRMVLSDVSASISSSFS

SDLVSSTPFYYIKAPPDREEQEENEQENQKKKRKVDELTAFGTYAGGTNKGEQYTYRVKK

SGAFGGYAIVKEDAHVERSREELLDIRSKKKGDRHCM

>contig19519 Frame-2F|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY53288.1|) 0.0

MQLKIQTGNASVNKKITFYSTEDRANFVQALEQGKVMINKKAATVATPSRVPAETIEETT

STVSSTHERTKLRDSIVSDHYQLLPGESVLEHVQRVTNLVVMSQSDRAVQGVLKITSYRI

TFVPYDASWKFGSFELPLAAIDLITRDGLMLLITCKDLRTLRLAMHDAYSRKKGYDQLPS

TPDFRWLNLLTLRMKPPNIIGALFAFDYHTEKAKSRGLSTPETHNGWFVYSPFAEYKRLG

FLSTRKQAEQDGVITWRLLKNSKFRFSPTYPQLMVVPSLMSEEQLVQSARFRSRARLPVV

VWRHPVNKSVLSRSSQPNYGMAGNRSEPDRI

>contig20137 Frame-1F|Blast-hypothetical protein PITG\_17492 [Phytophthora infestans T30-4](gb|EEY67002.1|) 2e-29

MCTYEALGGLSADNAKIWFPRLMSELVYEEQLLVLLFMAGNFQIIKDCFFQTKAGTQRIM

IECFPETGSIVNHDAMCPMMEHDPEILRLPSYSCYDAFKNGFLYVIRHTARAFHPE

>contig20667 Frame-0F|Blast-HD domain-containing protein 2 [Dictyostelium discoideum AX4]sp|Q54FK1.1|HDDC2\_DICDI RecName: Full=HD domain-containing protein 2 homologgb|EAL62031.1| HD domain-containing protein 2 [Dictyostelium discoideum AX4](ref|XP\_635539.1|) 4e-11

MATGAKALSAIEFLRLCGRLKTLKRTGWVNNKVALPESVADHMYRMSMCCMLLDDVNESV

NRF

>contig20713 Frame-2F|Blast-mitochondrial 2-oxoglutarate/malate carrier protein, putative [Phytophthora infestans T30-4](gb|EEY67662.1|) 6e-12

MLLKTGDLALGGGPLQWNPAATPRPPLASFTFGGVAAVGTVFFTHSFDLLKVHLQTSKKD

KLKLC

>contig21178 Frame-2R|Blast-ribosomal RNA-processing protein, putative [Phytophthora infestans T30-4](gb|EEY70390.1|) 3e-65

MGKSVREYVREVYRVLKPQGVLKIAEVQSRFESASIGGIDGFVQTLWAMGFDCRHTDARN

KMFVLFEFMKSSRKPQKVKPIEFKVC

>contig21545 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63947.1|) 1e-107

MNGRRAAWEPAMEQALMELFEKAREDSNLRTGRGIKARAWSDITTELNTRYKTSLFVEQL

KSKYARLMMDYDLFKDIGGEEGSLSEEQWKAIIAARPENASRIRQFKEHGCAYVDVCRRI

AATREEGKEGMPLIRKLKAERKPRMKRATSVMEAQAPLKKARTEDVGWTPERVEELLLFL

YWKAKNDEEGSKEEELTPQGWANVLMELNNVCSATFTEQEIKDKYVKLMERYHQFKHATG

FSGDLASIPKDEMDWERLIRERPGHYTELEELKELGGFPYVEVCSLITG

>contig21826 Frame-2F|Blast-mitochondrial import inner membrane translocase subunit Tim17, putative [Phytophthora infestans T30-4](gb|EEY55736.1|) 7e-85

MEREPCPFRIVEDAGGGFVLGAVFGSGWYTFKGARNSPSGQRFRGAIYNAKMRTPVLAGG

FAVWGLLFSSFDCSFEALRRKEDPWNSILAGAATGGALAARAGPRAAAGQALIGGVLLAA

IEGVSIMVNEWFAPQPDQGLSGNSMGNLDLDEQKLAPPSF

>contig22580 Frame-0R|Blast-hypothetical protein PITG\_14021 [Phytophthora infestans T30-4](gb|EEY62030.1|) 1e-44 NOT\_ORF

MDATHTQYLDHLLNRFFLLEKHMTVTQYISATLNHILHFVGRVDEIVSAVDRNLHRYFPN

CDNDEKPNGQLTQCVGKKPIFSFLEHPDFSILQSEMAQSFKEYKRQTHVLVIMLTAMQKH

GASPHVYEIVSQLNYNNFYQ\*QDGKTQRHS

>contig22746 Frame-2F

MVHLKQKNLRKTRLACTCQCKLLSRPPCIQLLRVGSLLFAQHCNANFITFF

>contig23455 Frame-1R|Blast-spastin and Fidgetin-like protein [Phytophthora infestans T30-4](gb|EEY65751.1|) 1e-125

MARELQPSVVFMDEVDALLSTRSASENDASRRIKNQFFTELDGAASSQEDRILVMGATNL

PQELDEAIIRRLEKRIYVPLPDATSREGLIKHLLSSQKCSLSAKDFQHIVKATNGYSGSD

LKAVCKDAALGPIRDLGAVIANVKAEDVRRINASDFQVALTRVRPSVSLKKIEDLIAWNE

RFGVSAV

>contig23622 Frame-0F

MLGLGGKNARSVCMINQLAHRRMSVAPSRLAQFPYLSELGLEEENCGVYNGRWFGSGNLY

TSLSPVNGQPIASIRSGTKSDYHKVVAAMDDAKPLWCNLPAPKRGEIVRQIGEELRNKRD

ALGKLIALEMGKIYVEGVGEVQEAIDICDFAVGLSRTLNGSVIPSERPGHFMMERFNPLK

GHVGIITSFNFPCAVLFWNAALSLVCGNTQLWKPSESLSLTSVACTKIIADVLERNGHPG

AIASLVCGTGVEVGEAMVHDKTMELISFTGSTKVGRRVNEVVSSRFGKTILELGGNNAMI

VDKDADLEMALRATLFSAVGTAGQRCTSLRRLLLHEKIHDDFLQRLVLAYQNVKIGDPLN

DGVLCGPLHNKMAVQNYLDGIDTIKKQGGKILTGGNKIESEGYFVEPAIVSIAHDAAIVQ

QEIFAPILYALKFRTLEEAIEMNNAVPQGLSSSLFTKSQAAIFKWTGPLGSDCGIVNINI

GPSGAEIGGAFGGEKDTGGGRESGSDAWKQYMRRSTCTINYSKELPLAQGINFN

>contig23697 Frame-2R

MSNHKTITVPSNTDYSFEEVLRNEDGQDNEGAGNGFSLEGEPENSLSLKAITAVTKNSNA

ATSMEAEEPPAELTTSGLIGMFVIGIGAVAGVLILVHVRKPAQH

>contig24065 Frame-0F|Blast-hypothetical protein PITG\_06232 [Phytophthora infestans T30-4](gb|EEY69745.1|) 3e-34

MTTITNFMRMTKPLKAHDKKGARSPVVKKQCLSKHEVISSPIEVARSDEKSDVYIPTFIY

ETVKYKREHETHNVPKEMQTIVAYIKKYYIVPKDFEINKKFGCHSGLTYETRLARAYEMG

HLSLKQFNKGPNLRKPICLTCATVGHTRK

>contig24223 Frame-1F

MLLLDRLMISMRNLTTDRIVIVSNYTQTLDVVATLCQERQLPFVRLDGATSAKKRKMLVD

TFNDPTTNSFAFLLSSKAGGCGLNLIGANRLVLFDPDWNPATDKQAAARVWREGQKKMCY

VYRFLATGTLEEKIFQRQLSKEGLQNIVDDKEEVNSLSSKDLKRLFVLRNDTMSDTHDQL

KCDRCPWRDNGDAGKIIEEDLSDDMIVDAINIEKETRGESVSVRGVRGDEDNDTYVNKDF

QPQIGMPPEEDLNSWGHHRSYASVDDEVMQAALQQVKSDLVSFAFSCRI

>contig24447 Frame-0R|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY60905.1|) 6e-51

MLKFFMEVQGKIPNKLIKKHRQTYLEQFAMEPHFTEDLKFCSRESDRVTGKPLLRFMGTI

KITNDLASSLMNAKSLMDDRKRILELSNLLSRMITLDPSKRISVKDALAHPFVKGS

>contig24573 Frame-2F

MWWKPLFRSVCDSLKFAVAIVRLFQRQTMAMLSRRLCAHMTQNCIRISRASFFSFPSPSR

SLVKSHTEKRVVPFSCTEMFDVVADVARYSEFLPFCVESRVLRRPNENVMEAALRVGFRI

FTESYTSRVIMIRPNKIATKAIDSPTFKRIESEWVFRPCPAPGSCEVDFKVTFEVSSFLR

ANAIKLFFDDVALTQLNAFINRARKIHGTAPRTRPHALVEDAVTKNKSAQTVTSECTANG

GSIAKPSLAEKDEKNQEVGPTASASPRIKGGISAQTYSDLAAVFVDYADKNGKLYYGGFT

AACMALSDEYDNMKDITESAALAGAVFTSFETHAMPKDWLSLDEFVEGVYLMTKGTFEQK

AHSLFVIVNKTGNGKITREELSQAMQRRIRAVKKLFPKLLRDQVQIQMAHEQVKELSSVQ

DAAMTSSVKAIEKLMEEVEKEIPLAVNQIFLEADFDQDDYIREQEWMFAWQAHPELVELM

TIDGMKKMVQWASVVQEAGKGNGDDNTTGSLEQSLDTRLTYVDFN

>contig24601 Frame-1F

MQLKTFMTFLIIVQPSRINQVPRHFRGNMVMGTHDYSSRSGHEQAFTTA

>contig24708 Frame-0F|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY60954.1|) 6e-94

MFQRTLIVNGFSKAHAMTGLRVGYLAASKHFIDPCTILQAQMTSCPNTIGQVAAVEALKY

ELESMANGKRRISKVMENLDTKRRYIVKRLSAMQNVCFAYPTSAFYVFLDLSSYFKGGKA

LIANKRVTLQSVDDLCAHLLQEMHIAVVPGSEFGDEFGMRISYASSMEAIKHAMDGMESL

LNSLICYH

>contig25080 Frame-1F|Blast-cathepsin, cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|EEY57990.1|) 3e-47

MAMHQFSSFQEPGDIDWRLKGAVTPVKDQGACGSCWTFGTTGAMEGAVFNQQKKLYNLSQ

QNLLDCSWDYGNNGC

>contig25174 Frame-0F|Blast-Equilibrative Nucleoside Transporter (ENT) Family [Phytophthora infestans T30-4](gb|EEY68424.1|) 1e-160

MLSPLPRTPGIRRLSFSYENENSLEDYGKGSAQVSVKDAQEEALACWLFALVGVGYLFPF

SALTQPVDYWNMLFPDFNIEFALTSIFMYTNLAVLSIIVIVFGKPWYKGRIVGGFVGQLF

VLVVVPTSYLFLQSENANIVAVLGSTVLVAIATAFIDSSTIALVSHYPQRVQESFQLGVG

LSTLISSLYRDITKLVFPVNKVLVSSLIFFYTGAITIALCIGAFYKVMSLKMTTKFLYRK

VSSSVELTERLPLLNVKRQSTSDPLSVAGSVRTKWTVLKKVWHLQALILMVYLATLSVWP

PLVTEIKTFNFPSLQNTGWWSLILLTLFSTSDCFGRFFVNRRFNLTPSNIWIPIMARSIL

VPIIIGIVKEWWLQSDIWSMICVVLLGIGNGYFGTLTIIFVSESVHTDEQHLIGPFTSLF

LNFGLVLGSTVGLVIKKSLLG

>contig25707 Frame-2R

MRTLVLMLLVAAFAAITLAQTTSSNAASSAATNSPPPMTAELAAIVECNTTQLDDGQITL

TSNQRAEQCEEALDLQAGTMLQVTTADATEMCETTSCRAALQELYNFLPNCRYELWGLQY

SAKRLLEYCGITPTNTTSAGRSRSSAGWSVTSSSASFADVGATEAPSTAAGESTPAAASS

DATTRMALTTFLMAVFGIITATVA

>contig26027-1 Frame-1R1

MANFDPFADCNQTISNGIAQNIL

>contig26027-2 Frame-2R2

MRFWAAEWQTLTLSQIAIRPLATGSRKIYC

>contig26092 Frame-2F

MSHLCHSSISVGLSYQRWNSVRKNRCFSS

>contig26838 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65158.1|) 1e-102

MVALLSSVNLVLFVIQLFVNGLFSRNIGPMSRHYETLITPAPFAFRIWGLIYAFLAASVA

VDCFWPSISFYESASNAKMLRALFAVACLMNMAWIVLFTNEYVNVATVTLMILWLSLFVL

YSQIIADRRCIGFDLKKFVLSELGLTIYFAWTCAAMLISLAVTAQYVAGGYLSLTFYVAL

LSLLAVGALFAVIYEGDLAFGLVVIWALVGLALKNATFKAHVNVIALSIRACASQSAAVV

ATFIVISVLRKLLDIKA

>contig27819 Frame-1F

MSFLPAATTSATFASIFRDTDDVAQYIGGCPYLSFWILLVETQKEVPLFLAMGQLMIKYE

PKTMKKIEKMKRVKGKLAAALGQYNVVENEEKEQRDKALDSTSRLSDAFQFSHTSMDSLS

QYKIYRWCNYCLDLPESEPLQIIYWQVFFALYFATAGSFRVYGHHFLDHTGVRSPKHVHL

RTCLQMKLRKLVSYCSNQAQVALTATGTSSHSQTDCHFGSSADLKEPKYAHYV

>contig28128 Frame-2F

MAYIFQKISFPNIAIGSNIFKILSTF

>contig28245 Frame-1F

MVALFTGQYKSLLECLICRYESARFEPFTFLQLSLPESNTRSIELTIFFRTDRVPMRFSV

RVRNNDKLKTIKEKVAELIKKTDDNDSNKENVLNEPLDEDDLMKVVIARTSNLHTVESLL

DDKVPLTQIHEKDQLSAYQLDCDDDLRPPEWKRINSTKTADVLHLETTSKTAEHDARASD

LLNKKPSSDESKTNIPTIAKANVYDEIGGSDEDKAFPVGASVYIHVEKSNEIMAARVIGS

SVSSGTVNVAYPSGARRYHIPLSKVVERRQSDAYIFLVHRRVERSTDSFTNAHITRLFGA

PLVVQISLHFTTAYNLYVLVWNRIRRIFNWQQPPPPSDFTGLNFSRDRMRTDTSSLALGK

HLPMAKFGFCLRLVTSNGIGCSRCEWLDGCLGCVLLPSYQTMIPLAAEETVAIDWDMRTL

KEEYDSIQASKLDLDASVQEHNRLDNQPLNLSHCMEIFTAKETIPEAYCGRCKTLRPATK

KMDLWRLPPLLVIHLKRFCFTQVARRKLHHLVDFPLRGLQFNDFVARKRDPRGRLFGLEY

WLFLGGKLKNDSESDKSESSQVSEDFVNSKSPRRNMSSALDAPAAATAVVRGDDGFLYDL

YAVVNHVGALGGGHYFAYVLSDHDGRWKCFNDHQCKDIDEKEVVSSMAYILFYRRRDTAT

MSIEELFPPLPMDSTGNGASTDEEAAKDKLQVEELIQQSKLSSGNGSSCNIS

>contig28487 Frame-2R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY60229.1|) 1e-18

MDIIRTRAQVFTQYGAVDTFKYILDTEGPLGFMKGLSA

>contig28696 Frame-1R

MHRTIAVEFADFMLVNVYAPNDYKDRELFYTALQQWSWQGKDSILASDLIVCNARSSTAS

GSYGPEGLRTRRSSGSFSVFGWRTRVRLWTQTTMTTRPWTRRLSSRIGDQVRIAVSTDLR

AAILDSSRPGGFSRGAISTFRP

>contig29619 Frame-2F

MSGQKKTGYLLWGAAFILARWIHKHRELFLNKSVLEVGSGLGLGGITAARYATVSTLTDY

QADTCVALEYNVQLNKFFTHELNSLKPEVQVSLLNWDCTDSVEAVPKADVVIASDII

>contig29736 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63797.1|) 7e-90

MFYPRTPDYNVCNREFEWDSILHSILGLKPKVEYQVLVSVINENRFGFVLESGSADIYHN

STLVGKWVLDKPWKAAAGSITDIVAGINITPGYTEGIALWKDFSKNQLIFRINATIAGSI

TWGRYK

>contig30172 Frame-0F|Blast-methylcrotonoyl-CoA carboxylase subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY68238.1|) 0.0

MLRRHLIQATLHHCKPLRAFSTSSRSFRKILIANRGEIALRVLRSAQKLNIETVAVYSDA

DANSQHVKLATESYRLGPSPATESYLNFPKIIEICRLSGAEAVHPGYGFLSENASFARAC

KEAGVEFIGPPVKAIEDMGSKSASKAIMIKAGVPVTPGYHGLNQSLEALQNEARKIGYPV

LIKAVLGGGGKGMRIVNEEKDFQESLDACVREGHASFGDGRVLIEKYLKRPRHVELQIFG

DKYGNVIHLFERDCSVQRRHQKVLEEAPAPNISEALRNKMGDAAVAAAKAVGYVGAGTVE

FLLDEDESFYFMEMNTRLQVEHPVTEMITKLDLVELQLKIAAGQELSIQQKDLKIYGHAV

EARIYAENPYKDFLPGSGTLQHVRLPCVSEAVRVDTGVIEGDEVPIFYDPMIAKLIVHGD

TRRAALDKLVKALHEYQIVGLSTNIEFVARTADHAAFRKGGVDTSFLNEFGDEVLGSLKA

YPPYATALGAISLLLLEQIAALHPSGTKNGNLQSSWSNGSLAHFRSFDTLERKLSLLHDN

EKTFVTIKCLSRDTYDVKLSGIAGLKICLVSGMIDKKGNFKFRVNNRTFKGTAVIFQQDL

HLFCDDNSQRYDYKFHISLPSFQATQGSMSAIEVSKIIAPMPGKVIKVLVKNGDSITADQ

PLLIMEAMKMEHTIRAPKNGKVKELLCEIDDFVTDGHVLVDLD

>contig30590 Frame-0R|Blast-sugar fermentation stimulation protein [Phytophthora infestans T30-4](gb|EEY70659.1|) 4e-60

MVEQALTLRWLTELGDYDTVRREVKFAKNSRVDFVLTAKADDGTVLHEKYVEVKSVTLAL

ESSCSSVSRCAVFPDTVSSRAQKHVKELTELVSTKARNYAKSNENVSGAIVFIVQREDCH

MFTPSIHYDKQFASLCSLAANSGIQLLCYSCGLTIDESSASGTVKLLGPLPFQH

>contig30969 Frame-0R

MADVGVPANSGDVQPATLPSPRPVVWSSDLSKTDYSLLLGLPVGSLLAIVFVLRVLWRPK

SGPKFRLPKQVPTYGSVGMDDDSYKYDGDSNDLIYAGQVAGRYDTRWTRTFDFVFLVGMM

LFAAFLTGFTTLIEPELWNNTSFWFYLLPKVLIMMGVSTLGGIICRFFCIVDEAGYVITE

RNSAFKVNYTRKFQLLAAYLVPLLVKPDEESCPACSGPVALAWGDFVTLLCFLLLIKPIR

ERSTLFMLQFNSLDRPEDRPHTLKWIVAGNIFPGLFVLLFFRWLFARTTQSDLVFILVFV

TSIGDGLAEPIGIAFGKHKYSTSTCCSKRKYTRSFEGSACVFLAGIVFPALQYTNFETPM

QLWLTMIILPFVVAYAEATAPHTMDAPVLMGATGLVLYTIIHIF

>contig31063 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61457.1|) 1e-08

MDSKRTLNVHVSIGNDLLEIILILNPLLMTV

>contig31618 Frame-0R

MPCCPYVRTRSTTLLAGQRMRNLHKINIKMRL

>contig31777 Frame-0R

MNEVHEAAIGGPLAIHFEAKRRILATVKQLSERGETLQEATPEEILEAANKAAKTVFKFD

FSISAEPAVDASTYKRTRKRSKKKRGKKSHGNDANKNENVKPTTQLASRRDNAKDSNDSV

RTQQQQINSTKSKLSGSSSLIKFRKATGTESEMAKMHLRYGHGRRNMVATNQREHRKQTA

SQKK

>contig32336 Frame-1F

MEQQGGLAFSSIDSGMEFSISSVTPSLASSRLAFGRKADLNASSCVIRLNKDRASKEQCF

ERHPLPELDEFGREIRHEPKGKLYDDRGERHKDRRKSSSKQNDRRDHLYTSHVGHPISEK

RRRLSGWDRTLPNKIATTSRVVLLK

>contig32457 Frame-1F

MAREAFNFDKAEDFDDGTRAFVHENSASGLDAEPHTSMRLRSSRKHRLQVEREGPGKYSD

QASALRIKNWEAEELLLSKEYAGRVVERKDLNDSNESPDEDAVAEWSDAKPFGTSDDEEV

DEITEEDVLSEKDSESEGKSAETIIRGFQREDSARLMGTQDTEKVVEKAKHIRHQKIFWE

RCLEVQIYTKRVLTTMKNAMSHETVGEETDGMTANKIKQQIVAELYESIDAVSSLQQNLC

NVSDLVASEAPMKKRTRTCDNLWEEITSSNLAMLPQYSNILNTYTRKTDLIAGGKNRQAK

KFKAVNQDILSQVESVLLDPQRVKRKAHAPLENEVAVDIEDQLDELMYDDSDFYQQLLKE

FIESSGSGTGLDAIRRTHRKKKKVVNRKASKGRQLRYTVHPKLENFMFPEPYPIPDMDLD

ELFRSLFP

>contig32549 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62310.1|) 1e-133

MHEEEERTIPGNAACVSPDLPFGGLSMFGTAFLNKFEVAQVPAPLLKELTIVDTPGILSG

EKQRIARGYDFTQVARWFAERSDLILLLFDAHKLDISDEFQRVIEILQGHSEKVRCVLNK

ADQVDQQRLLRVYGALMWSLGKVVKTPEVMRVYLGSFWSQPRQNHGDKNSSSTPEALFDA

EERDLLHELQALPQHAAVRKVNELVKRARLVKVHACILRISTYTDACDIWAGKKAARVAR

QDG

>contig32888 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65095.1|) 2e-40

MECQQEAEYEFNDPPLAVALDRYAVKQGIVVVAKLFFSNGHNTGEKDNFQEIIENVRLKK

PNVDIRVTQALGTHELLTEILQDRYSSIMSKEFADLTLNALG

>contig33821 Frame-2R

MNPVVTDERYRSFAYKDAVYFSGHKFVGGPGSPGVLIVKKRLITNAVPTVPGGGTVFFVT

DKDHRYLSNRVEREEGGTPDILGSIRIGLAFELKQRVGATNITELERRIVLRVRESFQAN

ENIVLLGRQDSSVTQLPIFSFLVRFRDRFLHYNFVCALLNDLFGIQTRGGCQCAGPYATR

LLGLTRQNLLALERALLDNKEILRPGFTRMSFPFFTNTAECDYLLAAVNFVASDGWKFLP

QYKFNHKSGAWKHRSRFTKFPDRKWLSHFATALEDKTRSLELADDEESLSAHRMANLADA

RRLADEIYMMNGISHAVAASATSMLDVDEEALRWFIYPFEAAEAIQSRDRPITTEIIFGP

YQPARYHTRELKDQWKTLISGSPAAGTASCDIALSATASIHVKSRSRTNNQQSGRMIGGK

YPLRITNSLDSGSSFKNCNLIHCEVLSSSSTEVTAQATASTMTKNAIINNLFPTPPKKLL

>contig34198 Frame-1F

MYSWCASDSPGSDKFILSAS

>contig34550 Frame-1R

MCLECSGRHRGLGVHISFVRSVTMDSWTDKQVLIMLKGGNDSFRSAFSSAGVPTDLSITE

KYNTPQAESYRHQLAAIVENRAPSPLPKWEFDMPCPASTTLSSSHADGVSLEGDKCGVEA

LKGESEQGYVTRQMKLREEARARMAAKFGENGMQGIGNNGETCAPQSGNLGDFSGALSYL

TNTVATAASSAVNIVKDRELKTKVSSGWSYLQSAIHDPALSESVKSSATSGWSLLSSSAS

SLLQSAHSAVSGRDDHGDLDEMSSFPRTNPDFFAASNDSERSSTINSNRDYNSASWLDSQ

PIDGSKNSIISSYTSIQQPNASPTTHLSSRKANKTSCDLVGLSLLPVSTASNKNGLASAV

APPVPVVHEAKKSQKNVDFFGEFGF

>contig35157 Frame-0F

MRIELRDGDHYPLNQQATIKL

>contig35993 Frame-2R

MQRHDVHVTKVSYFHVLNALLHDQNFTDFEKVLQLCEEMTTNLPGENVPLSLLPMIMMTA

AACGESERAMKLYNHPPDLPMTSFTENRFEMCLQQLNRLGEDSMLMEMYRNLLLSAHATR

GVKDRVSKYLFKVRVAETSNKDFCVAWEILRLMNLHKILVSHHAIYPLMYKLFSGPLILG

SIDGGVTIENGGDVPARIESADDLCNFFERFSCSLMWNEFALCEAIIAGVRADRAGLVDS

LCVYALENNMPIKYAALEQVVVYYYRLGFVNDFERVSTMVRALRLNKDIPVGIAVTEVGM

AANFRLNRYDEVIMLFEDFASIDGERRRALKRPFMLQTALNAYKHLGRGDEAMAIQ

>contig36215-1 Frame-1R1

MGKQSITEVIHKIKPFEKANKAMEWKEPQEEKIVMQLVKITTANETSLFFSLKQHKRCLF

NQKTCSLVL

>contig36260 Frame-0R

MVAYESHKSHQRQHRQMLMRTMNMFTEETSLKCGGGAWGNRLLF

>contig36758 Frame-0R

MSDTKTEDSARGVKRRRENSDDESEVRKGVKKQVTAEKIKEPVVSSHSVKRRREASDSDS

EERGAKKQKLKKQVATSEKVMKEVVNQEHEEKTAEKEVVEKQTEEDDKKTEDQENHAQKS

EEKVKNIDEADSIQKLTESVTPVRMRQESKISAKKVSRKVKKLKTKSKKIIRKPVKEVKS

TKPKRQPLQDITHLYVNEHSRLYERQQREESVKRLSTSVTIRFF

>contig37410 Frame-1R

MLMHDWQQRQERPFRSLKPSKDSFARDLDRLLEPTAVQAVPRRDRVSLHLDSLVQHAGSQ

WNGGLWVLSYSTIFPD

>contig37964 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64638.1|) 1e-106

MEKEYYLQDLGSTTGTFIFLKPDAPKRLHVGDRVKLGDTEFEVVAIDEHITTGMPYLRIC

FTDGPLTGVCQTIGKTSVTLGRHSSNALCIIEDDSISGRHVIVSYFGNGFFITDLHSTNG

TAIRLSSSGKRSRRRYLLHGDVFGVGSNRFMVEYSHQLASQCQLGKLVREDNGHA

>contig38914 Frame-2R|Blast-regulator of microtubule dynamics protein, putative [Phytophthora infestans T30-4](gb|EEY66712.1|) 2e-67

MAKEWLDKALAIPICGEEDEMAHEEAQALQKKL

>contig39391 Frame-2F|Blast-nitroreductase family, putative [Phytophthora infestans T30-4](gb|EEY55532.1|) 1e-103

MARRLATHQLRRNTRLLTDERSLSTGSTALKDAIEERYACKAFLPCHVSDETLKEILKLT

LRAPTSFNVQPYACILVRQEKDRKKLAEAMMGGNARKVIEAPVIAVFAADLEPTKRVPRL

QKLAYDSGAPADFVSNMPHVVRLFSGEGMISSMLRKIISTAVSPLQPAPSDVSTEAWSFK

QTSFAAATFLYAAQVHGLATCPMEGFDIIRVRNALDIPDRYSVPVVIALGYADPSAKPKK

LSERLDPTEMFFDGKFGDSCKKIFPDK

>contig39742 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53297.1|) 1e-108

MKVAIVGLNPEMQGLDFKESYSKRVTLPRMLIKIKKEVISMGIKEINPAVNGLSAHISAK

EFKTWMDNGKDMVVLDTRNDYEVRLGTFENAMNLNLKSFREFPHKAQTQLQNVPKDKPIV

MFCTGGVRCEKASYALQNEGHQNVYQLDGGILKYFEKVGGAYYKGDCYIFDDRVALQPDL

TEAAVIPCFTCRSPLTEEDQRSLDYKPNEHCPYCKNGKQDFRCIKKQQSPAIRS

>contig40243 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66270.1|) 3e-60

MGFQAIDDNSPDLRTNMKTINKELRAFEKFYKELDGLVVIKIDKLDWIYEWRDQPEQMLR

DAKKPAMTRDEVHDFVDRFMPSYKTYLKGLYTEPKASSSPLSTIPRLVFSITSVREPQGK

PVEYNFTSD

>contig40324 Frame-1R

MFNGQPKQENAAVLVDMLQHTFKSLCSICEELRKTADVLRLPSLRRFPYCTHIDHVCLIG

VVIKLSYHKCKLFRSELQA

>contig40636 Frame-2F

MYGPSNISSKRQMTQPITLQDVNKYSHAKKGLVCALD

>contig41198 Frame-2F

MKQLYAKVPKTSSSGSDGIDTQPIRRDRRRGKSLSKLSRMFVQLFLEKENCIIPLDEAAK

QLLQMEESENEDDRMLKTKIRRLYDVANVLVSVGLIEKLQLSSSRKPVFRWIERSTRGVL

NASSKSYSQSVDSVNKPLQL

>contig42173 Frame-1R|Blast-midasin-like protein [Phytophthora infestans T30-4](gb|EEY58697.1|) 4e-50

MAFARPSNRVYGVSPVISQAGTSKKCYDKQKLPVAVDVLKANSVHIGDIWHHLEKIVSVF

DTVTTPACFDKIMAEYACIIRADSIFEQT

>contig42308 Frame-0R

MADLTPTESSFTPPSIDPSVFAVLPQDIQQELLLSFPASTNLAAPVSRTLSLHTNPWTCH

VCTFRNHPELPECEK

>contig43062 Frame-0R

MPVGKLRLKIESQSACLLLERTNVNILGGVFPFKPFNVLANKSYLDIANVASDSDTSRML

YRLFVMGCQPVYDTF

>contig43758 Frame-2F|Blast-ADP/ATP translocase [Phytophthora infestans]gb|EEY68412.1| ADP/ATP translocase, putative [Phytophthora infestans T30-4](gb|AAN31467.1|) 1e-167

MSALTQYKPVATSEKKSGAVSFLMDLAAGGVAGGISKTVVAPIERVKLLLQVQAASSQIK

PEDQYKGIVDCFVRVSKEQGVSSLWRGNLANVIRYFPTQALNFAFKDKFKKIFMDGVTKD

QFWRFFMGNLASGGAAGATSLLFVYPLDFARTRLGADVGKGKSRMYTGLVNCIGTIYKSD

GIGGLYQGFGVSVGGIIVYRAAFFGGYDTMRDIALRDPKNAPVWQKWMVAQTVTTLAGII

SYPFDTVRRRMMMQAGRKDVLYTSTLDCATKIAKNEGSGAFFKGAGSNVLRGTGGAIVLV

LYDEFKKLMK

>contig44063 Frame-1F|Blast-serine hydroxymethyltransferase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY69906.1|) 0.0

MFSLLHYPARQAALLVRRHASTESLRWSAAMNKPLSESDPQLFDIIEREKQRQRNCISLI

ASENCTSVAVLDALGSVMSNKYSEGYPGRRYYGGNEFIDQAENLCRARALDAFNLDPEKW

GVNVQSLSGSPANFQVYTALLAPHDRIMALDLPHGGHLSHGYQLGRKKISATSIFFESMP

YRLDESTGLIDYDGLEKTAALFRPKLIVAGISAYSRHIEYARMREICDHQDAILLADMAH

ISGLVAAGVVPSPFEHADVVTTTTHKSLRGPRGAMIFYRKGLRQIDPKSGKDIMYDLQQK

IDFAVFPGLQGGPHNHTIAALSTALLQAQSPAFKAYQSQVIANARAMVSELMKRGYNVVS

NGTDNHLALVDVKRSRGIDGSRVEFVLESANMVINKNTVPGDKSAFVPGGIRLGTPALTT

RGCTEEDFLRVAAFIDDGVVLTAELNERARGQGAKKVKDFKDFVTDDAESKKKISALKNE

VTAFVRQFPTIGYSEESMKYAD

>contig44777 Frame-2R

MSRASQIVIRNLALLRRGKLLRIWYTDSRTTVTSTSPQNRRSSIQPTLAAFRCCSSTDRD

ATESWSKIAALGAAMGSLLFVISLWDQELDAATESTITQKIRCGGNIHDEYEILDEIVGE

GGYCVVQKGIDKRTGELVAVKMLSKSETSAREFWSEVDVLRVAGQHPNILQLRGTYETDC

CWFIVQELAQDGELFDHLIANGAYSEQQASNTIRQLCDALQYLHRKGIVHGDIKPENVLL

HKGRMCLVDFGVSFRMGERFFYDSHLMGTAAYAAPETLEHGELIYRRNSRDAQHKARMNG

EVILEIDESEDFESQAGPDAIKFGPKSDMFALGIVLYILLCGAHPFDTYNNLSDEEIRNR

ILKGQFCTQSLAWQSISPSARDLILKLLEIDPKKRLNAEQALQHPWLRNHAQLSSEPMAN

SVELLEKFQRGRRRLRASILAVLLLDAMAENLDDDEYQELESIKRSFAWGLSSSVESLTE

KTHALLSTLHFFDKEGKGFISKSDLARVSRSFGKQLSDNELNEMLVGGTGDPEQNASSVK

AVDYDTVKMTISTLR

>contig45172 Frame-1F|Blast-translational activator GCN1, putative [Phytophthora infestans T30-4](gb|EEY69168.1|) 1e-171

MFCLEAATIACAYKGKDNQPLSAADLADSFIVEHEDVKTAISEHLASVPNGKLYCTSPSQ

RLAAQRALASLLQYCGNGGGEEFALHDIIEDLLAKRLINEQVDTLSEDDIAIYLTPFDEL

YEDIKDAEAENDWRRQKRGGGRNNEDEKLEQGLRQDLKRKYQVKRETHTKEYTIEQKTLL

AEQQIVRRKVQETHRIVSAVLEAISMLAATRPDELHPALPSLFRSVRLLFACPLFQLEAS

NALMTLAKAINPKLLRSKYQDVGAALRIVLSLAQCSSDSAAAAHVAKMEALFFRLLAELM

EYVFGYQYNNEAEIGPDVSCNLIPPPTLHLLFPVLRDLLRFLPKIRRWALPLFAVHARMI

PEEEEEDVGDIAAQRLLRFEMLQLTLLLLSQQAAGLALPITNSNLFPTTLLTSLC

>contig45239 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60558.1|) 3e-81

MTTGESLLAQLKFLFEQDPLIDEVGLLFDIKQCDLSLENAFLLENHKLGVAFEAGTILFQ

AARTQFHSLNALLQQELANNSMSEDSERHAQLLHCTRAILLISADFYTAWNTRKSFVARG

WLNAQDEVQFTNLVFTLHPKSIDTWAYRRWLAARICASQLKDDVMIFHKQQIEVCGRLAE

QKPRNYHAWSFRHWIVSRLS

>contig45356 Frame-0F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY65546.1|) 1e-126

MSPHVDDYYNKVATPGPDTPSNDDIKTAALHIKPRRILYSSVLLALLQPFQSGWSTSQLN

FSDYNNTEECNARPVVEGTCILFPGHSKLEWTFAVNSWIFGAMIGSLLCGYFSDLIGRKK

LLYFNCFFMIGGAVIQVAVSNIWPFAVGRAIAGVASGAATGTIGAYVNELSPPHLRSYLG

LGLQISATIGILVPAICFFFFDSGNGYRYIAGFPIVLAASYMLLSPSLAVESPTWLLMQN

RREEAREVIARLYGEEHVQTALAW

>contig45604 Frame-2R

MQRLHASAKPSFRISLGRVLRRKPMEELPELKSIRAVQDLVARIPMQPRPLFINENDAYL

QWLNTHCSKSAYGAESQLGKDAFAVLIDGVGKYLLKREEIAFQECDKIGPMENDDLDCAK

ADAFVEAVKMKLSRHMCKQLEACFELLDKDKDGKVCFRDVEKLLQVVVHGNGTRWLKGQF

QLYDADGEDVVNEAESRLILNSIIATQKAVMAEVFATHVDYMPKKSEKLFAKSLSEEDYR

LKIPEKVRCVYHFANKVCKTNDWKLFLNSQKKEFPELHNLLAVYAKGFYNERYTYYERKQ

QR

>contig45969 Frame-0F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY68890.1|) 1e-41

MSGKRRKEGEPPTDSSEVASLVFSSTDLPPPAKAPRTTAVNATPSCARRFGFKGPSISQL

PASLVTMKTKPLLASDLHPIAEDFLGKNHIAIDASMENVNLQGLNLHISKTFREIFGQDT

VATLDQLLSFRPKANKFAVKARKEEQINYIKQLKTGLRNIVEKIQEFSKISTTMDETLSA

EKATLERRQ

>contig46151 Frame-1F

MELTANSENDYEDPWDDMAIVRAFEEALMDQRTRDSTHAKPYGGKHKVVTPTDAEKVSRN

ASTEKDRNFEEKPKSGNPSKPSAIMQERHGQANAASLSGFAAGSNPVPCSRKAQQENSGD

AYQAAYAQAYADFQAQFQAAYPSSSNQQLFRSCLHTPACSVQSAYLSPPPPVPVMPAPFP

NAPRTSASTSSSSAQSNDGLANVLLAWYQSGYYTGRFQAIQEMKMHSHP

>contig46403 Frame-2F

MIVHNACQTVRRPPTYYKPLVDKETKALKGSLMKVQMLMNHQHEFEMHMRSLALPASSST

GTFLNAGGSVAMSSSLKSQVPMIAGEDHPNDHTEAFPEGMVDVNGQQVDLRSRNSWLLRM

GEVATPEVAEVFAINTLAPFILNNRLVPLLEKSGKTEKKFIVNVSAMEGKFYRYKTPNHP

HTNMAKAALNMMTRTCAEDLSKRSIYMTSVDTGWINDENPLPKAHAHAQAHDFQTPIDEI

DAAARVLDPIFSGYTSDKPVFGKFLKD

>contig46821 Frame-1F

MTEKALAPPTALNAYIQQLHQCLQWDPIHGAAGKNKQDFVEALTEIAALPLDSSSSEIRR

LLIVSKCILTNGRKNQEPDAHLCNIIAALSARDVQLKCKAANAVGSLCISRVAGQELLHR

FGKKILHEVAKMATRRNQWVQGDAFFVLGWIIVIADQDTLRFISNLLPTVIKCLHRNVIL

SFQYQDGTQMPTIMATRESQAEFASRQSKAALASSEQASNVRIYALVLLLNFSQRHVDEF

ADLLAHVLPMLKDLLSKLLDVLPSAAFSTEQSDTISLPLLSDVFESAEVLRLGISLLSVL

CDQLESVALQLLQLQMLPLFLKLKHIDICAFVGEAGRQDFNERLEAIIETVL

>contig46959 Frame-0F

MKYLLCLVVTIAFLGSTNSQNPQATQALSCQGCTCSLRNQSLSIACLRCCQP

>contig47624 Frame-2R

MKARNVGRKNLQNKGESYTLTYSAVISMVRIRIIVVFSIIWLVPARHGDVPNAYVKASLE

KDYKILLQIPPGMNISDATLKIRVNSVKDLALELECGIYGFKQSRPFWNELLVSTLVNIG

FEQCTTDSCVFYKMDGSETVLLGVYVYDVICRGAKTDMVDRFLTDMHVLALKLSGALSKF

>contig47743 Frame-1F

MTCSFDGQLEMADEKEEEFDTVHAKRPGSKSTEMAVLGGNMVVCVAMAKVCLRCLQSVPL

GKDSTLRRRHSEVVRTEAFYRTDTAIGWHEELPQVGRPPNREVEELDGSSRYFKREPDMP

MLVMEDEDTDSIDELADLKRRSGSCAIDGRLKSFNFDYPGHTNQYLGPEDGTLDSLTNRK

RVIILSPHALLKSTSLPMRQRQDFKEESSYGSSGCSESYQSQYGSDAWSDSDDNNKQSIE

FCPTRALREELTFEDSQGRLPNCAENEVNSFLKSKNFQHTASAASSTE

>contig47888 Frame-1F

MREKLATADKWMLNVREIFTV

>contig48041 Frame-2R

MQLFVLTVVVVLLAPITALTSNLETSTSEHADDYGTEARSLHWIKLLWTKARGGGGDKIG

AQSQKVSKLESAVANNPSLLLTIKAIKDNPKLQRIVRKFEDNSKFVEKFVDNANVRNLVK

NIENGQKLNPDSVRKLQSDIVAYKNMHYVEALG

>contig48148 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54879.1|) 7e-21

MLVLVGDETGLLKSIALETKEQHILSNREHPQARSRGIQRLCWSSDGRDASDCENNVVLA

RANGIVESYEASHGITRICSEKLPMAYLL

>contig48575 Frame-2F

MPCQIHTKVFRLPYITIQLWRTTEWSEHLLQ

>contig48711 Frame-2R|Blast-reverse transcriptase [Phytophthora sojae](gb|ABG66532.1|) 3e-70 NOT\_ORF

MKQWPLPREQVLAIDKFFADRVKAGHVGKSTSPHSSPTFCVRKAIGGWRIVHAFNKLNAS

NVPAQTPIPRKDVIYDGMSKSTIFSSMDLMDEFYQILMRERDIPYTAVSTPSGMLWEWLL

IPQGLSNAPATFNICVTNHKTVETE

>contig49334 Frame-0R

MEPFVQITKLSVGIGLLAFFSSSVKIWMLERVSRSRSDAIVVKTLDAWTIVECLDFQRAF

VLLFIDSRGVLIANQMLVRGCLQYDKILVRLEQ

>contig49464 Frame-2F

MACRQQNAKFGRWPWFRAYTVFTHARFRQAPAPAAYARFEPLPLLNSSVLSTPMGSKSLL

DGSRSLSQRP

>contig49709 Frame-2F

MHFESLLSTQGKEYGMLEDFAAGARWLRTVFIQFRRHLSTGSFFSLKKYTPPNSHDNHCL

LLTIGINEDHKAVLPPSLGSGDGVVPIRCVLFTQGVNEKQSLVHAYKSSAVKLQERVNRD

NLAELKR

>contig49965 Frame-0F

MEALRHSPTLATTESIREEDEEDVQESGRRGMVKTVESSALEAGDDQNGEHCLRNFRRDS

GSDRPFSASQGLSASSHVANSVPSANSRPSRSGNLEVMETAFACAGSGSGALRRSSSSRL

ARSRRGSSSGSGLAGANTGTSPRCSPQMSPHVLPIPSPRINPFKQLSDKPYDSRAHQQLQ

QQQSLLNVASSQLRHNDGTGPSTLRNITGGGHALDSSGEYVLVDESSERRVADGADEFQD

GAKDRCMSCLSTQEDLMTRALTSGSGSNIPTETFSREYGQQLIDIVVLRTQAIAPLADQL

WALSTASATNSSCRADPTTESVGEVNRLSQQTAERILPSSAQGEKDFNCANLSTDFFMSS

SLASSIGVSHTLGGEEVGDDDEENYVKRVAECEYIYAAEALVLYVKCLRLVQRVVLYFRH

VRVSRVSPDSPLAGWSNTSLKISLAFLAEHLTHFLVRAEQCKVRMAHASRFRIPIRSIAS

QEELLYANALRIGRQGAIREVLGQARAAHDHYLQALLLLESLLLDAPGADGSSTIALAVD

DQKNINVFLRALEMRLKNVRTLLDEDKSSSGASRSNHMHQFRQQLTHLPSATAAVP

>contig50093 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56010.1|) 3e-31

MHAQQFTCQTETTLIARNVLVRSILHALSHAHLPKLAHFSLNCCYTEGLQSHVTRQIAAI

LIGPSNNFPRLQTLSLVGN

>contig50466 Frame-1F

MAKIKLIFVDQPITKFEASLRQLLISVSGVTGGASD

>contig50581 Frame-0R

MTPRAATGPLARLVVTNIAAGFAHSLATTNEGAVFSCGYNDNGQLGLGSRRNSAEFQRIT

ALEKYFIQHIACGQQHSLACSSLRDSTKAIKGKNECSDRSGVCFSWGLGVLGQLGTGENL

SWLPAEVKLARPAVSVAAGSHHSVAVTDDGKVYTWGHSEYGQHGAGE

>contig51003 Frame-2R

MLPAVNARIHQVSIPPVQSFHCNDTRPKQRPTLETVLAALADNDSIENIPILEDNGRSPP

TESDIILSWQTCAILDDSAAPL

>contig51735 Frame-1F|Blast-DNA replication licensing factor MCM9 [Phytophthora infestans T30-4](gb|EEY68481.1|) 6e-49

MLEVIEEEATGARFDRVAPQYEAAFARFLRRNYLISLQQLHRRLKRVPTSQFTHSDSVEQ

SHRFYSQPVCAQLLLDFNVQLGTLLFRHPEQLLPLFHSALAKEVGCNAGKPSDSGGLPSI

PATTLRKLKVRIENLPPIPSLR

>contig51814 Frame-0F

MDVVSSIIGGNEECQRMAKDEGLLRVILSNWNFMKTAHVHGSQVMLRALCLVANYIYGND

NAQVSLLISLPSGSSTLLSLLFDLVSQRSAVRCQGTHRDRAASEADLALSNAACQVLKAA

LVNVECVSPSIKTGLITK

>contig52042 Frame-1F

MSFLLCSEVPITADLTRLIFKFHSTCK

>contig52226 Frame-1R|Blast-impact-like protein [Phytophthora infestans T30-4](gb|EEY68401.1|) 3e-20

MLAYRIVGTFTIKDDDEDGEHGAGSKLSSL

>contig52644 Frame-2R

MEVLEEVCESVMKKQRLCVAQIERQLDDLLEHVESTQLQLVSRQQELYRKKNHQMTTSST

SESEICDNSTTTNAATRDPRCNEIGRLLFNSL

>contig52932 Frame-2F|Blast-TFIIH basal transcription factor complex helicase subunit [Phytophthora infestans T30-4](gb|EEY64472.1|) 5e-13

MYSEQLQYKRELKRSFDAHGHCMLGMLKGASKTVSLSSLVLSFTNTRIQTRRNSFSALGR

S

>contig52987 Frame-1R

MAASLLCRIAVGRDLSAHDRNADLRA

>contig53113-1 Frame-2R1

MSYILCLQWEKVSVPMIRVLWVLSNNRHDHSRMLLHAEW

>contig53395 Frame-1R

MAIVTSSFSALNGDMSLKRSHSLACGLKRRAIVWFRRDMRLHDNLALTAAMRAQEQLYRT

>contig53669 Frame-0F|Blast-phospholipase, putative [Phytophthora infestans T30-4](gb|EEY61139.1|) 8e-35

MYHVAEMVRDARRDMAERHDSASSGFVWNTLSTFTPFPFLLALCSQISSSLVRRAPDLAK

RAAGATRDCIVDAATETHDRVVELRLICTR

>contig53904 Frame-0R

MHHRRISRKCSFFDLASVLSGERERLEVILKIIDDELSVDDVNTIRNRVKVGDIVNVRGF

IERLEKGALVLLHARD

>contig54282 Frame-1R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY54564.1|) 3e-85

MGLVQLQIERCHGFLNVTHTDGANTIREGSAGFSTMNQYATTALSGGGQLIVVISHFNPE

TRDWHPMCTEWALDASVQGSLASEKELHVILTASHALNLTITHELLEVAASVGGA

>contig54369 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58430.1|) 1e-16 NOT\_ORF

MLLSMPNQFKPFRV\*KFDGTAIDHVTSVFDCLQTYCFVMIVLLLHQSELRLKGFWIEEPT

DDSVQALRDTTPT

>contig54695 Frame-2R|Blast-leucyl-tRNA synthetase, cytoplasmic, putative [Phytophthora infestans T30-4](gb|EEY57274.1|) 6e-25

MQFAAFVKTEAELRGREALELRWYRMPYDQKSVLVTNKVYLCRSLDLDDIEFYYVGEDIP

D

>contig55186 Frame-1R

MSSIVEAATSSLKGKDAGEERDSFGLRDAELRTRPI

>contig55494 Frame-2F

MVVNSPFGRGIVLNFREADHVYELQLFHSGLKTQNEEFSSPVHVFVQERHLQLSPVCPPR

SFFSMLRLGSSKNAIALPAGPVPVGSCVTTPYGKGIVRRYRASDEVYSIELTDWRLSQDN

YVTTYLMKDFINFVADADKDPRARTFATEDTALEKRISPSPGGGGILHLFRYGFSTFATA

NEIRNPFADEVGVNRDINTVFGRATTTMSKPYHGCLKATLVKTCFSDVVAYVQAKETSET

PSASSQGKRKKLELLVKNPFSYLMSGTSNNIEKCNPLVKAAQTLYVTGSLVETPFGEGIV

QTHRRIDGIYVVNFHGMHGYFHSSSLRRSVRGVVGQPVDTLFGSGILEEVREVDGVHVVS

LRLGLMSAHACAYLHPVSVIGLVKACRGDVVMTPFGSGVVMQRRLYDDYYHVALDWDTEG

CSHSSAYISEGSIVRTGLVKNSSKGCIVM

>contig55722-0 Frame-0F0

MAKRKFVSSKKNAPSRTLSSKEAALHRRIAGENDASSDSGDSAPSSDVGSSTLLSSEEEQ

EDGDVDINLNK

>contig55797 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63793.1|) 4e-22

MLAAFGGSLVTRASSKIAFDKHKRSMTAPDVLQSLGEGFIKAFPMSPV

>contig56309 Frame-1R

MAGRHPALSAWNCAPHNTEPEEEDIIHGYISSRETSELITKAPSRHSTALTEGAMWAEPM

HSWAYTGSDTVSVISESSIRMPTTLYPSVVHSNPCLRDSTALLGGNLRVQSQMEGYGSME

HRHSILRMGASKTSSGNGLRKSVSVEFVLDHALEHAPKYYTSTSLSGREPR

>contig56734 Frame-2F|Blast-3-isopropylmalate dehydratase large subunit, putative [Phytophthora infestans T30-4](gb|EEY68093.1|) 1e-92

MVAPPPMNVIEKILCHHAVGLTQPFVSVGDVLCVKADWTIASELTFQAMDTMHAAIGRPP

LHRPDRFWLALDHTVDPRVNHLPKQKALIEMSTNFAKTHGLTDFQPANTTIMHTEFARKR

AQPGQIVIGADSHTCSAGGMGAFAAGLGAGDVVMPLVTGQTWFKVPEVCY

>contig56873 Frame-1F|Blast-twinfilin-like protein [Phytophthora infestans T30-4](gb|EEY61597.1|) 1e-114

MLYSSSRESLKKQLGLNYFSGEFHATELCEVTLENFLEAKKKQAADAPLSESERLLKEAA

LLERDTNVKSSAMGVVPFEVTQNARDKLKLFQDHKFDWIAMKLDENNESVEAVLSLERVD

LIDIPDTLDRRTPSFVAYRYRGPVASGATTALIFMYVCPEDAPIRLKMVYSTCKATLIAA

ANDELNIKFDYTIEINHLSSAAEDIYLEVGPVKTNNEAKTREFARPAAPGRGRGRGRGRG

PSALH

>contig56947 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60552.1|) 2e-37

MAPVPHYVKAVALKNSTSHHVKVKATFGSDEFEAEGKAKIEETRELAPGAETIIKEREYD

MGGWKATAALFSLEVDHATDAGLLGKTLYTPSVSGIV

>contig57175-1 Frame-2R1

MSASRPESSSKVSNMHRSFAPCDAAM

>contig57441 Frame-2R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY53269.1|) 9e-58

MLSADVLKSRMQTASSVGSLSLNKAFHAVYSELGIHRFYRGWSAAVLRAFPAN

>contig57733 Frame-0R

MLLFCLKIATRTFLSPLPITSACVFYIHSNCIRALPTCTASVQVWCLTSLHVH

>contig58084 Frame-0R

MSPYVLLFRLLGQLITLNEKKHFVIQT

>contig58365-0 Frame-2F0

MTKISKLPERRTIFGSDGIPSLSNCNPVKKKI

>contig58365-1 Frame-1R1

MPSLPNMVRRSGSLLILVISNNSCNVTDPR

>contig59454 Frame-1R|Blast-phospho-2-dehydro-3-deoxyheptonate aldolase [Phytophthora infestans T30-4](gb|EEY69972.1|) 2e-23

MIQMSLVLVWGARMPTVRVARLAGQFAKPRSSDIDVVQGEQVP

>contig00587 Frame-2F

MESGVSEDAVSGHIQFLLPGRTACFECLPPLLVASGIDESTLKREGVCAASLPTTMGLVA

AMLVQNTLKYLLEFGQVSYYIGYSAMTDFFPTDVMRPNPECLNAQCREQQAKREHLEWTP

MVWRPLRSKEFDETQDMKHESNEWGIELHEEVEKRIEGTSVEDVASMKLTSGLSFAYPPS

VQSIKEDSLIETNADVCVEDLMRQLQSLSN

>contig01715 Frame-2R

MIVPSVNGLEDCQSAKQAANCCVETKEPESEMNLTTLARLEHDWTRACHLSTHLERMSMS

QIESTTRHRSTANGVPVVASFSMARDGSQWFQDATNSPLYGR

>contig03793 Frame-0F|Blast-predicted protein [Naegleria gruberi]gb|EFC37017.1| predicted protein [Naegleria gruberi](ref|XP\_002669761.1|) 3e-35

MDELVRVGIVAPTSASLLAYNALMSRQAKRVEYDKTNLPTAVDGDVVLSMELLQCAGKA

>contig05746 Frame-0F|Blast-methylmalonate-semialdehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY64588.1|) 1e-44 NOT\_ORF

MTLDTLDEAIALINRNPYGNGTSLFTSSGAKARWFQHAINVGQVGINVPIPVPLPMFSFT

SSKASIRGDCHFYGKSGINFYTQPKTITSLWDLQEATPYNTIMPML\*QISTNLFITQPCC

>contig09953 Frame-2R

MQINRSSGSLESSSTAVQSNNSSSPATLPAICLKNEIVLEFDLPFDTSDEAMTELLITTL

SFDNGDLIQYFELQRVTKLNYVQLHRVYDVFEPYMDNLMNSCIEKSTFDRCVGTLLPLNV

APSVAAAFHTNSNARMLAPQSMKQEKDSKMVADTLSRLFFAFNRGGTGKIDIIEFVSAFT

MFCAGSKSEKLAFAYRLFDADDDGCLTRREMWKFLRSFLTMLLALGNGSELSAKAIANVA

DTTAIEIADCIFKDTDKTFSTRESFTTHEERNPRHSLDASIQHESTSTTSTVRHHSNARY

EHRGSLPGNEKLHLFGAASHAAGAGAGSAFIRGGVVSFEEFAVWYSQQGYAIIAWIELLD

TKKWPEVPHSVSDAILRYISRQQHALENAIQAGNDDIGSGSSNDTVSSNESNNRLDTSEE

RNCSDSDLTVLDTTAFRAIDRLAVESDMDAVSGISNLITSLPTSAAGVKDLSSVALQFKL

TSYDNTFLRIRLKDVAIVYTISERMNLSRLTSGELVHLLKKKAHHRSLTKPGFLRAMRDL

VPRDELSSEDQEFLSFHLLRIFTLFESESILPSNESHHEEHGNGGSMNTISVETAQLAAA

LCVFCGTTKSAKLGVLFKLFASHGDGHVTRRRLFELFKSILVVLFAFSSLNATTSQSNDP

GSVQSWSTNSIAERAAGAVISKLFCEATCKRPDAISLAEFAAWYAAGGYMDCPWLELLDL

SKWPAKEAFEASKREKPLIYAFDAVEEGNILHFTESDISTYLFMLRSTKFGDLSVSKVYD

ALLAYATPSAEDALKMSKTVETQNRTGQMYSYAAVEEDEGAYLVLTRTNFYECIRSLVTK

HGMSEKAQQTSSKLLSRLFNVFDRKRCGRVNALELACGLSILGRGSKSQKLSLAFDFITK

MRQQRHKTLASYVVPPPSTRLNGFGAQGTSGFGLGFGGALSNQVFMPGTNGARFPSTRGF

GSIAQGMRSTKNRSVPSVSTTELNALPHSVLFIYLRSFLLALMALSDGTYRLGLEKIY

>contig10267 Frame-2F

MEVEINDERSWNYIKKKDGVKAYTKLDGSLTAAKGVGYLPYHPRAIWEQAIDVTKRSLVD

PQLACGIKLKTLNAQTTIDYLEYKSIFFVAGRDFCNLTHWRVMPDGAIIVVAQSIDLSEL

CPVKEPTIVRGILHFGCIKIVPNAMYDGAEVITMVKTDLRGDIPARIAGKAAAEQPFVIS

RMGGVIKARPDLDQIAAQGKLANTLFQIPHNINEPSSLSSAKSKLLARESGVKKTQMDSK

ISPKNSHPDLFEKISPAAPIEKQTKSSKCNVKDAVESLSKDGQTTASDLAMYAIQFGGAV

LALKTVSLHVVVHLTVVVLLIMLLTLKLKPMMP

>contig10605 Frame-2R

MVHSQLPGKSSAHVQLLLLLLGAVNTSVLSAGVILVANVFSSLCIACIKVGSFLPSTVNL

LLVGLLSRSCQVVSNYVDLYVLAPRKSTVRPLNEICRKKLLPS

>contig11130 Frame-2R

MCVLSIQRNKSFPKYRPTCLRSLSTHQINYNFDLGRPSPLFDSVHDLRSTLTAAVRVNAY

SWVKNIFN

>contig12258 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57497.1|) 4e-08

MTVLQTEVITESRYCRYPSEYYPVKAAVLFRDYS

>contig12427 Frame-1F

MRDDMSSKPVPSAASFTSFQSVVATSVDYASFVEGIQYGIHNEMLDTIGGDFATAAAARD

VLFYSWHASLDMYLHVYHLCRIGVPVTVDQVTQSLELYANASQTCGAIDGINATTPLVMR

TTDTNGTTIDVTDHPTLGQYFGYIGDDNWNYADIQQLGDHSYTYQLPEILRQQILSNNDM

CPGFNRAFAASYTSLNATAIKRTSSRRTTTRTTTRTTTRIVNGQRITTTNVTRVTTAANA

STSTTSRSTIRRGQLVSQFMYTYLGNFSTDDAMFTEGTFVTNGYTGYLPFYSNNVITTKH

NGIISVNTSSRNSVVNSNAVNTNVVNSNASSSTSVTLYGATTTVVANVTLGSRSVMRNVT

ASIATSGTYWAWLQAAYTGLYNRFNGSVDLVATHMKLLECSTFDRVYGTRNLTSAFVTNK

NLVSNRVDCGQRLDLVRSGLVQMAVQSTSFSASSLVFANTSVIQRILSSYRRVTTRRVTY

VTTTYIQRVRGLLIEAERELSNRSMIVTTGTNTNRISSSTVNTGFVSTNTTTSTIQSNAN

QSTQSTTTTTTTTTVTATTLSDATSQTNGTMTRQETSTIDRSTDMTPRSSMAPELTNSSS

TPTGSLMNPTTAPDVPDQSTTAPEGTPSSTPNVPDQFTIVPEEIPSSAPSGTPGSTIVMT

PGSSGNSSMTPTGSSVTSTTAPDVPDQSTTAPDVPNQSTTAPEEIPSPAPAGASGTPMLP

NASPNLPTGPTTSTGGDNLGNNTSTQTTTTTTNPSSTGALPPTTDFTVPVAPPSLATESP

ASEAPFPGVVPPSTIPTPTTSPGASPNLTPEITNPNGGGTPSGALPTPTPNVTTTPNVIM

PEEIFPGMTPTVAMPNSNPLAPTSMPGATPSPTPKITESIPSGSSPTSTPEGMTPSSVAE

GNFPGVTPAGSTPNDYPIVSTPIPGLSPNPKPEDPSSGVTPAVQMPNAMPNDTMSNPMPY

GVPATPAPTGDEDLPTPAVTMPGASPNDTMSNPMPYGVPATPAPTGDEDLPTPAVTMPDA

SPSGTVSNDMPFVSTNQSSDCTQVSVEFDATYCIAGPVCSGTSSSLTGTLCPRAGDVAVA

DCHENLLSYTNRSSSCVAPQDSVCAMVQTGVWGCTFQAVLPAPTAKNSTSPTPDMVTPAP

TPVDVPTSFVPTLNDSPLSPITPQPTLNDATPMSSTDMSMSSEEDKETTPFSRDTASPMT

PTPIPSTEASPSALATPVPTMRGNKVMTNTTQSSRSPMPIDNRQQPTKEGVIKPDSSNDA

PPSGEYGVVGTTTLNDGDMNQQQPLDAVSPPASRAVQATFATEEDTNDSNGSKTALAVVG

AIAGVVCIAAFAAHRYHRNAMNGHSSSNNYYSQREVM

>contig15178 Frame-2F

MELDALASQLKIRKGLRREFDFKKPLTRTFLTLACLNSETRHPTMLLEALRKSYDGYVPK

TIAVELWKDLMKQNSRFLAKIRSFLKQLPGKVIHPQATPPSVNARPGSSQTLKKTSSSVK

AGPGSSQTLKKPSSSVKARPGSSQTPIKPSSNAPHVDHENFQPVNPVHASNPPIRRSLLK

KMRDWFSTFYAKLQSFFKTWFSKRSKGHEDSI

>contig15260 Frame-0R|Blast-reverse transcriptase [Phytophthora ramorum](gb|ABG66535.1|) 4e-31

MRIPAMSYIRRSSGIGVTPRMTRCSRFRQPLAHTSRGLLLMAKYLIDRLSAYRLSLCNDL

RGRNIHEYHDSASKRPLETREDVPCAVSGFLLALHVQVGAALHTHDRLEGLGVSVDIVSG

LPADAQGRTEILVVVDRFSKMMYLLPIAVSITAEETGALFVDMVFRHHGIFATILSNRYP

RFTAAFWSRLFKLLATRLMLSTTAHSETDSQTEQVNRVFGRRVVQLRYIVCVME

>contig15772 Frame-2R

MRIHRRYFKAKVIRCALPQSSVDCNLNVKLCQVIHFRKSHCCRFSTIQLCDVFLNANLAG

CALLFLTQTTTFSATDTKNLRFRFCDGSRFTCCSSSRCFLFFFFLLRLLCFKTDHRFLRE

HVSMKFKKKK

>contig16063 Frame-1F|Blast-methylthioribose-1-phosphate isomerase, putative [Phytophthora infestans T30-4](gb|EEY62284.1|) 1e-164

MAKERMRSVLWTNGGLQLIDQRQLPTEFVLMRCETVVDVTRAIKDMVVRGAPAIGAAGAF

GLAIAAKTFPIVASTLKKDILEAVIEAKIMIDAARPTAVNLSWATERVVHELRSRERTAT

SVMDFVASTLVIAQALAEEDVAINTRLSKFGADVVPMGANIIHHCNTGTLATVDIGTALG

VIYECHAQGKNIHVWVDETRPRLQGARLSAWELLRENVPMHLIADNAAGYLMFMGKVDVV

LFGADRVAANGDVVNKIGTYKLAVVAKENTLPVYACVPTSTIDLDVLEGKSILIEERSAD

EVTCIRGVRIAPEDCPVFNPAFDITPNRYLTGIITEEGVCYPPFEQSLAKAVTAAEHRRA

QASSIL

>contig17305 Frame-1F

MVGHCSRYLKAILTLHNSEVLPEHHYEPNALQKLKKNS

>contig18775 Frame-0F|Blast-protein phosphatase PP2A regulatory subunit B [Phytophthora infestans T30-4](gb|EEY61246.1|) 7e-72

MHIRGHVTTSTAKRVYANAHTYHINSIAINSDGETFISADDLRVNLWSLGASNQS

>contig19354 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69224.1|) 1e-92

MCNALAALTDDSPSARVIKLFEAIYSNSRCFPVPPKETEAFKSRVEKLLRVLTDPIHNIY

HKNVVFNGPLAGFVLVTMLSCRDNVFATFKGQIWDNLIDNCCLRVVEDAVKLYKLRMSQK

LSSIVNISDPKESKQLLTANQDCQAAVQKCQKSI

>contig19758 Frame-2F

MLKAKFFLVIGKANAIFIAMGFFRKLPTFPWSFLKQSLRTSFGLTLSFLWA

>contig19857 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68172.1|) 7e-13

MLRSFVQGYKRLLATFVAQHTCPICLNNVPINSSCGVASEVNEVHTKLRCCHRFCA

>contig20181 Frame-2F

MFRNEWEAPFPVWIESIDIDEELPELMVTYPDYPIHTNLSPISTPEETALNTFLTFPTPV

NLHLDALLDGKFDK

>contig20268 Frame-1F|Blast-inositol monophosphatase, putative [Phytophthora infestans T30-4](gb|EEY55619.1|) 1e-168

MEVQYPAPYHVNTWFFVCGPLAVNTYLLGLAANLHVFHRYNFAIDQVFDMRPDEVPTASG

VFKTTIGMFLVQFLIFKGEASRRGDSFGQDEMRMEVLLLGYAAVAATVLLCPLEILHYKF

RMFVLRNLARCFWPFQHFSFKLPLHATPFAEVFMADGLTSLSKFIQDLFVALLLLSMSFN

TEPKHLRESYISKLKESPLPYFAASTPYIIRATQCLISFQQTKSVNDRFLHLLNTMKYCS

SLLVISVGAYPMLRGLARPEQSSFFLLCAVFNSMYSFLWDVVMDWGLGQPRLPRKFAFLR

HQLTFRPRKIYYIIIAIDFVLRILWVTKWWDWMHRGVHFKLISQVAEVLRRIIWNCVRVE

WQCIKLNILAVKKLSADNFELNENLENVPLIRDVHDAARDDGQSRLRTPSRPTTKFTTDL

NSHGLFRHEADNVEYQGNAPSTTPTTTFTGYVEKTVF

>contig20596 Frame-0F

MSSQLGLLVGMDGALLDDVDGLSVEDMIASPFSAQLSPAGLISIAAADIDEVAANSSPPV

NGQLDLAFIRSLRRSSSDMKTELGSRSYLHIVNEALRKVMGPLPATQRPENESPAMESED

KDSKHHFFSLVRRHLNMLGSASFSAATPENEVEVDATESQTKLRFLSLLRRINELHSQQV

HTESWDGLPYPQIIALPTFKYQVREHHGRGSQLDKGGEENNTVCAVCRDEFKAEEEVRAL

PCLHFYHRECIDQWLMYHRQCPICKHVIAVY

>contig20710 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67656.1|) 4e-22

MPVRPSGLQTARIARQVRAYTGLVNKESHIVDDQKLFTTVKRPTYLKRKSDGPLFTAMML

GLVFGFVQSFRGEMSMATGTNKKE

>contig21249 Frame-0F

MLNTEASADFKAIAITPIGFRGLNLEAPFSRKTASVTRATLHISPMTSRTILPQKRRKLT

RKQKLLDDMPQILQAELERDTFCYLEDVDELKLKRVRVPADADAFPWAARAASFRPAFYR

PTVMFGLRGHRHPRIDDINRLLVSQDKRSIKCFVQAFGTDTQCVHFGDLKLSSVFPYYVV

DLMTVRNFRDLDFIVRSRLVEVLEKHSRYTREHFGMDELQVQRWLEQHRRRKTSEQPPIT

LHYCLIDGARRRLELEQSFAKVSYKSKQAWLCFCANVCHLSVSIPISHQTLSGLTR

>contig21384 Frame-0F

MPTAPLAVGDRVDDGCGSLGTIRYVGHVATAKDHTAIYYGVEWDVWGRGKNDGSVKLPSG

ERVVHFSGPPGRKDIGHGGNISQKCSFVKASSFHKTTSRSSLLERLLERYAHKGCDQVHP

STSDVVVAGEVGTTLGSEKPIELVGARKLRTQQTLETIEKISLSACQIVDVGGKDLGKLA

PNLTELDLSNNLFSKWSDILSIALELPLLETLILSGNQFTVSETTSTCRTKYVVLKNLKV

LVLNQTLLSWKSVQLLVTRHFPKLQV

>contig21546 Frame-0F

MGTINVSDFLATGVLQLPTMNAISSQPQSANAIASAQASLSANALSYLLPATTSLVTSMA

TNGQQGPAGSVKDGSGATAVFSQELHDNLNMFLKTATAYLVMLINDHNSSGAAAQL

>contig22961 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY56910.1|) 0.0

MSCLFICIAFTYYPASIVTFLVKEKQSNHNSKHQQLVSGVSLGAFWLANYLWDFLLYLIP

CTAALILIQIFNIDAMTGSSACISCTSATFPAVVILFVLFGLAICPFTYCLSYLFKEHAS

SQTYTIMISFLLGVVLMITSFILDLLDSTKVLNEGLVFLWRISPLFNLGHGLLNLVLNEL

MTIRESDEDKTSPFSLDIMGYEMLFLFFSAIIYGLLAVGIDYAMTFPKVKDWMSGRNDSG

DDMYEEDDDVAKEAQRVASGEADSDIIKLAKLRKVYRGGKVAVRNLSFGLKRGECFGFLG

INGAGKTTTMKMLTGDELPTSGTATLGGYDILTQQIEVRRQIGYCPQFDALFDLLTVREH

LELFASIKGVSRSRLNDVVRDKIDQLNLASFEHKLAGSLSGGNKRKLSVAIAMIGNPRII

FLDEPSTGMDPVSRRFMWDVIADISTRGKNSTIVLTTHSMEESEALCSRVGIMVGGRLRC

LGSVQHLKSRFGDGLVFDVKLATPSQDELNDLIEQHFGEADECVTRADLKEKCRSFGDET

LAQRVVASHPTGYGLAAVMERDGYIRAEAFLTWCLEETRFDALLHFLTYSLSHVDVSVME

RQNDFCRLKLRGSNDELRLGNVFALVEEIKNKLH

>contig23298 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61870.1|) 5e-95

MVRTLWPDAVIDVYGSSYTGLALPVSDIDCVLVSRSLEEMQPLAVLEVLAAEVERRLWMK

KVELLRSAKIPVLKMTYSLDSTEQEVLLDLTCGHSAGHTGIEARDYIYSLKKEMPALRPL

VMVLKEHLVCKQLNAAYTGGISSYVLVVLVVRFLQACGGTHETSFVSNGKLRDINSRRSY

SESACGINFSEEDAHVSNFRDAVLVAQPRWCYTFSRGGHLTWQTDLGSLLMLFLETYIMF

DYRRFGISIKNEGSYFVLPPDKIVLTHCSVVIPFVADPMKPGRNICNCFRMH

>contig23306 Frame-1F|Blast-serine protease family S01B, putative [Phytophthora infestans T30-4](gb|EEY66041.1|) 1e-144

MISIGNSSELRAGEWVCALGSPFSLQNSVSAGIISAVARHSSELGFPQKGGEYIQTDAAI

NAGNSGGPLINLDGDVIGINTMKVDGSVGISFAIPADTAIQVIEQLRKHKKVVRPYLGMQ

MINFNRRELKEIGRMFPNVREGVIVKSVTPGSPAHKAGLLPGDVIVSFDGKKVLRTKDIL

TSLGYTIGRHISVHVQRRGEKQLVMLDVITEPLPTPLRG

>contig23579 Frame-1F

MRHSRRHVSYHDREPLPPPVPASPRDGTEDSAAHDDTVGSFDGKPGEYIANRYKIIREAG

LGTFGRVLECLDKQRNIVVAIKVVRKVDKYTDSAKIEAAILQDVNDKDKNNTSLCVRMFK

WFEYRGHVCMVFERLGCSLYDYLKNHDYKPFPLHCIRAYAWQLLTSLESIHSIRLIHTDL

KPENILLVDDEEERFSCDSSSPSSTSSYRSPDGTSGREQWSNGRQWKKRERDLSDVDSGR

FSLRPPANNAVKLIDFGGATYDDESKSSVINTRQYRSPEVILGLGWSYPSDIWSAGCIIA

ELYLGELLFATHENLEHLALIERCINPLPVKMVAQASKNSVSASYFHRGRLNWPAGSSSD

ESIDHVRRMRSLADLISPEDAKSGLLELLQLMLVLDPEKRVTAKEALRTPFFDEFSYRNI

VRPGRNG

>contig23621 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66702.1|) 1e-132

MFNDEKVAVKMLLPEMRKSISHLNAFLAEVKLMATLNHERIVHFVGVAWDSLHDLCVLSE

FMEGGDLRTLLENCERHETPVGFDRSKATIALHVAHALTYLHSLSPPVLHRDLKSKNILL

TSQLHAKLTDFGVSRERSDHTMTGGVGSSRWMAPEVMMGERYDHKADMFSFGVVLAELDQ

HLIPYANVKENSDSGRVMPDLAILQMVASGKLRIEFSSAAPEAIKELGMVCVSINPKERP

CASEALYKLHTIIAQGL

>contig24013 Frame-2R|Blast-importin subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY60346.1|) 9e-40

MPPRTSLKKHDAATESRALKAQRQRTSTQIRKDKRRATVQTKRRRVMSMEQGRHTDRSIT

ELVRVLGDTTNASSVHSQARFETLKEIRVLLARHEHDYEQVDQIIESG

>contig24138 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61152.1|) 1e-141

MMDMNSKDKSPGAVFIAKHKSNIALWSGFVVVVFFCYHLFSDGDFSFLMTMGSFIRAFGF

VFLIFKAFSQRSVAGLSLKTLELYAFVFLFRLSSILRYQGYLPYDRSGDWLYSLLEITAL

VLCCGVIYLILKRYNSTYELRYDTFGWMHLPTELGALYILIPCIFFGMLIHPNLNRNWFS

DVAWTIALYIEAVAILPQLFMFQKRGGGAVDSNISHFVYALAFGSFMHLVFWFSSYHELG

EKDAGHHVGYTVILVQVGHMLMMADFLYYYFK

>contig24387 Frame-0R

MRVTSPVGNISYSSMTPPRFKRMAITTDDSVQTCSSNLSRLRSCKFMMSRIASEDCENDH

>contig25704 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69607.1|) 9e-48 NOT\_ORF

MILESAELLRVSLTDLHRFLGLTKAISYGRSSRTIHFYFFSRETAKSLQDVQIPFQRRLY

TIENAHQPVRGAVWQNQRSPDGRLGHSRTEYTIFLHNVTRFNEVGRIAAYFRSKIPTDFE

FEEMDTCNPNSRTSTVWKVTFSLAGCPTFLQGIVRLL\*FGTAIIINHPNVGRSLQCL\*CG

TIGHPAARCQLTEAQLKGPGAIEVTEAELQDVKDLA

>contig26024 Frame-2F|Blast-DNA mismatch repair protein mutS, putative [Phytophthora infestans T30-4](gb|EEY69245.1|) 6e-22

MLDVARRTYLDTIEKIHDIVHSYKENVGIPIRLNYTAKRGYHLSLPANTRDLPASFIERV

TSKT

>contig26150 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY67460.1|) 1e-92

MEILQILGAVLHLGETEFTTRNGDVDASQLVDRTHFIVACRLLGVAVDALEQAVCNRNVF

VGREVILKPMTHDQAADCRDALAKSLYSKLFLWLVEQINQTIGVQTIRAGSFIGILDIFG

FEHFEVNSFEQFCINYANEKLQQKFVQDVLKTVQIEYEEENISWSHITFADNQDVLNLIE

GR

>contig26486 Frame-1F

MSFALGTPEWFSTRSVGWIGLAMVRTIVAYAVVVSMTVCLHQSVVPRLLRFLTAQEDVHK

APLILLGVVSVCLFMALFSEMIGLSLECGAFLAGLAFVHVAGSAKAAFTSIRVMENLFGS

MFFACVGMILHPMFLLRNAMEILSMVVMIVCIKTVSMTSVMTIFQISPRKAFMAAIGLCQ

IGELALIFMIKAHASKLVSRRTYLLFVAAISVFLACSSIFNRRIVLARRKSIFRLPSTRE

KEVVRHDIESHSTLKVRRNSESHVMDVTNEDGELASRRMRLER

>contig26622 Frame-1F|Blast-60S ribosomal protein L18-2 [Phytophthora infestans T30-4](gb|EEY57263.1|) 2e-97

MSLGKVVRFMKKHEGKTAVVVATVTDDIRLLNVPNLTVVALNFTETARARIVKAGGECLS

FDQLALRAPTGTNTVLLRGARKARGVYAHFGHKSTLESVHTHDHVKPYVRSKGRKFERAR

GRRKSRGFKV

>contig27265 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY68127.1|) 0.0

MGMLGPALIFFSTLAQQQSGLAAPVYGFGPIFAAHGGAALVTSFVSDFVLTYFKEKEFMK

PLIVVLLLCSSAWYACLAPVAAATGNLGVGILFISKGCWTALLNISLNRCSLWIAGEKDQ

RRRSIVTSMNIYYGHGCLLGAVIALILTELDSDLSYAFFGLAMTTMVPAVMIAILPCPRS

YYGREEHQTLLTFEDPSRRVPTVPSPIVGGVFLHAKHISGSKNFNPDTYDSKNNFIILLV

TIYATVLFGIQLGLAAFLYDYVGTVLTEGKTMAAPLEGSDTEATTESNEAVWQCAAMVLF

WGSLTLSYVVLPRFLFHDKNLYSIVVCAVVCGTSSFGFLFGSQVGVIPLAIFLFLFSVGL

APLFTLSIHCMTRVINEQLIRRVSSLIVFGCGMGEVFIPVLMGFFMSGQSGQANGAIAVS

YITFILAITLVSVSGVLLWMVKARLKELPEPVDELVGNSEIGRMRAARAAGLGTHKISHY

>contig27382 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61490.1|) 7e-16

MARAMRWASLLSLLGVDLVCAVELIWEDFYESAMYHTGLGYQCSFVDKPSQMVRQHLQVY

LKGQERATEAVVGAIEAWEFS

>contig27935 Frame-2R|Blast-vacuolar protein sorting-associating protein, putative [Phytophthora infestans T30-4](gb|EEY66878.1|) 9e-66

MEPLRKCQQAQFFTFCDDKAHPVRNGSFVTPCEDDPPCAYCHIQLSSCQPKCPDCKAPCL

HCGSIRMRLFDLPERGYRDDKLRPPMISMNDFTHVLEHLTATVAADELTRFVKWTQEFGQ

EG

>contig28431 Frame-2F|Blast-bloom syndrome protein [Phytophthora infestans T30-4](gb|EEY56970.1|) 3e-47

MGINKPDVRYVIHHTIPQSVTHYYQEAGRAGRDGEVANCILYYSFL

>contig28484 Frame-1R

MPGFRSWADNIALLFTNGEYSTALLSAILLHSALFQMFIWPLVIVTPFSVSNPLRPWIVN

LLMASSSYCGNDVPSF

>contig30355 Frame-1F

MEYRATRIRAILHVFSSSSVILSPYNGNEFSKVSEMGEVIRVCGYSDSL

>contig30881 Frame-0R|Blast-eukaryotic translation initiation factor 3 subunit, putative [Phytophthora infestans T30-4](gb|EEY60851.1|) 1e-177

MRPILLKGHSRSLTMIKYNREGDLLFSCAKDHTPNLWFSDTGERIGTYVGHSGAVWACDV

SYHSERLLTAAADSTVKLWDVQTGKELFSFPHTGPARSVNFSTGDKFFVSVADKFSDRPA

AVMVYALAENLNYQSAEPILTITNHGHEGRISGAYWMPLNKAIMTTGGDGSIKLFDPKTG

ELLESHSIHTGEITNVAFNKTKTLAITSSKDNTAKLLDVETLKVLKVYETDRPVNSAAIS

PTKEHVVLGGGQEAMSVTTTSGRVGKFEARFFHMVLQEEFGRVKGHFGPINTIAFHPNGK

SYASGAEDGYVRLHHFDNDYLKLDLNK

>contig31994 Frame-0R|Blast-aldose 1-epimerase, putative [Phytophthora infestans T30-4](gb|EEY63075.1|) 2e-72

MSKKSNMDGEKPIRGGIPIVWPNFGSAEGLPGHGFARITNWTLASHEDAKEKDGVSTAIF

KMEASESTRKMWPNEFKLEYWITLHANQLDTALHVRNTDKKSIQFHALLHNYLWIDDVRK

DGAQVNGLKGVDYFDKVSKTNVTETREYLTITKDTDSVYKNAPDRIDTVIKGVNAVDRTV

TVEKSGSIRNG

>contig32335 Frame-0F|Blast-PREDICTED: similar to splicing factor 45 [Tribolium castaneum]gb|EFA03164.1| hypothetical protein TcasGA2\_TC013083 [Tribolium castaneum](ref|XP\_975149.1|) 2e-21

MVGPGEVDEELQDEVKEECQEKYGLVTKCTIHEVTGKCPPEEAVWIFVQFKDVKHATKAL

TGLNGRFFGGRKVKALYYDEGKFERM

>contig32865 Frame-0F

MEVSEEDVCSFFASDDKDSSWMKHLHQLQIEENHVRQRIQRETNHQHALQGILKIEQDRL

SEMSLAYAETMSKLNTKTALTLKTYSRVSQDAKLVNLIQHSFNPILIDLLDKCEDALFTC

FQKLSRRFEDFSEEFEHYRSALLSFMESSKEQTMTEEGNASPQDASDLAMDNCVTIKSEN

IAKAVGEAVVAVPHPASGDADKLVDEGEVAVFEEGDGVSELDDSIGLRNAYVSFYVSEME

ALWKERSSSLEMLQAIQR

>contig33259 Frame-1F

MISGDVVGKHHVPVRVHDQCFTSEVFGSLKCDCKEQLEYAKSYTKQHGGVVIYMPQEGRG

IGLANKIMAYSMQERGFDTVDANRVLGFKDDYRSYEPVVDILQDLEIQSIRLLTNNPRKI

RLLRQLGIRVDGRQPVVIKAGEYSQDYLVAKAKRMSHLLPSDGSSDELLTDESQDEDERN

PQEAVALVSPTASSTSSSGDY

>contig33336 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70517.1|) 1e-133

MPTLYVGTYTHKEGHVDGHAKGIHAYSFDDTRGAMMLLKVSEGAGINPSYVCGTNTTLYV

VNESNEPSQLHPGETTGFVTAYAMGKKGELTQISRHETGGSYSCHVALSPNKDFVSVANY

GGGNLTLFPVNADGSLAPASDFHDYHGASMVIKARQEASHVHSTTWTPTGLVAADLGTDK

LVQYKLDVASKKLVDEEFLSCLPGSGPRHVALSTELGVGYVINELSSSVSVYPLDVKSGQ

LGLTPLQHISTLPRGYAGRAALASDIHISPNGKFVYAATRFCHSIAIFKILPDTRL

>contig34553 Frame-1F|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY67695.1|) 3e-60 NOT\_ORF

MTRAARTSFMSLATPNDVKNYTNDVGQIQWAQVPLNAALDKLKTSREGLTSSEAERRLAE

YGPNKLPEEKINKLSLFLGFMWNPLSWAMEVAGVLSIVLLDYADFALIMFLLLLNAVIGY

LEEVQAGD

>contig35990 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69965.1|) 9e-34

MGTTATKAREAHSKAKSKPKNNRSVQHQKIQSARITGVLALSESKLKTIPPEILELSTLR

TLDLSSNTLSELPCAMNSLTSLKILKVSFNVLVTLPNLSKLEALTS

>contig37044 Frame-0F|Blast-5'-3' exoribonuclease 1, putative [Phytophthora infestans T30-4](gb|EEY67074.1|) 1e-125

MEEQKRSKRRGNRHQSRQHEVEAEEVQNAMKLLLNDTNEDELPLSLPDDCVDMDEDERAL

LEALDGKDDTIISLELQQKDREILMLVGSESFQETKWKYYEHKYGILRGNGDADNKELEQ

VKKSYIEALVWCIAYYFQGPPSWAWYYPYHYAPMISDLTNIEDILTNVMFDKDSSIAGPL

LPFEQLMSNLPASSANLVPESYRFLMISPLSPIKHFYPETFAIDMEGKRNAWEGVNLLPF

IDVALLKQAI

>contig37170 Frame-2F

MSKRPKKEIFFGQPASTKFPITETTAFLANKNDENSDSSMQKGRIFNVKQLATIIEEYEK

NPRPTDARLEDLQKLLNKDDHMNEQAGDGVCVTKQQIKMWFSSRRAKERLDLINMKYNET

QAGLQGSRKLDFKGNEDEGIVSMRPSTHASLTQAGQTSNLIRNIAFDDSRESDNAEDMKV

DA

>contig37202 Frame-2R

MQSVAPWKWFFEFYLDFWLENDKAAAAAKTLPDSLARFSQNKAAAKAYSNKLVISVKFYE

SDAFRSLEKFVRRSVKGSQEEVDTIIISAFVNKYGNGKTIKLFTATILEKEKSPDDVKWI

SSLLEYFVRTDVDLLELSKEIFLHEV

>contig37413 Frame-0F

MFGNARDIERISRHLDSGNLGAAIDSFMALVSVVFSGMYITNTYIPYNSLPHTIWMAEII

CASLFSADFAFRGVYLAARRRWDYLISASSLIYFVNILPVLPASFFIRYHTFWYGETWWR

FVYPMRFAMCYITGKAVLSRCHPYLNPVRQFALLCYLQITCILLGAAGIIQIAETMDGTL

SVKNLGEWTFFNALFNSVMTFVTIDKPPSDNALSKVFVGVLVCVFILVIPYQISNVMDLS

QTVSSYEESSYKPFLNGQHVVLCGDLTVSRISNFFHEIFHNDHDFVGVHVIVLSEESPVT

SLKALLLDPFFAKRVWFIKGSLLNVDDCKRAACNSADAIFMLANRADGEDFSVSDHRTLM

RVLAAKRQSPKARIYAQLHQSIHCQLVRDMGVKNVLCLSEVTLSLLAQNCICPGFSTFMY

SLTSTSSYVDSNDGVGSEAKRLTRSSTVCKGEGSWVDRYLLGASHEVYVVELPPASVIAG

RTFSELASLAYSNCNGIVVFAVADGPQEKVVLNPGDTYMCVGGETAYVIAQTQADASALT

HLSRNVSLPPAWREMQAGPSSSFLSIDTVSNNETYARAPFKRHQARFIHWQSGDNKATES

EKESNCGDELVHDSDADVVSVQKTARDALIYDVNKLGFRVAPIVICVTGKSAFANDLEHL

IGPLRARSLKKYYPVVILMTKLPDDDTYDDFSHFPDVHFVIGDLYRHTTLKRAGVSEAYR

VLILGTSNSALESNAELLQDAEAIALHKFITSFIGVTRAPQVITEVGNRASVHFVAQNLL

ANGWFAGTEGKDELTMFSSSETFLRNFFLSPAFASGLTYSTSLCDSLLINQFFNGRIKKI

LGEFMFTSRATDAWATLRGDETTPRLQRSSLFAVEVPPDFVGRSFEYVFHYLLSSDDMLA

IGLYRCLSSMKTASGTEYQERVDVPGNSRSVPFGYVYINPQPFEVITGDDLLYVLSDSQP

CWAES

>contig37620 Frame-2R

MATKISHVVLNLFVPFQGGIVAESGDTAHEDSSMIHSERAKHPLIVTDGTACVGGNVLSF

CDFFAHVNAIENDFSRVQMLQHNLQVLQKTNVKCIHANYLDVMLQLKQDVVFLDPPWGGP

EYKDLERVNLFLGGQPLHEICSRLQGSTKCIVLKVPSNFDEVKFSQNVPGKVVIRRDLKK

MHLVLLDFR

>contig37787 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58401.1|) 4e-09

MTLNGFLDEYIIPSIEQDKAFASTSEAKTSLCNEKVGYLAQHCLFDQ

>contig37967 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59159.1|) 1e-168

MISIFQENDEVVMGIGSSMKECNAPLFSKADLAIALQGGIHAFFNKKFPQGKELPVFSDD

DIQFSNILNTLSCAFRLKCASDEARIQQSELDNNNNATVDGTASVAHLIELIRLGRRMLT

NFYQMNTFIFVSQLFIATIIVASYAIPFPHVPQLTCTSIFWLLWIFVPALSLSMLASASE

EGIMKKTPRKNEEFDIAEDLPRLVSYFVGRHVPSVLLSLAVFECLFGFSLEASNAANLNT

LRNVKFNEYRWTDFILDTELLALKPRPAIVVAAVDRAEAGMLLIICLCIVTSSCGYLYRC

ESMFKQSPFRNTIWVTTACFLMFLQLILSMLRAGVIGADGVSLWHFVSQSVPRTFWVITL

GVWPFAILGLDEAIKTHDKRYFVRYNKFLRMQFDTRLGMWSPK

>contig37989 Frame-0F

MAALPPASKVPSGKIKSRVRYCLGAAFDGEYFLSNMRSALQSSHVQTLLKVLTCLYNCID

LLPTAARKRLVAELILRDNFFQFFLHWNEEIRKIFSYMIVFKTSASNRLNLPSASDRILL

AQTPFFEIGPQEQTCHSSISAASPALSYFSALSELAQAMLRPTADSTMDPIKKAAVGQKA

LRRLINWDASARLKRPSTSGNTVFRESLVDEELSVDLSIASKLDANFKMIAEQIDLPKHR

GEIFKKSDANGTQKQYFPHELEAYVERALLQYVLILWEYYEAAFENPTNMPVAPSLEFTI

SVPFLSD

>contig38636 Frame-0F

MGSDQYFGSGLAGQRRWNVQWSPQVSAVASTCSLDGKVQIWGLFGGGNPACRPPKWMRRP

AGASFGFSGKLVTIANPQEPLDPNNRRLVHVQRVVSDAALVAEAEALDRSLETKDFKVYC

EQKITSADTAEERSVWSFMKVLFEKDARQYLLLHLGLDAEKINKLNAKFSPEAAAQQAEA

TQSSANSMAHVPGIKVDPATGAMLSDRIDSAIGADDVFSSGFYPKDGSAALAATPASPLL

DVSALAAANPSALDDDKSKRLEASPLPIYTEDSESTLMQALLVGNFEVAVNCCLAYHQLA

DALLLASCGGPELWEKTQRAYFAHQKRPVMRVVSAIIKNELNELVVESDLAEWRETLAIL

STYAKSEEFPSLCDKLATRLEGAGELHSAMLCFMCAVNIEKTVNAWCAESKVEASTYGHT

VALHRLVEKVSVFTMAVDQTDQPLGLEVAQRFHEYASLMAAEGRLDIAAKYARSPDLSCA

ILKDRIYNAYPTQGYQPPPFPFDAVQIKTEAQIQHQQQQYQQQQQQQQLQTSQQARGGYS

INSAYGAGINQRGSRAVPIPAPAAAAMPTAGVSGGIGYQPQQHTSAPTPAFSGRSNVSYQ

SAPQQPLYAATPSQRQQLVGFSKQQNPIQQQSGGITNQQQPGGYMNQQRPGGYSNQQQPA

YPQQPENPSPQQPAYPQQPAYPQHPAYPNPQQPAYPSPQQPAFQSQQPPANTSQPQPAYP

NQQKPSYLNQHQPTFPGQSTPSPYAGNVVQPPIPGQSSAPSQIQGQLKQPGYTRSQQPGF

PVQPPPQPGFPSGPTSSSGSRQPMYSDPRSASGTSHISGMASPAYLRAGVNLGAPAPAPA

PHAMHQGTVVNPLAAALGSSRIVKPSVDMNSHQRDGFVSSVGNKELTLKYGNATAASLSP

VANAGLKAGEFPPGVVPGSIENVGLQDIPIVNAFNDIVSQLQGLPLTMMEQKQLQEIQKG

KEIMFTKLNIGGLSPEVISRLHDMVACFGHRDFGSAQTIYVALTASDWALHKDWLRGLKS

LIHISMKRFR

>contig38643 Frame-0F

MDGDELKEFFEMALNKLLLSSDATLQELSLTVEGIHATLDQLKALKDYSTYQFQYLDEFD

LLKIGYKFAKSRIPEIQRTFDQLVTAESAQNREQAFETAVRLFQIAEDFSIAENEASIIN

DDTTSDDIIATD

>contig39147 Frame-1F

MLTRCLSAAFCVNETCAVNDRRRTLISNEDPEHHQRQQQEQQQHSSTMSGNQRQVLLAGE

YAQRRPVPPMTPLAGFALRMEVQQSRQKGSIIVQQEPELPEKPNLEWPEKVGIDVQVLFD

VDPAAVKIGREIGKGSFSIVYAGEYHGQHVAVKCQPKDVDGNIPAFVLREVQVLRLLHHP

RLVQFAGAADNVRTKQVWILSEYFNNGDVDLLLKSIRSGKKNHIGWHRITRIALDAARGI

EFLQKNHIVHRDIKSSNILLDDQHRAKLCDFGFAVEIKQLDAMTYDTAEMNSGKSLRKSY

CGTDAYMAPEMFLDEDYDQSVDIFSFGVVLMELLCCRVANSDGFLMRLPQFKFRVLLPQF

RDALPASCPLPLAALAEQCVSFEPTERLDITNIVRMLEDVLKNTAVSDNDIVKLVLFTPD

KSEPHIEEDDIAYYGENDENYDEDDDDCVNGDEEFDNGKNEEIGYSAYELQANGNYSTID

LESDEEDRAVRSQVLNHPFLVKGSIDSNIHSRPTLSAPHHEGVILKRGRRGRRLWVEKWY

ILDRAQLHYTDVPPGWRQHQQQIPQWRCKLPPISSLSLHECRIWKTTEMPELRFNVIDSN

WKIKRELQAV

>contig40240 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66270.1|) 4e-43

MAAITPELFQKLLQHIKVLIRRNASQHAIALDEHALQRRVNAYYLPLFSWIMEVVKAAQK

EQGDEKHCVCIGLSCPQGGGKTTLSYYFQEAMALLGVKCAIMSLDDVYLTYDQQVALAKA

NFNNPL

>contig40327 Frame-0R

MLGGAPLFFFRGCIYLMIMHVSAKGTIVNHERRVLMPKMLQVHTLWSILLMGYGIAGIWS

WYSRDMCNPDARFVLAVGGFLVAEVIFTTCLGLCMLGEVQLPEAIDFDKGLPASASDDPF

GNVCVSERQSLLDG

>contig40635 Frame-2F|Blast-N-acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56646.1|) 8e-53 NOT\_ORF

MTSMHDVLMRRGKRSESQLATKRTRSSKALRKENVSGKKSRTAILSWLSPTAHSRIARPA

ITPDPKATARVKESVSSSKALPSKQLYIDVGQHSFGKHVSCTKCGLLYTAGEEEDEIDHA

KFCKRMQRGVTFSKWKTERVLKRFNDPQARILEIRGDDPISHVKEAP\*RQTSA\*RRVGFR

RGEGVFATQPLCIYSGPSSRWMCHYRAHYKSLHAGYKRFLRGRTDRSGSRELLPRVCQF

>contig41175 Frame-1F

MDQEQKSVVYLETPLLSRLVNLFRERLEDDKAYVRKAAVHALEALLTAQNGETLNALSRH

DLFEIHARCTDASLIVRIQAIKSLSALVLKFPREKDAQTVWNLGVLPLCFDPETNVQSCA

LEAVGTVVFDRVVAWYNVREKERMREALDCVWMQVAYLDGVMARCVQKALRLLMKNNKLH

VETILQTCVYAIQESVRPYHSVAVHDDVEEETACRVLTRYWGFSWMILEELAHSGDLVKR

VQNEPQHLCIVIECWHKLQTQVLPFAFHDGSKRILRVLAALSTVIDARDAKSIATGILAS

LESFAIPLNVISDGIVALHSLCKAKTPVD

>contig42044 Frame-1F

MAHEDVATVVVTTPSFTSASHTYRMELQPRPHVTFDENVVNNEHLGRKRSNK

>contig42170 Frame-0R

MVGVDRQRLAVAHFKAIDSSFCSFSHFVSIPTQHPTWTQLMYFPALSLLAALALVDAAAT

SMSDALQIAPYSGTNVVSRQLDGNPAAVKELVAKLEGDDLVKFFRTEPEGGEGFSTTLSR

TLNHLQLRDDYNKLYGILDHLENDA

>contig42413 Frame-1R

MAKESSEEDHGVSAIYGGRCRKRPIPVVDMVAWTHDDKRLITLHSVKLDDESVDPDWEQR

IRIWNPESGSLIMTLGAIDKEKKNGHVNAAFALSTHPTDWRIVLTAGYDGRVFLWDISSG

RMLKSFTNLSSDSKPLSNLDGGFTPDGSGFCFTDQIGRLLIFGTGSGEQYAATPVQQYFS

HDYVMLITDGHYNVRDRETQELPSLMGSGPLMDASLVQYPHQPPHLLPNKMWTPREFAEN

RRLRILQSYESEIQCAVHHAPEGEEELCSFPLAIVKGEITVWGQEEGFAADVRALARTSF

RLNGAPVMISELQHRRSGSRRNADPRQRRRRASPVEERDTPV

>contig42466 Frame-2F

MTAAAVNDVAAPAQESLLDRLWPMLRMFLLYYAVTSAVNLFAPRPQHEPQNTNVVVKNAD

NSNSGPHSLEQLQHFHNSFHLGARINLRVYVTPDEHFSFIDVETKQEALRWFEEALSYDS

TPNADREDGVWNRKLNVTVDDHLLSNGSVYAHVFVTKDGCSPNPADSTYDAMGSLYRSIA

LTTFRSPPKIVKKRNLLETHTLEQEEAKTLQLADIDSGAYISMWKPSLTINVVLDHSTYS

TRQPPPSFVSTEMDIDNDTGLYSPVLFINEFWMLEEHLIPVNDTRTALPLDISFYTLPMY

KYALYTQIEQNFRNQEATGASSRRDTDNMKSLFIDTNPYLLAVTMVVSMLHSLFDFLAFK

NDVSFWKNQKSFAGLSLRTIVLNLFFQLVIFLYLMDNDTSWLILVQSGIGLAIEVWKIKK

AVVFSRDANNKIVISGAESYEDSPTAEHDRVAVAHLSYVLYPLIVGQAAYTLMYGVHKSW

YSWVIASLTSFVYAFGFIMMTPQLYINYKLKSVAHLPWRAMVYKSLNTFIDDLFAFVIKM

PWMHRLSCFRDDLIFFINLYQRWKYPVDVKRTNEFRTRPDGKQGCISFR

>contig42538 Frame-1R|Blast-inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY65488.1|) 2e-78

MLQRYFRVYQTQMTACANSDYKKYEADLADLSDLKTEIEELTGRLNIRTENVQKKLVNIL

IASSDICRRLGAGRTTCCKSGKDRTAMSVTLETSRLLVEHFHVKEGVHLCNAMRERGVRR

VNVLANTGKTKFAFNSFQLKYIPDCYKPPLACADSHVSS

>contig42880 Frame-1R|Blast-glycoside hydrolase-like protein [Phytophthora infestans T30-4](gb|EEY64375.1|) 7e-37

MLIAKSVSQLVDALGRIQYRTALFTSKRRSQAAGNANLLSPAGQKQRQQLNRLRATLAIE

PLSQLPLSLASVENSMHVQPFDHTAEEYVKIFKRTQRRKDAKYARALELPLFREGSALFR

HYGSRTLGDYDNLPTTKFDGLVTIIHSAQEEEEHTEYLRAQKVVGVDTEARPDFRPLKGA

KANPVCLIQVSTLERAFLYRLKRGKPLPSMLHELFADVGVLKVGHSLSDDFRLLKSSNLV

HSVNSTVDTLYITHKLGCMRPGLKTSCQVFLGGSLDKTMQVSDWEAPVLSNAQIRYAATD

AWAPLRVLLAMIQMEDTKQWLRTKSYNSSSRTIVNEDHDGILGKLLSFALSHQLPT

>contig42967 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61184.1|) 4e-72

MLSVLQTNSRPAVARSALQLYQRTAFSTSSKPKKLRGFYRLWDAYASLLVTHPLSTKIVT

GGTIAGLGDIGCQVLLEGERKDAKLDLKRTAIFTFLGGVAVSPILHVWYGFLGSRLPGIS

KATITKRLVLDQIIFAPVFLSIFLSSVQALEGHADDIQDKLRADWWPLTKANWVIWVPAQ

IINFRFV

>contig43061 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67728.1|) 2e-84

MEASFLVPLLVAFVVPATREVALQLVHRWLDSRAMVRELFDPIITRLKATAKNGDSDVST

DLLTDMEIDSEQFDSRKKQRDWHQSGSDAARLGFGLIFCYMLQVPFLGPFTWFVGFASAG

LYAPELVNLHAFGSANKKVL

>contig43263 Frame-0F|Blast-glucan 1,3-beta-glucosidase, putative [Phytophthora infestans T30-4](gb|EEY65324.1|) 2e-61

MTRTADFWQGVPSEDAGKGEFTAITKASDPDAIRLKLDQHHQTFITEGDIIEIAAAGLNT

VRVPVGYWIVGFDNDDPSKEAAWSKYSNGTLKYLD

>contig44378 Frame-0F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY57664.1|) 6e-24

MSQFFSGHEKLWHKLQGGCTIVKKGLEVNLTNVNAKLESASVLATKIIGEATDASAKEVQ

AIEMYTKKRKVCCTNGNYPN

>contig44428 Frame-1R|Blast-Phosphatidylinositol kinase (PIK-L2) [Phytophthora infestans T30-4](gb|EEY59643.1|) 1e-123

MRCLWAIGEWQKLNDHVQETWSKIYGERQDLDGEQVEGEKLLDVAPALKRELCSSGARVA

FSLQNWDSISKYINSDMDATESHLFKAVVCIRRMELDDALSSITECRKEMDPTLRSLVSE

SYARAYIPAIVNLQMLTELEEIVA

>contig44774 Frame-1F

MLRQGQSHTLMQISVWQWRFLTF

>contig44921 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65804.1|) 4e-09

MKKNVGMPTHKMMRNLVEICDTLQKKGKQVCLATVASADPTSSKRTLRLYCSIQPWSNFA

KGT

>contig44994 Frame-2R|Blast-Sulfate Permease (SulP) Family [Phytophthora infestans T30-4](gb|EEY55880.1|) 1e-149

MAKRLAIKEGYRIRPNQELIALGFSNLIGSFFQGMPSTGGLSRTAVNMQNARTQLASVIT

VLVVVFVLYTATSALAYLPKASLASIIIVAGFSLIELKEAKWLYRVKRDEFYVWLASFVL

SCLLGVLPGLLSSIFCSLIAVIYKTRRPIVSLLGEVPDEETGEIRIVDLDLYPDTAQSLS

DVVAIRVEGALYFANCEYIERVVEREVRKRHATTDVAVRGVVIDAASIMDWDSTTIQMMK

HLKEELRGQGIKLAIVNARDRLHDLLQTSEFLVGIVHNDARIPFSEAIQAIRDDSINLND

NHTLARSLRIQSI

>contig45881 Frame-2F

MILQVATPIKCERKTSTASRSSPDKATLTGTSSAASRSFRRSGPWSHDEEVYAAALIDSF

FKGALDVTEGTTLRAFLSSRLCCNPMRISKKLASESIAAIPIPKKLGSSTYVRDIEVTSE

EQS

>contig46152 Frame-2F

MEDDACLGDISLPLSRSNKPAPLKVTPTMEKTNGSNTYLKLDNATLERRSWASHQSEEEE

DEGWMVTPLAEYCNKSHDLMEENEADVEASVREALRMLDLSSDGEDGGKSDDEREGDQKE

AGRTDVSYMDFVQEVLNERWTQKDKKNEFCHWRTPAEPLDDDVEKSRMKKENSQQEMEEP

DEWQEAYTAKGRVYYYNRRTRESSWKR

>contig47982 Frame-1F

MCVNHSSQGNKVNNNLIVLMTRQRWRQSSISVYCTDRKRNCQRTWAILPKLHFFNRLSTL

VQ

>contig48330 Frame-1R|Blast-vesicle transporter GOT1B-like protein [Phytophthora infestans T30-4](gb|EEY55628.1|) 2e-63

MLDDNRKIGTLLLGLGFAFLLLGVLMIFDAAMLALGDVLFLSGVTLTIGLSRTVRFFTRK

ERWRGIVCFLGGILLVMLRYPVIGMIIQSFGFLNLFGSFFSVAVAFLRQTPVIGTVLCLP

GICHAVDRLAGVQKRGYQV

>contig48503-0 Frame-1F0

MNSLWSTWRRRRRKMPALDELEYVSISLQKILSRLTILKFSLKKKR

>contig49005 Frame-2F

MDHDDLDRQEGAHPLLESHSTSQELMMIRSGSFGSMPRAIAKTFRTSATFSQETTWQLYA

FSSTLRVDTERLSPLSSRGTFTVSIPALRTSIKVPASPRNVFEMLMNKESLFYTCNHVIQ

HARVVDE

>contig49148 Frame-2F|Blast-Sulfate Permease (SulP) Family [Phytophthora infestans T30-4](gb|EEY58082.1|) 0.0

MLLFFVVGPNAVSYLPRCMAGCVMMHLGWDLLREALIDTYDQLDTLELGTVWIIAGTMTF

WGMNQGLAVGALLACLTFVMQSARTPTNAPIRGSMSAATLRSHAWRLTAELNVLDRACRN

IHVVQLKGHLFFGNISQLCDYVNVVLQDGGVTVGYNDKNALLPSVLGIERRPRPEIRWLV

LDFTLVVGLDSSAADRLTKLKYVCRTHECTLVFAAVPAAYRKFTDHLMALFGDSADFYVA

LDLDSALEYCENAILRAYGGVCCEPRTLEAPEAHEHDEEGLHVLQFQRFMPDQPRAIQQR

LLAYFTRQIIAKDTVLWRQGDPSDQALVLLEGALTAVVEEEAGTTENVSVGSVVGDMCFL

TGEKRKTSLVATQKSVVYVLDRANFATMIAQDCYLAFLFQGISLRYTSYRLQYVGNRIWE

TKCLPI

>contig49467 Frame-2F

MKSTKRPRLADDSHDNSRIKNNGELTSVGIQTMVLQLLQHQPRVDDILGRILAMQKREQT

ARLQQRRDEELMRRLFSDEQRK

>contig49580 Frame-0R

MQNTNSIPARTRRGKGYTWVAYMAQRQADCAWSSRRRDTRELWPKYLSNLVSSQVLVAQD

GNHDGRLTALALHSQASKLGAVGASSGKLQILGLPRLRGLQLSSQRTLSICDYHVAGMIT

S

>contig49966 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53361.1|) 1e-14

MVEKEERKGSLGTKLSPVRLMQMAFAVTIVFSMIYMYQFVSISITLHSAKTSEDSDERGV

VRNRVLGHSVL

>contig50090 Frame-0F

MLIQSTICTSFVLHTARSIYQRRITILVYMRLASGQRCRSVAQMRNNDDYCGCLETVYGS

LLALNIRGTCSVESKSLVCQLP

>contig50357 Frame-2F|Blast-mediator of RNA polymerase II transcription subunit, putative [Phytophthora infestans T30-4](gb|EEY61185.1|) 2e-51

MRNPAMFNEKLDDIELLFLNMHNIINAFRPHQARETVIQMLKTQVQERRNAARNIRCIID

ESRQAVERVHGELHHSTDDSSSVDEAFPAGSNDEIKIDDVGDPVAMRNGNDIATDVAVVK

AAVLTSSRQDQV

>contig50465 Frame-0F

MAVYINNGRSTSVMEDGFEVVPMAKGFTIAEGVAALPRVTQNLRESIVDQGIAATNQEIV

DMAYFLLRSDGIFVGPSSALNVLGAVKMARELGPGHTIVTIFADGGVRYGSKLYSRDWLK

EKRLLPKEGSNSLEFVGN

>contig50582 Frame-2F

MPFRYILGQIVLDLNLSLKVSSGSNFIFCEHAIL

>contig51000 Frame-1R

MLLKQKSWARQNVLKALRSITTGQRGRLPSSLTLYIDDLMIRSIQQNAKSVDIPPGLKLA

SSYTPTTEGIRSVMSSKPSAR

>contig51109 Frame-0F|Blast-apoptosis-inducing factor 1, putative [Phytophthora infestans T30-4](gb|EEY59276.1|) 1e-156

MGRATRTGGGLERDEKNGGLVVNAQLEAISGLFVAGNAASYYDPYLGRRRVDRYDHAVNS

GLTAGRNMAKSLRGAGKMKTYRHQPLFRSHLPGVSLRMEGIGEVDSSFRTVGVWVQPPCI

GVDRNGSQRSSYERGVVYYLKGNKIMGILLWNASDVLESARQLMLSRPEIRDNVVEELKH

TISLAPNDWLHVVSTS

>contig51659 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57216.1|) 2e-50

MGYFVNAIVLVKNIVIGALEPAQIIAKLPVLQSDEENNPPMPVDVLRWLESNEASSKMLR

AETT

>contig51743 Frame-1R

MQDRIGAMETTSRAEANKLRRLQQKPSGHRVSENATNDGDEEGTDAGIEAEDGVTKTKPQ

R

>contig51817 Frame-2R|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58442.1|) 1e-22

MAKVLSMALPSHWRDPTQWCFTRAASSIQLGIICMRYLGYICQPFGMVLIFLISGYYMYA

VIPIMADTTLQLISHLSASLVVLFNISFNYVLCSATDPG

>contig52041 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53323.1|) 2e-22 NOT\_ORF

MNDFEQERFNLLQVIVSRAST\*IDRTLMHESCKLVAAVFGVRGAFLARVDKESIVMEHVI

GTCELSFQDEMVRQKSLCEYVLYQPPSQA

>contig52225 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59223.1|) 3e-23

MQSLIYHLQEEYSSYDSAISATIDGEKRQDISASKDVIQEAQCASNSTKSVTNSSVHAPE

DPSYTVIFTGTSTGDGSFDLLSLLKQQEIDSTAAVAKPTHHFVRELQNVLASRGIHEERD

FTKQIDQDISISPTLQALHLENDAVAYLDKAKTNSLPPCVL

>contig52492 Frame-0R

MCISSAARSPIGAAENAFGSASGEKLVSLSLSSYAMTSKSSELAMLDTTWLSHLFKFPLA

RSSALNFFLGEITRSPVMLLEDTSSSDVGDAAEASLSLRLRTTGRCTDSGDVLAVSATGE

DDDVVVVAGIFGVVCFTGLSQ

>contig52588 Frame-2F

MKMETWMGGYYRPRAFPFSTLLRLLIARYRVRIVCARLAKNRSARSRTSISIVRVSGVDG

TPSETLHPCTS

>contig53468 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60560.1|) 2e-58

MPSIELAAVFGALFDSIFLMFMGYNPPASSIPDGYKWLYQLVPHRYTFQSLTALVLGDCP

LDQLQLIAEAVATNTTINVSGWPLGCQPLTDAPP

>contig53532 Frame-2R|Blast-hypothetical protein PITG\_08805 [Phytophthora infestans T30-4](gb|EEY56044.1|) 2e-24

MLADLRHGSRTEIDALNGHIVAKGERHGIPTPVNRMLVLQIKALETERTRIVKEV

>contig54410 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55525.1|) 1e-86

MSDDARLMARYVRPIYEAIDTHQYRNAIKLCAHKRVTHLDIVQLLKAHSLERTGRVEEAL

EICRRIQLKKPTDEALLNTMNLVFKLSGCEHEMLPTFEYACVVSNPPNEELFQSLFMSYA

RCGAFLKQQQTALKMFKAFGNIRYMCWAALGMMLQVEHFGTPPRMLALAEKMLLKTLRES

KSNDGEVLQLTVLTLQLQG

>contig54564 Frame-0R

MWRDISPSTEWIDQHEVPAQLLHAYRSLKTHGKDMTRMKYMSSSKSSSDHHLICEAYANI

TAGACMSIGLRFAGTGDRSARATLRFFLLHFRELRSEASSSIVSERCNVVAAATQRATVE

RSLAVCAQALALVDAGSGHTETLSLLRSVTLRQRLDAAASYGNHMALSMAIGLLFLGGGR

ATVSRSKEAIAGLVIALYPMFPANTA

>contig54696 Frame-2F

MDGPSTQAASKDTSESKEVSKRQTESSRYLTDSVFLCAASVAQNLPDMWHYRILYDLLSQ

SWLLDLHIRPHM

>contig55185 Frame-1F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY56470.1|) 9e-10

MSATENALETLRLVIICTAAVISSVVAVLLFRRIPSRGYTTQWNDRDR

>contig55206 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67598.1|) 3e-16

MNMTCTRTPRELVAACMDHIALEGNAGISIALLFSRIEPSNDVSVRRQVWRLLRSCCGVL

RFFR

>contig55273 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55039.1|) 3e-24

MRTNLLNGRADENRSQMRKFQANCDTVLAALGEICTSIPPLPLQLDTSLIEEDQCDRSTS

SANTS

>contig55398 Frame-1F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY53555.1|) 3e-18

MQRMLELGFVDSAPEAYRMGNAFMSAGFLHHSHHCESYRNTSEQFYFDVNVLYRYASDTP

G

>contig55497 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61747.1|) 5e-40

MKQHSKLAPAALSYVARGAARTGGAFSGFFFLYCGFKTALATQRDDDLIGAGISTVAAAL

PFIRSTVMKQNLPYALMLVVLDHFHEELSEFRK

>contig55556 Frame-0F

MNSSPQKLIHSVLLGASIHQVIDVDTHHCARTAFVLVI

>contig56067 Frame-2F

MAPYDRVSKKRLTYIGSVSEEDNARCFAEDEEADETFLALQKLLQALNRSSRSSHGSFNS

NNGSFLGGGGNSAQTAPVCDTASQQRLSRDEMLETRRQERDRVRRSLFAKNGSSCRSRRR

HTLPGCYVSEEDEDEEVSVPSVESTISNRFMNGSFSALNVHVISRDRWSTEDHVMERLPI

VIQPKNGKHSTPTDNEKINVVHTDEFIELRESLVKNMSDEASTAHYLSPPRSTWYMQMHG

FEELNCS

>contig56870 Frame-1F|Blast-mitochondrial 2-oxoglutarate/malate carrier protein, putative [Phytophthora infestans T30-4](gb|EEY67662.1|) 3e-17

MAVTVPLQWNPTVTPRPPLASYTFGGVAAVGAVFFTHPFDLLKVHLQTSKKDNLKLGSAI

RHI

>contig57019 Frame-2F|Blast-endonuclease III-like, HhH-GPD superfamily base excision DNA repair enzyme, putative [Phytophthora infestans T30-4](gb|EEY57975.1|) 2e-26

MATLVMTYAWGNTMGICVDTHVHRISNRLQ

>contig57103 Frame-2F

MRFSLLSAVAACYIAVASSQPIDLDEVVPFPEIVPQSESDELMLKFKPQLHISSGCQPYP

AVDQNGYTSVGLGVSKVGTSCDGSPLGSQVYARFEEYNSHYAIMYAWFFPRDYMIRPIGN

RFSWENAVVWLSKEDHKLLAVSASGMFSYKKYEPVDNKNLDGDSFKLKYTYLVTSHHYLK

ATTEKGVKHDLVSWTNLTRPALHALQREDSFGDYPKMPLSDNLFGKNLEKAFPF

>contig57176 Frame-1R|Blast-15-hydroxyprostaglandin dehydrogenase [NAD+], putative [Phytophthora infestans T30-4](gb|EEY63919.1|) 2e-62

MELFEAIAIVTGGGRGFGRAFAEAILTKKGKVLITDVNVDELQQTCEEFQSQYGEQNVCW

VRQDVTEYDSFSRVFAFAREYFKKHVNVLVNNAGIAGNSFLDVPESTSWEAVMEIDLIAL

VRGTRFAIMEFKRTLKGHEGVIVNLGSTASLFPTPFAPDYAAAKA

>contig57730 Frame-0F

MQHGALLSKMCCPNGGTMSGDCGM

>contig58366 Frame-1F

MTPQWFQECIFPHRQVAAVHVVPNSMHSGPHSVVGKLEIHFADTDDTLVLFRKKSAKKEL

PGRSAAQWTRDIASYRNEAMFYAHFASSMLARGVALIRPFAVFESNASGQCTDNLLTRGP

SLVANSENFLLLLECLGVASPRSSVPSNPSLNRYEAADCLELTDTQQALRYLANLHASTY

GQEQLIVEARRKLWPSACWWTLSKRGEKELAQALDIWPLMLIKWRLEFESEGEFPLLSEL

ETLGERMVQHAAYISNCLVDCRFETLVHGDFKSANLFFETVTREVLAFDWQWTGVGLGVM

DVANLLNTSTSFSLLATDAMELELLHFYYDCLNARRQELGSGSLHDEYPFEAFERHYMLA

TLEYARVLISNFWKHMTPESCEAMSGYT

>contig58502 Frame-2F

MNYADKKENKEEEVIKNGELQSTKGSMVKISITFLLLE

>contig59282 Frame-1R|Blast-D-Tyr-tRNA(Tyr) deacylase [Phytophthora infestans T30-4](gb|EEY61053.1|) 3e-25

MDNGYEVLLVSQFTLHGQFAGNKPDFHLSMAPTPARVFYDAFCKRVRCAYV

>contig00586 Frame-0R

MTNKSFLQTKFFFSKTTHDLYFFSKTFFKCSNQLFFSKKKKSIQAKSISSYPTQHLQTHF

NQSIRKRLQLTHQILYTNVGICFNQRILFNRLDTRWIRKRQPRR

>contig02728 Frame-0F

MPSLFSRRFVTSLAISRPPHPLFRPIFACRALSIDALSAATTLTNTLRDLRASEHFDLIV

IGSGPAGQKCAIDSAKHGQSVAIIDKRDMTGGVCVHTGTMPSKTFREAALHLTGYRHRAF

YNGQVGPSKRFGVEDILQRVKKVEGAETDITRHQLLRNGVQLISGTARFLPGNQHMIAVL

SNESYETATDTSRHTSADICKRVLTADKFLVCVGTRPARRADIPFDGQMIFDSDQLLWGK

VKSVPRRLIVVGAGVVGMEYASMMTIIPGTDVTVIDGRQEILNMADNEVSEALCYSMAQT

GTRFLLGEIIEKVEKSEKEVLVHLKSGKTIVGDGLLYTVGRQGNVEGLNLEAVGLVPDKR

GYLKVDNNFQTAVPHIYAAGDIIGFPGLASTSMEQGRLASVHMRTCTPLNDHEISNDKLM

DDPDRVRTRMRSGEVFPFGIYTVPEISMVGKNEQQLTKEGVPYEVGVARYEELAKGQMLG

GVPGFLKIIFCPETLTVLGVHVIGEGATEIIHIGQVVMSTDGTLEYFRNAVFNYPTLAEA

YRVAALNGLRKIDRLRE

>contig04454 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56118.1|) 4e-20

MSKLFQRNPRNVRIASWVAALGLFAAWYKYDQMQQRRFSDKETQAWNEAILRQYPVKPRP

KKSPET

>contig05563 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61371.1|) 7e-37

MKVWKNWSGHLRPSQDRARELVTTIVGLDFSKTYVVRVRYEFRRGYGLGEWSSPSLPITT

ISQEEAMQYRMI

>contig05747 Frame-1R

MNKEEVMKVVPSKAEAVERKHKVEEVHEQDQVVQMNAKKHVVEGFERIKRVEALQTRTRA

ILDDVNPMVKKIRMQIRRQAGVCNQIAAAPSVIKSVVIKIHELFQMAKSFGDAYLMLALD

LVALNLSKQVASRDDY

>contig06908 Frame-0F|Blast-nonsense transcript regulator [Phytophthora infestans T30-4](gb|EEY69624.1|) 0.0

MSGSFDFSAYDDYLQTQPAQSQSSSMFPLTQASQSQYVFVDPSDPGNSADSFYDQYQAPG

GVGSSFFDQSRSAEDNPRSYPSPLDDTSLPNDFQSLTFDETVDEDALDYTTRELPKHACA

YCGLHDPASVVKCVTTEKWFCNSRGNTSGSHIIQHLVRSKNKEVSLHPESPLGETVLECY

NCGCRNAFLLGFIPAKQDSVVVLLCRDPCLQMNALKDMSWDMSQWLPVIEDRSFLPWLVK

VPSEHEQLRARQITSSQIAKLEELWRDNPLATVEDLDRPGIDDEPIQVTPIYDDGYQYQN

IFGPLVKMESDYDKKMKESQTQEGVMVRWDTGLNKKRNAIFTCSRPDSDLRLVPGDEIRL

RLGPTASMLYGKDWEGTGHVLRLEESEVTLEMRSNNVPTEIMDGYFVDFVWKSTSFDRMQ

AAMKTFAVDDTSLTGYLYHKILGHDVGVQPLRIPRSVGTHFSAPGLPELNTSQMEAVKGV

LEQPLSLIQGPPGTGKTVTSASIVFHMSKQNMGQVLVTAPSNIAVDHLTLKISATGLRVV

RLAAKSREAVASLVEHLSLHAMIKSLDSPDKADLRKLMQLKDDQGELSSQDEKRFKSLKR

QAEREILQAADVICTTCVGAGDPRLSNFRFRQVLIDEATQATEPECLIPIVQGAKHVVMV

GDHCQLGPVVMNKKAAKAGLNQSLFDRLLKIDLKHRPFRLRVQYRMHPFLSEFPSNEFYE

GDLQNGVAASERQLTSVEFPWPNPFKPTFFYICLGAEEISSSGTSYLNRTEASNVEKIVT

TFLRSGVLPSQIGVITPYEGQRAYVVSYMQRNGPMRSQLYKDVEVASVDSFQGREKDLII

LSCVRSNENQGIGFLSDERRLNVALTRAKYGVIVLGNPRVLAKQSLWNKLLNHYRDNQLI

MEGPLNNLTPSHMQFPPPRHSGRRAYRDGSSGFSRSRGPVPPLDSRFDPRYEQPGMPPFD

SLSSGFPPSHSQQRSGSRRGVSSYVPGSMGPLTQDGMTQSSLTMDGPFTQLAQTQSFSQL

SSDKFAMSQESFAYDHDFKTQNMPMSQEFRTPDSGFY

>contig07727 Frame-2R

MFIKRKTQLWHRFVTLLGIFCLLAWAKTDPIVVMASNAIANHTSRRLKKHHDGYHNRIAV

KAEERMFQIRSIFKGDTIADLVKVEQDLFQSEPFKNWWANSIKKGRSVKDLAAELVEHIV

GIAKYKFNDGNAEMDELKKSIIEVLTEKHGPKDPQDLNGLKDFFTNLGLNADTFEGQSFS

ILLKSFADYPKIRANDKAYYDTLFSMLSKIEQPLERIALHLLQERPKPGESTFAAKALSH

LLVRWHNEGKGLNDIYELIVVMPLQMRITWKDPLIFSGLRRMLKGCTG

>contig07943 Frame-0F|Blast-40S ribosomal protein S16 [Phytophthora infestans T30-4](gb|EEY62451.1|) 9e-29

MEGKIESVQVFGRKKNATAVAYCKRGHGLIKVNGTPIELVEPEILRVKTYEPVLLLGQQR

FANV

>contig08083 Frame-0R

MPHIKSNPLSLTGPKVSKSPRHLPPTSSSSLRFSMHCSHFNHSRRVLSMTRPQGIPAGSH

LSTLNPSRAPCRRWMPF

>contig08300 Frame-0F|Blast-rRNA biogenesis protein rrp5 [Phytophthora infestans T30-4](gb|EEY64678.1|) 9e-91

MFEIGETVMCSVEKIDTEKKRFTVGFRQSNFILPSTSANKVRPAFFQAYVREQAMVWNFA

KEKKLLFTVGKTEKAEFIGIRPYGAVFALEKDDDTVTVLVPMATDQKCEWSEGETVKLLL

IDYDFSKSVYYGATDEALVQSGFKKLRKQKQRVKAGATIAAA

>contig08656 Frame-2F

MTDVIRVLLLNPLTSTTSLVCLQRPLEWEGVLRDFYQVITNSDDDPAPSILAKCKVLLHP

TKSKTEKGVVIRKNALDRSIRDGDLLSLENFQLTEATGPPPELLSIMDTLDFDVPVDLND

NLTSFDSLNLSGSVPAKGGTEPFEGVTRPPVAASRGTSRTIKRGRSLSSKFWLVNKLAAS

GKISKEQKDSLKMLLLASDDSVLHEAFERYEETGDLETLLKLHLNAKKKTFVGLPPLSTE

AFDFQLTQTIEQELDLLSMQSFTLGMDTQDACSPVKQTPLATNNDPMPFLTVNDDELLDP

LHGLLDGTLASLPMPIGHGEDQRLPSALPGDLHGMEEWLQD

>contig10266 Frame-1F

MEKKDVPRQSSIKSFFSAGAAPSANKRKPTDADVTNSFKTPDKANKKRKVGKTKNKIIDS

VKKYDENEKAFVNELQGVKMITEGEGDEEEDTKSKMKPGRRRLRQRAVAEEDEDSDVNLP

MDTSKRKEKVTDTSSRPLSSERAKVQGDNRKVKATYPAVKTFCGQRADLEKNPEMAKELV

NADEIDQLKTNKAKKANNEAKRNEKACIKDTAVTVVETQTSFFTATSSQKLKAKSTVVDD

LEISKTLNKLKPDDVAEKNTGLRIESREVPYFELAHLFANIEEVTGRLVIQDLLTAFFRD

VILRSPNDLLACLYLCVCVDLAPPFENLKIGIGDAILMKAISEATGAA

>contig10288 Frame-2F|Blast-zinc transporter, putative [Phytophthora infestans T30-4](gb|EEY61698.1|) 2e-45

MTDAAHLLSDVAGFCISLFAIWVSTLPASNRLSFGFQRAEVIGAVTSVLVIWVLTGVLVY

AAVERFMECLKPDPKEHVNGKL

>contig10604 Frame-0F

MSATRVTRLTKDVMALGIHHAPLSSLLNSLVRLANVHFL

>contig10903 Frame-0R|Blast-acyl-CoA synthetase, putative [Phytophthora infestans T30-4](gb|EEY63260.1|) 0.0

MQYMLSDSGASLLVINESIITSDQTLRTFVNDLPTKLQIAILLSPDSVNPDNKTILSRTQ

HQIVQQWLANQDYNKAGALMIYTSGTTGRPKGVLTTHAALTAQIHDVTIAWEMTSSDHLI

HFLPLHHIHGVLNNLLCILYVGGSVEFLPHATPSLIWSKLSKSTTLIRPISILMAVPTVY

LKLLEEFDKYDPEDARTVNALVGARRLRVAISGSMACPVSILNRWEQLTGHRLLERYGMT

ELGMVLTNSLHGDRHLGYVGTTFPSIAVRVVDPETELEIPCQTEQEGELRVKGPTVFREY

WNKPDATAKAFDQSGWFKTGDLVQYCNEFQSFRIRGRMSADILKTAGYKVSALDVERVLL

MHPQVLECAVFGLADEMWGQVVAVVIRADVKGDKLGPEMFCPPLRTFSKQHLANYRVP

>contig11131 Frame-2F

MSTPTKVNPTRHMRIKKAADDKAGFTVAQIPKKSPFEGSEKVESSKLHPACEEVPSCGNE

DVM

>contig12800 Frame-2F

MAPSSRITLLSAFVQAAKVQARHFSVKAVNLGCFLPSQKQHGQCLSTFRFVTSSGGPKSY

GNKSIARIIALAGSIGVTSVIAQMEAGTDKNLEKRFEYAEAVDTIRQQVAEFRLTLRSFK

NRYPKEISINKIESTRICAPNGVSTIRIEFACPSFVNQEAILGRFLLQLHEASTFSSRQI

VEVIPTQLKELNKSIKTQPAVTYLYTNGSGSFQFLRNFSPKREITSKFIFYKDSYLTQAE

IDAVVGAYKEMYSLANVEAFNRYYLDQRQNSALIERSRSPTNIATAISG

>contig13308 Frame-1R|Blast-endoplasmic reticulum-Golgi intermediate compartment protein, putative [Phytophthora infestans T30-4](gb|EEY57043.1|) 5e-67

MKIVPTIYSEIDEEAIHSYQFSATQQGNYMDSSGLMTSLPGTFFVFDLSPFMVKIENDQM

PLTHFLTKICAIIGGVVSIAGFVDSFMYNSLHVRRQVSTNGGATKFG

>contig13542 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66748.1|) 1e-119

MTDSAKVWLVTACSTGFGREIVLAALARGDRVIATARDQRKLQNLVARGACAIALDVTAS

DAEIKSVVDKALSVYGVIDILVNNAGILLGGAIEECTDEEVFHQYNTNVFGTLRMLRAVL

PHMRAKRSGVIANIGSACAWFGLKSMGIYGSSKFALAGLTLALHAELQPFGINVTIIEPG

SFRTAMLGKGFLAMKNSIPDYHPITQPLHDRIKCVNSGRLDALQPGDPAKGAQIIVEVLT

KSGRCVGKTIPRRMLLGKDAVTVGEKSLEDNRCELEEWTHLASSTDYDDNTTCTPMTF

>contig15575 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY64501.1|) 0.0

MAAETGDIPTAKLLVTRGARIDAPNASGSLPVHLSPIGHPIRVLLGSGSNLAATNPSQPP

KPRNEMVAREGNATQVSHLAFKNKYQQDLALGPRDFEFVKVLGRGAFAKVYLVRGKGSNR

DKWYALKAYNKQAIVQKNQAQYIHTEKAALQACSDHPYIVTLYFAFQSQDRLFLVMEYCG

GGDLLSALTRRKAFTESEAAFYIGEIALALSHLHSKNIVFRDLKPENVVMDLDGHCLLTD

FGISKEGIKDHTSANTFCGSPMYLAPEMLSRSGHGFALDWYSVGALLFELLTGLPPFYTN

DKKQLFHNILRGHLVIPEYLSPNARDLIQRLLHRDPKQRLGSGPTGDREIFNHAFFASVN

WEKLRARELPPPFQPKIKKDPSGVPDTSNFPQAFTDQEISEMERGCDFLDPNSSKVQRPN

ANGHKDDKRLFKDFDFTPELQLDNEAKQFEQLALQQNSFKNLPPPALLETDEYSI

>contig15878 Frame-1R

MGIGLKKAMTTSKKSLFCKLLATPQPHFRLIRGMLPHHFHGYTSDGHLIVWDFVGRIKMD

KLYATGFTTADLRDHYRFFLAFAQENLLCTSSQKIVYIIDLDGLSLRDVDARAVDSACAV

VKLLQCDLPDRLQAIAVLNSPVWFSQVMTSIRPHLAKRTAEKVSFLSKSTMKQDLIALVG

VDSLPQRYGGRNGVEIGKSVQERSLDDLLKRTTASLESTIEIVATPRSQRSTSSRSRISS

VCSDEGSDEEAFFDCSEYGLQSVDDIEGQEPIISVVVHSHISPSSKTEAVTRSNTYKSGA

YRPLEKKQTMSSRPLSGKFDKPVSDLAITREPQACLVLLIYFLWSVFQLSFDELLPLWFF

KQISRTGDSTVDERPTSHLLSVTLTIAGTLASLSLFVLFGQILSNIVCHSSRNIMTPLAT

LRIGLLLQIPILGCFPLLDLFEVNKLPFSWLLVLGVLIAKQLVAGVALHGIMTLLDNSIA

VDKRLTIHRVAQRAHYVSHFIASSAAPALFALLGFFQQAFPFDQSLLYYIQALGLMLLFV

FTIAIPSRMNFPVLFSMGKR

>contig17515 Frame-2R

MPLFQFGKSDAEKARQRVLKEVKRQAKRQRKQAAKEVRQARKAQKKRRRPFGRNTRHERP

NGPNEPYERPNGPDERSFHSTMPDEQSYTSNARDERSSTHNARSSTPNAPYERRPSFANP

LCTETPAFSNSLQCHVCAKKFGRALHHRRHHCRACRHSC

>contig17986 Frame-0F|Blast-mitochondrial 39-S ribosomal protein L47, putative [Phytophthora infestans T30-4](gb|EEY58920.1|) 7e-64

MSLPLRRLFGGLRVNANQTVRRGLEDFFPVQKAVGEGAKASSLTQVPANVGSKQVIVGGD

WKAWMLREKSTEDLHKLWFVLLKERNALLTELQQCRAKNLVMPNPTRRTKVKKSMARIKH

VLHERSTIYKENQAKKAAAKI

>contig18110 Frame-1R

MDLKTAEDKLFELPEYLKPDLSSQSSMNYNDEAAEGGMLMGNAGIAEVELPASYAKKTET

ATQRALEANQLKPEAKLDAIGGLAKSFVPGNFSVDFNRHRADFVTELKNSNKDEQRTRGS

HQARNDKASDDRAVSHFRNFESRKFR

>contig18327 Frame-2R

MQIYGIPVDLLFVSLDLSSIPEDLDMLDDQILRGLDEAAVRSCNGVRVTERILQLVPNLE

RFRTTLIAVKHWARVRGIYSNVLGFLGGVNWAILVARICQFYPNSLPASLISRFFRIFQM

WTWPNPIMLDRVDNPFNLGFSVILLIFWIQDAVV

>contig18918 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63782.1|) 1e-91

MKWGCTMLRTFYYINALSGKSVIGGLRDRNTRYLFLQALVEMDELFQTVAASVASTEERS

SRGGGVKSSPDTSAATLFPVQSLMILLPLPNWIFNFFVLRAFDLGLVASSSDDTSVISSD

LKAIPPLQTNFDAELRDVFELAAKRNMALPVLTMLQNSLLYVKKQRHEEHQHLANCNTHL

HIDSGFLLAGVDLSPRCTDASRNFFLKVFVTFILTLLLGLYIFIW

>contig19126 Frame-1R

MYIFTIISTVPLTPKLTRLCLSLESQTCAWSLDIILPQQTSLHKRAASGVVLYHGAAICC

A

>contig19856 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66640.1|) 4e-78

MRIWKNEGCNHMTCTQCRYEYCWVCESTWDASHYACYDLPFIGASSACGQWLQRTLGYAG

IILIVVVVAAFGFYAFVGCYVFLFSLVHCIKLIQRAVNPSLQTA

>contig20438 Frame-2F

MYREFWKGENTLLREFVRRGSEAISVIPVDIQALNDSIQPVLFASEGEVTATDAMKTFSV

SSLNRSKAPLFHEFEAIQDIDAIGPMPACTRRRIRNTFKRLEVKEPWKLVFQFEKLTMPF

SMEQYPQVLANLKVFWNEHARAVWERNFGCRDRILILWSYTTSVDFDNAKRCSFLNSMCS

RHYCIETMGLRSLTLSMSVPKSLAAGFIVIRLLI

>contig20597-0 Frame-0F0

MLGTISTAKSLTCSLVTHRTDRLSARVAINAIRQRLKVLV

>contig20597-1 Frame-1R1

MPRKSPIASSNDSNPKKGGYADLETSPSGGYVWTGRVSFYLFKRYKVEQLPC

>contig21763 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67737.1|) 3e-10

MANFQAQPSLFRALLDTKASKNYHHLRVKAFGHAVLRTISTRPFPSTKEGPIAARLRYLY

PDLANIDYQSVLG

>contig21824 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54255.1|) 2e-64

MKDGREHVSGALLHVINSCGCPCPTERTVHLWNALQLFEDILADKIASMLVFVNDFKILI

DLIIRECADLPQKDITRLHYLEVLEQALQSQLFPMTQMYRKRELCELLESLLDAGAQDDS

FMPKAV

>contig22205 Frame-2F

MHEGVEHLKRTGPLSTVSLDSSYDEDGNRAKMHQRHDYTCWIPFVLLAGFILVAVFLVLA

LGHDANLHQGANNEDDPISMTKLSSLTSNKHLTAPQRKLSEWFNLASNASQLVVEGSNSN

ASFTGVLYPRVESNSLLPFDALLAIQMGEVLPNWQYIALQNDRGYKWVVTPMGDGNSIIT

NGCLNSNQISPLDGLDSVFFTASWASPFDKYSVTIVFNKIKYTISQVNDDSDDLMAEDTC

WLIESEDEDIGLSVCIRDLLLKSDLGELFRAARGCSRLALSSVHSLRQLMGFVPLPLWKW

YASFNGLS

>contig22476 Frame-1R

MSIDFLEFPEHCARRTKKKNRALHYLVHYVYFRISLSLSIPPRSFASHIPPNLVAPTSSS

QPFYSSLETSRYF

>contig22582 Frame-0F

MRQVFIQIADMLHYTKCLLRYLTSQVKLNCGRLA

>contig22744 Frame-1F

MAGGDLWSCLSIRRHTLNKHDPFQERGFGRT

>contig22960 Frame-0R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY70221.1|) 1e-42

MPLQHIRVVRDLKDVPDGYESLDEPLLNSDGSGVELRTYLCFRRLSYEDCLGSQWSILNQ

KAGDWIEIKELSSNKWNVGQILQQSPSEIRVHISTWNKGRDEFLSLSTCRNRVAKLGTFT

NFYMTPAYPFLKKQGGMWHANMMDLQHARDQFDTYFYDRERQKTYLLGSLLPFIEKSLLS

TFLSSDLANEMNAFHQHVLKNVVASILSNDAKHIEDHLLSLLRMILNGHSSCLFFYIKYT

GSYTSQKYQRLVYTSYLVSLDALAAIPVRHPCRSLYFIDNVDLFLQAGGFQLILDRLALS

>contig23307 Frame-2F|Blast-serine protease family S01B, putative [Phytophthora infestans T30-4](gb|EEY66041.1|) 4e-16

MFGCATVTANRRRSLMRLAVLAGANRRLSSRANTTCRTFAIGELSLAYAIGGAGLATAAV

ICCSKRDELNCSEAQPGKSSRMLSRDFIADAVEKVFPAVVNISIDSG

>contig23457 Frame-1F|Blast-U4/U6.U5 tri-snRNP-associated protein, putative [Phytophthora infestans T30-4](gb|EEY65752.1|) 3e-27

MLNELHKDLGGTQKPQSSIILKCFQGLVEVTTDDETKAASSELAERGSAVTKKVSPFLMM

ALDLPSTPLFKDSQGGNIIP

>contig23578 Frame-2F

MSSYDGGTFVSDLLQVKNLFGNYYLSDVLFVFSMDPQGAFASDGGESSSTRGHLIPAHRL

VLSFRSGAFQMAFLKAKSSHLPSQVRFPLKIHVQDTPYHVFYSLLKFLYTNELYLEESRS

ESLKEDYQLLLRAAYVYLVPSLVAICVQRIADTFDGTSNKVETTDVDGTANGQRQIQMNT

LEILVFLDTLLATKSEKTDVALLPNKQHSSRESEDVGADMLSQCTDSINQLQELCFKQLQ

HMEEVAFKNLLQSDIGRQSSTKQLCEILRLRSETPLIKAIRYQLGRVVHELLRQGEPLDR

VGKDETDLPLVVALQTGNNAIIRRLLIDETA

>contig23596 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63003.1|) 1e-93

MARMPTSMAKNPKPKVEEAKEAAVEATNEMLSQAEEMRQKSDVSERGRRTLEQLQEEAKN

LGNYARGKVEHVNDAMHEAAASARESTERTKAAAPSAEDISDTVMDSLKVASEKLSGEIS

DLGERVQSVKARVAQSMQNAGGKAKDTWQQSAEAAKTAGGKAKDTWHQSTEAVSTTGKNE

YCLPLPIDRICARHVAVVGIPLLALVLLVVLRRRYPKKWKASVNKMKDPSKMLARDMPSS

DKIKSQLGGVADTVGEKLEYVKQRGSTKMDEVRSMYGQPDNKKDL

>contig24012 Frame-2F

MDIQQLEQERRQRSREQEQLRRRLLQEQSRKEQSAKNQDLISKGLQSRKKEQNNCFPAAV

QSTKDSHSKLSRSKGGDTANVPLRMSECEKSDDFAFSMTRKGSSGGFSSIKRRRKRLLYS

QVNHDDDDGDDLADLFQLSSKSCQHDKLQDTSVTKSSCGKQSRKRKMLRLCDIDEGEKNI

VDLSQLPENINADEITLTASAAPILKESIRGDFIAVECSTVSSNPTEDNFNDFDADYDLE

PLNLSGRIRCICGALSAKGYRG

>contig24139 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60194.1|) 5e-57

MAKLQLEIDVLHLLPPSCDDGSLVARKQEHEELEEERQEELELLVHIRSMLQLHESTLNK

MKRMIAALTKELHRVRQREEVVVIATLRSRIVKVFAPKM

>contig24603 Frame-2R|Blast-vacuolar membrane-associated protein, putative [Phytophthora infestans T30-4](gb|EEY67603.1|) 6e-86

MSRRAKQLGLNLQRVTENGITSNLALHPFNCPIFFRIDGLSEQQMVEKRLVERFDFCCEA

LHPISSSPFHLKTEHATVTDDFQLPRAHRVTSCYHQYVHRSLACFARMTQTGLIWISNQK

ERGDEIQPVFDELREYIESLQVARSAVMSVLNGLFKSSTASAQIAVLPVKIDKDSLQNIK

SNKFDLALEGNVERAPKLLEIAATCRSTEYEGETEKENNPLGLKAHVSNAATRSFRHPTN

DIVATPDERSA

>contig25082 Frame-1F

MVEPLYIHMDEAKGLQKLSYYGGTDVYLFNTSGSSYQIIPVIHTRKCFKFGAEAIQHVFP

NVTFFEPQHGIYLVKGRPCFSWKFVTLIAEPTIDGLLGEYTLYVDQETDQPIRFHYVGRN

QMLGGSHIDEYYLDYVYVREGPVDEDVFTFLPSFMNCTDMSSDDERMQRNPKQDIHLLMP

EGIARKKELFINFTTTHNKTYMDNEDAAERMAIFHTNLRFINGENR

>contig25198 Frame-1F

MPPSLMACLQSQDESPTTFRPSYNAKQTPCLPSHPTPISATRARTHSLPGTDEQLLDRNS

SWMQLVIDRGLFRSFEGVSVEVARLRRIQNLDMYSSDIETVVEPHPDLALVQKELSRARR

KSVRIRDDQKQMIKQFEAQQDRGILKKYLAIATGSAIHHKIKMEELKKKLGRHMAEAAHA

DAELKRLERRSCSLVEDWKRRTSFSCRSSQSAHDNNVDLSIIQAKECTIYKENENDIIER

LEQLEMEKQKLLGLLLRTLRLPDALQMHSNVAVYASEVQSCESVKRQIDRALGLYHQALQ

LLRMAMATVVSSQYTGSVKEFASGPFALTVEAGQLMQAAAIGIQPEARRRYRFFALKLLN

LRLPKFPQVVSDFVRRARPNFDPRSALAQEFVRRLPACEYTMVQTHKFVIEKLELLDRWK

RTVEQDQAHAQDSQQRLETQLQQRLAVLARSISV

>contig25514 Frame-2R

MRMFSWMTFLHVIIGFCIAALSLIKILDRRIFYYRYFFSDEVLVSVLLILGFFITGAFVI

LFLGTESYLEGSRAATDLSGWVQDNFVNDERTRQVWRQQMETSRAMISQAISGVEGKYSD

TMWWPPLKSLIKTYYFDAKSSDGNVTSNVSLLSRLRLPENMTVVQAVSFAYSKVDSVNLT

SVQLTDWTSKGLDISRIAVGSLAQLVFLVVTLVLAFVSLGVRSFFFISSLFYLLCTNWDP

IERFVEDLLPIQVEKRPDVVRSLRRVIEGVFFLPLKMASIHAIVTMVSFTIMNADFMYLA

TTVTFFISIVPIIPPYLVCVPWVISIGLTSSIVKALALFVVQYVAFAVLDEMLYEKSIVA

LNAYVSALSVVFGVYVFGFEGVIFGPLIVCGVTYAYDVSNHGIQAAQDEYGKSDEARHEN

LHDGSDGDESHSNTTCSEDEGEKDNEPRNYQENDKCRSNDNANIFSNAVYRVMAGPLVDR

VRHRLSIDIATEGSVCVTFVVEGLKFSRKVRFVVKKSWTLKTLFDNIRRMLHVQSIER

>contig26151 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56555.1|) 1e-76

MLLFVEKQIPGMVESNVASLRINDDDDLLLSPDQADDFQMSWKDRSNVIEPSTLRFPTCI

VWSPIPILTWFLPFIGHMGLADSKGTIFDFAGPYTINRDNFTFGTATRYLQCIVEPENAD

KWDEAIAVGCKIYEKRMHNLCCDNCHSHVAVCLEQMNYAGRKRWNMVELCWWMFFCGKYV

SVAGFIKSWLPFIVVLALITIVRSSA

>contig26519 Frame-0F

MATFRYMAVIFVAKAFQSVANEYFEGDGTSYTLGQISSGNCNFMSAVPSAKTNYVALNQA

QWDNLGGCGRCLEVSCIDKRCKVQNKTAVVQVLDRCPECAFGALDLSPTVYKEITGMDPN

RLRMRWKFVECPNPGTLQVCLKDGSNPNWMAVQPANGLVGVQSVTVNGATTSMLDGAYYY

VSSKTGANLAAVEVSVTSIQGEKISGTYSLAAGKCTDTATQFGSSSVQRNPTLTSATPIQ

SITEPYDDIIGGESDSSFSSESSQITNTSTTDSTSQMEQTSPSSDTITQTINVLPSPSTN

TPASPATNTPEAPHTISGETNATTTAPTNTLQDTGAALKDTGATPTDIRAVVLPAFDATD

APSKAPTKLGVATSKCRVKTGNNKSVFRRL

>contig26623 Frame-1F

MTINERLKLDDTEKTKDVIVSPGKRALTFGGSWIMGHDKSIYPRETSSTLLCNVETDEES

EFEEFQFPFSSVSHLNEEKEDVGAVAESPRREKEEEDLERRKNEEKAERDRRNDEEAWLF

LSGSISRAKAEALLRNREQGTFLLRRKDSQTLILSYVGSDHAHHVLIEYSNQKYHIGSSK

ASLATSFTTLWKCLRSVRRYAYHGLVFNRNVDFSVVNKQELMLEDESFKLNSVIDVLNPS

APPTTSSVWHTRSRSGSSSSSGNRSSGSSRHSSPTPATRRARHKPSMQVNQEQVKIPPQT

RIDELSVEFYAHLASRLSYLAAQQKARTPEQDSDVSRCYAYEAITPLLEMAKQEKIELVQ

KRSHKADTQWRQLVKNIDAWNRVITN

>contig28063 Frame-0R|Blast-peptidyl-prolyl cis-trans isomerase 1 [Phytophthora infestans T30-4](gb|EEY61398.1|) 5e-99

MLMKLLLRPAQSAARKQRSGAPIALFSTARDQNPNVFFDVSIDGKPSGRLVFELRADIVP

KTAENFRQLCTGEAGVGQSGKALHYKGSSFHRIIPNFMCQGGDFTKGNGTGGESIYGEKF

ADEKFELKHEGAGILSMANAGPNTNGSQFFLTTVDCPWLDKAHVVFGKVTKGHDVLQKME

KEGSQSGATRVAVVIDDCGELKN

>contig28247 Frame-2F

MLRSIRRYVSHSRGCLLLFALRVIELVTL

>contig28485 Frame-0F|Blast-serine protease, putative [Phytophthora infestans T30-4](gb|EEY67871.1|) 2e-51

MRVTWGLWLSTGLFGCCFAALEDAEGLVFVDAAALCAFHCSHALLSPASQCSPELCGRRR

RTLEASDTSENPQQIDVLSCRNIEQNASTLAFSMTLSAADSAQVFEGFHHAFFEAYDAML

GGDSVTADACQLAFLQDKMLPTVEDD

>contig28548 Frame-2F

MRLLTSYSHQKTGLMYTQKENRRVTAYQYDLCVFIVHLR

>contig28694 Frame-1R

MHCCMPILVVSAYIALACVSNAELNAVDRRIPQSRALAILAETTTGKKSLRTENTSTSVT

EPRGLFDTIKQLWTRFCKWLASFMPAAEKVHMSPKAEFNGRPELSQSESNVVLDPTAKLE

KTRQDGPGTDTMPDTTKIKKSSSNKKKKSFFSFMKSSKRPRKSEKAQALKMQPG

>contig28889 Frame-2R

MIMRAVKRRVSARRLHASGLRMLSNEATPSEASPAKLEAVKKSEEDMGHLAGVPISQATE

AMRLKFFEFSKELQDQHFPEDLGRRMDNTFDLVGHRHIMLRDTVLQIISVLKSWDTVKSE

SVGAYLIDGERGTGKSFALHHIVQFARETNWVVLYIPNPRSWTHEAPYVMLSPYQQGKFD

IDVYGVDLLQKFLHCHGEQIKSIPLRGEYSDRYYQTDKHESKPKNAEDCKGAALTLYDIV

IGGIRDEELACQAVCDLKEELAQTTEFNVLIAVDDYNAWFQSTVFGYEGVDVGPDDISVI

SSLKDIGAKGYNESRKLKNGLFVAAVTENFPTKVHFKKQVDYRKIRATMRPYTAEELATV

ISYYNQVNFLHGMPTESELAYFRLMTKSLPLNVFDRASFS

>contig29459 Frame-2F|Blast-DNA repair and recombination protein radA, putative [Phytophthora infestans T30-4](gb|EEY68784.1|) 9e-34

MDLVIKLGMLFADPDQGPFRALIIDSVTALFRTDFSGREELTERQQRLNQHLVRLVKHA

>contig30835 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY59859.1|) 0.0

MPESTPTKYSEADTPQIGSTFDDANKAAARLIKPKAILYTTALLSWMQPFQSGWSTSQMN

LSQFHDTDECNARPVAEGTCLMFPGHTKLQWTFAVNTWIFGAMMGSLCCGHFSDRLGRKK

TLMMNCIFMIAGGLIQAIVSNIWLFSLGRFIAGIASGTATATIGGYINELSPPHMRNTLG

LGLQIFTTIGILGPAIGFFFLNTSTGWRYVAAFPVGLAGFYLILAPTMCIESPAWLLNQG

RRQEAKEVIARLYGEEHVQLALSWLEVSVKAENAEEGYAAPKQESMFSRRYRMQLLTGIL

LSCSQQLSGINAVFYYSGSIFSDAGISDSRVGTLIIDIINIWPAFFTGVLANRFGARTMI

LWGQIGMITMAIGMTVAFVADVSALSIVFTALYVVVFGMTLGPLVWVMTADIFPDSIRAS

ASSFCIGINWLCNLIVGVSYPYVSDALKDYAYVPFVALLAVFYLLSLKMVPETTGKSAEE

IQAEYDSRREK

>contig30880 Frame-0F

MDEKSSNAVGVTLFPADYEAVEMVTDQGKEILQREFLEAQLSLHSIRELERVRVERIKKK

RKTKVAAAEQDNEIETENADELIVTADKQKDAKEDVNEENDIIDPRIYYRPMVSELQAAT

AEL

>contig31920 Frame-1R

MVRIYVAALTVVLAFSASCSATSPLTLAKATPVTANGSGGRAQGRLRAHTTTNVEIDERS

ISDVIYAIARQVADHRSNLVQAPKRTYTTYLATLDLSLDKVLEQNWSELRLLYVKQTKRK

RPKDFVSMYELLVKKYGLLKLTDMMKKPDYISLSETDNFKYLYDEASVYWRKNSVLKQYA

SELYDSKGNSKTFDVTDFESLQPFFERIGRRGDYLEITAAEHEKWKTNKLRPT

>contig31995 Frame-0F

MSPNGGDVYTVNLHPSETHLVTGGYDQSVRLWDIATGAIVKTFHGHFASVCDAQFNRHAN

FIVSGSKDGSIRMWDILSGLCVHTLRQTLGEVTSISMASNGFALLSGSRNNSNRLWDLRM

LNTPRAHLSTGPTRGVSTSGSSGSLGSYTNKGNNRGSFSASGIGLSQGAGYGSSGNFSTN

GGLNSGSSIYSGSRNAEHRPLQRFKGHQNTAKNIVRASFGPRESFVLGGSEDGFVYVWEE

ATGKLLERLSGHCGVTYNAHWHEKQALLASSSHDGTVKTWWWRDKACQA

>contig32455 Frame-1R

MVMPCVQNLGRRRVVINCVPYSRAIALELDLERALRFPEFLHWPAVFVGSADIISVVFTG

IDHVLQRLVRSFTKALRTKLYKAKLFDLGVLKHGLFRRLD

>contig32864 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57924.1|) 3e-78

MATSNCFEHDDNQDTMYRGKPPPVPKVRAISSTDRLLKPTKASLAGSRKKVLTGKEKELV

EARDVALKRRRLARVAKENGRLTIPHSPKFHKLSKVTTRSRADMLTRTSRELLEIAAIRK

RVQAQKRKTRKYHDATTHGAATGKSDQFSQALSASGGVGVPAVRRPKLTTPKGFELEIDK

RAAAAEARKSGKRKYVVANPMKKEDNPSEEGKAADAKEQSLKQQRKSAAT

>contig32983 Frame-0F

MKNAFVSATALIAAAAYSSAADCDISTIEGLLSPKTMKGLADCGNATGINIFSVAEFPTL

DQVETLSENVKCSNSFNQINQVANTEIQCNITIEGVSINFGGLISSFLSGKTGNESDSGS

GSIQIQLDDSMGSSLDYFASKSNSTSASSSSGSTVASPSQVLTFIAYGIAIAVGMCL

>contig33258 Frame-0R

MADGRSSPVLEPGADLKHLESLLDDQNQKKRSKSKAPYEGKLEGWSPLEDAVETLSLNDT

IKPLTKAERKKHAAEAFAKAGGIPKREKRSKAERRAHQEAQQQKNESIKFKKIEVIGMST

LMPTNARLQYDDAKKMARRLKAAVVVRTQAQKQVEMFSHLPQYERESSLSLNVGFSTKED

VHAAVLALGLKYAEGRIVGSNARCIAMIQAFTQVIDDYVTPPETQLRRDLDKRLRPLIQY

LIDCRPHGIGMGNAIRWLRRVIGSTPSELSDEDAKRRIRDEMDEYVQSRILLASRAIVKN

LRTIVSPGDVLLTYARSNAVEALLLEIATASHELIATLRVIVVDSRPHYEGRKLVNVLAR

AGLQCTYLQIHALSYIMREVTKVFLGAAAFMSNGVAVARVGTALVAMTAHEANVPVLFCC

ETYKFSDRVQLDAITHNELGDSDELVSSYCIDKRRRTTNTTSRGHVLSDWRDLADLKLLN

LVYDVTPIEYVSMVVTELGMIPPTSIPAVLREYSRDGVVDGMLSRVQHV

>contig33342 Frame-2R|Blast-dolichyldiphosphatase, putative [Phytophthora infestans T30-4](gb|EEY56452.1|) 8e-85

MELAKTVQEFELTWVVYDPMDPFGALLALCTLFPIFLMIVYFTAITLRRDLDSISMLIGQ

LVSVVINKVVKKLINQPRPIGAYMSGPGMPSAHSQFMGFFATYSVVYTAKRLNERRHLEQ

WITICGVIFMAVLTCYSRIHLKYHSIDQVVVGAFFGILIGIFWYALVARISPKLFPLVTE

TRFARFFYMRDISHIQDLTVHQYDVCCKSYKKLQKLQCTIHVSNKEQ

>contig33401 Frame-0R|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY58730.1|) 1e-44

MDITDTNVKVFCRVRPPNERECGNLNLSSSNGPVNSKTRANVNASFAKKCVAVPVSDALQ

QTLFLHSKHGPSKTFTFDRVFDENSNQNDVFEVVGAPITRACLEGYNGTIFAYGQTGSGK

TFSMQGPDDFIDTNAH

>contig33508 Frame-1R

MSGLIIGIVVGIVVLCVIGYIVYINTKSQHQNHEKSFMHDFLPSKVTTSEPTYVSEMNVQ

DTPSEYDFTTLNAQSTKVTSDPLASSIAMLHALPSTSPSVEPKRYNFDPAQSTVNGAAPS

TSPFNKRLSIDASRPSHSNFDAHSMEFNAAPGSYAESYTESYAGSFVGSIAESYANSFSG

TYDKQGVLNSFDLSVDDLERDTVGTTVSEALDRQTEAPIGDQEQSHWMDDMRGTNDSYAM

LESGSFDRTSALSRFSTDSDLNGRPTT

>contig33823 Frame-2F

MMYMLTVTVASYLAQKIWTKRNLLTAGWYTEEQSELEQSMILAFEYIGFMGIVFVVGTAT

GVISSKMTKMVNSMASSTRC

>contig34174 Frame-2R

MEIYFGILSTCIYATFAFRSKVNCVFTLKD

>contig34527 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67783.1|) 0.0

MALALALLSHVDDTNVELLYRVTKPYILDDADASMQKRSYAALVAICDSHPKFLSEKSQL

QDLTRAICESLLTCSVPAKKMRLRVLAHLIRALQGQSANDGLAEKELIPNLVGEIMLCTK

EANGKAREAAFELLVAMAMLLRARDPQNGLMEFIKMVLGGLAAHTPHMRSAAVICLSRLV

FEFGREDSAIAQAMPELLKTVLMLLHEKAREVIKSVIGFMKLGIAVLPKDQLRQFLPDII

NGLLVWIGESKNRFRAKTRIILIKLCRKFGCEHVAALVPEEDRALIRHIKKTKEREDKKK

SELMADAAKRRTAKKDRHAFEEFMADSDEEVEDDEAAAMQVLKRKKNLHRKGKDGKIIHE

KEDDIVDFLEDNAAVKNIFSAFRGKDDDASSDDDFKMSKDGRLIIPGDDDDNMDDGGNEN

NDGNKLKRDVVSQLERMGIHHNKSKASNGQLKRTRDDDGSNGREYRAKKAGGDVKRKNKL

EPYAYIPLDPKLMAKRNKRKAVTRYGGSVGKRRGKK

>contig35241 Frame-2F

MDTVSTCFQDAVQFLVLVAQATGKLGKRGIPDRQAAARIVLQDWNRGKLPYFTAPPDQSV

QVLDTQLVSAFGHPLNVDDELLNPTSIFVPDTDVEHERKRGPQCSLPIQLSEELDGTKAT

KTAKTPVSARIMEMQDESDSEMDSEPENDSAAIDDVVVSTLTTHELGMKLAQDALNPFTA

MAARRK

>contig35326 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY59728.1|) 0.0 NOT\_ORF

MNRVENEGGAKVIDSLINYETVTYFSNKEHEAARYDKLLQGYQKAALKTQTSLAMLNAGQ

NGIFSVGLTAIMYMACEGIAAGSLTVGDLVLVNGLLFQLSIPLNFIGSIYREVRQSVTDM

ESMFQLGAVTPIITDPSTSLTLKGKGPKSIEFRDVSFGYRPELPILQKASFKIDAGKRVA

IVGTSGSGKSTVLRLLYRFYDPQNGLILIDGKDIRQLKLDDLRRALAIVPQDTILFNDTI

SYNINYGRLDATSDEVVNAARVSQIHRPIETFPEGYNTRVGERGLKLSGGEKQRVSIARA

ILKDSPIFLFDEATSALDSETEYEIVREFASIGANRT

>contig35559 Frame-0F|Blast-calpain-like protease [Phytophthora infestans T30-4](gb|EEY64790.1|) 9e-90

MIAGGGVNPLVVKQDIVTDCSFVASLCIAAAYEQRFKKRLITNIMFPADKRTKQLVYNPY

GKYVVKLWANGVPRKVVIDDLLPVSAISGQLLSSCTTRKNELWVSLIEKAYLKLNGGYDF

PGGNSGIDLFALTGWIPESILISELYDAPSKEERLWKQLQSAFHFGDCIITMSTGDI

>contig35634 Frame-1F

MIDEEEDESDVSIIMEDRSDDDCVTYSDKITEDEEELARGIDNAEEAQLAKKYQLDLSEE

DAILLAIQMSIESTKAAHTAASDAADSGTLVDIKSKTNNNNHADTTSALPSTITTVSCGA

RPSSSNESAVLDSQTSKALTIKKALPVAAKGKRKPKQFSNTDSEVEIVAKRHSSTNQGDE

QILNKPIEVIQTAAYDTKTTERSSITSKKVGPLPQQEKMTISGHQSECQGKASEAEACQA

VKEQMMADKLTAVSAMTDEAQELAVHLENTKSKAEATTTKHKYPATVPRGGHNSQSDTMS

TESYEDKEPVSATAGVLNETSQTEQENVTTTEDRRVLSNLALALEDSQSTYRKDGNEDVV

EEIEP

>contig37467 Frame-0R

MLHSVESANRLNEVVSHYMTLFGRFAVAYNVRQLHESLRHLKKAPRHSFPSFFFKYRQTF

>contig37786 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58401.1|) 8e-64

MVPDFCTLQRTDDDNDNEDITVNCWFGPRDTVSPLHYDPKDNLLCQVIGLKYIRLYAPEE

SDKLYPVAGLLANTSSVHVETPDDVCFPKFRSARYVECVLREGEMLFIPPKYWHYVKSLS

TSFSVSFWWS

>contig38453 Frame-1F

MTEDMVPEKLSRRTLALAKQQQVEEQTQLNKSKMQTSKLKQESDYSDESEDENMDEYDGQ

DLVRINGDYVEEVEICEDDEEALANFMIGAPERRNLADIIMEKISEKEAHERGETNETPQ

SNKFDPKIVEVYTGVGKILHRYTSGKLPKAFKVIPSLSYWEDILWLTNPAKWSPHAMYAA

TRLFASNLNPKMAQRFFNIFLLEHVRQDIHENKRLNFHLYMALKKALYKPQAFFKGIILP

LCESRNCTQREAAIIGSVLSKISVPVIHSAATLMKLSSMEYSGGNSMFIRVLLNKKYSLP

>contig38642 Frame-0F

MVQSFYLIALSVLVGMADLGASKKSNQAPNFLRENSSAQVRSAEDDDERAILNLPGRFYD

SLATATAVKELVAKRKNMKQVLEFLQIPLAATAEELVRHSNFEVFMLYCQMKMPKIFKNG

NPYGVLIKKGEPIYFSEEEFNGNLYFWLAEGYS

>contig39524 Frame-2F|Blast-leucyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY66974.1|) 1e-54

MVLGRTHKSSRSLRPLASSDYDEIIRDNHKVLVEKNTGVPVLTVWEKMSKSKKNGVDPEL

IRAHFGADVTRLAVLFKAPPAHELEWV

>contig39740 Frame-0F|Blast-dicarboxylate/amino acid:cation (Na or H ) symporter (DAACS) family protein [Phytophthora infestans T30-4](gb|EEY64697.1|) 1e-83

MPCFLTECDPMEEAKRFGLSIALLYAFHFLVDTLVIRPIVRYTVRNGWLSTDKEDKMRES

LYKNAAVGSLHIFGLYFCWNESWFLNKDEYFTDFPYVINEAQRWYYMIYLSYWIQSIDFM

LQITSNRYTIKRKDNAEMLVHHFATISLMLFSYSVDLTKIGICVLMIHDVNDLLLETAKM

FVYLQWETVANIFFGLFALVWYVVRWFFYSYNILHSSYAYAYRDIVASIMEAGSYHGINA

PVWFWTYVVFFGFLCLLLVLHVYWGVLIFKMAMKALGDGNVEKDIRSDSEDEEGSEEPQR

PAGEPAVGDVSKPRRRRAPKVE

>contig40155 Frame-2R

MTFKQLWPKTQCCFDTHFTSIESFLIANRKMPEPYNFSKRYWLACESGMTERLMTNFHPY

LTQVLLPPSRKVVGHVCESYSASFLYIYNT

>contig40850 Frame-0F

MTKRSRYGRRSGGRGQKKSRADGTRDDWRVDKFAEWVYENENFDAYYKAQNIMSDSDWPA

FKKALATPLPTTFRINSSCLFAERIREHIDQDFKFDTLVLENEPVEPIRAMSWYPDNRGF

TWSVERRRVRKLPILKEFQTWLVGLSTSGSITRQEAVSMIPPLVLGVKSHHKVLDMCAAP

GSKTSQLLESLHSQELATGQTPTGLVVANDVDLKRAYMLVHQSKRISSPALVVTCHEAQN

FP

>contig41174 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61405.1|) 1e-59

MIDNLKATYGQLLEENPNGKKLALAEEAVTKLCGKKLGAVDDKLCYNLEPLKKDVARQVT

FKKESFKICKSLEKMNPDFCSMRYPVKTDANTDYSKMRVKQLRKILGERGIECVGCVEKS

DFIAKIKESEAQFSDEL

>contig41831 Frame-2R

MKHAIVAHLKRIQEFYGEALLGISRNIEQEVAIISRRLYETVASLRQTNVFERVRARLGL

ADDVFDAYRERVLTYSPRMLIKQRPGCMVTHSL

>contig42045 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64889.1|) 1e-74

MDSLERKKAELLYDNEALSKRYDTLQHRLESLTSQYKKAVQLFLAQKNLMGDNEALEKLA

SAPIDDFYPTPFNMATKKNITQHIAASMEALDNKLKQLKHVICNELPSAEARSDKEVINR

LHQKLVNAHAIIKEQDQLIQASLSTPALTSHIDIENSHWRTETNWKGLKKISAVDAITSR

SSLDAAADEDIEQQKTELALSRHNLEKERKLLQEQAFKLDKDRLDFEIAKRDDLYGVERK

GVNMPSFREPISLTSSESADFLTPKRQRRKKRLDSDVGNSPFDLPISATPVTAALLKKIG

INVPTKP

>contig42203 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68638.1|) 1e-134

MFDACMAKIAAWGEDSRNQLAQRVKQSTATWKIVNSHYSPFNHYVEPGMHKWFNVLRGSG

VQVWLNGHTHGEKHDYSSSLRMHFIENGAGGGIQREGASGIPAYALPFVKTQWTYGGNEY

GFMSLQASKKWLKLQYHTADRSWQFGEDFQRTKIGGVETKHCWYIPVTGG

>contig42988 Frame-2R

MKNGKKHKKHHSQKNERKNLTANDIDETVQSTEALTKGPIESRKASECCSNQVQWNEPAA

ESPLLAERKPIDFKRKIYIAPLTTVGNLPFRRLLKQTGADITCGEMAMATNLLKAQQSEW

ALLRRHTSEDVFGVQIAGSFSDQIARVCELLARETDIDFVDINMGCPIDIVCRAGAGSAL

MTRPPRLLEVVSGALTGLELGTRMRTGGL

>contig43262 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58146.1|) 2e-08

MLACAMTNTLSSVPSRRLHINPQYQQVHKGPYTLVKELGSGLHGRVYLAYDERLQ

>contig43914 Frame-0F

MVTEEEEEEEINLQPAMDENVDVQTTQEDMDEDEAVHEISELEVVAPKEAEIQTQRSHEP

QLEKQKDLMQDDKELLDVPEHSVTRTASCFVSPKNQLSTPRRSDSKQKPLNSRSPSRDSR

SDSRERSPGFTRQSRKRGEKRVFLPGPSHQSKLLRISTSQRRRKSTSPSPHDSALTIINQ

KKTITLEEFEQLQKQLHDMVETTPQTQLAMTQAALANGLEHPFTRGFPGPTSFPGYVPGS

YSNHGAMVVHDENQSSDGTLQNEAIFGKRHRNQENGPILFPSSALRGQLTREQRLMRKPR

PSRLLTGAKRD

>contig44128 Frame-0R

MNEEQGSVAPGWMQEQAAEYQDLVGSFVDSVVDSDTDEIIEYQLIWEGGDLGVALTTIEG

GNGGVAVSRVTGKGFPFGIKNVGPGDLLLSINMKVTTKMTLDDVVAYLQVCDLPATLRFK

KLSPTTDQVPISVPRKSTYVITSDNGPTSPMGSQPPASYPRGSTKAVPPTSVPADPDRSS

MPVHEVPSEFSEPPAAPQRQSAKVPVNQQVVKSPPRPQSMPISEPVVYTDKHEEHLPTAA

APKPLKQKLAMPQEEMPSELDDLVLTSGVNDLGFDDSEDESVRLSSESRDSWRDESFDVD

MKHEEEKDNAMLEETQNDKKISQQQTLRESDSRVAMLKHLSSNPKKNAKTVLPDADEATS

VAVVDNESDFMPENHQSSPLAGSKVRPSDLSSSTVSSLSSSMNNTDGPRPSVRVTMDSTA

PMLKSHAIGTMHEMCAKGNLRGVVQYLRVEGPEALINREPNHGQTGLHLAVKSGKVSLVK

VILEQYSPIEDIINVEDDKGNTALHFAATKTPAMVHLLLENGASA

>contig44379 Frame-0F

MHVHGQQSVFGFQINTQGHGAFMVLVDSIDTRLTWLTEILVCVTNANALLPKQRLSLLSD

DAPKKRLSTATSSLSSLRSNKEEMKELVVEFYRNLFGPNLKFSSPQDAPASFWMEEKIDP

VSDDCVLSSNLPDCVPYWGEFHGYKRLCDYWKIRDETGERSSGRVLRILVDEDEETAVVM

TSTTFRILRNSEIVTEESCDLVSVSGGNIVSIHCTFDSHRIAQAFKREGISAS

>contig44429 Frame-1R

MKYELHDLVAQRRDEISIHQTKYCGDVLKRYGLTQAHACRILLELNARLYSGEASREETN

LLELDYRAAIERLMDLAIST

>contig44775 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62396.1|) 1e-103

MAMAKKNALLNLYLWAFNCVSCVGWAYVLYLTVKTGFHAHDAGQDWNQVAQSTWLVVSLP

LKIVQTLAVMEIVHAAAGFVRSPVISTLMQVSSRLWLVWGINVLCPVSRYQFGFPLMVAS

WGLVEVPRYAFYALNLYNAVPAALFYLRYHLFMVLYPSGVLGEVLCMVSSLSYLSKGAYS

IQLPNTHNVSISLFVVVILVLLVYIPGLPIMYTHMLTQRNR

>contig44995 Frame-0F|Blast-CorA Metal Ion Transporter (MIT) Family [Phytophthora infestans T30-4](gb|EEY64528.1|) 1e-31

MLLRWATSRRSLVFLSPVTASKNAPPCTTLNHSCHYLNRLTCRSFKSLTPDKPLSVSPTV

HGKDLLSLVSRARDSHPLDWSEGVSSVEDVDQWDLMDPHYDLTTAKLTKLFSLFQPNGIK

>contig45592 Frame-0F

MDRVERDDYGSDSYRRERHVVSLT

>contig45835 Frame-2F

MQQDKQIREHTTSSRASLLRRSRSASRGRHHRRSSRDNVKSSRESKSLSKESTATSERPK

KQEERHESTVKDVNLDQIAAPAIDLDFLAEPMEEEDMASDNEAPMTPAKLERKKSDESMK

DKELKVDDKQFSRSADGNLKKNDGKRNDSRSSSRRHDTTSNRSNRERDHVYDCKRERDRV

RDRDRERDHVYDCKRERDRVRDRDRERERNRARNRDRERSPALEKKVVSSSRSCRSRSRS

RSRREASKESFRRRADDKSSLLKAKDRRNGEDRYRERERRGRDRRRDRDRNRTRDRDDMR

NKDRLRDHDKDTNKGIAKSYERNHGNARDEAHEKVHEKTSVEAHPTTRDKIRDKAHEKSS

DEAHNTAHGGAHEKASDKSPGTAHEKTFDKSRDKIRGNSHGKSYDRANDKAYDKTRDHKP

RDDKVHDVNTHDKAYNDRHDGNAYHKAHDKSYEKSQDKTYKSREKPLEKTRDKGHEGKNS

DKTYDKAHKIPQERSRETYNDKGAEKAQERRDRPRDRKERERKRTSDAVDGKPVAGNERK

RRRSAEKERERRG

>contig45880 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70446.1|) 7e-07

MWAADEKVDRWSDLGLDQWVKDTA

>contig46153 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56554.1|) 1e-36

MERQDALYCTFCGDQQPSDRLAAHFQECASATFHKRQKSPLYRSFERALVVMSEDATLRA

LHYASSFPDPTPHPR

>contig46258 Frame-0F

MNKTHQAAQLSRAFTILRTGINVMRTASSYAAFRAKGLLVHPALRPALMCLIVLAFVFVA

LMSLERLDLWMTGAGLFMVVTSIISAVQEFNAPKLAQSYQDFLDENLKRCGSDNVTLPHL

SPVTCSTVNLKQQNTQVDIFSRFDASPSIINLVASTAAPNSSFEPAKNSRGASEYSIGAL

ESAVNTTTDNNMSPHVKSMTGVGDKKLDVLHCGTVIDLQGSRGFIIPHNLCLDAMVTSVA

VSSDVANRSHPKKRLKMPLVVPFNLNEEEPALRQDIAVGKTVEFAYSETAMNSKSTKVIR

ALNVTPIPTDDGIIKSRSALQSCKQAREVSFARAMEELTMISPRNIPVKHRIDLIKYAEE

LDDHDDHNNH

>contig46401 Frame-2F

MSKTAPGRGCKRADWVEWLYA

>contig47334 Frame-0F

MKDSHNCTPPQLLQCLRLDISNVATSLDGNENKSGNRFESYVVQISV

>contig47626 Frame-0R

MVKLPTAKRTLRTVKLQNSNDSVQRISTLVVSLIQCSAASQEIGFAEMLSESDTFAEGKC

MVTIDKFKIALEDTKNDARIFVRKLLKACWKKIDDRDNRVVLDNFVEDL

>contig47983 Frame-2R

MESRLLNTANGGDESTATTLRLERNLLPLCLPRDVVRQKDLSGIYEDLRRISHDFQSVDA

DISSLAKQSDTRGSQQEQHFEAR

>contig48043 Frame-1R

MGRNRMDCVLVVSDEGMLTGIVTDTDLTRRVVAGNRPLDSTVVGDVMTRHPVFVSMDDPA

IDALISMLQGKFRHLPVVERNGPVVGILSIAKCLYDAIRKMEKSEQSSMALRHTLEKEMK

SRVNGHARTGNVSQLLGSMVNKMFSPDIKTVIEDEGVEAPHVQRFTSVYDVAKLMASSKK

GALVVNTRGYYCGIFTPKEMLEKVLARGLPVHTTPVCEVMLDKDVSITGAMSVMDAMHTM

HDHKTLYLAVLETETSKQPPLGLIDVLSLSYGSFAKGKPSEWKAFWNASLEVADDDDVSS

QHSFRSGFSHSLASSSTSFNMKGRQATFATGNVRPVSKLRPCKAVTIPETFSVADAAKEM

SLTQTDAALIIGRDGGLLGILTDTDVTRRVVALGNDPVYVRVLDAMTPNPKFVDERDSAM

DAMFMMLEGKFRHLPVVDETGMVAGMLRIQKCLYDAITRIEKVQQSSSGSLRQRLEKQLH

ATGIGTGPGALKQLVGPMVEKLLSPTVDTILEDETLPPLVSEHDTVMEVARQMAASRKAA

LIVEDPMNDTSSSVSGGHRSSVSGGCYDIGTSALTRRVLGVFTPKDLLLRVIGAGLDAAE

TTVGQVMTPNPETAPPTTKLIEALHIMYEQKFLHLPVVNSETATIVGMLDVLSLCYGTFA

SGAAAVDEDSDWRSFWDVSLALGHDDDFSELASLTGSRVSRRRPGKYTESHHSSMRE

>contig48331 Frame-0R

MTLADIAVNVNALRCITYTRVGHNVNHTQVV

>contig48418 Frame-2F

MSPSHHELKGLEIGDKIGEGVAVVYLGKWRGANVAVKMKAVLAALESAADLEEFQHACNV

EIQAEAEVMRGLCHPNIVLFMEAGFYRGSICIISEYCARGSLRDVLKQHTPDVKNLNWPT

KLRLALGISHGIQYLHNANPPMIHRDLKSPNVLVDDSWHAKIADFGTLRFSEIVSSAAQL

QASQINPKSAANVPVVEMTGLVGTTRWMAPEVMRGERIYTSKVDIYSLALILWELIEGTL

PFENTRWNHEVEDFVLNGDRPTIRADLCPLRWKLLIVMCWQPDPQERPTIQQVIQSLQRI

GREEVWDPTGPRFTGVSQLGVSMYSTMSQSISSSYHDSPTNAGPIGRNFSRPPAALDENH

SASDSDSEAFAEEFSYVPTLESSTTSPVILG

>contig48713 Frame-1F

MGTPSACDECGKKFKVFGIKKKCKDCMDVVCKSCLASHLELKHAPSNRSRRSIMSREFVD

TDSHSDRDLEFMSPVGTSELELEYADLKLSADGIDASDEEEDDFAEHEEDEVFITTLSRH

SSLEEEKLKSRELYKIQAAVATWASKEKQAKLDLRRFKRERYCCMNPAATDVGDYENCDV

FAICYVVITTVVVWILWGTLV

>contig49336 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55527.1|) 1e-102

MNIGTKPQNGDERPSRQKSDFLNLFWTLAENDRNVRMQAVMQLLDHLKNSAKQESEVQYA

LKRLVRGLASSRDAARQGFSTALSGLLAMFPKQIALQRTHELLRDAMEVHSSMKPMEQRE

HMFGRLFGLLALYRSGRLQMDVPLLVTIIKELLEMATFKRWFRETCYEAALTLLADVPTD

QFVTELAALIQTCLQIQPLKSKEEESSGAWNADQVLLAVGVQRYMHVTKLDLDENKMQQL

PANFAAIGALKRRHVHTLIRP

>contig49488 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62605.1|) 3e-45

MSKLNEYVSVLVTELAKKEFMDKQLQQANEQLKLTGQLLRELASAQREIRELRRANYMQT

ILRRNSFVPTKLVYNSRMGSAGDHESMDSMSASDEPPSLLKARSNCFSALSDSTLLRLFS

FLDEESMVAMSVIDKVLVTRVNVLFGVITPTDMPNRSFPAQIKQRPASPHGR

>contig49615 Frame-2F

MLGVQTHSFSLAIINQSFDSLFFNVVTSNARRSEQIGKLASSILALLCRIRASNDRTPLW

QTASTVRFRSFRRTDILPSFISCDWTGIIATYIPKDTSWPRRPLSIFVKH

>contig49912 Frame-1F|Blast-DNA-directed RNA polymerase I subunit RPA1, putative [Phytophthora infestans T30-4](gb|EEY66296.1|) 4e-95

MMGKRVNYAARSVISPDPYISTSQIGVPLRFAKTLTYPQPVTPWNVEEMRQLVINGPDMH

PGANFVESESGRLIDLSKRTPHQREAISKTLLTRSASALGTSKNRVKRVWRHLKTGDVVL

MNRQPTLHKPSIMAHTTRVLTNPNMQTIRMHYANCNTFNAD

>contig50091 Frame-1F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY57665.1|) 6e-54

MAQPEVLRSLLDGQRPFAECEFGLDLRLSKAVAKMRFVHATLVQVHCIPLALQGKDLLVR

ARTGSGKTAAFALPLLHKILQQKKDTPVCEPAVRALVLVPTKELVEQTRHYIMELMYYCQ

DT

>contig50356 Frame-0F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY56121.1|) 1e-06

MARLGATCVALDASKRPSATHVSAELHKLLQQFDR

>contig50464 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67786.1|) 7e-86

MISRAQQMVNDSRSKDDVTSTLKKNVKELHNLANESRDAALRLESKDVDNFKASAQSWFA

DKLMVGQSVLMAFIEGYRSGKMLEMEREDALLVTFVKQAAEDHKDIIENQMKFFLEQQQD

KQIEEPMDAPRTGHSVVSVTVNLAQDTTTTSVRQITKSCVMKEHDEQVAVTEEKKS

>contig50583 Frame-1R

MCTQSQHLRSNSYFLTPFRPLAITHEYYPIRLDASSCFSLPPMHQCEM

>contig50600 Frame-0F

MNRYAPEVNTHMEVLRRFLFAEWAVKTPEQVYDLLRFDAKAHDFLKNPLLNLYMTYLDQY

HFGNYEIVRDKLMEA

>contig51108 Frame-0F

MNMWPLMANNIKCYSFCLNLDACASPKHAAGIKRCRSFKDGFIRVDCYAPH

>contig51553 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65824.1|) 5e-90

MKKTVGTQGCRRNSRHVFWEHQFRTMLRAHTSKVIAGNAAAPPKHQRLFENVVEILKVHG

REICQENCKLILSLGRLQRLEVHHPEQQNMCWKTMRQLIHEHLYLRELGFFHGKINDYQM

GQIRDTLMRSNFALSPKLTCHGITTLELVSVKIRHEGFCQLVSLVANMSQLLQLRLSNVI

TDFETKLLIDAAFCAPRLERLFLEHNELEDDAFIGLSTLQAPLPLRHLRLRDNNLSFNTV

EAICNASLNKVLNLAHLEFTNNVQIGNLG

>contig51658 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57216.1|) 1e-39

MVLPRKNVAQGLLFLPPVLVSVLLFFVCGASGVSALSIGMLSSFAFCDVWYFLRMGFDTL

RPAPRGSRKHLFAVSRIKGRIGLMDIDRNGHCNNARFLRECGFGRRDLW

>contig51737 Frame-2R|Blast-PNS1-like protein [Phytophthora infestans T30-4](gb|EEY67718.1|) 1e-24

MLRIVGLSAFASAGMSFVWMAVIMLLAEVVIWVALITAVFLNIAIAFIFTKKGLQQRFLL

VLVA

>contig52224 Frame-0F

MVNSNVRRFLPIVSIRIRMLVKVHQILVTNTFHALLLRVLEQCLELETKCIGTGTRQLLF

ILYKW

>contig53065 Frame-2F

MDRQYSRCSLIPVSSVTATSKYEDCDYQQLTKLRSSEEQSDNWYRHALRSLNGKRKQRGY

EHNLKAQSADKLGLVATTPHAAWKEAPFDDDQEFVRLLSVAKDGDDSTWYRQALQHLKNE

RKDRASLGDCDSLASTDPIYE

>contig53111 Frame-0F

MACIDTMQEQYSHVVAIELDSSMDDVSFTKAQPAPLFHERVIYFRDVDSSDIPQVRALHE

EWFPIRYNQAFYEGAAHGLWMETSCPLFARLAVEMQPALELQT

>contig53469 Frame-1F|Blast-UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase, putative [Phytophthora infestans T30-4](gb|EEY58960.1|) 9e-16

MPWQRSLKRPLRFAGVGLHSGKDVAIKVLPAPQDAGIVFCTGAPRSYVPAQIANVEACQH

QFCT

>contig53735 Frame-1F|Blast-acyl-CoA synthetase, putative [Phytophthora infestans T30-4](gb|EEY63260.1|) 8e-15

MLHIFEKLLEHEGLIAVTSTTNNQTIEWTYADLLTRALTLCDSIQEKLPTNVEQPRVALL

GARGASYV

>contig54235 Frame-2F

MWQMWENFALCAMETKRYGEAMYAMHQLLDMRGKHKRPIDTEMLAWLVEAIVYPDSLKQM

QHGVELMKTAGSDDERDEMSDAEDLLELDEGAIAMDATPLRSDSHYKKQLAMLLGRITSI

VTNDPKVWQVYARFNDGVAGRADKARDCRLKQCRALQVAGWEREQRKVEGLCAAAIRLAD

DYLKEGTKKSLYSCRLYIRGVLKKAQVDFHELEVVKMLAAKLDDVNAREAQARD

>contig54280 Frame-0R

MIYYVIKIYQATFRKPSDERVMTGRDDRTADNRKAFSEFIR

>contig54565 Frame-0R

MATLSHTHFRHLDENKQAKVSPWILNVSSDVFLQFNMTDALIANLVAAERAWQWIANASD

GSREMAEFSTYWIRNNTG

>contig54697 Frame-1R

MEAQNCALQKAFAPTPAAALAISDEAKKREQLETERKLQHRVDVLMLQLEINQADVASKT

RELERCSERISKLESDLLALQMKSGETHAATVSSNFNASSKHQLLITKCRNDSIYEMSA

>contig55207 Frame-0R

MKEMTAEDVSRAASSRFIVAGNVNLRHGQLNNKFWKVIT

>contig55272 Frame-0R|Blast-DCN1-like protein [Phytophthora infestans T30-4](gb|EEY61633.1|) 2e-39

MLALSCAMDAATMGVYTQTEFRRGMHRLYCNTIQDLRAALPVLRTQLRNRAELATIYAFT

FGFAKDPT

>contig55399 Frame-0F

MTSKLQPCDQRIIRNLKACNRRCFNRMLLQDLDNGVGLPAKINIPHAIHVSLSIVHTETI

HNCFRHCNIRSEQADAAPVLKEQCFDNDVMVELKHQIGRFRYPNPMDIRNLLNYPAEKIT

SYIPDVYDIIEDYLPTQPRDEQDDSL

>contig55795 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66324.1|) 2e-24

MLGSLLIFLKVWDPAALQRSSTTSLSPLASSAIFPFPDSLLLPSSRTKLRLAYGFATE

>contig56549 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57892.1|) 1e-165

MTAEGMRAKRRTTYQNMHEIVKLAKKYSPKLVKGYSAGNISVVDKKSWLEVCDRKHRYGA

NLRAYYKEWKRQPMEPTKPSFWEWLDDESIEVAGVPRTKLERETVLYCDTVAERQQFALM

VQNGVIVHVASQQIVDTGPDGWIFVLRDQVLYGSQKETKKNPRIHHTSFVGGECVQTAGM

MVITDGVIKTIYPHSGHYRPSEYELLVLLRFLVNNGVDLSNVNVDVQRIQKVYRQSLNGT

LVKKLDNAHFWNAYRVWHYLESKHRAWKVGLFDELAETVGRNSLQHVALERSEILGDNVL

ENTTIESCELSFKDKESHPLLLLCPGYDALNFEAGARHFSTREL

>contig57102 Frame-0F

MSIQRLGSLLTLFLTCACASDWLGISPELQQKLTSVS

>contig57810 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY70002.1|) 1e-61

MGADSFGTGLLVLSAFPIASALYHSFSLSGRPYALHESDFVANKGVGLLRIETPAGLIDV

YVTHLVAN

>contig58068 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61362.1|) 8e-58

MEVEALEAIYMNDFTKLSDTPLAYQIHIVPNQDGDNNFVGLLLQAEIPKTYPDSEPKIEI

IVKKGLASGQIKEIKQLVERQIKENMGMAMIYTLSEAAREYLVENNREDNDGSEHQEMLR

RMELKKKLDDKVEADKLEQV

>contig58086 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY59728.1|) 2e-11

MDAMGETATALTGSFEVAVPLAVVIGYGLARFSASASSELANAVFATGILNLNFTLTSKN

W

>contig58121 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54775.1|) 4e-07

MISVRIEASVAVAPLGTRIVVLFYTVQVCLIDGFRAR

>contig59283 Frame-0R

MSRVSDSNLATRILNSASQRQLIN

>contig04013 Frame-2F|Blast-3-phosphoinositide-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58380.1|) 3e-78

METATPPGTVDGVVPVRANSKKPSPADFMFGATLGEGAYARVVHARMKETGVEYAVKIME

KRFIRKEKKVKFVMMERKVFSKISHDRVVKLFFTFQDHSYLYMVMELCRGGELLDVITKH

HKEQVAANRPDHACSLELSRYYIAEIVVALEYLHKNGVIHRDLKPE

>contig05748 Frame-0R

MATSFGDAYLMLALDLVALNLSKQVASRDDYKYVSRIVLLSFKVFIVVSMV

>contig08721 Frame-0F

MNIKDVHLNSSCDGVFPNTIQHKCSQLDFDKLRQKQPCRPRDFQQSQMCGLHELKDQEDL

LKRFFRLMNQLKS

>contig08956 Frame-0F|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY59699.1|) 4e-53

MSEGTKLVAVIGDEDTVTGFILAGIGHRTADGTNFLVVKPTTPISVIEASFRLLSSRDDI

AIILINQHVAEEIRHLLNTYEKTIPTVLEIPSKDLPYDPAKDYIMKRVNLMLGES

>contig09106 Frame-2F

MRLETKGLRLLLRMLLAKRRSRRTTMKSRIRKSQKRSSRTRMTSRKASKVNGYPTKTTVV

Q

>contig09191 Frame-2R

MLSFLGTIFRSKELHLEAAKNYRVHIQETREKSSSGRLFDSERKNKATRVFNYWCFNPGI

AFLEICANNVYNVILTSGTLSPLNSTVKELGIEFPVRLENSHVVDADQVWVGVVGTGVTG

KRLNSSYNFRSTEAYLLELGHTIVNFTRLVPHGLLVFFPSYSILEESLEKWRQPTAGESA

LSVWDRIGQLKQTFVEPRGRTEFKAVVDEYHRAVADNLKGAVFFAVCRGKVSEGIDFSND

KGRAVVITGLPFPPTKDPKIILKKTILDECVVPPGESKLTGNAWYIQQASRAVNQAIGRV

IRHRHDYGAIILLDERFALKQQQECLSKWLQPYYQICKGYGEAHIGLTRFFKTNKTRAVP

ELSKQLLRQTRPTGLSKSALTKLPIAQFDGESERSCQQLNSMHVSISSSQSAIGDGQSYV

NPILLQNPSVSSEILEKGNEKAEPKASIERLLKPKKRSLGALLMSTSKSTMVGMTSSIPR

PIKLPKMFVGDEDASASNIDDEPSWQRVKQQFAARKVLKEATSKEIYSKTLSAEFPVLAR

RVLKASDVSKLYKSIRHLHDEIEVDSALREICILLRDPGCKDLLDLMPMILNGNICDRFI

KEANNHGLQVSVVTKAQSSSAQARPTDLSTFFEQLQQNKRKTRRPVGAVVKDPQCSVCYD

ITRKAYASPQCGHICCRPCWKKMEENGLTTCPVCKFAIKLQDLSLIRAAKNAKGNAKKKE

>contig09928 Frame-0F

MRLIENLTARLGVVTNAKHPWFQVGKTQVFCLLEAHQALNIARSKALYQSVLTMQRYCLG

YTIRARYQRKRQSSVRIQSTWRKYVCWQWYQEVMCRKRAAVILQSQIRGRLTRQRLKRIV

AATVIQSFVRGWLVRREYSGNTLSFEHDVSYVGSLDERSTTASSDESDSISKDRKNTTIS

FESSVSTSEYSDESASLCSNSHVSMRKKGMDEYEPPTRIPNEYEVVWECGLLGLYFESDP

VSGMPIVRRVHESLSNCADIFEVSRGDVLLAVGKVKVKKGDIRRILTLLQEVQKPVRLHF

LRNPTESFRLRSGSIELLGEEDYEVLWKEGVPLGLGFRPDASTGYPCVLQSQGNQSLPGM

FNVRGGDHLVFINEFSTQGVRFQKVIDILESGPRPAVLRFRHTDVVEGPQHPLDPPSSLI

TLMSNPQDDSHALGMSYLMRPTRVSMNPKHDHSLYYITWKHEDGPLGIVVKQESTSYYPR

VINVKTEGAVTRESQKNRVEIGDVLLSINNNNISKMGFGAAMKLLQKGPKPLLLMFQRPR

GSLTMTTRSCNL

>contig13538 Frame-0F

MLSSSVLQRQRILRNYTQRRGHGRTTMLQRDEVTQH

>contig13651 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58463.1|) 4e-72

MRNNSADAGAKNYVKINQKGRTLAYNEDKGVAYIKVDNSSVFKAQHNFRRSELVQFVKTN

PKGKTFFRASFIKQEPFLNEHVWQIFFAESQMFQVRVDAKAKPPTLIFLCNGEWDPKWQA

EFKYNTWYNFGVAISKDPKGDGAVVEFYTSMGDKDLKLEKTFTVVTKFALFEELHIGLLT

LSDSEKVAPVMNENGDFIGFNGVTVKDHVSTSAAGVTVGF

>contig15176 Frame-1R

MIASAVEVLRLNVPWSSTDVQCSNLISSLTTSHTSRSSNYHPHSGLPRGAD

>contig15460 Frame-1R|Blast-regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4](gb|EEY65787.1|) 1e-134

MALVASGAVYSWGWGSMGQLGHGDLKSVNVPKRITFFQQEGLQVKYISCGGCHSAAVTSD

GSLYIWGESHWGQLGLPKEHEAAHESRPVKCPVPEDKAFETIVKISCGGTHTAALTNFGR

VFVWGRGDSGQLGIGSVWLKDTDDERLLGASRPRLLDEFNGEKVIQVACGAFHSAAVTDQ

GHVYIWGKEDYGMLGVGLSSDQQTPKRIAFFDNIFIMRVSCGGWHTVAVAKSGECYAFGR

GEYGRLGLGDTKSRTRPHL

>contig15899 Frame-2F|Blast-DNA-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY69219.1|) 0.0

MLFLELLGVIERSKSVAYLKIIYPSLKEAEKHVFYTEIKQMLARFCITLGSGLQIESTVH

ADNMRLQLAELLEVLLDSTLDVSIRRVLLDEVFTPLLECQTGEVMLQFYLMESIPKRLSV

ISVLATLISASADVQSRGCQIGVYVAYSLVDILYRLVDGELIRTDINAAFLGHTNGKGRE

FTMLVCKCASKLVTKEYSNVDELNRMACCAAYRCLLSAVSRTQKQEKLYDQILFQPALWS

NIVDPARQYELAAETEIFTTIPLSTLSTVSLQSKLDTSNMASTNQKRTESTALQFFTSSS

LSMDAERVGPSTMTASIDIDQAVANFQNIIVKLDDLNQHPCMIPLLRVLVQMKTDFGSSW

STNSMPGWMKKIFNVIVEASTGLNVRLFLAKVVLNVPDVFFLYSESWLRAVIETLLDVNA

AQMAPEFNYILRDCCSLVLDSWQNVAVTPFIDTASQFVNELIHLCPNRNKLVCDNNVLLV

TKLIALWKNLIYIDARELIIHIISEDG

>contig16494 Frame-2F|Blast-isoleucyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY54996.1|) 0.0

MAQDSAMSRSLPERISFPEEELKILELWEDLDAFHKSIELSKDRKPYTFYDGPPFATGLP

HHGHILAGTIKDTVTRYAHQTGHYVERRFGWDCHGLPVENEINKKLGVTTKEQVLEMGID

KYNAECRSIVQRYTSEWERIVKRIGRWIDCKNDYKTMEPWYMESVWNVFRTIFDKDLVYR

GYKILPYSTACTTSLSNFEANLDYRDTPDPSVIVTFPLVDDPEVALLAWTTTPWTLPSNL

ALCVNSSIDYVKIKDLKTNKLYILGAARLCQLYPKMLKKGYKGGEYDVLSTFKGSTLVGK

AYVPLFDCFKEWPKAFRVLADNYVSDSGGTGIVHQSPTFGEDDYRVCVREGVADKFTLPD

PLDDNGIFTDVVPLVQGLHVKKADDVLCQDLKSRGRLVSKGTEVHSYPFCYRSGTPLIYR

AIPGWFVNVERIRDRIIANNKQTYWVPSFVQEKRFHNWLVDGKDWNISRGRFWGTPLPLW

VSDDYEEVVCVGSIAELKKLTGEKVTDLHREFIDHLTIPSTQGKGVLRRVPEVFDCWFES

GSMPYAQQHYPFENKEKFEANFPADFVAEGLDQTRGWFYTLMVLSTALFDKPAFKNLIVN

GLVLAEDGRKMSKSLKNFTDPEEILQKYGADALRLYLINSPVVRAEPVRFHAPGVLGVIR

EIFLPWFNSARFFAQQATRLQLETGVAFVPNREAALASTNVMDSWIIAALHNLIKFVHKE

MQAYRLYTVVPRLVSFIGQLTNWYVRLNRPRLKGSAGSAEAAVALSALYEVEYNLAKLMS

PFTPFFTEYMYQFLRQFHPNRGSKLQWILPRMPMACLVVSTSSCFQTLMPLALMKKSKN

>contig17404 Frame-2F|Blast-Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4](gb|EEY59471.1|) 1e-108

MIEGQHPVVQALLGTFVTWGFTALGSAMVFVLDVKDKHTSQQILDGMLGFAGGVMLAASY

WSLLAPAIEIAKESDLYGPNGRYSFIPAAIGFMLGALTLFGTERALPLFEKYLGVRIQSK

GGNTDFEVLKKKKNDDYISNNNNKRECYDKPTMNSTSSFRRVLLLVFAITLHNLPEGMAV

GVGFGSVGYSARASFANAVNLAIGIGLQNFPEGLAVSMPLKREGMSTFRAFMWGQASGLV

EPIGG

>contig17769 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57321.1|) 9e-96

MILPKPKVHGAIFDMDGTLLDTEELSRLAIDSIVRQFGREFTSDMHKTILGRPAVEWTQM

AITAAGLRESIITPDELLRKWETKMHDMVDSVQELPGGYEILSAMHARGIPIALATSNTK

RVVEQKIKHHSKLFAFFSTIVCGDDPAVKHGKPAPDIFRTAGQRLFGLKEGEDGDSPPYC

IVFEDSLNGYTAANAAGMHSIALPDVRIHTD

>contig17893 Frame-0R

MTQMHQLGISPSLVAFRRVMVIAAKAQQRHVLQKTVEFVMAKFVDIWTDGRALTDICQAF

LQVGDNQRVMDIYNQLDGNWLDTKGKTALFNQFLLAAIRSGDVRNETKQPQHDRAVNVSL

ATTIFHRMQNSERASPDDFTFATYMRELEKEGEWARVLDLFQTMVDMESTTSVFNALSCS

IVIRALHMQGEKADAKEPSRSICFPSFTNSQNLPCQLKQKLANVLKLLRTMQLKNVNHAS

TLIDTLDKYHLYTPARQIFQRVLDAKLLHETFWRRKNGCELDLHRFSRGMAKCAVVFAFD

ELTHAFAKGAVLQDVRIITGIGKHSQTFMKPVLRHEIVKLLTKSSRPLLLPTMHETNPGV

LLVRRNALQKWLFNGGTIRYF

>contig18063 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62701.1|) 1e-100

MSQRMIEYMVDDNCIEVEKDDLRFIQQLIIGAKKIHQGSRVDAHGFLYEIVANGRNSIDV

DKFDYLARDMLNLFGLRKVFDFSRLTMFNRVIGNEICYHESVNLDIYDMFQQRYQMHKQI

YNHRKSKAVKFMICDAMLLADKELEIYTATQSPEDFQFLTDHILH

>contig18531 Frame-0F

MQELRRVRSGALGESDSLVTMHDVLDAQYQYDTYKDESYLRRIVRPLEVLLTSYKRIVVK

DSSVNAICYGAKFMIPGMLRFADDIDVGEEVVLMTTKGEAIAVAIAQMTTAVMATCDHGV

VAKIKRVIMERDTYPRRWGLGPMAQKVKGMVKEGKIGKYGKVNENTPAAVSELYDHDEKK

GVVEEGNEEGTIEEGLKKKHKKEKKEKKEKKKHKRDSEDKTEESLEKKISKKKKKKSKET

SDLE

>contig19129-1 Frame-0R1

MGVATRIPRASFCAARSEQLLGSPVRVTGSSCPNVHSPH

>contig20437 Frame-0F

MQTRNFLVIALAAASQTAYGKAHIETISGPIEQHDNSQFAKQWTLQSDDYKNTLDSIRLS

FNGKALIHRANYLPEGVLGFVNVTGHSFAAVDAVSISHEDAYYDVADRFDDFDSEDVSDS

DFDFDSGDNLVGRYLDISVPSDRSSGHVRIEITLAPYRSVRRIKTERKANVVIENNVLIN

SGAKATLAIKSVDYSSVLVESPRAYVTLQVLSLKASNSASITYKAGYLVNVGLLKVSSIQ

HAAIAFVCDSIKVQRMQLKALVGGRMCFSAHQIKARKHDVDGKKMISMSNANKKYGTKGD

DSCRANDYRFL

>contig20598 Frame-0R|Blast-UTP-glucose-1-phosphate uridylyltransferase [Phytophthora infestans T30-4](gb|EEY65164.1|) 1e-177

MGNRQRKNFLKLFRKYSKVKKIAIDWNSVKPPTNSMMMSKASIENCPSDMNLRHELLDKL

VILKLNGGLGTTLGCEGPKSAIEVRQDLSFLDLTVRQVEYLNSVYGVDVPLVLMNSFNTH

EETVRIIRKYRMHNLSIHTFNQSCYPFIIKETMLPLPNTKYDRLTREKWFPPGHGDVYNA

LFESGLLESLINEGKEYIFISNVDNLGAMVDLDMLYHMINEDSEFVMEVTEKTRADVQGG

TLVSYKDKPHLLEASQVPPGHMDDFRAINKFETFNTNNLWVNLRAIQRLVAQDLIDIEPL

VTFRTVKNHKVVQLETAAG

>contig21175 Frame-2F

MRDIMMQLDKWENENMPKVRLLEDSGTIPSGGVFAFTELKYEVEQTIVVTIENSGVVVAH

FCFVPKLDEVTICKPWLKVTPMFGMIPPREKMDICITALVDQSVAHTLTSGQDTLDDTMI

LRVENGRDYFLVVSGQYAKSCFGSSLEQLVSCSEPIRYAKFPAPRSPVASVFSVWVGGAA

GVNANSLVASRPLENISTTSILSNDALKVPKELWRMVNDIYTCSMLEKNLFVEAGSKVEI

LDLREALDTGAPFSPHSGYSMAELLVRWLQSLQHSVVPDNVLAIASTNGNMAYGCRALLD

GLSSVRYNVVLYLVSFLREVIKNSASNKQSPDKLAFVFSRCLVSPCTLHNGKDLQYFKLG

RVLALNEYPPPNSHSSTASTVSSIGSNHQSTLPVSNKNGPPEERLRRDAYELEVAQTNAT

QRAEKMEKLLLHFLSVPMP

>contig21441 Frame-0R|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ32288.1|) 1e-76

MGERGFAIKSDLNKTVWESEEFPLLCESCLGDNLYVRMMKEAHGSACKICARPFTVFRWK

PGKRARYKKTEVCQTCARMKNVCQTCVLDLQYHLPVQVRDAVIAKEEGSDQLAVNVPESD

ANREWFSQQHSRMLEQDGVVSAYGKTSTSANNALLRMARREPYYKRNRAHLCSFYARGEC

NRGDECPYLHEMPREKADPLAMQNISDRFHGKNDPVAVKMLSGQKRDEAKPRGPPPTPEG

APKPKPPPLPPGTKPP

>contig21548 Frame-0F

MVDFVHVDLTRLQLKEKSLRSCRSLVFECETIVSNRSLTEVVMLMNDNPVPLSLTISQVH

KSDVVFVSLTATIVQIASQDLNTTQDTSTHFKQSLPDSVLIFCLDIKLI

>contig23915 Frame-0F

MRLHHILLASAVAVFSSRVLGAATQETRNLVAFDKLEGTADGPTDDDADVDAETTNKAFQ

SGATSDPADSPAVSTTAVAGSKSEEINSILTRLQSDLLDLIGSDDGSKPVDPNPLGENGS

KLTKLMNFSDPNFLKILKPLGLGGLIGADLNVKQEPEAPTAPENPVAPATPEAPLADDTD

RDELEAAVAAMIKKKKMQANGSDGPNDVDPTDPTLKKGLNDDETSGEDLLTTTKSSALPT

DDDGPDSTYLSSIAKTPVVPTSSDEDNDDDINSLNPTLDKKTGVANTKSSDTGVKSPTTA

GDGSGTDSDFDGKFDKLLQMSDSELDDLMTSDKNSSAAPYLAAAQKMLEPVESVPGENKT

AKGEAYLSKLDSMLKLSDSQLDDMLDSMDITSLEGLKKVAGTKDVAVSETTTTPPNTAKT

TPSSNTVSKSAPVLDDGQSDADVLFEKTPEKEDTLEVIPPAEESSYLKGLYALSDDDLKA

PAPAPDTKSPPKTIDDNSKTEDSMSDVEDFDTSECPTGFFGHIKSWWKNTVGGGDKCALE

RRLRVVV

>contig24389 Frame-0F

MRKVLNQKPNIMTAAMQQAPG

>contig24705 Frame-2F|Blast-plasma membrane H+-ATPase, putative [Phytophthora infestans T30-4](gb|EEY58081.1|) 0.0

MELQDDLPIFHPTATREEVLVTAALAAKWKEPPKDALDTLVLNAIDLRPLDQYTMMDHTP

FDPSVKRTESTIRGPDGTVFKVTKGAPQIILALAHNVSEIQEEVELKVLDLAKRGIRSLA

VARTSDDEANGGWVFLGILTFLDPPRHDTKRTIELAHQNGIGVKMITGDQAVIAVETCRM

LGMGTTILGTDVLPTANVQDGLSTTLGADYGAVVESADGFAQVFPEHKFLIVEVLRQRGW

VCGMTGDGVNDAPALKKADVGIAVEGSTDAARAAADIVLTQPGLSVIINAITLSRKIFQR

MRNYVTYRIACTIQLLVFFFISVLLIHPDSCRFQHFVPHIGDCAFNNNETTEGVDPYFKL

PVIALVLITILNDGTIISIAYDNVVPSKRPETWNLPRIYGVSTTLGLIAVASSLLLLFWG

LDSWNKNGVLAYFGIGDLPYDQVMMMMYLKISLSDFMTVFTARTNGLFFTRAPGRLLALA

ACFATVVSTLLAVFWPFTEMQAISIKLAGFVWVYCLCWFVIQDLGKVLLIFMLEHVDHMN

VYERKVSSKKYVKHEAQRQNRIRMGSTLLNNDSFMRGSFVAGRPVGTSFAERSMSLEQAM

DRLVRLEAEMKVIRAVIQNAAGNTRV

>contig24770 Frame-0F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY69845.1|) 2e-10 NOT\_ORF

MQYLNSSHDGASSSSYTSSDMESSSAINFL

>contig24990 Frame-2F

MGVVCQPLEHHQALQCELLTDLNAMQSWNCKYQHDATSITLAVTPCPVLSLGNTEPTMNV

CWLPNGCNLRQQVVFTTNAINHRHRKALKRVAGRPLVSRTRFKRQRVLVDCKNQLKASSK

EPRDQPSVASLRSLQFALPDLTSQDTLRVLHAMHAMPSELRHLNSRASRHYLRRRSKVRQ

VFGWRHLLCQEEEDEQSARRVVWKSAKTMEAMRMRPLAHQIWQAGVEATAQVPKEGSTKV

LYTVNRRARVVRAPNKEFRNRRDQVWLECFLDDGRQICVARKELRQFNGYCAPETSATEC

QGFLVRPVYTRAINVRVAGCSLQCLRAIDAKDSGVLSAVALKQQLLHDLPQLTLQWEEDH

IYDLVQAPQVLLDSVFAYDLNAG

>contig25012 Frame-1F

MRRKWTNPTAFVDFLNFAHGVAVHGLYERPLTCILNHLLAICCHALDVGAMTPCFLGEY

>contig25197 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60517.1|) 2e-10

MDEHRIREMAAILAQRHIEHGELQPADIIACRIIAKMFVYGVAVLFILISCMLIRMQFT

>contig25603 Frame-0R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY70002.1|) 4e-09

MVGMHMLSIVALKWSCIMVVGLAVICGIESVLEFLFLTFECSTFNELLNEVQLDLYLQEH

RMASDKELVRDK

>contig25971 Frame-1F

MITVAFEESMSRGIESYPEFADSPPKNIPKTSGLTPLRVRRSTGNDRNSRLSRGLDQSYS

SLERSRQSLACSSLDFSDDGSMMNVDDDE

>contig26332 Frame-2F

MKYAGEIATKHASTKPVSIKEANQSFSVGTSTVTTSFLPSAPSTSNTAISSGFSLDAAAP

NFDKVSEFSTSNSFSFGGSATKDHQTGISAAIATPKKASSSSLFSSKPSDSEETPILAFS

FGALPKPASTVSSTTGFSFSNLTAPPSNTTTSTSHYSSGVSAPSLSTNTSAAGNDDEDEN

TGREEATVIIKADSPDDDCKFEVKKAKIFEFKKNEKRWADKGVHPLKVLVSKKSKSARIL

VRNQIGKIVLNAALYKGMAVRPHEVKGKKTGVTLALQIENGELTQFLLKVNTERVDELIK

ALENAVS

>contig26581 Frame-0F

MTSTNRQLTDSELIEENGMVPMLLESQSQSIDDNTKAQSTQESITSVEDVPMALSEPSLV

PLSGEFDDFEFYYQQENIRETFIAESDLESSDKEYEEPKKVMPSQLQAKETALSSKNDSC

TPSFLENPPNLLATVDLPDTALESTQSLATAEQSKTQEHCTTDIDSFHKDNEDSKALVES

TNALPSTQIPMNKRKIAKGWRFLSTLTSIFSNEDDDNNLSEKPQNVESADFRQQSTHNLQ

EKPNELKNGLVEEEYLSSQATVVLQYAIDNDVDANAFEYEANSPDVVNSELNSPKTSNLE

NDVCVDNVTVPGEEKGTIYPLKKDLRIEQECGLLSTTSEVETTSRFSENQDLGHDADRLE

PRLIPEDPSKQNVIKNASSDLVILVTGNVSRASQTDFPSVKSQCSKRYHQKPALNNSSRN

ATSPKKGFKDAQLCVKRRRQEDLLTSQAPKMGSFSFSIGTTS

>contig26835 Frame-1F

MRPRKYIVVVLLSIAYTMCLAVGYPSDGTDDSTKSLKSGNRIRSHTPDIGTEERTLTWLK

SMLRPSSSSAKVTKEIPEVVKSASDFKVRQTLSAITRKLGLHSQRLKRFASWLRKTGERL

TRKKVYYAGYIAIVDSSSSQLKRLSVTYGSAFLFVIGFIVLLAFAMTAV

>contig27421 Frame-2F

MTRVGGIYLSRRYAWHEGGPGSEIYLAYPTLPL

>contig27559 Frame-1F|Blast-AMP deaminase 2 [Phytophthora infestans T30-4](gb|EEY55336.1|) 0.0

MDLTLAANLEHELNRFRLNGSPTSGYSPHTAHIDVIAAASAAAADAEDDDVPSPDEEESE

VASQRTRHEGLLKASILEKVATEKRLRCLSDGSMYDQIVDVGPGDLFETLPEPYGQLSAY

QKIKITAVTGEVDRETIESCELIRKCLALRKKWIAVNEPTLPQSTASKEGHSIPRTAGLA

TKLRHRDEIPYEPLKHPIPEATSHHYVMVDGVVWVYNDKDAIEPISRVGQMEEYYKDLFE

LKRIINFGPVKTLAFKRLQLLEARFNLHTLLNSEREFVAQKAVPHRDFYNVRKVDTHIHH

SACMNQKHLLRFIKSRLRNSPGEIVIFRDGRFMTLSEVFRSLNLTGYDLSVDTLDMHASN

TFHRFDRFNLKYNPAGQSRLREIFLKTDNLIAGKYLAEITKEVIADLQANKYQLVEWRVS

IYGRKHSEWDKLGRWFYVNKLTSPHVRWMVQIPRLYFLYKKLGEVDTFQQMLDHIFLPLF

EVTRDPSTNLPLHFFLETMVGFDCVDDESKADSLHAERGKKLPKPQDWAYEVSPPYDYWC

YYLYANIAALNEFRRQKGLNIFSFRPHSGEAGDPEHLAAAFLTANGINHGITLRKSVCLQ

YLYYLTQIGIAMSPLSNNRLFLAYHRNPFPIYHARGLNVSLSTDDPVMLHYTKDPLLEEY

SVAVQVWKLTSTDMCEIARNSVLQSGFEHKFKEHYLGPQYTLPGSQGNDIRMTNVPDIRV

DYRHTTLQGELDFIQT

>contig27814 Frame-2F

MKWSCKRAVYARQDVAAYLSISMEAFIWENDARVTIVWIKTSCGILA

>contig28150 Frame-1F

MADAASTSSLAALEHQRQRKEQFAMEKKTLTRQIDEERRRAIEAERVASSLKEQHVAAQR

ELESVKVELYSHMASRNPVLNENRPLSAVSLVQETVAVLKDEFKTKSRALQTRWKQQTLL

MTTKLERLSSQLRASEEKLKALERSILCAKELNQITDETWVREKEELRVEREKERR

>contig28547 Frame-0F

MVVSKPLTVQVQRLEADDNKRLDEKLSVQLAVGNDKRQTQFVSVGSKIGDTWKFDVSSMA

DSANVHIEVYEEGRETPLVSEKQSLREFASKNQMTFTYGTTSDPHTIRLVMDVDYKSSTQ

EGIVAAASTHRPWFMRASYYYTTTKNVYDYATSFVLVKPFARLGEATVNTVLATVTGKTL

ADVDQSLMVPVLGSVDSKVDATISMAFTKLYQGQLFAVNTKNKAVRAVSNVVHKTGSTAV

NATTYTTNKVLSTSGAAVGAVIGVAEFTSSQVKHASSSTFGAVRGVTYFFLSHVPILGPK

IRA

>contig28675 Frame-1R|Blast-NADH-cytochrome b5 reductase, putative [Phytophthora infestans T30-4](gb|EEY59645.1|) 1e-136

MWSTVIMRFPARAVLLSRGALVTAGLAALAALSVPSSAVQCEEKSKVALSPKEFRSFTVR

RVETLNHNTKRITFALPSLDHVMGLTTSSCLVARAKVNGTTVVRPYTPTNVNGEKGFLEL

VVKGYPNGNLSKHIVNLMEGDSLELKGPYLKFSYVPNRYKRIGMIAGGSGITPMLQLVKT

ICRNPEDRTEITLIYCSTSEEDIILREEVEALMYLYPQFYVVHVLSNPSADWKGLTGFAT

KEIIEKHMPEPSNDNLVCVCGPPPMMYHISGDKAKNGSQGELQGLLKDLNYTSTQVFKF

>contig29522 Frame-0R

MNGYGSHTFTNRNDKGETVYVKYHFKTDQGIRNLPVDKAATLAGSNPDYAICDLYESIAS

QKYPSWTPLVEVGRLVLNRNPTNYFAEIEQLAFSPSHMVPGIEPSPDKMLQGRLFSYQDT

QRYRLGVNYNQLPVNRPLFEPQTYQRDGLM

>contig29614 Frame-1F

MFTRKMAIREGHELLPLKAEDFRKQEYWDRFFKKRDKKAFEWYGDYATLRPCLHALLGLT

DDAPTSLLRRLKANVRVLVIGCGNSALSADLVKDGFSCLLSVDFSARVINEMQSKHPALK

WQVMDMTQMDALEDASFDLIMDKGALDALMAEDTPEIKLDATKMFREVRRLLATSGRYCC

ITMAQDFILRHLLEFFILKDFVETKPTYWGVGVQELPRDSRKLFAPFLVAALKCSKLHDK

AATMVQYNAKQFSIDVGEARLQWLTREVEATQWFAMTQAALRQLKSGRQEIIELIANDEK

YAAKSSGQVGEVRGQANPRFTLRLVDTHMRGPHGSCAVFLVPQGREHEWMFSTEEGAKEL

AARAGFSRLIIVTLGRGGHSFESLTKVQEELNVKVMELAPDTLGPDENIPYLTVEEGLGS

RNIVHQGTSPLSGNFFVEEVQTHGETTRRLVFLSNTNVIQSEVKLLTRDSAVSTSPEHSK

LAETSAPVNTFGMTSEEAAAVLKKKKKNKKKNQKKKKKNQARQASVDTSYLSFDYHKGMV

ASLHAMSLASRLPPDSPHRTLVLGLGGGCLAQYLHDNVPGIDVTACELDPTIVVVAEQYF

GFKQDDRMRVVIADALDYVAEQSMALEKQTFHSIIVDVDAKQRDVGMSCPPASFVENTFL

TCVHSLLAPRGVLLINISCRDSGLYKDIVARLQQFSGSGGVLTLKPSLQDVNSVVGVCML

NKNESDAKLMLQQLRNQGQQRGKVQNMPR

>contig30043 Frame-0F|Blast-prenyltransferase-like protein, putative [Phytophthora infestans T30-4](gb|EEY64646.1|) 4e-92

MAQYGDGTRAPVVLGDPSNLVGRTHPAYNIGYDKALQAIEYFRAKGPFKPNLSE

>contig30234 Frame-1F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY69528.1|) 8e-12

MVTLMCVIVGVAGKAFPVDIDDSKFVGHLKKAIKQENKNEMDKVDAKKLQLFLANTV

>contig31376 Frame-1R

MEDAVILLLMLFVLVMASYLMGRHSCMLLSQSSFALMFGLSVGLFMIMGGKHAALHTHLN

LDNSLFFNVLLPPIIYEGGFSIKSAVFFRNFPAIMSTAVLGTSISTTITGGVLYLAGVAG

MVTKLSWVEAFLFGTLISAVDTVATLSCFDKLNVPPLLFNLVFGESVMNDAVAIALYQTL

HKWEPESTFSAKQLLHVTLNTCGMFVGSLIASALITLGGAFLLKRKFFATLRYYPSYEIS

LCLIFSLLTYFVADSLKFSGIVALFFSGTMTAHYHFNTLSREAQHAFTHLLHTLAFVSEN

IVYVFMGTSVVMIFAGHGEENAGASLRVDDIDWSFIGLTLVACIAARFCNIFPLLSLCNL

LRSPGNRIPVKFMSIIWMAGLRGSMAFALAKNWNYIGLHGTSHRRLIESTTLVVILITTI

VIGGLMGPLLMNLHLTGNDKKRSHLSLSDTDRSSSEFDALRLDTRAKYHVDGKVRGALAF

PEEKQPNENSNGIGDEIPILTPRLQFLDDASNSEDGLNPSSPTHPAVERSRGDSLTGAFF

RNWQAFDTTYMQPVFGGSTQRRAQPASFDNPSEMELAKTQVDAVL

>contig31426 Frame-0F|Blast-glycerophosphoryl diester phosphodiesterase, putative [Phytophthora infestans T30-4](gb|EEY62069.1|) 1e-100

MLELLTEYGWNHADAPVLIQSFETESLRELNEITDVT

>contig31884 Frame-1F

MTNFDLTNISILNERMQKDKKLVEYLIQDKGDISHCRRYMCELQIEGQFMSLGEGVSKKV

AKARAAKIALQTLDGLNGTNQKQQKEPSGDVKKEELLLTENELATRMPLIMLGVDIDKKL

IERAAKKPVQVIGNDVMQFCHVDVMTNMFETKVASFIELAPRSTLERKFDLVTCFSVTMW

IHLNHGDDGLWKFLESISSMTEHLIIEPQTWKCYRNAQKRLNRLRVEIPESFHKIQVRMD

VVEKIDAFLLAVGRFRHKAFLGKTNWSRNVVLYSRTLVPGIAYTL

>contig32056 Frame-2F

MEAPNDKLKQPLVDPEMKAVSPRSLNSGAIFVLHNSSVDRDADEEKEEAHRRQGNRPQKH

KFQYTAPNVHPYAVPQYDPQGYGGGPANVWGGDQKMENGEQGSMVDIVFSGMYTLAAALT

IIQGFGMLIHFTFAA

>contig32544 Frame-2F|Blast-acyl-CoA synthetase short-chain family member, putative [Phytophthora infestans T30-4](gb|EEY56150.1|) 1e-103

MPAVLETTVAMLACARLGAIHSVVFGGFATLELAARIEDAAPKLIISASCGVEPKGIIDY

SPLLNGALEQTTWKPSKIVMLQRDICLFPMTKGRDVEWRDVMTMGHSVEAVPVLATDPLY

ILYTSGTTGRPKGIVRDNGGHAVALKWAMRNVFDIFPDDTFFAASDMGWTVGHSLAVYGP

LLNGCT

>contig32885 Frame-1F|Blast-hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY54427.1|) 1e-153

MLYPACRLLPRSIPSLLTRALTTSVGDIKIKKVGMVGLGLMGHGIAQTAASKGFDVVAVD

ANPQSLESGMKRIQSSLHKLLTRQVTKGSLTQQQADERTASTMARIKPTVELVELADCDL

VIEAIVENVAVKKEFYANLGNVTKPSAILASNTSSLAISDFASSSGRTSQVVGLHFFNPV

QLMKLVEVVRTDATDPTVFSACKQWVLDIGKAPGELQGHAWIYCESTACPVRGSSDRTV

>contig33635 Frame-0F

MARLSSLILCRGTINVLCSVKPSCLLGFHQKAPWPVKPTNLKL

>contig33640 Frame-0F|Blast-carbohydrate esterase, putative [Phytophthora infestans T30-4](gb|EEY62265.1|) 2e-71

MKHDCKLPSGRTAGYGAAYTLPIFVTVACISLWVNATHLQWLGLAHVFVLAKLIVLLGIH

ELLRPFCLSFKEVCTLTAHVGTAANTAVLQFIQRGFCPKFAEWTLWYEWFQAIALAAGQH

NGGHVLKMSNALAFRRNFELMGWLLGAFACWRHKHKLESFWYNGL

>contig33954 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61074.1|) 6e-41

MQCKGVSVGGLTAELNQLREGHLLVKHVAQASKNAIDDTANLALDAFNQFADEIDDKLRG

VQTSFNTMEVSVRFGIFRLSFKHMH

>contig34195 Frame-2F|Blast-digestive organ expansion factor [Phytophthora infestans T30-4](gb|EEY58822.1|) 1e-55

MAKDDEVAINDMQEEEEEEDMDPFRRRYLLSSFTEEEAKTFASATRKFVKIHVPMLDEGK

YEVGYKSGASMCASVASVITTPDVATTKKLYVRARLLSTWKERKVDVETMFSKGSVPRML

FQQMATYTDVFFAGQTYENTPVLRQLSAMHVLNHVFKTRDTILRNNERLRKQQERNVLTD

TLTEGEKEYR

>contig34331 Frame-1R

MHELEDIVHTTYESMEEARLAVSRRSKMRALCCCKRTRRVGHSSDGEIKTICLECSCSGN

ATLPRQQQRKRVRGSREIGCQSALTIRRMKLYGDLVHWVVEANKLAHNHESFADAAVHLQ

GRALKATSGNIYRTTVGVHSIV

>contig34461 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54654.1|) 4e-98

MSTYPLRGIFFFLRDQRLWRLSVLPVLLTVAVALCVATTLFAFTLHRQEEALYDAGLSSF

FAWLVAVIFVIVEVFIVTVVFGLVTLEWFKDKIFAHVLVERGYRDLVENEERHLPFLRVI

TSCCRVSILLRLGLLVITLPLNLVPVLGNVTYAWLNGTLMAWEAHLYYFEMKAFDFDQQK

DIIGRHKLQYSMFGMEALLLEMIPIAGA

>contig35556 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63917.1|) 1e-72

MESDCGGEEFIGYNEWATESLHVHIATDFVYETEDDPSATNRGVFIAEDVIPHTEVFRIP

LDSVLSVKSFHNIPALQSLAFFKQRTPEHEDDQLALALLYEKFIQCGQSKWAKHIELLPR

TYYNALYFEPEVLQALKGSNLYYMALHLKDHVAAEYARLKQSVLIELFEKCGEEINVDLF

HEYFSLENYKWALSTIWSRFVTLRLTNVLQFNIGEV

>contig35714 Frame-0F

MNRVNTFFWSRLNPTGELVRSVDVLLRELVPDAKLDAAFHNLSIAASPVVALPACKPDGE

EVDSVADGATNTCDTVYEDASPPEDESSDEESATEKTVPGELERKWAKIRAVFHDWDEEQ

GERAKKMDDLADLLLRHRILEKVLMPKVLGQLTFETRKYVGTVFRAMTVHNLRGFIELIG

ERPDIMRWLVEGYKSNETALICGSMLRDCFEYQKLTLIFMKELTFEFEFLFKVTMENSNF

DISADALINISRLLTVHKKASVQVLDESFDRVFGQLNNLLTSPNYATRRQTLQLLSELLL

DPINFAIMQRYVSSRSNLKQIMLLLREPSEALRMDAFHVFKIFVANPNKSLEVKQLLVRN

RDKLLAFVSDFGKAESGRDFLQERSLLLFALERMTEKAQVLEKTQDQARRKSTLTSVERT

PLSGPLSGMCVDQK

>contig36373 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70030.1|) 8e-79

MMLTLVNLLMDESVDEATCKQEMDLFFWELEQLQFEANKTEIWNYTCNCELEEYETLNSE

IDTHVAKATKEIHELQAKVQVEKTMRAYKEEYESIARVINELPSRKEIENDMIEQRKRLE

EASTAFDAVERKLDTRTKQFAVLMNTIQNLTATLEEDAKVEAEQQDDDDDISDERK

>contig36720 Frame-0R

MVEELVREDQICEVVARWTGIPVSRLTSSMGDRLMHLEERIHKRVIGQEEAVTAVCDAVL

RSRAGLARSGQPTGSFLFLGPTGVGKTELAKALAYELFDDDSHMVRIDMSEYMEEHSVSR

LIGAPPGFVGYQESGQLTEAVRRNPYNVVLLDEIEKAHPKVLNILLQVLDDGRLTDSHGR

TVDFANTVIIMTSNIGAEHLLFEKELSPRASKKFKTDNEFLDSESETKREFARQRQLVLQ

QLRHTVRPELLNRLDDIVVFEPLGRKELRQIVMLQFESVIHRLKESQISVKVTTPALDVI

LDESYEPQYGARPIKRYIEKHIVTDLSKLIIAGELHAKTHVEITKKNGKLAFGVSALDAD

VEMAP

>contig36755 Frame-2F

MSRATVTRVAALQLRRQIPRTLTTQHALLLNQHPAAQLRSFSVFSNIKKSVSSKLEERNQ

LKQGEAYKQQMIELSQKEKFDLNGFYDHLKKNAEATGATGWRSMIPGVSSMTAVQQMKAF

MAILESM

>contig36874 Frame-0R|Blast-GTP-binding protein [Rickettsia bellii OSU 85-389]gb|ABV79593.1| GTP-binding protein [Rickettsia bellii OSU 85-389](ref|YP\_001496630.1|) 2e-24

MFVKPGDEVYEGMIVGEHSRPTDIEINPTKEKKLTNMRA

>contig36980 Frame-1R

MAVIRTLLRQNSKDFDGGLDADCYGEDSYDFVDAKPKFQFVGTEAIEKVAKILSDEDRFT

PLEACKLGNAEERNYVLELPADPHIDVPRWPIPSNEDDRITSAAAFGILELANRLAPTDK

NTDLRGYIPDTKDLDLLCKLAVMTMNCSYSFVLVMAETHGHVLASTLPAFSGAAVPREQT

NCQHTLMSTHPFMVAHHEADVRFQNQTATNLLPVRFYVGFPVMIPPANGQQGDPEVIAGT

LCCVDSKPRAEITRTQYVTMIRLARTAKTFLIQKGRLLQQKLNEVAKVQEK

>contig37305 Frame-2F

MDRSTLGLRRVVSDVLKGGMERNGSAASPGQLSFSTFLMDEVASSVQLQKASKRPALPPL

PPLKAHTSMNAVSRRQEPSLLISRHRGESDGDIPVLEAARDSRGFRLDGTDRADAELHSN

GEEGVEAKVVLGEYDAEEDEFVPVLQTAEDAQRTVTPLGSKKFLWRASARMGVPMGKAVR

VPDQETLLSMSTRITDSMSIQSSNNAEGFRTTSSSCHIDRELIRSGWLYKQANVMKTWKR

RYFVLIKRTNLATGEYWASLQYYKGSNFGKLRGEMHLQDSMLSVRFLEPDETKRPFCFEI

AGGDFSFVCSGSNDDDASAWVCLLQSLSGGGSSSIPPTVAASNSIQSPHGIKSAQFRSSS

IDTRSIRIVAELRRVLHTSKSPEAVKFKSFIGSFDSRNSGALREFSEFHTTLTESIVKDH

GSRILSALTDPRNDNANGSITGADKFQMVSLDTLRSAVSRHVEEVLFVPLQSKINQFLRR

MYYEEESSINRKVRWLQGKDQMYFNIPLHQVSWKEWRKPSRILAQIAQVQLPAAKYDVLT

STIKEIQLTYADEHDPYTELDQLEPDDIIPIFTYVLSNSGLENLISLKTLLTELNGSWSA

ARSSDEETSLNILTHAVDFISNVNIPAVLEDIFKDQITLSIDGDWRRVLEFEVESTYRYG

AVVDHISPHGFSAVGNIITRGFVLVTVNGQNVVLWPFKDIMALLFGSASPHRLAFIPGSS

YFKILTSNKALWNVALMHACQRGDVFSVQMLLANGADVNYVAHECGSNTPLHVAVSALHF

NIVSYMLQHGAKVKMIGEFGRSALHMLGSPCTMPASVNTLHDVTKALTVTPAPLSDSDKA

VLIVKKLLDHGAPIDTVDIYGNNPVMLLAERGYLGAIDAILEVN

>contig37370 Frame-2R

MRAALNRCGVEPQDIDDDGFSTSHTQTIFSAATIPDYGKRSVRHYIDHKFPSVVFAMTEG

FHRTLPNLTLHTHNLQVFMASRVFDSEQHARCELLYEILTSKEKDSMAASAGGKTLVFTN

SIATADTLFHFLENDKGMDSCALFHKEVNRLQRQKLLKRLSSDDGADSHLVVICTDIAAR

GLDTTKVAHVVQFEFASDVVSYLHRIGRTGRAGTPGIVTNIESSENSLVVDKIRKAGAST

LQDAFSRKRSLRKKFKKTINSSSHRDYYG

>contig37482 Frame-2F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY58242.1|) 2e-67

MGRFESNIVYFFAYLFLWPYALLIRSVVNEKEKQLKEYLLIMGLPVMALLISWFLLYFIA

SVIVAGIGTWLLCGTVFIATIDGVLCFFLLLVLFITSLLLFGVAMTPIFNQTKTAATCAP

LIFFILSAGSFIQSLVGPD

>contig37833 Frame-0F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY61800.1|) 0.0

MAQWRRFAFFDKEVLKDSSGPWMKGVDITGMSANRGLICVGDSDGFVHLANRSLEARKFQ

AHEIFVSHVLMMKRSNVLVTIGDGIDPRPEGLREQSKAVAEAGRAPNAEEMYTPKPTGKS

TAIVRFWRTDQQDREGTPKIMQQIPIFAKKYPEEAVTAFAVSDDLSQFAVGLKNGAVILF

RSDLKRRADRPSHLLQPAGQFPVTGLAFTSKPVTATLSHVFLYASTRRGLTCYHCSHDDP

ALVKSAGGVAALPPRTTVLDERGVDTNCSCVNEEGEIAVGQTDAVYFYTTEDRSVCFGFE

GEKKFLSFFKHYLLVAHVDPRGRHQVNVYDLQNKFIAFNWTLTSTNTKGQIRKPPLASNA

RAPGARFGLDEMEEVRHVVCEFGAIFVVSSMGHVYRLSEKDTTSKLEILFRKNLYSIAIS

LAFSSNYDVNSIIDIFRMYGDHLYQKGDYDG

>contig38007 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57878.1|) 1e-91

MTLKNLKPITIKRNLSLADGYQLFPIADKWAELLPERIPLQFSFFRYVGFYVACIENGKP

TVVKSRAVAALRVTIQNEDKVVFNERVSTAFPNGVYYVQDICLENAGVHTVYVTVEGGLA

DELAPLVLKMEVFEFMELHECPDLVKGAYQPLREFVLKCIEEGNRDKLRDENFLATVVRT

KNHLLRNVDARWWLRTFVQHTINRNDLELSTCRTTHKRKQNHP

>contig38551 Frame-2F|Blast-Ca2 :Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4](gb|EEY61785.1|) 0.0

MHTAQALASIRRSRTNDVESSTSRVRKYPSEHSSLLHGNGHSGSNGHENSSSFQTCPGVT

SGDVKEEPLTLKEDAWAIYEMIKQQPLNLLLLSAPMAIWASLGGWRDLWVFVFNFLVMIP

LANLLGEATESLAFHTGDTVGGLVNATFGNAVEVIVAIFALKAGEINVVQSSLIGSVLSN

LLLVLGCAFIAGGLRNKESSFNAVGASANSSLLMLASFAMLLPSYIFYFSDNDSEETRVA

NTLTLSRIAAAFLLFMYLQLLFFQLKTHADFFVDVQDDSEETVALSMRASATVLLLATLL

VSMFSEFLVNSIDGFASEMHLSKSFIGIILLPVVGNAVEHVTAVRVALNNKMELAMGVAV

GSATQVSLFVVPVVVLSGWFMDRDMSLAFPQFEILIYLMSIIIVYAIIADGKSNWLEGSM

LLTAYALVATALVWV

>contig38757 Frame-1F|Blast-caltractin [Phytophthora infestans T30-4](gb|EEY60867.1|) 4e-23

MARRLSQKRNVKTYERPGLSDEELEEIRKAFNLFDTDGCGTIDPKELRAAMQSLSFEAKN

PT

>contig38832 Frame-0R

MTGPDRFEHLLDPLISGLSERQLSINDIQDVDLVTFPTLSTQLRLQSSNKEDVGSALILN

MMWKLAAHG

>contig39149 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60690.1|) 4e-58

MAADGGHNSSCHEIGKLFFHGSNEISQDLERALYYWTIAAANGHMAASYDLGYMYAKGLV

VTQDEAKAVQLYRQAAKQNMPEAHHALGTACL

>contig39286 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68796.1|) 1e-129

MSVVGIVTKRQFFWRISGQKQSFIQPPTIGVKHSRELLISNTGNSSRQLVCILHVRDLRC

LDTIEIRIDASRFGLLGTLEVNSVVEFSRLKGFVARITFKLFLNWCHLTAAKTKVSVVVP

HDAELYGELPTTFLSDLYSASCIDRLLHRFVVGVVHVSYVVLKRKCRLCYQPLEFVKRRG

VWRHFEGQALSKYSRCCACIGYQWNSSNSNFKRQTFMGMAVRCVVDDGSGQAELFLENDV

AWELLTCSAGQQKRFEDILSNYVEELSYYSGRTANESFASSKAAREQEYYQNELQAFVIN

AIPSLRSIVVFAHQFYKANVQETTSVLKFGKDIHLTTKTLPQLKLEAKRVDRLHVRSELQ

RRLAQLRQRM

>contig39624 Frame-1F|Blast-sulfite oxidase, putative [Phytophthora infestans T30-4](gb|EEY60062.1|) 1e-122

MNGETIPRDHGYPLRAIVPGTVGARNVKFVHRIILSSDESPSFWQQRDYKGFPPNVDYSR

DDYWKFAGASIQELPVQSAITEPKDGSVHVVTDTSDSSIVTVKGYAWSGGGRNIIRVDVS

VDGGKTWTPAELHELGKRQKYNRAWAWTPWELDVEVLSGTTTLDIMCKAIDASYNVQPDT

IPPIWNMRGVLNNAWHRVHVTVEHSVDEH

>contig39941 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56227.1|) 3e-44

MMDESGCVTEHRDVVKLDECSRRPALEESMILLETRPHSIDDHGFYFDDQDANGLPNIDE

AICADEQFEAM

>contig40329 Frame-1R

MLHKERRYSCDRTTRKQSHRIRPSRKSSILYSSKMNTCRRIRKRHDTGLVRSRACIVTAV

VLFSQGVSGQKTCALPELTLSTNCGNACAPYAPCLAY

>contig40556 Frame-1F

MDHHKFSLHGKHIYLMIAVFFEIEYIPVAEQIKFALDNTLKMVFGALGSSVSEFDILSFE

ESTAKSNEPSTVLLRVQRSGLKSLRSAVTMCTSLNGKNCKLEVLQIGDSLMDVASKRFL

>contig41195 Frame-0R|Blast-synaptic vesicle glycoprotein, putative [Phytophthora infestans T30-4](gb|EEY59841.1|) 4e-36

MGPPPHLAALLSVTASVMCTGAVASRWISHGTKDNGDALSKRSSGENASEAVPDISPVVS

RCGGDDDEEGEQSGLIRYDFLHREKNHALL

>contig41528 Frame-0F

MVQLLYFFHPLCEFGFYFLHSFKDLPVSWSLQFLHRAIDIDTRDAPSDEASTCDSRDFFN

KLVGDCFRLWTIGYCWQKRRCRSCHSIRRLLKKRCGHNEEGP

>contig41883 Frame-2R

MSPPSPNLLDLPLPESSKPPSSSPSPVDISPPSANLLDPPLPDLSKPPSSSSTPADMPSL

SPSIDIPTSGSPSPDILSTVPPSTEAPLLTQAPSSSVPPSTKAPSPMLPSTDVPSTGPPT

TDAPLLTKAPSSSVPPSTKAPTSVPPSTDILSSGPPATDVPLIVPSSTDAPLSTKDPSIV

PSSSKDPSSVPPSTAIPSSESPSSETSSSNAKTPSTEMPAQDKSFENEKPDEIVSSPVPV

TAKPIYVDDTLAASPPPVMNAPKATKSPIAIETNPVSEAEETDTMELNASQQKDQTQSDV

IMYDASATPIPIKKIGLNDPFFDSEPSKETSVKPVVLNIAGNTGENGSNNYKQYIRGKTA

ASDSNNALPYDTNVIGGRNAYVDTEASDVMSASAAAFQEFLRYASVAFAGISVALLLFFH

FVSLDANLVWVNTAWSPNTWEFLFYVGYLQQMQTISQLTLLKTPYFLWDYTDSFAWTSFL

IQKSTQSGFRRLETIVLGGLVSYSDRIGISESKILIHGAVGFAVIMGILVLVFLVLATLA

KRKAERALDETSDLTNYTSGVHRLRSISIRTLGLCVLVWYFALYPLSMLSSFEISMEVQA

AMAADPLVIAIIALVLICLGVLVVAARVIMHKTKDELEQFENLATWGSLYCEYTYRSRMF

FVIDVAVQMTTGILVGCVSADPTQLIVVIGMQALYLACVFIMSPFADKIVLRITYALGLL

KILNFGLAFAFLHSNTMSASARTSVAQAYIGINSIVLVVWFVRQLIVFSTYIRAWMARTN

VESRRTESMVKYDRSTDADEWGSHFTGNGMNNSRVDNSRLNQSLNGATLSLPLGSAIQPM

HATSAYGQSSSP

>contig42370 Frame-0R|Blast-beclin-1-like protein [Phytophthora infestans T30-4](gb|EEY60515.1|) 2e-33

MSGNSSLQPPVIITSLPRPPATTGAYRVIPTSSLSSSPSSVHASFSPYAKSPVPRTRRVA

MEGKSLFTCHQCGALLKFQYSPISIEEKIMKLRT

>contig42536 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53516.1|) 2e-35

MHDRRHINSSTLRRKRLAKLESLLKQGKEEADAIPMIADGVADEDMFISSNALDDGAEVE

LQQLCTDDAQHAREEEALAFMKEASALLGFRSCYACKSRFDKIHHFYDQLCPRCAELNFC

KRFQSSDLRGKVALITGARVKIGFQAAVKLLLAGAAVIATTRFPHDAAERFAKHPEFETF

KDR

>contig42693 Frame-1F|Blast-structural maintenance of chromosomes protein, putative [Phytophthora infestans T30-4](gb|EEY70359.1|) 0.0

MFAEFSEEVGVDSIRVYEERVLKRHHKAIEMRRKITEHEAKLRAQVDYLQSQDFQKPMLA

AKDRALQEAQHLKQLGEEEAELMKRIAALRKERSAQEEVRQHVSTKVNELEKELQEINLK

KTKYEERLGKIKRRIAAEEAVLERLKDHKTELFKRAALDHVKLPTIASDSGIKDVEMEDV

SESTSLENSDILLGNEAANQEVDFSSLPDAHVVVDDKEFDTMNAAYEKRIATLVSELEQM

QPNMRALDKFDAIQSRIGKEEEELDRIKQQALATATKFEEVKQARHNRFMEAFNHISGVI

NATYKQLTMSTKHPLGGTAYLNLENTEEPYLTGMKYNAMPPMKRFREMEELSGGEKTVAA

LALLFAIHNYRPSPFFVLDEVDAALDNVNVNKVSTYIAKCDFQCLVISLKDSFYEKADAL

VGICKDIHLQQSKSMTLDLTTFN

>contig42833 Frame-0F

MRLIKLRFRYRDERCDNNEPYNWNHHFTKFLRGMGNVQMVLNCAPVLFVASSVLCVLLGY

>contig42969 Frame-2R|Blast-50S ribosomal protein L13 [Phytophthora infestans T30-4](gb|EEY65891.1|) 1e-67

MSKVAQASKVVWHVVDAKGQVLGRLASQLAPILRGKHKPTYAPNVDCGDYVVVINAKHID

LTGNKWNNKLYRWHTGYPGGLKQRTAKELFERKPEDVLRKAVFGMLPRNRMRALQDKKLK

IFLDETHDYGKEVGENPVIL

>contig42987 Frame-2R

MGCLLPSRQADTDKKILENVSFKAERDDFYDLESRFPNGHWMSKAETADCEVKPFCAIDQ

YRNGTLPDSTELGNTLCDAATLKTCIVRLFVRDVAPPAQMQLEVARKARIPLFLHSPMYV

KTSASPLIDEINAEFTAESPENNYLVNAKSQVVNAVEAGGVNKPDAGANGGNYSRRRRPK

LSKAKNESLHVDFKELQIEEMIGQGAFGTVHRARWRGTAVAVKILVCQYLTAEILEEFEA

EVQIMSILRHPNICLLMGACLESPMRCLVIEYLPRGSLWNVLRQENVIDMGKQYGFARDT

ALGMNYLHAFQPPILHRDLKSPNLLVDSAYALKISDFGLARVRAHFQTMTGNCGTTQWMA

PEVLAAEKYTEKADVFSYGVVVWETVTQQCPYEGLTQIQAALGVLNNNLRPKIPEHCPPL

FRKLITMCWGSLPEQRPSFEVVLNILSS

>contig43218 Frame-1F|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY59568.1|) 7e-86

MVANLNDVLTPDVVSKSDFVNTEYLQTMIVVVPKNLEEQWLQEYSQIGDQIAEYGPKGSR

GNVRGSPIVPGSSRKLLEDGDCAIFTVTMLKGQYQSGFVDKEGNFESGTTVDYIGDFKTR

AKEKRFVVREFNYDPTSHASNEEAIAELEVEVDRLWSALLRWCKAHFGETFIAWMHIKMI

RIFVESVLRYGLPINFVVAMY

>contig43720 Frame-2R|Blast-transcription initiation factor TFIID subunit, putative [Phytophthora infestans T30-4](gb|EEY64604.1|) 6e-28

MPITTGPYDVDYMVRTAKGGAVTATGSMGYTVVDLHAIPIQWGVFPERKTHEPIAEEDED

DESKEGSVLFPNGTAATTSTTGNTEASGAEKTDRLKEKNKSHLETLRKQKRAKMSS

>contig43755 Frame-1R

MLHEDVRDSFEYQRHPDHSYYCESDDDIDEDEHNYKQHQDQYQS

>contig43874 Frame-0F

MLAGVDIGATGAKTRLELNDLEAVCVCCPGILEANGVICAAANFPSWKDVPLQQLFSDTL

GRS

>contig44127 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63758.1|) 1e-151

MLTCTACRLSFVSHLEQKGHFRMDWHRYNLKRKVVELPPISMEQFDYRMLQLREEKEALV

ANDPKQKQRIRIEEIRKAGSKTLLKCGPCNKTFTTTNAHENHLASKKHMTNAKKSPEILE

AVVTVEKKVDILFLSGSIALKAQTSETGKVTEEELSKEIEEYKKQVPLEKEDCIFCTHHA

ADFHACLSHMLKVHGFFIPDVEFLVDLQGLISYLAEKVKVGFYCLYCNGKGKSFRCYQDV

QKHMASLSHCKLRYETENLDELLTFYDFSNQYKNIKDASTDEIVEWETDSEASIDSNEDV

VEEEVVEQNENLVGENAVSVSETGELVLASGRRLGRREFRRYYRQHFRQDETRVSVLAAH

K

>contig44242 Frame-2R

MEGIRVFIPDEKLVWVPATVLSVDASGKVFRVRTQTLAEASESLHGYRQDVPAEERTIDL

NDDGMPDSLPMQNVLADGDEGGKHCVGAEDMCELGHLHEPAIVYNVRERFLARKPYTYTG

KIVVAVNPYQWIKEHYSEELRDRYTERPWDTMPPHVYATSAEAFHHMKQHRMPQSILVSG

ESGSGKTETVKIMMEHLASISMSIATRLHPTEHEETIVVKKVLKSNPLLEAFGNAKTVRN

DNSSRFGKFTQLQFNSDTCLVGAECRHYLLEKSRVVAQAAGERNYHIFYQLVDAKESTFG

FTNNTSAHEFRYLQDEALVLDGKTDLERYQITRDALSTIGLDEKEQHELFSALCGILRLG

QLDFVPL

>contig44884 Frame-0F

MTVEASAVKMDETVAIAEKEIVVETVAIAEKEIVVETEVKQPSDEVAKTIE

>contig45609 Frame-2R

MAGPVLPHQRSLLSYLYPMETIQATPRISVNAITRSNSRSLML

>contig46051 Frame-2R

MFIVALLAMHHRQPPINRYTLFLLVAS

>contig46257 Frame-1F

MSEDTWAADFAATIVAAVVVNQIVGPVLCAMGLSRAGETLKDRMADENDLKVEVDKEPDY

EGPNDSRMRPSRPSYRTSRYSVLDNGQTMPFYKVRNAVVIGDDEVAFEIALDLSLYGAHV

NVPLLDEERTKMWQQMNATIVNRCVQGDLISYKNALQDRDNTEAMSTADVIVFTGNADRT

RENIRLLKSLLGEGHPRMIVVAPDCQFSKEMRDQGILVIQPSIALANIATRMALLDQKSA

QALSNEISTTNDLSTAAYFLRPGGLRESVSEMAIEARRMALGRSVVNHHSVNYDRLYEVM

AAEKLPMPPPPSRVAMFGTSAADCDPFATRECDPFVARDTVVTRDNGSSFFVHDDDGEEV

PMSSTNAMLRSQSMPRPSGSRMSRPSFVNVTRDYH

>contig46507 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61797.1|) 2e-29

MAETKEVVRLYRLILKLAHRYPSIKRKAIIHEIKSEFHANKSITDAQKILEEMASVHAGI

KELSMYANLHPTQPNWNVEVGRDA

>contig47056 Frame-1F|Blast-phosphatidylinositide phosphatase SAC1-like protein [Phytophthora infestans T30-4](gb|EEY54523.1|) 2e-22 NOT\_ORF

MGTLILVLTHLVVRHPIQPAGDVAFTSSAARVQESNKSAIVSRLPSTLLAPFYIGAALAA

LTLVMTPFTQACLNPARDLGPRIVAAIAGWGVSCATG\*TARSLLGLFIWPITRGICGQYA

PRYSYLSSVTNTGPSCCGVDAAPTDGRGSNLRATGKESIGT

>contig47122 Frame-1F|Blast-CCR4-NOT transcription complex subunit, putative [Phytophthora infestans T30-4](gb|EEY67624.1|) 1e-135

MNILKAAVEAPSEVLSFSESPHKLAPFEGADASAVPKNGVWFSLDIVETLLQLSEHDCYS

DVRKLLDGAMKTCPDVLIANFAQASPCWNALRDDMFSELFSTYIMGRPNAPLIMRHLWSV

APKLVLYASVKCFYAATAPHIVSRLFALFRNTGDSFASAIHSNYFSFALALATMGANHDV

LNLESWLVERLASQRMAFAT

>contig48130 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57113.1|) 1e-72

MTDLPAFVSGSQLVFFDPQACHLPNVNPSNPGKMVDFIAHPNLVSNYSNQMAPFRCFGCN

FSGPFMGTIFRLALRTADQAQQSRLSNRIQTPAKVAEMLQEFAETLQTVLLFLRNVCKIT

IWEWKADDDAPTVQ

>contig48145 Frame-0F

MCLDDWHLFKTSGKCRYASRLEPSTIFLWLHVTLVEVEMVALAKILRNGKKHQVNCRFT

>contig48383 Frame-2F|Blast-fatty acyl-CoA reductase, putative [Phytophthora infestans T30-4](gb|EEY56496.1|) 3e-60

MSHVVATILLVYRQGISKQELVRQTDWLRREILQRGGRVMGTQGRSPTVVVDCALELLHE

LVMRRRKDLVEPAILSREQYPNMIGLGYYRNKLLHWFNLEGVLACAYNALVASNVQSGAN

STHIITSQPQKAGVDRQELLEGALFLHQM

>contig48578 Frame-2F

MTKFDKYGRLREAEALTYFTIRRIAPKKRQLGKV

>contig48691 Frame-1F

MLVIHSKCWNPPLSDSFLSELAEQTVGYCGADIKALCAEAALSSLRRVYPQVYASEDKLL

INLDKVVVARGDFAKAARKITPASHRAVSSFASPLPQAVKELLQEWLRQTLRDVERYFPL

FPRGKSAIDDAVTTVVEDCADRNDDNDEEDLDIYTRAHHEDCDICHGPGTDSLLRCDACP

GACHRACLLEMALSSEVVGEENSGLWFCLDCQQSGSAAMQRAGQRPQRCHDRSLASLQLP

RHVGFPRILVAGKPGMGQQYIGPALLHSLEGL

>contig49090 Frame-2F

MLHELWMVKTYLSVLRTQAVKKPHINGILFEKWCSLVKEPDWMCMNLGADPWFYLRTKNI

EFVAFFDSTRA

>contig49252 Frame-2R

MNMYQSTSTNSASLIDEAIQQWVVKKSQTTLKTITQPGATGVPVGAGTYDSYSQVLWAST

TSIGCAKAECPGGDLVVCKYAPAGNDGSSPWYIHAEMASKCPSGTKGLQGLCIVEGDAAN

NPIAPIPVAKLTYEVYPSYAADIQTILVDTARAIANGSAASFKEEKLTRLKEQTATTDGP

SPLSEDITTKNPSKSSTPSSSSTLPSSPPDASETSSKPTPGSSGKSNSVSISAGETKQGL

ADFSPKQISPKTVSEINISEDEEAPLQKPIGSFEKPSEKSNSDSPAALKTDKKMDTAELS

DDASKLDTVSSNSNDMAPGKVKASLDTGSQFSNQAAPESSTDVAPDDTPTTETPSEANSK

DTPPSPNVSQIISNQSNTADTSGGISAAGMAGVIVLVVVFVAAFGVVVSYRRNQKRQREI

MRDGG

>contig49533 Frame-0R

MQPLVTPNQPSDATLFVWHNGLTRPLEVLDASQQPLRVPLDEPQGLLASVQERILKQPQL

RRLFPHVTPETIHQAIQICERSGNGMKWTPLHEAVGPPALRKNQDQPRQLLVEAKFDEKK

QIELPDWRCGRFYSDIQENQWRFELGVGQFIDAQDANYKWFESRIVDTDVGFVQVHYRGW

SSQREEWLPRTSTRVAPLLTKTRNWRAFQVGDELLVGTEVVGKPNPEWRDAIVTACAYEG

KALHIEVFVNGTRQWMDAQDELLCPQGTHKVINADSNIVESVPYTINVDYFERSKKVLSV

AVHEDKSGRDAACITPVVANGVDANDWCA

>contig49968 Frame-1F

MNLICNLSMSTVNVHASRVKSGVDHWNGILTDAIVKCGRKSDRRLYLYGISSSRCPKCQL

RIVDKNVCSACHYELKTLRQCLRCSKKNEPVMWCVECDAYLCAHCHKKPHVLMLESSKPH

HCFAIDSASGKYLVEAAWSDKISSMVKAEYRLRLHDKMKTDKAKSKSNAASESADVEGRN

PPKDSVSASKLIAEDKALKASFSSVTAASLIERVKEQSRKRQHSRQDIEKGKKMGRASKA

SHSAELPADGMSLYDRVKAMHDMRAKAVQLIAFQASSLSANMNKSIPRQNDDRIEHKEDR

AIKKDDHSLLLQRKQDYQLEQAQKEQSKKDQENHEQEKSEQLKNEPRVLHKKELCQT

>contig49982 Frame-0R

MLIVREIITTMKVGILCAIILSGFIILFYLLRLLFRCVSKCKERANLREWFWRMENHEGK

SISRSESAVIAAGALCVNRNAQFGSSWDDSAIERKTLVSDMVGESRQQFRRHRTKRASQS

STTLHCSRK

>contig50023 Frame-0R|Blast-phosphoserine aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY57574.1|) 0.0

MMLRQAIRKQGHQLLQVQTQIATRDFRRSPRAMARILCSDPIDSMCPELLCAAGHDVTTV

ATSLSHAQLVAQICDYEVLIVRSASKVDRTVLDAAHQLQLIGRAGTGVENIDMVSATKQG

VLVLNAPRGNTISAAELAVGLITAVSRLGQATTEPSIRNSVIHGKTLGIVGLGRIGREVA

TRCNAFGMKIIGYDSILSSASSKAHGIEPVSLNELFSRSDYISLHVPLNANTKNLVNKQR

LALCKDGVKLINGAHAGLIDHEALLEAVESKKVANMAFDILAPSPPSDTWTKLVSHDNVI

VTPHIGALTTDAQQKVARDLAQKVIDALAGKSFKGVINAPNIGFGKRVEFMPLLSLAEKL

GSMQAQLLDDSRLKRVLVVAEGPKVTSSELSGQLVKGVLKGLLSHMLEEEVTFSNAKQIA

DVMGIQTV

>contig50359 Frame-0F

MQCTTLLRKPHAQNCREDKSLSWTLSLQPCTRLS

>contig50485 Frame-0F

MERGHRVSREESEDTFRVQDVKLSRNALTEWNLPNTNDLILDRPSFTKYIPHLDCAEV

>contig51235 Frame-0F|Blast-nucleolar GTP-binding protein 2 [Phytophthora infestans T30-4](gb|EEY65483.1|) 6e-28

MAKGINTTKASADNANRKIPKRQKAANMRDKSTIKRLNMYRNSGPIRNKAGKVVGGSLMM

KNKIGG

>contig51819-0 Frame-2F0

MFFVLISRDLFDNFTYSSRAIALLPFDAIICCCLAAGSIFLRRWAAVAVINRPVRREVPV

DIADFDISRRSVTKAIDRLNIGTDGWADGTNSGADSERLARPNCCSNCSPANIPLRARAR

LARSLDPPRAFTVASPFAARRMLRDIESHW

>contig51819-1 Frame-2R1

MSRNMRRAANGDATVKARGGSKLRASRARARNGIFAGEQLEQQFGRASLSESAPEFVPSA

QPSVPMFKRSMAFVTERRDMSKSAISTGTSRRTGRLMTATAAHLRKKIEPAAKQQQMMAS

KGSKAIAREEYVKLSNKSRLIRTKNISTPGKNAANR

>contig51932 Frame-1R|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY69813.1|) 5e-16

MTEEILRLQFGTAATTIGTQWLLLQQANKVANVPHVLAFEAKGRITRPIQATSKHEADPS

TWYIQIPHSEAK

>contig53237 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60187.1|) 1e-19

MSALLAGFTMSTIIEVQIADATSEPVLIMYGTVCCLE

>contig53372 Frame-1R

MGEYLPQVACLRSELWQLQQIAKHQTSVNTVLAATYVEQSLLNNEFSLTTLSTLIMLIDM

EPEEKRKEVFTVDAMLRVANLLLATLRSPAHDLRLVTLQLLAKYNRLNCLDSDDGMLSGP

SELLDVCVDLELSCKDISVDTEREVVRLLTRVKVLLRSPYTP

>contig53466 Frame-0R

MKSLRATRTMEKRWRSLTRLLVFANLDCIQKLSWPQLGWYDGHYEDEIKAHRVDDKVLTN

L

>contig54166 Frame-1F

MIASVRLAAASNFLSTRWTPKLRVKRTAWRAACSV

>contig54672 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54952.1|) 2e-23

MVRKKRKGVMKEAHATGAVVPNGVDLRLIMSQVPSNVALPAALGDSDLAAWYDTLCAAHG

SLYEQLKMLQLFRAKLKG

>contig54698 Frame-1R

MPSLGVQSCRTNTMLSRRRLLLLTVCCMHACNLVIAQAANELINVNSDVRCEAATDCILQ

SLKHSTCRNGVCVNNDLFPLSNKEIFGSMSAFVAIILASGSGLGGGGLLVPLYILIMTMS

SHEAVPLSKSTIFGGAIASFLLNVKKRHPLVHSRPLIDYETMLLMEPMTLAGTIVGVNLN

AVFPEWL

>contig55110 Frame-2F

MPQMPESCQARPVAIDVCEDLLTRREAFINDISAANTREVCATPHNLPLPVFDCHSTCND

EKD

>contig55301 Frame-0F|Blast-cryptochrome, putative [Phytophthora infestans T30-4](gb|EEY64676.1|) 4e-09

MVASLPPLEDAGDGESDTDFVEFAASLLDADDGESVLLESTLDAATLEAVHAAINDPQAS

ALDTILT

>contig55396 Frame-1F

MSRPRVYTPKLPMACNQKIEASAKCSMQCCTSFSVHEEH

>contig55815 Frame-0F

MFRKIGVTLSPFAILSIAEAAEQYDTDKKMLYAKENLLKSRSDFKSKPRIKDSKTTASTL

LGTGPPKFPYLLSVSAGDNPAIVINTLLTGIKLVGPYEEPARDTIKRITAPASALGLAAC

WVATQYSNLKKKMYRHISKGLNLHVNGKVSAEDVMMEAILLALRDLQMDNIKESTKNAYD

PINSPTSEVNNRLVFLLRDFDLFSDEEAERWLRWTHLVLHENLVHVILHITSTVTPSKMQ

WIQERHRLGLSGDASGKWNDFIGILVRPAHGLVDCSSANEKLHDLAVRL

>contig55860 Frame-1F

MSTDKNPPALKKNQRLIPEEAAKSTLAMT

>contig56069 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61457.1|) 6e-06

MGSLDVVGSHKKFGFYTRPRKLE

>contig56304 Frame-1R|Blast-hypothetical protein PITG\_21328 [Phytophthora infestans T30-4](gb|EEY60469.1|) 1e-23

MSAQSFRLWQLPGLRKFSKSIVGLFTLVICQDEH

>contig56546 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54845.1|) 7e-18

MRVPAIATCLRDIARHGSCITELQLSKSSDLVCRQLICEHVGDACSCRLALALERVPHLR

>contig57178-2 Frame-2R2

MYVKILVKHINGIVASSGAIGKELPDASDAPP

>contig57206 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68653.1|) 3e-77

MFARKCDLLLLGASSSGRRLSALVDSKWVRSAQISDNPALLIFDCNHPSLYHCGHIPDAI

PLPLATSLLKDPTPASTGVVSSRIFVDAVKKLRISNDITLVFYDDELSLKSTRMWWVFRH

YGYPLEQLKVLDGGLKQWQADGNAVETGNSKDRERQATPWTQVKNLHKLVGFEAVQKGIA

DPLTQFVDARSPDEFNGRVADGNSRSGHVPGAMNFDWSNSMNILQNGKFYKKEVLDKVFC

DSCHLDKDKPVITYCQRGIRAAHLAFALEQISGFKDVKVYEDSMLQYLNREDTEVA

>contig57783 Frame-1F

MKNVFIPLAVALAAVPSYGQNFEQCSSDGFKAGSFNVSRSTFSTNVMCITYLGASDTMIS

WM

>contig58368 Frame-0F

MFLSGDKKYIVKSLAENEARFLCEIATTYVAYLIAHPQSFITKFYGCFKITMYDRRFYFI

VMENLFDVMEVGVQIHHRFDIKGSWVNRSYKRPRQGAKVKCRHCSMMFQYNRTKNTPCPN

VVGLHEPNVVLKDNDLRTRMRIGREEGVVLYEQLRHDSLFLCQLGSMDYSLLLGVVDIEF

LVDPPSLVDSHGT

>contig58382 Frame-0R

MSCRPAKAPSCSSKEFKATSRSSQENDMCGRVIKPFLKQKFVELFLLFFIIKLL

>contig58470 Frame-2F

MLHLWILHFWLACAFSCDRLCPHASAFCGSITVDVGVRTSRRLRRIRRGTR

>contig58852 Frame-2F

MPTNDVHEREPILSSLEMKTHLLPTVPCDVPEHILLSTNQAGPTAV

>contig58939 Frame-1R|Blast-mevalonate kinase, putative [Phytophthora infestans T30-4](gb|EEY57207.1|) 5e-12

MSSHNKLPLRRTYSTSTHNKVVDGLEDEIHYVPIPSEKVMTRIES

>contig59521-1 Frame-0R1

MLMACRLVVDLYFNNFRKLEDFAPRSSDKIT

>contig00588 Frame-0R|Blast-ubiquitin activating enzyme, E1 family, putative [Phytophthora infestans T30-4](gb|EEY61480.1|) 4e-55

MSMEGELRALDRQIAELMQQKAAIQAKLEDNRKTLRSNEMSAEVVDSNPYSRLMALKRMG

IVEKYENIRDLTVLIVGLGGIGSVAAEMLTRCGIGKLILYDYDHVELANMNRLFFRPEQA

GMTKTAAAKQTLH

>contig04012 Frame-1R|Blast-3-phosphoinositide-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58380.1|) 1e-91

MACMVFQLLVGRPLFRAENEYLTFQQILNHPADEFAYPSGFPPVAQDLIDRILLQDPSKR

LGAGTDEDGMGYKALKAHLFFEGIDWDMVGSAQPLYMPEIGRLPPTDYDGAKEDWLFAGV

ATELQVSSGLV

>contig05301 Frame-1R

MAPSCVLCCNDIDNKSRFNTVGVCNHYGCCSICALRLRQLLGQTACVVCKTDMPRVICVI

HEDASFESFQDWGDNIGPAYVYDEQSAMFFFKENYMQHIRKLRDPICPKCGKSFATVEAL

RTHVLNVHDLQYCSICLEHKKVFIGELGLFTKEGLKKHHLKGSRYEGFIGHPRCDFCFSR

FYSTTELYEHLRKHHFECDLCLYHFHVQNRYYKDYPDLENHFRADHYLCEEPSCLEKKFV

VFPSHLDLQAHLTVDHPHIKTSRKINVHFTIRRASSQNTNSEVEDSQLIQSRSGTPTINV

ADFPSLSGSESAIAGPTFSLWENQSVSHRRNGEDFPALGSSVSNPSHSFQTAVIPPLSAA

VRAHLNTNQWTYENPDLASAAAVLGANNPLLKVLKPARKNFKGKKKGRPNAGLNEKVAAL

MTETNPLESKHDESSGNPSSKSALVLKIRQVLGSDATYEVFREHCKRFRLHQLHVPEFYA

IIRAMLSQQAFHDLFLPLMRLSPDHQQVKTFFAYHQERSQNHDQNKTTPKVPKTLSKKNK

KPMNLSPERSNVSLSHSGWGNAMKESGVSSALNRHASASVHNSNVGSILRREMSATSPWN

SSNQWQTSTRAASTEARAGHYDPSTSTMESYPSLHPTAASLSTELRTGASLNHLTTPLPS

SRELLPPSTNASFKVAKHDFPELPKASRPLGVQAVTRATWDDQVQAIAQHRSSSTWNASR

DTSKKKHKKKNMTLQEMAMHFG

>contig07729 Frame-2R

MAMKRSGGGYMRPCKFFAQGTCRNGNNCRFSHASFDNKQNNSGFNAPSVSPFGTSANRAT

SGVENAGMTEAGRALAIEELKNASIWLLSGFGIAKGLPNVVDGDVSAEEARWEAYQDLKT

SGNCMQSTQKLQALAKEQQNQRHRVLTLLENYQSAQKLFAGETLATTNSFNGQNPVASPF

TSGGAVNPFQSATPSTSPFGDRSVATNPFQTATVPTASPFSIPGNTEATGSTFRSNSLST

TFGTPSTSGAQGSVFGSSAATNSFGGNATTLKAATFGQPSTPTTSPFGALSTSTFGVTPA

PVSTVSPFGNVSNST

>contig07844 Frame-1F

MTYIDRKWVYGSPKQSEDQSLRRTSTKSVKKNEKKNDGDGDLFNFNSNVPETTDFADFSN

FEKGSKTATIEAQFLGDFATFDSPASTVKTDDDFAHFGDFAEFNSSAQKSTSKTTSSASA

SKFGLFTIAPPPNSTYTSSSVSTPSITNDLMGLSPPQKNNDNHFDSQARVSEPISQRHLV

SAASSSIKACNDVVPTSQAASLLNTVAILSAPAEQLSSPFVALDSNKASSTSVFDAFAVS

SPAPNEGSNVFDAFGNGADVFENFTGPNSSSRPNSANPPDSFFEKNDIPFANPVADPFAA

FNGMQSNCGAYPGINNGASTVNFGAPGGNLCQQSAAIYGQIGYASGTTGNSSGQMPAQHH

RPAYSAMIQGQNAFPAGYSQQQQPSNLIGSRTQQQPFYHGTPQQHGFSAQNKSLCTIGQQ

FSGQPPPRSAEPTPQPVSVDSMDDPFASLSINNLGYGSSKSHPALARTGSECAMSNHAGS

SALQWKPPASPMHSMSYSNAQHQSLGLSPPTVPLPNSLAQSYPD

>contig08658 Frame-0F|Blast-F-box protein, putative [Phytophthora infestans T30-4](gb|EEY54318.1|) 1e-111

MCTCHQLLLVARSEVLFEALCRRIFPIQNPNAAIAFARNTFRLRRFSTWFEMFHSRPRVR

YNGFYWLKVVYYKKPELSMWSDIVPGTILKCIYYRYFSFRRDGTVLYGMLLKTPFEVEAY

LGEQRKGVYCGRFHVHQDEVVVTVPTHCNNVNFRLQITQRKRGRNVKLILKEHFASSEPD

GTGWITYYDTAEEEFYYYRSCCL

>contig09279 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58290.1|) 1e-28

MDSIKTSLLGDVHSGGGDIDSLLSNEANVIKQSVRRLHEPYERHRAHDLRAECYRRGIRP

IKKGPNANDNKGGYVEFIAKIRCEWNHKYDGRTFFWYYIASSLETNGSRDWGRDYRGPFG

NSDN

>contig09316 Frame-1F

MAKTRSQTEATMLGDKERIPLSSSPPLAERHTTWQFIRTLLWKNWTLKRRHPVATCMEIA

LPCIFIFLLGLLKGFVDDVNVPSGWSDDEISGTKGTSYNLYQTSGTYLSGISADLPKFTM

HETSLWGILLYMGRLSILNGMKMGELSSTDYDNCTTGVTVRGLVDLDPTSSYAVPLSCRG

KVTPYKIAIAPDTTFTRDYLMQTMELWYPRINLRNTSTSAVIPSFMESVEFFKTEQALED

YISGTDYGSSLSKPLIYGAIVFNSYPIEDQIGSFRDIEYTVRLNSTVGRQDSTGSIPRTG

GDPSEMAFFQKAISVNHYPRYAITGFMTLQTLITRFLSCMPEWDSTNKTTTGECQRTQTT

AVESTELDDALLSSLDDDVIISSAIQQIMGPDVTYSSLIDLLPDETLEAFLKPLRQAPQP

YLGASVSPFPIEAFVSSPFYDDVADVFPIIFILSYLYSISRILVVLIQEKELRLREYMKI

LGVKEKAIVISWYMTYVFILFGGAALQTLMGTLNLFAYSSAILLFLFFFLFGLSILAYGF

MVSTIFSKARAGAFVGMVLFFLMYFVSSAYTPETPENQKMFGCLLSPVALTLGVKILSNL

EATGTGINFSNADVLNDNFRFSRSLLMFVFDTLLYTLLGLYFEKVIPKEHGTTLPWYFPV

TLSYWKKDRKKYEGVTSGIESEYAGEALLDNVAVDVTYNVESVSAELREQERQGQVLAVQ

HLRKVFSVPGGEKAAV

>contig10286 Frame-2F

MHALGDFVQSVGVCIAGGIIWYKPEWQIADPIATFIFSLLVLATTIGIVGDSIHVLMEGT

PEGIHADEIEQGLRRCSSVVAVHDLHIWSLSAGLPSLSVHLVSDDAETALHAAQRFLMSM

GITHTTIQIEKTATLYPRNCKSDLKCGQDSPKHNG

>contig10804 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57242.1|) 6e-26

MQRVPKLAPFIPSGNGVLDHALDLLALSNEDILFDLGCGDARVLVHAAEKTSARCIGVEY

DMDLIRRARTRV

>contig11616 Frame-0R

MPSVTLYRLLARNLMMLEPQKAAKDSDEALSKKDAKDCCRRDKGGRLLLQTYVPRLGCRR

VPLALIYT

>contig11779 Frame-2F

MDYELGDEKLINNEANGPTFEDLAIDDSLSDLQRVTKYVCSNIALQRVIHVKMLHETAIT

VGFQATCNQLLPLLEPLVCDVEYVVRQHVALQFPLLCQFLVEAEFDVGYKLMLAKLIPLV

SKLISDDQHEVRSAASESLVEMASMVKSEDQGQHILTIVLPLAHDDDNEQFRISAVSLYN

GLAEHFGPELCQQFCVPELISLSEDPVFRVRKSTALSFSNVCKTAGVEMGRIRLVPA

>contig13306 Frame-1F|Blast-endoplasmic reticulum-Golgi intermediate compartment protein, putative [Phytophthora infestans T30-4](gb|EEY57043.1|) 1e-108

MRQRATKNDVDDGGQGTHENDGGITRSVRSVLRKVDVYPKMHREFKVQTEFGATVSIVAG

IVMLILFLSELNAYWSIYTHEHMVVDSTLSEKLQINLDLTFLAINCHDAHINAMDVAGEL

QVNMHHTIIKTRIDSKGHEIATIEEKHVEKALPADYCGSCYGAKHPADISCCNTCDDVKE

AFLHSDLSLEEAEKKEQCVRETIETEKLAQDGEGCRFTGKMFVNRVAGNFHVALGRTFHR

KGRMV

>contig13650 Frame-2R

MNIAMPLCKAHRETPVPDMVSSLYIVTKERRHVSTANSLFEISYLSNLSLPISKRFYVIK

VADKVGSSSSHALMLKEPVKMVLAINDVVTGFFKEKGG

>contig14552 Frame-2R

MHYAASTGNAALVSLLVSRGANVNQRDSRGATALHWAVFEGFQYTAMLLVGYGANQKLCD

SEKQTPLMIASALGDAFLSKQLVVEGAPVHAKDKHGRTAMDIARQGAHFDTARALKAGAS

DRFVARASHQGASVVFFFGMVFTTAFLSLTFAVPCLQPQDTRYTEQYQAMMLVGLTITCI

LYIYVYVKDPGYVPHTTRPAYELLATEENNVPCPTCVTPKPQRSKHCSACRRCVYRFDHH

CPWINNCVGIGNHRTFLVFLVALSCFCLTIGWISFSILLGYLPLYPASNKGDGYNDLIVW

SWQWLEPPNWTLAGKFHKESSTVLLHSIHIFLLLCAVIFGVPTATLLLIQLRNVSRNLTT

NEVFNKDKYPYLKTPMDEFYNPFDKGCAHNFAEVCRGAIPNQEVNDWKTSGR

>contig15177 Frame-1F

MIIQVVLATDMAKHFEDVVLFKTNILSAALDDGAVLVKNVGDKKLLLKMILHTCDVSNPA

KERETMLRWTDLVLEEFFVQGDMEKQLGLPVSPFTDRDTIVIKKMQVGFTDFIVTTLFSV

WARILFNVNFSGYRALLVNREFWASVSDDFKPHMIKEVIRDLNCQQQRDFQAQNASLEEP

VFLASLLQHYGFATWY

>contig15326 Frame-0F

MKSIEEKWRYLKRCQTDCIGKYKDHSGTFEIFGWSKDATYSAADLRSRFRELCLKDGNVA

IVRQAFDSLCDILERQNEGDGGKTSDEVIECILKSQLYLLHKYGYQFYSYESSTLDLLIR

VLSSHLVEDSKVQSLAMQFLQRLLSVAPKNVPLLVVIEGSWKAILILVERCACGHDAADK

ENIFIILKLLLTAEEGVQSILKESKKKLANEVNLSKKLDLSTLADNDSSSYFHATEFTSQ

DSKYAQRVCSMLDDVILSFENIQPWHIQKMSFDIASSLSRSIELQQQIMASTRVFWKALY

LILASAENSSVVNNEQESTTALEKQERDMLESAFGALRSLALGPSGGSRSAGLEALANLL

PMDFLERLKKPNGHDFCAILLSDIREPTCVWNENTRTELSQLTEDFCTDPNGDGISFLEN

ASRYMYDCLSSEPYVGGVYLLILLEKSVGNLQTITEDILYPTTAVDFIESLLCFLNENRD

PKTGIYSDTMPALDCLSLLCDLPAFRPAIVECLEQHVDDEDAVLASFSVATLGRYLLPFD

GDSDAKVAASISSRRSLSAYGFRAKTDAPIAMDAEYGNVDYLARQEMAILIINKICGFKC

SLERMLAPFCQFTWCLQVISDHLGYEQAFYALSCLAELCDTCLVIAKYVQDSGLWVEILG

IALQSRQHVLHEHFLRAEALREPAFEVLYALLMKNLDLREKMYSGLCRFLPYPIVYQIHL

DPNKATRFFDDNHDKSDLIWNSHKRTEVRKKLDQVICRNRAERSIVKRDSVLLDDETDFI

PYPHNYVAGLYIDRFLSQPDAKKLTNPAYNLELLFQLWRKKLNQMIRFDLSNPPDNLKTT

VDEIDKYTMAMTHILRASLDVDESIANSRMAKQILKLVLYCNEHLITGFPYRCVLRIARR

LVQFPEITSKEFVELLICRVTMQHPDIPSLLKVLRRILEARNKMLMESETKDDPEYWLRD

LHYYHQMLAFLQGLLEKKEQIEAPVLSNVNRVLRIILAEEPKDNNLKHISRSFMGHWHNF

TLESRSIRNSINLSRQRGTKLPNNAKTTNVSSFKLNIMSTQGFDVDGAVIEDVASARSFD

VDNERKPSNRVEIKDESDDREVDIDGSFIQAPPRSINYTGNGVELTEAIAPSSFRYKGEV

AHNSPLPSPTSVRYSTLRARYEPIGTQYHSRKAAEYDDHDVNGVYAIRSRRGSLPMRVDD

TVKQVNGNGKFAATQGNIPLSSINVDSFVPQAPTICRRDLAMDGAELETPGQLNQQGRLG

AKKSERRYSLLDIWKAPSSAAPNSLLTTLTISRRSRRAAIVTNRLTSKKKRWFNR

>contig15898 Frame-0F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY61039.1|) 2e-16

MANRRAHAKEGAVPHINIREKVVIKEIE

>contig17405 Frame-0R|Blast-Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4](gb|EEY59471.1|) 7e-27

MIFVVVDDLVPETTQSGNQKLATFGTIVGFVVMMVMDVALG

>contig17632 Frame-2R

MPVKYYVFLHIAFVISRLTEGSAACRPMNPPSYPLHGPGGMAPPTSSIPGVQRPAGVSNP

NYFTDKKKGEVNELKNLLREVTIEKDLKRKREIIKKVIAYMTLGIDVSRLFSEMVLCVDT

KDLISKKMVYLYLTNYAQKNSELAIMCINTLLNDCRNEDPMVRGLALRSLCSLRLDSILE

YIHDPLQASLTDTSAYVRKTGVIGILKVYSLNPEIIKESDMIDTLYNMIRDRDPQVVSNC

LVALNEIMADEGGIAINQPIVMHLLSRISDFNEWGQCNILEIVAKYKPTGPDEVFTIMNT

LEQCLRVSNSAVVLGTAKCFFNLTQARGMEPIQDQVFERMRQPLLTLMAGGSHEINYCVL

HHILLLVGKKQQIFSRDYRQFYNRYNEPTHVKYVKIDILALVADGANVADIITELSEYVT

DVDQELARRAIRAIANIAGSSNLLVNTVPPQYLGTNVPDAYGQQAAEQLVEQTQDHILDT

MVDFLELDLDYVRDESLIVMKDLLRKYPDKRHDVFASALPHCCGRGSASSESCSRVDAWR

VRSRLASSAVRVGKAD

>contig17892 Frame-2R

MVWSKKSSKSWTGDRKVSIRTRICQCEEVILFLCPLIKRVDNRLVHSELVI

>contig18062 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62701.1|) 8e-59

MRHRELYEFIDEYLVPSDLTDRIPLFNATELATITSLDGVALNPDDIIVSDGRLNYNFRN

RNPVDNVSFFASRDLDSKFYIPKEKVSLLFPEKFEERIIRVYSRNKSPKVHAAIQHAFHS

YIRP

>contig18260 Frame-2F

MIILYLYIHYTKTTGSVTPFDRKKKLHLLGVMRLPTALLLAAVALLVDTDPVLSAELING

IPDAFKLAHTRQFNETKRVFKPLPNNHDERTNEDLMLLIRRGAQKLSDLLEHAAFDLKIS

EGVSAELGNDLAKLPRKRDVLSTSKRLLENWTSWLRTNWPQHSINQLIEKFGEEGLIWMS

IEWALRQPEPDIKTNALQLQDTLMKTWFVQPRNVMSVYDKLLFGDKKNNLLLRPLQTLFD

YGDKFNKEFKGKTIALKFSFAFYLFHGLSDKDLAKTMVEAGQSSVPKDIYRRLKSILFRM

WYNELKEIATNNELNFLWPEYKKTRDKISS

>contig19128 Frame-1R

MDTQQHFELSASPSDSSTSATMLRTSSSLASLSAAISSSTNTMSTSSASLSNGRPPLQDA

SALEIAYSTISPKVEQPQYPIHIKLNLIDQNPLTSSLSSNGELTSCESPYPMTPMTPGGY

SSSGGDLSKKQRHNLREQRRILRISNQFDILRNKLEAAGYSSSKKDKYSVLQATLEYISN

LERNRIGSVTPHPQLLHHLQHTSPHANGGVSQHLPSQCSESTGELSITAPPHSHVNNKSQ

AFMIDSMPSPVPALSMPGMPQATYPLDIDNMYSGSADSASDAGAGDIEGSAASYRDVFAS

SSMPSILAKLDGTIVEANALFLELCCKNIDELRLHSLYTMCTAMDAPKMYNLVGKILSCE

MASAQSKMMWHFSKSGNRK

>contig19858 Frame-2F

MQATPTKQNRVLIERQPLSRRAAPSQDRPFACPIPTCTGRFHRKFTLHEHMKTHTGEKPH

ECPVAGCGKRFSTSGNLGRHYKLHAVDKLCCPMPHCSRQFTSRQKLFRHLKVHVANTPQT

CDIRGCGKTFSTSGNLTRHRRTRHVDRMAKDSRRSQTLFFSKEPPPHQQLFMYGLPSRIM

HYPAVSGAMLVKGPIWSAAPAFDAVTAGLEPPRISDKDVQDLLDFLFVENPATAPDNYT

>contig19920 Frame-0F

MLWGLFLVAVVREALLILGVLRALQECGIHVDVVGGTSIGAFIGGMYAMHPNSLDLVEVK

VRQLSMRLSSIYEKLCDLTLPIASFFNGSRFNESIRALFYDLSIEDFMLNYFCVSTDIAK

SRMNVHRSGPAWKYVRASMSLQGYFPPIFENGSLLLDGGYMNNLPADVMKEEGGIKYIFA

VDVASESCTDFYDYGTTLSGWWVLWNKLNPFAKTVAVPSMGDVSAALAYVSSEQHKDRIK

EECVDLYLRPPVKDYGTLEFSKMEEIIEVGYKYALPRIKAWMTRVLDAEPDADIKKASVA

G

>contig20573 Frame-0F

MPETSTPVAHADEKAPSPSTVGNTFMRQYYHFLAKEPQSLHRFYKAESRWCHGVGSHMEE

PIAGQRAINDQILKRGYAGARVDLDAGSIDCQNSQGDGVLVLVTGVMTLRESPTPKPFVQ

TFFLAVQPKGYFVLNDCLRFLEFPGVSSYEVAVVGTKNGHKTATVLPPVKKVTAAIPVSP

KTSSSLPVKTANLTTTVNSLPNETASASPMKIPATTAASSPIKNSIEKVTAVAGKAPSPG

ESTEEVPTRQNKTPISTARPTSTIAPADPVVPVHAEPERPKSWAALFAASKTTMAVSSMA

TSVAASGKPTTPKIVVALASSPSSASANPSTSSPRIQKSPKNKASNGKEKEHKRLYSLFI

RDVPAQTRENDLRELFQGYGSIAGVGVVAQRGFAFVDYHEQGSMRAALAETKEFKVFDKV

LQVDERAERKEGQRSSLRGNDARGRGRGFNKGGRGERKEQNGDEAPYSTKSEQQFSRRVK

TGNRRSGKVDASVNDRAE

>contig20599 Frame-2R

MQETRSVGSSAGSAAKSYSHVRVNRWQNIDAPQYFESTYNTLNYAPARVVVFGGLAIIMG

VFVLIHTQHLVATAVLSRSSVGTTSPGARAALPRIRASASNCSELWIEQRIDHFSWLAAE

ALDPNKTNSTPSGLPAMYQQRYLVNSQFWDPQDEKAPVFFYTGNEGDVTLYANHTGLMWE

NAQTFKALVVFAEHRYYGKSLPFADKYMDHLG

>contig21174 Frame-1R

MPSDGADVADVQEAVLAKFFRRMLLIYPFQIVPNRLHVLDVDYTH

>contig21246 Frame-2F

MLTDVVAAYSARQNLKDSVSTTKCHLEFDQHGVYFSQLPDLQIDASFPLSNAFLLVFDHF

VEGTATLSRRNSFVLAPV

>contig22496 Frame-2F

MFCERTVGRSKMRSLLGARAFEWAKGVAVCTKISFPTRWMMLRIFVMTIILGLSQCVDGN

SLPPRTQ

>contig23961 Frame-1F

MPRFATFAVTITTLLPLIQGFTNPITVKGYKLFDLTTGDAFGVKGINYYPRPNAGELDTN

NVDFFTDDHEEIWRPDIEHLAQAGANVVRLYAVDPSKSHDLFMCALRAKGMYAIIDLGAN

CENCSITLDEFPTCYP

>contig24366 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62537.1|) 1e-157

MKLNLLPKAFDSWYLLVGEQTRNLAQLSLENTPNNELPTPLSIWLDMLDLLQRPGFSLSE

CSGTLSMTALSHQFFAVVFRINLTAQNEEICAFRQRIDVSMAFFMRFHLDDLKSSKEKSD

ALKTVDSLAISIVERFPESKTAAEYLLLRSEDQDTPLMIEKSKEIAKCLSASYPNSPMVL

VFQAIECLHVGDTNQVCFAMSCLIDG

>contig24704 Frame-1F|Blast-26S protease regulatory subunit 7 [Phytophthora infestans T30-4](gb|EEY56622.1|) 0.0

MTAGECQTSNTKQYDNEGDDLLAGPETVLDEGDIALLKTYGLGPYSRVIKQVEDDIKKAQ

KAVNDLIGIKESDTGLSLPSQWDLVSDKQMMQEEQPLQVARCTKIINAGEEDAKYMINVK

QIAKFVVGLGEKVAPTDIEEGMRVGVDRTKYAIQIPLPPKIDPTVSLMTVEDKPDVTYDD

VGGAKDALEKLREVVELPLLHPERFVNLGIDPPKGVLLYGPPGTGKTLSARAVANRTDAC

FIRVIGSELVQKYVGEGARMVRELFTMARSKKACIVFFDEIDAIGGARSSSEEGGTDNEV

QRTMLQIVTELDGFDPRGNIKVLMATNRPDTLDPALMRPGRLDRKVEFNLPELEGRTQIL

KIHAKSMNCDRGIRFELVSRLCPNTTGAELRSVCTEAGMFAIRARRKSVSEKDFLESVNK

VIKGYKKFSSTPKYMVYN

>contig24771 Frame-0F

MSKLIPRRSVLYILHFLRHKIFICNQFP

>contig25013 Frame-0F|Blast-DNA damage-inducible protein 1, putative [Phytophthora infestans T30-4](gb|EEY58045.1|) 2e-91

MALMQMHMKAASQKFEEQQEIEALERNPFDAEAQAKIAERIRLSNVQKNMEIAIEEMPEA

FGHVTMLYMPCEVNGMQVKAFVDSGAQSTIMSSSCAERCGIMRLVDKRFAGQAVGVGTAT

IIGKVHMAPLKIGDEFYNCSFTILDQQGVDFLFGLDMLKRHQ

>contig25178 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63589.1|) 6e-23 NOT\_ORF

MVTASRVLLPLVFLIKGLAHHSFLLDLNGISCAFYRVDI\*TF\*FRFVLRL\*TVTYLLYRI

SAENEKVLQFDFFLVAGDTGSSCCEIKPLGHTFFNTQLGQCLLAVCLGPELLVQWLQLTL

ALYSLHAMAATDDEW

>contig25581 Frame-1F

MAQICMKNDIMLKRTVSYSPQQKGVAER

>contig25970 Frame-1F

MPPPPTPCLPPTPSIRGSSWRQPSPIQTPECTTRTLAFDSAASSIANEASLQSKKRRRRV

DQSAAFITDRRPLDTEENEELDESKQMWTAKSAGNASRLSSSVRGQVEDNQQRTESPFNC

QKATPNAQQIFKADNRQMTVV

>contig26333 Frame-0F

MTKAPTYVVKTFPQHFLEDLDFRPQRIKKNAPHVCLYPINGVLNSESSLALYDCEKKKVY

LYSNFHWKLKVEYEVPNLLP

>contig26463 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY54846.1|) 8e-68

MVVFQVTLFNYSWVRLSIGGLILGVIIRLIAALPTIFNGLRSAWFILSILSFNGVSYAAV

LLVTTLPLVEITENCLEGATTGFVASFTILARMAALAVSDAIRTSSPELKQDFSKAVIVQ

DSPGTRKRVLCFVMANCAINLLALAPILYLLPRQKLEAQEMRTYGGSSRLARIAIIVLFV

GLITYTATVNVYAFLN

>contig26580 Frame-0F

MGVRSNVSARKMARIQQLRASMRFESSSSSFSDISTDGIDEKEVIGNLATRGYVVCLEDL

TAKEWKLMFGDLFEILGHETYKNGQEHEVDRIIEDEKEIDGVLVTNMCRIIKTFVTFPAV

HFLLCDGIDGDESTGIVARLAAHAYNPEIASLLHGLIYLGFHRSFDFIPIIRCLIERIVE

QMPPRLARSLSSVSSTSTVSSTSTTSPRSPTFRSLTVTPTALSSIEAVHSTSSSYAFRTK

PLIHARISGCAE

>contig27622 Frame-2R

MHFYRKALMYIQLQLIDCGAITARIVMSSEGLRARWKLRRTEPGNGIELGASSANAFFTS

NRIRQRGNRTTKAPPQNGQQATAKSDRLPLNDQNEKETKKEQPFGLDMPTHSQLLAELVA

VDELVESQTQGFDMYFSTWKGELLADFNLLFYGVGSKLALLQKFASTWLSDGFVLQVHGY

LPVVSLKYVLEILQKKILNMNVKPNQSLSQQCREMSKSVLPKNVTRIYLLVHSIDGVALR

TVEAQTCLSWLAKVPFISLVASMDHINGPSIWKEEDMHRFEWLSQNLDTCVPYTTEIELT

LVKHTKAADVTSSGVKFILQSLTPTDVATLQELARQQLAASNSIPRRRNVKLTKLVPY

>contig27815 Frame-0F

MAAPKMEDNNTLGRQLSVANEEAWLSLGRIAEMMGDDENTMVAYEKVLSHNRLNATALFA

IGCCYEKVEDYTKAADCFRGLVSLNEQNSDAWGHLGYCCLMMNDLTSAHTAYQYAMYNNP

MSQKDPNMWYGIGQLYERLGSLEHAQESFEAVLRFEPNFNMALEVKFRLGIIAKQRGDYD

GALERLKSVLHDVQANVQTTEMASDIWTQIGHVYELKDEIQLAKSSYLKVAELNPNNAKP

LQQLGWLCLKHSEHPSAIEFLKKAVTIDPQDGKGWYLLGRCYMAVQEFEEAYDSYKHAVT

TDSQNPNVWCSLGVLFYQLNQHLDALDAYSRAININPNICEVWYNVGTLYDTCNQTSDAR

DAYQKAAELGADAQFIRERLELLRVRETGQSTIGMAGANSAPGPSEPPTTSPMPTFSSRP

SPESQYQVPQGAPSQGNAPNGAPQVSQGAPMAHMLRTGEAPMNLSMGNASTSNSMSGSGP

DASSGLARGVPNASMNMMRGMGRSTPLNGGGMMPRGVMGGMVPGMQHPQQTQQMPSQHPQ

AQAHAQAQAQAHAHAQAQAAHHHAQMQAQMQAQQHHAQAVHMQQDGRRGMSGRPIKDENK

IGAMRYTMESDRKLQAPPQRLAGLNPKNLGGPTGVPQNGRRDRFPIPMSDPKQHQHPSLQ

PPPGRR

>contig29228 Frame-1R|Blast-Rab32 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY57913.1|) 6e-51

MSERRVNAAQDAVIKVLVLGDAATGKTSLIKRYVHDAFSEHHRTTIGVDFALKAVTVNGT

TVRLQLWDIAGQEHFRALNRVYYKDALGALLVYDMSRPETFDSI

>contig29822 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60562.1|) 1e-26

MVEQDGDHYLILPTDTLRLERVQSAIDRIEVALIQLQHDSA

>contig31126 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56317.1|) 0.0

MKSIVLAPYRVEVLFVLCTLLNGKRKVDFQERLAGMGLVQILNLMFDKFEWNSTVAPHPV

HEPLHGPGCDCSLDASLKIQFLRLIHNYCDRDYSDSSSKLLLLSELEIQLMKEGGSASIN

LDHADKGVLSKIIHALIQQPADSIYRFWLASCVEAFLRRAAPSEQLYVARTPLLQALIAE

ILSGGAFRSQGSFQSAFDMLGEMTKGNWETLQLFHGLLSNTQFAAFMEVVIFNLVDSNVF

IRSMLISSEKFARLPEFGTFEKANDFEMDRMSEFFNVNLVRLLRDLMTIVTMDDINHENI

CCLNTAIVILVYQHRRKRLPILLEALRDYEDASGKLGYVCDNFRGLLWFWIQYYTPRGRD

RLGLEHSSEVKFDEWRHVVSLLCADDGSATALISTPVRLPPSPYSRLYAASRERCT

>contig31377 Frame-0F

MGFVALARQTLIVSRFQIHASTRLSTAIPWQQMHKHRVPCSIDPPFLSTRTSSISFVRTK

VSERTLRRKKLRVNKSQKGVKVPILKETLRKLYLRTHPDLFGQYPTQQRANEESYKELLG

ILDAIEKHNQFPPAKTLKLPFFLKTPIEGEFKEVELQLRTTGGACNTLVEEALGQFFSNC

GLPEVFQWDKGSWGKSVGKNAVENPNLGFEMEDETHEDDRHDAKREELHSSAPAYNPVDR

KAPEDHSIEKVLNELDDTLQLIAVVPYLDDDDEQQQAIKTHFELGSGLDDLDAQGYSLKA

GVIQLWQGERNLQALIPGLDGDSAILMQRILLHTVDIEKRLENVIAQSSLDDKRFTAEAC

NKQSE

>contig32123 Frame-1R

MPQALVATLSPDLWTQLLMFLTWRDTNAMCCVCCVLNRIVNEAKKWHPEWRCSVLGPSVN

SVESLKLLQRNHLQWADTRFTPNLVILSAASKDSTPWRKGKYWENAIAAIEKSRLLPRAC

RIVGVFSMNAVLGSTEEVEMNDKRDEISVTLSISVAHLPETTIEMATFDRKDLRRSQQGD

HIENPFLTLKANDSPAFMLFGVNDQSARQLTRILAKWHPTATIIGAVSPLQHCCVPVATY

CKVSTDYQKPKARKTYRVKQEKYLTFPSTLLLCLNGSVGIRTSASSGYHVITPVMRCERV

RAAQDVSQALTYDTVSVVGAVASNAGSHYRMLDLVEPSERYAIQEEGRPLNNFLVKTVRR

LETWSIL

>contig33050 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65609.1|) 1e-115

MANTEPIETSSYGSPNRMHVLANGDIVDCGRLPQTARNNLYKTELCKHFTENGSCRYGTK

CQFAHGEEELRGVLRHPKYKTTRCKAFMSTGRCMYGSRCRFIHTRHVGDEDQRFFSYGNS

DLSSTSSESDDQEEQFKDLLVNPYGNPLEPIDLSLPFGGFNQQISMTSLSGPSPPSSELE

SYLSCDPFVDISFRSSDLDSFDVRSSISSSCNGDGLNAISPRSSSSSESTASKFSRLTIF

QRICREDN

>contig33634 Frame-2R|Blast-p21-activated protein kinase-interacting protein, putative [Phytophthora infestans T30-4](gb|EEY60549.1|) 2e-99

MIRVVAGTYEGLLYGWECPTDTSSKGTKMKLTFGYAAHAECIKSVALMAAKQGKTLLSGA

SDEMIKIYNVDKRVEVGSLMEQHGAITSLEFFGQSHVLSGSADYSICIWRTSDWNCLHIL

GGHKGEINSIAVHPSGKMCLSVARDRTLRMWNLVKGRIAFIRRLEKEAELVMFSQTGTHY

ALGFGKDLSVFNMNA

>contig33641 Frame-1R

MDSAGCLDPLLRPELRNSSERQRERRTTLSSRNSEGLTPRQAASVSAAMEAQDSALSIRD

LIATSPNTVSESGYSRRNIDVHIHAIVAPASLSAFTSLTRGNTETRNHERAANRRVETPS

TPPVGRPFASFDESQMSEEDGDQSRVPLLGAFRHDSQSETSQEQAVNQEMDTFISENFFG

TLFGHEEDENGRNLEPNALEGLQAGRLAYRPPSPSGQMHASATSTRDIPEAAAAEGQLHA

TEGNFSNGNDDDNEQTTSSSEESSTPTTLTFPTFFEIVRRTLSGVRHLAQNEESNNLPVE

ASSRVEMESDFALRSELLLPSSSSSPLSTPPVSPIVRSSIGSHMSNLSNSIINEELDLDE

VD

>contig34882 Frame-1R|Blast-receptor-type tyrosine-protein phosphatase, putative [Phytophthora infestans T30-4](gb|EEY55706.1|) 8e-69

MVWQCHVHVVLMLTNFVEHERLKAVRYWNPRGYAVTYGNLQVQLLDKKPQIEGLGFIVRR

FQLSHKIGLKTESRTLLHLQLTKWPDHGVLRDFRVIASMLDTVNCYRDEASRRLKVEAKV

VVHCSAGIGRSGTFIAIDILLKQLHRVLIGRKCETEGTQGIVPLDVSKVVYRLRSQRPGM

VQTPEQYQMIYHYLAAVISGNKPW

>contig35423 Frame-1F

MECNLYDIIMQRDRHFPESKIRNYMYQMMQGLAFMHQHHFFHRDLKPENILVKGDTVKIA

DFGLAENIRSRPPFTDYVSTRWYRAPEVLLRSTTYNSPIDAWAMGCIMAEMFMLRPLFPG

STEGDQLYKISSVLGNPTHCAWSEGLQLAAQRNYLFPQFIPTSLAHIIPHASKEALQLMT

DLLKYDPKQRPTSSQALQYAFFSVPLHVTSPLIEFIGVEKSKQHDREQPKENLATFTPPK

MAKSGIRPLRQMAMDTNENCNTRRSGFLSPISSCDMPRRSQQHAITAAGSSVLIPVSYGL

DNGYMGGTRGSGYMREAKDAPNTNGY

>contig36219 Frame-2R

MVRSTSKGLTSCTVRSLMLLAVFALSACVATLSTGPNTVTRSSYRHLRELPDTTTSALSE

NRINSYYDSLKAMAQQLEVGILTAIDGLFDVLLAPIGRPTPKKALDMIEFEVMSSLPRFA

DRDYYYNEVFKKLLATYGESQLESLINHPDLVNNPIRDAMNARLQQFRALNRSPAYFPTS

LNVEEVRSEVNSVIPSSLHAM

>contig36570 Frame-1F

MRYTYLKPSSYLIKVLASFNKGRLQGHVIFVIGGLAREDEDCCIRIQKEPFTSNCIDCGT

ADFVLMDLTSTVGYTVLAKQHFVV

>contig36695 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53701.1|) 4e-83

MKERHNVRLWPKEMRDAAMAKLGADSLQDKWSAMVKALHQVEREDGGDLICSHLPHINCK

TLVVSGGKNTFMPAFHGEYLSERIVHSRLEVLSNGGNDLITSEATRFNMLLETFLNEPDD

RLTQSREFVAVPTRKGK

>contig36754 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61002.1|) 1e-38

MLRNYEQLSALHMWLVKRVQRGLSIPETLDETTELVRQDPTGFPTKKFRMKQRRY

>contig36875 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65811.1|) 4e-57

MALSSEDERTYHMMVMQMQRDINCLTDPDRSVRRRAVDKLSRALKSESSHVSVPTLRVLC

TSNLKRPLLRCAENDVVEKCRERALDALLFLCERGALELSDATLNELVALADVRLGRIPY

PEPTEEIRLLILQLLYAFLKQFAAKEGTSKSLCDVITE

>contig37304 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62957.1|) 1e-57

MTFHENIENVYANSDFDLGIVAPLRDDVVTEGDCAEKVLANASERAGYYFKVPKVLQD

>contig37692 Frame-2R|Blast-Small Conductance Mechanosensitive Ion Channel (MscS) Family [Phytophthora infestans T30-4](gb|EEY61349.1|) 1e-153

MSLVLLSLAVSELAKFFCHLPMYIWGVFFLCWLYSLFNVVQSFAVRRFVGADGDFSKKMV

ITESVKILRLTTLLIVALIIYSSALGNSATLKYSVLGVIGLAIALGFVPSFHNVVGGLFL

AFNSQFKIDDFIRVGDAEGFVHRVSLRYTSVVSLEGTTLYVPNSFFLYKPMINFSQRPKR

DVDLHVRVSRTTPINTLRQALRRLESMLQSLHVGLTSHEENQSDLRHNEKWQRFCFVAME

ELYTIRIYSYTEELDARKYAMLKSEVWLAVTEIMEELAIS

>contig37788 Frame-1F

MYVPTQEKIVPSNDNKNASTDASTTSFGRLTNDEQEQLLDKQLWDLYHYGISDAAPKVKD

ANTNVDFTSKVEPNRFNSSISSRHASTCASDVLAYNELIQDMEGALQIKKELRPTSNGKF

AEVEQDQPQVVKITRPKSPIATPRKLHQKFRRLSKSTLNLIKPLDRLHSFCHDAKARASN

SSLASSSSIEHTSRRKKACSPKNSTVSPEQPLALKRDGIVLFDPQNLFCRVPFQPSTSRD

QALEATVKTEQAAEAGPRRRSLPVNTLAIQSKQTQQQQRKRSLRPLVEKCHGEMQASLLA

NVDPPLLSRAQSGSLHSLTDVYLPKNGDVLGVPVMTAAKKSFNNPATQRGATNRVTTRRQ

LGSNVIYINGAPLCVGKSINVGSVPGVVRYIGTTRFATGTWVGIELYERRGDNSGIVDGE

KYFNCAPDHGIFIRASRLDLSV

>contig37832 Frame-1R

MEKVTTVVVDDNLFDVYKSKDDDVTTFTYLSSKPLDHFCGNFIDFSKCLPEGSTSFPLYL

QSMSFGVEVYSGKDYFDATKLEVKIEKH

>contig38341 Frame-1R

MLRLRRHSKHMRCQRRRALLKLLRTTSTHLQAQQESGLTDFSHVQLGNWWVPKATSHKEL

VP

>contig38639 Frame-1F

MVKLFCAIVDVAGAAFPVDIDSKEAVRDLKKAVKAEKAATIACDAKDLRLFLAKTDKGRG

RWLTEFEVQNGVADISGLKMLDVTEAPLDMAGFNEENVRFTVTKELIKAKKTPVHVLVEP

PEPPREWWLVTGSVVDALGSTGIRSNLYWIATLCIGYYDPTRRVGNENGAFSYEGKNLCF

HVLFESQYAAQMFENNLALGTRTLHSPLNKHEVETRISRANGMPKDLKRIFHLDYDSNDS

ESFQSTSSSESLTTVAYFLEPSTKEFQFQRIEHEKIFPSCVKAECLYLVSKKECSDHERE

FGKYDRDPNNRLALSRDMYGWYDGVSVDVPIVNMLPGNVEEHPSIGSRRKVIFVSEALYT

MPENSDVFK

>contig38756 Frame-0F|Blast-caltractin [Phytophthora infestans T30-4](gb|EEY60867.1|) 2e-16

MARRLSQKRNVKTYERPGLSEEELEEIRKANNLFDTDVFGTIDPKELKAAYSQLASKPRI

RP

>contig39148 Frame-0R

MLWQRQMRLCRFQRYHVRFPLASSRFFSSSSSKANGDAEFALGVKYLLGKVQGEI

>contig39287 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53668.1|) 0.0

MKDLPNMSFNNPLGKFYVATVEPVRHQVTGSNYRLPVAPSDEFLRWGQPMTVVAKFNGRA

CGIRPREYYKDSDLYLTTEAKPTTMIPLREDGDLKCLAKESTRYLAHLEHRCVHLSVGTY

NVWMMPRKVSAFTSCSPKKNTRARLIGDVLPPCDVWVLTECFDHRARELLLQKLSNAGYF

FFSPTVGHKRLNKSNMRKLLNGGVVVASKYPILSVRVKLFEGASAGADKLADKGVLYCKI

LKNGLLVHVLSTHLQAWNDHLSRTMRKLQIKMVANLMRAMDIDPVNDVVLFVGDMNVDYW

LNKTNQEYDEMLEMFEAKDPSVVRPHQLGSMSDGPKRLSAADLKHRRKYSFDPRVNALA

>contig39849 Frame-1F

MVLGRNEAQQEIWNLAGLVKSQDIRTNEAMSYFIKEDDVIVLLQRYLPPNHSIRFLKFLP

ETIDNRVCVETRGYTRLLVATEQHAFLYYFLSEQVDSTRTKMAKKVLGKGEQMSSRGNHT

PINVAKGQERDWFLNGDEIEDDLNGKSESGRVVMHYNLTSLVTSITANSSFLFVATLSGL

QVWSIWSPCHYVAASRALKESLVPQPSQPQLLCIHPLPYPVSQLVALDSYVILLPQVASL

TSQRPNEIMHLASLSAAEQLPENEFELRRALTGQNDLSQRKILIFQQRPPSLIYSYVHQG

LLSTHGIMKPFQIDLLLSLFSLYRYRADVGFDLLRIAVNNDVAGKEVTASISDRKEKLAL

ELDTKLYDQLARKCAADLAEIFMSEPHRNLERAALLFVASNVSSTKVMQRLQIIVGTVDR

SEVIQATGKYLEAFVFLPP

>contig40557 Frame-2R

MLSLTALEQAHWDLDVHELFRNSWEASVEVVEGGLRVPLPVDKDGKFKVFHSINFLGGAL

WCNRSFD

>contig40715 Frame-1F

MVRKATPYRVDPPSQPRTTGNDVVLPIVLWTEPPQIEVCIIHVFRLPMTEASDVVHSEND

RKEGTWTQLCVFAGTVDGHVLYWRFHDKTVAQVNLLVFPGCNGHSVVGLVNGIDERG

>contig40922 Frame-0F

MFLRDNELTRGDGGGSRDDRARVLQLARKKRRERGQRKAQEDAATVLNSFVRGRLAAQRV

RKITRKELDQKLGDITKLKNILQLPTMPLPFDALFELLRLVLSFYSGSQEDAQRLQQMSA

LFADSVAATSEEIIGMLGTQRMWQLRRLVDLSLQCSFSLSSTVDVFIGLKLLPMLINVSP

ELHQYLLTKQLTAFYPQQASKGLYYEMPRASVTQIIREKIIVARSNFPTSSYATESLYCN

ALMDLLVHLLTTTSIILEAFLIEVLSIPLL

>contig41330 Frame-1F

MRRRTSLKVSKHMMHSSSSCPSSIYASPQNSIRTAMATIEIKNIV

>contig41460 Frame-2R

MKAHFGPLRTATSSVPASSSGASNFAVIKTPALASNVAFRGLEAQPPALQLSPFRSTRSP

ASPHQPFSSLLSDFKDTIYTPQVSQKYQDSTRQSTTRYGLNRPKSPMYYDATKAT

>contig41662 Frame-1F

MYQICFLTQSNPVFWYVQFLPWPA

>contig42537 Frame-0F

MAQTTKYDVLWELLAEEIVLVDCTRTLTDQVVNIYYIEDDFLTASGARKNSSATTGSHTV

AMNCRRTPSKPRGMILQKHVVVLPVTKVLFVRAMLQQQDRSFLTKMNIVTTEKSTSHQIN

PLSSLARSNSMEMSTRWPQHSCIPLRYPVFRLPAQTMSVHKPDHHDNEISA

>contig42692 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60564.1|) 4e-17

MTTTTIFQSPSFRPTLLKLTQGESVYECMRMTSENNKVHRVLAMDQRECWSDLLETLYAH

NLLKYFYKTMANSFACGDTMLVSDAMEGRDEALLLAIGEQGIEYGTMGQLNERGGLHRML

ATDLDAERSDCCSDATDTLYAIAMANYFASKTPSSL

>contig42968 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54226.1|) 6e-39

MLARSIRQVVRRSLSPMSRALSTATDSKYYILRYEYVSDILDRRGPFRAEHLERAVIAKK

DGHVIMGGALVNPLDAGVFIFNVTDKKIIEEFAKTDPYVQNHLVTSYSIREWTVVI

>contig42986 Frame-0R

MLAKYFRRMNGSVRRRSLRFLATTSDSAESVTSSVPKHRRKKTFQFSGEEPETTTPLEEF

AYPAYWDEDYPADFDNEMKHEVEKLQIFADFAPFLDLSWQTQIHPLFDGEAIKMTLNCPL

EDFDERLFVNDKNTYDTKVVVEVPMSCFKGLNTEAKEIVVQLAGPRYNANKKMIKIAEDR

YNKRVYNHKRICDILRDLTQTALELSGQTSEESIAKKNKDTKKEGTTDVVEQEVGRQS

>contig43372 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70219.1|) 2e-74

MNEGEHYVGFDRRDPESIIWWVSDPRNWIEIDRIRRAGMDFVRERHLVTNRVKALDLFIT

EGVAVYKTPSMLHLTSPCPSKALPDGHECQTRYDRESFYKCDRWFCGAQSLLPL

>contig43570 Frame-0R

MGAKQTRVVTSDTELRPKNEQAATTQGSVYLTPALVNQINGVQGTHNKTSQLVGGMSVEQ

QTVIKKQLQMAYSKGVDDCRKKMELENKQNTSKGLPSLAQKAQLAKEQEERESERVQQLV

SEISKKKYNAPLRDVQCSDEREACFQCYRNNGRDVLICKDVADAFVRCARQCTESFVSEK

>contig43695 Frame-0R

MAMLEGAVISDTLLDSRVAPLVALWSQDSEITSESNDQGEPRRQQLECYVARLKASMSVK

QNHIALNLGASASLGADTGAVIFLRVLKLPKSSPSSVTLFVNFARKSTEHPSMLFDSIQQ

AFLRWSNAIECSHVLSSGSIFRLELDNGIAVEALAHVQYEAEEDFSAEQLKGVPASALQK

YTVIGGNNGHCLTMDQVSVESAAGPQKLVLSKARNWGVLTDLSVLELSRSAKSYSLLKNF

VQTFMTVDALAVRVLLGTRPPGSALIHGERGSGKSTLVRAIVHEL

>contig43981 Frame-0F

MVETGDASVGLQYKQVWRNNMRIRGEPEINEFIGKDNKDFTKVSFAPDLKKFEMEKLTTS

MVRVLEKRVVDVAGCLADVKVTLNGKTVPLSGFESYIHAFCDSTTSLPAKPQ

>contig44377 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55829.1|) 8e-90

MTELQSKFQLKQTVEGITFVGREVRLLPFPMHTVARVLWSLLLYESKHMPGKIQTRVLNN

NHLNATIVDTLQLPKSHCTEIRTRIAVRRFFEANRVVVVWSGCIEIAGSMFVKLCEKGFA

TVSSFDFLGGDSGFSPRGSIHRVVIDIKPETVEYKTGTDAQGHIGVMTDLVLGTYHRNFG

LLNQVIENLLLNDLMGISGSNQECNL

>contig44427 Frame-1F

MKLVSVKEQAYASLDMDSPLVAPIRRNLSNIPSSPTPSTISVTSELGNGFSSDNGETRRF

YNSVTNEILAALDGPVRQLAFETKGALLATGLASTFYLLSWFQAVMVPFFLAIFLMYLVD

PLVEMMDVSPKYFLCVCTSRGRHARRKSRGCSRALASLVAVSLVCVFFGLLGYITVLSVH

ALDYSAYQTG

>contig44614 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59392.1|) 5e-19

MLSFCFLFRQYGVNQIQTFGCGFFDTRGDVPSRLSVSMSAESAISCVDVVAYAYIKKLLW

YMKHASTHASMEGNQSRVGQCDA

>contig44885 Frame-1R

MFRYRFCCAHCSSASLISNRFGLTPTQNMVLQLTQNKKNWAHIAIYYHV

>contig45042 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66319.1|) 2e-88

MSERWDFEGNDNLMDERGEVSESQASFTGVSPSLKVYGSHLGTHDNSLDATKVCTDFLRT

TVWAKASECGDVYMCFLIKYLLGERSDAIDILASPPAVEIQSMFSDANTDLSNLYWSAFG

KSLLGACDLLRFLRKTIVPIKLALKEKIVRLNTIAMLRLQGAGLGVLALIHQRDTFNLFQ

DFCRSSASSLDVAAFLACRERIIHAALGIQVDFLYATFTKSMCEAMTTSTSSASDTELDF

EDQLNQEI

>contig45503 Frame-0F|Blast-prohibitin [Phytophthora infestans T30-4](gb|EEY58193.1|) 1e-144

MSMASRFLNRVAGVGAAVSFGGFCLQECIYDVDGGHRAVIFDRKDGILEKSVGEGTHFKI

PFFQYPTILDVRSNYRLISSRTGTKDLQNVNISLRCLYRPNADKLSHIYAEYGADYADRI

LPSVGNEVLKSIVAQYDAVELLARRNQVSQQIAKEMNERCSNFFLLLDDVSITHLEYGPE

FTRAVEQKQVAQQDAERQKFVVMRSEQERQAAVIKAEGESEAARLVSDAVAKSGSGFIEV

QRIDAAREIAESLAKSRNVTYLPNQTGGNGGVLLGLQ

>contig45712 Frame-2F

MASRMDLEGRLRTLRVSKRSKPPITCLHMSKENTTSVLLPEISSSSDVNASSLSQPVFSR

TG

>contig46050 Frame-1R

MRRHGSLLSDMNDENFTLKTEVDAIITNNAGALSHWYTRWWLLLYVVLGSYAAFAIFSST

WLIRSSVQPHGQESYDQAANTDIIQVGTELRAGMKSLRDLEKGQRADTEEGADLVFDNTK

MPMPSEGSTTVVKDNMDAQEILNDDIVSGTSDATESIGSLSDERQPPERHSNDLFSGVLP

EIKPDGLNARVHQISHNLPDDEAT

>contig46256 Frame-1F

MAIEQDRIEKLEDFVFTDVSEELSRILLLYLLPALLTVIEGTQNQLQCFSRTYYKQTMDF

KVGMRQPVQLATVSGMTEKFTASRADFDATSPPMESPTLISFIAGTCGAKLNLASQRAEE

IMETEASHLFDCVELDRRGIACQSVSHGPRELHSTKAILVSRPINALTAASAVALSVKKA

KEKPATRRYTLTPKRSGPTFAVETRRPHTMTIGALPSPAQSPSSTGAIPLAFDGEVLPLV

PREKDGKIKKIVGSVFDRLSRHKSQSPQASTIKMISSSQASPVSLSGSIDSSVSGGIDD

>contig46339 Frame-0R

MRSHIFTSSESQIIGVMTQKAWRTFPALNSRTAAAYGLNATVNPNFDL

>contig47057 Frame-1F

MTPSDLNVKVGSSFKHQDGALEVIFSGVEKSIGFAAISNCLVIAIAITEAPSSVIDQLSW

SPDVLLDVKGDIKPTIIPSSQAKLRNLASAYCIELVNSGGYLKVIIRPLVVVINATDYDL

KCVPTDGQRQALAEDITESMVLGCNAGWSVPVCLLKQASERNITADVKSWLSSKLTRHPS

VSKVEYNEAKQ

>contig48144 Frame-0R

MGTTSSILPKFLKLRVILRILRVLRVLVVFERVKQRPKLMNLTHLSQRKKTSTVEQVLLV

LNELCFHPAIRPPLKNGLGFAIDAIKNNRLYVDNDEFLVVEGVDNNTQKWFPG

>contig48607 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65370.1|) 2e-71

MTKLWIREGNFSRAEEYLATACHFLRDNTNLLPPHFLSPASTESYSSSETP

>contig49705 Frame-0F

MLCCLSGQVPVEPVVSIKSGHVFEKRLLLKYLEQNQQHCPITNVELNENEDLLALHAAPM

AKASSATPVSLAPEAASIPQLLATFQNEWDAVMLETFTLKQHLEQTRQELSHALYQYDAA

CRVIARLNAENATCKERMAQLVSGKQDDVEMQDGTALAPEVLSTIEAKQKELAKKRKEFK

KQEGPQRAALLANIIDWHVVSSHTLHDSDKPGVTCVAIDSKHPTRVATAGVDKHAKIFDT

VKQQVVATLSGHTKKLSHVSFHPT

>contig49983 Frame-0F

MSILIALILTNAALAMKVVSIQMLTDPFALEHSTNACVKAAYRYASSMDVADPTGI

>contig50220 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63138.1|) 1e-77

MPVNFTDESLTQYLTRFWRANASAFMRWFLALPYAGQVSLLRNASPDMPLSYDPAEPRPQ

ATQLLTPELTLSALLEENGKALLRLMNARATKSEQCIRHDMLYLASLRATGTMPTFSGET

FKHVSLAFVDLADPEHHVQSLLPSATRESIEEKTKLINQGKLMEADVWLTLQMR

>contig51106 Frame-2F

MSWLLDQRGVRYKVNSASFARDKATLDDTSFMDLDRVRRSAVHTHRHHGNDAHREATALR

SLPASSPSSRHFLQRVLQSPPRPHQLRSPRVK

>contig51818 Frame-2F

MGVAVVHVIDENSPLYGMSESDFMQSDMLVEVSMSGVDSTLQDTVSERYIYTAASVRWGY

RFAELIDFDEDNAQVIMNFANLSSVETASIDDACYLETPAGDSIEESNTGLVRNVARRRS

HRKSRVTYFEAENDPYHDDAIHDVPAEFSESFMMSTRPESWDAQSLTDSVSSHSSKSGPT

IFSMGLEPLFEPLLHQPFGTQR

>contig52510 Frame-0R|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY59854.1|) 7e-44

MADLFPDEARPMGTCICVGCSWLSNFTVALSYPFVAAALGDYSFTPFMFTVTLAFIFVYL

FVPDTSKKTIQEIQNEFMARVLSKKNGKSHRHA

>contig52752 Frame-2R

MMRDVSARFKYSEREFQAQHKSGESSSGDGMEKKPPSTPSQIARSTGDEACPSRELIHSH

IQRFYRNVDSAAEVTT

>contig52846 Frame-1F

MPNAQVSAVSLSVQPDQLAAAHSQQAAMREMQRAQNASQLLGENTLKHSLSTSASPALTA

SVSAVGATTSAATSGNSAQTYVERLKEMKLKYWDDLVIVYREFERMVKQKPANQQQERIN

TFLVNLKRIIALLQQDPLKITSSNK

>contig53236 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60187.1|) 5e-62

MLMCMLTCMALLLALTRFVTHTLEGEVHALSSLELDVVSPFYGWWLSKCESEWILAYHLF

RSGLSLFLAQVALLGWTVFGEWKAAASCMTILCVLALAYLELRVASRWRYLVRFPESRTP

RSPVRRQPATS

>contig53399 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65489.1|) 3e-48

MVALTGTCSAYMELVDRSNEVSALIDNGKLREAATLLRYILDRKPAAGFDNVSLALTQHE

LGTVLRQLGELDNALELLMQAFVVRDHADENLGIVIALRDGNLTREEIAKVYEAKGNCAK

ALDVRQRGKRICSNDVCEALDYKDDELFACSRCKCVFYCGKTCQRQDWKNRHRPMCQQPM

RQI

>contig53665 Frame-1F

MLSLGIFCELIMRFRQSLGLRRPIKQCLFWNGTCDIDSRPAFSISNYV

>contig53812 Frame-0F

MCKITQKSIRLGKCQSFDDLVNRHNWFIELETLK

>contig53908 Frame-0F

MTGFVMVSSSPRRVRIKEAKAIAKAVRGNALALHKACSRISLVVGVFANN

>contig54167 Frame-2F

MAQRYEADVEWLDSEVEDSPCFSDEIGNMFSSSPNAKAGGKEHEQQMQRSVAGPSEHAED

FVDDTTSFDGQIAASRHYSAKISVPVKSVSQKRFQDVPIGLVADRGVAAKRALINRIRQE

SMTKLFMSCQAVLVRGASGNYYVYHLEISSDYYKQKWVVCKRYSEFYRLRKRLLAGLTIH

KKQRDCSLCGVVRNQLKDVGFPRRIVMFQDPSLLVGARTAGLEEFIVALCEYLAAEQEVE

VCSEIITTRY

>contig55164-0 Frame-2F0

MAPMSSDGEGFGCAMRASTYERSTACIAKRLRESMEKTTRLLDAFEHELGESSVPVGTYQ

RCCR

>contig55164-1 Frame-2R1

MLLIAHMYSLSLHSRILRRRYSLAPFLLFFY

>contig55209 Frame-2F

MAVALSGNFCFNLVRMICRICSTSAGGVASD

>contig55300 Frame-0F

MILMWLTMKGHERPSLHVFEGRRVISMAITPGCL

>contig55476 Frame-0R

MIPISAFWARTAIMTFPALHLLLQPWSRTIKML

>contig56068 Frame-1F|Blast-cathepsin-like cysteine protease [Phytophthora infestans]gb|EEY58999.1| cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|AAY43370.1|) 1e-156

MESAYALSTGRLESFSEQELVDCTLNGIDTCNHGGEMSEGYMEIIQHHGGKIDREIDYEY

NAESKGVCKAKDGKAVGHFTSYANVTSGDEDALQAAIATKGVQAVAIDASSFTFQLYHHG

VYNWPFCGNARDALDHGVAVTGYGLYKTKEYWLVKNSWGGSWGMKGYILMSRNKKNQCGI

ATDASYPIMTKEEDSIRKTSKVMDIM

>contig56305 Frame-0R

MASSDDYGPLAPMDDCEYPVALGQSLLNINDDLEELSDVYTSFSYEFQPASVDKSTPGLV

SVDGSNGVHVLMASSTGGVNFKGKVVEQKNTDCLLIFDGSGFRLERCAFSCVQLRHVRAP

TPRRRMPMQLKQKSVDPADGVVDDKTIPALSTKTVRKTGKKPLGRPKGSGKQTVQRVLKK

VVEPSVAKRPRGRPKKVT

>contig56547 Frame-0F

MQASPNMTTVAKVIDEAQDQNSDLFHVAVINDDRSFLRLMMTSLPLETLAEELLGLNSNG

VAAFQLAKTIAPSLAAEIETFLLSRGVVLLDENRQRFVIANCLPRQTSLSVGNPHLTRVE

VNPRRYTQCSNIAPTVGLVLRANNINYAASRAVYVQQVRSHALNELAFHRENLLAFLESD

TLFSVAWSGSKIADLAKKNSFRRTFKIFAACKNCKSTAGAGNDGVARP

>contig57016 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63888.1|) 2e-12

MYTQMMLRLQLFRRPLSTLARGSNASPFSLLENEVAVRRIESASYARFTRKIPSQIGILS

MEAVERTARYLMTRGFSHMQAIRAISLHVMV

>contig57179 Frame-1F

MQYVKTISFIALLCVASVTAQVRLQNQEQKEGLQTTDRFEGESGGNFSNVEKGFEVAQVN

FATSDTSEEIGENKTPGSNTVLIVAAVGACACVGVLGVVLMKRRKGNEKKLSGDIFTIDD

KNSVL

>contig57193 Frame-1R

MTSQRWRQSSISVNCTDSKRNCQRTWAILPKLHFFNRLSTLVQDSNSTQICREFFLFQSP

>contig57290 Frame-2F

MTGRRLQRRIGLDGAAKGSLAQQIASVVARSLQQTYEGSGKTLSDQRQGLLVSTLRLATQ

NAAEMATYVRRREQENAQLA

>contig58192 Frame-2R

MNDSNFRRLVQGIHDHIDAVFGQELLNYEGPCVAKD

>contig00918 Frame-1F

MCFVGFTHTKVGCCGTGLLEAGPICTYLTPLCTNPSNYLFFDSIHPTEAAYRYVTKTLLN

KILRHLNTSGHVF

>contig02017 Frame-1F

MRIHTWSAKMLSRCFKEIYGKYYANVSHC

>contig04011 Frame-2R|Blast-3-phosphoinositide-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58380.1|) 6e-09

MRQKGEIPWSDNLYVNSKSATAFDVVTVRSYSR

>contig04741-1 Frame-0R1

MPIVYLMLNTTKVGKLIAVLAALNYNRESQ

>contig05399 Frame-2R

MDYTMWRLPGRVVTMTAKESLLAVVYQGLYGEMLYQLVRIQIDSSRQRVVVISKGTVPMT

PPPRDVFASQHESNLIRQDAKNWAKLTWLGFDDREILYAVDSFACLQAISSSTGWNWFPI

GCVGNALQKKPEDRHGIFTLGLVNDSLLYFPLEKGANCPKLRGSHRPVPSTFPFRTASFP

KTLKETKEAGNGHMWQHVRLCGLESIANELNIDSISNEIVNEQAEMDKALILMMKTACTN

DEPARVLDLAKCLHLEKSHQIAQKLAIHFSLRQLQSQLYDLYRVKFENPRKEKETSLLSS

PPRRPLRFDGRKREESDQREMEPLCRSRSSLSRPLSAQLRDEIQAIDDVSIPVETAPGIV

NKDVNVSDDSAKRSVAPANPFLKKAGSVSVSPSGKGTGLQRLAKFASPPPVKKPRRSTWK

K

>contig07379 Frame-1R

MSASRNLRKPNDVFFPPARWKPTQDHVILVFLLPVDYRKTPQWQEPDPSVSPRIVY

>contig08723 Frame-0F|Blast-MtN3-like protein [Phytophthora infestans T30-4](gb|EEY67544.1|) 1e-108

MVSTNVVMAVRVWIWFSTLATIYMPSRFVRRIYSERAVGSASIDPILVVLANSHVWMLYG

YLGRVWFPSFPVFFIGDVVSLCYLFIYWRYSEQRHAVAKTIGFMFSWLVVATFYVIVASL

GLTGQSRPEIWKTHGLCFCDVTVISIHTPMLKKLVQVFKQQSVALIDTRALAVTTVNTLG

WFTYGQVTFNWIIAGPQVFVIALHVAAWTMYVVFTRRRTLEIDYAAMEEDPIALSVNLSP

KIDACTKEGVISYTPEYQSLRSPVALT

>contig09632 Frame-1F

MADQVDPSAGVETHVPSSTQWSEHNAPNGRKYYYNAVTGESTWECPVELSLPQTEMPRST

NPQQHLPVSGGFQQPQPQLADQQGATAYGGYPQPYGQPMQYPPPYGSSGYIYPFPQAYGY

PPQIVGPGPPIQTTESGQGPPGCNLFVFHIPNDMTNQDLFNYFATFGNVISARIMVEKET

GRSRGF

>contig10285 Frame-2F

MEGTPEGIHADVIEQGLRRCSSVVAVHDLHIWSLSAGLPSLSVHLVSDDAETALHAAQRF

LMSKGITHTTIQIEKTATLYPRNCKSDLKCGQDSPGNSD

>contig10744 Frame-1F

MVLLFCGIVDVKGPAFSVQLDENDTVDALKDAIKAKKPATITCDADNLQLFLAKKDNGLG

PWLTISEVHEGVEDASGFKSLLFEDEKLRDVGLARGQVVEVSAELRAVGKGFCHVLVQLP

DRGSTWQLLHNKCPPLAIEHNNPLVRIPTAYTVGSGVAADEGKDLLLYRRSQLIEEWQTL

NTCVCNSFAELWIVGPPGTGKSCAAFAFACSLDRTDWDVVWVHLPKDSISMVKCILFRGA

NEKWFCEIPSDELDTVLQSLKKKTILFVDGYMKDTESGEYIGKLCIAWRAKQRDRHRLVW

VSSMATHSKDDVQDQCDVISTNADAFRLRTTARLPEEASLLAVKDVMLFKLMSWTFEEYE

MAMKLDEFFEHVKSKFTNTLQPVPWEERKQLLEDKYFVAGGCARYMFAYSVSEAITELDA

AIYSISNITDFTEGQPCVVSKKIVHRLFSCFRDPTGLDTCIVSSYVARKYVKILGPDFVQ

KIATSLSRNPWMDGQFFDLWFFSTLQYGGVQCFKLGDNGETFVHDTWKTNDVPFFDPKGY

IPLNQTKQWLEPRSWNRGGYDAVYVKSSYNSTGALNGLVRFVQITRADKHSFKAHFLALL

LVKLTNFLRAHQSQTVEVYFVVPKRILPIFKLDVDVAQVRKNVVQAAGLNADDTRVIVDV

VGVNYKEFRLHDHLDRLETKRFRGALSGYGVNLLPLMC

>contig11181 Frame-2F

MILPDNRDQHGLISSGVRSFSFKDAVVGSKNDLAMSAKPLAPASRPIRSRSITKLVSRSS

FKKRCEALQSPNGRCQLNLKDQALAPCRSVMTEKDETMTRVQELCTQERRTDSATETGKD

RVNRLPSSSSTADRDDGTLVTPSSCDSSPMKAL

>contig11615 Frame-1F|Blast-hypothetical protein PITG\_09769 [Phytophthora infestans T30-4](gb|EEY55786.1|) 1e-38

MPPSVNLVKFWSKFGPEFGRTSRHLSPYEVHPVRSLINTLPYKTIRKIKENGLVLIPAAV

LLVTTVKWGNAANDAEHRTHWS

>contig11879 Frame-0F

MSYQVSSVFLQKFSPKEIHELKRVFKEHDHDYAAAVAVSDLATVLQKLGENVTPNQTSVM

LQQTKLARPEQISFQEFLELLYDFRNGAIALDPKLFEQFTSLTPTPVATPDFKPATAVEI

TPLFITKKTPLSTSQQTSQPPAFVQKTQWPPTGAPSTPLAAPTPVMNKLQWPSSGNNAAT

WGHLPSSAPQTDVPTHSVQSSKPQWPPTASHSSNSPVETAKWPRTTGDKSPAKPQALFNA

TSPSVTKSKGPAVESASKSAAFASNSSWQSAGNDAAKPQWPPSTASSSNPLETPHSDAPK

RAQWPPTATLASPPPPPLGRTSSESSASKAHEYVGTNVDAHTLSVLQRRASAAVQYNSTI

HEVKGTAGGLHSYSEEETAAFTEHINNTLHADKDVAAMIPIGLNAGLFHAVCDGVVLCKL

INAAVPETIDERALNFVPRTKELNVYQKTENQNLCINAAKSIGCSVVNIGPDDLIEGKPI

LVLGLVWQIIKIQLTSTINLKNHPELMRLLLENETLDAFMKLPPDQILLRWMNYHLKAAG

YSKKVSNFSTDVQDATAYSVLLHHIAPQHCDVCNELIPEERAAHVIQNARRLKVETFIKP

RDITSGNPKLNMSFVAQLFNTCPALDVIEEELKVLEEILYDDVGDTREERVFRMWINSLA

IDEVYVNHLYADLSDGMKLLKVLDKIQKGIVAWNKVNMVAPNKFKQVENCNYCVVLGKQL

KFSLVNVGGADIFEGAKKMILSIVWQSMRYQQLKILSELAAGRGEITDKDIIGWANTKVR

QSGRVKGNIVAFRDPTLSDGRFLLDLVHAVEPRAVNWDMVSQDDADDAKASNAKYAISCA

QKIGATVFLTYEDIVEVKPKMMMTFVASLMLVDHQRA

>contig12016 Frame-1F

MATTYSTTPFSSRFPFSLRTHYTSNADAAAQIQLQQVRYGSPGADNHIEVSSPGLTPPRA

TTGIISKQHMFAEPNAMHMSPPVYSLRQDVSAAMYMQSMMSKMYQPQPPHPPPMDMPHQL

>contig12320 Frame-1F|Blast-calreticulin precursor [Phytophthora infestans T30-4](gb|EEY70179.1|) 0.0

MLTKLVVALAAVAVTMARAETIFRETFDDADWESRWVASTWKPEAEVGKFEQVAGKFYVD

DDDKGIQTSEDARFYALSAKFAKPFNNKDKDLYLSYMVQHEQQLDCGGAYIKLLPADVDQ

TTFGGESPYSIMFGPDICGMNKKTHAILNYARPGEDAVNMDHKETLRTESDSDAHLYSFV

LKKDDTYEVKIDGKVIKEGKLAEDWPFQPEKKIKDPAQSKPKDWVDAVQIPDPEDLKPEG

WDDIPRTIPDPNAEKPEDWDDEDDGDWEPAVIENPEYKGEWKPKMIDNPDYKGEWEHPLI

DNPDYFEDDAMHNVAKNIGAIGFELWQVKSGTLFDDILVTDNEKDFIAHEEALFSKIEAM

MAKKKKIQDEEKARLDAEMKAKEAEKEDEDETDDEATEVEGEAKEDADKAKDEAKDEAKD

VADEKDEL

>contig13037 Frame-2R

MKKTPSSPCLAARHETFNEHSDLHRSLTKTADGDSTDFENECKTLSSGGDGTQAILSESM

FYCKLIPNTDAVSEFMIYFCGSFPVRMAPLVVEALVQRFTNMRFNWATKTLQSFLEMVCW

TSVTYATYSLYNDLLLALEVGTFVGAMMSVCDEIMLQLVRGLARVIRNQPGGGDLLQRIG

FDVPKNGKAPTDGQEISLIKNLVFGYLGVVAIRSWWDNFNDVKYFALLTVCTGVAFVIIA

EFFCLWLPTRRVGLTLQSRFTKVRQNWHENSVRSFLEMLCWTLSTIYMYYQLQDFWWAFQ

VGTLFAVGVSLCSGLDHLADIDTNLTDKPEYGVWEEHVLDDPYMTLAGRLIMIRQAVEAF

GRVVEAEAINMYENFGE

>contig13305 Frame-1R|Blast-endoplasmic reticulum-Golgi intermediate compartment protein, putative [Phytophthora infestans T30-4](gb|EEY57043.1|) 1e-67

MKIVPTIYSEIDEEVIHSYQFSATQQGNYMDSSGLMTSLPGTFFVFDLSPFMVKIENDQM

PFTHFLTKICAIIGGVVSIAGFVDSFMYNSLHVRRQVSTNGGATKFG

>contig14326 Frame-1F|Blast-sterol 3-beta-glucosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY55357.1|) 0.0

MLLDLQIPHAFMWSPALVPKPKDWGDLYDVVGTVALKDTASSYTPSPELEAFLGHEEGPI

FVGFGSMVLQDPKKTTDMIIEAAKQANVRVLIQSSWSDMAGSVRVPDFVFFLGNCPHDWL

LPRVSAVVHHGGAGTTAAGLLAGKPTFIVPFFGDQPFWGWAIHQAGVGVPPCPIEKLSIK

LLRLAFQALQRPKIRRQALELQQKMQQEDGVEEAVRSFYRHLPIQNMCCDLGDGRVATKW

CRTNQLKLCDVCDFVIASQPENFDRKVVEYHCVDYTARGPAHGFAGASSGAAAFFHELGG

AVKDVIVKPARGFREDGPKGAVIGVIKGMTGLVIRPVHGVALFADHIAAGHANYFSESGH

RRRGSVFDKTLMLALGMENGLVDSHALGGSSEELETFQLIGQKKVIRRKVELYVSDQDKV

SYQARFLEIVNEKENLEYSLDRIERSSSVSLGSSDRESETSPREKITIVSADFTASGNIG

VKFNVGSKVPDMISNAQMEKWQQYSRQQQIKSEQLLQSFSKTTV

>contig14977 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54890.1|) 4e-17

MTLSEEGLVAVAELRKHLVKVLFSTNDLLQSFRKDPFFSRLV

>contig15174 Frame-2F|Blast-hypothetical protein TRIADDRAFT\_60507 [Trichoplax adhaerens]gb|EDV20865.1| hypothetical protein TRIADDRAFT\_60507 [Trichoplax adhaerens](ref|XP\_002116509.1|) 1e-08

MAAVTKGLRNVFEVLTPTRGYGVGKRVTRGIWSKYAEPSFWEVVRIRPSPDLKHGKVFGK

FTFR

>contig17150 Frame-0F

MQKRLFALSFLQPKWTESSGRLTPCQENNPNPLTLSWTI

>contig18533 Frame-2F

MTEAALSVSISPLLPSSVEDETPLGVSDTDEGKRVRFQPTHAVFTPRLSETSSLRYRKPD

DRVVGSTSLAPPSSVSSIAQPNYDDFLRRVSVVLYQHIRRCEKRHRDQQRSNGVNNVVAT

FTTNRNASSILFAQRRSNVCDSRPPILTDDTATLVEKESATYFEVDESDEVGSQNPSSLP

SPRFVELPVEETFREEHFVTPQYKYTFVRLPRLHPLTVYRMEKITSKRHVPSVDEIFRFC

KNLFNKAQLSAECTIVCLIYIERLMEEANVPLLAATWRPIVVCGLLLASKVWQDLSSWNV

EISNIYPQFSLQSINRLERLFLHHIQWDLYISASVYAKYYFALRSLTEKKDFRRRYNYTM

RV

>contig19439 Frame-2R

MTTENTRELLTPSSATSYLSTPSSPLDTSGNVSNTAVKRNLLQQYVSASEVAQHQITRRN

DMQYSTCSTQSSPTVKGSTTAESSTSASYSPRFSSSVSSPMAETILKVVLIGDSAVGKSN

LVMRFTKNKYMPHSVQTVGFEFATKTIRVGDRRLKAQIWDTAGQERFQSLTAAYYRNAVG

AMIVYDITNRSSFEHVTGWLAQVLEHSHQSLVLILVGNKCDLAHLPQSRKVSTLEAARFA

AKHSMEFLETSALDATNVVDAFKKLIVPVGRLLSPTEPRKIAQLPPGWRRVLSRTRPGEY

SYENQYTKERISFSPKEPAKPSQQRFRPPCNELKNGFPNVVTVTRESLQRQHQKAYLAQN

QTAQCG

>contig19923 Frame-2R

MATVLHLAVVVATLALCMPLAVNAVPAELCSITPLSFEPAKTKYPKLASAITELEKYSIA

AWYTDRQSLADKETMLQKLVTECSEDQRMTIVVYGLPNKDCSGGHSTGGSVKTTADYEKF

IADLVKAVGDRKVLYVIEPDAIGLLAEKDGCGKDAGYLENIKIAIAALAVNKNAELYMDV

GYWTVKSETQLPVVVSAMKDLSASSKLRGIVLNTSNYRTTKEISELCSKFQKAMGNTEMN

CIADTSRNYLEPVDDEWCNVLTNGVGAVPTSDTKFKNLDYLMWIKVQGESDGVCNGGPDA

GLFYDKAFIKLWNQGYFVKELKMKPIGDGDSDVSQTDYSDADDPVQKTGLPEVGGESTVT

SEETSEIAPPPVMNCKLKRRMRKL

>contig20264 Frame-2F|Blast-hypothetical protein PITG\_03108 [Phytophthora infestans T30-4](gb|EEY65602.1|) 2e-39

MLGKRHLSEMEACVTEYYRLECLRALYAKQERPLDCAWVRKDMMAKPPRRVRKGVSFSMV

PEIIGCADPAVDRTPIDVSPISKFELFVLLSLRTFPIQA

>contig20668 Frame-0F

MCCMLLDDVNESVNRFKYTSSTEQLCARLTTNKAINGFY

>contig21177 Frame-2F|Blast-inositol polyphosphate 5-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY59786.1|) 7e-99

MDIIREDWIQQQLLLRRDAYTELRTTRVVVGTWNVNAKKPLIPAEASKIVQWLQPLRADS

SKDPPDLVVLGFQEIVDLNAVNVVVNSALTVQRSAAWKETVLTALNHYVGVSAACTGASE

TLGQYRIVMEKHLVGILVLVFVRMDHWDHVKEIKGATAGVGIMGVMGNKGGAAVRVKFYS

STLCFVCAHLAAHRDNVAGRNADYLNVLNKIQFEEMGDEGGATPMHD

>contig22749 Frame-2F

MMCGSRLKSAAALCTLALMGLQPSSVAEDPVKPAIVAPAGNSHNSLPAAGTPATTTPAEK

ASTVPAPDLGPHDTPEQPDYEWYWKHGEASMFGQDSGVFTTFKPNDTDQTCSLDTHATPF

NRQVRGVNLGGWLVLEPWITPTLFYQFLNTQQRFGDKAPEKTAMDMYTFCTALGKEEANR

QLRIHYDAWVTEKDIAELAAAGINSMRVPVGDWIFNPYEPFAGCTDGAVEALDRVAELAL

KYNLEILLDVHGLIGSQNGFDNSGRSSSVKWTSVASTQPVGTTTFEHWPIRQAEWAGTFD

VEKHNYSSINYSNLNHSIVAIEAIINRYKGHKAIMGLEPVNEPWELTPITVLKEYYWKSY

KRVKALAPAWKFVIHDSFRFGISFWADFLKGCPDIALDTHIYQAWNSPGTIADFFSNACQ

QKYVISDMENALMPVIVGEWSIGTDNCAMWLNGFNDNLPGFPKVACHLVDCPINSTYLGK

GFPGTPLDKTRPIQGPYGTGVSGPSFGKCPVTSQSSFGQKDDAALTRQLTLKKLNGFANG

HGWYFWNFKTEFATKWSFLDLVRLGAFPKNVSDYHESDGVGKACLKEDQGDFVCRAKRGV

KEFELKDGLAFACNFPDIDCTGIKKRFPTLQEQCDWVFNKYWHLKRENGATCDFGGAAHL

LSVPGSAPAKFPAVTPVSIDAPMTKAKSSHLFASMTMWGAGASVGFIALALTAVAASVFA

IVRWRQNRTRRQYSPIADQI

>contig23203 Frame-0F

MENERNYGNYPPLHRASSWQFWRTTSPPHRFYLLILMSCIPFGEHFVKNGMSSLEQLLLD

DKDFPISNTMYGALLSAVSVPSLCLPLLGGRLLDKSGHHSIRIFLAWICLGQAIFALGME

LKLYWLALFGRVFFGVGAGSVVVGARVLIASWFKSSELTFAMGVSVAITNVSKMLAKATV

APIALFYGGYVQALWCGLAVCVASTLVGVLVCHYTLNLQRIVESRVIDEEALDPTLLWLT

DYAEKKRRRHRWRKAHAQVKQISCESVQSFSRMFWVIALLHVNFINVFHLFQNVSASYLF

QRYNYSIVKAGVVSSFSHLFVVFAPFIGLVIDRFGGRIMLIIVAANLSVLAYVLMIFTEV

NPIVSMLLISICLSFTPTVLMAAIPNSVSCNSFGTAFGIVEITDAIGATSGNLMVGYLRD

ETGSYHVVMMMLLGMAFLVLLLALFLVFEDSRNGWVLSAPCGQSRAHSVDDEDSTNDSAA

LEARFGANEETDLMRGRRIEL

>contig23575 Frame-1F|Blast-exportin-6-like protein [Phytophthora infestans T30-4](gb|EEY55194.1|) 0.0

MRNSMQLLANLGFVLPYEDMAHIPSMIQLQAHIHQFSLHLPLAIQGDLYTSTSNSILSSG

VSLRGTSSASEGLLPWKNAYKALLVPIHESIDQSAVALQQNEQRVLEHPLVVQLKRDLYL

VRSLARSVETKPKVVKDAFFSVYDATFSSLMALLTTYFTVIRKLASSSVPQSKNHIKNAL

KVVNAIIRLYAQMLKSIRKEMPKSTVAEIMRTFVDIFDDSQLSEVLYNHSNAGLMVLCGF

LELLKTVVEEPTTVFSSFVQSILDLCFGPLKEVIFSHPESDSIILSYYVALIEQLLEKHY

RFFIVYSGQFTSDGVRERGYASDQAHAYFLSIFQSLASVLSREGSNLAPRLCKQVLELLD

RVDTAQGLFAFAGFQSELRLGFLSTLMNILTRGEMNLLQDEVIQLLLRVAAVDFASFYQV

FLDGYVQGILTQPQLEAASKMRGECLQWSGHVDLPTFTQEVVAFLNDLKVIKAQY

>contig23698 Frame-1F

MIASSKRCRAPNERDSYLPAAHNYQLAPMKALLRSARNEFYLESLHNSSSIETEAPPVVD

QASNQLNQSLDEQCRRLATFIANSRHLVAFTGAGISTSVGLPDYRGEHGIRTKTFKLSKR

QKVETTKPANRTNHDSEELPLILKSHAEIPDFNHLVPSTTHMALYELHRLGYLKHIVSQN

VDNLHLKSGVPARALTEVHGNATHAKCETCEKIYTSNFPWTGLCDDPECVSTKRSIEQRV

RARTRHGNGRLKRNVVGFDEPLGDIDVAIDECEAADVALVLGTSLRVEPFSEMAGEYAGS

LCIVNLQPTTTKLDRRAEETGVRVFAKTDIVMAKTMQYLMNDEKYSVPEWTGDHSALVFE

PEDESKNLVNVLAGRIVT

>contig24707 Frame-0R|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY60954.1|) 1e-139

MLTHALAVFAHYNLDLIKIEIRPCSSETVNQTSEVTMQSNRYQYFIYVDVQGNPTDNSLS

KAINRLSELCVFMRILGTCAILHSKDSMATAQLLPKTTRVQTPMQPSMSDKYPLNPIFQK

VTVAKTMLIHGQTKQMEAEGKKVWSLCVGEPDYNPHERVLTAGAKAMLEGNIKYTHMKGL

VELRDLISTYLQKAKGLQYDPATEILVSNGAQQSVYQALYTVCCPGQKVIIPTPYWLNYP

EIVKLVYAEPVPLRTTIEENYLINPKKLEKTLTMHPDTKAIILCNPNNPSGTLHSPDHLE

RIAAVLRKPQFCHVVVISDEIYEQ

>contig24909 Frame-2R|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY68453.1|) 1e-104

MENGTLTDLIRARRGSIDFFRLVAEIAMGMNYLHLCSIMHRDLKSGNVLIDSHGTAKISD

FGLSCALEIGSSSDLTAETGTYRWMAPEVIRHESYSNKADVYSFGIVLWELLTRDQPFRG

LTPIQAAFAVARQQMRPALPRQTPKKIGELIEHCWHHDPARRPDFGAILEALPLVKNSLK

KRDFKNMGILYLPS

>contig25010 Frame-2F

MRACGYAFAEAPDRKLSVKENEIASWFLGLLEMELAEKEDARPSLSASVCCEKSTSNISR

NVDEDTQDSAWKPDDLDMSGILILCTLHAMSRERATVFCLDNAMHMDGKSWVLVMIIAKY

FTNCMVAIGTRSPGLALGENTASCSFHKQLRLLKGLKSSSFKYLDTFSNSETEMLSRHIL

QVPVIPDDLLAILVSRCQGNPLFLHELITELQAQQVIKVYEKKGIRTCELHVQKSWGEKS

KAQFCFACHICFGCAKKEKEKDKKKVDIEKEMNESAETEGIKKTKHQCKCCGYYFCAECT

PKACRAKIPGKYSEPVRHCRTCYNFSSSRRPSGSSHAIGAAVGALNEKRSRSKGRLRSIF

HAGSSGDHYSLSSSSSNSLSVSNLQTLTNCIGLRPPRTVKSVITTMLDQLTCSQRMLMKT

ASAIGLVFDEEMLRGACPIEAHLSRLSQDLVDLEQLAMIRKIDTFIGGVPTSSKASLGAR

GARLTTSQTAPPSSFVKVKFEFCHGFMRSVIRDQLLRGQLDKLNARIADFREQQQRELRH

NFFAKANESLTRPVLLTISASFTEGRGFIQEVRRALTPTENGKKSSRSPILKNGRRRRLH

TRRNSHSGAHRISDASYYSSSEMSRTQGLYNSESEYGNDLATDSDSCLIASIPLTNNIFG

KQQLQVACKQTACIRLKADRVLVKKYCSMFSHLKLKGLKNARQWKSRYAVLESDCLLLQY

EDDDPVFGDTCRLAALQFGTVLFLKDAKVSACDPEVAAKVNCFQIQVTEWTKQGQVMKNQ

RRSFIIAAESEEEVDNWVYMIRFAIESLESSTR

>contig25708 Frame-0F

MRKRHVILSFVRLRLFSDVCKLS

>contig26028 Frame-0R|Blast-hypothetical protein PITG\_05455 [Phytophthora infestans T30-4](gb|EEY69244.1|) 2e-11 NOT\_ORF

MDQATISSLELVKGARERNDSQVLITAQIHHLWIVHFF\*HLTC\*SLCKMLNSPQTSAGNR

LLRSTVRSKSYCHCMHFE

>contig26330 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY66613.1|) 0.0

MRTGYPEVDFAGSMLDGNVVTAIFFGFGASMLGITGFESSSNYVEEQKPGVFRQTLRNMW

ALVTFFNVGLGIGILAVLPLEGEGGIYASSDHLLAVVAREAVGEWFDSWVCIDAFIVLSG

AVLTSYIGICGLVRRLSTDRVLPAFLARTNKLRGTNHYIIGLFLLLTSSLVLILDADAAT

VNGVYTYAFLGLMAMFSCACMLLKAKRSEIPRDIHAPWATVIIGFLLVVIAIFANLLGDP

AVLMYFAIYFIIVIFVMFVMFERVMILRCILAMMQTMAPSRYSKTAAFGLTPDSPSELEH

TGARGGQTIARSIASIRSAPIIFFCKVPDLTIINKAIIYVRRNEQTQTLRLVHVYGDAEA

DASVLLTFREMAALFDNIYPKIRIDFVAVPGEFGPAMIEWLSRSMNVPRNMMFITQPDIV

SVTDISAYYSA

>contig26583 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56187.1|) 4e-39

MFSSNENDAQERLLRAPLNSQNAAMGNTSGSGFIRQHGNNENNGFTSLSTLSAPTTYWQK

MMRMEAATLMRYLRYANVVLAVLQALAGFMGLFNLMMLDITCFLISFYAV

>contig28488 Frame-1R

MMLSGQGKTRERSNGLLSVTKHVYRTDGLRGFYRGYIPSIATYAPSSSIWWGSYGLLVPV

YYDLMQTWPRDPFWKQ

>contig28677 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58386.1|) 3e-86

MVDMQQLHAQRFAHDELLAVTYHSLAMHVERRLAREINYFEDEHTTLSLHKLVLLGGTFD

HLHTGHKKLLSLAVSICAHRLLVGMTADSMLTNKSHAELLEPMETRARAVREYLFFLNPH

IVAEIVPISDPYGPAIVIPESAAMVVSTETLAGAAKINRIRREHKLPKLIIFACRRSNSS

TLSSSCIRAKIAMSR

>contig29454 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63678.1|) 1e-35

MHAYHPRFLVLIDNQLMFFKYEVLAEESLHSHASMLDLRHVKDVREADSGFQENLDFTIQ

LTTTNGLLW

>contig29739 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY65960.1|) 1e-94

MSQVNDGDKNIIAEFGHQQTPLHIASRKGHCAVVELLLQHHAASNLPDDHGNTALHYAAN

IETVKVLLDRAFRTNANIPNKRGRTPLHIAAARGHVDVVAYLICHGAERDLVDDQGQNAF

HHAAANGHTAVALVLLQETDSNSRQLATGKSNEIITATDGTVVDELRQQKVEQHESDRVL

AIEDEPQTSRVFDINQEDLKGNTALHLAAMSPYDRCQQMLQFLLENNADPNRTNWFGYTP

LHMFCSHQPGPASLIQTF

>contig31240 Frame-1F

MLSSVIHFRRLPSSICRQFASMQASISTSTAVPTPETLLDEKLHGNTSYLQRPVTYPLHR

IKVVLLENIHPRAKQVFEREGYTVESHNPAMSGEELARVGGDAHILGIRSKTHLDPEFFN

SIGWHDHRLWAVGCFCIGTNQVALSAAAAKGIPVFNAPFSNTRSVAEKTLSEIIALHRKL

FQRSTELHQGIWTKSATGAHEVRGTTLGIIGYGRIGSQVSVLAELLGMKVVFFDPIKCLP

LGNARQVDTLEELLSHSDAVTLHIPATSSTKNMINRETIALMKDGALLVNNARGSVIDIE

AAKEAIESGKLSGMAVDVFPKEPAKNGEPFDTPLRGLPNVILTPHIGGSTEEAQGNIAVE

VATKLVRYLNDGSTTTSTNTPEIDMLPIRNNSMRILHMHQNVPGVLSKIHSVLSDYGINV

TSQYLQSDRRHGYIALEVEKFHAKVVTRELKKINETVFLRTII

>contig31374 Frame-1F

MGQVVLLLENLFGIQVRVYGDAETKAHESDMPRDRALWLCNHRTRIDWMLLWSVAWRTQT

LHQLRIVLKAPLRKIPIFGWAMQHFLFIFLKRRWVDDQVKLRKFLPFLKSVEPEASYLLF

PEGTDLSKNNLEKSAVFAKSNGLMLRQYTLYPRTNGWTFMFPLLSSQLSAVYDVTMFYVD

YASNERPSEASLLNGRLPRMIVFYIERVKISSLRGKSESELATWLERRFERKESFLRTFY

EENGKLPDDAQLLFQQSQRSATAVVVAFWLVLICATSIFISTFVSIVVSAVVATGYAMSI

AYGPGIDG

>contig31617 Frame-0F|Blast-pre-mRNA-splicing factor RSE1 [Phytophthora infestans T30-4](gb|EEY54384.1|) 0.0

MQLHPQKAPSGGCLRVYRLVEGMQLVLVHATEIDDIPHAMCEFQGRLLVSVGRALRIYDL

GKKKMLRKCENRNFPSILIELKAAGDRIYASDLHESFHFVKYKKEENQLVIFADDCVPRF

ITSSVLLDYDTLCGADKFGNIFVSRLPSEVSDEVDNPTGNRILWDSGLLNGAPNKLEQIA

QYHVGDVVTSMVRTSLVPGGIEAIVYATIMGRIGVLIPFTSREDVDFYTHLEMYMRQEQP

PLCGRDHLSYRSYFIPVKNVTDGDLCEQYSTLSVEKQASVAEDLDRTPAEVLKKLEDIRN

RLL

>contig31886 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59840.1|) 2e-38

MPNVHSNRSRSVFKSDPDIGRELAKSLPQYRVSRDQFMNWSSLTYVKPNQELPPLASSSL

ALEDQFCGWLWMRSGRFGRWRHRYFCLDGTMLSYFTSFPAEVFLKQAQTSVASACTSRHN

>contig32054 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67770.1|) 8e-35

MYDLNSAINGVSVESYLPFLGNYIGRATTILFFAVICAQTYEYSGWTKTIVLYNLLVAVL

QSFVYFTTKTVTPSQAQVDDLSDL

>contig32120 Frame-1F|Blast-CorA Metal Ion Transporter (MIT) Family [Phytophthora infestans T30-4](gb|EEY58043.1|) 0.0

MDFYPMDEDTPLLRDMGGPDASPHDSVKPASYPVATKSRDSSATPPNQQTTELELNVDKI

SVLFSPTARQDANTFNNYKSFAEIPSNGSLQNHDELNMLDPYFDVTPPRLRVAFEGAGPE

KNGELGYNGFRAALENLGIRCPNDVVFLKLVQNIDREKSGRITLQQFDAAVHHLKMMHMF

DENAIQEMESVGYRQAGLSVSDFSGTKLQTFALRQKQLQSFFTAHRPEWVNVRWINLDGR

NSLNLKRLAIKYRLHPLAIEDTIEGHERPKFDRYDGHLFLVFPVLRMQVMPDKGLPLERK

RSRFYSDTRETLMSNFVKRMSFRRSACTLPIDDTDDNDEDPLKLWIEHVFIFVVDNDTVI

TVKDGEGSNIWTELNRRLAVPYSKLRHNDAKFLVYSVLDVIVDQVTSVVDAVTECLIALE

NQLEQERHRFEMRSLRVLKNELFRLPRLLKPAREVLKNIIESKDFDASVTDYVRDVHDHV

VAALDDIEQQLQMCRQLTEEYRDAKSTQMNYVIYTLTVVTTVFLPGQFLTGVYGMNFDDM

PELHERYGYALFWVFAITIAAALQLYFRHKQWI

>contig32216 Frame-1R

MPFRGYVSSPNLDVKTAVDDNLKFLMEMGWRY

>contig32546 Frame-1R

MSTRQVSKARFGRSVALEQYVNIDVAPTNGIIRYLGYEIGIGTW

>contig33053 Frame-0R

MNVTERLRARHARLAPFCLVDPVKQHLRLQSYYQLARQLYRQSEAYFTECAFDNAYVFLA

KFIRLCSKVTTAHHDYELPQYHKDREWVRKQAEAGFKLFDEILDGMEAEENEYLEYEKSL

NNDQVSSIEDADKSLDVVDNSALEKQLQAMRLTKKSFERSNEHALGVQKNSSQTVSYPTV

GKASWMTVGATAPTIKPFPAPPRSRQRSQKLIANLT

>contig33642 Frame-1F

MLLRKSRLQTTKKTKFCRFLSYIADAEYAACQRGLGIVDDLDDDDGDFHDDTAIIATKIL

VDGAGSVLSSPAPVIPEIKATSTGSFYRTAMTRTAMKPLRDVYLTISLPSYSPAEPAGLR

QRSQSQLSQKINCGSDQGGMPLFLRITLSRVERLLHNSFQVNVAISGLIYALAQKPQRSA

VVFDLGEILPAGKSLRSILEEVYADASRRLNQLPNGAADLQEMRKRLVEKGNEAVLNDHE

AKTRLLCGYVLLDEILKELCSLLFARERVNNLPLKPEGHYLKPKRAELRASDFQRKRALS

SETLFSDDGSQTDLASPGRQRQIG

>contig33956 Frame-0F|Blast-ribosome biogenesis protein RLP24 [Phytophthora infestans T30-4]gb|EEY69571.1| ribosome biogenesis protein RLP24 [Phytophthora infestans T30-4](gb|EEY59297.1|) 1e-83

MRIHTCYFCSSPVYPGHGITFVRNDSKIFRFCRSKCHKNFNRKRNPRKVKWTKAFRKSAG

KEMALDTTFDFDKQRNRAVKYDRELMGATIHAIERVTQIKEKREVAFYKNRMKENKSKAK

ARDLRELEQNITLIEPAATTLKDQAQLVVSSSKQKDVAATETLSSMVLDN

>contig34197 Frame-1R

MIKWTTKATSKLVTFKSVPASKDGSSNGVFEAVKDKIPEASSVEVLQHVLKSAKELLKLP

I

>contig35046 Frame-2R|Blast-CDP-alcohol phosphatidyltransferase, putative [Phytophthora infestans T30-4](gb|EEY67777.1|) 1e-142

MVEEAPRWVYAYAGLSLLFYQVLDVADGKQARKTGNSSPLGLLFDHGCDALNVVISACTF

ASTLMLGPTYWSLLIFLAPAMVFFMATWEEYYTGTLALPIVNGPNEGLFIMYSIYIGTAI

TGPRVWTESNMLLPQLKNNQVFVLFTIVCALGQCLVSVMIAIRSMKRKTKDGTAALLSMM

PFVVLFFLSALWVFWSPSDVFTDHPRLLIWTVGLVFAKMVMHMMLSHMCEEPFWLLRKTF

LIQLVVSFLLVAGIVPWARESSVVKLFFLISLSAYAHMIYFVSTDLATILNIRIFKVKQG

>contig35158 Frame-0F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61857.1|) 0.0

MQYSNDEVVGENLVEKFITEDYREAVGAVLSRALDGIETANFEFPLVTKAGRRVEILLNA

TPRFNEHGTVIGMVGIGQDITDRIAQEQEYARLIEKANAPIFGVDSEGKINIWNHKTAEM

TQFSKEEAVGRDLMSWAIPEQYHDAVETILWKALEGDETSNFDVELKKKNGRTVNIRMNA

TARFDQHGQIVGVVGIGQDLTDRIVQEQEYTRLIDTANAPIFGVDANLCVNIWNKKAAQI

TKYSTAEVIGENLVETFISPEYRPAVADVFSKALNGIQTANFEFPLITRPGTRIEILLNA

TPRNDMHGNIVGVVGIGQDITDRIAQEHEYFRLIDTANAPIFGVDSFGCINEWNQKIEEI

TGYHKSTVLGLSLVDAFINAENRSEVRKLLNQALIGIDVEEMELPMTTAAGLSLLLLVNA

SSKKDMHGNIRGVIGVGQDYTAKKHMEAAKVNFLASFSHELRTPLNGVLGMLELLRDQKL

DKTSERYVHIAYISGSLLLNLINDILDLSKIEAGHMEISADPFQMEDLLEYSVEIFKFKA

REKHIKLKLDCSPKVPQRVIGDVSRLRQVLLNLLSNSIKFTNEGSITVRCTTVPSPDLPK

HCIKLLFQVIDTGVGMDEEEKSRLFSLFTKLERTRKNNPTGSGLGLAICKQLVELMDGDI

DVDSELGEGSEFFFYSRSGSP

>contig35420 Frame-0R

MDDEMTKHAVLTLSDQYNWRTGMQVVLFDGTNCDKLKQKMFPVELGGDRRRAKSASAVTR

PVHVESVGEGLDDLREGKVNTGTVYSIRGAGGLITPARKDSACISFRLIPDEDGNIDIRQ

GDYVSFTVGKNKKSGRKYASKVKLEFRPPANLTNDANNTSNPTGPFGGTAQKDYFSPSLS

RWESRSRAATVGAPPQPAPFRARSSSSGRIKLNLSSPRMAQSSLHIISPGANLLVPPPGI

GINGSTQIYRQASGPDGTRGFGFRRTGGEPSEMAPDLKLPVMERRRTRSSGGAW

>contig35554 Frame-1R

MWSFADYCDSSWIFSEVIFSSYSYSSASVKSLFFVTYVIGGFAGAEADNLVLFICISFLL

QVFQKILMLVAP

>contig36573 Frame-1F

MVARMSSKVGRSMTALDALQQSVKKSESDGVSSRAGSIATIQGHKSHYEQFEFIELGDDI

ALMKHTMAAARVAAGGVCVAVDRVLIAKNRTCNAFCAIRPPGHHAERCRTMGFCVFNNVA

IAALHAIAQHGLDRVAIVDLDVHHGNGTQDIVNQEPKLLYVSMHQTAPCFPRSGYACETG

KHGNLLNVPLKARCSARMYREHFLAKVCPRVRAFQPQLLIISMGFDGSSRDPLADFLLEG

DDFYWLTNELCAVAWEFCDGKVVSVLEGGYHLGALAEGAEQHMLALIHNSCRPDDLSLKA

A

>contig36722 Frame-1R

MLRLATQTPLPHRVTQFIQRHGHKKWFKAASTLDSWLARCSAVEIADLTSRVLPSNSSND

WNAILTSALVTARQRRDSWRLGWECFRAACVLFHVCPHDTDENDGMVLHLAFALEGRLYE

ARCFQAIIQTFETCTWAVAINLIQQWRASVGVLNLEGDTTLEPLLGELATLCAYASSQES

PASMLRALRRELVTVFTTRLVAVLLHPRGKRAKSKADTLVEKWSVVDNATVLDERLRLEY

HDHIRQILQDAGIEENSTPDGNSAWLHDVGLAFLFYQESASSTLNLLEWYECFSSELQEE

EEARNARQSTKVRKNDGLVKARFVRALCTLRHWGFLKNDGHRDFAQEYVEKLVFL

>contig37372 Frame-2R

MWIFDDENKRMCLKKINYVPGLYKIFDEIIVNACDNKQRDKSMNTLKVTIDVEKNEISVW

NNGKGIPIVLHKEHKVYVPELIFGHLLTGSNFDDQKKKTTGGRNGYGAKLANIFSNEFVV

ETADSSTKQRYKQVFEHNMGKKNPPSITKWAQKDFTCISFKPDLKRFKLKFLNDDIVSLF

KKRVYDVAGVSGKGLNVYLNAEKIDIKSFPQYVALYPGPHGFAPEAKDGEDSHSDEIKDD

DDDYSEGKLSKIKVAKTKPSNVTK

>contig37765 Frame-0F

MASTTNLLDDLMGLCVSSSTMSPRRYELLTSLAGNGLDIQYAFLRQPSSHSPEMNAIQLW

LANHSKEPIARVHIIGTINLDQVVSFPELPVLFPGGSTSIAQLQVDFHGRLDTVPLEVIT

STEKFRVDLCPLIGELLLPQQLSLDDFERRISQTDSTCLHTCEITLPAPVEMNAAVQAVQ

KECNMAQVYEINYMNGVMGKCKFAGRFRSGNDNAEIVLMAVEVQLQSGKGQLLVVMRDSV

LAQRLSTAITQALSTSVSS

>contig38342 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61862.1|) 2e-54

MQDDEVYLSDINWLPSTHQMAKLLMPFDFATATALNDSVKSLSALDMYVDFSMEELFSCL

SVEHVIDLITCMLLERQIVLVSSRYSVLTSVGETLKSLIAPLEWSHVFAPILPKSMLECL

QCPTPYLFGVHSSNRTDLREMLEREGCGDGIVVVDLDADAIDSPGRLQLPQNVRGPLTMQ

LLHLLKPKVFFSDLVPMLDSKSEASSVCGFPQDHVRLCFREAIATLLQTVEEFRFVLSDD

FDYVVVFDRLAFLHRLPPREQAFFRTFLETQIFSHEIASVTR

>contig38755 Frame-2F

MEKANSPRVELNEEAVRLPRYDIPPPYRAVSFATVNDFRPSSKLSSSGGSRGSTLSEVTA

RLSFLIMAVAENRAREIGICAIDLVSPYELLLWTIIDSHSYVDTISLLEAYKPVEVLVVE

TSKTRKINEEITKRFAGSSCRVIPLARKYFNQTKGAEDIKRVMANNVDINIGRNYVAMAS

V

>contig39051 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63221.1|) 1e-74

MDMKIKIESGAQNTAVCRIAAGKDHSLAISGEGVGFTWGRGDSGQLGHGCYMDVSKPKQV

MAITPAILDFCKLIDVAGGSNFSLFLSQNGTVFITGSDPSQDVESMYLSPTLLTLPMTLE

LKYFGQIASISCGEAHYALLSTSGALLLSNSSFFDPSPDAGLATAEVQERRVVWFKEAGI

VCRMVCGASHTLVVV

>contig39529 Frame-0F

MASPAEIYNWSVKPEKRLAVNMRVTEMNGISLTGYTYSEVLELLARMPRPVGIKFADVSK

GIVGRVEKEIPVEETEEEKEARAARVMQRSLHSEYFQILVSYELHKQVWATTRHHMRLQL

LDIQKKNEVVGIQVELEQQRRESLTKERELLVQETVSLTQVIDQLGKQLAGKIDSPEVLR

TAELARRNAVLEKEVTEIIAENDELQASRVRIEDALDDLQQELEAYGNLDVDRNGSNEVK

FFSPAFLGSMVHRGSIDTRAEDARERLLEKIKAQRSQFEEEIFLEEERARFVESEIYQFK

SQISLAAEAVKREDAFISGERPPQMIFLENKIALLKKNLRETVAGIVKARQSGDQQQTPY

LFTRRADLKDDLIAALEEMRRMENELSAYFDVVQKEKVESLPKDISLLTVNIDEAPHERA

LESSRLQKKLAKLQVQLHETVVQLAKAAAEMDEDHANYLGKRRLLLKDEMKAVQDQFEAL

TMGTLNVAVNNRESYVRPSLVGPPTIQDAPRRSTAGSRISLSGGFRGSITSTWTSMAPDR

ASNISQTSEIAPRSSERQDLPLGGRSSSNGSMALRTQCNALSSIHVP

>contig39626 Frame-1R

MTLGRSFSVLAIHALGFILLARYTSVGVRAHNLQRLQDFRGHEYFVQFGLHQSEDDPVEP

PVYEDYFPNAILDHFAPVSKRLLWNQRYQVNEEFWGGHGFPVFLYIGGEGPLGPKAITNH

TFIYFLAEQHHALLVALEHRFYGRSYPTTDMSLPNLAYLSSEQALADLAHFHAFITEKYS

LIDTKWVAFGGSYPGNLAAWVKLKYPALFTGTVASSAPLHAKKNFYEYMEVVGDGLRYFG

GGACYYQVEQAITKLGKALDGAQDDREQVLALFSPCYPMTTELDDSVFATSIIGAFQDIA

QYNRIHEEVMTLSDVCKHFSKPGDAINKLASFINSTRVGNCLDSKFQGVPNGTIEVLGRD

QFDGKSSARQWVYQTCNEFGYFQTTSSRESPFYALRAVTEANIGSTICSLVYQMDRAPDI

ATTNLEYGSLDIFVEHVTFPSGTIDPWHALAVRNSTKLPSMTAKAVYIEGTAHCADMYYP

STRDSPELVWAHDQIAARVKSYLVETDRVVAVE

>contig39943 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63802.1|) 1e-155

MAEFCSYFTAEQEYEHQWPEFQAAQLYCNFWVLLDILWPYLEVLWQILPTLNWEHPTHTF

LCFALCVWLCLFLQWLPVILHLAIIACMVRKYFELNFYSFAETKNHLTSGDTNIECDMSN

GAFRQCHLPPSFSHLMNKMTHVTIDQETKRTLQSVQNNMAWWSSNINILELIFNWEDTLY

STHVLLYVTLSCVLHIVIPNRYLLLAFTVYLFVQWTVPFIWLLHFLYAIHRAVCSIVYQH

RLQSSMAQADIKTRLPSVAVSGKLNLIDQARTMRRAVSNASARAHAHIIKKEEAFGAAAS

ALSERFVVSGEPALRKRPFLM

>contig40554 Frame-1F

MQSFRGTGNFTGEQPSGKPDVYALGVVLVEIVTGETRIINAQRLPMKRPGSENGLLSTAE

KIGVFTSMLQGNAESSLLLP

>contig41179 Frame-0F

MPEQQYHQQQPYSATGFEDRAGGVKQTQNHLADKHAFGAGLGYHAANTSQASHIVAAPFE

MTANKHKDPCVAPPSCLASFGFGGNVVTMFPDRKFRPNISGSSFRNNPRGTLPRSEFENG

GNSELCKGPVNFYRMDQLHSKDKEYSQMDTFPGPLTGNVSEDVIREYIDDRLKRSEAPTS

AIDAEDEDDRLLLGVLRIIIKCNGKLRSDPGTMKPNDPESPEAQLIILFDRSSKRRNGNQ

PPIFPEARNTHSAVHPELKVKHTNHLRELLLVGDRKGAISTAMSAHMWPEAMLIASFTNK

EEYKRVLRNYVDDTYAVGDPSRALFMAFADQQEKSVQEPKRLLHTNAQQSTESLVLSAWT

SHAQVLLANRTADTNKILTELGDRLWNEANLVTAAHICYLLAGIQVEAPIPTSKIALLGG

DHRTPTEARFYVSPGAVQRTEMYEWSQKLSKDAADNVMIPFQGYKLIYAMMLADLGKLEI

AFKYVTSMLILIKAVTATTKPGTSMYLEGMKNQLTVLDDRLRQHLGQDRVALVAASTSRE

SDRKQGKWGLGSALSIMGKIVNRVVEGNDSSSASISNSKAPSGLYASEAISPVAHLSESS

RCDRFKFDSEAFIRITANLATYSTAAFVDRSF

>contig41197 Frame-2F|Blast-SCP-like extracellular protein [Phytophthora infestans T30-4](gb|EEY56896.1|) 7e-50

MFVLQQSTLALLLSFASVSSATNLQQMAPDFSPVVSSQPSDLVAHVNMERANHGLANLCT

NHKLQAAAERHIMDQFKTDFMSDTGTDNSHPEQRITDAGFEWQSVAESVDAGDANATDVL

NWWMKGENRENVLGKYTMVGTAYVYNEMTFNKHYWVQVYATSSSEHCDS

>contig41881 Frame-2R

MLSHPAIDPKFATTRARNAVFPPVRGYGAL

>contig42048 Frame-1F

MEVHVEAMPINPNSNKRKSLFSVSSPIAPCGPVCNVVDSTPSSSISGALHSSSDSAKLSV

ALTALKVSLKRDLESFAPPTPAVSPAHGRGPVKRTRFDFESTQEIRASAETHPVLAATNA

PCKTVNALLAVSSHIKYELEKRRR

>contig42307 Frame-0R

MIWELETLALQYKFSLPAEEQSVGLQKIAVSDNNQVLVASGRAPCIYVWDFYSQTMIRII

ELPAPIKQVVYHAFLPGCKTVVSILADNGRLFFLDVAAKNPQIQLDISHQGRSISAFDIE

CHGRYLAACTSDGFLLLYDMAVARETAARAHKQWKGEGPVEYAQLRTRSGLQHMKSLTLD

PTREFNREFPEQGRPVPSKLIDSLFGEYSRRNSGAPKRSHGDITAAVHRELTPVQSTNA

>contig42534 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65714.1|) 1e-112

MTTELEANIQQALPSALKMALYAAKKQHLELLKYTIEGVDSLCNNAAFIKDLEDQEHLLQ

LDETAKGFALLKTRLTRYKTQLEELEPLVESGKLDQKKINKLHKDALTTPRINATKHDFY

KKFCDKAGIELAVDGDEDVFIQESESIRSMICPVTQMEMDDPLRNPSCGHTYSMKGIQAH

LQRNKKCPVAGCPQRLSIDNLERDVEMEVIIARSRHASKQHMSQVTAAATEDESDEEEYV

VV

>contig42691 Frame-1F

MWPQHYKFYGEDVGLVTYNFMWRSTVSFCGCITSKNSQMISSHICIFVSMRIQQNDYKKK

LANMTTVSELSSTREIKLLD

>contig42765 Frame-0F

MESHLFINLFRNLHTSLPRRSSTIRNATLSSAYSSRLDRNALPNPHMRFQQHQYSSRRRS

TSCHHSSDARIRVFVSSSLHRCRCANPKLPHSMLCRTTHGRSVQSTTCFHCQCPGLESHG

IIFFSTFVVVHPLNNNTVSRRRNEPFLAKLNLIVLFLPMSVLPSRQ

>contig43371 Frame-0R

MRERVSSGSPRTADIGSHEKVKNKLTAHQAGCNNNKISQTLLPVFFSRRHNTSDDDENDK

QGRRRKRRKGTAWFNRLRISTLSRLLIISRGLRWIRKVLLLLVVVMITVLTLEAIGRLRF

NGYLMPLRGHNGQLGFYHEMNYNMQTIKDATGEPQRKLFPASGLNASEVKAWIAKRRNVT

NGQKFLVGCSSQWKGYVLRSFLSLFQELKNEHGWKDLDTSKSSINTFLGMEQNEVPSIML

FCLNSFYYPMELLQTHSSYFHELRKQGTILAVWNDDLHYYDQFNPIVLRDEIFTKIDVLI

GTYAYFMGDYFSKVTESVDERDLPMTVWLPHSSGLDFINASFNEYPINKIILSGRLGSNW

YPLRHWLGL

>contig43696 Frame-2R|Blast-glycine dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63500.1|) 2e-53

MDRFCEALAIIRREIEDVATGAIAVKDSPLKHAPHTVDQVTAEVWDRKYSREQAAFPAPW

QQRGKNKTFWPSVGRVDNVHGDRHLVCSCPPLSDYE

>contig43722 Frame-1F

MSDNAERRILIPSPLSVIPSSSSHCHSLDKCNWSYRNPRVIVADPDDTLLGSRKDESRVW

IICDICFGEFPMIDVLGTDEVSAIPARPW

>contig43919-1 Frame-0R1

MLSRDGLLCVLKTTIYNRPWAKQIAER

>contig44125 Frame-2R

MYPSDDPWKEGLDTMLTTIMPYVCKFTQRKNPLETTVQAIESSSISATDEVVKEVKGSNE

KDAENLEWMGFSRVLRDIRRGFHMYPETGYQEFRTQAFIRRFCEQALHIPSKNIREIAST

GLVVDVYHDNATISMPEKRKLPIIAFRADMDALPVKELNQHLSYCSTEMGGHQRKRHKHK

KRKNSCCQDQTQVERVSVSNSNGIASSGTSDVGLNVSLYTTTTNLLPIPSTITTTTIGAP

TFGHDDDQDVQMSTPAAHMCGHDGHMAIILGLCAMVVRRAHLLPPNTFIRFLFQP

>contig44617 Frame-2F

MQMRIESKEIEVYDLQVDLEALKKRRDRRLPSHDQNASRNSRSTSCQSIRRRSRSHVQAR

SRPCIVDEDDEGSTEEDECIIIDSNEIKKEPTAVNQSTVVPIEDSIPDHFWGRSNIPKLL

ANHRFRAFPDGSLRKGRHFAFNPNQPKIFATSPDEGGLILWSYERQDQDISKVVTLAPSS

FRRENSCAEAIAWSPDGNRMAMAFRDPVQETGEFCIVQLHQLKLEDSNTPQKIPRNRVTS

KRTTLHSRGLSAIDWLPTGFGPETTSHRLITTGNSDHAVVLWEEHVDSERSGLDLKFNVL

HRDHRSEVKSLCIHSKRQCLYTGGMDGLLIRYDLNKGTSDVVMERRKPNISKINSVLEHP

HNPNLLLVSSVESSRYNLILHDLRQRYDSNEMALTWEGSSMSQYVVPRWSPAGYHVSCGS

KTGVVNIWDVRMRGESYPKVLPQQSLRVHHKTVLHATWHPRYDAMFSVSHDRTLGLLTFR

>contig44998 Frame-2F

MEDGQMCKWRGNPIIIIDECLKAMMKFRKREFITMHHRHFRNLLRQYFVAIYIVRAKCHF

VALQLNVYGLRLSGMADSCTFLRD

>contig45041 Frame-1F

MSCSNKLFVFGLGYSATRAARAFRSAGYLVSGTVRSVDAATRVSRSNADFLHFEDSKISN

VFLFDGDQWSRRNALTLEDALKGVTHVLISVPPRPLDGYEDPVMSALGNRLILATKDTVQ

WVGYLSTIGVYGETNGVTVDESAPVHSSVKRSQLT

>contig45236 Frame-0F|Blast-tRNA-dihydrouridine synthase 3 [Phytophthora infestans T30-4](gb|EEY64037.1|) 5e-92

MDPLDDKVVAHIPFVGGGDVLSFEEYHEHLQNGKLDTCMLARGALIKPWLPTEIKERRHW

DISASERLDLLKDFVRFGLEHWGSDQKGVNRTRRYLLEWQSFLCRYIPVGLLETLPQRIN

DRPSLYYGRNDLETLMASDQAVDWIKISEMLLGKVPDGFQFVPKHRANAYQT

>contig45359 Frame-2F

MSCIAILQATLLFIRRYNKFECSPIWYMSPNSL

>contig45838 Frame-2R

MYWLLLPARRLRQIKMSESNPDRRHACLFAHVQCQILAPCRAAPMELMGKPE

>contig46505 Frame-1F

MLTANYEVSNLRSAAAMNQPKTFDRIISSVADEPFISNVAIFGLITNTSSISTPYRAS

>contig46956 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65537.1|) 6e-51

MESIELPRCGPIFSQNHMQRQSLRKSGFVVEASEDKSSITTRVTFFITAPYRSHSLEQDR

AWLLRVAGCVRLVPSAIVNRRIRRNQLRDRRTWHFRNMCSVCG

>contig47120 Frame-2F

MPRPEYAPFITSPRNASVSMNGTLIGSSSPSTVLAAASGTFNAALSVAKFNLHRRRRQPQ

NGSGSNRSNGRRL

>contig47216 Frame-2R

MPPMGTLILTPGTVPSTAMDGGGYCVPRVSIKVHACWTAFHDYVAQYAFDTAQIFRTRST

VSVAARNARILASLAAKTRSEDHGVASYASYATAAPTSRLFPDEFKWFSKLLICTYGWKR

RVRGKVLKSGEHGSGPCSAMMLARLERNVDGMWQVVINRQVPEHNHELGGHVNDNVAKTY

RIGGIADVLSPARSLHTDSILQTSSNDNSILLKLHPITTPSSVDDIQMATSNQREIVVRV

PRLQSVFKSWDAFHASLKSYSDATYQLYRTRTTSSVQGRNQKIAQMKCRDDKNFDNNGNV

SDSETELSEVTAVRKIPESWRWYSKTLTCTHGWKERHRGSGKRNAHGVRSTSCPVKICAT

VQYHKCSKRQVNSSPLIESENTTSDRCWRVVVTKHVVDHNHNLSRELYQYYCENRRIYDP

ELLAIDTSTSSSVDSRDKFPDSGGISPEYHLHGIQLLSHSSVLPMQFEAGQTETVSHLQL

FATSRSSQSGSIETNAVALSASNPSQNVSSVVLVPYSPSIFC

>contig47458 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68139.1|) 5e-53

MKHKSVTQVSIEAFVGTNPITRVADDKYFKVPFLPLNAPKEPTPAGFRVSMPLYEHQSRS

LYRMLQIEARDENVNKFNFGMIDYISNGGVLADAIGMGKTATMLALIAGEPRDYASGANL

LVAPSHLLAQ

>contig47546 Frame-0R|Blast-calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type, putative [Phytophthora infestans T30-4](gb|EEY62297.1|) 1e-67

MAVGMPNPLEPLQILVLNLFADGMAAVALSLEKGDGTVMLDRPRPRNERIIFGRLWVIVL

VNAFLIACGALIVFTCGLYWNFKHILLDDIIADI

>contig47869 Frame-0F

MHQLVHRCVTTMILTTHLKQLTRASKTLNGRTLFRVHSLAHSLFPRDSTASLQEWKEIPL

PTDEILQKQGIVNASVRVDFSCTNCRYFCAIFNHGTIHVSAIVKIA

>contig48132 Frame-0R

MSMSAPLSSADTTTLSSVSSLARLSNSVLPPLQLNVGVFSRRKGVRYFRDGQVCSCRFCE

ILRTRTEPLLYEDDEIVVFRPLRPIVPSHVLIVPRAHIRNVNRLAARHRGLLMRMHHVAR

ALMTEEGPENRSIYERFGLQAKERDDSRKYPVRYSFHVPPFNSIDHVHMHAFHDDLRRLG

YYDRLKYRTQSWWCRSLEQVLEQLPPVPADTRQLEADASNSR

>contig48381 Frame-2R

MRASTFIVDFTRRNPFSSHVVKTYVREAHQMIQTLVKRTTKRLLNRKRLIYLLLYRTAS

>contig48415 Frame-2F|Blast-guanylate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY56424.1|) 2e-18

MATAMMPVCLIESSNIGLRVTDRGASLLESLKEPVAIICLAGQYRTGKSFFLNQLASRSD

DLPWISTGMESASVDSKGTPC

>contig48590 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64982.1|) 1e-163

MLSREFALARADSRDVAMSPRVVEMQLMYERVMRNLNEAQKAVDGIQTRIKSQDLALHED

ELRRLQAQNSRACQIVDEESRIATTIERRLNTVRVLKANQFLIGEHLQCADETVEFILAK

LNDAGFDVDNDLDVTIKLMEQYMKCARHLDKRLTQRQKHASLHMMHRVFKQVNLVSKAAR

SGGFDVEDTATRDKLVKFFEHAVCAAVRFWCQEETNALIRQQQRLLGMRHLTAREYDQLH

FSTRHKPGRPRSVLAVARDAFRRHEAVARSHSSHCPWIAA

>contig49092 Frame-2F

MKSQHFNSNSGSGGYGSSNGVPHPRGNLQPLEYRPKTAQQHDTHSQITSPGADGMDVNAP

VFKQSGGFNLQHTARPYDSAISHRPPPPMGHQPGGGMYQQMRGPPGGHHHQHPRLRIPRG

AMHHQQQVMPRGNMNSTSQGYYRPQMQISPHYMMDPGPYVRGPHMYGMPPVHDMSMGMGA

MPMPMSVQPNHQPPPKRERKRLEIVDPRTGKPIVIGNKSSSVSSTDNSIKLDDGKVAGSS

TSTSAQSTPQKKE

>contig49531 Frame-2R|Blast-F-box protein, putative [Phytophthora infestans T30-4](gb|EEY65520.1|) 1e-59

MSFTRLAREWKLHRPTSALETRMPERFGFEGQDRYADGTLRGSVSSLLTVHWVRVIVDEG

HKLGGQTPSDLMQLARMLYTG

>contig49834 Frame-1R

MSDENNERVREVGELEAASRHKGDDIVVRKTVESFMNENACCICQDFVDVLKQGHLSSCD

HHFHFDCIVAWAKVTNLCPLCKVKFNEVTREDTQGTIVHREVICDIKQVYRPDPFDHDLA

AQLRLVNQARCELCGSGEDEHVLLLCEVLGCGVANHTYCIGLRAVPNTSWYCTSHSITQH

RASDVIERPATTVSTRRRTRRLASLMSNVLRERHEVESPARRRRQRQEDFVAV

>contig49980 Frame-2F

MLSGGHDGYICRYVLDSDAFGALKATQVGRESIRNISTVRQLWWSKSAAHGKATHNLMVF

GFHANQAILYNLSAHYRLFNVECGGWRRPHALFTRAAEIMSSMLSHTFLFTLPAAQKQQI

VVKVHSTLFRETSDSNTVPRFLNLSLHGQYHGRMTTCVAFLGKDRMVTASDDNSLMLHRQ

RATNCTGLRWGVVATGIAHTTTVRALITFQRENVDGIFEHIILSGGGKQRLNLWCVCGES

DLLRHVCGQDRAGAAQDHRILGLATFVIPSVSGAYRLVAACNSEGSTQLSLLDFNHGKFI

EIGDLNSISRKPILSCVGFQDGDNDLVIAGLAVGTTDGIVTLWDLGALLREIGMSLQLSE

DIRHIKEKLKKLISELQPIFEYLAHDMGVNCINLVSCKSTEKGSLDVTLISGGDDQNLNL

RELRFPACLVLTEVRLINASGAAIKTVASIDSKAIFAAGYDQRVSRWSINHTDNGTKIER

QGAAFSECADIAKLAIRKASTRNAYEVVVVGQGLQMIQFQRK

>contig50021 Frame-2F

MLVAIQHLGIAASIIFTPLIRVDSMKEHATINPVIV

>contig50469 Frame-0F|Blast-adherance factor, putative [Phytophthora infestans T30-4](gb|EEY56141.1|) 2e-40

MGKARTTSRRRAQSAAADSSRMETWPPPPLTASERAYMIRKAKEASVALVDHAHTLDGPV

QWHYTGKFRGIQMYRGEGSFDHAGTIGTEFLCGV

>contig50487 Frame-2F

MHPFAAASELDVGTTELATAACFRIATRHLVQTGKMILREELEQAFKTYTSLQLKNCVEW

STVQSLLATLANGDIFTTKSESTRNAGVCWQPGRQFLTTPTFISSDASQIQTMVELEKEV

VASACDPDNSGLMSATLIKRRRQGLFLKHLLDDCSTIPTLSSVLCACIGVHSLTRQASNN

LRISYRSHAQMVDALQVAEIWLREQAEKIGHRSDLPPPFNKHNGPQDKFDRHISSRYAKP

FSVLNDSITKQLKRDAKKPFGSEKNDLMKVLCRYELNGVCNDKNCSNYHLKDYDLFVSTS

ADARDTIADSAEASRVDVNINELKQLMDSFAAFRERIKWPVITTTRT

>contig50858 Frame-2F

MPLFCLAIARSYYASCAGLRTTKSLSEKG

>contig50946 Frame-1R

MSTISKEQHDELCVAYASMILFDAEHEITSQSIEQIVQASGNEVEPYWPTLFSSLLSKEG

KVLEIISSGGAVAGGAPSTTGPSTGSSCEVDEKVVEKSKEEEDDAADLGGGIDMFGGEDY

>contig51105 Frame-1R

MGGECAPDHCRECGSKDVVTDFSAGDVVCRGCGMILGERIIDDSPEWRTFANDDRGGDPA

AKSRVGDVADARLDSLSLSTYLVDPKKSGGGADSSKHKRPNISSDSAKVKRMQRNMARIQ

EVADYLSLPKKIVEVALDIYADAEKQEINMRGPERESMAVAVLFIACRKASNARSLKEFE

EASGIPKRRIGKSFMSLQRQLKLEVKQATTEEYVQRFCSRLGLPNKTQMIAHTVAQK

>contig51655 Frame-0F|Blast-GlcNac transferase [Phytophthora infestans T30-4](gb|EEY68842.1|) 6e-59

MKAPAKTLLLLLGGLLVIYGVAVGVESHMSIINTKLSIKLDPSVQHIPLDPAKEQLRPPP

VQIPASFDIFVGISVFRDGYRCGKTILTGLKRAKYPKRLYFGVVDQVDDGDERCMDEYCK

MAEAEWPGKGSCPYNDHIRVDLRKA

>contig52584 Frame-1F

MLQTMMNNPMVQQVAQQNPMLAQVLQNPSFLAQSMQVLQQNPGMLQQMSQMMSDPNGMAR

MQQMMAGGGLGSSSFGAAAPLSAAATNPFSVGDNLFASNLSAPAPPASTPAPVSSSSPIP

TSSAATSTDHSNEAYDEDEIARAIARSLQDE

>contig52845 Frame-2F

MSLLSSPVQSLQMDANKREHMGTAKRSSSDTESESQANVAMSSSTLEKRVRNDALIAANG

KEKRKKAKPIQDLSDAMKFEASLVGADQIATVLTDDNKPIEIVITREEAAGLNAAVAASA

ELVNELQHQ

>contig53666 Frame-1R|Blast-para-aminobenzoate synthase, putative [Phytophthora infestans T30-4](gb|EEY53444.1|) 8e-48

MTGAPKKRTMKIIRELERAPRGIYSGGLGFISIDGSCDLNIIIRTAIVTPQSVTLGAGGA

IVALSDTGDEYDEMLLKARALVDTIGVYATRYGHGAGARVVFDS

>contig53738 Frame-1R

MKVLSKAIDDSSIYIEQLSHGGADSYRPKSVRQSETDRRKPPLSAIVPMTVMAFPCSAIY

RNTHFVIYMSLVVNVRHPHVAFMFDASSLTPSMYLPKLRIQMPCQLLSTERLL

>contig54164 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53272.1|) 8e-14

MPSGDIEVLVRALGEFAVLLRKRHSFDKIRNADKQAILKWLRSLRFEELASLCCVEDVGF

VKTLL

>contig54366 Frame-0R|Blast-exportin-4, putative [Phytophthora infestans T30-4](gb|EEY53544.1|) 4e-84

MAYLLHWPTEPVVMEKVIEFVLLLSTTRAITSILQMETWKSLVQANASAGPFIVAIDGKA

STLDAAVARIPSNLRGNLTEALCRAGMTAADQNIREAHFQAVSRPIAQRLQQLISMSNFE

SRQTANDARMQEELKLLVEMYSGIARSAESTSHARITSFCLPALPVLVKVFQIFQNDSQI

VNCILNFFCLMVEAQLCYLPP

>contig54735 Frame-1F

MSITFEDGGSTTESEDNSFYQELCVKSEPAAYGSDAPKVSHIAEIVESKAQVVKLEGDVV

EPHRDNASNSSKRLEVTPLDITMPPCCSACGYALLVVPQHKLLNSTNMMDCKCCLLMLPE

SSYSKTQRSESRIAIRKCKSCTGNGTRDAVRLVKPTRERPRAPPRLRTAEAEKR

>contig54836 Frame-0R|Blast-cytosol aminopeptidase, putative [Phytophthora infestans T30-4](gb|EEY68382.1|) 2e-36

MQVPTLEGCSMDSSRIVKLLSQASMLSNYQ

>contig54959 Frame-0R

MMASMAAAILPLFLSIVLRSLLSNPFPKLRLEFNQTILLISHTHCASHHHK

>contig55112 Frame-1F

MQNCYFPQPSQRQVPILTDDKLLKRLDNERASADDIRHPYMQLGAVSGASGSAYVEQGRT

RVVCAVYGPRTDTRARREFSKDGQLVCDVKFAPFADKLTRRERGQDPDEMELSAIVEEAL

APVVMLHKLPKCVLSVFVTILEDDGGALAAAINCTTLALADAAVEMYDLVTASSA

>contig55798 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61931.1|) 2e-28

MHGRRRSNKNIPTTRFSLLLLENGEIFLDDHNACRYLEEPNTLTHRKVPGRIKVCTRGLF

FVPQDLQLPILRFPFRCMTAEPMAECFQEFPENSKASISKTNDVALVYVMFQTKQVIEMR

ER

>contig55817 Frame-0R|Blast-hypothetical protein PITG\_00587 [Phytophthora infestans T30-4](gb|EEY57989.1|) 2e-13

MKQNDGTYWASVPQLPVSTSHRSTIV

>contig56409 Frame-2F

MNCRIKRDEIYTYTSSQDKASLVQQPWPPLVATNEVATSGQQLARLLQDDEFYMVACSDC

GTTVGVYDKHQRYHFFNALPST

>contig57293 Frame-0R

MSQSHQSCIEKVSKELIQTSALTLSIVFHFFMLCQ

>contig58065 Frame-2F

MATVTAPVSHKTPFFYRILTSGDAQQLPLQRPPRARVSNVTQYPS

>contig58191 Frame-1R

MNDSNFRRLVQGIHDHIDAVFVQELVKYEGPCVAKD

>contig58850 Frame-2F

METRLTDLPKSGQAPEPWSGPLWLSIDDGINYAWNDGQPSPSAKYALAFNMNVKEIMDKT

SARSGVDAFKTSKICTSSSQCDNAFCAIRTNAVSGRCLQPWFGLSHGLVPASILEKKPVC

SVKHNNVVFEPIDIMGLITFIYAEAVKPNVFIGERYRGEDGTEDAHGRFSVPSYRDVNPG

IFHITASNLLGKLKRSFIIDIHADALVWNQPVHTFKVTKQKLMTLKEAAQEFFKQDSYTW

NADATEIVHVNSQITTVDAVEIVNGKLSVTL

>contig02966 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53361.1|) 2e-81

MDTPRDVINYVSTYDNSYPLFLYFVSGYHDFNGRLWCPYCDRADVVVMHHFNYTAPDKAV

LVRVVVAPSFSKWKKKINPFKQPEFQEKVASIQSVPFLGFVKKDVPANKVIVHQFLPDYS

ETKKLQTFLKNKPRFIRPHSG

>contig04869 Frame-1F|Blast-predicted protein [Micromonas pusilla CCMP1545](gb|EEH50840.1|) 8e-41

MSTTGRGRHSVLRIFKGRRGRTGHRATCGALPAAGPYLRLSRFQGGQAVKQKR

>contig07662 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56029.1|) 0.0

MSANSDRRWSLARATEFFSGDGKPDMLDIRGMTAITKGAAGKRDKFRKSISRCGVSIYGP

KHSATSASDASTREKIYIEDPRAPCLNIDYSNDAYRLLPSSEKFSAHTGVCQILGTKCIR

GGKHRVRVGDIIRFGSVGLLVTEIDTGGTGPYDATLSPGEVNALIQRVVCHDEALADVDS

GMDTDDDNGDASGNDESKPRASLQRQSTSAICYVCYDETEDENPLIAPCKCSGDTKYIHL

NCLKRWNTNGEKNEICTVLDESNARTCSICKAPYPSKTRLPNGQVLSLLPDRLTPPSIMF

QVVTKHSSSTLNLSTRYQLSYKMLLENDIHRPLMVGRSSQCDLVLKYRTVSTIHAEIHFS

KGEFFLKDAGSSNGTLRYIYRPLTLHNNQSLHVKFGRTVLSIKPTKKIRLPHFFGTSGHL

HASGHRMEDSGVQEEGELSNHSTPRNNRYRLHHTAQQPMTTIPMQQTQRLNLQTQSQNTD

L

>contig09291 Frame-1F

MLCRLLRVRGARAVPTTTYRSLLQPTYGLPTDPKRWRSYGTSTTVSTATNESTTEIEATD

VDSMDRQPSDSGSPGVETAKVLTIADVLHAREHEWAQNKALVDFDEWESIAAT

>contig10284 Frame-2F

MVHNGYNSMGELTPLKGPALPQERKGFPLTKSAKRAQRKLQLACMCSLLFMCAEIFGGFL

AGSLAIMTDAAHLLSDVAGFCISLFAIWISTLPASSRLSFGFQRAEVIGAVTSVLVIWVL

TGVLVYAAVERFVECLKPDPKEHVDGKL

>contig10806-1 Frame-1R1

MATQRLSVVDIVLHPHVRHLDACPGSPNEIHIVLDTNTPAVKPMKE

>contig11405 Frame-0F|Blast-tRNA pseudouridine synthase D (TruD), putative [Phytophthora infestans T30-4](gb|EEY58382.1|) 2e-38

MGRSFKTRGGSNGGHRGGRGRGRGRRGRGGRERGERYDRPDFRATGYNDSDPYSVDESDV

GIQCFLRPEIPGFHGSTKHRFSDFVVREVTLDGRVVTLSDVPRFTPNVKPLRITEVFKLH

V

>contig12747 Frame-0F

MYVGFLSLNSFLKKLTSSRHGCHHNHHGSPDSRHGNHHTRHGNLYDGRRNILGYPAMSRP

FQHQMIQVRLQQGQHCRQQALQQWQKQQGSKAPPKSRKKTSS

>contig14028 Frame-2F

MPETIVHDKSSAIKNERNSFQSGPSTSADTNSHMTPKNEIIDLKEENNPKISDDVQPEFK

NRNPAANEDHTGHEISKGAPSDVILKINGETSSEVKPEINVETLYDDKPEIKVETLFDDK

PDISVKTPSKVNTGATSPRKLRH

>contig15324 Frame-2F

MDAILSRVGEDDLRHHCVAAVLEELVQSELHVKSVVLALERTLKVVLASREVHKTLVLNT

SGRVQTSFRRLGESCNQIGPLLRLLHHNMGARSSMTTDVIEAASAVPPKSTLVPTDSAST

TTSEYEYISEEEDDEEPIVVRVAPPKKSNKRKADALELSETIPMITKETIKADTELFQTQ

LAKELRNIRESSVSKYTVAIHKDLSLFLKSIFDAADQFHKWQPCNDPIIAQLLKEMEKRL

SIFKDSNAQKERKKIVSEWLDQMTALSFVSTFDLTSIPPKMDRKILRRRKNKTPQDMQVL

AKCARRISSKVRSDASGPKEKKRKFFKPLLDAFIMYFAALAGTKSVANQTGEAIECLLCL

PLLCQLTDSNEITRKECELLDELLYRIRFIMSLGKKIRKKAVKTNVVHDLLGMFPPSVRP

RFNLPVRR

>contig16556 Frame-0R|Blast-60S ribosomal protein L30, putative [Phytophthora infestans T30-4](gb|EEY58239.1|) 6e-54

MRSGKVALGYKQTLKNLRSGKAKLIIMASNTPPLRKSEVEYYSMLAKTGVHHFSGTNNDL

GTACGKYFRVSCMCILDAGDSDILRSMPSEN

>contig17308 Frame-0R

MRPSGFVSLSQLLALPLFQSVTSEQIKEVVRTNAKKRFSLTTDESGATTFIRANQGHTLQ

VVQDEELLTPLDDPCAIQKCVHGTYLDCWDSIWNLGLSKMQRNHIHFTEREVMDEQVVSG

MRSNCNLLLYIDFSLAVSDGIKFYKSSNNVVLSPGMGKTGVIDRKYFLQAVKRDGTVVYK

RD

>contig17393 Frame-1R

MFEQPYLYLTICSVTHLSNSCNLNHLPKLQHMFAKYYILDQRQPTFSQLNTSNLGGVSRA

KTWLGLDNPFKIITL

>contig17407 Frame-0F

MFASQNIKGIQQSQYQPHQTFHIPFGNFGQATKCQLPAGAPVYVGVAMQQPQQHQVFWNS

VAGQQHEVPKGVNNNISHLLNPASLDTDHSIQRGIDIDAFAGLG

>contig17890 Frame-2R

MNSKLPSQSDKSYTDGALGEIAIESLERFESITDFAARDDEEPFWSQKIQRQANAISNEA

RFDAFITPFFDKALANWNMVFVNSERYAWLTQSMNVSRSTDLKPDGFATHPGMYRAKEKP

KDKVPRSSNHKFRFGVAEEDLFDCVILFESKLSLTDAAFGQVVRYLQSLCPKTFGSAILY

DRRSFWLINSRAKFIGKVLKAHWTDGGSKSLFQKFIGANVSPWVAS

>contig18060 Frame-2F

MGDVAYVQLSGTPSTVTLGIHEGIAPQELQHLMRVALNYEDNVCVGFQVPPPTEKKKRQS

NSIPHLIPLSVACKVPKLLVGKVSALIAPALAPSYPQGIETEVPKAATDLQRLHKLLDAL

ISEEKLSNFECAILKDMCEQQNANVLASMA

>contig18778 Frame-0F|Blast-protein phosphatase PP2A regulatory subunit B [Phytophthora infestans T30-4](gb|EEY61246.1|) 6e-61

MPQRGIAQQIAAMPTSGDPDALDFSKKILQASWHPSLKEVAVSIRNSLFVYAA

>contig18796 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67918.1|) 2e-92

MPLLRTLYSKLSTPWATTIVESVLALGTRYRLLFTEQDRVEIDKWTKRMQDWRNAPAITR

SAGSDARRNLVPAKTSKMAEAGAKVPGIFNHPLFNKDV

>contig19438 Frame-1R|Blast-ATP-dependent RNA helicase dbp4, putative [Phytophthora infestans T30-4](gb|EEY57909.1|) 0.0

MALESHGLLDVTLEGAAPAPKLKQNELEPREIERLEARIAAETPARGSQLCDASSFDRFP

LSEASRRGLRSCGFTAPTKIQAGALPHALAGRDVLAAAKTGSGKTLAFLLPVLEQLFRLR

WSVEDGLGAVIISPTRELALQIFEVLRNVGKAHTFSAGLVIGGKNFHEEQLRLVRMNLLV

CTPGRLLQHMEQTPAFHASALQVLVLDEADRILDLGFQKQLRAILDHLPPAGTRQTLLFS

ATQTKRVKDLAALSLQNPEYVAVHEHSVKATPSGLQQTYVVTRLEHKCDVLLAFIKSHLK

HKTIVFLSTCRQVRFFHTVFCKLQPGLPLCALHGKYKQGKRVEVYYEFLNKPAAVLFATD

VAARGLDFPHVDWVVQLDCPEDAANYIHRVGRTARYNNHGKALLCLLPSEVDGMRKRLDD

AKIPIRAIQVNPAKTTSCRQKVASIVAGDKEIKALAQKAFLSYVRSVYLQPARDVFDASA

LALEAFAESLGLPGAPRMPFLANMQVEQETRG

>contig19621 Frame-2F

MLAKKSVEAIELKAKRVLEMQDRILSRKKVKYKDKEEEKLGRLAEDLGTTVRSAKEKLEK

LEKEDMALRRKEDALNKKKRGETHWRQGSEHVVELDKPVPQPCAFPKVEAPLIGKVLAVW

DCIYVFRQVLGLAEVTIDQFSHALASSKHSHLLTEIHLCFLEAILEDREDDEYVSDDEAP

IDDSERYRYEIQHAPLTVGVPTRSMLTALTWPCVLGGLIAAVPRYTAYATLTFLSAFEAL

QETEYLNLTVPQKLAILHFLVGRFLGTEKVRHVLGCHLDATIQGTKEYNRAVLLHKKVTI

EEEKKLREKQRAEVAEVMEPSKTAMKTWLGKTDVDEDVGFSEDEGASDADLQELTNREEA

VLQMEDELEKLQMQDFVSRHEYVARKKKLEKQREKWRQKIDATQRKQKVHEQLERKRKHA

KKSITDALTSKDGLLLRNAIERGKECNLPDRILVTARHVLEILDTEAIREEEAVEKKRKL

NALLRESFVRTEPIGRDYEQLKYWIFKGDSRRLYIEQVGRFNNLQCNDDAVFQKLSPRDH

LNHEKQGSTWSCYASQTEINLMMEALDVRHPREAPLRLALSDQMDDFKRDMPVSKPGLLI

SDLLNDETIKKRTPRTSRMSINGEEDMLEWRNDQHAKRKGSSRSVEPGIESFREEFLKGM

DWISKCLRTLGSTWPDRLENGGIEWRKAVAGITTWKDFARYVLILESELMATQTKHKEEG

KGSDETFEK

>contig20669 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58512.1|) 3e-29

MAIVHDLAESLVGDITPHDGVAEEDKHRMEKEALGEICKTLGNTPSALEIRELWNEYEAG

FTEEAKIV

>contig21103 Frame-2R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY54112.1|) 1e-180

MYFLLAIPAAFDLVATFVANLGLLYVTVSVFQLMKCTVIVFVALLKVFVLKDRLRSYMWI

GIGLNMLAAVLVGATSLADSTSQDNNSTTQHPAFGVLMIVLSCAIQAIQYVFEEKLMDEG

DSAPPLVVVGMEGVWGLLFTSLVVYPLAYLIPGNDLGSNERVDDAYVMLVNSTLAQIVVI

VYLLVILGYNVFAVSVTYLLNSIWHAILDNFRPITVWGADLVLFYGFTSGNFGERWTIWS

WLQLVGMLTLLLGTAVYNGTLRLPGFVYLEPIKQSMNLIRTPEILAASTFARSPLISRNA

MKAAEIARRTPNPNDRDRVRREFMTEYQPLTDPESRRRIDPAGHTYGSLEV

>contig21389 Frame-2F

MLLIALSLRHLGNLQIATSPH

>contig21653 Frame-0F|Blast-dTDP-D-glucose 4,6-dehydratase, putative [Phytophthora infestans T30-4](gb|EEY60760.1|) 1e-50

MTLHGNGRHTRNYLYISDVVSAFDVILHEGKVGEIYNLGGQNELSNEKVAMEILDVMKPQ

LLEGEKATMIAHVPDRPFNDHRYVIDATKIRRLGWSEKVTWREGLQKTIEWICQHGHCFN

KIVML

>contig22177 Frame-0F|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY66202.1|) 1e-102

MGFWLFPPSMGWLRSSMLVMASETYTSVASPIQHAARRAFVLDCVELASYKRKCQKTLQL

IGRWCAYQLQKMDVEVQVPEAGFYLFPCFRRHQKALSLRGIFTDEQMCAQLLQGTGVAIL

PGSAFGRAREEFFARLAFVDFKGDIALYL

>contig22494 Frame-2R

MNVVVGIDETGNEVDTPHHKPLKTTKIHEPDVESLLADFDRDGHVGRQEIEQIKDKLHRL

LDTDDSGGLDVSELKIRAQTDQDVDAALGKLDRD

>contig22748 Frame-1F

MVSYNGSSRAPTVSLSLLLILSVGNSLVASRRSIRPHLLQTRSMSLRTVNGAIASSRKQQ

LQQLQRIYCQGELLHEVQMQELFTDSKHFVDMPIKAQSSVSNVLTQFQELKASFDTKPKG

AEWKAQLETFVERHFDPPGSELVPIAPPDYKEGVVPPKIMKIRDERLRDWAMELHKLWNV

LARVPASASSDQTSRTSFLRSLPILSAPDASQNVLARQFNGENVLVVPGGRFRESYYWDS

YWIVQGLLVSGLHQTARGVVNHLLEYVAEFGFVPNGGRVYYLTRSQPPMLSDMVRVVSKI

EGVNETDNSAWDLQYLQAALPLLEREYEFWMQRGLHGHAIEISSGGETFVLNRYVAHSGM

PRPESYREDLYTASVSHINESDYSSLYNEIIAAAESGWDFCSRWFDDFSTLAATRTSQVI

PVDLNSILHRMELNVAKFYEVLGNPVASARFQDAAKARVKAMDAILWSEPDGCWKDYILE

SSMHSSVVSGSDYFPLWSGAFDASNSSRLDRIVTSLKASGLVQEGGIQSTTSITGQQWDA

PNAWPPLQDIIIEGLQAADTVSSRALANRLVQTWVKAGLIAWQETCLMFEKYNALQIGGV

GDGGEYASQFGFGWSNGVILTVLTKYQEQINLDDLAENARSNDTCHKFPNEG

>contig23088 Frame-0F

MLTQLNVDARPRFMENMGKQMAPAAFTFLPFGKISTIENTTTPRRRLTTEPMVQGMEKYA

LLIGVESGMLFYVAVAGIAVLVASLFGMYALAMAVCFWFVRDFTTFALKWLDKAIGGLVM

LLILSEYVIGATATFQICFCIEEALYDIRLVLAILTLGGLAFGTILYGVIVIQNNEDELR

DLGTKTHFNKQFHVRYGPLYDEHRFEGRFFFAPKLLLALFCGMTTGMVWIQGLWQIIVLI

ALHVAFLLYLEMKQPYPTAFVQKTSSFVILIKISALGLSFFLLSSATRFTASIPDDLRQG

VAFAIVGLQVLVLVCLMIRQVYIFYRTWQLKREGGESHEKRASIQTTNARDDSESFFAMD

PHAEMRQLKETTPRGTLTNGQYETP

>contig23787 Frame-0R

MTKSLQNLANHVKLQPPTLPGYPDRHTMLDVDVLVSLATRIKSSIKVLNVNTIMLSNRVS

HLLNTDV

>contig24081 Frame-2F|Blast-U3 small nucleolar RNA-associated protein, putative [Phytophthora infestans T30-4](gb|EEY64264.1|) 5e-80

MLQRQQHYCKNRRSSSAKEPVAPPESAILAQEVLQLLEQKLGATAFLEAYSFVQKKMAVR

RASRKLQRRTEAVSDPKRAAQRRLQKNERKHQVKKMRKRKFAVLKGSTSAAVRKKKVLRP

GAD

>contig24290 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70127.1|) 1e-142

MNDKEIGGRRLRVAFAVSHGTQRRFDGPAPSIQNPTSPMPHSMPHNSHYLAGASPNLFVA

NIPPHIKMSELDQAFGQFGEVKNVKVLPQARPDAPMSAFVDYTDISSAKKAHSATIIVAG

QQLRTDYNFRKYVEFKR

>contig24706 Frame-0F

MKIPSNCRVCCSFTVNMHDNPVYSAGKSPTLTAFRRAGQVKRYASPTRAFVCNTPQFFRL

FITLQPSGPQSHLSALPWQITKSRVTALVVK

>contig24773 Frame-0F

MKGSDDKDDDEEKQAIARIPVRLKNKKRKATRVIRMARI

>contig25709 Frame-2F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY66075.1|) 1e-109

MLGTQVVRPISGTSMTTPSCETTLVLYSLVGEDIEPVQESSAQHEPDTNWNAFVLPLPPA

INRVRLADVLAAFPLGSNFHFSFLCGDGTYLDLTFPESTVPFCGRKLLARVTPLDEEPSV

KYVRYEEPRKAVIPSRSARLNARKDRAESYGSSTMENFYRDEYVELESSTCESSTCESQD

EELSVRIELSPLRVKVRKDQAESDWNRGSYQSGEDEHQIVDDGNRRQKADCDDQYKRHEG

VSSRQSSEWAEAGIDAHIYLRKQTEQAYDFAKKISIDDAKKGASETAKKAKKWGGSLLST

ISATISNASANVSKTSNIQVGSVTVQVVRILAEGATAQVLMVRSLATNENFALKRVLCQS

EEVDIEVLMELQVFHSVKHLNIMPLVEFSDAPAQQGMEFFFLIPFFERGSLWDAIYAASQ

SSSPLWPFTQRAALHLFQGICSGVLALHRAGFCHRDIKPHNIMLSSSSSGEDFLAYIPVV

TDFGSCAPIHAEVNSRQNSLKLQDEANCKSSAPYQAPELIESTVGIALDGQSDVWSLGCV

LFAMAFGTSPFEDAQ

>contig26029 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69184.1|) 3e-57

MSLENVHVDDANSRIKVYFTPTIPHCSMATLIGLCIRVKLLRSLPSRFKVDILITPGSHS

SEAAVNKQLNDKERVAAALENSHLLTVVNKCIANTDK

>contig26582 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56187.1|) 3e-74

MEPWIRQQFGFLFTYRGRTAFIFIVGFMDFGMEGSLPFFVGFLMCANAILSLVIMLFHPQ

FREGTLNMNMDPTATYRPAVEETETLLRQHEGVAAKAGAFVLHEAEEHPEFMAKMAQPYA

AQHGYIPPAPL

>contig27286 Frame-0F

MMKLLDDAQNPEFQKVLEQAFRELGTDADAENIEQLLGSLKTENGTDETDDVNVGVAKTL

QDMAKAAEDMEDMGTAQVEAMGEDMMAEMMKKFEAMGEKNDFEGLVDGMMQQLLSKDVMY

DPIKQICERYPEWLADRKALLSKEDYERYGKQFQCFQQIVATYESEPDNFARLSELMQEM

QETGQPPSEIVKELAPGL

>contig27817 Frame-1F

MSYQSLSDDIESRLSNANFDSIETPKCDEKKELPNASVGALLVISMPRMAIRMAWAAQWA

AVGPYLQTMLPRYAVQLTQLSGPLCGILMAPIVGVYSDHSTSKFGRRRPYLFVSAVGSIL

CWILMIYTRQLGDALGDVGSGLPGEVTDRTYTGLLTIFFYLSMDITVNIAQTPALLLISD

FAGTRQTLGSALGQGWSTLGAIVVAMYTEIFGAAYNSMSFFFGMLSTCMVVAIGASCYVA

TEVPRMKETSANQSCCHNALMA

>contig28153 Frame-1F|Blast-acetolactate synthase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY64201.1|) 1e-168

MGRDDVLITTGVGQHQMWAAQFYRWSRPNSIITSGGLGTMGFGLPAAIGAKAAKPDNIVI

DIDGDASFSMTLAEMATAAEFKIGVKVLLLNNNFQGMVKQWQDLFYEERYSSTKMTNPDF

VKFAESMNCEGFRCSEENTLEEDMARFLAAEGPILGEFMVEKNEHCYPMVGAGRSLDEMI

IGDFDDCPGTTSV

>contig28342 Frame-0F

MEVSMNIYIIQIKSPLIFDDQPQPVLTRYPPDSSKSGGAWIWTICQWTSSFFQL

>contig28544 Frame-1F|Blast-ser/thr kinase [Phytophthora infestans T30-4](gb|EEY57565.1|) 5e-70

MINMYDKTRREQIIREINALFNAECPCLVTFYGAFLRDGAVVLALEYMDGGSLENVIHQL

GTIPEHVLASVAFQILHALSYLKTNKRVHRDIKPPNILLNSHGQVKLSDFGIASELGNSI

AMCGTFV

>contig28698 Frame-1F

MVSRWKLLLVLLSCTSHALIAEVANAANHTYFRPSGPDVSGFPRPNSAPFHRSPCPALNS

LANHAYLPRDGKLLTPQLIHDAVVNVFHIDSTLAERFTHSLPPQLTLADLSVHGLIEHDA

SLVHDDAWSHHDPAYINSTLFDCLIAQRKNGILNKRSLAMARRERERQCKKENPTYALPI

KTQVAAYGEAALLLIAMGNYETETITVEAMTSFLLEEKIPDKFKRSPKPITTATVLFVAA

QIRLLALLLKAEVDTTDASAGF

>contig28812 Frame-2R|Blast-50S ribosomal protein L7/L12, putative [Phytophthora infestans T30-4](gb|EEY67989.1|) 7e-71

MLSRLSQVAVRNAATRWIRNSTMRQHKVSFFSDDAAKVPTNAEEELALTHKVQIVLDQIL

DLNMVEIAELSHGIQTKFGIAESAFQVGMGGGAASGSAPVAEEAKIEKTAFDLKLASFDA

KSKIKVIKEVRAITGLGLKEAKELVEGAPSTLKKDVKKEEADALVEKLQAVGAVVELE

>contig29147 Frame-2F

MSRWLSKRGLQSWSASREEVRLHFRCTACGKCCTGKGGRVRVNDREIEELAAVTNSTIIE

FKRNFTHAIEDTVSGRKKMQFMLKQSPNQNQCVFLKGSKCSVYEARPTQCRTFPWWPQHL

VSDYDWQLAATECEGIQAHSVKKHDDMPAFSFNDVIPETLVYDIHQSGENFTYDELQELL

RDLQEVEPNVMAQYKAEFLENFSRNIIFRNENITVIDSNFNDDSKLTRCFVFNDRLHLTQ

SEVALVKKPIDSECEFDRSSLLLDVHRALCLPFAWLCKQEKALLPIRVCVLGAGACTLPL

FLLAHHSSQELTQLDAVEPNQFVIEVAQRYFGVEKALKSDSRLRMHKEFGQEFIQATAKD

SRFDMMLIDVEAGKSCDDVQAPPLDMLDLSFLQSVKQRLVPGGILAINVITRSNKALSAV

EATLQQVFSSGLRLSLPINTVFFLFHAQHKEFLVDVVELKRLVQESVFQTRFAQTPALLE

RYKLTGWNSGDKAKVETLYI

>contig29617 Frame-0R|Blast-FACT complex subunit SPT16, putative [Phytophthora infestans T30-4](gb|EEY54832.1|) 5e-12 NOT\_ORF

MTKNLGLGIGLEFREPCNLLRTKDTTTIQDGVAFMSRLG\*TKFRFPSPSAKKRRKNSITP

CFSLTRSSC

>contig30237 Frame-0R

MEVAQKLAPRILTAAPTTKTIGNNYFKHNLCKYYKCYQRKRTWVRCMLLDVAFPKSLVIA

SHLFRRSNEDLADRFLKISDIDDVKNGMLLFKPLKYAYDHFHISFVRDNTGAFRLKLFDP

NIRNTRLIDMVIENSRNKKVFDEIQITELHESISLTQEPCEFDVNTTFGDVDGTALAFIG

LERPFNRCLYIQASMARILAVKNGWVEESYDFPDFWDDVDL

>contig30710 Frame-2F|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY56593.1|) 1e-12

MQASKINNTVPTESQRKSRAVFWDKTIASTLQRVYIDEGPLALYHGLGPELT

>contig31124 Frame-0R

MASPELPTQDTLEPASPVLLEWPHQMSSVQYHTFVSNL

>contig31616 Frame-1F

MAPLAAHNTPVSRLPTTDMPSESKKTRTRKKKGRKLASTPAVAITAAIKTRLSASKALDD

GVDSRSMVGSNSTARRSFSPLSGSSQSYSSTDERDEEGEADEYSSESEDEGESSYKPGGY

HPVKVGEMFNSRFKVVEKLGWGHFSTVWKCIDRESGGFVAMKVQKSARHYMEAAKDEIEL

LECIVEASPKEYDSMEALKTIQVVRLVDSFEHTGPNGVHVCLVTEMMGDNLLTLIKYYNY

RGVPVQLVQRLTKDMMEGLAFLHDKCQIIHTDLKPENVLLSHRIPQLPKIRKNQWQAYRA

MRLEKCQAVATIQETGGIAKVCAVDNDTISKEEKKRRKNRQKKKRQRLKKQGGRAESNDS

KLLNETINSSILPSTVACVESLSSSLSHLTVSTCGTNKELIDSTFESNFALKPDTTDKSI

RLNTNQTWCQQVEHLGNEEEKDWVHLPQEFAARVMLLLPEGPVAGSKRKEREFTLSVEKK

TSERVARSSFDKDNEVVDTSFALRYLDHVDPDVMLSITDQVLELCSSCSATALVHKYRLW

KLEFDAR

>contig31779 Frame-0F

MVASKQILTGRKPPDCRIMENVTDNMNNVQIEDTYAPAKKMARRDHLIGMELQVIAKWEA

EKLFESDPDTSKPKYMVTFPFPYMNGYLHVGHLFTLLKVEFASRYHRLKGENVIFPFGFH

CTGMPIQAAANKLKREFEQFGNPPDFSRDLTTKFENAIENSLIKAQGKKSKAAAKTGGVV

HQYDILKISHIPENEIFKFQNPLHWLQYFPPHAIADLKRFGMTIDWRRSFITTDVNPFYN

AFVTWQLNKLNEQKRIVRGKRPNVYSIVDGQSCADHDRASGEGIGPQEYTLAKLRVQEPF

SNSLATLAGKKVYLAAATLRPETLYGQTNCFVLPEGDYGAFVINHDNDVLIMSHRAARNL

AHQEFSRVWGKEECLLELKGWDLLGLPLSSPKAPYDTIYTLPLLSISMGKGSGVVMSVPS

DSPDDFAAFRDLKQKPALRKKFGIADHMVLPYEPVPIIEIPGFGDMAAEKVCNELKIVSQ

NDKDKLAKAKELVYLKGFYEGVLLVGSQKGQKVCDAKAVMRQELMEAGHAIPYWETESLV

MSRSGDECVVAQLDQWYLTYGAEDWKNRVMDHISDPKSFNAYNPVALGEYKSTLGWLKEW

APCRQSGLGTRLPWDPEFVVESLTDSTIYMAYYTIAHHLHANLDGSLLGPHGIKPEQMTK

EVFDYIFLKASPPNESTIPLDVLKQFRDEFEYWYPVDVRASGKDLIRNHLSMCLYNHVEI

WRDDPSKWPRGFFTNGHVQVDGKKMSKSMGNFLTLKDCAAEFGADATRFACADAGDGMDD

ANYALDTCRMAILRLTTEEEWIKRVLEDKALLRYGEHNFNDKVFLNQMNNLITTTASFYE

RLQWREGLHSGFFEYQIARDSYRDICSRSEVPMHHDVTMRFIESQLVILSPICPHFCESM

WTAIGKTGFVSVAPWPVAEEVDHGLLRAGDFLNKVTRSFREVLAKNNSKKKGKKNAAPAE

VAKKVTHAHVYLTSEFPVWQQKVLLLMDGLFDDKTRQFSADFLQQLKGALLRDDSLKKLT

KNVMQFAAFVKTEAELRGREALELRMPYDQKSVLVTNKVYLCRSLDLDDIEFYYVGEDIP

DADLKRMETASPGKPALFVYA

>contig32217 Frame-1F

MDSLICNKKSIMLRPHVLRADKHRWMVVEG

>contig32886 Frame-2F|Blast-DNA primase small subunit, putative [Phytophthora infestans T30-4](gb|EEY61718.1|) 1e-78

MPQEEFSAELLHLYYDRLFPYKQMTQWLGYDGGEELLFRRELSYTLENDTYIRYKAFHNA

EELKSSMIKTLPFKIDIGAIFSVSPADKGKVSSTVFKPEQRELVFDIDLTDYDDIRTCCE

GAAICHRCWRFMVAAVKVLDDALREDFGFENLLWIYSGRR

>contig33052 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69371.1|) 5e-09

MVLQKLAMFSILMVLVPLSTFFGVRSLFRPG

>contig33636 Frame-2F|Blast-2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY66141.1|) 0.0

MSHLASSLRRCASTSTRNSFVDRLRKDLAGIAAAGTYKHERVIASPQGTGICVNGEIVLN

FCANNYLGLSNHQAVEKAAADALKERGFGLSSVRFICGTQDIHKQLEEAISVFHGTEDTI

LYPSCFDANAGLFEAILNHEDAILTDELNHASIIDGIRLCKAERHRFKHMDMTDLEQKLK

DTQHCRTRLIATDGVFSMDGVVAPLQEIAALAEKYNAQLFIDECHATGFFGPTGRGSDEY

CGIFGQVDVINSTLGKALGGSTGGYTTGCKEVVDLLRQRSRPYLFSNSLGPSVVGASLKV

FQMLSDSSELVDKIRVNTHHFRDRMAIAGFTLKGSRDHPIAPVMLGDARLASELADDMLK

RGIYVIGFSYPVVPKNTARIRVQLSAAHSIEDIDKAVDAFIECGKARGVIN

>contig34196 Frame-1F

MDSAGEERHRSCASLDGSSDYTTLSRIENDSLTSLTADDKVHTQEDLAMQQPSTSLTSLL

GKREADVVLREEEHENDEIEDECVPLLAMVEEEQTYVQCVGIDQCFDSWNDFHRAMDEYC

ESTHQPMRLRTSDSAKAVNSRAAKRNSMKKPIDESVGFVKKLYLCTHGVKTKPRGKGKRP

RQHYRYMGCPAMIRACISERKPNHLVGQENKYIVRVVAQINRHNHRLSEHLFKSYSESRV

VIDDELIVPNSQSRQKDEQTAVAPFVASVTQIDPRVASSVNSALEDSTTSKANVLLQTQG

IDLMSAASRVKIRWGLLFLS

>contig34462 Frame-2R|Blast-Ammonium Transporter (Amt) Family [Phytophthora infestans T30-4](gb|EEY56738.1|) 1e-143

MGWEGKMGALDFAQGTIVHVSSGFGALVAAIVVGKRYNHGESVKPHNVPLVMIGATLLWF

GWFGFNAGSQGAADGIAAIAAINTHLAACAGFLTWSILEFAFHQTFDPCGTIGGAMAGLA

AITPGCAYVYPWAAVLFGIIGAATGFGAVHLKNLLRYDDTLDSFGIHGCSGFMGGLLTGF

FATSEINPNIKGGAFYGHGEQFLHQLTSQCIAAGYSAVMTFIILMVLKYTLGLRVSDEKE

VNGMDISYHGGQAYGNTIVSGISTSVPEAACSTVGGFYNNDFGA

>contig35638 Frame-1R

MQWEPSRNGKSLNSWKILQRLIQHQLIILILSKQEEALLDRKCILKTTHLAGVILPHLNL

PKSCSFL

>contig35717 Frame-2F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY59592.1|) 1e-138

MQSLQTSGFSFPTCIQERALLPAILDNRDVVGAAPTGSGKTLAFGLPILSQLLREREQPG

YTKDCKAIILTPTRELAIQIQQHLENMVRKREIGVVTLVGGMAVQKQRRILSYRPEIVIG

TPGRLWDIIDSNHEHLKDLASTLRFLVVDEADRMLQPGSYPELEKIFHVLRRKSKPAASY

LSDLSCNGDDEVAIDEEKIME

>contig36572 Frame-0F

MAGKDAWKPFVKFEYQKLLPAGLRNK

>contig36756 Frame-2F

MPLLYQTAVQQMKAFMAILESMEACTMSDGSARLLTCESTYL

>contig37373 Frame-2F

MTEFTGITHPDLLPQRARRRSLSMIDRSNVATNFFAEQEEMN

>contig37481 Frame-1F

MSEATCCGCNSLDTDTEYDLEFHIGAIFILFVVAAAGTMVPIISQMIPQSKANSVIMEAI

NAFAYGVVIATGLIHMIAEGIEKLSDECLGPIVAEYESWGLAIVLMTIVVMHLIECESSV

FFGDKGSALHGHAHGEGIVTNHEGVVSPPPNDHPYYEKSVAQKDLNSKLRREIATLIFDA

GVLFHSVIIGVSLGVTTGSDFEILLAALSFHQF

>contig37764 Frame-2R

MVVKRRATEPVNNRSTTRQTSAPSIIRPPCQSGGQSGLSSSPRIGSISPSIDGLNRSPRR

LEKWQLRLQRSRSGTSSGTDEERSGREATSSRRVYRNLRSRQLMESPP

>contig37984 Frame-2R|Blast-Dicer-like 1 (DCL1) [Phytophthora infestans T30-4](gb|EEY55353.1|) 1e-177

MQRHNDEGSIAQFKTKFNERFLIPQYTSRLRLSKSRFFDAMGLVPLLYEFERKCQISHLM

EKIGLELDMNLLDEATTKPAYERLEILGDTYLKLETSWYMYEQRKDIHQEGQLTQLRRDI

IRNDRLNQFALAARLHHYILYPAEVEQHPFQCWKPSCMGKTPDPIVAPAKWIADVLEAIT

GAYLVGQGEQGARYFLKWIGVSVLEHPSSNFARPFYPDCFPNELYDAAITSRGGGTDSIE

S

>contig38004 Frame-0F

MRSYNLQRVRKSRKQSKSGAYTRTALPMDQHLKIVAKEEPNVAFIIQRSTNSNTVVYAGC

KSSDGKSLDATTPIQVYWIMYEKDGNPREDLNMIERNTAYGVTTRPSDVPGEYMAMIASL

RDRDCILRLDKHGNILALTTINGQSGILLRRVFVQMTTSWGIPTVDYVEIFGVNLITLAP

V

>contig38831 Frame-0F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 9e-10 NOT\_ORF

MAGIFTAVTILKDTTERLQRLAIPDFVSHKLVDMSRRSSTLAVAMVSNFVELDISWYSGE

GLKCLALYQ\*LCEVDIADQSRQLKSEF

>contig39050 Frame-2R

MRPLLQEAHFACFDDDDGVSQSSLPSFSIATPSSCSQPLKSFAHVRTVECTGSGTFYFQT

ERLRDRFVCWRVLQNVVVLREWSFNSALQHNGVRLEFATPVVSTGVFVVESWEADAVAIH

LVTHAGTIHRFSYSIPKDPRSSIFAQAKLKAFPDPQPATRS

>contig39212 Frame-1R

MPSVENPQKISAKSKLIELNEKEGKGQQRL

>contig39528 Frame-0F

MWLVASTFTLVVSAWMIPAQATIEQEGGMIMQLHRRPTQNNYPERYMRRLTKEGNSPELV

PLHLGLGTHYTWVYAGTPPQRASVIADTGSAYMAFPCSECDGCGNHTDAPFNINNSSTLI

HVTCAEPSIFQCTSCEKQSDSCMYSQSYLEGSTWKASVVEDIVYLGGDASFKDVDMRNQY

GTHFHFGCQNAETGLFVTQVADGIMGLSNTGNNIVAKLFEENKIGRNLFSLCFTENGGTM

AIGHPFKSAHRGEVSYVKMLTDRSSTHFYNVRMKDVRINNKSINAEKEAYTHGHYIVDSG

TTDSYLPRTMKNEFMKAFKKHTGRAYQSGNSCKSFTISDLAVLPTIQFVMEADGDDEAEV

VLNVPPEQYLVESNGAYCGSIYLTENHGGVIGANIMMHRDVIFDVGNHRVGFVDADCAFE

GGNATLPPSIHKSIQCIGRNTSRRV

>contig40047 Frame-0F

MLERRKFIEQHEMKTFPIKYVIPLVVSWLVVLVQSMLRGGHGASSLIGISCNSAAYWILT

LLPLLILFAITLWTGHQLRLLNRLKVLCNYPFIEGDVHWIRRRILLFPTLCSMAGVCAGL

LGIGGGMVKGPIMLEMGILPPVQSATANFMILFTASSTTLQFAINGQFPGEIQYDYIAWF

ALMGSIGGLCGQKVVACLVKKYKRESIMVYLLAATIGMSAVAMGIISMKSTIRDFARGVH

LGFSDICDNE

>contig41196 Frame-0F

MVLRATRRILQAALLVQVLQYKAVIVTSSDASPASFAQVASPATVKPYSVPSYNIQETVN

DEERAFGFDDRENAAPSPEDAAGNLITATPVPGTGDRPTYASLKSKYGSLVDDMREKMDL

GPVAAGPSAGSGSSGAAPAESTDVALTDTKAAAGAEAGSG

>contig42690 Frame-1R

MRRGLWLWPFGSTQPVKNPVYIITEVVFVIYDGKIVEQRSSNDKDGELKYKLHTKIRGNV

QSKRMVANTKKKLQARLQFQKCEFLSKPK

>contig43572 Frame-1R

MDVLKYVKNLSRRIMESVQIKFAMRVFIARHTSDYFQFFSLLRQATYLQSCLLFRYIPNV

RSSALLRMNRSYRSQIYPLEDLVEQLCFDDIEHAYFVCQEHHLRIAGRPGAGDDSLVHVK

FGGEFETDAQLRRNNTPLQTRSSKIYVGMKQGNYLRQDICRGVTEYARDDYPALSKSIQD

FECEERAQLYPEKPPYEDSYSRFVDFNLDALLTTTVSAQANGILNQHQLIEVNQKRHELD

AIARKKIELERKKVAMLERMRELEKAKEEKDNREQAKQVLAEQSAHFEAQKKRDFIAQSL

ANEEVAEATQLPKQTQQREEKEG

>contig43697 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57198.1|) 1e-74

MVLRTAAPDVVEIDLFPMKPGERRPPIP

>contig43877 Frame-1F

MRCHPRQLAKFISRHPPANCVRSVGGAATDTRRTLPTDAQFLDAKFYVHYSQVNGDGRTN

EASCVPRWTTDPKGFLKSNGWTNSVNTSIEQINNFSAEGLHDISVPITTTLERHHCSRFV

EKLPEPDRVVELEPAVLSATSSSNDLFTSISSTWESDTIFVPVSSLRF

>contig43918 Frame-0F

MVEAVSLNLTNARGLDASRLKAAKIL

>contig44616 Frame-0F|Blast-fatty acid synthase subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY57114.1|) 0.0

MTYGDVLSRLIDLMYVEVQGKPHRWVHETYFSRVSKLITRSEERLRLESDNKLFDQSTLR

KNPRETIRAFIAMYPNSVSTLFSVPDCDYFLELCRTGGKPVNFVPVIDTEFKGWFKKDSL

WYSEDLDAVPAQDAQRVFVLQGPMAVRYSTIVDEPVADILGGIVAGFANVARESGSIAAA

ITASVNQKINLMNVEVTENEKSVSVSLPTKLSALPSADEWLTSLAASVIGKDWLHALITS

PHIAEDKKWLANPVRQLLVPQVGQKYVIDNAGVRVFDSSVDLLGPVIEIMKKDNNVAVVV

NEVRPAMTGLQADIVALEMMFQYHPELSCVIHADGSGFIDKVKAFYARFWVA

>contig44779 Frame-1F

MSGIVTSVLSKLTEKNCASAQLFEIVSRIALMIFSQLSIANDESRLRALPESRYQQNMSY

LELLFHAVYSSAASTGNPSASRNSRTLLYSCIVHVLHVLPSRASHDSLLAKASRAMPSLS

QEQRIRHLLFNQVVDLVCQDASDGEDTLSMALAVSVLESLVAFEDNSLIVSVFRERGYLL

HFIEIFKKLSEMDAAAFERSSGSSTMVKSNVIRPELDATTIGTMYECFLSLFAKVADTQE

GAAALLEGGLIRVLSDARNLPTHRPQYLPQQNNSRSFASVEVFQRIEAVYYRKWLPVARL

LSACCASLPKNETLTRQVLHFVNKNRKLFTSALKLCADGLQMQPISVELLREVSYVTFVF

RYIIQFPDLCEQTLATAKWEKISQLILQVFLYFCVGLVPPSNDPDDMSDNANISWWNQSI

EEKENDAVKSFLCVDCEDKLLEQSDSTAVKSSGSASLLHLSLLDEEKLYASRMILCSAVA

FCASRMMIAVSESSKAGRAAPLLSITNKAQVQNKNHFPSMSSVDPHAFAAATDPLWTLAP

SLNEFATRFDSVVFAFETSKQLVDAVIAFKKEAAPINSTANSSARSEQRSILQDHQCETA

QLEHILEYQTDSLMFIVENMLMVLLFHFVHYLGQPEAAPSERVIQQTLDKVLVIISDIES

NPFIHATARRLRELASSE

>contig44999 Frame-1F

MSNHRIDACSSSDEELDFFGFSHCEDLFAETKIQHEKRNEAQRYKEQYAKRQWGLAARQR

HATKNKETEITLKLRDDKSIVFYEKEGQQAKVWDCALVLAKFLVNTAYFSPDFFVNKRVI

ELGCGVGVPGLAAAALGAKEVVLTD

>contig45501 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58981.1|) 5e-86

MATDAVVQELSISDVPSSDASDKEKINEADAVEATSSEDDVETHDAVGFGDAMSKILGQN

VAKNAQPILAKRTTARMREIKNEKKETKIARLSTAEKRERDLKDMAVPNHTTAIQDRKLR

TIATKGVVALFNAIEKHQHLGGKGEDKNEKKVKEMSKDNFLGLLKASKQKIAENPAVKSS

WSVVQDDFMMGAKLKDWDNEHGTEVGRVRKNGDADIEAVEDVAWRQTEVAMDSDNEAEDA

SEQPTKRRTSQPATKGRKKLKRS

>contig45710 Frame-0R

MFTTDPRFVPHARLIKHLDYREAQELAAMGAKVLHPRCIVPAQWGRVPLEIRNTNDPHGE

KTVIYPTSDADSMQHGSPKILAVVKRQNMTTLSITAFDMCGTSGFLAKVFAPFEACGISV

DLIATSQFSVTVTLDHIPGGVQGIPFKQLLKALTEHSKVRVFEDCSVVSIVGRRLRKALA

ELGCVFSVLENYDVLLLSESAEDLNLSFVLQQKEADEVVAQMHSFFFPEDTHVSSTIAAT

AYPKGLLTGDLPPLPPHSMTQTSASMPRGHSAFQSAAIRRSPSRDLLFGPTWQSLLDKA

>contig45839 Frame-2F|Blast-type I inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY60218.1|) 2e-34

MRQHLGGISEEQQPFDRYSRIDSTSSADSQAGIHEYDRFSQQVTFADDSHQNDSRRHARS

DSSPRRAWLSFQCFNLTLPSKSSIKSSSFVVLHLVEAETGKVLAKIGQTEISFSKDPC

>contig45967 Frame-1F

MTFKRNIRSSLQAGIQNSSQDEIRDAFELLFYLGDLKITAQACVNDVVQDVERACRAVIA

EDKLVRINSSLLNNSDSSARSIGSAVSKADVWKAVEEFFNVIRVYALQVWNMQRVLLKMI

ESQTNQSYLELVLDADEPSLFATYWEVTCVMVHEVLASTRGYSSAVQSVLIAEYPRMREQ

ATRVLNDLLMSTTQSAASDFLTVVPANEKGEIMEESFVKRELVPIAASIAERTQLLNAMS

PLYEAYIDRAYNRIMHPIQLMFPQSSNYHASPPSRSDMQTLSQTIFAELEHAGHDGVLLE

GMLQQVQKAVARFCDNVQKMIHHGKAAATPLLNFGRTPSQAHNVGLFNALSLLHDTIKAI

ETYIATATSSTENLDVSTATVDVKASSTTKLLSCQERIENLQYALLGSYLQTLAGLLEPI

FAKMHNESFGLGTDALKEASVKETIQSRSNVQTAQGTRGSKYMQEVSHVFAVILDEHLRR

LPKAALVMPCLVDFVERLMSTFVRHAALLRPLTERGKLRLANDMTQLELRLEQVVPLRKN

GAPYEELRAFRHMLFLENHEILRDATIDKIRPSNVWHHLISRAPAELQLPHRLRNWTATK

YIEWLDTCAAIDQSSLPSTSVVASSEKVLTHSWRDVPLGMACLKDPQLALQVEKQAWKVI

LECLDAYSQRASISTNAERSPIYDLLQESSALLLAGYEVLISR

>contig46052 Frame-1F|Blast-separin, putative [Phytophthora infestans T30-4](gb|EEY65966.1|) 3e-43

MAKIIQDSRELLSGHTAEEASSWTTEQKKEWWNSRNHLDGRIEETIGLLQKALGFWRCLL

VGGTSIERKCVEECWKILTHNTTSPIKLAQRNQSLLRAIADAQ

>contig46504 Frame-2F|Blast-3-hydroxy-3-methylglutaryl-coenzyme A reductase, putative [Phytophthora infestans T30-4](gb|EEY65495.1|) 0.0

MTIPCSDIGAVSALATPKMVLEATLDQTVALLRMALKTARGIEKDDALQHKAAQVAALAA

QVQRQCSHAANKQFLPLQSSNNGGKGCNSVAQQHKEDPQPVIWSGFYNKTLLERFDILAL

MYPEIKTLKAQQTSDVGAASGILAPIGSAARIGDLPLHTANLMIENCIGVLGVPLGLGLN

FIIDGKSLSVPMAVEEPSVVAAASSAAKLVATAGGGFCTATSGNIMTSQIQLLDTKDIPS

AIVAIERNRERLLMIANTTLCSSMKKRGGGAVDIYCRVVSQAARTALTSALGNVWYTPCS

DEVLVNAFEPQTQFLVVHIDVDVCEAMGANVVNTVAEGLSEEISKLTLSNVGLRILTNLC

MQRRARAEFEIPINKLGWKGVDGKDVAGRIVDAYNFAAIDPYRAVTHNKGIMNGVDAVAV

ATGQDWRAIEAAAHCYASRSGQYASLSHYEIGFSRDGGGTSVLRGSLEMPIAVGSKGGAL

MTHPGYTATHAILQQPSARNLSGIIVSVGLAQNFAAIRAIAVMGIQKGHMALHARNIAVA

AGAPCEVVSEVCSYMLLRNAINVETAKDYLHARAVI

>contig46643 Frame-1R|Blast-imidazole glycerol phosphate synthase hisHF, putative [Phytophthora infestans T30-4](gb|EEY69066.1|) 1e-84

MDPKRVYVASFYDEKAKGHNVIKLSQPGPNGEQYCWYQMTVRGGREARDIDVVQLAKAVE

ALGAGELLLNCVDMDGQKAGYDLDLTALVKNSVRIPVIASSGAGKPDHFTEVFKKTNCDA

ALAAGIFHRKEVVIQDIKTQLHADSINVRF

>contig47121 Frame-2R|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY65999.1|) 1e-29

MEKDVDFYPSNKPSADVVSQIDLLSILQKDIDGDWKLITGSWYFNGKAYQKYASLCLMAA

DSSVVGEDVTLLNKCLTKLKALVEP

>contig47459 Frame-0R

MPAMYLADKFVVRVRKKSAQGQQKISSRVRTEEENAILARWRHDNMIFSCRTDFLSDDLF

WLYASVLMASEGRVVSNDQGRDHVLALLNGDTNRLANARRQTNGKKSVAQAAGEQSGVPL

ISMDLIARWKDMTAVHVEIKHDESADPATTVLPIETIKLHHPLPFSRVPQVTTQQHFHFR

NGSVRIKKLL

>contig48133 Frame-1R

MVHGNRAHDSGLSGHCRWGLDNSFFGIACSVFGACYEISDTEAYTSKTVHPPSKKQRKNY

ATSSFDSFERSESRNSVMTEIRIMLSNSV

>contig48380 Frame-2R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY69304.1|) 2e-16

MNLPPSFHDKSARKFNVPVDIGSEGRDIVDANVTAVIASESPEDG

>contig48591 Frame-2R|Blast-phosphoenolpyruvate carboxykinase [Phytophthora infestans T30-4](gb|EEY57342.1|) 5e-49

MQHETTTAALGLDELGIQNSCKVFYNLTHEQLADHERTFNEGTFVANGTFAVDTGKYTGR

SPKDKFIVKQAPSQDNVWWGSINQPTTIDVFEALYAKVVNHFSSVDRMYVFDG

>contig48692 Frame-2F|Blast-serine/threonine-protein phosphatase 5 [Phytophthora infestans T30-4](gb|EEY66066.1|) 0.0

MASILVSEGTPHTVSNETRARADAFKAQGNDALAHFKYVTAIELYTNAIELLPTAIFYAN

RAAAHVKSENYGLAIDDASAAIQLDIAYVKAYYRRGSAELALGHHKKAVKDFRLVVRMKP

QDRDARAKLKLCEKIIKEAAFATAIQSERNLPLSETIDVHSLTVDPSYDGPCLPDDCSQT

QPDFIIALMDRFKRGKLLHRKFVIIILLKLKKMLCVLPSLLHVSLSADESDAHFTVCGDT

HGQFYDVCNIFTLNGLPSETNPYLFNGDFVDRGSFSFEVVMTLFAMKLVYPKHVHLLRGN

HESKNMNKIYGFEGEVKHKYDETVMQLFTEVFNWLPLAAVIEHKVIVVHGGLFSDENVTL

ADIEKVDRNREPPESGLMSDLMWSDPQPFHGRGPSKRGIGLSFGPDVTKAFLEQNNLDLL

VRSHEVKDEGYLVEHDGKCITVFSAPNYCDQMGNKGAYIRFERDMQPRFTQFVAVEHPPI

RPMAYAGNMGGMFA

>contig49008 Frame-0F

MTSIEEVALARNLLSSVLAIALPSGLPTNVAALKAFSIQQKTLCDAFERHNVFGIVTDGK

ALMKWQTRLLDLVNGLAPARRIGWELFSFTMRQSPFERLESLCPTLLEHAVKAFKRHQSN

KSEDEDTVETTSAVCNVVQVLVQHINRMNPETRREALDLLSKLLPPLVTRIASKNQQSPA

FLAPFELLQTVLIVSPTSVRHHILKIETACVTALFSKSTSNDMLLSITNCLALLSNASAS

PQLVWTQMAHNALKRAHEYLDVFAGNSPA

>contig49093 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66472.1|) 1e-108

MELLSVVQKLLPEILLSADTVLLLVKTVLQLLRYLLPPCRPVPTETIGNTLEEELVITLC

QLLRDVLLNGTDVLVRLDDCAPPLWPAFVFTDRFFHRDVYGANAIQFCIDRCQRKSQEIA

GRILRLQQACPSLSAVGAGGQVLASTMHNEAQILQTLDRFHRVDSTSDLHRVYNEVFSPL

PTMRASGSQLSKELPVDVATLFLV

>contig49251 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53668.1|) 3e-23

MWHNQPQYNLSDHFPVVSEFTFDM

>contig49530 Frame-1R

MQQRRPVENVGGSGGPQRSLMGPFAVQAAPPYPQQQQLHSTSYLQYSIPMEPPIRSYSHH

HQPTQQLISMQGLYWQPPTGLSTFSYTKQGRHDNSLELEELGGILDADSNSNAVTGRASP

DATLEMNMANFDVNSFHENMTASVGTSTGTTDAFSSAVVMTPVPSRPPSTPIEPSQTRLT

SNRKTKKARPLLSDVATKALVDAAYSQFSEASNDSDFQAGKPFKDRSERCQFHDCPNRAR

VSQSYGNFCNRHVI

>contig49619 Frame-1R

MQKGIWQYYTERVDWEKAVCPGMPATAPSTSLLLICNTAWRPVAPKIV

>contig49707 Frame-1F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY61775.1|) 1e-06

MTQLPDELPARIQTSVLEVGEIVGRTSKYKGQDPTESAEVNIVSFELELASKELMAGKED

NDHVTKVLADSVSIVADLKRTQTGAKVLMKMDNISDIINIKRDGKKLDQEPFVATHVDTA

SAGLESNNDMESRQIEADEAITKHVSIDEMTFFAYHPGIQAPAENSNVKAKIEQTVTDAS

LEVEINVL

>contig49835 Frame-0F

MASVIDQFLVHEIAKQARTVFSLSACKLLIARCLLPVIHNVKYTCGMSRRGWKGESSWVF

HSTRVTGVAWEMNSVGHNLNLIRGSLVSSLRRNVGLMGIAFRDQSFPCEAALPPVRSLWA

SSMALEFV

>contig50468-0 Frame-0F0

MCVEKRVLDTVRSYWFPRQTIERRIRLLMPCDFGAFAACSR

>contig50468-1 Frame-0R1

MNNKWSTKLITLAKDRLYCRFIF

>contig50486 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53416.1|) 7e-29

MMSKTNVTLLFAHGGGFCKETWNPIIRRLKESYVLQNVSTNFTTFDFPYHGDKHDSTVVL

SFKVDLSNPIAPRVWNESHDLVHWVAQAVQEQVAQSKDQIKKDDPEGL

>contig50859 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57705.1|) 2e-21

MHVFELILRLRQVCNACALVTADPLAEVHARAACAETLVENGKNEISLFSTKEVVLLERL

RQQQPTLCAEVASNLLESTKLAALMQELKKVRARHERVLVISQWTSFLDLIEEHLEAYNS

QCEISLASLETEYANDTILFAKLDGRMAANERDQVVRQFQQHEGNHEVGPNVGPSLDVLL

LSLRTGGLGLNITAAAHVFIMEPSWNPSLERQ

>contig51931 Frame-2F

MLNFVLVRRNVNGPSRQLSSNVLFDRMYWRKDLDQIEGSRKPRWRKEVVGLETRLGNGVS

LFLRQLTTDMESLLRHRQCKQI

>contig52228 Frame-2R

MKTKLWSCPRCTFENEAPASQCAICLCVHPNPKAMKFDAEQAKTTKSPHSPLHLNVGTSL

KKEQQVVDKKLQQLKDVGIKLSNGEIEALLQRNCFSVAAAASEYFEHVVSTDSPTPAHED

KRMLESVLNKFETTDSVGTNFQALGKITMRASINRRGVNVQVGDEVRLSAENAGKKRL

>contig52989 Frame-1R|Blast-BolA-like protein [Phytophthora infestans T30-4](gb|EEY65183.1|) 6e-49

MSFLLLLGRPTATYVFSRRLIMTEIVGPMARRIQEKLTAAFLPSHLDVINESHMHNVPKG

AETHFKIVVISDHFDGKPLLHRHRMVNDVLKQELEEGMHALSILSKTPAQWNANAQVKSS

PNCRGGMAVDATKREFLEILREKHHNK

>contig53234 Frame-0F|Blast-polycomb-like protein [Phytophthora infestans T30-4](gb|EEY56529.1|) 5e-42

MPRSTTCMLSRGTHRVEDDPILRFVPHFSPAISKDKMPEFSSTDSCKDTLGEMDNEVNEY

VLRYIVRACGGDQTVFEALRRCGSFTQPFASYIHILTRVTCAK

>contig53465 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66535.1|) 1e-14

MLSPTKLLPWGRLVLLTKKPSDTMPEKYNLLRSKHCVGRVASRSDIHIPKKFISSVHCII

RLLGTDDGKAPVVEIEDL

>contig54239 Frame-0R

MVELQQHIELLLTLVERFRPRLRVVAAALTQRDRTGGGPGAVPLAGSSSSSLPESATIES

RASDAAPVESVANSSHSTDYVSATATTEPTIHSGPV

>contig54367 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY70130.1|) 9e-29

MTKVLVESTLSGKPATIDVTKKSQLAIVIKGSPIPLSATCTASACERTGGDGSSASGSGT

SGSDSSSIEGLWIAIAVCGIVAVTLIV

>contig55113 Frame-1R

MIIMESSVAASAPVSQATDDTLIGA

>contig55188 Frame-0F

MIASSKRCRAPNERDSYLPAAHNYQLAPMKALLRSARHEFYLESLHNSSS

>contig55799 Frame-2R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY64147.1|) 3e-07

MLHGGFRPQMTQIVALLCYKEVQFLFFSATVSD

>contig55816-1 Frame-1R1

MSVISVYHQYCFHNVCRLAQGSKSLQLLPLTY

>contig55863 Frame-2R

MRLVAYVLAETMMHARLDVQDRIFAIGATSRKIGHTFRRIVNEAQADTNSQAEEQQVASL

VIIDRTADLASPCAFGNSLLDRILALLPQTPAVFALNEHNGLDIHAT

>contig56130 Frame-2F

MHRFSSCPFLCVCQQSLLKCIRRPQRLGVALTLLKKN

>contig56219 Frame-1F

MAPNLVTMIGTGVTMLTTVIQLYYAPHFLETCPAWVYILSALGLFIYQTMDALDGKQARR

TGASSPLGQLFDHGCDAVCTVFNVLSASATCQAGVGLRPYLALSSVSIAFYLAQWEEYHT

GVMSCGNGYFGVTEGQLTLMAVHLAAALFGSEFWTAELPLQVLPFTMTDVLVVALVASNV

LLAYGNISNVLRAAPDAMPSDELGNKHISKQLALFQLIPIGILLALGSLWICGPDAENYA

NYPVLFLFPMGIGYVYFS

>contig56408 Frame-1F

MSASVVVMRIDLRINTRMFPY

>contig56545 Frame-0R

MQKPMMSPGLTTSKSAMGEFGVGDVLRFRYFLYDHLALCVSRTRVIHYWAGRRKENFIRI

DKISYVLKVSKCSDPECYTAELDKWMDVEPFSRNIIVERARQKLNEKKYSLIFNNCEHFV

TWARYDHAYSPQVWWWVECGFWCVFAGCVIMKPIKIPYWVFVAAVGTHNIVDLRQFIKKL

YESKRKIKVVA

>contig57191-1 Frame-2F1

MKTITWKPRHFTKHRFSANLR

>contig57191-3 Frame-2R3

MSRLPSDCFHTVRGNSTTFRNFVVL

>contig57292 Frame-1R

MMEMQEDTLWNATDWIESRITLPWTPKLTYIFFSCAAALLQLK

>contig57960 Frame-1F

MDNILDAPNFAFWHEFVMWRDNLSLDGTIKAEVSFIRSTYSDDVLVKKFGLIKMAKMTTD

SSKRFQSYANAVIEVLGKKKFLQQILELLELKEDGMDLFTNSVFEKLDVYLRALNINIDV

FAEIYSVGALFKMLSAENPPELCRKQYMTDLVEWLKRYHASPAAVLVTLLIDEPFTVSQL

TSALERTKQMLNSENDKKFVKSLQ

>contig58190 Frame-1F

MRRSARLVATSRCVKAKTSRPISSVTKSSVASVAALSSHLHQKVENLDSDDWVSLCSTRE

L

>contig58235 Frame-2F

MQVLHNAWEKVDKDGHTSPFAHSSIIDNLRLRPNHGVEIGLLELVAFVLFLDTLEP

>contig58473 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57242.1|) 5e-09

MKARVDIRHGDALKVDLTLATALFLYLVPQGIKILLP

>contig59368 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64603.1|) 1e-07

MINRNEYPEKLLRVYRGLGWGLPGLILVYLVLRQL

>contig59522 Frame-1F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY68001.1|) 6e-22

MLGQMVQLDVSTILYPNRTLNRALVHEHAKLNIGSYLNTPGADLNDTLASSVQNFS

>contig03962 Frame-2F|Blast-histone H3.3 [Phytophthora infestans T30-4]gb|EEY58534.1| histone H3.3 type 1 [Phytophthora infestans T30-4](gb|EEY53312.1|) 6e-69

MARTKQTARKSTGGKAPRKQLATKAARKSAPTAGGVKKPHRYRPGTVALREIRKYQKSTD

LLIRKLPFQRLVREIAQDYKTDLRFQSTAILALQEASEAYLVGLFEDTNLCAIHAKRVTI

MPKDIQLARRIRGERT

>contig04747 Frame-0F|Blast-glutamate carboxypeptidase, putative [Phytophthora infestans T30-4](gb|EEY60401.1|) 0.0

MLAEQHGMVGVLIYSDPFDDGYTQGLVYPKGPWRPKGSFQRGSVQFNSIAGGDPLTPGFP

SLPGQPYLSLNESQTIPHLPALPLSYGQARFILESLGGKKAPTSWQGALSLKTRGYYIGD

DEATVLNVDVAMDNHIGPIWNVLGTIQGTEEPEQMVIIGNHRDAWVCGAVDPSSGSAVML

EVAHGFGKLLQEGWQPRRTLVLASWDGEELGLLGSTEFAEDHATFLKKQAVAYLNVDNLV

GSFVSVGGTPSIARLLQDTAQLLPGNTFHGTPVTETLYEQWVRQTAARRASLTIGMEDGT

LGPDHLIQLLGTGKDFTAFYQHLGIISADLGYTMGSAMYGTYHSSMDSLRYVETVGDPYY

ATHTNVAKWWGLLTLRLIDETIVPFDYSTYGLVMQESFVKYARNLTEMGRIVDLSNLQRA

IEVFQSKTEMFQAHIKAFTRQRVEKKKDNQQYEATRRRLNEKLVTLERYLIAESGLPHRP

WFKHLIFGPGFYEGYKGIAFPGISDCIVFKDDSATIQAHVDDVAAVIETASSYLMSK

>contig09641 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66335.1|) 2e-49

MRCIRENTAPKREELEYVVEAKRAHVKESGSILLNGVQALAKTVEKESIFFQGVTEMLRN

WKICAPIHGNIPKPFRAGEPLAVDCSYGSAGSLFVPQHRSIADLAYA

>contig09959 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69867.1|) 3e-15

MKSQNRGPLSTPAPMPVEPMQPIQQPTKPVTRRRQVRQSDIVSTSFVRGPFNPGFDDSKQ

RHGCESMNGRSVLSSDR

>contig10283 Frame-2R

MVKGYFTHKVNVPQQRFSNRRVPHYTLPHQTVDTE

>contig12252 Frame-2R|Blast-protein phosphatase 2C, putative [Phytophthora infestans T30-4](gb|EEY56002.1|) 2e-70

MFTQGKEIFVAHTGDSRAVLVHQSGNVSVLTSDHKPNRPDERRRIQDLGGSVVFWGVWRV

EGILAVSRAIGDRMLKPYVVAAPEVKQFTRTESDRYVVLASDGVWDILSNDEAAEVVLQY

KDPQLAAQHLMDEAYARGSMDNICVMVIDLRAEKNECILRDA

>contig13453 Frame-2F|Blast-60S ribosomal protein L10 [Phytophthora infestans T30-4](gb|EEY68744.1|) 1e-114

MGRRPAKCYRFQNKKPFIKSRFCRGVPDPKIRIYDVGNKKASVDAFPYVAHLVSDEKEQL

SSEALEAARIAANRYLTKFCGKDNFHMRIRCHPFQVLRINKMLSCAGADRLQTGMRHAYG

KPAGVAARVAIGQPIISVRSKDSFGPSVVEALRRAKFKFPGRQKVLGSKKWGFTKYEREV

YAEMRASGSLSVDGNHEKYCPNHGPLKL

>contig16490 Frame-2F

MFCRLLVQPFAEEKLTRGTLDGRNRGSCEGLSQIYESILEFITSKFEAVLALSICQGESK

CSVDILGNAIWKPIQKLLSSKHEIIFQAADPKRFHQSYTISMRFLRNIEERFCKSENMKS

RFRSHESVVEFKEKWNIDIYFQLQASILASSFSEPFNLKGNKSLDTTSSISSSVDKSTLA

YESSRRLWQAMQHCWSDQIFLAPLLPNLCKLCVQLLAYYIDFWKEPLLSTVALIKSGSKV

DYANVPPDILSSDENLLYAASDFHVLYRKISVDLLPIVTSRVDGFADDCQDFVAGLYQE

>contig18535 Frame-2F

MKTLIVFQAAVTALVTRYIAAFDLIPSVGEFLQDTTEKLVGLEKSSETIEYFAPFGTDEP

SRDLFVFNDSLKEIIPIINVAKEALNQPVPTNEWWANLIHVTDLGSESNFAAWANPYSVK

LPRERPYGLQTFYSFTYREFAKKINGTVKYYNHSRHNDLTLSSGEFFKRQPVYEIYEWDE

VGAKLRTCDKKSGKCMYSALVSGMAFVSAKYDGLVPRIDSEHNITHVDDSTPGKFVLYLN

NSQTWVMYTSKPVSFHIERKVNFSVNATGSSLVADNEYFGTIRVALLPEDARDDIYDEYA

TCTILGGTVSMESRTSYSFDWEVEGTTCDTTGLLHFALYHHLESMVGPVTTYTTPGAIIL

NAATRGRMVGQVCTVPKWSFYEPEADFEVDFYPIDRPTPYIVEKIDLLNTLKKDITANWT

GWDVDSWYFNGKTFQKFASLCIMASDKLIVGDDTKLLKFCLQKLERLIEPVLNNTLTPFL

MYDTLYHGLISTSIFRNNNIYEEFGNSIYNDHHYHYGYYLVASAMIKHLDPHWTRLPELE

RIIWTMIRDVANPSKLDPYFPRFRHFTWYLGHSYSHGATSIDNGKDEESTSEDINFCYGL

LLWGRMTGRKDIEDLGSLMLRLNAHAIRTYFLLKRDNPIHPPDIVRNHVTGIFFDNLVFY

NTFFLDEVYAIHGIQMIPVSPINRLARTSVFVEQEWVDIVSKTSIVLDQNSNNTWLSLLL

VNGATVEPMEALRRLPMATMDDGLTLSWALYNAATRCRDDVKVNNPSGISITIELLGNFL

TIEAL

>contig18913 Frame-2R|Blast-fatty acid desaturase, putative [Phytophthora infestans T30-4](gb|EEY68973.1|) 1e-84

MSLAQGLAFFMIAQMSCGAFLASVFSVGHNGMSVYERNDKPDFWTLQVTTTRNITPGIFI

NWFCGGLNYQIEHHLFPLMPRHNLQKVNPLVKSLCREFGLQYHETGFCRGLVEVVDELAN

ISQEFLLEFPAI

>contig20433 Frame-2F|Blast-hypothetical protein TRIADDRAFT\_60507 [Trichoplax adhaerens]gb|EDV20865.1| hypothetical protein TRIADDRAFT\_60507 [Trichoplax adhaerens](ref|XP\_002116509.1|) 2e-08

MAAVTKSHKNVFEVLTSTRGYGVGKRVTSGIWSKYAEPSFWEVVRIRPSPDLKHGKVFGK

FTFRGSFFVYT

>contig21171 Frame-1F|Blast-gamma-tubulin complex component 4, putative [Phytophthora infestans T30-4](gb|EEY58027.1|) 5e-84

MQTLLYTCHRVFLKQMMAWMIYGELLDPYAEFFIQKVETNPTNKTMTTKLWHEHFVINLN

AVPIEYVSTSVVENVFEIGKAVHILTQADQFTPDEVQKIRKTMSDLALRPVFDALILEHE

VRQVRQYVASRLHEEIVVKMNFVEYCMVLKDFFLLSRGEVFQTFIERSFQRMLVPPTTRS

EDDVNYRIWQDIIDECVPKDDNWSRAFHME

>contig22170 Frame-0R

MILSMVTVRAASLSQCVKAGFHFLFSRNSSEENARVDHSSFSTPIETDEELARRLQEEEY

KCQQVHEDSFDPQRLSPSEIRRRRLSRFGIYE

>contig22589 Frame-2R

MNRGYHMLKAMGWPGHGGLGPTGDGRVTPVAAIMKMDKVGIGGPSTSKRASSSPHKQQMQ

IAVDGSSQAQCMQHRLVRKRKLSVEQSKAQRKLQKRREKRLDQVIGNELYSEGLEGYEEY

LR

>contig23205 Frame-2F|Blast-apolipoprotein A-I-binding protein, putative [Phytophthora infestans T30-4](gb|EEY57115.1|) 8e-14

MGPQFQRLVTQCEQLNIPIAEHIQDA

>contig23429 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY66613.1|) 2e-74

MELNPNEDVNPIRSLQEPSTSYLELRSPRAHIPTTPLVPGTLRRRKIEIEIIEGACKGPT

WQFPGLGFAEHVHVPEEELSAIQQELDQPKKLLRQLPASSISGNDILSSVLYSAASVTSK

AGKLMPIPLLLVSIVLYFFRFIYEEVVTAIPLNGGTYNALLNTTSKRTAAVAACLSILSY

VATGVVSATSGVRYLKNLVDIPLVGST

>contig24086 Frame-2F|Blast-cyclin-like protein [Phytophthora infestans T30-4](gb|EEY60295.1|) 1e-119

MASDWIFSEHELHSTPSQRDGMKFTDELILRRKACDFIEKMAKSLELPKLAQISADNFLH

RFYMRQSLVRYDKYLVAAACVLLGSKAEESLKKIGYIARDYIAVRKVVEKDQVFAIQKHD

PQVTAGKIISMEGVVLHNLSYELTLSHPYKYINEKVDKVVRLQRLNEHETKIQSSKIKQV

AWSFLNDSAYTLACLRLESVDLAAGAVYLAGLYESYVPEHVCTASGLPWWSALATPLHTL

>contig24774 Frame-0F

MVGGSREARVRCRELGFMGRPFKEMVLLQPLGYCLVKLERMQEWLDNIEICSTTGTAN

>contig24994 Frame-2R

MLLDTESWLRVTASNTDVDDNADFLNLIEKRSGHSFKRKLRENLTANSIYSRRVFPSFFS

EGNPFNDANSIKWLSMKQGIRLKELGHINITKKVPLCAHDNQDLPVLEPHESEFVLISSS

LAGFVRLCGVYLKMMEYIPHIAWDTFCSLNNLFEFNLYAVLTNFVSTDSITQFLRSRSGC

VVNRDTAEWNVLRNGVCRIADDISSGNVLLQSSVEENLIQLQDSPTSKYLNLRKVIRAPA

TVEDAVEDNLYAVAERSIACEAIISQCRLLDAIEDLARSYLPDRHLCLMDEIYERNRVMA

RELRSLMYSTIATQLVNIPALKQSISAVSWNTSYISDQPNEYIVNLVQKCGETWGGLQIL

MDGSIPMNAREDVWAKMVQIILDSLLQAFSTISKPTPQGRALMLLDLHALQNGLDLINHI

GPRVVPRGREYVCNYIKAFYYDEKKLLEWAQNNKSLYSKVQYANLLKHGVGSTLVLDKLR

ELVISIDAIIS

>contig26336 Frame-1F

MAFLMAQSDVFTSFLMGGSSALGKEMSRSKAAKVAGSKRGKGSKQADAQTLQDMDDARYT

RITQQPSSIKFGTMKPYQLEGLNWMIRLHDSGVNGILADEMGLGKTLQSISLLAYLREAR

GIEGPHIIIVPKSTVGNWMREFKRWCPSIRAFKFMGSKEERAAQRETVVKKRFEALVLSY

EVAIIEKAVLQKIKWKYLLIDEAHRVKNENSKLSRVVREFKVEHRLLITGTPLQNNLHEL

WALLNFLLPDVFSDSEDFDAWFNVDEQEGQENVIKKLHTILRPFLLRRLKADVEHSLPPK

IETKLYVGLSEMQREWYMRVLHRDATHLNAIGGSDRVRLLNILMQLRKVCNHPYLFEGAE

PGPPYQEGPHLWENCGKMTLLHKLLPKLRAQGSRVLIFCQMTSMMDILEDYMRYFSHDYC

RLDGSTKGEDRDSMMEEFNTPGSTKFCFLLSTRAGGLGINLATADIVILFDSDWNPQVDL

QAMDRAHRIGQTKIVRVFRFITDGTVEEKIVERAERKLYLDAAIIQQGRLAQQNRKLSKD

ELMTMVRFGADEIFNARGSMITDDDIDAILARGEERTETMKGKIAADMQHNLANFSLSGD

NGNANVSSLYEFEGEVFSKDTNSGAVFPSTFIALPQRERKSNYNEDEYYRQQAGITKPKK

PKKSGSDAAKVPVVHDYQFFQQERMVALLTKKTQVENRRKELMRLIKEAKADEARVKARK

AKEEDSAEHAVEEEEEDNTRSAALEKELTETEMDPADAKVLEGLEKEGFGDWTRRDLKQF

ITSCERYGRADKTRVCEEVSLVLGKDRARVVQYYETFWSRFTELKEHAKYIEKIERGEKR

LERNEVVKQALARKCSRYSHPLRDMRLHYPAGYKSKGYILEEDVFLVVMMNKYGPLEHWG

EIRDEIRQAWQFRFDWFFKSRTIGELQKRGELLTRMIERENDELKSKNTKDEEELVKKAK

KRSSSSSKSKSKSSSRSKTSSSSKKRSASSKMSSSSKKQRSS

>contig26628 Frame-0F

MQNSTQAADSSTSKWMKMISSTFRGEGPSSSLFARRSSDIAHSNSACVSPTSFGPSANKK

GLDSMPEIKIALVGGPAVGKTSIVRRWLQRSYLTTYSPTVGVDILTTKHSHHGKEILLHI

WDVSSAEVDASASSLHSLLCEGFGWYLFCVQCTSRELHRGY

>contig26844 Frame-0F

MEEVFLDVPEKLWTMELLISLLPSTELLRQEFLMSLTIRHGQKPSNIVSIAQQICSHLSN

MDNKQISMEILEPKIAASAREISCATVGTETFISSVPHVSWDDIGGLERVKQNLIEMVVW

PLEKPHVFRRMGISPPSGIMLHGPPGTGKTMLAKAAAKASGCNFLNLSASDLMKAEVGES

EKAISRVFDTARALSPCMIFIDEFQSIFGNRLTAGQTTSRMISQLLIELDTLKAVSDVYT

SEMSAIASNCSEVNRTFVVAATNALSAIDPAFLQPGRYRKTFFAIQ

>contig27425-1 Frame-1R1

MILRLISTAKLWKDWTPCKQQA

>contig28068 Frame-2F

MLNAAANLFTRLKLHKNFLIQIGSWYCWIKFTEGFKARARYVFGIL

>contig28121 Frame-2R

MADATPAPAGERGGFGRGRGGRGGRGRGRGRGRGREESKEWVPVTKLGRLVKEGKISSLE

EIYLFSLPIKECEIVNYFLEASLKDEVMKIMPVQKQTTAGQRTRFKAFVAVGDSNGHIGL

GVKCAKEVATAIRGAIILAKISLVPVRRGYWGRMVGAPHTVPNKVTGKCGSVRVRLIPAP

RGTGLCAAPVPKKLLGMAGIEDCYTSARGHTRTLGNFVKATFYALRATYAYLTPDLWEQH

TFGQSPYQEYTDFLAKTAIKK

>contig28154 Frame-1F|Blast-thioredoxin-dependent peroxide reductase, putative [Phytophthora infestans T30-4](gb|EEY58212.1|) 0.0

MRALQIVRRLAATRALPLAVRLAPRATAPFLCNSLSASQQPLRLFSTIDEDLFQEDDEDE

DSFVHYPAVAARVQQQAPQFTAQAVVDGDITDVSLDTYRGQYVGLFFYRRDFTYVCPTEI

IAFNDRAEDFKALNTQLLAISCDSPESHLAWTRLPRNKGGLGKMDIPIVSDITKTISAKY

GVLVEQAGVALRGLFIMDKEGVLQQITINNMPIGRSVEETLRLIKALQFVEEHGEVCPAN

WQPGGKTIKATPTHSHEYFSTVKDDVEDDDAAVLTLIKDKAQFEALIQSGKPVVADFMAP

WCGKCAQIAPFVEELAEAHPEVTFVKCDVSIPEVEELKKDLHVGVFPEFRFYKNGKEVHE

KITGYKKTLLKKAVQTLL

>contig28239 Frame-2R

MKYMNPTFYGMELRDIFATGIR

>contig28543 Frame-0R|Blast-ser/thr kinase [Phytophthora infestans T30-4](gb|EEY57565.1|) 1e-57

MSPERIQHTEYSYSSDIWSLGLVLMETATGVYPYPKHQTCIDMLQNVLEAPPPALSPQYF

SQDFCDFLQQCLQKNSLDRASADTLLKSPWLQRCEAINLESSVANVRHWIASLQ

>contig28604 Frame-2F|Blast-ribosomal RNA assembly protein mis3 [Phytophthora infestans T30-4](gb|EEY63939.1|) 1e-84

MPGLLEESSFATLFPKYREKYLREVWPIVTKALDAHKIACELNLVEGSMTVRTTRKTSDP

YIVLKARDLIKLLARSIPVNQAVKILADDIQSDIIKIGGLVRNRERFVKRRQRLVGPDGA

TLK

>contig28998 Frame-0R

MQLQKSQKHWVCSPLQLVFPVAAASASASTLGTPMVVAMDMDQ

>contig29526 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59785.1|) 1e-79

MSTLLPNSIKQIKCYQELLVLVWKLLDENTEFLHYVLKRADVNQLVVPLLFLMYEGRQEP

AKVGMIHICTFILLLLSGERDFGVNLNKPFNNHLPLDLPPFSGNHADLLIVCLHKVIVTG

YEKLNSVYNCFL

>contig30506 Frame-2R

MTHVSGEFTNLAPLNNDDLQKLDVVAVSPFTACEPLRGQDLTGKVALVLRGDCNFVQKVW

HAQRAHAAAVIVMDNELRHEPPSHIIMTKDDMANTIHIPAVFISYVSGEWLLDALSRATP

WKPLQVSLNSNGELPRASPSYRVLKLVVAFILSTSSVCTLSIGLSLLSSVLFQWVRKIRR

TRVAKKLPIAKYERNMQRTLLEHLLKASIGLDRVALLKTNNVSKIQQVHESKLRSTESRN

SPHESKVAIADGEICRENERKAHELLKDNIADMDAEICTICLDDFEDGVDVKVLPCQHFF

HVNCINPWLEGRSGSCPLCKQDAIATSASASKRLFGIILPRIDQIFQQEHWAHTIFFILP

ASLVSCLIVNAATAIIYSMWP

>contig31123 Frame-0R

MASPELPTQDTLEPASPVLLEWPHQMNSVQYHTFVSNL

>contig31246 Frame-2R

MRSVSQSLSTSFFQTQKKNCPVASYRLCNLGEVGNRSKALILASYLDCHHRNLYGSGQIA

KCHERHANGSFLYPCSPCFSIYTITTSDCCVCWKKSALHARISELNLQLHNF

>contig31422 Frame-1F

MISLSWHALIELFTGLPAPSLLDTIVIPDDKTPRVLPVNLDRLDVHLQKLRNYLAEIKQE

VVDRKERKRLYQLGQAEGIVCNFAIGNSVLWSRVDKRMRGNKLLVRWGPFSCHGGSSIFI

YDNASFNKRYI

>contig31880 Frame-2R|Blast-GPI-anchor transamidase, putative [Phytophthora infestans T30-4](gb|EEY65990.1|) 1e-41

MNMSRPNISVWSLILLALHAALGENYHRHTNNWAVIVDTSRFWSNYRHIANALSLYHSVK

RLGIPDSQIILMLADQMPCNARNCFPGQVFNSRTQKINL

>contig32126 Frame-0F|Blast-centromere/kinetochore protein, putative [Phytophthora infestans T30-4](gb|EEY58042.1|) 3e-25

MARMLEPLVKKLVDGVLIQTNISETARARLHHLLSLLKE

>contig32210 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61925.1|) 3e-58

MAKNRWDRPLFRLTPDEYQKDGTGLPLDAITEAIRFGKTIKAGLATKAPLTAETSFLQAL

EDTTNAIVTALMTHQHEVGVADGVRVPPHSVKNELRISRPLSIAEARRHRRQFNKITCMR

PCVVATIGDHFIEYLNQQG

>contig32540 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57643.1|) 1e-45

MQSARIKSCRRATICGNAPFKRAFTTYSGGHPSEGQGGFYGSSKTRSEASSKFSPGARVE

PQDLTKLQNLMKHWEMRKKTLASEDQEKGLARIASEQEKLIKRLLIRGAPVWGLTTQQRE

FVAECNKVCH

>contig32988 Frame-2F

MNSQHCFDYARTRSLSTPSAPPADNRNYTIEPQAPFGGRRGSLTSQPQPPLYPDIGQRNG

PSAPRRESFVQQTHAQNFSLQPPNLASTYGPQHQSGQNFG

>contig33158 Frame-1F

MTCSGCCTRIEKFLMTQRGVMDVNVSLLTSRGIFQYDPQVVTAKQIIKVVATLGFESSVL

SSDELVSVVLHFGPSTSSLQAKNVALGTNGVVAAEEIDNGANSSSSILKALLVEYNPDVT

GARSIVRQLSHELGVDIQASSSQAPSVRAGVKEVRRARKLLLWSCFLSLPVLFIEFILPV

LYPSLVSNPANVGLWGTSNCLSIKNAVEMACATPMLFFVARHIHESASYALRYGGRVTMD

VLISLSACTAYAFSVVTVVSNAFATFRSEKAERTKVGSLSGLALPGPHKDTPASTDTFFQ

VTVLLITLILVGRFIESLVKARASNSVDALLRMQAKTALLLNEEDQNEVDIDVVLVERGD

LLKVLPGTRVPTDGVVTRGASSVDESMVTGEARKVAKEPGSIVIGGSVNSQGVLTMRVTH

TIHESMLAHMVRLVGDAQASRGVRQSIADAVAAYFTTCIIILAGAMFLLWYFLAKNGQVE

TQGWRPFPFALRFAITVLVISC

>contig33253 Frame-0R|Blast-aspartyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY67895.1|) 6e-68

MLSSRLRYAASTRALCIARSLSSFRTHSCGELRHDSHEGQCVTLSGWVDAIRPFGPISFL

SLRDRYGVTQLVLEKDFLKTANEVVKNLRPESVIQASGVVRTRPPNMRNDKMATGSIELV

VDGIIELNTCTNLPLQVAMGSEVANEDTRLRYRYLDLRRSALQHNLAVRS

>contig33631 Frame-0R|Blast-small nuclear ribonucleoprotein E [Phytophthora infestans T30-4](gb|EEY69432.1|) 7e-31

MGFDEYMNLVLDDAEELDIKNLKRTPLGRILLKGDTITLMMAVDISNGSS

>contig34465 Frame-0R

MLGLMMAGAIALVLLVALFVYKKTNQLVQDDDPGLERGRHDHTQGVAQASTVAANYHQNH

NMSPTGFSDDNYPPNPGNSQFDQEPYDHDGGRLTYNDPNLDMLTPRSQIALAHSQMSLPP

MAQTNSSHGTSQYSQYSSQSSSFYGQSMYSSGHSGNHFQSKYDSRHREDLASEDESDFGG

DSIQDLSNGWHGMGQKGSKKTTKRPDMSLDESFFEPKDSRSTSASDYHGQTRFQASGQTE

YRMSTADESRYMGDESFAATNSNYDQSHYNGDPSFQSSGFSEFEASGAPRRRGDSSNHDA

SSFYRTKDSRFTDASYY

>contig34559 Frame-1F|Blast-plasma membrane H+-ATPase 1a [Phytophthora nicotianae]gb|ABF85691.1| plasma membrane H+-ATPase 1b [Phytophthora nicotianae](gb|ABF85690.1|) 1e-169

MKEECHDFFKDRYQTCVMNNNNTGCGGMTGNVPQSASVSDVGTFREGVVIAYWRQYQQQF

DSRSQLFEDLADVHLNHLPNDAKPSAEVAYRQFVYSYTLGVGGQAYGHEYDVFNAAQMGR

GVEFIGDGEVPITNGVGFCDYVWGFSNWNSTWTRNNEMIGPGIQRKEGVLRSLVYLHVSI

SGQALIFVTRTAGSNNWFFAEKPCNLLLIAFIFAQVVASVVGWIGFGGYPTDRIAVIGCG

GGYTAIAWIWAIVWQFPLDVIKFMVNYILTKNTYASKAFTERINAGHPTVDALCRDKCST

IDTR

>contig35040 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66077.1|) 5e-62

MLKNRVGIFCTRSPHRPNPVGITLAKIQRVSMRERTVYLSGVDLLDETPVLDIKPYIAA

>contig35710 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53454.1|) 9e-11

MVLPALEVFVLYIIRSFPSV

>contig36377 Frame-1R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY67000.1|) 0.0

MCRGPTINQEERQEENEAVHCYPMEKKRDVRVMLRRHTTGVVTFGDTADVCTETDDVDVE

LVQQDALKQLMRHGSVLFAGGVAGSVGKTVTAPLSRLTILFQVHSMVSTRHTDRFSPTMG

SAFTKVLKNEGVLAFWKGNGASVLHRFPYSAVNFFTFEMVKNSIVAQHHPSFAYNSWTTM

FVSGALAGATATVACYPIDLIRTRLATQLNTDIRYTSIRHAVLRISTEEGLPGLYRGMGA

TLMVTVPNLAVNFTMYESLKNYVRSFRRNQVLSALNGVERKLAAASYDATPMCVADTLVC

GGTAGIASSLLTFPIDVVRRRLQISAIHAKPAGIKPTSLGIASELFQAQGIRGFYRGLTP

ELMKVVPMVGITFGTFERLKKLLTVED

>contig37208 Frame-1F

MPSHRLGAVSDSSCRNLSNKMRCFYTNRSSRRRMKVSK

>contig37532 Frame-1F

MKTRGEPHMLLIGDPGTGKSQFLRFTAELSPRSVLTTGIGTTSAGLTCTAVKDGGEWMLE

AGALVLADRGVCCIDEFSSIRSNDRTSIHEAMEQQTLSVAKAGLVCKLNARTTIFAVTNP

KGRYDPTADISANTNIASPLLSRFDLILMLLDRTNPSWDHAVSSFILNQAVDTNITCKEG

DERDAKESVFNSINSQGPASLPVDSELWTIPKLQAYICYVKEKYHPQISRGAMLILQRYY

QIQRASDSRSAARTTIRLLESLSRLAQAHARLVCHSDVAIMDAVLAVFVMEISKTTDGCS

DMLKGAAESVLHSTFSDTPEEEYALQEKLVLDYLGLQELRTATTSGLSSHLMSRPQHSHV

QDKLKNRGIDEAFDHGKLHGNTRHKMRTQQHFEASSSQQKQRCENDILLQDRQEHFLIPS

TPDVYEEGVNVMDDYRLGLSHNSKRQQCEKPNPRYDFGPWS

>contig37697 Frame-1F

MDSPEGSNMSPINSLYPEDFLLEAYSLEWEAIELRCQRLQKAWQQFLLLEKMELEELRYK

SLLRKIERKEQEKEAQERVEREEQAKQAREQVERGQAENFRRERDKERPRTKSIKKTKHV

AVGVTQANSRPEEANTMKLKQVSSKKQPTKAELLKRIIPTSMPSLQPEDQSSTKSMNDPR

EFDSPPPELPDDGLLDMLSLDKTSDSDENEPSMVSLILPVSQEKPMQVLPSPVMKKTLTG

QKRFKRPSGGPPMEFNFTNAEARRQAKIKESAAQVESDEVEIEPEPMPNPVIKKRLKRRK

DQNTSKAATLVEKNLALGRSTAVSIVSNKTITQAINARKSHGEIVGNQQPQAETENPGAE

RRAERSVKTTTQVLKRVKGKSEPMSIKQRLANAELLSRMNKMHDVCTPKVLNKKMKKAQK

EELSETGTAKQADVRKMSTSDSAESLVSRQIEDGDLSISLNSSGLISDDSPNNIIAASRM

RLRGGAESDVTPTKKLQFQEITKRLVKSPMPRFLRTPTPLMSPVAASGHAKQKALSPGPQ

STSIRSTVNTRRLNSAPVQLRKASNANRFGIPVGVSLGANTSAFSMFDAFVNSGSSASIP

KLKSKTRDVSPSV

>contig38003 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63343.1|) 1e-168

MEREVRTTMNGSRSLMNEASEQAGTPVTLCVGKIQGSLEDVVYGTVSTTSGDMCFNATYV

EDLTGAAVLATVVEPTIDDPLTTITLKWQELNLLLHSNKRDFVFMEATGFTHLRDGERVG

YRLMYSIGFPQTPELPHRVRGTVNVFFLYRQDHGHGVEMYASGVFANGSKVESLLVIPSA

MKFFTASKFAHCGEMKKLTWLMHRRYALDKQRGAPLSKGDCVSCGVSISSKIFGNFGRSR

DSCKLCHRLVCGSCRVKKRLNFVTLDMTFEERKTSFCPSCIKEALEINTADAARAQMAGS

HSHYALHSGTDYSFASSSDSESTT

>contig38458 Frame-1R

MKLVKVTLDDESTLQQNEATNRKKKLNQMDGPGLINGVRRLAFRTTWTMLDHSYVLLLLG

VAGL

>contig38836 Frame-2F

MNHIKPTPNGSNKKYIILIGLRLQSGVLLLLRATQDPLARLQWESAIVGFSQGLSSSPRI

CRGFDFYGDTSTNRSERLALVVDRISEEDHAHE

>contig39620 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61443.1|) 3e-12

MSQKDLAQWTKHEFGLKKTPAQSTISGILRRQHEFINMSTLELGIKKRRVVQHPQLDSAL

ANWVIQMAGRGQTVQGDLTKEKAKEFAHMLGIPENEQPEFSNGWLHSFQLRHNFSFRKFN

AEQHHPPSSFNDPRRLGAKVLYWTTMDALMAETDTYDLKDVFAVDETPVLYTMPP

>contig39839 Frame-1F

MLSRLASRTGKFLLSSIIRFKAGLRRTRNLAKRRLRRSQYTYSANHGKAESSPAWLQASP

ECELTAGEYFF

>contig40040 Frame-0F

MLHRRQFMIRCQYCNVHIHPECCISDIGSSAMIFKSNWICERCTQTDGNEVPSCLVCAKA

TEYLMPCVDPLVVESQSNGKTLFGSSTTSDARQYPGLQAHQKLLRQELKESVSGSKKSVL

QPRKQDRHGVGSSAVLNRWIHVYCCKWQKVKTVKRHHMLCAFVPAIKSNSMASRCELCDT

KGGLLANCAHCSRRFHPICAALKKLYFARSNRTEWRFYCEAHTPLDAAFDVSRQSWITKE

ILGQLQDLRRSLERGRMLLEMARQRDRQHKRLLHMCKLPLMEATINVILKKRPSPQMKEI

YNDFTGENLTDVPHRAKSAPPAQKSRSRVRNKSRAAARSRNTKYLGSQALSTPERNRKRQ

RSRIDSDGSSCGEHDTPNTRRHSRRKSLRFSRVVSENEDEWSEDEQAEDCEMIFANLAVP

KDGYFYSMLMTGIVD

>contig40426 Frame-1F

MNGSSVWRPHSFRARTKHNMLQLLTTLLLLYFLPLPVAATACVNASTLVEGESDLTAVVY

DANCVARSFLVVGNSAVERSLNLSNLNVVEVRSYPRVYQLLLNNNEIEILAPTNLDNDME

TLELASNVILDLSDFRFPKRLTYLDLSYNSIATLSYSTPWPESGELQTLLLHGNSLSSVS

VDSFSKLVALQSLSLSNTGISNLNDLILPVSLRKFNATRNSFTSASTNFSNLPTALQYLD

LSNNLLTVFPTIVSSLTTLVELNLESNGIKQIHGVTFASTLRKIYLNDNPLSTIEICRSD

VSVFQSLTEFSAPLSVSKDNDCIRSSVSNSAGGSNKDESSSSLDGTASSELRTRSKSWIF

SAESIGIIGTTFLVIGILLSALVFGYAWKKRQRNDDDLSHRGATKLQRDRPYGSSGGNFL

AFTSSGRVARAVGNNQYEYHDRDSKNGHNSSLEYSGTKAPGEDAAWSVYDSPLDNYTPVA

LLESSPKGSSFHGASTVSLQVRSKIKSKMNLDDLLVFEIPPEEIQMRQALHMSTSKSNSK

TAFALSSMGVRSLRKVDTALFLAEYQGYKVVIQALMRSKKRFEQHFVEQIRLAAALDHAS

IVHFIGVTTGCSATASRQRGSSATAVPFDITSSYGLNASKSRYPTMGAPAWHLGVVFEYM

QHGSLASMFKAERRRREGNGYYLSNNVAVAIGSGTGNIFSWYPVFVKSSTCANANPNTDW

RCKLSIALDVAMGLVYLHANNYAHGCVCARKVLVNEQGEAKLSAMDVLLPSDLASFDNTH

TTDDFHGSLRESARWTMQKLAGIRSMRVSKGPAKESS

>contig40710 Frame-2F|Blast-pyridine nucleotide-disulphide oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY70157.1|) 0.0

MTMMGIWTVSTRSMILRRGYGRMLSTMKPQVATYDLVVIGSGPSATQCALESAKLGKRVA

IVDKKKRLGGVCVHTGTIPSKTFREAVLHLSGYRHHGFYGKSYSMKTVTIEDILYRVQRV

VSSEEDVVRAQLKAARVDFIPGFAHFENEHEISIIRDFDTQEINNNDAAPGNSDTLDSLA

RVKADKFLIACGTRPAHNPLIPIDGKVIIDSDQILSRGMHQLPRTLIVLGAGVIGIEYAS

MINVIPGHSVTVVDGRPDILPFCDREIISNLTYEMQSNGARFLLGETVKKVETTEKRVKV

FFNSGKVLSADALLYTVGRQAATNGLNLEAVGLSRNLRGLINVNKNYQTDQSHIYAAGDC

IGAPALASTSMEQGRLASCLMWNSDEELTATSQLENGNYPYGIYTIPEISMVGQTEQQLT

SDCVNFEIGIAKYSELAKGQMMGAMDGGTLKILFDPDTLKLFGVHAIGEGATEIIHIGQV

AMAMGCTLTYFRDAVFNYPTLAEAYRVAALNGLGRLSRNTKKS

>contig41465 Frame-1R

MEATASDKLVHYRVSTILPICWQSVKETASGNDRRLYAPFEMPVHVDAARLAVKGSFVLV

AKLKVVDPHGEKWLLAATGCRRGFIVY

>contig42301 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69201.1|) 4e-38

MLKFHYQICSDADVRNGFDAPRGVANSDSVAIAKIQFNALLLQ

>contig42532 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68394.1|) 0.0

MPWNANNNPAGDIRAPAIATALRVKQQRKGTKSVVNAWTCLLRVEDLDTLDVSHEQRTIV

RHCALLHPEDFPIDAAGSDGTALIHPRRYAQYVVAVRSCEAITRGSIALSPAQMINLELC

RFQTEKWTLYTDHAPVASTVAIEIRPLLKTYKKVESDDEKDAADTVATALIVTDAKDFAA

AFARYTWQRVLSNHERLVMPYKDGHNYFIRVLEIDAEDENETELTMPDAYCGCIDEVTRV

TVSSEVDLSPTFSLLNEESFGATNLASMRSDVVTVLTNDEEEFPVKKRLLYPCIKLSSAV

LSGKGLHKEATSTIKVDVDCCTFDRVLLYLEHEARNDGSVFRFDPSVIDDLLAAAITVGC

IGLQEVCQKCFGEFETRVRKEAIRWEEVVQRNQSGEVLLVMQGMVLDITRWVPEHPGGSE

LIAQEAMNVDSTVMFEIYHASRQSFRYLKQFYIGELSEFDVSTIPKSREQPSSAFIQELQ

QFTKWRIKLKEQVFKSF

>contig42983 Frame-0R

MIDAEVAETLMSLSAPDERKFADNPLYASELPPPWQAGKKRGFAALDAVVASSLPSSSFL

QPHAKSFTSAMALLTHRIQERPLTSMIPDREHDSSSSDVDMEFNEASDGFSDRQAWPTYR

SSFDGLVAAAASKQEDNDRYSVPNSRPISIPVRCGNSRSSSARCREHLSTIDRKNTSSYG

KKYKSSSLSRVQEDKSFLGRDCSPTSVEDDETWYDSEYKQRARLPSVCSSDGSEYGGLGR

QHLEEFLRMEISAGNESDQRRGETLLSSDGKYIGSYSPDARRKRIERFLEKRKRRVWAKK

VDYDVRKNFANSRLRVKGRFVKKEDEELLCQLMSYT

>contig43269 Frame-2R

MSRSRTDAVIACPLSFLANGKPFVVLNVQQELQLRHVYDRGVRFVAGFPILAPNGTIVAC

LCTMDTGVHGNISTDDHTAMHALSKLASDLFEEEVNPYTPRH

>contig43377 Frame-2R

MVDKVDATLTVDELLPSGRQRVRRGKVPRRFTGRVVDVKVPPLRVPYTLPLAVMAAHAFS

IP

>contig43724 Frame-2R

MNYLGYLIKKYVNCLKMRGFACRQSHRCVRHSLLRS

>contig43751 Frame-1F

MAAKKRKLQSSGGDLVGRVFQLNRTVLRLLLPGHDIGDVGAKSMGNMLRVNTTLQHLDLR

GNKITAEGVGVITQALYGHETLVHLGLSSNKLGDDGARAVAEMLPYNSSLQCVGLARNEI

TEVGGKALLKAVLQNRTLFRIQLSNNDIPQEILDKIRAAVVVNKFMQKKAQRDHEIEKNN

AEHTLVQESVDQGTQDTSSDDDDESLWI

>contig43870 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69546.1|) 1e-129

MQTLFDMPCKTVANFLNLTLTPSNQIIHPARYYAIFRDWDGKKTYTLEELQNRKGLTLYA

DFDEFSAEQLAMLDNELQQIKLALLQRFSALDLSDVLPMGDRVVKHYGKDVLDHSSLLQI

FRTNIGYAGCLTPLEEPSKGRFQPATNSRLFWEDIPYGLCILKNMAELLGNLPTPRIDFL

IRWHQQYMDVEFLKPNGRLNPRELWRTGAPEKYGIHSLDDLVSASLPQKASNSHHLRSCI

>contig43984 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57692.1|) 1e-25

MIISEEYLEKTYNGAKTLSEEYVTSDVLSHSMNLEQASIIKASTEVSTTKNAHQAPLLIP

GKPMLKLKNVVVVKKMSRYQHETELYGNTGYEVFHLYCRLNHWFFCYIIN

>contig44123 Frame-1F

MAAQATIVSGRLTHSRSARNTAMHSTLWRNVYFETSPVNLLPLVSNVALPFFSEHERSLL

TYDAVDGYSSSLKSPPIAIVSSDPELFVTQDDMDARVN

>contig44611 Frame-2F

MELESALLADARAAFARSIEEALGRTALSQTKAILAVDVSHFAIFELLAYGSGGSEFYDK

LGISRLLSVQLQTGDTVQLQRQLSISSHMHLDQRQNVAIVAPPLPTVAKHLADALRPLEF

VASRRCAILWLPVATSDVSLEMERQGVAGFIHQANLALSLIPIDRGVAALCLDSVFSDLY

VKGDSRALTSVVKSILAIETHTGKLIVDVTSHGFFAERVKTMLELAHRQAQRLQSCQTNA

RDEIAVARSCTMDKLVVIDRMEDPLSMLLTPMTYEGLLDALVGVNHGVVTYEKEEEAAAV

GEEDGREILRAELNGATSTQKVVLNYLDVLFDEVRDVNFNLVSDQLVTIAKDLASQVRGS

SSESMSGVTPDSQAEFQKVKALLAKAPHLIKKKRSLAHHLQLVQRVRELSTQFALRGCVE

TEMTIMSAGPKVSSAAAKDVDQFLEEAILREPPLNLYDVLKLLCLCSLVRGGLKPDQLAW

YRQQLCHTYGHRILPLLAQLEKMDLLSLDNRFDFPKKRKQLVLMRGALDDEETRHPVDIH

FMFPYTGYAPMSIRLLQDSLGMKYKMLPKDSTSSLLRRGSGSGKHASSQISVAVDATVDP

NISGKRIHVLVYYVGGVTIAELTALRFLNQQENGFTFFIAATSICNGSRLLRAIY

>contig44664 Frame-1F

MDVWTYNDWNLACVIVLAAAIATTSATFLLAFKHVKVGESAVQYITYSICRLYLIYSLAH

LLLHVSILANFDGLQNALGNRKLSSTAYSEGKILRSLVVTVILIGDCALLCTAFFVTMLA

YEMKRLIIKSMDRGPKNESATIRRYCLCAYGGAMCFAILVAISAFLSYSNAEPLQSIACW

ILLTGIWVSVLYPVYATIYISIQKRARDPALLVLHRRIKIFVVVYCVLVFPYCIVQVLSR

TFDDP

>contig44880 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59509.1|) 1e-62

MLNFYDPVTIFVLRVFLVTILAEVAMSNRYIDVGGFEAYEDNDGQELTLKMLVNISAKKA

FNAWLRCGWLGRSSIIKQSEGRELVGLRRVILPGVEEQIVSAGPPDSSGRIPSVRYRIKK

SGPLLLRDHVAFVQFVADTTAPPSQPKTLILWNSKLTPSTVGSVLLCGGSISRLILRIVL

SDSLSKIPALLQQDQS

>contig45506 Frame-2R

MKREILPRSWRRKIGKRANRHHEVTIPNMFRVNLHKILQTLTK

>contig45599 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58056.1|) 4e-23

MAEFPAEFLSLEADFVDCKMSINNNINTMLREERSAVSKASQIGQAQVVEAQRCIKLMTV

EVRGRQPMLRKAMQTKVNLYREELQGLIRDIERAQLMAKEGSAVSSKNSQ

>contig45717 Frame-0F

MLLKGVGCIFFSKVALQKIELTSVFRRSAVCAQISLHLRQQVLGSHCRIAVKRNPDRVSA

TRFAAPEVLLSL

>contig46158 Frame-1F

MAISCCVCGAQIEANAMNMCTSCIASEVNVAEGITTSCELVQCRGCLRFQSRGKTQHYSS

ITGAWLDCEFESKELLALCLKNIPGLTKAKLVDAGFVWTEPHSKRIKLRLLLQREAANHA

VVQNTSMVTFTIQSVKCPDCTKQYHNNTWKAVVQIRQKANHKRTFLRLEQEILKQNAHQD

AISITTVKEGMDFYFGSKSTAERFLHFLAAHVPMRSKSSSKLVSENVHNATANVQLTYSV

ELSPICKDDLLILPRKVAQSCGNIADVTLCARTTSLVHLVDPFSGQHAELSTDKYWKTPF

LPLASSSDMVEFIVLDVEPVDTPSALIDSKSIVADVEVARASDFGVNDTTFYIRTHLGGV

LAAGDTVKGYDLSSAVFGASQTYSLQTELPELVLVRKIYPRDTMNKNKDDRKLKTLGASR

RNKVSKMEA

>contig46349 Frame-2R

MLDHKAYSCASVILNGPTQRTINSLPRRRSSTRDHSTKSPVLTFSSVPFFVIFWWSRVLS

LQSAIPSYIKRRLSRRACDSSSTPAHQ

>contig46828 Frame-2F

MASDFSLSKNWSEVSIPDKDMDNSGLGSTNSAGKLDRKSTNTLPDSILAINTSSGASDSF

SSTVAVILGLLGSCVVVALVVLRRKQTKERQAHLQAPFDQNASCYYAGPMRVKTTNSMTA

LSPEHHEEEEASSPIPELAAIPLDPRMSTTSSISVSESEVLRHIYRCSEVRNSNSLALLS

QQHMRYST

>contig46950 Frame-1F

MESLDTPLEVKITIVYALARFCVVANFEQYAGPRLLLPLARVASQVSAKGAFFFSRSSNV

TVTSNVSGSAGNGPTNTA

>contig47052 Frame-0R|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY62213.1|) 6e-46

MPVWQNLALALSVFFGYSAHARSLTATFDLLSYNDVYELQQDTVEGLKLGGPSRVVPIAN

AMRRANPNSLVLLAGDTISPSLWSARFNGQQMIKAHNAIGLDFASLGNHEFDYGLDNFLN

VSRTSNFT

>contig47126 Frame-0R|Blast-2-isopropylmalate synthase [Phytophthora infestans T30-4](gb|EEY66185.1|) 0.0

MLQTFVKGSARLVNATARRTLSSQAAAEAGKERLVIFDTTLRDGEQSPGATLNFKEKLDI

ARALSALGVDVCEAGFPISSPGDFDAVSAIAKEIGPITGKRASGEPMTICGLARAMEKDI

QRCFDAVKHAPKHRIHTFLATSDIHLKYKLKISRDECIRRAVDAIKFAKTLTSDVEFSTE

DAGRSDPDFLCDVLAEVIKAGATTLNIPDTVGYTVSGEYGSLFRYLIDNTEGSDKAIFSS

HCHNDLGLATANTLAAIQGGARQAEVTINGIGERAGNTALEELVMALKTRPQHFPVYTSV

DSTHIMRCSRMVSHYTGMSIQPNKAIVGLNAFAHESGIHQDGVLKHQATYEIMLPESVGL

SESKMVLGKHSGRHAYSKRLQQLGYTSLTPKELDYYVEKFKVLADEKKTVTDADMEAIVS

DELFKPESFWTLESVHVTAGNLVKPTATVTLVHKDGQEVSEAALGTGPIDAIYVAIKRAT

GIESIKLNDFSVESVTGGTYALGEVTVRVQEDKETKENVEAEKHVNAQTGVTRDRQFVGH

GANTDILVASATAYVNAVNRMMASQVRAAANDRVDA

>contig48134 Frame-1R

MLEDRKTRFTAFFDAIATHPAAFESNVWKAFLVQA

>contig48387 Frame-0R|Blast-F-box protein, putative [Phytophthora infestans T30-4](gb|EEY65518.1|) 5e-40

MPDKGSLGMIIFRNEDFAIERILVPRSVYDTIQRDPFSFVAAETLSTLEVFSNWQLAVVL

FAAMTLTFFGQLLSDLLHAYVLPPSFMWWGVR

>contig48509 Frame-1F

MKVTSSSRTSRQKLHTMIHWSWLHATAYASVIVVSVFYMHTQLTHYFTSLDARHLNEELL

YSLATIAAISSEHLDGLHLMLYNLSISLRWLLVVLSLAAWLGTLVLSRRYHKHSPLRRIT

NSLGFYMYFDNLRKWRLKHTKQRSKRHHSKPKKQSKSTTG

>contig48596 Frame-0F|Blast-carbamoyl-phosphate synthase [ammonia], putative [Phytophthora infestans T30-4](gb|EEY56914.1|) 0.0

MSERFIRTLKVNGFSDRQIAAKLSNTSAMQVRERRKQLGVVPCVKQIDTLAAEFPAQTNY

LYMTYGGSEDDIPASEEAIVVLGCGAYCIGSSVEFDWCGVSAVRTVRELGKPAIVINYNP

ETVSTDYDECDRLYFEELSLERVLDIWDRENPEGVIVSVGGQIPNNLAMPLSEAGVNILG

TSPESIDQCEDRNKFSALLDTLGVDQPRWTEVTDLDSALAFAQCVQYPVLVRPSYVLSGA

GMIVASDEEQLKVYLSSESVKISRSVTVSKFILNAKEIEFDGVAKDGAILNYAMSEHVEN

AGVHSGDATLVLPAQKLYVGTIKQVKRIASAIAQSLNITGPFNIQLMARDNDVKVIECNL

RASRTFPFISKTFDLNFINLATKAMIGLPVKSVPIALIDIDYVGVKAPQFSFTRLHGADP

SLGVEMASTGEVACFGTDMHEAYLKALLSAGFKMPKEKKVLISIGNKDIKREFAEGALIL

QELGYTIYATLGTHEYLTAQGITSIALRKPSDPESDLPSVIDYISSGKIELVINVPEGTN

REELTSGYKIRRAAVDFGVSLINNIKCALLFAQAIKKVQKLEICNISEYYAMPTMGWRPG

QKLSARKMSIF

>contig49094 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64527.1|) 2e-45

MFYKMTSMYGKIDRQRVNRYYQCPLAQTDGKEYVQCKPRGKGVLLRRYRKVGTAEELEHS

VKTAPFIVWLQLDH

>contig49256 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54281.1|) 2e-70

MHFVPEDAAHSAFRGYVRVDDDEFAVRVSNVMYDDSTGRTMLNLAQLDVESALATQLEPH

SATLKLRLVQASSLVGFATELEELVAICCRKKTNTQAKVPSAKYYERLLEELDIVGWNRL

GELSDDLRSLELNIKDQAGRNHTIRVKLPLQFETVGCAEKLECLVDAPEPFELEWPPKNK

KAVC

>contig49483 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66165.1|) 8e-06

MTFWKAARFCRVLQQLRGLVRTKNLELCPLRCEKFTPVFKS

>contig49537-1 Frame-1F1

MKPAMLGINNFKNVSPTALVAGTRHPF

>contig50027 Frame-1F

MSSDVSSSQEHSENEGDETIRLTSDTDTQIPLDCGSNLSDYEEHTIDGLGKIRTTTDLTR

WWHDQKQSSMASVQPQGRQSPRMSKPVNDHVRMAKLQHQAHNRRASIAISAVKRQDLVDM

VKYPEEGTYNIDAYHQPQRLSYDRRQQMPELEAQARYNAQQARCQQHSDFEEMAQYQE

>contig51103 Frame-1F

MHETGLHFELSPEKPLGRGRAARRETSGERLTLVLAVNADASDRMEPVFVGSGTLPKCTD

ELDDVSSLRPFQYQNNKRAWMTPVLFQDYVSALDTRMRDEGRYILLLVSPAPSHVTLGLE

LTNVRLEILPQLAETVPMALHVKEDSASLPESIAVDAPDAVAQSLTDSSMHESVLPDLNS

STTIVSTLTTTLQP

>contig51231 Frame-1R

MRKVLRKHSSTGRSFRILVGKFAERVLKNDFYSLP

>contig51558 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66022.1|) 7e-32

MTTIPRGKNKEVGDFDPYDSANSDSESSGSELSSHSRWRRSNQFDHPVADAKSGFGSSRT

NTLHFSLGAEATGRIVAYAIF

>contig51653 Frame-1R

MHKQAEVEGPRARAAANEGDRLRAIHVDRKELFVRASAAQRRRRQQENEERRLAKSRYSW

LFGGTRRLHEDEVESPSSFASNIVVSAKYSAWNFCPRVLFAQLKRPSNMYFLFIALLQTI

RDVSNTRGIPTILLPLAIVLVCSAIKEALEDRERHRADGVANGRPVMTLTPLGNWELRKW

KDLRVGDIVTSNE

>contig52120 Frame-2F

MENICYMILHDIEQNGLIIGTEVSLLSLQTIVSNVKTCFAMDVGQLTASNNDVHSTACLD

LCQHVASVDLASLTMELTLHFDEPKASIDEVTSAIVQRYQYAVDNLILRCMGGDNEDSFT

WMEELIWSWVMGSCAPSSGHLSELRSFLEAISSSNASARDLYQRVVKMLSESPSIRLKEV

GIRRLKDFQCQGGENAIENTSIGIAVRQAIFSQWEKITTNFDEDFKWAEAAILSHVLVDC

ANIDDATWHFGLYVKAIWSTLLAKFQLNSHREAQRLITMSSRNIFNQFA

>contig52498 Frame-0R

MQMHFPSIITSIEARLRGFKNVCIIRWKPHYLRP

>contig52582 Frame-2R

MQILPCVLQGHHVLVSAPTGTGKTASYLIPAIAQIMFAREGLKEVLALVLAPARELAI

>contig52757 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65743.1|) 6e-57

MSKSEARATVSKVDSQGDAIILKKPLLLCPEIVGNLVRRSLNVSVAPIWWDRQMVGIPAL

LEWLKSISIASDGLSKLVMEALWKQRSLAITGFNSLSSTLPKGKTIEEYIKELKLRLNNH

AWEALNALMPGD

>contig53233 Frame-2F

MNEQLRTEVADLTSALLARDLELTQLRERCQVLETAREQPDHGIKTLYTTNSITTDKEFL

KT

>contig53376 Frame-0R

MVAQEVRCESRILLLLYDKQI

>contig53538-0 Frame-0R0

MSGSLSANCRARRVSLHLLHKTQASQLASQCLCVRTFGTQLLLTFLPLRGLTVAPDVTHE

CQTTRGCPRDEKSQCSARTTSPAMNCSSAMPSSPSDNKNWAATAISGSIADLAMDTTDAT

NAEPRTSAKHNMEIPP

>contig53538-1 Frame-2R1

MRGRNIPASMTTETSADDQDDAYLAQRQSTMDSTTLGKLLMAEKNLAQAGQATTNVWKLI

GKLPSEESESPPPAQNPSLSVGQSMPVRQNLRDSAVVNFSASQGANCSPRRNTRMSDNTR

VSTRRKISMQCSDDKSRHELLVSNAV

>contig54830 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56573.1|) 1e-21

MRFLTQAIDASQCDMDDVSDTYTDAHQDELPRNTRLMTVDKLENEYMRRLTHAMESTDGG

AAWRAALNIFEEIQHANGRGLGLEVSSFLVEVLGTRRRANDCMRALAYSREQGIR

>contig55114 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66154.1|) 1e-08

MIQQNHQLQMQDFQIALSVASGHSMDVDEIECV

>contig55161 Frame-1R

MILAADFHSFAALGRVRARLEFKYACGATRIIRFCLGLRPCCIFEQLNDKMHHYKTLHRS

RYSLRSERTRQYL

>contig55305 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66899.1|) 9e-16

MADSDASSGSSSSSSSDSVLIRVPLDQNRRQKLRAQLQEDQRRQLERQLSAA

>contig55529 Frame-2F|Blast-sporangia induced predicted protein [Phytophthora infestans T30-4](gb|EEY57562.1|) 7e-16

MSVMYVKARRDSFISEPSTPDAFPDSDVLTPQGGHGYTPREGS

>contig56083 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60340.1|) 3e-64

MAATSEIPSELRRATYVKTTDLTPGSQGHNLVLQVVSSAPTVEKKRFDGTISRIAEVVLA

DETGCVTFTARNDQIDMLKDGQVVVLRNSNADIFNGFMRLNVTQWGKLSLHPDGIASTPP

PPPSVNTDNNISAVEYELVTADTHDE

>contig57013 Frame-0F|Blast-CCR4-NOT transcription complex subunit 7 [Phytophthora infestans T30-4](gb|EEY63848.1|) 1e-104

MLSARPMPADVEIRDVWATNLDETMKTIRGVVTKGCYVAMDTEYPGVVARPIGSFTTSTD

YQYQTLRCNVDLLRIIQLGVAFFNEDGSYMEGVPVWQFNFKFSLSEDMYAQDSIEILKQA

GIDFAQHEEKGIEVARFGELLVPSGLVLGDHVKWVSFHGSSDFGYLLKVLTCAPLPAEEE

TFFDLLNTYFPATYDLKHVGMDFDKVGGLSRLAEDLKVERIGTMHQAGSDALLTAATFFK

MVEVFFDGKVENAAKYSGQLYGLGNSIANLG

>contig57202-0 Frame-0F0

MPAMRSRSTMELKNRDNPEFRKC

>contig57202-2 Frame-1R2

MAGIVSSCKGDKASAGWSLSFRISV

>contig57295 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62998.1|) 7e-10

MSMESLSNAAYMTYFLAAKSIPVVAVGSSVVFAISP

>contig57318 Frame-0R

MGRGLTNLPTSVPFFDSCSYLECLRAHDKARLCSEPHLFR

>contig57448 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53195.1|) 1e-106

MQHLEQDETLLHVVDDVGNDEEEVEIFPARSSSSARVSVHSSDRLSLTPLAQRRCVSKEM

LEQMPTLSIDARYHDVAVCKPFGCFYLMQLIEKSIQVGALFSPKLYVPKEVWQQDRVRLA

GISLKVEVFHQLKQGLERISHALPILSDSANAAFVKELDALLKLAGQERMHLTRLFPFLP

QDKSDLTPQMMRRASSSEVEVGSTETSSSGIYIGKLTNLAFGFGRMVKKQAISAVERVGA

APIISVSIHELDEYAAVLCMFFNSTRSI

>contig57787 Frame-1F|Blast-hypothetical protein PITG\_01583 [Phytophthora infestans T30-4](gb|EEY61306.1|) 1e-16

MASTAQHDSHSATSNVVPLYEMRHGISSHSNALMCAAKC

>contig58232 Frame-2R

MVRRNHDYTQPLRTDSRSLARTFSFLQSSAANSYLSN

>contig58401 Frame-0F|Blast-Metal Ion (Mn2 -iron) Transporter (Nramp) Family [Phytophthora infestans T30-4](gb|EEY67411.1|) 0.0 NOT\_ORF

MSIAYVDPGNLESDLQSGAYAGYQLMWVLFGATAMGFFLQVLAARLGVVTGKNLAEMCTA

VYPRWASLTLWVMTEIAIVGSDVQEVLGSSIAFQVLFGFPLWIGCLITGFDTFTFLLLHR

YGIRKLEAFFLTLIIVMLLCFCANFVRGDVALNDVLSGFVPRVERYAVTQAVGILGAVIM

PHNIVLHSALVQTRQVNRQNDLKVREANKYFAIESGCALLISFLINMAVLAVFAKGFFSL

DCTASYEMNGVNTACVPHAITSGVTYGKCELVSGGSGMCQEIGLSQAGIALSGMLGKYAD

TIWAIGLLAAGQSSTMTGTYAGQFVMEGFLQLRLSPWKRVALTRCVSLVPAMTVAILSQQ

NSANSDHMDELLNVLQSIQLPFALLPVLIFTSSPDIMGDFVNGKTAIMSGWIMGGLVCVI

NMYLFLMNLEGLALGA

>contig58856 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62434.1|) 1e-18

MTVLPRHKSLTSMDYSVSTQAYVKLTLHAAKHPAYSVCGLLLGRVTENKIEILDAVPLFH

HDAPLAPLLEVACA

>contig04531 Frame-2R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60832.1|) 1e-35 NOT\_ORF

MLVGGLSVAQKKRVTIDVKVVANPSILFLDEPISGLEIGSALIVMRGVQSIVRTGYTVLC

TIHQRVFRSLNSLKGFSYF\*REEYTAYFGDLGDDSVMMLEYFESSPGTMEIRPQLSTALR

RWLRGASCDY

>contig05042 Frame-0F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY63962.1|) 0.0

MPTTDGLHRWVRQRSSKREVRIGGRDSLESDPGGRLSLSRYLDATERDSNLSVGYIRVRD

SMGRLVLNESDVVATDFHYRINIFDGAGSSELIMNLEGVHNLPFSDKIRWFTTEIHRLWL

PWESGHAELVIRRDHLLQDSFELVAAMKPYQLRQRWRVVFDGEPGLDAGGVMREWFTLLF

DELFDPSFGLFVHTVGDERSYWINASSDLLLGEEAHLRYYEFAGRLVGKAILEEHLMPVH

LALPFLKHVLGVPISFSDLQFLDDEIYHSALIVKSIQDIETLCLDFTATRVVNGHPEIVE

LVEGGGDLVVTNENRLRYLDVLFKYYVLGSVSNQLLSFLTALYDVVPEGLLKLFDYQELE

LLMCGVPSIDVKDWRKHTDFVFFTHNVPSDLELNNIQWFWEVVEKMRNEDRVRLLQFATG

TSRVPAQGFKGLISSDGRVRRFNVAFTGMNQSLLFPKAHTCFNRLDLPIYKSKRVLAEYV

KMIVQMDITGFTIE

>contig06137 Frame-2F

MVYFNSASGSDGTVLMFWRLAMQEMLRNERKINQLPRWGRRRRGLYAIKRRRNLRRRNDV

SIATCT

>contig07390 Frame-2F

MSAAVSASNNNNNSTQLSVGFCFIYCFICPWKNLHF

>contig09640 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66335.1|) 0.0

MDKLDDKPADLKVLSNRNESILKAVQFSIFCEELFYTLMKEALHDASKWTDTAYDISNYD

VKKHNKDDSSSSGTHISVLHVLDDEIHLRVNERYHLTIKLIDMESIPKNSADQTEDDTKT

EDDNFAAKEEQTNLCYTREEPQKVGSVSLSKRSSSETQCAASSLSAIPPSSDEAYLTQTC

RYAVLLLQQELRTRHGRNDISRALLYTGLNVSAMGGGTINLSNPGGGVAGMGHANETYKL

NNGPGTLATVLKVLAHNLLKKEVACFLDEISSVLSFQKQQTSASTRILDDGSLQPICDSV

RGIYLAYRWKTCAFDSTLSAFDLVIGKNFSTEVLITGARILLQTGMASQSEASGVEGLRE

FVKMNVCSQVALALHQDALSFGLKQSSMNLDRTSVRLVVAGEWDGSCIGEGRVSDTRKVG

TVFLRPYFSCDGSLAIKCSLQAIDTSRLAPVQATLSRSAAGEVHKLKWRRIPGSSDTMKL

LWLLQRTGVLKEPYKETIKSEKAPVSNGIEGLSGKGTR

>contig11519 Frame-2F

MNLTMNIAFQIVTPPNLAPTIKLVSPQIANEDTRPNDTCGLYDRELPIRNQALPLEY

>contig12253 Frame-0F

MRLFQSAMRASSPLLKTRSIATNASELRSVVFKDQLRTVQMADSKEVVLPGGRDLFPLLP

KAFAGIKQVGVIGWGSQGPAQAQNLRESLEGSDIKVKVGLRSGSSSIAKANAAGFSEDTG

NLGEMFDVIKESDMVILLISDAASVNLYPKIFPLLKPGATLGLSHGYLLGHLDSVNETFP

KDINVVMMAPKGMGPSVRRLYVQGKTVNGAGINSSVAIHQDVTGNATEIALGWSIGVGAP

YTFYTTMSDEYKSDIFGERCILLGGVHGLVESLFRRYVQNGMTPENAFKNTAECITGPLN

AKISHDGIKSVYESFKGEDKIIFEKAYTAAYMPCRDIIEEVYDDVACGNEIRSVNHAVAR

HDRFPFGKIDQTYTWKIGEKVRAARDGTFVMNPFTAGSYVAYDDGSD

>contig13030 Frame-0R|Blast-nuclear pore complex protein, putative [Phytophthora infestans T30-4](gb|EEY59245.1|) 1e-58

MSFGGFGSSNVPASGGFGGFGANGSGAGFNASTTASPFGGAPTTSGFGLGTSTFGAGAVK

PAFGGFGAAAPTTGSTFGAQPSTSTGFGGFGTSAPPQTGFGATANPATTSGFGASSAYGG

GTTTGGFGISGKSAFGATSPFGAKPATSP

>contig13654 Frame-1F|Blast-40S ribosomal protein S4 [Phytophthora infestans T30-4](gb|EEY60774.1|) 1e-107

MPRGPRKHLKRLSAPKHWMLGKLDGIWAPRPSSGPHKLRECLPIIIILRNRLKYALTKQE

VTMICMQKSVKVDGKIRVDPDFPAGFMDVVELPKTGDQFRLLYDTKGRFVLHRISDEEKK

YKLAKVIRQEFTKKAIPYIATNDGRTIRYPDPVIRVGDTVKIDLETGKIVDHIKFEVGNL

VAITRGRNAGRVGTLHHVE

>contig13759 Frame-2F

MCLYGFNLRCQSSLMRAIFHFTIVINASCVRFEKWQKPCESHHLAGAWSVTT

>contig15047 Frame-2F|Blast-dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69318.1|) 9e-91

MTFSTEATLLQRGLQYLDKSDEKRAGMWLVWLFLVLMRWIVGLHSYSGEHTPPMFGDYEA

QRHWMEITINLPVSDWYFNTTSNNLMYWGLDYPPLTAYISFLFGHAADTMDSSMVKLTSS

RGFESATSKVLMRTSVLLCDVMLFIPSIYYMSSVLYGSEQWTRRMTFLLLVLLQPAILLI

DHGHFQYNNVCLGLTA

>contig15623 Frame-2F

MPEKGIDKKTSFVLTIVKPGCRTMKILSLVALSDQQIKVPLEGNQGFFSGANYNVLRSGF

R

>contig16491 Frame-0F

MVLGKYCFNEEAFSEEVFEVGSFLESCRARSSMETIHQDLKHFQAALENQLVAIINQDYA

EFLQLSSKLKGVDEAVSSVRAPILEMIERVDNVQHTMSALNSKIQKQLLMADELQQQEKS

LKISIWISQKLLLLEDLLDAELPMTSDKVELNHCISADLEDSGDEEFENFERIKKTISST

NAVEGCAKLERAAQIFVQLDLEFMKAAHLGTN

>contig17157 Frame-0F

MEDELHPVMDTETAASRRPLGESKGLRRDRLASISSSGYSDASSVDEAIGAALELPPHLR

DHLVSVKHRNLPPVTSIEGELLPPIDHMRPPPMRIPLLPANMKMEPIPGINQRRQTKRVI

VCGAGIIGLTTCYYLAKHGHEVLCVEKERGVATQVSFCNSAFLDPSLYASWSDVASLRKD

LRSHSATRNTATLSTTSDGNSTARPAASFTSRLSTDVSISERPSHWKRSVREKPIQIEMS

ALRDAKFWKWGLRFWHNSRKNRSNEHSRTNRELGFYSMLKLRELQANTKKGEIVMDQTAQ

GTIEIFRAMSELQVTMESDRSVHLSELGMELQPLEAAQARNLEPALRSEMFASGAILSAF

GTSGDVHKLCQSLYRLCMRQGVMFRFNTEVQHILTDKTSVIAFQTRRGSLIEGDEFVLAL

GNSTAPVAKRAGVKLAIYPIKGYVLSVPVAKGFRAPLYNIYAGGQALIAPLGTSLLRISG

GVDFLSQKKTDDESPRDQQKRYDWLLKQATLMFPEGYLDVAKMQPHTCWRPVTADGVSLI

GRTKIRNLYVNAGHGSKGWTLSFGAGALLADEISGLRPQLDMSKFAVDRFGFFG

>contig17395 Frame-1F

MQFECLRWLGKHFQRPLRVLQYAASGIVSNQLLLLGLQKKQWISVELRALLVELRLDHIN

FLMYENHLFQFWVNLACIRNQEAEAVQILVEQAKTVYLSYNYPILAVNSIRLELLDTNKP

KNIMLNAAANLNTHLRLNDDDFLRDTRRQCWTKFTEGLQDRPRDEFLTLQKAIINWKTSG

KRALK

>contig17782 Frame-2F|Blast-hypothetical protein PITG\_06324 [Phytophthora infestans T30-4](gb|EEY69818.1|) 7e-31

MNRPSMSHRSSVSSSIAGAPTALRNDAILYLTILSARDLKKVQTLGEQDPYCSVYIATGG

KEQEKAAFKTDTHDNG

>contig18358 Frame-0F

MMEKLMQLEGSKGCAAHQSL

>contig21242 Frame-2F

MSEARKALESASRRGLQALAKQLELCKGNAKSDVIVSHAIKFLDSHPQDGEQLLLNVLSS

NGSVTPVTSPIPKGKIAVRESADADATSKVDTVVKKRKSDQMQPDKEPITSKDSIETKIP

KKEILTHETIIQKDQTTVAETTTPMRIAENNESSIKALSTTKTSKSSPPTKPKTSPLNKS

KPSPATKPKTSPLNKSKPSLATTASPPTKTNTPPSNKMLLQTTTKASSPTKKKGSFATKT

NSSPLSKTPPSSQTPSATKTKPSTKVSPSTEVSPQSKVSPVTKKSRSTSTLSTNEKPSPD

KAMPISNTTPASIEIKKTNATAKNKVVTSKKSALAEALKSSNAVEALVNANPDITFKGEM

RVRCLITGHEMKADVGIINEYIRGKRYQKARNLKLSFAKYAPMFVDHPDESKPDMLWCNV

TELAIIRDENCVKSHISGPKYQKQLPIWESEEAAKKKAA

>contig21655 Frame-0R

MALGAIHLWLERSLPEGTLRAKGVLYVAELPRFRFEVHWSGNRRLHVENTGEWVGTPKTQ

FVVIGSNQYSTESGFDKAQVVEKLETCLATIAGLSKKEIESSRTASAARLATDERFETLG

LFSEVTTIAFQLVCPVSALDETMLRHHHHVNTNELTKRLVREVNASGGGSLLLYMSLASS

DGEHQDTYAVASSVGPASVLSMWKDLDLRAQSIVDEVKQKLAGCLCGF

>contig22171 Frame-0F

MINMASHHFLSSSSAQPRSVSAGLKLDANLDELENRITSPRSYFEAGLRTGSFSKGPTTS

PPLKTAKRVGARDVRMWVGTWNMGAADPFEDGKGIIDEQRSAAMLVNFLPHGYQLYVLGI

QEGLAENVYHAVEAYLNRNEKGTRYYRMEMKNSKFLVNHKNYPLDAVIDAVHGRGDGAFV

GTKFTGIAVFYCAAIQNKIKLIRAGAHKFKLTSGSKGGVAVALMINHTTIVFVNCHLDAR

NDAYRREQIRNLNASLGRVMGHYSFDLTEQFHHVVWMGDMNYRIVLLDPQMVLHMLEEGR

NLELHDKFDGLLNDRRNGGVFEGFTEPHKFPDFYPTYKKFPKRGPVDETLPLWPSLVWRV

LYKEPFYKGGKVKKRVPGWCDRILIHSLLVSDSKLVPEKISDPTSREALPPFIDNYRSVN

HGVGMDVSDHSPVYGTFVLSFPQQDSDRQASGSPKPFLLRRNSLSLSTVKRMNDVDRFSS

SVNGSYFDQARVIQQMKAQHRSVSTVLRVFNMVLVWGGARSVVPKKTRIVAPLIGEDSKQ

CDVIGERCQGSNGLNLSLNAVIQHTRPLEQLHMLLWVKNESVNGHCTLSLKRVARQLDGG

EVKYRVPLYNDSMRVHLDGHPLLVVFSVRSKTFAK

>contig22517 Frame-1F

MHFQRLILSADQRQQLIHEAETVVRETLVANETFLSNKATFKDPRWKMVRVKDGLQVYYH

QVARLKNPAKARRPRYSSPYIPNGVDMSCKTDASDASSHDHSHDHTDRVSPSGTSKEARQ

MTGFQMVLYGHVIGTLDDAMFGTFAPTNESWMWRSSHINDRLDDARILASIQGPTKEDPF

RYLGVKWFVKERPAVLTGIMQQRDYLVLEATGLTHDSKGERVGYYLMHSILMPHQVPELT

QLGLLRGTLSLCFIDRQRGPNKVEKYCRSFNNPRGKLIDCVAVAVTAEALIAAANIVEYA

YVKKLTWLIKHKENLGLSSNAHGSRLKHCESCWKSFAKFSLSTAGIRAECQICHRVVCSK

CHVVKKMTVDVSITGAVKQCPLRFCLQCFQRAKELSVRGMLSETEARSTEGVSTY

>contig24133 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56938.1|) 1e-94

MVLGLLLRDEEERHLSFDFESILPEDGDDRMDLGEHRSGAIVGVGGATFGQQAAKKDFKR

GTVVCRHWLRALCMKGDNCEFLHQYDMSKMPECRWGMECQVPECPFRHVPDEERVECAFY

KQGFCSHGSSCRYRHIKLAREECPETADFALQAKAADEENVKRRKAQPV

>contig24609 Frame-2R|Blast-histidinol-phosphate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY66078.1|) 9e-37

MANRGIVIRYRGSQHLLTDCLRATIGSREENDRMLELLIEVSGEQ

>contig25585 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66062.1|) 1e-167

MRQRSLYATLRCLLHPAELEQMEIFALQQCLIEGGATIVESTIALESSTVTHIICHPKAY

RSFMELRNERFVALVRPEWVFRTFLLQQLLPVDRFSPNMALIFSTLTISACAMGKEDPRR

VINSLITHFGGQIIDQNEFCGGATHILHLDDSIVDSNFVNEPGAEKLQTLCQLKFSKRDL

VQGFDAWKLHLSTDSVKSTYKLPSCIIAYIGQNAGLDRQYHVKLKWIEECVMRRNRELEE

RFSPTAFEVARTALKSKPRSRKSCPEVQLEELNLGKFAQVYQLERTEHGIESSMVRKWSF

EKLEALKKNLQGTIVLLAQHLAPLLREKLSDMLKLVNAKVANVPFGDSYQEIVSKVVTKA

SFVVCRYRGGFEYKEAVRQDKKVVSIYWVLAGLSQASNPSPYNEIIQRPVKYFGSINGMQ

SFVITLSGYSSHSSPTREELQIAIHATGACLLPVLSRA

>contig25606 Frame-0R

MKCCTAYPIPSNSMKCCAAYPIPSNSMDLSEIPFNEPVIIWSVYKQLSLQNPLGSKKARC

LSDNRDIYEQLILRHVRDDKVAIQSVRNGRYLHVRTNGECVFDLKQPGPRELFSMETDSS

CALYFVSQHTGTTLQCTPNCDVRCVNDNRLGREAWRIVEPRTMTQVVGQLQNLAQLSHKL

LNLELARSGKTREQIEQIESEIFDAPLATVTTVNVALEAKKA

>contig26584 Frame-2R

MALCQDETWFRRRRFIRITVQRFQAYMSRRSLQHPRQDLKPIAMQSCLLVCHHSHVLNLG

P

>contig26629 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55023.1|) 1e-15

MGGYRGWMWTVGRANFGENEKKPAVREALERMIEIICTDRVAADQFRFSRSVRPQV

>contig26830 Frame-0F

MLQRVASVSDQWEFLNLILRAIDLTITADKVAQWKNSGKNSQFSFIDELVAVQNPRWNSF

VVEVVRVFRIGKLLPGHQKLDFTTGDARSVKKIFANFVEQEDWQ

>contig27424 Frame-0F

MKAQPRSTYAHTFRHSEEAV

>contig27626 Frame-0F

MHAWRSLTRSILVFTNVLFLLLGSVLVSIGGYMASLPALTQFSDGGVASSVIMCGSLIIL

IAMLGCCGAQWESKVFLFPYAILVLVSVIAQLSLAGFLLHVHSSLVEVASHNFDLSILAP

ADQETLRWINRRFKYVYYGCGFDVDIHGTNSHNYDLHASCTNPKFRWFATFVEENCPIGH

AQLQANSDFLKCAGPSFSLSTAMTEHTMLCACETRMISWVNDQSLLVAVFVFVIVFLEIM

LVALSCYIMHARRYRRFGYQEITMPVRPQSYTPHPRNYFGQSGQRQLLNSQPESTLYHPS

GGENPYAAAATKAAKKGKP

>contig28238 Frame-1R

MIFARRLPSLIWVDMHRTFIIAQMKGGLSQLQTQRTPYV

>contig28605 Frame-2R|Blast-acyl-protein thioesterase, putative [Phytophthora infestans T30-4](gb|EEY59172.1|) 1e-30

MCHGEQDQVVRFDYGNMSKEKLQAAGVKNIEFHSYADLEHGACMEELDHVLQWLQRVLPA

TPK

>contig29141 Frame-1R|Blast-Amino Acid-Polyamine-Organocation (APC) Family [Phytophthora infestans T30-4](gb|EEY59435.1|) 0.0

MQALRLAFWRKPLHLETLSHSVQEPKDAPELERTLGLFDLLMIGIGGTVGSGVFATSGLI

ASSYAGPAATLSWLLAGAGCLLSGLSFMELSCLIPSAGSSYAYAYHALGELPALIAGFLL

TLEYGVSSAGAARSWSEKLTHWMETQLGVQGPDWMKPQNSVLDVYAGLLTASSTAVVLCG

MQAGKVVINVVTMTKIAVVVFIIVMGLANFRFDRILPFVPESRVVDVHGKEQVAFGWSGV

LLGASASFFGYIGYDEVCCLAGEAKHPTRNIPRAVVGTILGAATLSILATLALVGMQEYT

DINDKESYGNAFTSIGLDWAATFVVTGEVLTMPITAFISFLAQPRVQYAMAKDGLLPATF

AQLDVNGTLFRGTLLSGIGVTLLAMFVPFHVLWNIISLGILVAFNITNSSLLLVRLSTAC

LYTTDDKPLVQSHGAMVVAYLVSSFMAAYHWQKGVIATVPVNAMTEWPIFDGYMRAFGPF

VAAFFTVVAIALVFALRDAEIKATVALATETAAQGQRCETVLNSKTQLTLNDANRQICSL

DREDNDTDSGNENDGQGEQLRVQEKKSASKNDTSTSLDDIDDIKLDESTFRAPLVPFTPC

VAIFFNWFLFAQMDGMSILLILLWLLLAVVVYFSYSRFHSLAFQQTQYHQLEQQ

>contig31122 Frame-0F

MGPRGAGRRLNDQERMEILEIIQRESKVKNVDLAKRYGVSEGAIRKLKQMKDTIRSRYHM

GNEHNRDKRKRGGFKRNAPFEEELYQWIVRMRESQPYQLMPLTQTAVRQQAIILSKNYEK

MTNFKASPGWFARFCSRHRLDPIITGAGGGDDVDTSAMTPAPPDISFVASVPQSVTAPPA

VSVSMTTGAPDETEFFMDTLTAAPVTPSQALEMINATAAIVDESKTDTPSINEQLQQAAR

QHNEAALR

>contig31373 Frame-0F

MIMRRSFFVRCFEIAKSCSKR

>contig31423 Frame-2R

MVTALQKCFAIDWLRLVADVIACYESMSTAVRLFSVLGAIRRKATHRNECMYFDYRWLVE

SYGTTSMFLS

>contig31610 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66218.1|) 2e-50

MEKANEKVRDAAKKAYIIEVRELVEFVCRRDPRVQKFNKTKEQEKAQEMEKQRLDYESLK

REKQAAYEIERRLFREHQDELWATSFMKTSHVADQDIEVELEKLRKKLDADVLACDLCNK

VFKSTNQLQNHLFSKKHR

>contig31665 Frame-2R

MAALHRSRLLLLLGLALLSLVANVHAFEFNFGFNGGRHDQVKEHEHVDFYEVLGLTMEAS

EAEIKKAYRKLSLKYHPDKNKGDEGAENRFHEISRAYEVLSDPQKRQVYDLEGFEGLERE

EKSADRPSSPFDAFFGGGGKQRGPDASVDVPVTLEELYNGATKEAQFTRSVICRKCRGTG

AKGGKTTTCKKCGGAGQILVQQKMGGFSMQMQQPCPKCNGRGKTFKKACPFCHGHKVVKE

NKVLVAEIERGMPSTHQIVFERESEQRPGIVPGDVIFRLHQVPHKNFRRVGDDLHYNLEI

SLEEALLGYEKPIKHLDDRTVLLASTKVTTPFEARTVEGEGMPVHNYPSQRGNLLVHHEI

IFPMTLSEELKELVKTLLPEDDPTVAVE

>contig31881 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58628.1|) 3e-32

MPPEYRLFPVDTQGTDATNPFCIYTNDCLTPGANTIGVPTAYYKKERGHESWYQGLRYGA

NNNCQQVLSEKQKYE

>contig32127 Frame-2F|Blast-centromere/kinetochore protein, putative [Phytophthora infestans T30-4](gb|EEY58042.1|) 9e-08

MVDMIFTFRELGERVLTSFTTAQAEEMLTGMSTLP

>contig32211 Frame-2F|Blast-pyruvate kinase, putative [Phytophthora infestans T30-4](gb|EEY53802.1|) 0.0

MSMLRRLVFGSIRPSARGFAASASELYKNPRSSKFSMTKIVATVGPASEQLDMLQKLTDE

GLRIMRINFSHAEYDEALQRIHNLRACRGVHAESHANFNLRAVLHDTKGPEIRTGTMRND

KKIKLESGKSVVLTTDPAFERDGTAEKFYVTYQQLSNTVKVGDTVLLSDGLIRLTCTGVG

KGEITCDIHNTEEIGNRKGVNLPGLIVELPALSEKDKCDLDWGVQQDIDFIAASFIRKAS

DVDEIRAFVDKCIQKHWASQPEYIAPKIISKIENLEGVQNFDAILDASDGIMCARGDLGV

EVPAQKVLTYQKMMVDRCNAVGKPIIVATQMLESMQYNPRPTRAEVSDVGNAVLDGADCV

MLSGESAQGKYPIESVATMNTVIKEADQLLLLPNYQAKFQFEPPTSDVESAVSSAVKIAN

EMRAQLLIVLTRTGYTARKVAKYKPTVPVMCFTTDQKVGRQLQIHRGLYPVVSSCLDRSP

TTAEAISHAKKMGWLSPGDRVVVISGDKLSRDLGGEILIGVAGVQ

>contig32541 Frame-2F|Blast-villin-like protein [Phytophthora infestans T30-4](gb|EEY57241.1|) 0.0

MVTFTEAGKKAGLEAWRIENFMLVAVSATDLHKLHSGDSYIFLKTSDAKTGLTWNVHFWL

GKNTSADESGVAAYKTVELDNALGGVPVQHRECQGHESALFLSYFKETGLQYLDGGVPSG

FHEVKRDDFVTRLYRIKGKRTVRVEQVPLQSSSLSVDDAFVLDAGLELYLYAGKQVNRLE

KAKALDFIAKIKEARGGRVIVTFIDEEPENSAFWKLLGGMQTVMCSSETDEQHESIVKKN

TTVLRVNGSTSENLRVQDVTPSSGVLTKDILNTEDVFLLDVGDEVFVWVGKMASASERAN

ALLAAVQYLKKENRSSQTPMTRVVEEGETPFFTALFKAWTEPKKLEFGYQSSKGVATMQS

DSNVDVVALVKAASLAEEEIGLDPNGDGKHDLTVWRVEELERVQVPKEQYGQFFDGDSYI

LLHEVTLLSSKVMQVIYFWQGRLSSTDEKAASALLATFLDDRLHGVPIQVRVTQGKEPAH

FRALFHGTMIVHAGGKASAFANRNDEDSYDNDGVSLFQVKGTNEKNTVATQVEEQTTSLT

SGDSYVLVTPNKVYEWHGVGSSSAECEIASKVAARLRKDRDIEVVKEGCESDEFWKFLGG

KGEYAKTKSSFEAPHEPRLFQCSNAYGYFDACEIVNFGQDDLNVDDVFLLDTYTTLYVWI

GSGANESERREAMTLAQKYLTLVKSDGRDAGTPIMAVHCNSEPLLFTSHFLAWNSNLFTK

NEFLDPYETRLQKLKEEKEKNALKDLAGTITNEGFIKDQAVALPKAADASSIAAPRVIPF

LPTDAPVINTPYESQVIPVVSASESETKATTPALVPPKIIPAPASKSGTATTAPAIAKAT

GSAGETFTYEQLTNGVEGIDITRKETYLSDAEFHTVMSVSKEEFQQLPKWKQQAKKREVD

LF

>contig32880 Frame-2F

MFPILPSDTTGHELQTYWSLPQIRDLFAQFVKSQGLVDESNKKFVLLNDPLKCVLYGKKV

PDGGYPDRLSRPEMLSLLLSKCTHYHKIKLFPTHAAKLHGGFLQPISIHAKKHRKNSACI

KISYYQQFGINGIIFAKEVRKKWGCSATVQKCEDTNKMEEICIHGNMVNEVMEYLASKHQ

IHAKYCRVTYGKNTKPRKINLDIQKIDDSHV

>contig32989 Frame-1F

MLDHTMGAQGDFERRRAELYLNQANHNEEITDEIVISSYADSIREDGVLREYLLQGSLAF

VMHQTLFVHGGIIDGDKDASFSALGFVPNEPLKRFDSVLEWVKHLNAWYREQIQEWIDHP

TWNEDRSSRGGNKLIRYVEPGYANSVVMGRHLLPSGMPTLMPDEIVSLLSNSGIRRIIMG

HTPHGNCPTVVKHPYKQHGTCAEGRSSDVVAFEDVIMCDTSYSDIRAPDNRGSAASEIVV

DATGRVSISGVLEDGRHIKYDPDVDPWVGRWLQDGRMVKARLVDDEARDTATYLIFHVEN

GYEYTYKYLTATELHRIGLKRL

>contig33252 Frame-0R

MSWQYNKSTTCVENTPLVALLAHCQSPLARVGEPQNVGEYSFQVNKVVAHDLFS

>contig33348 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56450.1|) 8e-11

MTDEPGTIMHLKSAQEILPALQKRKHDLLCRTTERCAFKRSKSERVGETTVDPIMSSKGE

EVMGERVIELKLQSKIAIVAGLVSDLFDCMFDSKWETRHGALLSLRQILLSAQFVAAVEA

VRSIVDNHGSREIVD

>contig33502 Frame-2F

MMKSTVAGGKVLEIRVWFHDTCVLDATSTTDDEKKLVIQKGAELRGESRRGDDVEMDYAT

LGLPDGWKDLWLSVPGNTEENGYTFDGTRNSLVTSRSFRSRLDRMYYYSASNHEASSCKL

ETIIIVGQQKIADGLWPSDHYGLLSSFAILEDEKNVLAESVGKKTKRMEP

>contig34190 Frame-2F

MDRFNDAPMLGVGSDAVLAALATVVRKPKRLSSVTRASKTSTSSSIASIKSLRTARGSWN

KDTQTLSKGHCTGTSHFAAVSSASLSSTDPQTVGIGSDAVLINTASVKSKRRKISLAKAA

PTLPLVAANPLVDDASAGDDTNAAQPPHINCSSNSRLVSATSNSCADNNLSTQISMKFDG

DTALSTSKSKRPAVTFCPSTNLTQAPNSGDLTSIAAPHAESISSFIVQYPDVNNFSKDSL

TGVTETCTGHEKVKRSLHNSDDKNEKLLPDVQFYDFEFNQAEDTETIPFTALQPFKRQTG

SVVVGYWFNSDRCGETEFVKFIQKAVKRIQ

>contig34334 Frame-1R

MADPDLPQPINLDALGTADDWKHFSFPPATCFITHPSP

>contig34464 Frame-0F

MEPHTVDAMMAASLSLKGTLNYERFGQKLGVERNVLKLIGKSDSDAGYDTDYRVAGSYFT

CMESTCDFKEAKDVFVFIYDFFPRSNCSALGHYEREQCGRLKQ

>contig34558 Frame-1F

MDQEAPTSNGAGKSKSGFKLHVPAINLPSSLSRKKVATVNFSTIPNVIVYFKDMVASKYL

SMNPSQSHGEILASFSIALCNMFDRLPPDLVA

>contig34886 Frame-0R

MQFLHLQYATAIGKVKDACAHLNYVVDKVLPALPSDGDLYPDSYVSVWINVLEVTVYCCG

VALNACPVDKVVGAEIQVKQIYPSRILLEWAARVLKSDGLRYQINQCCSVELRAKVWPFI

LRREFILSFSNQLVLNSTTLPWPSGYGRQKGCQRVLRNASQIMLFWRLSVQRL

>contig36268 Frame-2R|Blast-DNA-directed RNA polymerase III subunit RPC6, putative [Phytophthora infestans T30-4](gb|EEY57500.1|) 1e-152

MASKAGAPSIMSTFLGLLRNYREPVTDAEVRDYFQAKSGSGYEQLPDVINALLTEGKIKI

FTKGSVLSYGIVDAEEAERVRGLTLEQRLVLQEIERAGNQGIWTRDIKSHTNIPQQIVAK

TLRLLETRHLVKSVKSISSKNKKLYMLFDLVPSTEITGGPWYNEQEFDHVFIDTLSTFVY

EVIKASGMSTLNAITDKVHASGISKVALGPEEICSIIQTLMYDGRIEEVRSVRLTPGASH

EIQYKISSQITTFNHLSETPCGVCPVYEQCQEGNVISPRSCLYMNKWLGLKEHDF

>contig36376 Frame-1F

MLLDRIHFSLLAEEKDQALLGLQEILRIKSREVLTYLIPRLLVKPLTVSAIRAVPRVAQA

TGAVIHFHIERIFAVFFARNAELLEGKSTNAVNIELANEIRDSLRNVVRCVEAPGVHWLA

IELCKYCESGNVFDRTLAFELVADFCSTTILPYDDQAPLFLKQIILHYNDQNDAVVCAAS

AALKGMNVTTKPEQFAQHLDFIRQSINSMVSDARHRKGGVGDGEYLLPGFCIAKGLEPLL

PCYQWALINGQPELRQTAATGLGEIVELCSASVLRPYLIKLTGPLIRVAGDQIPGHVKTA

ILQTLEIILLKGGVALKPFLPQLQTTFVKALNDVAVDVRARGASALSLLVTLSPRVEPLL

AELTERLRTTTGGIREANLEAISSVVNCVGYKLSAAGRSALTDALDEMLNSREDALRDCA

GKCLASCVASTAKNGDLEAAQKQLLYYSLADADDVQAEPWQRRQSAAMFTALVLHKHSAL

LTTDITVPLTNMLVVLALDEQIAIRKNALNALGYVVKHQEHLKSVTTLVPVLVEGVAHKN

KDVVRGALQVIKAAVKRSPDQTREHLTTILPAVFQLIKSNNMAVKMPAERALLHLLEMHS

RPETLAELSRSSIADAKIIGEYARRVLSKLNPDSGDESI

>contig37209 Frame-2R

MDWSTATRRITECSKSLLCGNGGLGDELRVLQEYLEHEDVMVAYAAKEELLKVLASGKIA

NIYGFVHSLLLPPPFAWVRESSGFRFQLLRQLIQMKKEVNPNEDRSQSGSSSDTWNQSKH

YANVQIMLKHLNQIKTMVRSVFISTGCILISVPHSVQFEALVFVREFVKCLRGMKTIIYH

QVEFSDMISGLVEDVFVMMNYGFQSTYVSCAVLRLLSDFLEVLKYWNDRKDDNNWTSVRP

VYLMSLKQCTVWVLQSSCSTTALHLLTDKERNRSHENFIANMSFYSFTQHWLLFSSRVGV

AVVEASKPQTNDFSLELLPLTGACKKLYAQLPSRHQLFVVLAEQDSVLVKVLNNVTRIAD

GVDDFRFLLLPEFTELLAEYDPDLLFADLIDTIRHDHLILLDLLISNETEMLEYLMQHLR

RFCKRWTTSKQKLQSYNRLEDVMGVLIRLRLEIDRLVAADLFPYGAKPLTRRLMSIEKLS

KWRKKLIIASSK

>contig38002 Frame-0R|Blast-hypothetical protein PITG\_08495 [Phytophthora infestans T30-4](gb|EEY54925.1|) 3e-57

MAMQQPPLPPKQPPADSIPYLGSRISLVSKTDVRYEGFLFNIDTRQSIVALQNVRSFGTE

GRRADHVPPSPHVLQYATFKAAEIKDLHVCEAAPQPPANPPLPSAPPLPSAPSPPVVAPA

SPRKPTLLTPGSVSSAHNETPEPTPARRHNSNRSAQSNQARTIPGMGGHLLKRKERRAPG

GTEGTKVVPEAASGEFNFEERLHDFDKQQEFVKLEESTKKDSKGSYQKSMFFDTISCDAL

DRLEGQRSRMSGAEERKLNTETFGAVGLNNRRNLRGRGRGRRGGSRSSHWNGTRANGGSG

GGRNYHGSSSQHPSGP

>contig38330 Frame-0R|Blast-15-hydroxyprostaglandin dehydrogenase [NAD+], putative [Phytophthora infestans T30-4](gb|EEY63919.1|) 9e-35

MGRQAHDAIPEYTNRTGGLMPVKVVVDAFVAAMRDPNNAGRVLRITKKATMYHDFQGDKI

LFPTSKL

>contig38837 Frame-2R

MCVILPPNRLTVYDAEDIENDDDSEVCGETDEN

>contig39056 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53073.1|) 4e-67

MAQRQDQIPLKVAFNGDIHRTRVDLRSLSLEVMTQLIAKTFRLPVGEFVVQFVDIEGDCV

NVTTDAEFEEALCVLLNSAKPLQSLKFSAATRHQIEFQEQVTAPLVKSVELLMQALGTML

EQLKGDANFSSCATTSSAKLAQSEHVDSLKTAASGFSTFAQGLVGQINRLIPEKKNEETT

AVAAAASLPSLESKQKQSLLEPVMTTMPPVLMTEATPAQKLEELPPNTSSAAFSEKEVKW

AEQLSIVRGIFPNAKPAHVIDILEKRDGNLNVVLNILTEEN

>contig39838 Frame-2F

MWERWADFPIEICHHQVVAIGDKLLVLGGEKNCATSRHMDLYTCSTIRNADGSLPTWALI

QPSNMSMPPSRAFHTASVVSVRRNSVVFMYGGKSVENEVLGDAWHLSVDDYKWFKLPSTM

SLNPGPRLGCSSAVIGECVYLFGGMDRDESYRSDLWRYNTFDRLWHLCHDDQFQGAKDVA

SSGSMGKFQRKFQHMIPEGRVQYSMCSDAGSIWIFGGVNKVNTLLCDMWYYSVSLQHWNQ

IQMDTQG

>contig39944 Frame-1F

MASAFVSSAQIDAVAACSTLHASSGETTHKSLLAVAQSHLEGNLWSGGVALFDVVSSERL

CELQLESGVASLAWCSSEGNVIALGCDDGDVRLASLSTDSTLSFVPFGASSNDDAKITGW

GHDDVVTGVSVSQIDKNQLATSSWDLT

>contig41558 Frame-2R

MAKRIRATKQEGFAPASAVSSDLAKSAPKSTHTCSDGKHVMLPAFLSKTYEIFSMPEFLQ

VCGWNANGDTIIVSQLETFVATVLPRFFKHRNFPSFVRQLNLYGFHKTVLDSKRLEFQHP

YFKRGRPDLLHHIKR

>contig41666 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63948.1|) 5e-09

MVQLALLSAAEIRGTPLDIVAAAVYQNSKEAFGITTI

>contig42300 Frame-0R

MSIDIVLHLCGSKSQSQNPCISIGTLLFYLFPIDI

>contig42533 Frame-2R|Blast-Sulfate Permease (SulP) Family [Phytophthora infestans T30-4](gb|EEY65009.1|) 6e-74

MFWLRELIGMQSHQPSERYALPKRTWNQQLQHYAPIFRWLPHYNIQRDLKYDLVAGVTVA

MMLIPQEVSLSIIMHVPANHGLYTAATAPFVYAIFGSSTVLSVSSGSEVSLLVGATLENI

QDVHERVATSTLMAFLSGCILLVVRILNLSLIADFFSRPVMGGFISAGGFLIMLS

>contig42982 Frame-1F

MKTKTWNPESAIAVARRVFRDDSRPQKHQRHVHGSRLKDDQDIAAVMSLLLYDQRERVPL

TWRGQFFLTSAFRESVIDHVNRFLLERTDLVGPQGSSFETFYAVSKRCNTSV

>contig43268 Frame-2F|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY68213.1|) 0.0

MENASLLRTTSAAQSPSQKLSTVTIASSLPTSTEAHFPAHFFVEGSAFSSFLGLATTMTG

ACILTLPSVIQAVGQLPALLLFGISAWLAFRACEMLTICCDAAFAYSYEALSSRLVGATG

VWAVRLLTVALLFGAIVSYMVIAMDLFEPFLLGIMSRRAISLVFMLLSIPLCLPETIHEL

RFANILVLLCLLYILVALAIRTIQNDPDFAAQIPKNLADEFNSEVAALAYALPIVTLSFT

CQLNVPRAYQEIRVKTQMTQVHKALMSWGLVIYLFFAYLGYACFHGQPPSDILTGFKTDD

KLINGARLALGISMVLKTPMTFQPLRQLVEICCLGHDRESLLFRTGITVAFLLIAHLFSV

SSRDLGIVMAFVGSVSGNVLALTVPGLFLYEVSRGYLVERDAFYSPRLALSFVFAGAVFA

AASLTYVLYHALIS

>contig43574 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63049.1|) 1e-06 NOT\_ORF

MVKIDKGASTKQVSIRQFFLCYRFEPHGGSMTCQLDVF

>contig43871 Frame-0F|Blast-RNA polymerase II-associated factor 1 [Phytophthora infestans T30-4](gb|EEY65838.1|) 5e-58

MLPSEDVKSKAMISREERALLCGVNKKMQAGNELIQGSILLPTGSADDEESNDREKFSCL

REYLMSVESLDSRESQHIVFMLNPESDQFTYSDVLNRIKLRKAK

>contig44122 Frame-0F

MDRFRLDGVDQDGVDTVEPMRPSSFDMTFSLGSYPSAQGLSRGSDEKHSSNQDEIDNKDT

RRLLRGGEKGRLHMDKQLESVCPQNVEATGVMSSSVNTRATVSPPVSSSTAHKDVANIAF

RLEEKAHEAIDAASLCGKVSWKLAKRTQDVHVYRPATLPLEEEASSKLYFRISCEMKAHL

GTIMEYLTPSNSR

>contig44610 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54879.1|) 1e-21

MRVLVGDETGLLKSIVLETKEQRILSNREHPQARSRGIQRLCWSSDGRDASNCQPNVVLA

RANGLVESYEASHGNTLRASRCQLGHGLLSTTTTAIHVA

>contig44665 Frame-0F|Blast-striatin-3 family protein [Phytophthora infestans T30-4](gb|EEY64163.1|) 6e-41

MGEAVHSVTYHPSRNFIATGGADSTIKIFQ

>contig45507 Frame-1F|Blast-guanylate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY62385.1|) 2e-52

MKKARGGAKVESLLIFSETKYAEAMRILLSRQEEGYEKKIRTLQGNVSKVNEELGSVGGR

EQIYKEQIEQMQVQTSQNMTERANFEVEAEAQRERIANLESMLHEESTTQQQAEPGRNSA

ACRTSSVATPGGIIDSE

>contig45598 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58056.1|) 7e-16

MLTEARRLLQRMTRRILTNTIVLYTTIFILGVAICYVLYADFIRTPR

>contig46252 Frame-2F

MIKKGRLRSHKRVAKLGPNLLYFLAVLEVVRGLCSDIDLTGSNVPFPMMRDVMTY

>contig46502 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69280.1|) 1e-61

MIGPYFAQVPLSSTMKAVAFAVAAILPGARGWTDRWDYSQRFAIAGHAQLYCDGENQLAS

CCICKAIVNEVETQLNNTQNDYVMEVVFRISEEKKQIKYSRSEVRILDVLDDICDRLPLK

LQGDSHRTKRIMSDACNGFVGEYEDELTRTFFDDFTPAKDRMCGGTLQVCSHADKRLKHD

DL

>contig46645 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY69205.1|) 4e-46

MEVKHHMRRGEKSIIKQINASNHILHDIMKSEKEAAKKQELKKILLEQKLQDPPLVRVAG

KYTKLERETPVSFSEELTGSMRTLKPKGHPLLDRFDSLHKRNLIQIGRPKKTRKAKVRII

EV

>contig47053 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60075.1|) 9e-16

MLDKRGQLVREIVNTSKAHTHFLAPYDQESRVCVFTGDMRAVFRAQRLVLQVLAGDALST

KRMVCHGNASAQKRTITLFCRRNTRMKSMKKKHPKTTILRGPIRRQQARRCQLDDNIEET

KHGLIARLECTSSDHETFSEEEHKDDRLTVARRLDSKQPSVPTAGRKVIVTLRRTSHELR

RRRTLATVRYGKPRVRPTKC

>contig47880 Frame-2F|Blast-cyclophilin B [Phytophthora nicotianae](gb|ACR82294.1|) 3e-91

MASPLISVLVVFLAALALKVEAGKKPKITNQVFFDVSIDGNHAGRIVMGLYGNTVPKTVE

NFRALCTGEKGLGESGKPLHYKGSIFHRVIPNFMLQGGDFTSFNGMGGESIYGKKFPDEN

FKLKHAGKGTLSMANSGVNTNGSQFFICTTKTSWLDGRHVVFGRVISGFDVLDNIEAVGS

QSGTPSKKVVITESGEHLGNDIVAVE

>contig48049 Frame-2R|Blast-reverse transcriptase [Phytophthora ramorum](gb|ABG66535.1|) 2e-12 NOT\_ORF

MYSLNQIHASCLKIKALYMRSSSNGARSTVSWIYQWIS

>contig48386 Frame-2F

MGERVRSLVYEAITLVIPKIVGAREPAQVLTSCTEVNRALKWVYLNADWIRKQNLPRYDK

DEVKDSALIS

>contig48508 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66319.1|) 2e-37

MYCVLSNGDFCIYRVETIHFTGNSPKLSILLHYHSLREQLVNAIVYNVCSSDYIDYNGSA

GFILEVLYQQKNKKSQLFCAKLLLKAESCFGKTRNGSEPFCVQSCEVYPVCSSLMSATEK

EHVEAASISSVNETPGCHFESQDDPAGLPVKVAVTNMANRLNVFMGSGSLRRQSVASQSN

TDNVEGSLTQTA

>contig48694 Frame-0F

MLIISIVFHNRLVRSRNALSPSFEQCFFLMNCSFYKLLYGINNQIKTLRNSIKMRVLLCC

MLLAFISSTAAENFLDSFINSVKDATSTAIDDAIEKGMTKATDSVFNFPNKSIDVLNSSS

EAADKDEE

>contig48719 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61846.1|) 1e-42

MSTSVPRGSGGLVMAIGMLRKSTGSEAQFRQSMQNLVVVVNNICNSPENLTFRQIPKDND

SFHKDLGQYTGGYHCLIALGFQELEQLDTSQPRTVFWMEESNLHF

>contig48834 Frame-2F|Blast-thiamin pyrophosphokinase, putative [Phytophthora infestans T30-4](gb|EEY54260.1|) 2e-82

MMTDLPIQHHSNLFWSAPKAAPRLAVLVLNASHESWCVTQNEVDSITPDLFWSMWSNAQL

KVCADGGANRLYDRSMALGVQQQVVPHYIKGDLDSLRPDVCAFFTAKGTTVLSDPDQNSN

DLDKCLQLIFEKQANEDKNRFVVMIFGAMGGRFDQEMQNVNALFRWNDKFQHIVLLSDDT

TATLLKPHTRHVITPNFDFETRTCGLIPIAGTCKETTTSGLKWNLSPGMETGFGGLLSSS

NYVDDSCVHVTVLASHALIWTTELKKSNYKSLVEGHGP

>contig49095 Frame-1F

MNGCTSLLLKLMLVGVAMCLSFHTVGNLQNYRLDSLVNG

>contig49257 Frame-0R

MPECTELCDISLHELPCGVPLIMMTWLRDTLLPQKAPFVELIGTSDNYVTIQKVEDKWQR

VICNDGVVCTFGRPAEAIKFKLRVTPG

>contig49482 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66165.1|) 8e-30

MFVMINATDNPWMVALLLFVQVVMPLLQSNAAENEGASLALNVALLFLLGLSLMTFWKAA

RFCRVLQQLRGL

>contig49536 Frame-1R

MFLKDKKITTYTSVQQLNPSTAETTTLQYKFHRNTCVICGGRDFTGMKQWTEHMRSKGHK

YHLKRIEIQKEREKCG

>contig49987 Frame-1R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY61153.1|) 7e-90

MAKRIDLVSLKSYKQEQLALHIAAKFGNLEAVRLLAEPEFRKFINMPDRNGNTPLHFAAT

CSALSAATVVALLLLRGADPTIKNKQGVFPIVAHLLTTQKDDIEIVQQLLKNGSNP

>contig51454 Frame-0R

MKEHICVVCECEGDNLVVCAGPCISAFHVKCLPPSSEAADAVQGVWLCPNCKSKTHACFH

CKETGMETLTDESMSSEVGHKPVRKCRALSCGKFYHHECITQFPLARIAINTHFICPLHT

CATCNQSGAQ

>contig51748 Frame-0R

MNASNNGVCRPSDDSDSDPVAKAPQLQLLPVQVTDDSEHEQEAIVTQSRDGCEMFEPDLC

RGTHDKLKPHRKRLMAAAPQSSQYKCF

>contig52499 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67218.1|) 7e-82

MRIAAQFNHEIVVKWLHSHTAPPFVGMNAIEMAAKNGNLHLVKWLHKERNQWSGYGAGEA

AAWGHKAVYRFMIKGHSVLRESALNDAAANGHLWAVKNLIRRKPTLVTTRTTTAAAENGH

LHICKWLHGKKFN

>contig52514 Frame-2F|Blast-chromodomain protein, putative [Phytophthora infestans T30-4](gb|EEY63490.1|) 4e-47

MLLSTRAGGVGINLTAADTVIIYDSDWNPQNDLQAQARCHRIGQKKSVKIYRLLTSKTYE

LHMFHKASLKLGLDQAVLGGIKNDDPV

>contig52756 Frame-1R|Blast-proteasome subunit alpha type-3, putative [Phytophthora infestans T30-4](gb|EEY65638.1|) 1e-28

MLHDEVRHPFELELSWICQETKWQHHLVPDNLRDEVNEWAIQSIKEDEMADDDDDDDE

>contig53232 Frame-1F

MDATVVVCFSMGVISVVLALESAACVGGLKCACILSQSATIMTLILSSVTLVPVVACLVT

AWLDTRAKL

>contig53377-2 Frame-1R2

MPDTTYNTSHVLQNLSAKITMYTHPGGRANWQLLKA

>contig53539 Frame-0R

MVNALMDRLCLDASNGGAMEEQVDIYDTLCDLAAQTLACKYAVVSLVDENRQWFKSAVNV

KV

>contig53661 Frame-1F

MHSTDAQVHCRPGLSCKPNDWLRERFSLIVDHPLALKHRCCIRVFHWVSKS

>contig54163 Frame-0R

MATICVNGAAVVTKDERCILYTSAVDDAHKYVRVSCKDRAAFCLLRHQEVIGSVASFGLV

EALQLSENRENLQVEPATHDNNLTGAATCKCKCGIITGIRVRFLDRTRPSGAVLRGLQHI

ASRLFDGAIVWKGR

>contig54732 Frame-2F

MSSEDHAAVIPILRALVLLLRNGFFQEAVIESRCTDSVSIKDVIEECGGNIRTKKALLGH

VEYYLEYLYTVSPTEGHVFTDIQELSMEVDTLLRNPAKGKIDDTSATFNQEDHVKLDAGA

AFRDQTSSFDCVLCQYNVA

>contig55115 Frame-0F

MRLDNDDGIAHVYRQFQEVLISKQTPWCLQRRRG

>contig55278 Frame-1F

MAEAAEITRPLVGSMSGAPSTFRNSEFTRDAMETSRLTESGGRESASYGPGGQRQ

>contig56657 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55806.1|) 2e-19

MEDSKWHLETAFKASMEEIRRLKSVLEAPKDVLLSESNEVLKGMVQEERLRWVALVNESM

KAMVVQLHELLEEEKNVDGTHVLHVIRKVLKAGTRRMIEELQEKVYRVKNGEEEGGWEDG

EVVLKEDFVSEKEIGE

>contig57108 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64003.1|) 2e-90

MYCFGGYDGSYRNDFHEFNFDTNTWSIVAPIGRVPRPRYRSSLVVHNHKCILFGGHDGSR

HLNDVHVFDFNTREW

>contig57197 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67653.1|) 2e-57

MTSLPDCVSFVEAYDRFMAIESPLSHLSDSSTKAFQEQLIATILYMKKCIQQRQIDGMLS

ANERLLELQNAQLYALCVEYYLGILIPKQTFFQQASSGHTRAGPSDNTHNVIYRHQYLRE

ADVYLTEFLDRAESVGLLTETKRREQYERLENNQLSLSR

>contig57203 Frame-0F|Blast-N-acetylglucosamine-1-phosphotransferase, putative [Phytophthora infestans T30-4](gb|EEY58130.1|) 2e-87

MSSPQGPSCKARSSCYIASFTFFLGVFATYLSIILSRWKPLNRNNIGNVNSEDFLSYGPI

DVVYTWVNGTDPRWKREKEFWHKHWIASLTGQPLPVWGHEADVKGKDDSNADNRFRDNEE

LRYSLRSLEKYAPWVRHIYVVTDGQIPSWLDIESPRLSIIKHQEIFTDPSDLPVFSSPAI

EWNLANIPGLSD

>contig57294 Frame-0F

MRHKCLLVMAVVASMAFYSVTSTKNVTQVDTEQQENRRLRPHVEPTANELDKQSDVDTKL

EADQRLGYPGESGFMLEGELEERGGFPWRTLFLGLFASVIGVSVISACYGIT

>contig57319 Frame-2R

MLTDEALGKESSDDETDDTPQSRLSENEVEEKILLTEENADKSNRLTDDVQETPIFVYDE

TRMAKVLTELVSRTANWSVDMLRDELLELNRLAYPFRHHFDRTELMTLVEAHV

>contig57449 Frame-0F

MFFNSTRSIGTTVLRLTGATIL

>contig57535 Frame-0R|Blast-crinkler (CRN) family protein, putative [Phytophthora infestans T30-4](gb|EEY60146.1|) 4e-07

MRNIFRSFGLVVIVSSTSGTARNLVSDSAGSRNTLDYLWCIVHPLLPRTAIDSDIMILPT

ILQGIIANSRPLFAWTAVQYMRKSRWSEGSNTANYLNALVGHLAPMFADMKPKRLHEFKI

GQLCLLLCSSYRAEDGKVNLIDSHYACLDEKTMFRLMLTPTGELYKVAEIKANEAKIKAE

DKRTWECRSVFPHPANDVLLHLTLTGGLDYRPFDHPLREVLASVSTTTM

>contig57786 Frame-0F

MLTRQMLQAGVALKEILTSLRQVDPMTKAVRRTVYNKRKRLRAEELQDRTSMEALLDFLH

REVWSPQSKVDEDERVSRLFYAAPESVTLLLRYPHAPVLDCTYKTNRFKALMLHIIGMTS

FNTSFTIAVAFLKREREADYSWALEKLRLLFHQILPTANH

>contig58233 Frame-0F

MMLTSLPLPLPMPKRGMERSASFHDYCESSGCNSVWLRQRSRIQATAPISVIKNRTSP

>contig59524 Frame-0R

MPSLVVIRSGSKHVDYLENRNG

>contig00802 Frame-0F

MHYRIDRFIVYLTSISNFEKYHSLFHHHVIVTNKTDFYVM

>contig03032 Frame-1R

MRFDAPLLRTAVIYQIWQEILHPRLHQASVLKTYRESFDSTEKFSRRRARSSETPDNCSS

FEHILTVRKQPINSPLARLKELSKNNHTASL

>contig06299 Frame-0R|Blast-30S ribosomal protein S16, putative [Phytophthora infestans T30-4](gb|EEY63084.1|) 3e-28

MSVGAQPSDRVAHLLGLSNILPMPPTRQYTKKNVPKKDRQ

>contig06710 Frame-1R

MHVYTSVSVVLVAVSVCSVPLVRSKALNVRDTVSHESQFEFVSKNTTGEENHSLRSAETA

HEDRMPTGFGKKLSNLLNKSSRNDLPFAISTDGEPLSKPLLSKSLNEKFSAIENEFKLLS

KNCQSMVPRLSRINKRDAERLIEWIEWFSKARDPPAMDPRTALEFLGLLTSFKVNSMNIV

TAFKLLSYNPKLVQFANVALKEMGSDWAFIETLFQSWKKNKKDPMKFLKLLPISDAVMNN

MLVMWLKHFQDYYDVSSKPTIQTIFESLKKPNPNLSSATLFYRLQWLLAHSTLEINETIT

RLMLSGFMDETTSRFMKETWEAQNIGFDKILDTMGILQNGHSVDSSLLRQCLVYADDWTE

KVSVAMINRKRDDLEKEIESKLHENVESARNAIVKRFNLEDETIKETLISLSRTEVIETS

DVNEILEIVSPIKKRVVHVKLKDSSPVTKKDVDIILNKLVPTKKRVANEILKNPFPTNK

>contig06808 Frame-1F

MPDVVRLALNNTKFGAANVPMNDHNFINKIEEAWPWEWPPKDSK

>contig07137 Frame-2F

MRGQVLSQFSSTFWNEIKQKE

>contig09438 Frame-2R

MGPPSFLPILPAQGSKIQSFTMTINFQKAHLRSLRIRDASNCPSDLSVFLVII

>contig09643 Frame-0R|Blast-CUG-BP- and ETR-3-like factor, putative [Phytophthora infestans T30-4](gb|EEY55767.1|) 2e-21

MNGFQVGRKRLKVQHKKEKNQNPMFGDMPSHMDNDDIDMAAQDTRASSLPTGN

>contig10388 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54895.1|) 0.0

MGGVYTRVLHVASLRPGDHVCIWDFSRWPITYQHHGIVWASGATAADMRVCHVWSPLEGF

QAAQADSCFRISTLEEFMGKRKFNHLRLVEYNTSGLREILSKWGEVHLRKADLPQVVLAR

CKFLLGLGRGDFKLFTQNCEHAAHWCMTGEQWCKQTLTKARGRVPFENRLAKEDVDALVK

EIEEVKDISRVVLGNILKLSGSRVYLRVNGYFYVHVNLDGNVKIVPEGVDPTLCGRTAFR

IECYARGYNSVRVRFFHQDSGCYMFSRSTFSCFRDLRMKKPMTIRGKSGLTWEYSTLGYL

RSMNQHRRYVGVRDDGVLLDVSMRGDAARIEFVAFEGTAAIYTPPDIHQIPRTYNHDKSI

QVTESQSMRDYKAAELLYL

>contig11343 Frame-1F

MMYEFMTQQTKNEMLVFNSFVDLFKARFPNGNIKSLIHEGRRVIKRKINLSQTYYLDVFV

EFLTRNVIYDDASLIFHDISLLSSYDVIQTASSQLRTLLVGVTDVSRFADQLVNELFSQK

KDVELFLVMHVRIFGKKYPDFKSAVFKL

>contig12742 Frame-2R|Blast-ras-specific guanine nucleotide-releasing factor, putative [Phytophthora infestans T30-4](gb|EEY66820.1|) 1e-163

MEIITEGMRRRMSLAGVWRTGVAKESFVVKPDEALDSLSETPSTTITPWQPRGVTVGRAF

SSEQRMARLWLLDLDPSIVAQQFTLMQHYLFSKIKVSEVLASRRNAEKTPGYQRLRLLHN

HISVWVVSQILMRGDVDQRAEILAYFIRVAGVLLSPLQNLDGFMAVMNAANDSSVFRLKK

TWGRLPPQARDLWQQLMPLTEKGARSLNKFTKEATPPLIPYMGVVIQNVLALQEYPDRVE

GDLINFKKISSIGLLIQRILYFQKTPYLLPTDKRVLDFICSTVAFVDGESCFERSLKIEP

RVADGGSETR

>contig13046 Frame-2F

MEFEKGFLDTTLEFYRAEAQMMLDVATCPEYLEKAEQRLNEESARVLQYLHPSTEHKLKS

IVETQLIKNQAQALVEMEASGCNALFRDHKTQALRRMYALFRRVPSTLPRMSECLLQYVI

SEGNEFVKTQSCADTALDASQFVDKLLTLRETLLNFLSNCFLEDTQFYKSMKQGFEAFMN

TNTICAGYLAHYLDELLRSKNRFQEEMDTRVTQIIALFRYLQDKDVFEEFYKVLLAKRLL

NSRGTSDEAEKLVISKLKAECGYQFTSKLEGMFKDMNISKDLMELFKKAGNTDRSTGLEI

DLPVPPMVLSVHVLTSGFWPTEMAPTCALPLELIQLTRTFEAFYYTRHNGRKLAWMANMG

TVDLRATFASPSDNALHRHELNVSTYQAVILMLFNSRSKWRFNDLLDVTRIHVNDLKRHL

ISLCTPKYKILIKSSKGKRIDEASDSFIVNDLYKSKLRRIRIPLVSQKETSLLPVVTLHA

TKEGLPPTVAEDRKHLIEAAIVRIMKTRKQMPHNQLIAEVTRQMVGRFTPMPQLIKLRIE

SLIEREYLQRSVTDRR

>contig13958 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56394.1|) 1e-171

MPLTAASARVNSAWASDELNYLVDAWEEVVDDPKDRLLLSTGERATLHARFCVISGSNKR

SLSSVTRQHHRLCTSYRLIVATNKKSLKRGTPGWYELSAAEQHELRRVHSKKEKGVTIVS

QELFRRLDRICRGGGKNRKGKDFRKKASSKRSPPRQKKTIEPEEETDSVETVKVAWTAED

WALFVGAWQDAVDEFIDYGNEPDEKVKLPNWLIRQKFVALGGPEDTTVGSITAKKRCIIH

SYNFICQCVTALEALDGSDWFDYTTGERFRLQRKLVSPKSSQRVGCEIDRETFHKISSIL

EKEEILGTVTATGRKRKRGHRILRKSSVSSESSSDESVARSPSPSPSNDVDDESEVEEDH

SKNSSFAVDDVEESHIDEQVVEVLLEAQNARFEQLMHELREERMAERKQNQAMLLAILHQ

RNPQEISNQNLNYMETLVEKQQEQLLNVFTQMHKERQQEREDFHALLRQLCTRP

>contig14717 Frame-2R

MALLKNKYMPLSEANVSPERVATYDGQRITLSSTPDTAAFVMGNYLGGGIAGVVYEAFDQ

RMKRPVAVKILNPVGYKLTTPGALRRAEIVKPGVPILGHVRGMTLDNVYWVHLPHRRELL

ACYVTSTPLPVLRELTLEMCVSLWLVDHDDDAFQNPPLSQRRRRPRTTDQRSTSEEPVQE

FSQRSVASASVAVAASARPVPPHNRDEDDSIVMLHDVSYVIPQLPAKYRAFLQARQTIYR

EIAHMHKLTGNTITGV

>contig14973 Frame-2R|Blast-phosphatidylinositol kinase (PIK-D) [Phytophthora infestans T30-4](gb|EEY61947.1|) 0.0

MIITCTGVDRTEEDAEEAADATIKSQRNTWSRRTHTLPHYRLMYKRDDLRKDSIVQNIIN

VMYLILKQETKLEIPLVTYRVLPTSSFDGLIEIVENAHTLYAIIRDHGSILNFLHHYNGH

RTLSDISSSFRESLAAYIVITFLLGVGDRHADNVMLTKDGILFHIDYGFILGKDPKPLQP

PMRLDHYMIEALGGTQTPQFEQFKQLCVIAFNCLRRHVSLFMIMLTLVVKALPEITDFGV

NYTQSDLEAFVIERFLPGQSDDEAATALMLKDGRQIE

>contig15268 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64029.1|) 2e-48

MLAINCVGSFHAIDMMTVKSVGTGLALLDQVHIFLKQFIRHHSPIVFANKEITNGTRSPW

EHAEYLPSSWTSQVFKRIMLRVPSPSKLSS

>contig17781 Frame-1R|Blast-hypothetical protein PITG\_06324 [Phytophthora infestans T30-4](gb|EEY69818.1|) 3e-32

MRDLSRGRSMEKEFALAPQGFLKVLMYLSLGH

>contig18119 Frame-0F|Blast-endothelin-converting enzyme, metalloprotease family M13, putative [Phytophthora infestans T30-4](gb|EEY56805.1|) 1e-106

MERGKGSKWTKVTEKDKTLGSVDDSQVAQTQQNDEQPLVAIEEDSLGHAMPPAPMLQKPL

AAWAVGGLVALFLLVVVLVVRSGILQTQQRVKFATFGPKWVDLLPSEVKVHMNVDIDPCH

DFYEFSCGAWQAQSKIPDDKGSLSLSFTTVHDANQEVLNTVMQQGWPLVGELYDSCMNFT

TTSPAIADTTSRRILEPALQLIAATTSKTELFQVAGYLSQEGPNFLTGLYVTADAKEATQ

YALYATQSGLSLPDPEYYLNKKHFESLREAFFTFVLDLFRLTGFEADAAASHATKVLAFE

QLVAPLYVPKETLQDPVATYHRERIA

>contig19512 Frame-1R

MLSSFAITRCGASHWEGKELLQRVYAISFPTKAQLNEWHHLQEEAKKRDHRSIGRAQQLF

MFHPLSPGSSFFLPHGTRIFNTLADFIRREYRRRGYEEVITPLIYKKELWEISGHLENYC

EDMFMVSQGIVAEDDGSDNKQALGDQKTIDQFGLKPMNCPGHCLMFREAKKYSYRDLPVR

FADFSALHRNEASGALTGLTRVRRFHQDDAHIFCTAAQVQSEISHVLDFIKYVYGVFDFT

LQLRLSTRPDKFMGELELWDDAEDQLRVALDEFGEPWTVNEGDGAFYGPKIDIVVTDALK

RQHQCGTIQLDFQLPINFELEYDGPDGKAHAPIIIHRAVLGSIERMMAILIEHTGGKWPL

WLSPRQVAVLPIAEAHRDYAHKVAAKLQLAIPSGLCVSVKDDSKTLKKRVREAQVAGYNY

IVVVGDKEQASGEVNVRTRDNQVHGAKPLTDFIENIKAAIDRME

>contig19624-0 Frame-0F0

MSDDMIPHREWYCKMCSYVIRSSLFKKSGGFEVDDFHWCVCFGLIMF

>contig19624-1 Frame-2R1

MKIINLKATTLLEKTASNHVRTHFAVPFTMWNHIVTHTQASIPQASFNE

>contig20718 Frame-2F|Blast-phosphatidylinositol-3-phosphate 5-kinase [Phytophthora infestans T30-4](gb|EEY69411.1|) 3e-86

MPLHVSLLAGKTSSTASCVCWEMSMIAYYPLQFEVLRELFFGKSQSYIFSISHVAQWDAS

GGKSGASFFRTLDDRFIIKHISSKEMQ

>contig22969 Frame-1F

MALGVKESVSVKLYHLTADGDEIRVCGGKGAVYLSGPKVGLRCCGKTSIVVTRQAKQSVL

RQGDVQLLGPRDAFYANGTLTKYIVVDMEKSPPKMALHVLPTRVPSIIMSSAATNCSVAR

AKRASKPAGPKFVSSFYRSKASGPSPNMHGSKSKSDTVDVNNNTRLSHARDAEEEEDELA

PSTRRRGKRARAIIESDDETESSSFTKEELSVLSSPKNDDMFEMNLARSTSAARDWMDAF

KRGAGKKAKGDR

>contig23782 Frame-1F

MSDLKAEFESAAALVKTFTKNP

>contig24130 Frame-2R

MEALLKVMAAKKREVSIVKEKKQETKEKYLRRADVESLLEAQDQEAQTSTKKRKLEASNI

SGTPAEAVEDVKETEQQQLYESESVLSWPDLRRRLRELGEPIHLFGESLSDRMNRLRRVE

MDVVIKHDEELEAGHGIRNRFVNGDLGMHGDAKDSAEDAAEDAEEFEATTDRTTHHGTNH

TTNTSEDTSHEDDAKDADKMVYRFFKRMLQEWENDLATRPDYVKRTAQGKVAVKTMKQCK

DYIRPLFKLCKHRQVPPDILPKLVDIVTFCRQGEFVLANDAYIKLAIGNAAWPIGVTMVG

IHERSGREKIHSNKQAHVMNNESQRKYLTSVKRLMSYAQSISNVMPSKRVL

>contig24295 Frame-0F|Blast-exosome complex exonuclease RRP4 [Phytophthora infestans T30-4](gb|EEY55753.1|) 1e-135

MEVRVRQWSSMTEDAPLELADESQIVVVTPGEVISTDTGAFLRGHGTYLSRQNELVASVA

GVVEKVNQLITVRPLVSRYIGEVGDIVVGRVTDVASKRWKVDVNGQQDASLMLSSMTLPG

GAQRRRTYADQLQMRAFFVENDLISAEIQEVRYDGSLSLHTRSLRYGKLENGQFVAVAAP

LVKRMKQHMATLPGIGVDVILGTNGYIWVSRTMADVGGEDTASNMETRVEILTAKRQLHA

VTPMSVEDRRKIARVAQALLRLNEQFRMITPDNRIGHFLSEICRIGFFYSQDTF

>contig24776 Frame-2F

MTLFNPNSQCPSWSKFQYYLATLAFIRASQDSKSMVARGPFL

>contig25977 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66113.1|) 4e-37

MPPTPAEQELPHFWCHECSATVDTQVDDSTEEVCCEQCGGNFVEEIEEDDLPQNFHVDQV

EETHSQTQSVVSAENTRAEIRNEFGSTRPMPRPTGRATRFAASDDGQNGLTPLP

>contig26334 Frame-0F

MSKRRNENGQMRREEYDAAEDDATADSFELGFQRASEESIRKRKIVKARVGSRTAVSETK

SNPFGSF

>contig26752 Frame-1F|Blast-AP-2 complex subunit sigma [Phytophthora infestans T30-4](gb|EEY61359.1|) 5e-37 NOT\_ORF

MIKGILIVNNHGKPRIVKFYEHVVHCWMRGLYNLDVSFC\*YTV\*N\*\*PDAEQQAVIRDIY

TQVSKRPDTLCNFLEGTYVFLFSNKLLQLHKWLIEVEVA

>contig27698 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61726.1|) 9e-38

MSSKRFTVNPFGDFKLSSKDRSRLLEITDALVQLKVEEYESYIKTKKSVDPIYWKRFVSD

GPVTTFTERKAFQSAGNMLSTLMVGPLVGTLDEVMFGLVSPTLESMRIKASYLHDFSAAA

VLATIIEPTLEKPFRSV

>contig27759 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69382.1|) 1e-119 NOT\_ORF

MARGQAGGAQSSSYKEMKLFLRNRMWRDYLCALVSVGVIVVALFGSAFLQFSTSPDHVYR

IEVTDSVLMKRVFHSGEPWVVLCLSPDELLPEVFDKASSRLAGKSFAGVLDCKQKLPTPG

KSVLKRYSIRSSVSPTVFTVANGKKPKQVYLDYLQSAIALAKHVTERNKPTMQQVQTSAQ

LKNRCLSKSNCMLFLRGHRFKRQEKLWIDKLMDKHRLMTFAWLDSTSLRLSLESMLPNAQ

NDKHRIVFFQRQHDLGQSKKVLAAKAFRGHVFDETSVRKFLVQCAQEKDFTPLKKAVKIS

RLEKVRQSSQPGHHREYRHANGRHHHGNAERDQEKELKDNDAYYFSQHKSQDHDVEDSSS

FDDA\*DDVLDLDAYVDNE

>contig28123 Frame-0F

MEISQFYQCSSFSSHCKTLGPSKSNIILLKNFV

>contig28347 Frame-1R

MSIQNNLLNEPEFESVFKYLTDVRGLTKEVLQKYCVGAIEQPFWDDNVGERVTAQCISFP

WMARQTDLDAMGVVCHDENKPSTEDKNLYDVIRLKLRAVDDKSKQQLVPKGGSWGLFGWN

SVPSTAHELVLTEGEFDAMAVHQETGLAAVSLPNGCQSLPPSVLPLLERFERIYLWMDND

TSGQSNVEKFASKLGMARCYIVRMPKSITNPHLKDANDALRAGLDLTAIINAAERMPHSQ

ITTFEELRRDVYEEIVNPLKACGVQSRAFPSLNRLMKGHRMGEVTVLTGPTGCGKTTLLS

QLSLDLCCQGVSTLWGSFEIKNTRLMHKMLTQLAQRNLLGDVKAFEAAADRFEALPMHFL

RFYGSTNVDEVLDAMDYAVYAHDVQHILLDNVQFMMAGQGRGFDKFERQDAALDKFRKFA

SSKNVHLTLVIHPRKEQEDQELTLSSVFGTAKATQEADNVLILQRLRGVSKLDIRKNRFD

GSLGSIPLKYDAFSGSLREIATEGMSEGVASVDHEVEMEQAQRRRLHKSLRDDEDIHPAY

DKKYEDDPFSQAYQYVAAPVLESESRRLYESHHFRINGSLPTLNGDDAEEQYRNTSGGGL

NGNNGYSGPNRSGNYPNGPRACGEGEPFASFTPIITR

>contig28541 Frame-1R

MWFKLIYIFKKKSNSEVVSKHESPKNKNSKPLKNNINDEAAKSPVTSSRNAVENAAVVSH

PPEYTGIKVIKLELPGIKHPTKQDFHKFLKSWMDSVIASFKALKSTKNKFA

>contig28673 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65898.1|) 1e-57

MDAQVRATVTPTPPINDTLVMAYAEANSTVIESRAIPIKQYCRRKCKVEGCIKFARFNNA

CSGHGGRRLCAEAGCERVAQFGHKCSSHGGVKFCSIEGCFRAVQSRGCCKTHGGGVRCQH

QECTKGAISKGFCRSHGGGSRCAEQDCQKWAQRHGYCVRHSKSATECAEIANQPDPELFK

SEKISLPQPIFKYRQ

>contig29142 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55548.1|) 2e-54

MFVGIFHYVATVLSVVIDPGFIQLYEFTASRWAMSVVGIVIYFIAFYHQSRCNYLLAKQK

RASTMKYVIPKGDWFRAVRSPLYTTETMLYIAFVLVTGGTIKILYFVLTWVVVNQVLLAH

INSQWVENKFREKIHEFPKWKLLPYVW

>contig29959 Frame-2F|Blast-WD domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY66788.1|) 1e-166 NOT\_ORF

MDISKAPELIEQVNQSVSFMPNDSKWIPGSACFVAMGVYPKATGALTVFGLNQTEITTHA

ELEKTYGIKCGTFGASAFENRHLATGDYKGFISVWDLEKPAVPVFSAQAHESIVNSIDGC

GGQIAGRGAPEIVTGSRDGCIRVWDVRVPEPVVTLAPNEQDTARDCWTVCFGNAYDDTER

CVVGGYANGDIKMFDLRTKTLRWETTCINGVVNVQFDCKNNIMNKLLVTTLESEFHMYDL

RTLHPEKGFASVTEKAHKSTIWQGRFLPQNRDFFVTSGGNGGLNFYK\*YVMLVQGVKCLN

>contig30045 Frame-1R

MQSAVLLPTGVLSNLAKARIKKLIDRVYKASTNSVSIARLSAPLLMPAAMPASTYSAVPS

VKF

>contig30232 Frame-1R

MPIDPVTSLTAPEPTESTPSENSQPPMASKPTQLTPELTFPERTEAPTFVPPTEYAPVPE

WTVMPTQINSTTPEFTQESKSPTTLKPTEQSMPPTPIKPQKTEMPFIEESYPMPLPTSKP

TEVPTTPDFTTPESTQEPESTQEPKSTPPMEKLPIPEQVPISTTPEFTEEPTLEPPFEYY

PTFPPTTTAPIEPQKTEMPFMKVPTESYPTPMPTSKPTETPSTELPTESPSTLIPTTTTP

TLTPESTIPEVNNEPKSVPPTTLKPTLASTPPAPIEPQSTEMPFTESPTESQLTPIPTMS

TLMPEFTIPEVNKEPKSVPPTTLEPTVAPMPPAPIQPQLTEMPFTEPPTEFPSTPIPTKE

STEMPFTELPPESYPTPVSTPKSKSFCQCLRTLRWILSRRSHRQ

>contig30889 Frame-2F

MLELISFSFDSHEDGLTKNILSNGTYAGESGWPDRPVLLNGNNLEYTFLGDENNVGDHFG

IAFTVTAFGISLEKQLSKATIIDMEELLVKLVSMQAVPDGWTPEMDLQLVDWVNNYVEVK

ASLQSNPMTTPKHSADVKPAEIRLKQAQDGLRCSHLLGLPLERLQLRFALLKYLNQSLRH

CLSLLDLRDTKSPWTIAHRLRQLSHCIFFDVKSTLVDAAIEATNVTDIGGDFHKQTARIT

LDRMQALESRDDREVEPSVSECFFAQAFRQLHFVDPALFRRQIDSKGRLFNVKFRGEEGV

DWGGVYREGATSMVDDLFSPHFALFVLCPNGQHDTGNNRGMYLPNPKCTSPVAMQMFAFV

GQLLGISLRTHGDFPFMLPSLVWKQLLGQTLTRADLEDTDAMFIQMLDGIAHCESDGILT

EEEFATAFAGLELRYTASSCTGEEIELVPGGITRKVDFLNRLEYCRLAERARLEECSAQV

AAMARGFATLFPRRVLTLLTWQELEILACGSPKIDLDLWKSHTRYDGYAEEDVTVQLFWE

VLGELSDEQRADFVRFAWGRSRLPRGKWPQPFKLSKKSGRDATRSLPVAHTCFFSVELPP

YTSLETMRSMLLATITFGLGGILMA

>contig31370 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61358.1|) 1e-27

MLLILGIEYPTSFISHLRTQKLNVFNIGVAFLTLSLSSQMVSYKQRYEIALKEKESIGEK

VAVLEEIVLGLGGKLPDDEALS

>contig31666 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53883.1|) 4e-99 NOT\_ORF

MSLLSLVLFVALASPDTVLSTYQGYGTVYSLSTPSSGNCNFMHWPSEAVTKYAALNAAQW

NETMNCGRCAQVSCTDPSCSGMPSEIVYILDQCPGCAYGDLDLSPEMFQSITGQSYTKLS

IEWNFVECPVSNNVQYCLKTGSSEFWVAVQPANFISGVQSMTINHQEASLVDSAYYFLID

GKGKSVADLHSLQISITGVNGEVLEETLSMAADSCTNGHSQFSSSSSVYQSTSTSTSTSF

SSFSSSESTSTHVSQTIQDPSNTEVPVTDPPLPSASPIDSHNVTTNGIAIIDDSNRKPFH

SSCDSAN\*SPNDVSYDRIAVNCLPN

>contig31882 Frame-0R|Blast-imidazole glycerol phosphate synthase hisHF, putative [Phytophthora infestans T30-4](gb|EEY69066.1|) 1e-168

MVEVTVLDYGAGNVRSLKNAIYATGHSVKTVKCAQDIQDAEVLIFPGVGNFRAAMEFLNR

SGYVEKLKNYIMADRRFLGICLGMQTLFEGSEECPELKGLGIVKGEVARFPSDQIAVPHI

GWNGINAWKKSSLFSALTTRTENIKVYFVHSFRALKMDRNADWVLSTTNYGDLEFVSSVQ

KGNVMAVQFHPEKSGAVGLALLKGFLEKSTFVDHDAPILTAATALRTKLSKRIIAYVGSS

>contig32050 Frame-1F

MGSMAYMNASQQLANVEVETVQSNNKAYRMTPNEAIRLGLGMSMANSTVKHPIESCEDAL

IAADSKEIDEAKMMVENDTANVDVEVAHHSSAYTKKEPSINFGTISVEWSQNGEPDVQVS

TTKRAHVRANSERSKTDLLSNVGSDSIKLRSNSSLSIGLPNGTRCGRSMEIIRADLTPLV

NTVQENKQANCKQQQGELSKIAYVDILQQTRRPILDRRASSSAIQGNTQLSSPESWHGGS

KTSSVGERISTDAQLLKSCRKGVVKRKKGRHDDWKRDNTSTTELLRAESSVSMKASSLQQ

LSSAFETGDLSANDIQSLSRRGIGDHQCLHKQDDPPALPNIPLPSAESHKNSAPPFRSNA

LLTKRERPRLGWGQGLVVQLTPRQSTKRPRIGWGQGLMQQKADIWSRKHEVSYMDPSADV

ISINSGKTILANPTAIGQGHNSREDEITGILFGTSGFSALTNETFQSKNQLAPTLRDKNQ

PKPASLNKCTIREIIKSSDMEMAERFDIKQGDIMPTKPSKEEILSAIDLLDSEIANAKKQ

LKSLVRTIVNAKAKQALSVASPMDVSSDKENHVFCTHSHALNELATNESSPNLLPKKTLH

HPFVSPLLKTTIDSGLLELLAGVFSENLRKVAAANEHLPKRREQEPYAAKNYKQPSDYDF

FQDNINRGSKIAEKVRLKVRMRNRARYEILKNLARDYIDMKKSWKLSVKKVEKDRKRQDK

LRLKQLQKQRLKFLSESGPIRTTNTNHQSPHVQQLVAAEKAAEVSGEGTMVRTSSRLTNN

SSADIENNDLEKIEMAKAQAVADQEVRKKRLRNALSTLIPDMIITPTERQRRCFTRFANS

QSCMGDGLVTDWKLKEKEEMKVNPW

>contig33057 Frame-0F

MELKGEVAILTRLSNEISAVQQLKQSNPYIANVIVLNVSQDSNLVQMLASNAAAKANAFD

AVVSFNEHVVQLDVELAAVIPLIKPNGILQLYVNNVQEEDKRVILMALMIGGLVDTTEKH

ESSPFFPTFSNAVTYSCKKQSLESPSISLTKKYTEPRPIKKWTVLADDFEGDEQDDDIID

EDTLLDDTDEVLLAAKADCGEKIGGKKRACKNCTC

>contig33633 Frame-0F

MAKVSHEDIDARIRCLQVVYPHGKDELPWIVLATSSGAFQIWDFASITLDESLPEESNKS

VKPIASTILLTKPRVTCLSACVASEQHVEEGDKGDTALVESKKAKKKISQKTPVPPSLNT

PHVIVELNDDNSNATDEDNRNKKRKLTEKKTTK

>contig33646 Frame-2R

MSRERVFLCSKMPLFMSIALGRLLERIDNSVSVQDYVHLTQHSPLNLTEKGLHNNQNPAS

HSFISLYNSIN

>contig34337 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54214.1|) 0.0

MRIGGDNRVGIERQLHRISVMRSKSDEVYGLTMRVGRALCNAACVLTDLLLSGKHANKSV

LILGHPGSGKTTLIRDVARCVSKTMENVCIIDTSNEIGGDGLVPHECVGWARRMMVPSLE

AQARVMVECVQNHTVETLIVDEIGRKAEVLAASTVRQRGPRLIASAHGDFRALLRNPDLK

GLVGGSQQVTLGDKEAKESSKGKLQTQRAGNPIFDVIVELDHVARGRCRIIWDVAKAVDT

VLEGKVYPVETRRWDRSTRGVQVLKNSHEIAI

>contig34838 Frame-1F

MIFNGSTTGCVCKGFFRALLNCIHSVGYCNSANLLLLYMYRWLNARNTPSSLGDSGSRCS

RNARAMSIVAWLW

>contig35424 Frame-2R

MQRRSMRSLPKHHSRISSTTSEKLTVDQRIQKIRDVLINTAPNCIWCLDELTLRHRTTSI

RPDTAVNMDARSLEGISVALAVSAMGEKLHLQVVGKNPMPESMKDVDTLTTYGVYYREQY

RATHDASTIVHFIQAMNHEAMLRKQVWFVVLDSCTAHVAAAHSLTSTGSFRNGFRFDSMV

LLFLPPGPTSEAQPLHQGIFRFFKLRFRQEMLQTLLYEYEQYALQSHERMNENIVVEDAL

GRDV

>contig35925 Frame-0F

MSPESAVALQRYSAFVEETLRPQLKQTLANRDALALEVQEYQELQELLEELSHNDNKKTL

HTLLDVGERFYVRAKVPDTSLVTVDIGLNFHVEMTVLEAQQFVQNHLIHLTGKRNKWQKK

AREVSEHVNVVISSIQQLAALQ

>contig35998 Frame-2R

MANPIISSIACLSCSSAGVLLFISFISSFRALVPFRYLAILFASFQSCSLGLCVC

>contig36069 Frame-2R|Blast-acyl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY63794.1|) 5e-99

MTSGRFADVFSSLYLGFSTMWFYKNNRHIDGIDVLFDYAMTQLCYEAQQGIVGISKNFPM

PVVGPFMRRLSFPFGLPYNAPTDKQMRQVSELITVDSGVRSLLSENVFVSKDLNDRVALL

NATLPKAVKAGRTLTAMRKQKRTATIDEQKFIDEVEAAREVIIQVDSFEGLGAEIGKPKD

FVRPGMIGNKFEKN

>contig36577 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61879.1|) 8e-43

MNSLLFLYLNFVRGPKIVAARRAKEEEEKRAQLKADIASGKVPRVASCKKCDVLVDRLAV

PMGIMPTCVACLAKESQELYIPQVDVQRKIAMSPFLWFQIFIMLLGLTVFIHRNVVSLF

>contig37303 Frame-0R

MVLRSSIFSNVGLNRVLLSCRHL

>contig37484 Frame-1F

MHARGYSPLFGVAHWYWKSVQ

>contig37628 Frame-1R

MNLVSSQRLILLLRQLARTGRTIIVTMNTPLSHQVALFDTLNLLIDGVTVFHGNVTEVVP

FIASLGYECPFNWNPIDFFISILSKQDMTSEARREVLNRFKACGNYHLPLPHLNGFHDEN

EMWRTKELDVKRSSGFPLVVLMVLHRQFLVLIRCRCFYYWQAFWMLCLGLVVGLVFRQLD

LKDQEDIPNWTGAFYVLIVLQMMVNGTRTFVLIPYEWALMEYEPRYTRFVLFIWCCIKES

TELVLLLVFSIILFVPAYLLMGIRHGFQLYFYMQLVLWMAGWSATGMATLVLGLVRHVRS

AGFVFMVVLLFMAICGGLLIHVDDIPDYFSWVHYISPVKYGYEALMKLFWGRIGLLACNR

GNASGSGSMAAVMVGDTFSHSMSSA

>contig38333 Frame-1F|Blast-casein kinase I, putative [Phytophthora infestans T30-4](gb|EEY54211.1|) 1e-136

MEGIKLKTWILGKKLGSGACSDVFAVKSASSLDSDKNHEYVIKLSPLPQIPGSKLKNKKR

KKTSAERNADALYAEHLLYKNHLSALSGIPYVPNGAYGEDKGYRFLVIERLGRTLETVLQ

EQGPIPSITAARLGQEILVTLQQMHVKNILYVDVKPENFMLDKDKEYKVYCVDFGISDRY

VLASGKHKELKQGTVVGTPTFLSLNCHNGATSSRRDDIESLLYVLIYMMRGNLPWQEASS

DAEGARIKKSTSVTQLCASLPREWAIVLKHVRTCGFEHRPDYDFYEQQFLKLGGEKGLTT

P

>contig38751 Frame-1F

MKQPRSDDSGRVMSIQSHVVHGYVGNKSAVFPLQLLGMDVDPINSVQFSNHTGYSKFTGR

RLTGEELHELLDGMEANGILQDAHTHLLTGYIGSTSLLDAIVHAYERLRAAQTHPARFVY

VCDPVMGDLGKLYVPKELVDLYRFKVLPICDVLTPNHYECELLAEMKLHTVADAMRACKK

IHLLGPKVVVITSFQEASREETPTELVVIGSKVSGEDLCEQYEVRFPLIDSYYTGIGDLF

AALLLAWLYRFPNNFKSALETVVSTIQEVLQITLQSGGKNCELKLIASRHVIVNPNIQFV

ANPLAVPVLHVLVDVDFLLGTTSTSQVVDVPSDASILRLQLLRTFESLVGVQHVSIVTNY

TVSSTLKLLDQIPTNGPAWTVLSFTDILPMASNVVDCLDNSNCKTLVVTSSTTLSNLASR

AMYQITPEPTTEEAILTYIKERKARCRLC

>contig39622 Frame-0F

MMHGVLESATSATDASVKDVDTAAVLARIRAPSTLDPFASLGVKWMEFDVRRRSMGTVTN

RDYVYVEATGIKCFPSGEPLGYHVMHSIGIGEAHNLPRRVRSKLSICSFFRQVNKTVSIH

SLAIVEPMSDLVRQFVLPRVIQTLQSSFKPASLSSVSKVKKFAQTLSHRPSEHETQRLSG

FDQHCVTCSKRVGRFVKFASRHATCATCCRPICSACKIEKKQKVLAADIKLTTKKVAFCF

PCLTEAMTTNEAQFYCADKPDNAFEPQASANTWAWATKLPTWGSKGGETPIDLTCT

>contig39749 Frame-2F|Blast-bifunctional folD protein [Phytophthora infestans T30-4](gb|EEY68282.1|) 2e-59

MRHLRCPCTPVGCLELLDHHNISLEGKHVVVLGRSRIVGLPVPLLCLHHNATVTICHSHT

KNLKARVHEADIVIAAVGRPNFAGGEWLKSGATVIDVGMNSVKDTTKKSGYRLVGDVDFD

AAFQVVHAITPVPGGVGPMTVLMLIRMPSNVLFDVCKQ

>contig40042 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53379.1|) 4e-73

MWYKNIGMYKALDLVRQARPSVDPNVGFVFQLTEWEHLHPEGKLKFPKTIVFRMDIAYAD

SKESCNRDGLKATKTPLFEGPLLSVSQDYFRDPTKDIGGLCLIVACADYMFVWCGTDVTN

DQVEVAKSGAQLLQCYEAFPVHWETVRQGQEPVAFWNLVGDDPSR

>contig40424 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64342.1|) 1e-33

MVLPLFIAGTLGAGTATAYNVYQAGRRFALPSSKNEIPANTARSFPAGVITAVAAYSIQS

RLLKRYVLRFITYEVPKNVTKWAFRHFFKIATPIVAPRLAILSTSVGLMSYVRTKINLRG

NKHHSQK

>contig40550 Frame-0F

MAWRDLRVAQRLGLRVPLLQSPMAGVQASALAIAVSYAGGLGAIPCALMSVDAVRAHVQN

FRKATNAPLNLNFFCHTLPPGNATADKQW

>contig40859 Frame-2R

MMAASSPSADSDDSTVFPSSTATKVYGINAADNDFGSFVAASGLQLDPFGDVYAAEADFG

DFVGQKQSHEPTAITTTSSLLSPLSASEALSSPMSGEVDPFADITGGFRAATGNTKEVKT

RSNSGASATASSSTSAILDLVWG

>contig40998 Frame-1R|Blast-hypothetical protein PITG\_08092 [Phytophthora infestans T30-4](gb|EEY54448.1|) 2e-32

MDWKPQRALVLILSVLVCWCRSDEILDMLSPFINFKELADQVAKETAESPVANKDVDHTY

PVASVEMDALMKMYRECRTQNSQAMRSWCTGFDEDYYRFESIESTNSCPRGVTTHPCTGQ

ILNTTKSPSKPDSKLLWSWKGLRCDVLTEPT

>contig41337 Frame-0F|Blast-Cyclin B [Phytophthora infestans T30-4](gb|EEY67764.1|) 1e-174

MSTSLSTAGAVFKKKITAGKRSLRNVNIGSRSLNTANSSKRDLENINESNCFVATANISK

RNLDHVSVGCRHAIPAPSVAPILCARGSSSSSITEPMSRSTSSVTLVVNTCETMGQISKL

SPKFNIVSPTIEKKEHDIDSKDKNDPTACWQYAEEITKYHLETEKNRRPNGSYMAHQSNI

NSKMRAILVDWLVDVHYKYGLLSQTLHIAILLIDYFLEKNLSIGRRRLQLVGVTAMFIAS

KYEDIYPPEAEEFVKITDNAYTREEVFQMEAKMLATIGFRVTFPTAFQFMRRFIKASRTC

NDRVEHFAHYVIDRSLQEYKLIKYLPSTIAASAVYVARTQMRDIPAWSSTMEHHSTYSEQ

SLTSCVNDIKEMLWNAHNGVGKLAKLTAVRRKFSKARFLAVAAEPLAFRKSI

>contig41467 Frame-0R

MNAARRCTIETVYRLLHRDKSVSSMSPLVQFHPLSAMRYSTAPEFCVFQELVLTSKPFMR

NAVAVEHHWVLQYSTDKLHVSIAQLYALCGRKSIVNRKETEQTTSETKEVDSIDIANSRC

KVTTATVNAARARYLARKKGRYDYPDVAL

>contig41665 Frame-1R

MQSFLKLQGMKIFISLNAKQLTHPTMKKAVACCKNVPLKAL

>contig41838 Frame-2R|Blast-phosphoserine aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY57574.1|) 3e-96

MGMSALQLPALRQLHTVNQRLWTFITCYVQSRRINTLFECHQAFLQQEGLRFFHELKLGN

SFLHTEAVQNLYFSPRVMYPIATRDVLACLRQYGDMLSQDAFRPLSHVDLHEFLQYIAQH

YRQSSAQAMGIFIDSSGFGIYVGMLRRIANYEMKELKTLEQQFQSEVAERMFRLSKEKFS

AEN

>contig41885 Frame-0F|Blast-DNA ligase, putative [Phytophthora infestans T30-4](gb|EEY65982.1|) 3e-55

MEAAVDQNAALGLSFTALCSVLKATEATNKSDLKLELLFSANLRAQVGEGNLYPLIRLVL

PHLDRERTYMLKEKKIAKLYIDILGLAPMSKDAQKLEHFNDPKIVNSKSVGDFAAVLYEV

VLYQSMRTKSKVP

>contig42178 Frame-0R

MVISCSITPASVGVWRVNRARDRLPHANSLEYFPRNIT

>contig42303 Frame-2F|Blast-guanylate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY56424.1|) 3e-95

MRSQRAAHIARLQTRSGKFCLKVLAKLRGKFLTRPLAAGVWDAAANKEKAFQATMQIIEE

VYERKARGPAMKTVFHQFLRVDSLAFFEMLYQRIVADHEQKTLEWCHARKQLEQQHALET

IKWKHQLHEKSLNVQQLIEAKAHNEEKAALLAERLTELQSTSVQQAAVIADLENERKHQN

GKIEKLRSAAMELTREVEKTQIWLQRKEEDLVKVEAESRSAKIELT

>contig42484 Frame-0R

MTKLALPRSTSDPKREPSMVKLRTKNTNGDIFQLRSRPTPTGAEDHAKIAAPHASIAAAP

ALIHRTQRHGAKPLSGATVAPKMMRGITTGSAEALSLASAQAGGLDAVIQDTLQRARVTA

SSRRSARISYDNIEPLSGLSAQEL

>contig42695 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY64165.1|) 6e-88

MAQNASREAIPLLRSTKEHLIAKEKQDAFSRWRIDNVDDQSSSDDSLTHRRRRKSAQRQM

LCMQFSLLLLLAWDLVSLLVISSWSLGSAVFFRFECLLNVQTLQWRFWGLPIWATVIKSV

LFLLANSWPDVRVVTWIANVFCLAFLCVLAVDAFKLDAISRLDEEKTALVDANVANSLPL

IFTVLEVVNMSYLRDSIKSPLPADDATLPQNAASNSIEPQKPRGISFVKLVY

>contig42835 Frame-1F

MEIYNTLVQALLAAAARMEDIEMELSDLQLALLEDHEEVEVYTDEIADCCDRIGAIDDFV

SEIDAGHVPAIADLASVVSNMAEEREDEEAMLQRLGEVRACHEQQIQHMTSKLTTLQEER

LLLQKKSAHVWCALHRTGVLKLRLVEPHVKVV

>contig42888 Frame-1F|Blast-hydroxymethylglutaryl-CoA synthase [Phytophthora infestans T30-4](gb|EEY60171.1|) 0.0

MSSARPNNVGILAMEVHFPSNYVDQSEMEAFDGASSGKYTQGLGQFGMAVPGDREDVNAL

AFTALSRLLFKYEVSINTIGRLEVGTETLVDKSKSTKTVLMQLFEENTDVDGATVINACY

GGTAALLNAVAWVESSFWDGRYALVVAADIAVYAKGAARPSGGCGAVAMLIGADAPLVVD

CQTKSTHASNSWDFYKPHCSSEYPMVDGKQSNACYLHALDECYQLYCKKDDKRLKERGLQ

TGVAMVDFAVFHSPYYKLVQKSFARLVYLDAVRVFKSGKEDSTGKLDTLKKWRNIPVNDT

LYDRELDLAARAVAHEDFQAKVAPSCTTSQMLGNSYTAAVYINLATLVHARSKDLAREAR

VLVFSYGSGSLASMFVIKTREPTDSAKGLFTLEKMAKSLDLTTRLEQRHKLTPHEYTARM

KLRQSAYGVINDQKLTQSIGSIRTGDFYLDRIDEMGRRFYARAESIIATEGKSSEQQLIQ

TTMQELGGAVYVVGTSVGLPGQAHVFDG

>contig43375 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53261.1|) 4e-29

MYHPSESELSSQLSKLSHLVHVISKTTLSFDGMKEAALKELIVFIEMASVEMFRLLEELN

KLTELMDLLRG

>contig43692 Frame-2F

MTSLLNKLIDNYASIFCMSERRVSPQNASQCQALLDRRSLSRHKKLSKLSIDDRLRALIG

DVISEEELNQHLSFVRVLGTGATSKVYEAVETKSGRYVSVKVFDKASMVEARRSMVADGQ

YVIEKAVDRVRRRLLKLVSELEIAKSLDHPNIVKYLGAYETSHRICIVQEFVRGSDLLEH

LLENGKMPENVAVGVFQQLLSALEYFHHRNIYHRDLKLENVMITKDLKVKLIDFGLSEVV

TCPDQPLKTVCGTPLYCSPEILFLHTSIEAARNGFLGGPADVWSVGVLIFALLTGCAPFD

DSNFHRLRRDVSRNRINFPAYISNQARDLLMKILVADAQMRPTITDLLSHNWFERSVENN

VTAISSYQAEDLCSKLSSQLNDDVRYRSLSYRRTSSSDCTYSSSASLEDTLKRRLTMPAQ

S

>contig43753 Frame-2F

MGALVKDLENDVKETISHEASSMVAVGVEEETSVPTLSTEACYEKWKPNKKLREIRQVLK

KMKIMAEWSRNQSDETVVEKMLKYVCTIGDAIDRIVIQSQDKMERHHVEAMPREMDELCT

SLWTYAASFTCFTPQGFERLYDDICADGKSLRATA

>contig43872 Frame-1F|Blast-glucokinase, putative [Phytophthora infestans T30-4](gb|EEY65839.1|) 6e-89 NOT\_ORF

MLSMTSFELV\*SF\*LAIYKSFNLSIHKALGTGIGFGIVANGKLVRGSNNAIEGGHMIVER

NGRPCGCSQNGCLEAYSSASALTSEVQKHLRAGKMSSLSRHSEADINAGLVFRHASEGDE

LCQRLIEEAADYLGFACVTFCRIFDPEIIVFSGGIAEAGEMYIDKIRLAYAKYTWTKFSN

SVRIEKASAGYNSGIIGAVALHIFKM

>contig44420 Frame-2F

MFQHVASADQRRARSPSIILEWRVLAECGFGYFFKPGIRCHGGSLGAAFMGRETHQRARG

SMDIN

>contig44613 Frame-0F

MLAASKPSQSSQTRERVQMNSFVDLHFSIRKEMYLRFCQLEEEGNLTRDSAHVLRSLVYP

TSDRFQDLKFVYLVNKALSSTQLTKRLLEVVSYPVTRSSIANKNIARLSVPIGVFSTGLY

CSPSSLAGSSHMGVLESSLGHAKPEAARLDDSSNSSSDSTGLPQSLRSSTYPNTAALSGL

KG

>contig45179 Frame-2R

MILAETFYMPKIKPRHAQSNEDEQDPDGSPRHERSQTQMDDADVLAWRRPYLCADSKSLS

SNNCKELLQHVDHTHPLLHGGGIGRGATRTYLQMEVKNHIIWKSPSFWEKALLIAIGEEL

HRTPQPCPWEELSSEIAKHNGLSSRKEAVCRVHNIVFGQLGSYTLSMLEFDVPLPQIESF

VETMCDAHELTEDQRFLLRKNLREIYATLQ

>contig46057 Frame-1F

MAICLLILATLNACLSMNAIASHSSGQLQRWDFWPPLVAGARITRYLSSQPRGIHLIRQS

FEPINLFQLQNNKLTINELLYGGILLKPIYPLDLTSNSAVQVAFQAGVKSIRAHANVHVS

PEITLVAATVYPLKVTGDNGESEMSILQESMGTNGQRYQFTSHVTFGFNYYLTLEDAKFN

LRHHIVVALDRESEHNVFQHTFSPLKKRILDETLEAAICGPGDDGCSTARVGPRILSYNV

WNTNPSSGVYGAGRRWKQYVKRLD

>contig46251 Frame-0R|Blast-pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731emb|CAA30503.1| unnamed protein product [Drosophila melanogaster](pir||S00954) 1e-09

MKTDVLCDVCATSKQVCKSFKASVEDKGLRESARFDGIVCSDVFGPITLASRSRFKYIVS

FIMMKSWYVMAYSLRKKSEVVSAFARLYRKTRIASGTKIKVIRSDNGGEYRNAFF

>contig46408 Frame-2F

MASFLTEEENASFITLSQDPDYTNFLTVDENSKIVESGSFSGKSNIEVIPVHLEELTIEE

IHPVNIGLESEEFNLSEAEHTNARNLSLLYMEPEEIVMPMVVRKVVKKLVVSSNVRRLRD

MKPAPRAPPPKVAEMVTSSMARASATIKASAAPPSALLTAEDITQSSKEARSTMEPDDEV

LKVEYLQVHLDRMNQISANLRDLRKEMNSTTETPASTQTAMAALTSFESKANADRAAKIA

ANFISLLDWNAAPAARRAQQHLKQHNEPRTSLFNLTLAMGDGSFVDYLMDSTFEDVGESP

DGTGIGWQAVISQTTGKQYFFNQNCALASWTLPGPDVFRGMLYKVL

>contig46633 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63337.1|) 6e-57

MSKLAPRVFLALDDLSRAGKHVIQFAKINGAGPHSVPQTIAETLLPPHLSPYVRLYQWLN

YEAVAIIVATNEMQVSQYWELADALVSVLSEADVQWLTIVAALHLPYAKHDGLSVFYSNL

NGAEDQEVDVTVLPRADPSWEVKDPWLSAFLRLIKLEQWPRTHLLLAKGYKPG

>contig47050 Frame-0F|Blast-pre-mRNA-splicing factor 38A, putative [Phytophthora infestans T30-4](gb|EEY58957.1|) 3e-99

MNATDPSAQSVHGVNPQSLVEKIMRNRIYASIYWKEECFGLTAETLVDKATELQEFGGTF

GGNQQPTHFLCLLLKMLQIQPDLEVVRHFIENEDYKYVTVLGAVYLRLIGKPIEVYTLLE

PLLSDYRKIRKRNVIGWDVTHVDEIADALLHEEYYIDLALPRLVEREILEKIEGLPPRRS

PIEDELDADSDSSSSNVE

>contig47124 Frame-0F|Blast-U2-associated splicing factor, putative [Phytophthora infestans T30-4](gb|EEY54549.1|) 2e-40

MASNMSSLPAMPTSILPSLRANPAGKDAIVVEIPNDSEVRRLVDRLAEYVATDGLQFENA

VRIHEGHNQLYRFLLEPQSAVGLYYRWRVYSFAMGDDAFSWRESPFQMTLEGPIWQPPKM

PSRVSRSYRQDSPLRLLKRSGRLDRSPSSSPRPTHRR

>contig47212 Frame-2R|Blast-phosphatidylinositol synthase (PIS) [Phytophthora infestans T30-4](gb|EEY58436.1|) 1e-110

MAEEKQRTVTGVFFYVPNLIGYTRVMLSIYSLSVAFTNYKASVLCYTLSFVCDYFDGFFA

RLCDQCSTFGAVLDMVTDRCSTAGLLVVLSHLYPKYMLFFLYLLILDFSSHWYHMYSSRG

HHKVISAKRNILLRFYYGFYPFFGFCCVGAELFYILLYVLHFNPTLLLPVFNIPVLQLCY

YVCLPACVSKNLINLAQLCSAAHSIASEDVANANKTK

>contig47883 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56448.1|) 2e-33

MELQKGYKVNGQGALTGVEYQSPLGLKTCVIADSCAPKPPSNPACGADAKSGGTEFKPGE

VRKLRKCYACKETILGRTKVCK

>contig48143 Frame-2R

MHAVNIEGADKLRACEAFSIENAGDTSVLKQATPSAFNESDNKLSDAILILVRGSGEEGL

TLISLIKQLCVQRQFERESRFVVRSLDSLVDQGELVAVNAYYDQRYVVKEHGDMWMLRPY

YLAPSVASSSTPHIMFEEHKKKLSFPW

>contig48338 Frame-2F

MAQEPMSSPRMRRPSASSERSTRPATSIVGADGRIVLTPTELHDGNGSYGHLSSPLYGSI

SQSQPQHTNASNLHHISPVRKRSLRDLIVSPSVAKVLYALCLLAAVGARASLVSLYYLLV

LCYGVVQSFQSRRVTLLTIVVSFVACVCHIAIKLAYGDESRYNGAEIARLFGFYTMRTTK

TY

>contig48385 Frame-1F|Blast-peroxisomal acyl-coenzyme A oxidase, putative [Phytophthora infestans T30-4](gb|EEY56904.1|) 1e-110 NOT\_ORF

MMFRNHTERYEFGLKKVYHYVKLLQEGSYADAVDQQILYKALGEPLSVEVHRSMFIPTLE

NQATDDQRATWLPLAKSFRILGAYAQTELGHGSNVQGIETVATYDKTTQEFIIDSPTLTS

RKWWPGGLGKTANYAIVHAKLLLEGKEVGVQAFLVQIRSLKDHQPLPGIEMGDIGPKVGF

NSVDNGYL\*FTRFVFHVNT

>contig48600 Frame-1R|Blast-sedoheptulokinase, putative [Phytophthora infestans T30-4](gb|EEY60294.1|) 2e-11

MIGTGNALVKNELLQRFLLHHLAQPSNFHVQTAVDAAVGASLSSSLQGGRYAV

>contig49254 Frame-2R

MEEQVHLRMHSKNNFHCPGLNTIRWLLQFFLFGYKDKIDAVKRSFVPFRCCHGIMAQLEF

NSFDFCTIEVCLLIVVSLFTIGRCPNTIFVVRVNGFPFYDR

>contig49481 Frame-1R

MSWMACFREAYTQVSAEAQRGTNFNRTAHNESRSETFNRTLRTIQVMPTEQFKTPEELKE

ASISELKQRLERRNVDFAGCVERLDLVELLIKFRGGPANNDTCCICCEEYETGDVLRLLR

KCKHEFHLECLDKWAFTSVNSQRAPFCPLCNQGLD

>contig49535 Frame-1R|Blast-carbohydrate esterase, putative [Phytophthora infestans T30-4](gb|EEY54423.1|) 3e-13

MFSHHFTFCMEKMTRYAYLRPWWFCLLLNNQLMQAVPMKSSRKFALALRQAGHNAMFREV

SKCTHQDILFALMGDSVDCRMEVLNLLQQILSGAEKLAFDGIQALPFKP

>contig49984 Frame-0F

MECPCRTNRQDAPLLSQSPPLATVPLLVANNFESFHRRHLPQTCVSFSSPEGRKLFTEAI

NCPQNYMHIYFPLA

>contig50025 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY54846.1|) 1e-29

MILLIMAIVTLVPIPAVLFRLGEEPRQLRVDSVDRLLLARHLWNILQQQAVWRILLFVCT

SVL

>contig50098 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61936.1|) 8e-28

MNSEAWLALHLPQLDHYDVPSHLYQQIYECVHDKIGNWNYLDAISTSQDATKDTRGSRKR

RVKSSMPLPAAKMVLRVSHEWEFQSISDAQTQLRHDNSLRQKISNLIDEIIIKNTADIGF

KKENHIEAEVDTIVKHLHLMAYSIRFRA

>contig50609 Frame-2R

MVLPGRGELLVAHSNFQIFGTTTHEHQMPKGFQDSVWTRVNVATLANNEIEQILLARFSM

IPPQVVSKIMTTFNAVSGGTSKEIGGAAIFWKETRRNYGRNFCLRDLLKWCKRIYRFSYY

SSSEKSIFSH

>contig50942 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56889.1|) 1e-69

MVFLQLDTNNYCIMATATALEVELRKKLLQDAQFTPNMDHLIRNEIGLFQRSMYKNHSQH

RRAFFFQNLQKVKRCLRDFKIEAFNVMLKEARDVLTKLEPENGAYCISWKLLASDLKVRT

DAVLRKFVAVSHAATEIIRAAQKAYKSLMVQFAMTYFMPFVLTMNSILARLTVLFKTVLV

RAIELHGGITLLYLHAVAVSNPLRAKITAVQLQGYRIPSEILKIA

>contig51101 Frame-0F

MHAVATHTEASSVASWTGKSPRDHLESYCLKNGLQKPQYTKMPRSPGGDHLYSVVLSSKS

CEKQVMSLRDPRDAARGYKSITEAKDAVATSALFELAPNLPLYRVLPPIYRDMWQAWTKK

EQEMDAAVAAANREEQDELLTAIFNALPAELAAKRALIETPTPISQSLNKESKSCDNALQ

NWNVNDW

>contig51233 Frame-0R

MKTIARRELIVSYALESASLASDDDARELYFRAPVAELFQVSLVLCMSFHDELKREPAGH

TLKCE

>contig51651 Frame-0R

MKAAAVAGTTATTTDSQRASSLASQSSSRSSASDVSIESTEAAQDTAESVRWRNQQRTKY

SVKQKRELIALAKTVGVRDVCRMEGVPRRTLRHWLNDAEKITSFEGLDSRKSIGRCGCRE

LVPFGRKLSRFLKQGQQEGKEMTSSHMMKFIRQNHQQWLESYMASKKSPESGHAALARLC

QRFVERHGMIHVATDSDAMVSSYKGASVTASRELSLLEDHPLLFGLDIGTTAIKCVVVRA

DNKLTVAMVTVSLRDVMELGTPKNTPGVQKVDQILIAVQRAVAKLPEKALQRVISIGICG

QMHGILWWCSRAVHESAERLLTTQGIKKKWDETSDDAVWTELVTWQDQRCSSLFLQACRE

KIGTSIGMGSSSRLATGYGLATFAHVLEHAPRMLVGMDACGTIQDFVAFVLCGHQLPSEA

FIDTTDAHSWGGFDLSTHAWDSKVLQTLRIPAAMLPSVKKPGTCIGHTSAGCTGFGLPIE

LPVYVPMGDHPCSVLAAVTKQASSEARLTLVNIGTSAQVAMILSKSDALKLSVEETTGFE

VRPFLFENYYVGVAASLSGGNIFAWFVRQWQQWIEEIGLTSVYNGDEEQIYARLIELGLR

CQDTQLVIKPTLLGERADPDASGKIQNLRMNNWSMGDISAALCRGLIDNLFEMIPKALQL

MMSSQ

>contig52580 Frame-2F

MSSDSSASVGISQGSNGAYKHGHGDGGESIGGGLQMATQPLVATLRAHTRPINDVAWSPM

EPSV

>contig52755 Frame-0R|Blast-proteasome subunit alpha type-3, putative [Phytophthora infestans T30-4](gb|EEY65638.1|) 1e-104

MSSTGAGYDYSAGTFSPEGRIFQVEYARKAVENSGTTIGIKCTDGVVMGVEKTLLSKMLV

PGTHRRIFAIDRHVGLSMGGLVADGRQLVNRAREEALNYKKNYGCSIPPQLLAERMGQFV

HYYTLYGSIRPFGTAIMLAGYDQDTEKTSLYMVEPSGVTYSYRGCALGKGQQSAKTEIEK

YKLFDMTCREAMKYVAKI

>contig53374 Frame-2F

MTTHNACWWLRPWKKLDQDWQASCMKGQQLLGAVADSMQKTTYLLSESLDGFQQLPVRAS

T

>contig53460 Frame-1F

MQVCFKITALVMINALSISSLISAESSLGTAAFALKTPHMESHEAMRSLRARHTSTLNVD

EERLRLKLLRRV

>contig53789 Frame-1R

MIYLRSLVFNVHWTQYIENIQKLSLDDATIFSSIYHLVVFSTCSFALHADRCPSLC

>contig53815 Frame-1F

MLQRCSCRLFTPLPLFRSTRTLQMKVSALHPPNCRRLSDSVITGVVQQRLKASRHVHVAG

ACAMNIKTMPLAPLVPLSHPL

>contig54731 Frame-2R

MNGLMILCKRSAASSSKVWSTTSWRLPLA

>contig55116 Frame-1F

MLLHHHMTRPIIVFKIAGIHFEQLHREASDTVA

>contig55163 Frame-2F

MVESSSSASSGSESPSSDSSASPLISQPKSEALTTQDGALMDKSVPVEENGATGDQDTDT

PENAKKT

>contig56081 Frame-0F

MIIKPILLDQIGWDSLNRLKIWKGFARLTKQRIEM

>contig56302 Frame-2F

MYILVRVFSIRRALPLRFRKSSSRRVVITTMCICF

>contig56496 Frame-2F

MIYFDVSSQFYLRMIFFSIALFQRQAWQQITISFQLRKVFYKQRPRNFFRTMSYAIAESV

VQVPVNLVVAFILGTFFYFMSGLTRTFEKYIVFFIVLVAFQHAISAYMTMLSALSPSITV

GQALAAISVSFFLLFSGNIILAELIPEYWIWMYWFSPVAWALRSNMLSEFSSDRYTPVES

RTLLDNFSITEGTEFIWFGIIVLVAYYFLFTTLNGMALHFIRYEKYKGVSVKPLTDNATD

DDAVYVEVSTPGTIDVKNAKKGGLPFTPSNLCIKDLEYFVTLPSGEEKQLLCGITAHFEP

GRMVALMGATGAGKTTLMDVIAGRKTGGRVAGEIIVNGELKNPSNFSRIAAYCEQMDIHS

EAATIHEALVFSANLRLPPNFSKEQRMNLVHETLDLLELTAMSGALVGSLSVEQKKRVTI

GVEVVANPSILFLDEPTSGLDGRSALIVMRGVQSIARTGRTVLCTIHQPSISIFELFDGL

LLLQRGGYTAYFGDLGDDSVKMLEYFESIPGTMEIRPQYNPATYMLEVIGAGIGRDVKDY

SVEYKKSPLYQLNRERTLLLAEKSDEFVCHSTLNYTPIATGFWNQMTALAKKQQLTYWRN

PQYNFMRMFLFPLFGVIFGTTFYQLSADSVMRINSHIGLIYNSMDFIGVINLMTVLEVTC

AERAVFYRERMSNYYGPLPYSLSLWFAEVPYLIVVIILFVTIEYWLVGWSSSAEDYLFFM

FVFYLYTSACTYVGQWMSALTPNEKVANVAVGGL

>contig56654 Frame-2R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY57969.1|) 2e-11

MESYRYFLCQLITFLYIPPLFCLVSYKATHKNDQ

>contig57200 Frame-0F|Blast-ATPase WRNIP1 [Phytophthora infestans T30-4](gb|EEY53542.1|) 9e-29

MHYDCISALHKSVRGSDENATLYWLARMLEGGENPLYIARRLIRI

>contig57536 Frame-2R

MQIDCLNWLNKLFRGELKVLQ

>contig57738 Frame-0F|Blast-CDK5 regulatory subunit-associated protein 1 [Phytophthora infestans T30-4](gb|EEY55916.1|) 2e-64

MCSYCIVPFTRGRERSRVMTSIVDEVRALSDKGVKEVVLLGQNVNSYHDRKSEGAIENGR

NYIPSAGFSNMFRLRDAPGYRFADLLDQVSRVDSEMRIRFTSPHPKDFPDEVLDLVYERS

NICKQIHMPA

>contig58230 Frame-0F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY67459.1|) 5e-53

MMPQQINFGASFNPNLVYKSGRITARDTEAAGMSLLFAPILDVSHSKLWARTYETFGEDP

YLNSVLGVAIVRGIQSFNQS

>contig58678 Frame-0R

MPKQPHWSFLSCRRNSSSNGERHDEVGNDPSPWRSNYLSRSKRTVSSDKWSPASPSYLHL

DAQEHLPL

>contig01215 Frame-0R|Blast-croquemort-like mating protein M82, putative [Phytophthora infestans T30-4](gb|EEY60216.1|) 6e-28

MSDVVWPSLPLNVVLPTYWVQEAGEANDSLIDEFKKLRMIIQTFLPGLVVFLIVGVAEIG

AGLFLWRREKLKL

>contig02012 Frame-1F

MKFAQNNHRKHHHLKVYFAYFSLDFQRNGLSEQNVDVFIEFISKKIKGTIQQAKEFKE

>contig03033 Frame-2R

MFVFQLLTSAVPRTLILFFKSIRLLSTHINSCLSNLQICASI

>contig08599 Frame-1F

MSKLVVSIGHAEFTANRDVLYVIKVQQDEDEWEVRRTYSDFRKLRDDVQRTMKDARAHIL

DDSCSNEFALGLQELVFPSKRLFGSKKDHVVKERAVELYRFLIKLLFLTHKYRKAQKTRY

EQYMHALPNHQKEAFAALQNRSQASISVFYQLRDFLKPHSSPSDGLVHSGDLPKSDLSGQ

GDSDHFRLIRESRMLAMTTSSPKEPNLVPHKSANHVLGPTRKESRTCLPQTKEETHEMAH

RTKNHTTIPYRSKKTTTILESAPFNEPPKPRHYSTPDGTTVASQRRNARAKTSVTAPRTV

ASSSFDEPEPEHEKALKPPFSTSSSTLSNKERNVSNQTFSTRFSKSSKRDSLDQSQRKSS

QTSKPLLDPTSFSLSILDKKRFSRTKRKAKTVLTTSLTESERLSRMSSALKAQAISISAQ

RELEKHLNEYSAIMVLRYVDRFINRAVMKAPGCYRVDTSDRLVIDAQRFLHELEDTFTDL

PPTFGTLFQIGTLKHDDEWGIPSALNQYVQLKWDSFQAMNSSRFSYENDQSSVADHTSDS

EDSEYEYEEVSTSGYLSTPKHHFSTDEESMLQEMIANGTAGREQMLRLRRQTNEQGWHRR

QAPVSKSHCVVEEASSSGSDDDREGFKNPLEKRRSKRVEAKRSVSCVVEKYQQEQNARRK

DRLSQFGSQSIGGFV

>contig08726 Frame-1F

MGSSTITTNDASGRRPESILLSPIAVDHS

>contig11401 Frame-2R

MSGCRVIRRFASIHNITTHSLHRNSTNLIHTFSQFQLPASRSFMNASEQVQSLINSLEAD

LGIDADAPVKNFTQQNDQTKNTKTPFVSKAPSPVASSQPEITKLDIRVGQIVKVWKHESA

EKLYCEEIDVGEDTPRLIASGLVPHYTLETMQNHRVLVLCNLKPRNLVGFRSHGMVLCAA

IELPNGKEHVAFVMPPKEANIGERITFSGLVGDPLTPNQVEKKKVLTILGNDMKTDQHGV

AKWKEYVFETSAGPCTAPVNNGVIR

>contig11496 Frame-1F

MLRNAWPRHGRRLLSTAPIVSVTEAMERFQDVPNFRQYPNFFPVTMSVREYQHKFKSLEP

KSRCTEESVALAGRVVAIRHASKNLIFLDLQSDGHTVQVLSEAKHFIGCEGNRNGDKEAA

KREFRALHDSLRRGDIIGVQGFPGKSGKGELSVIPRQLEILAPCIQPFPNTKYGVKEPEI

RFRKKYLDLLTNPEVRPIFEIRAKIVQSLRKYLEARDFIEVETPLLFSAAGGAAAQPFMT

NSRALKTDLCLRIAPELFLKQLVIGGLDRVFEIGKVFRNEGMDASHNPEFTMCEFYQAYA

DYYSLMETSEDMISSIVNNVTGSFKIEFPMHEEDTSTTVEIDFTPPFKRLPILETLENCL

HEKLP

>contig12743 Frame-2F

MSALALAAKSDRAVVVEGLLNYGAKVDIHTLHGETPLHFAAASASERVCQLLVEKGCCVD

VRTSKGLTPLMIAVAQGHGMAMEKFTANALSMPSPKGDINHDGHNHHQNTTLELRNSDRV

DMASAISVIDYLIRSGAEASAVCELYRTPLHYAALYGCDESYACILAKLGDECIAERCDL

FGVSVAVAKANRYTHVVANAMLPDNLCAVRSDDDDDSDDDLDEVEQADIPMSLSGRRTTV

SVKNLVTEEKNGVEEIIAGTFDAIANVLLHIRNYRMEELSALIWSCAYASNGSGDKFSEM

VGILRNFWKQHSAESDTGVYVRRIILSALNKLVEILKHSVECDMQVCSHVAELYADVVSH

ENQLVEEDPQCAQWVRASLLPEFVEACQSNRVRDYQ

>contig12808 Frame-0F

MNHERITNGFIPAKSYFYSFNLPACLLSVS

>contig14323 Frame-1F

MTVPAEEYSSQEFMEKELSSGSTLHRESEKSALRRWWQCNHNRSSENGSRLAAGHEAFSS

TTSESDHRSRQLSIPHTVTEKNGGQELWVKAPVVSGSLEKRGFRWRKKWKVRFVELNGRQ

LAYYEDSSKIHRPTTATANRSKKNRTLKMNVEITADAVLTDVDALTLSITPA

>contig14781 Frame-1R

MSNGVGFTVFQVPGAKTAKRSTSTKLGGGFVLSSVGSSHSVGEPYAASPHVGSSFDLSES

SNVPPQRTSDATFASFQPPGGLQPVSTQSLRSTTALLMPSVGPMPPLSSSSLHSPASFNA

KPSDEQVRGGAGWMRSGRIIRVKDSGDCFRFPLDADYLPTLNMSSDQFATLKSKCHNLAQ

LYINSTATWLDNPIQSPQYRNQNWKLQLEKKNIVIYRQKEMSDAPNVHRKMIVRAKLDTT

LEEVEYAVNCCTTESQRAYMAHCYQGNFLDAAVVQVQEKATKDDPFQFLGVKWLAFQSPM

DSIMSCRDTMVLEYSKTLLDAKRQKILVKVQQSVNMVDYHGNEHNFGFLRVSGTWVWLFR

GLGPSSGKVDVSMFGEDWFEGPRNPPSWFASRVLSTLYTVTIHHATAADAKFFVQHRRIT

DKAWVPNHERPACSICYKSFNLLRSRHHCRVCAEIMCGTCTYELGIQASHLPPNMLPDSG

NSIIVSVEKFCLKCINKARQERRSAESQEMDLSTEELSASLVVSTTVLREDEKRSKPFMT

DLLEPQLQQDLSVASISSTSSVLEANATNGEWSGISYTGWSTKVLSAINREKTCDGTKER

ALVTLTPAGNSESLDLVGSSTALQQESNDRRRQSNSSTNHRVMRNFSSVDSKGRKDLNAG

DAIRLLEEHHDVQKNMTPLPTSFSKMEEQIAAQQALLRSMFIEGKKIMKQQQALNEQVHP

PYVNQMSPMPSIVEGKNTLTLPPPSSASIEYIE

>contig15269 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64029.1|) 1e-24

MQRLKFDETALELFARRPTSSFLTGLEFIDAATTRNDEKIAGYKPRQVVEICGASDTPKT

EVLEHVVASFLTSSS

>contig17241 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54794.1|) 1e-136

MQCVQQNNGCMRENAAKVSAVAMSALSSATFGVFGEFAKFGKRVGWGIICADYLLIFVRA

VIRFTRNQLVNEPETTEEKLLLLLYQTNWVVVDLPATILVCSGKVPHKNLQLTRLLLPTA

QYLLLLAMTNKDNIIENWAMLKAFMIHANFSAAAEQLTEGEISSLEAGMKQNSTCGEDLK

TLTTHVWSTVSAYRHQNPKIKEGDLRFKVSESTLVKVRHSHSN

>contig17634 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65920.1|) 2e-83

MVGFLRKKKSDRAVLSGDTVLDRKGKVDGASLLNGDGEPTEGTLYDMHGKRVSHTQRNSD

EENRSKPVKNASYPPVMATGMYPPQHSGFGQQQIGVYGFNPNQPQQYGQPQQQPYGQQQQ

QYVQTQQQFRPQYGQPQQYGQPQQGQQQYRQPSQQFGQPLQQYGQPQQQSGQPQQQYGQP

SQQYGQPQQQHGQSHQQFGQPQQQYPPTTLGGQYQYPVRYGQMPPPMPSASSKKARFRLP

GMGKKN

>contig17894 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63496.1|) 1e-126

MADAAASVTDAAATEDLTPSKTILNGMRVYFVIGAIGWLAFEVGRRKLQCAYYCREGNLE

TTNRFVTKCHDAKVFGWLKLLYFTRDDDIFESCGMDTLFFLRFLRLCEKVTAVGILCSVA

NFPIYYYAQKGSFDALYRMTLSHLVTDQRWRFWFTVGTMYLVSLVTCWLLWKEYEEYIRR

RHEFMSRRSPQQYTVVFNGLPPHLCTPQTLRNYLELLFPKSVLHVYVAVECEALEKLVAE

RVKVRNKLEHVLASCAKTG

>contig20063 Frame-0F

MMHSPLDASELTDGTSVKEVAPFLKSLRRMLDSESARILRWTPDGKAFEIHDMAAMTSYV

LPKYFKHRKYASFQRQLNYFHFRKWTKSRAVVCTFSNQFFQRDQPALTWRITRKRALSPP

HSTTVNETLSMSDVHFSKDVAPVVTVEASLPLTNCPADEDASLAWVDVLYAALDFDDSTP

TRTDCFA

>contig20188 Frame-1F

MMRTRHCSRIFLTSLRRLTKHRRHMQDAQECRESGHLHRNGGIISFSL

>contig20261 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57429.1|) 2e-75

MGDKSLFQVGSDVEFWRVLVHLSILALCLVFFESALHYVEHHLARYDKYQHMLRKAYREL

MILGLISLGLKLFKEVPGVAPDSKTMLAFQVADLTIIILALALILQAIVVFLQLRKCNKL

ADRTELITAQDLVDGISPPAGTPPTAATPTHPLASKWWFQSSRMIQGFDNEVMERRLLRH

LFLRRFGLPQLFPFSKYLRRAQANQISHMIEVEPTMWLLLLAVAWGICGVLSTLHQVQLD

LSNGHELVEVFVVF

>contig21622 Frame-2R

MNVRIYCEVFLQTFRVTEAGKACIKGFQYIF

>contig22087 Frame-1F|Blast-pre-mRNA-processing factor 19, putative [Phytophthora infestans T30-4](gb|EEY52940.1|) 1e-100

MPAISAGQPTKSTNETRCACFHPDGGIFGTAAKSKLVQMWAMTSLSNVVTFEGHAAPVTA

LSFSENGYHLASGSEDGVVKLWDLRKAASFGEIDFKKEHPTLHVGAIYSMNFDASGSHLA

VASAQSVQVLKEVRKNQWEVIKSLEDHTATVTSVQFAPDSSYLASTSMDRSLKIYR

>contig22490 Frame-0R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY64252.1|) 8e-87

MDVGTNVWVKSKDTFVWAAGEVIGYRDAGTLVQVRLQDTDKVVVYRYPGTNDDICLRNMS

VDFSVMTSLTSLEHLHEAALLQALNERFDHDHIYTSIGDILVALNPLKPLPNLYSEKQLN

AYMQVMTCAGPALKGKELPPHVFSVGGKAFSGLLKPERRNQCILVSGESGSGKTESTKFL

MQFLTSVGRDPSHPKEDKGGAVEIGKRILQTNPILESFGNA

>contig22515 Frame-1F

MQTNKHANRAVGVWSSDEHDRFLEALKNFPQGPWKTITACVGTRSVRQVQTHAQKYQEKV

SRRLHGLQTGKATRLRREHRIDHDILGLHTLISSPSNVSYNCFNTTQVQLLSNSPVIERL

SFSSTPRIKASSSEHCGNTSSDGASPSSTSSLFLFENPMFALMETDDLPSLSESLDFFIE

TLI

>contig22968 Frame-0R

MTRRFILCFYQDYNIRLAGSICWLERSGFTGETPQRVVVSWPILLEGANREVRPKNKKRY

SHTHPLRQVFEKL

>contig23291 Frame-1R|Blast-tryptophanyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY61871.1|) 0.0

MVRKQKQKEKQSKPSESAKPAEIAAVPSDAELLLRQSTFQYQKESTGVANSTQLVTPWDV

EAEDGVDYDKLVEQFGSTKIPPEMVTRMENLTAHKAHRYLRRGYFFSHRDLDVILNAYEK

GEKFFLYTGRGPSSGSLHMGHLIPFTFTAWLQKVFDVPLVIQLTNDEKFLFKNQTLEESE

VMAWENAKDIIACGFDVKKTFIFTNTDYIKEMYPQILKVQKCVTYNQVRGIFGFTGSDNI

GKSAFPAVQAVPSFSETFPVVLGGRKGLRCLIPHAIDQDPYFRMTRDVAPRIGYLKPASM

HSKFFPALQGSTTKMSASKASTTIYVSDSPEDIANKIKKFAFSGGGETKADHEKYGANLE

ADIPYQYLSFMLEDDEELERIGLEYGAGRIMSGEVKQKLIDVMSEYTLDFQKRRAAITDE

LVAEFMKVRTLEF

>contig23570 Frame-0R

MSPSGDKKSVMYDVNWQKVWPDRMPVILRDLAPTNPFNPRNLWPEEQEEEAPSTQDKKGI

VKEDKKAVLNAASGKLKKADLIRMQLAKEKAQKQSKVDEEKLANVKKSKNLIDMKMVTPT

GRLKQLYEILRDSCKKKEYTDAVDTLWEIQRIKFIPERTTGPLARTKHDKQKTMTEIDDG

KLLEEINAVHKKYRKYVKVINEYLADKDLIEWQLTEMSDRLPPLNMHHMNKFILDDWQRT

VLTHIDQNHSVIVCAPTSSGKTVLSSYVSVVGGKVLFIVPTDPLAWQVAALFQAMVKGSV

ALITEGTVFLPPGFRIAVGTPRAVESTLVEIGYDFQYAVYDEVHDLNGSEGDALERIIKA

VTCPFLALSATIGNAEKLKEWWETHLERDVHLLEYKGRFINLQRIIWYEEKVEGDQTNKK

QEMVYLHPCAGVTLEYLTTIGFDAGDLAFTPRDAFALWQAMEKFYPSELIEDVDPHKFFK

LEAETEGEATAAAASCKNDKRSKKDKKIKKDKKSKKGDNDDEEYIVDLGKRTHRITLMES

KKYEDQIKKRLEDLASQEPKATQSLLDFFAPPTNLQNITVKLHNPRDMNPTSLVDVYSLV

CQLCTKNLVPAIFFQLNSVRCRQLFNQLLSAIEASESAKYPNFREKVQLEYAEWEKNQIA

MKKREAKIKAKGKEEDDREAQAFEEKSPPDIYAPHPDFVLTPVGSRLTATEFKEIKWQLR

RELSEDSDDGHALVRSLRRGIAIYNQNLAGGVLANCTSTCSGRPSGGRVFR

>contig24702 Frame-0F|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY60954.1|) 6e-25

MGAESKIAYEAEEPKKIAHNLADNSIPAVGLNRIEDECFSGKKQEADFAVLPIETSFPCS

TYANYELDLQCKSHVVSESTQRAPLTPEHQPDQTLYNRFFLQPNIKDMTLDNKISGEQYK

TSLVFGFKDSTVND

>contig24841 Frame-1F

MGVQPQLTHLHVHEAPTFRKRALGSIHHTVRRHRHPETPAETLPKEAQQLKEKILRTHGA

KRTRFSLSHMKKRVMPPVEIPRAMGSHRALTTTVSGRSVPLTRCMWDNTKRKTHHMEQIP

ELYPLRCTLFR

>contig25015 Frame-2R

MCDMCELNFYVTGYAGAGKLQRGRRHGGG

>contig25604 Frame-0F

MFRTFSATTAVFIALGLATEGRLWQWIPASYTKLEESERKILSSAISTFFEMKKVAQLGT

VVVPCSVENNRKSAENLVLIHGFAGGNAVWAMNLEKLSKRFNVYAVEWIGVGRSDRPDFN

FKDYDSANDFIVNSFETWRQEIKLESFNLCGHSMGAIFASSYALKHPA

>contig26159 Frame-2F

MESYERKLQRHKKELESERMKNMLPFERLEDFSIAFKRLCSSKYLYHGSSSKIDTESLRS

STSSSAPPSSGAQGGRPPTSPIKETTTAIQEPSKGSTTDEHGNRHSVIMHTAGSQICISR

ASFRRDILGVFPDMPSSFAMRFMKAVSDRQGSDINMDEFLRAVAILNCGTMEDRLQFIFN

MCDLDHAGKVQSTGLSNFLVSLHGRHVLDRPENRRLLSEGFDQGRVRMSCDDFIKIVPDL

EAHHTLVDWMKSFADILCETADPQLLESQEEFNPIVQQKILANETHFSVKEVTVLRDAFN

NYRASGGGDAVDVDALTSDFPLEMSEDRFCRVFASFGSRANGSEIDVFSFVSALSIACRG

TTKEKAEFAFKLFASAGDGSFMTREDIYGMLRLDITQNSELESQITSIIEKKHLALNATK

SLSSSSLMDSMGPRTPSVSGSELGIFVDGLLKGYGQRRSIRDVSTASTKALMLTLDEFTL

WAIKQKYEMSTLRIMREVAFIDLGLVPSTKEEELLIATGCYTPYDPATLVEDDRWYLVER

KWFIHWCRYIQIHVKESLALSHSASNSTLITTSASTSTPSTSKVQVIGSNTPQKDNYMKN

LKGEIVRPKCINNYPLLTSDRRDRILKTSDGIKFGRHYFIICEQLWMALKLWYGGGPEIQ

RRVVIASNGEPVLDIWETKSKLLKKKLKETETPSIDLNKKEDGEDVEDDFSSVPSEEESR

RKQELALPRRMRSGGSVGLANLGNTCYMNSALQCLTNTKLLAEYFLSGMYMEDINRTSTL

GLQGKLAG

>contig26511 Frame-2R|Blast-COP9 signalosome complex subunit, putative [Phytophthora infestans T30-4](gb|EEY63010.1|) 6e-61

MDNLVMTLETQRDELLAAYATTGNREIAQKTILKLKSVFEELELVIAASTTSPRPAALTP

GLYATYLLVVLLSKNLNDARFLWKRIPNEIKQASEELRNIWEVGKALWERNLAQAYAAMD

YDWSLTLDGLVKALKTSTREDATELLSRAYTTIAISDASIALGFARHEDAAH

>contig26753 Frame-0F

MTDGVDDVNAKLGVHVEDLCNETPPNPFLFPRSFLSMHTLHDIVGVHPFLPTYPPQILQW

QQPNPITESCVGKFFVSAAMGYVMGNVFGLVLGSYEGITPPVPLPGQREMPKVPWRES

>contig26847 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65632.1|) 0.0 NOT\_ORF

MGFAHSLEVLYALLRLYVNGVVSSFEFSNIPYPHLQQRLQQTLRAVALTVFGAVITPLVV

LCFEPLLSPLEFPGFTAFILVTIALWVVTIFHLTLRFALLPTPRRIETEPVRGRLQAAVC

VIVDAVKRVQQQPQLPILIIMCVAHSYAWKLVLYNAMASNAFVAMDFESFAISGGLVAFI

SFMLFENSLVDDPFVLDPRAAFSRAMKRDIVRAIRRGVLVYVVGRVWSWLFSSNIEAKLT

VPETWFFSLNVVRVSFQVTTSVLENFALLSATSVFRILLFRPSHQVVSAAILKTNNLWDA

LATVKAKNEDGLDALFSTVIVANPQTTLALHEQYVQGLRNRMDAAAKMISDKRTPKAPAD

AEDVQIIDSLFKFDNLLCGCKFNAAARGTLFVSRDRWNVLFSSTTAVVDEFTLMLQMLNS

LPEKKGDADDNSPTGPLALEQSVAALHHFLNTQRDVHSLFLLQQYPHLANLRISTASVKS

SIRFFVESKLQFAIRRNLMIEARRRVFDRVKVVNAAVSLLCHLVSASRSEDKQGFVQVRL

GMY\*KTMFFTIYSMPRQL\*HTVPAVLTSLVECHNALIAYMETCLNESKTTKVYVKQATGL

A

>contig27008 Frame-1F|Blast-Rio kinase [Phytophthora infestans T30-4](gb|EEY65501.1|) 0.0

MKGDDDFCLSKVAENQLMRSLRDEESGRTRHTGRDDRATTEQVLDPRTRMILYKMLNYGI

VTEINGCLSTGKEANVYHARLPNGREGAIKVYKTSILVFKDREKYVSGEFRFRHGYSKSN

PRKMVKLWAEKEMRNLRRLHDADINCPAPLLLRSHVLLMDFIGQDGWAAPRLKDAKISDS

RYRECYISCIKMMRTMYQKCHLVHGDLSEYNILYYQTKLFFIDVSQSVEHEHPSANDFLR

KDCRNIADFFRKTGALNPMTTQELFDFVTDPRIADEGVDDRLEAIQCLIADRPIERTNEE

QVDEAVFMSTFIPRSLGEVLHSEREQLAYQEGTMEKSLVTAISRLEAERGVTPAPVMRGM

RVMDLLNEEDEQDISSCEERDEEEAETPIDESSDSENDSEEEDIKELLSETHLTDEQRSA

FRQEKREEREKQKARDKLNKKIRKQESKEEKKTKRQTKIPKHV

>contig27282 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66740.1|) 2e-17 NOT\_ORF

MLNKALYTVAQRKTNSNHDVGAVGNISHRRDIPAILNRCIFLLDFRKAYETLDREFLHPT

LQRFGFNKRFIALLRRMHTGTKA\*VLINGKMLDAIPVRSGIRQGYPLAPLPFPIVVKLL\*

LALKQGPTLQGPS

>contig27813 Frame-2R

MICIFSLHRKAHLDPNNCLLGRINCIPSYRPK

>contig28122 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60031.1|) 2e-21 NOT\_ORF

MVKALPVTDLRSALSAA\*FESIRLAKFTFVSFNLWDNHLELDVLGLL

>contig28438 Frame-2F

MPLLSRLVSFVAIISTARGSFIDFRSVDGHLTANNESFQIKGINWFGAESIELVVQGLWP

SATSIGDALDLFVTHGFNALRLPLAMDSVMKDPIVASTQTAGTPSLAGQTYLEVLDFIVR

EARDRNLLIMFDSHRITASEPDFPDIAVPSDISPALQKLATRYCNDPGAWNVFAMDIKNE

PKGKASWGKGVEATDWNLQAAKIGNAVLKQCPRLLIFVQGVQTNVKGVSLTWGQAGGSLQ

GAKTYPVKLSNMERLVYSPHVISPGVDYKSPWWSDSSFPENLPEIWDAYFGFIPKETGQA

VVVGSWGARMKDKDKEWANALSTYLTDKSIGSFYWAFNPQSADTGGFVKDDWITPIDERV

ALLDPLPTTNVDTFVAVYAKCSGTCAGNGGCEGGKCVCYAGWSGPQCEICSVGDTTACND

MGACLRNSTCACEDDADGKYCAGTECDEVDCGAGSTAGCFNGECTCLYNCVGTSCAVCAA

NEVALADASIGATLLCDACDAQTRSDFSTAQALAAFIPGIAALALIFTIIL

>contig28540 Frame-1F

MHSKYKNSILSTSTWYHSVPKCASHFQVPSMAARLRPRTRNHSNDPEKSLPIQKALLKSW

SPQTRRWVCLMLLTFVLITLLMVSNNTFEKRPDNFISSSLQDKKTLSYLHAHEDLELRTN

ITFAELESSYSNWNHVLKAQDERTIAEAEAHAKNVLPFPVWEAKRRRLRCIGWKATSNCT

PDGFRVPGLDFPCNTVVPYGSSGYCEVTDKDTGESFRVMHRYCSSMRDGGKFRCSDAWEF

ALVPQKAREVVRKAQISNLLLPNIAPNPLQQTEPRNGIVMVV

>contig28607 Frame-2F|Blast-acyl-protein thioesterase, putative [Phytophthora infestans T30-4](gb|EEY59172.1|) 4e-67

MLVARARKPFASIYLRAMNTCRMTTNANNNIVLSSGHPTAAVVFLHGLGDTGQGWSDAMT

MLAKDLPHVKFVLPTASSMPVSLNMGMRMPAWYDIKSLSHVNADNADGIDASRDRIMAII

QQEVAEGIPLSRIVLGGFSQGAALSLFSGYQSKTVLGGIIALSGYLPRHD

>contig28672 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60956.1|) 3e-09

MSSICVTHLWCERNDAVFRSVQSTTTQSVLSNIFSKQQKNSAIQSQTITV

>contig28881 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67986.1|) 3e-47

MAASTGNASLNSYTITNTSKTRNLIFKSMSEKREREPSSTSLSGIWNPMVEPLVDSASCK

IDNAAAARVVSLAKEVARQQTIRALCNKIRRASEDLGINKLTSSAFETWQIISKLTGNEQ

DPLIPHAGSDYSGLFEELRKAGATKSGATKKCKELMHESERMLHKFNHQEFVSGKKRKVQ

KVISEDSMCHLTYGHVVVKLSVRHYVKLREMYARKQGLICDGSSMAPKDQHEFERALFCM

LLRYDTLNGGGT

>contig29143 Frame-2F

MDLLLLLQLAWLFAVLIGLLSFSSHFCRCFVLHGKTRTSAAIPQFLRIEVPKSYYTWFYL

IGALHSNLILALVIIWKDTRMVQKALHLAHPLAGLVGNGAIPIQPHSILFLTLFSVHTTR

RFLESLLVTEFGDSMMHAS

>contig29824 Frame-1R

MQHSRSDVALGTNGSWADLKVAEGLKKRSNTAQNLQFYVEEQKRLYQELPFSVLPGMRRQ

SFQRERSFSNLKSRSSWGSFTNLVARGEDQPLLGADDEFPEPGYTFPLLLSCGVALMSAF

QFGYNTGVTGGINPDVIFPGHSDMQWAFCVSIFAIGGPIGSLTAGNMSTVLGRKKALLVD

SFLFIFAGAIMALSVDIYALIFGRFLVGFASGTVSVVVPLYLGELAPPNLRGALGTGYQL

FMVIGILAADLLAFKFSGESEGLSQPGWRFLFGFTVVPGILQLAFASLLTESPRWLLTKN

RPKEAADILRRLRGSNDVYEEIDSICSASDNESGANTGIWDVLNDQSIRFSLVTAVVLQV

AQQLSGINAVMFYASSFFKNVGLKDPLVGATLVYTVNVISTAVALVLMDTAGRRPLLIYS

AIGMIFSSVVLTLGLMNVLPFASMASVGGVMCFVWFFEIGLGPIPWLIVAEMFPAKPRPT

AMSIATMVNWSCSFLVGLMFPTMQRVLGEYTFVPFCAALCMALAFTLKYVPETKGKTIQE

IQAELHSNKQHPIKA

>contig29899 Frame-2F

MQPHNLPPRGFGGPPSSQQHQGPQSGGGYASPGIGYGNMQYNQQQQQPMSQPTGSFPGRE

FPGVQASHSGIGGNRPGFQPTQQPLSSGTYRPLQQAGSSSLSGPLSNGNRAMAGPPGAPH

GQRAAYPGPPTQLTAASGPLLAGSQNLPGPPRPPFQQGIPPGRFGAAPPPQGARSGPFPP

QYNVPTQDMPLPGAAPHLQPNRNAGPYPGVNAPPYSGPEAVGPYGQPQPGGNMPPQQSQA

SQAPKQRIDPTQIPRPIVSAERQQYIAHGHTVTMPPAASSDYVCVDEGCCNPRFIRPTLN

HVPSTKEILNQCGLPLAAVICPLAVLQEDERPIPLVDFGPSGPLRCTRCAAYVNSFTKFI

QGGRKFVCNICLLNNETPREYYCSVDQYGSRRDTQERLELSRGSVEYVVPAAYTIRPPQE

PILVFLLDVSHFAFQTGLATSALQSIQYLLPSLAQNRRKKIGLITFDSAVHYYRMDNDVS

SISISICPDVDDPAAPLPLSSWLVSMDDPAASDKITGLADVIVRTFENTSNNQAVSGAAL

WSVADALSVSGGRVVLLHAGAPRVGIGRVKREEVSGAYGTTKEVDLYTPEDNNVYENLAR

LCAERHISVDVFSVANTFASLADVGRVCELTGGRVQYMPQFEKEQSSNHHHLTSMLQRLV

DRDCGYEAVLKVRCSAGLRVDHSYGNFYSARGANVFTTDEMEFAVIDQDRSMCVTFAYDE

PLAEGTDAFIQAALLYTRSDGLRCVRVHNLALQVEPLLSNVFRFADLDATCSVWQRWAAR

QFVDKQLMRTTPLAVKESLVDQCVTVLFNYRKFCASSSASGQLILPESLKLLPLYTLATL

KSRALRENIMGNPPRGFIDVRADERVMMMGLLNSLPVEFCVSAVYPKLYSVHDLAEDCCT

LDEDGKFLLPHQLPPTAEKLDEEGIFLLHSAMCCYIYIGPKVSADLLLELFGVDHADTAE

QTLHLFGAPETEASDGDTMTARERLRSLVEYLNSTIPISQPLEILSKNDWRANRFMSALV

EDRTRNDVSYVEFLVQVHKKIQYKFHKT

>contig30044 Frame-0R

MTRLIFLTVQFLDVTNLINQLHSITRVFYQSLCVICCKSTSHLPPVRVTMLSCKAFLKLL

GIAVALSASTEHTGRAYATSYGDASPSVSNTANAATQTAQPKSAFSPEPASPSVDSSKAQ

SSSNVKEGIPQDAVLGNNDGGTRSSSNVKTVTAQVNDGTTSSPNPNQPITKGEGPFGTGN

NDNLPNSKSATTSSSNGFSTTTESHSSTTSQVQGNPSVTKVGGSSVNTNSASNSDVNVGR

GVDQGKTATASASTNNGVNSVGSTNSNVDRNVGQDKTVTASASTNSGAEQGNNPF

>contig30178 Frame-2R

MRPSMTIWWYCSLQAFLADARESEVNKIQISALDCIAFKYWTATLTRDPAKLKINKAADD

AADLWIGQRFSKKVLRKGLKKPLLSSIQPAFEAVPSYDNKNVRLRVVK

>contig30233 Frame-1R

MLKLFKPLHWHLLLFKIKRGPAT

>contig31421 Frame-1R

MHDNFSLLASANKALPALIKFEDCHSIPWQQIAPNNPQTATFSHPLPPRAPSPVAKTTHK

QLFVCTEVHCGKQFPRSFALRRHMRIHTGTKPYECDYEGCTQRFNTSGNLSRHKRIHSGE

RPYPCIFESCDKRFNTSTKLKRHMRVHFPDGQHVFRCMGYDCTWSCDNYKEFAQHQKVQH

HVITGASPKDSYRHQETGSEQKKNLYLSTSNGTRGHLNETVSECHASMTPTTTFLCAKTS

VKTYLDCTKRIGSPIGLDSDLPIFSTTRHKNLCKLVAEPKSPYGLDSFRVKLSSAFPSMH

LRSPGRSFSINSNHVVNHQSFSSNCSHFLPRRCDEERGTRSSYYPNHSQQMFLLPGNHML

RPPPDSHPECSYSGLAVPSPMNHAAPDLTGEELNVVLQLMNETY

>contig31612 Frame-0R|Blast-CCR4-NOT transcription complex subunit, putative [Phytophthora infestans T30-4](gb|EEY67624.1|) 0.0

METHPVISASTHPAGEVGNFLKTGIVGAAGAIGAIAAAGANVGAESDIASTDGNPSTYTA

ELIEEQANAYFQQIYTSEQNINDVVAMLKRFQGSRDERERQIFFCMIHNLFDEYRFFPRY

PEMELRITGVLFGKLIEHQVLPSNFLQTALRSVLESLREPINSKFFFFGACALQQFVPRL

RELPAYCTNLSQISHLQHALPEIMRQVNQVTRAIAVSGSSSVELSPDGNVALSLGDSLQS

ISTAVSRDGVPKVISNAVSFGAKLPLPTNSITKALDDIEIQIPPSILSHSAGPSMTSTSP

QAPTISPPSPVTSKPVLSVDHIFHESSKMVENEKVEQPDENVKDRIHFIVNNMSISNLEV

KISEMRKMLLPVFHGWLAKYLVVKRISTQPNYHTVYLIFIEKLMRPELEREILERTFQNA

RKLLTSGTITTNSQQRSLLKNLGSWLGVFTLARNKPLLQRDLDLKELLYVGYETGHLIAV

TPFVAKILEGCKKSKIFKPPNPWVMGLIHAMSEIYDVPDLKLNLKFEIEVLFKLFKLNVE

DQRKTHLLHTRRPPPRTANPDFNVKIPKNLGIGQRSATPPPSSGIALARPFTPSKAKKPS

NTFAPTGSP

>contig31928 Frame-2R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY57874.1|) 1e-154

MSPPPASGKKVGPRDLINGGLLQCVEAATLGMPFEVWKTRMGRFRTETTLQAFRNVMQEG

GGISAFWAGTGPKMVESGSKGAILLYSKEAIADSLLAAGVGKSATGFLAGAGGGVCQVVV

MGPCTFLVTGAVTGDRSISTMQRIHNVYGAHGIKGFYPGGTAIAFRQATNWASRQGFTEI

VRGQFKVLFHGDKDAKLTVAQEASAGIVGGGLACWNHPFEVARIQMQSAADRGEPKQNMM

QVFRTVIKEQGYGGLFKGIVPRLGLGIWQTLFMVTGAKLVRQALEDREAGKK

>contig32051 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57868.1|) 0.0

MVAKKDLPLLQHGSYAAPSPTASSVSSSYSRVASEELIVPAPDSVNSVYYGVDAFSPTLV

DFYTMDQKRIVWSSRAHRKMMTTLHRAWHGKAWKMYSLSFWASLFAIVAFLFFITGATGE

AMAHSVRGFNAAREPGNQIHTSVDLPLLFAAVFFFAYHAVTYLEVINCCHNLEIWLEEYF

HGTEPVLERQYVGFFPSRIDFWTAIMGMLGSMLYVFARAYVWARSDSENFGIVNVERDEL

SLIMGYWVPFFAGSFLLLLSAYLAHVEVVHQWFSCRLTTLETWVTGFNMMAMFGFFASST

LQFMDPFSVLFPFQACVVPFATGCLLGLASSVLSLVELENIHKRHKHPEYSLYDSPAGRG

SWSYGSFKQQV

>contig32543 Frame-1R

MFTAPTALRAIRKEDPQALLLKIKKDEIRRTLKTMFVAGERGNPKTFSFFSGELGVPIID

HWWQTETGWPITAPCFGMQNDDITEDGNPRIKVGSVARPVPGWDVRVLKGASADKDENYN

HEFEDQDAELVVKLPLPPGALTTLYNNSDSFRAKYFKRYPGYYHTGDTGHIDDDGFVYV

>contig33056 Frame-1F|Blast-metalloprotease family M67C, putative [Phytophthora infestans T30-4](gb|EEY69372.1|) 7e-57

MCSMTNEEELFDFCFSNELLTLGWIHTHPRQACFLSSVDVHTQCGFQSLMPEAIAIVVAP

SDANKTVGVYRLTEPSGLQLIQNCNLTGFHTHPSDNQIYSEAFEFKWLEQVTARLVDMR

>contig33632 Frame-1F

MSSKVQKLMTQPINLMFRFLQN

>contig33953 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61074.1|) 2e-27

MNYKARFSLQSLFSLNHTKAFDKKTTIFDGFLYVL

>contig34192 Frame-1F

MDDSATASDRRGMWSMVKEGYEGLVSTVIRPLRAQYAPSELGPKRVQIGEILMQRTDLKL

KNPAGYTLECSWWKPRKSKTGHQGKLPCIVVLHGNSSCRLGALEIVMYALPAGFTVFAMD

FCGSGLSEGKYVSLGYHEQTDIAMAVKYIRKTKETSSLCLWGRSMGAVAALMYADTNSTV

NAMVLDSPFSSLPKLATELVEDGRLGVPKIAVKLVMRLIRRDIKKRAKFDIFKLKPINTI

HKCVVPAFFVVGLQDELVGPHHVEALYKVHNGPNQLYKFPGGHNSPRPFNFFIQALQFLR

VMVGLMPLPDDLSTFDLSPAQRRQIQSNQSDIKVFPKRKKPIRVYKNPLEPGISIESVHK

MSIKELKQCIDRAGYSDVTCIEKCDMVDLVLKLYARYRRSSKYANDDRRQKRTVLAPEID

ENGATSASKASPTSIESEPMTLKIADAAKHRRRSEGDTFPPVGKGTRTSSSPRLPSIQST

TPSILSDAELARRLSIDHSCDTDTEDKLAEEVSMDY

>contig34839 Frame-2R|Blast-50S ribosomal protein L15 [Phytophthora infestans T30-4]gb|EEY55120.1| 50S ribosomal protein L15 [Phytophthora infestans T30-4](gb|EEY55118.1|) 1e-118

MWKFKALDRTLPAICGVRVAFASSAPPVSAFEVVRLNTLRDNDGAHKRGKRLGRGIGSGK

GKTSGRGHKGQKARSGGGSGRGPGFEGGQTPLYQRVPKRGFNNNFATPMETVNLDKLQLF

VDMGRLDAKKTITIKSLVDSGLATCSRVKHGIKLLGNGGQHLTAKIDIEVSQASKSAIKA

VEAVGGTITSVYHNRLALRALLKPHKFEILPQPARPNPKKLTYYTNYDKRGYLSPKIQVK

QALANASNTN

>contig34884 Frame-2F|Blast-DNA replication complex GINS protein PSF2, putative [Phytophthora infestans T30-4](gb|EEY56943.1|) 6e-33 NOT\_ORF

MPHFQVRDNNGMLNFICVILDHFTPALRCMCHYGWPLC\*SSFTSAAFWPHLGSQSVSGMV

DATQRE\*CSRSLYHIDLTVEYLTAQLEREKTSDVFEELPFHYLEVASLLLKK\*VQIYNV\*

TLSLPHVASVKICSAPEDLEQGEHLRLLVEDLQNVRQDKIRNGLAKIANDVQSGGTAISN

QRVI\*FVSNVALQSLNQFYQLSQLTADSSACFDCWCHKYTNMYNVPFSL

>contig35043 Frame-2R|Blast-alpha-actinin-1, putative [Phytophthora infestans T30-4](gb|EEY60523.1|) 1e-126

MKKFVAMAEEMVEGVKSNLQDCLRVQQNMDAVAKDAKTLMRNLKYVIEEMDEEIEAATKL

QDVSTAGVVAAKHQFDTVLVPKVQNAV

>contig36374 Frame-1R|Blast-60S ribosomal protein L15-1 [Phytophthora infestans T30-4](gb|EEY64058.1|) 1e-113

MGAYKYLEELWKRKQSDVLRFLLRVRAWEYRQLPVIHRVTGPTRVDKARRLGYKAKQGFV

IVRVAVRRGGRKRPNSKGIVYGKPKHHGINQLKFERNLRSVAEERAGNKFSNLRVLNSYW

VNQDATHKYFEIIMVDHSHKVIRRDPRINWIVDAVHKGRQQRGLTSAGRQGRGLRKRGHR

ANKIIGSSFRQNWKRRNTLSLRRYRS

>contig36576 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62825.1|) 3e-73

MSAADMAKLRTVLSASSNETQRFIQPLLPLKGVQELLLTFVQDSTRTFEDWVWDPQVRQS

LVHMRDFEPQTRAQGHEFDQWYMQAAKERLEAIALQEPDDVTPREFLAEADTAQSDGKVK

FQEKNYYAAKNAFLKSISAILKHQQSEYYGKSLPPIEWEDSFDLQERYVQLCNNVAICGL

KMKDSGNYERICCKSFDRGEKV

>contig36693 Frame-0F|Blast-glutamyl-tRNA(Gln) amidotransferase subunit A, putative [Phytophthora infestans T30-4](gb|EEY63475.1|) 0.0

MAPSVTSMAVAAVVLLASVLLMLGDPTNLPVMENLKRQWATNSSYDLVDLSAPILYGQPL

LALAYVARLPVLGRILCNQLAKDNKIIEARKFAASISDQPLYYPYLEPNQSDVRLDEISL

SLEEFTQKGVKSENVGALFKHWSIADYTSRYASGEVTPVQVAKALLAAVEKNQQSEYPLN

VFVEKHDNDILSQAKASMERYARGEPLGVLDGVPVVIKDELRVKGHRMFTGTSFLGYEEE

PATKDDPPVARLRAEGAIVVGTTNMHEIGAGVTGFNMHFGTVRNPYNPKCYSGGSSSGSA

AAVASGLVPLAVGVDGGGSIRIPSSSVWYCRY

>contig36752 Frame-2F

MHSRAARAMTKAAVAAGTAGTIATAYWLLNRIFHNDGYKRIKVANEILYGDDGNDEMNSD

ASFLMLPVVSESDESINDSLGYTDECFPPHHDICMLSVCIETVDPFLSPISLSDDRVCLA

PSETESTTFPSKKRRVLSFTERDGQCRQTVIFGADGDVKEWKNSLQSSGTTSQRLYVRL

>contig36873 Frame-0F|Blast-GTP-binding protein TypA/BipA, putative [Phytophthora infestans T30-4](gb|EEY65810.1|) 1e-115

MNRESKKLESGRVTKMFVTRGVVKSEVKSATAGDIITIAGVNAYVSDTIADVSVTDPIPS

PQLDPPTISMTFGVNDAPNAGKEGKFLTSSHIKQRLERECENNVAISISPSASSEAFDVH

GRGELQLAILIEEMRREGFEMSISAPQVIFQKDPETNQKLEPIEEVTIDVDSDFSGTVID

KLSTRGGEIVEFKEVHDKVRLQFKIPSRCLMGYRSE

>contig37377 Frame-1F|Blast-NPP1-like protein [Phytophthora infestans T30-4](gb|EEY58144.1|) 2e-19

MVRLFIQVMVTGALLACSYYNQLATAAFAGQPVHTQIAGKEFGDKYGGQFDYRFSKNFGD

ILKGVTISTGKRVDSIGVIFQTPQHKQVKYSYGGDGGNLQTLMLQQRERITGIEAHSTVK

DGRKRISFIKISTNLNRSIQGGTKTDDVDKEDAENGFQLMGFYGRRGDEVNSVGALWQHA

G

>contig37485 Frame-1F

MISATTFQHVFGRLCRRVGIQFRILFPHDSVQHKARGRDGVTTLEEDGSQGEGQVCIHLD

SLYSRHRSTVPYNNSTL

>contig37694 Frame-0R|Blast-Small Conductance Mechanosensitive Ion Channel (MscS) Family [Phytophthora infestans T30-4](gb|EEY61349.1|) 1e-22

MPKRLFVLALLQWANVIHAESCNDDCASVSCLPSWWRSIAAPQLVVAAVLVFFATFLPRV

LVRLLIFVITKLPFMR

>contig37889 Frame-1R|Blast-proliferating cell nuclear antigen [Phytophthora infestans T30-4](gb|EEY62624.1|) 1e-141

MFEARLPQGRIVKLIVEAMKDLISEGNIDCTKSGLALQSMDGSHVSLVSLLLRAEGFEHY

RCDRNISLGVQTASLSKILKCSGNDDALSLSAEDNGDALNIMFEATSGDRVSDFSLKLMD

IDSEHLGIPGTEYVATVRMPASEFQRICRDLQTMGDTCTISVGKEGVKFSVSGDLGAGNI

TLKNNTAAEKESDRVIITMEEPVELTFALRYLNMFAKATPLSETVTLSMSPGIPVVVEYA

IGDMGYMRFYLAPKVEEDD

>contig38109 Frame-0R

MLRTSELTPLVVESPRPLPSVISVSTLRRSAALTSLFLITGVASLLMLSLVTQQNSSVSS

VENLPSTESVNNHDDTFCGITNYETGYIKLPNKNDDHFFYWFVESKSDPTRDPLVLWLTG

GPGCSGMLALLAENGPCHVLPDLSTTYNPYSWNRRANVIWLDQPSGVGYSYGLTEDINSD

IVAENIYWFLQAFYKKRPDLADREFFITGESFGGHFVPNAASYILKANMLRHLYQSTVHI

SLAGIAVGNGMTDPAVQSQHSVDMVHNSYNISLLSGKSIEDMRNAQPVCQKLIDRCQDER

PSCIDAKDFCFGALEVPYFRSGRNPYDIREPCTEVNIMQCFHFEHIETYLNLPKVQGRLG

INVNKSKPWRECDAAIGEGFALKSFHSSANEVKLLLDAGVRVLIYAGDADLMCNWVGNQA

WVMALDWSGKSGFNSALNRQFVTSETRDAGRVRSFENLAFIRLFNAGHMVPMDQPAVSVD

MIDKFFQNEEF

>contig38332 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55552.1|) 0.0

MIAVAWIVMFLCLFNSSSALKSTAKSAAQARPRVVFSFTTTPRGIQELQPTVDALVHQEG

DGFKAIYVIIPHMYQNKVVDIPSWLLSDASILKRTNFYGITFSTGASSYDTKIQIIVIDT

DFGPASKVLGTLLVEQDPDTIIVYGDDDRIYPPQLCERALYYTHKYPNDAIAVLGGWISS

EDRLYCGRSLEIGVNSVSFVGGAGGVAVKRRYFGMGEATLLAFAVANMSKACFLGDDFYL

SHLLSRNSIRRRLVADSCWNVETLDETFSHGGLSHAPSNHSGGANVEHYQQCIRELGKDQ

DLSYDGEFGIACMFVLSRTWGMFRGLKNLMYGGKFVSC

>contig39748 Frame-0F

MMSDPVATAGVEDRRRKIESSRLTKSWMAIRFSRSGVSLRMVTTEYLYWPYMQGDAELPT

HRDHMLEVIMV

>contig39946 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY55851.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55122.1|) 1e-103

MMKSTTVVINTDSVSGSMAAAAPPKRSFIQKVNDVNKMELPKLLRYMRLGNVGCSILQII

AGIVGITSFITLNITGTLVSIYVIMFGILFLLFECRLSRMETVIRSNFGFLYSYKGRAAF

IFFIGFLDFGIGSALATIAGVFMCLNAFINLLVMCRHPQFRSTLSAGADPTAGYTMSSQE

AANFMGKNPELAAKAGQYAFQQAAVTRH

>contig40249 Frame-1R

MECKKIILDCDSEDPTLSSGGGLFIYSSFALICRLLSNHQFICEILSISMLSGAEAVRHR

TIFTLLFIGLTRSFAEMSDLFVGARFLSQRKTKGKNSLACMPAKLILNAPVFGRNSL

>contig40713 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53608.1|) 3e-14 NOT\_ORF

MPIEHFSGKEEYPGLGPGFKE\*GL\*FLEGLVAAQLVSGGDWPEEFNLRTLNAYLDGPARK

YFDKMKADWAAEPCTVANLINKMLEVYIFIYCGQSDEITASQKAKRLDMG

>contig40858 Frame-2F

MVQIVEVRDINDLVDEVQMASNNWSYESAKQEVIKSFGSEDEDDVVAYVTMLSVRCPLGL

CVINLPARGLHCKHLQCFDLRTFLLFSKKARSKAWRCTVCHKYIKASDLRIDPFLKKLLL

EVQGEEELEEVEIFPDGSWRRRLEEESVTEPPAKKVKAEHSETLNTATNVSASLVPAPIN

DAPGSSAMAPVEIDLLSSDDDDGIEATTACRAATVTTSAPILLDDDIDILTVTSDAWDTS

SALVPASALTNTTSDGNCGEYFPFPLDENLFPPSANST

>contig40999 Frame-0F|Blast-tyrosyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY64400.1|) 1e-55

MLQRDSVKKRLQTDQGISFLEFSYQLFQAYDFLHLYKTYGCVAQIGGSDQWGNIASGIEL

VRKSTGKEVYGATFNLLTTATGDKYGKSAGNAIWLDKEKTSV

>contig41192 Frame-0R|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY57593.1|) 6e-52

MKSFYEQKMAKMVAEVHTAQVDRDRLVGEIQQIEKKAACEGDTSGGNKLLAKLSRDLRVK

EDEIDGLQKKQNDINRFMAQKKKNEMQLRVLNSEISNMKRQKVDLVKKMQEERKRY

>contig41336 Frame-0F

MSFVRRSIRINNENEVLTNRDGFRPAK

>contig41718 Frame-1F

MILPMTVNPEGLLMFGMVSPSSTQYFDLLFPKWGVMKNEQLQEAILRELLEEGGWEGDIL

QYLPSFMSGDDTIFPAIVMVDKAEISTSENLRTAAFFSATDSIIAGSLRQESLDILGLAF

QFLNDVAKGNSRITKTTQPDPTIATIKDSHTFPSSSSFFTENKMETIKKLLPPYYATEKK

VKEVLSL

>contig41884 Frame-2F

MASNNVDFQALYQSSLKLTTSLKDMGIPRLERRLEQLDDVLLISRNQIPSSRSRKRPATA

GADKAKFLLASKGIDAGKLSKELQQFGIAPESESETPLGETDLEGYLAHHHEMIVLTAIE

DVSRRTVEATHDRMNRAMIDDFEDAKQRLLEDLGSAKQLGIRNYPHALVASEAAGNIFSS

AAREKRQALEPASGLGLSGASFVGQPLFDSFIGSAFGTPSLHMSQQKIENAMTQEMKQYY

MVIKELNRSRVPNTRSQFDLAHQFQKTCLSNVSVSVAGSKWVAVHKCWQLVNHLLAGGDT

LMDNAPKLAEREFQAARQSIDEGQRIIFQHRLVFGARVFLEKQFRDYVHETVQKNGLATG

GIPSLVSNIRGFVKHLHSSRYSADGSGNSTDVNNIWAIVYYCLRCGGDDEAFKLVSSGDE

SAIDADVICALKYRAHQKNLYTNSSASPLNTFSKQYPAESDRLIDRYHRLESSSIDAVSV

INPFERCVVNLLCFGNVNANEQRITTTVEDYLWQRLCFIQPVASSVSTSNSVYTITKLSR

SMQSFGPTHFERGAQLDGNNYSAFMYFEILLISQEFEKAINYLASKNFLLEAVHFAITLN

HYGLLECTSFSMAEEDETTVDLVRLIRQYIHGFQRANAVEAADYVACISDLTAKKELLAE

LLLDTRMFDVLAGFTNNTDGSRARGLYDQLLRDEPEDEVKDLILLAARKAEARGRPHDAF

ALLKSVGDIEGVIVLLNLQLSSTISATRPEREEWFREAKEFAEKWMRFPWVQTIANRYAR

MAAIAFQTLLNISIFLEIFEKQKYEDAIGFVDELALIPTQSSTNLSLCVDRFLAFDETVR

QNFHILLLGYMECLVRDADRLKTQVSGDVRRASVAILRKKAELLVTFAGMIKFRLPSGTN

ERLNRMEAMIH

>contig42179 Frame-2F

MTTTALSSSSKPGSPPQSIAEPMANKITTAMSPSNFTSDEVSNMDQTIDTNYDMEHTDSA

MFAAHYGGVGVNEDSFWDILADSHMEAGKLRHSVLRPRDD

>contig42302 Frame-0F

MATTDTHAVHVSLPPGASHLTMQLRINNDRKRFFRPCCEKLERVRYRLQILASDQQTVGG

STSKHRHGGTAPLVSVKFFDMNDQEISPKMTVGDALMRTKRLQLDKENFVVLYNQPLVTD

LKVLEPVMIGIPIFPVPKTQFLEVEECSWRWFRMCYNEKSFDENLATLICSERSYTPLED

EVGCSLYIECRVPATHSEYAEDSKAVIMTMPLQPGPNRDVFKSRRLMGYKIAPYTFFNLD

AFRVMSYNVLYNGYATTEYAKKNLFPHADANVIKETRRIQLQILEITENNSDIVCLQEMG

EHAYTNFFKPIMASFGYHGFYSEKTGTTKEGCATFIRTMWFEVITEHTVDLANAIKHSSN

AATRSFLIAYPEIAKGIKRIPSIAQVLVLRSKQDPARNLIVSNTHLFYREDAHLIRLLQG

VAVVDSVCQYKYGAFEDAAVVICGV

>contig42377 Frame-1F|Blast-DNA replication licensing factor MCM6, putative [Phytophthora infestans T30-4](gb|EEY63344.1|) 1e-126

MPRSIDVILRHENVEQAKAGDRVVFTGTFIVVPDVSKFAKAGGETAMANRSNTQARRQTG

EHSTQGMQGEGVRGLKALGVRELTYKTCFLACSVQTMEQRFNSISIRSDVPDDSVDRDAH

DEAGLEDFSDEELASIRTMQQDPDRYLKMAKSICPSVYGHDEDS

>contig42760 Frame-0F

MSHRRGRLQCCCVGHAHYSYSLISSRSRTL

>contig42889 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66287.1|) 5e-59

MADAENKRKFMQLLRLGVQDKIRALQLIKILFTEDEVNTDIGLKAQLADGDRQTLLPSCG

TKLAEVAAWQTLAWRDAFSMAPYFLEVINNKPLRIKQVLQGELNGFGTGLTVWPAACVLI

KYLEYQSAHTVKELVNSDNPFLLELGSGTGAVGISAAMLLQAGRVVLTDLDNVRFIMEAN

VALAQQDEAVNKHVTLQVDTYEWGLLPSENLILPSENVYPDLILVSDCILPRLYPIEPLV

EALTKLSRSHTRIIISYECRHFQHFDPKQRFWELMEAKNFLLREIDTNEYHPQFIAADIE

VWEIINSSERNL

>contig42980 Frame-1F

MRLKNVNTVEDGVDTTSQHLPITSTTLRNFSSFTSSPASSERSRKRPRN

>contig43374 Frame-1R

MIPAAHMLLHHQVALSTQDQLTASVRRLVIQLKNDSDEVKRPLTQTHGIQFKSKISTRRR

AGSCPTSYDLGVQSPIDGSLMSTQPHLCPTRVPQEMPPGKKHKKSAFSRIGPRVLESLHL

RKKPKTYLFTDEELETIEGARWKIVELAFRFGGKHRSYLVQAVNMFFPLLKYGRRGGAHT

TRLHCNCCGTLQWQHKRGGLSKAVDLAEVLQVLGGRQTSVFRKYTSNNELAACSFSVVFR

GRTLDLETQSLNHRDWLISALRTLVAYARRQRRIEQQAIAERTKLPLEEELPLFLSPVVS

ARERAAPLPFPMFT

>contig43576 Frame-0F

MSPQAIIIGYPSFSTIYQFRCAPKSRPLRQMSNSWCCSSTGTFYYQWRTCVSNRAWPVSD

ASVNIQTVMAS

>contig44120 Frame-0F|Blast-choline/Carnitine O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69430.1|) 1e-121

MPFSSRTFRTQHRALSSAMGMQKPGWFNRMLLTNEYNLPRLPVPQLEETVQRYLESVRPL

VSTKEWEAHKEVTSAFKYKEGPQLQEILLRRELNQAMGRAYPFSYIEKDWDDMYLAARYQ

SPINVNPSYGLLDETEGNLKGMIPRSAAFVRSMMKWWTKVKMSELEQDKNQCMAGFARQF

GTARIPKRKTDTLVSYPHAVHIVVMSGNNYYKLNVLSPDGKHLMAQQQLEEQLDFILNSS

TQNDNNDVDLSTLTAEKRDIWAQIRNSLVAYHPLNAETLEVIDS

>contig44371 Frame-2F

MFYVHAGAPSIRVPSFKPSHWKFCAKRLKHYGASPNTIDALNPFFRLPEDGLTSLNMIEL

EIQKLFATNRNFGAGDSIKRSDKASAIPSADPKHFLKRDLQLQRIVKEVNEGLTSLRLLL

QSMQYLQVSGPVCTRLDLGLSPRPERYTSGFIFQAILLDETSCKENESASLLVTATGNRI

IIAEGGRYDALVSRFQLTTAYAKSSTVAAMGVRFAIDKIVSMLADSMVPTLLERKALALK

DLRGGCRILVCSVETTSDTMLFRMQIAMLLWNHGIGADYLHPEPLDLEDLEVHCAQQNVN

WMVIVQLRTINEKQQVKIRTVRNYTEADVVVSVVSLPEYMSELLANSGKSGYVDCMAGGR

GITHVGDALARNTNNGTICVSSSSGSTPQPMFEVRVVDAKYQTRDRNYRNHQLDTQRVQR

RVSKWISSCFSSRGDEAMKVISVDLPFALIREMSTALMEIGSDGINTVCANNPRYRKQLK

YTMEELLDLTPESTSRGRVRYVLLHSLVDDRYDMMSLGPPSKGGGRKAMKSFGVSQ

>contig44421 Frame-0F

MCIASVTIRGPRQGYSSPLQYAAIFITSNIPDPMTYQEADNMTPEQFAALPFPPCNGFCS

RDESLPVAFIVLDGSGANVSKQLAYPVIGRYILVKAICPSAGTNIDIGYIGFFGLFNVEN

GPAYCGTAIASDNMVGKSYCCDECNISFKAGMFYYGQEENRNKLCVACYDDNRGDVNCKY

YASFAGSSQGDTLNLETLLCPTRRSWTEKIEAFCDGLIQSETVNVATQQQNSLSDIFFSD

SSFEECELFSCGQNNYGELCLGHCNSSSQLERVPHFSAKAIRDIVGGNEVLAVVMKDGRV

LTCGLNKSGQCGIGTFEERVIMATPVRALNGISIRLVAAANGCEHMLAVTMEGTVYSWGY

NDRGQLGLGLTLSKSHTPRKIESLRDKYLITTAAVSYHHSAVISSNGELLMFGMNDCGQL

GLNHTQHQSTPQFVDSLSSQFVTKVACGLYHTIVSTRNGDVYSFGKNDYGQLGLGHTRNI

QLPTLVKISFGEDD

>contig44612 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54204.1|) 1e-132

MDQVTLPADQLRKRHYSRPTHLSSAVADGLESLGSSFVGAATGLVTTPIAIYKERQMQGL

DTGFRNVVGSVGMGLVGIVAQPVGGIASLVSMTSDGLLYGLKENRAKLHDSPSRVNARPN

ELLRYKLKVLSNAFESYLVFAHGVWIIPDENSQLVLEHQAECIIEEKPKSPENDSLRGLL

LPRDVTRPLAQVTVVCSKELVYVVGVTKAQNQVVLIRTSLKSIEAVEESLQEPTMFDLGI

KTSSSAEWLHFRLPPQQRRHLSHHLRLLLAGDASIQV

>contig44667 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY61153.1|) 6e-41

MVCSRKFGLLVRRHHCRLCGRICCGPCSKYKRRLPFADVSNQGTSKGGHAKVKVCSTCIT

VHEAAKDDLSWSNTTVDRLIASDAVIDY

>contig44883 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY59587.1|) 0.0

MLGSNHLDIDMPNLKDFRSSFLTTSTASSGVSSGGMEPTMLDLEALSNSRLSSLYGATSS

ACQRLTILEENMEKDASLRSQKAIQKELFELHEVRALKQVPLPDWMKIFVPRIIRLQTGP

KPYMEYARSEKGVVRQRQTITVWTRVDRLSKNRLSIDFRNPADVERSAPKRSSLNSLDAS

DKVAPDKWILKFEAKNERDSWAKLVQDATDLLGWIAKFTLGNVMMDTENSSVVECSTWMD

LNHPSYVMKITEASTSKQSQSARSEIEIQRILTNYSSHPNVVALYDSFYQKDRTYLVIEN

CVGDDLYEFISQNGAVDEDEAKTLFHHISSAINHCHEHGIAHLDIKPENLFFKVSSTQLE

TIKLGDFGSAMQLDKCAVKKAVSCTVGYAAPEVLQNRPISAASDVFSAGAVLYTILCGYS

PFSAPSEEEVLERTISCEVSFDELEWWRISKEAKDLVRQMLHPEAEFRPSMEDVLEHAWF

LKQ

>contig44928 Frame-1F

MATLSFAEASRRVGVKRDIFFRRVLVSDADVQKQMLARVTDELQELLKRDDATLLTDFFP

TALRLTLDAPFLAIREALAKIVDVVEKKYPDARELRAKQMQVSHFFRNGDAPEDADEAVP

RVDIDDDEDLSALFKQAFLRTGRVNHLTQILAWHRSYLALFDRSLAATMTRDGTLPLQWR

SYIAVMGASELRCHYLADLQQYDFIVNGGEGEWIKGLDYVPPKLFRLHELSSLLAHRPWL

LTAEHVAELLRSDQDDSWSVSELVHAIIVLCQAHSMASIALGVGCAEEVDLAVFGQFGYA

LEAETVEGVDNQECADASSCSGIDLSTLDRDDDMLLKQLKKNCGLDSDTADEEEETGEVQ

EEGGGNDHGNEYGADDGFEIVVDEANDRINTAIASRRKDTLWRFCGGSVIRYADFDVRSE

EYEVLHTEDFSWDEHCFSLVKRYFPGEAGQILEDLFNLTSKLTYDYFGSQKEECVDTSPY

RDAVWYYVHRIFGICHDDYDYCQVNTYLNRPTKIFLKKVACTPWKVRQDDFAHFDRTLSS

SEKCHVILLVAEARKQAGLMYGLRAVMNHMR

>contig45233 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69475.1|) 4e-42

MPTERSSRRDRSRDPEDNAGSETGARLRRSMRSMVADSDGADTDASSAGHRSDEPQHRLG

RRSRARKAVEDARKSLRSTEDRHIAHFGNEDDEIDDNNREQTDVRGRQRSLSNLSNTSSV

SASSLNSESLAGNQCRTRIDQQLAELEQKKKMVEDGTLAEFCRRVAAFKEERNRLLQTAE

LHKNLQLKNGQDLYKFEVQRAYHLWENDQKEYKDKLLINLETIMAKLQAEMKALCDIKEI

VTTNRSKSKQTVESSNADNVSVHVATIKERTNASNVNVEPKQEEGEV

>contig45963 Frame-2R

MRFYCVVAAAIHLACVALGSSVGMPKAIIESPLDSDTNTQVITMLRRTTAVALNKKAEPV

SRRLIRSLWRKFNDRILHLRSEKALARLSKVSS

>contig46409 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68629.1|) 1e-142

MNLLQGKSNQYLREAILEGSLEKVRRYLTLKIGKADVAAHTESGGFSMLHCACLVGNTQI

AMMLLQFGADVLALTDDGYSALDLAIWKGHLQIIELLRSQGCVAPMKEPESLNGKVISHL

GRKATVVFFEPSTSIYACSLRGLYYADKGEAKLVSLWAGLDYKIVGSNPYYRELRDLEYH

YAEISMTRPEKYDAMLEGALQGAAFFDNDSDSESDNETEEIVEVRVPPGPLGVLLNSGIQ

ECAVVHGFTNLSTGEKGPIELHGDVYPGMYILSIDETNASLMSLQQ

>contig46500 Frame-0F

MVYISTHSKISDVVTALPLKETVKLCLCVKTA

>contig47125 Frame-2R

MKEMQRCQDQKDLPAALEHVWLNFPKLSNKIAAPQADTVVTLKTRLRQKEDELRQTFV

>contig48137 Frame-1F

MKMLVEAPNQFKTFHPKLIEPCGPRLHNLRCASAAHRANLGWASCQIKLLPRFYLHFYCG

PAQCLGVCKDMAR

>contig48339 Frame-0R

MCIRYPQRRRTRSVCGRRMPVGVPFSSARRRKVGNLDLFLTPARLTRNIVRCADCGGSCI

IISQVAIRTGEEITVDYTGRAGGLLWLNCQPTHCRANIAAMRLMSFKKEARDQDVDEVAK

N

>contig49097 Frame-0R

MGEVKADFTKLLKWQLLYANVADQRMQRLTGGEMLQFLSVIDPTRLRMLFTNENFTSPS

>contig49141 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66701.1|) 5e-08

MLAMACVGGALSFLVLLVTASSIDSGANWFAREVFDTETCSSTPVIVNLSKAVQCRSCQC

SSFKSNNVTR

>contig49255 Frame-2R|Blast-proteasomal ubiquitin receptor ADRM1-like protein [Phytophthora infestans T30-4](gb|EEY68626.1|) 8e-21

MASFKHLAQPKSVSLNKLLNADNLISILNDPACVEALLPHLPEGSQTSAELSATLRSPQL

RQSIGSLVNALHSNAFYTVVANFGLDPAAGADKFNFGDSVGALLAVIQAWADQQNTSMGV

TDDSNNEDL

>contig49480 Frame-1F|Blast-Rab32/38 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY55584.1|) 2e-85

MLAQYSSDSESSGSEDDEHETIILKVLIVGNARCGKTSTIRRFTKNEFKEEYVSTIGADF

VEKIIRYDANLTISLQLWDIAGQDRFAKFTRGYFREARGAVIVCDITRTNTIDAVVKWKH

EIDTCCKDLKHETAIPVVMIANKSDLLMDPIKALDIGVNMQKCVEKNKIVEWFRASAKSG

ERIPEAFQCLIDRMVDTYRIEKESTRNNDSSSSVKGSEQATPGVIHLTEAPP

>contig49703 Frame-1R

MCVVYGNYDAVRAEKVATSDWHTCVVLRCARNGRSFGQIWQFGYGSFRPSRVVFPSAVKT

SGSGALTCDTWIPNCKQRDLDIVEVSCAVNHSIALSACGSVFTWGHNVSALSHKASESFR

PPFSACKASPTTSPSAPQKVSLASYGPVINVCASQDHCAVVTEQGDLVTWGCGQQGVLGH

GRGNTWQLSPKRVAGVKKAVMVATGHQHTAVLIAPVRPSFKSGIDAANQKVVPPLLEIVE

RTIASYVDVANCIFVWQVAERHAAFRLLRYCAKYMQINWDAVLD

>contig49831 Frame-0F|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY60954.1|) 4e-13

MVDNSISAIEFERIEDASIDVKNQQVDLVILCIETFFLGSNGANYDLGLQCNLHFLSEYT

QQATLTPVQQLNQYPH

>contig49985 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65736.1|) 1e-114

MGTAWEAQDRSHLGIVRADNHVDAAIAIALLFSVVGLPPLIGIRTMYTNCWLVFTTFAHL

LASEAALGMATSMGITIMVGWYSLRIFDRYAFTAILNGWIGVWASSPLLGVAARIGDFVL

HLIVPILLVTCYLPLVRIWMSVPALISSRLWSHFVVGGGLFPKADHIYRFSPPRSQHFWN

AAFKMELMLNLLVPLFCVLAHQDPSGSMSLRRSQEQFYFAFS

>contig51009 Frame-1F

MVDLRPITDVPVTLPPPPASESVEDDELECRVCRSEAEPDRRLYAPCKCSGSIRFTHSDC

LEQWLEHSG

>contig51232 Frame-1R

MERSHPILRKQQNSKPFLLRHALRCWQQRLAVFLDSRDHLLYHTNIQDRMEVSKQFCSCR

DRILITDSDLATASNFRLTDPVSHAKTKPLSVVSLQESIRPDN

>contig51456 Frame-2R|Blast-UDP-N-acetylglucosamine transporter, putative [Phytophthora infestans T30-4](gb|EEY55436.1|) 7e-63

MYGFGVLFNALGLMLVDGNRLLSGGFFYGYSCWTVVIVVVNSIGGIFMACILKYLDNIAC

VYSHSMAMMFTTLLSIIFFSFSPSLEFACGLGILVISMYLYHHPLAQV

>contig51650 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59236.1|) 9e-83

MAGKQSPMRMLIMLPMMFLMNKIDFENETTLMAARIAFFVCQITALLMGLYLKQLIQRKH

DTRKIYVPGVKSPFDQSPNYGDLTETTYETHELAKAKEFLKQTLIGAGISSLIHFKMGVN

HVVMIQSVMMPINLWDNPLVQAYILGRRNGRIWNERFEGESAEDA

>contig52516 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56303.1|) 8e-42

MMQQSVQTEINLDGQWIAGVMERPSALVVPLRDLDAQPSEVKSLVYHLNSKAIPRWYYDW

ESGANKAQRLMKHTLKAYVMERVAVDRDDNFTTCASPKALTQLFKVLHVVSSTEFTVISY

RRAPLDASHTPAHLVKAERLQLLR

>contig52840 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70526.1|) 2e-62

MNPPVFGAEQRHDATGVFPVVDKDGEAYESFDLSQVDHLFSAPDSLKGGSAPMKDDPLF

>contig52938 Frame-0F

MYLMRKGNLQNFSTQARPRLNSALRVKSRDRCVIAPLLNTHVMRCISSHGTRRLGHEDLT

TKSTTHCIHSHS

>contig53230 Frame-1F

MGKNKRKQQHKRHVLPTAPASSCDTNAKRIKTTKKHKTQKLTTTTEIQVELDTLSFDDAF

SAGLAFEQLES

>contig53375 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53679.1|) 6e-18 NOT\_ORF

MYERELIAKSLIANDVFECDKHETVTVYLASWQMQPHIDRERLLELETLL\*EATHEAKKS

GCLRQDLNCLCQNKA

>contig54161 Frame-2F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY63452.1|) 2e-53

MNVGDERALRHDIKLIDEFIMKIIATAIECRRQRQEDLLAGKVVSKRDKDIVSIALECME

EDGDLISPTDVRNIAVAALGAGRDTSADAMSWLLHTLTLHPDVETKLRAELHEKLPKLTT

D

>contig54288 Frame-2F

MEFYPHDASNAADANACAAMFSNTTLLLPAISNANLGQLTLDLVINTLLQNGDKFGAKLT

RVGHLLSQVAPPIAGSAAFTGQHGLCLNLEVYQCKEKNLTIIQQRALVLP

>contig54363 Frame-0F|Blast-phosphatidylinositol kinase (PIK-L1) [Phytophthora infestans T30-4](gb|EEY63188.1|) 2e-36

MDSELEPDPTELSPASEAYFPTVAIHALLRILREQSLNAHHHGVIQAIMFIFKSLSTQCV

PFLKYILPP

>contig54730 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64437.1|) 4e-49

MVLGLGGLIGYVSSGSTMSLTAGGLSGAFLSFVGYCSYNEYKQSPVTSKMWPAISLIVSA

PLTVMMAKRYNETNHFFPAGFVASYSAGMSIFYVWILTKKSKPHYKKKA

>contig54833 Frame-2F

MNQKDQHSSSDHVLERENDPAVLPSNRFKTSWTLSGCVIGSSFVLLVVLSAFLNATFLLW

PLTILR

>contig55117 Frame-1F

MTDGSSAPAVSCGATRRQYQQQPIAQLEHHYHHQHQWPTITQHEMPYDSNSNL

>contig55812 Frame-1F|Blast-DNA replication complex GINS protein PSF1 [Phytophthora infestans T30-4](gb|EEY57519.1|) 8e-17

MKKIKALRWEIGTIIPAQLAE

>contig56080 Frame-1F|Blast-putative chitin synthase (Chitin-UDP-GlcNac-transferase) [Phytophthora infestans T30-4](gb|EEY61714.1|) 2e-77

MKLAYYAVCTTFALIVIASILVGLSAYMSMQVTVQSIVSTTLTAGVFIIGPALHGELHHI

LLTYAHYITLVPSFINVFTIYSFCNLHDLSWGTKGLHSDPLLAASLENRGMGTCKGGAAE

RRALKKSSSEESERLKDRKERFEAFRTKMLFLWISANLSIAVYVVYFSSSSAFFPKIFNF

MAGINSCRLLGCIGHCLYIHTNVLRDSVFDKVKVFMVPTAIRKIRACTSTPLLQAITVPI

PHYQGLEITTDYFGSRVKRGITRRGERRP

>contig56541 Frame-1R

MASKSQASSSFRRVLGHCKLFGADSNGGAASLKSFVFTSFGSEKPLEEDESVKEQVCSGK

IQSRGGLKRRSGLSGASPN

>contig57542 Frame-2F

MGVWQNVAKVALWLPVGVTVNALV

>contig57784 Frame-2R

MPISKDRKLSMELQTLKEAKRLVDNLQVQLVGSNILSRFKVTIGDLTKELEQAVHLQVAQ

NFNPFRASSGAR

>contig57818 Frame-2R

MSSRPGSESRPSEDYRATEESRDSKNSFTGDFSEALGQSRLQSEVSVDSYGFRASRLSVD

SYSSGMSFYSREGSRISGFSSASSFDRSSTLSKY

>contig01025 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55522.1|) 6e-49

MNRLVAAIRPLSRAVMRPQFVTFRFMPVRLLSAQTFIDRNEVSERVLSVVKNFEKVDGDA

VKENAKFQEDLGLDSLDVVEVIMAMEEEFTIEISDNESDKLLTPAQVIDYIAAHPMAK

>contig01292 Frame-2F

MKVCTTILLAAVATQVVLGGGGGGISFPNENPYTPSGTGSGSNRQNDDQDGMKTTPPTLP

SSPLSTPMPTNPDSNSTPTGNNNPPTPDQTPSSPPSPPVEVPMSKNDPSNSPNLDENTPC

PTLSYNYPSPGPSDKPKDEASSPPTPTTPTANSPPASTPPAPDGNPTESGPPNPTQQDDD

SSQKPSGSHTGENIPSTPDVKNPPISSPPEESPSGPNAPPSGIPPVGTPNPEENTPCPTL

PYNYPTEAPSVPTNPTATIFPPVDPSNPAGSPPPGVPSSSPPTGPSPPGQSPPGQSPPGQ

SPPGQSPPGQSPPGQSPPGQSPPPATPPTGQSPPPETPPTANDPTATPPTVPTVPSPPGL

TPPGQYPPGQSPPAATPPTGQSPPSGTPPT

>contig04237 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55957.1|) 2e-06

MSSSGIAVGLNKGYPVNKKQVAPRPASRKG

>contig06833 Frame-1F

MSVRYYQQLFREYALADLSRYKEGKIGLRWRTETEVVAGKGQFSCGNKHCDERTALRSYE

LLFTYIEHKKRKQCLVKVRACTLCAKKLFYKKIIARSSQDGYIKNEVRQRKRQRLVNMAT

NDATEIHDLCAKLHAEQMATSNLQATTIPAKKRDPQFDALFP

>contig07478 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61679.1|) 1e-13

MLGAYVGAFPIPLDWDRPWQVCKPITCVHTNRLTYSC

>contig09403 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66279.1|) 0.0

MSLKHAALWDEVQGSCEASKLKAILSTDLDPSSLLDGWTPLHFICENYSVKPTARAEGLR

LLLHAGFDANAVDENGWSALHLLCKNKSGSGEDFFLSIHQLLSAGANVDLQTLDNKKCAL

HNLCENEMLKEDTLEALLKAKPDINCVDNHGNVPLHYLSENPSVSDRLFSLMLAAKANIN

IQNHFLSTPAHYICQNSHVTQLVIRELLNHRANFNLKNNIGNTPVHYLCENNVLTVDMLK

ELMRDKHVNVTIINSLGKLASDYIPSPKHECLEFLQKFAAPNLDSSIWNSNAPALIGGED

ASNLPEPLKETLNAWNASLPPFDAAFYNAISCEAAFQSIYDEVQNASGLVCDSPRNVAAF

DAWKKSLIKWRACIMLAYAALVPHNAWHQYAEQFQRPVPSDLTKLLIKVEAVWKQFPEQT

QRRGRFEALTGLFIKP

>contig09731 Frame-0R

MKPSLKWANLIMRIRGMKVCDHGTLHWDVSVLGAANNSKRVKMAH

>contig09942 Frame-1F

MWICTQRWIRRRITFQWALKPCTYNISTASYITINTILSCFYSGL

>contig12155 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY68960.1|) 0.0

MVFGTNIWRAASLFLLLRSSQLHAQECTALRNNVLTSAGCPTRCNDNPCVLYSPSQNNTC

IELGASGPCYSENDFALPGASATCNITYQCLDSILWDGNQWLLALGANTATDSKTMAYVT

QITELTYSSATLSVQLQGAPTGSANKSILKEIMLDQTFFDTPPPVASMFLLDVNLRNIIN

TVTLATTYATFYLTNVNLEAVPEQLGSFTALMKLDLSSNYIQELPPNTSSVWTGLNTVAD

LNLAANELTDFPVVLTKLQSLNLTGNRYTTIPENVYTMAESGVLRFLFMNSCNLTNLEVS

PAQQVLLENLATFSADVAITGCRDGLSVVTLSNSNVQVCTVSTASTNGGGGSGSTVAIVL

GVVGALLVLAVLGFLWYRRTYGSHSGSSKGGSTIFGTDMGSSLTGGDTMFGSSIWDDPDL

LAARIEHRDIEAIKMLSRGGFGEVWLGLYMNENVAIKRLLNDKKSMQDALAFATEIKTMA

RLDHPKIVHFIGVSWTNALTIQAVTEFMDCGDLKSLLDSSRANSLTWANLKCQIAIDVAD

ALVYLHTLNPKLIHRDMKSRNILIDAQSGAKLSDFGISRNRSFDETMTAGVGTARWIAPE

VILGGHYTEFADIYSFGVVLSELDTCKAPFYDATNTNGGKMQDVTILQLVSAGKLQPSFR

DSCPPSIVKLARACLSFDPAQRPSAIHISYELRKVMKDEL

>contig12573 Frame-0R|Blast-pre-mRNA branch site protein p14, putative [Phytophthora infestans T30-4](gb|EEY56776.1|) 1e-56

MQQRKTTVDINKQKQELQDLKDKYGV

>contig13646 Frame-1F|Blast-programmed cell death protein, putative [Phytophthora infestans T30-4](gb|EEY62221.1|) 0.0

MSASPKEAATAMEESLRPTTMHFTATSSGGTGSASASVNLLPPRRERSKSRDAGKRMGGG

QKAAWKVTEIPHVVPADKRDPNYDSEAEDNVILVSTIADSPTKTTPTLEPDELAAKELAL

NPPPAIKKRILAILDEYFTNGDADEVLSSIHDMDKPEFHFEVVKRTITMAMDKHDKEREL

ASRLLSNLYLDGLTASQIIMGFRRVLLLAGDLQIDIPTAKHMLAIFCARAVVDEILPPSF

LEDPFITRYAPEIAAEAIKKLSINHATARMEKAWGPGDGRPVEELKVAIDQLTKEYLLSR

DLDEAARCVRELNVPHFHHEVVKRGLMNSLEEGGEANGAAMASLLAYLVSNEVVSTGQLV

KGFQRFQFVLNDVALDIPNASKLFQDIVADGIRDGILPKDFDASAVKK

>contig13884 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60985.1|) 1e-106

MSNSRQKNVVVSKPILYGSVATFMGRKAEETKTHRWSIYLRGVNNEDLSYMISKVVISLH

VSFANPVRVLTEPPYEVTELGWGEFEARIQIYFHDSNERPISIIHLLVLYPPNSQPASTK

KPVVSEFYDELVFNEPTEFFYKKLMAGPDRQSPPLAMQEQLPTYSDVEVLKTLARAETFV

KKELQDIKNLLLNADLEIYDLKERIAKHTKIKKEADKLGNSIGSSWPL

>contig13963 Frame-2R

MAQPDLVPSLSSLYQLLETRLQVHGPMQKLSGRLSLVLGQIHVSKEDSHEQEIEESRAAV

VYHEENDEVDENESNSQDEEDDEDVESEDE

>contig15701 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69573.1|) 6e-85

MQQCSSEYSQLAEKHAQECAKSFVEYEADEEHFKILRDVGETGLAPKSNEREDAGLYFRY

>contig15987 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54483.1|) 2e-80

MHPMDLTRMKEKVEHAEYTKIDQFTADIKLMAANAKTFNRVGEPVHQMAVEIEQLYESKL

QVYRKMFDDLQQERKRRKKEKKKRKEKKKEK

>contig16883 Frame-1F

MLSNNEQRDGHVAATAPDARMQFEAKRSNVHRPRKNLKSIALSEDDEDVLLSARTEPVST

TDNLGCFCFCKFKKIGQSY

>contig18104 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62783.1|) 2e-51

MDTFLQGRLHTLIRGRTLSMSVKTGRIAFVHPLDIAECLSAILSLNKRDGFYKFTGPEAF

SFQEVAKILSEGIGDTVTFSYFPLWAVQPARWVQGVPGDVTEEELGVLRALEAGAQDEVE

TSGMEKLMGHKPRTFREFVLENSDKWPRADPY

>contig18526 Frame-2R

MATRYGDDFRGRGRDRSRDRGYGGSGGDRSHGGRSSGGGFSRDRVGGRRGEQSGGGAEHL

ARIHGTEEDRVNCPFYFKIGACRHGDRCSRLHNKPVFSQTILVSHMYQNPIAQVIAQNGD

PTSLDQRQVDEEFEDFYEEIFEELCKFGKLEELNICDNLGDHLVGNVYAKYEDEEHAAAA

QKALYGRFYAGRPLVCEFSPVTDFREARCRQFDEGTCNRGGYCNFMHIKTVPRSMQRELE

RMFNRGKREKSRSHSRSRSRSGSRGQHVRGHSRSRSGSRDVLKGASSRRRGSRSRSPSPV

KKSRRTRSRSQSPRLHTRGTSLEALKTEKGFIEK

>contig19420 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59231.1|) 2e-07

MPESTQLQLLYSQIDAAIDKLRTSFPSRISEQVYGALRLGIIVKRLIKHLADCHRSIVSS

AVTSNVQNYVQTIKEETAA

>contig20019 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54081.1|) 0.0

MCGVSWPDDTVGNMYRWKILGIVTHQGCAQFTADVLAQKSDIITRDEFLSMSKTSVASLN

KPGTFHITVHRAMELPGTQLIGKQAPYAKLSLLPWKEPMQTKPVENGGRNPVWSSAHDNV

MQFTHMYNSTITPIPLLEVEVFNYNYLADDQVACTLVDMSPLLRYPNIEVKRWFTLSSRA

LLTQSTGQPKIMLAIKFISTKREISTSNAHKFRVHQLKSIGLAMPACAVCDRSIMNALKS

AWGYRCELCGIDVHKGCMMKATISCICTAQELLRVGQKEKALRGIHFLVLNESVLRPSGE

LYVSFRGLHLCTKYCREDLHAKNIFEGDTYCRLKFDDIVHETSPVLKSADPMYMEFLCFK

ARHPNSDFSIDVIDFNSNQCIAHLKVSLFQLLQREADKFIFSDPKMMQLRYLVRYFSLNS

ETNQAAINDSWTMLPKLDDKGYYKLYPPARTKHQSGDNLGFALIDFEYVEHKDDLLRERV

NDNSYLLEREDKAFSVESLRITIERFGRAVKIFQRIDAEYASIISWKNRKKSAFFLFRFC

LDVFLPTWSTRFLTYLEGFLCGCFINCILG

>contig20341 Frame-0R|Blast-cyclin-C, putative [Phytophthora infestans T30-4](gb|EEY69286.1|) 3e-39

MVAYAAAYISCRDAGYDAAQVFATVNIKKDLQLKIVGEFQKAVETEKRLYAVQLSALEKL

DEIIPDVSAGDAEATIGGPADK

>contig20723 Frame-2F

MVETPIDGPPRATAFRIKNAVFSMLSLYLAHSLAGYILNREDPIVCDVNVNDQSWFGARR

YESLRFFDPKKTHHKTQYVAMRDGIELAVDTYLADYLWDKQQKVPSVLFPTRHGRGYTLD

FPFSIFSHYERKFTNPRVNAYVQRFVTNGYAWISVDVRGTGASAGSKTFDFHDTEVLDAY

DIIQWIVKQPWSNGEVAVFGQGLDGVGALLVAACGHPALKAISVNSVPIDVFQDALFPGG

VKNVKAVNDWASFTGATDRQTRWNNIPTFKPRLMLKYFGGEVYRVDDDDAKFQKYINEHM

QNPDLSRELLHTRFRDDPFASISGVVEHLDATRHLPAIAASGVALQTSTGFFDMGVARSS

ILLYKYLTNTLDVTTASLLPALPEEALEALNKGPSYHRLTLGPWSHAGVDNADPFAEGKQ

KCFYHLDEVSRFFDRHMYANRRQITKIDEELPVHYFTMVHNRWKEAELWPPVYVSDVVLY

LGVNNGFQSEPTLEVSTVIHNISHKPTLETVSRWNMLDHLFGLRPTYYLDRTPLAEHYMT

FLTPMMPLTEITGEAELRIFFSVDHSNVSLVAYLEDVDLTAPFPNENKRPGVTYMTEALL

DPVHMTVHPDSSVYSFKQKNSRNIVPGQVYEAVLRFQPTSYVVKRDHQIRVSLGAAGSPD

FGSPGENEATKLSIHFGGVYSTKLTLPSYVGVYDANVVPRAEPENNPVTVPACETTNGER

EIVRDELAEAKAEL

>contig21180 Frame-0F|Blast-ribosomal RNA-processing protein, putative [Phytophthora infestans T30-4](gb|EEY70390.1|) 2e-44

MYFFRLRRKVLFFQMTKKNRNGLAKGKRATTGSSKKRTKKAKSRVINSVLKSQKVSQMHD

RKGKKKSHTNALTPAERLAEMRRKIDGGKFRMLNEQLYTTTGDAAFSTFQQDPELFDVYH

QGFREMANKWPTNPLDTFIDFV

>contig22000 Frame-1F|Blast-oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY53324.1|) 7e-42

MSTRNTPLSGKVAVITGASGGIGAAIALELAQAGAKIVLGARRLEALETISTQINQTIGL

ENSVLIVQTDVTKRNEVQHLVLRAEETFGAVDILVNNAGIMPFELMKNVNQDSWER

>contig22109 Frame-2F

MPKGEDIDVPLLQSNSFRQTVPRTKTDLHHSTMDTDEYICYGDRVAFLCEGQLLALTHKF

NLTYQQMALLAASTLATGGLMGIAGFFVWRKGLFRKRYAALFGNDVYNEGNDSCGQCESV

PLLGG

>contig22318 Frame-2F

MHELVTRIFVESCSPLLASVSHLNLAGSVDESNPCHEFEATTWSRNMLAITAQGGGDGLI

ESDLLTEVTEMLPKFLNDMAPVIFHLCQTRAIVQSMNASLTHSLATRTRKHAFSGCLEMW

KQKVDCSMILLDNTFCLDCARTEKIISSEISADRLGQNFNFEDAEEKRSSCSERRKIDRQ

VPKLKQHQLQQIHQEAPGGAKRLKDKAIVDQSYGHELLVKKFSVLMKKAEERRNYMRWRR

NRAVRLSTAKEQLKWRRAKDIAIWASGARIDFTGKDKFLLANLMTGVVPTVKGTTFKRIA

SLNSKHKTSIYSIMTSDEEIRKALEKAQIISRSGTSATLDNDVERVSNIVMREVSEPRLG

DIHDSFIDEMALREMENIIRNLARENDADVLPESFDASTLENQNAKAGGTIAVHDDIEMV

HSLAVMDEPLFNALASTRHEKIVYDDNAMHIISEEEGFMSQSSKYGDAQLSNTTVASISA

KSARLPPVHPLFSMANKANESELLKKALIGTASTAELNLLKPVTDCLINIPIRLAAKQLE

QLAVMWLRNSLQVHEQFRWLRKLMLLSERLFMDIFARDFLVNMKSFSCGTSGIRKCLSFA

LNSAMVDYSVTLGAIVHAFHYKSTSEVSQSSGGLSLIDEIEIVYDVRWPLGCLITTHLLD

RYKQIHQFLLRVRLTSLELRETWATIRIVCKKKQLSSSLERLCGGILYMINACLRAYNET

FATTV

>contig22527 Frame-0F|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY54291.1|) 2e-12

MTASLNRGLDLQEPVDLEVVDLDSQTETFSSTSSLSVHSDDDNDGKSRSVPKRLQTPNLH

QHAEAALHLTS

>contig23090 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65538.1|) 1e-57

MALRVAAEKAAAASTNSPAVTLYRYIIKQVPRVLTLYDIPMEPAEARLAVQALFRQHADV

KDPRVVDMLITKANMELEETLMQWKQKVHLLTLLEHAQTLRQPTPLENTADLALEKFFAG

VDDDEDEL

>contig23634 Frame-2F

MRYPSRAVALLIALSWLPGSHFDVSEALSSDPISPPSPLVETLNRENAAVRDLSDSALSP

LVPRAERRDALVQLGDIYFYGNSSLDTSVNGTLAMSLYAEAAALGAPRAQFHVGVALSYG

LWGFPLDEAAAMSHYYFAALGGDIGATMVLGHNHMLGINAPMKCESAARYYEVAANEAVA

RRERNVIHPIIYDVPHRRLKTVADSLHKKSSPDDAAVADYYQFSAEKGDPESTLNLATLY

FYGSRGIAQDVERAAALFQKAYELGAPEGAYHLGHIYNFGIGVPQNNATAFKYLQEAVKE

GSAAAHNELGRMYLEGKGTNRDEEKAVELFKAAIKQGSIEAFHNLGILFMQGRVSKDVAH

PEYDVARSYFLIAAYQGHTLSKHKLGHMHLHGIGGTRSCKQAVESFKTVAEFGEWDDVLN

QAYADFKNQDYEASFMKYAVMAQQGYEVAQHNAAYLLDSDFLTPSAFSTSHILTSSKTEL

KKDVIASTAVKLYRLAAQQGNVDANLKIGDYYYYGKGGHAVDYVKASAHYSIACKHSNAQ

AMFNLALMYEHGIGVDQDFYLAKRFFDKAHLAHNDAKVPVMLAMWKLRAHKALRAWMRWW

NELVGYNFSSNTTDVLPNKAELSAIDAVDSGLSLVFGEIKKWRESLDFEDYVVVLLVVAL

AIVVYIRSERHYLHVPPPQYI

>contig23995 Frame-1F

MNVSQLRDLHLLHAHPDTLRCAYTRCIACCYKIVLYGDRGLLPNVRPEMCPRMTSLVKAA

TATGLDVTVAISGKNDQHFIGLYNADQVKSILTVGDGNFSYSLALARSLGPESGVRLVFS

SHESKKTVLETYPDCNYILNELSAIKNVRVLYEVDATDAEQMKTLGKFDRVIWNFPCVRA

PGGMDGQNREMEANKKLLNDFFAHVSQMLTPTGEVHVTHKTKMPFGQWGIEKIAKTNKLR

HEQSIVFDRCLYPGYANKKVLSKESFPIWDSLTFIFLPEDRALGDASRLREGDKENYVVP

ITKDILTKLYVLLTPNLDDMLGLKKKKKGKKGTNCSNEIMSKYKRGSEHCQNGLRLNKGN

GNKRMQASHGELKRGRRKISRRS

>contig24671 Frame-2F

MSLKVNVSYKDQAYALIFSDKLSPSVADLQAQIESFMGVQKDAQRLFQKRHRIDCSDPSR

LLRDVCDTTMSLRLMTGASMKQIEEMEASHRVMQRNNTIRETRRVVNIAKRNEKTQARDA

LSTNYRFHAIEPLNHFAEKEKAQEILEKLANDRGILAVMAKHKWSVGVLAEMPPDGKVGV

DPVCVMGLNQNMGQKILLRLRTDDLLGFRKYLSIKKVLFHELSHNVYSVHNNQFYQLMRQ

VEKECNELDWTNGGGATVGELSLISPQNNFSQSGLSGNRLGGGTLSSSRLLRIAPIEPRT

QEEALYLSPNLDELLAKEVTAIASRTEP

>contig24910 Frame-1F|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY68453.1|) 1e-70

MKGNILDADVMTTSDGTLLDRFVVRGSFMSDERQLELRSQIEQNLRRLTLEEDSRINPTI

MPNVVVSQNVSLAEKLGVLKMVDKNEIKAEWKLDLREVRLTDAVGSGRSGCTYSAWWRGT

HVAAKVVGSSTNSELVGEELLNEFYRE

>contig24965 Frame-0F

MRLRGSFVTLVAIIAVFYQGEGMDFQAASATFKHVRSPIQNPPNFEMESVPSAQMTRSLR

VDENRNGGQLGSDAKTIITKVKFPKKAFENLTMKIKHNPFYPAKHIN

>contig25250 Frame-0R

MRLSQRFRRQVRAKGIAPEKNVLHNRLWCSFHLGVTNTTHTSPALANVIVIDIEDPKAII

FTLVEGIFGPHPFEL

>contig25575 Frame-0R

MNIMLIASVKASQRKCTKSVS

>contig25966 Frame-0F

MVCLFFACMQQTAYFSRSETNYSRKSFYLSNGKFASLCISCYKCLKFGI

>contig26084 Frame-2F|Blast-pyruvate dehydrogenase E1 component subunit alpha [Phytophthora infestans T30-4](gb|EEY65753.1|) 0.0

MMMLRRSTAALARSVTPSNRKFTAAANASGEVKFDLPVPFELHRLEQGPPKFAVTNREEM

LDFYQLMYTMRRMEITNDNEYKARTIRGFCHLYDGQEAVATGVEAALDRTDSWITSYRNH

CIMLARGGEVKDILAELFGMSTGATGGKGGSMHFYKKENNFYGGQGIVGAQVPVGAGLAF

ASKYNHKGDGPMPCAITMFGDGASNQGQVFEAANMASLWKLPVIFCIENNQYGMGTSTQR

SSYNTDYYTMGNKIPGIKCDGNDVLAVRECTRFLKQWCGAGNGPIFVEMNTYRYHGHSMS

DPGVTYRNRDEISQMRASRDPIEMTKKRMIEAELATADEIKELEKKVRAEVVKATKEAKA

AGKPDESMAFKDVYSDGNGYNVYPPFIRFPDYSKSMYNGKPLQ

>contig26307 Frame-1F|Blast-aspartate-semialdehyde dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY64301.1|) 0.0

MTTPNGKAVGICGATGAVGIEIISVLAELKFPVKQLVLFASTRSAGKKVDTPFGAVSISL

YSVEKAAKLDYIFLAVSGDFSLKYAKELAAVPNGPVVIDNSSAFRRDPEVPLAIPEINGH

VLIQKEGQPHAKLIANPNCTTAIAAMALWPLHCEFGIKKLIVSTYQAASGAGAAGMEELA

NGAKAFLADEPVTYKVFSYPLPFNLIPHIDKFQENGYTKEEMKVTWETRKIFNEPHLAVS

CTAARIPIMRAHSEALTIETIKPVNIARAREILAKADGVDLVDEPDKLLYPMPKNATKKF

NIEAGRLRKSLVFGDYGLELFVSGDQLLRGAALNAVLIVSFLENPRSIPQFTKKVSMFTL

SKDQQQTMLSVVAGVAVGVASVLAYGV

>contig27014 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70033.1|) 4e-32

MTQFYTQIQHISLVDAPVKKPSWGTFRGLRTCRLPTKFLRFRGSLNAQRRVVFDSFLRQT

AALV

>contig27199 Frame-2F

MAEDMLTELYAWDSEIEDVSALAADDPKRDEDKAEDAYEKIIHAASGADANDVVLSLAAQ

LLHKHFFRFPHVQLNVVDVLLKLCGPKRSQAVRIHTLRALLQIVKTPPDTAVSTLTSANS

IVRDNSRMWMLRIDEAVSHILESEKSSVILRQVTPLRQALEERLQPNVIQEKSNSAIGND

QRDNQALILECSRKQPRDEKDITEGNDGVAVSERDTKKPKLDDEINKFQNKPAEAKFVQL

KRDWSSSRGNGNNDIVSRKSESSNGRIVESEGRRPKVNAFSPRNCPPCPYLFLGSVPRHT

PSGEIVEFLSPVWPEIDNMSVQIKQPDHNATAYAFVSMPTIEHARLAIHYVNENKFRGRA

FLNANFARGPPVDTILFVERTGDNVSMEDKDAVRDFNFDKYDPEVWDVMCQQLERFGPLS

FAEKGCVRFRSAEHAKAAIRKQLFTVMGHDIFPVYDIKEQFAIDSTRRGSNVQPKQGFAL

KSGRL

>contig27869 Frame-0F|Blast-exportin-2-like protein [Phytophthora infestans T30-4](gb|EEY65961.1|) 0.0

MAEPNMLLLRQSLEGTLSPFAETRKSAEAYLKTLSAQSNYVLLLLQVLESANEKQEVRLA

AALLFKNYIKHNWDPEKEGCVSLNEKNLVKQHLVDLMCRMPETLQKQLIEALTTIGEYDF

PAQWTDLLAQLVQKLQTEPDWQVRIGVLMTANTIFKRFRNAFKSDELFRELKHCLEIFQE

PLLVCFKDTGAALRAPSASHVQQMQMMTALRYMSRIFYSLNWQDLPEYFEDHLSEWMGEF

LSYMSYESNALVKTDDDDEEEPNLMDRLLVAIVENINLYAEKYDEEFKPFLQKFIEVIWH

LLAHRITLYPKHDDFAAKCMKFLTSVASRSFHRTLFESPQVLTELCGIVVMNLQLRSSDE

ELFEDNPMDYIRRDIEGSDGDSRRSAARDLVRGLLGNFNEAVTQICMNTVHTHLQQYKAD

SARNWAMKDVSMNLIIAISAVKQSRLRGVSEVNTRVPLMDFFMNEVLPELATPNQASLIL

KADAIKFVSTFRSQLPVEVMDQLFPLLMNCMDPSHFVVHTYAAACFERLLTVKDPSGSLR

FNKERLAPYLAKLLDHVFRILEQANYPENDYLMKVIMRVMNVAKEDILPLTDMVVNKLTN

ILTRICANPSNPSFSHYLFESLSVLILNVCKTNPAATERFEALLFPPFQKVLTNDVEALS

PYVYQVLAQMLELRPHGVSDAYKSMFPVLLNPALWERISNVPAIVKLIEAYMHQAPNDVA

PSVPGILGVFQKLISSRITEGNAFSLLRGLVAFMPQEAYAPFLNEIIKILMLRLQTRMAG

RNSVGYVKELIYTMSVIIGKLGPNTVLASLESLQKGMASMFLRSVWLPCNARGRKRAEQK

ACIIGLTRLMCETELCLADLELWIELLIRAIQVLEEGGESTSAIKDEDESLLELEETGYE

AGYAKLFFASVVSLDHLQEYPVPTRYLVESIAKLSASRPGVHLAYAQTKISTPATLVALQ

SYFAQHNVPFQ

>contig27920-1 Frame-0R1

MLEAAEAQSGLPTFGLYSIVVRLFRSIITSYRCYR

>contig27955 Frame-2R|Blast-trimethyllysine dioxygenase, putative [Phytophthora infestans T30-4](gb|EEY68209.1|) 4e-09

MSTPPGLQIVNYIDQAGKGDESRYVDAFHVVQKLKNEHREAFKRLKTNIVRLFNFEVRCL

FPISLWTITPNLATMDYPGIDKFD

>contig28297 Frame-2F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY64568.1|) 0.0

MKRTVSLVSAVMFMFSCGADALNVKMPGANYNSRKGPDWAPTASKCKTASEVQKDMFALK

GITDKVRIYSLVDCNQAELVLPAAKNAGLKVHLGIWTSKSHDYLLEELAKLAGLLDKGLY

DNNVVAMHVGSETIYRGEISVATAISYMNEIRNYIRGRGKNTPITIADVIDVYDANPQLI

DAVDFVSVNQFSFWERSDVNEAAAVTLDRLRKLRIIAAQKSKKIVLSEVGWSSGGWDPAA

GIASPANQAKFFADFFKMAHSHNFEYYWYVAFDSKWRVTNGGKEVEADFGVFKEDDTMKS

NFQQLTIGYNAPRAIRNTGTKLLLSENEGKLYMSGKSSNWLVQEQQVWFFDSATQQVRSK

SSDRCLDAYQGWNGGIVHVYRCMEHEVNQKWRLESSTGKLLHTKHQGYCLDTDPAQGHKL

QLYGCSPNNANQHWMMIDPANA

>contig29755 Frame-1F|Blast-phospholipase D, Pi-PLD-like-1 [Phytophthora infestans T30-4](gb|EEY58277.1|) 0.0

MSGLSRAFHFIMDPFQKEERPEKAATAPFDQPFLEPSRWFLTEEEMSTSRDGYKREGIHL

YTRGNRVKLYVASAPYFNDVADNMMEVRRGDVVYLTGWGTCNVPFKPHEPDTKLCDLAKS

AVMRGADWRMLVWSNITERDQNHEVRDLVNALPPPERSGPARFVYDDRLPHATSSHHQKS

VIIRKGRDLVAYVGGVDLTNDRWDTIEHDQAEVRERTGIKALWNGWVDAHARLEGPAAKD

VAQNFFDRWNMDKKPSEDLMDDLLDFENPEFSSLPPIHHADVSLNIPTDGTHAVQLCRTF

SPDYDHYTFAPQGEQSIFHARIKAIRNAQNYIFIQDQYFILVPELLEAIMDMMPSIERLI

VIVQRTVEAGYTGYAKYLYDMVFPIQKAYPDKFKLYSTKESKQLYIHSKLVIVDDVYVSL

GSANWNRRSMTSDSEIGINIVDTELVQSPDNITVNKLARNFRIQKFAEATKLRFDELDAM

TFLEACDALEAAAHDDGTSLIETYSVVDQPLFDYVPDSLRQIVDPDVERD

>contig29838 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65717.1|) 1e-119

MDDTSMIPTRPFFQSSRSVPRQMLLFFVTFTCSFWLLFFIRLNYPILGERRVNQHMWPMQ

RIVEVLIMLAGAGLGCVVAFTESTPRSMSQSEKTRLMPTIGRNSPHEEMDNGLYESDYSH

SLSFDGQEIQFNHPVSRARLNVKELFNEVVKEQSHNFAVNITGIGTWVSGPMGLIHAVET

EASNFAGIFDVHYEEFEM

>contig29944 Frame-0R|Blast-cleavage induced hypothetical protein [Phytophthora infestans T30-4](gb|EEY65820.1|) 1e-42

MNSTSRYSYSRNGDRGRVDEKCLVRVQIPNVDTSDGGNVRYHVRVTNLRCGKMWEVLHRF

SEFLELRNELIDFFDKTDKKCPGCRNYEKVLNLFEFPR

>contig30058 Frame-0R|Blast-Resistance-Nodulation-Cell Division (RND) Superfamily [Phytophthora infestans T30-4](gb|EEY54105.1|) 1e-115

MVTGTSNPTQQHYIDSYKQNLAAAEWISKKTGVDVWVYSLTYVYFEQYLTVINDAYRLIG

LALAAIFVITMLYLGSIFYALIIAFMATNLVALLLGLMQPLNIMLNGLSIVNLIIAAGIA

VEFCGHYVRFFAKAHGTGDERARAALHQVFTSVIFGITLTKIIGLSVLTLADSRVFKKYY

FRMYMMVVLCGVLNGMLLLPVVLSTITDVKNFFSSWHSRKASLSSAPMTRAE

>contig30894 Frame-2R

MKNTSRVVENPISSMAILIRDKLFMRLTGLIALTSFVVNGVFQIQPFFLNTIVEFDIQDF

SKLTLLGGILALVGQILILKPLVNCVREKGVIVIALVANTIGASGFALTAYYPHKWLIYA

LCIPGCISDLSLPAISALKSMNVSEKEQGRLQGSIYGARSIFEALGPVIFASLYGAMTTQ

SIWSQAFPYMLASLLYLLGIGMALWLPAGKGVSSRDFVAASAPLMSPTNEKFLPSTYFEI

NHDDKIEKEDKFDNVLCASLDEDVNESLVKPLLGTR

>contig30919 Frame-0F

MRWSQALVNVLAVLCLVALVASDLTERDRNDQSDRFKDVGFVRPKESLRLDNAVKEDALN

QERVGSNYFKNLFDDLGKQIDHHLPTLSKLYKSRAVSPDATVH

>contig31053 Frame-1F

MLIRKRLENGSDFFATTVSRKQVTIFLNAAFFDRQQ

>contig31277 Frame-2F

MSSNELLKLLLQAYDKQIEVLIEHEGPITPLLKELQKARASAANISPNKADRGFRKVLKS

YAELEREINEVEALALKDANEDNEVNENVADAAED

>contig32539 Frame-1R

MRVFSKGIFEFSLNASVFNTMVRSIDGLVTLAVLVPSTVTGYAKYSELVPNGGNVPGNEN

IGHLDPAGETGLSTFGEAFSKAGNAWGATLCQADDDGDGFTNGQELGDPCCVWTTASAIG

LITDGISDPADASKTPS

>contig33433 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66533.1|) 1e-131

MPFFKEEWETLVVAAELVAALCTSFWLITLRVGRADSRPLSNEPAALLQPRRCWSLRAIL

AFRVGAATFFLLVQIWDICRTRGRCLAFYTSWNFALQGLYFGGAAWRTKRHRQRQLNQRN

AIYTALVDTGDDGTGSPFAGRQRIMRDSGIPWMDLELLLDLCLATSLLICGVVWTVLYPY

AIKIGHPEQILNGVSYFQHGINVLLLQIDFHATRHLVSRDALPLVMGWPSLYAVFAWIVH

GTVARGFWPYPFLDLDTPWAPFWYGGLLGAHIVALLLMLFFSRFQARKSKGGDILQLKMT

>contig34115 Frame-0F

MSARRGSRSRRRPTTIYQIEGTQYSAIGIDGYAEGKSAQLADNLGEESSEDGPEGKDEEF

TPAGTKVKKPESARKATWTPAALAKSSRPKRSPWSQTRSLRSAEGDSMVKERVTAEVSGA

EGNGINDNREAVIDSLFDAIQVGKRSLENVLKKWHDRFKTDDKKAMKEILNLVLQACGGT

GQCVPESEPLDQLDMGGLVGHVVEELEKANGKYPLVSRGKGMRKFQLNFEEFWKAFVTEC

YESEILFTSEVINNLIDWLTTLSSSNLRPIRHTSTVAVLALSNSLVRTAANISEKLSIAT

RQLNAEINSPVSTPGGKKSTNVQKVSLLKGNKVQNETRLQQVLQLVNLIFTGVVVHRYRD

IMPEIRVAAMQCLGHWITILPDQFLKDNFLKYLGWLLSDKSALVRLEVIEILCELYENDA

FTERLALFTSRFLARYLELCSDVDDNVVEQCIHLLIAVDKHNLISSDIELQSVEKLVFDA

EHEAIRKVAAEFVCLQYDAFGVAVLKTKNATLKKEQLITQAIALVEFVEEYIRNYSVPEN

AVETLVDAFWGLEDCIVLQDWRLMTDLLLVDKSTPDLSNDQQAILLRILVASVKKLVVDV

NRSASKKAFEQLQEEITVAYCKDIPSLFNLYQADSDKLVLLLELIPMLALKSEVIGHNSS

HMKELLEKLKHAFLLHADQELLISLTLSIIHFLQTEHASLKREAEVIAHELIRVVMDSID

RFLEADVKLFDEVINWTNGTPTTRSKNLKGKRKKSYKSKEVSDVEYGLRIALARFSCLVK

YLNIREYLFSDASFQKLGKDDSINALNLRSGRVDTFIIAVGDLVHRRTKSTMGLDEGFRH

VDTIKHGLAIIYFDMLWTTVPVFKATDVAKNCSSSYAVHESFEANVDPLIEVQIQQICRL

RSTLEEALVSVLEMHLSSTNEAADEEHKEDGKACELQVMASLEKIELEDENVKAYVREAQ

RFAFLTFCDARCLFVEKFQDATAPYDVLEWPLPKRLIHLTQMYFESEMDDAEEDEPKFED

EEVENVSEITEEKSSALRMWQEKQRRKAEMLVALGRVALCNPSKKHQAAAVLQYLTSSGK

PSVEVVKAFGKKVKIDAPVRYLEIQMTALRRMYASILVWKQDIEAGQASEDFNEDTSTEQ

KEMKEKVRRSEQELRELAKRFSQSLGIGKIAASLRAPFLRFLCEGVRYAVSQLVHFEFLE

IMRVYLPRLDSSGLAQLRDYFLEQLKTICDIPDDAEGLDSRWRSLFDFQALVTTAGANGG

KGGSTNTMLSPPLSNKRQFLKPTSVQTISIAEEQEDEMGNCGDDVGAITEKVCFDNISVD

KSDQHDRISRKRSSNNEPAVMADNKLDDTDTLPLRKRTRRSRNANKVTSGD

>contig34326 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62195.1|) 2e-50 NOT\_ORF

MNVAAASSTTMAMQTDAVASAISPRKKKHFGHKNKKIIRDGMPIARENKSKRRRNNLKQP

LTKEMPRTLSQLLKEPKVALLHRVVKTIGPKLAWQLLRETLRL\*KDGGQSVNAVGSGKPE

LFFVVDEVSQEYKPRRRTSGGVFFTLLKEKVSKE

>contig36074 Frame-0F

MRSFPRLAHAAVAAVRPFYQRISPGRILITGGTGQIGMELVPYMRHLFGFDVIVNSDIKA

PAGPRDRNFFYCDVQDRTSMARIVAEQGIETIVHMASLLSAVGEANPSLALSVNTRGIQN

VLELAKQYQLRVFAPSTIAVFGPSTPQDETPDTTIMRPTTMYGLTKVHVELLGEYYFQKF

GVDFRSVRYPGVVSSEALPGGGTTDYAVEIFYNALRRGKYTCYLARDAKLPMMYMPDCLK

ATMGLLMAPNDCLSQRTYNITAMSFSPEEIVASIQKVMPRFTCTYTPDFRQQIAATWPRS

IDDSSARRDWNWQHDFDLDSMVEDMLMKLDAKLTKPEAVEETA

>contig36272 Frame-1F

MAYAPCYREATFSCTHVQNEVSLGHWLPTIPSMSLTEDLL

>contig36368 Frame-0F

MADATHPKKLTKKELRILERQKATTEASAPSLTESYGDLPLVQSQERPLHDYKSIKDLNP

ELQGQSFWVRGYLQALRAKSKIAFVTLREQTATIQATLHESDIVSRPMIKYAAGVSKESV

VDVFVTLRVPERPVLSTTQKDVELDVEKFFVVSKALSELPFQVEDAARPDAIVKAKGSGY

VNVGIETRLNTRPLDLRTPANQCIMRIQAAVGHLFREFLVDRDFVEIHTPKLVGGASESG

ANCFTLKYFDQDAALAQSPQTYKQMACAVAGLERVFEIGPVFRAENSNTHRHMCEFVGLD

LEMTIKEHYHEVLEVFSDLFIYIFDGLNQRYAKELSIINEQHPFEPLQYLEPSLIISFEE

GVKMLKDAGADQDPEDDLSTENEKWLGRLVKEKYATDFYILDKFPLAVRPFYTMPDPKDK

RWSNSYDMMIRGEEIVSGAQRVHDPKLLIQRMDELGVPQESMRNYIDSFRLGALPHGGGG

IGLERVVMLYLGLGNIRKASMFPRDPKRLFP

>contig36900 Frame-0R

MLRKLTVTAFAHKCAQQQRVRAVQMLHTRQAFSTRSFTSTRFRLNPEKITKEGEKAADAL

VLTPYEKVTATATGGFWLGLIGLGAVGVYFVARELLPNRMSPNGLFSESLDFLSSNTDVT

SRLGLPIHGYGHDHGGHREGRRNRIEHVNLTAKDGTPRLRVKYNIKGPSGHGYVFAEVNK

NMKKNEYVYLIVQLTKTGELLKIVDNRQILAAETKEEQDALRQLLGN

>contig37143 Frame-0F

MYPLFRLRNTPRPKLSVRRLLPVVMVLLIIVDMGVVFWIMVEFNCVQIRDPTAQDSGCSR

TALWSVVGILPAAIAGSPVFGLIFITRKNIFYGKLFAVWNASSIVNLGAAFICGLLFVTY

IHDDILLVAVGGV

>contig37271 Frame-0F

MTAELEGALRRVLDPTTPSGEKQQLEEQLNRFKETPAACLPVLFQILSTSQNEYALWFAA

TTLEEYVAKRWIHLSASEQLQVRKFAWSYLISNAITAVSPLAFVRRKVRKVVADIARIQW

PGAEQGESKWPDFMSQVEALIISEPTRESGLKLLSVVVEEFGRDDALVFATVKRRAKLRL

SAELPILLSLLANVLKECNQLMLTSGENQVIAQQDQIANAALATLNHFATWASVAEHVDE

AWITLLFAVARNWEGIMKRGGTIFVGASCVTALQCLAEFMGKRFLPVKADGIVGHVMLGL

CTLLQETAENQLLNRATDQYRDKLSEFIELFVAQHLKRVEASTYKYLLQSFLQSMLVFTT

QQPHVEGFLNCLKVWEVVVSYIEEMEVSEGASNEQVRDVLMTYEKGLVAVMLHLVERVRY

ESNRAQLEELDDGDDAGTHGDHEDLETVAALEMNSMGEAYGQSSYQDLAQMRTDVATGDS

SATMVELSERKQFVVDCVAIIRRIAALPGCAIPLLEMMLPCVQRVAEQVLFHIHEMAVLS

QQSDQWEQQQCIIRDLTINCAVLSSACATHYSVSEDVKLQMAGWQILYLFITISDYTV

>contig37385 Frame-0R

MLLSALQHCSGIESLAKDGTGHVVNFTNEVQALEALRKLDGTLCGGQRLRVVRITSSRHR

GAGGGKPRTGSSGRRKRQRIDLRSRK

>contig37828 Frame-2R

MALWGTLRHRMGGSVPTDSSEFIDDFFNATPQDPRWELSAIQSKVENFITTQLDNQRRGI

AFITSGATIVPLDPETSTFVDMAPQLLEHRGPACAEYLLQVGYAVIFVHRLHSMKPFTRH

FQKYTQNGALMDMFQIKDDGIVFSGMGIPQQLQLQKITQLYTECSNRILYISFTSVQQYL

MLTRITAKAMEAAKDRGIVLLAASLMDFYVPVDPSVPEVDFSTIASKTVTSSILSPSFAP

KHPKSKHLKKLSKKKNSGDFSVNFVRVP

>contig39659 Frame-2F

MMGDILEVIAAQRRLDIAAAKLLIPAEDLIEKIRIRESSYGSSLHVLDRLNAPVEEGRLN

VALAAEFKRASPSKGNIAMELNLREQVQAYADVGASMISVLTEPKWFKGSLDDLMTARDV

VEGMHQRPAILRKDFIIDVYQLLEARVYGADCVLLIVSLLSQDHLVELINATHNLGMCAL

VEVNSVQELDNALAAKARLIGVNNRDLRSFKVDMDTTARVADAIRERGLSLGRDGITLFA

LSGIRSHADVVKYEMCGARGILIGEFLMKSNNIVKTVEDLLQKDTCRIESGDFCLPPPLS

KVCGITKVEYALAALRSGANMIGIVMVSSSPRCVQMEEAKAIAKAVRKYGERSGPILADI

LKTHLVGRNDWFFRNALALHEACSRAPLLVGVFANNTAAEMNAAADDIGLDLVQLHGNEG

FEICKDIHFPTIRTLHVPDTALSERTAYLQEIQEGLANYVLLDTTVKGQQGGTGVTFDWK

IAATFAHARVPCLMAGGLTPNNVQMAISAGLPIGVDVSSGVEVSKSPGVKDLNKMAAFLK

AVKNS

>contig39754 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70078.1|) 0.0

MDDCVQAAANTGMFSLCSELTLRRICSRAKAVSYPKNAIVYRQGETQNEMLLLKQGSVES

TKIIEGQEHTLGITSSGAVSSNHALVQDPAAVTVRCLTPVSGFSLQSAELNEVLEDRTAA

REVMHSLSKEIRRQASLLQTPLFEQHAKPTPYFATSVAASIESFYRSGMNSLLNARLTGQ

PVARLFPEMHLQIPTRMLYINGFKGIRHLLERNVDVEQYEYPLLVRLLEAVSPGVIMTPV

SSMLEAFNAGHMNPESLATRWIRGTAPRMLREVIFGVGLNQLSDYFEERLSLTSSPALNN

AIGSMAAGVVSGYLSHVPHNLSTMKLMHPQKSYGQHMDDFIRRAEVRVPNTVSPRQRYMA

ATALALLFPKGLTVRTSQIVGSFIILNGTINSLKDIDFNTIKGYLST

>contig40273 Frame-0R|Blast-aminoacylase, metalloprotease family M20A, putative [Phytophthora infestans T30-4](gb|EEY64299.1|) 1e-177

MAEHWQYEPFEAKVLEDGRIYGRGTQDMKSVCIQYVEAVHLLINSGYQPQRNIYLLFVPD

EEIGGVDGMSKFLESEQFNAIMPIAFAFDEGLANIGDAFTVFYGERSPWWVYVKAKGPTG

HGSRFIKDTATMKVIDICNKALAFRDEQGKALGADNGCKHGDMKKKKLGDVTTINITALQ

SGVSNDGGVTHALNVIPTEAVAGFDIRVSPDMALEAMKDKLDKWCLTEGVSWEFASWTDP

LHKHYVTSLDNGNVWWQLFQKACAQMGEKLEVEIFPAATDSRFLRKMGIPAIGFSPMKQT

EILLHEHNESLSKDTFLHGINVYVGIFQEMFAYK

>contig40417 Frame-1R

MGQVYCPVRNDATNCVLMTHSIWHKNSLLLLQQTPTHLNEAPRVASMEAIQKYRKVSSVV

MIDPGQGHIGSVYSGQSPEWLHLHGVQQSQFFLLPHARVAGIQTSVSVPMIWKLSTVAVL

SWYSYQAMEEDIHVVQR

>contig40655 Frame-1F|Blast-phosphatidylinositol-4-phosphate-5-kinase (PIPK-D1/GPCR-PIPK) [Phytophthora infestans T30-4](gb|EEY69098.1|) 1e-111

MSEPVMKRKASKPREYPKNHGCNGRTASNTSSSGRRLPRSGMRMANTVVGPAYYHLGVID

ILQTWTFQKRMERLFKIVFRGVDGDGLSAIPPKLYQARFQLKMADILGVEDLVSGDNSNL

DLFTQQNSHMDVDTQQADQQYNIQSIRSLASSELVAINPMDSHYANSRSSSILRQRSTEN

SQSVGQDTEEYTGIDYHL

>contig40844 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65515.1|) 3e-11

MQIPKAAICRRRPFCRFLRSQNPLLIIPLLPAHTSAMPVANNSTFLPSCILQETELKSQR

KFKHHQHDVSRRLAERRSEPRFKHHRRHQNRANIA

>contig40938 Frame-1F|Blast-importin subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY62298.1|) 1e-56

MRAFVYLLSSGVPPLFDECDSQHKGLWDTILAAIPSFVAILNEDLLDANAVQLHSDAAFA

MRFISSMDKASAVIASGV

>contig41115 Frame-2F

MNLYYFNSTHVCGSAFLPSNRRVLGHFFTHHGRKLATTPFMFQVHRLPLVLSLLKSILLL

SNSITQILRSIFAGLLCY

>contig41281 Frame-1F|Blast-cyclin-dependent kinase, putative [Phytophthora infestans T30-4](gb|EEY54371.1|) 1e-142

MELLDVFVANETISVVYELLPSNLDDVIKDKAVVLTAADIKAYMQMLLKGLAYCHEQYVL

HRDLKPENLLIGPDGHVKIGDFGLARVYGSPNRNMTSMVCTIWYRPPELLFGAREYSGSV

DMWGAGCVFAELMLRVPYLTGISELDQLGKIFHALGTPTEEEWPGMTSLANFIEFTPSSA

PPLASIFSAASEDALDLLAKLLKFDPMKRITAVEALKHPYFSNSPAPTSVEKLPSTSAPQ

QA

>contig41326 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65944.1|) 2e-30

MCLDTFNEENPKVRTLCHCGMNRTNFHMSCLLEWLNRNANCPVCREYLFFEDT

>contig41476 Frame-0R

MSMEPEQIKATGPELHDESTQQLWRLEQENDRLNSCVRRFEALKIDSEHKLEQAEEKV

>contig41704 Frame-0F

MRDKEAQTETQVLAIEGNSDAGGQFHLGEWNDAMNGCDLRQQIKEQQTFIKELEEKQVKL

VTERNMFRAKSMNLSKELQKLVKANNNESLDDLKTQLAERHFLKNEVVRVKAKAEKTADK

VTHLSSLLKNRDKDRGTKRLAAQVVELQRTVHQLQDSLTEARDQVDAVKQINTALASRLA

TLQSESSRQY

>contig41898 Frame-0F

MAALQAVSQAFGNVSNASGGVGMSNYAEEKAKCSEFLRNFTSNLADPALGPKYAQMMQEV

ANRERTSIPVALDDVEIFEKDDPTFVTRIVRNARRYIALFSDAIDESLPPPTKDISDSQD

VLDVLRMSRAQELAQQRQQQDNETPTSTVNAFASTVFPPALMRRFEVHLIPGVKLKAVPI

RAVKAAKVGALVRIKGMVTRVSTVKPLLTVATYTCEACANEVYQEVKARQFNPLTQCPSE

RCETNKAQGRLIMQTKASKFDKYQEVKFQELPDQVPMGHIPRSLTVYLRGELTRTCEPGA

LVTISGIFLPLPYSPQRQMQMGLVTETYLEATDVVNHKKRYSAMESSEPMESAVLRLQEA

SENVYEVLSQSLAPEIYGHEDVKKALLLLLIGGVTKRMDEGMKLRGDLNVLLMGDPGVAK

SQLLKHIATIAPRGIYTTGKGSSGVGLTAAVVRDATTKEMTLEGGALVLADMGVCCIDEF

DKMEEGDRTAIHEVMEQQTVSIAKAGITTTLNARTSVLAAANPIYGRYNKKLSASQNINL

PNALLSRFDLLFLLLDTANYEKDEALARHVTYVHRFSRNPEMKFEPVRPEVLRYFIAIAK

QYQPSIPEHLCGYIVEAYVTLRQQDVNDHARERQRQQFRQKYGDGGANDAQTAMTARQLL

SILRLAQALARLRFSTEVIHQDVDEAIRLVYVSKASLIEQDDANGTDRG

>contig42271 Frame-1R

MAPELYDESYDEKVDVYAFGMCVLEMVTKEVPYSECINPAQIYKKVTAGIRPKGLQRVVS

QAARDFIELCLSRGNGLVDVTAQYLLDHPFLKAQDDDNDMVECLDEDKVERDSKVEQQRL

ERVAEESFAEEFNMEGRLKDGVVLAMSERSNSMSFEMKDELT

>contig42385 Frame-0R

MPVHVSKISKVITLFALDDSANIMTRTYEIQVFLDYMFTKWPEDALAMLNNWRKATLPPK

TF

>contig43368 Frame-2F|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61120.1|) 9e-78

MCSRGKYTCGLQSSQFPGKLGSWILAAAAVFGLFCSLMLLMELYNIYQDPLFTLIADQLA

ARRGGDKSTSRLERHLSVICGTDGMRASWCFPPSDRRALHDLEIVQGFRCRLEDADIC

>contig43900 Frame-2F

MSMITRCVEYDIVVTRPMQLEVDSRMLGRRRVGITACVFNSHLTLSLAVQDLDIHLEQLS

RQNASNTGDLTRFCVVSVETVLFPVVLQPQERYKFLFVLEPFRDVQHHESLKCVSGDDKT

TIKDSPPIETRPIVPTQQQIVLTLSWLASAYAMDAITEDRTVVWSPMHSISSLLMDGNKW

RPHIEKLMAYVQTGDLRRKAKPSADFKCVQLFPDSVLQATLAPLTCDVSLGTAAVVCVTI

VNRSAHVDYDLTLVWPSQENSGIEGDTPAV

>contig43975 Frame-2F|Blast-translation initiation factor eIF-2B subunit gamma, putative [Phytophthora infestans T30-4](gb|EEY54236.1|) 1e-127

MAEFQAIILAGGRGIRLYPLTEETPKALLPANGKPLIWYQLQLLETSGFTEVLVVTVPDL

LLPIQDYVTREFDGKIHVELCEVADNTETADALREIADKIKCDFVVLAGDLVTDVVLHNV

ADFHRINDASVTMLLRQEAPAHKGKGEKARRDKDMTDCIGLVAGQRDEENRVVLISQAVH

MNEDLFVAKSLLKRRSHFVLHTDLYDGHFYFFSHWVLDLLRERKYIANIKADLVPHLVRR

QFRGKEA

>contig45249 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60699.1|) 1e-40

MIVVFGSSNAFGRDVSETEMMVLSGTVFVISVLLVLVYKLARGWDELEKEDFGASLLPLH

APRITNRWVISRKTHFGRLSTIEENEIFSVSTKMH

>contig45335 Frame-2R|Blast-gamma-tubulin complex component, putative [Phytophthora infestans T30-4](gb|EEY58484.1|) 7e-63

MDEETIKAEREAERDRRAEKKAREEAEVALASYQRQKGLFGVKTKGGVLKHTQASHFDMR

RTRIKEMSNNVKRALTERKGDAENPFVRMTNDLENQFDSLLGEFMQQLLRRSLLQQNSHL

SNLCTRLDYNCFYTK

>contig45537 Frame-0R|Blast-glycine cleavage system H protein, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY58729.1|) 3e-30

MAGGWFIKVELDEVKDLDDLLGEDAYKEHCENEEH

>contig45582-0 Frame-2F0

MLLSGFSFGATPAIPVSSSGLNFGATASASAPPAGNSFGGG

>contig45919 Frame-0F

MADQTSESASLNIVSCPLRFIVCTLATSVVRGSLFLCYKCIDGSTLYASTCVMDSSAMAT

SSPSKRRKHCRFLFRPTQFFPLLMPLSTSCTVL

>contig46046 Frame-1R|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY64036.1|) 1e-174

MMVMGIAGVACAWLTRFPMTPERLYNMQVDIFRAKHEHADFFYHSCLYLGTVFGAVIGGY

CGDRLGRAGTLELAAIPLIVGWVLIGVAYGELTVLIGRYLLGGAAGILNVIVPVYLAEVS

AAHTRGRVLCAQMLVSALGGMCYLLLGALFMYLSHQYLGFNLMEWKVLALAGVIPGLLLL

LVAQKLPDSPTWLISRHDDREAAFKVLLKLYDRNQRVAENETNAIIHAKVLGATEQRHHG

AFFRPVLLCATLFTLRTVSAFLLEPAITSSLANARVRGNNGTSTSTSFVLTLIGVAVTGA

KEELLAITFVAAVASIMGMIACFYFVDTRGRPAALQCGCSLVTLACVFLLLSLYQSVPPT

RDHGVSLNAFGYAAMLLANAGHQLGLGVVPVIILSELFAVKHRMNAVSLV

>contig47117 Frame-0F

MWNVLRSVTLHLLWSARNSRLYSPMPTIPALWVIYATFSFHIRAFFRRTYDDLEQPSLRW

VLQEFKRSPFLGGFVQQNEALFHVRCLA

>contig47320 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70570.1|) 1e-84

MPYESFKSSQLVSIRGLVQDRKTGTWRYLLQVTRHMQDDAFGQNTRRASTSKSDSASAYA

TRPCTTQSYAIRRSFEDFKRLHEALTPLMAKCGKSQLPKLPNDSLLTFFVGETQTALQKK

RLALERVLAAIEAHPAASEAPEYIEFLANLNSYDGVAKALMSPSISSRSSFSVSEDGTMT

PRDFGAQNMLTTSRSANALRRAYFQHEAPSERETHLRFSH

>contig47870 Frame-0R

MKRGHACNRTCSCSRDCRNRFQGCKCFVGNCHTSACPCWSAGRECDPDFCFTCGASDAAV

VAFHALGKSWGSNQLRLCHNVNMLLGSIQKNVGVSFSSTHGWGAFALEPISKDEFVLEYT

GELISDEEAERR

>contig48303 Frame-1R

MYVATALSDECAANSIINGDNIEILSQCNSICTNMISGLLNRMPKCFFGYEYINKKESFS

SQLNKCNQGASLISIAMLGESFVFFASSSGPGSVEADDSVSRSAEDDYDSISLGSTSENS

NSKSESNAASPRRINFLLWVLLAATMTLPITS

>contig48686 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69521.1|) 5e-24

MLSIAFSPNSSSDVDTRRESVAFNLGPKRPALKKKKKVSKARALSTERSRQCRERQKFYS

ENLEAIVRALRADVYDLFALRDLRREQCLQFRGSVSGSLAKIVQEYMT

>contig48761 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61322.1|) 5e-32

MTVDYFFGALQKKMNMSSTADKKLFSSLVAQLPQISVEILRIITLLCREKVGLVLGITLL

RDLCKERKACQRPCLLLLLR

>contig48981 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54845.1|) 1e-29

MLPDAVYALQSLKTLNVQQNQLTTLSTHVQNLTHLQTLDMRHNQCKTLPVQQLETLERLQ

TVSIAGNKHLIQALENQELMLSDELLHKLVLT

>contig49065 Frame-2R

MSLSSRMKTRQRRSRDGSPYGHHVSFVISHDRIWSPGRRTIRHASPKTRTLATSCANMHE

NELANLIPSRL

>contig49267 Frame-0F|Blast-FACT complex subunit SPT16, putative [Phytophthora infestans T30-4](gb|EEY54832.1|) 9e-25

MVQKDLIITRDCRVQRLIDLSARLHLTERKTHGTFEAHSNGVRSTTNKNQKVDIFCMQIS

SSRR

>contig49528 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67022.1|) 1e-86

MTAGACERRQLPYDALNPEWEKREFKKFRATSGNARQQAPYGSYLFGRLMQSDLHESCLP

ALPADIAKCNGATVQGMCILQLVDVANIGANFEYRTEFSTAGPARTLKLGLTDGHQLVFG

FEFTPLPQLSVNVTRGTKIVVENVPVRHGLLLLGHDNCQLLENSTVRPKRATGIKHHPPK

TDGLKVLEFTRLPS

>contig49779 Frame-0F|Blast-adenylate cyclase, putative [Phytophthora infestans T30-4](gb|EEY56781.1|) 2e-83

MVEEPRMEMRKASRERASSGMLRKELDMRLTAYLPAVVRRHLEKQDMQSPLRMPTTHRMT

VVSMFADVSGFTAMTELLASRGPVGAEDLGKHLNSYFEQLLRLVSSAGGDVFKFAGDAML

IFWPESKEDTMDSLLRRALQCALRIQSHLHEAELAPGVILSVKVGVGIGEATIAH

>contig50038 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58324.1|) 6e-22

MTPTAVATSLTRDNIKFLAIARATDKVIIASYLHMSTGKPIRGAEVEINTFRAMLDKVLR

APTWQAQVTPNVR

>contig50799 Frame-2F

MPVTTSTLLHVLDRMPEIKNKIQSILNRTDCSESQKVAMIARLLSNTNAISNTNAICSST

ASAAPSPRSSSVLSALAVDASLLNSSDMLVNTETPTSSVDVTPSRAMASPEELQSPPS

>contig50939 Frame-0R|Blast-APS kinase/ATP sulfurlyase/pyrophosphatase fusion protein [Phytophthora infestans T30-4](gb|EEY66435.1|) 2e-91

MPVPIVLPINNATKTRIGKFRQVVLVSPSGEELALLSDPEVYDHRKEERITRTFGAIDDG

HPYIAKIHKSGEYLLGGEIELLSRVKYHDGLDKYRLTPTELRKRFKEKGADVVLAFQTRN

PTHAGHAYLMNTAREQLISKGFKNPVLWLSPLGGWTKK

>contig51446 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57049.1|) 1e-43

MTDIAALLVPPQDIHPNNAVFATQSLPRPLTWQRREHMMHRRTILTRIGQLLVRKTHRVL

SEPNCATSTGGVDVHKTWIVARKLEVLMFLQSASLLEYINMDSLTRRVQALTARIVNKKI

RRATT

>contig52054 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70095.1|) 1e-119

MSYINSDMPYERIEEGPSIFSKNSIVKTDYLLLSRNPNDPNDLHQRLCLHAVIDYPNWGL

IDVYVTHLSLSERSREQTMVEIWDYMRQGEGKAQVLLGDLNSEPQSLGIRFLSGTAELLG

QTTDMKDAWLEMHAEAEPRSLDPNDRMHKFTFPSDSPSKRIDFVLYRGEVQVKECEIIGQ

KPTKDTEEFPNHVGMTHVSSPIYASDHRGIIVQFE

>contig52159 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65228.1|) 3e-43

MEWQLLDERDSIVDRLTRTFIQSNKRRQLRILLQAVTEAHYDDWIAIIQFVMEQ

>contig52230 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65824.1|) 6e-14

MPRKKFKSLVELSIVTVARYTPVQDVLKYVEYLPTAIRYQLFNELSNVRLREMEVALELA

AQHEPPELCDG

>contig52245 Frame-0R|Blast-pre-mRNA-processing-splicing factor 8 [Phytophthora infestans T30-4](gb|EEY57153.1|) 1e-170

MILRYVKSKADWWTNVAHYNRERIKRGATVDKTVCKKNLGRLTRLWLKAEQERQHNYLKD

GPYVSAEEAVAVYTTTVHWLESRKFAPIPFPPLSYKHDTKLLILALERLKENYSVNNRLN

QTNREELGLIEQAYDNPHEALSRIKRHLLTQRAFKELHIEFMDLYSHLVPVYDIEPLEKI

TDAYLDQYLWYEADKRHLFPCWIKPSDSEPPPLLVYKWCQGINNLQKIWDTSEEECVVML

ESKLEKVYEKIDLTLLNRLLRLILDHNIADYMTAKNNIVIAYKDMMHTNSYGLIRGL

>contig52924 Frame-0R

MYQTQYQPPCHQPSLPYQQQSCGDDGRGYTIVTPRPSPAQPERYLQPMNKFQHFQQHVQQ

PQPSTIPQQHMQQFQDKMPEFFNNLQVPLVPSQSPSDYADAVRKRKQAYAPVLSTSDQQH

AAYQEISQFSQQPPLPP

>contig53123 Frame-0F

MTSIVKHCCVGIPRKSSYYLLGAPRSLECYLLVKRTKFFQYLIADHVINKALSIVLAKVN

YNLLADNIRPQLCRFHP

>contig53541 Frame-2R|Blast-CDK5 regulatory subunit-associated protein 1 [Phytophthora infestans T30-4](gb|EEY53383.1|) 2e-66

MLRLGMTNPPYILNHLNSIAQVLNHDRVYSFLHVPVQSGSDEVLLAMKREYTTAEFRRVA

DELLAKVPDLTLATDIICGFPTETEAQFDETMELVEKYR

>contig53619 Frame-1F

MLELLQKLEGCNFIRPSSVCRVLLRLIQEYLT

>contig53808 Frame-2F

MGNVLIKLDVQWCECDVGVATRVL

>contig54041 Frame-2F

MDLEPALRRSKREHQPSAKAAASSASVFNFPASPRSSRRSQRRRISSMSPVSTIVPTCHS

SPILNV

>contig54423 Frame-2F

MLHLILAMRQRRYHEEKWIEKLLFVDIGISIRQSFSMLQSSLVINKLTSRLRLCKTVSFT

FSAVQTIFDTYPA

>contig54935 Frame-0F

MRQHELYYSYIQPVTSRTSSFHLSSWYPKRLLSAYPSSQSLTN

>contig55734 Frame-0F|Blast-ATPase [Phytophthora infestans T30-4](gb|EEY66204.1|) 1e-84

MIHIPIESVVSKWYGESERKMSTIFEACDKLEGVIIFIDEIDALAGDRSCGTMHEASRRL

LSVLLQKVEGFASAKKTTLVCATNR

>contig55895 Frame-1R

MVLTTDRDITVKKEFSSLALVLEHTADDAVQCLKMLKKSLAEYDFRHGHKFLSSAKSYMN

SDIRYAKDISSDLKHVAQQINKSKNHSKSEVELAQSSMNATANAMNVLKTRSRIYDETDG

RATGVKGMIQNIVGGANKGIDKVVYTDNQIDLDGVNGSSDTVESLVEITLQNSFDLNVLK

HQISTAENSLIPSIVERAQEAVHEAEETLKCDMTTPTPERMYVAFS

>contig57286 Frame-1F

MGVPLGNTGIDVANIGITALPEFFTYYLGSEPSFVPK

>contig57703 Frame-1F

MAYLNNYISALPTQLNYTVQGAHMIHAGPKVST

>contig57798 Frame-2R

MDADDNQPKLRHVVYCPVDTFPPEYCEYGPMFNECKPWLAEHCPNLMLTKYNRTVTELLE

VEQQIADGVEGISLEVKGKTVKKKKKNKIEEAAKRKENCMVTISKSSRKGRKRLTFVTGL

EDFEGVNIKEACKSMGKKFACSSSLSKTDLGQQ

>contig58485 Frame-1R|Blast-reverse transcriptase [Phytophthora sojae](gb|ABG66531.1|) 2e-11 NOT\_ORF

MMQLFRPHRGYAQA\*LMTFFVHRRAE\*GRSDVETT\*TICEQCSSVCAQIN\*YANASKCIF

GADEI

>contig59305 Frame-1R

MALALATQEIVWIRYLLMEMGVACKSAT

>contig59370 Frame-0F

MFLLYSALTLQVASLFVDATATSMQNESLTVL

>contig00603 Frame-2R

MAHHLLLAALGVVSVQLVSSLVRVPLTLTPQSRSTEDLLQFHTQPSEALLSGVHEDHVLS

ALRFQQDNAQNPFQNDRIVHNAQELAAQGHVPLENFMEFQFFGPIAIGTPPQEVLVCFDT

GSSDLWVPGTKCDACAGIERYNHSQSRTYHESKAHPGFAVQYGSGKVSGHFGNDVVQLAT

FEVNHTAVGIVRREEKSMAKMKADGLLGLAFDGLSTFSHPPFFFALLEQHADLDSVFAFY

LSPYPNSLGSELHVGGYDKALLTSLNATWQLTDVLPQFGQWTFWRIHLHRVNVGRHGNAC

PDGCVAFVDSGTSLIGIPGTLYLNFLYQVATFAQNQGCYCGFVQYGFQCFLCAPQDFPPL

HLGIGHQHFYTLEGPDYTLCVGLTCIVLVQPSGQDMWVLGDVFMKKFYSLYDVEKKQIGF

ACASNSSLCGMDEFIETPTSDPLPAYTSPLFESSFNMYTMDTHAVVVLFLSGCSFLGALF

IVASFWQYPVLRTFPSFSLVFWLAMCLLAYHSTLWIAGVLWRTHQTHAVFCAWLQSTQQF

LGTAILMFSGAMGLELIRTVRWTRCSTVNFNVAYHIVIWGTAFCTGVFALVTR

>contig01024-0 Frame-0F0

MPMVRMGSDPAPPIQAAPLMGLGEDAVARHRGFGEDAVAR

>contig01774 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63346.1|) 2e-67

MYASPRYSRHHGSNNSYQTPYTSSPTKYSHPPYTSSPTKYNTYNSYTSPEKSTSYHQRNY

TDYYSSPSSPTYYHQKQELYNSSASTASSSSQDGPFYADELDELDDYTMGLASPDMTTVP

TVPTPLKLSLYEHGKIPSGRVMVSAGNQTIEFFSSVVNAPLSRCMIVQE

>contig05288 Frame-2F

MTADSCLRYLLTCVPVKVVKLAELDSSLTPVPIVFKYDISKTAHRSPNSVTAEITRTGRI

VGCCYGSVEAGKSRYITNEDSAFLHVSPFNAPTRDQLLAVPDQAAKPSKVRSSKSDQIRH

MILKQYAVNSRASRSSANITGYILLDALRNI

>contig06285 Frame-1F

MSTLNPNAGEWVPPSSAPLAFLNKSLAAVSPVKATGLTGAANTVKEVEVAPVMLSSHSKT

TLERAGEFNMASDEKGEAISYEGYSPVHDRLIYSKEYLLAFQPICDQVLKSISDVVKNLI

PLKKIGNRVKGRRVYSIANLLKFQPLYEMMPEDFTWA

>contig06797 Frame-0F

MLCIGSKNPRLPLKKTMLVTPLEDWPRPPTFIHGGIRWTRSDEPQSFGWNSLCKYYKVVY

SSAYEKSQEEFQLLQRSHDPNVIAHFLQRYPYHIEALVTMTEVYQHHGQMDHASDCIQRC

IYVLELAWTDDFEVTKGHCRMDIRIETNGGVFKALFLLMKQAGRRGCVRSAFETAKLVLG

LDPEGDPMSVVLAIDYYALTSRQCQFVIDLVHSKTLVVDRYADEEMVLSKNQARLKAIKK

NSLHDIATLPNLQFSLGLAHFYLGNEVEGKEKVAIALLHFPTLLEKLLHRMAAISS

>contig07479 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61679.1|) 1e-11

MLGAYVGAFPIPLDWDRPWQ

>contig08104 Frame-1R

MSMSDWRANALDDAEYAFLLFHPDPRPSTTPPYLSTTSYPVVVPPRQPPLGLSDDDMLDE

IFQEIMSPGPQDPPNHHHSNDLHSFPISATSALLSPIVASSSAPSTPQLATSQRRGSIPS

ASLGSISPNMTVSLRSPLSMHTNSTRSTSVFFPMLSDPKVRNIPTHYNAHPPSLLFPSPT

ARRNYRRMARMQKKKPASRICRMPGCTKGIRSRGLCKAHGGGRRCTTPGCEISDQGGGHC

IAHGGGRRCS

>contig09402 Frame-0F

MATSASSPSSSPVAAAITAPAAVTTSTASNSSATGAPQPFHTASLYVGDIHPDVTEALLF

EIFNAVGPVASIRVCRDAVTRRSLGYAYVNFHNVADAERALDTMNFTSIKGVPCRIMWSQ

RDPSLRKSGVGNIFVKNLDTSIDNKALYDTFSLFGNILSCKVAIDHTNGNSKGYGYVHYE

TAEAATEAIAKINGMLIAGTEVFVGHFQKRQDRPDADDWTNCYVKNVPVEWTDADLLKEF

EPFGKVLSAVVMKDNANPDQNRGFGFVNYEDSDSAHKSVQALNGKVYPTGESGETELYVG

KAQKRSERERELRNKFEQLKMERINKYQGVNLYVKNLDDQLSDEELRDAFTDCGMITSSR

VMRDPNGNSRGFGFVCFATPEEANKAVADMNGKLIAGKPVYVALAQRKEVRRAQLEAQHA

QQRAGMVVGRGMPMGQPPMYGAAPMFYGQPGQLPPQARQGFMYPQQMMPRGVQRGPIPYG

ARMPGAPAPTGYPMPGYGMPMQQQRGQPRRGRQGPGPQGPQGAPANRRNFKYTANARNHQ

ARDMPPQGVMPPAAPVLNAGPEPLTSAALAAASPELQKNMIGERLYPLIHCQQPELAGKI

TGMLLEMDNGELLHLLESPEALEAKIQEAMAVLEAHQG

>contig10178 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54392.1|) 1e-170

MKFLCGDRIQRLKQLQSEGLVDRGAIHDSVNATIQEMLNGKNPEELKALQEEVKKTIASV

STGATGVDIDYWEAVAQQIQVYQSRARLTELHEEMLTKLADLMEEHETLTAEVAAARAAE

DEIHGVVDENGRDAGREAREMEKMFAEKEMDESEAKLEASEEVHLPDPKKAPRWSEKYQP

RKPRYFNRVKTGFDWNKYNQTHYDRDNPPPKVVQGYKFNLFYPDLIDKHKAPRFFLEKTN

SDEFCIIRFSAGPPYQDIAFKIVNREWENSQKRGFKSVFERGILQLYFNFKRHRYRR

>contig10611 Frame-1R

MGSKHSRLSHSSQGDRRASVDSQKAVVDAISAEARAEFTVGDINRPENTRRAQSLYCNDR

DRFCKYRNYFKNHHMSLAREVGRETRKSKTELLQWVQTVVGPLENGENFTKDEILELAMV

SAALSEYGESVLAKMYDRGELDALPNVPLHTHNLRMPGKQQACRNGSDALNKDKLEAAHY

IGLEVMLRLNERLPVEHRMGEELRVILNHPSNLRLMLASSNQILHKKVDALLIRANDPIS

ENKMQVGGTKSSSREYARLVQIAKHAQDLAFQEAMIAANGHYLYQSLRNQFQRLEVSGRI

KLWEIEKDKPELRQIPRSRYRSPSPVPRNLRLPGSPEKKPEPKPRMVDETTTSSPLLEKE

HRNPFSRFAAKIFRSRHQKKNLAIPRSSATPAPKLHDRTVSIKRRGGKGANVAIVAKAKA

KSHKANNGRKPHRNKYEKGKRVSRPVANETATLSHDSNSDDHDSD

>contig11102 Frame-2R

MLHLRRSVRCPQSCLRVGLFSSSAKLSPTFISTPIFYVNAAPHIGHVHSAVLADALSRWH

KIKGSDVLFTTGTDEHGLKVQEAAENSGTTDYKAFCNEVSSRYIDVFQKANVLYSRFIRT

SDSDHHEAVNAFWRVLRDNGHIYLGNHESWYCKSDESFLTEMQVEDKVEACGNVIKVSKE

SGHPVEMLHEENYKFRLSNFQNRLLEWLDANPDVIVPKTRYNEVRAAITGGLKDLSVSRL

SNKICWAIKVPDDDKHCVYVWLDALTNYLTSAGYPKNIDHYWPTAYHIVGKDILKFHAII

WPAFLMAANLPLPKKVVAHAHWTVGGVKMSKSLRNVVDPYEVLSKYGSDYVRFFLMREGV

LTNDGDFNVEKLEDRVNSELADTLGNLVSRSTGKSVLEKGIIPLRPELNRLTVEDMKIVT

KGRALRTKVELYFDTPDFARGLEEIFFYLHDVNR

>contig12572 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56790.1|) 9e-10

MASFLLGDEYASSSSSEGEYASIATSDIFISSSGADSTTKQLLPSAEELFASETSSLLTS

HVVPTSK

>contig12815 Frame-2R

MRAVSGYDRKDLNDDEEALVRNLKYRIGIMVLL

>contig12998 Frame-0R

MAPKTVVVAGAGVVGLAIARAAACRGLEVIVLEKNAQVGQEASARSSEVVHAGIYYAPTS

WKAHLCVKGREQLYAFCHAHGVPYSKCGKLIVAHSHQSNELRLLLQRGRANGVSDLKLLT

RSEVFAMEPFIECHEAVYSPSTGIVDSHGLMMALQGEAETYGAMVVCATAVEGGTFDLKT

KTFTIQVVQHDCKHEIQGDYFVNATGLFAPTLLTKVGVLNRPINSTSELPTVFNLFAKGT

YFKLQTRPFTHLVYPIPEVGGLGVHATIDLSGNVRFGPDVEWIDKIEYCPDSSKAETFAT

KIRTYWPDVRTEMLTVDYCGIRPKNCNAWPNL

>contig13885 Frame-1F

MIQCDSCSHWVHAKCANKQPEAVAQEKFLCFRCGWIFDCECDIRRQPNHDDGHRMVECDS

CKTWQHTMCVGIPMTEEPADDYQCPRCIMKGRQCEPASESGESRDRQLMRSRKGKRIGRR

LSRNASLLDGRSAASSVEPTTISTQVKRRLTKRNKELTADKGKSLTQLSYSRPVSAAYSS

SIPPPPVSPPPGLAQMLTRSPSYDRNRVHVEGRRSCTQGLQTTQFVDSHQRKRGRPMPNA

DITTTKTSGRVRIALSQSEVSPSLRGKGLMLQRYSSNPSVPSTPSGKVRPSRPLSSGTDQ

THGSHGVSSRRRKGDSARDRLAKKLKVRRASSR

>contig13962 Frame-2R

MTVLQNQIHKRQLHRQWLSSRLIRRCIS

>contig14981 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54890.1|) 4e-79

MISKSFGSEEEAFKAIERATSRHLKTSTTMILILDEIDMLLQHNQIEKDLCRLFELAHRR

SNRFFLVGISNQVDFTERYLPMLQQRLPDCVPQVVIFKPYTHQTIEHILMERLGGQVLAS

KMVSLHGISFLARKIASTSGDIRLAVDTCRRVLQHQFNQTNQANAENPIGENVVERPLPL

TDMLRIIKHALESKSALVIPS

>contig15076 Frame-2R

MHSSRRRRGEWQTRIGNVAHGAYNTDIRHDFRAQRHQNNKVTLNNPLTIVSSQSKLNTTL

AIRLLTFANECHVLSRIRPRGAQKPLLRFERWWPVVAWMSTRPDTFACLRRDDSKTVVGP

YERH

>contig15252 Frame-1F

MRQRFRLRCGRRHLCATALLLLSLASAAESGEEADVLDFGPAHRVAEQRATELEYEQEKS

MDKIDVVDIAHQRGSQSRKSSQVSPHLKERSIADTFERDRDECVRETKTKKNPQGMHHMA

SKSVRKHQGFDSKIGKRQVTRIDLTLDVNSQNHSINKA

>contig16275 Frame-0F|Blast-UDP-glucose 4-epimerase, putative [Phytophthora infestans T30-4](gb|EEY69388.1|) 0.0

MLPTRHGHTNRPETRWLLLPKLYVYLGALAIFAVGALFGGGYYQTRGGLSTMTPGFRRFA

SPKPIVLVTGGLGFIGSHVVEDLLANDFEVVVYDDMSNGKNFNRGAAAVLVKDITIVDDF

SFIIYKVDYVVHLAAAISVEESTRFPEKYERINVEGSRKVLEWAVKNNVKRVVAASSAAT

YGIPLPENLPLSEETATGGICAYATTKFQMEKLMQYFNEEHGLPSTALRFFNVYGPRQDP

HSSYSGVVSWFMEQAKINGSLKVTGDGDQYRDFVYVKDVARAIRTAMLLEDNKFDVFNVC

TGVKTTITSVAQRIVEKFQSTAAIVNVPFRSGDVKESVCSSTKATSKLGFTATYDFSDGI

GETRDWFLSQ

>contig16882-0 Frame-1F0

MRNVYELSRGSLQSNIVIFSTV

>contig17478 Frame-2R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY69433.1|) 7e-29

MRGITHSTLKLHAVLHPILSSPQMKDVMSRVFDMFTQKLPECFKLVQPRTAAGKNR

>contig17889 Frame-2R

MLLRHRPRITVSPRPSFFFLECDLQM

>contig18480 Frame-2R|Blast-nucleoredoxin, putative [Phytophthora infestans T30-4](gb|EEY57948.1|) 3e-61

MEALLENELMLKSGEVVSTSQALANKQIIGLYFSGHYCPPCRKFTPLLTSVYHTIKEAGH

DDLEIVFVSSDKEEAKFTGYYDEMPWIALPYARRDVKLALCEQFNIKTVPTLVFFNAKGD

LVEREGRHFITHHCNNIHAILAHLQPRAK

>contig18761 Frame-0F

METPEPPTYDESCDETGTGHRRGRFAFRTRSFTAVPKQAQRFVGGLTAQIRRRMSVESSP

RWNWAFGTTGDASLWAPSVHYMLHTGEVTSLVLGKDGRALFSTSKDAMFKVTATLDGTLR

RTLMCNLALSCCDVSPDEKYVFIGSWDNCIYMYSMDVGRVIDQISAHDDGISAICVVEDR

VLSSSWDGSIKLWQYTHKGLATVPLLTFMECEESVVKLCVGSDGVVAAAATKNGLVYLID

LRTCELIRKLIASPIHQAEICGLTFCGGTSTIACMTTANELSVYHTDGTRIVTIHVAVEG

LI

>contig20018 Frame-2F

MKPKTRSDREKKERKQSDEMETMKQDVVELEKNDERASGFEPDKEVKDDVRHRSRKSSRR

SRSGSLPSPSRSLRRRRHRRSSYSRSHSLSRPRRPRRGGSRSRSRSAPRDRRPRGRERRT

RRRGRSYSRSPSYSRRRNRTDRSSSRDRPRRDTKDVAEPLQPAPDAAPPATMETPPAAPT

TSVNPTITQLMAQYPTMSLQDIIAKMQASNVTMAAAVAQKPARELYVGNLPPSVTGPQLQ

EFLSTIVQQVGLTTQPGNPIINTWISTDGHFAFCEMRSVEECNLALLLNQLSLLGQPLKF

GRPRSFMGPPQPMPQISARTQTALINLGCSPNPAWFAQPTLPGMETNMAESTLAEATLSA

IAAAQPTNLSSGVANLEHHRLLMSNIPVVLTEAQIKELVEPFGKLQLFTLVKDPVTGASL

GNALFEYEDNSVAAQAVEGLNGLSIGGILLSVQRQPSTNGVRMIQADQLSAVLKMENMVM

IEELNDDDEYADLAEDVEEECKRFGNVIGMEIPRPKDGEEVAGLGCIYVRFEKQEEAVSA

>contig20340 Frame-1F

MADTGLGSSAFLESEERVSDNPTTIELLPVDEERYESLTAPPEVFSTMESALNLECDGGD

SSVPPRLPRSQKPRKRSKTPRSKSNDLTRHKKGTTRGSSGATTLFETPDVTAMFMAPLQP

ERPLLSESPWEVEIAGFGTVLNNVLHCVTNRELVAKTAEYMAAYPHHALRFQIKMKQVLF

SI

>contig20722 Frame-0F|Blast-diphthine synthase [Phytophthora infestans T30-4](gb|EEY58907.1|) 1e-131

MVLYVVGLGLGDDQDVTLRGLNAIKKSQKVFLENYTSVLGIELTKLTEFYGREIILADRD

CVETGADEIFADAKNNDVAFLVVGDPLCATTHADLILRAKKLGIQVEVIHNASVMGAAAS

CGLQLYSFGQTVSIPFFRDEWRPDSFYEKIKYNRLGGMHTLCLLDIKVKEPDFEAMCRGR

TVFLPPRFMTVNQAIEQLLEIEAKRQEEAYTKSTLCVGMARLGQKDQTIIAGTMEELLIQ

EFGAPLHCLAIAGDVHPLEQ

>contig21181 Frame-1F

MGMLLLPGRTLGEYGIEKNGLIDSVVTYA

>contig21325 Frame-2F

MFASLSEMLAWKSSGYNSKHSKSRCGPTADSSNEESETESASSSHSNAPNLRRQQSCPSS

VSQKARMNTQSEDENASFPQNVYLLARAGFTTSSKLFLARPRDTPKTPTDISPPTPPNHS

TELLTDYGVHSRCAGARVATPFGLGKIMAIRN

>contig21523 Frame-1R

MAIESDNQDKNVAAHDRMLPVTPVAVPDVSESEDSPSSKMLGEFLTLDGSDLATQNQRRA

ANQVLEHLLVVDQDQTQDKELGPIEAVKRAFDVSKCPTHVEACEFAGTDYHSSETEKEPS

TFPIPANEEARVAAIEHLSLHDVVNVPELNVICSLAAAEVNCPHGIVTLVERDIVTIAAA

NDSKFWTIGSGNPRAQTFCQHFVMDDKPLLVHHAEADKRFGHIAPVKMLSLQFYTGFPIT

VSCTSKPTGQSEKVIVGALCCLDVNPHDMTRSQYWRLKRLADAASSILEKSANEYIANYG

ATSTT

>contig22108 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69194.1|) 1e-122

MQIDYIYQGKNQASVLRFQTQLDMFLWWWSIEVAARVPMEAQMLHKCMSRSFLSPDQIQL

GTYQVNNVLFPKVLQPEEIIFSKSMQNPQGVIHLFFIRHGETENMNFRVCDKDKRLTKRG

EEQAKITAMSVTKMLHLRGKENPDVTLIYGGLRRTRDTAAIFAKVIPWISHKYECCFLED

GAPKNVDVANRFNYRESMHKMAFQNICRWGDDVALTCGPKGYPEKFMLIIAHTSFIQYCM

AQCYSVPREIIHLGAPICHCSITRIDLRPN

>contig22319 Frame-2R

MIMRIELIATYYFQDAFREGKMLQRTGEALQLYLTAHRNLIEALAKQCLESSSSENYQKS

ARISIANLLCKSRKLCHVAQTIGTIFGCDADIFRPLLQS

>contig22382 Frame-0F|Blast-U3 small nucleolar RNA-associated protein, putative [Phytophthora infestans T30-4](gb|EEY64264.1|) 1e-13

MKPVPAVSFVQPSRILGFLNLLEDLFAQLGVKLAPFVPHLADVLVAILNLSIASSDKVDR

DASKNKDSNEIKTV

>contig22526 Frame-1F|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY54291.1|) 1e-40

MMGFVTLVGVAAVSTYSMMLVVQCKYKLKEQGHIVSKYGEIGYFAVGQIGSIIVDAALVI

SQTGFCTA

>contig22975 Frame-0R|Blast-NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, putative [Phytophthora infestans T30-4](gb|EEY61787.1|) 1e-106

MPVCMFQAPTRATASALAKRAGAILPRAFSGISKDEEAAKSAAIAAEEKLMAKLREQHFS

EAERTVLPYHASEACFPTIDDSPMPFPEEAAIVSGTSQWSVGRKGKLFKPARNQMQSGMQ

QTKHWEIRFQSPRTWENPLMGWTSTADPYVGLTASFDTKEAAEAFAKKQGWVLEAADPAP

SGDFNGKISYSYNFLPEHIETLIKQKGKKSAVQFKHPTSRRSNWVKTLKYHGDGVVGQHG

GEAKD

>contig23217 Frame-1F

MQVRALWPFLLQLLHRRRRGPLTNFQRAQTGKDHVTPILLALLLSGSLRGHAWYHPKPAV

HGQAIPFFNDY

>contig23433 Frame-1F

MRQHNGYRAHKGTSGQDETRREASDMPSISYDDSSKGDDKHANSRTHREEDRFAFRDYRR

SYDKEQNRRSEDKNWPDHRHYRNDRRDYGNRRRDSHREGSKSSRNVSREMSQPFSRKEYC

QPSETLLPLKAESNRSTSPNTRRKRPYLEPKLFPPRPDRFTSRSSYRPMEKEPKRHDSKS

KTSSGGSTNVLSNILSSAKQ

>contig23635 Frame-1F

MGFADHMRENTSSNESPGWHQWEPDHEPSIDDKPDFPDVTCPAESFPQLGPPVLRPSLSG

NAQAPLNHHNQVTRFMAKQALGYIPKLNALSPERSSVLSFQLPSIGTPPLSPQKWAGPSP

FVTPEESEHGRLSLPALGPSASNFIQRSSSFSEPRGLPMPPLKLAQSEVTHHTMSIADLC

QPFRYVRAASCPSDTNPLSSDPTTPQQAVEQSWRPAVEALKFTRTQSCGGEGDMLRGNLP

LSPSPLKKERQPSRLERSSSMDAPTLMRHLKRTAAESIDLTQWLDQPSRDSLSSLADSAD

SMYQLEQAGRSMRISDSPCSDQEAKREKKLCAFPQCASNAVTRGLCISHGGGRRCQR

>contig24911 Frame-2R

MHGSENKHYQQQIQSQLDRLSVPSLPGHKNSADDLVAEVAASPPYHSPSDARLLYREWRT

GSHVGVDFTRLETGETSSSNSCSYNGMSSEDVLNRSPFGVCDRSPNSLPRIAERFETLPL

RVNTLPVAPVASHDVEEHTRLLSQKIAAMDSTQSGASISTAKLQSGSYGSSDSNELFQGI

KKAQSNQALADLEKKGYFPVAPKPSALGVQRGLKNSVVNDMCRAVVKHMVGDVYVSASGS

YGQRKVLNHLYEPVFTSVQAHFRRLPARYALSVNPDDVPLHMRLLAKNQRDPTAIAVNAQ

LKKDDNG

>contig24964 Frame-0F

MHAEAVILTIAGVPASFHISTVKYYSKLKEYKAALASR

>contig25501 Frame-0F|Blast-RMD5 family protein [Phytophthora infestans T30-4](gb|EEY65014.1|) 7e-55

MDLEFELLRLKYVDILEFSPDMMEAIDFANKELSGFHKTHSEEIGVLMSCVLYKGKLEES

PYKKLFSLDQWSKVYDTINQAFCWLHRVPHQSYLDT

>contig25574 Frame-0F|Blast-hypothetical protein PITG\_22552 [Phytophthora infestans T30-4](gb|EEY63445.1|) 2e-13

MCRKFMKNECKDTECLLSHLHDE

>contig25967 Frame-1F

MQSANSSKKVLHVLLRKFFGSPRDVILLRILREIVASGWLASEEFELLTKSICSHVMNTP

RLTEELLDDNLPSAAHAIGDLLFSRLAPLLVLRMFPRIFVADMCSEVVPDLRHCNKLLHR

HLHLNENGQEAVTTSELLFHLLAQSMVNPLEFKEVKMLATECLSSFPPPLVLPFVQAYLV

AFLREIVGPESQDSSFIVQEDSIPSSCGLVTAKLMVYCLNRMFAEDTDVSKDFDSSARSI

AILVQILAVPVEDEFLDLQRGCVDCMALIIFKFAADACKVGKLEASQANDFTLMLLLISW

IFGPQNGEHVNIRSGGEVIGLKVHALLENIWNDARLDRLPHHARICYCNVLVRAICRAER

RILARWKSQGLLLRIALAIQSCSDESIAAGGFQIIFSFFVKACDMLSMQHTSDLNFVEIC

CEAITARLELTRSESVAV

>contig26085 Frame-0R

MNVHANISTDNQAALIMCKDLTYSRRTRHIELKKHFVREVVKQGKLTLAKVASKINSAAM

FTKHCQETDYDTYVYS

>contig27198 Frame-2R

MKEHRMPRSRSRSPLSLVKHVGRHKSGYGTSADKENFRELRSKFVHRSPSPIDVRSYEKD

ILDEECRGRQYGRKSSGVDLRLVENFRDRRELAGEGQSHKIIPRVDSPTSSSSRRYRKNE

IGSHHFNEQRHNLKASRHPYRREELMEDVRGRMPPSPPGGVLHLPRSLSRSPPRFAKNGG

SIKSRVRSRSRSPHVDVRAKSRANQRPGGYHRHEDLSAGSQLSEDRPAFQVERPRYADDR

SIAEVARDEQHERQRFFQQQSHGRRDFIDADLSRYGSGRVAGRGGCRGDKYDNKQPSRGD

RNPGLYHQEVVPMARRSRSPLPLITHHRSVSPLPQPHRRSLSPFPPTQQKRETYGREHRE

EFKTRGRNSRFSPPQSPLLPSVFIPGHAGSSDIHASKSATDDLGNRLEQRYHSRHDKSRD

DKSYHHQFREKRPSHLERSLTPSPARRERPSGSVGRKASVPSPHRSVNRRNEGDNILEEV

SAKEISSRPKDGEDAVLQQKEIKSGGARMAREELFAGMDDLTVDYEEDDE

>contig27204 Frame-2R|Blast-40S ribosomal protein S15 [Phytophthora infestans T30-4](gb|EEY53513.1|) 4e-54

MATEEEKNLELAALRKKRTFRKFSYRGVDLDKLLDLNHEELMELVNARARRRFSRGLKRK

PMALIKRLRKAKAAAKPMERPEGIKTHLRNMIIVPEMIGSVVGVYNGKEFNGIEI

>contig27921 Frame-2F

MMKLCRLKKVFHPKWMNFAEHSSKVATNNLLLYKMIEPLSHSSVFNGDDSYVIQVDSPVV

SSRSHEFLHKGNAYPHAVQLNT

>contig28010 Frame-2R

MMHQKSTRLIVDLNDLREYDSSFTDPAVGSHVNLVSRLLRHPAEFVPPFEEAIQERVFNL

DSLYGSKETESIKDLRFHVGFEGDFGHHNVNPRGLLASYLTQLVCVHGIVTKCSAVRPKV

VRSVHYCKQTNAILSREYRDTTSIAGAPTSSVYPTKDENGNLLETEYGLCQYKDYQILSM

QETPETAPLGQLPRSCEVIVENDIVDKCKPGDRVRVIGMYRPLGGNSTASSTAVFRTVLL

ANNIQLMGKEVNGIVMTSSDLVNVREFAKRDDAFDMLARSIAPSIYGHAEIKQALLLQLL

SGVEKNLENGTHLRGDVNILMVGDPSTAKSQLLRFVRTIAPLAVNTTGRGSSGVGLTAAV

TIDPDTKERRLEAGAMVLADRGIVCIDEFDKMSEADRVAIHEVMEQQTVTIAKAGIHATL

NARCSVLAAANPVYGQYNKNKKPQENIGLPDSLLSRFDLLFVVLDRLDRGADRNISDHVL

RMHRYTCPGQEGVPLSFDVCSTDHMALLTEAAGDQLDEAKKSIFQKFDPLLHGGYQSLSY

AGNGILTLDFLKKYIYYAKTRYQPVLTDNAIELIAEGYAELRSQQNARTLPVTARSLETL

IRLASAHAKARLSKTIEAVDAEKAMALVSFALYHDASEPHATNDVVSQVEVTAELPEIST

QKAMVELAIDVPVSPKKSVEMSRKRDRGSWSSATLADDVLRILSDMGTNGNLDDENDSIK

LTEILARLNVSRSKGDNVPLTELEKVLVELEEQNKVMYIQDGGDPMVMLI

>contig29372 Frame-1F|Blast-phosphatidylserine synthase, putative [Phytophthora infestans T30-4](gb|EEY57971.1|) 0.0

MEDKVAQSPVLRSRRDSDVDDAAAIYGTDSSKNYKNRKWSVDETVEVSDDNESQWISSPH

TLTAGFLLILWIVYAAFHESVASYTDPNEQFAADVKRGVKYACVFFLTYCSLQLPDGHFK

RPHPIVWRLLTGMFILYEMLLIVLLFLKTHDARQFMKGFDSTLGVELPETSYAGDCRVYT

PENPDSHFANIKATLLDRFVLMHFFGWIVGSIMVRSKMISWLLSILFELYEITFSHWLAN

FNECWWDHLFFDIFTCNAAGIYLGMQICHFFEMRRFNWVGIRKIPNLSGKAKRALAQFTP

AYWMAYDWKIFRSADRFWRVMSMVAILSMMMLNSFFLKTVLWVPASSNVNLYRLAIWYSA

>contig29516 Frame-0F

MGPSIDRRDRTRRRSPSRSPRHNRHKSSIKSANSPSHQRYRRHGPHVVDDSPNPQNK

>contig29668 Frame-2R

MKLWPIVIFALTSIATTPAEKIDFEEVEPFPEFEPKTIEGKVALHFKPQLFIKPMRKSCH

APYPAVNAEGDTSKGIKVPFVRCWGSPLGSQIYGRMVEYEGYVAIMYAFYFPKDAILLVR

VHDWEYAIVWLDSLSVDAKVLAVSTQDTLTHETYHAPFPGYLDGPNFKLDYTRVYRAQHR

LVATAERGTAHNLVMWEDMTEKAREALNKSDFWLTSVPINDDHFQGYVEECFPFKRKAEQ

>contig29721 Frame-1F|Blast-Mitochondrial Tricarboxylate Carrier (MTC) Family [Phytophthora infestans T30-4](gb|EEY57963.1|) 1e-131

MANNEVPPFSLDKPRFDTSTYRGRWRTFAELVSPKWLFLSSKQIQYATKTLDDYRSGKLA

PGQVTPAELWNLRQVQEAAVHPQSGETIPALFRLSAFVPVNIPICVGMLLATPTLGNTIL

WQWINQSYSAGFNYANRNASSDQDTVTILKSYATATFVSCSTAVGLGKLVDSAKNLSPNM

RSFLAKMVPFVAVASAGAFNAVSMRFNEFTEGIDIMDEHGTVHCRSVAAGRHSLGQVALT

RVALPMPILLLPPYLYEVMKKNNLMPQAKYPKLAVEL

>contig29839 Frame-1F

MVNVGTQTQLIRPATVVGVEEDILIGVRVRKSFGSRSFWGSVVGCYWVSGGLFYKVSFDD

GDVDIFTADEVLQDTEAAKTHAKEDPRTKESNTTSKSSAVADEYIDLMRQYTLKRKRDEH

VSVSLPNICRVSLWGQRLYASIFTNEKNETFIRELLKTDTGKMGEMEATGLVEVGDLLLA

VNEIRVLGMSNKQLAELIRKPTRPVVLTLYRPQRFQRPQEPLKMQQPNYVLSTVTSIPTT

REMTADVVVSQPLSTQAPFVLLPSPSTALHGHLKPANQFAQQFSHALQRIADKELIRQRN

HKNLVAHQSTCIPTTLNHVGGTPQPVQTHSTDAVRALPVVQTVQSTHQLPNSTATIRHDV

PD

>contig29945 Frame-0F

MDLFMRHCSEKMKLRAVKTRKDVEKALEDRAASGKKPFIFFLDEFPRYIDRETASSDHQS

RMPAPTTQEAYDHKRRLRLMLNVFRSFGLVVIASSTSGTARTSALVSSGSRTDSDYLWCT

VHPLFPRTVIGCDIGMLPTVIQNIIANSRPLFTEIA

>contig30059 Frame-1F|Blast-orotidine 5'-phosphate decarboxylase, putative [Phytophthora infestans T30-4](gb|EEY55676.1|) 0.0

MPASFFSFLRARVSAVDSLLCVGLDPHITELPEATAIAAQAFCINLIQQTQHVAAAYKPN

SAFFEAFGAEGITALHAVIKAIPVGIPVLLDAKRGDISTTAAAYAVSAFEKLEAHAITLA

PYMGVDSIDPFVRGHPERGCFVLCKTSNPSANDFQTLSIGSRALYEEVAAKCQQWNSEDN

VGLVVGATDINALHRVRTLTPHLWILAPGIGAQGGNLEEAVEAGLSANGLGLLVPVSRGI

SKATNPKKAAENLRDAINAVRKKKMATLTVAVAKLNCNVFIKFALSFGVLKFGEFTLKSG

RKSPYFFNAGLFRTGRALSQLGRFYAEAIYNSGVQFDVLFGPAYKGITLVAAVAIAYADM

YGVDIPFAYNRKEAKDHGEGGVLVGADMTGKKVFIIDDVITAGTAIREAFDLLQTTNAQV

SGVCISLDRQEKVSSEDVRSAIDHVRESFNIPVVSIATLDSLVEYLETLDANVDTNASFL

PVIRAYRADYGVLQQ

>contig30165 Frame-1F

MNEQHGEIWQLRTRKLLKQAPCDPSRFLVMTIHIEVSTPTYTRTDTPPHRESFALGLIDH

PPRLSTFSHLDLNDGGEHNHMVGCSVPMLVLLSLPRMATNMAWSAQWAALGPYLGTMLPP

FAVQLTQVIGPLSGIVVAPIIGVLSDRSRSPWGRRRPYLVFGAITSAACWTLMGYTRELG

EFFGDFGEHRPYTAWLTIVFYTCMDVTVNVVQTPAFLMISDFAGDRQTLGASIGQASSTL

GSIWVAGYIYFFGAAHMTLRWFLGMLSVTMLIAVSAVCVFATEEVSVLSKDIEMTSDETQ

GTMSRIRDAFSSTLLGIKTLPRTLSVFCLIFFCIQFGFTAYNGSKGQFFGIEVFHGNSTE

ADVCGLSHCTNDQELYNDGVQIAGGLADLLFNILGYVYSWVLPFLVSRQGARWIITVACI

PQILLMAMAFSHNVAINVTIVTLTAITQATIFALIVPMIVHVFGTSTPVGMYVGAVNSAN

CVGQLVNFVLGAALVETSFGYALPVFVGGAFSLVGALISLGMLRIDVHSI

>contig30334 Frame-0F

MNEDVIEIKRQQGVSTGEHPYTTAIANGDRSISTNRNLFHFYPIKILKVSRVFVSPKHGE

MVKKIAATTVLVFLTAVAVLQILMNYAIGCQSTISGSDGRSRSP

>contig30341 Frame-1R

MSSFSKHVRLFVLAGSVSGITSVAVRHLFDTTCQRLQVFPAHSRCFFHCIQRTVQRETTR

GLFKASYSILKSGSVQSHHLYHIVHAS

>contig30709 Frame-1R

MALSKPMETLAAALAAGCGGILSTSILYPLETIKTRIQSGQSLFPSVKVDEASFPNKELA

LLKSLYQGIQYKALESSTSKFLYFYAYTMLAQWAAPKDGKPIGTFTDMSIGYLSELCHLP

ITMPMELVGTRMQTDSNSGCIVDIVSSIVRESGIRGFYKGLGAYFVLCLQPAFQYTVFDR

LKSIYLHKYNKASETLGALE

>contig30895 Frame-0F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY53509.1|) 3e-20

MKSSTTDAPMQSQRKQSIARSLSAILGLQVLIAGAFGILSPILSIIMTEYFAKLHRNGSQ

IDCEVNPHDEACIAGSQQAAWLS

>contig30918 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66615.1|) 9e-49

MVGYRALGSKFKSLQYFLNHTAVLKQYREFLRTTLPLDEDVRLNVRRQIRAGFDANQNEK

DERRIRLLLHQAHAELKSVRDLVFTAQAQQRSGRNDIFENWSRADSICSTDTRMDTPCKD

KDGKEDLKGRLGTGWPWKSERGTKKVDLKGIKRR

>contig31276 Frame-1F

MFASKIPPPKSRKLRTALVRKRSSNSTTRIRTSCYSNSNLHQPLYVPPPTPISTRIRCPR

TSFVAFTTRIEK

>contig31500 Frame-2R

MHQTSRRKTWLAQFRDCLAEKAQLRYESNALRETMA

>contig31694 Frame-2R

MYSPTTTSSHQAIMKCPWQWRQPFLDEKRESRKRKVGDGYFYDPVDPNFVDHLLPGYAKK

FCGADVLESDEKENIQREIERLMMKKSDDPRDDAKRDDAFHDFAASHENQALVDSILLMS

KSVEASSLSLLASPKSVISSSSDEGSDDDELSSNGEELFDLAEDRPAKLIAFHSSSLELV

SDNLQEEYFAFGDSELLDFPSSEAIEID

>contig32321 Frame-1R

MTFIYQWISLPEYYQITDNLLINNVSSVNFM

>contig33928 Frame-2R

MENNRRGTSENVFVVGSAYHTGESLMKGLQSMSLGDICRYHTDDVGVVTAFFHFITQLGH

QQDGGQVMLEEMQRQWGEARLRQWWKEWQLPFPEKYLPELVRQHVALPTLLSASSENLVS

WGIWDRQVRERILALCGQTQQCNNSDMSSTDALARDGSTQLLRLVLQVLGSFLRTSLGTS

DDGENKTYLSFVNASLLTLQTLLATSFGVSVLMTSLRQFERDESVEVIIQSAKKIFEVNE

RLYGVYSVVLATQEIIMSVVRWFLANEAQALADAPFDNVQSPAFVAMERLWFVSAADFAI

QVLLTQESWKFASGRERCEILERCYRLLYVLISPRKCLSEQNEIIPAFEAALRETLATDM

LLLNNLLHSCSVALPLMEATHWNSAKL

>contig34161 Frame-1F

MKEVIGGGNSTSVDLVTKDVTTVMPNKRTQASYGNTISVHVSELNRNSGVNAAERTGKGS

AWWNIKRRRLVKTWLPQFVSYVQRRGRSLSKAMPRKELLNFARDFCDLNFSSFENGFFSS

GTYEEKHATWIIARSLSFHYPGVAVQQLGLGVGKFKRTLVIDEVCRSRNDESGASFVEME

FILSALQVVPKKCAYYEDVMILESGEVLFHGNGESLIVYFQELGFVCPSDVNMPNYLLNL

NQQQQIQHQVTMIQGFNNQRQLRRSRMFCGIMNFSDDIMLITGGPGAGAPSRASTPIGSP

VQSASTARLGTSSSPFQRRLKTGSFSRSPLKSPQRSPQRAAMASVSPQSSTMIKSLKISA

YLAPGSKTSQAGGNTDFAAILEKKSTKLD

>contig34543-0 Frame-2F0

MAPTGGTRLRFKNARSKKPQQAKKVPSLKNRIRGLERFLSRG

>contig34543-1 Frame-2R1

MRFLSDGTFLACCGFFDRAFLKRRRVPPVGAIAISNKII

>contig34705 Frame-1R|Blast-N(2),N(2)-dimethylguanosine tRNA methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56619.1|) 1e-144

MAGPIWSAPLHSLDVVRRIRDRVETSTSEFSTKARLHGLLTSIAEELVDAPLHYTLPGLS

KVLHCSNPRMSQIQGAIRHAGYEVSQFHKVSEAIKTTAPNDVIWDIMRCWVKKHPLNKKR

DGVETPGSRILAKEPKFEASFSFKRSGPDNKPKALRYPLNPEPNWGPKARAVGNRSDVAV

SIVEN

>contig34802 Frame-1F

MGLLFCASKCCGCIALSQLYALLLPLGILAALGLFFYAYALPYSEKQIQQALNLTADVEI

GNLNASYIAANSCSGCVFGSNTQWPTDTTGPLHFLDSKAGNTASGVIATALASAAVVGTG

SMLWASAMPSATAALSSSGGFYEMTHIFEQAQFAGMISQLRIEGAPTFLMQFSVELSWTN

FNLIKGSSDASRNSESDHNATRRLAESSSNVIGVVTEGGESGPARYATMIGVDADDLFYY

TLVNFAGVIAALHVLYLVFVVIVSGISKKESFGEVARKWYRKIIWAGVLALLLAQYIFSM

AGCYFISKGSPANSANRFTLRFMLGIVALVGVIFLALGLGVFVVAKNTDELKDIGTYEHD

QRAFSSKYSAYYDEYNFDNRFFFVPRILLAVLTGAIVGIVHDAVVQLICILAIMLLYLTL

LLSRQPNLLRVLYYMGIMSVGSKAILICFMFVLAKDDYFPQKVRDNVAYGIIGVNMLIFF

LLFMRQAYMIIYKVVIACRHKNDGKINSDLNATDINLEFSNNMSNIPIYDEVEPTPSNQS

VNWYANNQQKDQQEKLYSQQQHQAKSGTISSYTTQSSHSGLLENVPMLEPAPEGFS

>contig35416 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64179.1|) 1e-134

MKKSSQPNDYRKCVAFWFYSAWEFFAGDNARAAFRSCNMYLEEKSVWNAESREDVV

>contig35654 Frame-2F|Blast-26S proteasome non-ATPase regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY54294.1|) 1e-101

MTAFERSMIQLKIYYHAGLEPSPLHYPILGTRLLQLLVENRMAEFHNELELLPEQSRQDP

NIAFAVKLEQYLMEGTYNKVLEARTNVPNPYFPFFLSQLLQTVRENIADCAEVAYQCLSL

ADAQKMLIFNSAAELSSYMQEDRTEWTVREGYVWFKAPEKSLGASDIPSLRLVGETLAYA

TELDRIV

>contig35845 Frame-2F

MEEAKTLTSMSNAAYAFDEEVLKDVRNNKVWTQDPKYFKKVIISPAATMKMLNHANSGVE

KGIKAGGKPVEIMGLIMGRPSTGTDRDAGDAHTLVVTDCFPLPIEGAETRVLADDAEVIN

YMISLGEAVEQTRKEKFMGWYHSHPFDVEVHSHCFLSATDVSTQLQWQRSEDPHG

>contig36075 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68763.1|) 1e-109

MYIMVRLTHQMPPPVTVENDNQDALHRRERRRQQCRASQRRYRDKQSSIEYNLKLDVNNL

REHVQRLQGMRELIETKIWGTRLAREGAVVKAARQYYTVFSHGMHNPEAGGDRVRKCYDV

QVGFVIAFMDKDVEFGDSRGVSAVLNQWYLYTQFHAFLSVSMESAEVCGTEEAPIVFAKG

ILKVSLNRLSIENMFPHILAYEEIVQVLLHHEIEYPTSTTYVFNSRLQVKRQDLDVDFMT

GINRCLGSAYASSCVMQRALISDCCKLGMKCKQKLLLD

>contig36273 Frame-2R

MSRYPFAPRPVDDNLMSLMYQQKLAHRLHTNAYWPTTPFLASKGPKDASDKLSFLDTQGD

FRVRTLSY

>contig36567 Frame-0F

MFTWAIIGSHSRQLVCIDVLNAGQEKWRVILDDRIEASAALCRKHKIVYVGTYSGSFYAL

DLYTGNVRWQFQAKESIKASAVVIDQENLVLCGAYDQNLYALNAIDGHLHWVYPLQGSMF

ASPFYCVWTKQLFVATTKGIVECLVVSTCDQIKSHWKLQLPAPCLLD

>contig36901 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY67838.1|) 3e-10

MSPNGLFSESLDFLSSNTDVRSAVVEMTFCELSTNFTIVIITGHVASWSSNSWIWPRSRW

>contig37142 Frame-0F|Blast-peroxisomal (S)-2-hydroxy-acid oxidase, putative [Phytophthora infestans T30-4](gb|EEY54193.1|) 0.0

MVKIVPGSDGTPLNLLEFEEYAKEYLPKNAFDYYASGADDMVTLKENREAFKRLVLHPRV

LRDVSNMDITTTLLGHHVSSPVCVAPTAMHRMAHPDGEIASSTATAKADTCYILSTISTT

TLEAVGKANSRANPHALRWFQLYVFKDRELTRSLVQRAECAGYKAIVLTVDTPMLGHREA

DVRNHFSLPDHLTTANFSQVGGEHEHGIKSLKDSGLAHYVSELFDLTLNWNDVKWLKSIT

SLPIVVKGILSPEDAKIAVELGCEGILVSNHGARQLDGVAATIDALPAIVKAVNSRAEVY

LDGGIRRGTDVFKALALGARAVFVGRPVLFGLAHSGEAGVSNVLRILNDELKHTMLFSGT

ATLTDISPAYVRRELPALQSSL

>contig37689 Frame-1R|Blast-50S ribosomal protein L20, putative [Phytophthora infestans T30-4](gb|EEY57220.1|) 2e-52

MSWSKHKKILAMAKGYRGRANSCYRTAINRVEKGLQYQYRDRKQKKREMRSLWIQKINAG

ARQENLSYSRLYGIMNGSGIELNRKVLADIAATEPFSFKSVLDVVKQMEGVNSSGIAKLS

ERN

>contig39049 Frame-1R|Blast-proteasome subunit beta type-5, putative [Phytophthora infestans T30-4](gb|EEY61142.1|) 1e-155

MSAPIVNLNFLRAGSRGASFNYGGAMPNTYMSAIDDLTPAAPDALAAGFMLPPVSDPAAY

SREHFKVAYTDDNEQSLKFAKGTTTLAFIYNGGIVVAVDSRSTQGPFVASQQVKKVNPIN

DYILATLAGGAADCQFWQRNLAVQCRMYELRNRHRISVRAASKLIANTCNYYKRYGMSLG

MMMMGYDDGKPVLYYVDDEGSRIPASKVMPKFSVGSGSTYAYGILDTNWRWDLTDDEAVE

LGKRAIYHATHRDAYSGGFCNVYVFKPEGFKHVVHQDVKEMHDYSNNS

>contig39658 Frame-0R|Blast-putative exo-1,3-beta-glucanase [Phytophthora infestans](gb|AAM18484.1|AF494015\_1) 0.0

MSCAASDSLQARLRRGDLPCRGVNLGGWLVAEHWMTWDSCIWHGVPDEIKDQGEFATMKF

LGHDEGDRRFGQHRRTWITEYDIAEMKRFGLNTVRVPVGYWIMGFDPTDFPNKQEWTVFA

PRALLYLDELVNNWCINHDMAVIVDIHAAKGSQNGRDHSAAVDSGAKYWSQYPENVDNTV

YLAGFLASRYRYCPSFLGVGLLNEPEHPTDPHVLRTYYERAYSEIRATGNDCVLTVAPLL

TEQCPPFMEDFMRYPNYYNVWHERHPYFLWGYEGQNRKQVLQAVHRYGDQISSWGGNWLL

IDEWSLGAQSCAFPCEDRHGLQQFASAQLEIFSKAHSGWIFWSWRHSDDGHNRPTGWSLR

QLLRDGVMRLFEV

>contig39896 Frame-1F|Blast-deoxyuridine 5'-triphosphate nucleotidohydrolase [Phytophthora infestans T30-4](gb|EEY66733.1|) 8e-86

MIPSKRIRVAPILRVKKATPNAILPTRGSSLAAGLDLSAAYETIIPASGKGLVKTDLVIA

VPHGCYGRVAPRSGLALRKFIDTGAGVIDADYRGNVSVILFNHSSEDFCIKRGDRIAQLI

LEKIEYAEVQEVEDIEDTVRGSGAFGSTGVNVPVAVDQHVECNRLGQSDKSVDPDSLFRG

IQVLSEKKLLDETSRRLLIEKLLTASDRQYKLLYTSVSEFLNDGEDAKVMEWIEAFLRSN

>contig40621 Frame-1F

MANNEQKTPMAQKSANALACPSSDTAHAFAPLPFDESFMTSTRTSETVNSSTIVTSTKSA

ADFFLDQIAAVMSDEKKLSDNIMDLIPPVEAPMSQAAVTQAMTTSSVSIGMPLQPPPDLM

RALSPPTSLLPDFGDLASLALLGDAITSNAATIPTTTTALKRDLSMMKHGTNVALPRKVE

TVSQSLKKPKNETSGVENESHAAMHVPLSTRHSSYSPPASGAATAREKGMKEPQSGDLYE

CVIT

>contig41114 Frame-0F|Blast-beta-secretase, putative [Phytophthora infestans T30-4](gb|EEY53259.1|) 1e-122

MYYSGQMFYTPVTREAWYVVTVTDIGYGGTSLGLSCDHYNDPHAILDSGTSNLSFPPDVY

NALMDQIKLATLAAIPDFDARYFDDSTSCCNEVYCDPTSATAALLELPSIYFTLGMETSD

GSTSHQFTVEIPPEYYWRPEMNGDNSSTPCRALGISEGTSTVLGDVFMDGLYSYHDRVNG

KIGLAVASNCPNNVTSHKKVYASVESIDWCSCFSKSLQKRSTWTT

>contig41705 Frame-2F|Blast-phosphatidylinositol transfer protein beta isoform [Phytophthora infestans T30-4](gb|EEY59784.1|) 5e-86

MVLIYEFRVPLHMSVEEFQVAQLYMVVNASEQLTGDGEGVEILVNEPYDNTDGHLGVSTI

SGWTIPRNKGQYTRKHYYAKSKIPSFVSAFCPEDSMVLIEEAWNSYPHCVTVIVNGYLAK

HKFYISIESIHKADRGDSENVLKLTTKELSQRKVEVLDIAATLPKQTLKEDCDPAT

>contig42270 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63504.1|) 1e-106

MATPQCKEVVNGIRLAEQFGLNKSTVSRILKRKEEFKKAYYKDNVSGCSKHINKKSKFDK

LNRLVENWFEMNREKNDTITDTLIRDVGKQYAQELGIEDFRGSNGWVRSLRNRKQHTTRN

GLTIEAQEVEKRKKDHEAIERMRRIFPNGVKDMAGFFKDLSTYLENDGADMGSSNGVNGN

LFAKNNDSARDAVVVVTGASYTAINSNNVSNIDDGATTNEFLKKKMIDSLRLWSQELMAC

ELDKLKKRMKPAFL

>contig42384 Frame-1R|Blast-vesicle-associated membrane protein, putative [Phytophthora infestans T30-4](gb|EEY62335.1|) 1e-111

MPIVYALVAREKTVLAEYTATSGNFPTVTRVLLAKIPSTDGCMSYVYDRHIFHYIVEGGV

TYLCMADDDLKRRVPFLFLQDMKNRFQETYGGHALTAIAFAMNDHFQHEIRRLLDYYNAN

PDTDSLSRVKQQIDDVKDIMVENIEKVLERGEKFELLVDRTDKLNRQSVKFERSSTHLRK

SMWRRNLKLWLLFVVFGLFVVYLFISMACGFDFSGCSGKHDDK

>contig42612 Frame-1F|Blast-Phosphatidylinositol kinase (PIK-L2) [Phytophthora infestans T30-4](gb|EEY59643.1|) 2e-85

MLGVERNIQVWQSLMLVRSLVFDPKEDVDIWLKYARLCLKSGHLNLAASALWRVGAQPFI

RSVERDPNVPIPINLGGNAGASQGFANGLLSLADSAAQDPRV

>contig42689 Frame-0R

MASSLHEAVKVQQHLAKISVCAIADAMAKLNIQGHLLDISLVRGFEVADICGPALTVQVV

PTKGSKVNKLPYHYIDEIDQGQVIVISAPESSTFGVFGGLLATAAKARGAAGVITDGRVR

DVQEIRSIGLPTFSRGTSVHGQQGKSTVADVNCPVVVGGCVIRCNDIIRADCNGVIVIPN

EHATEIASKAEVIEKQDDKIAEAVKQGAMLEHSFERFRAKM

>contig43075 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59154.1|) 6e-61

MAPAKRKCDTKALKKNPSSLSSNAVDLVPQNSVKSVVSATKALVEPLARLKDEHVPILEL

LQGKYSFIRALLIEFWPEMVRDPRDETQLLIEGDTQWFWFVEMQFMVIFLFEIAFMEFSM

SVTKPDSITLEPPELEKTTRAHRQDMEERVTFLARLKTYVNDLAQCRLIATTNAGKRLPR

VFRL

>contig43273 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59734.1|) 2e-57

MSRKGLKGSSTIGGNDVLTIDQLRHQDDWVLDTERYRCHVCTRNFTRFRRKHHCRKCGEV

VCGNCTLKKEAELPVIGRSLVRVCMSCILSHANGQANPQAPPPA

>contig43369 Frame-0F|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61120.1|) 4e-41

MLAVHRPLWFLWDLPGIAIALFAWILVIGMLLAVLASISQWVGLLSPMGSSEAIWFIGLF

GMCLWCHIVVLTSNPGTVPYQHKGMPFLKCDALGDDMEEIEEVMPLQEYEEFEDDGSLLV

YCDECA

>contig43567 Frame-0R|Blast-ubiquitin carboxyl-terminal hydrolase, putative [Phytophthora infestans T30-4](gb|EEY56259.1|) 6e-60

MSDVERKPKRWFPLESNPAVLNSYVEKMGFPTSQFSFYDVLSTEEWALAMVPAPVTAVIM

LFPIKPHTKEAEKQEAANIEKYGQKVSSNVFFMHQTVGNACGTVGILHAIGNMRHLVHLA

PESYLCKFLDKTKAKTPIEIAQHLEHDD

>contig44935 Frame-0F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY61593.1|) 1e-112

MMRIRSTAAAKMTTLELVDGLNESQFVAPKGLGKHKVELLPSYIHHLLPSFKRDFIGKGI

RRDKSPIILILCSSALRCVQVIKPLASFKCKVAKLFAKHMKADEQAKQLARNFLPIAVGT

PARVKKLLETEALSLQHTTHVIFDMQKDKKQLTVLDLKDTALEMVDLLQFYLIPL

>contig45165 Frame-1F

MPRLHKQIQQSMKMSTHVNYFVSTIAPRLASEASKPSAFPFICNTSTALAPLLNFQCGEC

ARRFSRRYALQEHLATHTGEKAYKCPAPSCGKRFTTTSNLARHRRVHGGELLPLACPALA

CSKTFTTQHKLQRHMRVHMHPPARRCSFADCAKTFSSAGNLNRHMRNQHLRFG

>contig45334 Frame-2F

MPKESGYFAPLPSASTCCAWICALLDAHLSTLVLRASQSANIARTLRQLDQLVQLQLDAT

AQFESVHGVLCNILSGVQLPRAPGLPDYCIEELCL

>contig45895 Frame-0F

MATDAITKPQHAIFQKIQASLEGRLQSPMMGTIKLPPMLDIRSKEEENTPEMQAQTLEEQ

YEGETVGMSAAERLRFLRKKRKKSMITKRVSVAEDDFMAEVANNMKKKGTVMKHHGGERE

QSEKHQKRQQIQKEMEEKKTEKRQSQERTEHLKLEQDAEDDKKKRQENESAKSKKKKDTN

LFDTTIITEDTNPVASWQLNSADRSNAPAEDVLDVSALERKAQKKHKKSKSGKSIRLEEH

KNGQLGRNSESLIIDAHNANTEAELDLAHTKQEKKEARIERRARRMLDGKLAVATLSARG

ATLPSEASLTTQKQVLSIESKLEGNQSCREQRRIAKMEAAFAAQSLESNKNENVHSEHVQ

RVNNTSEADSSSGHVGGHTMHGQPLSSQAAPDQPIVNGGLFPLYPYVIMSPLPPYGYYNP

YTQMPVVPMPVYSPGTVQPGYQFMPSTSPPLTDSIAALVAYSAESTLASSYELNLSVGQQ

ALPKLTKCEHCKGIGVGLVEKNGICAHCNRLRLAFIVDSAQMRRRCSRCGGWGYQLLQAN

GMCTHCNRQTAQKAQAKLLAK

>contig46120 Frame-1F

MDSTIVIFLNDSTFSMNGTSHL

>contig46850 Frame-2R

MFVCLRPDTVTVDIYLVLICLVHPPQHGTFTNAYIWCDWPSRIVIHTNKTCAKILYDK

>contig46928 Frame-2F|Blast-hypothetical protein PITG\_16925 [Phytophthora infestans T30-4](gb|EEY65282.1|) 3e-15

MAITCGDIPRLICSVIIPPVGVFFQVGCTKDLAINCLLTLL

>contig47321 Frame-2F|Blast-phosphoinositide 3-kinase regulatory subunit [Phytophthora infestans T30-4](gb|EEY53006.1|) 2e-38

MKEKENDLRGLSSTLQKKKIEKLHDQFNALIQKKNNLLLLDYACESSTVRFDGESANNAE

AIHPDASNTINCSTKTGTSTTLPPSSKPRRIKPPI

>contig47354 Frame-2R

MVLLNLHQKLPTSRPERYKDSYYSNTKLETALLNRFYFPNGFACPKLTN

>contig48302 Frame-0R

MEDILPQSKKQHRKQEKARWLAERKSLQILEGLASSRRKSRNHRQRIVPPSAAVHFEPCM

STNCDNRVAGHSCVVRRIEPYVHRFALFAKDRWTDCSLRDLFASEFSTLSSEYCARAAQL

GLIRVNGQEAKLDTILKRGSFFEHVVHRHEPAIHFPIKTAMELSTLASLSTTWILFETDD

LMVVNKPSGVPVHPTG

>contig48687 Frame-0F|Blast-Poly(U)-binding-splicing factor PUF60, putative [Phytophthora infestans T30-4](gb|EEY60629.1|) 1e-113

MNPNDSLSIGQQAIKNVPTKCIYIANVRVELNSQHLESIFSPFGAICSCVMTAVSSLESG

THRGYGFMQFFEESCAQSAVQHMNGFELAGQPLKVGKASEAAMFINIALSQDKVVRDASG

ASTNRAIELTAQDSKPFEEEDVDKVLDTTDMDDNCCLCLVNLVKCGEVDNELEDEVRGEC

GKYGVINKVEIHELADHVRVFVLFNDAVGAVKAKQALHGRFFGGNEVQALYYARRELEQQ

HYTSKFL

>contig48760 Frame-2R

MAPPTDYICKLCGQSGHFLKNCQKYTPDTEFYSCNTEKLDKEKNSISIKKRETLYRVVND

DTWQQLRGFYGFEDDMWKNRLWCRSDTAATINYVDQEISDACLSGNALDIVNTGLKVFTK

ITERGKVFYRPSEDSLGFIANFFTKRCLDVSIADFSSLFENADHHVAFNTLSIELQEALN

GMPMGPAVGRVQAHEQLRMNLWVGQGSLLPRISKAMRSEVHDMLQHCLEKTIGSR

>contig49903-0 Frame-2F0

MASANEEEREAPDAWKMDVSGNKVEKALPVVSKREMMLRKAREQQLQTTAPTARALAPVK

EPMLSFQEDALMDIVPSNEVAEWWQVADPD

>contig49903-1 Frame-1R1

MGSFTGANALAVGAVVWSCCSRAFRSIISRLLTTGKAFSTLFPLTSIFHASGASRSSSLA

LAMTSSSFSSYAAFSFSTPFPLSFCSACFNDVKV

>contig50237 Frame-0R

MDDLAQLSADAEKEFVKLAMVLYQTANDTIKCLRILKQTLATYDSRHRLHFRSTSNYFIR

SDIRVVKGTTTDLRHVAKRISKSKISTNSEINAARLSMNATADAIKDLIQAGRVFDQNTS

SGVSITRDSVESVVRSTLNNNFHGIGALKRQIRATEIAISPSFATCTKNAVVDVANNIAS

LGSIHGDNQCEHTREAEPTK

>contig50404 Frame-1F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72305.1|) 8e-20 NOT\_ORF

MC\*ETVIILLTLYFAITAAKIIVSDRNNKFTSALRPSMLDLL\*TKLQMSNAAHPETNG\*T

KRVYRVPEDVLRSYALYFTS

>contig50471 Frame-1F

MAAPVRFAIKPSKKRQRDIENDSIRRRQNLSGSVFSDAEMLKQVECNALPGRAQSHIRLL

EDVPEKVRRLKNEGNILAEAERFRKAMGRWQEALAIDLNNAALYDLMAQASMAVYEDFQA

VQFARKSTELAPAWSDGLLTLARCHLNFGELTLALDALNRXIERNEGVMTDEMASDRRVI

NELLSKQSVVLRKRDQDAAREVNMDKLQVISCFKHLSLRAKIIGLGDKGRM

>contig51447 Frame-1F

MSSTLLSFLFVGALWGCTNPFIKRG

>contig52231 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY62502.1|) 4e-07

MSLGPQGSQRSFQRSTVRKESRKSSKSHLVLIEDVDIALLSSVRQDHVQYCL

>contig52749 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59445.1|) 3e-48

MDASIWFRLGLTYAAMGQLLQATKAYQRSVQIYTKEFDSAKGFNQEDVLELQKAYGITLA

ALAETFGELGDFNSAVQVFKTATAKFPNNANMHYNLANMRLARMESTGKKAFDIKVVQNL

ERAVLLSPDTLEFVNDLNLYLVAHDQQPDRVR

>contig52925 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64653.1|) 4e-67

MLESGEKNPSVFCLGRAMLAYTGANRSQHAWACWHKIVAMKESNPVPMKYNKILQGLSHA

KDTQLALSVFEHLQKLFEPGQIHQGAYATAIRAQGRSGNTQKAVDLFNEYVESCKDTRRV

SQYVG

>contig53122 Frame-2F

MLLLRVDPVDMSVSKAESEPTMPSSTVTFFKRGSTHKHALDFNQLYKKSPSQDQSQVMEN

NQANGTN

>contig53346 Frame-0F

MHGLFIQQHQDADPMITKIKTACLSGSNNSDRQLIAFRGCTLVTYYKRVIVHATLRDDLM

HLYYESLGLPASSRLYKTMHQILYCPSVRTTIVEYVKQCVICKPTKLMAASRIMVLLHLE

IPRP

>contig53618-0 Frame-1F0

MMLQQTHQRLNLAITSCASRLK

>contig53809 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66381.1|) 3e-88

MYSPEKLERLLRQAKVTTQSIQRVSQWMLTHRQHLAEIVTIWSGLIREGETEHQIVYLYV

ANDAMQVGVRKFGRHIAAAFEHNLVDIFHLIMRDGEEKVKRCAIKVVGIWKERGVVTPPL

LAMLENVCAGKSPVVEVPETDEELEERKAKVLQEMTSDRTVEHVLEDMPEVVESSVTTQL

ATHLQDLVNATISA

>contig54295 Frame-2R|Blast-ribosomal protein S6 kinase, putative [Phytophthora infestans T30-4](gb|EEY64993.1|) 5e-80

MLSYLKKALSENYGVIIMNPAAQSCHPRTHVETAWDQLIAPLLSDVFIVAFSRGAQMVLH

LLNHDNGQGVVQDRVKALALVEPSHYVSDHDTYFARRILARRAVSWILNSEIDVGCKIPQ

GPLRHGCVCVSAGTVPSNVLGSSGAYALEMVKSPV

>contig54934 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60068.1|) 1e-26

MSWFWGNETAEQAHFVVSALQSELDERESKIKALEAALKREQHDMTSLLEDEVKELEARR

KAVEKELA

>contig54941 Frame-0F

MKFLLQRQGEEHQRCTSNAMDGAASNGFIRTVQYLHDQRSEGCTVAAMDRAAANGYIEVV

HFLHTQRREGCTIAALD

>contig55191 Frame-1F|Blast-ribose-phosphate pyrophosphokinase [Phytophthora infestans T30-4](gb|EEY56308.1|) 9e-18

MFRQFVARHGRLTTTAVAMSIAAAGSALGAQKHQPQYAVALSEEAFPRAAPVAKQPKING

LKIFSG

>contig55263 Frame-0R

MDPFEELRKHAGGAHPHKAKLNVVLEAVCDVIHERRSNDNCRVPISPTEYFAALMTALEA

ASDSHRQEITQLLNMALPEVPDAVLRGKFSAISKCLTTILQEAEDVALLRSASACLSLTL

LAQEPSAIAWG

>contig55317 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54283.1|) 1e-24 NOT\_ORF

MTRAQKDMEICVGRCVDSHVSLLPNISARIEQAIA\*VQQQQ

>contig55894 Frame-2F

MISYWDVNIFLFISILGRRGRVRLAKRG

>contig57287-1 Frame-0R1

MAMDTLSNKNERTTDLYDVCAIEIVHAICTHHTRLS

>contig57360 Frame-0R

MLSYPLEDSFLTLRKYTRSLKLAKNILGKMSFDCIYLPRPGHYLTIEDGLSCRDVNDFVL

WGLTLRAVVSIFAAAGSPLPMRSSAQRLDSNILGNIVLYCVRYADKVIAGTATISAMVLV

GIAYINL

>contig57799 Frame-1R

MYTMLLILNCMPYMARSMYPYYKMSHWSALFFVLFVLLTNLFLLKLTIAVSYKSYKRNTE

NMLYKRLQKRKAALYAAFDILAQNINFSEEVLANPPPSVSKPIDINLISNAPMLNAANRR

GSSRFFLGTFDRRASFNVLNSAVNTSLVTPVNKRQISLSSWITVCEYLKPNWTATDAELV

FNTVDIEHVGFLPLTDFYQLCSLLSVKLERPTLFSNSLMRRCCTSRQRQLIRRFRAHVRS

TLLNEIYILGRYRVVLAELVVGMLICLSVVQAVQVNNIQLAFSTNHSWRLLGFFLLHLFT

LEVLVKMFAFGYNEFFTRPFCKLDLAVVSVGWSFYVLTALSKPPNISLV

>contig57979 Frame-0F

MLAVIQTAHHIRCKRQIRFWHSQLISLHSYHTILQARDPSTRRDCSHHAVA

>contig58189 Frame-1F

MRRSARLVATSRCVKAKTSRPVSSVTKSSVASVATSSSHLPQKVENLDSDEWVSLCSTRE

L

>contig58484 Frame-0R

MPALWKNTIASRPGDWDVSSWIPDVVVINLGVNDLSPPASAETDLIAGYTSFLLDVRSCR

PNAHIFCVVYDKGCLSLANSNFVSLQLQEIVKVAISKVSKHDNNVHYTFIKVEEGLKKED

FASMMHYAVSGHIKIAKLLAEEIALRTGWSIDHEPLTMPYPQAKDRILMPRDHLRPS

>contig58570-0 Frame-1R0

MLYLDAENKKGWRLKRAKYNDLSWLSDYWE

>contig59098 Frame-1F

MQVRYNAWEMVDKDGHTSSFARSTTIDNLLQRLIHGVE

>contig59115-0 Frame-2F0

MLLPRVVPSLRYPMRVLPFFSIRETAKELMCSSFSKR

>contig59304 Frame-1R

MWKACEYFDAATAMPTSVAVRTLF

>contig01702 Frame-0F

MSVSIKSMTFHDNAANCTNFYEIKVLGEFSTSVLTRPESLQTNHYEYRRRM

>contig04442 Frame-0F

MTSSSYSSNHNPKAFLSPTDVAELAAAAVAALPSTLSQANLALEQSTTSAHRTENGDIVH

HHQATHRGGNATLVTSTTTTIHHMGSASKTSFSDLNGSTPSPPYSLHPHTHHHHHHVSHG

SNLLANGSLSGLPHATLGTSSYEKPLGGVRLVASPTFQGDLNQIDAGLSSEDATVQVEAA

KKLRVLLSSERDLLIRQMLEKNWTPRLIQWLRLRDRPTLQVEALWALTNIAAGATDNTSV

LLQNGVIPTLVSLLDSSNEEVLEQSVWVLGNLAGEGAATRDLVLSAGALTPLVNNLKKTS

WDRLSLLRILTWTISNLCDGQPRPVFEIAVILPYLAKMLTSTDTEILSHVCWAFSHLCDG

PSTHIQAVVDSEVCFRLVELLSHSSWRVTKPALRAIGNIVCAEDDHDYTQHIIECGAVPS

LRRLIAHSNREIQKEACWTLSNIAAGTVNQIQCVLDSGCIPSLMGLAASDATDAEVKSEA

CWVVLNATSCGSDTQIEYLVNQGCIQILGNLLEETSMVMMALEGLERILQVGELEAKRTK

CPNPYASLMASANIETLVSHKSATVAKRASRIWQQHFVTCAICLGPFSKHSKDTFFCAEC

KCNVCTTCDCTVFHLKYQESLWLEETVKETNEKQARQASKRSKRQKKRQRTKERKAALLR

GQKIALSTDKGFKQRPLLHKAQDEHVSSDEESSSKSGEEYRRRRQESDDLGSEHGFNGSN

EEEEETTSLGEEEDAMIGKNRNGNVLDEMVTANDKLVSYLLETGSIMALAERLDLEDDSM

WLVAEKDRRALHA

>contig04921 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64016.1|) 3e-99

MTEAFMGYSEDFEQCRDDAMEDIRSIAKANDQRERTERTERAQGNISEAERYMRILESES

RAGDSQDRRQMHQQLRTFKSQLDKLKANLERSKLMDGSQQRQQAAAPQDNVARYHQRADR

VDDHLGDAQAIIAQTEATAQNINRNLADQREQLINVRTNVDETREDTAEAGMHLKKLKCK

MASQIFLLYFVILGLCVVIVWQVISKFV

>contig05126 Frame-1F|Blast-superoxide dismutase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY53396.1|) 1e-103

MRAPSLVLNPRRALNLRVAGTRAISSVKVPDLPYDFGALEPSISGTIMEIHHQKHHQAYV

NNYNSAMEQYAEAENKNNHGKMLSLLTALKFNGGGHVNHSIFWTNLAPKNHGGGGEPEGA

LRKAIEEDFGSFDNLKNTMAAKSVGVQGSGWGWLGYSPETERVGVVTTANQDPCSTTGFI

PLLGIDVWEHAYYLQYKNVRPDYLKAIWQVVNWKNVEERYLAAKK

>contig08789 Frame-1R

MAKTLPLPPHFFQCPELTEREEQYLVGKAKESAKSLVDATRNDEGPVRWEEAGMHRGVQM

YRGEARYPNAVVGESISYGCAATTIQSTLEEVADFFDVSTDAKVAELVELHPDVLDAQLL

YVLEDPNLLNDPRYNARSHRSGSSKMLNANQVTVSWVAMDMGSKLVKNRDFLTVECQSTF

LDVSGRRGWVRSFHSIKLPCCPELSAYNLVRGSFYHTGYVFVESDRPGFLDVIFSAQVHM

KGSLKVPTPLHATIQKKRLCRVADLQKLITRRRLGAQKFLGDLDLVPKHQRTRCHLCASK

FGLLTRKSRCRKCGEVVCASSCSTEWEVAITGQGVRKVRVCTKCAQHTDPNAFGTLTPSE

QYSESYDDETSVRTPGYTSETYPPHASRRRSRENDETLSRRGPYTASFEASEESYYDASS

TGFERYSTDSMEPDEHMISTRRRRDERNQDGYDYGASSPRDRDLDPRR

>contig09733 Frame-2R

MLYPCSRRHHVKTRALYLLTTVVKFDPPDNFLKWYARYRVWKG

>contig09940 Frame-2R

MMVCIKSHEDTMESKTSSDEDRDLHGLNDSHSPADANEPVGRQTLCNLMGHYLLGYPSST

QGVKRLANDPERAAEMLARAKFIPVRLTYEERKLLRVLEAALSVSSYTDKLDTRTYLPPG

KRVRAQLQNVCGFLSALAVALNYKAGQTVLDDKNFAESAFMYQELFELGRRYKIMNPEKM

RSEYGKLMYLLQDAVSPELQELLGFSCMKKIRTVFDVLETGDALELLTDSRLDVATMVVA

PKGKSRHQIQRQIKQKELAIRALSDQYESSRLSRETLQQCLYSIADNKYHLYFERDPIDR

IIHLLTTHFHPENENQDTSLAITSGNDGARLSHSHSRQYHYVLQSLTLWREIAHDLFRLW

YLTDEDLLADGTRYELTETGQGLHRIQSAPRVSRAMHMLLYSTQRTLDAWVGSSVIHLGD

KNVPNALMFIDKYTQVGHILRPIINAIDTIESLCESSEAIQKYVETTFGGFVKLQRTILA

DFFREAFDGSGADNFFDAGSCIDGRLTSAWNWCSNLSTKSFFPIFKLTGFVGFDGKFE

>contig10973 Frame-2R

MFMNITAWLTSVLDTLCSQAYGAKRFAKIVLYFQAGVQIISVRLGPIYHFNWYAETFLLA

MGQDAKVAQFAQSFSR

>contig11101 Frame-0R|Blast-acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase [Phytophthora infestans T30-4](gb|EEY53465.1|) 7e-18

MLLGVGRSLCQRFCSSVPSARALSSIAEAHAELIAHATHQKSRPANKRRELVGNLQKYKI

SASVERAAEVHATSVVHPNAELGPNVLVGPYSFIG

>contig11439 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67962.1|) 2e-21

MINYRKKATADGVLALFYMYGKIAVLASLYYLNITLFGWYLVFCL

>contig13231 Frame-0R

MQASSASKKRDLKAREQMVEVVMEELGVPALFCAKSAVLACYANARTSGLVVEMGATYTS

VTSVHEGYAFAYPKSQATLFGGHDLDAFLGTKVAPQLATNFERKVAVTSMEVEMAKKKRQ

TWSYVVEAKESGLCRVADGPFDEVQNAQLPLISYELPDKTIVSLGTERFSVAEHYFRTPT

IPNDVDNSNAIGSGMKLPKIICDVSGLTTESELRRELFQNIVLTGGSSCFENMPTRIERE

VVTTLSGMPLPLPGSSHSGVAGGFTSTLRVKVVAAHVQERRVGSFLGGSILASLGSFHEM

WMSKAEYAEHGATLIHKKCP

>contig13886 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY65269.1|) 7e-68

MMHVIGATVPHYIIGIALGAGIFGMFMLCEGFMVPRESIPTYWIWGYYLAFHSYSFESFV

FKQFEHETSSVARNVLTKYGMENVHVERNMLLLIGYVFAFQTMFALILWKFHTGRR

>contig16070 Frame-0F

MTHYLGSVYKLLHALDPSCERNLSMSSGTLAAVTADEIFKVADVDQNGKLTFEDFKYWYS

SPEHAPSIDNLAPLDLEEVRHLTNLGNLDVVEVLERFAQHANEAGMVNRESFDKCFFEIY

KLAHLCFQNENEVAKKVADRLYSVFNQDENGQINFSELASGLSVLCKGPRDAKVKAAFRL

FDNNTDEFISSDGLKRYLTSALKVLYEVHPCIKDEAGISAAKLALVTVEHVFLESNRSFD

AKLSSDDFLKWCDSPSVDGVSSSVTKKALFESLMPLNEMKQLSFLASLEPNEVFKIFACG

ADNNGLLSQSRFYKSFCEVIYAHQSKQTQAFGLDMQQKLQNALSSLFALFDKKNIGAVSF

IELAHGVSVFCDGTKYQMVETAFSLIDYNDDGFISLDEMTRYLTSLFRVLILASPDSQSL

DVSPEELGDVTAQQVFAEADQDHDGQLTLEEFKLWYQQADGIGGVAKNAEQLLNSAKARR

PTKMQVASPIEQLKSFTDCTNEQRIVSQERINGLIQTILSKETKPEWKQQIHLALNRLKN

DFDVDQKGMIDLSEISSGLLILCGGLSEDRIPTAFASHDYNADGYISTEEMKRYLNSAFQ

IFKVALPSRLQHFTLASTEELGALTADQAFSKADLDEDGRMGLAEFRMWYARSNAAVIER

FIQNSIPEWLLVQELQHLTNLGLLSTQQLFETLADFAAADGFMGKDVFRQSIDHFVVTSA

TQEKKSRLHFVADQVFELLDKDKNGLVDLNEVVNVLSMLCCDTQADNVRFAFNLYDLNHD

GYISLGEMRLYLTSMLDVLFEARPTIIKQIDVTPEELGNITAEQAFAEADQGRDGKLSFA

EFSLWFLQLSSLSDLPVSAALGEYVGKLQKEVVLTDRPIPEWVSLDVVKQMTNLGNYSAD

EVFEIFANRCSENGTLAREAFEECFEQLVDEQLKNDEVSLARLRLILNRLFVIFDENNTG

TVDFCELSSGLSVLCGGSREEKVRAAFSLYDLNRDGLISLDEMVRYLASVFKVLYETSPG

TDEKLGVQPEDLAIISAEQCFLEANLNEDGKLSFDEFVSWYSKSARFEAPIADVSSRLVQ

QRATRQLIQGSTSSTPCDGSPLHKAIETSAHELPKEIFFHSATIDSPPALYSSEKIHRMT

GFNDDSLLPPKSASALKVDSSNMEHVRQLLKLGTYEVNEMLEIFAEAAPSGELTFAAFKK

CFDRIIRLAGGHESHAERQEADEMVRRLFRVFDTNNSNTVNFNELGCGLSVLSGSSMDDK

IFAAFQLNHRNGNGFITQEEMIEYLASIFKVMYQTTDTTKTDVGMAPEEFARIKANDCFK

KADLNGDEKFSIEEFKKWCTSEL

>contig16764 Frame-0F|Blast-lysophospholipid acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY53424.1|) 4e-95

MDILRGPIDAIALSGNFPVSGFRLMVVLAGCIFVAPIIHLMRCETSRHLFNVVLGLFAGV

FVFDVAVLHTIGTALTVYLLMMVAPRELVGRMVLFLLLAYLVGIHYYREFHSPDIVWDSA

QMVLTLKLSSIAINYSDGGLSKEKKTPTMLKNELQEIPALIPYFGFIFFFPTYLAGPTFE

YKDYICWMKEIRVAPLSVHLRNLFVI

>contig17279 Frame-1F|Blast-glu/Leu/Phe/Val dehydrogenase family, putative [Phytophthora infestans T30-4](gb|EEY58921.1|) 0.0

MSFQEASPRPQIRHSRSMDLGVARTLDLSHQMEEVKALIRSTKILNEEAVTSEVEWFYGP

LGVHDFYFMGQSPAVIAHHVESFIAAKLLSKASNRPDVKLEQEREKDAFFAVLSNVVGSA

DKPSRRAARYEAGITETELLERRLEKHYLSGSSGVIGDGVKAGYQYLEKAESSKQRTYRM

QCYRSSGVLDPVSVPYHVRMYFLQEPQYADPTASATETDITKVADKTFLERSGPRLREVY

QECIIQAMHQMTPAFHTEVWTEADGSKMARVAIAHRSGATHSYFSSIADVYRQHGLFSQR

KYAEFFANGIVIYCFYLQMLETPRLGNGSFEDRLVAVVNDASMHFTLPRTSLTPMLTDGL

LTPQQIAYAYAAWKFSFHFMHRLPESFAIVSQSLRDKDPHAFARLEQLRSTMKLNTYTES

QILDHILSSAEIVRILYAEFKALHEPMKTGERPQVDTSGTLSTLRKSIVAEQALEIFSLF

HLFNTHTRKTNFFANDKAALSFRLDPTFLSKTEFPDQPFAIIFVIGSEFRGFHVRFLDVA

RGGIRMIRSSHAQVYLNNASSLFDECYGLASTQHRKNKDIPEGGSKGVILLNQAHQNKAD

VAFRKYIDAVLDLMLMKEPEEDILFLGPDEGTAHLMDWASSHAKVRGYSYWKAITTGKSA

SRGGIPHDVYGMTTHSVREYVLGIQRKLQLKAPITKVQTGGPDGDLGSNEIKMSPQEATI

AVVDGSGVLYDPKGISRDALVELAEARSPISGFNTSLLSSDGYAVLVTQNDVTLPSGEVV

ENGTEFRNIFHLRPSLTADFFVPCGGRPAAVNLNNIEHFMFREDGRALRFKYIVEGANLF

FTQDARLRLEDAGVILFKDASANKGGVTSSSLEVLAALSMTDDEFAEHMQVDEATGKRPA

FYAAYVEEVQKRIDLNAQREFECLWREHERSGTYYSVLTDQLSERITDLSAKIQHSKLWH

NQTLRTKILADGFPESLLQMTSKEELIQRLPQSYTRAFFASQLASRFIYSVGLGAPEFSF

YEFIQDLTGDE

>contig18340 Frame-2F

MVRDKMFQRYKDTHKYTSEHRFKSKCICMFQEIDGVSVLLFGMYVHEFDEQEAECNSRRV

YISYLDSVNYFNPPHLRTKVYHELLIAYFDFVKMRGFHTAHLWACPPLKGDDYILYCHPE

TQKTPKSDRLRAWYVDMLVKAEEEGVVWQITNMYDDYWRNDNTPCALPYFEGDYWVGLAE

DLIEKLDAEKPKLVVNKRGNKSHKRKNLETKKTANKKSKVKKPKRRKSATCGEIISDDEE

EGDDGNEGSRVLTVKSLDVPDRKLSDPLMLKLGEVIEPMKDDFLVVKLIPCCRVCNTSVV

RGLLWRDHNVKTEHGLSPKVVQTALCDGCYQKLRLLSVQGSSALHSKLVTRLNVLTQETV

ALPDRCTDPDEINDSEFFDTRQAFLSLCQGNHYQFDELRRAKHSSMMALYHLGNPNPNAY

VYECNACTRDIVAGNRWHCHSCPD

>contig18524 Frame-2F

MGKKRNGRHTRHGKRDDEESMSLESVKTLASNDSEFDGILRKGGEDRIDDVIEELNEERT

TTRVAALAKLKSKLLQYLAPEDLSESFVANVLGCLRKPSEDEAVLGSQILAITAIILGND

EERFYQRSKNVLMPLIKASRKAKVMVP

>contig19934 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57755.1|) 1e-129

MMVSGFAEDHQTATRYGNVLVRLGFIEHVSRTDDQLHNSKDNFYRFTKMLEYDDLAEAFA

LDTAMRRRTSINANNYRESVVSNESGDVVDYDFATATDEVHALVTDESLQVMARVLHQVF

ERKNKLLFYKGFVGCFLGAEAVNVMREMRIATTLIDAVLIGQALLDEGLIEPIATTISTF

QDKYVFYRLTNISAS

>contig20259 Frame-2R

MDAVETGTIGYDPMDLLHVIRQGKCEYFTRYRLQETLMLMGCRPKDAVIVTKEALLAYEM

HLQREKSKNKDNQLSINLDIDDDTAERKIQKLTSRIALPWHVLHQCIYSSLARLDYVKPH

HLLDFEIAKEITQRRQSFAVLLGGTSGTGKSTLASLLAARLRLTTVLPTDSVRHVLRSFT

SKEENPCAFVSTYQAGDALTPAMIAAMQGDRKDLSAARLHQKMVLKGYKMQSTLVLEKLD

RVLTMFEARKQSLVVEGVHLNTNDLLTLVKKHPTCVPFVIYISNENKHRERFAVRARHMT

IDPQENKYIKHFGNIRIIQRHLCKHADRYLIPKIDNTNVDRSIATIQSTLVRVLRKLDRG

EELVDNQLGKFVTLSREYENSTKKAWSSKGVRKAMRPLLKQRVSKRLLLRRLLAEQATNL

LGARDSHQGDDSSSSEEDEDDASREADDERNADEDDEDEQTTIVGSLVSGTNAQELSSTV

NGPTLTTELITPTRVAAQKQLFIDEIEEHSTNTSDKAKLISQAVRQAAVWRASQPLSKYT

DWDSHVPPPSPEVTFSDVMETLPEFAAVVEKGKRSTWSFEERRKTWMARGKQPADALNGL

VNQVRSSTTPPPLASRQFKAFAESQRVEGEAQLQLQRTQQQLQQQQVYRMHHQRPPIGRQ

TKALARRAPSLQLQDSSSSLEFDFDSVSMTDVNEDGDHVSQTSSPLDECISPFEHSYDDT

DSHFEVSSQSSVE

>contig21326 Frame-0R

MASSTPKGPAFSSPVKSVGSPYFSSSKAPLPIGFSSGIESCSHSESSALIVVSDAKRMPH

NDNNSAAAAESAHQGTYSFVAAGTNFQIDEKYKFVKVIGRGAYGVVISAENSETHEQVAV

KKISKAFEDLVDAKRILREIKLLQHFDHENVITIMDLLPPPSLGQFEDVYIIADLMETDL

HRIIYSRQPLTDDHVQYFLYQILRALKYIHSANVLHRDLKPSNLLLNSNCDLKICDFGLS

RGVAPEEDNMELTEYVVTRWYRAPEIMLSSREYTKAIDIWSTGCIFAELLGRTPLFPGDD

YIHQLQIICDKIGSPSEEDLQFVVSERAKRFMKNQPMRPGVQFCNLFPEAKPEAIDLLQR

MLLFDPAKRITVEEALEHPYLASLHNLEDEPLADSCFSFDFEKEDLTGPRLKELILEEIY

KIHPIKPSSYKSLKNGISSPPTEQLLSPTMTHLQN

>contig21454 Frame-0F

MKIVYVLATFLTLLGSVQSVNIESGFTLDGSTTYCMGVSAINGSVGTLNFDTLEAGNVGR

CPVGVTLTLTDSKFRISDPIIVKWAATAIVGLPNAIFSNAIDAATGLPAPVTMSTLFACT

VGTNCATSIRGTPTGDGTSSGAFPPGGFKTLETNTLTFGTAGDYIIVGLVTLPGDSALNL

LAEEYLVFKSISIVPDDSAFSSSTSSRAGTLVKSSEVTSGKPDSTSDSDKTGLAKGITPN

DNISSNTIASPSADTAKQMDAEYMGVVKTASVFSGSSTFVKDNGVLIIAAVILCCILGFL

GAGLLLRRRKNQQKGLDGNTSSDADDDGCKTDLTYIANMSARNIEKTTDNMMDEELPVIM

MPSMKHGSEHYLRTRSSRQSLTMNGSDTDDFFDKASHGAAAYLNAAAIDPHRMSSASSVA

GGQSEASMSNFGDSIVSARQKKYLQPNDGKDAVSARTDAQTTLFDQAQLK

>contig21595 Frame-2F

MVCFLFKCALVAFAAAAATAEEEVPNPLFVALQANNDIGDITVEANPNLTPANSNAQSLS

SPFETTTTAAISDSISNVTTEMELPPETPDDADGSDNSVSDADSPAPSVTSSAS

>contig21847 Frame-1F

MTTEQNTPLGALRALRAHLIAGKAVEVEGEDLVFRNVSGLELYRLPKHTATAYHSKKLDK

SYDLLAVHTCFKHADLSFSDYVLKCREEKAAMVSTVDKKELVAYLKGDIDSGPQILNANG

QPSALSSENDRKLKKAKEAEDEARAVKKSKLAQESPRLPLGESHKIPEANDVLKTILDRE

SMTRTRTTVLEAHKTTFESVLKTLEVVNAETKEKIEKASKASALEATTTTRKEQLPLHRL

VKEKLLGTPIIVVPAGFSDLFTMLNAREFLEDGVYVSNGQKKATGQRKQQSMMITHEEEG

HAYTFKVVDTINRFKDKDWRLVVGVIVSGQSWQFKGWKWHFPLEVFKKVCGVHIYNQGSQ

LNPDVKQWDVKVLMIHPDKRHLDKVAAKEFWRYLFAFIKHKLQ

>contig22727 Frame-1R

MGMKVDTRTRGVHDFSFDLVSAGDGMNVYICISGWLDNEDPPMKGFRRAWGDSREYLRAF

YRQQKSDKVDQVDQVMDRYKGREDEFFAISRRTYNIKAGSIDNDPLGIADLSTMAEASQY

DDITSLNGDSNAIASSCTDSEVKRSSSTSLWELGTKYEPLRAWRWKDRFPQGDQYCLVWE

EAGLRRFGKSMRTFAAEQVSSYATTEFVRYTALAALFTAVAIPRVILRLADIIDNVWTIT

MNAADTSGRMLADALRKREQGLRPVTLVGYGMGARLIFSCLKELAKSELIDVSCGIVENA

ILLGSPVSMAREDWANARRVVSGRLINGYSEKDWMLGIMYRYQGWELHSAGIAPIDIAGV

ENVDLSAIIGGHLEYKSKIGAIMDLLQLEV

>contig23908 Frame-1R|Blast-molybdenum cofactor synthesis protein 2 large subunit [Phytophthora infestans T30-4](gb|EEY57331.1|) 8e-76

MRLHFSTNMATHRSHTSVEEGRGDFVEIGYEPLDNQKAVTLVTHPSAGAISTFIGTTRNN

FQGKKVVRLEYEGYTSMAVSELHKICATVRKKWPDVVGIAVFHRLGVVEVATASVIVAIS

SPHRLEALQACAFAIDALKATVPIWKNEQYEGDLKVWKENIEWRDGAAVRSSCCDNKRVA

K

>contig23997 Frame-0F|Blast-SNF1-related protein kinase catalytic subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY63063.1|) 0.0

MSDIPIQLGHYHLGKTLGIGSFGKVKLAEHDITGHKVAIKILNRHKIRSLDMSEKVRREI

ALLRKMRHPHIIRLYEVIDTPTDIFMVLEYIAGGELFDYIVSKGRLAPEEARHFFHQIIS

GVEYCHFHRIVHRDLKPENLLLDADNNIKIADFGLSNSMEDGDFLRTSCGSPNYAAPEVI

SGSLYAGPEVDVWSCGVILYALLCGSLPFDDESIPNLFKKIRGGMYSLPSHLSEMARDLI

PRMLVVDPMKRITIPEIRQHPWFQIDLPPYLQHPPEIVEHQIFQIDKECLSQCLALNYAA

NVGHEQLVALLMTRESHALRVAYELILDHKNAKIRIDELRDVRAVNTKPKTFSTPEPSTL

LLPGRGPLPMAASPLVMPSSALQEARNFGGRGLVNAGLGPRLSMGSNGTSLSGFDDSHAS

NAAPTPKRRRWYLGIQSKKEPAHVMSEVYKALFVLHFEWKVVAPYRVKCRWQVPTVDTTT

ATLQSAEKTQLQQQMQQIKIGLQLYKVQQHIYLLDFQRLDGNAFTYMNLCARIITELKTL

SGIRPVSNGLDPRFGQDGNLHAMPMHQQIPHAM

>contig24673 Frame-1F|Blast-pectinesterase, putative [Phytophthora infestans T30-4](gb|EEY69622.1|) 3e-24

MRLFAYSLAVCVTLLLSTYGKDCKDSPNARTEPPPGAVVVDRTGKYEGSVKTIKLGVDQL

KASSSPQSLFIFPGTFNEQIFIRDHVKSLSIQGYTCDTTDYKHNQVTITHSKAQKDLASD

VED

>contig24718 Frame-0F

MVLRRAAEGEGAYDEEIELGPMQAIDRLSLEAALAKKAEKWTRCAAVNRLLLEEYNADDW

TFLKEYLAARFQEKSCCSANELLALGQEVIVFFDNLTSRPGNERIRGPALARIHVRSEIL

SRLKIDDSAVVQVEEKLQEEIVAYADRFYAKTCCFTDLKQYYTLYLKEIKSVSARAKLKL

IQHFVNLSVRSALLLQKKPKGDCVVEGARKDGQGNLSKRLLALKTLRFLGYYDLASIKSL

DELVSELEDEYVALNWLNIGSAGGQREVQLTDDLLLLATHFLLDMYQLSSGDRTYLERAA

GLLEYGLEQSAYNFQMKLLLSRVYGYMGAAEAMLNRHVELDIKYVQLDSLSFLVLDKMLD

LCQYTEARQLTNRNRSDASKHGKGHT

>contig25090 Frame-1F

MLMHLFELTETVEFTDSRSTGGNAAASVGIDCLNFLCSTHLMRKGKLLVRKKLKNEMQLC

QVSLNCMMGLRMTTLREDQGSASTSFDQAFAPNLGNQSVIILDEMENVRSSEWHEFGFEV

TVKKKVPNSNKNLLATQHAALNPANAMVLHQRRVGKGNDAQTMEVRLTQDFAASSEEERQ

AWITLLQAVIDGDLNELEIFCSDDWRSNVREYRRLRECLITCMERKGHELMVFLKQVITF

NTRRASGFHLWSVIQCLNSVLSNESKRLDRMFVGAHVITTLITCYEKYPMWNLLLGEITK

MLVFCIGDFKSKRSRKCPIIGRILQTEGEDAKLAPLLCKVYLSRDTRNSNNEQEYDKLAG

TDALANLKLIMEALKMCYKEPKTRSQERIQCDMKMNSVWRDLVKASDKMTKEDPNSCIMK

VEIRPSSSFMPSSAPTPPTFQEDIFNQISRPNFSTTNGFGSSYLEGDGCAFGYLFKERHG

SREWKKALVVYEYVSHKLWYFYPSEVDETHAIQWKWIVPLSVRSRYTHGQDETHTSVGHH

GLYISAYDNQQSDEDTKVSAKEMHFSVTKLEDRDLWKDLLSNAADIIRKMACDYSVLSQR

LKKPDKKTITHCQNQSCKTPFKLFRRPHSCKRCGKWMCAKCTSQRISIPEVGLLHPVRHC

RECFEANGGVHAETDPFNLFHLRSKQAAIASQNGSLSNAELYELAHGKVSPRTLMQINRR

LTRLSSIDSPTASEYGGNSYLVDEINAPGNLGAENLSSFTDDEEDLYPISLSLSRRSLLN

PREDIRG

>contig25227 Frame-0F

MYMMFSTFMAPPHQEIQYPGVDFPLPFSSPSLHIHKHTKAHIQTLPFVVNLSGSYFPNIP

SPPPPPPPPTTTIAEFRYLKWLPYTKPSYFSSI

>contig26529 Frame-0R|Blast-carbohydrate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY58254.1|) 1e-24

MQLRGIITTLSLAALTTEASVLVTIFNACSENVELFDNVVIETITPGFATTRVLPEGFAG

MFRNGVNPQATLAQFSVAGGALLYNIGIVPTGNVG

>contig27016 Frame-2R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY61994.1|) 3e-30

MEVLTPIDHSSIQYEPFRKNFYSIHRATSILSTNDVATLQTNLRICVDGDNVPAPVQSFT

HLNFDRKLLHTLTKLKLDTPTAIQAQTFPIALSGRDFIG

>contig27746 Frame-1F|Blast-protein mago nashi [Phytophthora infestans T30-4](gb|EEY54593.1|) 6e-14

MEFEFRTNGKLRYANNSNYKKDSMIRK

>contig28426 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56486.1|) 9e-39

MTSSNSSASKGMVFLCSGLEKNRIQQILKWAELLKATVVRSWSKDVTHLIVKCVSWDGSD

EGTPLPDDSRSERVLQDYDRGNLNLPDDSKCGRWVKIRSLKYLKALVGGRWIVSDYWLQA

CANCGGYVSELKYEVDGHWKGRTIKEAVKRSRLAREKLLQLAMPDIDHSNIGTMLFAGFC

FHVTGDFLSPMPPISELNTLIMTGGGKLIAFLDEIFDEMQKLENSSRKLIIVSDKINPLA

LRQQAKQLTAQLQINSISSPIIVNYLWLINSISEAKLRELC

>contig29469 Frame-1R|Blast-phenylalanyl-tRNA synthetase alpha chain [Phytophthora infestans T30-4](gb|EEY58374.1|) 0.0

MKNKWIRLDKADGRFYRCIDQVEDEVTNTLQRLEQASGVLSAVSKDEANTLKRRKLVEMR

TRKSYALSKGVNFAVQRTKQAAGLTKEMLEGNAWTNESFKPYNFKALGLNVGGGHLHPLM

KVRAEFRRVLMDMGFQEMPTNRYVEISFWNFDSLFQPQSHPARDAHDTFFLSHPKYCLRV

PEDYYKRVHDMHENGGFGSIGHGKGAFKRETSMTNILRTHTTAISAQMLYKLANQPGGFT

PQKYFSIDRVFRNESMDATHLAEFHQVEGVVADYDLSLGDLIGIIKAFFMKIGITQMRFK

PAYNPYTEPSMEIFAFHPDLKKWTEIGNSGVFRPEMLLPMGLPENVRVIAWGLSLERPTM

IKYRLNNIRDLFGHKIDLEQTRSAKLYRN

>contig29757 Frame-2F|Blast-bloom syndrome protein [Phytophthora infestans T30-4](gb|EEY56970.1|) 1e-115

MHQAKKVLRDVFGHNTFRPNQERTVMEAFSGRDVFVLMPTGGGKSLCFQLPACINDGVSI

VISPLVSLIQDQVQQLEALDVGVANLKSDQDYATEQRPIIAELFSNCSRIKMLYVTPEKI

ASSNMLNNLFESLDKRGLLARFVIDEAHCISQWGHDFRKDYMNLGMLRTKFPSVPIMALT

ATANTQTEADIVKNLKLRNPFITRSSFNRPNLTYDVRKKTSKFMT

>contig29946 Frame-2F

MEPAIWECRNVFPHPANDVLLHLTLTGGKSYHPFGRPLREVLLSLSTTTLYLHGTNEPMN

DGQRLEALVSAAVVMA

>contig30342 Frame-0R

MQNNEKELHCLVDTIAPGAFGSWAEFSLYYGQDIKYGRKKSAAPEAVERSRQKEKELRQK

LIPYYLRREKAINPTFQTVKKNDQVVFCDLTPLQLAAYQRVMAMPEFQLLQRGEEKCDCG

RDSMEKRKKCCYKTPADLGNGRGLLYERFHEQEPCKNCPNCMGLPCVAMLLKISNHLELL

KVNPHDSSELQNYQREFARIAFDSDLDEVGGVNQVSSFQEMCAISTKTCGKMIVLEKLLA

VWEKRRQKTLIFSRSTRMLDIIQLFLITKAVRYSRLDGNTKVEERLKMVNEFNSGDSDMT

VFLISTRAGGVGLNLQSATNVVIFDPSWNPAHDCQAQDRAYRIGQTKDVQVYRLITLGTI

EEMIYVRQIYKQQLSDTTLKGSNAPRYFEGVQGNPQQRGELFGVANLICWKPGGVLKGIQ

DAYIQCRDGFTMQQNQVRHEAATMKRMVKSSTPKLHHVADDDGEMIEIAGELVSNIMIPD

EPPTQTLRKEKPVAEDISNSEDDLKALSGATTFYHEEIFGKQDGEGDGHHEEVYNGSCSE

VEADSDICRTTSSTSHASNQQALLSHPLFHEKSCISSPMKATKGPKVASKETQKRMYVPA

YL

>contig31275 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59438.1|) 0.0

MKNYEARQPSYFATPSVNHLFALNVALDILLDNGGMEQRFREHQLVGDAIKEAMTTLGCF

LVTADDSGANTLTCVRYPAGIGAADFLPKVVKRGVSLAGGLHKAIKTEYFRIGHMGPSTR

CVDHILKTVDAIEGAFLECGHAVKEPGKAAKDLKKKLHGKLAMHPESGLEATHLSCLLPP

KCQVYSIAAVVLAFASGLLITKLRSN

>contig31503 Frame-0F

MVCFGLDRPLLPMPPTATGSSLVTRTRVPQASASGRPLSVGSDGLPLLPCHDAPVVMAPP

PAPCPTAVTLFGHVDTTQNVRTQLLAHFSRTQQLN

>contig31697 Frame-0R

MALTMLLASEMDRVARNAENWQERMVALGEMQRAFATLETDLPSGTVAANLSTEMWKTLR

PLKGMVQDLRSQIVKEVCALLTTISRVTRDAMAPFLRDVLPTLVEVRGSGNKVCSTYCGK

CLEEIVTHTVVKGATLRLFVDLLLDSKNALIRLCCISCLRRVLVTWSTVLEKSDIQQLEK

SLQHALYDASSSCRAQAHELFLTFHTLFPTRALVVMSMVDFKIQKRLEALASTNINASGT

AAGLASNVSEDGDVTPVVPRVQALAGLYLEIGDRVCIPDKELFGYVRFLGEILGTKGIWV

GIELDEACGKNDGSVKGRYYFQCKLKHGVFARPQQVFLTMSSSKMLNFQQAQPAQINESA

TQKEENVPTEIEAFKVIDDLSEPEEVELSTPSSPPLAPTPASVSSLPVPIDTSEPSKLSL

VLQQASLAHRRYLNRLLIFVRTELEEHERFENYGATASSADAVQYLQQLQNSAQDKIVLS

DEFIQQIIQSQQAARES

>contig32115 Frame-2F

MVLINPAGGNGGAQQTFEKEVAPMLKQANVEVEQVITREAGHATEILAQVPLYQYECIVA

VGGDGLLSEMLQGLMGRKDWQQAILQPLGIIPGGSGNGLSASLLSRANERFEALNAAFSL

VKGCVQELDLFSATNGIGTTMFGFLSFEWAFIADMDIRSEQYRFMGDMRFFVATILQIFG

FGQTKYHGQLRYLLSHDKEPQPIKHHAMHQSGKALAQQACISLRTEADDENWLEMDGPFY

MFWSMNVSHAAADAYIAPSADIADGYFQIMLVSGENYSRFGLAKLMMGIEKGSHIHEKRV

QLIRTRAFSVRSSNADDRMCIDGEPFQGPEVKIEMHRALGRVLCLPATK

>contig32322 Frame-1R|Blast-tRNA pseudouridine synthase, putative [Phytophthora infestans T30-4](gb|EEY57959.1|) 0.0

MAPATPLTTIDVGSLTANNTTTEQLLAILRELRNSVGPKIVCNAIAKVMHFRENKFKQLA

LSDDSTPMMMEKQLLKQKNEIMANKLGANIPKKCKKREFMMSNYIMRSVAMKFLYLGEKY

AGFARQDHMPETVERYLLEALVRAKLITNVDEANYSRCGRTDRGVSAFGQVIALRVRSNM

PATAKLLTFPCIDDVRPGSKFRVRLATGEEKVLTEIDYASQLNRALPVDIQIYSVASCRP

DFSARFNCTARMYRYYFIRRDLDIGTMQEAAQNLVGKHDFRNFCRIDPNCHVFERNVHSF

EIVPCLGQRAHDPSQQMYRCEVFGRAFLWHQVRCMVEVLFLIGTGQEEANVIRKLLDITQ

TPRKPQYQMASDLPLVLHECYFPDPDDPERPGPRFEYTPLALMQVHAQLTEKWEKRSMQA

AMLRSHLDALENFQVSADRVVKDLNHYAPVLEQLMRKRNL

>contig32807 Frame-0F|Blast-phosphatidylinositol kinase (PIK-G3) [Phytophthora infestans T30-4](gb|EEY55051.1|) 4e-55

MRAPTLIFVEVVPLQSAQPVGLYDSNRDHLRPFVFNTHP

>contig32872 Frame-1F

MEPQESRFANCCRWQERLRNVEIYNALHFDMDLLLTDAYATLKRS

>contig33044 Frame-0R

MVPFAKTPVMKSNHLTPDTIDVVQSTHVLLGSTCFFALVFHIVNRLSDRYVRAYRDFSIP

EQGDWCSR

>contig33350 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56451.1|) 4e-09

MNLNEQERRCYAVKQRRLLLRRLSGADGAIWNTREDSFKDNSSATYLGPYAKCL

>contig34801 Frame-2R

MAARKGKKAPSARKVTTKRKNVKSRGRSADVFSDDEKEVVQQERVMDARADVDVVFDYEE

PTFDQEDSEVDEDEAFNSDDETAYGMIFNKQKVKELKADDEDGGDLLSDLLGTTAASRLS

TASDDDETQDQKIPNLQKMVDALVNEKSRTKVREIDAQYVNESTEGELTLGTLLGTQPLN

SGEEDVRKEGDDKATMSEFEVRRVRQ

>contig35657 Frame-0F|Blast-26S proteasome non-ATPase regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY54294.1|) 8e-06

MMANLEALDEEAQALRAAIDNKQVDEAIKILAKLQ

>contig36076 Frame-0F

MVSQKVATQLKKLEGDEWDSDSDTETNNAAVSSSTFDAGSDLVILPTEAEAATFGKKRKS

KMQRRKEAAAQVKEQQVETKQLKPSNVIYLGHIPHGFYEKQMMGFFKQFGVVRRVRLSRN

KRSGNSKHYAFIQFDEPEVAQIVANTMNEYRLFDHTLSCHIIPSHAVHESMFVGANKEFK

PLPRQAINRNRHNAEKSYEQTIINHNRLVKKERQKRKVLRAIGVDYDFPGYEAQMPAKKQ

HIGFTE

>contig37273 Frame-2R|Blast-importin subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY62298.1|) 1e-133

MATPSLRRASVLALTESCRVPEVMAKRRIMGEDIKRETMQVLVSIIQQLSNEKVPHCISG

TGGLKRETLSFPLGDAEIAPWRIFEISTGKPAPNDIAVVRYVRHVDAMTVEVMDVDVNFE

TGENLVFKAKKADMRPLQVMDDALGQDDELNEEETELLDEQGLTLCDTCWALVEMTLHDS

DIVGGIVQAGLCPRLVELLYISQSSILLAPVLRLLGNIVSAEIVYSQAVLDAKLLEVMPR

VLNTTSRAVREEACWMLSNIAGGQEEQVVAMMNTPGVIAGLVEQMSW

>contig38423 Frame-0F|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY63233.1|) 2e-79

MATRGRVNSALRAQHMPNHFRHFDGTFTNTRGQKLSYLALFPPTSAPLRAVVLYLHGIGD

HSRRYFHLYERLCTAGFGVLAYDLVSHGASDSDRHGLRAHSARFQNFVDDTNEFISMAKS

ELYPKVALSLDTEPKMILSGMSYGTLVSLHTILSGTHHFSGVVLVAPALLVEMTPVLRVQ

A

>contig38544 Frame-0R

MMTFRTFLPLSQPSYIDMPQLLGLKSIQQSKPVNKCSLDFILSSNKVLTPPKLLPSFPWT

SPQRGSSNKTFAPIVAPPTGPSKIAKRRRLQKTSATNGRAKVSGQSEVMLQNGAIVKKGS

KYCMVEGCTSRAKHARRCWRHGGSVKCKVQDCANRAKTKGVCWSHGGGTLCSFQGCTTIS

VSNGVCWAHGGGKRCAIDGCARPAYERTNHLCTLHFEEQQLVAPVPKFAEEIKF

>contig38805 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66541.1|) 1e-15

MIETFRQVGQGTANEVELLDLREELERKEEKYVREKDRKVNTAQGSVDLFNAAVSAYYFS

AWYDG

>contig39820 Frame-2F|Blast-L-aminoadipate-semialdehyde dehydrogenase large subunit, putative [Phytophthora infestans T30-4](gb|EEY68241.1|) 1e-151

MVSLPPRNVFLTGATGFLGVHLLHALLKFTTTIVFCLVRAEDEDAALVRIKSALKEFALL

DEARNFHLEDRVIPVPGNLAQPLLGLTANTFKMLATEIDAILHNGAEVNLAKPYSALKSV

NVLGTQEVLRLAVTNGLTKTRVKPVHYISTNGVFPSTSNTPIFFESADISELSDELENGY

AQSKWVAERMCQEAALRGLPVSILRPGNMAPSSSTGQWNSSDFMYLLLKGCADLNAVPAC

SDWYFDMTPVDYAARAIVHFTALHPKEALGQTLHIQNPSLPIRSDSF

>contig40569 Frame-0F

MHEVIPSRIGDRFGSHVDRRCKRLRFLPFFGATTRPGRGDRQVTICEEISNV

>contig40846 Frame-0R|Blast-hypothetical protein PITG\_15577 [Phytophthora infestans T30-4](gb|EEY64798.1|) 7e-15

MVTAINVIFLMAIVLVSTYFIAAFYYTHRNADSKPRKKSVHKKIRSSPPHATSKFLSTGQ

RIHVMNASEFDDLRRKLRMQTASRRYRKRKKEEARQQRAQILELQAELTRLKEIEAQTKQ

YQQRSIESLEKELKMHNDEVTDLSKKIQDAAKEEQECLQFAS

>contig41162 Frame-0F|Blast-thioredoxin H-type [Phytophthora infestans T30-4](gb|EEY55747.1|) 6e-07

MDERSGAIRDALVSMISKHCDGTTASTDIF

>contig41188 Frame-1R

MRCCSISSSPNCDRSVTRRSGNEKSVKSYDFKADLVCQRISPLRKCKLNTFFPPIASTIV

TVEEGESYSWKDSLYACHRLFG

>contig41324 Frame-1F

MPTRTRRKNLQKRRKRRLFAAIASEILSG

>contig41399 Frame-1R|Blast-Resistance-Nodulation-Cell Division (RND) Superfamily [Phytophthora infestans T30-4](gb|EEY54105.1|) 1e-109

MWTLLSIYSMESLEQGLPQKEAMPSNSYMIEYFNALDVYLATGVPVYFIVETGYGRNPDN

WLLNKESVERIFCKSKDVCDTYSIPNIINALANHGDKLITHISPGTTYSWMDDFWGFVNP

DSECCRVNSENAYLPLERGNNTYTTLRSEANTCLSTSVTVPPVSDAQYMSLFSMFATASA

GSSCSYGG

>contig41474 Frame-2F|Blast-RNA pseudouridylate synthase, putative [Phytophthora infestans T30-4](gb|EEY69313.1|) 4e-45

MELEKALAPVLAAEEGKGISKRQIKKLRHKKLNSSDRKAKKLKSQRETRNTNRIQAEAPV

YSIANGYRMVKPYVYEFRTYAKARWFDRELLEIFTREFGANSPEYYKFAIASGRISVNHK

IVPPDIIIKNGDLIIHT

>contig41540 Frame-1F

MAELKEYRHLDIEQSKFLGGDLEHTHLVKGLDFALLGQLKREKQQLLATKQKQLDNTTSS

GVQKMSMPQNGNITFKTRLGRLVHYHACQSTFKNTESTQSELFLPGRMYYTFILSRTEVE

SIPVSVQCSKEDAPVSDDVVSGFVDDSLIGQVVDIMKMKQTGKLKHKRVNDHHHSPAVQQ

SDGLGHETEIAMDETKAAVDDEDIFPDLEEYVPIDLRSDDAINEKLNKETIAKVGYFSNL

SAALTEKEDVARKKEKIKERAWEATLENAVESQKRVEREKERREKAARMTGEGDDYAEYQ

SIGALGGDSDNEDDEETVRRRKAAGLQNRKDLSDPEERIRRKKQKQSSKLANALHKINKI

LADKSNK

>contig43076 Frame-1F

MKMASLEKPQAWSSNPVRFMRLILAITMLLSLWYMWQFTSESVVSNKLKATNANDAQEEP

LE

>contig43270 Frame-1R

MEKWNLSMFKRNFTEFQDKLLLPFDKVSECELFGSIVGHNSD

>contig44503 Frame-1R

MEDYDRLEQEALMADREDVMLKQTDDTHAFSCNLLNREVSKKMLLAEDPSGGAIFEKNFL

RESASGILQNERDLFSRRGSVPGKLHPDNSLRNTGDQLPLTSRRRNSFETPIENNLSKAR

MLHKLKSSRTTTIPPSLYSFNRSSRV

>contig44608 Frame-0F

MEMNKGEAEKCLEIGKKHLRLGNWEKAIKFFDKSHRMYPLAGVEAMRDRARTEMEKVSAS

KRPPTSPRGGMRHRSATAPSRSPSSEPSRPYTAEQLQMVRQIKACKTHYEVLSARQDATD

NEIKKAYRKLALKLHPDKNSAPGAEDAFKAVGKAFAILSDPEKRAHYDQYGDDATIQQQP

QHRRGYAPDGDITPEEIFNMFFGGNFRPRGHRPQPQHQDHRQPQEQRGGMATLAQFLPLL

LIFLVSLLSYPSTPEIPFTLDPTPQFNIQRTTQMANVAKGIPYYVEQDFDQRYTTHWRDL

SRVEQMVEQALTSKLTESCENLQLRQKRMIYRARNSRSDNREVAMRKALDMKMPPCDQLR

KLRRTRRY

>contig45166 Frame-1F|Blast-electron transfer flavoprotein beta subunit [Phytophthora infestans]gb|EEY56791.1| electron transfer flavoprotein subunit beta [Phytophthora infestans T30-4](gb|AAN31477.1|) 1e-123

MKILVPVKRVVDYAVKIRVEPKGVDLKNVKMSMNPFCEIAVEEAIRLKEKKVATEIVAVS

IGPKQAQETLRTALAMGADRGIHINTDMRTDQELQPLAVAKLLKEIVAKEDPQIVMCGKQ

SIDADAAQTGPLLAGLLDWSQGTFASDITIEGDCLNITRETDSGIETLKLCLPAVVTADL

RLNEPRYATLPNIMKAKKKKIETFEADSFGVDLAPRIEVVEVKNPASRKAGIKVSTVDEL

VDKLKNEVGVI

>contig45535 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69886.1|) 5e-13 NOT\_ORF

MFEDYARVHLSE\*FLINALN\*RVDALKNVDLIHARSSDPYVCMLLLIFHVVRAFARRFG

>contig45580 Frame-1R|Blast-SDA1 family protein [Phytophthora infestans T30-4](gb|EEY68850.1|) 5e-94

MDVLVCDLIQYNRARDKTIVMAARGVLNLIRDIHPALLKRKDRGKLYNDSAKPHRFGELV

ASEGVDGADLLAEAEAAGRFDGENNKDGWDVASSTLCEEDSADEWVDVSCEEGDSECGSN

ISADDNAAKLEEPIIIQQRDQLDARRILTPLDFERIEILKKERDAALKDPKSRSKRMAEK

AAVMASSDATKVNPTDLEGYSKKKRMTQEERLRIVLEGREEFKHSRSGGG

>contig45896 Frame-0F

MVAEVMALLRLFGVPYLVSPMEAEAQCAALEQLGLVDGVITDDSDIFPFGGQRVYKNIFH

HQKFVEAFSARDIENELGFSREQIIALALLLGSDYTDGVRGIGIVNASEIAASYPGLEGL

CDFKQWVRDYNVAEEAQRVASKKHTKSRQKSLAKDSATASDSDDSDNESIRARFQRVHAS

ARRKWDLGEEFPSKQVVQAYMAPQVDRSDARFTWSAPDMDALRKYCARAFGWDAAKSDGV

LKPLEEKARKDGGHIQTRLDRFFTSYKDQVHYAQIKSKRLRSAVNQRQSSKKRKAKLQ

>contig46853 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65988.1|) 1e-108

MKNVKYPSDEELEKTSREAILEMLEYQVSGEAVTYMGWQTKRESKSMYMHAFSEKSFNEV

DMACVFNETWKMFYDDAKQELLHRRRNKFCILKKLNDNMYLTRNIHQFVGESFPRHAMTL

VYRISIDKNTFAIVSKSVVPATNDAQHLVWTDEFFMWKFARNMDGQGGFQISIRGKYGST

SAVAGNRLPMLESYFQLVEWESLVIRPIFDFTVS

>contig47069 Frame-0F

MRSRVCLEDKSNVTGSECYKHFGAGRKTSECKRFNTSTGTNDTNSSWATRLQFVKQDLRQ

RAASHQNLRVPAQSLEHQPTRAEPIDLSYLNELVTPRARTTTCAVDKE

>contig47115 Frame-2R

MNNIAMAVRMLLDKQADTTIVNKEQRTPLAVARLGCHAESMAYHLLAEDEQLYSFARR

>contig47872 Frame-0R|Blast-DNA replication licensing factor mcm4, putative [Phytophthora infestans T30-4](gb|EEY68142.1|) 0.0

MLAAFRRIAAHPRVYENLAHSLAPSIWELDDVKKGILCMLFGGTRKDGSSGSVNEVESEH

EYSGVAPKRRNMRSDMNILLCGDPGTSKSQLLSYVHKLSPRSIYTSGKGSSAVGLTASLI

RDLETNDLVLESGALVLSDDGICCIDEFDKMSDSARSVLHEVMEQQTVSIAKAGIICSLN

ARASILASANPIESRYNPNKSVVENVNIVPTLLSRFDLIYLILDKPQAESDRKLAKHIVA

LYYDEETRTRVRAQTRRGEDTPQLISMKLLTEYISYAKRHIHPTLSAEARVSLIRAYLDL

RRMGGASAASAKKNITATPRQLESLIRISEALAKLKLCKTVTSNDVKEALRLMNVATQRA

AMDPRTGTIDMDMINTGHSVLEREVLAELMTGVKEILGETPNQSMTVYETRRRLEEKRKS

EIKGANFQMALRSLEDENFIQVSHGVIRYFGDSNE

>contig48301 Frame-1F|Blast-regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4](gb|EEY65901.1|) 3e-59

MAFGRNNKGQLGTGPRTLASADLPLPVPSNALVNVEAVKIAAGFYSSYILIGCSDENHQR

EGAHDKTKQTQHLPEDSLIENYDCLFLSLMEEIDANYKLKSRSKRAPLQVKRKFSCRKVP

LLKLHAAGWAMTRALMYRSLQDADDKTRDRSAGCVNPILAT

>contig48510 Frame-0F

MGRRTQEQIMRVQEGHNWSNEPQKIGLMKVKKFKSVKSLLEMLSNLSIKTIKIVDGTLIR

GPMHISQRAASTPRRCKAWKIARGTHLSRNLLTASIPKRKG

>contig48684 Frame-1F|Blast-syntaxin, putative [Phytophthora infestans T30-4](gb|EEY66829.1|) 2e-13 NOT\_ORF

MNSIRDHICALS\*RKKYECRRNIKRFNKSTRAI\*RIRSKRQLEIVKPAASDADIDAVMRS

GDPGSIKKTAIMQGGAAGTISDIFFTFVLR

>contig48763 Frame-1R

MFKQESSVDVAKKVLRAFVSSNLKNSSVRSRSLRLHVVGSEAAVAHTLLVVCRRVHDSLD

SLSSLSERDEATRDISAFITRLGDTLKSKTATERAQDEEADALLMLYTDCRRAFYKLEPI

IVLLCTKILQLAMYVHKRINNGTASGIGMTKRASLQRGFLQSCLAFAHVTIPSIDSPLTK

LQLLILAASGALVMNCIPQMDALVKASIVLIAELNYKALQPENQPEEELNTSTFRHRVAG

GLLGAGSNSALQRLVQLCAQLMNLLVYAPSLNDEDAFYFVNATRKALFKSLASRDLEAGI

ARVRVLFMFIQLYYLWGQRLLPPCLHGVDSNDRLYAGDDTYRMEVYNRFSLCVEEVVREI

RALSESPDDASKQFAEAQTELMLDFINLVAPMLQYGEFQVGENIRHRKKSRSGVVLIHKC

>contig48899 Frame-0R|Blast-iron-sulfur cluster assembly protein, putative [Phytophthora infestans T30-4](gb|EEY66911.1|) 2e-46

MLRVAVEGGGCSGFQYVIEFEKDTTPDVEEDVVFEQNGGKVVVDKESLELIRGSTLDFEE

ELIRSAFAVINNPNAVSGCGCGTSFDLKE

>contig49067 Frame-1R

MERLRKENDRLRQSNELLQAAATSPAHIEAPSTKHSCSFADKVDPIDASMLKSVHSYLES

AAYDCDEIKKQP

>contig49809-1 Frame-1R1

MAQNPHSFAQTLAPALLMAKYRTLGYVLHCLYRQTSQSRCEIRLTCQELGTVGRVSLWYR

DPLQHGPLIVAQIDTLFRAPNTKKTLHT

>contig49900 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64539.1|) 8e-68

MQREVLELLESSHRASHALYQGFGKKSLKQQWQGRKNKPAVKWIRKTFRNPARASLPGES

VDEGLTLSHWGKAHLEQPDYIFSRFNVKCETTSFTEKEYEAALAPHQDLMMM

>contig50234 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65900.1|) 6e-55

MGQHISQPSAVIESPSDRTQLRPLQAPYAPLCDVPKPGDSSVTDDTKDTMDKILEFGAAL

RYLPKESEVSESLAVRNLKQELNDIMSPVDSMDELFQLISQLAGLPTQDGHDPSQCHANR

EVSETMPGIFDARVASYVKHLQALYQMTKKEKSRYEHQLGAAREQALSLRKVSPP

>contig50289 Frame-2F

MFEALHGDVLRLWVSGKLDGNNTIFTPHNGALLLLYFAPCTFL

>contig50407 Frame-0F

MRFRGTLAKDALVVLLDVAQSFARLGLHSSAKTNCVFTLTPETLTIALKSGGAELQSFAR

LQTTRLFHDVVVQSQAANHIGFLCDIRHFQQALTSGKDASAVMLRLLKRDGHNFLCLRTR

AVDIDIIQSIPIDVLSMSLVEHYKEPSVPAPQMAIEMPPLRAMRSIVDRLKVMHKTMTVE

ASKSGTLVLRIDTNTLTLQTLFAHLRYRDDLIEDDEEDEEEKNRRQQQRSSSVTVDSKVL

SQAILVDGQSTRSVLCCISENQAMVLHSILIDSFGSFTCYIPVLTPDL

>contig50472 Frame-1R

MRAAHNAPFPNVIIEVAYKNESLTALRAKLLRWMDPEWSSVQVAIGIKIFSANFRRVAIL

NKHGQPVEEVEFG

>contig51031 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54554.1|) 5e-67

MDKQTSQRLVKMTNYALVQVLKASVARLHNIEVEIGDLELALEDVQEEVESYSDDIDDCH

ERMDDIDEFVRELEAGNIGTVTDIAAARAEMIEERQEEHKLLQGLNDARANHEQQFEQVQ

SQLAALKAEHELLVMTRFEICRHFRRNGVFDLVRRRLALFDPNLL

>contig51444 Frame-0R

MFIGRDRLVAHMTKTEVCEVDWMLLDNQAYTQKLVPNTVLATDSIPTTTRFKLLYTIDPE

ATNFHAFLARLRLRK

>contig51523 Frame-2F

MSRESTNSRRKSMHLTTSCDRLVSQSFNPQYGDNLLYHPCSCSMLLRNYVLLHITILKAY

TQITLAAGSRSALFTKKRAA

>contig51750 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59852.1|) 2e-32

MKKRNISSEQEKWNCYQGQWKIALEKLRLHPRNAQVAVTAREIANFLLKATSVELHCDAI

NFCLAELHAVEWLLPHLKLPSRGLLHYQIGKLLYGNVRDFYHTMSPLNRIEQLEKAAIHL

QESISV

>contig51905 Frame-0R

MTTESGAMMWRVPRIMRRYPSWETFHKYLDEYSAATFQLYRVRTTYSVRSRNVRLRQLAA

SRGLLVR

>contig52232 Frame-2F

MNRDEEKKNRKRRQQQLTMQAMHTRILEKNQERARARNRIGYFIACSGVTLSVFVVAAVF

IAKVGVNIQSKSFDTKNSTTISNSSGGDGFVTISGSGGSKADLTSKSSRIATDGDDMWTD

LDDNTHARMYTDSYTYVHCFLMVLSLWMSLVVVVMHVLFQSFRTYSHPFVLTLSSVQCGY

WITSLLRVMLETSSLPGVTYSVFCIFECFFNFAQISFACAIAFDMYRSVVSYVDVLIDLQ

SAKRRYHRYTLNVLIFSVMSAVALALAGSKPHDSTIQSKSTSSSTDLTEDLILDEETFSP

CLNPTCR

>contig52247 Frame-2R

MSAGSDAPPLTTNGVSAIVRKLSFSGAVTDEMEEEERRDDEKEQSLDQPRQSEAIKMDAT

KVQIVIRLRPLDKSSHVTESDCFRVLSDVTLLAQPPKTSQSYRSTGTATSFHFTH

>contig52504 Frame-2R

MRVKKLNVNRRYKVGEDEVVAVSGDSDQRKCVSPTESQRKAAASNSSGSSSPTDVQQQYL

SDQSPFSFHSCRNSQNYAVVETLIEPNATATDVVMHEIEAVQRDAMVDRLVETLRSMKPH

APEKVL

>contig52926 Frame-1R

MLEVIGMEGFKGMVASSKRPLIVTFRKLLPDAAGVIKASENIAGRSAEYPVNASLQIAVA

SASNQLLTTVIQQERLSNGYNQQQLHLNNNTIRGSQQPSSGLITASIPYAVIDGNCFNSA

PVQSPLMNDDVNLYSNLSPLNQSPREMMADLTGQTIPPAAMVTQNYNSIPKVNNGVNAAI

MSDQLSEKWQAAPLNSVMQHIPLEQAQNAITSKGGGSVLQSSMPTESATMSYSSLALPAL

GVSDSSQSDASIEELATFVARNDPLFPIEDLSDTACRVIGDVDTKEIASTPLYQRLSKSA

DDKVIANVDTKPKSLTMSQAIIPT

>contig53121 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54952.1|) 2e-08 NOT\_ORF

MNRVSLRTSELHSDHVSYFTFEMAQCVAKLC\*TRFLN\*STRGAVVMAYQAFEG

>contig53459 Frame-0F

MTTPGAKSSESEQPAIPGNTNARAAAEPSLPQIYPKPVTVLVIGMAGSGKTTLMQRLTAY

GVDAGLRNYVI

>contig53796 Frame-1F|Blast-SUMO ligase, putative [Phytophthora infestans T30-4](gb|EEY57558.1|) 5e-10

MSATPPQMLDLRARLNQLRMPELRNILVDLNLARSGRKSEL

>contig53891 Frame-2R

MWRPTRQTPVKFVLWGRDRCRIHFSVCGRNIF

>contig54043 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66264.1|) 1e-37

MEQKLQHAKSAFATGELTDLERFELRDLQKLVNCSVCQDRRKDVIITKCFHIFCKECIEN

NLKSRNRKCPTC

>contig54421 Frame-2R|Blast-nucleolar complex protein 3 [Phytophthora infestans T30-4](gb|EEY59642.1|) 3e-48

MSKKVEIAQLCESILESPEEAFKKNKEHPQQLSKIQQLQQLCHDPDFTVQRLSLLSQLAV

FLDILPDYRIRLESTEKGVEKKGRQNHGRPMKKKVQDMQDYE

>contig55192 Frame-2F|Blast-CENP-B protein; Homeodomain-like [Medicago truncatula](gb|ABN09791.1|) 6e-06

MTDDVRVALCKYHAENPALTQAQLVDRLQENYQLRFSQATVSNSLKRK

>contig55314 Frame-1F

MNSRRDRDQKLKMTQDAFTSVAVAFERSSHLKLRTSNRVAAAAANIAMAAQAQEEAASLT

RDLAMSFSHRARPCGAQNSIQKEQVA

>contig55585 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54480.1|) 1e-18

MGTSHEEYQNLAKKNQMDDLHLSIVKLRDRVSAIQRNQDYAKV

>contig55897 Frame-0F|Blast-succinate dehydrogenase iron-sulfur protein, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57141.1|) 6e-23

MVLDALIKIKCDQDPTLTFR

>contig57110 Frame-0R

MSSRHEWKAKQFLTLKKNLFIIHLKLYKINTQPIFCVRKVRLPRY

>contig57239 Frame-2F|Blast-cyclin-dependent kinase, putative [Phytophthora infestans T30-4](gb|EEY54371.1|) 8e-06

MDRYDRGDILGEGTFGIVYAAVQKRTGR

>contig57284 Frame-0R

MMINRVAIESPQCNTKILSISA

>contig57806-0 Frame-0F0

MMPRSILKTLSAYASPPRPNCAARSDLKRKPLRQNSGMRRRVRFSPFTKPRGESSRMLLF

A

>contig57806-1 Frame-1R1

MPLFCLKGLRFKSLLAAQFGRGGLAYADNVFRIDRGIISLLHSRLKFSFSFC

>contig58865 Frame-0F

MVAKRASNSSRSEGVDLLDENNEMIDVQGFLLKDCQAMS

>contig59372-1 Frame-0R1

MDALMYRCFPTCASANARSSSRRSSKLARAMFVPNKSLYN

>contig59398-1 Frame-2R1

MRRPPLINDFLLLLLSAANAMYSHLPSHTNCCAVSCGD

>contig07316 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68702.1|) 1e-103

MPIMSPDQTEEDVRPSHVLNSRLSNFNHFAPTSSGGLGASQVANDSHAPRPSMMASLLRP

SSMMRSTVVTDLSNNFSESKLQDARVQIFKTDVLMEGQLLKKGESGLQSWKNRIFVLRGQ

ELSYYTIDSKQRYGAIKGAWDISGATVDRQDNSSFCLKLANGSTRNLAAVSVHVLMDWMT

AIAVAAEARVIAPSSNLSLVDQSRSTHVIFVRHGHYNTSPTPSTDLRGPLTELGVQQARA

TGTFLYKYLSDRMVLKRYP

>contig10972 Frame-2R

MWAPIFCGAGQQKVAATVNGVAYYVVGIPLAGILGFYRS

>contig11100 Frame-0F|Blast-acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase [Phytophthora infestans T30-4](gb|EEY53465.1|) 1e-108

MVGGYSALDGDVIPYGLVVGNRAKLAGLNLVGLRRAHVARNNIKMLLRVYRYVFGMPSTK

TTGFAPPLDLAYKDTICERALQAKQFLVREGLDSERIPQVDEMVEFVVTSPQRLQSSLCL

AKVANTPRSSDNNSLASKMRKR

>contig11438 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67962.1|) 9e-53

MLADLSLSFTSKTLQFGRVDVDKWSDLAVEHRINVSTSSWQLPTLILFQHGKELGRLPSI

DGNNKVTKTVLDRARLLMAFKLHDLKDGKRANFAQ

>contig12817 Frame-1F

MRLNYAVQATTETKAIVLNHDRANFCCTKGFTTMKLRSDSPDAGEERIIFNLWRWKKSVN

WMDIWVADNVPYLTSRHKSEVEKWLTWNLSLKELLKRLKFSKLTAPDAIRTKIVQLDHYC

NLIDTISSAKTMNKIKKNRLELLSLLGGNHASEKRKVLAHVWASKRIPLEDVFTALKMDD

LDSLKKLILINSGQATLEFFVRLFFASHKYGQEEKELANVFLKTYDHATLVHILRDGYHI

KSAKVFQHR

>contig13887 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY65269.1|) 7e-68

MMHVIGATVPHYIIGIALGAGIFGMFMLCEGFMVPRESIPTYWIWGYYLAFHSYSFESFV

FKQFEHETSSVARNVLTKYGMENVHVERNMLLLIGYVFAFQTMFALILWKFHTGRR

>contig13960 Frame-0F

MDRSRARTRQHTINALPTTCENEESAKMMRESHLRLVKSTHKKCSSYFVVHCAAHNSCNF

SSERINKMRMLCKNCNRSHCNKDDDKLFRMI

>contig15250 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63823.1|) 1e-42

MYVFKVDSTTGLLQCTGKSYKINTAVCLHVAEF

>contig15702 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69573.1|) 1e-24

MLLRKAGKAIRSLGQTIDRVGVLLEGKLTYTEHLNPSTRAIKNLGRSPKFGDGVFVAPNA

SVIGDVKV

>contig17164 Frame-0R|Blast-tyrosine-protein phosphatase, putative [Phytophthora infestans T30-4](gb|EEY57974.1|) 4e-46

MHGIKLLQFGVPGNKEPFVDIPEDGIVAALKAVLDRRNHPMLIHCNKGKHRTGCLVGSLR

KVQRWAFSSIFDEYIRFSAPKPRMMDQQFIELFKTERVLEEESLVEHLPSWPGL

>contig18763 Frame-2F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY53225.1|) 0.0

MAKTSEQRRIPSHESGAALMAFGPEVLHSYMATRFEAALGRTMPQMEIRYHNLSISADVV

VVEEGGTTSELPTIYNTMKKFLAKVTAKKHVIRNEILHNVSGVFKPGTITLVLGQPGSGK

SSLMKVLSGRFPREKNITIDGTVTYNGMTQTEFRRRLPQFVSYVTQRDKHFPTLTVKETL

EYANRFCGGEMFQRATEKFAKGTPEANKAALEAAQALYAHYPDVVIRQLGLENCQDTIVG

NGMIRGVSGGERKRVTTGEMEFGMKYATLMDEISTGLDSAATYDIIKTQRSIAKTLQKTV

VVALLQPAPEVFELFDDVILLNDGEVMYHGTREQIVPYFESLGFRCVSGRDVADYLLDLG

TNQQYKYQVELPSGMPFHPRQANEFAEYFCRSKIYRDMVEALEAPYDPKLLENISNDIDP

MPEFHQSFWENTWTLMERQNKVTMRNTAFLKGRSFMVIVMGLINASTFWNVDPMNIQVLL

GVLFQAVLFLSLGQASQIPTYMAAREIFYKQRGANFYRTASYVLSCSVAQVPLAFIETMV

FGPLVYWLCGFVASTSAFVIYSVMLFLSTLSFAAWFFFIASVTPNLHVAKPTSMVTILIF

VLFAGFIVAKGQMPDWLVWIYWINPFAWCLRGLAVNQYRSSIFEVCVYDGIDYCSDFGTL

FGEYYLSLYDIPSAKSWIIYGIIYLLVAYVLFMMLGCLALEYMRYESPEHATVVKKTVSE

PEDENYVSVATPKKSNRELDGEAFVVEVKEREKNFVPVTLAFQDLWYSVPNPKNSKESLN

LLKGVSGYAMPGSVTALMGSSGAGKTTLMDVIAGRKTGGTIKGKILLNGYEANDLAIRRC

TGYCEQMDVHSEASTFREAFTFCAFLRQDSSVSDRKKYDSVEEVLDLLDMRDIADHIIRG

SSVEQMKRLTIGVELAAQPSVIFLDEPTSGLDARSAQLIMEGIRKVANSGRTIICTIHQP

SMEVFYLFDQLLLLKRGGETVFVGELGEKCCNLVKYFESIAGVPPLPAGYNPATWMLEVI

GAGVGHGAGTTDFIEAFQNSKEKRTLDANLAKDGVTIPSPAFPELLFTKKRAASSMMQAR

FLIVRFMNMYWRTPSYNLTRAIVTFLLALVFGLLFFDSDYTTFQGINGGMGMVFISTVFN

GVVSFNSVLPITCEERESFYRERAAQTYNALWYFLGASIAEIPYVFYKWLYLYICVVLYG

RIHGI

>contig20197 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56440.1|) 1e-158

MKAPLADELHVVRCALHQRLKHKLSRVISSDCVRNANESAKDWGASFKLEQLFERTVQFG

ENQSGLLLGAAGSERNVIVKRAMHNLRCKFGKFTLIYLNGMILQNELEAFRELTAQLTRA

TAVKHPVLSYWNMYEYLRGLLIAKAKTGDHVIVILDALEQFVLETSNKKQLLLYNLLDWL

QDFDIKMGVLGVTDNYNVVDNLEKRVLSRFSNIQIVIERPSFVQIQRDLFCMLSLDDFNW

TSFSTMQQPSVNYIALLSQSLKELQSKHNKVLTSLEFDYDIGKPQAFFIRLVFAAVCYLD

VNTPLLTAQNIRRARNLLEQDHQLAVLRSVTDHGLALLIGMGHLEKADQCVFTLEMVYAR

WEIFLRQHDMLVQLPTRSEAQKALEHLLQLKLVKDAGDAFNTGRGGDFHMRLGRAGSLQP

EFRVVHLIFAPRTLKGMLLNGSIDCSTILREWALNGN

>contig21169 Frame-2R

MHTQRRSHIFTRRSLNIFAEKNSLGEHFGHTLADVLKSVATSNSTTGKSSLTVPTPGVPQ

NQ

>contig21183 Frame-2F

MSRRLQILALVVRLLRNRSLWSLKFPLFPLQLLFTMSGGSLTIS

>contig22591 Frame-0F

MNHRNHVVRRGGTSVSIPGLNVDIEMLVQSTQGSAMHFGRKTTGEKFHGWLWKKCGRFSK

WRNQHFVLDGALLTYYDAFPTDQFVSESSLLPIQGDTLFTTKSESTPAGAVRVAHVETSS

KSKIAFKVYAVSGKIIDVRAKNETLCQQWVDRLNEAAVLAKRQESLNSSTTSTVSSVISL

GYSDSELDVQCNIVDKSGWIEVGDRKSKRARFCVLQGTMLTVYDTEDAWAVPLRRAYVTN

AEKLSEASCEFSVSTSAGKSTKTLVCKARSQDEMHVWIEALQSAFE

>contig22692 Frame-2F

MKLSRAYIAIPALFMLMDTSTTALDVKMHGVNYNMRKGADWEPDELRCKSPDQLQRDMFA

IKQVTDRVRIFSLVDCNQGEYVLRAAKTAGLQVHLGIWTTTSMNYLLRERDALGRVIDMG

LYDSNIIGLQVGSEAIYRREITPETAINYLNVIRDYLRGRGINTPCTIADVIDIYIEYPE

IPAQVDYYNINIFSYWEGVDVNEGAARTLDRIRAARKMAEDTGKQLTVAEVGWSSGGYNI

TTGESTPEAQAKFFADWYKVATSINLAYYWFSASDSLWRVTNGGYSVEAYFGIFQEDDTM

KSNFQALTIGAPRYYQAIRSDVTNLLLTESNAAVSITGTTNSPLAKEHQRWFFDPTTQQI

RSQSGDRCLDGYQPWDGGIVHCYRCMDNEMNQKWMYESTTGKLKHGTYTAFCLDVDPAQN

NKVQLQGCSPNNPNQRFTILDGASI

>contig23215 Frame-1F

MDSVAYSSILLGLLPEIMAKALTHRTMKAAGEIYLVPLTVEQAQSGRDALAKAIYASIFD

WLVAGINASLGAKAQQTTSTIGVLDIFGFESFEHNSFEQLCINYANEKLQQKFTQDVFRS

VQEEYEREQITWAHIAYADNSETLGLIESRMGLLALLNEEIVRPRGHEEGFVSKLSSAYC

KHKTLIEFPRISKTQFAIHHYAGTVLYDATGFLEKHKDALLTDLSDLMCQSHEPFPQMLF

QVRKEMEAAAPKHPLSSLGIRKAGADRTVGMQFKKSLNALMTTINDTNVNYIRCIKPNCR

KSASLLEDKMVATQLRCAGVIEAICIARVGYPNRLVHGEFAAQFDLFLTKEQQQQLQNDP

KTYGVLCCRDVVEQFHLETPEEYQMGQSKIYLQKGVLETLEYAKAQKLYAYVARIQARWR

GMRARVEYCNQRIAVRMIQRRVRVFIARRHFQRARVALALIQRVWRGLR

>contig23909 Frame-0F

MVDLHLYIGRRLEDSCPDVIRTGKKPYTLRTMTVADVHYGAFPNELIDQENEAIQEIVAN

HPHVSPLIKVCDNAYKAYARTRADPSKHSIHRGKELVVKKVHPLFQQEYVLETNKAEKAA

YIDSLQTFRPPQTIFEIAVGAHSSAKRSSPGVQMMVKKRQVHGKIIHIETIKGAAKEKTK

EARYMDAKAEESVLASGKKVEMIKSMDRVNKNESVEATMEEGLGFKKKSIFLSKHQRKQL

KKRVAAGENEVDVIQEYAVSNESTKIETGLPEFDERGGHAFKDDDNYIGYMKDGESTIEG

FLATNADGGKVNAFAEARLEEAILDVNPDEAIEMNKKRRILHWDVRKKKFVKTTAGELTS

QGTLKRRNESGVNFRKKQQFGEVYRKWQQKQHKRVAGGGMEVEDDSGSQRLDYRNGRKPR

NGAAMTNRSSVNKHAKNELSTEGKIRKEEKRKARSRGVKVTNGIRSKRGKGNIKGKSHGA

PTRSKAIIKKK

>contig23996 Frame-1F|Blast-alpha-glucosidase, putative [Phytophthora infestans T30-4](gb|EEY61906.1|) 0.0

MTWVHYYFYRAFACLGYLALVSSLLGSSTSTQGTHVKVGGGYVDGPGYSVTSASENEGVL

TINLALNKPSTSTPYGADLSALVVTVFMTEVESIRVKIVDMKKQRWEVPKALFSAGTLGM

NDTATSASEEPLYSFHYTKNPFAFQVVRKFDNYSLFDSSSTSLVMKDQYLEVSTAINKNL

SIYGIGESTRDNFRMSTGDKQTLWARDEPSATANVNTYGSHPFFLGVNSAGQAHGVLLLN

SNGMDVTLEKKSLVYQAIGGVLDFNIVVGPTPAKVLSQYTKLIGRPKLMPYWAYGFHQCR

WGYDSVDALHTAVSEYKRNKLPLDVIWADIDYMKRFHDFTVDPLNFPQARMASFLDKIHA

DGQRFVPIIDPGIPDDTKDYAFTKGLTMDIFIKDTSGKPYLGQVWPGPTVFPDFFHPKTK

SYWSEQLQLMYNSCEFDGLWIDMNELANFCPGTSCVRNSAETCPKQGNSSTMTVCCLTCT

NKKSRYDSPPFAIHNAGTYDAITSKGISTSALQYGGIRQYDAHNLYGISESIVTNAVQEE

LTKKRSFVLSRSTFPGSGVHAAHWTGDNAATWADLRWSIPAILKFGLFGVPMVGADICGF

LGPSNMELCARWTALGSFYPFARNHNNLDAPPQEPYVWPEVAKVGQKFIGMRYRLLPYIY

TLGYHAHVHGIPIARPLVMEFPTDIATHNINYQFMLGSALLITPVVTKNAKKVTGYHPSG

VWYDIFSYSKILSSGGLVTTKVSLYDMPVHIRGGKILAMHQAALTSTAGPPNIL

>contig24672 Frame-0F

MVVYPKIVPSAYASIRALREVLLCSLPIELWYRKKEMDAAPYSMAPLHQLAQVHRNVTFR

EIINKKAIGFDAKVFAIYHSHFDSILFLDSDNVPVRDPSFLFESQEFTDTGAIFWPDFWH

PKHSIFNIHSQSLLWELLDQAFVDMFEQESGQLVIDRRRHGAALELVKFYSFHTPNFFKN

LKLVHGDKDLFRLAWLKLKLPFYMIDVPPAVAGKAINNSFCGIAMAQHDIYGDVLFLHRN

TRKLTGELKRVHPKTATSLPVTPERL

>contig25091 Frame-2F

MHQPTRKVYVHKDVTGCSYRVENGMTDGDQLPVSTIFR

>contig25253 Frame-1F

MNGNKAHSVHFDSSVETELGSGRSLALTSVAVPAVASDKAPGPAAFLTKRNSVVRKIMMQ

TIGEQCEDTTLHAVQSFVSSIENYCASTESLMSLGKALYTSLSLVFVVDESMRVILWNDY

AVKLCGYSRDEVAGRNLHHDLQYLVPPSTATVLANALAHCIQGSAVASVRLEFITRNQTK

MMLLGSCSPLIGSSVRAEMLVVAQEFTHLPFAMVSSEALAATPAVLNQTQETPTEKSLVT

IAVPSVPVVVQKMPSVTASVPAVVTSNASTIPGWSEIAPNYSIECVLGQGSYGQVVRCKH

LPTGEIVAIKKIQNVFSDPIDAKRILRELCILRQLRHPNIVQIREIIAPGDMNRFQDLFV

VFEYLPSDLEKLLHSPQFLTAEHLRWLLLDLLKALKYMHSAEIVHRDLKPANVLLNLSPV

AIKICDFGLARGLSSSASTTGRKRKRLSDGSTLDESTLQGVGVHPRTPAGRIKRQLTEHV

VTRWYRAPEIIFRDHDYSAAIDVWSVGCIFAELLSMQKSSVPSHYQREPLFPGVSCFPLS

PGAGQVALPQDSRDQLNTILDVLGTMEEDDIAEIADPDVQFYLRSLPPRPKRNLQEMYSG

AEPEAIELLTWMLKMNPRKRATLDEALSHKYLASIRSLEEEIVAPGTIQLEFDEKKMNVT

EIRQRMMCEIRFYHPTAGTAAAKSQPAVGITSKKPKQG

>contig25965-0 Frame-1F0

MGKISLGPVALRGRMYPVALSAGSRLWDLRRTLRKGQVALRSRQTPGNNPISPDRPLMPW

TSRSVPF

>contig25965-1 Frame-1R1

MRPRRATGPRDILPIKTLQIDNLCLS

>contig26160 Frame-1F

MKSSVPSWAVTPADMNRKANLKVEKEGKVIELISIGTRSCYVFGRSKDQSDVWLQHPSIS

RQHAIVAHNEQNRICIMDLGSAQGTFVNDHEIEPNRPQALMIGDRIRFGTSARTYLYQNV

ATEQAEIAALDPELQRMKHELKSFGDHSKSSQNQAIDAKEQRNKREAEIVAITAQMMMAS

KQGSESIIEKPENTKNEISEAESDTEDEDNVTLRYGLPTSHEVRLESHAKALACIAADAP

GARVATGSMDYHVKLWDFAGMARHVRPFRDIEVDDGHPLVAVSYSPSGDRLLAIMGSSQP

KILTREGVEELHFAKGDMYVVDMAHTNGHTHTTTSGQWHPNVRDQVLTSSLDGTVRLWHL

DGKQTFEKLINTSVLKFKDRRGRRCGVTTCRYNSEGTLIAGGTMDGQIQCIDPRKACAGA

ALTLSNAHADGGGDLGISSIRFTLDNKYMATRSCADDTIKIWDLRQTKASLKTFHGIEGV

FGSCNLAFNHNGTAIAAGTCIRKGTGQCGHVVFLDVHTPSLMEPIATIDMEVDESAVCVE

WHHGINQIFVGTSKGSCRVLYDPRQSTKGVLLSATKKLKVHKNDSGVRIDGAGKVYNPHA

LPMYRDETSGSSKRKYDKVRADPKKSRAPERPLTGPGVGGKIRGSSTFTQYFMSSHIRTS

FREEDPREAILKYAKKAITDPQFLGAAYDQNEKIDPRYQLAKQTLEEEKLAKEEETRKFL

QP

>contig26528 Frame-0F|Blast-peptidylprolyl isomerase [Phytophthora infestans T30-4](gb|EEY68840.1|) 2e-59

MLKELINLHFSKNIKGDYHCPVTYKVFTDNTKIAAIATTGNVYCYEAIGELNIKAKNWTD

LITGTKFKRIDVIVLQDPQDFSNREIKKFEHLRQAKSSISVRWHMQLFTDHVLH

>contig27017 Frame-2F

MDQLQREYLRDARRKAPATDYFEAKDCAEEHTHILPPASGSGDDVDPLDAFMQDIDKQVK

QERKAPSKRVADKPPVLNLADEEEDASCYMGGFAQS

>contig27435 Frame-2F|Blast-prohibitin-2 [Phytophthora infestans T30-4](gb|EEY55580.1|) 1e-154

METGKAAMENMKNMKMPPGSKGPATALVKVAVFTGAAVYGAYLSIYNVPPGHRAVVYSRL

DGVGHQVIEQGTHFLIPWVQRPLIMDVRTRPRTYASLTGTKDLQMINISIRVLSKPDRSR

LQWLYQNLGTDFDDKVLPSIVNEVTKQVVAQFTAAELIFQRDHVSRLIIENLKRRADRFA

IMLEDVSIIHLTFGAEYTAAIEAKQVAQQDAERARFIVERAIQEKKSTVIRALGVAKSAE

LVGEAIKKNPAFVQLRRLDAAKEIATVISRSANKVYLDSDSLLLNILHDTDQS

>contig27488 Frame-0R|Blast-small cysteine rich protein SCR108-like protein [Phytophthora infestans T30-4](gb|EEY64712.1|) 4e-16

MKLSFIAFLVGAVAVPVSVISLHLRLTMHSKIAEYLEQCEWEDKAVRCNQTYLFCLRTSS

TYGQCLKTNPGIGDRCCGVKHRGATWSRSCIGENVECKVDAKGEGTCQKKENRKALKMFD

HRKENAVDVP

>contig27747 Frame-2R|Blast-transcription factor Dp-1 [Phytophthora infestans T30-4](gb|EEY54594.1|) 7e-13

MSADGTPESVILSSLIQRPSKSKVPAKGVGKRRAGAGVNRSIKRVTRRELKKLVEMDLEE

KDDVSTVPVKKEAIG

>contig28221 Frame-0F

MAFNPEGSQLDVVLTSFQTSRTTVFVQRLMKFGYDRQDAVSVATAFVEEHFALCEEEFKT

PTLKTLFALLEMLFPYVQSYFGLKTRVEPIEAMELLFEQRQDELMALESIYDDKLQITVL

DDVFKSQLLEFKVSDSLRLF

>contig28355 Frame-0F

MRRRQNTMDLLLCGKQYAIILTISEEEEQTDEMESKYCGIFDNDAPLWDEWNAPMINLTS

RLCVKVEKKFAYDTAPRAAYYHHPFLLLDQADQTTVYNMGSLQLVQAIPLEVPYGVCAAI

NVASATVGGWNANFRDDRPATLFTVSPPFVVQKHEMLPLSHQVAASIGNRRLEDAVALCK

LCPDESPLSNDNQRDLYADYGFMLFRSRNRQQAMNFFFESDIDVMEVLLLFPRNLLPRTA

SALRNSKSENGVLEGDELVESLLALIGYLRRKRNTYLRNEDNVSAIECVSYSGESALEVV

DTMLVKCLVLMTEKDGYREQAKRSLLEVVTGQNWCEIGEAEVFLRAHRRFKTLLAFYSAR

KLHRKALELLEDLERSAASTAVISEATTAGRNNNLSQNTNELQSSHEYMVLIAQYLRRLG

NKHAELVFEFSRRVLSVNPELGLSIFTQRDVAESRQDIDHAAVLQHLKSCPISASNSNEL

HLEIEIGAEADVPSSTMPLISSQMLCIEYLTQIIYEGTCHLTPRLHDEVVFLLLALIHAN

TAHHNLTSRVESQRGITRLLRRKLLQFLEFPGAVYHPERMLSRTPIEMVDEHAALLSKLG

RHLEVLQLYAITLNDAALAEAYCNRCYESKTAGSSIYTTLLRIYLGPHKHTEESALSVVN

STHPHQISSSESQNEAVNAAINVLNKHAERIDVSTALELLPPNVLAAPLAAFFRCVLEHR

VERFRNGQVMKQLSKMENFKVREQLTTKRKESVTVWASQCCQSCGKKLGVGTFVRLPNRK

LLHYACQPIS

>contig28427 Frame-0R

MVSQPLVEDNTRLLSMTPLQSFDSLPPTSPRATSDTESLPSMNKLLLGSTSAGASI

>contig29514 Frame-1F|Blast-transaldolase [Phytophthora infestans](gb|AAN31490.1|) 1e-169

MAVSPNKKFREASQLDQLKQYTTVVADTGDFDQIKKYKPQDATTNPSLLFKAAQMDQYSA

LVDDAVAYGKGLSADLSEKERLGFVVDKLAVNFGLEILKVVPGYVSTEVDARMSFDTEAT

IARAHRIIELYEKAGIKKDRILIKIASTWEGIQACRHLQKEGISCNMTLLFGFAQAVSCA

EAGATLISPFVGRILDWHKAKTGKTSYEPHEDPGVVSVTKIYQYYKKYEYETIVMGASFR

NTGEITELAGCDRLTISPALLEELNTATAKLVKKLDPETAIKAYTGEKISYAEKEFRLSM

NEDAMATEKLAEGIRGFSADIVKLEQILKIMLSA

>contig29756 Frame-1R

MKALRCVLLLSSVALLTCVETAVENAVATSQSLGHRSLLQSTMTSDSDLADERLLQGLIE

KFKGTWLGRMLAKTWIGKWLQPEVYLAHASNKQAAITNLFPRFNKKSLETSNPFESTKFT

TWYNIVNKQFKTNFRDGHMYMLETLKTTFGELKLV

>contig29947 Frame-1F

MFFSERINHKQDGSGKARSTAHGCGCWNTLVKLIFNFARRWGVPAKPPTPMLMHTRTRTW

RFIFVFHKVWNCLTELPRTLAWIMRKV

>contig30581 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61862.1|) 1e-60

MPTVEPLVTLDAVVTDPHLHAMFLQHLSSSDAKGFARLLFLVSVDEFKKGCVFDKHSLEP

ESDAEVYRQRYASKIIAKYMSPDAFLDIASENLRILNKSVWNFGKLLRNDLMLYSGLAAK

TDLFQEAEAAVKKALQPSFSQFVATPEFAAL

>contig30897 Frame-1R|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY53508.1|) 3e-14

MSAAVADVVAPEDRATAFGILFASLSVGYCLSAFAAPFFSR

>contig31418 Frame-0R|Blast-dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69318.1|) 1e-70

MALYYAPAFGVFLIARCLHRNLCILHLLKLATAVISTFALIWYPICAYTSLGESCLSSMA

QVVHRIFPFSRGLFEDKVANFWCITDAFFKIRRRVDFTAQMRLCVAMTFIGFFLSVVDLL

RRRPTSLRFILSLAICSLSFFLFSF

>contig32873 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58299.1|) 1e-109

MLRCFRGARERPHALQSKGYNIFQSLKVTFATTTSRIVGTRIFNARDWIDKVAPSLHTFL

AQKKHLLVPNKFKVPHGDPQWPQKAWGYRLGLYCKMLRARRSSGKSLPLFALEELEALGF

PWTMWQYKWDLLVLPSLIRFREINGHCDVPWNFVVPEGDNAWPKCLWGLKLGYLVRGIKH

SNTYRAQVERSHEILMDIGFSTQRWDTRMWDNKIFPALKAFKREFGHCNVPNYFIVPNES

PWPEATRGLRLGKVIINIHSVGNYERMTSRDKEKLKELGVVWSQFDDRWTNRILPALRTF

RQLHQSGWVPASFVVPHEEPWPKASYGLRLGNTFRNVRYYDAFSSYVERDREQLNEIKID

FKVDMKSAR

>contig33045 Frame-0F

MASPVLEGNVHPTSAARSCRSFLWQLQARESLSS

>contig33122 Frame-0F|Blast-glutamine synthetase [Phytophthora infestans](gb|AAN31463.1|) 0.0

MSKLDRAVYDQYMTLEVPDSVTLAEYVWIGGTGQDLRCKTKTLTTPVTSLADLPIWNFDG

SSTGQAPGEDSEVLLRPVAIFKDPFRRGQHILVLCDCLKPDMTPIANNTRADAARVMKAA

TNDEPWFGIEQEYTLFEKDGVTPYGWPKGGFPGPQGPYYCGAGAHSVFGRVIVDAHYRAS

LYAGINVSGINAEVMPGQWEYQVGPCTGIESGDHLWMSRYILLRVCEDFGVNVSWDPKPI

PGDWNGAGCHTNYSTKAMREEGGMGKIIEAIEKMKLKHKEHIAAYGAGNERRLTGRHETA

SMDTFSYGVANRGASIRIPRVAEAEGKGYFEDRRPASNMDPYVVTSRIIKTTILNEA

>contig33629 Frame-0F|Blast-serine/threonine-protein phosphatase, putative [Phytophthora infestans T30-4](gb|EEY61625.1|) 4e-82

MRTADANDDGRIDFQEFAQRFEVIFTDLGPKRDNGVAKHRATVSDLLKLPNASATPAKDV

MLEPEPLLIRREVPRENQSTFTRHAATNLDVETMQALLQIGKTLFARRGSLQYHFYHFDK

NQDGVLSHSEFQSALKQLGFAFEPQVLDRIMAAVDKDGGHSIDYKEFVAAFSVHDLKEHE

ALESGNLSWQNSVLQQVSNVFYQHRIHIRNAFRMFDANNSGT

>contig34189 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53335.1|) 1e-106

MLEDPVMLTTCHHVYCFECLSTWSHSQALHGVEVPTCPLCKKSFQEVYANVRSEVDFELL

RFQGRCIRDQTGRLRLKDHNDCNQERLRRRSLVYRRHMRLARVANQPIIDSNAFPRMHKV

KGEYEVWMKRELRACIGRDVDVTVLIAIIECCLNKVSQCGPQHCYSELQNALSPFLYDDA

SHFVRELAFFLGSRLNVDAYDDAVEYRCESASECSNALCCGG

>contig34398 Frame-0F

MKNELDHQQALMRSLYIFIDALRDIKSIQNFTTENSDVLAAVRELCGLSETACVVQWQDE

AWRHRLVPTMQRLCLCILRLEKLEAQQKKVESQEVNYPKAPAGLLSLRDYSVLQAAVEVL

FCWGAHPRVSAGVLMPIEKRKPTRTLEISKDVLMWGTRRYKQEIGDSNVNTEETMKELLL

ISQTLFQLLTLPQLFPILLPKYVVELLALLIYGEVAVNTAQRTEFTRLRILMLQMLPLRM

SMSSVRAVLGQVSPLAKDQLVGQRFKSQCGRILSRLLMKDGGIVATIEMLLEAVEEGNTQ

ARTQVASLICQCPSDADPITYATALCAQMRELLLTVITSEMGSRSNLLGEMASLLADQLA

NRHPEIFDAQILSALFYPLLIYEDSRLDTDGLKGDTSEEALNRCVSIARLLLCGPPCSQH

FLKALTPLMRPFLHMYAFASSSKSFLKAPLRALLAVWIRSCSNAAFLLQLAVLPVTISLR

PTLLACGFERNSDRGLWEPLRKFGAGENGGLSLRLQSSITNRAEELDTATSLKFLIQPIV

ELLGDKELESSNVVGELFSLLLSTYMNLRKRGEATLSDLNTSNENLRTPSFTLHDSLKNS

LGAEGVEMIILFLLALIEYLGPSVLRSAGIILQCVGTVLETFDTPSANIVDEVEERESLR

KTASAEETEDESEILTICLGVTLTILEAGSSHRCESEEHQLRAMLPVLQSLSCHPRPEVA

ELASNSRVHILSRRAKDAV

>contig34475 Frame-1R|Blast-GTPase [Phytophthora infestans T30-4](gb|EEY65768.1|) 3e-45

MLRVSSMLQGLSAVPFLRRGPLSHLFIRLNNSFISNKEDGDGNDDKLDWNALAIVKDQSD

EMTGKTVEHVKQKVRVQRAKHSKRRFVDRIRVKATGGHGGNGCASFFSESATRKRPNGGH

GGAGGDVVIEASAQMQNLANATHHFKGGSGTNGM

>contig34800 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64319.1|) 8e-61

MAFIEVKDNKALGAALSRHHTLLFGRRINVELTAGGGGKKSEIRRQKIDSLRSKQSIVQV

KKAKALIQKRIDSPEYKLTQEDVDDRMIDFLSWFDYETAKKALDELDRCVSDNVNNRKAF

FMGILKRFRQTDGLE

>contig35414 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64179.1|) 5e-35

MARGKADRALTVGKKLEIIDEAERTGLLSITAQKYGVKAGQIRDWKKNVNRLRATDPTRL

VCASTIQRGHLVFNETYAQY

>contig37272 Frame-2F|Blast-3'(2'),5'-bisphosphate nucleotidase, putative [Phytophthora infestans T30-4](gb|EEY70569.1|) 1e-123

MASTAPGPSLRPLLAACFSASVHGGCVIREVVQQHVSLDLVNKQENVYDPQTIADRRSQQ

RIIYALRHAFPQLTIVGEEGELASPASQDVVHCDLQVLDAVVDLNDHEAFDWNDLVVWVD

PLDGTKRFAAEIYDEVSVLIGITYQMRPIAGVVHLPFHGKCGVTYWGARNWRLPQRTRRN

KRPGVTCEVYNAVAAVPAPPSGLHSFVHGVRFGGQGYAFDGPFSCHDGRGNWHDGTWCNH

WA

>contig37508-0 Frame-1F0

MRGGMKKAVKCITVTEMFFNVQLIAAFSHKVRR

>contig37610 Frame-1R

MVVAVLLWLLVLLVGSFVVALLSSAKLRRNFFIWLSYATITGWYYFRVFQKKYMSDDIEK

DGEAASMSPPPSANDKPVKTSQPCAAKILRHPNFGNLEPRDDIEKRQQGCQGESGRVFES

DRFLNCSNAADEGAKCHENEACFTENVTESNGCITALSKGATRRTYIGRKKPASWAD

>contig38804 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66541.1|) 1e-35

MTTAHRPTWHAAVGQSNEGGWHAGGKNSDQLSARDLPAHRRLKMRQVGQGTANEVELLDL

REELERKEEKYVREKDRKVNTA

>contig39533 Frame-2R|Blast-ribulose-phosphate 3-epimerase [Phytophthora infestans T30-4](gb|EEY66420.1|) 1e-107

MCHSCVCKIGPSLLASDLSCLKDESLKVTAAGADYLHLDVMDGHFVPNISWGPPVIKSLR

PHTKAYFDCHMMVSKPEQWITDIAAAGGNQFTFHLEATQDPVALIKQIREAGMKVGLAIK

PGTSAEAAFPYVELVDMVLVMTVEPGFGGQSFMADMMPKVWTIRAKYPTLDIEVDGGLSP

STIDAAAKAGANMIVAGSSVFKAADPKAIIL

>contig39757 Frame-0R|Blast-eukaryotic translation initiation factor 5B [Phytophthora infestans T30-4](gb|EEY54719.1|) 0.0

MKLEYRLPGLLVIDTPGHESFTNLRSRGSSLCDIAILVVDIMHGLEPQTLESLRLLRQKK

APFVVALNKIDRCYGWKTMLDMPVQEALKHQNEHVIREFEDRMKSIIVEFAEQKLNAEVY

WRNKDLAHTVSLIPTSAISGEGVSDLLMMLTRLTQERMVKSLAFIDILQCTVLEVKVIEG

LGTTIDTILVNGTLEEGATIVVCTLDGPVVTTIRSLLTPHPMKEIRVKGEYIHHQKIKAA

MGVKICAQGLEKAVAGTQIHVVGPDDDIEELKDSVMSDLTSILDSVKSARRGVMVQASTL

GALEALLEFLRTCDPPIPVSCVNIGPVHKKDVMRASVQLEHQPEFATILAFDVKVHSDAT

ELATELGVRIFTADIIYHLFDQFTAYMDNFRSARREEFAEVAVFPCVLKILPNCIFNKKD

PIILGVDVEEGIVKVGTPLVVPSAGGLLVGKVGSIEREHKEVDRAKKGASVAVRIDNESS

VMYGRHFDHKNQLVSRLTRESIDALKENFRDDLQKEDWQLVIKLKKVFDII

>contig39821 Frame-0F

MLLDLMQCYDKFHEPLPRQCAEFQFQLHAWLGAGGGVFDTKTLVDYAMKKVDAFATHLTH

TTLENCYEVLSKHPFYGPEIQATPLNLEDNVSSPSQIPLQAHQAGYDAFMTGYVFLRVCS

GLGVSNECIASLEKGSDGAEIISNAALKTLRNALFVSHFVPTFVLHLPGPYPLPTRTP

>contig39894 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66999.1|) 1e-83

MNKSRGQVLRQINSLLDKGDGAAIVLTWKHTEEIEVVSWENELCMPPPEGVYMPLENEWG

PARPSKISSVSI

>contig40656 Frame-2R

MPSSIAFSHTSSVTSAQTVPLSKVEAVTSVNDDFVVHFQKQKIGLHLETDLFSNHVFVVD

CDKDSEAAATWNKRIVPGILVTSINGVSVRDFYFTDILSEIQRANRPLTLGFTHPGRDVS

FEYRRFQEPPNVLRCLLSRDSKTLIKALCPLDNNAVVSAVLQCDFIARAASVNERGNGSS

RVFVPHIEIEQVFVPAGSVIYEINDVVV

>contig41163 Frame-2F|Blast-thioredoxin H-type [Phytophthora infestans T30-4](gb|EEY55747.1|) 8e-19

MSLQTDVTTYQQLSSVVRVTSETQWEQLWQQNRESSIALVVNFEATWCKPCVMIAPFFQA

LSQKFPFAIFAIVDIDELE

>contig41398 Frame-0R|Blast-hypothetical protein PITG\_05634 [Phytophthora infestans T30-4](gb|EEY69402.1|) 5e-38

MKNRWERKDDVRSTKKALAESKFKCA

>contig41475 Frame-1F

MEPEQIKVTGPELHDESIQQLWRLEQENDRLNSCVRRFEATKIDLEHKLEQAEEKI

>contig41707 Frame-0F

MIGSRFLALLMVSMFGVSSSTLSLSDCIHAFNASKLFTLQPEGDPSLVWFEYERFLLSPD

RTTPLLLFFISSSICSGGEVFEENFNDEKLFLVDQEVCLRHQMLVEAAMTLAAETVSTPQ

LPFIRIDVQTWPEMLQY

>contig42140 Frame-1F

MPKNGYYAVAVGRSTGIFTTWDECNEQVKRFSGCKHKKFKTQIEAQAYLDAFTRLQLETN

TRCPPKASAEVEENATSSLALSHTKIESRVPIDRGTESWYAVARGRKTGVYRTWNDAKRQ

VDAIPGARFRKFATKSEAKEFVSQHVAAETRDPDPKDPNTLVAFCDGRSALKTYY

>contig42508 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55546.1|) 8e-62

MPGGSLFMRNAPIPLDVCFPDGVIPDDVELSPLEGINIDMTPLPAKDSVFVDFSKKGYD

>contig42610 Frame-2F

MESQNGQWHDASRFSPLRNSGHSNPYTGVDREQMSFSSQVNRYSSRDQYQVPLPRPGRRT

RWDSMPEERSNNNFEDRRW

>contig43271 Frame-0R

MSLISKKSMATSRRGASFWGIIVSTVATCSPSSAVHYAELNATTSSNDPQLIVLSAYIDG

ASRPRRTSKCFRCNGVGVRYFKSHKRSYEEA

>contig43565 Frame-2R

MKKQDNQEVMQITENPILVSPLLNGCTEKVETKEKESLKMSSHKFTVRSIERPLPMEEIL

VHPMLSHSTSGDWNASNQPLDDNFSSTKAANDESSVVHQAAALQEPALFAHGQEEGSVAT

LTSVPVQVDIGFPPIVAASVKDDAIHTNSIETLPVSQAQIDGEVLPVPVDRDQVDVLATK

GSGRWGKRKRPVHLDGPNGYLWE

>contig43749 Frame-2F

MELVRSLAGMLAVAILMCSGNLCITASKQGDKIPYIITTVTLLIEILKLTFMLTTIAITE

TPPPARFISIEAFYYAIPSFLYTIDNNLNYIILRYMDAATLSMLWNLKIVVTAVLFRIIL

KQTLSDLRMAAILLLVVGVLMSQSNHVRQMQEAMITKDGSGSEMDMQSMTADKSAKDLGI

GVVLVLLGIILSSCASVFTEWTFKRKSSCPFLWQNLQMYAFGVFFNATGVVLIDRNEVLL

NGFFHGYNNWTLTVVVINSIGGIGMGLILKYIDNIACVFSHSMAMMLTMLFSMLFFSFQP

SLEFGCGFTVLIISMYIYHHPQAHIDTIHSTNATKTSAIWTAKEETSNQNEMVSSSDEKP

TSQPRERRSDEDTETDTISIALSSDASLSSRQPTSMRGLQLKKSQYAMLPSDSDDLESAR

ANAKAMDTS

>contig45336 Frame-2F

MEGPVSSIKLHQTAVAPDLAISLSTFDKRLTRRTTSSVSSGSCLDSIDSTRTRDVAGDEM

KSSIPPAPLSIDEDERLATSARIHSVQSASNVLALASRTRSKDNLLASVPIRRYNSSTAM

VHASLERKRSLGHSTAPARVVKGNSGDVRTGFARIYFENNTFTSSTVFKLVSTTTVLEVR

QSMAA

>contig45534 Frame-1R

MCNQLLSYSPSALRHPLATHRPIPLHPEAPTTAEQFGFGDIASASLISTSLSQTWQKMKS

MGKATWARNLLEKAGLRRLHDGNKVNDRSDSDLHNTSKEARHLALGEAYACKTDTFPRAA

TVKLSESSDPFVLENVKALSCLCGTFLFRWGHDVGKRHSYATRLLNTLAFYHVEVVTREH

SGMRHVSFVQLLWCVLQDTKMFEDYARNVDLIHARSSDPYVCMLLLFFMSYEHLLVVLDD

N

>contig45790 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64066.1|) 1e-106

MKAITTPADVFAQRRGPANRPVSGQESYDVLGVSKDATPEEIAAQFKIKSRSMDPTKVED

QETLERINDAYRNLQDPMARSRNDSERARDSSQVPSDPTSHFVSETARSDQTECQVCFRP

FKLGRRQHHCRRCTRSVCNQCSVESKPIPELGFPMPVRHCTSCNENPPKFIKPVMDPVA

>contig46852 Frame-2F|Blast-U3 small nucleolar RNA-associated protein, putative [Phytophthora infestans T30-4](gb|EEY66799.1|) 1e-116

MSSLRNVVKRREHKERGQLRERQKLGLLEKHKDYVKRARDYNSKQKRLKTLQLKASLRNP

DEFYHRMREVSTEAGVHVSTHNHKNSVETKALRLLKTQDLAYMHMKHAVDMRKAERLNCS

LHFVDAPKINKHTLFVNEREEVNSFDVARHFDTAPELADRAFNRIRTRDLETTELRDLVS

NPKQKYKMQVEKDAVYRELRNRLVRATKIGRISAKLDLERKVQSKGRKVKVKGAEHGMPA

VYRWKQQRQK

>contig47323 Frame-2F

MEEFDKQRAAIARQQNGDGVTSLSAMYDDNLSQGETLASTNERNSSAMLVAFNNEVNLAG

EFEAEFSLPSSGQAVSLAMSECMSAAAPMSKGSETVKATSAMPSTNLLDDYPSVV

>contig47356 Frame-1F

MASPDGRVDREEWPSVWCASGYEWPVTAETSYPLVHSGTEAWLNTVRMEPNLLLHHVRRF

VFPDELLASLADQVLVQWTSKWRQECLLSGLQAYRIRVKDATTSQWLDQWISLAQWSQSS

SSLATLIDNGDDWNKLRDCNYAKDKILRLCDPRRRIRLSHHLLCDDLFDKEIRALTGDDV

HSLTLPDKLRCHVHLLRRNSHYQGAYYSSDYHRVNWRTLVHFFLHRWQLRRRGSFLNTEG

SSRLHLFSCLCTCSLEEVDAYGRARLLQDWTTFPDTNKETDQRRVGDEVIITQNVRGFKE

STRAGWMAAWRRQTPGQRVLARCIQETHVQAV

>contig48685 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57206.1|) 4e-72

MVLGYTFNYNLKLQHFARHHSSLQWLSVGMYAKRCFRNWFCETSSIRNPSRLLGLSNEAV

AQFMEDILAFKEHKNPFDFESTNDFENPKLFYMLISESHPLMHMFGSRLFSFVTSTPYLG

SVLSNMCFIPSAPSTTCPQHTLMPLLKMKLFFQQHSGL

>contig48762 Frame-0F

MVLQRNKGMNVGKVGDPNHSGAKRFDEFLNSLRIHFITLHILRHFLHQFNNERACIIK

>contig49066 Frame-1R

MADQLLEDLTPYFWRSVSLEKENIPQPVASDPAV

>contig49264 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59936.1|) 8e-18

MIKKPELLVTVLFGKQSTRFSVPADDPRALDIVKLHIYNEFQLESKFQRLVLRGRDVKSA

TALTNNCKLLVLRNRAYHEKNSASKQDETTFTDSS

>contig49808 Frame-1R

MYHFLERNESHEFHGETSRN

>contig49901 Frame-1R

MYKFDIYVLSCIKFVVVSSDHKQLWYRKHETNSLTRNNIMFYVLLWIVVTDLFYKTGFQ

>contig50147 Frame-0R

MSHAFWKASFIKLYALESMSTGLKFVRALINGIAQSSLEVKEDSENMVLDEGVAVLKELM

KDIQKPDQNDVVEENDAIINLFISAGAHISLLELLRDSAVREISRNRQGQANFEMDEYAF

EASHEYVATRALELLGLLARSRRIRLLILEAGAALDALVIAYEAATSEYTNSSPVR

>contig50235 Frame-0F

MYTTRNVVRQHKMKLNYTLMLVLPAAVCKKPGEHNILKYRCSQYVAISDSICSASRADRY

TSLGMQRLDTNVVFIDVFFINKSECKPRCSVTSA

>contig50406 Frame-0F

MKLLTDAVAVLTLGPKLTKDKMMQGAGRMRQLGCNQSLYIASFDEVAQSIFQFSGHQSSA

LVSPADVLNWVIDNTKAEAVRGLLEWGGNGLHFQRTQLDQDCEFVDDDWALEVLYRGQLE

VNKISEVILSKAQHYFEKEDLSDEQVKQICNRGFQYGLDDEVCVTSHTDECERELQVEEE

VQQQREIEMHKCTPSKEQRWVYSRILGVQSVKGLCGVVGIIEMTQFVRQSIDPEEMAILN

WARAHIYGTSNFFATIQTHDSSRLNMYLRLIDVVLVFKNGDVLLVSECEADHILELLWST

QNSAACNFCFFNLAFAHEGLSRVGKLVMYKDLHLAMGSRLHAKLPKLSIIACDVFNGETM

MVKGQEKIMEVACRLFIGPLAQRESVLSNFVASRGNSHKWTRSLLHELCCRLDLEDCN

>contig50473 Frame-2F|Blast-enoyl-[acyl-carrier-protein] reductase [NADH], putative [Phytophthora infestans T30-4](gb|EEY61640.1|) 2e-55

MSPSPFVKYDSILTMLLEGKRALVVGLMNKHSLAAKIAQSFLLNGANVILSSKTPLSDSH

LRSCAFQISPTSGAAIHFVSCDVASDESIDQLMHYCGMTFKGELDILVHSVAFASGQAFT

DGLLGTSRDVWAQALDISAYSLVALTRAATPLLLTRGQEKRDRSVLALTYAGSTKV

>contig50499 Frame-1R|Blast-resistance-Nodulation-Cell Division (RND) superfamily [Phytophthora infestans T30-4](gb|EEY58769.1|) 3e-20

MRVSAFSTLLLPAAMVSQTATATSPSSPVIASSSTSSVSGHVPWTLSDNASVLAGIRSQL

TTCSYSKVKECLHDPALMRELGLLVRAPGHCVAFDSSYVNVTTPSAAIPNRYYPTSVEDA

YRAGFANKFSEWSDSNREQFQVDCP

>contig50617 Frame-0F|Blast-mannose-6-phosphate isomerase, putative [Phytophthora infestans T30-4](gb|EEY53727.1|) 4e-57

MQELQCVVQNYAWGKFGLESSVAQLREAADKSFKVDAAIPYAELWMGTHPNGPSKVLHEN

DDNATLLSEWIRTLRAGETDDLPFLFKVLSVRTALSIQAHPDNKLARELHAKFPQIYKDP

NHKPEIAIALTPFEALCQFREINEIVAHLQAIPELSALVPKDVSQRLVIEQNEAALREFF

RCFIHAKPENI

>contig51522 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68139.1|) 1e-29

MASSGLSRYFNQSGETEAGFRMLYKHN

>contig52057 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69140.1|) 5e-49

MKSGSNVNKQTRQGSTALLLAAKRGHTAAVEALMTAGADIFLKDDRDKTAAETAQRRGHV

DLFLKISVQNQLRLMREDLRRQRCYMLIRVSTLYVLSRAEIIPAMNCRKRQQYNTLMDRT

LRLPKPLLQNIALFLPLSRMWDRQLRYLIYEAIPQPNRVVQQGIRILDEVLLSVSLEQRP

SLYAIKQKCGGLLHITGQLGLLRDSDEYRGLFTRKCYTPMSPRMLHQLRRMADIQGALST

YAAGSAIQFGVEVAQDVVALLTELLSWDANRRKAELLE

>contig52505 Frame-1F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY69908.1|) 4e-37

MEAQDLEIVSADTAVLSSSAYTNESGPIENAPLNSYEIASQNEAWGVGDEEDGWMPKPAR

LHSGRTRSCAVCFAPLQRTSFASWDDYLQSQEYLTQLQTSFLQDAFISSLLCGENMAGDL

PTEHRMHKNRKLKCRQNVSD

>contig53458-0 Frame-2F0

MAFAAATARAMTATHGFRVQRIARRTRTSAPRPRLLACRMRLCAMRW

>contig53542 Frame-0R

MLRITFIGQCIRWYIAITWVPNAKQTILHIRGHLLAVIRVWAMTFSRSSSFNGVGRNDLA

TAFEVMRCWQRSDIYERRCNNTSILVLSAVALRSSSSSSLSATDNKLSSSESSASGAAS

>contig53797 Frame-0F

MSDAVVVFGCNDDGQLGTGIKRRPTISIDGVSASNFPQQLDSLVNEAVVAVSCGSRHSMA

LV

>contig54042 Frame-0R|Blast-serine protease, putative [Phytophthora infestans T30-4](gb|EEY67871.1|) 1e-106

MAHGRSNNASLVVAPALEIRLVQEADQLAVLSSLQQRASDLVGLLNVFERNSLQPRSIFT

KPLQDLQTWIQIVALAVAESSVEWIDEQHKLTHNSLQGQEHERWSRLQNHRRLDAYVPSL

VGVDSAREAGIRGNDVVVGITDTGLYLYHDQFDQDNRDVYSGMVLSARKVVMYNAWANRN

DESETITCGHGTHIAGLLAGSSFSGNYPDLGIADRARIAFMDIGTQSETCAGRQNCPVSL

ATPADASDLVRSQLAAG

>contig54158 Frame-0R

MSLSVERLGNGGAFCLREERSGVNVLIGCGEANNGAPDDSNVEDFEALTTQYRRDLKHLL

RRDGGTLDAILVPDYRPGVCYLLPYMTEKCGVSWGSTATTAAQDLAPKRPPLIIMTHSTR

AIAPHLLAEYWTGCHSKVKDRGSGLPAPYDLQDIASA

>contig54297 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64249.1|) 5e-71

MYVDLAKWETANLPNGLNAINLASFFDSLPLRLVAYEVNQEGVETFDVHRQRDKDYLFSF

EVKYDKYGREHNNHHAVDRKQEGDDGGQALTASRTRLSLMSSDLSTMSTTRSEISLLTEE

DSQQAQEHASFLQLEHARRLKQLSFSYLCWMEEVDVALDVRRVHYIFAIKDKVGEYDSND

NCIRPERLA

>contig54943 Frame-0F

MGEYSSRLYQCELSVPFLDYDKRSGVTQHHVTVLHLAILCESC

>contig55315 Frame-1R

MIACAIIKLHRLSLSTLYRVTVRADSSRILLMSSLRMVCCFHSKLGANNDH

>contig55896 Frame-0F

MQRVRMRNIVWILPLSLFSVLATTLTYWSYNAVPISITQTCKASQPLFNVVLAFMAYRSR

FSVATYLSVVPIVFGVVMASVSEMSIN

>contig56664 Frame-1F

MTSETTNDKVATKKEGGVTRTGIASKARNGARKRQSTFGFHAHQPPPITISRNDELPSCN

RLR

>contig57238 Frame-1F|Blast-cyclin-dependent kinase, putative [Phytophthora infestans T30-4](gb|EEY54371.1|) 6e-07

MDRYDRGDILGEGTFGIVYAAVQKSTGR

>contig57362-0 Frame-0F0

MTEEWAIQAEGFKAEGNKLLAAKQLSDAVEMYTRAIELDPENAV

>contig58864 Frame-2R

MASFLPTQPRCVRQLLSPVMTLVVKIECLVATQ

>contig59117-0 Frame-2F0

MRTRQHESALQHKNIISLEANEALKSPELVPATSEPTSPVASLAFPP

>contig59535-0 Frame-0F0

MLVGYDSRLLELFQCWFLMHLCSTLHLHLNDN

>contig59535-1 Frame-1R1

MHEEPALKKLKQSTVISYEHMNSIGHNLDIRTWQIGGIDLEICS

>contig01296 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70028.1|) 3e-11

MVELSEVSRILGCNSHYEVLHLVGTGECPVFIDALKVRKRYKELAILVHPDKNPAF

>contig03786 Frame-2F

MCCRSPILIAKAKNEAMLIGKIILRQKISSSRGILAEKVAPKEYRCNDDVGRWH

>contig07122 Frame-0F

MSLVLVGSLLLNIVTASVDTFRLELEKNGQYDIVSRIHEDGSAVVVVRQDGLLHLLYDET

IIGAEFQDSSLRDQTVYPGFTIMQCAAYLKRKPTKALQIGLGIGTVPTFLREMGIPTDVV

EISHAVVTQAADYFQYDWCTQEDDDEEELCIQGQTFVMDGLKFLASTSVALGIQTNEEKK

NPYDLFIVDVYTGRNPFAFVLREQILRIHKEWLTPDGVLVMNFVGYIKGVHAVAPKSIYR

TLQSVFQYVKCFPELEESTIEALNIVFYASNQPIDFILPSTGMYENPLSETHFY

>contig07409 Frame-2F|Blast-protein farnesyltransferase/geranylgeranyltransferase, putative [Phytophthora infestans T30-4](gb|EEY57304.1|) 0.0 NOT\_ORF

MAAKARVGHRVKGEEREAIELSVQEALNQKVLQHYTKTVYFNDLWVSFLSKMAGLVALMS

YLEVQRMRHSPRGISFIVGFEALSVIIGLSTVLFIRRWFDSLLAFKTAFAFSLLQGFWFV

ASYSSRFMDLPRQAGDLRPDQAPFGLMYFLVCWISDRFMIRSQTIAKQTAEDMHSVLQGK

TD\*SEVSLSYVAEI\*EL\*AAIIKLLERLLCCCVSLCKKNAMKYSEDPAWADVVKVPQDDG

PNPIVSIAYSAEFTDVMDCFRGVLKLNEYSERTLALTLDVIDVNPANYTVWIFRRRVLQE

LGSDLHQELQFTADMAIQHPKNYQIWHHRREICSMLHDGSAEKDFCALAITEDSKNYHAW

AHRQWAIKTFALWDGEIEFVDKMLLEDIRNNSAWNHRWFVHSNTLGFETIAMRQQEIEYA

LDKIALAVHNESPWNYLRGLIRNYEAAFAAHIKEKAHAILQTTGDCIFAAALLVDLYAKE

GTDEAREIARKLATTLMKETDHIRKAYWQYRLSTLKQRS

>contig07746 Frame-2R

MENPIIASTPVAPGQCLVHAVSINSKPVISLEPAPNGNVEMHPPSSDPAEASTNSANLRP

TTAELLFQQETIRRDKSTVDAARRRGEAQSLLPLTLKRSSVNM

>contig08440 Frame-1F

MVFSACHIIRPHCTMGSIEIFSRGFMDTRGYIAERLCTYIYCDKLTTIPQTVAEANTKKL

AWLLSVQTRAREVKPFIVALNASDACPCCHQKLSKGLVKLLEGHCRCQLCGKSMCRKCSV

KKALPIITGSLKQVTQMTMDFCLNCYLEALNLPAWRVAMNTTVVSPTANLCS

>contig10661 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53359.1|) 1e-106

MLSKGQPSISRPQRWFIVAVGIAALYYMIHFQVWIWSSTVVVDMRTNVITAERDTVVIQR

SLIKPVAIKTSDKIKPSVVVAEKPAPVAMKVANTANQPSESTVGPFLRSPKKQETSNSLS

IADLKNPISQFPFSVPNRHDIVFGYAAAIKYLANYSIPVTSTERLFLFFVCGMEHGQETT

WRKICVDASTVVYTCFAKSSAPNRLVTIYAGTQIDWSSSNAFYNDGDLKVKMIPALMEWH

GGRPHAKRATSNMMLEETILYEPLVRYLFKTTDRPDLLLDPEMIASKEIVVLQGHAHYRE

YIQAIATERNVLITIPKGELFFFFISGRLQGNNRYWCPYCRYSEISVEYAFYAFAPPGSR

LVKVETTNSYAIWKNPTNEWKSDTTVSLRGVPWMFRATVDTLAHTVSLNRVIERFDHPEA

MR

>contig11716 Frame-1F

MTDNIGSVPRTKFFLRGRNGIEVLWGPPSSSKDEVKIEPDERFESLASADLMEFTEDGEL

VVLVRTASGFTVRHADTGALVTEVANPGIHAVAWSPLGSQLLTWQRPQKDSDAGNLIVWD

AATGQDLARFHHKSYTRDKWPVLQWTLDETICARQSANGVVLYHGRDIPSGSIGHIHEPS

VSNFSVAPASAPYKVAIFVPEKKGKPASVKIYQFPNHLDAPIASKSFYKAQDVTLKWSPT

GSALIIETRTDIDTSGKSYYGETGLFFLQSDGEYDCIVPLTKEGTVHDVAWDPTGRGFVV

IAGAMPAHATLYDIKALPIFEFGAAPRNHVSWSPHGRFLCLAGFGNLRGDMDFWERNKLK

KLGSATSNAATTFAWSPDSRYFTTATTFPRLRVDNGFKVFRYDGSGPIYQEERKELYDLK

FRPAALETYPNRPQSPRRKGEAAGFGSLTDPQAATKRQAYRPPNSTGALAAMMRKDEGGS

QKLDRNKYAVSRTIGLSIPGAASRPIPGMALVAGPKKLSKSARKKKAQEAAEAKAAVEKA

LAKVAPVLEEQTNVCLLALTPEEKAKKEKNLLKKLKQIDAIKAKQEVGESLNPDQLQKLT

TEQSLRDEVSALSL

>contig13318 Frame-1F

MVEPKTIDHLKGSAKENSLIRESPAMHSESEVKSHLPSVDDTIEIHADEISPHKPSPVRN

GPESSRTSTHVVDPPSDGAVPPKSVLSTIRRWFSNFWAKLRSIFKKSDNVVNDDHKLRH

>contig13556 Frame-0R

MGFGKIYVILLVAIAFITSIYAVAVAVTDDNPMAVLNNDLSDSNRLLLVANPIITNYFNR

RNLRQITQVPRKLANLGNGFHNVKETLNFFIKRYLLPWLYSSH

>contig13880 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64185.1|) 5e-31

MKKGLIWPCVFNEHIEMDAMQHEATKQQMMLERFQEENPGFDFSNAEFNGAAPDPRTFMG

GVKYT

>contig14539 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53214.1|) 1e-74

MTEMQVKKQCDHPRVRLGHRFCRDCGTAVTEADAKPGADELSGAMGAGNMRYSTPVAGSD

VNQPVSYRASSHGALVRCPQCQMQMRVLPHMYNMRVACPSGHMFLVQVAGQTRISGRGRG

GHGYGSRGGLVGSQIPLRGVSMGFPGSYHRSTNNYSEL

>contig14984 Frame-1F

MNSIAMIPVFKMAFGKLECELKRRGWYWKSGGLQWKYYQPYCKTKDPKTLEPNVDYFCGR

ENLETYLDRSGEYEHIRAKLEEAHRRQYIVESESEEENDLVNNESSSLDGPHSLNETTLS

FKHRPNRSTSVDPSKRPRSKSSGFSSQTTLAEVKFGEIWRVLSDDGWHYRYGKLECDYFK

PHCASTNEGIPGHDYFRTKDQLIEYLHGSGLWEETAARVRAEAAMSSSDGEISEMDDEET

SCSRKRKHEELTPGLSRKTKRKSLDWTPMEKVMTFTDCQSEEKDIGTMSPPTVETNENER

HGRNRQPLRNLANSFTPSPIPKESNLDCLKNA

>contig15073 Frame-2F

MRVLRKSFTFAFTCFFFHSKTSLRRELIRQVDPK

>contig15338 Frame-0F

MSSSRRRSRNSSISLASSPPIPKSKPWFSGHLRAMHVSDRLPRKIKVRGEGDGIDFESNS

PDLGSQRSRLNSVASTKSRNANEDADDIFGEQHVDSVENKSVERQEGSSRSESLKQEESV

LAISVKSIVGSESTTSLRLERNKRRSKFLRSASFDLTHLQSALSPDSSSEVPRLIHRTTF

GLDEGQIVVSDIVSNVSGCPSSVRPKKAFDDSDIVDKRARLDSADTHMKSQAKCSAAVLR

FAVYEMSGKETAGLRRTFGFAKANPVLDRYTLELDCRQRIVQAKSVFMHRFWSFHCDSVQ

SFLFGTSDGMASLIVSNGGQGNQSFELKFANDDEREQFKQAIDNCRSLSLQKMRAFATQD

HVSLPAQLKAPTSPVLDGLDSPTLKEPNTTFSADLCTTIESDLSITHNIRRSTATDLPVL

QSILVPLLPGETVVEDTELQATLLIGPASETYESALVWGRIPGKVAVTNYRVIFIPFNQV

LEQPRCGGQGGVAYIPLFNITHVHLLHPNGRRTKAGHTHDAGKTGSASIISIICKDIRVM

RFQLDTHPSMSNDHIRSLRATISKLADASQRYTVRECVMGIAGMPNSSNDSDLLSFREGE

SSDGYPHQEMNLTMPRERSGMFAIAYSISSVSSKLNGWNLFVDEREFQRQIGGDTAVSPF

LKYYKNDRGNICKTYPSLLLLPASMNSVTLAKVANSRAKNRLPVITYYHRRNRCVLTRSS

QPLLGNLLSGTSNVSDQLLLGVYRRLPDIILNQSQSSQSSRPIYIFDARKPKASTGNRLM

GKGGVETPQDYPGAVIHHLNIANMYRMQSSFVGLLKLHLPGSVDDTDRTWLSSVESTKWL

DHVRLVLDGALKIARVLELEGASVLVHCSDGWDRTAQLCALAQLMIDPFYRTIRGFAILV

EKDWLAFGHKFAERLGSDRNRDPQRNKSSPIMFQFLDAVWQIQRQYPHSFEFNERFLLHL

ANALTSGLYGTFMYDSRLQRDVNEIKHSTVSVWTPVLMKTALYSNSTYEANDGPIWPWVS

CNMIRLWENYFFQWHPKFYKCQWVCNLIYHNPAGSTTSANKHQEVVYIPSNESFTSRDSP

LSKLLAPSTVGNKKEDTRNEMPALSLYSEEDAPRITRPASDNYTQNLSMRIVSGLKIGTH

QLVQSETTNSQEVG

>contig15868-1 Frame-0R1

MPTHPSRQLDVGVLSCGYSSRNGQIYLGI

>contig16887 Frame-0F

MRAALILLVAFPASTVASSVMTAGMTGNWRSGEVTVADTEVLDGALKGDSFSQSVGDTRV

CHTSLKKVEKQVVAGTNYRFYMEGCSVQESTGTCAPSSCVKPECCMVQIFSQTWTNTLRV

TNITIGGSVCVSPSSESKETITFPI

>contig18272 Frame-2F

MVADSTSTRKSLRKQIKRQLEFYLSESNLRQDKFLQKAMDEMGFVPVSVILSFNKLKGLN

ATERMILDEADKSPMIRVDRVKCCIAPKIFLETSQGDEAVIDARTIYFDNFCATDDHDSL

RRVFARFGKVTLVTLPRFRLSKKFKGFGFVEFADQTAAENAAAESLNLDLRGIRVLSKTR

WIQMKEDLKRQLTCVDAKVESGKARESASGSSIVGNVTGGDACIGNKKRKLQQTARGDSH

LIFTFDKDSDISGNIQL

>contig18711 Frame-1R

MEYARLCVSTFCFGLTGLTGLNADNYARHWRCMRTGRCCGNPCHIK

>contig19424 Frame-0F

MRLVDTQMQEEAYTMARDRGGNDNNGKLNSLMLLPTVQLMAVFRRHSNVVEFDYIFGQLQ

ELEIKLEDATLVALAHVFSGVNWSHTASKSRVNKEQMKSEDEFGSNLALKLLEIEWSTPT

LLSTAAGGRLASSRNGGGSNTKVLLHWLLLCPVKVNVTFTSTTDRSLLLSLLSPDMSPLL

STLISAAAALVSNLDQAPIRVPEFYVENLLETTHTLAFYAMQHYLHHGLRSWYSIMGSVD

FLGNPIGLVSTLGTGVKDFFYTPAQMLLEDENGLRIDNLRTGMTKGSKSLLRNTAVGIFH

TTGKITETLGKGIALLAMDEQYNVQRQRASTRQIKKINDLGDAIAEGSKGLVGGVWDGIK

GVVAAPVRGAEQNGASGFVVGIGKGVAGLIVKPTAGFLDLLTSLSRGAKTSAESLDGTDR

NAFDTVTRFRLPRRFCPDGVLVSYSDREARGYAVLLLTSLDATD

>contig20428 Frame-2F

MVQLLRIASQTLQVSSLLNLSIRENAIRQVFASKMLLTPAAASSQIVHCVAKSVSTNSGL

FWASIVQEWCNCSDLSILSWHQRVIVIGNVVELTTLCSFEQTLVTVVSYVLSELIRPSLC

HWAFDVKGIEHKDHLLEDKDAMNDPEVLTSPRLFMTSRDLNVDKEIQDGIVALGESEGSV

HVQWQLLCHSSFSARCLDILLRRDTAQMHDEKNAVALFCHTLSMILLSTGRSYVLNIAAQ

FTTPSAAIFALLSSMTVEQFGGTLDGKITDLSLVNRLWMWIKLTIESVRGQRKGYATNQF

VFTTSQMHVLLVFNVVYSHTLLGLDDETFYDKQWPLVVTEVMDVVTFLKQLIYETCWMTT

SETSFLNDCMSENEVVRFSAVVSSIKLFNQLYDRDCRRPFMPESAWLWPLMPVVKEIVDL

GFMKEDESRDAQAIFMLMTGKVASPFARAALILVSIPQVLSFNERVQLFQKLLEDSKAHV

SSIRDEFSRALVMKIKRDEIVDMSFFYFKEFCDTMSLGALKLRMKIIFINEQGLVEAGID

GGGVFKEYMDCLTKNAFAPELGLFLETEAHLLYPNPGVRYMVDSQMEAFERYRFLGRVLA

KAVYENILVEPQFAAFFLNKLLGKLNYIDDLHSFDPALYTSLMHLKHFEGNVEDLALTFS

VTENEFHDVVTRNLVPNGENIPVTTANRIRYIHLMAHYKLNVLSSQESAAFLKGFRDLIP

GTWIQMFSPTELQMLIGGTGTHVDIQDWKEHTVYGGGYHPSQRQIEWFWAIVKDDFTSDD

RAALLKFITSCSRQPLLGFAKLTPKICIHQVRVEDNERLPSSATCMNLLKLPAYSSKEAM

RKKLLYAIRSNAGFDLS

>contig21593 Frame-2R

MPSLKLLGVALAMVHLAVVNATYMASERKSFVSAFYANPDGRRLVEVKPVSWLGFGTYAS

TSENRRLGEHNEEERVFGMSGSTFSKLAKEPELLGVEDVLKTRFGDDFVQVFKKNDKATK

AMKDSLASFMKRSKAGDLTPDEVGKFANDMLAAVKNSKKWSKKKKFV

>contig21834 Frame-2F|Blast-26S proteasome non-ATPase regulatory subunit 2 [Phytophthora infestans T30-4](gb|EEY65582.1|) 0.0

MKEAPPIPVPSKDPQLKEDLEPKSSLSTKRIESAPSEEELSEEDRKLKEDLNTSVARVCD

PQEEIGVKQLALELLRREIRSATSSMTSVPKPLKFLRPSYETLKAAYDTFEASDAKMLMA

DILAVLAMTMAKEGSRESLKFKLLGHSTDLGSWGHEFVRSVAGEVGAEYNARITAGDASD

PDVRDLLAIVNAIVPFHMQHNAEPEAIDILIEVQQLAKLLELPDIDEKNYQRVCLYLLAC

ADFMSDAEDLASLLNTAYSLFVRLEHYPDALRVALRVNNEEFVAEVLQKCPNENVRTQMG

FILGRQRYVYEDENEISVNEIIGNSDLSGKFITLARDLDVLEAKTPEDIYKSHLSETASI

GRGRDSGVQPADSARANLASTFVNALVNAGYGTDKLMTPEGNTWLYKHKKHGMLSAAASL

GMIMLWNVEEGITQIDKYLYSGDEYVKAGAILGVGIVSAGIRNDCDPALALLSEHIDSGN

CSIRCASCLGLGIAYAGSAREDVSELLIPVVSHADENADIQEVSYAALALGMVEVGTCDE

EAGSVLMQRLMESSDAELSSSCARFLALGLGLLYLGRQERVEAMLEAAKTIEHKMSKYLA

ITLETCAYAGSGNVLKVQQLLRTCAEHIEDPMEAQHQSVAVLGIALVTMGENIGSDMAMR

SFDHLLQYGEVAVRRAVPLAFALLSVSNPEYALIDTLSRLTHDADFGVAQNAILALGLIA

AGTNNSRVAGLLRQLSEFYSREANHLFVVRIAQGLLHMGKGLMTLHPFHSDRLIMSRVAV

SGLLTILHASLDMEHTILDTSHYILYCIATAMQPRMLITLDEDLNPLPVSVRVGQAVEIV

GQAGRPKSITGFQTHMTPVLLNVKDRAELATDEYFPLTNVLEGVVILRKNPDYEPET

>contig21841 Frame-1F|Blast-autophagy-related protein, putative [Phytophthora infestans T30-4](gb|EEY64085.1|) 1e-87 NOT\_ORF

MSAYLPSSLSGIAEGTRDFAYARLRSTGVPNKCAVHGPRDAKTPIVQLYVATTDGYFYEY

SLNLAIGGKCKLERVRDLSDVETFSRI\*CSCQ\*I\*ENVLRDTTSEEIEAIYIS

>contig22721 Frame-2F

MDQDATWRSWKLMLSKLLDGCNKRGKNSCGESVVLNDGIFAKLLQEDEFQRLIYPGIPKE

QLVYAPKNLQTLLEDPWYEQELLTLMPKVQAKAASVLINVKKKGADLGDVMDMATERMFM

PQVLQEAFGREVLAMVHRVNYQKHVQLANDTRLLADPNSDFASWDQLNENFVDELLNDQG

NERGIAVMDNFMGNEWTQLLLNDVTRMAKNGLFMSPVPNIGAVRRQAVGSETVAGAKLCF

VELQDCKIEYPALAELIEKLHALPYEINKKRPTKAKLCAQFGHSTAIQYLPSGHMQPLRL

DCGTGDKDNGVKITCIYFFNQIAAEKTSILRLQMNAVKNASVRDIIPKADCLVAFQSQSV

LNEITVVPDGEDLFYLSFWIHGRAIVMTK

>contig23212 Frame-1F|Blast-apolipoprotein A-I-binding protein, putative [Phytophthora infestans T30-4](gb|EEY57115.1|) 1e-13

MLISLTAPKLCARYFIGPNKVHYVGGRFVPK

>contig23568 Frame-0R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY62053.1|) 2e-61

MRVALTDPLDGYVFRTVVENLIPQGLGTSQLNQIKKRLRHVGDRLRLMHNLLMYSGRFNE

LEEIVRKCFRRIKWILIDSEV

>contig23630 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57026.1|) 1e-17 NOT\_ORF

MDT\*TPDSRTSTAWRLTLKMAGCPESLRDITRISGLADRSFFCTSSLEGVSTTPQTWQSR

AHHSSVPI

>contig24006 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61431.1|) 6e-22

MTLQKMKQWYNHVRNIMESVSGLEVTTISENSLEVRVLKSHLVQLFCHPESAILQRVQ

>contig25221 Frame-1F

MVPILVGQCNSKERFHRLTAVTWVHEFVTLGREKLVEFYADVLAAIMHCISDAEHEIRQV

AERGNEDLLQLVKSTTENVALLPLMEKLTMELSSDHVPTRMAALRWIAMVLEKYPTQLSA

PMNQLLPALLRTLSDTSDNVVLLDLEVLARISLNQKEFENVLNAILLLFAQDRRLLEVRG

SLIIRKLCVLLNSKHIYLMFAKVLTTEAVYLNRPAECEFAAVMVQTLNLILFTANELEHL

RTILRRSFESRASRDDVAVFIALFQSWCHNPIAAYSLCLFAQSYSLSAALIRKFANIDAS

VGFLLQIDKLVQLLESPIFIPMRLQLLEIHNEFHTDLVKSLYGLLMLLPQSAAFRVLRDR

LASVTSMATTIGRIDDLHLAIPRHGLTTQELCHDTKEESKTLPRIDVEALLVHFDRIQAT

HTELRTKG

>contig25395 Frame-1F

MLRSSWCLRRLRCLSTMAMPTPPSPFRRLQYVTSDTIDRRLLQGLTAADDDSRPVNLIQD

EESARHVLKIIEKLGPHHFHACDTEVGQIDVKAVGPVGNGFVTCLSLYSGPEVDFGNGPY

VWVDNLDSAEGTLQYFKSFLESKQYLKVWHNYSFDRHVLFNHGINVQGLGGDTMHMARLW

NTARFRREGYSLESLTADLLLQRKKPMKELFGIPKLKKDGSNGKERSMPTIEELQRFPEF

RKRWIRYSVYDAESTWFLHRVLQDKLDQTFWSEDFQEGESMAGSMYDFYRQYIVPFGECL

TDIERKGM

>contig25571 Frame-0F

MEEATLRAKIQAMKNLLEANSQTQVPKATHYYRYRSSRGRFNTVAGPVNRSWNRYSSPDA

ATKRSDVVERSINKVWRRKDYTDPSLASAKNKPCKRPVKMTASKCNSIQVQVPKDGEYAM

VNGGFGLVRAVVKKPTMTRRPQAQVDAKPILTQTHSKNGGLELYLALIILN

>contig25962 Frame-1R

MLALRAGMHQLQGGDASFRYTMMTARWRHVPTFAQL

>contig26189 Frame-1F

MKLATILVLAALAVTTAKGGNPNSLRATDFEPVDVSKTENVDQLELDSLDATDNGSVESR

PLNGVNNEDSADLSTKSTVSSKSSKKGGEPFSLGPVYNDDLDNTLRTQDDVTKDGMLDPS

IEPTVASKSSKKGGEPYSVGNVYDDDFFGTTGDQDNDMDNDMTHSLRKETSQQNRRGWEQ

KDADYIDESSITDENIDAIMDKYAIAKASTYSSGSGYDIEGKNGMSPDDLMSNLKDFES

>contig26303 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58754.1|) 2e-14 NOT\_ORF

MWFTGIIGTLGSAMLAYQNSTLRLQGFGRNEAELERHLHKIRDK

>contig26655 Frame-2R|Blast-transglutaminase elicitor, putative [Phytophthora infestans T30-4](gb|EEY65316.1|) 3e-79

MVRAIFTGVRYKHGKKDLDEYGRAHDPILRDLNPGFFHITICNLLGIFQKSFVVDISADE

EVWNQPVRGYEIAEQTEMTPQEAARTFYGLEEYPWNAEAKRIVYVQTRLTWVLESYDDGS

LVESGRVDNYTTGEWYYYLLELDEFGTIIGGEWLYHSCTNHPDF

>contig27201 Frame-1F

MQSTFAYGLAKNRVNGLPSVRRVATAAQVGGRLSSPSSPLHAENGATSRWSSDDVLNEFA

TSSPPSQSVKPVDVPRVASSPIAFAGLCSEQVATPRGNSEIRNLTTTTSESESEVYPSKR

GTLVDKTNPFIGYFQIGTEENDADVHAAKATPTVCPVPLPPSVHRGPLRTHSSATLSSLS

ALLTPQKNMTKWLQARGSCFPTFLNQRNESKYSKQQPQDKKLSHKAFLESLKWKHAAFVT

TNDCQEEHKQLKPFKRTVSLPAA

>contig27951 Frame-0F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY63452.1|) 4e-80

MDDVQGLVYLEATIRELLRLQTPVPFTMRECVQDTVFSDGTFVPKGTTVGLCHFGAARRT

EVWGPDASAFKPERFIDPYTGKLLSTPAAKFNAFSGGQRVCVGKTLAMVEMKLVIATLVS

RFHFTELPNQKVQYAMGITIGMKNSLYMTVEPVNEQAPGAAA

>contig28015 Frame-0R|Blast-serine protease family S01A, putative [Phytophthora infestans T30-4](gb|EEY64173.1|) 2e-40

MKLNIVFLPAVFAALVNCISFTDPDERIFGGTIAELDKYTYIAALHPDGVRSNLTCAGTL

IAPQFVLTSGLCLEYTLVDVYVTLGSKFRSNVGIGNYEAIRAVEAFRHPRYILNPDTLDY

AYDVAILKLETPSTQQPAKLPAVDGSSNRPGVMATALGWGEMETGENANVLRAVDVQVIT

NKQCSRIWSTIVDKSFICAGNGTNKGINVGDWGGPLIVKDVVVGSASLSSNKNDSLHNLY

ARVSHALDFIHDILDGGSTGDVTELLTK

>contig29940 Frame-2R

MAKLSVGIESLHKLRSTYLHPLAECRQIRGLSYTIFN

>contig30331 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68199.1|) 1e-180

MGSGRDSLRWPDKNGTDVFNTSSFVASITGLRDRNANDVFEIIASKVNEDGVLSREAFFS

IVDELVEEHAANTNQALSADENNELQRIIETIFDGFDTDHDGFVDFCQLSSGISVLCAGS

QQEKISSAFSLFDINQDGFISRDEMVTYLASVYRIVFMTSPGMVQQLYGISPEELARITT

TDAFSLADANHDDRLSFEDFTKWYSSHEASRLPTLQQPQQDVPPAFVESALPYVRVSSVY

SKGVLARMGKLTNLCAYDVSEMFEIFRASADSEGKISQTIFNKCFQKLLAKGGLISRQTQ

METQELLKELFELFDSDMDGIVDVQELSAGLSILCGGNRADKTKSMFTMYDVNHDGVISP

DEMNSYLTSVFKVMFKASPDLPSKMGMMPKQLARTTTRECFRIFDKNEDGQLSFDEFQGW

FQLHNPDVQRQQG

>contig30344 Frame-2R

MMSALDFATTEYAALNNEQWDGLQNCGRCAQVSCDDDRCDDTSKTIVVQILDRCPECKYG

DLDLSPSVFTALTGSMPSRYTIKWKFVDCPVSGNVNYCLKGGSNNYWMGVQPTNCATGVK

SMQINGHDTTMLGSAYYYLLDGASQTQTDLTSLTISITDVNGYSIEDTVSLTANMCTEGS

NQFPTNAAISPKVPLNPSTILKPVFTVSPMTKAPQITKLGTLAPIETVAHTQAPT

>contig30797 Frame-0R

MKVSKMMIDYSLRFGIPIALCYAFWHPKSDEEIRRDVESKLKPDLEARKKNRAKFAELLL

QKDGISNDSKQQIDQVTSFTRTKKQLLAEKTKEK

>contig30890 Frame-0R|Blast-serine hydrolase (FSH1)-like protein, putative [Phytophthora infestans T30-4](gb|EEY54817.1|) 5e-85

MTRPIRVLCLHGWRTSGSILRHQTSALRRAFDSRAELLYLDAPWSATGPAPELVRSFYGE

TGPFFQWWDALKREDGTTYRYEGYEHSLDYLTAQIQALGTVDAILGFSQGAAVATLVTAH

YLTSYGYVPWKICILVGGFYPHISETQELLDSSKSSVDGAIDIPSIHVIGKADPLLPLME

NLYKSYTSTQRT

>contig31273 Frame-0R

MCDSDQAARPDINTVVEELQALAEEEHKRDGDNNSFEDDSPPALPLHRASSADYLNQVIA

SPFVTPVNSVPNGLELVRRQSSPSSISLVNSPMAIGNSVRKSVSPLHDSVVATVELRQKW

LCVKISSIGNRVVVSKFLRTESGAAGEIEASGRVERGDVLVAINGQSVSGLDRLQISAIV

QTSSRPLELSFQRDLQLLTDSFRFRGLPTDRRWRDRGSAIPLPGTLSQLLTGSRDDGNFE

LESRTATDAFSIEMWFSLVGLKDTFLGGVLLGAQALPFQETSDTSMWPHVHQALLTIDPL

CSLYCSFLNRPSPACVVRELSLNHWYHLVVTYSGDADKVSFSRNDQPEQLLTLYLNGEQR

LSDAGPLLADWEKFRHVNVGSGCISATAPAKPEPHFSGWFGFSGLLFDMRIWRRKELTSS

QVQQLFRGSSDLVDEATYSLRRDLLGEAADLTTSKARKKHLSSVRSTKLQGSPFAELVRS

TWPRQVNAQVYS

>contig32324 Frame-2F|Blast-alpha,alpha-trehalose-phosphate synthase [UDP-forming], putative [Phytophthora infestans T30-4](gb|EEY68908.1|) 0.0

MAPPDGWTPKTPVIVASNRLPVRLYKTNDGHWSVKWAGDRMIDSHNGLSHYEVSQRASIK

FVGSVPDVDIPLQDQDDIEALLREFNCFPVFLELQEAKLYYEEFCKQTLWPAFHNVVDVY

SPVDVVLDVEAQQNVTPTAHYWNPDRQKVAWQAYVNVNQLYAHKICELYDQGDVVWIQDY

HLLLTPSYIVRKLRAANVGLFLHVPFPSSEVFRTLSMRKELLRGMLNADHIGFHLFEYAR

HFMSACRRILGLRYRPVLRGQLGIDYGGRRVAVTCSHMAIDVSNIENTLNTKDVRDLIVI

LRQKYRDKKIFAGCDTIERLKGIPSKMLAFDGFLSRCPDFIEKAVLVQKGIHRRGRVTDY

LQSKKEIGLVVQAINQKYYDVAKGNVIDYEEVEEFPFQERVALWRVADVQITTVLRDGLN

MTPFEYIATHKSSPGVLILSEFSGSSRLLSGALTVNPWELDQVIDALRDAVYMPANEREH

RRNDDYQFVVANPPRRWAKCVLTDIVNARKKDESFVYMGTGFGLDFRLMEVSAHF

>contig32777 Frame-0F|Blast-glucose-6-phosphate 1-dehydrogenase [Phytophthora infestans T30-4](gb|EEY57587.1|) 1e-133

MQNHLLQVLSLVAMEAPVYAAGNDYSNYIRDEKVKVLNCIEPIKLENTVLGQYIGDQTLN

EPGYLEDPTVPNDSSTPTFATAIMYVNNKRWAGVPFIMKAGKALNERKGEIRVQFRPPPG

VEHMFPGIKIPVQELVLRLQPEEAVYLKINVKSPGLQTQAISSELDLSYAERYEGTEVPD

AYTRLILDVLRGKQAAFVRDDELHAAWKIFTPLLNEIESRKVQPLPYAFGSRGPKESDEL

VNSAGFHYHDGDYQWQPRVRTNSAL

>contig33042 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69362.1|) 1e-23

MTPQLWIIGVSLSLTATLFGTLGKVLLKLAHTSPQALSVKAAATVCVFLLNPVFDALSYA

YAA

>contig34285 Frame-1F

MILIGCAMIIVLTVAFLYRRVFRRPRQPYMNISSLEQPTRSIINSIDDEDYDGNDDDTNE

GPRIARHAQTSRSVL

>contig34472 Frame-2F|Blast-GTPase [Phytophthora infestans T30-4](gb|EEY65768.1|) 1e-131

MEIVADLDKPGTTFLAASGGKPGLGNRILAGKTTMFGQLRKHMPENKTTGLPGTSQYYEL

ELKTIADVGLVGYPNAGKSTLLSVLSCATPEIAPYPFTTLHPYVGIVEFPDTYRLSVADI

PGLIDGAHRNVGLGHDFLRHIERTKILLYVLDTAGSEGRDPLEDFAHLRHELELYAPGIS

SRPSLIVANKMDEQGAEDNFHKLCQSTDLAVLPI

>contig35299 Frame-2R|Blast-GPI inositol-deacylase, putative [Phytophthora infestans T30-4](gb|EEY53553.1|) 2e-63

MTASQLLLPLLAFSSVLLTALYVFDEVATRKYVSACEMTWSWPVFSPVKWRSTPSHDKYQ

FYRVDMKSARNSLSGVPVLFVPGHMGSYKQARSLSRHLWDTNETLFDIFALDLNDEPTGL

NGNYITDQALYLNDVVRAILKEYKRQHIKSKKQLNSP

>contig35413 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY63448.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60716.1|) 5e-40

MKSQYVKPIVNEPEMSKSESSVIDQFSEQEFAEQSDNEDEEAGDAEDELKFKSPTDEALF

NLRKDMSRLRETTRLADISRDVSLKSVHVPPLRHAVSTASNSFSLQIAPAMGTVQYPNEL

AKEPLNLFQSAQADELDRNPLEAAFFDTPERRGSFSIDKQASSKTLEFLKCHRSHFDDEH

DGSKDNNKSDYQAKKLPPLPFFEQTAAKDYETMSNIPETFMKAQNPRPTFVVGLEMEDQI

QESSSADADQTSRFHAAEKLFATNSNAHIYNETGQIPLQQFETLQSPEELPDQQYMHPEH

CYPPPVRMGAILDPAYELNTIADCKDAFAEINEEANKNDQDFLKQTLEQAVDETLPLYPS

ESRYAQPAVLTEAKEKHDVDAASVKTSPTSDGPLQIPLAKKPNRFYSFGKSFFVLLSAIF

CIAGLLNASRKMSESYQYHLDLKSRIGNFEAVVAESHAKMLELERNYNIWTEYVRKLAEE

DETNAMMQLQSLQTEVQKWKQDMHEDIVKFQQALSVDSIEAAFADLRVSEMETD

>contig35840 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61691.1|) 0.0

MKLVLNSIREARFGSIINESDLEVVRDKMRNDAPDKRYSVIVHYNELQTSQEFATALNKA

HPAIAYQMLKIVGETSSQKQSIVRANAPRDDVVELAASLHKYGIVTSIVSCDYKARMPLI

NSLLQWLAMLANLSDGLCRLICEKLFAVGSFENNENSMDVDAAYDYPMLRAVIMVDSFLP

KTESDALHSLLMALLADPLFKQAFAISFTSSYRQLYREFAAGVGSSTSTILAFSVQFFNR

ATFVKKLVAEYDLLEVLVSSVLETLRKKPRTNFTDITLYESWGGVAHSLHPDHNHEFDIW

DVFAMGIHRSRGSTLKDVNMKILILEAERAGFSIRHKREDSPFLRLPPETELTGRFELDV

ASPVFVCRRYMSGLLDLRYVLQIDGISEAFVLQKEGTRYARFLLYLAYLQSACSEVRRFG

DHVEMESRGWVVTVEFVSTTSDVSSWVVSNAFKSSKGFETMRSLNTSQRLIAKLAKPLFE

AYYFWLASAGKYYPPPDYQVGGTLQNDQIETAVSCHFPLQRTLSQLIRVISDTTDGLENL

LSLVKNRVSEDNEVVWIHDCDSTIGFWHRVNLIEPVLQAIVWDAQVHSGLWIRNGMSVMN

HSMNYGEPPFCARFRDLDLLLLQFSFQLLGVDWIMASIVERYDVKEWYEAAHSSDAKEAE

LMVTECLTLLSQLASELPPKVNEDEVVRSLIPYLRREIVQRLCVGPCAHSDLSKITNEFF

VSRENLFPTSFSGGPVLDLILKEVCVDAGNIASSGAGNSSASNGGKYQYRLKPELYAEYN

PTFAHLTRKQHESAHE

>contig36070 Frame-0R

MYRHEEVNHASKGQWYLHVNEGEMVLLGAAVEESDAFCET

>contig36971 Frame-2F

MQKQKDSIDHLRLLVDKLRQCRVGTVISSKLEKRIQRFNAELFWAKEGQAKRDQVRTFET

KRGSPRVKQKLNDAQYDVSIWEEKQIFFKQELNSYHQSKKKQ

>contig37275 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59177.1|) 3e-57

MAEPLFLLRIALTLLLLALSAFLYKWLKTPSTPALQTFSKRPKKRNKKKPAKKYASPGSS

SPPPQSPTQTPQPSVASAIPSALTAAVSPNYGDSASESDADDGLSAAQVLTTRKFKPKNL

GGTHLARTIKASLPPANALKFSIDQKVVARFQGGTQWFPATVMEQRKGNEYHLKYDDGEV

EYRVPVELIKAWPILSDDEVNTGRHSLIEEANKSAENAVAHEDSSGSDSSESDDDDGWQV

VGTSSAAKRHTRS

>contig37406 Frame-0R

MGNCCSTEASAVVARRSGANKEEVQAMPYTNLPPLRKHTDTEDTESHIKEKEPLSALSPS

SSEGPEDDFIPG

>contig37778 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59983.1|) 8e-96

MVEQESGQVLIDRSRSKPMLEQLMYYATHKPNLFTKLKLVWGDKDLFRLTWLQMRKPFFY

NDRRIPGTLGVINDGRQRYCGVTMVQYDLNGDQMLFWHRNTIKLSGQGDDRRVWNRLQEF

PLNVIDPNQVPRIQSFDGKKLFNETSCFGVKRFNMNPLVHMQRVEELNSDLATMEQTLIT

YAREAYVLLYETD

>contig38018 Frame-2F

MNTILLRFRRCPRASRQLTHLPRRWINYGHDMHQ

>contig38137 Frame-1F

MWIAYEELCELGANLEASRFFGVANYFKTSKLVNKAKNFSLKPESSDFIADDGHYVGEKL

GIHAEDSLTETTISSQEAFCLNMPFSGLSPRSYTVSAIADKEPNVGSNNRSYTRSTSTII

QSRKEKNRAPARQRRAYRRPLAASDENDQESNSSKMLVSLLSPLSTRRSFQEKAKTTGSK

HTYQTSSSVHGRHELLRLLSSFGSIYSKINEYLCREALKMLEQLPASQLASGWVQLQIGR

AYYEMADYVRAQEVFRGLHRAEPHQMKGLDLYSTTLWHLKNEVELSYLAQQATDFDKLSC

EAWCVAGNCFSLQKEHDTALSFFQRAIQLDPSFTYAYTLSGHEYVANEDFEKAVSCYRHA

VRTDSRHYNAWYGLGTIYYRQEKFEFAEYHFKRAIQINPRSSLLHCFLGMVFHAVHRYDE

ALSSLAVAASMQPLNPQARFQRANVLVTLQQYDEALAELHVVKTFAPRESSVYFMMGKVA

KKLGNLEEAMKYFTLALHFHSKDNKQIKEAIEKINEPDHDDEDRI

>contig38748-1 Frame-2F1

MLIRLQRQMSALEAVLIPNPT

>contig39039-1 Frame-2F1

MAPISAYWASTAIMHFQHYFCSCNLGPEQ

>contig39534 Frame-0R

MILDAVAAKNKAACFLTPPPSTKKSYIDGNAMSGGRKRKLEMSKKKMSSSSKNGSTTTSP

GENKASPQSFFLSDHEKKQLKEIEAVSMLREQLRQTREKDLAYFAGKTANPFFQTRSGIL

PGGKAESATAVIERDEAGLCYEAKQRVEYAEIRWIKMLPLFPEVQHVVDLYPDVDAIVTN

RKPFERSTPTINGKTRDETLYRGGKLPSGIMSQLKVAINGQVCTESSFCEQFWFRSYLDS

SRHTCNEAIGDTTSQELCAGSAVAKLPKQETELIDELVETHGMGENLMRELLIGLEQARK

KRLGRVQNLSLVDRYMPVSASGLIGNYEPLHTLSSWLSAWKIGGGERERLSCFASELFNF

EDCDSNSEDESRDLCRLFILEGESGSGKSAAVYACAEELGYEIIEINAAQNRSGKNILEL

CGEATQSTRVLHVGGQGESKKLHKKKRRRQSESRKSLDKATAASFSLVLFEDVDLIFDED

KGFFNAICSIAKHSKCPIVVTCAQVPDGFPSKPGRLCRKISKPSMDEFATWMRLVAFVEG

LQVAPSLVDALGKFFGRDVRRSLLFLEVNLPTLKVNTTTHWRWQHVSKDICEKNQALQIN

IPAWTVWALGPSTFDALTSNLLAELDVAADAEESALENKSIQEKQKDLDAMSELAEILDS

SSIADTWMAPNAISCNEEDLFFFSERLRLAALELRRSSLYRLGASTSSLNALYMRRQRTC

ASACIQRTLDSAFKATHRRSQQVALAQLKAKFELPLAYKGCGRSEPRFTLDYMPMVGRLL

SSTGLQGGRRRTSRRNHYLSDVLRDMTLIDELPAFNAYLRLNEDDIIAATSTHC

>contig39826 Frame-1F

MGNKVTSDEESLDVVGIEADDETIPTHVYGTLDKNRKSNEGSRHLALQKLALVIDGQALE

YAFRPQLRKLFYEVTRRCGSAVICCRVSPKQKADIVEFIREFEPDSITLAIGDGANDVAM

IQTAHIGVGISGQEGAQAVNASDYALAQFRYLQRLLFVHGRWAYRRVAKLMSYMLYKNVT

YVLTTFWFGCFSGFSGQPLLLDVAAQSFNVLYTSMPLILFAVLDQDVSSASATKFPRLYA

LGQTNALLARRVFWPWIFNGIWHSIVIFFISAWAFEGFGFCIRDSPVIATKAGKSGGLVT

LGFVVFTNLVLVVNLKLCIETFLLTWPFVLTVTISILLWFAVGTLISLPNAGFLQATGEM

EYLQKLPTFWLACLLVLALSLLRDGLWKIVRRLALPKLYHILQERELLGLPITPSRLQQE

RRQSVADKFWFDNPDIIDCPSANKSLSRVENPEEALLRSSPLGERLIASPYASSFNGGEV

TSSKQAVEFQSREMRRNIRVRGSFLDGFNTDIAVSSQVPSGYLAATNSANSVVGNRSFKS

GVGGGGSYHGYAFSEDENVDSDVEAASSKTRQGDVDPGKAAIGAHVAIKKVLKSVRG

>contig40299 Frame-0F

MIVVGIYVDDFFTTATNQKELEV

>contig40840 Frame-1F|Blast-SWI/SNF-related matrix-associated actin-dependent regulator of chromatin, putative [Phytophthora infestans T30-4](gb|EEY61707.1|) 1e-137

MRPLSRPTIHLTPSLPIIAKPNRPPKPVNTFLMFCRQNRKKIMADHPSTSAKDASKVLGD

MWQKLSEKERA

>contig40949 Frame-0F

MLNLHKRHFLWSDVSESKKRIQEFLLKYIGYKLHIAAEQEVFLDAKILNLRSCDRVLRSF

ILPKSS

>contig41111 Frame-2R

MPYALKIIDEKLHVSYPFRVVMERDIELGFMAQIVVSSQAALTSSAALMHQVIDFDALST

TVRFSRAQTEEFRVYLVRGSPYITMEFMRSRPLVETWDGLRIDHFTKLEGLKLLNGHSVG

FATFAANLSNGQTWYIFASDQLLTLRLNEDGQVTSDVEFTGVLRIALCLDAHVMPYLLES

APVYVVGGEVAHSMSLLDSNQMALEFRWKTSTFAIFHNKTDAVTEPENNKLLMLALPHHM

DVMQVQTDNRMLQVGKNKALLRLRYTSIRGLMEGVYGAVWHMTESLPAIEWNYADDGLFI

EDVSGELSSHKQLRLDMRATVMAALLNQLPIDAEKYTMPMSPDSYNFGKQVSRDARLLLI

ADKLEQEELKQRLLTKIETEIVVWLEGTNVDHFVYDKTYGGVVTKDGLNNEQADYGNGYY

NDHHFHYGYFIYALAAIRKFNPAFIEKHAQACAMIIGDIGTPLHDSNTTFFTDLPVRSMF

PATRHKDWFVGHSYASGLFLMETGKSQESSSEGLNAYYALALFSSLDTSVGQEESSYYQY

ARLLLAMELRSVKKYWHMSANSQIYEPIFSKNAMVGVVGEMSVVYNTWFGDHVVYIHGIN

MLPFTPFTTQLLDEEYVSREYS

>contig41285 Frame-1F|Blast-carbohydrate esterase, putative [Phytophthora infestans T30-4](gb|EEY65286.1|) 5e-56

MECTSDCESLESLSSLAQPITWNLRQIRSYIGISGPYNMEASIATFHRHGFDRSVVERIM

AHRLAYYSPSLRLLALSELPSRIRQTLLEDFPPCVLIHGTEDKTVSYRSSEQLTAALQSC

NIPV

>contig41322 Frame-0R

MEHSRKGLAIIGERMLRLWTEKGRSEVLARLVPALADYSRNETSDLSRLLYELVWIVLHA

KLTKHEVLGLLKEAKLTKHKKACDLLTDLLWVIGNEVETLERGHEHHTSREWRNLCTLVK

AIAEENLVSVLSLKGLLEFDLLHDANLTPEPQLLAKKLVRINTKTLYTQTKYNLLREETE

GFSKVLCLLHTGVTESQLEATKTDLIALIGFFDLDANRVLDLVLDAYEMHSRNDCFLQLL

DVFKRESLPHILGFKFQFYKRDPPAVEGVTTPRSLYRLAALLLSKGVLDLDALLPHL

>contig42381 Frame-1F|Blast-phosphoserine aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY57574.1|) 1e-124

MSGLIKSQLQIEHLHASHLMRLLSLSAEKNDVDWTVRMLSLLAKLWRKDRHSGLLRQELR

LIKCFPLKQDESANGMSRWISLAGGHDSFFLSNIQTGNNASREDSDAHFSDLRILDGKVT

DAASKNLELRAFFLNDVGLHVMEDHELIRHHILPKMTELHDYNQASNAKKADFGAMIQYG

RYLAFHLAMCNNCPLLMDVKSSMVVATSCSRLVRVDCQNLFGILPSTYCEVTDLFAWVKL

KGEALNESGNSLLILTDNYFSNSSNSTLSKDLVDKQWHYLFVETCDLPILVNISSFETDV

RSQAGMRQLLTWIEDEKDVSVKRRISMQLAQYLDKHWTTTKDGPGANGIVSTDDKDAALD

VFRKYCWLEGSDTKFHRSIDLWLSTDETTRLFAPDMVTFSSLMWRSDDFSKRILGMKSAA

TVADALAAIS

>contig42406 Frame-0R|Blast-DNA topoisomerase 2 DNA gyrase B [Phytophthora infestans T30-4](gb|EEY61057.1|) 1e-102

MAQDFVSSNNLPLLYPSGQFGTRLQGGKDAASPRYIFTLLQKYTRMVFPEEDDALLRYAD

DDGFPVEPV

>contig42617 Frame-2R|Blast-cGMP-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY55415.1|) 4e-34

MLENPIYVELTGLDYGEDKTVGKMIHYNRCKVQYVSCKWFNNEEVYSRNAHIKMKKGASA

EIKEDTILLGRNKRLPKTRPRDDMVRQLESKNEQAERQKLSEE

>contig42998 Frame-0R

MRPEEATMISKSGMQSVETGYALQRVTWRTNIDHAIIKLY

>contig43276 Frame-1F

MKAFVAGTPSTRCVCKRKNREEEASSGDHDEMTQLDEEEDGSTSRTPLTQHVESPSGFYR

RK

>contig43319 Frame-1F

MIITSSLFDVNTKCCHKSVLNPSQDNTGVSPEHVVSSISRLFILYVAESDLVNGNEDTLT

KLLRRAQLVNHIGSQCDTLRLLCIQKSQVSSPLLNSVMLSRMQNWFCIFSSHIFDDMVVL

PQPPSCQSLEKAIDEYVITAGHESFKKVTLMTSVKESEEWPLSKMKSLFCEASFSLVHVR

DQADHFQSLITCQTILSALDLLGTNIQEDVQSTISAGMKAINEACAHVFGKIDDKELLRI

DTALPALNSSVIEVAVLLPSGVASSETEAYKIKMMRALNDIPSIHHVVGSNLPNQVYFSL

CSALSNAPHFCVMMEWHGRTAQMLFVERQLVTSRAACDIEAYSVLCGMLRPVLWTQCTMD

LRSVCRRSSLINLISERLVVYYLDSFSEGRDGRPTADDATSGRIVITFYDMISYLSKLES

DQWAAVFDTSLEKLQGNDEAQLMWRNAMTSMMRNCVAILASHRCLSDKTISSSQLDFKSH

LSALVALMKTDAAVATHGSLERAYIKVLTPSWSPLHSLAYCDKLRNAASMALSQADDANS

PGFFSCAPCLVSRRLDVTCSSRDHLRIVMEKIKEVEAALGADCDGGVHAEHVICRSDADE

EVDFGDAEQQKNKQLC

>contig43904 Frame-1R

MLRTKKELAKKRKLRFKKLQRRQALRLGGGGGSGKPLSSDRQRCHMA

>contig43971 Frame-2F|Blast-hcp beta-lactamase-like protein [Phytophthora infestans T30-4](gb|EEY53607.1|) 1e-104

MNNPNLSDADIRRVNQELEERHYEFRSNCNEGEGDASACHSWGEWLSVVDKNYKDAAAMY

ELNCSRNDYPASCFNLGRLKLAGKGVGQNDFDALKLFEKSCAGGHAAGCHHVGFMRIQGI

GCEKNFTQALAALKEGCKRDDANSCNRVATMYMSPALDSPIKRDIQQAKAYLEKACDANF

APACHNLAVMYKKGDESIQKDQFKYEEYRVKTEKLIDQAGGISSIKSS

>contig44691 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56920.1|) 4e-90

MRAGRVEELIKAQKAYNETITKIETVRHQSNVELLKSMQLIGMTATGAAKNYKMLAAVQP

LVVICEDAGVILEAQLMTCLFPSCQQLVLIGDHQQLRPHISDHNLSVESAMGKRFALDVS

LLQRLVAPASALPFYVLTNQHRMHPQISQLLRMLFYPNIRDARETLEYPRLL

>contig44930 Frame-0F

MPHLGYTFTVAIVVCTTLQVLTSAATCTDDEQTTVDKLYMELSSSSACENLVFNSGVTSL

DYCMNRECLSVLSDAVDQLPDCTSNDEIDRKKGLATIITFCIGANELLDSSASASASTSA

SGSNNDFITSGTSKSAVVRGNMVFWLPIALYVFGAW

>contig45331 Frame-1F|Blast-hypothetical protein PITG\_01169 [Phytophthora infestans T30-4](gb|EEY60933.1|) 7e-13

MPLKRAFVALQDRFVSSLAVACCPTMDLIAVLTLDHHLLVY

>contig45533 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60943.1|) 2e-55

MARSNDVNQALLLNPELWTSTQLKEWLQHFEGGRYARFVGPLHGRKGAEVLRFTAANWAQ

LTPKNLATSLRFTLLGMAQVASSTDDSLAIVTDFVPLATSPRKLNQTQPGNVAAVKFPPI

IELPSMLVLVAAILFIILTILCFTVLRGPLADIG

>contig46042 Frame-0F|Blast-phosphatidylinositol kinase (PIK-J) [Phytophthora infestans T30-4](gb|EEY61830.1|) 8e-70

MAFEQAPFKLTADFVELMGGPRSAHFQRFRSLCVRSFLVARKYRYRFALLVEMMLHGNEH

LPCFAGDPKGTVERLAARFQPDLDINSCEDFVHELIDASLDNWRTRWYDKYQRWIVGVF

>contig46125 Frame-2R|Blast-exosome complex exonuclease RRP6-like protein [Phytophthora infestans T30-4](gb|EEY64044.1|) 3e-64

MVELDEASYLWVDTEENLLLMMKSLRAPEARVIAVDLEHHSYRSYMGLTCLMQISTARED

FLVDTLALRSKLQTLNHVFCDPSKVKVLHGSDMDILWLQRDLGLYIVNLFDTGRAARVLQ

YPRFSLAYLLKRHCN

>contig47351 Frame-2F

MLSTVSDKNTTHDALGDSNLSLKASILLAPPVFESDQTKTHLSLSADCIRDVDEMAESPD

RSDEWYDRALLNQLD

>contig48035 Frame-2R

MEQDTNISSEMCRRMAEMMHSTVPSNLFRATVTVNGCDDGN

>contig48408 Frame-1R

MRVLFNVRHPISCLRDSNERGTSAALAAAYP

>contig48516 Frame-1F

MADGYDPQKSRVAEDTLADFLRAPLTGDLLEVPGIGKAAIAKLSSEDGEDAVTNTFQLIG

KFLILKENSDDNDDGLIDCAAHCDAFWFWLKSKGITAYRRSELKLFVDFYMGSAYTLTHN

EFN

>contig49061 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67860.1|) 1e-18

MMMKNKYFYFQPFANLSFSNLETDLRRYAMNAAQITRTNKKEPNDLVN

>contig49263 Frame-0R|Blast-FKBP-type peptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-4](gb|EEY56079.1|) 1e-130

MPALELVAKMLHVGEVCEVRCDARFAYGDVGLEPHVAPGDEIKLEVELCRVGKRITTDMS

SQELLVEATQKKESGNRYFCEKNYEQAAKLYKRALKLLESWDQSDDDQTQCKELLIALGN

NVGNVQHKLKQYKEARQSSLEVLQLDGKNVKAMYRIGQIALDQNEFEEANVFLRKALEME

PKNTKVRQLLVQLKKQKREMKALERTLYAKLGGVKKPERVEMGTIAALIEWVRQNAMILA

AVWTLLAAIVIYALTSN

>contig49498 Frame-2R

MTVPGLQNLGNTCFFNAILQALASLSSVHEYLEDIVQSERAGKCDIAFTSTLLDCLDALA

PRESSSVVAPRVLNAELTHQLSYFRGNKQQDAQELLQFIFKLVSGEQRRCIVQDRGLLDL

ISDNVSISSSISELRLSQAVNERSWNPFQGLQVNVLQCTRCNCFRPLMNQPFLDVSLSLV

TPGGKNVSRLIDALQLYTANEVIKDVDCSICSVKHELKAAKEEYTQALEEIKACNTNGAV

STNRREHDDWIDTLEHFANFSTNFDLQELPRPIPRSQGDCIKRLLFSRSPDVFCFHLNRK

MYMKRG

>contig50049 Frame-1F|Blast-thioredoxin reductase 1 [Phytophthora infestans T30-4](gb|EEY67612.1|) 7e-84

MSLSENSPSLFLVYIASVLIICIAGHRRLNFGLVEGQVVLHPPPFFIVDGMDFQGMALAY

LEEHGVNTSIEVQSWMHQHGYTSLRAMLDDESLYDVTEEAIFECGLTSPGTETQQIPTSN

SFVTSGYTLDGPCEVWLSDSKVASGQSCCTEFPRGQHQIDYSLCGESCTLAWYWLGIKYV

KGTYSWQVYKNCVKLVKGNFTHMR

>contig50401 Frame-1F

MTTPADAARLEELMLLEAIRRSMQEFSVDKNGEERSKSQSSHHPTKKSGEHGTLAGYADL

LPISASQITTNASGTMPCSSSSSAESSQNVVRRTAIDA

>contig50474 Frame-0R

MALNPPSALQLYPERILSAQQIPTITHYTKLTVDCLPRDGCRQIARQERSNRSDITAVAY

GSMIFSVLPHF

>contig51037 Frame-2R|Blast-chromodomain protein, putative [Phytophthora infestans T30-4](gb|EEY56540.1|) 2e-18

MPLSVDTEMQSNDDHQMQFPFAPSNFLAPSPTPIRPLDGDPRAMKPHKQEGASVASNNTQ

KSANVNLQNETTAPYCDFACSNTVSQSQMFFH

>contig51525 Frame-0R

MALLLSPLWIHAARNGNAFHSYSHGTV

>contig51648 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59236.1|) 2e-59

MVACGSPVDTDNFIRQVIRAGADVLAVDGDGWSALHWSAFHGRPEAAEALLSSISGTDRE

QLLAITASDGRTAAEVAKGRRKCRRG

>contig51756 Frame-0F

MLTRALRSSYSVSRRYIGGLAADSSAPTVAENVVNVVLVDYEGNRHVVQGRAGMTLRQAC

ETNKIGYVKDDSMGGGGVYDARRADYYTESLFGEGSTSPQSHVVVSNEWIAKLPPANNQE

RHIIDTYVPAEDRSDNSRLGTEIVLQKELNGLVVAVPEAPPIEEYKYEHEYDEDDYESYD

DEVHHT

>contig52234 Frame-0F

MAMDFFIQLQRSAWAELKIPSESSTNKTMRTFKLLDSKHQFTRSVMKIVADCYSIVSELL

DYEDAHLYQYLFSRVSSRRKLSRQTWVDCVNLHPSFGIISAEQLQVVTHHREYPDGSNVI

VAMIATAAIDVSECGLLFGFFIAPSDRNNELNSVNVSCITALSNENHPQYFNLSLELLRQ

LNEKISMPRFVRLPSEMGTSMTSSISQEKVLSDSDRRRIWKENQESKHDRNESRRSYVSS

NTSATSSRGETSEQYVPAGNYAAQVSPYDFTHVTHLDTNEQL

>contig52241 Frame-2F

MIDQHVHPSQVDSGLLTMRQQLTDHSNSVQLKQTIEIIIKNTKFKKSELYEDLSTKYGED

LVVALSIKQKKAGKKLRTWSD

>contig52502 Frame-2R

MVQPAKTILTLLLVAVAKSKCAHANPCTSIELGVFNDVRGQVSKCLQDSKLNFLIPPRTS

LTKTQQTALCKSKTCQEMIGSMDDLDIPSCEATFDNQNMTL

>contig52739 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54890.1|) 8e-41

MTRHDCEQCTTLQWVKLRSMSFFWPACVYKSYSAAVAHAHDVWTLRNAKPVLDTEDCVLY

FFGVGPRACHVVAPGASPSLQLCVVHEEDLTLASWTAPDDFTRLCKNFNVPMAMITRAQN

NVCFIRACNEA

>contig52858 Frame-2F

MGESRQRALERWLVEKRRQKDYKSRKATATSHSTCHAVSQRTAQVTLRGMMKARKSRKAS

PASVTIES

>contig52920 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70211.1|) 7e-57

MSMYEVEKLCYYNVLDVTVDASPAEIVKAYRSMALKYHPDKTRSEDLNQFQAITEAYEVL

SDPEKRRLYDRYGPALKPRVGEAITQLAPLLLSFTTGLIGSSVRTCNGALSYQVIYSCEI

CFMGFAGMYFCHRPGYKENIKSPVNQQTKIQREVMSVSDYVTM

>contig53127 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64236.1|) 5e-59

MTHLLQTQQQHDFTQAEAMALRMVHEKTPQLEKVLSWSDKPLIIFRALELLEALARVSGT

AARELVRLFDFQSSAFV

>contig53790 Frame-1F

MCSHFNLSAPHEPLQANQLGGNCGVYLQDVFYMLAHFHLHAPSEHTINGKAMSGEIHFVH

KSSVSDDLLVIGVFLVIDVTSDPWLAPLLDALEQVNSAAQTEAVLVQLSP

>contig54045 Frame-1F

MELAENISMDLEGRVLVLLDEISDRSLRVDATLLVLRSAVPPYSEALKKYATDFKQ

>contig54427 Frame-1R|Blast-60S ribosomal protein L44 [Phytophthora infestans T30-4](gb|EEY69005.1|) 8e-11

MKRTKHFELGEKKKSAGHQY

>contig54643 Frame-0F

MDAELRISGFKRILVRLDESTRRKYCCRALEEDLQHAKRQMRACAAAMAEAKEVDEATRK

LHASQR

>contig54728 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66317.1|) 5e-16

MTARLSGGAKCQVRVAGEVNRMIQKDVGELYDQLEIVRAEMHFPSFAPINVPMVLVLGNH

SSGK

>contig54931 Frame-1F

MWCFRQQPEWERRECDAHRAQTSRQYSNDCSRSETSFNHDSLGRSHQELLDLSSRCGTCV

KRLTKLSGNKPCALCCQATCSRCRVPRTLKEVSKELWMRKADVLVCKRCVLRVDNIAAVD

VARAEVNAHWLPKESVHSTSNTYVARLVSSAMTTDARTPS

>contig55194 Frame-2F

MHMVTTTFDRELHASYFLKNLRSLPSPYAHQDMYPWPSAAE

>contig55891 Frame-1R|Blast-phytanoyl-CoA dioxygenase domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY60398.1|) 1e-111

MSGLTSAQLDAFHRDGFLILRKALTPSTCDELRSRAGDYVAQCDVHDHRSIFTTNDQTRR

MNDTYFLESGDTIRYFFEEHAFDKDHTTLVVPLTGAINKIGHNLHNLDSVFQKVSYSTQV

QNILKSLKYVRPVVVQSMYIFKQPNIGGEVKAHQDGSYLYTEPQSVVGFLVGVGGLYS

>contig56663 Frame-2F

MTSETTNDKVATKKEGGVTRTGIASKARNGARKRQSTFGFHAHQPPPITISRNDEVPSFN

RLR

>contig56847 Frame-2R

MNTLYWRDRPSPCHSIMMRSKQQPIAMKIYEESHCETRKQAFSKVTNKPVY

>contig57008 Frame-2R

MAVNENSPLLHDRSDQQRTRPPLRRALYVIVPLALVAIATIFLLVDSNKSSILSKRAPAT

T

>contig57116 Frame-1F

MQMSRASTGNSLPFERRARQRSFGDLPRSVQFSHAPMRNTYRETSMTVPRTFHDLRSAPL

PIASGLHPPPILLPRHEHSSLAPPQLSYEDSQILRVNRQGSMEIFYGNGEQSLQTTFSEP

VMQGGFQYRSLPMSPSRSTLDEFNYLSHRSLCEPPPPPRAVYLNQATCSEPILKEKSSST

EVINLDDLRAAALRSKVDRSLPLLASTTATKIQDSPISTAAPIGATSSLTSSSSPSRSLH

MDEKIVQDASPNSENELRLEILRSMTRYRKQTITDTKDGSQVLASPLSVTNIAKKLKDAK

EARDSVGNDITKNPVHLSNSCAPQKVLELTPSNGHESANAGHVVNCESSKFILKNGKSDK

ISTSASNSANLFAQGSKTSPKLRPLTASTQSVVIWLNTEDFSPRQGKTDAHLQSTRLQEE

INEMRRKIAEREQERINRSLKNTPAKWSGDLSSRAPSSPTSLHHSSLGKQVSTVSIKPPN

ASAILPEENEVESVLDGIHVQVSLNDGNQPTGLGNKSQPLEK

>contig57282 Frame-2F

MTMAHIICEFRNQEAKSLCH

>contig57435 Frame-1R|Blast-hypothetical protein PITG\_09549 [Phytophthora infestans T30-4](gb|EEY55606.1|) 4e-36

MNGFPMETGWQKMKRRCQEEPLVPIGCLATAGVLMGGLASFRRAADAATQQKFMRLRVLA

QGATVLAMALGGFIALKPSEKNGGTRH

>contig58481 Frame-2F

MTLAVILCTYTKVGHFVHHTQLGGLRGHQFRCSSKEGHVYSTIDEDHFKCTA

>contig59110 Frame-0R

MKDNVTLDTEYSYTETDNLKLITFPVWKEAVELVLQWREQDYKAFWLLLAQFHRMIPVDN

NGMDLSGPH

>contig59532 Frame-1R

MTFLLPHISNDKEELSSSRRIE

>contig01055 Frame-0F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY65942.1|) 0.0

MARSGSDVDSDDAMHSSKLLQQQKKLCDEAMELVNAGVAMQNASPPDAAGADAKLSRAVT

LMEQALTIEYPTQEERDASQRLTNKMNRYVKMIRSQREKGSAGGATGRAHNTKNNILPMD

KLPPTYKVIVELLTNSSILGDVFESLKTTFGFQDANVANQKEHVMLMLTNFKLQEDEPNP

TNVAIQRLDYQQELDMATKGIKRFHTRIFANYTKWCKYVSTKPAFTSDPVVDIVLFFLIW

GEAGNFRQMPECLCFLLHTSLPQASSRGGGKHPGDFFNEIIRPMFEEFRKDNDKKTARGA

RAPHAEIRNYDDFNEFFWSKKCLKYTPLNLHEAFGQVDKKGRPNVIKKSFVEKRTWFRAL

MSFRRIFCFNCALFLAVCGFALNMVMYCPDTPILYGADLSTGDSRGFTVFGKNFTASDVT

SIGSGDGGEDKTNSDTGPSCNQQVLATCLGMSYTSGVFDDIPIDFKALLQILPFTDCVEK

TTGRCGCYLDLLDNCFEEKGVTTKVTEDELAFSAASEFDQSLCVVNWRASVESIIKKPGP

GKLNCEICQLDLKALITNGKIGELFSGLLEFGDGTPLLPGEMDNPKRTDMGGLAMAAGGA

CLVLVFACEFVNKMVSRVGSGYVGRSLPVPFRAYCRYTCFWLLLFMCKLTFDYQYMIKAL

VETTLFIWYAKEDEYLPYSNFILQMTFHNIAYILFLWIPAFFVFMYDAQIFYSVLSVIFG

SFAGFNLRIGELRSFRVLRLSFKSIPRMFNKKIVPNIQDTAADGKKTKKKKKQGDKEIAE

MPVRHFERVSMADGIKPLTVKAQMYSNLLDQSGDHLYNEVKTPMDKDDVSSTGRQSQLGS

VTGVSGADFERTIAFAMAWNRCLGSLREADVISDRELNVLSYLIDSKDAEDRKLYPPAFL

TAGKLDESLDIIVDCSAVYEKLSSDKKKKDKTLQKIENTMRDRLTKDDLRVESILGSYKF

TSQAVRFLLGDEHRDLNECFEFMEEMAAQKSILKGLNLKSLHECRAACAELMKALLEVPK

TTSDNSIKFQRSLYRVIDCVESVLNCMKKILTKQEHLVQILTNTPLKQSSFFFPGDAQQY

ANVQLQRLVNSEGCIGYCFARISF

>contig06793 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59688.1|) 2e-29

MLQPPELENGQLLDAEARAALVQAQEELNAGNLPADANPLLLFLQTLLPWNQVQGAGQRP

PL

>contig07934 Frame-0F|Blast-luminal-binding protein 3 precursor [Phytophthora infestans T30-4](gb|EEY57932.1|) 1e-116

MVLTKMKQISEGYIGREVFDAVVTVPAYFNDAQRQATKDAGTIAGLTVQRIINEPTAAAI

AYGIDKKTQGEKNVLVFDLGGGTFDVTLLAIDGGVFEVLATNGDTHLGGEDFDQRIMQYF

IKKWKKDKNIDISK

>contig10660 Frame-0F|Blast-peptidase, putative [Phytophthora infestans T30-4](gb|EEY53248.1|) 2e-83

MLESVLSEAPKRKQEGGVSAMKDYLTQQSDAFAQHAHLASYNLFEYLVTAFHDGYQVSDF

YAQKLQVQSLFYPKWWLQQVGFFKSV

>contig10974-1 Frame-2R1

MFGVSVTFATVLYGLRKDLPYLFVNTEKGAS

>contig11810 Frame-2F|Blast-60S ribosomal protein L12, putative [Phytophthora infestans T30-4](gb|EEY56048.1|) 4e-83

MGAPPPAGEEKVVILRTVGGEVAPASALAPKVGPLGLSPKKIGEDICKATQDWKGLNVTV

KLTIINRQATVTLIPSASSLLVKELKEPPRDRKKVKNIKHDGNLSLDQVIAVARIMRERS

MARHLAGTVKEILGTASSLGCTVNGEAPTEIQRLITEGELDIPEN

>contig12312 Frame-2F|Blast-ATP phosphoribosyltransferase [Phytophthora infestans T30-4]gb|EEY55681.1| ATP phosphoribosyltransferase [Phytophthora infestans T30-4](gb|EEY55632.1|) 1e-138

MSDERLLFAVPKKGRLHDKILKLLMGAGLDYYRPNRVDIALCSSLPVTLVFLPASDIATY

VGEGKLDLGITGQDIVAESRTNVNELQLLGFGQCTLGVQTPVKDAITSPKFLAGKRIVTS

FPNVTRDYFKQFETEITGRTKIKYVSGSVEAACSLGLADGIVDLVETGTTMKAAGLELLS

TILTTEAVLIANPHTAHQDLVDKVHQRILGYITATKYRMVTYNVDKDLLDKVSTITPGRR

SPTINGLVGGGYAVSAMVEVKDVSNVMDQLHDVGATDIMVLYIENCRA

>contig12576 Frame-2F

MRVDDGFDEREDVEIRRPCRRNVRVLDDSMGFSDRDSEEDVGSRKTIRAIEDDSNDEGPS

SWRGGTTRIVDSDNEVCEEIGRNAIEGVNEDEMEKAVGSEESQLWCEEDGARPRKRVCPP

MRLVEGESEEDNDSRGGRL

>contig12811 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54298.1|) 1e-10

MPFKLKHQYYLLRNPRILLCSKPAQHHLSRIVLWWGGWV

>contig13643 Frame-2R

MTDRSIRVVVAALEVTGGIGLRHQIPWHLPSDMKHFRALTTAQSNASVQHAVIMGRKTWE

SLPEPVRPMPKRYNVVLTRDTGYRKKKKLPENVGVAESFLAALELVQQQGDKVDQIFVIG

GGAVYAEALSYPKCTKVHLTRVRGTFECDAFFPLELLQQNFKVTEESEIKNENGIKFQFV

ELERKKGTMQDVVTESLVDTTMPHEEMQYLDLIRKILEQGVKREDRTRTGTLSLFGAQMR

FSLRDNVFPLLTTKRVFWRGVAEELLWFISGDTNAQTLMQKNINIWDGNGSREYLDSRGL

YHREIGDLGPVYGFQWRHFGAKYTDMQADYTNQGVDQLAEVIQKLRTNPTDRRIVLSAWN

PIDLNEMALPPCHMFCQFYVANEELSCQMYQRSADMGLGVPFNIASYALLTRLIAQVTGL

KPGELIHVIGDAHVYMNHVKPLQQQLTRTPRPFPKLYINSVKTSSIDDFKFTDFDIRDYN

PYGTIKMAMSV

>contig14040 Frame-0R

MVSKPKTTPLLYLYMLLSHTVVTPIKMADSYDAPHPSEESLENFRHIADVTDPSLIKDSP

ESLRHVSHVTTPTLSKKSSENLRHVSKLTVSPLSNDAIENLQTNLQVAASPLLKVFPVNQ

TQDSHGFEDRSYYHDELRLSAISLAKSLDNSQFHPTGIYKYVPKFLRGSYLNRVEGFQRF

TLLWNDFRHDCLDKMTNNALNDKFLIKWIKKIKERLPMRQDEAFAIIAILLSDQFKVPMS

LRAIAGLIRDYPNDYHLIFTALKQLEKKEGPRLMTSFEHPNGPGMVVKN

>contig14538 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54568.1|) 2e-33 NOT\_ORF

MLDAITPTTNVMDEDLRETLVNDEAF

>contig16271 Frame-0R|Blast-1,3-beta-glucanosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62229.1|) 1e-32

MNEEEEMTAEIVGGNVFEFTTEIANLAKSKKLTKAGDAGKYGIGYLFPETCDNNSSDCVF

TPYPEYDNLKS

>contig16886 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53439.1|) 7e-50

MVSFWGCTVTETKTASVNVPEGFVLNVVNATCDATAADAQVTIGLETNQLDGKAWKGAVA

HLGAKQPLQVKLDLVFAQSVKFYLAKGLGSVNLSGYFQPGPSAGLPKANTTTQPSNAPKK

SKKRANVEVKEPLKSVKE

>contig17315 Frame-2F|Blast-alpha kinase [Phytophthora infestans T30-4](gb|EEY63164.1|) 1e-07

MNNAGSSSSVNRRRVSKPPSDKMNAHYGNRNAPLAVAVAIPSHQSPFEKL

>contig17360 Frame-0F|Blast-sphingosine kinase, putative [Phytophthora infestans T30-4](gb|EEY53016.1|) 3e-49

MLEQPDGLREVTLLNRKKIRYFPDGQVACVTSNGVESRVSSDVELQQLL

>contig17979 Frame-1F

MSSDLSILLYPSAVQSPSPSVKRFLKETPEEKKTSSKHHFRKEKLNPLKDTKKTKTSTSA

KPRKNWIMRKAALFSQWIQEWLVRILNFLGLRPNKGGKALALYKWFEIKMNFKRLKNAMK

WFRGGLPL

>contig18523 Frame-2F

MPRKKKLQRSPSFDSSTSSTSSSSTTNNLAADDLSKIRRFPHVPAPVYPRKIEHIIHSAK

KKHRSDLTPDYWNREGFAGSDVCDLPLDESNAIKREHCSDLSVERFIDEFELPAVPVVIE

GIPESEKWGALKHWSFKKLRRKYKRVEFKCGEDDYGKSIRMKLKYFLIYLTYQIDDSPLY

IFDSSFDDHVDTKSLLEDYQVPKYFPEDLFSLVGEDRRPPYRWFLIGPKRSGTTLHIDPL

GTSAWNTLIVGRKRWILFPPHLPKHVVNGKKHVRGNEDDEAVNYFMDLLPRIKQANSSKS

LQCIEFMQYPGETVFIPGGWWHAVLNVEDTVAITQNFCSSQNFPAVWCKTRKGRKRMAVK

WLRKLELQYPELAVVATKLNQKDKYVMYSKEQKIHTHEFSKQKKSEHPASMNSGNISEMC

TSVKRRKRNFAEV

>contig18710 Frame-1R

MFSMPVIEIKHHTWVNNCILLSLFPQIHAIILTNKLECHQNGDFQKM

>contig20542 Frame-0R

MSKREYFLRKGLQMQRLDEQISSAPISGNASREVTKYRDLCPPATPDNHIQKVIAQCKGD

TQRMETAISELWENYRGSEQDAWATVSKKATKKKNEHPLHFSQRSNSTPQHQNEHVELPQ

NGDLQSSKLSERYSTRGRGSLRGRGLVSLRGGRGGRGGRSRGGAIIATDSTREPLTGDES

PDNDTESTTNSTNEMQLSRTVKDTKRDRGANTTTKAANARAASQIPPVVHPVLTGAWTKK

LNVNSVSAKPEPTKHIPSSASSPTPASPKPADKTTVSVTDRDAAVDAIAQETLDAVGPLK

KEKLAKESKKTQKRSNYDASEPFAAMNKPVDAVEKVASPKNSPQKMGEKQTTTKRIESTG

EATPSANIATGWGNLDVAASSMSDWSSSVPAASCEAKMVPTSNAWTRNNPILSSPATKIN

TSTPSSPVADTRLIVSPDSPKDTEGPRSSKSASTSPRPYLKMGKWDRAATPNLSLQFGSF

SLNGMESLEPATPVAAPVSWSSSNVTTSGSKNVVKQVTKTTTAQTTPVQSGWGTATKTVS

PKSILSPDHSEQQQQTITSKSASSAPPGLSVDSGRVTPTTGHSPRFAPSAPSPASLPKPD

EVKRGTPSRAQGGSFQTQLQEGAATQNNKLNIGYGTGLYQASYGQYSMDLGRSTAASAPG

QHHAGSGTPKTASTRGSAVGQVAIQSPSLGKQAVSQMQQIPLQQQVQQQQQQQQAQEQSH

QKQIHHQQSQQGQQNPTQQQTAAQLHQQAQASMQQSYHYAPPPPPGMALPYNPYNYNGYY

QGYG

>contig20861 Frame-1F

MKLQFQVFSTIALVASGGTFEFLDNLDQLESSSTGETSRDASYICQQYSFEETVNTSKVF

GGLGGEEFTDVKQVRYGVPLNKVILYSGERLDGISLIAEPVSDPFSLLHHGGKGGREQIF

NLETGEFINKFTVQTGRKDGSDRIRYIKLDTNRNRSFEGGTRAKDDFGLHQVDAPPGFMM

TGCHGRAKDEIDALGAVFVKVSDHICKSSKKT

>contig21185 Frame-2F

MEQKNEEIRLKQIESELNVIQERQNKDMTLAEAMEEMRNRLERLEEITASQEKAAQVEHA

AMSQRDEKEVEKATTSTKKIEAALAMLHANQESQEQPTLPKWLTSSLDGAQGRREIRRQD

MLQQDVANYVAKQKK

>contig21592 Frame-2R

MFFSHDQQLIVKSMSDEESVFLRSIAAEYASFLLTNPDSLLTRFYGCHAIRLYGNTFNFV

VMANLFSTEKVIHRRYDIKGSWVNRSAKHPSKGKRVTCRHCNAKYVFGSTDAENCRARVG

RHEPNVILKDNDLTAKVRLDTSVAEELYHQVIKDANFLSRLGIMDYSLLLGIHNVEYMVN

PDLEEEQIVLTKDMVGPRRTINNSTMNLSGSTAPRSESKLPAHLPRLATGTRRANTVVGP

SIYYFGLIDILQTWNMDKKLERFAKTKFLAKDADGLSAIPPAAYCERFKRKMGEILSVTT

RDDYAECFVGERRGSNSNNGETDPNRRFF

>contig21714 Frame-2R

MADTGHDARENGLSHRKRHDADFGGESASKKIKLEEDTPPEANPNTIEAVREKNKALEID

MKEKNRRIAYLTKKCESLYRSRGVASASFRCLRRHWFQLQDELLTAVNAFSYSDEASLKT

WQVALDAVNGFGQPRLLKNELTINLPEWFMIVAKDAKQEEPDADVSLPTDENTLDNTFIK

ADDLTNIENDVLEQLQERSEKTKELLQKLLATVGSASHDKAKMIEYAHVLKSKRAAVAEL

LVLKSQLQACKTCIADLEFDIEAKEIERHRACRDFDRLSTFVKQQGAVDAENVVDANLKL

ERITDDSNSLDKLPDSSSSEVVEHEEIIKKEKEHEKLVATMRENMSILSKKLYQERHKLE

SMDRELDKYRALESAWKNDEAVLIQGHEEKLNQLRQEKCHSNEEYTKLLHKTKDLQHHIT

EKWEKKITKIQAEMSKTKSQMDGLNLKNVSLREKVFNASKYRDQLIEAKSELQSVKRENT

KLKAHVENITKQAQAAVDNHKIQTLTIKVAHLEKENLEIQQAYNTIKQAEMKKAHEKAID

VLKPLIELEKKYDHEKRELSACTLELATLRAKMENMKASCESAREENDALLLEIESMAKN

IETLRLARKKLIQQIEDKRNANKKLNTLLAREEQAKSHCFEELAAVRLQVSTLSTVHKHQ

KTLIESSKELLQAKTCELEKLKTYIHVIESQCEATDAEKR

>contig21840 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62725.1|) 8e-41

MVSPRSTASFFARTSCVASGHSVFITDTLPSRQKSPMVLHGTLDGSLNDCMFGSLATTEE

AWRWRSSHIFEKIHDGRLLATIKGPSLEDPFRFLGLKWYTNDVPLVLSGILQRRDYLIIE

ATGLTRDAHGDVVGYFLSHSVTLPGVAPDLSHLGG

>contig22070 Frame-0R

MRAARSIRRSWRTFQTAPLSTNSASISKFPTATYMAVGSGAAAAVVAVYNGVAPLEWVIR

QLAEPM

>contig23213 Frame-2F|Blast-phosphatidylinositol kinase (PIK-I) [Phytophthora infestans T30-4](gb|EEY57127.1|) 5e-08

MGMTRYEGLVRIRKRANLHSSSSAYFLDKTADGLFTSSSSNSHLPSSSHLSDDVWYF

>contig25022 Frame-2F|Blast-hypothetical protein PITG\_05283 [Phytophthora infestans T30-4](gb|EEY69099.1|) 3e-08 NOT\_ORF

MKLCTAKVPFVFARRFRVPAKL\*DIPNAY

>contig25097 Frame-0F|Blast-Folate-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4](gb|EEY60612.1|) 0.0

MATSDRSTAMEDEEAELEQTDERSSLRQGATSDDHSPSSSIQERTTDKDIKKKLKKQQDG

QGEATSTNGALRQGSAPQLLSMESIGLISQYAAVGMVYGVLPSTITPFLTYYLNMEGTAT

TSARALLSIPWSCKVFIGILSDCFPLFGYRRRPYMVLGWTVTVSCLLAMAASPLEEPYFP

DPAMRNIKPAEYSLELTQSFNKSAPNSGAKYIVLMMFATLGYLFADVAADAVVVEYAQRE

LEETRGRTQTAIYTVRTLFNVVAQIITGFGLNLPEYGGSFDFGLSFPDTMLILAIFCLPV

IPMTWCFVREEVVSKQPVFKQYIGDLWTAIQSRAIYQVIAYSFLSGVFSGFTYVAQDPMT

SYWVHATSFNLSLSSIFGSFVTVVTLTLTGKYGLNWNWRTMQVVTMCSVIALDAVCTMLV

TWNIVRKQWFWLGVPIVEAVPDAVGFIISTYVVVELAGHGNEGAIYGLLTTVSNLGGPFA

LTLTKNVNASFKVFNENILNDTTEVRRDVTITIVISYVMKLLALVFLPLLPRQKHEAQAL

KRSGGSSRRMGVLTIMYLSFALVWAVLTNLLGIFESTRCWVITGGCKE

>contig25394 Frame-2F|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY66689.1|) 1e-113

MLPYGGGFNPSWGNFEHDSGGECGVPMHHRWHAPGTGNGIYWYSFDYSGIHVIQMSTEHN

WTRGSEQYEWLRHDLEQVNRSVTPWVVLTAHRMMYTTQMYIDGDMNVSYKFQEEVEDLIY

KHRVNLMMVGHEHAYERSCPLYKNECIADGRGTVHIVVGTAGFPMGDEPFSSTYGNWSLS

HVNDYGYLRIATSPDDIHIQFVLNQNGS

>contig25668 Frame-2R|Blast-V-type proton ATPase subunit B, putative [Phytophthora infestans T30-4](gb|EEY70646.1|) 0.0

MVTADQAFRANTAAVVRDYYVEPRIDYRTISGVNGPLVILENVKLPKFAEIVNLTLANGE

KRQGKVLEVQGSKAVVQVFEGTDGIDNRHTHCEFTGDVLKMAISEEMLGRAFNGSGKAID

GAPAVVAEEYLDIEGQPINPSCRDYPKEMIQTGISAIDVMNSIARGQKIPLFSAAGLPHN

EIAAQIVRQAGLVQRKDVIDSHDDNFAIVFGAMGVNMETARFFRNDFEESGSMQKTALFM

NLANDPTIERIVTPRLALTTAEYLAYERDMHVLVILTDMSSYADALREVSAAREGSAWTS

WLSWLYVHGSFDVVRACWSSHGP

>contig25963-1 Frame-2R1

MPSPLLVSSIDLDLIHKSLRLMLAIAAS

>contig27011 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63417.1|) 2e-36

MNMANGNLVDRVLRSRTLEPGNSFPRKVGWLGFSRNAEIARTIQCRCCQHGYTYDEFVHH

AGISVTALKTKARHLLYVVERTDESALVPFSAFALTLSVAGASHELETLLKELQPPPFAS

RVL

>contig27433 Frame-0R|Blast-rRNA-processing protein, putative [Phytophthora infestans T30-4](gb|EEY59702.1|) 1e-99

MRYLRAKSIRKALRQFHILCGIKPPYKVLLDGNFIAMCLQMKLDVRERVPKYLQVKPHEC

EFYVPGAALEELKMLGEATKAAYDLAKSFKIAETHNQLDDDEQRSVDVSKTIQSIIGDRN

VGKFVVCTQEVELRKALRLVHGVPLIYLNRSVLVFEDISRATLAIVRQEEKSNMAKLDVN

EKRKLNQMVEAGDNDNDAKLQRTTKKRAKGPNPLSVKKSTKVKVRVKKKKN

>contig27925 Frame-1R

MDSRKSELCRLFIVCGRNCKEDELRALFSPCGAIKHLHLVLDRSKKSRGFAFLQYENSSN

AVKAIEKLDHLELQDGHILKVTAAKERPAGGNGKQKRDQHAQQGLDEKAKEKIQEDEKSI

DARLHGKRQRSSPPIYSLSRKPRRVVPSFVLENGQLDEYGCDNATLTRLKMKSSDDEVPL

PNIMTKSNFPDVCQTNVAIVMHMMISAIEQIETHKVASSKSFFTYKRLSTSLSDVYAQMH

DARISAPKESIKKETSAHSLASSIRSVSLAPTSITNQGSQFESPD

>contig27950 Frame-2F

MEEPLVSRGQQLEAALDRLPESYFAATPLLSPIKVLSTTFYASPEPENKPQTLGSDSASP

RKHPASNATMSCTDDELELEKFDGSRRQQSNALQQCRQQTLGHSMVSSRPSTASSVGACS

DLVLSGFSMRGREKRVMYHIDVVHPDAPLQTYTIRRSYTDFKTLHTQLTELLESRKAYDR

SKAVSRLARGVVPVSQEAMTQEDKLEQALVTFTLPPLPHAGFLTFWKRHDQSHVKYRCES

FQYLLQSVQQMPFLRESFAMQKFLSVAPCTIRDRGSSYVSLCEYSVPA

>contig28014 Frame-0R

MDFGANFPSLPPRISELYGANRSALRVGEAKAYQQDLNELEREEYAFMSTIQELVNRQAA

VPIGVKFHREGAGNVVLQTHSQVTSDQIRSSSSEEEEDSDEEDDNEEQEITGRATIERED

AQQSGEDSFSPDVDTEDDSMELDEVHSPRNDSRGF

>contig28353 Frame-1R

MAPIELTKSNAMASQPTIVYIPKNNESVTQNGTLMTPQVDDLPTQNIALTNPIDVVMQGS

STTAPDQGRIDDTIALSLAPVLDQVEPPRSITVMDAIPDKPHVDVNVVNSC

>contig28421 Frame-0F

MRPPFEEKTHPVLPKLASRNDFGRALPTNAFWSNLMAADGHGLNAGAGEITLSPYTVRSL

PKRLEISYGDSRRVATKDAVTEYFNVDASFLAYSHKVLTSSNSTLLGYGNSTSRYIVDFD

VLSVSLQYNYGKSNQWMLVPMVRGSPYITVEYQNVLPVLELNATVLTINGEHVEESDPMM

SRTKLQTWTNKRFELEIEVYGAGESASNTSKSLQKWILYFETARTLQVQVVNEKDYRPYN

SQGELRTPTTIRLVDTDFYTGAARLAIVPQQMAQEALDTAAGIYPVSSSLTTNITTNTAS

YSFCWQTKRFSDRGDFKQRSSSTLELLMLANVHHIATLKKESNLRVLGKFGHRTLKSYMT

AVLGDCWEMEESLPTTSFTEEMVAIQPQYRDAIKLALANDSLYKPEANDPYYFGKEISRQ

ARLVLIADELQEIKLRDDMLDSLVEWVTPWMLGQNSDYFVYDRSWGGLCSQNGLKGVFYM

TDFGNGWYNDHHFHYGYMLYAVAVIGNFRPEFVTKHKTVVMSIVRDIASLDEKDTYFPFT

RHFSWFDSHSFASGIYTLDGGKSQESVSEAINAYYGVYLVGKAFNVPQVEHMGHLLLALE

IRGAQTYWQMPSTSRIYEPIYTANKMTGQVAATKVSYTTWFGPQAEHMHLINMIPFTPIT

SAFLHPAYVQEEYPVLQQQAFDRIQDPMNDRWKGYAYLDLAIIDPATAWKKVQSMTFFDD

GSSRTNSLFWIATRPIS

>contig29725 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54118.1|) 4e-34

MRIFSRDTITDFVRRGDLEGVRRRLEKGDDVNERRSFNNTPLIEAARYNVVDILELLIAR

GADLELTNRNDLTALHAAIDEQRSA

>contig29848 Frame-2F|Blast-CTP synthase, putative [Phytophthora infestans T30-4](gb|EEY64095.1|) 1e-156

MARFCEPDLQAWSSMAHRVDAFDQKCIIALVGKYTGLQDSYLSVIKALKHATMKCDRELE

ILWIEASDLEMEMQETNAKAYDEAWTKLRSVDGIVVPGGFGDRGVDGKVLAAKYAREHRI

PFLGVCLGMQVAVIEYARNVVGWLDANSEEFDANAGHKVIVFMPEINPDVMGGTMRCGER

QTIVHEKEDVIKRSLVSYLYGKDQPILERHRHRYEVNPTFVSKMRESGLNFVGTDVTGER

MQVIELDRDVHPFYFATQYHPEFKSHPNDPSPPFYGLILAATSKLEQFIKDVEAKESEA

>contig29941 Frame-0F

MPNEWRKVTRRNIVSNFLPLPSRDLDIQSRRGTLESFVNESEEEPIEEEEEMMEQMERTG

RAVASDRNHGDQTIRDKEEESDTDTVSLYQTPCSKRKNELNFREAIQDEVKKKETQSDEA

NCFTEKDNDMCLVCDASPRNSGVVHGLYLHVYCCYACAKRQYRVKSGCMVCNRPIDQVLR

LLPLTYDARKAIRNRPKKT

>contig30161 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54890.1|) 1e-35

MHLKASQNVPPSTVKHTTTTTNVLPLLKTPDKTTLVATCWSQMLQNGWETMTQGDGQVLY

KMPNTRFVAFKPNVNLFDSLEKACVHYIRDWIQQTRLNSSTEASSDFIALFWSMAAASGW

ESIETTTETLYKH

>contig30891 Frame-1R

MQRISGRALSSTASIAAALRYRPRETMPVFSTHLSNNEHREPSDPAIATAVQEMQSLTPT

MNRMKISRAKSPVEHRREPSGRLSSSSSSFVKIPEAVSENGEPEQEADTKQKEVAPERQS

EMKPRRSSIFDVRSEWI

>contig31272 Frame-2R

MEAQQTKIYVPDPKVSWVEASITKGHVVSENTIEVVIEGDSAEENASNQPEAGSIRKIDK

STMLLQNELMSDDGCADMVSLNYLHEPAILFNLKHRFLRRIPYTYTGAICIAVNPYSWLD

IYTKALQEQYMERDRSELPPHVYATSAGAFQHMRIFGENQSILVSGESGAGKTETTKILM

SHLASAGSHSTSDAQAKEANIIERVLDANPLMESFGNAKTSRNDNSSRFGKFSELQFDAL

GQLIGARSRTYLLEKSRVSLQGLGERNYHIFYQLLAAPADVTTEIKVTGLQAKDFMFIKP

HEEDIENGIDVSAGMKDAERFQQTVSCLETMGVSKEDQRSIFKVVAAILHLSCLQFESMP

GNEDASQLTGTPENQQASELVSHLLELDDNQLQTALCTREMTAVADTYEVPLNVSQAEGA

RTALGVALYSHMFSWLIHRVNVSTSAAAADVAHKICILDIFGFEIFEKNSFEQLCINYAN

EKLQQKFTQDVFKSIQQEYEDEGIPWTRIEFADNVNVLSLLEGRFGVLSLLNEECMRPKG

SDAAFANKLKAHYSDNDRFECPRFARDAFVIKHYAGPVQYDTMGFLIKNTDALQNDLIIL

IKKSRAPFLKKLFPDEHVGDAMTGIPGTAALAATSALRGRSMLKRKNSIVADTVGTQFKS

QLNGLMEDIRRTNVHYIRCIKPNGKKSPLVFNKLRVTEQLQCAGVVEAVRISRMAYPNRV

LQTMFLERFRGVASSSTASSALAGLTASVDENPSDDEKIAAAVRELLANLMPGKMNEYEI

GKTRVFFRQGALEGLEELRTRKFNAAAVVLQRYAKKWMAMAMFQRVKEATLVVQKVFRGH

RAMAQYKSQRMAAISVQKYVRRHCARQLLVHMREEYRATKIQNVCKMFVARRQYLVKIKA

IRTMQSVVRMHLAVKAFSGLQKQAKEDAKLENQIQLLKKRLQQEREARIELEQQAQHGSR

ASVHMRSEEALEDADLVIDQLRRENAALKDANTNLKAFGVQLRKEKDVMERGAYVNGASF

AAANQRATKLQDENEVLKSELARYKTGHRNLKAQHAGVMEKISLMQSSLSEALNERQALR

HTVDHLKQHTEHLQGENMALAKANARLRLILRQDPELSRKHREEVPRLTKLALSSKQPQQ

IGTVYKTTAAPSKAIELSELSVGMRTLSTLQPPTPPMENTISITQPMTTPIKRANSLSIR

KLSHESHKSIRVVNIRELSSAGPEEEPAVLVSSPTDEAAGERLSFAEVIKGRDRRSSSIS

STGSSSESQAPIATCTNIRQPTGEDGPLESPAKVMGIVLEGESEDSTDRVSFSVTLAVDM

LDDAKQQQNQRLSLTGATSIAKQGTNNAAGKSKGRSRRSSYDRADNGENRRSASSRQSFS

GSMEGSRTNRHSYDSYGGNNDGLRNSSLRQSLTGGGHHNGGNHHNNGNHYNGNNRGRTRR

GSYDRNGGYKSRPTSDTMSNASNSSGGGGKRIEL

>contig31690 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69693.1|) 2e-50

MRSTQRSVVAKVAADTSSQRSVTFEASWLQKMNRIGIGARLIDAGNGWFLCERLEGKNIV

EFMGECDQVTTPANAMWVLREILCQ

>contig32112 Frame-0F

MPTFTTIARGHTDAFFPVYTSSRYEKLGGQHVIFLV

>contig32325 Frame-1F|Blast-SCP-like extracellular protein [Phytophthora infestans T30-4](gb|EEY63799.1|) 1e-45

MLNFTRSPLGLWLLISASFNNSVAKELLHKKPRKLQIYSSYDDYYQEMLNAVNAERAKLS

LSALCANEKLAAAAARHSEDMASNDFMGHTGANGSTLSERVSGAEFAWTKVAENVAAGQK

DVASVMQSWMSSKGHRDNILSADYIMLGTSYVYR

>contig32798 Frame-0R|Blast-serine protease family S10, putative [Phytophthora infestans T30-4](gb|EEY53504.1|) 0.0

MVSESTPLTSSYSLQQYARREARNRQFYHALVAVLSLIGVCLFVVYAIEPLLLRTHKVDY

AGKLEGVPVAMGNESENIFCGLTTQDSGYIKLPNKVDDHYFYWYFESRNQPATDPLVLWL

TGGPGCSSMLALLTENGPCHVLPDLSTKLNLYSWTNQSNVVWLDQPTTVGFTYGDKSDAD

NSEYSVGENIYFFLQGFLEKHPELGMREFYITGESYGGHFVPVAAHYIWKQNKINNGTSK

HINLKGIAIGNGITQASIQLPHYIDMAEKNAYDILLVNATQLEAMKLEAPKCKAILDQCP

QDKIACFDGVNFCTEKLFIPLLSANRNPYDIRMPCTRMDDPTKCYDISYVSKYLDSANVR

ESLGVDSQRVGAWQECNMKVNMAFYMTADLAKPFNMYVADLLDANLRVLVYAGDADLMCN

WNGNLAWMLALDWNGKSGFNAAPETAFISAEGMNAGIVRSFKNQLTFLKVFNAGHMVPQD

QPAVALDMMNKFLRNEPF

>contig32800 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64453.1|) 2e-30

MRFGESWDAGHLFPPRELILTRSDMDVYEMLSDQLVAETIQASEDFIADRRAVDLDRWKV

VMEKGTTSAYRYRSRGHRRVKRNRL

>contig32875 Frame-1F

MEAFKADKKDEIEQLEAGLKDRVALVAESQRLWNEELEKTQQLETLIASLKMALEHMETK

KTEDERLEKEEKDKRVAARKNDIYSQLGLLDLTKEQLLSIILEIGRHGVSTKDDLLSIIR

KEREAAQEDECQQLFLKKKLRRSASAMKRGR

>contig33043-0 Frame-0F0

MKCGSVNSCDRSNISSPALRKHN

>contig33249 Frame-2F|Blast-C2 domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY63774.1|) 1e-131

MSGMHTLQVTLICAGDLAASDFGFMGMGGKSDPYVVFKLGRVSQKSSVVPNSLHPRWEPP

ETFQFQVDRPKEKCLEVHVMDYDRFLKDDCIGNANLALAPFLEKKQSEVVSYEIEVPPDF

DRQKRKSILFLEIKLTPNEQVDQMLELWENQRYHIVKKWTTDTLISGSNERKRWSSVTDA

NVSSDAFEKVAPKVPSHLRAEGWTLDVSQGDDNGWIYAPSFSGPWQKDPFTLAMVRRRKW

INRCTVVDK

>contig33436 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54919.1|) 7e-18

MSSVCEGLLAKLNELMDFLRFAKHRDANFHGVVTFMFRASSEDKNTIVCMRTIDMRQ

>contig33854 Frame-0F

MITYSRAKPDDVQVLLDMVSVFLHQTPIDFSFLQLFYREEVATKYSAANKRNLIQLFLRM

LREPGTSEDLKVHAAQLIIAPVLTISFEDPNVSNIDVMDLDTIMWMLREILAIKEHSPDA

MQSLRIELLKLGTLLIQHMSNYVTDYRKEVIKFAWNHLKAQDLTSKLWAYVNVCRFISVY

DTPPKIVLQVYVALLRTHEMDARFLVRKAFDILLPALPSRLPSNEFIKAIKWTKKIAYEE

GHALGQLVHIWFLIIRHPALFYPFRGQFVPLMVNSLNRLAIPPSSTPDNRRLAVNIVDLV

ISWEHTRQDRLILRGTSFGIKAATPGEELKRSPSAMNETNIGTSPDEQAAKKRRLLTSRV

ADLPDIQSSDKVSKGEESSSCAPDKQQEQISDYSYLEMNRVANSEDDFELSGAMVDLVVN

FAFRFALASADKQETSRLAKTCGELFDKALRLWPSAAIRFSYFDKLIAVTAETIIRQQQQ

LQASLNAAAAASGEAGQQISVSDPPPLTVMPQFLTVPKGAPLSSLAILDAVLGILNSLVT

SDVVIKSKRPISYVIQYAPR

>contig34165-0 Frame-1F0

MVKTDVLVLLEFDDVLTDVDSDRYLTNKLHADAANQIWALFAADKTIGRANAMDAFFAQV

AQDYPTTKIFDNIRKHVENLPCNERIVEAICLAVDTYGATIK

>contig34165-1 Frame-1R1

MKFVGKVTVRVHIGQDVIELEEHEHVCFYHAEKRQKNWNLF

>contig34284 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61831.1|) 2e-52

MSYRERDDRRGGSEGLSSSRYGSKGSQDRNYDRPRERETYRHENTRDRSRERGRMNREAP

RRSGPSSSNTSVRDNEREDDYGEGLEDHQDESQPKASGAWDPAKEALDDPTWARIYISNL

PADITSDELQEMFGAIGIVAREKQKRGYKDQWPYKIKIYSDADGVPKGDAVLTYEDSNAA

RTAPDFFNGTEIRGRAVKVELAGKPEPPAGGWHVGGGGGGRRGGGNGGGRYGGGGRYGGG

GRGGGGGRGGGYSRYG

>contig34806 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68215.1|) 9e-18

MATLWSSSSDVVWATVWARYDLVLQSMHSDLVALDTWYVDSYPPILRAREPQPYMTQEEL

KKLMQ

>contig35625 Frame-2R|Blast-SpoU rRNA Methylase family [Phytophthora infestans T30-4](gb|EEY66677.1|) 6e-32

MLPRKMVLVLGCEKEGIPLEILQLVDVCVEIPQFGLVRSLNVHVSGALVLWEYTQQQLMS

KGSRIKSLGDKIA

>contig35948 Frame-0F

MEQRRLKPSLSTKRKAPFVAAYSSTKRQRPHPAPGGFPAAAATVSKHKLPYSNPTKPTKV

TNSGNTNERKPPLFSRYADPSVQSPKPIKNKYNTIAKTVASRQSMEP

>contig36071 Frame-1F

MSAEFPNSSGAPGSPEYVRGPTIASQWPADVDLDALYLSERSEVDELVRSASDMSVWTME

TRKDQAIVYVHSKNSERLSYSVRAVTKVAGSVADVLECLRAVDNASLRGFQKVLHSRNFL

DGEVLHAHQADTTSDHEGVSTESMTLKWLVFSSPKTLGRSKEFCIREYCILRPSHPVHGN

VGVLKFESYDGAAARYGIRGKPDSNSLTVFEPSSYVVQQTAEDPNLCNVTLTFAMRKARG

AESVSAGVRMTSLRLAGDLAGLERAVQQVLFAPAVLAQRQEWVNDAKRTNCSLCVQSFGL

LKRRHHCRVCGEVVCSACTVFKMVKGDQDVAVKMRVCKACLAKNSNSNGTNTNFGSTTVG

GFSLPSSRKLSSDVEVEMNGSTGLAPLSNCMGVSIGSTSSLTSEESYSPPNDHLASSYPL

SMQFNKGSALSFSELDANAQPNDDGESSPPPYRKPASSITSQGRGTSYEVRPNGSMGRTV

SNASIATSRKKNVDCRIQYFNEDMEEICLLAMETLTCPMAGIRTEDFELVRYYDGKPAPG

LPRSLPTFRRLATRGKPCIVLDVSSDKRISGEKRFTAKLQFFVGIPLLVNGEVVGDLCVA

DRYARDNIDHKQVEVLNVLGETVTQYMQSEDYQEDLEEFKAGNYAARRVVPMVDSSSQPP

EKEDSGLLTGSKEVAF

>contig36277 Frame-0R|Blast-hypothetical protein PITG\_14851 [Phytophthora infestans T30-4](gb|EEY62411.1|) 8e-14

MLRCTTSGLCQSIRQVRREAARKQQKQQRLQTVLKRSKGTKRTVCGPAREQSIITNQQKQ

TFGRIRHTET

>contig36563 Frame-0F

MYVPQNLLRSTIPSEPLVEKQENKVLPFLTLMTPTRHAAVRASLITDEVVPDALSPLVPT

RALKTLPKQTERGRVKTKKSRQRKKIKKGCKRLKLCGATLYGYQLLVDVRYRAEQYAEAR

ILDLDPATKLLLVHYIGWNARYDAWVGIEVVAAHGSHCQGVVKKDASWNGMTSLFATNKE

IGAQRECGFAIVKDTPKKRLAMSPALTSGTGHCEKIAAENDTQLVVHQAEENCCNYTQEA

ETPTLTERTPRRVQVEVETTDEDSERKKDSKTADLVLDVEIATMSEVLNEKGDDHSAPEE

FQTETSQRRLESASRSGWKRKRATRAEAKNNQLFNPTTSTFEASHWNQFCKAMATSTRRG

GKFNARETCCNLSTSSATKTADGAVACNFKETAVVAGFRDKARRFTHE

>contig36905 Frame-2F

MNKFPSSIIVKLFLSVLLYGRREADVSFGRCCTMVRRKASVT

>contig37616 Frame-1R|Blast-regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4](gb|EEY68375.1|) 0.0

MLGAFRSAKRLASAARLASAHKVHRISFYTTQSSVYTWGNGTLGQLGHGSVLKSGIRNTY

EELTPKLVEALEGKAITRVEFGASHSAAIDEDGKLYMWGSNEYSKLGLGESSELESLPRE

VEALKGIRIVDVSCGDYFTAAVDEDGKMYSWGWGGSTMKGAGGLGHAGGRDEPTPRLLAT

LVDQGVPIATVECGEFHTVALTRDGEIWAWGNGEYGRLGNGESDTCEVPEPIEFFANNNI

VSIAAGRDFSFALTDKGELYSWGGNSHNQLGIGGGLAMDVYNIESIPVLVDAFYGLTVKQ

IAAGYDHAAAVTEDGRLYMWGAKIWIEPHEMTAVSEHKMVQVACGRQYTAALADDGKVYT

FGKGSCICLGHGDRKNQLQPKQIEALTDIQITSVSCGDYHMGAIATPHAEAADKDFSFRE

>contig37858 Frame-2R

MKTIILSARIIISEQCDQSWKVPMTSFAESGQLGITCNVLI

>contig38424 Frame-0R

MADALRHLLGRTYVRASFESMRCL

>contig38802 Frame-1F|Blast-elongation factor Tu GTP-binding domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY65087.1|) 1e-125

MATRVTPEVLAALQHTPERIRNICIVAHVDHGKTTLSDSLVSSNGLISERLAGKVRYLDN

TEEEQIRGITMKSSAISLVYQPDPGPENDLEAPYLINLVDSPGHVDFSFDVSTAVRLCDG

ALVLIDAVEGVCAQTHAVIRQAWNEGIRPCLVINKMDRLIQELQLSPQEAYQRLHRILEQ

ANAVSSAMIKMEVLKKYEDKASHPLLVSNDPMVESIKEFDVISIETEQLEHDMLFSPSTG

NVIFASATDGWAFGIGSFAIRYAKKCNVPLRVMRKALWGDYYYNHKTQRLSL

>contig39535 Frame-0F

MQLLEIPKRSSQLTTKFLQEILIESYPLQRVLDFQWKPMNAGVIAEVVVIAIVFKSLDEN

DKSKRNTRHFVGKFMRPELPFDSMFRVESFFYKNFVTKLVSASISAEDFPFAIPSAIFTS

NGLIVLECVENMRTHMCVKGSPPHLTPMLLTKLAKMHARFWNDDCDGLASPAGIGSQLTG

EEKCLQFPSCWKDFLDDVSLKRNDKEKLTALCQRLCQNSGQLILVHELVNSGPSCLIHGD

FHIENMLLTADGTENGATWLLDWATCGKGNPLRDVAFFFIVSVRASDRRAQEARCLEIYY

KALIAESNVVSLSQNELYWQYKMCVLNQFLILVVYDSLSKSFATNAKTDDSRKQLESHFR

EVNYRMCLSVLDNFCEKDLNLLESHG

>contig39751 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64149.1|) 1e-121

MALPRVHRGFWIAYESIRDELKDVTRLILDENPGISVYITGHSMGGALAVIAAYDFAVNF

SIQVAMYNFGGPRVGNPSFRQPYDRCVPTSYRVVMDGDIVPGWPKFWGLYQHVGTEISLD

LAGNLIVDPSFIERHLHISSRRKTTMHGTNIYRMALAKCLDILTTS

>contig39953 Frame-1F

MERISLLEVDKIAVDIDSSVTASYLESIKGSSDVAEAAEDLDTSITNEIDDSEAMFTGVE

PTTANDVSAEPEEKQRVENLDLADNEFEADDMDIESLDELLSIVKSKPIAFADDETENSL

TILEADFLDKFAVSDDALDFDATNQISLIRRSVSDFIVDEAAETSGEDFAAFESASPAAT

SDLLVTKPDKNAQNNSDMKSTIEADPIVSEQDQALHDNKREEDEHATITAVTEEPAKATS

ADENLVDVLAKIRYKLACESVQVLDSGEIVALPKGWTTRQSKTNDGKTYFVSPFGHTQWL

RPPMKTGIIYNWVHEIEVTFGPGRLGLNLKQIAGIPGTQFTDLQVHIAEIYKLP

>contig40298 Frame-2F

MLSGWIRKNRNVMCARNFTIALLQSSSCVD

>contig40841 Frame-0F

MLSQWMLGRYKGNIGRINGLMEAWLIRRRGGKPMDKGMMLFTSTTSSPKLKGRLEDMSDP

LQAVRRKESMILAQRTLYNYP

>contig41806 Frame-1F

MSGKVEPTLMTRELKGAAVVVEALAVYRTTMPGYCMEEEAFFEKFVEIVILGKVCETMTS

PLSFEVFTAIVKYQSFLLNYGKGLPMLVNFVENALTASMKLVVMSDSTSNSKLQGAAWFF

FENFCNDYSSFRSFLPPLKTYGCLLAVSLSLGSRDVSELKVKGAMQALVANANREEFCLL

LSTVLQELVSCVGRRKLSALLALCLLLDGDQKLNASRRLLLNERKNSILEALLQIFTINA

LEAEGNSSDICGGRENVYLWNLKVFVLVFCKADFFTWNSFELQHVFKGFEPLLVALSELQ

SGTPKYKVQDLHELWTLSYTLLLRIVRNHFISLVNGIPHLIQATNALLQLLVLASASPEY

SRYCSDWSSNLARLYGYMKEHDVQLRKHVVYLLMAYFVGVTRDKLAVRYQQKLRPGVFAL

FDVCSSYEKEQLFGALDSTGKSVFKALDTNYKLTHRYVGKV

>contig42274 Frame-2R|Blast-hypothetical protein TcasGA2\_TC003750 [Tribolium castaneum](gb|EFA00849.1|) 2e-13

MKYSDLKGPAPSNTTAGELALGITKLPTLPSYSSGSTLIKRKRVVLSIHDKQQVLQRLEG

GEQPMAIARIFGISRQQVSDIKKNKDRIVAFCTDAKHMSTLKRKTLKTTSEYHPGVEQEL

YRWLIRQRKLGRDVTAESLAAKTTDIFMQYSPDDAHITLKAASNWLRQFRKAHGIRSLTK

EEIQQLPEKFTPAMEMTRPGNISATSLINSTPEMTTVTSGMDTESYYDSSSVTHPINAAI

LTASISPSVDINLFVHSGIHGYAHSMGNSIASLQYTLNTVQQLNALLAKFEREMETKLDY

LDERVAKLCCFVISARLGVD

>contig42380 Frame-0R

MLRNSNARHLVRVMAVTYTCGSAYAARPHRARNKNDAARHFYTFWHEVTEIYPPIPRYKQ

LVEFALAVLS

>contig42407 Frame-1R

MYLTRQAKDVANRESSKCEAEETVDNIIESDDVDFIPKEAEILHLLLQRRVNLDHRDENG

WTALHHACFVQNAVAVKMLIHAGAKPMRENYGLLPQDLLQRGHMSEWVAQAQELKEILDQ

ITDKSAYTIKLLAFRPSGVVQLDMGGQVEKGSLVTLEYDAPEHHSIKDYIQVLVSEEDSA

EIATGSYHYVPAGAHGQLTINTKDIPPASTVRFVYVKSDINTMSREVVASGCNAVVQASV

GEIFQYELFLYERVVEVESIPDFELIDQPLIVLKRIGIVEGDDIDWITLRPYNHIVAVND

IRIDEMEFAEAVHVLQENNGRQCTRLLMQNYSACGDFIPEKILGVGVVGKYASLHPIDED

YDVGSNEHTHEELGQRCPDECHDDNGESRSCNNASLKPVNKSVSAVQLPTETSPPPSAVS

QLFSAEEREVVSKVLDDYEIDNPAAINSSYKVSASSTIETVVPLHNSLQLVAQLQHGISI

SHKSS

>contig42858 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70054.1|) 1e-131

MQSRADWFATSGARELRDSSTLEYREYLNRSQYCLKRHFEEDLRQIELDLPRTDESIRLF

LLSHDERQSLATNEELPECVMQQYLPKLKNVLVAYSMRNPRVGYIQGHADVLCFILGNSN

KRRNEEEAFWVYASVIERVFPEDFFSRTPKLHGFQVDCKLYHELVLEILVPLFPTLSKVD

LPLVTTLLSCKWFVSLWVGELPLALLYEVWDAMLRQDDGSILHLLVALHFFHLAIEKIQL

YMETDQWDSSYIYKIILNQCQNATNIAPQTLLQQARTLYGLRDESIEDMRATIHRL

>contig43318 Frame-0F|Blast-proteasome subunit beta type-6, putative [Phytophthora infestans T30-4](gb|EEY63713.1|) 1e-109

MTKQEVDEGSYLKPGEVDAGTSIIAMRFKGGVVLAADSRTSMGAYVANRVSDKLTPLHDR

LYCCRSGSAADTQALSDYVRYYLSSHSIELGRLPKVGTAATLFRSLCYQNKGRLLAGIIV

AGWDPVKGGQVFSIPIGGAMVEQDYSIGGSGSTYIYGLMDSEYRPDMTQDECQRLVKKAL

AHAMARDGSSGGIIRTVTITEKDVVREYTCGDDLPFTI

>contig43563 Frame-1R

MKTLHSLGQPNPASDEFGDHLIVYINPKESSCHHTFNDWNAKFGEESFWRQHVVELTGDS

TADLRLLASANILLATPTQWDVLSRRWKQRKRIQHICLLLLDEAHFVGGGDYGPTIEVVM

SRMRFIAAGMEKKTREVGEQSERMRILAMSNSIANARDVGEWLGASASDGIFNFHPNVRP

QPLEIRVQGFEINDFSSRMLAMAKPLYNTIANHAAKKPVIVFVPSAKQAQLSAIDLITFA

LAENDPRKFVSSSGDDLVELPLEDTALLHTMENGVGYCTDTMSLRNRDYVLKRFAIGKIQ

VLIVPQSMAWDLQSSQASAFMVMIMGTQFYDGREHRYVDYQLADVLKMTKYASHAASGAV

KCVLYCHASKKKFYTQFLYDPLPVESQLAHFLSDHINAEIVTKVIESKQDAVDYLTWTFM

YRRFMKNPNYYNLQGATNVHLSDHLSELVEASVNALVESRCIQVVEEEEDEGREGEEGLA

PQNLGMIAAYYYIKYTTVELFACSLKADSKVRALLTILSSATEFSDLPSRYGEDKKLESF

AKQLKFPVAAGGDYEQAHVKTNVLLQMHFSKQHDRLSLALRQDLDFILKHAVRLVHAMVD

VISSNGWLKPALAAMDLTQMVVQAQWSSESPLLQIPFFTQEMLQKLSDMDLEQEVETPID

ILSMDDKARFELLPLDAEKMSTVAKFCNAFPDVTVQTTVQHDGKNLTQGSTVSVTVQLER

EGVDEEDTEDAAKELGLVNACYYPVAKAENWWVVLGDSKKNTLLSIKRVPFASAQANVAL

QFAAPEEVDEHIFQLYVICDGYAGCDLENEVKITVVQSEDTDQDEDEN

>contig43970 Frame-1F|Blast-Mitochondrial Protein Translocase (MPT) Family [Phytophthora infestans T30-4](gb|EEY66046.1|) 1e-105

MALYKSGSTYHAKDVFKKASQKFPESAEVHLFHGEVLADQGNYADAMRHFLFAWELSPQC

PLPFLYAGRVYISTNDPMRAIAHFKQALEVDPRCSSAHLDIAQVLFAQGRTGEAFKHYEE

AASCCRFLPELEEVCACQKMATMQLKVTEILGVELRHIMRSNC

>contig44056 Frame-0F

MFSAASISQCLTINRFRCRSRRLLSLGCFPGTEMPFVPNIVFRDPRNDDPIPCFRILDEN

GDFVKGAKDPQLSRDFCTRIYSQMIRLNTMDTILYDAQRQGRISFYLTSYGEEAISFGSA

SALRLGDVVFAQYREPGVLMWRGFTLQNFADQCFSNEDGHGKGRQMPVHYGSKALNHQTI

SSPLATQLPQAVGAAYAFKLTKEDRIAVCYCGEGAASEGDFHAALNFAATKDCPILFLVR

NNGFAISTPTSEQFRGDGIASRGSGYGIPIMRVDGNDFLAVHEATRQARTFILKENRPVL

IEAMSYRQGHHSTSDDSTQYRAVAEIKHWKETCDPINRTKRYLLQRGWLTEEQDRHMQDH

ERTNVLAALQQAESKKFPALDTMFEDVYDKKLPHLREQERAMLEHVSKYPDYYAVEH

>contig44272 Frame-1F

MIEEIKVYVANAPTDSLFEPPPRSTPILDLMSTSRHLDLVGAINELAHFNIKGDSADPHS

VVNGSFEDKLQAVVDHRTRLELSSRNEKQKLAHHIRDLVTTRSPWLTGDANNQVDTAENV

PAQLDVLQNARYVKRKVLLSNEENRVVSNAQIENMHGNVAEPT

>contig44690 Frame-1F

MCTTTTRPKGMTMGFCTKSLLDLSTLHIKVSEVRQSVDGTWLYLLQVSCSSARWMVHKRY

NEIRGLWLEISKSLGDSATQNSCAEHCHFLAGFEDEKFPRRHLLLTQHKLEARASELNQL

FLKLVMRLNLCKPHVLQTCRMRGCPLLTLITSFFEVNAEQAREYAALSFSRSISMQRGAG

RHDDQHFTQKRRGSISVSMGFSRRSPYVFSEGHRSVAALAQ

>contig45345 Frame-2F

MGTPSTADAGLMSTSKIASKQRARKLYPMSPQTPPQVSSILSDHASDGFEDFATELKQAQ

KYSAVKRKPNLSSKRRSSRLHNRSAVTKVMPSVSAPLRLVVPTTPIVSIGARHSARSSSV

ASDSESDDLKKLIAELDNCRATFQPSGLRIAKVK

>contig46043 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67449.1|) 8e-97

MPLYKQVLITNLKSSPKDVANVFQDCAALITSHGGVIRATENRGEKRLGYGIEDRRWGAL

QRHYEGKLVVQQFNTSPAVLKEVEAKLKNSFPIIRFQTFKVRDPLDKLMNTRMTLEEAQL

MLNPAAKAKAEQAAREAKEARRPRNPDLSTMKPEDFFNLDDEKEAAQFKQYVPEWKRDAL

FTPDVPAHIKDKVQE

>contig46124 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65706.1|) 1e-141

MSRKLEKKQSIKYYSVEKISHARRSVPKADLAVLFVTWIGLVLFSMTRGGHGTPSVIGLS

CGSTSYWLLTFVSLSFFMSVTLYFGMKINRSHTILQSSDYLYIKGEMVWTREAIVKFPAL

CTVAGIAAGLLGIGGGMVKGPILLDMGLLPQVSSATSSSMILFTSSATTIQFIILGTLSL

DHALWHGVVGFVAGLIGQLGMSYLIKKYRKSALVIFFIAFIVGVSGLVMGVLGAIRTWRV

GFEGFCSLCGTG

>contig46249 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64677.1|) 2e-89

MDITVRVEVQYHAPANAITRDVLERFRSTTWVRFMMRFISPRLKVSSPADQAILDELQGQ

ETVDVTNGNECIICMSERPCDGLVALPCSHLFHYPCITSWLQNRSTCPVCRFQFPKAFTG

KYAVQKLKTSMVLTDEQSKMPKFQILALDIGKQVVVAIVNVTLVKVMTERDDRDFPCELS

AWLLDPSSGEAFSEVDCLASAVGLS

>contig46436 Frame-0R|Blast-CorA Metal Ion Transporter (MIT) Family [Phytophthora infestans T30-4](gb|EEY64528.1|) 1e-101

MLSRLLHHDPLNFEADRLAKCSKEIKGLKLLAKPLSEMITQLVESNDFEGETLRYFRDVQ

DHVRVIDETCDRLLDRCRLLLDDFHNARHAQQSEVSYTLTLVATVFLPAQFLTGLYGMNF

VNMPELQCENGYMIWWGVVSTIATGTLSYFKFYKKWL

>contig46854 Frame-1F

MALDVENEQHTLAVLGSDDYYDERHLASRPYSKNSTGV

>contig47112 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63467.1|) 1e-30

MHAMNLEADISSHSTSELQSISKMFNDRPQEKDVKTDNENELVWNP

>contig47325 Frame-0F

MTNKRATFYTSNESGNGLGKWQWSQLLRKTTNVGSNAETVRVHERECFMDASSRLVSLIT

KQQNAKSRTSSILPLKDTTTKDAFLPAD

>contig47350 Frame-2R

METFDRRVEEKTKATLQALEHQTQTKEQENRCHETSERDSDDNGILQTLRAKPQAAWYPS

VGKMVEFPDLSRSLKATKSTDSTANFDTTP

>contig47798 Frame-1F

MREAMYTCFWADVRCPSLICQSNSLQHCDFPKLINAFTKQSSCKKPIDASSMPQKFRIYP

RHTASFLRLHLAGGKEA

>contig48409 Frame-1R

MKDVVDYEKANAALVGLVNNKNNNVKIKAQLNEIINEQGQYHLTSL

>contig48764 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68702.1|) 2e-77

MVSDCARLKMAYRMMFRHLIPQDLEVDERELSEEDQKLYASTFGVHSTQTRPKDRFRVVV

CHANVIRWFVCKALGVDPDGTWGRMRYNHCGITAMDIDSVGNVQLTYMNQTGHLETAQLT

EV

>contig48823 Frame-0R|Blast-haloacid dehalogenase-like hydrolase, putative [Phytophthora infestans T30-4](gb|EEY53928.1|) 1e-102

MPVVLGVTFDLDDTLWCGKTVLQNASGAFHAYVAQELPELAEQFPPASFDALLVQFQRAL

PEHAHDYTFLRKHTLRHCVTTFGAQKLHLHDESKLTAFVDAAFRAFVVPRSQPELFDGVE

HLFRELTTEITLLNRPKNATATILGIITNGNCDITSLPEFFQHYIHFIISAELVGCAKPS

QAIFDAAVSKFSTSCRRHHFVHVGDHYTCDVEGAKRAGFRTIWVNSQWPRHDAFTRADLI

DDDAAQYTAADAIVKDVKTVVFVVQHWNALALETEGPWCST

>contig49015 Frame-1R

MFSALDMPLGTSMYTSSLRKLFKMPCRHPAVQSRIHSQPLPFCLKPFATNRAL

>contig49060 Frame-2F

MTRTPLDRYNFSIKSIKIIPISRILTSWSRKRNYDDMQCHRLCPT

>contig50141 Frame-1F|Blast-lipid-A-disaccharide synthase, putative [Phytophthora infestans T30-4](gb|EEY61944.1|) 2e-47

MGWWDRLNWVLPRREQLRRFSTTHDAIDAFKKIYVIAGEASGDGIGAKVIRALLRRQAQV

RWKFRGIGGPEMCHVGDFTSLFPMQELSVMGLAEVLPHLWRFQRRIHDTLRDIEEFDPDM

ILTIDSKGFTFRVLQALHVNEQKIKGKRMIKVHYVAPSIWAYKHRNARDVFKLQQLLDAM

FTILPFENHLFKLQSSKAD

>contig50233 Frame-2R

MRCYILVVPSLLALASSALPNLILTTESSLADASADSPLRSSSTSPDDHSERGN

>contig50475 Frame-1F|Blast-enoyl-[acyl-carrier-protein] reductase [NADH], putative [Phytophthora infestans T30-4](gb|EEY61640.1|) 6e-23

MGPAKAALEATARQLAYELGPDGIRVNCLSPGPINTVSARGIPGISVLSRRFNEPLCR

>contig51036 Frame-0F

MKCLLSLAVIAGALTISAVADDDAAYFCDSDSYCEKTFPDTACISVNNYGDVVSKCTPNT

SKRPACRGATPGLCPSFQSADIGYLNAHCVFVSEENLSLSSSGSMSSSRRLMALAANTSA

VLSNSTLAASSMLSSLSASQGDDVMIPEGKNGMFSAEVDGVAVSGQFICLDVSDCANKAA

DPSTCEPTTCQSPDSKEVCTYHGTCTYKSKSKINKRSCMCYAGFDGDKCEKEVSNACDVD

CGTGGDCVDGECVCKEGFNGVEHNGKKGKPNQRCTRCTNDLACQNKNTCNTETGKCICGP

GFTGDTCGATEDSCTTRMDCGIGACQVLTNGSSACFCPMCNPTCNLCDINVDASFDCSTC

QANSATTMQSFNLLMVASMVVTILLTNLAL

>contig51443 Frame-2F

MQQTPMQQQSSHLGPQGHGKGGSGSVTGGPMSQQSQGQRGNASMQNYQNGGGREHVIPPV

PNASAAMTGSYNQHYGWAGNYGAQPVGGWGHMVPQGYQQSPSHQQQHTSQQQ

>contig51757 Frame-2R|Blast-acyl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY65023.1|) 3e-26

MVPGLSDVSIKKLGIPSEREWIQGYCSRASCFPPLTKTWNWYTGMSIYRFAAICHGVYAR

ALLGNASSANAA

>contig52235 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64311.1|) 5e-76

MVSVLPSFTPGKCFFCSKNDAEHFVPACGMWGKWTHWRMNQQNNLNHAFIAGALSDNTVS

KRTANVSMCTSYYDLENDKMLLEAQVRNEAQKQAALLKKLTAFEEQQGALSMENARLLAE

IHAVKEKIALERRQSEAQYQEKLKVMQKEANRAAHERKLQVKRADAIHVTALQKRLEASE

RRVQDQSARAQAAEEDATNARQRLQLSENRVVKWKLNAEELQR

>contig52240 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62031.1|) 1e-50

MTPVPAWTREWRPLVRKLFLRLNGIVHAHSEEQCSFSKETLLLHADRIVDQLYSHRFVDT

VPQDVQAQIQALATKFHLHLLEDRAEKVLQLALKCDYQVLKLLLELAMSPMTATDEEVAL

DLDLTSKWTAELQQEQLKFKQQDALQKQMVT

>contig52503 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64362.1|) 2e-08

MVAIAPNIQRHSAQLDDNLMQLCNYQIAKALVITQQPPEIWYKDQYGRKATFELKVERTK

IHCVQ

>contig52738 Frame-2F

MTAQWSLWRLPLRAAALCIRCIPYFKANRFCSVCNFVLDGDVLAIKVDLLTCLTCNHYVH

AACEPDPNVAFHAFSNSSEFTLDVVMEMET

>contig53126 Frame-0R

MDVGTMLNKSVTYQLLSDFERDCKGSHFGCTNRPRCLDNYFFVYFCIR

>contig53229 Frame-1F

MEAAGPNTGLTTEHLKSHLQKYRLNYERSRMEFLEFYDRSAKRNLKRRRCQAQQRSNDAC

TENNTMFVFPITNSKRQKSRKSNSDSDASRSDTDGRSQIGKRLSTIANCQVTPQKQRESP

AAEASIHAQNMNYAQLMQNAQQQVLLDESTCVQQQSPIINARLMPIVTAPISMGKMPIGL

HHLPPAYAAHAQRKQVYGHDCDLAAGAVGTCRHSLGHASNSTEPLGMAELSDPQWNILNS

LMSPQLAGITEPVEEGMFATSEAMAHASSNASGYNMFQGQLIDLRLKMHLAMQAQMNLHR

QMLTRKVEVAQHQHRVANLHQVTRISSIETVDV

>contig53896 Frame-1F|Blast-aminomethyltransferase [Phytophthora infestans T30-4](gb|EEY62888.1|) 4e-55

MGQLRITGHDRLRFLESVVVGDLEALDSGEAKLSLITNDQGGIIDDCVISRYDDHLYVVV

NSGNHDIDLAHMHQLLKAFQGDAAIEQMPDHALVALQGPGARDVIESLCPTVNLNELGFM

HGM

>contig54291 Frame-1R

MLLELHSAYSICYGTKVGRRLLFLFDVGSLNSKDATS

>contig54729 Frame-1F

MMMDQVELVTSAVQSTTLNSSIITEQTSTLASTNASSTADPMPQLLTPEKAKKVLHLVID

SGAI

>contig55469 Frame-1R

MAMAPPFVEFDDNHLTNLYFQFQLTSTHAS

>contig56460 Frame-1R|Blast-15-hydroxyprostaglandin dehydrogenase [NAD+], putative [Phytophthora infestans T30-4](gb|EEY63919.1|) 6e-20

MEIDLIALVRGTRFAIMEFKRTLKGHEGVIVNLGSTASLFPMPFAPDYAAAKA

>contig56846 Frame-1R

MKIYEESHCETRKQAFSKVTNKPVYIR

>contig57283 Frame-2F|Blast-cysteine protease family C26, putative [Phytophthora infestans T30-4](gb|EEY65931.1|) 3e-37

MLSRFSRRYCQQSSSALRALSSAKCLSSPLNILIIDGYALEGRADLEAGGASTAGKLYTN

LLNEAAPTGVVIAADVVYPADSDFEMPTIHNYTPLHGRAAR

>contig57364 Frame-2F

MCHCCFIYRLRRRSSRIVLGGSVHEELVKLWFNSWLKMSR

>contig57434 Frame-0R

MLQKSSAPAIVSLTSHMLLIVSN

>contig58480 Frame-2R

MPGRKPQLKSSNAFPRLSRVEISSMYTASVGSSSSTELPS

>contig58574 Frame-1F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY64330.1|) 8e-06

MPQRMTEKFLQFALSISRAMNRQDFAL

>contig58862 Frame-0F

MLVGPTLKKLRISTVIKDEDLKSIRDSLDINTWTVGGVSLDICRIISGFPEWFYVRKETI

DIIKIFQGQMKANYNTVLTGSSGVGTSTLVVLFAFYMALIQKKRVVLFRIRCGCSLLYLD

TEKKNCWQMDYTCFEDLYKHRQLFKGAELCLDGLDYDDVEKHFGMLSRFRLLATSAPFNF

TDGDYAVRRKCLVPFWSLSDLNAIGAHRKWTEHEIKMRYFCSGGILAIFLSDKVGYSNYI

YRAVLQVKSIGAEFLSTQYGSAPENQIDRLPTTGIPTTNDHRDLKQYMSGKHWICVITSE

YALRLLCKNVSLSYCEKLWLTGRMLGDDGVMDIAFKNYVHTLARDGKKIGLQVRAYDQVK

ATEHFYVAVELEAKLCRNDNVYAT

>contig59300 Frame-1F

MFSQFYGYAFVLSSKGKLSFETTESIESSLLKIYKDSTSDVAFDMLIQIRLARRFQIPK

>contig03146 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58299.1|) 6e-53

MYDHSDVPHFFVVPEGDAAWPISAWGRRLGATVVDMRAGKAYASQMAQSKKDLEKINFCF

TTIPERDWTEKIIPSLKIHQQEFGHCIVRQNFKIPSCHPWPKRAWGISLGQIVSDVRLKH

AYVKQAARSKDILDKMGFAWSRSEAVWYQNILPSVRVYHQIFKNGNIFRDFIVPSEFPWP

EQAWGIRLGVICSEMRSRGTYFRYFGRNADVLDTLGFNLRLSRRAWLNRVVPLIDVYALQ

SGGKSEVPDDFVIPSADSWPREAWGIRLGLIVQRNTHN

>contig07502 Frame-1R|Blast-anthranilate synthase component I, putative [Phytophthora infestans T30-4](gb|EEY61414.1|) 1e-159

MAYQEAIDKIIAVNSALDKPLVRLSSQSSKKASNAFTMDLETASNVGKVGYMNLVETLKH

HIVEGDIFQAVPSQRLTFNLPDDVTSLDLYRQMRVINPSPYMFFLDLGEDFQIVGASPEM

LVKVDHNAIVETHPIAGTRPRGATEAEDEEFMNDLLADEKERAEHIMLVDLGRNDVGRVA

EPGSVRVEQLMQIEKYSHVMHIVSVVKGDLRTNQSVYDAYRAMFPAGTLSGAPKVRAMEL

ICSLETERRGVYSGSVGYFSFSGFLDTAIAIRTMVVKDGKVYLQAGGGIVYDSDPLDEYT

ETINKLGSAVKTLEKCIAHVAPTTLKIESQ

>contig08208 Frame-0R

MTMQYACNLSSLQLKPSVDKSALDEANKVKINEERTRISEKQDAGLFILPNDSNLSDDSF

SDGESSSEEEIRSCADRKEYTTPPTKRRRQ

>contig09405 Frame-0R

MHACENEMVYKSTNDKVPYFNAGAFLENKTRIGKVDEILGSINEVMFTVKPDSGVSASSF

QAGDKVFISPDKLLPLSRFTEKPGKKPAGAGGRGGRGGARGGRGGGGRGGFGGRGASRGG

FSGRGGGRGGGFSGRGGFGGRGGGFGGRGGGRGR

>contig09944 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58037.1|) 1e-82

MAKTRLFVNDIKSVWSDTIGSSLTANWKALPVVCEGKPSVQTKASTVQPNGGCPEVYTKA

NVSCTCLEGYDTATEWEFYIQSRTRLENQPLVLEFGATLGLTSLVTIVAPSNITSIKIVG

VGEDIVTLNTTAEATGWQNYDTSNPSLIEGSTTSVLKKITLENVDLYAAMDTSSNYIPMG

IET

>contig11048 Frame-0R

MPSAAKLTLIQNFLIVKKGV

>contig11714 Frame-2R

MEPDNVFLLQPTDYVLCSSWGQCKLQLQPSEKWWILGDVFIKTYYTLFDAERMRVGFACN

GDVCQGGRGKVYGNTGESGAFYDWEHVFLVTSCVAAAYMLVCVFNHHKNKKTHLNHDTSS

S

>contig11813 Frame-1F

MVKARWGSFILICSLALHACNEAVRVRGMSVSYAVNESTKGEESRSHFEERAPGDMNSIS

EILQTALSNIQSGLNGQLVKNEIEFVNLIKDALHDWVMGTKISLFDDWRVGTKNSASKAE

IEEMYQQSVQLFNAFKAQFSEFDRARIIATSLNVRAGRLVIDQHIKDMWELLMEEWKAKS

QEQVYNMLRLDATHSDFLTSSMFQLFVKFLDKYHNKNYNILRDKLMEAYVDNRQILRDRL

KNVKGIGKTLLGMIPPKYWDSPTFYPAILQLGRFEFVHLSVKELVRSPSLEAWCFLAESN

GEKPYRILVDKLLVERDNLEFTKELEAALKEEPSGNLYGKLKQLENALFQHWMDVVKFTP

IEFEKFLLLDTVKEDAFFRTPLSWIYLSYINFRGFNVRNTILQKLETKYGGVRQVIDVAK

EIDPRIASMVITMYYRHWKNLKNALMDLNLMDLNLTFGVLNGRWVAHWIEFVFESKKTQN

PTNYVISFAKRKYTEQGAAVLLISAIEKAPTIIVKELVLSVFLEYMKQTPAKNVLAGLGL

DQAGDNLFSTRNIIYWIIGTKPWNEARLKFDPFRDFYTEDKLLKLSSSASTAANSVAAVK

SFADEMIQYLEALSVEPPNKRLRTSAHTP

>contig12575 Frame-0F

MDVRKECHNAEGEAPAEKASFSDIAESKTQLDEVVDLDEENDYEEKKDVHNTNESEDEMQ

FISNDDTSIDNQDNKSNITKENDVIQNSVLTRNPLISSGQSSANTDAVMAANGYITPATL

EAELQCIICQYTMFKPISAICGHSFCRVCLLNSILSRPMEEMQCPICRCDIMAQFSPNGS

VTSFFSINVTLWNLVQLLIPSMAARISTHQITEEDAFQQQVDHFKAQWSIFVLEKNAAQY

HRDNDDTTRLMQDEFPVLKTDETQDGHLHVSRTIVLDTTDENEDGYIHMRVGLAIVDFPN

VFKVCTEHQMCSINVLKMEEDEEMADGMPFFMNEDGDDDVLVCSSYFNELCLSVWDEA

>contig13158 Frame-1R

MFGDMTFDHSCVKFPAYLPTQLPSHVFVQQPLLHYCMKDISRRESITCACARIAEPG

>contig13882 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64185.1|) 8e-17

MQEVNIFIRPPPGVTAQQIQCVIKTNHVTLGLQGVTDKFF

>contig14036 Frame-0R|Blast-ribosome maturation protein SBDS, putative [Phytophthora infestans T30-4](gb|EEY57818.1|) 1e-152

MSGGRISQPVGKIVLTNVAIVRMRKEGKRFEIACYKNKVFNWRNGVEEDIGEVLQIAKVY

ENVSKGKFAKKSDWSKAFNVQSEEQACRAILDHGELQVSEGERKALVENMYRDIATIIAD

KCVNPTSNRPYPYTVIERVMKEIHYAVIPNRSAKQQALELMKRLPQIMPLARAKMKLVVT

TPQIQVDAIKQGLREEGAEILEQSGLESVRMIVLITPRSYRIVNTLVQTCTHGQGSLEVI

DLKSHQEGEHTIDDELSLKTERLGLTSVLSSTSVVTPVRTSAKSREMNTTRPCSTCGGDF

SADLKAYREHFRSDWHRYNLKRKARKQPVKNQEAFNELDQKEVEALLASVS

>contig14609-1 Frame-0R1

MLHSQRSPANFFTACVCNVASGTSKVQKKSFYLEDTFGAPTINNTFVAGENGV

>contig16328 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69136.1|) 2e-18

MLDELSDDTDKAKQMLQKVTKQTQELIKQSGGMKNFVVIIVLVLILLLLTYLVIMS

>contig16629 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65879.1|) 3e-58

MAVSYTDYKTDLKAACRAAARAFLLAYGAKTFTAVLLAYKRGIHRKSSYTDVVKVLLLED

NLRFGALFGSLVGIFRATELMTRLARGGKRDAASLAFAGAFSGLALLLDTPSRRSTISLY

IFVRMLDVVCRHLMSIGFISTWQNSTEVLFALTNAAIMYAFVVDPTLLPKSYYLWICHIG

AVTHQGLEYTLRHRMRGQLDACGVPLPFRLCQPHYH

>contig17316 Frame-2F|Blast-inosine-5'-monophosphate dehydrogenase 2 [Phytophthora infestans T30-4](gb|EEY53372.1|) 0.0 NOT\_ORF

MASSVLSDRELLDGCTALDIFVKNNKGQGYTYDDLILMPGHISFGVDAVNLETKVSRNIS

LHLPLVSSPMDTVTEHAMAIGMALHGGIGIIHYNMTIEEQVKEVNLVKKFKNGFISNPKC

LSPENTLEDVDRIKAEFGFAGIPITLSGKVGSVLVGIVSNRDIDFIEDRKTKLKEVMSKD

LVTAPEGVSLKEANSILRESKKGKLPIINTNGEFVSLISRRDLVKSRDFPHASMDANQQL

LVGAAIGTRPNDRDRCAELVKAGVNLIVIDSSQGDSTFQVDLIRWIKTTYPQVDVIGGNV

VTRMQCKRLIDAGADGLKVGMGVGSICTTQEVCAVGRAQASTVFNTARYARQFGVPVIAD

GGIASSGHIVKALTVGASAVMCGSLFAGTEESPGQYFFQDGVRLKKYRGMGSIEAMTAGS

SKRYFATHAAVRVAQGVSGAVVDKGSLMKYVPYLQQGIKHGLQDLGQLSLETVHASLYAG

VLRFELRTPAAQREGNVHSLHTYEKRLF\*GTYKRFCLCKVLVSKEKTDI\*CSH\*ARKAEN

CMVI

>contig18102 Frame-0F

MEGLEFQGRDLRVQFAKQRRPDNPREFYSRGGGNSDRYGGDGGDRHGGGGGDRYRERRDD

RRDRRDDRSRHRSRSRSPARRGHTDGDRGGRGRESSRSPRPRSRSPRPRSRSPRPRSRSP

RPRSRSPRPSSSPPPRRD

>contig18469 Frame-0R|Blast-GTPase, putative [Phytophthora infestans T30-4](gb|EEY69406.1|) 0.0

MLSQLTETQSETNAVEFTTLTCIPGNLLYNDVRIQLLDLPGIIEGAAHGRGRGREVIAVA

KSADMILMVLDAGREAGNRHREILENELETVGLRLNRQPPDIYFRRKNGGGITFNSTIRL

NKLGDDPYQTVYKILHEYKIHNCEVLFREDCTTDDLIDVIEGNRKYVKCLYVYNKIDVVS

IEDVDRLARLPNSTVIACAHGDRPALNFDTLLAKMWDYMGLTRVYTKRRGEVPQFDEPVV

LGSERKGVSVHSACMSISKDMLDNFNYALVWGSSTKYNPQRVGKDHMLHDEDVLQVIVKT

ANQQKRDKNYNQKVQAYFDKYKKKKKALKT

>contig18520 Frame-1F

MSVPKISNAKEASRDSRSRTALPLILLVVIGSSVLIIETISLLGSPLGLGRTIGLKWRNR

FHSSLSADEIVPDDDLLHLNLLHEACTADANVSLTWLYGSPGNQAKGGFATNPHDLILET

DKDLLRKLRQCPSVDVFLPNDMHTSAYCEDAVAYIKYLQSRLLPQWMLEIKLFDRDIQRE

VDYFDLCPKTPVLFLDHHWGVFGREWNGVTASLRWPKDKPIYMMPNIDIVELTPNHYWGV

DAILCKTGVCHDRVTKWFKQEGNPRNARVFYTKHTSLHPGVFVRKRLGEHVVAEKDFSNI

KFFHMAGTSTAKGTREVLDCWSSIPNLPPLEVYIARNTFTNCFKLRTS

>contig18814 Frame-0R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY67460.1|) 1e-81

MEAFFNMREKQENQSILVSGESGAGKTETTKIVMSHLAALATNTNSKVIQQIIQANPLLE

SFGNAKTVRNDNSSRFGKFTELQFTIEGQLIGARSRTYLLEKSRVTTQAENERNFHIFYQ

LLAQRHHLPDLELKLVDSFKYVSERANAPRGDEEGV

>contig19611 Frame-0F

MKVELKYEVFCYFVDTTVRKDKKRLSMKMFQQHQQQHLTDSSVDAIVTNGATGATLSANN

ASFLPFPQAGTTGFPLIQSYADMSIEGALTPGGTATKNRTLTGLKNGPRDDNLSGPDRPR

KIARSTQIGIGPDQLPLDGNGDDAVFHTIPFRIHGFVVPLEVDVSALKRSLGLTRPLSDT

SVTGESIDATSHI

>contig20192 Frame-0F

MTSCNDNERVVYYDLEAGSHTKNLLLSPTTKPAFTLPIVGTLALEVTGQNSEISPHRQHP

WFILG

>contig20347 Frame-0F

MAKRLAAASSSPSKKQRSEAPRLVMPNALECSVNLTRAEENLFAFLLNVASQPAANGAVL

RVAGGWVRDKLLGRDSDDIDIVLDCMTGRAFADLINAYETTQGRSARAVGVIKANPEQSK

HLETATMQIGDDMHWVDFVNLRAEAYASEDNRIPTVSIGTPQQDAERRDFTINSLYYNLS

TKQVEDYTGRGINDLIKLHLRTPLEPRVTFLDDPLRVLRAVRFASRFNCTLDDELRAAAQ

LEEVRKAFVRKVSRERVGKELTSMLIGSAAHPERALRLLHDLNLCESVFLPSILLEKMPL

CHSDGKLAELEENVWNSSYKCGKEMHRLVAATDENLDTDALSAEEKHDVLVRVLAALLLP

FRRLCVRDKRRRSVALVVVQDFLKLPNRDAKDVAIAVASVDDFLMATKDAFDRVKVGLLI

RRIGAQWKICCDAARVQEITNAKGSLDDARASVATRYDYFYSQVQDADLHDVWKLKPLLN

GNDLAKHCDIKPGPQMKELLDRIISWQLVNPAKTRDECLHHFMTSIAANTT

>contig20541 Frame-0F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY64330.1|) 6e-14

MTSSLSEVLLRRWDLAEAARVMRTSVTDTMRRRIPGDLGLVIQFNPNHIKVRLEANISE

>contig20862 Frame-0F

MGLAYQNQAKREAYVRECRRVLNEWWKEPLQTFERPKYFQPPSEDKSLSVSDQIVRKGSK

YHILNSTTVDAGKLTSTRKASHQSPYSDDFLHMYHPEELTTFDKVLGYKFMLPMEVSDEV

NDKEKRRSESTVVAHLTSSPSSSSISGSGHVDEENLSGIGVYARRSTIKKNRSYRSMSAP

DFGEDQPLFTRKERQSGYPAEYSSIRSSESHRASRLAIAEAINKYGGHGSAMLKAVVKRN

DDQMSVDDYVTRRGRRHKFVGDCATPGPDPIYLQYVLRKDSPQMWEKESESVKIYFEMYM

RDNQISPDDARSLRDAQARGGATFKLQVGPYTGLEQHVKARVLVSKKLHTEPEDRTMYED

FVDVKRLVKTGETSVPSESLALYKTFFDEDLPSVEIFRPTPNMKAPISTTADDFAPLMAK

RCMSATALSSVLAQSIQRISISRKNHTRFSTGELISVGPLFKMDGGKDRDFIIFNEAAAD

NAFGEVTRNEKELSFYSK

>contig21018 Frame-1F

MSLLVPDYASSSDDEELSTGTASAADTFHPLPTPKQSVVLNDIALETSNSKKNIKSKTTL

YLPPEIQQLLERGTSGGAFSDSSDEDSELLAKHRRARLAANKRPRTSTRDKDSLLSFLPP

PKHKLPAVKNPEQTLDSAEIQPNEPPVSDTAAAGTVAAWHPQHHYPSSTSADFKDFSIAQ

G

>contig21524-0 Frame-0F0

MEDDASAGYAWEGTLERSWDVIEEDDSGNLKITQAMQNQHRQ

>contig21524-1 Frame-1F1

MRGKARLSAAGMSLKKTTRAISRLLRPCKINIAS

>contig21524-2 Frame-1R2

MLILHGLSNLEIARVVFFNDIPAALKRAFPRISGRCVVFHGLFRK

>contig21959 Frame-2F

MRTLRLTCVSLVLVCCGSTLATIETYQDTLFTATSTKPVKTSEQNLSGRSTLRSLKAVRH

DRNYDLEPLEEGRMMSQHPPSHVPLPASSKEVIKELRGRLRKRKGFKQPLRN

>contig22679 Frame-1R

MATPTSSNATAALVLPAYKWNSAISARSKSMAERRCCAPLFTQPVEANTDFVRYCPTVGE

APTTDRKDRKAFYEDLRERHCNLVRRQRLAQEMFAYKAKEEFAYKAKEE

>contig22828 Frame-2F

MDGRLTNFRSSCRQRTESLLRHYQSRL

>contig22972 Frame-2F|Blast-thioredoxin-like protein [Phytophthora infestans T30-4](gb|EEY60565.1|) 7e-98

MPKLDFFRRVPEDLKVHTSTGRFFSLLSFAAIILLLLRNWDAYQHQRTKTTVIMDEHQED

RLRVNFNVSLLNVPCFVASVDLEDHMGQRFTNLTRHIRHFQLAVDRSSNHVQRLNEVIID

NHEKGIPVWGGVHHDIEGTHVQYSTPLTSKTFDDFLAKYELVLVNYHAPWCPFSRQLHPE

WERAAAQLPDHPEYSEMVRMASVDCNDP

>contig23434 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57214.1|) 4e-48 NOT\_ORF

MKDAMADSLQAQARIVSLVIRVLYTFVNYINKICQAGHKIRARRA\*GGAVRARV\*LHAQV

WYIVHIYKHCLKTLMIVTDIAQRHSRELLVRDFNTLKHDIRMLEKIDFDKIRMEIAELEK

KFLLQKQAEDETLNELRLSMEKVEKRMLQYAVGFAGTIMAVGAALMRLVL

>contig24004 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61431.1|) 5e-63

MSSKMELEAPPSDDQVFTALYMTKTLAKLRANEKTPQAAGVELQTALRELHTLQQEFVTK

QAKQNLLDHLAQVDELDVLQKVAASRKAQAEADYDQEKRELQKAVRERKDTLELLEKIAG

EVEQQKSKVLEHERTKNMHEKELAQLNEVWKELQRRNAHRKAAVQVATGVMITDEEDCGR

VLDQQTQNIQEMHQRQKQLE

>contig24677 Frame-0F

MEDGAHDPDSEKQSSLAGSSDN

>contig24916 Frame-1F

MSGWLIAVHCGAGRCSSSTEASYLSLIRSTLKDAHDVITNSTSPPTAAQLAVRLLHSFEH

SPLTNAGFGSNLTEEGRVECEASVVCGQTHLVGCCGAVTGVKEPSALALKLLEQVQRNDS

TSSFAFGRQPPLVVVGEHARRLAREFGLETAAEDGEVLKKYQITAKAHEHFIKWHERFQA

LRGSTDDDDERLDTVGAICMDPKGNVAAALSSGGVAYKIPGRLGLAACPRMGCDASNGQF

CALKCRKRKRRKQKKVKNAFAVACTGRGERFIQSALVTLLTLRLRKSTNLEQCLRKAFIE

ASDANGGVGVEGGVLAFVSPHEATSGLRRIQLGAAFTTPCMGVGYLQCQDDATKLQVHAQ

ILRQPASSFVVGKKQSLSTHVSILHLDVEK

>contig25397 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55926.1|) 1e-151

MLSKPVRSSSPSVSLGSSSVKSHCGYSDFSLSTGCAPSLSILVGTTCERSTISSTTALPF

ALAAYERTATSSGLVSLRVIAGILHHSLGFLKYEIGFLSLFINTMGKPKKRKGARSSNAG

KAQVFAQICMDNMSSHSEKKQRNLRRMRVVQLQRSVDRKLQDLRTFPTHSPPPKPLLRKG

PKPPSEWKLKGAARPAALLAKIAAGELDECGDEYPKPVETFDLYEKALKEGKFAEYKETK

EYLSILKQLAAACCEAGMPDRGIKTYELCMNLDTIGSIQTCEDFACALVNESRGEEVRKL

IEEHKDENSAMLAYCEVIIEYVSWEVLEEEGSSEEVVRKALHKAYKLNPFIAVVIAYHET

FFQVIEYVNEITDPKRGSIEEAFRYVSQNIGVWVDTVGAWQWIEKELHEMAEPAATKDNV

SDEMFLGMYTTAIEMHKEMLADAEADSHDIVADDGDGL

>contig25960 Frame-2R

MMPEDFTWADTIGADAVLGDLKGRNPKKDKSRQHDAMSYDASLVCYFNPSEYATAMNMGL

YTGPPAATLANGSTLMIEPVNPVEEAIFAKRQMAT

>contig27203 Frame-0R|Blast-40S ribosomal protein S15 [Phytophthora infestans T30-4](gb|EEY53513.1|) 2e-07

MIIVPEMIGSVVGVYNGKEFNGIEIKVCVQNCSQLSGDVRLTTQRVVLIGALNDESPDYI

PGCHPLVRLSVYGVTQRAFLSTLLHLFQP

>contig27319 Frame-0F

MSVDVASIRAAFAACNLELEEDAASTCVSLCAEFDMNPDDIAAQWDAFSMNKQLPGAAND

DGLVAFRSHLKQEKQHMKILESIFKESSQKISSLKTPVIKLESLYNIKSPQGKRGHSFSS

PAGNFKVQRKDGMKSPSFMQSPPGGGYEKRTDAGKMVSEFNAHLKIQLMGMDTNMRLPVN

IEVPFPNRNLAPDSSYMYTPLFQRAVALDEQLVEYEELVKDKYNIKELKPIGDPSPAQVT

VVGRIVCEAAEGKLNPSVVQIEGSRKSCGGQRVLLDLSGLPNFQVFPGKIVAIEGVFPDT

RSSMVVKRFLDPIPAPVQTALPASVIDEQGVLGSPIRVLIACGPFTTMSNVNYLPLNDLL

QVALGQKPDVLILVGPFIDSMHTMFQDGLVKYDDMMLSYEEIFLFKVMTLLNNVLAQNDR

IQIVMVPSLRDANHEYVYPQPPLNKHKACEAFENAEYA

>contig27430 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58746.1|) 5e-17

MSSSPAPLTSALSLTEPSSSVLVHTAKSGSDPVAIRVMIRICRKGVNLSDHVQARDPREP

RFPVIVKHPAFDDIKGNFNAGDYTRWLGTSLLSFPAGYVF

>contig28017 Frame-2R

MEIVDNGDPTTFDDIAGLDFAKKCVNELVIWPMARPDIFTGLRSLPKGLLLFGPPGTGKT

LIGKAIASQSGATFFNISASSLTSKW

>contig28350 Frame-1R

MLQDSNCVLDASQTEELQRMTITFPKYNYVVSLDAEQVYVVKRTSL

>contig28422 Frame-0F

MSENNQRIREVTEKHLEAFAQDGLRTLVVCAKKIRPEDWEQFHAQYRLVSSDLSVVEAKS

RGEPNAINKIEDQVESNLEILGATAIEDRLQDGVPESMEALAKAGICIWVLTGDMEETAI

NIGYACRLLNNDMQRHVINEAKYRTKGSILRKLDKIFHSIYDAKENSVESSLAATPSDSS

LLLDQAEHALVIDGASLTKILEDPLFNLHLLRVALLCKVVVACRVSPQQKAQLVELVKLN

VPESHTLSIGDGANDVPMIQSDHIGVGISGQEGLQAVNSSDYALAQFRFLSNLILVHGRW

NYNRVTALVVYTFYTNIAYNTSMFWYTLWPTAYSGTMIYSALIQQGFNVIFTALPILIYS

AYDKDIPKNTVLEYPALYHAELRKSSFFSHLMFWKWVFLGIIDSVGVYFATLAAGWNIER

GGNTVEYLSLGTLGWTILCIVMNARFCLLANSWDVLTCSSMVVTVVSIYLAQYVVDQINW

SFDTDSLPWQYGRAQFWFGQLIAVAGILLKDILYEGYRRRFNPDYIDLVTESLTDKASMS

REELKNFQPPQANYLNPELAGMMDFQDRRVHESTPVRYAAPGRSKLYTGFAFDQPANIIN

WILTGTNNSGGQNSRKSINANMRHAILNSDDPVFFENQRYQPFCGYGSSFPGYLLPTDRK

RWSDRSGKVSAQAIPLAGLELDLEVPGCDAEGWVYEKDFAFFPSTIENEEDEIEDEDDFQ

ISDSRRSSIGAFRMSRKKSKKKKGKKMRPHHGLVRRREWKLSSEYKAQTSEDARRCRESN

ESRSSVVDDPDEHRRQSTTQSPMQSSG

>contig28909 Frame-1F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 1e-155

MRINIFNRKAQQITNFSSEEVVGEMYVDTIISPEFKTVTYDIMCRALQGNETASFELALN

TKTGRKVNILLNATARFDQHGRIVGVVGIGQDITDRIAQEQEYTRLIDSANAPIFGVDVN

GCVNIWNKKAAEITQYTPNDVMGENLVEKFITEDYREAVGLVLSKACEGTETANFEFPLM

TKTGRRVEILLNATSRFNEIGEVMGMVGIGQDITERIAQEQEYTRLIDTANAPIFGVDIN

GHVNIWNRKAANIMQYTNEDVLGKDLVAEFISNEYKVPVRSVLEKAFQGIETA

>contig29942 Frame-1R

MIQAKEGGVLDFAAIRQINWNVHLGDLITACGILQRKPREPGRPMEWLFVVHSIQVDELW

SLHHDKNMLNYTMNTDLKSTTTSVAVVKTNKYTNMVILDGFNTCKYFFSSSGGTNCLRGE

QCHFWHGPLENFKTNQRRWIAKRLEQRANAAHLAGDSCDPHSKVEKVQRSRLFCDWLVAS

MGEARLAAGTGVIDVAGGKGDIPIQLWIQRGIPTTLVDP

>contig30162 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67683.1|) 1e-100

MLGQCVYVGRTVEVLGIRSQVDAILAGNVFLKCGVIGNATKIVVRSRSSRLFWLVQMSTE

MWEFAPNGEIYYEKLLHQLLRVLIAKWNESSVSHSVTIIAFSRSFYDSNQFPDTFDLTKA

PFSDPCRQSFNSGYDPRGYNMANRCGPTIHLDPETGRFYEDFYKVVVANFTGPDWNQLLQ

LLKLEFVSYHKTHRWRTPEQVSYAQYEICH

>contig30988 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58473.1|) 1e-120 NOT\_ORF

MVTSRYETEASLRTAIFGDILLCRDWVTKTRVVVKTVDLQLALKQTSRSQEPVQENVLHE

VEVLTRVRLLGGHPNVINLLNYHVDKGSGILHMVLDYCEGGDLLDVCVQPPATKDNDGAM

YNRNRDSRQENQEEDATTLKGVKRFLKQIPQPDQSGRNARLLNGTNGFKRLNENVVRAYL

VDVLSGLRFLHAHGIAHRDISLENILLRKGRAVITDFGLCVQQLPVTSNPALGTSFYCVE

AVGKNYYMAPEVLAHKPYDPRRADIWSTAISFFILLTLSPPFERADVSDSGFRYVKKHGI

KAVLSAWGLQYKVSEAMQDLLSRMLRVDPMERISMEDIWQHPVLRGK\*CLKIVFVELACS

KDGTINNTT

>contig31055 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57375.1|) 7e-87

MNLNNPFYDPSVVQMQSPATPSMNFPTMAPPAPFMPVGGTIPSVYDATPGVPHQNLMDEI

GAQIKSTNSQTIIKVMRTLNLVLASATIVVGVLAWLLGQVNNFQKVIAGIYIIMFGALLL

LFELRTEKMDEILRKNFGFMYGNKTRTIFLVFIAIWPLSMGNFWLTILDAVLLFLNAFFN

YFVISKHPAFSSVLPVYDIHQPPHAGGYAPAPQVIV

>contig31271 Frame-1R|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY62871.1|) 7e-66

MAPEVVASDNKYDPKAADVWSLGIILFILLTGSPLVPLAAEENVAFRAFRTVGVRDLLKT

WHMKELLEESALGLLEGMLECDPKVRLTIAQVLNHDAFKRCAVGG

>contig31507 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58776.1|) 7e-22

MSGGSEYPYPKYTWSPAGGWWLKTKNWQRKTGLALAAVACVAGSISHYSNSNQIKYPSKE

RRKL

>contig31693 Frame-0R

MCQSHLSEVKELTPEFYASDGTFLRNSNTYELGKRHDHQIVHDVVLPPWASTPEEFIRLH

RAALESDYVSRHLHLWIDLIFGAKQRGRASLDANNVFYYLTYYGVVDLDQINDPFLRESM

ELQIAHFGQCPMQLFQTCHPSRYGTSHSQTKVPVSVVEHSTTIVSNSDRTSSSGFQTIVP

RSLSLSFHDLSVLAHEKRRQWTCQATVQSITCHSIRAIQILSDRVVSINEHGILEVFQWT

LVPKDKTMHSRIVSIHHEPYEPVPCSPIQDEWHECPWLLELHRDESIKASIPCIPMYEHF

IINGIHTSLKRSPLVISDNGRVVISGGARNGALHIRLVDLDTNHVIGKASVVGHTAAITC

LSLTRRMSRTHELNTLLTLPDKDDEHVLVSGSEDGTVALWHLSRLERDGRSPLPRISSRP

VHLFRGLTTSIVDCCVNTWLNLVVVCTTRVGMALFLHDKGHVAFVLEPADVQGVFVRVCI

SKKGYVVALTRLKHVLDANESTVCQVFNVSGVLLQSHHLRMEEVMEVDIDATGELLVLTL

VPGIIRIYRLEDFETVQEYVSSTSCVISATCLGPKEAVVLLAVGHEDGTLSMHLLPDASG

SVSFVANVRRLFGVSSKLERVKGTVHQAQTLAMSTLGNAKAVTNTARDIAEEALGEAKGM

MRDLFLYLQK

>contig32775 Frame-2F

MLLAHLRKTATVTRRFQAREFASMLGSFTNKMEKEAAGASPSHSRGDIVLDGFAKRQFQD

KTYAGTRLDYDEDEFVKKVNEIYESNNKQLVDGYAPFCKHLFVKNFTGARHTMVPITQAN

AHLLMSDYEARAKYELPVLTRWFPSHSVTPRVAEYLDIILYSRDQIMKENEAMDLPADPS

HVDAPWGIVSIKAQDVDHELPMKPITMMRNAIGKEQGGSGVPIDRDEYMKAVEYWRNHVT

IKKM

>contig33127 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62786.1|) 2e-46

MRSRTRVARLDKNYMGSQYTMYDATGQVSLELEAIQYAATLGKSPRQMRVALPLVASLEN

VDSATEGIASWAVEPWRHESKEDAILAQVENPDTTRAVHWINKPPVSIESLAASIA

>contig33435 Frame-2R

MYSGDATATEIAGMVMSGRVSVPWSSYSHLKAFAECFDFSTEKWNDYYATTKASGSTRIV

CTQKCCVQSRKEDIEANWLLIADTTTTSGDWEVISDLQCLNVAKDKRPEMDRVFDFAPLE

EWLTKLWNGNGAQVGDTRSAGLLKSNVKNSLCDLKSMAGRLFVSLEA

>contig34038 Frame-0R

MENRHGERLSTTSPPVMYVMIKRFTTELEFDKVEYFRQYVIIDRLLVENSPSLSNLVDSL

VLNFMYLLLYTL

>contig35626 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60181.1|) 4e-18

MPTSNSQQLEDYKRMRKQDLSEALAKRSDTLELIELQHRLHEKTMARVKHYERMEQAMHK

PKK

>contig35653 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66067.1|) 1e-144

MLESLPESKDELSAFMRTEISAVDVAKDVILTKLHDEVRANYNALIQGMKVVQDVDLDLV

RAQIHVKNGRRHLATVKHDLVLSSLKIVKTKQNLNRVCEIVNLGSQILSFFSQEKEMNLA

LQEHQFLTAVDICIYLRQGLAREEMQKLTILEDIRLRMQNFIPKLRDQFDQSLRKIAGRF

DPLEYKELLKAYITLADHSESLGFDFSSYTLTDVLSKIPEKIIRSIDDMTRECMRQVFID

VSPKKLRLGNQNIRSDNFCNRKGGVESDPMLTPSSQTIKNVKRCYENLTDLMHTYYLLVQ

WHRDPFNSLNDDVAYLHRCG

>contig35842 Frame-1F

MRQPKHWTFQEEKAFETALARCAGSTSYPWATIAAAIPGKNAKDVCSRYHNMVREIALIE

SGAGSISTTNGSKFTLSQRAIPPPPIKVPPRSSGKEKVAGIFPSSRKGSLSGITMLSPTF

LDFLAKEAESEEKSTIPAMFLAKPAPSPLFSPTLLPSGSPGFFSPGTKKAAARGQQGRRF

ASTNDMTMKEIEGAGSTTAANKTEAGQNPREWTNFSRPITNARTLSDQSI

>contig36274 Frame-1R|Blast-40S ribosomal protein S7 [Phytophthora infestans T30-4](gb|EEY62410.1|) 4e-62

MSSKIVKPEGQTPDEFELQVAQELSNLEQSAAEIKNELKDLYITAAKQVDISSGRKAIVI

FVPFRLHASFKKIQARLVRELEKKFSGRHVVIIAQRTILGKGYSRANHGSGPRPRSRTLT

HVQEQILD

>contig36429 Frame-0R

MSTNATCSEVTSQLIHPLERLEFQPKTSLDGSTLPYASAPRSHATNYSSFTKDFRFNRAR

VKFLHYKEKWTPNLKALNSVTGSVQHLMVEQNTFKKNFQSFIGPSRSPNSYSSFCMEKLS

RHHRRAENLMNRFPLP

>contig36560 Frame-1F

MVKVDCLPKVALATCLSAAVASAANVNFINKCPHSVELYHSQLGSAVAKVADIAVGASTS

IYVTGPSHMYRHGQDPSATLVELSVDKHVWMDISIIPPMPAYCDSYIACKAGGKVGFNLP

ISIVPKTNNGSGSTCHGIECAADSPKTCADAYHFPLDNSKTHSCPMDTELDVTFCYVQLS

PSPPPYEQQSPVQQDYEQQSPVQQDYDQQKPDQQKPDQQKPDQQKPDQQSSDQQDPEQQA

PIRQDDSYLPLPTVIPVDTDVTQTLGNALTLGTVKSKYTYAGKNAGNVPGSYDRVTDLCQ

CKKERVTINSPVGPLSEAVTMVFRGPLILFDVAVYIMDTTTTKWLRVSSYSKKDQTVENM

TFMNNKNVDYSGQDRHSPQGYATADGMSKADNATVFNGVLKEAADVSKIGGGSGISTGVE

VNILTGTKCVDGGECVGFHGDNDYQGWVGGKKIFVTKVMMPHDTAPNQPAIWMLNAQVVH

SNQYGCNCRGMGPVGGCGELDLTEVIETNAKRDMITTHYYFYDGSILSPLGDNFAPRRHD

KPTVYLTIIDDSKDGLVKIVEVDDFDFSQVDITSLYQQLVDC

>contig37145 Frame-1R

MVFFSSTLHTLAGGVFYALLIYTLTSVVDHYQDDALNTSSSVLNTSVSHLLRTDGHRDGG

EAAYVSKLTHEAM

>contig38135 Frame-0F|Blast-phosphoserine aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY57574.1|) 5e-81

MDSNSVPSPKVEQIIRLYMFLWEESQISDANRVNIFEEFSRKAMIFVPSKEKAQCCFIRT

INAVWSASIQKGELVVLEALYPLSLSNFFIEVCGVQRKPSTTLLCNIISSQQDQIWTKGG

NSKQPHDIKVWKKTMLPLLCALARNFKKRSLAKGEKKIIKKALKSTLWLPVRSLSGRNSG

IVFCSSRDKPVRATTEDERKLQTLALSLTKKAAESGGGSYKGEDMRGEDDIHLIQYDLIA

ENTDFNPLLSLMKVSTLSSHLKDHADLWGKLIARLTKFFQPDYNKYRKKLLKISQLLVKL

WAKAFSMTSIEERSEFQAVMQYLMLFPTIGESLQWVSGNGMFINDQTELSKEVLEHSGQS

QRLQILGLFPLSYFVI

>contig39309 Frame-1F

MLLETINTALEMARLPIESPHPHQSVCKSLDCDHPLLRFKRYHYVIENFGYVLGIPAMSS

GFLLQSNLLEKWLAALAKMQGLDPQVRIQDGRAHVTYETQSWLTAFAFHASVSKIHTLIS

KGLRHFEAKNTETCNQDRERMVLNMLEAFWHQLDQAAMTTTRFQLYISPCGRLLGSNCAD

KIVKYDVSAQPVSFHNPLHGLMANFLIESLYYGPCSAPGSGLPWIRSWSTLFERSMAKQL

HFDKIEGDEKSLLVQQKKRMLIYGMMEFPLRSLILCAQISCGLWIRNGQNMQRQMLNYTS

PPWCSELRDLDLFLVQLSATIISFPTFLTIFFDRFGMSEWLVTWANIRNTSDESSNFFAR

EAIGTASEDIKLVGILEAALLQLLWIVTELRPPADAVELMDTILRREVIHRLCQHPCRLS

ELLDQTAFVVSTPSNGIVARQERQHLSRLERILEEVADEQVKRSVTMASLGKDADESMED

EPTQYIIRKAFYKEYDPSYYHLSRSGHEKAQFARQEALFKTWKVEDPPIPIVTQIPPPHF

VSWPSAISRAGQRFAQYLAARVGRCTLS

>contig39536 Frame-2R|Blast-eukaryotic translation initiation factor 3 subunit G, putative [Phytophthora infestans T30-4](gb|EEY60945.1|) 1e-170

MAISGMRWGDDEDDLLPQRVESEPDSNGVRQIVEWKLNEAGDKVKITKKVKKVTEVEQIS

KRALERKKWAKFGDALGDGGGSNVTYMSYEDIKLDDPNADQVLPGEKKEEENIFAGVKNS

SIVVCRHCGMVGDHWTLKCPYKDTPKDELEQDMAKRAESGDVAGPAGSSADPGARGSALD

GAFGSGKYVPPSLRGRAGAGGDAGVVETTRDDSATLRVTNVSPDTGEDDLKELFRAFGPV

ARVYLAKDRETFQSRGFAFVSFMYREDAEKALEKLQGYGYDHLILKLEWAKPSNKPATED

AGSMGTTFRSGYGKALPQNVAPPPRK

>contig39543 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64094.1|) 6e-34

MYFLLERKDVQRRKLVDARNLEGATPLHLACHVNHIEGIKLLLMHHADINVKGEKGVSQD

KTPLELASLQEVKDLFSQSVKESEEPANALIQNDLHANESTEISESSSCVLPKKNEQVSG

TCIQNEQDSKLLLQLEEKRFVGESVEGDD

>contig39950 Frame-0R

MQATEIYSDESCDLPVTLSATFTASCLESDCNPIIIGGATYYSETSCSSNIVSHAEDFFE

DSQYIIVDSYSDISCTTYVETVVVAASGRCQLAGSSGQSVIATVSTNGSTQLTYYSDRLC

TSPALATHVVTQEELVRRACLSGRTYLASFNGADTGDDSDSVSSTISRDGRFEINSAVLA

GIIVGVLFLIVLVGFCVFRRCRRRRNSSSPAADNFRPTHVEGHVDYEAQVSPEKPYTQTT

STTISDFDRCHSIQLWKDDLIVAARIPREEIQVGQLINRGGYGEVYIGNFRGKDVAVKML

LPETKKTMSQVNAFLSEVKLMASLDHPCIVSFVGVAWDQLIDICVVSEYMAGGDLKALLT

LYEQSGHPVGFNPTKVKIALHVAMALGYLHSCAPPVIHRDLKSKNILLDEVLNAKVTDFG

ISRERIDATMTGGIGTSFWMAPEVMMGERYDDKADMFSFGVVLSELDSHVTPYALSTNRN

LTTSSSSAEPNKLPNAAIMQMVAAGKLRIHFSDVSPQSIVKLGYACVSVDPLMRPTAVEA

LKKLRQILAKDV

>contig40626 Frame-2R

MATQREEDIKMMLAAQVHIGTRNADSKMADYIWRRRNDGIHIINVGKTWEKLMLAARVIV

AIENPEDVIAISARPYGQRAVLKFAHHTGCNAIASRFTPGTFTNQITKQFREPRLLIITD

PRTDSQAVRESSFVNVPVIALCDSDSPLQFVDVAIPANNKGKLSIGLLYWLLAREVLRLR

GTISRALPWDVAVDLFLYRDPEELKKAEEAQATAAEEALAPVNWGEASAQTPAEPALYAA

EPAVPAVAATEWTATGNTEWSGEAGAGSNWNAAAPSGGSGWD

>contig41113 Frame-1F

MCYGEPLCAAAKLDCCDVPGGCCSASNSELDCCFHAKPFTAHSSASYSSSTNTCQGQPKC

GAADLDCCEWDGGCCKPDPATATTLDCCIDVSSNNNRTGSSEESDTTPAASNADYTIVRI

LVGVGGALVLVAMVYAGGLCYRRRGYSAIDVDTRAIYCAALLCGLAAFFIFLVVT

>contig41269 Frame-0R|Blast-carbohydrate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY55480.1|) 1e-25

MAVVGTIALAAIAFVVKKKKLDDKRIDRDEAMIRAFDSYSSPVEINATNIARI

>contig41470 Frame-0F|Blast-RNA pseudouridylate synthase, putative [Phytophthora infestans T30-4](gb|EEY69313.1|) 1e-132

MPTHPCGAYRHNSLHSIVQASRPDLPQLNIVHRLDRLTSGVVLLAKNAAKARALSSLIAD

RQASKTYLARVRGKFPDISIAEVQDKLVIQAKEKCSACIITYPEHKAALISCPLRCLCAR

DGVWEYHPDGKPSETFVQLIRIDKDTSLMKCKPITGRTHQIRLHLQLIGFPIANDPCYGG

EIHFGESVERIQKIAAARLRKADLAPTEPVDFSTPQQENECEKKFMERTCTWCNTSEAEA

FSETQLHCSKIWLHALEYKLDGKTYKVPEPDWARPSSEHLFQDGQK

>contig41544 Frame-2F

MLSNCTSSSSQSIVAIKNLYRKDKHKLSLYLAIPLRTLRNLPHRKPYQMTKRQMPCQ

>contig41805 Frame-2F

MAWGLETTPTPTRMPATTVAADDSSSLSAATFQTPSPDSADAFDVFQGVALVTSVALEGV

ALLQVIKHCHESLPGSVAGSLLGVDTDQVLEVTNSIPSPPSSDRKKEADEYQLDMLKSLR

EVGMDNNIVGWYQSVAMGTFCSASFIEHQYQYQKSLGPNAICLIYDSAETSKGSLSLRAL

RLTKAFIETYKSSSFTKESFSKSDIRSATIVEEIPVVIRNSDIITCWLQQSSGKAAFSSF

DRLDLATNAYLESSLKNMTLWADELAQEHYKFQGYERALSKQRAAYQLWQNKQREENKIR

RENGEDLLPEEDPAFFKSVNQPSRLESLLITKQMNTYCEHINRYAGMSFQKLFLAAKIHQ

NE

>contig42277 Frame-2F|Blast-small nuclear ribonucleoprotein-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68847.1|) 8e-85

MAPMRGIGGPGSGMIQPGQVAAMAQPQVYGRGRGISVPAGGMMPPPRPMPGMGMPIPGMG

MPPGMGPPPGMMPPPGMRGPPGPPPGMRGPPGQ

>contig42404 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56606.1|) 1e-144

MAQPLAAPPSALAPWRERLINSKSYMRYDYAWKAVEFQQAEHRMTGVSCRLLYLHAVWIE

TYNHTTSSCASRPRAKAYIEGNGFQVFEEQVAEACELMGYDIVANKLTADLVFVYVAPLN

EQRCKGSQFETFQAVVAHSKNLVDNEKPMFCFLLGDAGFLPPSKTEEDEHIRSLSDFAIS

QELAPIASESGYGPVAQFAVEFVPSSAATLSNEFREKTTLTLDSLMNRFGCVGQNLMHQN

EKWEFYASCGSVFCHGEDDLNGVTHPSEEDTLFWLRKMKGKACDHCFALSEKLSKCSKCR

DAMYCSRDCQKAAWMLHKRLCGKPVEEMQVSHETTRSSRPS

>contig43128 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58151.1|) 1e-105

MLLQVVDNDLERSHLEEAKLIMTINSAHVSGDFVQALQGRIHEFSCISFSNDPPILESLP

TPLSDLIDAFHSIVSNEIQEVLSRTLHKRLPRVLNHEMDEHLQYVLTSTQYDILSSQGSP

LVKVVEQEILSNGELKRYERALCRGPFEDLVEAATQFLTKCVEMALLRSKKPCNELGALQ

LEREVTDMLTRMSSLVSQKSLRGAFTRLFQVAFVLNLMQPSHILDSIDKLRVDFAIDVIE

TLLRMRVEYTSQDIAHVMDVISK

>contig43274 Frame-1F

MRQIASGVQFLHANGFAHRDLSLENVLVSDEDQCQVCDFGLAASTAMPCHETVGKLFYMA

PEVLAGVQYDATKADVWSLGVMLFIMLIGAPPVETASLSDARFRLMSEKGVRNLIDRWGL

TNELSASAIDLIAEMLQVDPRQRMSMTGVVAHPFLQRCIPINSLLSPIISLSQTRLASPI

KQTLPVEICSSTPMHSTVILRSPIDGIQRSGCRLLLYKIHRFFSRRRNKRVMAVNRTSRS

LKRMRSKRLATAA

>contig43560 Frame-1F|Blast-Ca2 :Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4](gb|EEY69209.1|) 1e-124

MRVVWNPFEIFTVFVRRLTIPLVDEDTWNKNLVVVCPPFAMLLFGISVFSFSIEDPFFLM

TVVVLGGFASAFVEYSTSPLGPPEGWQLALLISLAFGMSVVWIMNIANEVLAVLETLGAL

FGISSSVLGVSVLAWGNSIGDLVSNMAIARDGFPTMAFAGCFAGPMFNLLVGVGLSLTIN

IISRGPLIMSMPSPLMYLGFGYLLLSLLLNFGMASWDNFRYRPRLCYTLMALYASFAIIS

IFIVLNYPEE

>contig43906 Frame-2R

MSSVYPASVSPVSVPSSGSQIPNQTPTITFSAIQSVSESYNVKTNDSELIFSSSDAYDSE

MLSERQLIARGRALLQAYQSQKQQWLKRTETDGNHSSVNIFEHLEPLTLEHSSPITRHLQ

YNRSVLHRYKRKTMTPLPISFLNSTTTEIDSRNNGPLSTSERTVPEPLLVTHDEQHWTDF

MQLLKTHARTMEMLDTQLNQLWGDLVSVDENASESVKLLHIAG

>contig44693 Frame-2F

MPYLQDRVALNLDRRYTRNSGASTCFRRRRNIPINYVRVTCLPLLLIYHLPAFQPPLFRS

FSL

>contig44868 Frame-1F

MEALVSLFPTLGKDSRTRHIIQPLVDDLATLDDNKDPEEVLRILQFNVENSQSEDITLFC

MRAKVWMSFVTSYRKTIGNSFSAMKSLRKVYGDKKLAAMLAKAENTPGFRELAKHLQDEF

LRALLNHDLPIENIKNKRTTTRAKPVADDSSLQTLLSDYHALRRDIHNMLRMPQEMTLV

>contig45333 Frame-1F|Blast-histone arginine demethylase, putative [Phytophthora infestans T30-4](gb|EEY54346.1|) 3e-40

MEWFVTFYKDVENLPSHRKPLEGICREGETVFVPHGWWHTVLNIDESIAITQNFVSSGNV

RSVFEFITEQPELVSGCPREQRCKLGEMFRDAMAKSAPDMYAKVINDLKTKNERQHRQSK

WEKIVTSKPNQEAESTLLTSSIDDVATPKNFTFGFKFE

>contig45449 Frame-1R

MISKRVYTSCTYCSASKHVAGDTLHRAHSRIV

>contig45795 Frame-1R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY56572.1|) 0.0

MKDLIHVGVFCDTNVSKKDAPQIEEQYIEEILATQTAETELDEDAFVQWASRAVAVQQLL

HQLAFAACHLFGLKPEAGNLEKRLVEWHWLEATRDIKTGQTYNLVGAEWWRKWCDFVSMD

PKNGSPYGSLPLPRLPPSTEVEAARNIRGNIALRSASLGGNVSGSMLSRPGPVSNWCLLL

QSGCRRLKDKLLLARDFYIIPSQAYSILLTWYSGGPDLVRYVVEVSTETGPELQIELFPL

VLRVARVDPANGCVVRSGEEVLLGNLSTPASLLEATCRALLMLNVMDKARLWYFNEKTPH

HKVRLRDEYPNELKKLTQDSVFLLEVQDNDSSWPLSQASDSVVTLPINGVHQPVEKNGCS

NESDVNASKKRQRDHRPSMRTSDICSRGNLGEALGQRGVVIDAGSPTKEENPMLASPVMR

KRFLKDAFKGTGLVGLDNLGNTCYMSSALQCLSHTRLLMEYFKKEAYVKDIN

>contig46040 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67179.1|) 3e-36

MWTALAVVSMALSSLSTGLTMVSLRRSWDLHVSSVRWLFFLFFLYLWLWSSARVLYLLWI

SIYPIDTTIADNASSSSNAAEVAYDRYSSMGIYTILQLDETHDALATALLCFGDAALFAV

ALWMFPLTFELSRIAATSMDRGAEKERQQIRVYAWTIHASIFL

>contig46435 Frame-0F

MEERDGAQSIGNVAEVLILLLNMAFMVVGCLLVYFSHRVETSGWMDAFQSDFEWIGSSTL

TFLLVLGAIVIALAAFGCLGALLHQKLLLTIYAMVLLVTIILFIVVAVGATTANSKADDW

GMKVYPTTDQEASLGANFNKLYCYAQIPYYCEDASVNSVLDMFNVSLSGYFTDSTTNFSR

VCGTMSLPVIYDSCAVCDLIPQYSRYSVVLDWIKASCPRSPTNQVWCGDFLLTTTAAGDM

FTNAPFMECRITFYDLVKKWTNVVTVGSFVSIVAAVMVLIITGALRSRVRAASQDKPALP

APVPPHQFR

>contig46758 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62786.1|) 0.0

MLECAICQEVFTNATEATCCGQIFCKECIERWVSERGSCPMCRETIGFTLLATSRHAQRM

ANEMNVTCPYCVAVMKKASAADHLVTCDQAPVEPPPPADVALRHLLIQTARLNSSLLAQF

LMAPSPPLSLMMQCYIRTRGGGNYELYTQDTDTLLCTAVRRRQYDMSVSFIISLATNLDA

ASHGMEVNGLDYPLNAPVPVARLDKNYMGSQYTMYDTTGHVPLELGAVQYAATFGKSPRQ

MRVALPQVASLENVDSALTGIASWAVEPWHPETKEDTLLAQVEMPNTTRAVHLINKPPVW

IESLEAYCLDFGGRVAAASVKNFLLSYPNEMDKTLMLFGRTQDRQVYSMDYAHPFTPVQA

FAIALSSMDSHLVTFD

>contig47803 Frame-1R

MVHDASCALSAAWRLPTDAESTTFCGQATLPKLPIPDLKSTCQRFLKSVQALQTFEEQQQ

TKQSVKDFLIRDGPRLQQQLLDYAGDKSSYIEDFWYEAYLNHRSSVVLNVNPFFVLEDDP

TPSRNRQLLRAASLVLSTLKFVNALRRGTLEPDMWRGDMTLCMHQYKHLFGCARIPSPGA

DNVMVNELSKHIIVVCRNQFYWFDVIWEDGITAITERELLANLKAINDDALLADDVDVAS

NAVGVLTTERRATWATLRTKLQAENKDTLDVIDGALFLVCLDNTSPPDAAAFAATALHGT

YSITKDGVQTGTCMNRWYDKLQLIICKNGVAGCNFEHAFVDGHTVLRFVSDVFTDTIIRF

AQTIRAGTYAFLEASYRAPHLSPPDAVNLPHVQPYKLEWQLNRELQEGIKFAEARLTDLM

LQNEVKVLEFTAFGKLFITQHNMSPDAFVQMAFVAAYYFQYGTAPCIYEPVLTKRFLHGR

TEAARAMTPSALEFVETFFSDAAPLDKIGSLRKAIQAHVTNVRDCAAGLGPERHLFALKC

LWQHERAADSSKPTPALFADDAWRKLNHSVLSTSNCGNPSLRLFGFGPVVPDGFGIGYII

KDEGIQFCASSRHRQTERYLMNLESYLLRIQDLLMHEEEIRFPHSTAEKKNMQAAFKGYG

FFDDGGHLTETKALASIAVGKPLL

>contig48248 Frame-1R

MWCLLLLLSVALLTCVKPGSWDATTDATVESQVHRRVRLTTNSSVGQEPGYNEERLP

>contig48514 Frame-2F

MRVDLEGIPVPDISEFADDDFWGDTNLDALDSAEWDDPALLGGLLGGGVNGTAASSVLSS

GLATNMNLSSTGGASGSASGGGAHVDVGHVKAGYPKSSKKSKTGIGRARKSSISSSDSGR

DVWSVHDDIVLKKLFELYGANWTLIAQVFNSSSAVSRFVCKKRSPRQCYDRYGNIVSSSL

TTPTSSAFNAPSSTLKDGKASIKAHRAAAAASMATAQLSPAVLDARIGLPPEELLLKFPS

RHSLPGLPPPSIKSAAFAHKQSQVRKDTKKLSGGMTDLKSIITSFDAIIQCMKHKTSPPP

IPIPVGVDAASTSRAIPAKSSDLGTKASLTAASFLPAPSSASVTT

>contig48820 Frame-1F

MTSQPFTTAEENLALLFERSRQRSFATPIQLKSASPSSKEKSALLQSYLHRLTRMHGILF

ALSSPRGSPLASSGRQNRKAIKPIYPREMEAVLFKDMQTLLHAGGLGDALLLKIVVINIF

CVLRASGSDSPLKDALRLSICTITSVMEILLASLEAHTNDKSSRNSVISAFRLAGPVAVF

CDFLQLHPDILESFKQLTAHRQKKLYRDAATSDQETSTDQFALAFIETLAKLVNHARVRE

LYAPLIESSRQQNNDGVTNRQYLLKESLELRGFTPLEQDGH

>contig49261 Frame-0R

MDILHATTYRSLDEAEKAVKSYAIQNGLSTNRGRSETNKAGTEVRKVWLKCVYAREHEGS

GGKIRRTSTLKTACEWQGTI

>contig49904 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58452.1|) 1e-34

MGGGNGQKSAAKRDRNNAKKMKEAKNKNHAESKAKMEADRTGLKCKICMTTFLITANKAQ

LNDHYESKHSSKGLSFEQCFPA

>contig50476 Frame-1R|Blast-enoyl-[acyl-carrier-protein] reductase [NADH], putative [Phytophthora infestans T30-4](gb|EEY61640.1|) 2e-21

MGPAKAALEATARQLAYELGPDGIRVNCLSPGPINTVSARGIPGIS

>contig51035 Frame-2F

MVYMSLICTRSWSQGLARRLSTFKPDIEAVKKLRAESLAPFKDVRDALVATEGDFPAAFE

WLRMKGIALASKKSGRQTAEGLVSIKLSCNGLAAAMVEVNSETDFVAMNDKFQALAISVA

DALAEVPTTNIVTQYSTDKLAAIMVDGATVAEKVPELVGVVGENVVVNRAVQFQLEEGTI

CKYLHNTIAPGIGRTGALVALRFPIKTASAEQVAGVKKLGHRLAMHVAAAKPKFLSREDV

PDDLVNKERAFLCDQVKDTGKPAHIVAKMTEGRLNKFFGEIALLEQDHLIEEGNPQVSAF

VAEQSKK

>contig51358 Frame-0R|Blast-DNA polymerase epsilon catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY63268.1|) 7e-50

MYPNIILTNRLQPCAIVNEADCAACTYNTECGRAAIKDKEAACQREMEWVWRGDFYPATR

PEYYSIKTQIEYENFPLEYKGGGTTG

>contig51527 Frame-2R

MQDLLNLFMLFRLIILDTHPIDPALQNMKRCGNRLLVFSATSLSLKNQAKQVEAVNKEHR

GSMLLNDHFTNYKWVAYAAVLSICYILRKLDVTLT

>contig52052 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68297.1|) 2e-23

MEVLVCLKRLRSQHYAKMSTATQLPPAELQSRAFQSLKYHKSGVTSKCVVEVRADGIFQR

>contig52236 Frame-1F

MAKCSEKDERMLQLKNELSSLFKQLQAALGEVEALDASARDEACKFRSEKSVLEISLSAN

KLKLDELQAMGFNCEETIRVLLCDISSIKRSRSEAIARCCEKNEEIVQLKSMLSSLSMQL

QAATAKLEAAAVKAGKEISALQSEKSALENRLSAKSAQLQDLRENQLISLTTVDEKREST

RNACAMTCIRQDKLPKLVVPSGIFSLSFARDRSEVEAEKRQINEANLLQRRLRRQKRQ

>contig52359 Frame-2F|Blast-vacuolar protein sorting-associated protein 35, putative [Phytophthora infestans T30-4](gb|EEY60193.1|) 2e-24

MAQQYLMDCIIQVFPDEFHLETLEKLMNTMHKLQATVDVALLLTVLVERLIKFRQTQGNI

QIANQEEDRVDDCDNVNPHNELFVCQQ

>contig52500 Frame-2F|Blast-leucyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY66974.1|) 1e-62

MTSAKATAAINARLVKIGTGGAMTQFRLRDWLVSRQRYWGTPVPIIHCLKCGPVGVPIEE

LPVELPPVGVDVAENLRGKESTDSPLARMSQWKHCKCPHCGGEAERDTDTLDTFVDSSWY

YMRYCDARNNTAAFNPG

>contig53547 Frame-0R|Blast-anaphase-promoting complex subunit 7, putative [Phytophthora infestans T30-4](gb|EEY63812.1|) 2e-34

MFAAAIESYNTLDEIFPRNLYCILRKGSLELKQDLLHQANVTFKRARQVDEFNLTYMDRY

ANCLRKGKSQNNLNDLVHELFQISSTCAESWLAAAYYN

>contig54047 Frame-1F

MLNTRPIFAETYQHLQGQGQMGNRKIPTADAMIKEDASVKDKELAHLKRLKACITFESIM

SFECYFYSESTSMHDYVWQNILQYSQSVWSRSEGDEESKTWY

>contig54292 Frame-0R

MSVSSVLLCLEYAKTSPLCRYWCSSEREHIALNLSYDVVLVLDERLHSNVLLWALYANRR

QAS

>contig54425 Frame-0R

MSLSSFTASSGRAFAVSHSSCPSVSCNLVNHPLSSLRANASICDSTEHPTSHLLIGTQLL

LIAFSALLAPAVCASPATSLRF

>contig54946 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53722.1|) 3e-16

MMTMTKLTRPMLQLYAQCLRSARRCPQWEQREMMKAYLRMKFRDEVNAQNPDRLQALLAD

GREE

>contig55039 Frame-2R|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY61535.1|) 1e-29

MDEAVQISLLDKSRSTLRCLICGLRGGCIQCVSGRCAKAFHVLCAFRAPSSLLFTGS

>contig55581 Frame-2F|Blast-T-complex protein 1 subunit theta [Phytophthora infestans T30-4](gb|EEY63968.1|) 0.0

MSKSMGLNVAGGLSSLLKEGHKHFEGVDEAVAKNIDAVKQLAAITRSSLGPNGMNKLVIN

HLERIFVTSDTATIVKELEVVHPAARMVVMAAKMQENDYGDGTCLVVALAGELLLEAASL

LRMGLHASEIVTGYEKAHEKCQEILQTLQCVHVQDPRDEIELQKAIRTSLASKQYGYETL

LSKLVAEACLNVMPAAPKKPSINVDNIRVAKIMGGNLNDSTVIRGMVIQRNTEGSIKKAL

NAKVAIFGCGLEISSTEAKSTVLIKDAKELMNYNKGEEAKLEEAIRAIYDSGATVVVSGG

SISEMALHFLEKYHLLTLKIQSKWELRRLCRAVNANALVRLGAPTPDEMGFCDSIVVKEI

GGKKVTVFQQDQEDAKIATIVLRASTDNVLNDIERAIDDGVNCVKALCRDNRLVSGAGST

EIELSRQIRSYGDATPGLDQYAIKKFGDALEIVPRILAENSGQMATEVLSSLYAAHAAGN

KHAGVDVDNEQSSHVIPDAMVKGIWDHLETKMSAIRLGADAAITVLRVDQIIMAKAAGGP

KPRGM

>contig57280 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56645.1|) 6e-07

MSITHGTPAESLECMATMDDITIDDGNYCEF

>contig57389 Frame-1F|Blast-general transcription factor IIH subunit, putative [Phytophthora infestans T30-4](gb|EEY65991.1|) 1e-09

MSEVLVAVVRVKKRDGRAEFSPNGLRWTADASPEVPDGQCLPIVVP

>contig57437 Frame-2F

MLHFSTSSYFLIVLPFKIVLATNLADRI

>contig57648 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60999.1|) 3e-23

MVQFWPTVMFPSPPTDTLAAPEADVQRIVWAIAGVFVAASVVSSALLIRGHLNHFTQPIV

QS

>contig58861 Frame-1R

MWLCRFQRYHVRFPLASSRFFSSSSSKANGDAEFALGVKYLLGKVQGEI

>contig59219 Frame-1F

MSLFWNISQSSHVGDGIRMDSDRFDNYFFHWSAFGVYG

>contig00076 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60111.1|) 1e-61

MSLVKRVFTPFASSARGAVRRLASTGGIPDDLEHAVGRERQELEAAEIGVAQFNRDPLES

DETQGNSKDDPILVPSFNNVRTVGVSHNDASYVYWFNMEKGKVHYLPEIEKYFMLYNPEE

LAKLVQEVEAKQQ

>contig01295 Frame-0F

MYEETFPETKQNAKDASLRTEKQQQILDSCLDIKSKKWVAWTQPNCKRKRTETLIPEPAP

ATKDVAPSSIDCLLCRRTFSSLEILRKHEQFSKLHIANLSNKL

>contig08102 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65813.1|) 4e-62

MKDSPEESQGIITIEIPQHALQKLSKQLLNAVDIRNVRGISQFFGLGQEKPFNIPGRDVL

TSRCRKNALYFCANYAISAALVGVVTILLNPFFLFVLICLGGFWLYMSTATANDSPENPT

KIMGHTVTPDQRKVGMLG

>contig09088 Frame-1F

MWRQIKKDMVIYLRIPLGMRVPDSTIKVSGVDADKEHLLRLVKCYNKPKDCEVDFFTIN

>contig09404-0 Frame-0F0

MSFRGGRGGARGGRGGRGMGRGGGRGGGRGGFREVEGP

>contig09871 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64363.1|) 1e-180

MGKHDFLTPKAIGIRIKAKGLQKLRWFCQVCQKQCRDENGFKCHTTSESHQRQMLIVANN

PNKFMSGYSEMFESAFLENLRRRHGTKRMRATHVYNEYIADKLHIHMNATQWTTLGGFVQ

YLGRTGKCVVDETEKGWHIQYIDRDPKAIARQEELAKKKKAELDHEERNRLFIERQLKIA

TEKEVVETQFQPTKLQRGENGEKITLMLAGKKEIVKKDGMKAAVFKVAGPNGFEDTEKLA

HESGEVLLGKRHAVDVVMEEDERRRMGKRKQLQDESKRQRKENWITTGIVVKVTNKKVGN

GVYFKCKGVVKDVQDKFCATVELLDSGDVLRLDQDDLETVIPRPGSTVKIVNGLGRGYTA

ELLDVSIDDFCARIRIDSGSHRGEILDNVEYEDICRLAAAV

>contig10617 Frame-1F

MYRIMYSKPLQHKLWTRSNGRRPVAHSIRFSMNMKKERIFERFFVTGLDINEASQHQESL

NRTKFWKPHVLYDFPD

>contig10998 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61623.1|) 9e-43

MSDSRVALEYCGEFLSHIGALDEANAIAEILCKTGVELPESSSFRRRALLAAMRREVDAN

PMDSVFVFERLLYLDAVQPSRSSHALFDSPLFFHLLVERYAAAFHGLDAELFKLESDDLC

YTDEIYETCLLIRDTMNESGYGANLTQFLTAFELLFKQNEP

>contig12152 Frame-0R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY70256.1|) 6e-44

MLDQVHSIRTQELQYLKQTILWNVCGKVFLQAGPVLVSVGTFAAYSYIQTEPLTPDKAFT

AITLFSIFRLPLTLLPQVFSLLFQANVSIHRLESFLYRKSHVNVATLLSP

>contig12813 Frame-2F

MGCKSSQYLWFGTSTNRFLRPRFSRAGGFHKESCALRFMAFQQLLCSLTKKSCRIYQLTT

PSSVIRKTVATRHF

>contig13641 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66271.1|) 7e-37

MVGCTGRTNLLKRLGTSLSNYPEFFLGADGSIRPGNLVDYLKKHQHENGEVSITRLWNVI

LYGLQDIWPTSRTQIDGHNMGDVWEL

>contig16075 Frame-2R

MLLLTAVISLTFVVASANKPILDHSTLSSSPDANLDEHRLANSTSNTEERNWFMTLFKPW

KGLNENFGQIGKSLASDKSRTMLRDASTKFQKHKVFSPVVNVARDNPNFIVNVMQKGGDK

AIEKYVRQDPRKGEH

>contig16273 Frame-1F|Blast-1,3-beta-glucanosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62229.1|) 1e-179

MVFSSCVQRLCAAMAICTAIAISSTTAWVPPIITKGNKFFDSVTGVEFRLKGIAYYPRPN

DGEMAGVGNYDWAADEHEAVWKPHLEIMKDLGVNTIRLYSVDPSKPHDNFMCACSDAGIY

VLVGITAPCENCSVLDYKPPACYPEDLFTRAQMVYNAFAVYDNTLGFSVGNENNLQVEHG

AHGTTTAPCVKAFLRDTRSYAASCAGAVRPVPIGLDIADIPPREQWIAYYDCAAEEDENT

RAEWLGFNPYVECDPTTHLKYSQSTGLKKLMTEYASVGYARPIMFGEFGCNKGINTIDGY

ENQRSFLDAKWMNEEEEMTAEIVGGNVFEFTTEIANLA

>contig16884 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53438.1|) 7e-28

MKNKLVLIGPHWIGVVMTFGTILVATFMFLSQHMQTMAWYNTIITLGLCGSTLYYLFQTA

CTDPGIIQTSRYKDLSQTDFESGVMVMEAPIASDESMPPIEKALAQGLHAGRWYCDICRI

IDRDVTAFHCEDCGVCVAGYDHHCPWVGKCIGRDNMHAFQKFNASWVIYVCFVLFMAITS

INWGLAL

>contig17814 Frame-0F

MEQNTVKLMGKRCCHIGNNMCFQKGAVTYKDNNVLLPVYCAESITSPSY

>contig18103 Frame-2R|Blast-succinyl-CoA ligase beta-chain, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY56104.1|) 0.0

MLGRSLYHAKLLALPMRQCAQVRRLNLHEFQSLEIMKRFGVATPLGIPADTPAEAKAAFE

QIRGDREGVDVVIKAQALTGGRGLGTFQNGFKGGVHMCTRPEQAEEIANKMLNETLVTKQ

TGPKGIQVAKVFLMERVWMRREMYFSILMDRASQGPVMVASPAGGTSIEDVAAATPELIF

KEIIDISTGPTPTQVTRLAKALGGHGSVLLKLETQIQNLYKMFIGVDATLVEINPLAETR

EGAIFACDAKLNYDDNAAFRHAEIFSQRDTTQEDPREVEASAYDLNYIGLDGNIGCLVNG

AGLAMATMDIISLYGGSPANFLDVGGGASETQVKKAFELLDRDVQVKSILVNIFGGIMRC

DVIAAGIVAAAKDLGLQKPVIIRLQGTNVELARQIIADSGVKMIVADDLEDAAEKAVKIA

DIVAQAEQVQLGVAFQA

>contig18271 Frame-2F

MLQDPRKHIDVVLEIKSWWLAGLIKEGHYDNAASVLDQIGDLDELPVLGGSTSFVHIRLL

LLQALLSKCQGKIVNHEKQLFHLILRLQGARQQNNWQVFENVDKEIFARWLRIAQFALAN

HLVHQQKFRLALRVSSQIDAHY

>contig18345 Frame-0R

MYRVELDLSAFVGLLVVHRFKSLLDNSWLQRFFYTSWKLKTRFATLIIQLVLRRCSF

>contig18486 Frame-1F

MSTQSNVFSALRPERKKKTVEPPPSKMFASFVNKSSTSAWGDDSDDEMHAAVAPVADTAV

EDDDEEESESESEDDEDEHERETATAVAPKKVSTARTLSKKEKKELEMKEFEAALADLGV

RTETSRDEDAKAENKVVETQLTISGSVDKKKKKKKGKKPLKTDPESTVTEVMDIKAIVKA

KTKKKKATEPAAVRIAREEKAKAKAKGKKDKSGFNEFSI

>contig19610 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54400.1|) 0.0

MAGSCGEMAEILLLQLAEHGILWYLSLLVFQYQLNNDKSDNDLQRISIGAAKALNRILEA

NAREETIAVFVKRMQATIEQVFTRPLIDILRRSGPISMLDVLAAEVREPHVMWTKRMRKE

LMNLAHRAIDFHTKLDQNDVDLHKVFELPPKFIYAAQEKELCVAGIYVNFFNENPKNGIL

AQIAGTVNSYGNRAELFQSKPATKKQIQAAAAAAAILEKRSISGHVMHGLLAALSYDLSS

VRAQPQALDSVLFQRLLPIATAIRNLLQYTPDMDGQLVQADGLVTLLFVLDSETQPQGFS

FANSPLLLVRCMECVHILSFSGKCIEPLATSVPPFIRSAFQVVYKNLARTEASIEGQLAR

VTLQLLGNLCLIPACIDNLVKGMDPASLSNLLPHVWLGDSTEMQLLLCLHMIPLKRHTQA

ATEFAKAAVSSQLASALLNLLSTLVPKSKVGESTATKQYAARFLSVLSSNPGSGGAISSL

LIASRVWETHGDTTQATSEDLRRLLVPPHAPALLKGPHANPNKVG

>contig20193 Frame-1R

MLLLQGGLRPLTLTFKRFMPVQEALVLNDDNVKETDLDEEVVLDEGTLVDLEQLRVPVLP

LLPESTQNNEMNAADVLLSSLFSLFWNPPTTTTAVADTI

>contig20863 Frame-0F

MRAEDTAKADPDTSTMEKSWESEKGIRKMADLLRGRKGMPSRHAVELGKRVEYFRGDRLA

TFLLCSQRVKKYFPELITKEDAYSVGRELAQNSYIHRSERDAKNKKILQPTPKQDFSPDG

YYTWMYEGSRTFRNFLTALLIIGFLIITCFPIWPQWAKVALWYMSVTFLIFVAIFVVIRL

FIFFILWMIGYEYWLLPNIFDDNLSVADSFVPLYSLRSTDSSERIYRLVGLIAFLCFCVW

VKNQPTDFDEYMELTKQFTDDIYSGKLLSDMSQKDQDNIDGVKVPDLKDLLMDEDEDDED

QDVKFTKILDDDDIEDSNVPQATNDNGEPGDRD

>contig21525 Frame-0F|Blast-ribosomal protein L34 [Phytophthora infestans](gb|AAY43421.1|) 1e-55

MVKNVRITYRRRHSYATKSNVIKAVKTPGGKLVAHYRTKRAAGPKCGDCKQSLKGIKHLQ

SKEYKNVSKTQRTVSRAYGGSRCAHCVRQRIVRAFLIEEQKIVKKVLMEKLKKSKSA

>contig22678 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY58242.1|) 0.0

MKHIKSDANYLRNHLETPTSIRWTQFSPQKRLMSQLGALLLKRFKVTIRDKKLLFAQYIW

PLAFFAIIMAVLQHILDATGVTETITALKPSQKDTMVYIASPSFLTASVADLVAQFTVDT

HRIVVNTNITTATAMIEEIIADKATTFAAAFFVSHINYTANNALMAPVFTYDLYYNDTLK

HSLPVSLQWMSQAYCQARQMHENAMPYFPCTLIVKRGSLPLTKALGTAITTDGNQGWAVD

PDEAASVMRRIMVAFYLLMAMNSVTGSYVGPIVRERANGLKRMQYQHLTTSFVSSVYWLA

NFIFDFLLYLMAVMVLIGILLLFSGCLTVEIIVAWFVSLVLFGVAILPAEYLSSLVFASQ

SSAQSYMMYASIFQIMAASAVFALSMIPGVCVKVHLVSSIMQVLPLFALSLVTLNAATPS

WGPMRYQCLTLGSDVEKIDAMALLKGFLDFHPFPCGVGTSRDARGHFFLVRVLSIRVCF

>contig22696 Frame-0R

MGSETSNVDKCEIVTVVMTKSETVADPVGCTTTLPRKAKKSKEKAKAIVATQELSEADRL

GSISVDHPYLSVLYKRIRSHRKKLEKIKSLEQAQLQEGKVLNAQQLDLMSNKATLEKLVA

ELEMLREQFIGVFSEELDLKKQLETKDAIVADVTQSEEDQHVIEKINVAAESEKETQELQ

EEVASAVKETDYTDVYELLKTLHVVNLHQVLNKEVPMVLDFFSKVLLGKTRPPAELSYDE

NLMESLEEAKKYLMKSDKTFACDTTYCELKAFVDKFASMSSSEKKTEEGNDIGEERMVTC

NTVEIKKEKPGVEEVVAVPEVPAEINMMPQISFFTESQLEIERGGEPIRVSASQLEEAVE

LQIEPVKIDQSNNLVISEIGEEDNSALLTAEVASASQLSFAAVAAGEAGDCATSVSALSG

AEKYESGKSALKNGRRRAQNRWREKGSSSSG

>contig23211 Frame-0F|Blast-apolipoprotein A-I binding protein, putative [Toxoplasma gondii GT1](gb|EEE23211.1|) 8e-09

MSATHGFSIDQVMELAGLSVAAAVGKEFHRLIKQNGAINENRRLLVVAGPGNN

>contig23769 Frame-2F|Blast-DNA ligase, putative [Phytophthora infestans T30-4](gb|EEY65982.1|) 0.0

MPLSWSQSSMAKGSRVMSVKEVQFISRNGINYTDKYGPSITPHVLSQLEQGVDCILDGEM

MVWDNTEYRLREFGLLKNTANAVRKGERTNRWLCYVVWDIVYLGGSPKANQLIHEVFQGP

GEISAVMGLPLHARRKLLLRILKPLDHRIVIVEQKLVNDASAKVRHDKVMAEVDLQLSNG

GEGVIMKDLNAHYMCGESSRKTKKWLKLKPDYAGMTTDLDTIIVGGFYGTGRRRSGNVSV

FLLGVLAHSLDEMGAAEAMKPGAACPIVYTFAKVGTGYNLEELEQMRQELAPHWQPWDDT

NIAPHLSGWKPPKSDLRPDVWIDPRHSKILEVYGFELSFTTQYQTGLTIRFPRCKAIRND

KEWYQCISLQDLNAARGSQSTKRASEVVLGQKGALKRPTKRQTVSNLRATGVLQEYSRAD

LEGIAQERNVFEGLEFCVLPGKYQMPSSDTMSFIPASVIEKNAMHLSKQAVEKMLYSFGG

TIVQNPIAGSTHYVVAAADDGLKVA

>contig23992 Frame-0R

MEALYLRQSRPDMAFMSDQGRMPIKVPKLQQTRTVKNFPTIKKTSIRLQQSSSHPHQYSL

EFKFDAVKPCQVSVYMVALERTYAVTDSSSLALMSSYKRILLTKQLSAGSGQQFGLKKIE

NSSTTTTRIKKKHENILPQLEFSHCKLDKLMNKPNTAQFPLKIVLETLSDKCSQSQTTFC

TFVKGCNEAWNVKVLKQNVL

>contig24005 Frame-1R

MILWMLPCAIIMSSIYYASIANVFASIWHGKLAVKRSIKCEHVKRNCIVYTAVAFPDVII

SFTDLKLLILSLKKYYG

>contig24214 Frame-0F|Blast-pre-mRNA-processing factor, putative [Phytophthora infestans T30-4](gb|EEY56427.1|) 1e-137

MKSVVLEREYAENRKDEEDLVLEGIKMYPDFPKLYMMAGQFYEALNSPDYDKAKKMYRQG

IQNCPKSIPLWTLSSRLEETVNGVTKARSVLEMARLKNQKNEILWLEAARLEARWNNPKG

QEMLMAKALQECPESGILLAESIDIAPRAQQKRASFTALKKKNNDPSVCLSVAKLFWQER

KYSKARKWLERTIQLDSDFGDAWAYYYLFELKHGTKDATEKILKRAVSKDPHHGEKWTRV

SKQTQNRRKKTEELVKLVSLTLPFAEQP

>contig24544 Frame-1F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY65513.1|) 0.0

MTMSCQCAPQHFGTHCRSCPICAPHGHCNSGVDGDGRCICDIGWSDSNNCVGCMSGYFGE

TCVACRNCGEGRCDDGLRGSGKCNCHRGWDFRTDCYDCEEGFYGESCNPCPLDCGHGTCS

SGLNGTGECTCHEGWKLEGKHMCNSCADGYIGATCQLCPGFLESEVACNGHGQCIMLGTQ

AVCECDARYGGDGCESYDFPFAMVAILGTIALSTLGFCMCTMRRLARQPHALQGPFLNRQ

HSFSQSEYVEISNMADLEYFVSNDSRDWLIPFDSLSLQHEVGNGTSGQVFRSLLHSGGGS

SVVAVKRLYSPVTGQEYFQSFFRREVSILSRLHHPYVVRFYGVSYYNRVLYIVTDFCPNS

LSGLIENPAMKGPLQEAVFMKVISQIVSGMGFLHSRNVVHRDLKPANVLISETEDVNICD

FGLSRLIEPDATTMTAEVGTPSYMAPEMATMGGIQCSTKGDVYSFGILLYSTWSRSKPYG

DQGMNPFQLMTAVVNGLRPVIPISCPPALSHLMRSCWHENPDRRPSFPEISQILKDQWLL

SMYAEEGVYKCSETSKNLPPKFASTTGSTNSVGIDRPARGSKDDATAVSLFASPQPDGDG

GCDTYEIAEKKVEGNSPRENDCLLGEDENRPR

>contig24698-0 Frame-0F0

MMIACSLYPSSSPLNGHNVDSLAVFAFFRIQSGYLVAKKLRCIHPIKLKKNIILHQTYLS

SGQLLLDHCHQ

>contig25020 Frame-2R|Blast-nuclease, putative [Phytophthora infestans T30-4](gb|EEY58702.1|) 0.0

MASGTATVKAVLSGDTLVLMGSGANGPPQELVLTLSSLQAPRLARSPEQSNEPYAWASRE

HLRKLCVGKVVHFKVEYRVPSINRDFGSVWLPPNARGIKENLCVIQARTGFARVKTLEQS

RDGVCVDHEKMLQQEQVAMNEKKGMYADANSESNATVQWQGADTAALLEEHKGKLVPAIV

EAVRDGASLRVILKPTLQLINFGLSGVQCPRLNPPLNTADAQEKTSTPSGPAPYAQEAKH

FTEVRLLHRDVELKFEGVDKFGNLFGSVVHPSGRNISVELLQNGLGRMADWSSAFTSASV

RATMRNAEKEAKQQKLRVWREYEAPVLQSPKHVKGVVVEVISGDCLVVYVPDTALLAAQE

KRIYLSSLRAPRLGNARRNEPNAPYANEAKEYLRHRAIAKTVHIEVEYEKPSPAGQGDVM

TFGSVFLEPTANAVKKNPEAKGVNLAMDIVAAGLAEVVRHRPEEEKSEYYDDLVTAETKA

QTQKKNLHSNKEPPATERRVTDLCFDATKAKQFLPFLKREQSIRAVVEHVYSATRVKLYV

SKENCLINFVVAGIKCPQPARHGAQGVILQPAEPLGEEAKLFTKRNVMQREVMVEIEDMD

RGGNAFGPLFVVPSSGGKPVRDDQHNYGVRLLDEGLAWVDSFSVERTALGNVLQRAEERA

KSQKKKYWATYEAQAKAQAAQAIKVKTKDEIIPRVKLSEIVNGTHFYFQNVGDRNCAAVE

EKMKIFTRTHGLSGKTFEVRRNAVCAALFDDGNGSTWNRAKVEHVASDGSARVRFLDYGN

QATVTANCLRPLDADALQYPPQAKEAVFAWIKPLAATEEFGSDAAIRLGEVAWGKILSCR

IHGNDDHGRMQVSLYLPDGKSVAGNLVEAGLLRTDRKALRSVLSFQKPLVEGILTAQEVA

KKQRRCLWQYGDIESDDEQDL

>contig25378 Frame-1F|Blast-integrator complex subunit, putative [Phytophthora infestans T30-4](gb|EEY64022.1|) 0.0

MLLDTGIKLQSLQRSVKQNGGYLYRIQLPALTSVDVKALDVVLLSNHQTLLALPLLTETL

GFQGQIYATQLTIDFGRIFLNELATLNQGKNSTFFTFENVTDNQELPMFSFEEIENCCRK

IHCVEYNEVIKLEYGVEITALSSGFTLGSSLWLIEGPNDKLAYVAAASGDYNRHPKELDL

LPLVNCETLLVTDLKPDRDPHSTTERMVERVLSSVTNVLERGGICVVPTSPCGVLFDLIE

AVYTASVLKNQHVPMYLISDFATQILELTQLGAEWLCEKKVDKLYAGEHAFVHESLLKNK

VFHPVADLSAITATTFQNGSLVFVGHPSLQFGHGVEIIQMLGNDSRNAILLIDPSVNSAE

ALGNFQELSIEKIVCPIDPRLSCGDANQLIARCCPHHLILPYEFTIAPLETTAVDDVKRS

SHFSRVLPLHELSASSPKTELLTFPLKPLQPIVVEKPAKYLDGKLDPKVMRRR

>contig25499 Frame-2F

MAAKVVLEMQQARQAAEEAEAVKQEQLAVEQAVVSETERARDISSSQDQKENIGLILDND

NDANQNAQDDAIALRNGGATNMEVDNSDSEESPDITLSAIANMVNEDNDVIAATGAIVAA

SGDRMNTKGSGRRAKLPIPELLQENTFELRLPEKDLIFDTSMLNQEEIVFLEAAKRGIIG

EGHRGWKHGNNVGVLADSHSQLWSGLLTQNRLRQKQEVTNEIELKVGCKVIRGPNWKWRD

QDGGDGSVGVVEGVSPWSGVDGEGMSVRWPNDSLYTYRWGADGNFDLIHVEVDDDGNITH

QYATPKAKQEDEESFGFELHLGVLLYLFEEDATIGENAKVVKLAGLMEWPDYGAAVRIVG

MRYIDGSICIQELQLVRGDPDMGWMLRFGTEKWQPGTKYLLRPIKLSDSEKGSSACDASN

VDTLRGEYTHPGLKGGETVEIRGELQVSTKYLFTMDHYNHFSTLEISSDGLSVTCHNGES

RNLALGTVGFTTGVHYWEVHVEQAEFGSVFIGVCEKAGPPGSQAALSSRLNRWHGWGFVN

FRATYHNSTERIYGDHFNASDTIGVRLDMEQGKLSFFMDGIKFGEHVVSDLGIAFENIKG

ERNSRTLYPCIGMRKGGDRVTLNQKWTSMPGIAPSQILLDAVDVSRSLHSWYVSIQQEQA

ASSAGASASAKIGAKNLLTSPPEDARVVLPATLLRESWSEWKRWSDNHWQRCHVRPRGIS

VDFDTSPAACIRVSNAAGLVAPFLTGDRVRMCSKCGQELNQPEEAVILGVYRGFIWYRTE

TQGNEGADEGRSWAWYWLLTELPGLLLIRRGDKDMTLIENTATVILDCESAPEHSPFKPQ

SDLENRARTDFDAFVELATRAHSTSSDMQLVDRLNAYCATIGVDVTNLKITDVMTTDENE

GNASSTIVSHGRSRARSLIPDNYFASPGLKNITGPELRARAAVLRVLNNKILRVLPIIAI

QPDDGSCAQPIEVAESANKTSAEFLSTSLKLRLLRRLLFTSTKRTFWDDVLRATTTNTPL

PSDEYEDPREIRVIRINRIQAQASKLSLLTQPGDRLRRSVFGQLYREMRAWNDSFFRRAY

CGKGHGGQRRAFKVKFLGEGVNDYGGPYRAVFEQIVDELQMDNLELAKGEQGLLPLLIPC

PNRRSATGINQDKFLLNPSCGTALPANGPVALDLHRFLGKLIGTAVRHGLQMGLDLSALV

WRPLSGLKVSRAHLESIDVAAANNLTRVEELSKNTATTAQEAAVVFGYLTLSTTLSDGVE

ILLVPHGEKMAVTLANSDLYVQLVEKTRLTESSQQLAALKDGLAAVLPMELTPLFTPKEL

EVLICGRREVDVDLLHQCTEYSEGADESMPHVQHFWEVLREMTSEERTSFLRFVWARSRM

PNSAKDFPMNFKLQTAQDPGASSQPDLYLPHAQTCFFALRLPVYTSKEVLRTKLLYAIQN

SPNMDADVRLHNAEGWADA

>contig25572 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66328.1|) 6e-30

MFLRGFCTRESCKYRHVKVSVTADLCEAFTNGFCQQGSACPLRHELSCKPPSTVAIRHNT

SSDAIPISCALSTSIASSEPGTASGSSRSGGPEVLSIRPNIRFASKHSTRFPAFFGQPNV

LS

>contig25828 Frame-1F

MEPTYHVSDNNLPAFRLIFSSPNVVASVARRPEQTNCRRHAVNLILNLPLGNQATYD

>contig25961 Frame-1F

MDRNLVFMVAMTAITQSMRYCSKSRTNCFKWGPQAEKLHVLIYWMMSYESISGENRPSTC

DYVRQLLLEWIQPTATKQNQLSACLTLFEMLRRHRSMLQSQSSRNEYWCVFGDRFSAYKD

ALRGIVEQGTTYTESHKLKLSKLALIALESIGFLCGEVALQHFNCFEAKRTKCFAKGEVM

YKAVGCMGFFLLTLQKWHQYSIHRQFLHCAVKHLQSYVEICDIVLANGAGEDCGDGSIQG

ALNVLYWHWDLAVSLFCTRADSFCRGQKHQPYNVLSRILKKWTFDTFIVEKTDSQQNPEF

VYAQMRYVCMLFDVIGGTGCTKAFQMISDEMKLQILYFYVRGLAIAVTNTNTATVRLCVH

VLRAVLLPSEVLNRAISRDDEQGLLSQLLSIMSDSPTACGGLNIGLEFLTDLGVFIADFI

ISRGLFLSNLLRRLNDTHSSNV

>contig26083 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63644.1|) 1e-29

MKRDDPVTYAGWVFKEGSLVRSWKKRFLVCKRAELAYYKNTDEENRAQLLGALTAAHIER

LPEITNGLRIHGTEGRQLKIFTESKPECDRCYEAIFKYCRMQNVTDGAQQQRVGWLEKEG

QHFRTWKRRYFVLSGTQLTYSATMGTERLGGGTIIEVKRDPSRPFTLVVTFGGGREMRIG

GKSEGDIDSWHKALRRGLSSAQDLQTNKLKRASMDSDPSNSRDREFAKRQASARAVSVTS

YEGIDKKSGLAPKENLDSKDGEKRLSLPELYAANSFRRHIVVETMPDNTASFVEVAEERG

RDENFEKPFSPTAPGTSTIRRMRLAEKLLQEELEEERREAMMKEKKTVLMRTPSKSEEQV

PRHACCCVMM

>contig27013 Frame-2F

MSGRWGWKGMFVVFLTLQVTNAALTVTRTPVENSSTEPESLAALKAQRQECLKSPPQQVT

LMQSRSLPDAAYVIYKDCAILTIRATTLSDGSVSMDASRQKIEVVRSFPNVDLLNLSGNW

IQMIQKVDKASVMTLDLSDNGINALGNISLPRSVRVLNLDSNQLTGIFKDNVPDTVTSIS

IRNNSLKSLQSFQLSDETQFIDISGNAIVKLSSWKMPPRLQSFRCQNCGIKLIGGVVFPT

TKSLSVFDLSGSNVELFEITHSSLAVLNEVQDLVVTTVGVSCKDRYATWKIARSMNLCVL

PDTYFGIKYLINGTDVSKRADPFVSKSDTHSTRLSNWMMLAVTCLGAMFVCILGGVVFFI

FRRRQLDRDVELEEAETLAYNPESLSAFKVPQYLPRHVSGTSQTGQTDSIPEAGLSPSRA

SYVLHDIRMNDDILQCRLLQKEVVRGDLLAKGGYGAVYLATFQNDLVVVKQLLPERARNK

RCLGNFLDEIRLCSTLDHPKIVHFIGVTWSSLLDICMVLEYVPHGDLSTMLQQQLDREEE

NDVAREKYGWFHSNEQGIRCKSLLALDIAEALVYLHSFESPIIHRDLKSKNVLLNDVWEA

KLTDFGISRELTEDETMTAEVGTVSWIAPEVLRGEHYSEKADVYSLGVILTELDTCRRPY

ALGIVGESNRSGKIQTSNTRIAVLVSAGALRPNVHGDCPRSVRKLVDKCLAFHPEDRPSA

LQIHFELRNLELQREERCTSARRMSSI

>contig27202 Frame-0R|Blast-40S ribosomal protein S15 [Phytophthora infestans T30-4](gb|EEY53513.1|) 3e-14

MIGHYLGEFAISYKPVTHGRPGIGATNSSRFIPLK

>contig27318 Frame-2R

MNIYPQETNFIALGDFGTGDENQRKVALALEKFLATMHPPPAFVLSTGDQIYDHG

>contig28016 Frame-0F|Blast-polycomb protein, putative [Phytophthora infestans T30-4](gb|EEY69291.1|) 1e-111

MVDVGVSKRKRDGSYERKVPINKDCRTRIRQEQMEQEFAETYHGLTALYKLLEIKHLQSP

LFLPRTLSYRLKTVGHKKDLKNNSNSKVVKHALAGAIFKDLKIGMKPETMEVFKGQKHRF

GILLSLYKANGRAFLENNYTLLTSCLTSVPCYKDLMLPKEFVLLDAEIYVLVFQVVDISD

IGDAIASQSPIRFVAPQKALTVSGKNLLSTCFNERKPLFGNIMRISVSRRRVGFVTIEMP

AIASSMHGGVRCEFYVSWDPLPKTRKMKRLASICDAKLNFDGKRKHIDENFALALPKRNV

ASADHKPCAGMVSFSLPFHAA

>contig28351 Frame-1F

MAAYRAVAGTTSSLALTIKSADQSLESMIRADVSVNHIDIPPLPSEDATEVGSEHVKKGK

GVGKRLTDRERVEILELLEKSGGSLSNAEIGRRYGITRAAVQKLKQKGPEVRARYRYGSE

ATRDGRKRGGHILSVPFEREIFEWVRGLKARKVPVPPSLIKEKAKLLVPKYGLGSFQASN

GWYYNFCKR

>contig28908 Frame-1F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 1e-126 NOT\_ORF

MQYTNKDVLGKDLVAEFILNEYKVPVRSVLEKAFEGIETANFEFPLITKAGRRVEILLNA

TPRYNERGEVMGMVGIGQDITERIAQEQEYSRLIDTANAPIFGVDINGRVNIWNRKAADI

MQYSNEDVLGKDLVAEFISKEYKVPVRSVLEKAFEGVDTANFEFPLITKAGRRVEILLNA

TPRYNEHGEVKGMVGIGQDITERIAQEQEYSRLIDTANAPIFGV

>contig29374 Frame-2R

MNFKQRELGSAPLQPVCMSLAWLPLSTFSLVLEYAVCGFTRDLGPERRSLHGRSLKDVAL

VSKRWYHAVDELVALIRRDTMQLTFKYGSRTEVMAIRRKVQLRGRLVRDLRIRMGRSDGA

RFVTGVWWWMEDRELPWNVILSLTPGLKRLDLRFMPLDSRHLIDLLEVAAKCCLQVEFLI

LPKKQNFGVTDNCKAIARLMEALKYAMARWYLKGKCGGLKQLTVPTREKTDTFRNSTKFI

EGVIEFCPNVWYLDGYKDTIDELNDVACDEKWMISLETWENFNKSCTHLREFNWILVPFT

DPFFQMFGKYVKPNLKILSLTPNMSWGWDNYLSQDELTNHATTIPDHELPANDVVALFNG

CPALIELKIRISMEKDEDVLLYAEVFGDKFWETVVSCCPLLQNLCFDDCSTYNEIQPVKT

IRSFTDRGLLALAGHLRLTTIKLPAVCCSGDGLFEFLQHLFRMKDFGGGTRTLVLSLAGP

TDYNNLPPHPFYVEIVRLLKCLAQTSEEQMGITTCCFKASLIIHNPQGSLVDQRWSYSYV

HNELKPILKKICETQLSLDLHIVLCRDDESTFRRIDNLELNWCLGSQQGDVFIEDEFAGS

AGSNYYSSDVEDDYNDD

>contig29727 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65357.1|) 7e-83

MELSRAESALRTLKNRPKVSQASIDTAFSIKTLLFPSKSLNESPTQPPLVLSSDVDETRR

EMLETDLLTLLAYGKERWEPVAVFFVVVRDLLSRYLDVADLDTSPDLNLSVPLPPLYVST

IAPLSDKFVKQTVKDAVHAYLEYYEPRVRMAVAKLLGVLAHSDLLWVTQEFTPQIVDSIV

SNLSRSPDFEETGFDELDDNISTNGMSTPPPSPESTP

>contig29752 Frame-2F|Blast-protein phosphatase 1E, putative [Phytophthora infestans T30-4](gb|EEY59029.1|) 1e-103

MDLSDPEIQQRAERVVKWVTIYRVNGELAVSRAIGDLDYKGKALSKYEYWAYPEGHDRVF

HGDLVISVPECQEIEITPEFDFLILACDGLWDTIKSKEAVKYVADRLNEGYSAKQASQSL

ANLAIRSGSSDNVSVVIVLLNTEQMSIFLER

>contig29943 Frame-2R|Blast-ATP-binding Cassette (ABC) superfamily [Phytophthora infestans T30-4](gb|EEY54021.1|) 1e-48

MIFFLFAGFNPPGSSIPSGYKWLYHITPHNYALALAAALVFGDCPSDGDGLDIGCQIVSG

TPPQLAVNLMVKDYISDNFWMNHNEIYKNFGIMCFFIVGFRILALLSLRFVNHQKK

>contig30163 Frame-0F

MRIVAVLLANGYIWATSVAQPTPTWLTDEKTVATPVSCVFRYVLPTGTNLPSAVIDQFPP

ALPITSEHETDTSRSTTDGSDDSLEPASTESDTMNLPTDANVPKVTIRNTSMATLNTTVL

VPSTSAPHAPTSLLNASTPATSNTTTPKSASKPPVLATNATKVLDVFNTTTTPQKSLNTT

SLEKDRRLQVTNVLPFTPENDSDASNDSSRDKPTTMDTIKASNATTPALIPTVTNSSSRN

ALSPSLIKSFVPINSSTESSSNGYIKDLESTATLATFQCDATFYNAWSRMGLQCGNVDLD

VASAISASVCSIYSGTSTSTV

>contig30989 Frame-0R

MWRPVAKQMPVLTYAHLRSLQTVALSSFQDCVTPHLSTSRSRLTIASIASLQIRALSSKA

NKDYALNLAKVLASEAILEEYKQLYRNPNAKHTTVIKIGGDVIIHELETLIESLRFMKDT

GLFPILVHGAGPQMNAELSKQGVEPQYVGGNRVTDQKTLTIAQNIFIDTNATLVEALNKA

GVPAKGITSGVVQAHFKNKEVYGFVGEVNKIDGGPVQAVIDAGEIPVLSCMGKSVDGQTL

NINADVAARQLALKLQPLKTIFVNAKGGWIEDDGTKLKIINMAKDYERMAARDYTGRQGT

LLKLNEINTLLQGLPSTSSVVLTSAAELMREIISKKSAGTTCIKGEKPATRDAKPSGKAS

AVRCGPNGKYRVGLLGARGYVGRELIRVIGSHSKLELVCASSRALKGRNILKVVSAPPLN

PHTSLPAKKVEDVMLQINTELQFCELGLEDIATSPFADSVDVWVLALPNGHCEDYAKALD

ALPRKDKIIIDLSADQRFNAEWTYGLPEAPDRRTRLQGAKHIANPGCYATGAQIGLMPLL

GGKPEVSSKLIDESIPPHIFGVSGYSGAGTNPSMANNPNFLEDNIMAYKSVKHIHEIEIS

HQLNTMVRFMPHVAPYFQGIHLTLSAQLANNGLITSASQAEELYREFYANEALVKIQSNV

PLVKDNSYHPHVAVGGFQLDPDTGRLVVITTIDNLLKGAATQAIQNINVALGIDEFAGIE

VE

>contig32352 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64448.1|) 6e-39

MALDSDGERIFYYLVHSVELQECPPLDARHQIRRVQVSVAYISRQLNQNTVELFG

>contig33434 Frame-1F|Blast-eukaryotic translation initiation factor 3, putative [Phytophthora infestans T30-4](gb|EEY58778.1|) 1e-125

MSPVEQLQQRTWLLHWSLFVFAWHEEGRDAIVDFMLQSRSVEAIQSNAPWLLRYLCAGVI

LHKRRRNLIKDLLRVLRVDDKGYNDPIVDFVECLFVNFDFDSAQEKLRECEILLASDFFL

YEKNSTDFMEAARLAIFEMYCRVHCTINMKTLSSKLAMHEDGEAEKWIVNMIRNARLDAK

IDSQEGRIVMGMPHNSVHRLVIDKTRDLAARTCSLVAQFERMGKRKCFQ

>contig34039 Frame-1R

MTIKDHHSSIGSKTARLCIIFIKIKIYHNARLGRAQNNYCSLPSFEHLTTELLSCSMSAF

FHHSRDSLAT

>contig34167 Frame-0F

MPSDRDLAISVADVFSISLFVHSKTPGGNSYLMTYCSFHRIVIGVGGLEDISCCTSGFTF

SYGNPAKYPIFYNKYRKF

>contig34268 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53845.1|) 4e-37

MLRLPQIQFALYNLSNSLNSEVTVETNSFLENLKAMSQGEMEHLCNLYVDAFAPCLTSQL

LPSLATLRATTANGCCNAWESESVSNYGYTLTGQYAQMAQLLGDTLCAVQTPA

>contig34286 Frame-2F|Blast-exportin-4, putative [Phytophthora infestans T30-4](gb|EEY53544.1|) 5e-91

MELCAVEVLTEQDEDKDVEDNAASSTQEQYDLAAALARLNPYASASLLVSLLQSLITEIQ

QELANLQGRDEMTITLSQLFEKLYFIILFSGLFLADDFKGERPGIPSRIGVHLRSIASAE

ESSVVNLIVLILNHVLEFETLRLAHNPTSICVSPFVSEGLIETITRLCATYLAPDI

>contig34321 Frame-2R

MKNKASKKKVKEDGRKRKESRYFVTDLATKCFHCGEIGHTASVCSNDKLQRPCHYCALRG

HQAWECPNLPCTKCLQLGHQEKDCNNRAMIVIPCSICGCPGHSVAKCDNVGNPAEVTCMV

CTEKGHLHCVPMPPPADRSVYCPHCARNHTLDECRRYREPVATDFATRTASGRTVQTCFV

CNAPGHIAAECPMRSNGYDRRGGTCYRCGKQGHFAADCSESANNGNNYGRRVAGHKRGRD

VEEEYVDFNGYDYDDDENYDSYDRSSKGSRKHRNRGSSSFSTNHISKKGYARLNEALPTR

PYRGSDSRGNRKRHNLSH

>contig35410 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY61430.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55084.1|) 5e-71

MASPKKLPTPSNDDGVPLLDAEQEPWGRGSAAIMEDRTPEILFHEDAIGDTDSNNDDDDG

ASRDGATALDNDASVIMYQSMGKVGSKQKWGFEHLAIDLQMLSVGIDMANNTIVKVEGYY

RPEEQKAAKVTQMFVLLLNECIVKVHLFRVRREIHAIQFVTNLRTSERFGVIKHGELCKV

VEAPKGKYITSFFGDMTTDEDEMNLCVRFAEWTIEAEAFEEEVDV

>contig35627 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60181.1|) 2e-43

MFVRAFSTGRRVLCSLQKLKNLQGKGIKFPLQPIEEVNRYCANANAKSRRHLDRLATGFV

FYHETMQQPRAFVNRCPHALLELDFDDSDFFCEGFIHCKAHAAFFDPDTGICLQGPVSTR

KEL

>contig35652 Frame-1F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY60678.1|) 6e-82

MVTLETFRAFLMIYVSATRTQVFYDVIGCLLGFSDGIITIFSLIPATEIAENGSEGATQG

MLLSFRSTIAVAMRTLSSDWMADVAPVTLDDGTDHLLSLLLIAYSVHALALFSVLLLPRQ

KLDAQQLRVYGGYSKIACIAIWIIFFVFFAYAMFINLKAVVDMTERVLVR

>contig36428 Frame-0F

MGAEEYMNFLAIEPGRVSEHQELGVGMTYILKQSISVSSL

>contig36679 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58946.1|) 3e-12

MHHVSVSLENVIAEKSEIEATIEGQCSTEFAIQVRLSDEKKAV

>contig36899 Frame-2R

MKTSESSNSANVLSHKTTALESRLGGNGLNASAGKSLHNGTPSVDTEDLHRVHYPTGSGR

ALSLRADPMNSTYFPTDASILTLGATTVASSNFTSSSSSFGDLQSCWRANEEEKERYYAE

CRALRHELGRAVAAQRIQKRLAEKYTQQLQNVVDKFQVQIQEFVSSSRSDDVVKLRQQLV

EAHQALAKQ

>contig37298 Frame-0F

MFRVVCVPVLSSCYRFPSKFCRVDNPPSLSAGLYINVSRLLKRDPIIAATRSQSAFPLLY

VDTPAF

>contig37382 Frame-1F

MDAAGGLLTRLAPNGLDAPMLILAAVLILALSGIIAAVSHSCQNVLKDTTHSSRKLTRKL

SNIGLTTLVTEVPTNLSIPITVITVYGNLTKADLVERLRSRLQHDSFFLRWRSVVRGDYV

KGVFKFVEVPEYDIEQNVVEHTITEGETIMSYIESALVNVPLHFNKPLWEMHVICDPGNA

GITSVGWKVHHCLGDGASLAMAMEKLSDQSKASNAMLEKRTGAKPNQKTFKAKKSLAQIV

RDILIFFYVCLWSTYVITYHTIALFARHEPATAFKRPGGRLKRLSYSMVYSVETTKAVGK

LFQSTVNDVMLTIVAGAMRKTLLAVGESVAPSLKVRCAIPVDMRTSTEVIRHTSNRFSSL

LIDLPIGIENPVQRLHHVTASMNEAKSSLEKYFVYWSNHLISMLPAPLMRIIVHFVTSRM

SVATTNVRSSAVAMSLCKKQVSGFYGFVPPPPYVNLGVAILSMGDELGLNALVDPCVGVD

AKQFLDFAKEEFEALREAVAAIEAKPVVDKSIKQGWCRQL

>contig38134 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65801.1|) 3e-69

MTLTVLGKPALQFAASIYDEELALLIWSGLVQFHATYQDFDLTRQVLDNSADSNGYSALH

YAVEAQMKCFLLDICSDLKEYNLAPVVIRVVTQDVTLPINTAQSIGKNIASGGCTLLHLA

ARNNELDIAKMLIDVPMLMNPKTLHDWDDNSPARVAAIHGHDDLATFFE

>contig39201 Frame-2F

MVSLTMESETMPITMPLCNIGDIFNLPSSMELLRDEDFEKAMMLLDCPDFQKEDITNSDQ

YMVGLADTFNSQATKSTFNRNEQQSATGEFNLPYGAHSCLSPDLKIQISDRRPVICDQHI

KRECDVSGYSPVMESFLREHWDDIVGTGSRPVWPLKASSSCSSPLVILTASESEKPLFPN

CFTPPSGDYSMKKRILEASLFLPPTTLPSACRTPLFFTAKSHTSTIKSKSTRRAKQCVSD

GCTRRAQSNDRCKTHGGGARCQMEGCDKSSQGGGLCRAHGGGKKCRVSGCSKGTQRLGLC

YLHGGIRRCIMEGCKKKDRGSGYCISHGGGRRCETQNCNRSVRKRNHCQMHQTLDEDIIV

>contig39537 Frame-2R

MTNGNELQIAAGWNRILLEDSVSDAYAKLLMVAKRCYKGLYPKALYNIWPTLQKRKTDLG

AIVQAFVYHSVAKRDLFLCTDGIFRPLSNSYQLDFSCINIQVSSFAQLHFPALDIPAIIL

QDCARFLPSHLNAVTPKLMRHFLRSFSRSDILLSVCLPLLEYCLSDLPFPLPSETDLIWA

EFHGLPLLPLEDGSIGVLQANQRRMSYIIGSYDQIELLG

>contig39542 Frame-0R

MSSLSLHQLEKQMERVTDAFQKPQAHPLKLDAWTSKTEREKDIHNRYIEKHGSDIWSTVW

NGIWAGSVENEQDEDGEIIMTV

>contig39753 Frame-0F

MSDKLSPLVPPPSISAFSQSSSCRPKRQSFSRFFSRSSYSKRRSRAVVPADSITHPHLEI

NTHKRRNDRAMIKICDATVHVRALHRIRRILGEFMRQLSVEVFFVMIVLLYGVFVTVQLT

LADGMLSSYMLAIDATDLIVGSILLLEIFLNVFAYGL

>contig39825 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56863.1|) 9e-48

MGVHVKRDFLPRIQRLQHRATHSPRGLAKRSKFRRQSSPVATDLPKDVRQLKQKILQNHP

AKLTRFSLSHMRHMTVPPVTIPDTLDDSHALRTVVSGKSVPLTMRMWNNCKRRIKHLDMI

DEYVTYR

>contig39951 Frame-1R|Blast-glyceraldehyde-3-phosphate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY66508.1|) 1e-118

MVITETGAAAAVAKCLPTLEGKLTANAIRVPTPNVSLAILNLTLDPVKAIGITKDSINSL

MSKVSVDSPLQNQIDFVNSAEVASTDFIGSRAAGTVDGKATIVDGNKVILYIWYDNEFGY

SCQVIRVVQRLMGINHTRFPTKDQVAAIDRSLALTWSH

>contig40274 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65829.1|) 1e-172

MTRSIPKPNPILDTLLLSLLVCELGIIMYTFAKDKQMLYILIAMIVVVALAVRLTKTSFA

IGGRWFSRTFLQHLNDPLKKTVALKKWCDQSWQLVIHVSMTIFELYVLRDEKWWQDQTTL

WNQGTDTGVFPTQKFSTKLLYITQMAIWIYTAFSCKFLEEIRKDYLVMMTHHVVTIALVT

WSYAIGFLPVGVIVLLLHDMTDVPLDMLKMSNYLKMEGVPGLFTTEILFVTTIALWFYYR

IYQYPMKLLYTTIWDSREATMPIADAHDFTQLFPHPGPQSWLLFNMLLTTLYCLHIYWGI

LLVRILIGVVTKGTHDSAKEEYEGTSSDSDNDGKDD

>contig40627 Frame-1F

MANVGGGRVLVGEDSEEDDDDEEEMNFHLDGFGLQSSSVAPRFALQADGPHSAAVGGKVD

ERSNEEEKAVLLKEEVEKEIKEHGEEQKDEEQTKNTIGQSPESKLTSTKVAGLNDSNNLW

QIDQSINGIEIMSNAFVKTVQPSLDATIYRIADLKESQQQLLEMLIEQNNGLRSKRQLED

AAVVLQKLPLYIKKVQKIKAAMQEISVSSEKMKRRVEGLRIDAQSYAIKKENERDKQSQW

NKLYAAKNTGASSR

>contig40843 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61280.1|) 8e-11

MASVSLILCICSFVNLKPQDMISSQVAMSFFFSISALVSTTIGRVRPSMSMPASAQAAEP

AS

>contig41167-0 Frame-1F0

MPFRGIVASATTLVDDRVRLARTRRELHFLFEHICTIDTTNTRVRQFPPICYLAWISIRI

RFSVDLS

>contig41167-1 Frame-2R1

MLEKEVKFSTRSSQTNSVVDKRCCTCDNSTKRHIRRFSRCFRRSITPPIIASKVAFPAIL

KFNLSLLQNQLFVESP

>contig41286 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59513.1|) 5e-24

MTLKIVNTVEDSINMTTCQYLPMSSTTLRNFSSFTSSPASSERSKKRPRNAQMIDDYECE

ASPKKMKKRLRWSTMTIHEFGIGLGSSTVPGQGGPSIGLSEKPEFTWTT

>contig41321 Frame-1R

MGQSCSCLQHPHKYQRQPSDDHNDLDIEQSEDGQELDMVEGHELLRTRIRTNSNGRNSLW

DGIKRLSLLVGIGNSSDAQNEAKKALKEPQLRHSRPSMRLMGHADHLLTPSARPEELLIK

LLRLYQEKTGV

>contig41471 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63560.1|) 1e-103

MVPNYGIGVVAHSSMTQRDDGKRRQRQLRLRLGFFAVLLTTVVSLLFLLPVRRYMEITSA

WADEHVVLGTLGFILVFWVAVPLCLPATALEMMVGSLFGVPIAVVVITIGKTGGSTLAFL

LGRCMGKELIGTYLSTNYPAFRAFSEILNSPSWKPVLLFQLSSIPNLVKVYSLAVTHVSI

SRFAVSSAIGTLPHAVLWASVGEQATDIAAIITGETKVSTSRMVVVVTGLALTTLAITFL

VVYTSGSSRCFRNEKAAVVERKGI

>contig41545 Frame-2F

MYEGMSTPQGATAPLRPRLSDLDAKTLSSEGRQFSVSIGGHGSAREKDVDDPLRLPVFPL

GGHGYTKSFASSRFSRGSHVSLHQLGTSHAGHLRRRPPSSLSSKKRSFHVAYPNVALQGK

MPHVPR

>contig42298 Frame-1R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY66891.1|) 4e-25

MIPTATIAGVIAAFCYLKAFWTVWGLITPGLLGLLFIGVLMTAHFLPSI

>contig42382 Frame-0R|Blast-60S ribosomal protein L9 [Phytophthora infestans T30-4](gb|EEY65665.1|) 3e-99

MPRQLLATRFVAIPDDVKLVLDGRKVTVTGKRGTLNRDFRHLTLDMRRINKEQLRVDLWF

GNRKQLACVRTVCSLIENMITGVRVGYLYKMRFVYAHFPINVTFENNVVEIRNFLGEKRV

RRVALSEGVQYVRTGDVKDQIELSGIDLQKVSQDAANITQACLVRRKDIRKFLDGIYVSE

KTNIEIEEK

>contig43275 Frame-1F

MRAQVARKDKANCCELIVIVLACYILMVLLSMIEPSRMYLISPRLYLNVPHGSNSGLDAT

EGIFWQVLYTVLVN

>contig43428 Frame-1R

MTGCTPVNAATPSTVKTGCVAMALLAIQYGLQPMIYKKFVGECNNRSLLVIACEVCKLLL

SLLSLRFTGTLRKVVKTWSLHDSIMASGFPACTYAVQNVLIQTAYQHLPSFVFNLINQTK

LISTALFLYILVGTRFSMQQFFAMLLLLSAAVLLSIAKDGGANDASAIPIKLGLVPVLLA

SMLSGLGSALIQRSMQQTKRNSALVTMELSVYGSLFLVLPAIWSTINKTPVLESPATNFF

INGLEGCNYFTLIPVMSNAVGGLLVSTVTKYVGGVHKSFALICGIAFAAFVESYTYGTVL

PDEVFVAAGLVTMSTIIYFKYPYVKWDEKVKKK

>contig43679 Frame-2R|Blast-regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4](gb|EEY65901.1|) 3e-28

MKSASVHWNLTARVPPKIWHATSANSLATPNITGGLIAIPPNEATISWNRKRKGKHLEVG

PNGTTVIAGTYCSIDNSFETIAASQGFDKESIFIEVRVIAAGKDGISILHFGIIGCDPVN

FEAPLKHKLNVTFQHEEEVVECGVFGVLFDLENASITLYSESMKPRACQL

>contig43907 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54990.1|) 1e-20

MQYQVEALSLAQSPPKSPSRETQRLSNSDVSPSSSVAMRGPRSVNLKLTRGTTSDGVGFY

TCNKWEDFYPNQEVAMVTSIRQPPIPPEGYVPVRLGYCRTQQTPEAALAFDEDTPNG

>contig44054 Frame-1R|Blast-calpain-like protease [Phytophthora infestans T30-4](gb|EEY64790.1|) 2e-32

MLSSNPKLAFAGVTSGGGMYVSNARSGVLAKSFQRYSPGWYIIVPSTFESRDLSFELRIY

ASNHVDVRLL

>contig44692 Frame-0R

MTTLNPSSLSVDDMLIGEILMSLKRDIPTRMPLKLESETIYRSKATGLSVEVALPSIFPS

LANSSAGVFSFDAFGSVSPMSCAQLLPIATPSIPVDPSSAQTTAVTPRGSSKRHGPVIQL

DDLKQCFNMPIAAVARKFGICATLLKKICRRHGIQRWPHRQIRSLQKSIDMLRESLRVAK

GTNKDYIAKKIGAFEYTLECIMKDPNTAAKGISAGQLASPAMEEMIKRGIRMKNRQETNK

SSVSISDDEAATTSASLAQSEKPITCDAPESSIQRLTTRRASVPMSLQSILC

>contig45530 Frame-1F

MLASFDGPVTSVDSVGNLRLSPQVRTISYVRTPPPVRRIQAPFATTQFGEQAAIPAHSWD

IATCSRFERRSNGFVMAIPGSISMVYPTALNSVRTAPECVKSLHHRTASRSWSHRSSHRS

YSVVHFDANALRSPSSPIDYRIVRTPPTCPTKIRANAPTLSA

>contig45585 Frame-1R|Blast-ATP-binding Cassette (ABC) superfamily [Phytophthora infestans T30-4](gb|EEY56570.1|) 5e-13

MRNLNDDKVSLAAQLSRVVVLSHGGVLYYRGAKIDFLYISINGRNLYRMCSLHVSRNRFV

RLMQ

>contig45794 Frame-1R|Blast-hypothetical protein PITG\_16835 [Phytophthora infestans T30-4](gb|EEY65214.1|) 2e-11

MARDPASGIKLTDTTRVKCLACAQGKQTKKRQLQKDSGLNSPIDVIGCVVCSDL

>contig46041 Frame-2F|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY63578.1|) 1e-121

MQIDKIPAITDLGIHTERHLEALYSVSKHFPKDRIQRATLRTGLTLEYAIESSADEPESE

DLPAENLVMINGFVMTKEGCAPIIDMLLDKWDTKARGKKLNILSFDNRGAGGSDTPYTRY

TTTQMAQDTLALMDHVGWNSAHFMGISMGGMIAQELAATVPHRVRSLSLVVTTRGAYIPH

MRMWRPFLGSIFGQSMRCLLELLYPAAILEKTLEGRNGLTVQNALTQYHSTPQSANQSSS

YFAMLAQGMAILTHWVSNERLATVAKSNFPILIIGSKHDIMIPPENFVTLVEHLKGEHVR

AMFFETGGHGVPFQFVEEVADALQDSIERSWL

>contig46856 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65988.1|) 2e-49

MRIEIVRLENLLANRIAARATQDKSNLSLERSNKIEKYVEVMELTKCLRRQKEFLLTENR

KRQRFAEKIQQAMPPSTDSIQFMKNVKYPSDEELEKTSREAILEMLEYQ

>contig47110 Frame-0F

MICSMGWPCVHRFLLPAPLSVEISNKHWWHDQSAPTTSIRLNLTLPVAYTSQAPSFHQSV

ERITAEY

>contig47327 Frame-1R|Blast-histone deacetylase, putative [Phytophthora infestans T30-4](gb|EEY68123.1|) 0.0

MSSGSMALTSGGTVAAKRRVAYFYDSEIGNYHYGQNHPMKPHRVRMAHNLITNYGLTKHM

EVFRPRMVDWTELTRFHSDDYIHFLRLVTPDNMHEYLRQLQRFNVGEDCPVFDGLFEFCQ

LYASASIGGAAKLNSGSADIVINWSGGLHHGKRSEASGFCYVNDCVLGILELLKTHQRVL

YIDIDIHHGDGVEEAFYTTNRVMTCSFHKYGEFFPGTGDIKDIGHGDGKHYAVNFPCRDG

MDDESFTGIFRSVISKVMEHFAPGAVLLQCGTDSLSGDRLGSFNLSAKGHADCVSYVKSF

NMPTLVVGGGGYTLRNVARAWCYESSLLVGVDIPDAMPYNDYFEYYGPEYRLHLPVSNME

NLNTPAYLDEIKRQIHENLRQIEPVPSVPFMVAPESGSIQEEKEAIARD

>contig48249 Frame-0F|Blast-protein transporter Sec31A, putative [Phytophthora infestans T30-4](gb|EEY66053.1|) 1e-120

MSLLKEIQANANVAWSPIKRRGELLALGSKGDGGVGFENNGGVFMLVSMNLSEPGRGMIT

LGSVKTTSRFTSLAWRDVPRHHDTCPYGIIAGGMADGSVSLWNPALMLDRDPENDAPVSC

EIGRITRHKGAVNALQFNPHEDSAHLLASGGSDGEVFIMSLEKLASPGVFTPGVPTSPQT

QANEIVSVAWNTQVNYILATGSQNGSVVVWDLKQKKPWCELRDPARGAATAL

>contig48304 Frame-1F

MTRICSKHCTCSKMNSRKTSAALVGWMLQAKKRNHTCDVIALQETRIKSYDGAARL

>contig48515 Frame-0F|Blast-threonine protease family T01A, putative [Phytophthora infestans T30-4](gb|EEY63538.1|) 1e-07

MADSAYSFSLTTFNPSGKLLQIEYALNAV

>contig48766 Frame-1R

MPLLRPNYYCTSNYVDDSICEQTILSQLKISDIATARARQNLCLLVA

>contig48821 Frame-2R

MCLSMFRQIQYYLPTHRLSEREKNLLIINRHFLGGHTKWLLQLVKAIDFSAENERFEREG

QTGFFPTHRDTTNPQLIQEVLNLLTQERKYTCMLTMCSRLCKPQIGSVDALEILADDTIY

NDQLRGMAVNALLKTATENEWWSYLHVLLHSLSVETNATGSKLGQSLIRQAQCDIRFCYE

LYWGLTVMAEDPSCRRKFDGMKQRLLLTLSHFQDNSSTGRQNESSHQGTRDDVAEQLLQG

QELVDLLWKIPPRIPVE

>contig49260 Frame-1R

MPPLPRTSSNSSRSDSLIVTISSVFHELLPYRLFA

>contig50143 Frame-2R

MLYALDRFEAGRQHVFHVDQLQAMRWARHCWKQEISDEIIRKCWAATAILVPPPPSETME

AFELIEHEIDKEICDTVSALEILRPLPIDEFVSPRDEDSG

>contig51034 Frame-2F|Blast-chromodomain-helicase-DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY65872.1|) 3e-62

MRLGVSSSNNISVLGFQNLANNIMGPAEASGTISVGDVLAAVNKTSVSGRSFQDVIGSIS

ASPS

>contig51755 Frame-0F

MGMHVQWSFLPRLQPSQLHAFKSPLSKKHSQLRHLAIQVDMKLPDDVRKLKQKIIESHPS

KLMHFSLTQMRYKATPPVLIPDVFNNHHAVVVSGKTVPLTMRMWRNCKRNIQHLEIINER

VTYR

>contig51900 Frame-2R|Blast-hypothetical protein PITG\_15528 [Phytophthora infestans T30-4](gb|EEY64756.1|) 3e-08

MDGYRQTLLGRSLADALHDIEMNCGDADVDRHVNGDLIFSLFDEAMMFELHDKRNAQTYT

HDLLQLTGEVTAFNRFVDDWSVLACVKSHEIHLNRSVAIFHLRQQSQDHEKEQGIAVRLK

LRKIAKNANKEVQSSK

>contig52053 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68165.1|) 6e-83

MSEVWGYWADPIQLYLHPAERVDVQDLIKTDNELFNKVLTVFSVLCDEISELKVTVEDNF

YPALIMFGQARHGDESEVKAGDDEVYIGRMLAFFQDISNFVDRCNAITINMIHQLASLYQ

SFQKLWKSTFKLVHLYPVFDALAALLEI

>contig52237 Frame-0F

MVELEIEMSILSEQLQAVTAKAEASAAKAGDELRALQSEKSLLEEHLSAKKAQEEKLLAK

QNELEKEKHLLLSEVSALKSVQS

>contig52242 Frame-2F

MEHEIHKLLELELNQTNASACSEDALSFGMTQTNTQAAISNGTQSGYEISQSQSYEYAQA

LAKAQGQEQTDPCIQSSPFSTPRVSMSLEA

>contig52408 Frame-0R

MDIDPLSTRAQFAEVPTPAELASFKVSKSPYLPSPSVAQMDTPNAPEFIVGDGVAAGSWA

AGLFNCFDNLVPNCFMVTFCPCVALAQLSTRLGVAPYRVILSMLVLASTIILTMVLLMCV

TATEDYYSIDGAIGHVHDKMAESVFLVLMLLVVVLLLSFISYLRAITRRRFQIPGNSAID

CLSSWFCSCCAVAQLRTHVRVYQPGSCTFGPPNVLPAYPDKSYAV

>contig53124 Frame-2F|Blast-anthranilate phosphoribosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65373.1|) 3e-21

MTMKLSTLLAKLTLREDLTDAEATFAVQQIASEKAAGNPVAVGVFLALLAAKGESAAEVA

AFANFMR

>contig53340 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53335.1|) 3e-11

MSLGNRVDSEAAAHDEGEWVSRGEAEALITTVTTQITVAPPASSNGQVIVSSEDEIDPRA

ADLAVLG

>contig54046 Frame-2F

MTNEQNVPILRGQVLLNGFEATELAIRRCTGYCEQTDVHSEASTFREALQFSAYLRQDKR

LAPDRVEAIVDECLNLLDLEAIAHQLIRGSSSEQLKRLTLGVELVAQPSLLFFDEPTSGL

DAPAAKKLMDGVRKVADSGCTVICTIHQPSADVFLLFDMLLLL

>contig54947 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63747.1|) 7e-21

MDKNDFEHWKVIVERHESEKQQLESRLQEVMLRTTEQIEMQRNSAALSTEEGRADLQILK

AQLLQRDTQIDEGRQQVRSMQENARL

>contig55038 Frame-1F|Blast-DNA-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY69219.1|) 3e-23

MSENSKEFKQPLFASSLGSGEYSETQIDASWESKSQSMLPLFSVEADALSAHSESRQQLN

SSTKYSA

>contig55733 Frame-2R

MCGKLGFKLDFTDLLADSVVTFQRKHYMKTAVVMCYVVPTIIGYYLGDACSGFWVGGVFR

HVWVLHMTWMVNSVAHVFGYKPYDLKLKPVENLIVAIGALGEGYHNY

>contig55892 Frame-0R|Blast-TATA-box-binding protein [Phytophthora infestans T30-4](gb|EEY53626.1|) 7e-13

MATCDTRFPIRLEGLLNDHARFCS

>contig56417-1 Frame-2R1

MLKFIFMSFCCKSKRLDVCKPQMFHKLAEIFNFDPNRQIL

>contig56844-1 Frame-0R1

MTKMEGGRSQSSTKKEEWSTLLQAPRRSRCNCARRIVTTWTSTA

>contig57366 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62986.1|) 5e-17

MSRGRGRGRVRFGGSRDSMLADIMDETREDLGLSHTQMELLHAETG

>contig57436 Frame-1R|Blast-hypothetical protein PITG\_09549 [Phytophthora infestans T30-4](gb|EEY55606.1|) 3e-36

MNGFPMETGWQKMKRRCQEEPLVPIGCLATAGVLMGGLASFRRAADAATQQKFMRLRVLA

QGATVLAMALGGFIAIKPSEKNGGTRH

>contig57649-0 Frame-2F0

MIKIFLFLVLAKLMVASANS

>contig57649-1 Frame-1R1

MKRHLGARRKLVNENLEQSKRNVVATKCR

>contig58576 Frame-2F

MLRRFYFQLVNREGNAIGTVDFVRMPSDEADVGE

>contig58860 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69730.1|) 4e-33

MSSSPLWHESRPSSPFSAAGMVDLALDSLGLTTGQISTRSFVPSPLQADLFTHSEMYALI

LLDKAYSLSSMDAVHTALDGTQAFHK

>contig59218 Frame-0R

MFQKRLILLTETRHIKRDVIWLLRLHLCH

>contig01058 Frame-2R|Blast-predicted protein [Populus trichocarpa]gb|EEE86229.1| predicted protein [Populus trichocarpa](ref|XP\_002305718.1|) 3e-17

MGLVVEKTYDVKTGKGMPDL

>contig06385 Frame-0F|Blast-DNA-directed RNA polymerase I subunit RPA2, putative [Phytophthora infestans T30-4](gb|EEY63911.1|) 2e-83

MIPVGLVLKALYPLTDREIYERVLRGDHANTYLSARVELILREAKTFALYSREAALAYLG

KHFRQAMPYVYDNMTNLDVGSKLLDDFLFVHIPKGEKGRTQKVELLCLMLRKLYAFAKGD

VPEDNADSVMNHELLLPGHLYLMILKEKLQESVAALRANILKETQ

>contig09133 Frame-0F|Blast-bifunctional polynucleotide phosphatase/kinase, putative [Phytophthora infestans T30-4](gb|EEY67995.1|) 1e-165

MDANQLFAEDVVFFPFVEGNQETIALVKSHGGVVVDDSEASSKPITVVFLSTPTQDDTLN

LLIARFAKAEILHTQWIYDSIKTNARLATNSYRLREFESSTFKRQKVTALSAAYFAVRDT

KETTTAALPEPHLRPWKILKKSLYVLDARAEQHQGNAAANTYKIAGFDLDGTLIVTKSGA

VHAKAIDDWKLFHATLVRDKLISLAKKGYTLCIFSNQNGIAKGHVTAAEVQRKIEAIIGR

LKLPLLVFLGTADDMMRKPRIGAWHEMASLLSGKGEECIDKDTSFYCGDAAGRPKIPGRA

KDFAATDYKFALNAEIPFFTPEHLFLGSKQRIHTQFDTWDLGFEPKLIKFNHSKEPVLDP

IGAQAAKPGQEMIILVGSPASGKSFFASNYLSSYVAVSQDELRTKIKCKIKCLDAIEKKE

SVVIDDTNRDPRSRNLWIAIAKDKNLPVRCFVMDVNKPLSMHLNTFRALTKQKNVPLVAI

HGFYKNYVVPTVKEGFVEVIKVQFQIDCNISNEHKALLRSYI

>contig09652 Frame-0F

MEYFIIFLAFERTHSKKKSIYFGFETALIKRLTKFMECSIMRPRCTPTCSCTTIITLGLT

RQKSEKARYFEAIQDLDKEQKQEMVLL

>contig10618 Frame-2F

MLSIASKLNVTLLERKALLSEDETILIGESQPRTQPTNPASHFRKSFSTDDIAHGNLANG

PIVDKFMVKRIDSSQPKEYERVQVGDILEATDSIATTSMSLDQTLALLDNGNRPLRLRFR

RPVSSTSLLSRNSQFLLASSIDILHRARRLQLNDPGHWSSVRLPTFNFSYQFPKRASDHW

SVGVMLRFLSPDQVVEIVAYLLLEKQVVIMSDSPAKISAVCTALLLLLAPFQWQSTYIPL

>contig10997 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61623.1|) 5e-11

MKRALWMIESVTLGPTKLELVLPAVPAESFKKRISRTILEKKFRGTREEWQHFAQIYSIP

GDTQHQRDVIDHERQQEDVGCTG

>contig11352 Frame-2F

MGKSRRTERAEITRLNGVVANQVSQIQSLQDKLAAELELRKKYEKRLEDYRQEEHRRRSK

GEEARKALQQMRTPSPPEFPPPITSRRWSLYAQKERLANAQGLNGIENVAENILRGNESS

PDLAELLISSNGKPSRISPPTNFSRRLSMSALDQNAQGGPKTKQKDRLLSFQGKRKRSSA

SEKIRSILKKQRGNGKSAIGTDADVSLASKQVSFDLSLVTIDTTLPPRDVNEGIAAPRIP

VGGAVRVLASNNRPVTLPPQAKRVAHFKRVKRKSIGWR

>contig11882 Frame-2R

MFAAKARACVQHALANSSDTRAAPSYLQRASDHFIHSASEKRT

>contig12128 Frame-2F

MDNLLVGLFGNKFKTLAHKAITGPTDCPAFEAALDLVVFHWLRRQKSSEINILISDMLKD

NKLSKNFMALSKREKEWLAKLNNYA

>contig13314 Frame-1F

MDSSNEHESLPYKKRRKSAPAAIQKVKIPVKPFMSPPAAAKQKWPEETCDSSRDKKATAE

KDPALLNSVAGAGNHIHDSFPWLYENRHDINGNPPDSPDFDPRTLEVPLDFLKKETPAMV

QWWEVKSKNMDTVLFFKVGKFYELFHMDADVGYKELNLIYMKGDKAHSGFPEIAYSKMSA

QLVAKGYRVARVEQTETPEMLKTRNKSLAKKAKVVRREMCSLLSIGTNTGSFLDAPITSQ

SQAATYLLALKELCDVTQRSVRFGICMVDCATGAFQVSEFDDTEQRDRLKTLFAQFHIME

IVTERFNLCHDSKMLLQHAAPAAIHSALRVGKEFWDASKTIDEIERAGYFKEHGWPDEML

YFLEMDKAVKPKGQLAISALGGCIWHLRRSLIDQELLSLCNFKRYKPSDEEAREARASKI

SVSAAKSELGQHYVVLDSRTIQNLELLCNNSNGLRSGSLIDIMDKTVTSFGRRMFQEWVL

KPLCKISDIQERLDAVEALGQNGNLMMNIREFLRNLPDLERLLARIHALGSAHRSKEHPD

SRAIMYESQIYNVRKIKDFLAVLNGFDAAMTLTLEVGPRLLQSSSPILQTLLKRYNIVDG

VHPGSKHGHFPDLTEKLEFFKRSFDQASAKKSGVIVPRAEVDQEFDAACAEIAQVENELA

AYLSDQRKALQCHQIAYWGKKKEDRYQLEVPESALSKQPREYELKSRKKGYKRFHTATIR

ALLKRLANAEDQKEEALKDQTRRIFHKF

>contig14038 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53393.1|) 1e-180

MAREMIAKVTSKSDFCYIIKELCNRCRHHQVANPSVHLVKLCQKVLATRNPMKAYSSAMK

SMISRQMKIYAAFDKDIKKKRRLESSSASSSPVTESEASSSPHSELTDAELAAVKRRIPR

PPRLNFKKVNLRTITYQETNDNGTVGVAISGIPNAGRGLFNLSNHPWPAFSVVCIFGVRR

ITKEMHHDGLNKVARCGELGETFVVVNGTVRDVDKFQTQYGHRLMPFDGLVDADGSAGGF

PNDRVYEYPANIYWDASGFLQQLHPCARLRDRESTGHDKLDYFKSIVYCHVEGGGSARGV

FLGIRHIVLRG

>contig14535 Frame-1R

MVTSVIVFHTSLRHKHRLFRPCDIDFCRLLCGQVEPYLQRIALEDAMKKAQLKAQAVLAV

SDLVFRQLEQVPKASTLLDTVAHEIERQAWIQTTKCTVYLRDPFTHELYVPRDAMDRESR

TNVPSGSACAMAAVRTGNIVNIRETETGLLFCTKHGKFVMAVPIKDPSSGAVLAVLEFQD

KSPDTIESSALMWLEKGYFDLHDEDIARAIAHQLASALRHIQRLDAARIAERKSAALLAL

RLPA

>contig15334 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65790.1|) 1e-07

MAFNFPVAHETKKKLQVFECPVETWKERKPRISKVRNFFRRKALNFFINTLWSD

>contig15402 Frame-2F|Blast-glutamyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY69415.1|) 2e-98

MYDRACHGLDEKEVNARVARKVPHTIRLKVPEGKTIVKDLLRGYVQFDHAGIDDQVLMKS

DGYPTYHLANVIDDHAMRISHIIRGEEWLPSTPKHVILYKAMGFKVPTWAHLGLLLNEDR

SKLSKRQGDVAVEDFRDKGFLSSSIVNFVALLGWNPANGSNQEIFQMQELMNH

>contig19095 Frame-0F

MPCKLKSSVVARKWARTSLAFDDTLPLGCPQAPKLLFDLKAAEDFIDLVVRVLHVVDSDE

AVRLIIWDGSGNAAESDHALVSALQNKGVDIPPHGLLKEVIMSSCWSVVQEMGFVDEMLA

SWCRFRNLAVGRNELLPDTALASGIREILRFREVTSFVLMPEFSLDVQRRCSLNKCSNPN

PTINFQRRRSNENVAEPNQVVEIRTIIPDHIFKSVPVTPLREILNSLQIPRKYHCRAFFR

SVWPDIEKICKPKSDKSDEYIYSFALAVQEGNESMNIIVYGNDAAHFLHGIPPCDLSKST

SSKTLLQKRFAALFQASKASHLCIKSYHVSLPPGHSSGSINAVRYRLFQTLLQYEEHE

>contig20349 Frame-2F|Blast-cyclin-C, putative [Phytophthora infestans T30-4](gb|EEY69286.1|) 1e-56

MYTFQDKDILECEFYVIEALQFDLILHHPFPSLL

>contig20925 Frame-0F

MRVAHMSAFVAAMGTLSASAKEYSFSEISTNEKNFIFGGTEADINDFPFVANLVDNLLQQ

PFCVGTLISKQYILTAGHCIRSDTFGIIARFGRNESTGVEAFSVPVVEGFRHPMYRKKTH

>contig20950 Frame-1R

MEARNDRFLAVLFCIQPFLPCDRVSCSSLCNEFETAAQKARSQLWKYALKVLVLLISNGL

VAVRLAEACWRPLLATIVAFIEPQSGHFPSCVQSEEDQVVVLSLLECIVNSSTKLLRESD

EYIQKHSRAFLHELVAVLCSGINAVHYDKLMLQSCVGQLTTLCLQVLDKDMALFLQKQFV

TCCKMAMQHFMTFENGFDSTILMKNKDLVAAQETVVVLLTSILEAALPRSCVLEMYSSLC

GCITSSDEEVRQWVQRLLLRLEDDSLVVLGMK

>contig21081 Frame-2R

MFGATTGATQPANSGFNFSTGASTTPAAASGGFGFGATSAAPTGGFSFGGTAASATSAAT

SSGFNFSATPAHAATPAPAASSSFSFGGPIAATPSPASSGFSFGGTTATPSVSNTGFGFS

GTSAAPAASSGFNFGGTSATPAASNPGFQFGGTASTVPTGFGATANPSIFGQTPATGSGF

GFNAKPITPSTGFGFNTGASTTGTSAFGAPSTTKSSLFGNFGAPSSSAIPSPFGAAPGAL

TTLTPIIVGADASVAQLNSVQAAYQDPVQSRFKFFMYNTVDPTLRHLYTRP

>contig21188 Frame-0R

MDPRKNIYGSKATKSSMASPRMRGLTYDIGIDSLPSSPEQRLQAETKKRYITPVEDSSAS

NFLVEIIDLPPGVERTIIIWYSPAPIGSNLEDLCGETSEAVDLKATRLTKQTFRVSFRCF

FMQGAWQQAQSRVYDRTLGKTIHIRARTCTSVVTVTPSILHLGDCNIGELRSSVCMLTNH

SELPTVVKPLVTSKVISTVPNDDMILGPKQSAELKIEIIPRKTNQNYTRLISIINLKNKS

NIPQICVRSSNMDAHLVIYHSLFYKLLTQSRSAFLNFEHVTANSVGIQVFDLDNITNAPL

HLNIQSSAPLKVHLYCIRHPFSDLTNISNVCQVGNQPFFSSMNLQNSAGCGNPNTSSMQK

YKPPLGRPIRRRRSFGSLSEISDGKVTSKKKKILSTSRTFDEKADRGISSSSRNFANYHT

>contig22758 Frame-2F

MEVVSVSSAYFLVLFRSTYLKPFLELY

>contig23564 Frame-1F

MDGSNLPKKPLQATAKEFSFNPGATTWTPPAAFASPPPAPAVPRTFDVAMPAPKKGVTTV

LGATSEPSEIPPSSPVSRLEEKMQEVNVNEEEIEKARTETLENDQPKKDDHDMEERGEAA

DENDHFDEEEEVGDEDPREHLNVVLIGHVDAGKSTLSGNLLYLMDMVDKRTIERYEREAK

QRHRESWFLAFIMDTGEEERAKGKTVEVGRAHFETETRRFTILDAPGHKSYVPNMIQGAS

QADVGILVISARKGEFETGFERGGQTREHAVLAKTLGINKLIVAINKMDECNWSFDRFEE

CATKLRPYLRMCGFAVKRDVSFIPVSGLHGDNVKVRVDKSKAPWYEGESLIDHMDTMHVT

NRNPDGPLRVPVLDRYGERGTVALGKVE

>contig24103-0 Frame-0F0

MVITFKDAFYCTSSYQEPQSLRPSRAMLGSKRPHNQSFNTAWCRSGHR

>contig24918 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61365.1|) 1e-95

MVTVVSLRRTFFPLVLLLNTRHVVKGHAWIDCFEKDWNKIYDQSASYIFGGAGGNGFCSG

YGAGYPGRGDHGIGPGYTHKMLQNEVEAGVPVCQTVDPNTYSDWRKRLSMAPGETTFFAY

LPNGHIVKDKKGVGTQHGIYWTGKPGTSLSTTREMKPEHLINGHTMNFDDGNCGETVDFN

NVPSGRAGDGKPCIGSFMIPPGTAPGIYNMVWYWTFWLNNESAYKDQNMAKGYFGAAYST

CFEVEVTSGGAQAPNSAPQASNPAPQAPNPAPQAPNPAPQAPIPASPSCTQTVAPGDAAN

GIGIMTDTNCKSGGLGCINYICRYCQVTMTD

>contig25401 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62954.1|) 2e-92

MLTWKSKTGLVFDLKKNEDGKTDGFILKREFTFDTTTSEGWGITFDGENYVVSDGSWTLI

FWDPMTMKEVRRIDVTTRSGVQKIAHINELEYAKGFIYANVWYQPYIVKIDPVTGIVITV

FDLSNVIADAGVDVNAGAVLNGIIYNEVEDVFYITGKLWKNVYKVHLIDSGQ

>contig25496 Frame-1R

MDRENTPQKQRQKRSSTNRRIGSSSTAQGVSSRAGTSSVSNLTRVSRSRGRAVGASGPLS

SAAMTKTPSILLRPLSGGTLGSTGVLYEPDAHKRSSLYVSDRESHNNTRSKTLDRHNDND

TSSVFLRPHHPSSVQQTKTVPPLTRVKLITPQMQFATDLSIKLGSCLELENFTVVGVLGL

EGVGKSTILSLLQEKKASEKEVDLTQRVEALALDRYGTTGVDLAISLIGGAGHPTVLLDS

QPLLSSSMLVDLLDRNDAHRYGALSPDQQVEIVSYQLAVFLCAICHYVVLVHDDLAYQVS

VNELLRIIDLKMTQCRLPSVTGNNHRHAAQLLYVANNMADSELLYRENELLSAHERALEA

AWSQALVRVPHKVSSYSSSADTDKYVQNVAYFVFPCQQQQSIRKDIKTHVQLSSASPTSG

HKIEIDRNTKRRSSKYSEFDEVAEDFRRFVLSLPSSPSFTFPVTVKNAASKTLPHALTLR

EWLSNASRVFEALRKASCFTAEYASSRDHQ

>contig25827 Frame-2F

MYIDKSTLYSLQIFNHEAHPSLVKGAGRAKEGFSLFGLLNRTVTKSGGSMLRQWMLTPLV

SSAHINERQNSVAFFFDAGNDEFRQLLLNKLKHFRDVAGIFQRIKRRCASTGDWCRFITS

IGSYLETQSLIESANKTNSSSLPSVFSKVIAEREIIYLSNLLGNVVDFEMSQLESTVVVR

SGVSEALDAARERYEDLDN

>contig26185 Frame-2F

MSPSNKSFSSDDDNSDELDVEKSQPRHGKASKSSSLSESSSVSDSSFSDEEGETVTITNA

VHMKVRKASLSGQERHDKRVPTLSNPREKNKSQSGADTIHSTSKSRMNEYMEDRARKRNE

KLKLKQEKEHEETKKKEEYEKEWEIMAQEERERKRKQQQTRRNGRRRPASMKTVRVSQIR

QQMNSKHQKEQREPSTSSPLYSNDPPRPREDEGVDVNGQASRHFRRKSECKTSESEAEEE

RQSDPRTLSTEMPPLPPEPALADTELYLRQQARLRERHEMQMKKKLEADEADSVRGVIHR

RVEMWAFGKELLHMILTLDQISSSDALKKCQLMVVQSPDNDTVRKAYRSIIRVVHPDKLR

GATIPEQLEAKELFTVLNQAFEKFKSHST

>contig26659 Frame-2F

MILWAGLWALVATIALADQTSYFTGQGTSYQLNQVSSGSCNLMYESGDADNYAALNDAQW

NSTRNCGRCAEISCGDDRCKDKTSSALVYLVDRCPNCQPGDLDLSPTVFQKLTGSTSSRY

SIKWKFVACPVRGNIQYCTKSGSNSSWLALQPTNLATGVANLRIAHQSVTMVDSCYYYLL

AGGQNVDLDAVPVEVTSVTGEILTETVKLSPNSCTEGTANFDASSTQQMDTNSSISVKQK

VALDSSEGGTYKAGKVSASDVSILEPEKNSIADMLETQHMDASNVQQATTSSGETSVGTS

PVAVLIVLAVVATVAAVAIAFSVKKKIFGGKRVDFSASLNRSFDTFSSPVRLDESVIAKI

>contig26956 Frame-2F

MSTVVCVRKSDNDEKSEQRVLTKGAPEVLELIFTNKPSYYRRVYRYYASKGCRVLALGFR

VLSEDIALPELRRKPREELEKGLTFAGFLILDCPLKEDTKRTIQELVISKHKVCMITGDN

PLTACDVARQVGINAGYSKQPLVLSSDAEKGYLQWNSIDDSSLDIEKEILPFNVEQVEKM

QARYDLCVTGEALEMLYKQQEKEQNDNVAALERFLSILEKMCLSITVFARTSPQQKEHII

MAMNRRGKITAMCGDGTNDVGALKQAHIGISILNASSSENAFEDQNAALGDKNAAVQGNL

RHRRQAGNQRRLTEGLQQSNSGDQASIVRLGDASIASPFTSKSSSIRVVKKLIRQGRCTL

VTTIQMYKILGINCLLTAYYLSSLFIYGVKSGDQQLTISGLSIAIFFLFLSRAKPARKLS

HQRPPSGVFCTSVMVSIFGQFAIHLAFLAAALNVATPFIEHGDPAMHPDGKFTPNVVNSI

MFLMSSIMQVNTFVANYRGQPFMEGFWENKQFSYSALLNYAVLAMIIAEVFTPLNAMLEL

VTLPNQETRYKVAALMAGDTLLALVFESAVQTIVSTSA

>contig27317 Frame-1R|Blast-tartrate-resistant acid phosphatase type 5, putative [Phytophthora infestans T30-4](gb|EEY53559.1|) 1e-89

MYRSRKLQIPWYVTIGNHDCEGSIDAMLEYAKTKNSLWHLPRRYYSVDHPVAPKTIVRLI

VIDACDLVCGREPRDFRCTQSMNDQTSVASRQSQYDWIEQTLSASKPLGVERMWTIVMGH

WAVYSFAGNGDTPELIDKLDPLLMKYKVHAYFNGHDHSLQHIKKVNDDGSVRNYFISGAG

GYSIHTLKPNARANPELIHAALKYGFMTVHITPTYFRVQFVDDASDIIYTTDVRYE

>contig27483 Frame-2R

MQLRFRSNQFESVNERLEEALKEKRTLEVKLTALEGQLFEQRGRTINPGNSCSSANDVKK

TAKLAEMQHELDKKSAQLMIAKRDIDQLRSQVKEDFVSSSRSSSIDEVADKVKQCEDEIS

RLCQRNDEQTRKLQTLGDRVKIAVRERNELEKIVQQMVTEMSLLGKDVKYSFESCNSPTS

ATSMIDQIEEKSYTVTHSRSSPSVVATGKITDRYDVAVASSSNTSHTPSSLAPIVTSSKV

AELMKTFSPNDADLKRPAKVDTRNRKASSISNDNSSL

>contig27630 Frame-1R

MSFFSSGSLKMITVEFSGLWVRILFYRRKRPVQGYVRHANHLGKRDKN

>contig28019 Frame-1R|Blast-fidgetin-like protein [Phytophthora infestans T30-4](gb|EEY54210.1|) 7e-45

MGPIRSCTDIRTIDAGFVRSINLDDFKEALRGVR

>contig28554 Frame-1R

MELRKDLTHKVLAGDEWFETALERLWRVVGDRNKDVLYDRNDVDWVKLGFQNASPETDFR

GGGVLAMKCLLYAFEAHPVEMRAIYYTEMPDATQRKRWYPVCVAGINLTCLLAGLLQLGD

GKFTEKKDVFWPLFQDPASFYELFYLAFIKMDAIWHRLSATYMEFGVVLQITRKVVVCML

EQAPASLRELREASDQTYLERFVINLSARSMAEWEKGECPGPFCMLETEDALVIAKTRTV

SN

>contig29463 Frame-2R

MFPLYRRTQPFLRTSSRAQLWVYLDSASSISI

>contig29845 Frame-2R

MSRMPCKNSPYDTCKLVRKIILRRIIKK

>contig30025 Frame-2F

MDAKEIIYNEFVDINVAVASERGYVLTLTAVFTCLKILFAYVLSTCR

>contig30050 Frame-0R

MDVFGNSFEHLRRTRSQRMKDRGANHEYVPCDHEGVSCDSALCSCMRRDHYCEKSCGCSP

DCSNRFAGCRCEFGQCRTAECPCYYAARECDPDSCISCGASVLPVLIADGSKNVSQLKAC

ENVNIMRGQMSKIAVSASKTHGWGAYALENVKKGEFIYEYTGSLLSQDEAERRGNVYDQT

TVSFLFDLTEDSVVDATRKGNKSKFANHDSNAPKCFARIMLVNGDHRIGIYAKQDISVGD

ELFFDYGYSGVIPDWSQARIGSSKETESVKNIETYPSSVDHN

>contig31134 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69735.1|) 3e-48

MKHTTVKNMLSAVNLGEEVLSGIVQVAEHLQGSIIAADTGCIESLRWSGAMPLLLRDFNV

SNIVSASDLLTCASPQDLRRFLLVQEHETIDHVVFFLSGFLWDYETAFKKLLTLNIIHRV

TICSSLSESAHECYDFYKLRPSTALDATEKVEEMHFD

>contig31602 Frame-2R

MIDHFVIFSKTGTILWSRTLCLLSGDPVDKLISRVLMEDRAGEKKFIDDAYSMQWVFENK

LDLVFVVVYQKILQLLYIEELLDIVKKDFVAMFPQQIINQTPVKYNEKFAKILKATELKF

TSNQMRKGPRAFHASNKVRAKGALTDVSSATSSSLRSAKTANSSDDESDGRTSDALNSSA

GEPDNKGALKSKVRAMRTGPRRKGKDMVVKEPKVSTKKMTKWDDTKVSKKEAEALDRSKL

TTMEEEVAQLREKREAYIGEMVDSDSDGSSDSDDDLANSGVDFDSRWSFSKTRLGNFLST

VSGNKILEREDLESVIIPMHQMLITKNVASEVADELCESIITTVIGQKLESFTRISTVVR

KALEAALLRILTPKKSTDVLREILQAKADGRAYSIVFVGVNGVGKSTSLSKVCYYLKSKG

INVMIAACDTFRSGAVEQLNQHAKVLDVKLFQMGYSKDPASVAKEAIKYGTNNGFDCVLI

DTAGRMQNNEPLMRALAKLVSNNEPDLVLFVGEALVGNDGIDQISMFDRALADYSDRREP

HCIDGIVITKFDTIDDKVGAAVSMVYKTGQPIMFVGTGQKYTHLKKLNVRTVLRHLLQ

>contig32917-1 Frame-2R1

MRLPFHVLALVTTYALSMTSQTSAESSLVRATVAHEQSHMESLEAKRSLRAQQTSPLNAN

DERISFKNLMGKIKGIVQKFYRRKTTGLRRIKNMKSVR

>contig33244 Frame-2R|Blast-metalloprotease family M12A, putative [Phytophthora infestans T30-4](gb|EEY56315.1|) 1e-132

MLLSVLLLMSTTARAWSRPAGCNLDGMEIDHGSMKYVTGRAHRPGSIYSRCSYGIATCFE

DRGLVDAPQWINSREVSCFESLQRRRLGVAIILEEDIWPDHIVWYRITGSFSDDELDMIK

MAVDVYANVDVNVTLKECEPVTMCNGKYVSIEQNEDACYGLVGYVNDGKPQIMNLGETCF

DGGPGNVVHEFGHALGLYHEHTHPEREVIVLTDLDLPVSAENYAKKSSQVATLTPYDPKS

IMHYGRAAGLCFPKSHYPLKAFCDVEHVRNCIQPVVQ

>contig34036 Frame-0R|Blast-2-dehydro-3-deoxyphosphooctonate aldolase [Phytophthora infestans T30-4](gb|EEY66546.1|) 7e-29

MAAAVGVDGFFFETHLNPKNARCDAATMLPIDELEPLLNELLAIARASKALL

>contig34267 Frame-1R

MAESFQAIPGTLASSVQDSDDDYDDEEDVYLLHNLAEKGQIDRLRSLLPLPFECSNPPLR

QSVLSSETSLLEKDDMGFLPLHIAVLHQQTACALHLLRYSSALTSAMLRLKGGDFGTPLL

HLILRVGAINASCSKELIHELLTERTQDSGVFHDDMRALMLEKVAAKDEEGNTVFHLCAR

YDLVACMDELALFYRKQCAVVNGASLEREKKKRPLTLEKLLEKGNKIGFRPLHEAMKYQA

AAAVKKLIHEYNVDVNSVTTLRQTPAHIAALVGFADGIDLLHASSRHVRADLTRQDMQGF

TAAQVANHCGFIALEKRLVAVEAVKSIPKEPCEMDQIYLNNQTRLYFHPEVYRHLPMAYH

YRGGPDPPPENPERIDTLVDPVFGVLRSREFQRPNVKWHDKIERADLADILRVHEFHYVD

RLRRTCAGLAASIGGKKPVEFKNVGLRSIQRLDPLKSMSCSSLEDSEECCATHSLDSDTA

LSDGSYEAATRAAGAVCQAVDDVVAGKCRNAFCIVRPPGHHAGPVGKVVCKNDREGSLGF

CLFNNVAVGAAFARAHYKHEGIHKVAIVDFDVHHGNGTEEIVRQLVPSMKEIDYETPYGT

GKQVVHQYKPWRNDNDAENVFFSSVHGYGQKDQDDMVHQETPSWFYPGSGESRVKEFPVI

WNEGLGLDCQGSSVSRLKWRSAFRDRILPKLCEFHPDLIFLSAGFDAHKKELVNWGYLAL

LEQDYEWLVDHIKRVANTCCQGRLISVLEGGYNFHGRMISPFARSVAAHTRALINPARKL

WDKDEIAKEAAHEQALLAHYQEPTATNVTILQTKRSTLNTAEMTRKRPRKEVDYVLLAKE

LAEQRQESLD

>contig34393 Frame-0F

MPANIPQKVSKLTPNNKPLLKVQESMFHNKPPPKFKEMPSHFRNDAKVALSGQKDDVATK

TFETWLNSNSKGQMPFLSDLADKLSLSDAGMAKALANAKSTEQNGDNVIKAYQRQLIRDT

VKKKRTKDPVALYLKSRFPD

>contig35761 Frame-2F|Blast-scavenger mRNA-decapping enzyme DcpS, putative [Phytophthora infestans T30-4](gb|EEY57723.1|) 1e-29

MILSLLWFWKMSLSRHRTSSMLHDFSLVRVLKRTDTELTLLGNFKSDNHKNAAILIIQTA

VMDIRSLDLLLAEMSLHKVLVNDIYSTFQGDVSRDIKPYKVRVNASTVSIQRVDLSKYV

>contig35945 Frame-2F|Blast-Voltage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4](gb|EEY65674.1|) 0.0

MAATAVACSIADYSAGCYTASWYLIWDQVRFWLLVQVPIIVLSIVYEWLDIASHKFVERF

RQLCDLPLTNVVNYIVQIITSIYVCIVWIVRGGSLAVSISSWSIESLFLIATGIGYAIRW

LAAKNKLTFVLQLHNLFDLLAVVAHFAISFQTVVVGNKRLRSWLDFGFLRSYVGYVVMDH

LFTRYQHKTFLSQVLLVVLKALCLVFFFSAVLFSLEQLGELPHTNSFLFHVYKCSNEDGS

RSVLRAIKEGTDEYPTCTESWSFFSSIYFMFVTVSTVGYGDFSPHTVLGQLTVCVIIVFG

IYTFANESAAFMTIYGDQRNMLLKYDCSRNTVHVIVTGNPSVAQTKDFIREFFHPDHQEA

FQGHDMDTEDSDDDAHQFVASIKTMASLSRREILQKNHHRYEA

>contig36427 Frame-0R

MSLCKLLLRPVSPLVAKHGRGHIVSHGPLSVASSSFCTFRASNGLLRSRFAMPSKTPLSS

PHARALDTKNVVLILSIPQKQFYSRGRNSWQRKSDWKAALKTGGLVLLGTGALVASTSLA

FGLILAGAAGYGVYTLYQRLRGPYRSRSNDVFRNLNSNIDTLNDLLNRKRPRTSKAPVQD

DLNAFLQSMPFMVRGFVKTVFSFVGKAMQHSITRAP

>contig36676 Frame-2R

MLLLEFNDVYFFCGNFLRALQTLQPATLPFLEYLAPETPPEPGLLPMEAPLYCLSDGFTF

DLSPILQRHPRRTLMRPKPLRLSPLSQASHDECEAALVRYSRLENDQAKALVKALSSRVA

CIQGLPGSGKSYIGSMLTHIIVKAQVSPVLVVCYTNHALDQFLCHLLDTGLTNLVRIGGQ

SKEPRLAKYNLNKLPKSYPGYALKLLYETLDENADAIAIALKDLDKHTRRPTW

>contig36742 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60158.1|) 2e-16

MAKAKWNLSVEESLRQLHSNGILFISRGLQRALTSGKDFGFVFQLALVDDYTFGSPYRQE

YTAEVEQIKWSSSSFEPQSCLVKRKLPDAASFGDSARRRPTRSDQEEK

>contig36801 Frame-2R

MAEVAALRAENALLLKDVDRKDEELQRLEDQVNTHKARITGLEQALKQEQNAGMERLKAK

QDLVVAMEKQIQQMQLRRRSSVAAALAQAELEGRDTVGFGLKERLKTNRESVECSDEEPD

TPPGTPPPIASGLLPPEDPTADQTIRDWSENRKIKAARSYDEALDLDRLDELIRKLPYEH

QEGASRVLMGALDPDSSAEPVYESQIVLRHLSSERQAELREYLVPL

>contig36896 Frame-2F

MSYERLYGHGGECAGLQHAETRYAWFYKLLANIEDIINAFFPIHWRMARRMCIRYCEKTR

THLLAQIGALAPDEMDVTRLLKSLQRALMFERDAVRRFEETADEEDSPQYKIDENGEAVD

PLPTVEITTNYRRKKCEVGQKALVEEMKKNCQLVDDNSRSLPTIRGMISCSFDPFMTAYI

SLERKNMEQMINEDMSAELVDWNGQLPVFSSSVNMFAYIRNSIKRCTALTNGQTFFDLHN

EFKYCFRLYSQRLLSKLPPSASAGLSGGLEISSCNANNHLKLRDKQEDELCFVINTAEYC

AETLPSLEEVIQTKINKAFFEAIELSEEVDTFHFVGAAAMKCIVAGLETSLERELAALYK

TNWQVWETVDDESLYVTRMGEKLQVFVQRLRQMLSGLYFTNFCDKFTASFVPKILQAVLK

CRKMNQVATQQLLLDVYALKTLFLQLPVLSQDGNHISSVSTTTITSRYTKFVTNEMATVE

NVLKLIGTPNDMLVESFKIMLPDGTAEDFQGIMVVKGLRKCEQSAYLEMLGMQCKPTGKI

AEMEGKVSDMTENWRKNMQNLAKA

>contig36908 Frame-2R

MLSEWQLFFNNYDNYWLCGMLSTISSLTIRVRRFSVCCCTHSPNRYVGHFLPEDRLLLQL

RGHGRFI

>contig37297 Frame-2F

MVHNPPIEYEKVGSPIFDLRRSSVTSDCINKNEADVESDEDDSYSKKTLPEKIVWGLVYF

IASLAALYFFMVAVKLIGEGFTLALGCDTKGAFDFADNPVAGLMIGTIATALLHSSGTVT

SIVVALVGSGGMTIRQGVYVIMGANIGTCITCIMVAFGQVGDRARFQRAMAAATVHDMYN

LWSVFVLFPIEIVLHPLEKLSLAMSNAQTNGGAFSSPVDTIVNPLAKEILVVDKKAIYAV

ATGSEVCEPSQTFVEGGMFKGSSMSDGAIGSITALIGFCILVCSLLTLVKMLAKVFKGPT

KRLISKLLNYNGYINIVVGTMITFCVHSSTVVTSTLTPLAGLGVISLEQVYPLVIGANLG

TTGTALLAALVTGKSDSVAIALVHFWFNFFGILLFYPIPITRRPILSWARSLAFSSAAWP

LTAVIFLVVLFLLAPGILLGLVYMCTADSAVVQVIGYVLGTIVVVDLAGFVFWYTRKGGR

AVWHAFLEKKRLEREGSAESHDPTMTPPSNFALQVV

>contig37503 Frame-1R

MWHVLSKPIPGFSEVIDVIEA

>contig37680 Frame-1F

MQKIGDGESSASIAPTSTDFANDTCKPKNSSKKRSNAGWIWTLTKEERVPLAIGVTGMTI

ASAMNLIFPRIMGKAIDVAAGKPAPGGLSRKGFVVVVFATFVTGSVGSFLRTYSLGMVAE

RIAAKLRKKLYKVLLSQDLLFYNDRKVGELVTRLSSDCQQTANAVVDVLSNGYRSLNSAI

GASCMLMTISPKLTLVSLTILPLVGTGAMLSSKFSSRLAKKHQNSVANMTGVAEESLNNI

LTVKLFSAEQNELNRFEKINKIILANSKRAKRARGLFMGGLSLSTNCSLFSVLYFGGSLV

KSGELTIGTLTSFALYSGFMGLGFSGVSSCLSDIKKTRMSSEALFDLLSLPAAADGEGTL

AAVKGHVCFNNVSYAYPSRPQIMVLDRLNAEMKPDEVVAIVGKSGAGKSTLASLISKIIK

PTSGSVTLDGVDIATLNTSWLRSQIGVVNQEPSLFASSIAENIAYGCEIHNYEQLVSAAK

EAYAHDFIMKLPNQYKTFVGEKGVELSGGQKQRIAIARALYKTTNILVFDEATSSLDGHS

EEMIRRAMLQAAKNRTVLIVAHRLNTIKHADRIILLEEGVIAETGTYGELNQEGTRFYDL

AHNQSSFVIDTADL

>contig37855 Frame-0F

MGSQPGQSYRPPTSSYVEEFARVKAMMMQHPDLIPPPMEVLRISMSQSAASQQNLAMGTN

AYMQQRGNPGMNRGGASGNAAYAQYGNQNMMMCGPQQNPQQAGMLNAARMRAAQLAQQQA

QQRPAVIRTPGGSNVAQSAWQSENDLPLRRKMIGKIVSLLQQRKPDAPAEWIRRLPDMAR

RLEDSLYRTAKNRDEYGDFSSLKTRLQHLAVTMGARAQHKTVGNPRAAGAASVPGNSTEL

VGNATLMASNAPSGMTMNASTGAMGAQGHVVGNIPYGNRLTQQQLMQQQHLQLQMQQNPQ

MRQQLTPQQLQQFQEAQLQRRQLQLQQAQQQAQMHRQNSLHQQQYQHNQAFQRQNSMRQM

QQQMQQRQNPNYMQQQQAQVQAQARAQAQAQVQRNGASNNNANQQRMSSDMSLGESSDFL

NLDLSSSMLGSDDLHDDVNSGLTGGDSMKNGTNEPANMGGQKRTLSQSQQQMAAAANAAA

FKRTKVGGAVDQAGNQPGVAPHQQHSGATTSGIQVSKPSQTSMQKPVTSTSGSSKTPPMS

TVNAK

>contig37994 Frame-1R|Blast-conserved oligomeric Golgi complex subunit, putative [Phytophthora infestans T30-4](gb|EEY66064.1|) 1e-107

MTPVQRKEHTPDVILNSLEVTSGYIEQLKSEFENELPETFPVVPQHIVTCLNGLEDASVE

LQQLLFASRKKLLKLLEPKIASYLYTLLSTSSSAASAASVLAASATGLSSSGSAPSRRNP

FQYELTEAMFTLNEANDPFAHSFVRGLRSLLKSFRGYLSHSNYCAVVHGVASISATQLES

WFLSHY

>contig38014 Frame-2F|Blast-phosphatidyl inositol kinase (PIK-G1) [Phytophthora infestans T30-4](gb|EEY65922.1|) 1e-120

MKASRASCEGYLTFRTSPSSPPPMLRRYCFLVGTSFHYYSTQEDAYHMLRIKGEVDVLGV

QEWDGKGNMHIYQHGFLFATAQSKVFYAYADTAMDKEKWIRAIQTAVVTTAPRLVAAFFH

QATLDQLISPVSTFTVPSTETDVTCKCPDCTRVAAEAASTGSVLPAVAVLLYKCNSCDNL

FCDKFTGHKVPLPQRSHYYAKRVCDRCYEAQNYINYLRAMVERLKAGICLYPKPLNAD

>contig38256 Frame-2F

MMVFVSRLYLQKMIRCGTIQISSWKKVRLLQNSSVQQCFYLIHLYAVIIFTPTKNLLLYP

ATMTQLQVQSFLSMRKSVSWRLWLLNNLREIYTRGNTSYKVRRLRHWNA

>contig38322 Frame-1F|Blast-carbohydrate esterase, putative [Phytophthora infestans T30-4](gb|EEY64329.1|) 1e-105

MNAAELFNVKDKVVVVTGGGRGIGRMIADGFVQNGAKVYIASRKLEACQATAKELNAKGP

GRCIALKVNLTSEEECKAFANEIIKRESRLDVLINNSGDGFESPVESTPASIWEKTFALN

VTSAYLLTRFLLPLLDVAAVTSEGARVINVGSVGGLVPQKINVMVYDSSKAALHHLTRVL

AAKLARRPNGGHILVNAVALGYVPTRLAEGIAHVTGMSFHNISQTIPLERMGDSSDMAGL

TIFLASKASGWITGQVITSDGGTIGAAEIGVGPSKL

>contig38744 Frame-0R

MLNTAAMEKMITEAAMESGRMVTEAAMQVTPHTAVIMEITVAMQPVGLALMVQDLIPTMV

IVQTDTDTVTVITDLLVITPVRLDTVVKTRDTIHIRQITTA

>contig39538 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65940.1|) 0.0

MDEQKPTGVSPLMVACSVGNVEAARALMMFGASLDLEDVHGMTALMVAVRDGHLICVRLL

IKKGARINLSRNRNRGTTALHIAARGGLEKCCLILIRGGADLETQSPNSTTALMEAARAG

NLGCVTILVQEGANLFAKDREGNTAEHLARLAGHTDIEDLLREQAESESVKNHRRKIEDT

VAMADSTLQDLLQIAKNNSMSVDILYREMIREHKSSVWLEQPRIIYEVFRLLTVPVTSSE

SDPTNDPYYGKYTVQHFCSEVALWYSPKIFQKGYRPGGADWTPNAGDAYDITTSSGYLKV

LFNFVCTADSLDEVLLVLFCKVVNHLIVNQNLGELVWQFLAEDGAFVVPWLVCHIGLDSI

RDTVVWLLYSDMSETGQINVQKSRMFACLFTRLYSWQRTLGWGVGTAFQRDSVENICSLI

NYIIYPPSVYIMNNIATFVENTDHSLPLITDQHFPLHHNELLKSLLIYLLNTTDVSFGTL

LDLGFAEVCRQCTHGCTMLVIREGGALSIMMMLLGTLGYHKKKRDVTGVEGLLKTVNVYV

INALIPRIETIVKLCRAVVTSDVPALRVMSIIHNPGSIKAVNTKGSAMLHIITFLKRCVF

LQNGDIDRLLADFGLMPCLLACYGSHPNNNMLHHTLTDVIRFVLMDPDQKRLPSSPLLNS

LFIEDANILDFVIRAYDENVQYKGHMTTIANSVFTLTNTPNRKSESATITCQDVVRKFTS

QHQKWVEFEKVLAEQNRLEMLPLGQRHAPLCHGCLKLKQSAIEYVGTALSNADVDEYTGY

LETIFSDAASHYCKVTYTDEFITGFMYKKDKIHDHIPIPEPTRVSSFIQFPVPMPFHALT

FTITFFGLCQVCDKLWYCDTLQSANWTNRMKWIIPTSVRKWYSFGVTEGPGSGAHGLQFS

SKGYKNFIVLTDTWGRQEQWMHAIEDAIQSLTTQMSRGNIESAMAIEIDNEVDADEFDVM

RIKEVTVGLNNVGGLLIGSAPKGDLSSRCSQDDESARRPRSNTLTSIESDT

>contig39651 Frame-1F|Blast-mitogen-activated protein kinase kinase, putative [Phytophthora infestans T30-4](gb|EEY59831.1|) 3e-60

MAPERISGGMYSYPSDIWSFGLAIMACAIGKLPVSSNNGYWGVVHAVQEEPAPRLEDFSD

AFSPELSDFLDQCLQKNPMHRPPAVRLLEHPFITKNYSLKDQASVCMSPKEPFATAKAME

RSRHELQTIAEKAELWCHDHADA

>contig40295 Frame-0R

MRDKMINTIKTGLGSRKHKVTIVFAERRYYAGFTNFNYY

>contig40628 Frame-0R

MVLNLLPPKDVKESSRILYEKLSVYRRQNRSATREIEDLQNAIKLYKNAITDRDDAIANY

KAMLLKLSTQLPHRIHFKHVNDELMKQLHQTKRIIALTFSNLLDCRALPASARSHLKSMH

GDHLANLKTQLQHLQAEITHDPIAPTSQSTV

>contig40761 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57851.1|) 2e-40

MDACLKNYENCWSSTPITPTISTSSEVETPRRVAKWDSIREKCNNCHHIYLKTLSKHLGF

CSVDCKSNMAYLQKVNRTIRAMKDAVDERQRPRQQSRKEKPVMQQPTDESSRLSLKIARN

IKHAQSFAEFDREARATSTCDVEWSFSVY

>contig41267 Frame-0R|Blast-beta-glucan synthesis-associated protein, putative [Phytophthora infestans T30-4](gb|EEY62157.1|) 2e-10

MRQCITFERNMQQRATPNSLGRRQNKILKSRERLSYCIQSNGKGIARPKSMSPSIITSCR

VEKFSCITFAFNKEGLAAMALQRLWVTSSIMWLAAGYFTWALKMNRKNDHQLATQSGLKM

WVDPDTPEEHYSWTTSRGDTWDLVMSDEFNIP

>contig41890 Frame-1F

MLDELFTSAMHSTWDQRRQLAIDISNLAPPDLPGVLLLIRKYAQGLEVHELLPHEQRLLP

WELQQQPMPLKESLNTIQLRCDFLLDHADDALLFQLRQYVDNCHMPHFVPKENCSICEGL

WSCGRVIFCSNDACPVRLHEDCFGVILREQKNGPWLCPSCLLGKQLVCAVCMQHGGPLKP

LAISESSSADEQKWVHVLCALAIPELCLRDVPTMEPVDGFEEIENGRFRYLCAICRKRGG

ASVICESEGCNVGVHPQCAADAGLMIGNEGNLLGVYCDKHLPASRIPGAKRWISDEDLVE

EIMSEYSIDEEVDADELDTPHYSDVERYAFVLESTPFLNCYQQLLGDTATLHYKSISLGA

KDIDHKIFLGVKIIANAYVPPAMVVQGMKMQRPVVFPSPAIYARKERLGLPKFPEGTLVV

GAIVDYLAVAQEMWQRARVVQWDKEKKMHLVHIVASNQKLWTKLDVKNTLILYLPDEENL

LDGPIVKLIRPVTKGVVQWRPKPRSFES

>contig42820 Frame-0R|Blast-predicted protein [Physcomitrella patens subsp. patens]gb|EDQ59858.1| predicted protein [Physcomitrella patens subsp. patens](ref|XP\_001775388.1|) 6e-09

MDAGIPMISVVTATACSIFVDGNMNLDPTSAEEEKAVSWVTLTRSSTSNGVLSLHHKWIA

IRRAILCMFRSVPEGIGKCGSILSHRPAKKVSTRVR

>contig42994 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62288.1|) 1e-80

MERDEAFVVVLFYKYVRLSETPKELEVFAATQEHLCSSLGLTGRVRLAQEGINGTLGGSI

ASVQSYMDTMKQQPLFSNVDWKTSKSHVLPFPALQVRIVAEIVALELPDDAFDLSLRGHH

LSPEEFRFEQLNADPASIALIDVRNAYEYNIGHFVGALNPKTRRFGQFPHWVRHELPMLQ

QKEKVLMYCTG

>contig43126 Frame-0F

MVHYTCFHIQLVIIICPKSGDTSYYCRITLKLYRGC

>contig43676 Frame-0F|Blast-Rab21/Rab5 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY64754.1|) 1e-53

MEDVGLDRKLVIIGPTDVGKTSITMRYCHGSFSTPTSATIGASFLQKRVIVGDDSGARRK

LTLQIWDTAGQERFRSMAPMYYRNAKAAILVFDLQSEASFEKIQEWL

>contig43742 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61639.1|) 4e-89

MKSFLTSHVIALATYVSSVSAHGYLSQPKASYVPGSIYTDYTSLTNSSVNKGFDGGVYNG

APANNYKEFSKHWSATGYKSLRDMVDPIAPGYGFSLDTADPVDVSSYKEMWWQNNELKEG

FLASHHGPCEGWIDNKKVFHYDDCVTEFPENPAKIPTDYSSCKSSKCLFVFYWLALHSPK

WQIYKQCVPITNGG

>contig43801 Frame-1R

MEVEASDELPSHASSRPMAPSLQKGVAQDFIMKYNIRQHSSSLDNERLWRPASGFALKHK

ADLEAKRLLRERKQQRARQIQEGKNWRNTDSAKGSKPNDHHVVKDVSHDCRGPDEYYLAT

DISPDVPSDLLDFDLSLSVDGLSVSSECSLSQEEIEATEVTRRKRRQQMKRRQNKALSDT

RDEAMTGIPHPSLLGKVLFLRRSTLQRLADELYLKKAIAMHSERKVRANPQSCNFPGAAS

FADGLLRKTKSTSSMAH

>contig43896 Frame-0R

MLVTFNLHFDDDNWKMMPKV

>contig43908 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54990.1|) 2e-12

MQLTAWTRQSPLSRRQKFDRINRLVNKSTIASAGT

>contig44134 Frame-0F|Blast-Resistance-Nodulation-Cell Division (RND) Superfamily [Phytophthora infestans T30-4](gb|EEY58756.1|) 1e-112

MTENVSIIGSRMRFQLKALRNQSMYINSYYYLHKVTRQWSTRHNIMAFPYALVFVYEEQY

TYIQGVALQCMLLALAIVFGAVFVLFNGCMRLSAVVTLCVFSMTFSQLGLLYAWNSIADS

EAKTSINAIFVVNLLASIGLGVEFCIHLAHQFAFSRKHYFRKSGNDHTRYALTSVGASIF

SGITLTKCCGIGVLAFAPSMLFRVYFFRMYLGIVLLGCFHGLVLLPVLLSLLGQPQQYFD

DLNALLLSETRDEGRLDKVNLLDEQRS

>contig44343 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66707.1|) 5e-62

MTPCPCLDKNKTSVCAPRYGKCEKGTRYIPVKLLDVAGLIPGASEGAGLGNKFLNDLRHA

QVLLHIIDVSGHTNEKGEETVGYDP

>contig45025 Frame-2R

MGTAEEDLLNLLWFPATKPKEDFVTDTGISYATVLALTEESLKCGETVTSPVDVDTLVIE

GSTYLKMPTKEVKDTANRTRITPFAHDSTTEAVETNATEIEAPYPHETETPYPHETEAPY

PHDTETPYPHETVAPYPNET

>contig45050 Frame-1F|Blast-anaphase promoting complex subunit 11 [Arabidopsis thaliana](gb|AAL13436.1|) 4e-33

MKVKIKRWHGVATWNWGVEEECCGICRYAFEACCPDCIMPGDGCPPVWGACNHAFHMHCL

MKWLESLQSMRQHCPMCRQDWKFRN

>contig45447 Frame-0R

MPKSLTMAALSFNPPLVSSIQTIPVEFDYDYSCPANDLEAVVIFGMFLSYAPNTAATYEV

VVLLNTYGASKIAGNFVNTVTIGETLCDVYRSEDNTIFTFVVKTPTFDLKADAKLFLNNL

PINSNLVDMQYLVYIYGGSKIYRGTEAQFDVLNLSVV

>contig45911 Frame-1F|Blast-endoribonuclease L-PSP, putative [Phytophthora infestans T30-4](gb|EEY61980.1|) 1e-84

MNVLVRRTKSRSLASAVRNVHIERKIKELGYTLPAVAEPKGNYRTSVRSGNTIFLAGHLP

QPAGGELILGKVGKDLTPEQGYEAAHYVALSLMATLKHEVGDLDKIKRIVKLVGFVNCVE

GFTQQPAVINGASDTIGKVFGDRGIHARSAVGTNALPLNVAVEVEAIVEVEE

>contig46129 Frame-0F

MGGGFVWMQSSQSESDACRRRKKELQDITNQQTQGDDYKSVDVLHVPMKYVTSVQPSSLQ

KRAQGVEVILMGHNRFEFTFMPGPFACPTHRDDFLQALEKQALDKQAHDGSKYSVKCTPV

AAERHERIKPKVKTPDETATSQKVKFRRLVRKHTKLEAMSVEAIDIAKTVHAGTYQLGAL

AAKILKYSEGAEYCTENVEKLADNLKQIKQESQEADAHRTTHMKVNYSKNIDGLFEYSEK

VTGMLMSSAAYEQRYLEYLETHEINHVTKMHPVQDKKECQHILKHHINELAVSTESAKTL

YMETLGIDISSSSIVDADFFRSVSNKSSGSQICKNDKTPFRTAVDNARIKLWNSWAEEFT

QVFQTTNLEPR

>contig46244 Frame-1F

MFRKSVLALARACTQPHSTVTPSCTASYRLSRCFSSAKQTQRHVIAALVVNQPGCLAEIA

NLFAARGYNIDSLVVGRTEVQELSRMTVVVNGTAQSVVNMKKQLEDVVYVAVVNILSSMD

AQKSFVERDLMLAKVSTAEEGSRAEVVELANLFDAKVIDVRAHQIMVQLAGTPGRIEAFL

DLLRPLGITEIHRSGVIAMARSTTVTDNLGDLSTFEGATRTLLDKADDDEIDISRLPPG

>contig46514 Frame-1F|Blast-pol protein [Phytophthora infestans](gb|AAV92918.1|) 4e-38 NOT\_ORF

MSAKGICADSKKVLFICSWPAPKD\*KHLRQCLGMAQLPLSMLGTFRQ\*FIRCSSY\*RRTP

RKRWRQEYQDGFDIMKTKHSTAPVLALP

>contig46859 Frame-2F|Blast-patatin-like phospholipase, putative [Phytophthora infestans T30-4](gb|EEY69210.1|) 0.0

MVTDCYSKRQNSSAVPPSLSFSFACGGWLKMYLFGVAKALQEFELEKDARLIGCSAGALT

ATGLALHCDFVAIRDYVLQCIIPKAHVSLASYFRVRTYLRDTLLCHCRTHEFETLNKSQQ

LTIVYTSLTSMKSRRVTTFESTEHLTETLLASCCATPIAGLPFKLNGEWVMDGGMLDFQP

VYDSKTVTISPFYCVGADIKPSVYVPMWWAMIPPGVRDVEWLFDLGYEDGLKWIVKNGLA

GSHKNFVIPSKSTNYANGWNTTVGRVVGYRACESHILDALFVGLFVCLWRPLAFICLYLE

LYIQAILSGGKAVVFGAAAKLLISNIIMASLAMALATLGLQNTMHFLLSLTVIGIFLGGM

VLLVGGLQQAGAMASADWKRCRSYMRSITSLSLFLHSMPVIGPKVQIKRHEFLLKHSLVY

RVAMHFV

>contig47531 Frame-1F

MDAFVLASSCDGNRSKINVIRPNNSRQLAATVEELSRFFVISTPEKHCVALTPYGWRGKM

ACFISKLMR

>contig47878 Frame-2F|Blast-kinesin heavy chain, putative [Phytophthora infestans T30-4](gb|EEY57642.1|) 6e-54

MAKLAYLKSDLEVKANECEELRHLLAKCCERLCISPMPCDSTTSTANSKLRVKTTSEKID

PYNKKLDQVDCVPSSEVAVLDANSLAIENEHLRQKLAAKDEELRLSTLQLGKLNKELTSR

RINCNAQMEKPPNLQNL

>contig47892 Frame-0F

MSQFGRAPVSMRAELATSALLTSPAEATECIHFVNNCQQNCQEVKSAFLGEASFAS

>contig48039 Frame-1F

MLFGMLYVLNDPSCIIILVRKLIIATYNTMYVAYNTNNAHKARDMIHSQRACPCELILSH

PSTYLDALTVIDGL

>contig50478 Frame-1R|Blast-neurobeachin-like protein [Phytophthora infestans T30-4](gb|EEY55313.1|) 2e-64

MEARDRDDNETNDWRPYFPIANELDKRQACRHEETWDTRSTYSSVVSRNDSERVVWAASE

VEENRMVALMQDVRNREQQRSLTAKSIQCMEKVPWTHELWLTHELTFRSQHEYKSLRDIA

PATLLALHETHVWRLGGYETPFPSRIRQTIAIDVHLSAAKLWAKEVHETLGQDDSTPLRR

ETDGGTEGTRLTEAFGEQLLVRVGRVVAQQRGGEIRDITSEDRMV

>contig50517 Frame-1F|Blast-trans-2-enoyl-CoA reductase, putative [Phytophthora infestans T30-4](gb|EEY63336.1|) 1e-159

MISTVAKRLVAQGKRSMSTVRYSEFGHPLSVLQMEADDKDVALTKGQVALKFLAAPINVS

DLSQIQGAYAIKPTFPAVAGNEGVAIVTAVGAGVTTVKVNDRVIPTSPGFGTWRSKAVAK

STEVMKISEKITIQDAATLAVNPSAAYRMLADFVPLHKGDVVIQNGANSAVGQAVIQLAA

LRGLQTINIIRDDGDYDVTVTHLKNLGATIVCTAEYMGSAKFKELVSDLPRPKLALNCVG

GKTSYEMAQVLAKKGVHVTYGGMSKEAVSVGTGSLVFHDITLKGFWLSQWVHDSSVEERT

TMLSELAKLVETGKLRTWIQTYKFADFDDALLAAIHRTTKRKVVLLME

>contig50706 Frame-0F

MRKKLDHLILISKIRARLMQKVYERRAKKAAEAYGDAGGGPNDVTGEIEVQEGESDENEV

FDFQDLQLSTSMNTPSITEEDKWPQKLDFLNELHGRIGLPPIDHSLREFELLTNDLLIEE

K

>contig51222 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65749.1|) 8e-12

MANMTEVVSRPQDKLKHHLIDDCPHAVALTMIQRHRNNRQRFDSADYEMSKYGSSSCAGC

S

>contig51356 Frame-1F

MHVYYVSSLVSHRQNFSENFATTLMHQVTGFTPRGCPWTRQLLLRATH

>contig51529 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61504.1|) 1e-133

MVLNTQEPDEVRVNALYSIIVQDDVDFVRGLLALHGDGDRKKQGVSASCFNDMSSRMKLA

LVELMPVCQPSGCVDFITLMSYDVISSMICLEVKTNEMAWFLLQDPFTTLSRFITSTQEL

EVVVVSLLKITLDKMNEMLSAEMNLRFNEGTPSRESILWRNAESLASLAAAVVLHYDPDT

LGQIDPSQLLNSSGLEDEADVLVFWKCERTIWHEAELVDSILGIWQHFASHFHSNSDASF

ARRSSTAHRRHSAALRPMENGLPSPPSLSSAARTNTGP

>contig51644 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66962.1|) 9e-18

MDGQPSSIGFLQITTSIENGIDSVAVEKYARLFPNGSRFIALVPNKETCDNFRFVPADPA

TQVSLDVAYISTLSF

>contig52238 Frame-2F

MRRKSARIFRKRRLQEASVPESSRWRRTPRPESSSSTSYESIVWLAPKGSRQKTSSRDRT

LEDTHPLT

>contig52740 Frame-2F

MTFPDENTRVKHVNTDALQAAMDERAQYQVAKAESDEELKDEHEAIKLSSCVDFSDVQED

ELYYIGTSGIKVTD

>contig53549 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56303.1|) 6e-55

MDPNSHVPPMSLMSLVDILSQIIRLEIAIDIQENSLRVRAPNGVAGSLDCMHLVLDGKAR

VYRMLPSGLSTCAGVGVLGDYFGEMRVDDPNQLVILLELFYWSLDDGNPSFHVRMCIEGS

RNGQLTGTGDILATTGLNLFSADEIPHVREMSLRAKRELVDTAIARRHHGATPPKDTHIM

PWDEYGRFRLCYHK

>contig54049 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64463.1|) 1e-18

MQKSMLFCLECLLKAKHTSAREVAIDLQKWHLLAQN

>contig54153 Frame-0F|Blast-ryanodine-inositol 1,4,5-triphosphate receptor Ca2 channel (RIR-CaC) family protein [Phytophthora infestans T30-4](gb|EEY58028.1|) 9e-34

MYREFSVLQLCGLWKYVQSLWNVLDMLQLVLLFAFLAHWVLFVVKSENIRKDLHRVGSQN

CSVPANEQDAARACFIDIAPLASLSRAVTNYAL

>contig54386 Frame-1R

MPPTSASTQMKTAAASLNSSTVSIASQFDRVASVAVAI

>contig54948 Frame-2F

MSESSSSVSLDELLRDENCTELALESTAVDRLMDGYCLVEHLSHKATRKPRRRARTVDAD

TELVDLQEDEQPEPMPRCCLSDTEEDTFQFHDQKQPQVLRKKHSNTSSSSVVHVCRCSKL

SRSSDVENEAYDPHSATREYLD

>contig55037 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67097.1|) 2e-27

MGKLSWQLSPLHIRHDAACADDGEQQCVGLSLPLGISEDILLIGKKALSTQHLANP

>contig55172 Frame-1F|Blast-aspartokinase, putative [Phytophthora infestans T30-4](gb|EEY60689.1|) 6e-22

MSLMASSWVVLKFGGTSVSTAGRWRCICDQIRSHLESPSSPRVWVTISALSQVTNKLTRA

>contig56094 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62332.1|) 1e-06

MTRYVRLLGARGLSNHAKSHVHMPETAMLSNN

>contig56155 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55164.1|) 5e-29

MNWPIRTRNFRLGQWITRVRSGQIVLSSKLR

>contig56573-0 Frame-1R0

MPPFKTIPQDFEWTNSLVFQVQS

>contig57369 Frame-1F

MRHYDARKSRHISAIKQKVSIDVSPHAIVPKIVHPSLKPLCSQEPVA

>contig57905 Frame-0F|Blast-crinkler (CRN) family protein, putative [Phytophthora infestans T30-4](gb|EEY67040.1|) 2e-06

MDEVKLLCAVYGEGTLFFVKIARDADVIALQTAIVNEKKGV

>contig57970-1 Frame-1R1

MGSTWATTTLKVDDHGQDDGV

>contig58074 Frame-2R

MVFPVLFLLAAFALGDAGGTSMFDP

>contig58203 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65892.1|) 4e-06

MRAKTMEEVPETPGGVTEIPNDGSFLKKMLALQQV

>contig58579 Frame-0R|Blast-Type II (General) Secretory Pathway (IISP) Family [Phytophthora infestans T30-4](gb|EEY67050.1|) 3e-14

MMGFIGFFVKLVHIPINNILVGGSA

>contig59091 Frame-1F

MQKEGSSLEQLRKERDEARSERDALLKQVNKLNYRVQHLKKHVPVPLSADMKL

>contig59217 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61946.1|) 2e-08

MSHIDSALKRGEDAAKKIAAKIEEKSQ

>contig59378 Frame-1R

MKAYPFPVLCLLLSLMLYAGLCERNIKR

>contig59583-1 Frame-1R1

MLKKRSKRWRRRHKKSAWEVGARFLSFIYVDLLAWGFATSIS

>contig04449 Frame-0F|Blast-protein transport Sec23/Sec24-like protein [Phytophthora infestans T30-4](gb|EEY56434.1|) 0.0

MSVSVGLLEATFRGQGARIMMFVGGPPTVGPGAIVSRDRKEDIRSHTDLQKDKAPLTKKA

LAHYNELAARCVASSHVVDIFACSLDQSGVMEMAACVQKTGGVIVLADSFGQSVFRESFR

RMFSKFSEEAADCDKDQLTMAFAASVEVLTSREFKVAGAIGPCAPLKRQGAAPKNVSEVE

IGFGGTNAWSMGGIDPNTTVAIYFDIANQSPLAPGKARYIQLITRYQHASGRYRTRVTTI

CGPWTVDSNDTVSLGRGFDQEAAAVLLARIAVHRSDQGEEQLDIMRWIDRSLIRLAARFA

EYRKDDPSSFRLSPEFAIFPQFMFHLRRSQFLTVFGYSPDESAYYRHCLLRESTTNSLVM

IQPSLLSYSFNGPPVPALLDAASVRSDTILLLDSFFYVVVFHGDTIAAWRDQKFHEDPAH

ENFKNLLEAPQADAQLIMDSRFPVPRYVVCDQHKSQSRFLMAKLNPSVTHNSMDGQGEVI

FTDDVSLKVFMEHLMNLSVKS

>contig04540 Frame-2F

MSEIRAKQLHDAMTAASVMPRVVTQEEREQQRLETRQVKEKKTPLPTREDDLFAAARLYR

YFSTIKQQMMVEILPCYEADKGEMPLFKCTIVHGGTGDVLAADVRAISKKLVKNEASKLA

IEKLWSDKQKAGTLTLEDLTYLEKFQALNASTPQVDDKGNEALKGAIDNEPQLPMRVTWL

DRQLQPVALLNQLTQRHALEACFDITDVSPSKEVTEFNCTGILNGETIATATGVSKKKAR

NKVASLVLAAAFEKNLIVKYDEPTDEKKEEKKIVDGKTLEMT

>contig06722 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62925.1|) 1e-18

MFGRFFKNKEDGKNGPPGHQRQGGQNGTIDDPPVGGGFFNLPPPVAKPYGTSNPTALNNF

VPSSGTGGYPPSVTYGNSSTQDNTAVHGSDMFGGMAVREPSAAKPIARYQPQHPNQYGGN

GGAPQSAANAPHGTSGNSLFTGLAVASVPMVS

>contig07066 Frame-1F|Blast-FKBP-type peptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-4]gb|EEY63710.1| FKBP-type peptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-4](gb|EEY59149.1|) 1e-35

MGFQIDTIKAGDGENFPKPGQTVSVHYVGTLTDGTKFDSSRDRGRPFQFELGAGQVIRGW

DEGVAKLSKGQIAKLT

>contig07192 Frame-2R

MAEGGRSTYIPPHMRGGGGGDRGRHDEDRRGGNEDRRGGNEDRRGGNDERRSGGGGYDRR

GGSREGGRSGSHERGDAPPRATNSRWSGFESDRRDDRRGGYGDDRRGGYGGGYGRGGGGC

GGGSVRVNEMGYHGDVRRNERLEHELFGDAKSSGINFDKYDDIPVETSGENVPDPVSEFA

EEQLGPEVIRNLELCKYAKPTPVQKYSIPIGLAGRDMMACAQTGSGKTGGFLFPTLAAML

RVGGTPPPDVGHGRSRKIFPAGLILSPTRELASQIHEEAKKFCYCTGIAPVVIYGGAEVG

RQLRELERGCDLLVATPGRLVDLMERGRISLSCIRFLILDEADRMLDMGFEPQIRRIVEQ

EDMPRERQTFMFSATFPREIQRLASDFLRDYIFLTVGRVGSASKDVKQTVEYIEQYDKED

YLVRFLNQVQDGLILVFVETKRGADFLEDMLCREGFPATSIHGDRSQREREQALASFKSG

RTPVLVATDVAARGLDIDGVTQVINFDLPNNIDDYVHRIGRTGRVGNIGNALSMMNEKNR

NIAREMYELMAENGQEIPAFLDQMANSGFRGTGGRSGRGGRGGRSGSRFGARDFRSEDRG

GGNRGGGGSYGGGGGGYGGGGGGYGGGYGGGGGGGGGSGYGGGGGRSGSARGGEDNSAW

>contig07938 Frame-2R|Blast-luminal-binding protein 3 precursor [Phytophthora infestans T30-4](gb|EEY57932.1|) 0.0

MKDADLKKSEVDEIVLVGGSTRIPKVQQLIKDYFNGKEPSRGVNPDEAVAYGAAVQGGIL

GGEQDDLTKDVLLIDVVPLSQGIETVGGVMTKLINRNTVIPTKKSQTFSTYQDNQPAVLI

QVFEGERAMTKDNRLLGKFELTGLPPAPRGVPQIEVTFEIDANGILQVSAEDKGTGKAET

ITITAEKGRLSQDEIDRMVQEAAEFADEDKKVKDRIDGRNALEGYLYSLKNSVEEKLDDK

LEEDDKDTVLTAVQDAMDWLEDNQEVDKEDYEAKQKEVEKLVNPIMSKVYQSGGAPETQD

DEEDEDERDEL

>contig09068 Frame-0R

MAKGFVDFFALARGCVTNVCCGTNDAFVLDVAGRRVFSWGTYLGGREVG

>contig09132 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58112.1|) 3e-35

MLRPSLRSYFNAACKPRPGKQHKKKNHFLTAGLPLVLFIVGGYVTLTQFVGGKFEAKDHL

IKSQSVHTFNLEEEHTKMTKKLALDDFELKPIPKPKDL

>contig09653 Frame-0F

MDTPLLTGHPHALQLSIYEKSVMVAFYWYYPPSQKLIQAKVNNFLPPKTSLHDASFQLNV

SSCSIGCPFLSLFL

>contig10996 Frame-1F|Blast-cleavage induced hypothetical protein [Phytophthora infestans T30-4](gb|EEY58548.1|) 7e-35

MGVQHLVRTTATALLPKNLVAFSKVSTCNQKASLEIVALISHVFMKFPLPSDTFPTLSLP

QTDQDALKHLAQAFVDDAIVDYRTFRSPQLKGHVDESNWKFIKKRDGLSSYWDRKLLERE

LGGPASLRNSVPGEIGLHVVYKKSSRGTDRRNDPGIAPRFNVWHA

>contig11047 Frame-0F

MNLRQIGSANMVRSDALGTASLNIRPLSHLEERERCSYQTVVTCQYSINRGYCVRV

>contig11191 Frame-1R

MKIHHFNDKRTLLQRVRQCGGTCDPFSGARE

>contig12907 Frame-2R|Blast-PREDICTED: similar to pol-like protein, partial [Hydra magnipapillata](ref|XP\_002165882.1|) 2e-08 NOT\_ORF

MIAAFAELNRHKAAGPDWLNNDFYLDK\*ALLASAMVAIGNEILDGKDPPPSFLNRLIIPL

RKKGNSADVLTTGPIYLL\*TG\*KIIR

>contig13728 Frame-0F

MSEKEEGKSSGDEFENRERKSSEELDTRGIAAFEEPVEQPKLKQNIHSSTQISERLNKKD

IYNFMEKELDFTPQFVPSADSPVRCRFYSSMAYTSAKKVILFLSDSGPLGLWKQDPDNKP

LTKDHKWSMTPYFSRAQDEGYGIVVCNPFSNNAMVYEAGGFEREIPVPNSATPKEHVLFV

WDQFMSNCKGQISIIAYARGGALVKSILETYEESSRDKIHRIALIESKHEIDHNESPGIL

ELLGRRSINWEASYEPLGAQIVDSQARVNCVCLSLGFMPSQEADNTPKTLEKAEDPAFAF

IDANPSQPGMTAVVKHVRLELRKRKTVVKPVARTRRQSNIIVIGETDGDESSDVSAGADE

GKHKIKTNGSSLDSEDDGKIKATYYLPKPVPKPKRNPGFGSSGSGDKQQRLISDKDFELL

KVVGQGGFGKVFLCRKITPPRQGEHYAMKVLKKQQVVSSGLVNTTMAERKILTDISHPFV

VKLHYAFQSESKLYLVMDYLSGGSLATHLRRRRKFPEEWARFYAAEVAAAIAHLHSANII

YRDAKLENVLMDHDGHVRITDFGLSKVGVSGLKGATTFCGTAAYIAPELLKGMAYGKAAD

WWSFGILLYEMIGGKPPYYHRNRDIMFQTILKQDWVTFSPSFSDAAIALINGLLTRDPMM

RLGSGPRGADEVLTHPFFDSIDWPELLERRMLPPFNPGVGKMDTHYAPRNMNEITARDRE

PSVMMAKTDRPNDFDGFSFVGRPSSLSNV

>contig14880 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67919.1|) 1e-122

MFSLRSLCIHKLAQQLRTFASGRKTRLTWRQKAKIEERKRNPPPPRQQPRTRAHRQNFLV

SPPVDDGKKWRVLSAGVLERLPIIQPDLKDWEMDFEVMQHEKALREDQRLEEDFWYMEPG

AKHVSPDEQPWPNAEENPDDIVGAGFHLAPRETEDDATNNRKSLNRALKGRVFLLVKNDQ

KDAKYPWFFPVGEKNESEKMRDAALRHVSETVGDKVETIPVGFAPMGYVKYLHDEKDSDF

DGTKVFFYKSQHL

>contig15335 Frame-0F

MLRSSIMPALVLLCFASAESTSPAISYRTYAEMTRFLLELNTTFPDIVQVSVAQETYGLP

YPKELQCIEDDEFNTLRHCKQYVVHLTNHSTVANDPKRPEVFISGALHGDERIGPNAAIE

LVALFAYGTSMYSTQSKKQPTVNTRRWLKELINTRNILVMPMTNAHGYSHHVRKELEVDP

NRDYNYMRSQGDCMQAMTSRVVNEIWRDHIFQLAVTFHAGTRAVAYEWGSPDHYLNGSKE

NMSEKSPDHMAQLQISSTLAKFAGVFPDGQLFPTGTMNDVVYGVTGGMEDWGYAASWENQ

FYKPNKQPFRPCEPTTFGGYPKEKTIYNNITHRAFNMLVETSNKKEPQAKDLGFSNELYE

ANVDFFRTEDLITEVVGHVPRNVRLALMMIELVQPMVRWIDGAKKPRNEEVVDVFPAISL

FASNANQVMKMGCSASAWMRNQVATCNVSRCSILDTRHSKVQLAWEVLGALTVDRTLVQI

SSSKTFEEDAILMETTAQAGITRRFYSFTPNASQTTP

>contig16864 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54480.1|) 3e-15

MKTNLAFYAPNSNKGVDEKALLKNEPTSQ

>contig17621 Frame-2R

MQQVQTSLDEWRYQQRRRDAARYSCSLQQDFPVDLLKPSLAAEACITNLSVREEVSNPEQ

LSFDKFRRRLEEFDREEYSPSPLKKQKVVFEKVDHVREQVKVNQDIFKRLKSELRGNTDG

RRSRKTVASITRMKTPIVEKHTRFESRKKDKNHDIACENEAKEDHSSKHGHKIETNGEFL

STIRHDSFHDISMSAKFREEEIAEL

>contig19094 Frame-2F

MALPTSLINQTVLRSYCSIGFEPVRTHSRRSAASSPSMEKTADSNHLQRSFGQPPKMLIF

RQRWIISLKRFFRLPLLARFATFFRRMWFKLISIFNKKSTPAVVSNQEIPKSEIPETTLT

DVVDDTSNILKTPVNDDIAATSEIPSSAGRSTVINAADNPNGDASAVSRTPAADSAKVLP

EVPKKAGIEITEPTILSSVDGEITWLRENEKNLMNSVAESETELEAVRSTYAAAKNNLEA

MKGMIEQALERSEFPMALSSKDFATINVLSAYEEAFNKYGSGLKEHGQHIGTQMRSLEIS

LNNLHDLVRNLKAMDEVGKVPEAGPAISNINFVKRQKQMEVEKTLGEFRSKLESVRESYA

KVKSDEVELSTQKEKLLTSRMVGFLKNKKTKASDHFNDEPIIKAQVEGTATTDAGLDLTR

TAEGGGGLNSFVGAIAPKQPDSLNLKSLKRSGAGYDFDGISFTNELPPVSGYSSNSFVKG

PNKRHLREDTVESIPSTSVDVTSAATPTRNFAPKTKLT

>contig20924 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66324.1|) 4e-22

MQMGLDMYFRLQELKPLLRTLLDLG

>contig21163 Frame-0R

MHILKLLYQSQYKNKTFLIVSSNRS

>contig21189 Frame-2F

MGSASSKAGDTHPKNLGANPNDPDAFPHHRPNYNQVPQQGRTHEGKMEGKQPQKPYYVEQ

HSSTEAMEVDQPTDTSSDANGAMADAAQDGGPSSMTNLETKDVALPPGEDVVPMVFKWEH

GGRNVFITGTFNGWDKQCFMHRSGNDFTYIANLTRGKHMYKFVVDDDWRFAPDQLTMADV

EGNVNNYVDVSDFVPLSDFDGKDGPQEDDEDPENPYARYIPEIDEYTKEPPPLPPHLRHI

ILNKAPPTVDGRLLPVPQHVALNHLYCTAIKDGMMVLGITNRYKQKFVTTVYYSLMPGAN

>contig21839-0 Frame-1F0

MPFLLQLILLTALAVSVAFAIESEQSQHTRLRGLLDRIVSSESTPEPVRVLSASWEEGKT

GVPRQLVPISEKIMGGGTVVLFNDRRVPTVGEKESAVVNFDVRSIPNCVVSVCGEMSQWY

LGSKEKCFDLRIAPKSADRQENGLIRGLSAAYSGLRPVATTLYLKFDETNFIDGSKCEYE

ILAGTKTVREDQVASGSEAAIA

>contig21839-1 Frame-1R1

MAASEPLATWSSRTVFVPARISYSHLEPSIKFVSSNFKYKVVATGRKPEYAAERPRIKPF

SCRSADLGAIRKSKHFSFEPRYHWLISPHTLTTQLGIERTSKFTTADSFSPTVGTRRSLN

NTTVPPPMIFSEMGTSWRGTPVLPSSHDAESTRTGSGVDSLLTIRSRRPRRRVCCDCSDS

IAKATETAKAVKSISCNRNGIMTTVCGWISAGGS

>contig22311 Frame-2R

MRLVELIQAQSVVYQLQDLYCIKCHLPAEHKMREYCPCSGTYALMPGVRESFLETLRLLK

RIAQQHHFEQLKEAVQRLGREAVLPLQM

>contig23136 Frame-2F

MQSNFIRFRRPVRTIFLTFNLMNLLYIIFKPILG

>contig23767 Frame-1R

MAVARKQLPAKESALFRSIVKCYEIKQYKKGLKAADAILKKHPDHGETLAMKGLTLNCMG

RKEEAYEFVKNGLRHDLRSHVCWHVFGLLYRSDRNYHEAIKCYRNALRIDPENLQILRDL

YLLQVQMRDLKGFAETRRTMLTLKPNNRNNWIGFAIAHHLVGNYQMAIDIIVKYFSTLDS

ERVATYEDSEIYLYQNQLIEETGDVHKALSHLEESKTRILDTLAWRQKKGQYLLQLLRYE

EARGIFEELLEINFDNHEYHCGLQCAILKRHDFYVTNASLKTLLMPSERIDSFNEEKLVS

TLLGFYTDKMATHTNTTLVSLRFLIDFTKGAAFQKYTDVYLKKQLKKQVPSLGADLKPLY

VQEDKVKVLEELLLGYLATLKAQKPLDEDDLTATSSTEQVLVWTYYLAAQHYDRLGKYVE

AMKYINLCITREPTQLDFYQRKARILKHMGDLNKAADVMVAGRKLDLADRYINNKAT

>contig24678 Frame-0F

MLEIRELRPLLAILNEDDKPLEQVTSLFLRTFTKNDHFKVGCTICILLQDNLLTSSQRIV

SFSILCDLYRSEGTTTNPFLLVFVDALEKGSDPCEQNFIVHLLTTSGAPRDSSKKSAKQW

MADFRTNPSPPLHIDVEALRQNYLERTPLVPQFRAAGIRNVVTDSEFDLQEHVNNGANLQ

VPPNEVSSLNLPCSEALSLEEMSLLSDADTSSGPASSSAASASCTGSLSLLSFEPKFMRL

PPSILEPDMTEFIWLNPDYCPTLLWDSTMLDSTHNIALRELMTCAFQKPLVPSLQQKVLA

ELEADPKLVYHCSLTPQRLPDLVENNPMLAINCLLKLMSSNQITEYLSALVNMDMSLHSM

EVVNRLTTAVDLPTEFIHLYISNCISSCENIKDKYMQNRLVRLVCVFLQSLIRNKIINVQ

DLIIEVQAFCIEFSRIREAAGLFRLLKTLE

>contig24696 Frame-0F

MIYWMGNGLTAYNMEDGILRVKDISGFSWSHADLRVFNWHPLFMTFGLVFCVMQASLAYI

SLPFSHAAN

>contig24713 Frame-2F

MAGPTCQMPYESIRKASQELRVKAPCQLRRVDFLTTVANNLLSNSPVTASFASSLQYSAM

KAELKIAYEGDNAKNVALEFVDNLVLMVPYKCIEDACAAVKTQEVDFAVLPIETSTSGSI

YTNYDLMLQYCLHVVGEYDQEELLTPEQHPGYISHTRYLLLSKKGDITLNKQNSGLPFKT

LLVFSLKDSTIKGMLTRALEIFSRYNLDLIKIETRPWDGRKSNRTSKSILETGIYQYLFY

VDVKGHLTDCHLSKAMYRLSKLCAFMRILGSYAISSSKTSATAVSSLVLANTNRSMADKY

PLNPIFQKVTVAKTML

>contig25185 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65779.1|) 1e-103

MGSRQLFCGMATSLALMLIMAPSYSNALFVNLNGRVEECFHEYVRTKRTAYLKIGVLESS

GAYDVRLKAYGPFSAYPEDEKVEKKFFDQIVATPYEEKSQNVEHSGFNFESEHRGGWYRF

CLDNTHDSSMKTIEWYTAFDLSNKDDLGVEDRVDEQTRQAHMEGLKTTLDHLKTLLNLIR

NEQDYYRVRVHRHVQTLDSSNYRVVYYTIVELIILGAIYGGQSFLLHKWFNDRGYLSKRQ

WA

>contig25400 Frame-2R

MRNQAGRNKYELLAEDGETSTSSLPRRTYLFKRAAFLLIIALCGVAIVGVLLITFGRDVV

PLSSRM

>contig25664 Frame-2R

MFTRCCVCQQPNHLQYNVNSHVVPFPYQNRWTCLHNLQLQTFKQIKSDLIWFDIT

>contig26184 Frame-2F

MHRPQTNKIPQAFKLTQLIKRRSSDNKCCQPILTRPVPTTLAIWQGAWSAFLKKGVVFKR

GI

>contig26522 Frame-0F|Blast-bifunctional aspartokinase/homoserine dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY61951.1|) 0.0

MIIDCSGQRNTLELYAACFQRGIHVVASNARSVYRLPPTLSRESLATTRAKTGRTFFMYT

STIGASLPVIDTLGNILRTGDRVLTIETSLSGSMNYVANEVMKGTKVSQAIGSVLRKGYC

ECDPREDFLGMDIVAKTIVLMRALGVNLDSKAIELEPFLPTNVVEAISVVERDSSGRYYC

WI

>contig26957 Frame-0F

MALADNCPNGVASGKRIIIENMTSKTSFCDCVGSSDRKNSLISSVFPFSSRPCFFWQWWM

YVVIVALTIALLMAIAYVYVWWRHRKLTQQLQNETSFRNTVDSVERLDPNLFDTPTHSSS

VYMEESLSPLQKTAAVRHARRGNTFAPNANRTELRAFTRPL

>contig27644 Frame-0R

MAYRKPEERTPLLASVPRPNNDAKNTSTWLRADTSGLGDRIPSQESGCVGSIFFTWVTPL

MKLGSERPLKSEDLFQLDPHNRAVNVSKQFAKAWTHETQSRNPSLVWALGKAFGFKFLVA

GFLKLIHDSLQFVGPIIIKDIIAYLKDPTASLSEGLTYAAVIFTSGVVQSFALRQYFFYC

YETGLQCRSAIVTAVFEKSLVLSAAARQQRTSG

>contig28906 Frame-0F|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY65818.1|) 7e-45

MSTATDELFNQGWGDVLSNISPYAWGSMGVALGLSLSIVGAAWGIFITGSSLLGAAVKAP

RVRSKNLVSIIFCEATAIYGLIIAIILQSKMNQPELRNRGDEPISEHALYFAAYAVFGSG

IAVGFTNLAS

>contig29130 Frame-2R|Blast-isoprenylcysteine carboxyl methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62713.1|) 6e-79

MSTAASNFSHRIEYFKRKEHQLVTHGVYRYIRHPSYLGWFWWIVGSQILLANPLCAIGYT

LVAWSFFHDRIPYEEQLLLHFFPNEYQAYRARTISGIPFV

>contig29394 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57619.1|) 9e-73

MRALLELPLDPNRAKTIVENALSIIPSHEKNSWSILMCTYGRIFAAMGDYQQAVAAFQRS

FKLRPKNWETHMIYADSVLTPNKAWSEAVKHLTAARQLLSRTDQRRDKIESKLRAAEDRL

NAHNK

>contig29462-0 Frame-1F0

MTLKHAEVKYVVFPELFWVKLLIKT

>contig29660 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63358.1|) 6e-84

MASHSSKSSNKFGYALNFDWKHPWPRAPRPKNEDERLEELARYHILDSEPDEKFDKLCRI

ACKEMKCPIAAVSFIDKQKQWFKANSGLTQRQIPRDVALCAHTIMHAKRALVVEDTSLDE

RFQHNPLVTRASAVRFYAGVPITTPSGFCIGSVFVFDVKCH

>contig30240 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62218.1|) 8e-23

MHRTIMNMVRCMLFGSGIALTF

>contig30349 Frame-0R

MIPGRMTCIYGLESNVEILNYEPFPNDLHRYFDAEQWATQCTLLTHAVFCKIPVQDLIKP

GSKKLSLEFISIKRWFQHLSAYVINAILVQDTPEERAYVISFFLQAADFCISFHNHDTLA

SILYALQSTAVQRLRKTIDCLSLSAKKKMNEMQLLSDKGCREINRLMRKTANPSMPYIGL

YLQSFASLIELPASDKDGFVNFYRLQKMGELAMEILHRQSVAYTLQFDGNVDKMLHVSLP

YSSEESRYSRSLELEPREANAAPLDDRSSCVVINDDLDLESEVRESIGGDGTFGIRQWIR

KHQVVHRNRSRSSLVASYVWV

>contig31342 Frame-0F

MIMWLFVMLEHNDFIMLHAVTSAWSLQQLKHLISPKKKAWRVWLQVALSALVTSRVCDFR

SEDICKPSDNLKDRLAALPSWSQLREKALTVPGFPDEHVFKMVFIAQDYAKSDMNGYFLT

RMEREFVARTAALVVISKPFQTVAKPK

>contig31412 Frame-2F

MVCFIGKRHIALRRLSYGGSAPHAGGQDKSSISSLLKITGFV

>contig33623 Frame-2F|Blast-ATP-dependent helicase, putative [Phytophthora infestans T30-4](gb|EEY61840.1|) 1e-176

MGSYTAKPGGDLSTMSIFTQLRKAANHPVLLRRHFVSEEALQTMSRCLHRAEAFGNQCSM

SRVLQEIESYSDFELHDLCVQYGAIDELRQLQLPIGTLLASAKFDFLRTLLPKLEKENHR

VLIFSQWTKLLDLLEVLMGHMEYRYLRLDGSTDVQERQGLIDTYNEDKSIFVFLLSTRAG

GLGINLTAADTVILHDLDFNPTADEQACDRCHRIGQTKPVSIYKLVSEDTVDEDIYKLGI

AKTELNHKILGKLNAHSDDTKKAKTSDAVTVEMMLASVISNYKSDQSKVKHEEILDG

>contig33858 Frame-0R|Blast-monothiol glutaredoxin-5, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY61465.1|) 1e-68

MITTIVHRSARAALRGSLRTGLAVQHISMPVAVVQMQQLRMFSAAGDKDSHSDFQPQFHA

AKSSEPNEIQKMIESHVKKYPVMVYMKGTPSAPQCGFSMQVVRILHSQGVSFDSVNVLDH

PEIREGVKKFSQWPTIPQLYVNGEFVGGCDIITDMNKSGELGELLAEFKQK

>contig34037 Frame-0F|Blast-2-dehydro-3-deoxyphosphooctonate aldolase [Phytophthora infestans T30-4](gb|EEY66546.1|) 2e-19

MFGYGDLVVDARNLPKLRRSNGLVVQDVTH

>contig34169 Frame-1R|Blast-phosphatidylinositol kinase [Phytophthora infestans T30-4](gb|EEY53601.1|) 0.0

MFGLNQRQSMQSVLQSSGNSNHPVRNSASSFISASYNSYESGPKSCRNVDAGLVPSFEAL

NPYAKAGRSMMGDDKRWQPVPDLFHSKESLYFRSAVGKVLKMAHEEISPAELEVRANTPE

FKVEEGDWIAHNSNQKNQFALITPLKTVARIPANLVISDQPISLTQPINNHMGGYLRKKG

EKNKAFKKRYMELSGSVLAYYKRKPEKNGIPLSRDEKKTLERGRIDLDRVSSLQPMDSKT

EPYGILLVTTTRTWAISADSEPEYQRWLKGLCDVVKFSAVHVTYKRMFQLQEVSAKAITD

VRMVVTTGDTVGQIVEHIFNCYEQALDAAPLRPYNPAEYRLKITGYRDY

>contig34604 Frame-2F

MYYEGIICDVNTLKWQLSKNGTFKQQTRSVDIRAFKLVQWSNSQAAYLHAQLYSLAKWKA

FMELCCLRNGVTGDTEKTSAPVQLKRPESIYSSPRIMNNVSNGMSTSIAPNSVDLLSDSR

FIDDRTIFGMIQMLVDVIKIRVKRFDTQDKTLDYFMLIYFRDLTQLLISMLHHQLCFATT

IEIESFQTRQHSEMSSTDSDLQLDANTTLDVLAVIEKMMCLVHASIKQETRDLQISSGNS

TLSDKLTVVPLLCRIITNFASKVDIVATDMHASLFIVTLLLIRHWRKLSTQTTGFDDNVS

PFKPLLQAKLIGHCKAVIDLYHERKHFEQSVQSLYELSCCLFQEILSSCGFADSHKSPLS

MGIVTSPLFKKLEHELEGLDTFFHLLVQQLRLGSFEKEDIARHEAVYHVLQGLTAVVWDP

ANGELCRHVMLHNIKSRPSTGLLTILAIELLPVLQDQMKREALSSKLRGYVKSGTDKLQR

SMAHRMWCLVLNFVSGLLCMSTRLDVAYVWVFMSHAEPLLLAAIEPGNCSRLTRAIVAEH

QAYLRFLYGLSKTAVTRRSWRQAFPKNFVVLMEQSRHLLRRACVLLSTLSFEKSRLCKEK

SQKQHSRGSGKAGVKLPKSPRSPSSFPLVHEDLLHDQLQAIDAKDKQEVTQFRRAMEAEL

VEIVRISSLMLVKWTASITDRDAILVVNGVRYVDEEQLVPLLSFDPPSEARSMDSSPSLG

HLGLAMKFIFDELLMGNEMTSTTPKKSKEVMENAMDACALLFLKTYMLHLEQYELADRDC

KEFKTLFSQLCARLCSVENVGFDKDLLNHIG

>contig34891 Frame-0F|Blast-bzip transcription factor [Phytophthora infestans T30-4](gb|EEY64830.1|) 5e-10

MMTSRRNLDDNHQPFSDAVIRSVLPRTATHRFVATKSNSRIFDPNVSQTAQRPIQNSSPP

RVILPPLRNISSLVGLATRNTEVSDECEHRSKAARHHSDAVAAPFAP

>contig34947-1 Frame-0R1

MASIRIVKDSRIAKHFMKKTKTCEYIGMQGREHEQYSLLPAACTEGARC

>contig35030 Frame-1F

MVLSRIKVVTTALHRQRLVQTSRFNFSNEATDAAAAALRLGFKNAQVEEDPLNVNKGEGN

KFPKDKSAPQLSAEKQFVPPARSSTQPLWLTQDHPVTDLSGFAPKIVVVGVGGAGGNAVN

NMIARGLQGVEFLVCNTDAQHLRTTLTENRVQMAPELTGGLGCGANPEIG

>contig35629 Frame-1F

MGFDDLGNRWTQIAELLPGRTEDAVKLRWKALNPNEMVKAKPGRPKLLPGMTTTKQRSIA

LPTPIDVAASFVHTSPMMMPEIPTFDEQYEVSLPMDNRLSIQPMLLSSQVAEGDLVATNQ

PLLRNQYVEPLMKPLSEELMAESELDDVAMLKELLHSHSNSLLISFGSTRGFNSLTDISP

EELLASGELDEMFRATVSISKERTDQSRLLSSSTWMDTLTDSFKTPESLQKAVKNLNQQD

QHLFREITAQKGMTNALSIEGDCIAPLPVEPVAYSHYKVDTSRSQKLSLDRDKTRSLPRQ

NSNGILYELGHITNDIDDLLNSDLMRPIRKGKMC

>contig35931 Frame-1R|Blast-phosphoserine aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY57574.1|) 0.0

MGAIPSGSMLLFNNTDEPGVLHKVTSVLANHQINIGCFGLARENSGAAAVGVLNVDEAIP

DTAMEELEALGMLTNLRRVNLLELNTATSGCIWDKFLQPSTVADENSPDITSGEMARVIS

RHPKPRVKPTSPNFGSGPCKKRPGYSLASISDVVLGRSHRSKLGKSLLEEAIVRTKKILK

LPEDYHLGIVPASDTGAFEMAMWSMLGARPVDVCYWESFGKQWFKDVTTELKLDNVREFE

APFGQLPDLSKVDCDHDVLFTWNGTTSGVCIPDGDWIPDNRKGLTFNDATSAAFAMEMPW

NKIDVCTFSWQKVLGGEGGHGVIILGPRAVERLESFVPKNRPIPKIFRLTNVSTGKILKG

IFEGSTINTPSMLCVEDYLDALRWTESVGGQDGLIAISQRNLKVLEDFAAENSEWFKFLA

AEKTIRSNTSVCLLINGFSQSEVNQMQALLEREQVAYDIGSYRDAPPGLRIWCGATVEMK

DLEALLPWIKWAYQEVKSARDTTSK

>contig36127 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61095.1|) 1e-110

MVSVRLQRQHQVSVNDRLAPESTPEDDKMTPPAAPKLAECSDFPRLLVALALRPQLAQTV

DAFGMTALHWVCSDPKAPARVVWTVARVFPAAAATRNLAGLLPLHVAIRKRLALEVIQAL

LHVYPEAVIVCTPDGKTPFMLAKQKPVASSAIISLLRLLEAQAKTGAPTLSPSRWAAKLM

SRKNRDVKLSNGLSSSRMDTQEGTMVTRMAPRVTPPRWAMGSNVACVRTPLATFDSGIIV

AIAVHPSVDDTRDITSH

>contig36800 Frame-2F|Blast-heat shock protein 70 [Phytophthora infestans T30-4](gb|EEY57401.1|) 4e-72

MNAHNTVFDVKRLIGRKFSDPEVQSDMKHWPFKVVCGPGGKPLVEVQYQNETKTFQPEEI

SSMVLTKMREIAETFIGKQVSNAVVTVPAYFNDSQRQATKDAGAIAGLNILRMINEPTAA

AI

>contig37313 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65175.1|) 2e-76

MERIHNFQPSTLESLPSSSLSIANLSPLSVQKSLLKNENELGDVDEAGMVVDYAGTKRSK

NIDLSEVTYYKFPRELLPMLHGDDGETMSKFQEHTGTYIVLPSYAASSSPSTSSSSLTRP

QSSVLTLSIYGY

>contig37681 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60849.1|) 1e-103

MAFESTVEITRGGIENKLGAPQESPVNETESSALGFCIPASIASVRANVLAFEDDSIRSL

LTRYEGTDVLPNGWRDGPGKNGIQVVYGEVAGKGSEWYTMKTTGTLPVSAAEAARTLMRS

DMVPKFDEMTKEVKMMQKLSDDSEVRRVTAKSVMFTTARDFSVVSTYREEASGRMLIATR

SVEYVPERKGYVRAIVLISGYVVTPNPTDPNMCEMSVIAHMDLGGNLPAMVVRYLGLSAP

IKLVEKIREITLNA

>contig37854 Frame-2F

MARALAGETPHQIEERKKRIVERKERQEKRFEARLQHQMELSTEKKERRKLCHARNDRAS

RSPSPTRD

>contig38323 Frame-1R

MLRAKHIGFKSVRRVEVKAETTTPGELRASTDAAGARVSAPRGRRTLPKLEFTVDEDGAI

LHGPQRGSFPFQCASSSGSHAAMPTDAPFHAALERDLAASFQTLHMRDFPS

>contig39539 Frame-0R

MSLERAHRNVALPAVVHRVANDISASTRLIIIGDVHGCFDELQLLLRACQFSSTNDRLVF

VGELVNKGPKSLDVVRFVRESNSLCVRGNHEDAALSAYYQWVRNGRIANSAQYSYVEHFE

PQDVKFLEHLPFSLTFPNHANSIVVHAGVVPGIELKDQRPVDLYKMRFVERETKEWKALE

KIKFQREREAVLWAKAWNGPRHVFFGHAASVGLQEERFATGLDTGCCYGKKLTACIVPSN

TLVHVDAIKQYEVPRGD

>contig40030 Frame-2F

MELWWLLLAARVGTEVGFARLVQDVACRTCLCLKTSQSRRDVKLRQRILSLGKFESASCV

LDALHEGDGALMIIC

>contig40294 Frame-0F

MEIVAPAKGQTTLRAPQKLSSLNTGKKRSWHSEQGHHSVCSHAQDFYDLLVKVRFVLQQN

SDKVLVEALYKLNIGLAE

>contig40931 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60289.1|) 7e-36

MGLRSAALRMRVLCPILSISGTPSFAKQNTILNAPIEHNRLTADCMSTTALLVFRGLGAG

LAWTIAVDAYILASAKESTWTQKSVTRGGSCKTRNAFKLLSSLCKRNMLGFASFLGIFAG

VSCSLEKAREKNDVLNEFAGGFTAGLVCMLRELRDPRALLTSAFVCGSASMALHFFIPAL

>contig40944 Frame-1F

MKKYNTRPIQTVMGSIAYIPVFVVMAYSARDMVRSGNTAGFDSGGFWYWKNLMEIDSTYV

LPILAAASTYGNLELSTRTKSGFWTKLLQGGQYVTILAVPIMANLPQGVFFYWLGASWSS

MVQTVAMNNNTFRRRIGLKPRIGLTQSPAAAAAEMLGTTLDEIGGTKETDTMASTSPQRR

R

>contig41266 Frame-2F|Blast-DNA replication licensing factor MCM6, putative [Phytophthora infestans T30-4](gb|EEY63344.1|) 1e-180

MLADNGICCIDEFDKMDPMDQVAIHEAMEQQTISITKAGIQATLNARTSILAAANPYHGR

YDKTKTLKYNVNISAPIMSRFDLFFVVLDDGDESTDAKIAEHIVNLHMPVALQVETTSTG

AYSEEELKRYIKFARTLNPVITRSRRNEQWLRVIEVYAKTMS

>contig41288 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59513.1|) 5e-55

MAECVEGVHRFTSEERMRLLEGAGVSEGMILRFSRETSIINCSRRQTLLEDITAKKEARK

LFRQQKRRCKANLPRSPCASPILGNHQMILVNNV

>contig41392 Frame-1F

MQVAIPEYSSIHGPDGVLAPVLWSSDDQEILDILLLTGADGLNDVDIHEVQQDSHSSSHV

TAHTHQKCANDMPKGKNLALERRVRHREVVKRAYHRNKAALKGLRETVNELEKQLEQLSL

SRRQMNTLASKRESIDSIQRRYVLLRREQEELSYEATRICLLLKNRQRFATTVETLAQRA

AFMSSNDLDCSSTNSDEATTSSATSLFVTSPSSPPVSSNKLHGIDCDVSPLKAMKKTKTS

FSIESPTFLGPPTTEKSPLMMLMRKQLGYKPLSSSESSSLVNDIYRSILSFALCGTAISS

GASIMGWEDKRLFDGTGLKFSLRKNFVNQNALQLMMRTWQCLSDPECIEAKFRGLISLRI

LQCVNDDTIVALRESRSEDDTTIYRCVHLLFRVRTRQGFFICVQSLAPENLTDPALSCSS

RDGRIVQWTELSGWFRFDPVDDGLARDQLSFQERAQVEYGGYVDHGDVKSVATLAMNTLS

IVFKWESMMIGPIFSLSSYSW

>contig41947 Frame-0R

MSAKGVGGYHAIALPLPHSPFRRFVYVKKHEAKKSDSNVKANADTALAAGYTAYFVNLPA

NASVQWLHACLGPLGAIQNITVGKTEHSSHKVAEKGAGTNGRTAHVVFQTKNSLDQLLHV

DALETPAPSESSGLQAYATTYRQNRPGIVAIKDVADRYMALFEKLETENTRRREEVKNQV

QEDGFQTVVNTKKRSSEDVLSRPAKKQKSKELSNFYRFQTREKKRDQLKRLRERFEEDRE

QVEKMKHANHFCPE

>contig42502 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59584.1|) 4e-35

MTEKRKLPIDIQYKQLLETLIDRHIVPQKWLEQYEEIREAIATLYPELPLASEALSKFRA

KVISHEAINYFDCKLLFQYLEQSEEGATKNFFGQ

>contig42821 Frame-1F

MLRKPILVSPKESCYAILNEFQKGHSHIALVTESIDIVSRCWRSGDEIPESVIFEGIVTI

EDVIEELIQEEIEDESDVFVHGIVDYWQSHIRKTVKGTGSAFVKKRLRLLADRARCRVKS

RYSKQVEGGSSKRSSGMLKSNSTVEINVITENTPLL

>contig42854 Frame-2R|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY69560.1|) 1e-141

MDSEGFTSRAWLGHWVSGEDEPVNNYYEDHKLMEGALIKLGDYAHFRYFLLFRNGRFCYY

ELPMPTVAPGSGPEGPKCVRLTLTSKNLRGVMMLNASVNAKDLAKSEDEYDADLIKRGLV

FNRKKLEMQLTGYSPTGQLMCWKLRAGKDAVFVKWERAFRLALRPIWVQNSKCCMVCKKE

FGFFIRPHHCRKCGTCMCDECSVFVPRLPMQGYYDEVRICRDCSPMKIQRSSLKLGTRVL

VYGILVGRVVQVDA

>contig43314 Frame-1F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61857.1|) 1e-93

MPYSTPNSFSSSDGNNHYEAGDMANNSTIVANKPARAYSTTMAPGEVVIPAGDPIDYSLG

VEQCGASESLFVSLLEKYADLSDEFMRRIEEAYLKSDLIVLRRESHSLKGSSAYVAAMRV

SKAAFRLQLATEHVMDESVTSDDYTTLDDAFHLLKSEHRALRGYLRRNFSFRASIISGNQ

EIKKKSTGVGDNACAVM

>contig43743 Frame-1F

MEPLSLTASSFPEHLSSPSLERDRSKSGDGRKETSYSESGRYASVSLLQLSMLSELFDGI

SIGDLELILRRFDGQESAAIDYILHNHPSFNPVIGTGGRVETGVVTSPSRTSSFGQGKAS

LHRSSSQSGSTGPPLGPSSNWKTEICMYYMQGKCNKTRRTCSFAHGESDLVRPTGLSTTV

GSSKHAPNYKTRLCQAFENGTCIKSRRDCLMAHGISDLREGGSGSVGPANPPNLQATTPR

LQSYKTELCYYFLKGNCNYSKDECRFAHGQSDLRTVESNTA

>contig43897 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56645.1|) 1e-50

MKKVQEADCKAELRRLVAKGPPIWLEDKHALPVPEEDSHIIQVWFAKKNVERSAKLDGAL

EGSARDSLWIELRQLLHAMDDDKEVN

>contig43909 Frame-1F|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY68993.1|) 1e-65

MQFGSETRDNILLNFSPAYVAQYPSVRAPLLLGQLCMALALILTTPIAMWPFRSCVLSVY

LRVKNGVQTPSHKATYSEYVWVTVVGLSLIVTCSIFVPSVKIPLSIVGSVSGSLLIFIMP

ALFYLLQSPGPICT

>contig44867 Frame-0F

MRDWHSRHNRATVCIHLKWLTSRHRVATGHVHGLRRLLRVHLRYNNWKCSSGTSKCAV

>contig45051 Frame-1R

MTYTTEVLLLLNLRLVHKRLF

>contig45446 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54760.1|) 4e-60

MLKSFSRQCSVDTSAAGALSYASAKSTVEHAASIDTLVSSLAACDQTSDVTGTTTEAASA

FILCQILSSLQNGVFTNTSTPVREFFGAIQSDLPKCVSDLAAITSAEVTVIPSSTCREAL

YSDTSISTKTDFNLRKNGFAIVTRGEQDGSIRFMNPPGK

>contig45701 Frame-1F|Blast-glycine dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63500.1|) 2e-81

MMFGGPHAAFLATTKTYHRKMPGRIIGVSRDARGEPAVRMAMQTREQHIRRDKATSNICT

AQALLANMAAAYAIYHGPTGLDAIATRVHLYASTLVAGLEAYAPFCDVTNSAFFDTIRID

VTRSGRCAADVAMEATKRGVNVRVINDTCVGVSVGESVDFKDLKTLLLAFGAKENDLPLD

LELALSARARAIQKESLPERLCLTTAYMTHGV

>contig46128 Frame-2R

MSVRTQYNGSRDYRHLHSLKTTATILTHLTTQATPAIPGRYKKTPPRLPGIHSLFFIRAA

PTVVLPPLQCTVGRQNLDVTCARRQSPVANQVKPAVSSPTSPAMTLFRPDCSRKAATPIH

PIISLKLRRPLSLRDLLTSESPSSISTQRSTHVHHRRQCGIADCQKYALTGGFCIRHGGG

KRCNYEGCQTVAQSGGRCKAHGGGSKCNVSGCSNVARRKGFCMTHGGRQQCKVRGCNKCA

HGGGFCISHGGGKRCSSSACNKSAQAGGFCYSHGGGKRCAAPECFQAARKGGLCIRHRKL

AADNEVATRR

>contig46245 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68287.1|) 3e-27 NOT\_ORF

MGPKSIPQFFARLPVQFATPAT\*KQYHADMDQVSQYVCAKFGGLDEASRQLLGVHDSNTR

HSYEDIQEFLVRKQGVEQRRRQHHQQHQKRIAPMMTESVLICGLDEYLNELDPTLFVELA

PVTPIAS

>contig46757 Frame-2F

MTDFEKEMTSIQNGTNAGMNASPKASHKVLDRMSSLMSTDSQGISGGARTQYKIVKINDG

HNAPKREPLDGDGDESDEYFFVSNEVTTSQYTWWSFVPVFLYLTFQKTANLYFLLIGIFQ

MIPSVSPTNGVPLQFMPLAFVIIIDGLFAGYEDHKRHQADDFANSAITRVFNRQLREFEE

VEWRELKVGDFVKVANHEILPADVMILAVIPAEGARSGGNMGLCYVETKNLDGETNLKLR

EAPS

>contig47260 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66089.1|) 3e-54

MKCFQCDQEFCWSCLCSWSTHDEIMCLPLSFLRSKSHKYGCWAPMRVVTKSAVLGTAVVA

LIAGIGIAVVVAPPVLGYKYAKGSYRRHKYKRPSYLHLMEGDVM

>contig47879 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61492.1|) 7e-66

MATLRSVGSLRSFGSLRSIGSMHTISEGYATLVTPVSESAGGSTSLDEAEADVAVLVDEE

TLSDGAISESSARLASEKAARRYQMNHYLLVAMSVIIGAYVGVGIRVLLTEFAHVMYDSQ

TALLQLLGVEYFLPNVCGCFIMGFVTRLKPVLRGQYDILLTGVTTGFCGSCTTFASWDLG

AALLFVHGRWLDAILMLSVHVASAISSLRFGIHVAEGVVHYLTLQEYPFHKPPVDLLQLN

LGLERHMNL

>contig48966 Frame-0F

MAPQNKPRNDSKASADGNEPAIQRRNPSHIKNKMKRQLVMQTFRKEKKEAKKAAKLKRQR

DAEELGEE

>contig49172 Frame-0R|Blast-Glycoside-Pentoside-Hexuronide (GPH):Cation Symporter Family [Phytophthora infestans T30-4](gb|EEY58262.1|) 9e-88

MFFGLEVFHGDATNAATCGNQCSKEQLDYNRGVRLGGGLADILFCSVGYLYSWVLPPLVR

RFGAQTIATLATIPQILLMLMAFWNVVAVNLVIVALTSITISTFFALVVPIVVHTLGQSA

DIGVYVGVINSANSLGQLLNFIVGSALVETSMGYRLPVFVGGAVSLVSFLVCITFFRITM

HAI

>contig49495 Frame-1R|Blast-N-acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69879.1|) 3e-23

MELVVLTVFKKNTGAMRFYRERMGFEIDETSPSASGDDSKDYEILSKSVRSKINR

>contig49554 Frame-0R

MRQIHERPVDKASWDRLAPVVSALSVPVLANGDVFRYEDMDKLREISGVSSFLVARGALS

NPSIFRRQGRLPVDEVVREYLLAAAETDNVFQNTKYNVMRMVPSSLEIASSNKFGYGKHT

QVVTVSEVAATKNALQLYSLWDLQNTYNEHQNQFRAIAAALKTDSTQKEDAFAALTSLPV

AHDRYAADCRSQKSDFYTTIPDHYCGTCNLQLLSEQDVKLHVKGRKHKNVLRRQSSATIS

KFVAKVQMEQIPGGAQSDIDALEKEFDRDLKRTKLEDAGNSSCVVAKVVTNGF

>contig50044-0 Frame-2F0

MFEDGRRRCRMLLLSPTGRLAALSDTLGRILLVDTLRMIVIR

>contig50479 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54957.1|) 6e-68

MKCNADTSPAVYLFVLLFDVLTVTSLCPQFGSFRLNAFGSKAFAFLWNSTLKKLPYVCFA

DWSWLEDQSTGGKLPALAFCHLLATILLSNSPMDHYCQRSCKNYAAVVKHILCKLYVGGQ

AIQKSVDTVPSTSLMLAEWEITHIELHDLDSTFASILGLDGFFEVTEAMKTICWP

>contig50790 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59083.1|) 3e-40

MYGTVATTDEAMKIQTACTKNSVRDSKVLREIVHPNFHNPFRTVAVKWRLYEGCDYVSLD

ATGITQVRGCERIGYS

>contig50930 Frame-1R

MPKSCANSSYANSTHLPEDICSITDTVSARMSDSILSFGTCSHVYGLIGAYSTPIAAPLD

SPSTNSIFMNYKTNA

>contig51115 Frame-1R

MSFESRSTSSTHVVQVKKQIGRKCEIKRQFGSQVFSCIRDRARHSFRLKRKLLNENTVSA

FLVLLKSFLVELFAAKRDTFGSNKLNPSSFNDHHSVWWSL

>contig51223 Frame-2R

MQHYFLRFRFGRPESSLQALAAAQHCYRPRAAYVAV

>contig51645 Frame-0R

MTAKVNVRKLVMQGAIAKIVYTNAVAAIPNNVDFRLEFVKIRDLFGAFMAASLSDFILQD

CQNAFPKSEQVFAANAMRPLLVAEEHGKEQVQEESEAVRQAERNVVQNFETSVKELDTVR

MKELFGAWMINRLASCRPSSFLLEYARAKLHDFVFSKTSVASSTLAINYVDLIHRLDGTN

DALTIVRKICDNVLPQSSELWLLQSQLMLHLDYDNEITRPLVKRRRSSSDSHAKTSSTPL

DEA

>contig52150 Frame-2F

MNAQLSQWGAPKVSRLWSAKGDERCSPPRSDDYKEWSLMQLKREITQRQIKTNPRRRNKD

AFVRVLLANDQEQTQTPRIALNQPQQTLDDSVLFVAAPTSELQSVYANNGGP

>contig52406 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62392.1|) 1e-21

MCKRFKGSSGRAKKRPAYIRAQIEHLPD

>contig53225 Frame-1F

MPPNDARIRQLFDLNRFASAVKINATTCRVLLAQSATSNGSILQAVYFS

>contig53452 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66740.1|) 1e-07

MLAILATSRAEPALSDGLSRVILLLDFRKAYGMAARDTLFVVLQKFDLSR

>contig53687 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66910.1|) 1e-45

MTKQLDEEMVLSQAKDKALKELQDALRTTGEELARHRALLEQSEAEGSRLRRRNTELETQ

VLEKNALLHEWLEANSGENIGKSPSPALVAMATQEAAERMSHLTLNGDDGGTAHSP

>contig53874 Frame-2F

MMPLFVPSSSLFSSVVLQAKSTNAFRASLLSDASTSYEAEDVDDAETIDLHSL

>contig54310 Frame-1F

MARLGLSDSMRSTASVDDNKSFVPPLHCQSPRAKIVYAPSGQHVQMKTFALGLTKPLRNV

ISHSQRNAQIERLERSMELLSSDNTKL

>contig54840 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70265.1|) 6e-27

MGIDAEALAQVAATGLAGIFSGASIYITVAQHPALIEMDALVFQAPFFRRMYFYAARMQG

PLAVGSSLSA

>contig55199 Frame-1F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68035.1|) 1e-22

MLQHAIALLLQRLLGKFVSFDSSMLKLSLWQGDLSFQDLQLRLSYGKGTIGHLSVRIPWR

>contig56095 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62314.1|) 2e-22

MPQDHSNTYTVDNGTTQAREIPPDTSTDTSKLFKNPPV

>contig56370-0 Frame-1F0

MPRRTLALSTDTHRSAILERVDLRIRYDSND

>contig56370-1 Frame-0R1

MADLWVSVLSASVLLGICTA

>contig56419 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61301.1|) 5e-09

MVTLENVGALRQTALADEHLMICICGVDVTRDCSNAQVLRDALQKMVRIKMQMGTNHQIC

LARFQASSLIIEQE

>contig57232 Frame-2F

MQCARLVRPTQQAVHLFRSFSTGRTLVKTVQSSRYAQTHTTSDVINFGLGQPSASLLPPL

EMFRDAAIAKFQPTQDSMMLQYGVAKGFIGFRKEIAQVVRGINPTKAVDPETLMVTAGNS

QAISHAAMLFSKTRKRVFVEDPTYFLAHDIFRELGLSMTSIRTKTDGIDLDELEAKLIAG

DVPALLYTVPFFHNPTGSVMSPMRCQRLVTLARTYGFHIISDEPYNLLHFDGSAYSSLAS

YDDSGLIVSLGSFSKILAPGLRLG

>contig57386 Frame-1R

MRSRGLSRYQSWDPITNCFIIKRIGNSFHIRIRVVTWNEAHLLEGDLPYSLRKKQWSSSS

ESSATR

>contig57553 Frame-1R

MYAPVDVEIRHHSPPDIVKSYRQQLMRTLLALAVVVVGLTAGVLLFRFVRSDNFDPVVQW

LKSHEALGAVLYVCSFTCSVVLCFPSTAFELLAGYVFGLWLGLLLATTGKLLGSVLSYII

GRYLCRQRVHAYMARGHPALQGLQNLLRKRQILVV

>contig57791 Frame-1F

MSWPALRSLKLILCFQNGIRANRGSIYGTIGHKHRKPLKTIAFVSMTASAPSLIGIFKLP

NLTPLLHTRNGRACTSRILATHSGVAKASFQVDALEAHKASPFFHSCGHSASRRGAKTQA

KSTQVAPNKAHALQPHPLASL

>contig57904 Frame-1R

MSWLLALVDELNFHFLLFMYRWDTLS

>contig58075 Frame-0F

MLIALSICTSPIWISGFVVLVARLLLRDTSTIEDEFHPDFEEEEVTSPHHPNSMYRRAHL

TNHYIQRE

>contig59090 Frame-0F

MSHKSRTLRLLCLHGMYQDASTFAGKIMPLRCDNMNVEFVCIDGPFTVVPPIVKRTKGKR

SRVVSSKTGIKNKFRAWWRQQGPHQNDLCGSMYERSVLISFLREKLAEAGI

>contig59216 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61946.1|) 2e-08

MSHIDSALKRGEDAAKKIAAKIEEKSQ

>contig02970 Frame-2F

MMTLSDRPRRKAKRTDVDYAVLSSGQQIPEYSDENDDSNDESYGSNYRKKRRKQKTECFI

CHRPPRTYKRTMLQCDSCSRLYHAACGKPFQSASILGNTSCYECLQEAKVDSLSALPREP

LNSIADFVKILKKAKKILIIAGAGISVSCGIPDFRSKDGIYAMARKMDVVLPEPECLFQI

DYFRDDPAPFFEVVRHAFATSPKPSLTHWFFKLLQNKNKLLRVYTQNIDGLEQAAGVTRC

IPCHGSFAYSACMRCKKRMLTSSLMPVIQAGIVPSCSEAHCRGVFKPEITFFGEMLPDKV

STMITKDRVRADLLLVMGTSLKVAPVMEIPSYLPSHIPQVVINKTALTKKKLKAKVRVTN

GMGTPKSGFLNDKLETRDEEDFDMSLLGNCDDILRYVCAQAGWELEPLAHQVAMTEATTL

ENQVVLHENTCRKRVYCFGTCQCKNKVATNMDKKDEGQDEEQEKQELHDIACNYCRQRID

TEAEPIIGSKTVHYRC

>contig05360 Frame-2F

MEVDAPQRPSDEIDMATTTSVFSVAPSSPSQSRHVLNRSAGTATDTGASTFSVSPSPLSS

PISSILHPSIHRAATPPPTVSTDTHSRLQSASRTLAKPQEPKISRRVSIEYPHDNPSAAS

STVNPFVTNDSRSHRNPFTMSNRMNSFHLRDSMLSKMSSNVGNFRDSFLGVLGKSLPGID

PLEISPHQEFNLAVIDETGGLNETIGQILKPPINFRNWSNEGYSVLVFGLFFVLLLFSLT

QSTEKLQGYSIDPGLVFGSLVTLVLCTCVFVTYHGVQSFQKHPNPLIYYKCVIDMLVALR

FLLDPVFLDLGMYRRNDSNSCAYLSGMTQFLFLSSDCWYFAQIVDLYWSLTNPFMSVQAN

RKTFKLLIYSAGTFTGFITLTIPTIHGLADGNFCWTRQKTSIKVMERNFFQLNRGSWLLF

YSWMLLFYLSGIAVLFFGIKRLRSGLRDTLQSRR

>contig07234 Frame-1R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY66029.1|) 9e-13

MPGEENKEFDDELVDYEEEEDTTTDASKAAAEGKDAK

>contig09409 Frame-2F

MKVRIYCEVFCRQFELACVKISQHHQQVATITVDNKGVWLRQFPNVIKRGVYQSPKGIER

LL

>contig10296 Frame-2F

MYDLLWLFSECPRLKQVPVLLVHGERDRHGMAKECREYPNVTAIAPPLPIPFGTHHTKML

IALYSDKVRVAIFTANFLANDWNCKTQGLWYQDFGLKRLAEENCEEITNVPVAEFEADLV

NYLSSLGVPVKLFCQELFKFDFTSARVALIPSIPGVHKGKDMKKYGHLRVRKLLKSYRIS

STDHPLICQFSSLGSLDEYWLFGEFAESLLPGVANISSTRMRVQTLHLIWPSVEDV

>contig12904 Frame-1F|Blast-V-type proton ATPase 16 kDa proteolipid subunit, putative [Phytophthora infestans T30-4]gb|EEY61710.1| V-type proton ATPase 16 kDa proteolipid subunit, putative [Phytophthora infestans T30-4](gb|EEY61709.1|) 6e-07

MLTQLVADVCPSSASFFGFMGVASALVFA

>contig13239 Frame-0F

MNPRPLYQVFLLFIEDAPVYSSDAANC

>contig13558 Frame-1R

MIRVRPSLDQTTRLIRQQRAAASAPVSRMTRLGASGFGADTFADITRCGTYTNDRPKLLR

CRGIFVDEAIGRE

>contig13987 Frame-0F

MLERKQMVSDTTLSLLHIQRMQPTCLRLQDWRLCFRKTTKRCCIQAEQLTRSNSLFTIGM

LPPQEVGWDSREELLSASQE

>contig14605 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55346.1|) 0.0

MDEIALLQQQLAAVQHQDAALKLSDHNVVDLLLKLQQLGKLHVIHTRTGKQFLTFLQVQR

EIADYVALYGGRVSLTELEKLIDVDRVHVEKQAIALCRGSKSHKDTYSIVNSGEELLTSW

YLDGIIEDTNILLQQVGTTTIGDLAQQFGFAVDYMRDVVRTRLGSILKAKERDNVLYTDT

YVTAQKAQLRGVFAAITRPVFVPDILRSYGIDESVANEALTELLQTQAIMGTLRGREYVP

YVFMTAQKESVYSFFQQNGYLEHARAKKLQVARPYDFLKKRFRDAVPLQESVVSHELQLQ

LEGAIEAVINDKSLVDVRTLLPSALSESDVGLLLSMSPLLDNAGRVSKAFQIAEFYAVSA

GFFALCLEKFGENATLKASHVAAQQKSTTVQSGVRDRKQETEKDYGSDGDECDKKRGKKG

KRVKDWNTRDQKELEAHSAKTRKSKTGKRGSKGSGNTGGDRDSAAASTEVSIVPSRAETI

ELLVEWFPALEDYEGDDDFFDGILAFLKPKIHELHSAALTKALSCIIRGDAASLRELRKS

FEEQFDEQFTKLLVLEKGFNKFSALVDVKNLVSMAQLALVETHLLDSIAVKLAALVTCFI

AESNNIELQGVPLLSSLNNNSEGKSNSVAPITSLSKENKKVLEASISQSTASTLVRLWTL

ATAGRRSINDFVAHIPVLAGALNIPLHKLDRKTERQVIFSYRQDTLAELDRNLLLVHENS

LQYSLLVSLILQLYFQQRVGLPITFPSDTL

>contig14814 Frame-0R

MGFLCLYEMLPFELCASPAFQQLLFECSGSTNAWATDTNSFALVTKENASTSAKKLAAAS

NEKTMVLMRDSDFMHLMISEWRISTDQVFLALFGIGLNHEFCLFRRCLHVVSIDYYRVGH

KKAIAELARDYQPKKDTTRINSCQYMPDILAVNPPSSNYQLFSVELKVPILECIPKVLQN

IMIATITGIHVSGNYCLSSNNSIEADYTRSVGFQTWRLNKDEYIESTLNASSTALSNEAL

YGGHFVEELASTVLEELPTSLTGHTYRDLISKVMYLLAHFKQSPTSRNVLRSLSLKQ

>contig15400 Frame-1F|Blast-glutamyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY69415.1|) 2e-26

MISSSLKAAGRSLTSADLVEKFGVSYIWEALSLM

>contig16117 Frame-2F

MAGQKVIFRSGSSIERLRLSFSLNMTSFIIIDDYRFTLWPTVIRFVVDFSEKSSIHRLSL

SQVDRGTEDHRFYLYT

>contig16625 Frame-0R

MLYCFTRALDIVWQLSKRRGLVRYIKHSEVVVFCFSMSLIMSSPTRYLKPTYLQILRFIF

GRNII

>contig16812 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68822.1|) 1e-119

MTDQPTRARSLPILRLRLDSRAPPSFHILTSMFASLEFGLGTLALYQHTPDFAAIKSAVE

SSCQLSFTPAHLQQILHILPGAYVLEWKKNTRTARRQAREEGGASLQAHRQRLTHCPSVL

TLRKQQLPSPYESCEGIEARLNLFVERLNIFLEDQLGAIKKEFSDMNEDELNHALKLVEI

EKAELPKIPVEIMADHEKLAFLHLKSSNGQTGTTQKSKTKKMHEEVMAKPVPQTLKSLPE

WLIYKVRKNEVYRKGVVDHNTKALKKRMLSSLPHLSDQLQSLVIVTKKSIFLKSEVVCRL

AVRAPVKGKVEEQLYMLESMVPEWLTVVLSDGKEFVKISTSCKYSAVKASIRRAISVGA

>contig17819-0 Frame-0F0

MGVPLGNTGIDVANIGITALPEFFTNYLGSEPSFEPK

>contig17882 Frame-0F

MNMASDEVFANYLLEKRNSVQHDARKEEGTNQQSVLFQQTPKFVEALTDLAEKMIPTPRA

ERNKQLREGLTAIEAQMLPSDVIYLPIGNSYHRVKGIQIDECFTFSTKERVPYFLCVEVL

DYSSSSCAAVSKQQRKRRRSVASRNSSRVFSLRLPFKKSDSDLLQEDDSPVSSSTSLESE

LSLVPSPSVASPLPEMEKDRPVLNGVALQRTTSASVVRLGKEVVKEVGGWSGSKSFHGVE

GIHSDGGDQQDRLGQWNLPRSRRRNNKDYYSSASSRSGEKFDTFYSSWCTQMAQKGTDDD

YNDLIRRRKELLDIDSSVNENVDTAMTGVKPADMTMSAARTESPPSDSQTVVEDLSSLLQ

KPQNGGNLNQCTDNLKDFERDAFIDQDTQAFQVGVTPCASTISAQTARPPVFVKKPTNLP

ALKSERTSIQNGTSEKQTVTSNAPANMFAAIFAKKLQEKTEASALNDDVTDTLMSTLEIK

AATRNKLTVHVPMKNMETDFEAYTAKCEPNGRISVVLEAEEGDAEDTDSNGGIFSDDDSV

ACEPEPSPAKIPTPSFVSWFSRKPASSLSDIRIEEGTSSAIDEPPLSSHQELEPSKTVED

NITSPSNEPFQHRQRDLNGSLDFADPSAWKEKFELEDGFTDDDPEPEAGDTDASEEEFGD

ESLKIGEDEEKPMIVFREHWSEKEERIRRESPFGDHPGWRLLSVIVKSNDDLRQEQFAAQ

LIAQCDRIFREYSLPLSLRPYNVIATSAKTGLIEAVPDTVSLDSLKRNDPSYTTLLDFYY

RLHGDKDTASFARAQRNFVESLAAYSIVCYVFQIKDRHNGNILIDTDGHVIHIDFGFLLT

NSPGSNWNFERAPFKLTDEFVELMGGPRSSTFRYFRSLCIRAYLALRRNMDQIVLLVEMM

LVGNADLPCFAGGKKAVTEGLRARLKPGARTSACQVFVNQLIDQSINNWRTRWYDKYQRA

YLGIL

>contig18007 Frame-0F

MVRAWLRPCASAVTVLGRRVGPNVKVAIKQTQTSATLSVSTTVSPLLSGVRSLATKGKDG

GKKEFKKKSTFDKVESVDDITELPEEVKYLSRQLDENDFLYTEKIELDDDDDDEEDTDLN

PTEWAKNFEREVAQWDQEAHDSDEDGELFDLPSDVEDDRLYVEMPGYDASLSLAESQIGG

HEEKNGSDPFRNWEQGMAISPEMLNWMLPPEQRKPFRKETTKPWKYFVAANHPDVVELAL

DVDLLRLFISPTGRIRPRRFTGLTAKQQRRLAQAIKVSRQLALLPYLSRYPEPTPEQWQA

IDKELIAAAELDENSGNFDDDDEDFDEDFEYD

>contig18465 Frame-1F

MEKVKLNDAKAFFTRLRQEKVSQEVGFKLQARLVMQLATTDDGIQSLKELANPGLLYTYL

KDKLTSRSDLRLQWLQYVNKYWILKGEVAGHEQFSYDDVIRVLLEVVPHQNKLAFFKTLK

DTNGMESFADEMMAYVTNVPSWLVNKRKPQDVFAKFPYKNGAITDFGFLQWLIYAKAYKA

KDANFNYGELYEFLETKNMIPRAKTLLEMHSKNTKVSDFARGMLDYMLTKTNKWTTLRNS

IKWIFPF

>contig18780 Frame-1F|Blast-ubiquitin, putative [Toxoplasma gondii ME49]gb|EEB02374.1| ubiquitin, putative [Toxoplasma gondii ME49](ref|XP\_002369514.1|) 7e-11 NOT\_ORF

M\*TLTGRKQTFNFEPDNTVWSFPWSGGYICDNNARLVVVWEQILHVKQALQEKEGIQVDQ

IRLIYSGKQLYVMP

>contig19079 Frame-0F

MVVEEMTPKDFKVTKESLEDFPRAMLVRYASREGASEADAEILASAALMEHFKDKVDTKD

TLNAVLPNLKAIQGLSPSDLAAVFRVKMDATATLFNQPNGFAFLLFDRLRANQDPFKTFH

RVQSLYGKDGELKSFATKFWPSTKDVDFVSKMDQFVKDVLPTTYAGKIRNFFRRIWFKLS

SIFKETSTSAGRSNHESPRSEIHADSANDLRDVSKKVGIDIDDPKSFDSINARMELYLQR

LAAFNDNVEKSAKTLEVSRTTFSNAKNDLEINKDPIEQALIRMFDPTKTVLPEDASAIEK

LIAYDKASSHYESDFERHDKLTFERINVFEGFTALSIDIQEKLKTIPKVDEAPDADPSFA

KRQDPSKFIMNALDHFQSDFNRVKKDYAKFQSDRLEFLNDKEKSLTPRMTTYLIKRNTGD

LNMSTSKVLEKGQEGM

>contig19981 Frame-0R

MLQEAWNAAPNFKKNSILLQSIGTL

>contig20927 Frame-0R

MATPLDSKVLLALQRATQNP

>contig21083 Frame-2F|Blast-Phosphatidylinositol 4-phosphate 5-kinase (PIPK-D12/GPCR-PIPK) [Phytophthora infestans T30-4](gb|EEY54682.1|) 1e-122

MQLPVGWNKMFFVVMENIFPDGPVDERYDLKGIFHQSNFRYQEGVLTPLSSSRSRSGRAE

EEGSVHGVDDDEAAMNKSQSADSGWEQFAEKQPLLRRGSSRPSLRYDNDFVIRRASLRVN

PTTRANLLAQVTSDCGFLQELGIMDYSCLLGIRHYHRRIEPDILDNLAHNAVVSANQSTV

YYLGFVDILQHYTIGWKMQHCLLAAVVDKRKITALPPAEYALRFLNFIHEYLLRDPDGLN

VRSYGSIGYSPSNFIP

>contig21256 Frame-0F|Blast-Rab18 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY61856.1|) 8e-34

MTHSTTICKVQLVRIKASRERLNFGKLVAYTNLRDVQGVDFKVKMMQVDGKKIKMTIWDT

AGQERFRTLTSSYYRGAQGIVL

>contig22103 Frame-2R

MHYVLDITKHTIMRPCSGRSYDYDQIGGTFRTFWFNGFQFFQLLV

>contig22367 Frame-1F

MSLKIEFNPIAKRPDYRREVLFYLSERIELDGKRWSDVELRSMKNMRMLMMLNGMNGNIG

HSTIWRQTAEDQVYPKARVQSGSNLKSSTLVLGYPLLPPNQSVSANCVTIQKLSSTLPTK

SDCLKKATASGAESGESFDKKPLSRQSSRATRLSAQTVDDYFRTQRDDIGMRGRNESDNR

VKDSEMEASNEFDTRAAQNNLQTYGASGLKCNLEKKKSAFSGRPRFKKW

>contig22389 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53130.1|) 1e-94

MMIPEYPPRGTSITYGDPMAMPTVVYRLSLKPASSALPASSTSSASPSTSTTSSTTSPEI

TITRVQNSRLTIPSSSSTGTLMTTENDFSGRRGKSHSETASRLERMLNSSASSRDLLRGR

PYSAGDEVDLARSVTISGFSKNSHGTWVFKVDVGGPSDSNAYVVRRRFTDFKLLHEGLSK

LSKLPELPPHGIVSVFQMFVSPEKLLAARVARLQEILLVIRAHPILRTSQAFVAFIGKNP

SRYDAGYVSLSGYEVPASQRPNPAGSLDSL

>contig22486 Frame-1F

MSLGKRLKVLLLLCFSNISLCTAVGEQYQSLNGSEVKLSVRPSATTSKKDAKVFPDPDKD

SKNTITNTEDDVQEARSPNKKLLNSIARSVKGNPRQSVVSTIASTMERNPRLKVTRTSAS

STKRISREKKISTIASATQRNSKQQDNAEPTRSHVSVLFAMISNQITSEEYKKALKQTQS

NLIQQWQEKNTPPR

>contig22598 Frame-2F

MERRALDVTPPMAKSPCLSPGTYFGVNELVYARAAEHVEMAAPHPELLQNYVPPSVYQHR

QVPQNVPSYTRAPGARPRKLFIFLSNYDFSRDFLQ

>contig23764 Frame-2F

MKKTGLWRNTSNSDESGNSTAITAAKSNSTTKASKVPSQSSTDANPQNGARGSSTGRRST

GNTTPEGDKLPPGWTRKESKSQKGRYYFISPAGKTQWVPPPAKTSSVKVKKSFNWVSEVE

ICFQEGRLGVSLREVHQMETILYAQFQAEVDDLPKINGKAGPAELHNWSVKPHKRLTIGM

RVISIEDTSLAGLTYKEVVAKLKSASRPVRIKFADVQKGTMEEHGGR

>contig24376 Frame-2R

MTKTNLSNNHVHTSKGEYDDLVNESCGNDGRSCCSINGNGKNSDVDCGSVSQTMVMVADE

SSQKEPIESVSTVITRLADKWNCYIREDKVTLLALATLAGSISVVTARLLTHK

>contig24549 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53885.1|) 8e-46

METMGFERLRNGERVGYHIVHSVQFPETPVLDTHFRGNCSISMFYHQRASNRIDVYVKGF

FNPAGGIMRAIVIKLAARTLLCVAKHVYCGQMKKLAWALKRRRSGDLSSSDSESTGRSSN

DSADDRLCCGCRKKQSVLVQAVLKTNPGTKLLQKKRHC

>contig24710 Frame-2F|Blast-calcium-transporting ATPase 1, endoplasmic reticulum-type, putative [Phytophthora infestans T30-4](gb|EEY55343.1|) 1e-101

MVVGIYVGFACVGVFAYWYMYYEASGDGHTLITYDQLSHWTKCHEWQNFTVANFDGMDFS

KDPCRYFTDGKKTASTLSLSVLVAIEMFNALNALSEDGSLLTMPPWANPYLLIAMVVSFA

MHFVILYVDVLADTFSVIPLDLNEWLVVLAFSLPVILIDEVLKFLGRRIHARELKHRMDE

WEKKTQ

>contig25375 Frame-0F|Blast-3-phosphoinositide-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY67623.1|) 3e-16

MDCAVKVMDQTFIRKENKSAFVITERKVMSRLSHPNVVKFYCSFR

>contig25494 Frame-0F

MQSIERVNQALRALNVSEDDVSPGNLVLSVAGEWELKSMAAGSIPAQQYHLTLSQGKDGS

MQGHSSGSFTTVTLNGIARGTKVSFVETWRQGGTCLVEGRLRADGAVFAGSYEDTKSHTS

GCIVGNKISRNTKDVESRQWVSNHLVILEMVIANLVGYFGHALITLTNDDILVDNLAERA

LSLTRSADRETGANDDVDLPRISSAECPLDEIDEWVNSSLLKGGLPLHNIQTHLKNMLDR

CSDITGFGPAATIRSLPILTKATKCWMQFVLPETLSLPLSNAETLLTAGARVNSLYLKDL

IESCGDAATLDRWVSSHVGESPFVRLGGEPMKAARRTVCAAMIWHTGSLNSIKNQNDNMQ

SDLAASGARPHDKLMQIWRAAQRVIEWAIRAKNSKGFSYSVIAGLVIRKAQFLLELEPNA

KALMAAEFVFALASVDSGNQRIGSKLSVSECAERVYSDVLVQVARFVESPVRVSMLQSKM

LGNCSAACLRTIGMLSFRSFVGDSSNSNRDILNAERVEVIQSSCALSSALQWLSPTLADS

KANGGRGTSLGKDFGEYGASVVSASSTPSQAKYIEASYYLSGLGGCGKHLRNDLRDSFES

LYGYLSASLSKATWAHDVDLQLVILLAWGIIIEPDDHSFLSRVGIFRVLQTVLDEARGSS

DATFADNPRGLTPSSNDVAAMVAKNKKKIVQAALKAVHLLAAQVAHASDAADGLLSASEH

SLTSGLGFGSIPLLRKPSGPETLGKSVFHMLYSELKNSLEQMQKNESNAAVHITSTVSVT

DPTQSGDASTPKSEADPGVGMDDAQEYCYQICSLLYSVSGSPVCRSHLSSSRWLRLLLAL

VDVNSPHIQRRILKLLRRLLPSLDPSLIKVRYEEVEGFDMDSEDEFDADGLEQSDHASTL

INFFMGLVRMNRPPSVAEVMLHRLNSFSAPESTEAKKLVTDSGFNGGSLAAEVVLLLRSL

YESNKWAQYLDRAISDALASIPLLCITEQDRGAADIADSDVEMEDVSKEIPSLESWTSQI

TNYERALSALCILDGHIEGIHIGGTVKIVPRVGSSLQEIALRGARGVIVAYEVDKSAAEV

LLRGNRADEFNNEQVSMLPNRSVPTRPIRVPIDDLFAVPEVELSNDVFSSEVLQSLLVAR

FPYFLVEVKKSLQEVDLCYALSGADEGGDNDGDSEDDDEMSNDGSSSPSAMDSDMPSGAV

DESDCEVGEFPCHQKNRTELTSPAEPTDILVELEKESRLYRMLLCQHGLRASATLLKNDK

CAALFIKGVGSGGLKNLLKVAISETPTTAGAGDISSLEESWLMLWSRWYAIRSAHAAPSP

YTYTNKGKIKTSDGVNATDDLGILVQQMMEMGFPKEWCDVALARCSQNVESAINFCFEHS

SDMERLVTEYQSSRSSGDGSVKLSRKDDLEAISPLLEQLSEMGFPFNWCKKALAANRNNV

DAALTWILSNGEALEAEDRRDEDMKLRAPGDDDANEIAICATEGEDHVLMPNPLRAISGQ

ACIGEHDLMVEGLIGGGFASVGAPDCLVSSGRWYYEAILHTNGCIQIGWADVAFCGAADR

GDGVGDGAHSWAYDGWRQQRWHGRSSHWGSKWKQGDVIGCGIDADAGTVIFSINGKMRSA

NMGVAFRAIDFARGVYPCASFNRRERLQFNLGGSPFRYTPPPGFQPILNVLSETCDLSSV

PNGFGVIGSREDCLEENVGEEHYPSDTRYFARDMHPSMLRTSGHSRSSGFTPGSGMTKAD

ALAEIKALPDNRVYVELLVITRSLAILQARRALLTLLAKWPKDEVGTFSVAACLTGGSQC

AAVESEDSACFIEFIKLVASLSATHVSNPLPSTSFTRPDSDALHFLDCGATGRFALSLLS

RVVLSALSKALLTLTSGTIDHNPLVNTILSCISSEVKRASQRRYARIPWNSSEAAITATL

FQITAESGQTWSDKEVLNHPNLFLAEWISGLLLQSLELHKAKLYAPVHDQIRQQLLQAWI

SALKSPSICVKERGATIIGGILQNMLPKDCIVTNEENTQTFNGETKLQLRMALDVLPLKR

LVSLSQERILREYPNAPVFSKYVQSVVELVAAAGLVLSAVGQSTDKLLRNSMSMQLEACK

QIEMDLEPIDKQEYEEA

>contig25825 Frame-2F

MKATQARHPLQELLVEHYIPNGIFLDSTDSLKIVTGHNGS

>contig26169 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57991.1|) 7e-24

MTIIRSAGRVAASYTLLTSHRRLSTALRFQPNAKLSDESILKHLVCPISKFPLRYDAKRG

SLVCDEIHVEYPIWKGIPMLVPSEGRIINPSEPNSSAKQSATS

>contig26521 Frame-0F

MLVVDGLEVAWSVCLPACRSCRS

>contig26820 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61385.1|) 2e-65 NOT\_ORF

MKLWCRCLSRKRGDLPQRMLFQEQFERIKAVYPGTSYVCLLDGTSGDMIAQSEITEIHTD

EIARTIITLKNAALQFAATLNQIDPQVVHVRGSQGMFSCYGTAQMILAFYSEMPGMDLEG

FDCFEADKRIESITGELHRVLDAS\*SVNGRHREFGGI

>contig27315 Frame-2F|Blast-animal inward rectifier K channel (IRK-C) family protein [Phytophthora infestans T30-4](gb|EEY64136.1|) 2e-87

MPASKKRIQNRGPLNVGTQQVPAALKDWVHIWHGVQVNNSVDETSIFHAGSRFEEMPFWK

QFIRLPANSLFPRVLTFANPRKKYKDFLYVLLNMRWPMLLAVLFGIFMVNIFIFAMIACV

ICGQPKQFFQAFNLSYQTFTTIGFGVVYPTDTCSNIAMSVESFASMMMVSAITGLVFAKF

AKPRQKWHLAKFASCNRMEKSISPSSCALPMRHNLKT

>contig27647 Frame-0R

MAVGMTLNQRYAPSSATPNVNAVLSPPHGRSPRYQEDAKIHHANVLSLPPQQMDRIYQMP

FLNQSPYAPLYPSSSTAMNFHPLAKPGPSISEDYAADPLPFEYSRKYSPSHRDDGRGSIS

IVTSSAPMHYNNSYGSHSDYAPPPSSQRLSPYHHLQYPEPRTYHHSELNPQVPRPHFPRS

SSTQMYSPMLPLPHQFPLTTVTKKEVDAYPHPPTSIYGDVRGTAQEAMIKVKTPLKLKYW

RNGRRNLQCFPSCKVFGDYSAIKIEDLKQHDFMWGKCRGSLITEVTLNSSMSFDDIVLLG

RVHSLENIPVAFEEAVIRECMLGQTVEADALDLMKDQWITGERLPNFVQQDANVTCFEFK

PKSVEVHRRHDPRQMQTPKRQVLCAV

>contig29461 Frame-2R

MLLAYELLRYVYYYSPLVRVCDSAGVKFNGAFCFGHARTIDNFT

>contig30243 Frame-1F|Blast-alpha,alpha-trehalose-phosphate synthase [UDP-forming], putative [Phytophthora infestans T30-4](gb|EEY61781.1|) 0.0

MEEEHTALHVVAASPPISGAMSPRNDFFVSQRASTDFELSRLDTLSLEEQEILASIQMLQ

LQLVQLRAEQEEDSDEDSTDKPLDTTGNQLIVVSNNLPVLLERQPQTGRWKVTKTTGGLD

KLMCLTGVRTDLDFLWVGWVGQHIPKSDHEAVRRLLLQHNCLPVFLSSEVASRHTSFSSE

VLWSLFHYVSEPISFTSTTCSSSSFHSTKRFNKQDWRAYESANESFADAIAEIYKEGDSV

WVHDHHLMLLPSLLRERIPPCRIGWFLHTPFPASDVYCRLPVRSQLLSGVLQADLVGFQT

FDYERHFLSTCHRLLEVECSHKGIRSILPDRDHFTSIGVFPIGINLEPFARTASSVTTIN

RVNELHEKFGGKRIILGIDRLDNIKGIPHKMLAMEMLLDRFPEWQHNVVLVQIGISSRSG

VVESTSISMNAAGENIKRSGAKSATKDQNAALRRTSSFPIVKAVDSSAGSGSPMKGVSES

PTTAASPIASGKSNIGYDSCHQLEMSSHSYHNIVTQVNQIVGRINGVFGTLDYAPIHFIQ

QHATSHDELCALYDLADVCLVTSTRDGMNLVSHEFIVCQQHFMRNKDERDKAVRVTAKSN

RFENDSGETLAGKLGRNLKIKTAQEGQTEGAVLSPISSPRQSSSFVLSDWEGKTGGPGVL

IVSEFAGCSQSLSGAIVVNPWNVEDVAHSIHQALSMCRTEREIRQQKLYRYVSSNTASAW

GKQFLDELSEAVEKKRKSSTQLPKLDKQTIVQAYRSAKNRVIILDYDRALIPQHSLLPLA

AVGPNFKAILDALSTDERNTVFIVSGRERKFLETWLNGVRVGVAAEDGFFYRMNLSNARE

HWKTMSKFQYDVATARAGGSSATVMGAGSISDDNLDISYSGDVHSMMHMSMGSLPAYSQQ

TSIRGSSDAGDDLTIANSIAPIDNLLDGDDMSWKDLVLPTMLLFTDRTPGSYIEDKESSL

TWHFGDADPHFGSWQAKDIQIILERQLIGTALEVYQGHMSVSVEHEGCTKSRVLEGILKH

LSLSDQITKKNGHAVDFVLCVCDDVKDDQMFQTLNALVAESNERHDVRKRNEEIQAATER

TRENTDAKNKFALSQLHALPVPSAAHVSKAKSRMPRLREKCGVSDDSGLPLNLQENLEKR

HRNDQLIRAAAAAVRGHEEYSTDDDDNFNVDEFLDDDNKVAFSRLQKIPVDLADKVATFA

VIVGSDVQHSGGRHVSSFAVDSLADVREVLKDFVDESRKDKL

>contig31059 Frame-0R

MIHAYVFVATSVRDHEDHGPLFQSHMNRINRAAQTKITVFHTFHDEVNSYRNHVWQCSGA

CRRKSPHFGLVKRSMNRAPGPTDRWWADHERNCGGSYSKIKEPKEFTAKQVKKREREKAR

DDKVKEKMGAVKAAPSVKDFFATLSGSFDGKNDFDKTTASSESAAPRTESKIPALPRNDR

HKKRNRNYKNADWSRLKFPLPSPVVIPAGDDKVTSLFLRDIPALLQTPLVQMFSTYSQNQ

VGRKIATSVTEAKPGDSCPIVDLVTDSDESDSEQLKKAIKLSLVGHSQSVDKSLRTSRTG

EENIIEIE

>contig31411 Frame-0R|Blast-dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69318.1|) 6e-62

MPFSQDGSASFRLLGMYSLLKKDGLVVPYILLQSAYVGVVVVPFLTSGTSKLLHIKQSKR

APGLKEDGSAHPVLKAYIMFSLLGITVIHAAQVIIIPPARYPHIHDYIFAAYSCSHFLVA

LGYLTYWQLTAETQSEETKNE

>contig31600 Frame-2F

MGKIHCSAIANQEFAALKKVLCQTADDAKQCIRLLKQHLLRVDSCHGKLFIHSATVFMRN

DMRKAKDTSFELKRVANAISQISEPSDMEIEAARNGMEAIAKAMDVLHTTARNYDKVHNQ

SEVVQSTFKVRKRDREQDHLEMFVCDTNTLESLVKSIVRDNFNLSALSHQITIT

>contig32263 Frame-0F

MRGVFVHSADHHENWICSAVRIIFTRLSSSAEETKLGCITFEKDRRQSQGIPCSRQFYVY

KAP

>contig32533 Frame-2F

MQGSKRVVLRAAVRANGAAHRPITSLTSRAGVFIARSSNIKALNGTSGYALPACVQRLSA

ASPIRVCGFASSGGPTDVPVPSMGDSISEGTVVEWIKQPGDAVAEDDVVVVLETDKVSVD

VRAPFAGAMGKHLAEIDDNVMVGSPLFQIIKGAAGTESVQETTAPENTATAVGIEPTGEE

VTVPVPTMGDSISEGTVVEWVKKIGDSVAEDDVVVVLETDKVSVDVRAPKSGTITSILAD

VDQTVEIGVPLFSILPGNEGSSTTASKPAPASTPAVAPTPTPAAVTPPSTPDPPALTSPS

IPESTAGVNPLLAMSGRSVRREKMSRMRLRTAERLKESQNTAASLTTFQEVDMSKLMDLR

KQYKDTFEAKHGVKLGFMSAFVKASASALLEVPGVNAMIDEERQEIVYRDYVDMSVAVST

PKGLVTPVLKNCESMSFADVEKGLAELAIRARDGKLTLEEMTGGNFTISNGGVFGSLMGT

PIINLPQSGILGMHGTKLRPVVVNGEVVARPMMYLALTYDHRLVDGREGVTCLKSIADKI

ENPERLLLDI

>contig32890 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66418.1|) 2e-66

MGTAPVWLPLTLVVGLMGFPIWITFGFLTAMLVVLSAISAVVTVKLVSSERVKSACQHLL

TSQQGQLLLFEGMPGEELLSPSVMSVRAKEFINANPSRKLVASLAIDFLGNATFVVPGLG

EVIDVLWAPVSSKMVDALYKESSPRAKYVASYGRAAAIY

>contig33439 Frame-1R

MKETVASSNSALVPSTPAGSRRPRATSMQHFSELCSVPRECCSSGSFVSKLFRMVDTEPS

SIVSWCRDGSAFCIVDPKMMADHCLPKYFRHRRFSSLIRQLNFYSFYRVQEGQLTIYQHS

FFRKGRPDLLLHIKRRGAGKAKDPWFDPLANSSSKTSNSMVNSPLKNVMQTPTMAPTPLG

LTACYSPMAKSITLDNMSPALKPAMVQACLPSVELNSSGMSDGPSKIDTDHACPLPSALS

MKNEMLFGDMLDSSLTKAASSLSAPLDIDIQDFLTDDCSITSGQADDPLCGANQNKFAMV

SRNCLKLDNLQHLELSPTLESQGDSESISFENGLLMGLANVEPGTWEVPLSPLNDEEDVM

PWLDLCF

>contig33516 Frame-0R

MDEFTCPFCGVMDDKFDAENLDQHFWSSCQMLTPCKTCGQIVEISTLNEHLLKRCELQNH

CECPRCGEAITVKFFERHVSLNDCQPRVPLNCASRCPLCHNDIAIGTAGWQRHLLEEGCP

QNPRS

>contig33620 Frame-0R

MKFWTVPIASLFAAGFLQVHDQVRAQGKWQPEAISHNQVQPFPERPATTISEKAALAFKP

QLKVASGCVPYPVVNDKGEVSDGLRNSGKAAGSCRGSGYGSQVYSRSTWMADKWAIMYMW

YFPKNAPESGRGHRHGFEHVVVFVNNPGTEEPQIIGCSTSKDHRYAPCPLKKVFSKT

>contig34265 Frame-1R

MTPLCKPRLDMHTFLLLRSSSCVLELLGELPLLTVFWLREPFRHSASCSLDTILKFLDMI

VEVWFGVSAETGAPALLAGRTGMSRGSLRKFYKNFFMRHVSVDASAYVVLLFHKLVTWDV

RTGRRKGSMRVGYSWSFEKVL

>contig34672 Frame-2F

MIRLSQKSCFTRTLSTLSSVNPVGIIGLGQMGGRMADNLRKHGYNLVVCDPVAANVQKHV

DQGAIAAVTAREVAEQCDTIITMLPSTATVEKVYLGKDGMHEVLRSEHLLLDSSTIDPIF

TKQLSKELHDRGATFVDAPVSGGVAGAQNGTLTFMVGGEPEEFERVKPLLKAMGKNLVYC

GGS

>contig34809 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68215.1|) 8e-30

MTQEELKKLMQWKLKKGKWRPQLMKYISELTVSEVKQASLTGYSEIKRGNLRAATEAFCA

LK

>contig35297 Frame-0F|Blast-structural maintenance of chromosomes protein 6, putative [Phytophthora infestans T30-4](gb|EEY55333.1|) 2e-88

MKLVTSRRSTAKAQKTQHKDPDTSTTSETEDETDIVDNHANVNEYENCVGIGHKRRLKTS

LAHLPQLDAHVDTEMGIVEEIYCENFMCHRKLRVALCPHVNFITGENGSGKSAIIAAIQI

CLGASARSTHRGKSIKNLIRHGCDGNALVRITLRNDAVGSDAFRPELYGRKIQIERLIRR

DGSAEYRLKDERGLLVSKLKTDLEAMLDHLNIQT

>contig36674 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59576.1|) 1e-104

MTEYRHSRRPPSTDPRHKRRSRSKSRSASSVASPKHIRRRHRGEHGCHDRHEKAKGAEKE

KFENRREAKHRSRMWTVVDSESGAASSLKQEVRKIRDVRRSSCSKHQSPSRSPSFKSLLD

SDSKNSESSYDKSSSKRKRKHIKSEKDKKRRKKDKKKKDKTSKKSSKKSALNQDEYGKYG

ILHESDFHSKSVSFQAWLRNVKKMGEFNGPKWEAMELFKEYMEDFNTCTLPHEKYYDIEK

YEMLQYQKQQRKAHAKLESASDMAMDIQADEDRVRRERQALREKKEKEEFRLVLQLMDKE

KIEAMREQERLRAQMQMFYKSGNVEEARRLEQLINKVDEDPRLNR

>contig37295 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62982.1|) 3e-78

METRLIESWNNNQKVEALRIAIKCVKLLADTDTAPQLYPCVFALVSEILDVFGNLVFNRI

RSRASEDENGQPLPEPLSDHFMSSDINIQATEMCRNWFYKTACIRELLPRIYIELALLRC

YRFLCDGEYFQITSRLSNMI

>contig37682 Frame-0F

MSEPILAFIDCSAGIAGDMLLGALIDAGAPLEEITRGLESLQGIEGEWKLHIRQVWKGPG

SIAGTKVDVESMYRHKGAGAPAPNNRGHEHSHSHGHSHGHHHRHNHNMPTQNEIKNTQAA

SIEMTHDHSHDHVHDHDSRAQENPIGENEKEPMRNLNDIKKLIAESDLSEWVKEKSVAVF

TLLAQAEAHTHGTLLEEIHFHEVGAIDSIVDTIGSILALDLLHVRQVHASFLPFSSGTVS

CMHGVLPVPPPATFRLMIGVPVCPAPKGATGELVTPTGISLVKALASTFGEPPPFIPTHT

GVGAGTKDFPQHANIVRVAIGMKVDPMATAKSYVNPAI

>contig37822 Frame-0R|Blast-protein phosphatase 1 regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY62012.1|) 7e-85

MGSVASLRQLQHLELYDNQIQTLEGVQSLVNLQVLDLSFNEIRIIPDLSHLTILEELYVA

NNKLKKITGLENLKRLKKLDLGANRLRVMENLDGLVDLQELWLGKNKITTIQGLETLTKL

RIISVQSNRVVQMTGFAENLALEELYLSHNGIEKIENIEHL

>contig37857 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65133.1|) 9e-29

MRLSSFKLQLLLPLWVGLGGYVWPQKQAPGKSLRSRRKARPWCVKRAWCDSLIYSNVVYA

LAAIFSFSCGQKCCGGLQMGAAIASVMFHRSKETKFLLLDALISGLLG

>contig37996 Frame-0F

MREGDVCSGTYPGLCPSFSTWKTVFQSISSVCAYQLPSGTDQCLNDSFSGSNTDGFVSCM

SLQDTSNTSARETYGVIFGCVDFDGSNLLFDKDSDNWALSAQMNYTGVINDACRSTNDSN

SDIACSGRGTCTPNSSGSLDYACVCNVGYNGTFCEEIESNRCTLESQCQAGTCNLVTQEC

ECEEGTTGDQCAYCDPSSSKACGGRGQCVPAPSLSNKSNATDANTSDATADSSSLSSAVG

SLDSDTILAGSDVSADASTRFLQVSMGNATTSSDAMVCECEDGYTGDQCTRKVDSSSSGD

GKKSRGTSTSDATSLATSIAIVASAIAVISLLN

>contig38016 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65139.1|) 6e-62

MEEIVDTDEAALDDAILFNLRKGSTTLNEVEELLRKLTAEKWLAPIARQLQVRSFTLGPR

AYLELIAFLRDLQVKKCLICQYELLQGAKCYSETCDILVHHSCIDKYENNGISYKCPTCQ

HKLRR

>contig38254 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61115.1|) 5e-94

MADYNDEPECCPLCMEELDLTDQTFNACPCGYQVCLWCWHQIKNEYNGLCPACRQPYAEL

SKQKNPLDRDEVVRRTKQRKLKEKSDRRSAAQAKTVMGSRKSLQNVRVMQRNLVYVIGLP

VPYAEEELLRSNACFGQYGKIVKAVVNKSHLNTDRANATASAYITFAQKEDALCCILAID

GFYLDKCLL

>contig38320 Frame-2F

MKKASRLSSLRLLLFIALFCIALLSGSFCLAESTESQNELERDSSNPVVDDLKELTGGET

FAFQAEVSRLMDILINSLYRTKEIFLRELISNASDALDKIRFLALSNNELLKEQRHLDIR

INFDKDARTLTIRDTGVGMTKEDLIANLGTIAKSGTAKFVEAMQGGSDDSSLIGQFGVGF

YSVYLVADRVRVVSKNNDDDQYIWESDANASFAIAKDPRGDTLGRGTEITLFLKSDASEI

LDQDKLKSLVGHYSDFITFPIYVNATYTESYEVDEEPADNEDDIEKNADTTSEDDEEKDT

EATSEADEELEIMEETEESNSSKTRTETRTVWKWERVNEVKAIWTRSKDDIADEEYESFY

RSLQKTDTTDPLTWIHFQAEGEIEFKSILYVPGQAPRDMYTRFESKKADIKLYVRKVLIT

DDFDDFLPRYLNFIAGVVDSDDLPINVSRETLQENKILRVIRKKLVRKILEMLRKLSEND

GEYGEEEDDETEVIDPSAEVDFKTSEESVKDAKIEVEEEKEKENATYNKFWEQFGKNIKL

GIIDDAANRGKLVKLLRFVSSGSDGKWTSLEQYVDRMKDWQGSIYYIAADNAEACEKSPF

MEKMRAKGLEVLYFVDALDEYVVSHISEFDGKKLVSIAKEGVKFGDDDESLIQKRDQLYA

DKFLALTTSLKALYGDKISRVTMSQRVVDSPAVMVTSQWGYSANMQRIMKAQTFSNGDKN

SPMYGTASAILELNPRHPIVCKLHELMVNDSQKEETKDLAWLLYDTALVNSGFDMSDTSQ

FSARVHRVMRSVMGIDSFELEPEIEVPEEEKDVEEVDNLDKAENSPSLDAEIYAEADDDQ

SEKDEL

>contig39455 Frame-1R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY57772.1|) 2e-67

MVLLEKVVAKKTCLPESQRWLLTWLGPLQQILYMQQQWKRLLTQFTAKRGFLWLLETVRK

KRSTICLQSNVRAMLARMRYRVLKKKALARSRWHKAFLQITIFSLFCRCLRRIHVNRLEK

DNAKLTSGLASAMNRLTAIQDEAKVARLQLKELHVSFDHVQQNAKCHFQRVEELEQALER

KGREVAELQRQMTTGRGFVERIVCFFTCSAAVSPPVSPREMVTSSSR

>contig39828 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY66518.1|) 0.0

MDKNYFNAVSEESQYLPKKHYIIIRILSFAMALSPSRLRRSCSLVAGMLLMLGVGSTYAL

SSWNAQLKMLLHFTQAGISTVSSMTMLGTYMSYLPGVIFDRLGPSTSLLLSGNIMLLIYL

VLFTTLQFAPERTSPLSIGCAMMLFGLLSSFCVFSSIVANESLWGASNRGKVMAALMSAY

SCGGAFFTFVFHEGFDSSDVPGYFLFVGIYLFVVCVFAWYVFPRPICGEEEMSTRERSKS

VEIGLCRSETEVNGHVYAKLNCEKPDDITGVVLLMDMRFWMLFIPVMIVVGVGLFVMSNV

SFIVESLGGQIQQIPLMVALFSVANTLGRLLAGTISDIYRLRYPRAYFAGISTLLTAVTQ

MAFLFVPPNWLVLPVALAGFSEGVMFGTFPVIIREEFGLHNFGKNFGLLSIANCVGYPLF

FGPLASYMYQHSAGVRVVDGVEKCFGAQCFAHIFVVAIVLSALSLACCAQLAQIQRHQLP

FNFQQIQ

>contig40033 Frame-2R

MDGIATFSSCNRGDIGQNIADVVPARLLNKPHLWLSDWEVDHSLLDCDEGGWVYAASNAH

FGSLEGLVRTDDNETNLKTPEQIEGERLVRRRRLIRKRRIDGSDLSWFQELLDCSTLLLK

KRLPTCHDCEASLLSQFT

>contig40297 Frame-0R

MQNAHGILTPIGMDHDERVCVTLLAKYSNGNGGTAKPCQSLVGSLLWLARCTRPDIANAV

HKATRRSHAPTKDDWRPAKRIVRYLLDNIF

>contig40947 Frame-2R|Blast-endo-1,3(4)-beta-glucanase 1, putative [Phytophthora infestans T30-4](gb|EEY65979.1|) 5e-07

MTSHNTDAECYADISHTYDGHIPRINTEHNVTHLDESIPGRYVHIPQQ

>contig41809 Frame-1F|Blast-cathepsin B, cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|EEY57812.1|) 0.0

MSSAQDRIKIANKRQNYTGADVMLGRQSFLNCAPGHGLSSGCDGGEASDVYEFMLRYGLP

DESCLPYNATDHTKFHATNGTCPPHGYCMNCMYTPESRTAPVCFPVTKMVRYRAKSYGHL

SGELAMMKELMKGGPITCGIACSYEFNYEYKAGILEDKTGFLDLDHDVEVVGWGEEDGVK

YWHVRNSWGTYWGMNGFFKIVRGTNNLGIEADCAYMEPDISKEELVWEEKEVYGGSIFGI

VPFKETAKEHPILDTSADITRPENDVLGHELPLLESDATRRRKEDGISTVLATLFFASGC

GFAALVAVVALKVRGHRYVYRAIA

>contig42295 Frame-0F

MRVMATRNRTSYSHVPPMADDENVSNDGSDEQSSGLRMSRSQKAALWSTRLPAFLWVVTA

GLGAYGADFFGIIFTDPRIDR

>contig42501 Frame-0F

MGILGHNFRDELRRLPLELPFMFDGVGKAICSEKIDAAMKYHQALQTYLHDCDTPAVASV

SEFSNATALSKDKMTKIRGNQHVEVFDNANDWPSELTGIPHGFFGAIKELQIARDGLMEV

APPLNFEIEAVDINWDITCDGSATADVEKIDWDIGPAAYTNAAAAIDDVPVEIDWGITSS

DVEEPLGDVNTSEAADIIEAISEITITNERPSRGSLLDCSDFRTRILNDLLEMRAFFLQR

LAEITGGDSVAFANQYQGSSPHLEDQSKAQIEDYQSAVNQAISLLTSKRLQQLVLLKTSD

RYLDRLVANFEMLTKHMDKCRREIFSLEDKIGNLIDATKNTQFQVEALVVTTKTLKKELE

AALPSLFKGHKINIVGEVNTL

>contig43124 Frame-2F

METEMTEMTEELIAKSQEIRTRDENIENLQLALFKLQSEMATANDGGIAFTNEREKMRSQ

LEEKDTDIARLKDELDLLKSHYDDLSENERQLKASFERESEAVDEWKEQVESLARSLEDS

KEDRMELEQKLCVDMGEISQTRKKVEELNTLNLNLQKQLDVAKKLNSELEGKLALLAVST

VSPGFEKEAAESKRLIIELQTLRNSLNSLSAENKRLRNQEGLSSVVTAKRVSADILQVNF

TPEQLARKYLAERTRNASLLSRLQTVCGNIQVFCRVRPVINDEIKKSWGLKLAVNVINQA

DLAAMDIRPDRLSDGSIGSDNKMEALVSTSSWKVFTFDRILGPEETQNDVFREMEPIAQS

VMDGFKACIFAYGQTGSGKTYTMEGTSSDPGLNYRIINHVFQSAQLRGSIYTPESERNSS

EDDEMNGLHGTSELSVYHIQVGVLEIYNDSLRDLINTNNLKGLEIRHDSLTGDICVPDLT

MATVSSPQQTIDVLRNAQSNRVTGKTNSNAHSSRSHSIVIVQILKRRSEPEDGVNDPAEV

EFEEEGCGKLYLVDLAGSERVKKSNVSGDMLKEAAHINKSLSALADVMEALDKKMAHVPY

RNSKLTYLLQDVLNSSCKTVMIVNVGPAVESASETFRSLQLAERVRNIVVGRNQIVKNKK

DILSAKKAFAELQSLKQQMQISKRKYMQSQQSVVAMKRDQKNQSEKQSATLQTRLKLWET

QNESLKIQNDSLKMLVDDLSAQLKAERDHKKRELEQREAVQRSLRQQSAKNRVSSLQKEA

HQQLLCEREEEIKKLRQQLTEIRRRSTSSLIPRLPLSSPPMKKSKSASSSSAYQQDKDST

STVIALSAGGSRALKARTVLSKTSEARSSNEFCTDQSLPGSKRRSLLGSTRQLSSSRTTP

ISTSGVWK

>contig43278 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57474.1|) 3e-07

MQRKLYGLIELSSIFFRSLLASVPWCSMYQACA

>contig43362 Frame-2R

MSPDAAKLGFWSESRTPSSPTRLRSFSNHISNKMVQPTELLHGLIDSFVNKNPTEKTLDP

KAEALLSKDHNEEASRCRHLSATSQLVSKSKIAFSKRSLTVDTSEAGLRSTHSSQAVSAS

DVSVRTDYHNLNSATSPSGGLWSPKSELVLSPQSETSPSSPHHLARFDSTDRFLQNLSER

DSKLEEDDEEAERSDSSVRSGHQLGVEPPCVIFKERWAEKERRIQLTSPYGKLPGWRLLP

VIVKSDDDLRQEQLALQLIHQFAKVFEESKVPVFIRPYDVIAISATSGLVEAISDTISID

SLKRNDREFTTLLDFFTRHFGDPSMPEFRKARANFVSSMAGYAIVCYLLQIKDRHNGNIL

LDAEGHIIHIDFGFIL

>contig43425 Frame-0R|Blast-DNA-directed RNA polymerase I subunit RPA2, putative [Phytophthora infestans T30-4](gb|EEY63911.1|) 4e-62

MVRSKRCHLNNLSPLELVNAREEATEMGGYFICNGNERCVRMLQMPRRHHIMAVRRGAFA

NRGD

>contig43674 Frame-1F

MSGKPPYLACLEGIAISIVWSFYIIYNGTLFLSKGFNRAGITYLHLMWSAIMLTIISTVF

LTYGLRVLSRLLAYERDSKLRESTTMSDRVINHSYDMEGMSEEDSRTTKRLEPKKGHSAK

IRKILLVTEMLSLTVVAAQIFMAVSHTAKESEELRCANGIGCESITAGISYLNILQVTCV

WVVLWIFRTIKKKEVIPHPRTRALV

>contig44059 Frame-2F|Blast-eukaryotic translation initiation factor 3 subunit F, putative [Phytophthora infestans T30-4](gb|EEY55350.1|) 1e-130

MSAFLLRTEPVTEVKLHPVVVLQALDRSLRRAKGQERVIGTLLGRVEGGVAEITDSFAVP

HLENGDEVAVGRDFHTHMYELHQRVNESEVVVGWYAAGPGHVDDHSALIHQFYSSVCELP

IHLVLDTTLSKDQLNVSAYVSSPLEIAHTASVHQFKQIPVTQKVSEPEAIALSVMNPKSE

ETQAVALPKELEALEESMEQLYECIDSASSFVDDVVAGKHPADAKLGREIADALATIPIL

REEQFDQLFNTGLQDLLMVSYLSGLTQAQLSMAEKLINT

>contig44136 Frame-0F

MVRSLPLRKGFFKATVLSDADQTELLSWGRSLVPDLVRQPDVEWTMIHERKGVQLCEDRQ

KGGLTYSIRAVAPVHASLDDIMDIFLAQNTVDYRALMQLQLRDLFADAAVLFHKEQNESE

ALSIKWMAARTKKSVTSLVGQAGVDLCLLEYAGVISSEFIDGHSLSICGSTTPSSPVGVC

LYESIDQAECPSL

>contig45027 Frame-1F

MFDELAFSRATNQIIVPCNIDFMSQLMSRADQEVVGDWGDRHARTIAEAQDEVLICLGMV

IWDKLHNLWTKSRSEKRSEELLVHCVVSTLRRNFDVAVEALHGEEMIEQLLAEEDDEFRR

LEKRKEKRKEKKKKRKSASKQKQVVRSESSKGQQTKKQDRPQTNMRMQSDSTNTVTSQSS

TSSFSSQGDDDDGSTSSRSIDQARLHLCDSTCEESCLHVNWTYDERMEWQLLSSMGWNAS

DQMNSSLPELDVDTDDENHGIPEDEIRLWKENRSILVRRRMAQRRKLQERFDQFVLRMNS

LDTQSVSVKP

>contig45702-1 Frame-2F1

MVSGGTYFFCILLMHVRLASTCLSYLVNGLLKSRWR

>contig45799 Frame-0F

MHRQSKLHLQQTKFAFTVKYKLTPFQTFRKREVRAKGKDHSLL

>contig45913 Frame-0R

MRSSVPSKRTNLLKACTNWWARTHRIHKLTRFMKTLCVFELALMPAAPTVFGKDH

>contig45984 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57662.1|) 1e-50

MAACSRARNLRGANHVLEGMKAGGIMPDARIYSFLINCCARKQGFVKTAEKYLDDMLTTK

VNPTVFVINSLLRVYSRDRGRSKEMLNLIHRAFVEYELVSDTITSRTMVHYLLHEGDVGS

AVTYLREIENEIFRIGMKFLPVKRKVVNFVIDACRQRG

>contig46620 Frame-0F

MERLKRGRVESASYEQKHPDDCELRVDYSMQSCSSNVAHMVDSASILPRAGRAPHHAAFL

GHKDSLIRPKSAPNLTKQTDDKVISRIFPDICPR

>contig47061 Frame-0F

MLQTRLKLEQWAASQLPIAEARKRLKLKHGLPSKDMDFDNSLA

>contig47915 Frame-1R|Blast-glyceraldehyde-3-phosphate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY66508.1|) 3e-83

MSNSHLTCDQMNALRNDELEQWKLQENAADLMVPLIGRLYRENNVVSVLFGKGLVHKNSI

DIIKLHNYVCKYVGKSLQPTETLVVLLAVAQYATNARDIRIDLGRTFVFMEKEVLDVQAQ

TTIETRESKILMLGEILNEKMASLTQAPTLIPRDVILYGFGRIGRLLARLLIEKSGPGVK

LMLRAIVVRQGSNKGDLMKRA

>contig48150 Frame-2R

MTVCIAVFILLGHGGTSVVYKCHERRTGTVRAY

>contig48392 Frame-1F

MKFIIACVVLCSIAVVGHSTSFDFQS

>contig48518 Frame-2R

MRRSDGRGFGRTSSNRLKILRARRRALRLSSAALAPSVPCVKAVAR

>contig48785 Frame-2R

MSCRCDTIVSLLLALLLGYHALSEPTILPEPQNPDSSTTSSSEAASRWNELYSESPVLSS

THASLHGSQAIVPTITSATDVSINQVEKHLDIVHQIELSVDKSLHHLENNEQFATFTTLQ

RQEIHHLHYELTTMQLNLRRLARGLNGT

>contig48891 Frame-0R

MHGSAQFEWDCERCRIKSIRSQSNMMSPVLRLLGDLHTVSRVFRDALVTLNFQCRALEVE

>contig49171 Frame-2F

MSRLHSSSTSSSRVTTTPNHFSVYTSGPPLSQPLVMTNENQAFQLELVPLEPISISTIFP

LPSEDVYALQRKVYEVAHLVQNGFQSSARVDDDEESQLAYTNYRTVAWKDAMSNGVTHSA

ITKAVNGGVHIAISIEAEKGYGGQGVLCLKESD

>contig49496 Frame-1R

MVRKELDEMENWCRMHVTDHSGWNHRQHTLNKLIKKCLVSNEENSSWKLILAEYQFLSEI

MTLYPTYEALWCHRRFIMQHLLDKVARNNDNLNLAYLNDSVSRVAKNVLVASRDETILSA

SWRKFLNDCSNYTSTSAISTIIHEIGIAWTCNNQYSRRYGAWCMMRLRAFFHRKQELGEM

TLQILLIRELNSLGSFFQKVLTEKDGMRQDLWRSILNCNYIC

>contig49522 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65494.1|) 4e-39

MARQVFGIGVDVALVSRFERSYARFKERLLKRAFHPQEIDEFFARPSSERAKFLASRWAV

KEATFKAFQRYRLLFPEIYTMRGDINELAISTSLPATKKSKALRLMFSGETEFLAKRLQL

V

>contig49908 Frame-1R

MWPTRAEFIAMVERNLDAVYMKWSGSMRRRWEMNTWRMKTWRGRRLDSVRLRLSSGLLMK

QQQQNGVAVFRPRKVVARVSWCLRLHCRRNKSCCRLVLARHTIFGLNTSSISVLTARSVT

MLGI

>contig50281 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68023.1|) 7e-16

MVSCEAMVNFKLLEVCLFLLT

>contig50704 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65687.1|) 3e-24

MDTPPNIRRQYASPPRESTEQRRRRLANRRAAKYRHFRSLSHASEPVAESQREQNTRRQR

ERRSLLNDEARDR

>contig50793 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58146.1|) 2e-81

MAPEIKSKHLYRGTPVDVWSVGVVLFILITGLPPFNEAQKGDVWYDDLLKGDLQHFWDSQ

PDEVCQMMPPSAQDLISMMLVSPDKRVTVVQALQHPWLRDADCVDLSLIRDAVSTHIAAA

LAVRKMETNA

>contig51039 Frame-0F|Blast-Cullin-associated NEDD8-dissociated protein, putative [Phytophthora infestans T30-4](gb|EEY61245.1|) 1e-115

MRANEDKIAQLLDKTTDFDKDERYMATSDLCVELQKNVDLGSYLEPKVCVAVLKQLDDKS

NDVQSIAVKCLGILVTKVQENQVEDICAKLCNLILNGKAELRDIYSIGLKTIVSDVSQNT

GASIATGICTRLLTGLGKGKDAAIKVETLEILTDLLRRFGYDVATEHATVMELLMVRLTD

ESPLVRKRATACVGSLGVMMSDVLLSRLVEHLIKSIQCSSDSANIRTWIQTIGMLSRTAG

HRFGQHL

>contig51220 Frame-2F|Blast-aldose 1-epimerase, putative [Phytophthora infestans T30-4](gb|EEY60571.1|) 1e-124

MNAEKEAVVELRHPSGSRAEVHLYGATVTSFYAAQEPDRNVLFLSSKASLDCSKPIRGGI

PLVFPVFGAADGYPNHGFARTSKWKLIQFNEATGDEKVPTVATFSLDISTKMKTMYPHDF

GLLYEVKLYANALTTAFHVENKSEGEMDFQALLHTYLSADSVCDQGVEVEGLQNITYHDK

VANAEKKETRAVLHFEQETDSIYANAPSSIVVRMKRSDGKERVVTIEKEAIVKNGTTHMD

SRATWSYGTRGLTRPKA

>contig51354 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59539.1|) 1e-98

MQKEMVVKRMARLDELESKMLAMRLLYLRSLSLGWTIPNGGSPLPFVSEEDVERGNLRHF

IENSVDHYVDKNKIPATPPTFHLLRLSLKMSRMNTRLIMNNEKKLMTFFVHDVSFEMHYR

MTKTDKNDTMIELALDAARFGLLDDRGAASNVFCQVMDRNPEADDMLGLVILQRGDGYMD

IGVKLKHLSLLLVFDPLLFTLYQFLPAIGIDEKEQMRFIAHEMANCMDSPEHRDAVKR

>contig52737 Frame-0F

MATEGGIDMLIDLLSSTNEHVQRQAAKALANLGVNVDNKERIAKAGGIQPLIDLASSRQI

GVAVEAVAALANLAVNDANEVEIARKGGLKPIINGAHAESVELQSQVARALR

>contig52742 Frame-0R

MGDSSAGASAAELFAACVVLYKPAPPLSRRALETSRIDPESGSRWVPYGVCVLSNFPIVD

LLRERLAEAYEFLLELETIAASAAAKTDDLNSSRHSFQLDKKVLAKLTRSISKEHISKYH

QPSPLPESPLLEASGLTPKATAASLLAALPRLDHSVRLLFDTLDISTVLLVFTA

>contig53129 Frame-0R

MHAPKPSRNLSIASTVNWLTTSHATNHNSYIHEDNVLRYIWLPITSHCKFNIEKGVSSRK

KAVNIAIYRGDILELRISRLRYISFNKIISVWL

>contig53226 Frame-2F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72292.1|) 1e-63 NOT\_ORF

MPAVKQSYEKLCGGCVKGKQTVEPFPARSITKSSHVMELVHTDVMGSMQKTSKGGAR\*VL

TFVDDYSRYVVAYFLKTKSEVATKFCEYKALYENQ\*GQHIKILRSDNGTEFDNKKLPRYV

QGAALCISVPCHITLSRTGQQKG

>contig53451 Frame-0F

MIKVPGRMYPVKQFYLEDVLEMTQYIVDEESPAYVGVDQSGANRKSTQIKVSGRGGTSYT

QQILWTSTSESSSTKSAVQETLKKPYSESTLRTLERIDPSIVNYELIQALLEQLITETEL

LSLAERNQTSASVLIFLPGLQEITTLLGLLEASRLLRHDSQGRAFELLPLHSSLSAQEQQ

RI

>contig53684-1 Frame-1R1

MECQFLEMLSRCSTATGSVRCAYLHLKKRQSSTF

>contig53899 Frame-2R

MQTIGDLCEEATLHAVHRLESSIENCCASTESLTSLGKALFTSLSLVIVVDMRDSLTDRV

EKPWHHSQRKVASRN

>contig54726 Frame-0F|Blast-Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4]gb|EEY68576.1| Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4](gb|EEY61751.1|) 5e-18

MVIEDARSLDLYTTFGINALAALTTILGGCIVFSNKLLQLASPKCMAVLLSVSGGITLFQ

ALF

>contig54843 Frame-1R

MDPLTFVHRQTQGNVPVSLVDSDTHDCFLLPLLTGPNLKSNFDRNGHQPSQHQNTHRTPL

DHWT

>contig55268 Frame-0F

MLSIRSVVSRGVSRVSLSSVARRSSKPFSQYLINLNQSSSLLSNCRHCSSTHASNSAKAL

ST

>contig55538-0 Frame-1F0

MSIVSTSRSFASLLTSTHDEHEPEMVLL

>contig55538-1 Frame-2R1

MAVRTKRTEKEKKKTNELAEEFLLTRESETRLV

>contig56122 Frame-1R

MNDETPTDVAFEMASPAVFDALFRSFERCVLTLSKMGASCLWVHLRLRDSFKQFY

>contig56571 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70376.1|) 0.0

MSTPSNPIEKVAPPALKATVGPNPTTHRGAPSVLGIHPQEPKLIYCSGKLVIVRNLDDPT

DTFVYKGHNEPTTVAKFSPNGYWVASGDVSGKVRVWSYDNPEHTLKLEIPVFAGEIKDLS

WDPESKRIVAVGDGRGVMARVFMWDTGNSIGEIVGHQKRILSVDYRPTRPFRILTASEDF

NVCVYEGPPFKFKQNNNHLHSNFVNCIRYSPTGDFAISVGSDKLMCLYDGTTGEFVDKFP

IEHQASIYSVCWSPDGTQVLTSSADKTVLLWDVASRQVLTKFTFGGLHPQLQDMQVAVQW

CHDHIISLSLSGDLNFLDLQNPSKPKRIVQGHQVSILALATDPRQHRTLTGSYDGVVCTW

SSKVATKLGGSHHTAKITGIAARAEEIASSGWDDHVRFATEKEYTGATALHAQPNGVAMT

ASGLVVVSTNKGVKLVQDQKLVYELPECSWTPTCVAIAPSADLVAVGAHDDMKIHLFDVV

KGSSLVECGEITGHLGALTCLAFSPDGTLLAAGDTYREVRVWDVASRSAKVQSMWVFHST

RVTSVAWAPSGLFVASGSLDERIYIWDVDHPMKKRLFDFSHKDGVTGVSFLSETELVSSG

NDACIKYWDLTV

>contig56849 Frame-1R

MSAHSTFSQTPSYKAHHINAKELASEEAKVYEELKRTLFLLETVVKTNAKEKIPRIFRAT

SRLRKTLSVAQLQQVVEQLLPTQNPSKPVLLALLDQIEAKVQADVMKSLDAVTTGEDVEM

TEASPEVEAALPSATLVVTLPVVDLIEVEIYLYLFVLAALVKYKLGQEALDTVDRVVARC

QQFNRRTLDLFHAKVLTYYSNIHEQFGHDLPTIRNTLLKAHRTSCLRYDEAGQATLINLL

LRNYLEENLYEQAYKFVSKTTFPESVSNNQFVRYLYYVGKIQAVQLEYTEAYTKLMQSIR

KAPANTAFGFRCTVHKLAVIVQLLMGEVPERSVFHQDELRQALAPYLQLTNAVRVGNLEE

FNVVLADHGAAFKADNTYSLVLRLRHNVIKTGLRKISTSYSRILLSDICEKLALENVQNA

EFVCAKAIRDGVIDAVIDHENGWLQLKETVDVYTTNDPQSAFQRRITFCLDVHNEAVKAM

RYPPDAYKKDLESAEERLEREMQEEELAKEIEDEMDEGL

>contig57550 Frame-0R|Blast-prefoldin subunit 3, putative [Phytophthora infestans T30-4](gb|EEY58258.1|) 3e-97

MSSSSPTPLVLESPEVLARLNATISGERNTRGIPSAVFVDSVEVFMDACGVSTIEPLVGA

LQQMYSKYKFMETSLQKNRETFKRKIPDTQKDLDMVRHLVAKRDEGETLQTHFSLADNVY

AKASVDCQIGKVCIWLGAQVMVEYPYGEAKELLESNVASATEKLAQIEEDLSFLRDQIIT

TEVNIARIFNHDVRRRRQEKDNMLAVELEAK

>contig57709 Frame-1F|Blast-proteasome subunit alpha type-5, putative [Phytophthora infestans T30-4](gb|EEY59553.1|) 6e-94

MEVDKHVGVAMSGITADAQTLVDHARVEATNHWFSYNEPVRVQALTQSICDLALSFGEGS

DENNHKQKMSRPFGVALLLAGVDEAGPQLFFSEPSGTYWPVKAHAIGSGSEGALSNLKDG

YTDELTLHDAETLAIGALKQHMEEKLTSINVEMAVITHERGFHVCTADELEIVIGRL

>contig57907 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57497.1|) 4e-18 NOT\_ORF

MRQSTISLKIMTFNLRFAGNGDGLNDWEHRKGFVAGLIDQHPPVLLGTQ\*GLKLQLAEME

VPSDFFQKGV

>contig58076 Frame-1R

MVCLQLALIKIHVQRCSCRQKYNSCEGGGAVYTQRRKSR

>contig58182 Frame-1F

MSFLRTYKTIETTITLISSFISDALRSTTKMKRRITPSLGIPSRSSTSLRLVKVSGKSTI

ATCSSKP

>contig58308-1 Frame-2F1

MFRVSKRQICRQGPAKLSLPL

>contig59215 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67986.1|) 1e-32

MECFASPLNCRYSRFCSAFLDTDYVFGSVGSFFHFSPRSGCFEANPPFIPKV

>contig03789 Frame-1R

MRSNDSQKILVVGLPKTLNDAQLSDLFSEFGAVAEAKVVIDAASSISRGFGFVTFTAASA

MRVAIKSMDKKEIQGRTLNVRQLVPKDEFQSQKKDVPDASQRPCWLLRKGKCTKGANCVF

SHDIKDGHFGHCFEFRQTGACKRGNTCKFLHPVQEPVEDGVEPELLVVKPVDKRVCYSFQ

NGRCHRGKQCMFAHELLLNGETKDVKLTQEHNTTEL

>contig04289 Frame-0F

MGESLTVRLFVRTQTYDIPCDPRQPARWLLYQAKNIERANHKTASDEFEVLFNRTTRRVV

DLEASIGSSISAMDVVDARTLLPTFETSYNSALFPWVRSYPETLLSSETQNSANGLFFQQ

LYAFTLIGKRTPVITASHRKQKDDQEAFLSLLQKYVVGSYDPNLYGHLKSVHRAIIPSSP

AYTPPCGTNTFSDSGSDSSGDLLPPSTPHIVSKTHSMLVPTPASPVHKFLLKSSNKTLNQ

LDNVFDIVFKQQAIGMKLGADESKQLAIVKECFDGSEAKRYPEIQCGVIILAVNGQEVTG

LGLSRVLYRLREAPR

>contig06838 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57288.1|) 3e-41

MEGCDNTNRGGGYCKAHGGGKKCTISCCNEWALGGGMCPNHEVFAAAAVCV

>contig07190 Frame-2F|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY60432.1|) 1e-164

MPTPKMHHPHDGLLATSALKDAMGAEMKNRHVPVYVKMMAGMAGGVAEACILQPLDVTKT

RLQLDRTGQYKGMFHCGSHIYKTEGGMALYKGLSPFVTNMVLKYALRFGSFAWFKEQIAG

GKENPITPRINFTAGLLAGCIESIIIVTPFEVIKTRMQQEVGIGRFRGPVDCTRHIIRHE

GVQALWKGNVPTMARQGSNQAFNFMAFAWLNHHVWDKQDGDGKRLPTYATVANGLIAGSL

GPMCNTPMDVLKTRLMAQETVKGQELKYKGFVDALKVIAREEGVGALWKGLLPRLTRMAP

GQAITWSVVMHVTALFENQDLDLEQKIPL

>contig09408 Frame-2F|Blast-small nuclear ribonucleoprotein G [Phytophthora infestans T30-4](gb|EEY64434.1|) 2e-18

MVKTAGPDLKRYMDKRLSLKLNGNRKVSGVLRGFDQFMNVTLDETIEEVSTTESNRIGMV

V

>contig10172 Frame-0R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY57969.1|) 3e-99

MLYKERVIRDQPVDMSYLNAWVSVNQFIAGVLAAPLIFDINFLHLDQQSNGLLCLIHGES

QVSTDHCYMGLCILLLYVFSNIVVNSLLLQLLRLTSVSTMYGCTLLGFVTSFVVLAWYQV

DPDNFGLINLHDGLRNWIPDSVFVDVFACLIILTGKVLYQWDPDPEVETTTLSAEDKEAM

SLLDGAEDYGLRYT

>contig11045 Frame-2F

MLRLIYSTSVTVLLLIQCSNATTIKKDERFGGAETNCQTAKDPRRTVTGLMVCSGDRVDR

IGVFYQGVNEPETLGGPGGKCHNYMLGKDEYFNRIEASADFRNGEERIFFVRFDTNKGNQ

LKGGTNSGRVGVSAHPNFKLAGIEGCHGNDVDSISPIWISI

>contig11351 Frame-0F

MSKSDEMHKFVSSMKDKKLRDDPKYAKYFKMLQMGLTEEAVRQKMISESVDERALDLGGD

EVASKLVSLKDNVKLQDDPGYSKYFKKLKNGLPEGALKQKMVTENFYVQALELGPEDSRS

QLHAGENAMESSIATMVKPKRARKKLHWQAISEERISNINKQTIWEDENENVNFEMDMEE

LEALFFANSNTRSAKSNSTFGQSKPIQRKQTVTLIDGKRAMNAAISLARVKLSYSEIADA

VAKFDSTGLSLEQLIGISEFLPTKEEIVLVCGYVGDKELLGEAEKFITEIAKVKRYASRM

DCLVYKSSFASRSADLSHSVANLQKAAEEVKGSRLFKTLLAMVLKLGNTLNGSGEENEIK

GFTVDSLLRLGQTKAVNQKTTVLHYLVRLIKKNHPQILNFQEELPSVSLAARESFETIDK

DFKKLKRGLANLYTELKLQEK

>contig13559 Frame-1R

MTRRGESGSGADTFADSTRCGTYTNDRPKLLRCRSIFVDEAIGRE

>contig14352 Frame-1F

MGTQLIKLSFWSLVARGQVTPIAYQEFFIRDLFYAANTFFERQKRARHSLQDEKLENETA

AVKIIGITLETRPDCITPDELRRFRKYGCTRVQLGIQHTDDGILKKINRGHTVAQAIEAL

KLLRDCCYKTDIHLMPNLPGSDPEKDRKMFQYVLESPDLQADQWKIYPCEITPWTVIKKW

FDEGTYRPYGDDQLIDLLMNVKAQVHPWIRLNRVIRDIPSQYILGGMDEPNLRQVIGVKM

KQRGTSCKCIRCREVKTDDVAIANAELVLRQYQANEGDEYFLSFETPDRSKICGFVRLRL

SKTSGGGVFEELQGAALVRELHVYGQLVAATTNTTLKTSELSNRAHAQHTGFGTQLMMKA

EEIARAHGYTKMAVIAGVGVRNFYRRLGFEVKGDGELMIKHFVPASRWSEVVSFRVFNRS

SRQLLTALIAGSAILGIVTVGALRRK

>contig14536 Frame-0R

MSTGGQFTCTIKKPIHNRDRLASAGSALSQIPVSTALMGHGIIWTSSFKWEAFV

>contig15610 Frame-0R

MAEEKAVKAQANAEESLRFFNRIVTEANEALAYYKAVSQEAKEFFVKNKDFFKAQETTYF

QMVNKAASNLDVVKVDDKVPKLNAGKAKGTLETAGIATKDSFHIAPGDLPHIAREDFPRI

AKEDLFIIIQRAQAKRNAHVSQIKADKAQNNIGMADSDVNRAKASYTEHYGAYSDFNNVI

AEGSKLHKDAVILNRNADILNASASKRMLRH

>contig15867 Frame-1F|Blast-PREDICTED: hypothetical protein [Mus musculus](ref|XP\_001003060.2|) 2e-07

MDVFPQILPFSPLSESLSEPMPESTQEASERKLLLLPLLLPSLVPLPPLPFSPLPFSMSD

MPVTLPPAALSSRRLRSL

>contig16888 Frame-2F|Blast-predicted protein [Micromonas pusilla CCMP1545](gb|EEH56938.1|) 2e-11

MLIDAWIQANRLNEFGDHVMTMYSGGTPLFNESTGTVIDRYVYIVKKHSDRPWQEGKMDY

TEETVYATKSQGSVAGVFSMLGVFTVVMAAVAIMKMYKEQRNRFRYSHIRTRG

>contig17656 Frame-2F|Blast-eukaryotic translation initiation factor 4 gamma 2, putative [Phytophthora infestans T30-4](gb|EEY56620.1|) 1e-176

MSIRIKSTIEEYLSILDLDEVITCIQELPGKPYNVEFAEQILNRALEGKADEREHAVELL

VGLYERGTLDANSIQTALVNVMEFLVDMKIDLPLIHQYSALIFGRLVSAGCFGLSWIFSH

ALSNCIECELTSMVFAEVLSVLEMETDERTVIRMLTNEEITPESVLPTAMKNKIGVEEYV

RKHGIDNYFIDSEDDLDEEIAEKMRSTLEEYLSINDYDELVRCIEELTAVPDRWRHFVHI

MLIFSLEVKQSVRRNVSELLLQLFTAGNISADDITAGLEIILDDFNDLHVDIPQLAVNLS

DLWTPLFAKKVLSIQWLSEACSHLIENGVATDVFDALLSAYESQNGLEALVSWWKWQANT

KAIWKQLSPSEPKDKRVTKWELVLQ

>contig19562 Frame-2F|Blast-rRNA 2'-O-methyltransferase fibrillarin, putative [Phytophthora infestans T30-4](gb|EEY53622.1|) 1e-165

MAGGAKVIVEPHRHAGIFIARGKEDALVTLNSTPGKSVYGEKRISVDVPSASGEGTEKIE

YRVWNPFRSKIAAAILGGVDNIWIQPGAKVLYLGGASGTTVSHVSDIVGPAGAVYAVEFS

HRVGRDLINMAKSRTNVVPIIEDARHPLKYRMLVPMVDVVFADVAQPDQARIVALNASHF

LKNGGHFVISIKASCIDSTAPPEAVFAREVKKLQQEQFKPAEQLTLEPYERDHAVVVGSY

RVPKKEKK

>contig20926 Frame-0R

MLNTDEHNTSIKSQHLELERAQIRTKAKL

>contig21529 Frame-0F

MFRRKAAAKLGLAVTTTLSSVAPFREELQEQNLIVIPSVYVGGDPTVSDSNAFSQKSSLE

ALEKYRRALEKRVPHANRAIALLELAIQHLNIYVAARNTSHNRIICRLLVHLGSERLALG

EYDRSRAELQKAKVIYAVEHCWAQMAQILKLLLVCTFRQGDIAAYLDNSLQLLSPVLEEF

VSLKERSRIQDAFMIAWKDPAALGESFTMTMPLGNGFELALDRSRPVFALLAQFDRACAC

VKEDLTLELRLRSHFPLPLVISKLELLFNDERYHTVIYHQAEINGNLLSFAKEKTSASLE

FTHKAMKELQIPLRILDGRQLLSIQEVRFYLSRDSNKALVADENREDEFLIFSLLVERAS

IEERATPLPYLATGRVPAMGNGSASPSFSRRRAMFSLIEGRRPDPIDRAEPIKEDGTAHL

RGTSLFILQPRAKATLMLLSRESLLTGDYRELVFKLSANEDTLQNVTCHLMCEPSPESLS

LDDAFFFSMQSETLMPMVMNQKFQPRDFIALPDIDRSGRSFELLYARQNHCLCH

>contig22195 Frame-0F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY69908.1|) 1e-112

MIGLWHLTEGEGICGYDSASTLKATKEGTKVKEGLKLTIFHCHWVPSCLPVFGNDAVSGM

LSNEWNKTIKCICLLQRKIRLWLMKEFDDAVRLSKLMCDYHERKSIQKYSQIIRINGDDD

SEAVLESDEAVLESDEAYIGSIENERCP

>contig22313 Frame-2F

MESTNSGTAALLSYAIDACVCLLVLLFSTALFQLLRVYTRRRGYIEIQQDDRSMYSNVLL

TASDSWENIRAADSNKLDVNSILVATS

>contig23567 Frame-0R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY62053.1|) 1e-59

MRVALTDQLDGYVFRTVVENLIPQGLGTSQLNQIKKRLRHVGDRLRLMHNLLMYSGRFNE

LEEIVRKCFRRIKWILIDSEV

>contig23901 Frame-2F|Blast-myb-like DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY58393.1|) 9e-73

MPTPLGFQPPHSLRRSPRFMSPAGFLKVDGTKFSFDDLDFPTELDSNTLEFEILSETGGF

LRRSPRLRTDVSVAFPHANASTFGIGRQPSPHKRFAPPTIDVALQQETFDFDHSITPTLK

SPQLRQWLDGSPKNFVASV

>contig24100 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64003.1|) 1e-58

MLESRAREIPITDVRRPIFISLMEYLYTDCLDVAVEVAMELFVTADQYGVERLKRICENK

MLGSLCIENAASLFHAADLHNATVLRDQCVTFMLHHFDAVTKTDAFEEMGRTNVELVFEL

LKLR

>contig24283 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57196.1|) 2e-22

MKPSYQSRLSVSKIASEFLLAYTKRNVSIDYVLDTAKNFGFEWKSPINDEGIYTFYLV

>contig24711 Frame-0R|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY60954.1|) 8e-33

MFERTLLVNGFSKAHAMTGLRVGYLAAPKHFIDPCTILQAQVTSCPNTVGQI

>contig25374 Frame-1F|Blast-3-phosphoinositide-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY67623.1|) 9e-86

MLFMLQHVIHRDIKPDNLLLSKHGHLKVTDFGTAKDQDGERGDICQFCGTASYVSPEILH

DKPATRAVDLWAMGCLIFQMFTGRTPFVGENDYLTFQMIISHSSDKFEFPGSVPETAQDL

VRKLLAQ

>contig25613 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53606.1|) 4e-23

MIYYDTSKLWQILCRLHGSALNGQAPMRAVIMAIIAFLVAIANHYCPFVVATQKSTAFTD

SLTVFNTFLGL

>contig25824 Frame-1R|Blast-MutS protein homolog 5 [Ectocarpus siliculosus](emb|CBJ29342.1|) 2e-22

MKMVGLLQYMTQIGSFVPAATAEIGLVTKLFTRIQSIESATVPQSSFTIDCNQMAWMLNH

GDDRSLFLIDEFGKGTAELDGIALLVPQQT

>contig26520 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55968.1|) 3e-87

MAEELLSESDGAVYAFAGVMLALYVVPATLFTIYRVVRTPSKVRSRGFALHLALLAVGVS

SLWRCLSALQSVDTSGVFDPYDILGVSESTSIREIKKAFRELGRQLHPDKNLDNPLATAQ

FARVTKAYEALTNPKSIENFRKYGHPDGHQSMLMGVAFGSWVRGTSSSTGSAVVLLYFSI

IFASLAYLVYWLRQRAGRSDRTRVSRATLASFVDALSEKMSVHDLVELLLSCDEMAGAAA

GIVPEAQNSAQLRVKTHEKFAKKLEAAKALPSDVISRIRKHPNPVARENMLALYQFLRRD

KLRSVSRPSWVESRFQKVLLELPFLVDIFSKMAAEQLVKRAYSAMTLVRALALLSSIGQG

SMVPDEAALRAQNERLAATNGQLPRLELKDTTLVVLDESRILPGDWLTLETTLERQHVEI

NKRAGLAATVYDHVDPKSPFRKEHVWFLVIDKRTGRLYSAWKCFDLSQHVVEKSGFLGPE

MPG

>contig27291 Frame-1R

MAEEEDINAGAFVNALYQKVLLSVKASNAIPSENDGFHYHSQFTADFAARSKHSGAKVEE

LVRLLIQPPRSDADESEDNHIEELFDGPEPNARIIDYADMLLDEASKHLANFMRGNKTTS

SALDSKLRPLENKPQIFEKKQNVEKELQSFQKSSWGSQDKPQTQFDEKIDNSDVPFVSKL

RDKVHAGVNAVDN

>contig28715 Frame-1F

MASAALGNQPLVIDNGSGTMKAGFAGGETPQVVFPSFVGTTKHVRMMPGGAYEGGEVFVG

NRVQHHRGLFKIHYAMEHGVVTDWKSMHRIWQHVYSKDMLNVQSEDHPVLLTEAPLNPVA

NRQRAGEVFFEAFNVPSLFVSPQAVLSLYASGRTTGVVLDVGDGVAHVVPVYEGFTLPHA

ITRMDIAGRDVTHHLQLLLRRSGYNFHTSAEREVVREIKEKLCYVAFNPTKEEQLEAEKS

ALAVKNMHRTNSTPSNASGDDTSAYYLPDGQLLNIGPETFRAPEVLFRPDIIGSEARGVH

ECLVQAIMKSDMDLRKTLFSQIILSGGSTLFPGFGDRLLAEVRKKAPKNMKIRISAPPTR

MYSTWVGGSILASLATFKNMWITKTEYEEYGASILHRKNL

>contig29460 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55992.1|) 5e-42

MMEKGSVSAAVQAFTRAVEIRPDDPALHSLLGRAYYADENLEDAVASIAKSLDLEPSATN

STLLGKILFEKGDHEKAIAAYQQSLDMQK

>contig30026 Frame-1R

MSFQALRKSLRSGRPAAHHAFIAVTRYTRSQAALNARQQLRSISVIVLQPKRVSCLHLPG

RSLNRPFSSAADEVVPVPTMGDSISEGTVVEWLKAPGEFVKIDEVVVVIETDKVSVDVRA

PSSGVLEAQLAQVDETVLVGSPLFSMKKQFTGNAPVAASMSKEQATSVVSPEENFETVNV

PSMGDSISEGTVVAILKSVGDHVRADEAVLIVETDKVSVDVKAPVSGKLVSVLAKLEDVV

EVESPLFVIDKAFKATAESAKSEAPSKSTVSVAHPSPDAASEEVPIVSLKSSTTTSTAPA

ISSERTFGSYNRNEIRVQMSALKVRASQRLKDTQNSAAMLSTFQECDLGNLIALRDELGE

TFNKSHGVRLGIMSAFLIASAQALLRIPAANSVVDMDAKEIIYNEFVDINVAVASERG

>contig30053 Frame-2F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY63946.1|) 2e-41

MITLWQIMVPSRSPWEDKSHLQVYRAVAQGERPPLLSIIPKACADILVAGWAANPNERVA

VEDIIPAVHRLWLLAMHQKPLKRTKGY

>contig30242 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61782.1|) 6e-19

MLPIERQKVLMGLPFYGYDNS

>contig30589 Frame-2F

MQLNSGKRDVPLSASVDNSMRLKKRAVLSGSQALKAKLVGQMPLSSQSKNAASALNDTRI

LLHYPNLVPARLIRRYKRFLADVVLLDKTSKIELTDQEEVTVYCPNTGPMVGLLDGLPNT

RVQLSKSDDPKRKYAYTLEMIQIH

>contig30776 Frame-2R

MTERKRKIDVGDQNGTKKRKSRFSDVPPSATSFDTGVNPMTGAPFSPRYKSLLSQRQKLP

VHQFLNQIQDAVNAHQVVVIEGETGSGKTTQIPQFLTLLHAKNGKVVACTQPRRVAAMSI

AKRVAEEMDVQLGQEVGYTIRFEDVTSARTKLRFLTDGMLLQHAMSDPLLSNYSTILLDE

AHERTLSTDILFGLLKEVLPKRPDLKVVVMSATLDAVKFQKYFEDAPLITIPGRTFPVEI

FYTPEPERDYLEAAVRTAVQIHLCEDEGDVLLFLTGQEEIENACRQIRAEAEALDSSKYG

PLDVYPLYSSLPPQQQQLIFNDAPQSRYPGGPKGRKIVVSTNVAETSLTIDGIVYVVDPG

FSKQKVYNPRIRVESLLVSPISRASAKQRSGRAGRTRPGKCFRLYTEQSFIRDLEEQTYP

EILCSEMSGVVLTLKQLGIDDLVHFDFMDPPAPETLMRALEMLNYLGALDDDGDLTDLGR

QMAMLPVLPQLAKMLISSSKYQVPQEVIIIVAMLSVQEPFIRPKNDAKAANIAKANFAHV

DGDHLTLLNVFHAYKLNVGDANWCFQNYLNSRSLQSASNVRDQLIRNMKRLEMPTQSALD

IHSPLYYPNIIKSLVSGFFMQVAHKAVSGNYVTVKDNQVVHLHPSCVLDTPPDWVVYNEF

VLTSRNYIRLNTRIMGEWLIDIAPHYFDLTNFPPGEAKRELEMLYRRMNASKKLKES

>contig31058 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60572.1|) 5e-09

MDKIAIARGDMLGTPRCDLLAPENEYLDPNPDLHSLFK

>contig32796 Frame-2R

MAVHLKCWDSCTSRIFLRKRFYVGFLDEVFISTVYIRTNHLASCCCRIGMNGSLYHSWYA

LWWSLNDLRRNILFFFNHCDTFFSIGIGNNVSIVTLHKCKSVKGSITCVSLFCF

>contig32891 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66418.1|) 4e-31

MELSLLKADVLWLAKPRESKLTKLQAPQATRLIVQLPYAEKKDQGVSFPCKILIPVEEVA

AKNEASLLEKNVTFKLLDEEELVATHTFKLRDCIPVLNTGSLHWEQLVLYRD

>contig33438 Frame-0F

MCGGWRLQTLPWRNSPTRSLLLP

>contig33517 Frame-2F|Blast-Cation Diffusion Facilitator (CDF) Family [Phytophthora infestans T30-4](gb|EEY68628.1|) 3e-32

MMFASKVMKTEHATINIGCSANYEQNSGGKSTYEIHADYGI

>contig33922 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66395.1|) 1e-95

MDTIGLRFFTVYGPRGRPDMAPFKFMDRIARDVAIDQYGDGSSSRDYTFIDDIVQGVLLS

LDRGHGCEVFNLGRGTPVLLTDFIAIIERLVGKKAKINIIPDQPGDVPRTSANISKAERM

LGYKPTTSLEQGLAKTWKWYSKFHNDELANAA

>contig34893 Frame-0R

MVHGLSAATFYPLISWLYTKKTLRRLSGPLRADEVIIQKLTL

>contig36279 Frame-0R|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY63175.1|) 7e-29

MEQLQKSNQIEDPNSTFCNVPLLVLQGTEDKVTSVKSVEHFFARAAHMDKELKLFPGLFH

CLYNEPEKQDVMDYAS

>contig36316 Frame-2R|Blast-phosducin-like protein [Phytophthora infestans T30-4](gb|EEY62958.1|) 1e-100

MGDRGNVFYAPTGETTEWEDILVKKGILAPKSKVPEEEEQEEEQHVDPRENATLEELDEM

EDDDDDDAELARIRQRRIEEMMTQAARNKFGDVQPISKDEWAKEVTESSNDHWVIAYLWD

DALEECKVMAHVLREVAKKHRDVKFVSIQAQACIENWPSRNCPTLFMYNNGSLQNQLLSI

RKLNGLDMKLEDLEKYLAKADVFKPRA

>contig36363 Frame-0F

METPRNDSTSESQRTAQTEYLPQHILVLVHGNNGAAADFDAFESVFINKFGNRQMLIIKS

KINEPDTSLGVEFGGQRLAKEVVEAVFKYDLSPGVSRYKLSVISHSLGGLYARYALIQIM

ESLTCLDVEYIDFVTMCTPHLGSRRARGPSTVK

>contig37148 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69515.1|) 2e-87

MQAELVIDVTSSVTVTTAKKGLKRKREEANGFSCKRLSSDETEITMPPGGYCMETEAVPS

YLKVLFSKPMTSDAAFDWVKDSYGDIMDLKAQQKNTNAVASSFLGWREDKRDLIQPKQKD

GECSLELMMTQNFPGMVSGELVFHTWNLLTLLKNFKKLFPLTKDLAVLQMINDDCLVVRI

GLAPNHETAVVHSIVVLARGQIDGGYLVSMRSVPLSAGQKAFADNEQKYFSVLAWFMLLD

KFDENAQPVCEVIVGASTQHKSQRVLRRVATDFVAGAVRWQEAVSRCSHWLF

>contig37683 Frame-2F

MSLRGRTGGVNNPRISNSLHRCAIALCSNQSVAEGVCSMHLSCNGRVSSRQGAVIDSRIA

GLRGALPSSAVMVTDMSDDRYYRAKALAAMQPRVGPSIKKHKASPIEPLNRYRMENAGSS

NSLTRESLNEMVSQMQYSKNTAMSAYESDPYVSAQASASTNGSIRSESDGSVDETNLRRE

RNRIAARKSRQRKLDRISNLEDEKMRLEQHRDMLVQEIRNLEKKDSGTVSNVVLTITDKE

YQHLQNKRLQIIKHIEEAYNSGDILSTVKYFRDDSIVSGPQNSSVHLRGRDALVLDYLCT

AYLFGDIYLHHAKVDCGGPRSQHFRVHWVLSGTIKSAGVSMNKEFLELIESVKGLRVTIE

GVSNFSFSGDKIVYVHRTADQAKFLSALVNLSK

>contig37997 Frame-0F|Blast-mitotic checkpoint protein, putative [Phytophthora infestans T30-4](gb|EEY56318.1|) 1e-69

MLVYPVNCIAFHPTYGTFATGGCDGIVNLWDGANKKRITHLRQHPTSIAAMDFNHDGSVL

AIAASYTYEQGEKDHPNDAIFLHAVQDSEVRPKKKIAS

>contig38321 Frame-0F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY69845.1|) 4e-26

MASRSDGRARTPMRRQAESNYIDVDREQALHRLESFHATASGPFELLQSKFGFQHSSVAN

QKENLGCWTT

>contig38747 Frame-0F

MQAQLLRRRPVRPQRLLSALEAVLILKPDDSKTETGGNADHGAYGKTDDVSTPAAGSGSS

TNGKTDEVKPVTTATEASPAPATDASPAPATVVSAGSGTDSKATDASPAPATNVSPAPAT

I

>contig39043 Frame-0R|Blast-40S ribosomal protein S13 [Phytophthora infestans T30-4](gb|EEY55889.1|) 2e-34

MLIKKAVAVRKHLERNRQDKDSKFRLILIESRIHRLARYYRKNRKLSPNWKYESATASTL

VA

>contig39652 Frame-0F

MAWKNLRKAYDLCIDRVEGRIINSLTSRLSATSNADEMFRVFSKYNALFFRPRIRSAVQQ

FQMQLIENVKKDVSNLQAKFRARYAYSEASRTSKLRDIPPIAGAVMWAKQIERKLKMLLS

RVESVLGIGWEQHVEGKALKAAAEAFVAKLNPQLIFDQWVHELAAMPIFDTKNIILNIVT

ENTPQGEKKTLAVAFNQQIVTLFKEVRNLEWLGYHVNFTLKMIAEDAKSKYPFAMSLDAS

LKTYTSSCRRIKPIFEALTAAYVRDVRATIGKTFTKGSEMRWHADGLGEYVIELAAKVER

LHDKVDELLQKSSDIDTLLDGVRSSSDFQVENAHSVLVKVQGHVDELSLAGYANLAVFVK

NLNTLISEILGKKLEMLLQRWVICFGPQSDDKSFQAALSETRLDITTHQILLKNQVLYLE

PSIGDARTNWLAQL

>contig39829-0 Frame-1F0

MSACTAIYDPVIHVHAVSVSCKRPSSLVADHCTVLLLLRFALPG

>contig39829-1 Frame-1R1

MVGDKTRWALAAHGDGVNMDHWIVDSGASRHLVRDVSMLENAVDCDEPNWLLLPNGERLQ

VTKKGTVSLAGIAEGKEF

>contig40032 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58205.1|) 3e-99

MAKTALYVFLFIEYTASLIPADVTQVHLGISGPSVGCANGIAVSFATNEAKPYKVIATTG

DSTITTESTYTNYAVTEPQYNYSYVSPQLHTALLCDLADTTRYTYTIGDSDFTGSFVSLP

HPGSDSKETIIGIIGDPGDTNSSETTFSEQAKTFEDKRFKLWSSWAISRMPMANICNGTI

GFGRNRTSLRSSRSRVSTVTTRLSRQRVI

>contig40278 Frame-0F

MGPPEQIALYQKVTSNSYGAVPVADPRHPYDDNQDNWKLTPRLLSAEVLALLIQYAGIGF

INGVLPATLYPVLQGYLNAEGTTVVSATVLIQLPWSYKLFLGILSDCFPIGGFRRRPYML

LGWLLSCSMLFLLASFPEAAPYYGDPNMHFSSPDEWTEAQRQSINDNAPDAAGKYV

>contig40560 Frame-1R

MTLQRHKCFNLFTLVLRWIVIISKPHVKNTTDGVGNREGDDNQGLDKRTKHCSNAKLIGT

SKDGGRNDLTEKQHARDGQDVETASGTNFVRKMGNASFALAFTISRVTSKRWCLVSTGST

CLASIFSLSEPSNSRMRTLSMSSDKRPIVRPAIIPAIQISTIDIVRYR

>contig40762 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54284.1|) 1e-48 NOT\_ORF

MVRCSRVTKQASALTLRLSL\*TVVFVVLHVVNTTILVCSWRSCELIDPAAPVEETLPNGW

FGIRLDGPRWEKTRYCALCRKAVPGLDHHCTWLQTCIGKSNYAQFVTVACTGTIQFVLQV

TYAACCLLWLCDSSLEEIDTFG

>contig40946 Frame-0R

MASPHGFLRSSFHLRLVDFNLLCLAIASSFGVLLLRSRAIPKRIFDVRRALLRRSVASLG

SIYSENCSIFRLSTPQTELH

>contig41181 Frame-2R

MASEVQHEFMKHRQQLAHEQKRRLGSGVPTYHLDSEQEAEKDPILNAAEYGNALEEDRYL

IAAAFIKDGVHGRKIGYRLDRDALFLNEIFHSETYRLV

>contig41390 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65906.1|) 2e-73

MKFGKELLLRIVQSNPQWAPFWLSYNILKKRIKTATSTAHRATKQQNIAESKVEVAFFRD

LQVELKKISLFYVAEEKRCFLRYQKLHSMLKSHRKERNIEASKLQRLLFAFVHFYHKCIR

LESFAVMNYQGFSKVKLNA

>contig41549 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55374.1|) 5e-96

MQQSRKAFRLGKSITYYQKIQTLSNTKNLTETQRSLQILQNLGMLGYFITDNVAFASTAK

VLHLDAQKLARYGGILWFGANVAGFFNAVDSLNADVEKEKCVRDILTTEDYAARIKTLQM

ELETLQNGRLKKLLVVLKVTCDLVVSSNTGSVRLAERITGTKLHDGIIGSIGCVSAAVVL

YNTWLNAAKTSERNVEPLTGVRMKELKL

>contig41606 Frame-2F

MPSRSSIFASRLINSASSSLANCKLDGPSRRLLKARHHGMEKMEIQTNTLTAVLHCETIR

FTIYKLQIRSIASVAEGGEWTLMKRYSEFFYFRQTLLKLLKKWNLQFRSESERLQCKELA

IASALLLPALELPAFPRKHMRCDTAAIIKERRTKLQQFVRKMLDAYSDISIFLYNVQSLN

TCAFVNLKEILEVLEDFMIVPPQQKEINRRLTSAVLALEDVDRHAVKSQTSTCCICLCGE

SDTNEWEVFADRMVKLPCSHQFHEDCVINWFSTSTTCPLCRKPAFKDDHRSFDVSINSA

>contig41673 Frame-0F

MAAVEACVVVVDGANVACQKDGKVHIPKLVAAIQYFCSLEKASGRNPIKCVAFAPNFWLN

VK

>contig41808 Frame-0R

MFKQDKQQHEQSYPYNIVAISRQLHHFASLNPRKTSKMSLH

>contig41945 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54233.1|) 2e-45

MFTMSQMAVFVAAFMQTVTSHSSYSELIPNGENILKPLGHTETAYTGFGQLFSDEGTDWS

NVCNMTWPGGSVTCGEALGDPCCRWKNGVPDYTLTEPSLDGTICATSSDASSGDSSAATY

GPDTTESTVATKESPIQTDITFSSDAVTDSSEYCG

>contig42148 Frame-2F

MQMMQRNNSSASNAFDGQAAYGQSQRMVNQEQPYVKADLSRFDLNEKNARAPETAPIAQV

NKPPSTAYVNPPMPGDTRQRDSDSVSEITPSSAAISDKNLHNSTMRREENMRITKRPQSI

DGFAGFSSQGSSEQRPPTDFFSNLPAQTHNATSSHQFAQLAYYQQ

>contig42294 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY57626.1|) 9e-10

MSGSLDPTAQYELIERVGGGAFGEVYKGVDTHTD

>contig42409 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69108.1|) 1e-101

MDSTMQAWRKKMPSKRAIASTLNQLVQQKSVAVLYTPTEVERIKQMTDMIREATSEFKVE

EDWDRILKVVDALSNVSNRAVLKESIWYLKLRLGDPSCRVVILSLTLTESIVKNCGDLVH

LEIATEHFMNEMEALYKAHANKRGRESMEISSRVLDMIQAWGEAFLPFRHELPLFVDTYH

NMRKKGIKFPDQYDQTKVPVLTPSVDLREGVQNRALDSWSMLSNKSQNFSSIDTSSYLEL

WTGWTFDARITSCRNQCAGNVRRHAFCGANEFIFD

>contig42683 Frame-0R

MVGEKLAAQIEEELNTGKLRDETSEQNVSSDVNQHQRPELVLEIHNSRANRPGNQHLVDE

LTKFGEHELYFGNSGKGVSHLRAAREIQLTPTLIKSGSSAVSNVPLVGEVIADKIDQILK

HGRIVKDVGETTGSRGRSRGGYTVAPIVKDLRENPAKCSENQPIVDALVDYG

>contig42823 Frame-0F

MKMASLEKPQVWSSNPVRFMRLILAITMLLSLWYMWQFTSKSVVSNNLKATNANDAQEEP

LEV

>contig42856 Frame-0R|Blast-serine protease family S08A, putative [Phytophthora infestans T30-4](gb|EEY60762.1|) 6e-55

MDHRKVFMFSLTLLLSSVQAFNHVLLVHLHPCLNARELLLSSELSRSERREKVFQTLTRS

VSDVQRSVSSFIEAQNEVNLTVSRLWIQNTLIVRYQSDHHGFHSVLKQNLRWFPGVLQVE

EDTRVLRLIEAHQDKNIASLDLEKPQSNIKLLHAPQLWNKGVKGKHVIVASIDSGVRYTH

DALR

>contig42997 Frame-1R

MPKILCHEHVSLRCATFPSLPENKLIACSLDFLDMRDTIVAALNINEIVEMLKEHVKWPK

PAGKRVALIIEAIATYPEGSVDTNDVDHWIQQFMWMTQYYSVITPALTILIAAHSFGTES

VEKKTALLQETMLQAYLDLANTYVTREDEVSADTVKPTRQLDGKTVQTRLGPGASQAIAR

ALGVLQVYYKVHPNATLEDALAFLDRLAPRLRKSPV

>contig43741 Frame-1F

MSFHFYFVPPFSRNMPCMQLRDFHEYSGFSASTLGNVIWYVMDEVVDKDPFNKHRISWRI

KA

>contig43895 Frame-1R

MLCVCCKLMYLVKVPFLGAFFSASAIDDTSHSQKGQNCDKGALCGLWYWRLGAQLDNGTF

VFAADIYRHSKHKMIPFRAEINGKLHNISVAARISNQHPTRHHLYSRRNNSFRDIQLSVG

AIQVVERHLYDTIRSKFGKFLNIPEL

>contig44137 Frame-1F

MRVACWALFAVSLVVSVLAKGKAKSKDNLTCLAPSAVASFESKIAELQESNAALQLQLET

AKAQLEDKAPNHEVDVSELQKEIHELKKNVASEKQGFTLELNSALNKLSTETKRAATLDN

QVTKLKKDLATEQAAASTASTELKAAVAEKARQAKKIAQLEKTIQSMDKKNKALLKDLSD

STPVDLSLASLLSSYYDEALVLAEDAAGIAQQKLHEQSDTLDFVQRPD

>contig44340 Frame-2R

MEWLFGSKAPAAMVVKAKLSSSTPQGRSAPSRDDDSWHKNCGNEFFKSKDFEAAVHEYSL

GIELNPTATLHSNRSAAYCALGNYEMAKKDADVAITLDPDWAKTYSRKGKALYGLKSYKR

AADAYARGLEICIRGAVDEANQRDTELEALKRQTDSQAKAYLRLLEENDHLKTANNGLPA

RLWRMDEEGNVTRICLVQIFERYCYYKFFMRLLSLT

>contig45026 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57522.1|) 1e-145

MLSRAILRKAALSSSTLSSLNMLRPLSLHTTGFVNKEEGSGGEIPVPTQGLLEQAGLTDW

KISAPIIGALAIPAISNHFYVLNEESQLACCFLLFCSATYKYGGDMIASFFDERAAAILS

EHNAVEDANLDLAKETLETHKSMLHIHEDIASVAEAHKEAVALMCEVQAYKLRHKTRETF

IKNLEAVREIEGNYNLELQKSMVAAATSKVRAFVQKGDKKLKDAAFKHALDILGNVDMDE

TKEDDVAALFSKELRAYASDLEAKQGQLVKLTSEEQSELQADLDAYMKRFGLEDANFKAP

TEAKFKLM

>contig45053 Frame-0R

MANMMLALQQQHQRADMASYLYEKHLDHQDGVAGTLSIRLVAARNLRAAASLFRVRKCNP

YVIFRVGKQSVRSATISGNDSPTWRRELLEVKLTKLDHTRQPLCEHSDVRMELIIDVMNE

DSLTGKATEAVGMANGSVIGTAVVDFTPLVEGKEDVMDQWIPLSGALPMAGFTKGASTAK

KQPMEANLNLGEIRIVLQYEPHGMEPCVGDVVKFEGFGQYPSAILGPVEELEMHVKKTSG

SYLLCSYTSQSGYEAAIRVHRNNVFVVHRGSFFDRVYESCVVEPLEFVVNTPIGRSAKEM

LRPYMNVARAFSGPALIATKATLMTTYRASSAAIGAIVASLDD

>contig45242 Frame-2F

MRLRSVCRSAKVLTPLFVTSLQLSCNAVQQALATRIDGNACILRECIHLRHLEIVSLAAG

MTFGKLSMRATNCPQRFVVTHDDHEQIVLSLAEQMRLNTFVGLSRLSHTCLFTNEEANGE

ADVLLNTLMLGCCPNIEELCLPGNSFGDYGATKVAEMLWSQVCPKLTRLDLRRNFIGEDG

IRILCHALADGCAPNLAELCLGGNTITDSSFHHILFAMESRQMRCLRFLGVEMNYLTAKS

MEMLGRTVGKLVCPALTQISYSDNSVDNDAAKRLLTTAIYRERVLRASKESNFICDSITS

EDESSSNEPLLSDEGV

>contig45444 Frame-0R|Blast-signal peptide peptidase-like, aspartyl protease family A22B, putative [Phytophthora infestans T30-4](gb|EEY56587.1|) 0.0

MWSCMLLLLVLALPSVVAVLPTGVLSLQILQESPQKPLELAKQLCSPSAIAGWGMPLPAR

SDSQWKTLVQSPASNYDGCAPYHFQPEKFSARGSVVLVDRGNCSFVTKAFAAQAAGAIGL

IVRGTKRAVYEAIMSNRTTNSSTYLIKHDAEFNGINVAVENKPVFEYDCSKGVAFVDELA

IPVWNTDAKKCSEDVRCSSRSCVLTGHTMMQGSSTKHQVCCMWDTFVIMGAMNETGVAKL

AIPVVYVTINDGQELQNAIVKYPTSLVARTYQRERPLIDVSSILLWALGVATALGATYYS

TRDLRHRNEWDAAFRDQKERGDQDQVSLTYGRDDVYELNARHAVGFMALAGVVLIGLYYA

KIGGVIPVLFAVSGAVTLAQVVGTPLMEWLVPSIASRELPIPLSGGTASVSECLGFLPSI

AVAVVWYLHRRTYWVLQDLMGISLCFFILTDCPVAEPQSGNCAAYSSICIRCLFRVPVAN

LLWLKCHG

>contig45776 Frame-1R

MYNYEAQFSVILMDWIMEELEAICWILGKWSFLLPNSFRNGPIQDLHRAKGCASINLACQ

QLVLTLIVLHASARQQYRIALACCQFLFKKVRGISLALPEVQGIVNLLSGCRIVLNEPTL

LNPAHMQKSYNLLVGQLRSLSLSSACLESSFFLT

>contig45985 Frame-2F|Blast-cysteine desulfurase, putative [Phytophthora infestans T30-4](gb|EEY55031.1|) 1e-128

MEEREEGGTPDILGSIRLGLAFELKRRIGVQHIMDLERQHVRYVRAVLSKNANIVLLGHD

NLDQLPIFSFLVRFGGRFLHHNFVCALLNDLFGIQARGGCQCAGPFGARLLGISREHITA

LGYAVVAEDVVLKPGVSRISFPYFADANEIEYILEAVNFVADHGWKFLPQYDYYPHNGVW

SHISRTTASSPPEKYLASMQLDDVETLRLSVSVAPICSITAHRRENLTQAAALANACIEK

AVAIDE

>contig46247 Frame-1F

MTTFTSDKLSNWQTFYHMLSFITGTGMLCLPLALVEINWYGVLLLVAAALVSAYTSKLLV

DALEAVRWRKGTSVSYSDLGQECFGAVGKIFTSLLVHSSLLILSTGYLALASSCLVDVLG

LRYGTVILLVAGCVWFQVLVPSLKALAVISAVNVALSFWIESFILGDAMYPLKQIALKHS

DFVFVTPDLSNVTIMGKFSYTFSLLLGGLFGHSVVPTLYDAMADPSQCSSVVARTKLGVT

ALLYVPICCVTFAVYGATLQAPVFFNMRNTVVRNMAIVLYSIHLLLSYTVTLFPIQRAFE

HWIVQPSNRSGLNGPLEAAAAGALPFVYSSPTYQINRQCKGVITTARVFCRSILVLATLF

LGYYTAPSTIDVFAWMLIPTALLALVLPCIFDWQLCGEDFSRIKRVISVFISVLAIVTAC

WSL

>contig46621 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65512.1|) 2e-48

MVEPSGLQGTDEEDEVRFLETRNEDLILVDKTQHSTADEEEEGEEDDESESEEDKMGLSN

SASMLRIMRSLPEAEARRYEHFRRSHFERGAIKRCMAQAIHECSATDKKVAGVTNVMAIV

MAGISKVFVSEITSEARRIMEMNGETGPIRPRHLRQAHWKYYKRRPLARGRHTRRLLR

>contig46755-0 Frame-1F0

MLKLRHTNVRTSTNFIFVTTECTKTQFVYGRDRERNVAWFRSGLRHERACEQSCRSSHGG

A

>contig46755-1 Frame-2R1

MNISSIIDKTHMVTEVTGDGYSSEKL

>contig47060 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66324.1|) 8e-71

MLVFSKSVSKPDLNLVTLYGGTYLVYIDTNSTKLLLYLVGPTMVTCVRSLNVMLPPRTAL

EFSVVDNLLVCHSLEFEVSVFFDIKCDENPSDPFSAPLPISMRPPGHKGDRLPLKATRWQ

F

>contig47262 Frame-0R

MNRADSGMYSPTYSKQNIVHFDDISMPFPALTRRFEVHLVSLEHIGLVVSSGFAGIFTTC

LKNGILPLLQVELKMQSYQVVAASVLILLPWSYSFIWG

>contig47532 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60288.1|) 0.0

MREVFEAFLTDPIHVNDDVFALWLEGHNTNDALAARLHLPSAVRMPFLGGNAAAKLRELL

WRDTVDQYRLYDKLEHYLSQPSLFRSQLLFQIPPLQQYYMVECYYTRDVDVDRWLLGKKL

SGRLEKDLDDVAERSCRTLKSCCRQLENLRRVYAAVEDRNFSGLACRAVSEQFLLSGQLA

SMYACLLFILHTRLQVHPLHPVTGFLTSSDLHFIASLLMTHWLTQRKKLAKVHYSQTTDT

KFDDLVVKCGAQIALRSPSTKEWPTLELLRDRLQPTSVMETIGLDLSHPLTNCLRDLKAH

LINDTDVLQLYRDSIISRLRSWAIASDAQEEKGIFLTKLESNLLLVVHGFLTIGAGLSQP

KELQLFVEYLITRVVRVLHRSKIPFSMLDDFFSAVIDALVELDVWYLNGQETRGLLLSSW

NRFISVCRAIVIIMYDRCHPFP

>contig47778 Frame-1F

METESALIDDPNRVCTTSVLPKDAPDIVDESVAPEELLPKTKYHATAEI

>contig47891 Frame-1F

MASMAPHPNVVRYHTAWTEIDACSTQTLKSSESVRGSVVSLIDSQCSAQNLQRQQLELLD

EEAELRMSNVEAESLSFSLDFSSDSLSFDEYSVPGFVFEDEREGQDVSCRTSEGTNDDNR

VSPLLTAEPVVMKPQIILYIQMELCGTAANAVPLTATEAGDHKPVHQFLNQLMSPLQERQ

QLEIETHSNLGAWLRSSLKERSAWTHTSEIHQVGLNYFLGAVQGVAHMHSYDVIHRDIKP

DNIFLHGDLAKIGDFGLSKSVYEDSMSDKALSPRERLQQYGFDDGNHTTALGTFTYASPE

QLGYRFNRSDALLKDRFSL

>contig48151 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY53521.1|) 1e-160

MEQFQVEIQVLQSLKHPNIIHIEDVFLSDCKICMVTEYMGGGELFDYVVDRGTLSEVEAS

TIVRQITSAVAYLHARGIIHRDLKPENLMLTSKSRGAAVKIIDFGLAKLLDADDKTASFL

GTRGYLAPEMLQRQAYSMSVDMWALGIIVYVLLCGCLPFEDDGGKVANEKAARAKFGLRF

PRWASGLSESAKDLLRNLLEVDSANRYTAEQALAHPWVTGARTPNMFLKSPNYLRSIKQE

QVSQKIDGRVPHESNIDVEVYDDNRPAINVRRQSR

>contig48308 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55096.1|) 7e-24

MLELLTLPPFRELSLTVSFTSNEIHDVARKLSAQYVASYCETRSLEFFVGFEKEMNRKQC

YICEDGLITTTRDEGRSDGVVKCFYQSCKMCCHVSCLRDHFHTLGQDDNNTKKGGSCPKC

HQLLRWQSLTQQCEPKQIQNDGVHQIESSNASRDVKVNENDAKPSDLIAVRKSESQLDVS

LTVSKRMMKESYLKNRWIKECEDVGRETSQKAYNDYTAVEVIDLT

>contig48407 Frame-1R

MDKLEHLPIAFDASATGAEIASHGYGSGVMNFAEAALLIQGTSVIYSRKVEYLHALVYQT

LAHLSHQGDMYSNSEVTTTESTNRVAIDTEESAFSCPLPLYDELEEARPGSITLKRATEA

HATTQTNARA

>contig49772 Frame-0F

MGRYYARVAMASLTCTVLEGEARLLESVWIKCLLWDVLERGLMLLPGLQPQRQIEYLIQS

SHILETLGHGRRVAFLLHEAAAILLARNAPCIGVESKGLRSHFAVAKGSQQERDLEAALL

LERMAARCLNIQDIRTLRSEQQWHVSTVNQRNCRKNSSKASSDNSWPIIRFHVLRQLLAI

AELLGDALLVGTYCLQLLDMLIWCDSIVQPSIIKKQISTSKTSNPLDHLQQPALSLRKPY

SLAERAALGLHAKSGIFCSPPPRADTKTRRNFTASPSATMTNAAASLSSTLSNTPRILAT

PRQQFSA

>contig50033 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61288.1|) 1e-122

MKQKACRLIDHTMSNLDLHEIVGSRAKKMFAEFRDVREHVHQFDAMVAGCVIAAYMETSK

EMYSAQNSIRIGQNKQPGIATLALLPNKAVDEKKLHPFLCSLCDMKFNARRGMQFHACAG

KLEDDKEKTKSTNNLAPVVFPDELQPIIEMKNGKKWFKCPVCSRVYGKEESLTEHMVRHQ

NQSKKRMYHIENRTVDSTRLAKTTKLASANPSVQVNTHEQVMFRGGGRRVWLQHLTEN

>contig50046 Frame-1R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY54022.1|) 3e-63

MLEVIGAGVGSSNGDKTNFVRAFQTSKKYEVLLSNLKREGVTCPSKEFAELTYGDKRAAT

EINQAKFLLQRFFRMYWRTASYNLTRFILYLVLGLVFGITYIDAEYTSYAGINSGMGMLF

CSTSFVGFISFSSVMPIA

>contig50705 Frame-0F

MDQITILLRTATKRDEHDAAHIFLVIARRKIPVQSEKCSSSFPNTPMPELSMALYRRTGN

LSTKL

>contig50792 Frame-2R

MSQINRYELKRVYISYISILDRKTRRTSLSCNISSMTQSARLSLDRQQTSSH

>contig50932 Frame-1R|Blast-polycomb protein EZH2, putative [Phytophthora infestans T30-4](gb|EEY61878.1|) 7e-45

MSYLFDLNEDAVLDAIRCGNKSKFINHESDSPNCTAKVLSVCGAHHITIWALRDIAVGEE

LRFDYGYKRSVGPDWSQLQAASKGSS

>contig51038 Frame-1R

MAAAGIFLASSCMHLLPDAQNNVALTEWGCKHTIEDLLTANSKGEGKSCFNWANFFYGSG

FLMILLIEVTAHSLQRNYNKVHGCEQEERESLITVDTCAVEVNNFAKESLCSRSQLDCGE

YGTCGASIELAALADGVKKEIPSHSHGIVDGNLILALVIFIALSFHSVMEGMGMGASSSP

AWDILIAVMAHKSLAAFALVLEFLHHNVPTKQLILTVAVFSLMTPTGILFGRLLIDSNHA

TPASGICAALAGGTFLFVA

>contig51117 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57062.1|) 8e-38

MGANGQAVQTMNKKKVKLLNKKRAAHRNQKKVAVLQKGKRSVLRKHRPSKKKQQKDAKRS

RIYVESEKNKLLSSGLITKEDIEKMGADRGDDYEVDTCDSAMPVED

>contig51355 Frame-0F

MSRMENEKYSPPSSASSKTTFSPLDETVQLLLHSPSASPQSVPALTPVDLPQLAPFSLAV

VPTSPAEDRRVATSALIRRSEEELLYGPETYEVIMSNSNFCWEICNISGRAVVQQVQPLG

PAAAAGIQKSDVLLFFRDTVITKENCAAVVQQLLEERVTIPSVLRFRRVSSFAATATSSP

AQDSDGDIVMASANTDASTFLESVDPKYGLQVLCKAVESMQDAVAGPATVELKVLVDLLL

KSDFNLDRAVNMFLTEDRIVSDFRGIVGSEWNIDQPNATVMESYAASIPAGPLGLTVENI

LERTIVVDIKSGGAAERANVKRSSWLVGLNGQRVTHLTHKETLRLIETAIRPLQLQLVLV

PPKDYKALRRQLSMNIRQQKTERPIPEQDRMSFR

>contig51647 Frame-2R

MIQQAQNEDFAMNSARVQAISQSLVALSKKTASEVDVVVNSMLSQQTKKSKNDKKLNCFL

SKTFENVANSAHFVSSNTDANTSLALALDHPTEHIRYQALVSLAKIYDTKAETVSGKNQV

LNSGDVLVRRFLDDSKRIACFMVSSSLGDMMVNLSTKQEILIAIAQAARKWNSRGDAVVV

QAVVDFALQQYRKKAVSSDIDENLLTLLVSLLDEKCGVSVEAVWSWMSALNHPFVQSDSK

LVIKTLTEIADKFGLALADNIQDLLPYCLRWSQESDYNEIPLTAFLIETLSAARAQLASK

KPRSKKTKEQQLFLDQAFLILLKKEFARLCNDPASEAQGAYSILVASKMTEIAYDIFTIS

RDDFDVCVATLLESPIAVFIRMQECLLDLFHAKLEAQLLPTMARIVTKPAIHKDVPNVLA

KTRSLDIISAVLEGISYETQSEELRQLVIMVPVVMAALSDKSKSVRQSAVACLDRWIVSL

HCGNVKSSQLVADVKTLKKASEFLLKSKQDILMDSNSVVSLCGTYSTHADSSSFYQLLMD

FVSSASSDEIGVAVKLLELLAPVK

>contig52404 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57883.1|) 3e-45

MGVLPEVASATTALMVLYSSAAATAKFAVFNMIAWDWALLLFALAFVITAISQVVILGFV

RKSGRQSVIILCIGATICVGAVLMTYQAIKTTIQHAGESFEVHVCN

>contig53227 Frame-0R|Blast-ribonuclease HII [Phytophthora infestans T30-4](gb|EEY59579.1|) 1e-96

MGKTVNRTVKVAAAMVPRRSPRLMKIKMHLNNDAVPINTRRIMILKKSKHLAPCTLSRGF

ETRYEAKGYSTVIGVDEAGRGPLAGPVVAAACHIPPEVTITGINDSKTISEPQREALFEL

LTTHPGVTYAVHVNSAQRIDEINVLQATLESMTKSVNLLAKQLHQNDKIFVLVDGNTLPP

MLKLPAEAVVKGDAKVLSIAAASIIAKVTRDRIMRKYDIEYPQYGLAQHKGYPTRAHVAA

ISKHGPSEIHRMTFAPLRHKM

>contig53450 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56011.1|) 1e-27

MLSTSMLGGIGEYISTENVLLAVLAPHQTDQQFGATVQVERFSIEAHNGRMTGTAKQRFR

LVEQLPANGSLQFLYGKVQILPHDRAQSIPF

>contig53612 Frame-2R

MRFLGVCIKQSTRDFPRKIQRLGQWGRLVGPLLPVVRNAPASSPSKLH

>contig53803 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60059.1|) 2e-27

MKILVSDDPKTVIGYDSDKEVLVIVTVNMEAAQTITFDLASFAAVRGPIKAWTTETSGKG

ALYEESTLSLTDKSIAVNFPAASVMT

>contig53876 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70239.1|) 9e-53

MTVKKPQSSYLIFCNEQRRHVMNDNAGVRIGEIQKIISAQWNQLTPKEKDFYVQLAANDK

ARYNQELLDNPQIKEEPSDIDKTALISNTCLYPLGRVRKIVQSDSDVSKVSKDALVAIAK

ASELFAQLLGIKSYEQALYR

>contig53898 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65898.1|) 7e-10

MSQIADVHASKQVVPALKTPMGSDGRPVREWIDTLLQAAVIAKDKQKKHTTAEVEIH

>contig54150 Frame-1F

MRMDDSDRLILSNTALAVTSKELDAGTKDSTEQTSVN

>contig54385 Frame-1R

MSYARQARLEERSIHEPLTPISESTLKA

>contig54842 Frame-0F

MEERRTKRFGAARKRTARMREQLNLNDFDMESSHYGNTREFDAVVINHSDPQNLRYSSDW

ED

>contig55034 Frame-0F

MQSKCMTREAAQERCCKHPNYHVVSRRTVKYHPVASLQRSHVSQYCFSYDGRVCHRISVA

LRRFT

>contig56097 Frame-0F|Blast-PREDICTED: similar to ubiquitin-fold modifier 1 [Ciona intestinalis](ref|XP\_002128704.1|) 5e-09

MAAKVTFKVILTSDPKHPYRVVNVPEQAPFTAVLKYVAEE

>contig56372 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61160.1|) 1e-08

MLPMELPVVDQLLERQRHHPPLDGFPMAARIGDLPLFLGEAGAA

>contig57007 Frame-0F|Blast-inositol-3-phosphate synthase, putative [Phytophthora infestans T30-4](gb|EEY61403.1|) 0.0

MASSDFFREPFTVNSKNVVYTNDEITSQYTYTTTRVEGTVATPLEEKFTFKTQRKIPKLG

VMIVGLGGNNGSTLLASTIANKHHITWQTKEGVQEPNYFGSVTQASTIRLGTNVNGEGVY

IPFHNLLPMVSPNDLVIGGWDISSHNMAEAMKRAMVLDHDLQRQLVPHLEKIKPLPSIYY

PDFIAANQADRADNLLQGSKQENLDAIRKQIRDFKQSNSLDKGHCALVCQHRALFRHR

>contig57119-0 Frame-2F0

MTKSYRNGVFFFHILYSSLMSFSCKAASLAAATSTAVAAVSGWSVVSAMF

>contig57119-1 Frame-1R1

MADTTDHPETAATAVDVAAASDAALQEKLINEEYKIWKKNTPFLYDLVMTHALEWPSLTV

QWLPS

>contig57230 Frame-1F

MDHAIVDAAKAWNELNRTVKTFDTWSSRSNAMHWIATRSSWLAHKNRSAFSNPASDIDNL

CFGFPACASAGENGTALTCCSTLPGCCPSALGCCPLEDPALLPNNACFR

>contig57708 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54689.1|) 5e-17

MHFSILLLKRMRLVIDTDAGVDDAVAILLALHAFPGEQVVGITTVFGNVNVHQANHNVK

>contig57906 Frame-0R

MLSLSTSICDSSASPIIKRCLTTSP

>contig58077 Frame-2F

MDDDGSTSKTTTNMAVSEGTLISSSTEDVSGKDGLPVAVATTDVYRSTDANG

>contig58118 Frame-1R

MELEKELYAKWDMLPGNLKKGDRLDDLIKRHYYSWLAWK

>contig58200 Frame-0F

MRLTADVILRAHVSINPLRERELSLRGIHLVPSHYRDRLLTCW

>contig59092 Frame-1R

MKRHLGARRKLVNEKSYAIEEKCSRYEMSLKWDSPMILCSQLMPSH

>contig59214 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64471.1|) 2e-09

MTPYVGGLSSYELLLMVVYVPQEQKALNSTVDRHQRMHDAGDDDDVDDFQAALPAARTHW

NSRYEAQRL

>contig59391 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68478.1|) 6e-06

MDEPTLELPPPPRSLWEFVAILTPVLKYYVALLV

>contig59580 Frame-1F

MSRIHKYLESCNVSGRKRLSSMIVQRLDFSICLLWAWLHKC

>contig05858 Frame-0F

MVLYNAKALVRGAASIKYINLVMRQIHRKFYCG

>contig06525 Frame-1R

MHDIVFLGTDSRESRWLPTVIAASTKTLVVNTALGFDSYVVMRHGVYTDLNQIALGCYFC

NDIVSPRDSLTDRTLDQMCTVTRPGLAPIAAALAVELVVAVLHAPEGKYVNAMKPNDPMA

PMAYIPHQLRGFLNAFHHISITGEAFAQCIACSRLVVQAYETNAMELLSHACNTTAYLEK

LTGVQDLTNQVDAMTFEVEDSEEDEEMM

>contig08448 Frame-1F|Blast-pectinesterase, putative [Phytophthora infestans T30-4](gb|EEY69622.1|) 1e-111

MKIYVLPLVALASLAINASATSIANECSGPVDVPIASPASCSGEYARTTPPAGAIVVDIT

GKHEGSFKTVTEAMASISNTTEVTTVFILPGTYHEQVVVDKLKSPLVIQGYTCNTMKYSE

NQVTITQAKAQADLPVEIKQNRNFLTSTMGFKSESGVKVYNLNVANTAGEIQKDGQAVAV

YVDNTDYGFYACNFTGFKSVVGANKGRELYAKSYFHGADNIVFGRHAMAWFESCDIETIS

KGSITSHGNQNESIKSEYVFSKANVFGSEKNLTMLGTPWGEYARVVFQECKLSDVVNPKG

WKASEEVNSTETVYFKEFKNTGPGAKFDQRVEFSGQLDMAKKMTETLGEGISNYWWVDSK

FL

>contig08967 Frame-1R|Blast-ATP-dependent DNA helicase, putative [Phytophthora infestans T30-4](gb|EEY60960.1|) 1e-124

MQSRVFRSSALLRTTRCRKTSTCSQALDDVYRKLLERGEFEDFQVTEAQSTAVSLASQGY

SVFLHLPTGAGKSLAFQAPALLTAPNQITLVVSPLIALLNDQVAALKRKGIHAIQVSGGN

RNKSVPLSQLLSGQKLVYTTPEFLQLNAEMTEWVREATKEDRLARIVLDEAHCVLEWGNT

FRPSYMRLSHWKAQLIRDVPLTFVTASVSNEAIAKMAHLFQLQMLPSVPVKTNTQVATRH

RQMVVIQQITDRPNLRLEIVAKPFQPALWIARRVAKETTIVYCMTQKEAEETCMALLSSG

SHAGVYHGGLSLKRREFVRKQWMGGKLTIMCATSAFG

>contig09656 Frame-0F

MAIFLFIQTVKPYSWKYSLESFNTVWYREPAENMATTVTMETPKIMATPKSPILHGSPLL

RGSASPPPSQSPHTVGMADRSTADSYYLAFVREKLDDLFGLLYPSVELTDESSTSIRNDQ

MDLLGFLLCWGDQTLVDHHLKLSSCYAKWKVSEFAINDSKIGQEGVFHVENGAKL

>contig13888 Frame-1F

MPAHRDIVCLVLRCHPTPVRRNSVTPSHLVNTETPLLLTLPGLVDLLVSIPVALYVNSNT

RGWYIYSFSTRI

>contig13981 Frame-1F

MLKMPSLHGAWYAAVLWNESGEAWKLSDGKLNTCEKILAAEGTHSVKLLAENRIVRKVPA

DCIRPRAFQPQVGSVVDLVGGTLGEVVHVYENDCLSRTGILLDVKASSNGEIIRVKRDSI

RYPPHEASTSALENKKNRIDIQQFLPAHENSLLVGSVGDRVWVKPMSGTPVKNFCVAGTV

KNFHSRLGSVAGSHTVVVEVAFGSTQAPLVLKVDQDQVLNFAVGNGVLSGRGSSRLLAAL

QMASGHRDLNKTFGGGRSVHNINTTAIHRAFGRVAGSLQQNRQESRLGSAGTAMDQIRNL

ISSNTTIDATNAPSDVEIIEQPPLISESEAGLIASDGLI

>contig15499 Frame-1F|Blast-trifunctional enzyme subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY70125.1|) 0.0

MVLQTASILRRVAHFSERVSLRGLSTTTASPGAFLTMEKRPDGVAIVRLDDKAAKVNTIS

SKMTAEMSSMLDTVENDPNIKSVVLISAKPGVFIAGADITELNACNTEEEMRAMSSTGQA

FMNRLSSSKKPFVAAIEGSCMGGGLEVALACHYRVASQSKKTQLSLPEVMLGLLPGAGGT

QRLPKLVGIQAALDMMLTGKNIRPDKALKMGLVNQVADSYALESAAISAAQGLAAGKLSL

SKNEKGLVNRILEDTPLRKIVFKKAEEMVEKKTGGHYPAPKLILNAVQTGVEQGTAKGFE

VEAANFAKLGMTSEAKALMGIFFGQTALKKNRYGKPAKPVKTMAVIGAGLMGAGIAQISA

AKGVRVLLKDRESATAARGEDYIRSNLDQKVKRKRMTIHDRDSVMANVVPLSDEDEIWKK

HFKTADLVIEAVFEDLALKHKVLSSMENNVPNECVLATNTSALPIADIASACKRPENVIG

MHYFSPVPSMPLLEIIRHAGTSDATAAKAVDLGLRQGKTAIVVKDVPGFYVNRCLGPYIA

ETLALVGDGVDPEKLDKLMTNWGLPVGPITLADEVGLDVVFHVNQTLSKALGERIGGGDA

RLFEEMIEKGFLGKKSGKGFFVQPPKGKKGEKKFNGDAMNLVKKFQTKDLKLSEEDTVNR

LMSRFVNEAVLCVQDEIIASPLEGDIGAVFGIGFPPFIGGPFRYIDKMGSAKFADMMQRF

ADQYGPQFTPAPLLQDMAKSNKKFHSS

>contig16623 Frame-2F

MSSSTKSLDKGYTEILIWYSPRFTHLFCHLSFAIACATFFR

>contig18597 Frame-2F

MANSGDVCAFFFEPVYDSSGPLAPEFSTSPPALKKRGRKKSASLGETNRHRCKKCYNIYT

QAVSTGYTNLLTHLRIKHPDWEEIFESQKLESPSPLVLEKTTTETDSQSHSIPTTSSAPK

QNPSAGRKRGPVYEHFEEVALSSGKKKKTMLCRYCREVSQQLSARLKLHLATQCPRVPED

VKSKYAGAVGLKSNMSHENHSMAVVSTNVPS

>contig18719 Frame-2F

MREHALFAVCGVLAIASSALASHQALGAQASMFGFSGSTCKCKSTPRPCLFIHGQNNGYQ

AKALQPMSTMFGDMKDHAPCCSSIKYASLNTIDTPWTDDNLQATVCAHALSVSKSSDLDK

KIIANTILVTHSMGALIVAGALANAKCFLDKHTTWVSMSAPMMGTMASNYAQEVCTDDNT

QAFQKIFAVLGKCPVGVGMKSLAAMGGKFSNVDLNRAYVAAQKVYRKHVSAVMCSNSAFG

IVSTEQAGYIYLGFSAKHNSSEHDGFVTYDSCRGGLPRSQFTSSYKSRFYVSKCNHADTA

FRHADSFFRDSTKPVKWFECLL

>contig18900 Frame-2R

MFQQDAALALKGLECLTATAASLKKAANFVDVERLSFQHEREDLSSNNGGDEDTVAPLNY

IPKVSSTMFAVEAFESKKKRQEEMATGILKFNVKPSAGIAYLVAHGHMGEGSPRDVAQFL

YTSTDKLDKTMVGDYLGNGVHYQGGFCVNVLHEYVDMMDFTGMEIDVAIRHFLAGFRLPG

ESQKIDRMMEKFAERFFSSCPPGLFPSADTAFILAFSIIMLQTDLHNPSIAEEKKMDKAG

FLRNNRGINDGKDLPEEYMGAIFDRIKTTPISLKEDDDFRSRRGGTASSATSSLFGASNA

VTDRMRRDAYIKERESMVRQSEALFKRRAPVSARAQQHFSLTPRVLRSSSASNLSHKPPP

TRKSGGSSSLLTSGRLSSTFHEVSGLQERSHVRPMFEMLWAPLLAACSVTFESSDSAEAI

QLCLDSFRHAVHLSARTG

>contig19091 Frame-1F

MGDCTSETAFSLGDVGCEKKPRAPALDLQVIRSIKKQQVEHEKEVELEIATRVGGALLRM

HVS

>contig19459 Frame-2F

MSSTFDFVLLVLSLVWSLLAPSMAQSATPECCNTCIGKTSSAPYSYDPVIFAQCTSVTGG

VCCFECGNMGDPTFGDTIAYDDDGVTAIVKAGTFISFTWPGVANVTYISLKTGQKKTITP

SESDEAADVKSDTFLICARSAGIIYFRGWGKDACREASIEHAVTVEAGDSSANTCNANDV

VVPTPSPESSSSVPKDGTVDTCNPQRASVQVVDGTRTCLCVSDWTNPPVCDQWPVWKWLV

TIGGGVAALFSIIISVRAFLAGRKKKEEAAYQENMAPIGTKSDVETLQVTPDSVYMEPSR

KYNPETDRTHGGAKKTDDREFTL

>contig19767 Frame-0F

MHPSDTFQRGITVIPPPRRRNGAATWAIVGIGLFFIGRASGIQAEVRTSQVHRRLQDATP

SSDWIDELPTSVVTYINRDVDPCDDLYEFSCGAWLEQVKIPEDKTNVALAFTTVQ

>contig19987 Frame-0F

MESLKTADLNLEPFIKWFKGIETGLPNLPEVAHVIAAVVLSKELGNWDAARVLAKCSTTH

FVDSQKIKKALFEYWLFEKVMLLDLLSDVNWQQNFLEVIRTISDPAFSLFYNYAHVLEEN

EEAVVYDSFMEVLEMYNLDGKIDKIIIWGEIIADIAVFNGQEQIPFGLPVFIKYMEGKYI

RENPNFILERIVLPLKKVAINYAYDQFSSIFQEKKDFSKLAEELVKQLTNPGDDFKLFVV

MHEAAFGDSPPEFSVEVMKQLLYRWKESDRSSSLAVELFG

>contig20082 Frame-2R

MASASSFNAALAVLLAVKYCRQNPLFHWKEEALPSMGRRAMKYCFRVDMLNLQQERCGEM

LLALLPSQLSLLNCQKDNILYRLKALLVTL

>contig20257 Frame-0F

MIRRLLVRRKFLREKKMATRIEAFGRMVIYRQRYHDKRMNIILLQSLWRMHWNRKKYRKC

VRQIILLQSLWRCHAHAQKYRKTRRMIITIKAFLRMAIARTSYLKMRSAACVVQNAIRTF

LGRRRYIRCRHGVVKTQTLYRGYVLRKKYHQSRRQIIMIQNVYRQKKFRALAAVRRRSMA

RVLGVIQIYLSRLRMRKRTQALFGAANSYDLAKILRIAQEMPGMLRVRDREHEMMSIAHV

AAKNGDLNLARFILEENSQLEDLVFSKDTTGSTPLHYASRLAHLDMIRLLSKVANRHYNF

GAHFNYGGNRIRSASSASTASDDSRELKLRAISCASTASMTTVLSRSPSKSMNLANFNSF

ESHTRTKPSASFSMQPAFQPGDHNAPKRHGRRTLVSSKTETSRRLSSSSCGLPSVLPATL

QIKVYKEGYLRKISGDRRASKRYVIVDEVCLSYYKSEMDKIPLMVVELCDAMIKRMSDVD

FCFKIQSPRLKSSRNIDGTLSFGADSEKVVHEWMLAIRKVHGVRVVTTNPPNHNMICIDT

GLRREYVSMQNKLGFTPLHLAVQNDEDEGFEAVKACVWLIENGADPNAIDVNGDTALHYA

VELERFDLVETLMKRGANSSIKNLKGLSALEIAEDEDLIKILSASYNAFGVEEFSAVSGL

PLADGLEPLKLTSLTSSLLPPPERLHDSTYVSVFLGAIAVATGPIMETPHYKLYIMDCRG

AVIDTAQRTPTSLIQTGGNYWWFGNTWYLQTPLEHLKDGCVAVVELRHRSLVTLEVEVGC

WTFFHLDLSKITTAPATFEMYAPPVDPLSKILARIPGDSFLQAELNVSL

>contig20921 Frame-2F|Blast-proteasome subunit alpha type-7, threonine protease family T01A, putative [Phytophthora infestans T30-4](gb|EEY58026.1|) 1e-121

MSSYDRAITVFSPDGHLFQVEYAMEAVKKGAVVVGVRGKNAVVLAVERKETAKLQDPRTV

RKICKVDDHISIAFAGLTADARVLVNKARLECQSYRLTVEDAPSVEYVARYVARVQQKYT

QRGGVRPFGISMLLAGCNGQGVPQLYQTDPSGTFSAWKANATGRNSTNIREFLEKNYIEN

ASEKDAISLAIKALLEVVEAGSKNIEIVVVRMDGKVTPLEDSQVNEWCNQIEAEKEAARQ

ASSESKSSV

>contig21166 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY66268.1|) 1e-68

MQHHSQEKDCRKPRPQQLIYSTKEAGRKAKARQLQKLHETVAESVKSASEQEEQHHKTLS

NDGQTRGRHRWNRSYSRSVRRMHPSRALLQSDHAVVALCVRTMVERKTDAALIVDSSGLL

TGILTDRDVAIKVVAAGKNPDTTLVHEVMTHNPSCISASSGAIDALKKMISGQFRHLPVT

DNDKVVGIFDIAKCLYEAIAKLEHAYQKSSDRLEETI

>contig21250 Frame-0R

MQIKARNATVRYPTPVTSLTVEGEVVAVDREKKEFLPFQVLQTKTTTEFCLFLFDLLVLN

GTNLLQAPLRKRRNLLHDSMEEVSGYVEFVKRIDITLSTNDAMSLQSNIANETAAVQECL

ERAVTSGCEGLMVKILDDDDSQYRAGHRTYSWMKLKHDYIFSAPKMESKSKKRIATTGNG

TFLADTLDLVPIGAFHGKGRRAGVFGSFLMATYNSTSGNIVDDW

>contig21328 Frame-2R|Blast-diphthamide biosynthesis protein 1 [Phytophthora infestans T30-4](gb|EEY59612.1|) 1e-53

MNPDLVAYRYDPYPKVLTIEKYDLPQMMEVRRAAIDQAKGAKKFGIVLGTLGRQGNPQIL

DHIKQLLEYSGRNYFVLLLSELFPDKLARFKDIDAWIQIACPRLSIDWGYAFS

>contig21953 Frame-1R

MSHFVRQSKFRHVYIEPAKLESCYTNVRLATATGEQNYIKGNTKFFAVSIQAGGGAMAVV

PYEKVGKFDPDFPLISGHRGAILDFDFNPFHEHLIASASDDSTIKIWGIPEGGLTETCVD

PLVDLTGHGRKVTLIKFHPTANNVLASTSSDFSVRLWDIEKGSETVKMDDHGENLIQDLA

WSWTGSMLATSCKDKVVRLYDARTGQIALQKDDAHMGTKSVKMSFLGDKETFVTVGFTRQ

SQRQFKVWDPRNLDKELKKVDIDQAAGVIMPFYDPDTNLLYLCGKGDGNIRYYEMSEGEP

FAFPISEYRSTTSAKGMAMIPKRGCDIMKCETTRLLKLTSNAIEPLHVFVPRKSDAFQDD

IFPDTYAGIPSMSADDWLNGADNSPVLMSLRPEQQGKITNDGKRTRTASKTSVGAGIAAR

VARFARGGGKTDSTPEGKLKTELETANARIALLEKLLRENGISY

>contig22729 Frame-0F

MCLQKLAESTAFTTNLKFASMVATDEVCRLLVTKLASYVSLEKSTSSHVSPLGILRFLSN

FLTCVSNESSQENVPTASQLHFVDLPPIVTALLDKKVILSECQLLGETLKLAIVLLPVPG

ETQSTTTVPRLVLTLAHDLMPRMIRVYDFTSRAKLRYDCLHVIYRSCWVVYGSQQMLAAD

QHTELSQLGAFLARVLSPKRNGRATAGEAEVAVIEMALRITEVPLLHSGVREAANDSFER

HGLASIIRLHALKVEDSSSYNVQSVQTTATRLVDEYIGASSSTNCRMTQLRRLVNELQET

LETSQIVSDDNDVSLVHVLLKLRDFVAKGDDFLTAHEIACSGLVKVLISLLSDTKGQHAF

SQILENQIAGSDGLEFVSLLSQYLQDAISSDKDVFCISGTDNLGLSSVSISTDLELLTQH

IKVHVLIDACKPAVEPDNEDQSHQEAGFHGEQTSSHAEIKKSYGQSLNISTVHDTVVLVE

PLARIETIENFIADKLYGRNGNVKPILDALAEADTDIEDEGEVDECGEFANNVAKPRKVV

AIYNEHVLPNNISLLEAILKFGEAGKKTIKTINASPSKFLTRILTASPHDITFRLVTLAE

SSLSGDAVKYTIKAIDVNPSVPAVSNQKWEDVWDFLLLLKLLQKHCIGKMIDTDFKFVNS

YLSLQVLRVLEQPVAVLTNSLPLWCFRLINEFSFLVEFEMLCQFIYATTSGCSRAIQYLC

RTVWRKAVQEDLALVHPPRLNASGSRRRLRDGTSRTRASGLEILLQTVKLPRLKVRVARS

RLLQSAVKLMAMYGGKKAVIEVEFLGEVGTGLGPTTEFFTLVCQQIQSKQLQLWLDEDGG

RRLSDEEQKRVTINESPETNSSLVVRGYHRIAVYHCFQCKVLHIPTCSLHRQLLTHEKPA

IKDKDTPFDKAKNSASPLLAQFRSWKISIPQCAQCLDDHDWHSTAMSCDCESQLNEASET

VSKTTSGCTLKWWILSD

>contig22978 Frame-1R

MMLSHRNCVLHALRVLHTSAIVLLRLLSRGANRLHHANVLACCACRVHTFFYPQIRPLAN

AGSSPQPHERKANLPTNRF

>contig23560 Frame-1F

MAEPNPDIATYPQKMLLKVLTDWEDNNPKSLQDAHAFFMSATNDPTSVSFAWLLKYARLK

EMPILSGKPMRVLSLIDDIHLEEAFKYAKTANIQKIVGKKMAYVWNLKGLSLFQVKSILD

RLTKNQALSDVKVTVLLAFVSYSQQRNAAKKLYTQLQRWFGRKEVLRLFFDDTLGFDMSL

KELFRKLEELQVADWNKFILKDIVNDFQLQDAEETIFETSKLLVLLKLAIRKMRENEDEV

MATQPLRVLLKENLGAQYDSALLLANANTIPSISVLNPAVKEWLHFFQQLDEGKLSEDLA

SKMSDKYVSLLETLKKLKQEPILHRSF

>contig24107 Frame-0F

MPSSRRHRHGKVTYSSSIRDSIAIMSDVNLPSIIPFSSCVLQLTFGLYPSNHRFSRTLLP

IFAPIQ

>contig24370 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63938.1|) 7e-08

MFGGMISVILLLVFYFICQRS

>contig24693 Frame-0F|Blast-cytochrome b ascorbate-dependent protein, putative [Phytophthora infestans T30-4](gb|EEY64794.1|) 1e-41

MEKLTFNSSCNVNGKLNGQNVKGFMAPDCVLGNIIGLLVALSFISILITIWHAKHQDSTA

HVEEEVTPLLNENDD

>contig24716 Frame-1R

MAHMLEAHLLLRNSSGTSLATSSRSNRRKPGANGSNGGSGSSTPRSRRPSFSRGTNSSSG

SNLTANFVAASLSSGKNRQGKCRDVMSMPNLIDLKTVTVEEVEWEGYLYKQRKIVKSWTP

RYVTLQNRTVSVYKTKNHALAKEQYRGRWMIKELLSSLPSAGFGGSKLRPEALGFNFLAT

NGNLIHFVAASGVEKAMWMHMMQLSLENAAAKETKGQPQVRHMLPSPNPYSGDDVASRES

TVTTHIAKKFLADLILLLAEKSAEKVIERLPSFLRQLSKDVELLFDLETCETTQPSCVFK

GIYHGREGFVHFAALYVSKYVLDTDRTEEATHKADDDDHHAFVFLAHRLVNIVSGSTTEG

KFGLQMTFTPARRVSRVVLSFRQRALSASRFRRVTTNPMVVAEHPACFHQYCLTKRSLAL

SFSDFDVVGVLGQGGFGTVVLVQRHLNPDEYFAIKIIDKHSGAESALKERRILSGVHHPF

LTCLRFAFQTQTKLYLGMDYYKGGNLYLHMHSSKMDPNVSMSSGRRFSVERARFYAAELA

IALSYLHAHGIIYRDLKPDNIMLDKTGNIRLVDFGISKQLRLQGAPGSHNYSQAGTLAGS

PAYIAPEQLLTQKPQYGMAADWWSYGVLLYEMLTGSTPFFDANISQMYKKIQTADVKYDR

YPPIDDDAIDLLKKLLVRDPVERIGIDAIRSHPFFNAIDWERLEMKEVEPPFIPPTRELM

QNVHEHFRNMNVDETIGEDRKNINGKKATTVANANDESYFDEFSFAYDTTRDTFDNLSMA

DEGWLVRQLQEGAAMRGVLNASDTDPVADELGSEDDLSHPILNGRRSSESDEPEVEVTNI

>contig24877 Frame-0F

MSVYVPHSVDYKSTSEISSRGTRLCIIATFFFEKK

>contig24969 Frame-0F|Blast-phosphoribosylglycinamide synthetase, putative [Phytophthora infestans T30-4](gb|EEY59710.1|) 0.0

MCPSTPLVVLCGDRAPENFIKVATSLQDGGQRVASLCSPAVEAALLAAKVPHVAVLTPAD

VQLMLSDRVAVVLALPPRITDGGIALHTRVSQWVSGAYSFVRTAAWNYKQISVIVDEADL

DKVVSNISRDGSLGFSLRERRSLAQKAFALFAELDSAIAASLSGDDELVHDVLLVGNGGR

EHAIAWKLAQSVSSGRIYVAPGNAGTEDIAAGIANANIDINSHEELIAFAKNKGVSFCVI

GSEAPLIDGLADKMNAAGIPTFGPSKVAAQLEASKAFSKDFMHRNEIPTAAYQKFTEYEK

AKEFVDSIDYPIVVKASGIAAGKGVLIPTTKSETYDALREVMLEKAFGVAGDTVVLEEFM

TGEEVSLLAFCDGERVVCMPGVQDHKRIADGDQGPNTGGMGAYGPAPCLTSELERKCVEI

VERVIAAMKKEGMPYVGVLYPGFMLTPTGPKIVEFNCRFGDPETQVLLPLLNSDLFEIML

ACVEHRLEPSLVSWKSGVAATVVMASQGYPNSYPRGKVITGLVDAQSLKDIHVFHAGTST

ATDGSIVTSGGRVLAVTALGSSLQCALDSAYKGVSKIDFEEAQYRSDIGLKGLLHGAKKL

KLAVLGSTRGSSMQPIIDAIRAGELNASIDIVVSDKAGAGILERAKTHHIESMALSAKGL

SRAEFDDQVLEVLRNKHVDFVLLIGYMRILSGKFCKEWENKVLNVHPSLLPEFAGGMDLA

VHRAVLDAKKDESGCTVHFVTEEVDAGPIAVQMKCPVLTHDTPETLKARVQQLEGAAFLH

AIKLAQTGLLRKSKAETKEMTYADSGVSIDAGNELVNRIKPLCKSTIRVGCDADLGGFGG

IFDLQAAGYDQDTALVACTDGVGTKLRVAQLAKKHDTVGIDLVAMCVNDLIVQGAEPLFF

LDYYACGKLEVDEATDVVKGIAEGCRQSNCGLIGGETAEMPSMYHGGDYDLAGFCVGAVC

KNSILPQPVEAGFAVLGLASSGVHSNGFSLVRKLVEMSGLAYSDPCPFEAGKTLGECLLT

PTKIYVKQLMPTIKSGRINALAHITGGGLLENIPRVLTKDLAVKIDCSSWPLPPVFKWLQ

KLGNVSNTELSRTFNCGIGMVMLLPEANVAEVTRQVAATGEKVYRLGTTIARAFNADQVQ

LDGILA

>contig25180 Frame-0F|Blast-60S ribosomal protein L7a-2 [Phytophthora infestans T30-4](gb|EEY65946.1|) 1e-11

MPTKKIKRTTTTTTTTTKMAKKSAKVSSGSKKNPLFASTPKNFRKGGDI

>contig25492 Frame-1R|Blast-cytochrome c oxidase assembly protein COX11, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY58733.1|) 1e-107

MLQIQVIRQIARCPLLQQPLQFKYLNVTRYISRRAAEEARRESVKKRNRRAVMYLAGTAV

AWVGISYAAVPLYKIFCQMTGFGGTTRRVDEFVENKLTPRGDARPIRVTFDGGVSANMPW

VFRPQQRDILLVPGETALAFYTARNKSDKAITGVATYNVYPPSSGVYFNKIQCFCFEEQR

LKPNEEIDMPVFFFIDPEICDDPSMSGVHNITLSYTFFKTDDVSEDEVNDDN

>contig25579 Frame-1F

MFSLKNSVHAFFLLIRAVSKTKLSYFLPLTYCQTMKVIEEPLPTEWEIAMSRSKNMPYYH

NVLTKKVYWVDDELPRGWSHQFDRDGRRFYFHVKDKNATISYDKPVLYQSPSPSPSPPTQ

FYDIPSTEPPPVAAPSFDDSKSLSPRAFAPLDSSDPSPLVKKKYNSLSDLLSPGPPALGA

EQLQETLRPSRAMTISNLVSTSERMPEKISSNKRSFDVMSRSHDSDKETDPDAAAAFYNQ

LQRRAQSDRADSLLFHMRALNNWVKSILINEFSRHEDDCVLDLACGKGGDLMKWTKRNLA

RYVGVDIAQKS

>contig26181 Frame-2R

MHVDAGGQVGKLSSESDSDAIEMIFDVRERWRRGKRQRQVNVALNMSDFYGREYPGFGRH

ATLQALIHPEIKHGALTSLEHPCFFKDHVSMVEGVNVTLKGTGDAVKCLTLLKSHVLSSN

ANCPPETFCFIGSAPQLQGGESFYASGVLREAVLRAHCVLKSIKDKRQESHVEPLLLPTP

TLWSLRKAAITLCMLPYEDIVDGATLTHVLCCCKCDFEFDGRK

>contig26527 Frame-0F|Blast-peptidylprolyl isomerase [Phytophthora infestans T30-4](gb|EEY68840.1|) 8e-20

MRKNRHSKDRLFITQTEHKYLYGGKKHEVRHAYKRLPFNCCAITLCPF

>contig27102 Frame-2F|Blast-cyclin-dependent kinase, putative [Phytophthora infestans T30-4](gb|EEY57985.1|) 3e-94

MWSVGCIFAEMLLLKPLFSGRGELEQIDQIFKLVGAPNEHNWPGVNHDVPDASVRVRGKW

PKYSRLRDKFPLSATFSGSGCSLSKAGFDLLRQMLTLSPRHRISAKKALAHEYFMESPPP

KQQELMPTFPS

>contig27195 Frame-0R|Blast-glycosyl hydrolase, putative [Phytophthora infestans T30-4](gb|EEY61621.1|) 1e-133

MRRILPHTLLFVELPPLEFSIEEFPEINDHVIPRAVNATHWYDGVTLFLQAWHPYFTVDP

RTRRPAFGYTAVRQTHLKQLASIKKYGSEQMKNAPTLIGETGIPFNMNHGQAFRTGDFTC

QRSALDHTISCLEATLVSFTLWCYTPDNCNEFGDQWNREDLSLVSIDKPPRLLEEARLTH

SERDACARAAHAFVRPYATRIVGIPFKSAFSLERVRYELEYVSDCSKSREVAMPSTEVFV

PYLQYPKGYVVTTSDGHWSIQSHDGWDIINYLHDALKDKHWLVITSKDLRIEKLYRARIR

RQRVLVVALLALGASIVYLILEAAEAL

>contig27209 Frame-2R

MHYVESSVEEEKMRGMRVLIVGNIVVATDQA

>contig27296 Frame-0F

MHCPIAIQQQLQISKTYIQFMSSWMSPSLPQYCRRRRKIKSLQEIRLQLI

>contig27865 Frame-1F|Blast-cell differentiation protein rcd1 [Phytophthora infestans T30-4](gb|EEY62849.1|) 1e-150

MEAPEQLYSLVLELSSPEQREGALLELSKKREEFPELAPILWHSFGTVAALLQEIVAIYP

LLSPPQLTAHASNRVCNALALLQCVASHSETRTHFLNAHIPLYLYPFLNTVSKNRPFEYL

RLTSLGVIGALVKIDDSDVINFLLQTEIIPLCLRIMEAGSELSKTVATFILQKILLDDMG

LTYICHTPERFYAVGTVLSKMVTTLVEAPAPRLLKHIIRCYLRLSDNPRAKEALRQCLPD

ALRNHMFDEALKEDATTSRWLAQLLFNITTEAGAGAWAAQGARLTN

>contig28550 Frame-1R

MRLLTRSRPQRNKIYRDFDVETAHGRRGKKAAPSSQSCF

>contig28903 Frame-1F|Blast-hypothetical protein PITG\_18705 [Phytophthora infestans T30-4](gb|EEY68804.1|) 4e-39

MGLRVPRQQQRRHLFSAFVDDSTLFLEKAQQIPHALRLVRQFGRLSGLHVQSAKSKVIFL

NTAVSLATWHGIDIVSPADTTRYLGYEVGTGELTNKNWAQRIRKIQRRLLTATKVATSVE

NRVLILNSIVLPSILFTAIAFDLPRWAEVELSNLYKQFLWAHATSTERCRHKVNPGILVT

PKKAGGVGLVSITVAIKTQRLKHAVVWLTQKEDRYFGAWRTWA

>contig29759 Frame-1F|Blast-structural maintenance of chromosomes protein, putative [Phytophthora infestans T30-4](gb|EEY70359.1|) 1e-131

MAITVATGKHMEAIVVNDYRTGQDCIQYLRDSRAGSAQFIPLDKIRVKPINERFRGLGHN

IKMVVDVIECDAEIEPALHYAVGDTVVCDSIDVARDICFRQNEKVKAVTLNGMVVSKNGS

MTGGKTQNDLRRAGRWDEKEVVALQQEKEELIDTIRAMERHGASYAKQQTLRTHLEGLTS

RLTHAKADLVITETKRPKIQVRMENATKRV

>contig29834 Frame-0R

MDWLTKKKKVAAAKISKKRTAFSGDGNVLGGGEASTTASLETAVPQRPSMINSVKSSFHK

KPPALTAEDQQKRREQQAKALEQRTGAWDKRVATARKARLQQDEEKDSKFQYEEPPVAPT

SGPPPTVLSNEQVKARELQSVQQQMGFNPYAATFSSSTQAASVMNGIGGGSAAPLNAVSS

FPASMQALGSNFSSLDGDENGAVYV

>contig30443 Frame-1R

MFALGSAIKTWKFNYNLIWEGN

>contig30771 Frame-0R

MAGVTNERYCTVLLQQATGEKAIPPSQDEILKGLESPKVELKIRAVKNAILALLQGEKLH

KVLMHIIRFCSTQSDHTLKKLLMVYWEIAPKYEQQSPGEKSVPKLLPEMILVCNALLNDL

NHPNEYIRGCMLRFLCKIKEKEILEPLKDAVKSNLTHRHSYVRKNAVMTVYMMYKTSGDL

LIPDAPELIERFILNESDLAARRNAFIMLNDCAQDRAVVFLMNAMDQVPKFGDGFSLVIL

ETTRKVCRQDPAQKARFVRCVFQLLNSSSPAVSYEAAWTLVTLSAAPTAVRAAAKTYCGL

LNSQSDNNVKLIVLDRLADLKKYHTKVLQEILMDIMRALSSPNLDICKKVLEIAMDLVSV

RNIDEVVTHLKREVVKTQDKTREKAGEYRQLLIKAIHACAVKFPEVANAVVHLLMEFLNQ

PDGAMDVILFVRAMCESHPDLRESVLQKLMISFSDISLAKVYRVGLWILGEYATLPHVGG

TEDETSVFEAASTIFTAIGSLPLAAETSLKALTESLEGAENPAIAGTAYANSVTKSVVLA

DGTYATETSYAAPAAKAAISEEDTAPGLRRLLLSGDFFLGAAVASTLTKLCLRVSNGNVA

SATARNATIKKLVMDSARCMCAIVASGQSKASQHEIDQDSVRRILMSVRVLLDPASAHAT

HTIITEECRAAYRRLLDAQKAQEAEAARDNGGATSEPVTQTDDLINFRQLRGKKALGSTD

IDIDDGADINRALGQQSDGSNNEYAGAMRHVHQLTGFADPVYAEACVTVHDYDIVLEILV

VNRIPQTLTNLIVDLSTIGDLKLVERPQPQTIGPLDQRTIRANIKVSSTETGHIFGTIMY

DSASGAEKTYVNLNDIHLDIMDYIKPATCTDTAFRAMWAEFEWENKVAVQTELSNVFEFL

QHVVDKTNMRCMTPTASLGGDTNFLAANLYAKSVFGEDALVNLSVEKQDSGRIAGYIRIR

SKTQGIALSLGDRITAVQRVKDDHGKRKKLLA

>contig30915 Frame-1F

MRPNLCFQLSLYAVLLVVTATTILDRTSSPDDNDVIRRLTGAGNDLDTTIPFNSWNNTIK

TFRNGLAFVIVLVAAHPLGVFFPRYFRLPLITGYLIIGIIAGPFVANVLTEDIVTMLSNY

VSALALSFISFQAGQEIYLPELRPQLKSIFILLSTLYITAMVILTCVHLLVESAFFYDDL

ALSCQLGIALMFGSISVLGSPATVMAIKIELNSVGPFTSLMLGATMTAEFVVLLSFSIAR

IVSSIYCAELNVSMLNLMFTLSIVMSNVVVGVILACATYLIFQIPGGESHHHAHEPAMEG

SPSQEFYYNQKTDVKASSVDMEYTPAHARHEQPSSSSFLSPQASLSIKGFIWLSMGYVFY

ISTATVAKVTDVMYGLTWEVKFEPLLVLMIAACITGHHTAIRHDMHVILDTAAPY

>contig31130 Frame-1R

MTRRPGEKVRGRDVVWRRICKILEAGEPRNREHSSLIELGIIVLETLERMDCCQTRWDTC

RQRIVRQLELCQQGKSEWILVEVADEMQRESMDNHEVVCSLQERLTVLVHAFACTADTLL

DKCTIALIKQALCKTLLQAVRTDPVSVQLALPELYAQVVPYMGTIGHLSTEVESRKDDWE

WNEDQRSDMSLEAITERIEAYGQDMMKVL

>contig31938 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62486.1|) 5e-14 NOT\_ORF

MSGLVHRATQSSDPISDEHFFLLVIHS

>contig32359 Frame-2F

MRLNSLVAVIFIACVATSFAGAHSDALDKIDYGKKKRLRNHIPTSFGKTSAKSEERNYYY

THPGSPMIHVVTDSMSWWRKLVVALVAIPAVLVAACAACLWSTIFVAVA

>contig32791 Frame-0F|Blast-sphingosine kinase, putative [Phytophthora infestans T30-4](gb|EEY60809.1|) 0.0

MAMPTSESSAAAALVPLSTSNASAEPTESMALLNSLLTELQLEQVVKNLWLVTCYERVQL

RLSPSHCIVEATSTKKQTLCLSWTNVLGAHVHTADYDLLEKPSDVANDGKFLLGIFACMC

SSHKPNAMKKRRLYKFFFRFDGKQMPQVLKLLKVINYVTDPRHGEIISKVESLEQLQVID

RQPRKYLVLINPVSGPGRALQIYKDKVAPVLRYASIETEVKIMDHANHAMEIVRDIPLDV

YDCVVAVGGDGSLYEIVQGLMTRSDWNDAIRQPLGIVPGGSGNGLAHSIAHHSEEKSKPV

NAAFILAKGTPQNLDIASVRNGKDTTYSFLSLEWASIADVDIGSEKLRMLGGMRFTVAFI

NQLVFQRPEYPGKIWYLDEGKTNSPTHYFTAHDSNSTDRPRMDLFDGEGQGPPNETSLES

MPGGESQAESAIPEAREGSWKELSGHFRIVWVMNVSHAASDALVAPKAKLDDGYFYITYM

DGNHSRKDLLAMMLAIETGSHMDKKGVQQVRTRAFKLFPERPTDLMCVDGEVVEGPYLEA

QVHRGMARIITLSA

>contig32896 Frame-2R

MLAQQTDCHKIISKFTHSFNAKYFWCSCRIITSAPRCALMSDYKHARNKYLCLRENPHIS

VYENKSSVSELCRYRSRALVTLLCRHHFIKRRPNQISSLGGRRCEISREDQARTVFTATG

CRSDAGNHRDTRSAQTLSQTLTCLISDR

>contig32913 Frame-1F|Blast-Annexin (Annexin) Family [Phytophthora infestans T30-4](gb|EEY59585.1|) 1e-157

MLKLYPPSTFDAYKKEKTRFPSSVDAVVEQIHAACDGVGTDDKALLRLIGPLSPQDRALV

SLRYKDLHGQTLRELVKSETSGDFGYLLQLMTFPLPQAEAYIVFHAMKGAGTSDHLLYSV

LMGRSNEEIDFLKKVYFEMYDADLSVAVSDEISNNFLAVILKALQEPMVEYKSSFHTKEK

AAEDAELIYKAGEGKWGTDENGFVRVLLSSPPEHLRNINAAYQAKYEHDLVYVIENEFSG

SECAALTYFARISLNAWSFLAEHIESTMAGIGTDSSALSAALVRYHSYLPNIMPIYEKTY

QMTLQDRIKGETSGLYQELLLHLLDAPSPIGKMA

>contig33240 Frame-2R|Blast-choline/Carnitine O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69639.1|) 1e-135

MLPPSASMRPAVVRAFSSARSYVQETIIPTYHFQKSLLRLPIPKLEDTLSRYLAAVEPVV

SPQQLHDSKRTVAEFQRGIGRELHQALVARDSANKHTSYINQWWLDMYLQDRQPLPINYN

PQIKLKMDPVAAKNTQHQRAASLISSTVRVFRTLRDKKLEPDIFHTKPHVTKTKAFQYFC

KLLPESVSFYGAAAFGAYPLDMSQHQYLFGSTRVPKIGKDELQITRKARHVVVQRGTRFY

AFDVLTVTGDAIPDAHILAQVEAILALPLTKHTPQDPGMGLLTTMNRNAWANVRQKLEIS

GINKAT

>contig33752 Frame-0F

MSSVVQTVKAAGNASNASVDVCPMCQQRFAYVSQLIAHINRAHPDTADPRRLSASTVPRR

TDQVGPSGNEVCPQCRAIFSTVTALIQHAETAHTGAVTTEQNVRDQDKCCMM

>contig34263 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY55699.1|) 1e-110

METGDLRDYLVDPTSPRHWSQEVLQIAVDIIEALVYVHSFTPPLVHRDLKSRNVLLTAEL

RAKVTDFGTSRYKSVDDTMTANVGTCRWLAPEVITGSSNYDQSVDIFSFGIVLSELDTHL

LPYENMRNLSGNCFSDIAILQLVATGQLSPQFGASCPPELHDLAKQCLEQDPTKRPRAHV

VAYELREIQRSLYTLL

>contig34708 Frame-2R|Blast-N(2),N(2)-dimethylguanosine tRNA methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56619.1|) 5e-08

MALRVVLQTIESSANRYARHIVPIASYSIYFY

>contig35035 Frame-2F|Blast-oligopeptidase A, putative [Phytophthora infestans T30-4](gb|EEY64174.1|) 1e-38

MAAISGHYKTGEALPDELFEKLKSARKYMVATAMLRQLGFGALDMYLHSQYSATQEPLFD

VQERLITDYSVVSPLKEDRFLCSFAHIFAGGYAASYYR

>contig35848 Frame-0F

MSLLLSLWVPLLLITGVQAFEISGTVYLQESVSKKIGPLKVQLNGGEHTTFVRADGLFVF

RDLAPGRYVVDIPSTHFLFSQYKVDIGVDGLTRALEYKYMGAPKMHASYPLVVEPVKQLD

YFEQREKFNLLSLIMNPSFLTIIVPIGLLYILPKLSEGMDPEEMKKAQAEMGSADPSSLL

AGMLGGGQGNAEDSDDD

>contig36364 Frame-0R

MCMISGIAFAMLSALVDLRADLGLAQVSLVTLSVRAQVTRACSMAPLIDVDTCACSLV

>contig36423 Frame-0R

MTALLISLLQLVFLAMASMPQPLILRVEFQQQHNLPDTLQGPMTLRLSNHPASLAELHEV

LDRQLVAHLLDFRVDNRQMMKLNMTIEIYNQEKQRFVTLKEISQLGERRSRLSITLANAD

AVFPGHTCLALPSKNFTDIAGDNKIEIDGRVVFISEVANSGKGTGLTTWDGSVVLAKYLE

HNRHSGIAGSRVVELGSGTGLVGIAAAILGANQVILSDLPYVVDNLAKNVAETVKLAARI

GRPIESEVSVEVLDWFKPPTDLGDIDILLASDVVWVEELIPPLVATFDTLLRHSTAKTRI

LMSHQKRSNRSDRLFLIELNRYKLIRSRVPASNFHPDFFSDHIEVWEIVRAV

>contig36892 Frame-0R|Blast-cleavage and polyadenylation specificity factor subunit, putative [Phytophthora infestans T30-4](gb|EEY70241.1|) 1e-123

MKNAGQDTTIEIRPTKTVTNEIVVNIAARIMRVDFDGVADGRAIRNCLSNVKPRKLILVH

GTEKTTKDLKLFVESSIPMCEAVFTPNVMECIDIESDTNVYKLSVKESLYTAAVFRKIGS

HEVAYVTGQLVLSENSSVPMLQSLDENDGLTTHKPILLSDGKMKLDVMKQVLGKAGFQAK

FRGGMLVCNDGVALKRAKNNEIVMEGTLSKNYYRIRALLYEQFTLV

>contig37293 Frame-2F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY64287.1|) 2e-99

MLKNLGFQAICLHGQMPQPNRLAALNKFKAKARNVIVCTDVASRGLDIPSVDVVINYDIP

THGKDYIHRVGRTARAGRAGVAISFVTQYDVELYQRIEHLLGTKLDAYPCEEETVLVMSE

RVNEAQRIATIEMKEAAANGTGTKRGRYSRDENDDENDDEGEEKRYKSASRVQKGGRGND

RGRDVRGRGGRGRSGRGRGGRGKRN

>contig37770 Frame-1F

MLCMKARRANKSWVWLFRSLNGCSANVKLGAKFKLSAMLYWKKNIDGQWYVEFARVKIPL

LGRIFFIVCLYNIMVKSDEFGEDDHHSSRGTSEMDVAIRLRREQELGQAEATVLKCRAEL

GYQLSNHLTGTSTRLERVAKDMAATKQQYEEQMQLWEHERLQLKQQLVKARGQRRVLVTE

IRNLRTQSEGQIAVAMAEASEARMVNTRLKKQNEILLTQIRTLLDEVNEHEKKCLTNLQP

REVDGQGAQVADALNKVTMPAVSATTAKSCNKNCFDGDYHSEVVAKDDHLPIPYTLNEKD

IAMLNGRAPVVNFANELLPTQQEQAPSLSIALRGHDTVFRARLVAFFEERDPDKVAEVDE

MLANYQGVEESLFESLELKYNFMELTRRIAQTL

>contig38252-0 Frame-0R0

MAATLCACRCRSPNGSSQCEWIKSVALAGDNARSCDGLDNSIGLCGGGKHVPSRSCINSC

GSDISRNAALPECNA

>contig38252-1 Frame-1R1

MDLRNVNGSSRWLLQETMRALVMVLTIVLVSVEVESTFLLVPASILVAVIYLETLLCRNA

MP

>contig39655 Frame-1R

MSISGLLRCLERAVGQLQRRCENVHGVNSLILMFFFKRTEIHVK

>contig39758 Frame-2F|Blast-importin-like protein [Phytophthora infestans T30-4](gb|EEY63321.1|) 4e-61

MEPDLIQAAAFGVGICASHGGDAFTPYAKQCLKLLDPIVTHPNAQKQTRRNATDNAVAAL

GKLCEYHAEAVDASKLFPQWLTLLPLRGDLEESFAVCRRLCGYIQDSHTLVLGGREYLHV

DKVVAVLAAYAEENFSQQLSQSVGEAQVVNLRLELASCLATLCGSVPEKVINYAWTSLSI

AQQTALQALLPKVF

>contig40291 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66295.1|) 2e-36

MRFEKEVELRERELALREKHMDRQVALQEKLCEANRKNAQIEGAKFYRLAEVLRNIVTEA

QTSLDAASVV

>contig40567 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61935.1|) 3e-52

MRYPKLKLARGIELDEALVGLSNRRIIERTNQGNLYKSEMEQHCKQEKSALAVTTLSERT

EIIHADFMDVNMTDADVVVLFFLPHIEIAHTLQNKLRPGTRVVTYVFQIAQWKPMRTVLT

VPFMTARGSSSIFLYKVPSTK

>contig41032 Frame-0F

MAYRTKFHKDVIIDLITYRRHGHNEVDEPRFTQPIMYARVDQSEAFPIKFAHELEIMGLV

SRQSFENTRKQLTDHLDREFSKITSGNYKPTELEAFQGKWATMKQPNRHDLYVNNATGVD

VNTLLQVGMASVKLPEDFQLHYRLQRNHVTARHKMLHVERNDDPANVRVDW

>contig41674-1 Frame-1R1

MLSLSCIRAVDSSTFRLSTSGDLRLLHRLEYAQLRT

>contig41708 Frame-0R

MLPATPSLLWVPGRTSEHFQRYPYLESNFLDLSAAEDIISKQDKENKNIYDSLSHDAASQ

TVAQKITKFVHLCQERSGYLAHGRLSPKLSVDSHIIAISALELLPILAFAAFIAFAVHEN

RAFALEVVQMRHFWFLVCIVIIYVALSGLCHSIIHRQAWYYFGPLHGFVFVHPSSRRQFV

LEGLVNGSWSFWLSLGLMGVSDVAPAIKSRLAKEEVFRWSLLLVIIP

>contig42389 Frame-1R|Blast-RNA-dependent RNA Polymerase1 (RDR1) [Phytophthora infestans T30-4](gb|EEY56917.1|) 9e-94

MQLRRLMNGQAMPFEKNYDTDDMELSQFLAKLRILRLEADKKARRILAESDVSGSEKKQR

QLSDLELILEHLQKVASSFYSLSIHGAGTVADGLRRIFSDLKVAETKKGKRTYVLVEQTY

YDVMNPALDHFSSDTFTGTDISNRVHLVADCIRNANFDHNSRAIVFVRRRKTA

>contig42770 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65793.1|) 1e-38 NOT\_ORF

MFHYLTCVAVSRGDFDSAG\*LLSSTVELYLLCSS\*KSRDK\*VLQILAMSRKGSPLHAAVH

KRQLTAITLLIFMGADANVCNRKGRRSLHVVEQSIDMATFIQSLIDAVADIDATEKHGFT

PMNHFRLTCTGR

>contig43078 Frame-0R|Blast-hypothetical protein OsJ\_13054 [Oryza sativa Japonica Group](gb|EEE60152.1|) 4e-16

MGIEYDLDIKEGDLIVAGTDGLFDNLFPKEIASLLDLFLPSLTKRDRRSVQEVATHIAHK

AQKAAQVTNTKTPFAVAAQEAGYEYLGGKMDDITVVASLVTS

>contig43746 Frame-1F

MHLIRTVLFVAAAFVAIADCKSFKGTDLDESSQQATNANLPNEIEERRGRGGGGGKGRGT

RGGREAYRANGIGMFTPFMYSSETPHLDRERDRFYRHMFAKYVKMKKDNQAA

>contig43805 Frame-1F

MMTAQPGADRVKAFACEHANATSPPLATIPSVIANEAAELAISEVSSISPATSPSIASRK

RKEHLSLFDDINASVSVDANDYSDECKDQQLQPSKKSRRELPPHTVAILKGWMLSREHVK

HPYPTDEDKQMLLKKTGISMKQLTNWFTNARKRIWKPMMRREHSRQIQSAMEFDQTAVRE

FPGAGLNQQFAGSSYAPRSVLRHSFDAGSLSAPPRTAALSRYARPQASPINAPLYPTRAG

RSMSEVSARTDVDDYLDAVRIRERVSELGNDNRVPRNSLLPHGHKILQDWVNSNLRRDFP

YLNDIERLKLARDTGLDVSQVDGWITSLREQMGGHSMHLPQALVATKMAFPPLPAYGERR

SIPASGNLMFPSRATSISSAGNLMGPPPSSRQKLSDTRYANFSSVVRYPGRSVSRMRSMT

MTASPYLNHPTSISSVGSSQQQSAGSALPSLSSRNLMSRSPPTVTSNGPTMGQPRDSRSR

TLDMGQFADARRRKMTFQDILASTNGISAPPAPKQASLSRTPSQSVASSNNVENMYLNDS

VQLAKVYQSAAFSGFERKHSPASVKHESKRVAC

>contig43892 Frame-1F

MVLLLHIQSSHNYRKRAATNVAQETVATVMQQRLPFHQKLHFITTIVSAFQ

>contig44417 Frame-0F

MPTLACESTHQEAKHVMITEANTEICRSYIEDLRKKQFGVGLKVQDDVTTSVLLKQQQRL

ERALKRLSDELYSESTHFVLELLQNADDNTYEEMVTPRGEFSLTADNELIFYNNEQGFSY

SNIQAICDVGASTKALVDSEASIGRKGIGFKSVFKVSDNPQIHSNGFHICFHAKSSSYGN

GVGYILPHWLDDRTQWKKKTWHDICIAVKHLVDARCERYFCITFCAEAVSFALP

>contig44606 Frame-0R

MPTKRNVEDHAVNDFTMLKGKNLSPKFLEMQLTRSRKQTMRTFNFKHLSNGVLPTPTRIV

TDVMNEREKLQKCRARDKEMKLASKECKDSSKHVAVDEDGQKLRLGKKDGDLIHETIGIG

EAVILKSQLSEQDFYGYVSAITRGEVKLRLVCGSHARVAIDRLRTGQCTLHKQPQNINLI

NKPLGDCNEKWDAKTPLSVATSLEELMRDPPDERRRAAAVLSTS

>contig44862 Frame-1F

MNVPRQQFATYNPQQQFLVGAAAKQGGNNSGSLYAWQPPSPLEQQYYDVLFTHADDQRRN

AISGKQAVAFFFRSHLDKAILREIWSLADSQQRSELSRNEFYVAMRLISMGQRGEEVSIQ

RFSQYAAMQYPLPVIEGFPPPLEMSQPTQLHQNYPQNLSSMPLQSSRSYALTAEEKSKYD

LVFRKYDTDRDGLLMGGEAVALFQMSGLDRNVLRDIWAMADITQDSKLNLQEFYVAMHLI

VCVSKRGLPMPPSLPPELRQAVFGSSNSTAQDTP

>contig44938 Frame-2R

MPMHALSGGQMARVGLAWATFPYSPHVLLLDEPTNHLDMQTIQLLGEALWKYEGAVVLIS

HDLHFLEILTNASQLKQVNTKEIDNARARVFEVSKKKGVVSLVPLDGFQVYRDKEASRLM

SLGKI

>contig45054 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54799.1|) 3e-16

MAKRYYYRQVEGWWDEQPTLEHAT

>contig45168 Frame-1F

MDVLGKIVQGTGCAVDGTVATQNPLSRALESIVQSHSRGHQSRGATPHFGTQSDLQMQMQ

RLKATPQADSRFLSASDQEAVSRLNMEAAYRSGEVQQHMTFAHHASMEAAFKEAQHSHFQ

HYSELEVQHSRRQHEAWNEGLRASYFDDAWQKSGKLDGDEAWRDLKRTVLVKNQSLDHET

LVASQQASTEMTHTMLQNPDPKFQKSQFLKFMNQVSNGEVLIDDEKNEAVGGEHKIDNVL

ENVWKDTMNVRSNQGVLDASWKQTSKASAGAYRNAVAQASAPHVYPLIKAWDDKNTAQSK

GLEVALKTAEEKTDERAWSESDDLEAIWDKAMAGAQTTDSFEDAWDNATNQSYAYKAENP

YLALAENYHNGVEYFRSGHLNDAILVFEA

>contig45339 Frame-0R|Blast-carbohydrate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY58254.1|) 1e-37

MQIAPWGCTTVTCLQDGCADACLFPTNDLKTHMCVDSTAVALTFCPEGSTGLPLSDLNPA

QVPKQPEIYNADPNAALPTIEPATTQLPTEAYDSQAYANVDTTPPLTTLNSQLPTEPLIK

VSLPPLNPVAVTTLATTQDPSKCSMDEPLPVSPVPTPAPSNPTVPTNAPIAPHA

>contig46626 Frame-0R

MTESIDAFVLERALFCEKNVWFYQVPAGQVTNLAPRADAWDPEHPLLTGSVRVLQKGDAC

FVQLFEPVSDDAETSASPTLFAQCPLHITRELSLDVYVHDCVDSSRYFMLRVEDETSGRC

AFVGIGFPDRTVAFNFKATLLDYAKYVLRQFNVRHMETIEKTEVADGMSSQKKDMSLPKG

TTIRMNLKTSANEDGEKLTRHRSCNNGGAVKNVPLIPPPPTESTKTAAPSLAVAEFVTTG

TDEDWGDFTSA

>contig47067 Frame-2F|Blast-DNA replication licensing factor MCM5 [Phytophthora infestans T30-4](gb|EEY53798.1|) 6e-90

MHLLNEASREHVQEAIRLFSVSTMNAAKDGGTQGLFGGLHEKAHEVEQSINRTLRIGTRV

ETSALYSRLEAQGYNPNAIQRAIRAMVQKGSLRQLSQYKFVSRIK

>contig47809 Frame-0F

MSSSPSLTTSILYLVDSNKENLKLIQDALHCCILTRCSRRPPQPQ

>contig47913 Frame-0R

MPLETCIRILNAILFSLHTSVRHVFVLEWNISSNSDRQNGLHCRLGHDDSESECVTHAEN

YSFL

>contig48400 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57727.1|) 2e-10

MIRRAYDNAVATLSGHVSWVLSVACSPDGTQFATG

>contig48637 Frame-0F|Blast-anthranilate synthase component I, putative [Phytophthora infestans T30-4](gb|EEY61414.1|) 9e-24

MSFEPSLERITQLQQQHADKNLVPVYLNAAADLDTPVSVLLKLRAGQTHSFLLESVAPGE

KIARYSF

>contig48897 Frame-2R

MRTEAADSWWNFTTAPILAAARGDHFAVLEWFQANRFERYDRCAMGSAASEGHLEVIKWL

HKNGSEICSNWAIDQAASRGHLDVVEWLRANYSYKCTSFSICRAAENGHLSMVKWLYANM

PESHTARAFNCAVRYCHLDVATWLRSRFLEDDVVFDLTNPTLRIVADFEANSFEMLLWLQ

TYANDVFTPDFVSFIRSETCKPISNWLEENY

>contig48963 Frame-1F

MFTRVSRRVALKLCSTRSFASQARTAAAIKAPVTFAVAAAVGMTAFAITAAPVAENKAAG

KPTTPLAGVAGTSKERTFIAIKPDGVQRGLISEVIGRFEKKGYKLVALKQMTATEERAKA

HYADLSGRPFFPGLVKYFSSGPIVCMVWEGTDVILTGRKILGATNPNQAAPGTLRGD

>contig49069 Frame-1F

MITDFEQDGAYEVRSPIIAGQELTPTDSRCDFKNSTLYRKLYLEKPKQMHWCAALRVLHY

LMGTQSHGIVYTRSDG

>contig49177 Frame-2R|Blast-calcium/calmodulin-dependent protein kinase kinase, putative [Phytophthora infestans T30-4](gb|EEY66793.1|) 4e-71

MMVIGHPPWMADNEILLAERVQRVELRFPKDVERTMEPHLKNLLQRMLTKDPALRISVTE

CFTHEWITKEGSDPLGLITPEKNLTVSMDESERAIENIPERIDQRLSERLAQAHLLVKTR

QESVGPGFVRTSSGRYFTGTAVSGT

>contig49490 Frame-1R

MVRVYVTALIAYLALHAAVSATSQTTLAGDSPVDAEETDTPVQRRLRAHAETNLESDERA

LVNLSEPLFYRAIRFLPLPKPDMAAIINLVKDLDLSSSEALNNNLAQLQHLKTLVQRYNW

CYYDKPISLFELLEKKYGAAVMEKMMETAKDDITDMSISKVLYKERQVYLKQFSRLGTKR

AMDLQ

>contig49524 Frame-2R

MFKSFATLHRILYYVLKCIIYFPNTSIFCLA

>contig50041 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63467.1|) 1e-119

MEEFLADLRELDETQERVEAVSDGMMRVQRLNDAFKAKEMAEYWIQALRASDFQSERVAF

LYVANHVLQKTLFGEVDSCKAPLFVDLFSQYLEEAVALVCNSPMDRQNVTRLLELWHEKQ

IFTDAQLLKMWRCTGENLPPFLQVAAAEDGSEDCKHRSLTSNNAYRVELPDSHDTASEFY

HVLPIKLNSHSVNPVLDVLKKIDHFKTAVKFLDQQIRERHQTLLKESIMKYQTAADLVAD

RVIAASQIKQKAEDCLKLVKVRNKYIREVEHLKTQLTDAIADMIDYEEEAATKIEQKLEQ

CDEIDIELMDLADHQKKFPE

>contig50148 Frame-1F|Blast-GPN-loop GTPase 2, putative [Phytophthora infestans T30-4](gb|EEY55424.1|) 1e-134

MSFGQVVLGPPGSGKTTYCNGMQQFLQANHRDVAVINMDPANEQLPYAADIDVSEMVCLE

NVMEELDLGPNGGLVYCMDYIDVNFDWLKEKLAALKNKYVLFDFPGQVELYTHETSVHSL

LHKLQSIGYRLAVVHLVDAHHCTDSSKFVSVVMLSLSSMVRLELPHINVLSKIDLMQQYG

KLAFNLDFYTDVLDLRYLLNRLEEPDDADDEDQIALEPRHVPIPTSRLAERFRRLNEVLV

DVIEDYSLVSFVPLQIQDP

>contig50287 Frame-2F

MLPKGLTSISDDIICGVCGAGVDARGLIASRKELKRVNYIEKESKFVQSGCYINAGGAKV

KFNFCNGSGSNASSRKPPRPSDGKLTDSLMGQHIAHQALGPPKMERINVQRTTKWLACVA

QIIRQAGAPNSNTPLPAASPAIATVAGAKSLANKPAESDLAAALCLNDTSSYRDAEDTST

LIVPTSKLSGLYVEATESHNQAKYERFAVYKGEPEEERTPTAATSFMHSTRSSTVKNASL

VSPAMQALFDEAMRLVQP

>contig50496 Frame-2F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY69908.1|) 1e-47 NOT\_ORF

MSSNTRLSTERDDCCGCEDSDDLQPNKKYDYTNRFSAMMKACELYIRDGIGAPPEILTML

LEKRQRRSDSRLFGFQAMKSILSLLSYDSAIHNALIFLRPL\*EDFQRVKKNLANLMTAKS

LQRHFEQQFATII

>contig50618 Frame-0F

MSYRINRSLLANFVELVDVLMRNPAMF

>contig50702 Frame-1F|Blast-phosphatidylinositol kinase (PIK-5) [Phytophthora infestans T30-4](gb|EEY58194.1|) 9e-45

MSESVLHTLRKLQTILLVLQGKQKLEKCRHPCADPIAMRTPPELRP

>contig50935 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57730.1|) 5e-17

MVTQGEELSISPPLRRASCGQQTGEARAKDSNGWFYHTVSAATPPDKRNAKCFHQDAGEC

QSDEE

>contig51110 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56317.1|) 1e-111

MILQELIQRLLDPNGVHAEPDELALAGSVNRYVAAEREMFLRMGGDECLLRVLHALRDEE

PKIRKQPARESDVRTLWEIPVPVTIAPSKSGMDGSLRKHALNDTMALLRELCYFSVNLAV

HLCDKDGLVVYLFQLMGDVRFFDNASGLVEEILAVRDEAFDLSRVPNVHVIMQSLSSRQL

AFFCRVLALVVFEPEDRKLLETAKVIKSVELLRLRRNRMIRADNIIDRNHALIYNSPLIL

QRLLLVLQVQNFYFAL

>contig52155 Frame-1F|Blast-alpha-1,3-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY57731.1|) 7e-16

MESHGTRWITAFGLQGGALEAQRERYERLKQHMVFQINAEGNADPLTALTAAKNSAPNSA

ASW

>contig52403 Frame-1R

MVKGDAFPLLILSGLILPVIDSN

>contig52850 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58267.1|) 5e-45

MCANWHEWIYDRHHTKDDNEEINTEGVQYNAPPVAAVHEAQRLLRRDLDSFASFAKQIFI

DPTKSAIPEEFQEHMKQLKRIQENEKAVRQMHTKKL

>contig53871 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60517.1|) 5e-16

MIVDAVLWATKKMDEAVVNPVATRLAGSVANPAVLSFLLWDRLKTLAPQPARR

>contig54157 Frame-2F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY56168.1|) 1e-18

MENDSRRESCRRCNRPLCVCYCSSLPSVPLVTDFTHVLVLQHQHEKERRRAISSVPVLAQ

TIANV

>contig54298 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56013.1|) 1e-46

MSTMEVKALTGSDGEEETPQEQIKSKKDESTAMENLTDLVEEKQMDENKMKVAFQALHKQ

EEADKEAERLLEKKLAAVKINKDDVALVAQEMEISVQLADRKLREADGDVVQCLHTLIAA

>contig54315 Frame-2R|Blast-peptidase, putative [Phytophthora infestans T30-4](gb|EEY53249.1|) 9e-26

MVTTIVCGAIETLDQISRLQSNTTMLQQIIEGIIIGLGRLLHNFEAARSLSIELGLGEII

QRLNVSPGLHAIELLVSEVVQWL

>contig54382 Frame-0R

MAQQQAPFMANQLKCKLNSGTGLHTLRTHSTNNASCTDLIEARDRRMRTCKNDEPMQQAR

MPPSN

>contig54720-0 Frame-0R0

MMEKQEDTLWNATDWIESRSTLPWTPKLTNIFFSCAAALLQLKLPSHLNLTTKYRYDC

>contig54720-1 Frame-0R1

MQANGELHSAQVLKSGHDVGSSHYAGGVPPHKRMRKPIVRKSVDPNATFINYVTQRRFVL

ARSVR

>contig54939 Frame-1R

MLIICLTFDLWPSLCMMSITVLNVLLTRGYNA

>contig55738 Frame-2F

MSSPSSPRRPLTLPEKILTHWAVGLTKPEVSPGQMLCVKAQWTLACEITWKSMDKTYQDM

GRPRIWRNDRFWLAVDHTVDPRVNHQPRQQMMIQASADFANEAQLTNYQPPNTTILHTEF

YRQRAQPGQIVVGADSHSCSTGGLGAFAIGLGAADVVMPLVTGETWIKVPETVLIEFCGS

PPLGMGGKDVMLYTLGQLKCNTVAINRCVEWGGNIAALSCDARFAISNMTAEFGGIAGVF

PADERTAAYLQKRPDHNQDALFFRADKEAKYVETYQIHLNALEPQIALFPSPDNVKPVSE

VVGMKLDGCFIGACTTAEEDLVLGALVLEVCLKQGMIPVRQGHRRVTPGSQVIIENLRTH

GLLQVYEDAGFTIGAPGCSFCLGIAADVAGEKEVWLSSQNRNYRNRMGKGSIANLASAIT

VAASSFTMQVTDPRPFLKHIDRAKLKAAVPELPAVPITITDVKPELVNHTRENPGMDVDA

TASLETFTGSIRGRVQVFGDNIDTDAILPGEFLCENDMAALGKVAFLHTHPDFRTKVQEG

QDILVAGHGFGCGSSREQAVTALKGAGIKALIARSFGYIFSRNYQNFSLVGIQLDNDRFY

ELAKENVDMIVNMTGRTIDVGGETFRFQMSLFEERLLAGGGILPLYKKFGNRLFRV

>contig56090 Frame-2F

MVRVYVAALTAFLAFSASATVQLTLASDPPVNGTGRDAPASRSLQGFATINEKTEERDVM

EIIKASARAIKSHLSRPNVDIQASSVRELDISLNKVLHMNSEQLHQLIKRLKKSNKYPVS

LYEQLVLKHGALNVENAMRIAKSGKNDADVMKYLLEEEKAYRKNWAKAGTIYARELKIHE

DGVKAFETNKISELQAYLARISPDPSEDLQHQKLVKVLSEEYGGDKFLAPCIAQASSLGL

ETFSLKLALVSKWEKNDVPLDYVWWYFCKDVTAPTEEEAEMFSQFYGYAFVRSSKGKLLF

ETTALVEPNLMKVYKDSASDVALDMLIQIRLARRFQMGK

>contig56375 Frame-0R

MVTLPETMDQMQELEEINLDGNKLTTLPAIFGRCNKLKILSARRNLLAGDVLIQSIAAEV

LGEGSTVQVLNLDGNSMSKEHLQRMKGFDAFLTRRTKLKNKEIHGGLNSDLSLCGLD

>contig56577 Frame-0R

MGLLIVLHLCAATLLGHAFAWDPQPDGYQVINGPDSPDALDTWRREWGQWKKMELITNRY

DPNDACTVYNLPQTQWTQRNFVQVFLMMTDRAIFDRDTQQYTVDKYVDNMMERVGPIDSV

VLWSGYPNLGIDNRNQWDHIRDLPGGLEGVKGVIADFQRRAIRVILPYNPWDIGTEDESG

LEDTVRMYTADITALSKILAALQADGFNGDTMYGVPKAFFNCSNPMVATPEGGVPSAYLN

HNPMSWGYIFGYSKFPPVLRPKFLESRHLVEVCARWSLDRMVEFQIAFFNGGGYVLWENV

WGIWNAMTEREDQTLKRMFAILRQFGAIVSTGTWTPYYNWKGDEVYASAFILSDDKALYT

MISTSEQSLSYELVLVANQSSTDVRVYDVYHGVELQKETGSASNRMVVKIEIEPRGFGAV

YATTSTNPDLTAFLRDMQALTLKPLAEYSMERQLLQQELVGGSTFLNSNSGMDSTTDMVR

ISGMKDWWFNVTGVQIEPVSAWTPTFAQFGTGVQFPWESRPWNNHSSILSIDDFMIDKYP

VTNAQYATFLKASGYVPKSLQRFLMHWENRQGAVASWTIPTSLEQTPVVYVAVEDARAYA

TFYGKRLTHDYEWQYVVSNGDKYDSYPWGSNLDRSKLPKLYHGKELPPLRPVGSFQSSRS

STFEVEDLVGYVWQMTDQFCDSHTCGILLRGGSSYYPVAATHSDPNWYFPQALDAQHHNR

FLMISEGYDRSPMVGFRCAKSVTS

>contig57000 Frame-2F

MQRFAGNRQSRGVGTVSGTTCLNWSKCGTVVFVEIDVLLRDYASCPKAFAKPKETALCGD

HVAIGNKDVAKTGDARTPS

>contig57383 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59952.1|) 0.0

MNTQAGDAVVKPKAILGQGDNFYWTGINSEAGRDSRFTATFETKFDGENIANIPFINVMG

NHDYGGASFICSKGDNNAECPSTEALLSALDDKFKWQQEYTSPNDDRWILQDHFYVYSIE

DATSGVSIDVFNVDSGDADVHAAQQVCCQCYGYSKGDSDSCESVTRGHEFCAGGDTDMYD

ACFAKFTEWSDDSRKQLAEKVKTSSATWKIVNSHYSPSVHYAEAGMKVWFDILKDSGIHA

WVYGHTHGEKHDYSESLGVHFVENGAGGGIQKESASGLTTYAAEYVSNVWTYSGDEYGFF

SLTVSEEWLQLQYHTADDSWSFGLNMGTTTLGGVETKHCWYIPADGAKGVEC

>contig57556 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70409.1|) 7e-42

MWAAIQLAPDDKLLKHRFQECVKRGRTNHQTKLQTLGT

>contig57794 Frame-2R

MHTTVLMAGFLVLLFKMDRKALAWDKEYDRDEVEGDDDDSFDFVTSKLEFIKNEDIVEVE

CDSQHCAANAATGVPSVFVRGLVTTKPKPKLILQEHARAATNIEKQFKGETLGYVTPWNN

RGYEWAKKFRAKLTYISPVWLQVREDTHRAPIITGLHDIDRQWMRDIRDEIKGNIVPAIV

PRIVYERNRLSSEDVSVIIDDILALMDEHDFDGIVFEIPVMAGTVDMLQQIARACQNADK

LLILVLSRSSQEG

>contig57808 Frame-1R

MWFAKRSVKHWRMAYLRWLLVLLGLSLLASIEIETVGTRLTSTSGQVHGHLKVLSSSSRR

DHERRLGEVWTTGIMGKMKQWFTRFVKKIKRTRLWQYLWPT

>contig57901 Frame-0R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY54955.1|) 2e-14

MSGTLTVVFCAFLPLAICWTSPLETSVGCMLTIPLSAGLDLFIRHTSFSWQSIAGSVFVM

AGFGILECSSSSSVPLCIQEESRRPSAVA

>contig57974 Frame-2F

MGLQGQPTTSAFVLHERPRSGGWSTSLSKP

>contig59396 Frame-2R

MQKTVRSIYISTLAVTLLSQKSHQTGDLLKLYASAIATCDLPKSSACDFVS

>contig01028 Frame-0R|Blast-unnamed protein product [Ostreococcus tauri](emb|CAL57182.1|) 2e-10 NOT\_ORF

MHPFQKSGFVARISSRITTVIRVADTIKQTITDLMSHSQFHSLNLFILTHAWLNL\*DKHM

TTGRINQV

>contig04438 Frame-0R

MEGMRMLPRPTRLFEQLVDLLLAALLVVAGIVLVVSDYVANCSVYGYMLRCNHLKTAVVF

TFLASFSYFVTFLLDCCEDFAGSGTTHASGESMSEVGHGGGYTGGSTPTGASTPKDVSSR

V

>contig05859 Frame-0R

MVRTLFFLYLYLNHITHVVYNAMAILKLAFYFFQFQRLFPSATVKLTMNLTHHEVNVLY

>contig07233 Frame-2F

MSLTTLGWSPGRSYTYLGFLRDKENSMLTTSSVNHDRRKILST

>contig08535 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57889.1|) 0.0

MRVIGLMKMLQQPENSIDNGVDLLTASSVLAPVIAFKNDSGLILQSEESRMSTHSQFQEV

RYAAVGAQVVERMIEHFSIIFNGVRVQVDDALERLEVKKKALGMVSHQMKLQPNMASLSD

RQRVNEMTRFFRDYLLKGDNKLWPGKVCNSLTMYSDSECGLNMEALSSSEQLPTQTSSPL

SSTSSGATSSAACDPIERELVGIWEQFGFNRPSILSNFEKGGMLLLGALLSWLKSDSNAL

SLLKMRALPSELPTYDAGLVASSICESLVKLLKLVIDSKHSEIDIVALSLEPFWKLFDEE

MYFNKLFMLMFQVFDHLWSKLDPKAASFTRVITETEEIIQKLLNRSPSTVKDLQAAWKEE

TRIRHFYKNEEAGKMERQAKLVEKEVKKATVLSEPSHDSSLFCISKKKPSIAYDLNDYTS

KLIDSSSILTIEHLAYIDRALPITSQLCRWFRIYSVETNGSSLETLLLLAKKQSPTLLVV

KDTKANVFGGFASDEWHRAFHYYGTGESFLFSFANQSAAGGFVKYHWSRKNSYFMLCSDE

SLIMGGGGNFGLFLDSDFSRGTSGACETFNSPPLTVSQEFSCVQVELWGFTLGEKPTELN

QRHKKSVLG

>contig09543 Frame-2F

MCLWKAFNSYRSLPQAPEDTERLDQKTFILKLELPPNHFLVAATSHPYKT

>contig09657 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58408.1|) 4e-37

MERPFPIPSEYNAVLQNHYETVEKLRQLVTSDEFDLTKKRTMEVVIQYKFKEWLSSTSNV

RQILDLVHLDRTLHDPPTTK

>contig10817 Frame-0F

MVMASDGKRRINKLTSEKLQQYRNEILSLDGKHVDLTSRGIERILSLEGIDAATKLDLSH

NKLTKLSELKSVPRVTMLKLTDNKLNGDGLAEIQHLKKLVILNASENHVTRVPFEVIRNA

RTLKALVLNNNSISTLDWIPKLPNLNSLILSHNNITKIPQRVVDGLPSLKKISISHNLIE

EIPNLSQLSEITELRLSHNRIKAIPAHLAQLKNLRVLELSHNDIDDWSGLDALSTLENLR

QLNLAGNPICGRTLTTLAQPVEENCSESDDEGDKVDSDDEKKEKNNIQDYGNVKQMGKEA

KKLDAKHKQYNFKMKRLFPHLVVRDAVRVLDKRVHGYVAPPKEDKTAKSFSNPKIVTRKR

MGDDSDKQKTNLTSTRVDAIDATKLSKKEKKGKKQRKTERLAADRLTMDAGVFSEPERKK

LKFHAEKNKATKKLITEVLETASVNAVKEKKWKDKRDKLKDQRQPKEVASGVVALKHLKM

TKQVQRGTKVNAVDLSQINLTPDVGFGGPSAWDNFITT

>contig11195 Frame-1F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY64900.1|) 0.0

MGYWINPASASKVPNHLEYYECIGRLLAKALIEGYNMKMSLALPLIKHVLGVPISFSDLE

FLDEELYRNAMWMKHNDHADHLAIDFTVQVITSEGKSHTVELVPGGADRDVTDDNKKEYL

ELLLKHYMFESISEQLGALLMGFYDIMPQFLITVFDYQEFDLLLSGIPELDVNDWHTHSE

VRWIKLERPSPVETRVLKWFWDCMREFTSEERARLLQFATGTSRVPVQGFKALTSSDGRV

RRFTIQFVHRGAPPTGLMPKGHTCFNRIDLPLYHTKEEMVNYLTLVMNMEISGFWME

>contig11436 Frame-2R

MKSPLLSSHTRSEDSSSVSNSFDYSSSSQFSNTNEPVKTLEKVPYSPPPVTSPPQKQILT

DTTKRSQKSSIKGKESSDHSASSGSDTASADLLNATDTPKSPPPVSWSPPPVAAPSKISK

APSKLIFMSSGSDDLANSGDAASADSSEASNLVEFTSSDSSSYLKDKISSPAPVTRPPEI

TVKTIKATGNENDKRKSTFLSSSTGSSDSGNNKNQANFSSALTASDDKYEVGQVKSPSKS

TAASDEGNKIWQTELVLNSSEKTTPSPVQRTRVPRSAGLVVPPSLDSLESLGTVAPANAV

DIENASAEVVSNEADLESGKNTFNHDTLILLGDTGSTIVYTDGSATTTYEKYTRGDVNLK

AIHDANGSYGKIVVGGGNRVNLPPGASILLSATSQEIHNALLYASYALGIVSAVLLIFFH

LLALQRPPWLSNQSNGHGRVSMEWFMPNVWELVVAVGYMQHVNSISMLELTKAPQIVLDF

TDSFSFVNLHITPLTTTTATEASRRLQLIILTGTVAFADRIGISEDEALLSSFWIFLAVV

AALVVLFILIAGYSYYRHSISADASLTFYPRQLRKSFAMCVVGLGVAFWALSIFPLMSMA

SYELVMELRYRMGIGLAVALFCLWAVAVGGLCYVFISVQAIPTSEAFRFRNFSIWGTMYG

ASKMTFRYFFVVAVVIQGLLGIITGAVSGIPAQLVALIATHLLFVIVTVIIRPFASRWVV

IVVVGLRVVAITNLICSFAFLTSNGLSLEWRSVVAQGFVIFNSLVFFVLFARYVTIFVLV

LKRWSSYAAPESLMHSLQTCDMEQQLNHTPRDVRDYDQSHEGGRFDTSRAHFTPPQGSIS

IYSSSRTKRYKFTPTNLSSNSNVAPTPL

>contig12266 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69796.1|) 4e-93

MGGLHAAMVASVFSGDVGAIAWLAPPSAAPVFADGLLSGSCNWPSLYKQHELQLLDHKML

AGHALVESYKKLVSPVTDGFKEKIDFLNGTLDPVNEAKKRLRLFLSITDIENFLPPRRPD

AVIFVYGTEDEYIGFSEPQWQRLREQWRPAQFRKIKRGHVSGILLEQEEYRKTVLEVVEL

LKEQPIFMP

>contig12734 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56515.1|) 8e-17

MIDSSTMSDSQNWSSFENPETPKHPTEVVDSSDNKRLGADKRGSPLRALTDPVALRHVRN

RLIFGGLVGFVTGATFGG

>contig12819 Frame-1F

MTKSFRQGNISCSRKRNLEQYEWEHSKENVVPLKRGRNVTDLNKALRTHDSYLSKLQLED

EFHAKKNYVMNYNGDDPLAPWLELVRWLEDNMPEDTQKKFAVLENCTRKLKKNPQYKNDM

RYIRLWIQYADLVSNPKDIFKYLYHNKIGERVSLFYIGWAYVLETMANYPQAHKIYLKAS

QKSAEPQDLLEKKYKEFQRRMSRQWLKMTEGTENNDINEVTYRRALESLPTYGILELSDA

QRQQLHQRRASARSERVQKTNAHKPVFIIYEDTEAPFIDPFDGNNGWKKLKPMLQQDKEN

KVAPSGWNVVKFQNDTQAGPDLQSDHQSHSSIRASSVQIFDDENLTLPIKKCEKTLLTLC

PRKLRQQVDGKAAEEGLLVKATLKNSIDCDNTAQKGAKIELEKRMYDVKQITSTTGEHTS

FEEIRAHSYEQTAGRRRQLEHRDLQNMTCDNQSVCNATLSSLTAPSKFSACTAFDEVKAT

MRTSPTPTIDSCKHHYFNTENLPIVAPRKLALTAFNGDHEDVTINTQVALEDVNNMFCSP

PQPKSNVRIAVEEAPVELKPHFSVFDDSVDRVAASQSVQIDPIESVTREGRQVVSGNAFT

TPSKKKQTSRIFSNDKYGEYQLRKKQGKQIFQESVQREAWTGKKALSEKRKPLGARDDLV

RNKRLTNKDIFMNAQIDSTAKGSAGR

>contig13889 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY65271.1|) 1e-142

MCMAAKLSLPCSVTSTQIVTRVNDVIEAMGLNTCRHTLVGDMFRKGLSGGQKRRLSIAME

LLANPSILILDEPTSGLDSCATHNVMKLLEKLCTQGKTIVCTIHQPSSLVYNFFTNVIVL

SAGSTVYCGPRSQMMAHFASVGHDCPLYVNPAEFFLSLVNTDFEDHADVSTLVHLYNESD

IYKGLETRLMNECKTLPHVSDMEKTLPPSAMRQFRVLLYRNMLNNIRNPGIYWIRLLMYF

CLSFMVGTMYLSTNNNLTEEDLVPLLFYVQAFLVFMSVAVLPFFIEQRAVFARERANSSL

SVLSYVGANFVATLP

>contig14259 Frame-2F

MVETRRTSQRLQAKAALSLSPQKSPLLLDKKVHHMPSPTTPTTTNVDAIVMTEVEPTIED

ETSPLEDDEDIAHY

>contig15146 Frame-2F|Blast-choline/Carnitine O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69639.1|) 1e-147

MYRDSIQDPVLKASGHAAIQELKWEIQSDTKQVLNEAKTTYAKWVRSLLLACAETPVTRA

IGKQYDIGTDGLMQMAIQLAHFRLHQRFVATYESASTAAFKHGRTETVRSCTNEAVAFVH

AMTNASVSDADKAAALRTAVKKHSELTKNGVMGQGFDRHLFALRAMANIQGVDVPELYTL

PAHDIMSKIILSTSTLSSPALEGGSFGPVNDECYGIGYGIENEGSAFQLSSYRKDLPQLK

DLLVQSLIDLECLLADTSSKN

>contig15407 Frame-0F

MILKLVNDPVRAREFGITLAMANKMKATRSAMEFLDTMTDTERMASITTAWNDWLKDYIA

RIQDEFNPTSDVLRRERMLQVNPLFILRNHVAQSAIDFALHGEYDKVQHIFQLVTNPFKE

PVNESDFVYAVPQDSSVAPLCVSCSS

>contig15498 Frame-0R|Blast-UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Phytophthora infestans T30-4](gb|EEY58445.1|) 4e-87

MRSLALGRGRSVAILRWNRVANFTEAFYNASSNTSKLHPSAIIHSSAKIGSGCHIGALSY

IGEDVIIGDNTVISANVTLQNVTIGNNVVVHPGARIGQDGFGFMLHSNGEHAKKPQQLRV

EVHDYVEIGANCTIDRGSWRDTVIGQNCKLDNLIQIGHNVQLGTGCVIAAQTGIAGSTML

GNNVHIGGQVGVAQHLQIGDNVRIAAKSGVMHHLESNATYGGSPAVPIMEYRRQMAFFRQ

QGHKKRNDGTSDLRSLG

>contig15861 Frame-1F

MTKFKTNLKRISLENSWRSAKEISVAEPEIDQDPLSLQSRVLLSNEQLLQIVHEASEKVD

FRRLSNRQASLSHWKYKTIANNFTTFSHGDGIEAACEVLATGEMKASLNELNHILSTNTT

KDHGMVMRGLYKDYIHGAVVHIIDPSQEATFVKTSEMDTRLTVKTSAFERSRMFRNHEQW

CFLEHFEKGSSSDSFTVTLASVPEQYLVAGKMKADRVDDLPDLTAAYLIEKIPASNSVRV

VFFAQAAFNEPNARFDQSIRNVMGGMNPTSQLHFSKKRQKRLMRLATGVSRLPDVVRRRR

FGVQSLADRTSFEATNSRCTCCAKSLSFLRRKRRCHMCGYITCYQCWSLHSMESRDGRIT

SVRACIRCVGFVNNGDYSQVNQRKLGRVEIFSDSTFPSADPPGKALTNCLHDALQNSSGS

KRKTIMAVIRHILNQEQAEASSNPTRSSLTSSIRLTDEDFDLYNDALDKGIFHVDPLPVE

KCVLANVKGRNYPLKTAAEPTKMNEFPMPYDEQKRLSAIQNGGFANITDTEELDLICELL

VREMNCNIGIVTLITKEEQHILASNLLPLRQLHMPREESFCQHTIMNEEPLLVPHPEADI

RFQNLPALHAFNVKFYFGFPLKDNCGQVVGSVCCFDGKTHDVTASQYSSMKKLAETASKV

VQIKGKQARAI

>contig16110 Frame-2R|Blast-pre-mRNA cleavage complex II protein Clp1, putative [Phytophthora infestans T30-4](gb|EEY67582.1|) 1e-160

MADSPRKVVLSCEGEYRVEVPPHTEVFIRLTSGSAELFGVELAIDREYAFRDRKLAIFTW

YGCTLEVRGAPDEAYTSEETPMESYLNIHAQLQRRRELAKAKQSAGPRVLVCGPVDSGKS

TLAQILVNYALRLSEKPTLVELDVGRGFLSVPGTLSATPLDLNSLSIEEDFVLTNPLVYF

YGHAASSENVELFRYQQKQLARTVNIRMENDKEVNASGCVINTCGWVDGAGFELLLHAIK

DFVVDVVLIIGQDRLYSRLQSALTGANANGVERSIVKLSRSGGVVPLNSKLRSAARISCI

REYFYGVHSLTDSIPTFSPCINEVSFDDVSFFSIEDIRVSDVMLPVGQMESQNERLRVVP

VEKTSDLSHTLAAVAHSRSSQDTSCSTSANLSWLIGVPAAGFVFI

>contig16622 Frame-0F|Blast-Proton-dependent Oligopeptide Transporter (POT) Family [Phytophthora infestans T30-4](gb|EEY57830.1|) 0.0

MPDSQSSTRSKSAMYSPLSPTLDELGNTPSASSSYFIEGPWEQRNRRYQNVLLHVCSFIL

ILEFAERVSYYGINQGLKNFLGMLGWSQVGSNSLKSTWTSICYLSPLLGGYIADEKWGRF

TTLWVFGVWYTLGAFLVTASAHPKFMELENGNHVAANLMCHIGLFLGIAVGTGAIKANVI

TFGADQFDPNDPNEVTQKEHFFSYFYIVINLGAIFSYGYLSVLCIEGSGTISEEYGYFAS

FFICGGVMVLAYLLFFFGASRYVHFVPQDSALTKLCTIVKGNCAFSFEARMLYYGLIAFG

VAFPLNLLASFLSDWLSVSQYLSYIVVICCVFGMYAWIRYGMTTAYMDKSKASNGGKFND

ETVDEIKMVIRVLPFASFMIMWECAYDQLDANFQSIAQQCDLRIASQRMSDSDAMQIPGA

SLGIFDPLTIILLIPILDGFVYPLWGKIFGRPPSAFGKVLTGLFVAMFTMVWSGFFEIIR

RNSGEILYLDSTGSLQTISNNGSGQPMNHTYWAYAVPMYVLIAVAECLINVTAYELFYTE

VPVYLKSTCQAINLFMVAMGSNLTSTFTLLFDRYITDNLNDGHFEYMYWTLGLLS

>contig17625 Frame-0F

MRGRAIVLVLLAVLAHATAVSMTNQRVGTLVWCPSVRTEDSSCQWAGESGRVIDSRALRE

LFLKRSNVPFSIREAYSRNLQEHMTYLEDVNMYARQVRHEFSYDMGVNERHLSVPSTRKL

SAFQFVDQEIYSAYSRRLQEVSGTTNSTSSSSNSSVYWNWCDKENAMGHSVCSPVKSQKS

CGSCWSFVAADAIETAVVIAENASTAVSLSPQQFLTCSSLRTTQTFQYCWATENGVDGAT

WMQSEIIWESQNDGCNGGMTHGAFMDAAQNGWGLVTELTMPYDDANPASFSNSTSVCQTI

PSEAAASITGYEQVVGLDCTVSNSCTVLLRSALQKQPIAVAITSNGGFGEYAGGFYNCPN

NGNMASKNDLNHALLLVGYGTDSTVGDYWILKNSYGSSWGESGFIKLVADSKINCGLNVF

PVVPTGAKAGAQASTSVDSGGDKKFVGLSPTAWITVAAATTIFTVVSTAIGIMVSHQKVK

MIRKQNAAQISVNGQQRH

>contig18075 Frame-2R

MSLVVGVIFPPKKIARLQEVLTVDRDDIRFILIDLEDLTPTKRLISNLELEAATERFAAQ

YGLLDALLHKLSHEMVFEGMGDFGAVNRVKLVQNYLQHHPSVCVVDPFDSVRLLTDRHAA

CKLLQSMEHSETPATQRFKVPKFFEANCPEQFQTLLKDLNTGRTVLPLICKSIEACATER

SHMMSVITKLDDLQYDGYPTLYQEFINHSGRLFKGYVLGNAIDVAERRSLPNLVAGTAQH

VRFNTQQNYPTSEDFHPHVDLKILESRLDDKYSQQNVFAAVRAIGKRLREELNLTLFGFD

VILADDGSCDLYVIDINYFPSYRELADFSTILRTHIKQLCGRQ

>contig18596 Frame-0R

MAQDDFKKPALKKQASLGNISEEIEDDLSTLPDMKISQLHFLLQHQHADSSTLTPEAAAA

AKTQVLELVKQNDMTPFYRMICSEFSWTVDAVLEAQMSNKNTTELTALDERLADAEQNLG

DIEVLEALLTKARMYSRIGDKEKALEAFEVAGEKPQSINQKILVALHIIRIGLFFSDLEL

VEAYIKKATALIDEGGDWDRRNRLKVYEGCYMLMARDFKRASTPFQESVATFTATELMPY

NTMVFYCVITCVLSMSRVDLKTKIVDSPEILAVIKEIPYLTDFLNGLYDCDYKKFFTAMV

DIQPQILRDKYLSTHSRYLYRELRVLAYAQFLEAYRSVTIASMAAAFGVSIEFLDKELAR

FIAAGRLNAKIDKVAGVIETNRPDAKNAQYQDAIKKGDLLLNRIQKLARVINV

>contig19564 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58605.1|) 1e-61

MKAPSAEEVLALVNAATGPDGTLDPVMQSLLRQMQEQHVLNQANRRAQASADQINSETKS

HADEANGKNNPIIANLTLFEAAKAIEAPKSGAFENARSTVEVASEVALMETAATFPPKVM

KRKSIPLSMKKEAIQWIMGPGKGIPSRAEKHFIALNWDVRASSFRKWWKNREKILGDAGG

KKRIRGGGRKPYLEDSEEKLLVVVIQERAKKDRVTRKWIAKTAQHMFQRCDATFKASENW

VTKFIRRNGLTLKRSYVTDEPQQGALEPLQLAQSSNEASMIV

>contig19766 Frame-0F|Blast-endothelin-converting enzyme, metalloprotease family M13, putative [Phytophthora infestans T30-4](gb|EEY56805.1|) 2e-20

MEQGWPLIGELYDSCMNYTNTSDPTANEASVAILVPTLLQIAATTSKEELFQLAGNISRV

GP

>contig20014 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54486.1|) 0.0

MTCVMGLRLINIVLETAGTGLGNHLCLVSVLQGDLSKFLLQNSETEELGILSLTLRVVFN

LFNSIKDHLKVQLEVFFTSVHMRIIDSPSCSNEQKELALESLLEFCREPALMLDLYINYD

CDVHCTNLFEVLCKSLAKNCQLMSGPDGNLNALTLLCLEGLLAVVESIARRCPLNTVAKT

SGSKYFGNHAGILTLKGSDLARFTSGASPGTESSSSEFSMDDISPLSSVRDLMHRVMSGS

ESDSDSEQSESDNPRDQLAWLHTARERTAEVLQQRKSIKKRYGLAADKFNHDQKNWMAFS

QQIGLLPDELTPESVASFLVHTPGLSKTLIGDYIGDGPVEKYPFNAAVRDAYVAMFDFSS

LSTLDEALRMFLAKFRLPGEAQKIDRMMEAFSKHFYLQAGASGPLADADAAYVLAFSLIM

LNTDLHSDHIVKKMTLDEFVRNNRGINAGKDLPLEYLTDLFHNILEKEIQMQHDVSDFMD

SPSSTVDRYSMQWDGVLKRSKNVVGASFSSNTSILKLRAGLYEKDMFNLIYESTIKSILL

AFERTCDFTNMERSLEGLSNCAKIMLYYDMVDEFNKVMGALASYFLTFAHGIMSGEKVYI

PPRTSSNLLTSPLPSAAPFGSTETVGERVICRQDDGSEIELLAVSRQLDGSIDEDLLQGA

KTRRALLALKKLFQFVQNKSEYFRKGWANVVECMLMFNELDAVPTS

>contig20869 Frame-2F|Blast-alkyldihydroxyacetonephosphate synthase, peroxisomal, putative [Phytophthora infestans T30-4](gb|EEY67127.1|) 0.0

MSDATPSVARMRAILRHISAGGKSATISSLPSTSPPVALNFATRWNGWGFADTKLYVNAD

KIVEISGSRYAEVFASAPDRTLPLLLPWAERRIGLHLERRSPPSITVSEDLRLQNQLLQD

GETYQRLLQFLHVASLDLGMKTSTTVKERVRHGHGQTCEDIYRLRHVQDVERVPDAVIWP

TSQNQVERIVHEVAQNYADCVCLIPYGGGTNVTSALACDPNETRAIVSLDLREMRRIVSV

DRENLTAVVEAGITGLDLHERLRHHGLTLGHEPDSWEFSTLGGWIATRASGMKKNMYGNI

EDMVLNITTVTPQGTMQRAANAPRAAMGPDMNNAVMGSEGIFGVHTLATLRLREYPSVQV

YDSLLFPSLEQGLASLKEITRAGCVPASLRLLDNTQFQLGQALKTSSTISKFTAGVIDFA

KKTYLTQIRGYDVNAMCAATVLLEGTNQLKVAAQQKLIQKIAKRHDGISGGVENGKRGYF

FTYIIAYLRDFALDYYFMSESFETSVPWTNALQLITDIKLAINLVAAKRDVKVAPLIACR

ISQVYDTGVCLYVYYGINYFGINEPLTLFRETELAAVDAIVRNGGALSHHHGVGKHRLAW

LSAAVSPPAIAAIQGIKNALDPTNVFAVKNLQPSQ

>contig21084 Frame-0F|Blast-60S ribosomal protein L7 [Phytophthora infestans T30-4](gb|EEY53584.1|) 1e-124

MLRLVEPFVTYGYPNLKVTRELIYKRGFGKVRGQRIPLTDNAVIEKSLGHVGIICIEDLI

HEIFTVGEHFKQAANFLWPFQLSSPNGGYTKKLLHFAEGGDAGNRGAEIHKFIKQCL

>contig22193 Frame-2F

MTPLSTDPTLFAATVSPRDPAAKVAAGASSLISKSQCSPMVNAFASHRLCIPSSGSSDDA

SDDEYDDSEDVPCTASGKSMKGNTGRWTEAEHKLFLQGLEAFPYRAWKKIATLIKTRTVV

QIRTHAQKYYQKLEKEESRMKEREAQDRAAIATGAAPLSIPTSPAAQKKKINLMRKRKCS

MISMDSVIESDSIVLPSIPKRIAREHLLAGMSPKQKVSSISGNKAFLSNSMDSRFMFARN

LKSHAVMQPPHQLPLDFADAAAEAMILDFAEEKALSDYTLDCVDQTLASIDNEDLLQLTE

EELEWFSTSNTDLSTSIDETKSDAMQTGIGPHSGFNFDALDSENFALNLCLDDADDDFVL

DPEKFLSSYFAPSEMS

>contig22360 Frame-0R|Blast-phosphoacetylglucosamine mutase, putative [Phytophthora infestans T30-4](gb|EEY59263.1|) 0.0

MSSVSVLDKTPRVAEETTKYPRADRLGARELLYGTAGFREDASLLVSTCHRMGMLAVLRS

RNLGKIVGVMITASHNAAEDNGLKIIDAKGEMLSQAWEQYAVQLANAPQEKVVEVLDAVV

AAENIDLDQTGNVFIAKDSRPSSEHLAELAREGALVIGGNVLDFGLQTTPQLHHLVRMWN

YEHYNKGDWASEVGYYNMLSDAFKQLTAGHDSKRLDTRPPLYVDCAHGVGALQMAKLSKD

LGESLRLEIVNTPGDGELNLLCGAEHCEKSRQPPINVTRETDRGKRYCSMDGDGDRVVFH

YFSEEGVWHLLDGNKIACLFAEFLAEKLHALELDQEGVTFGCVMTAYANGAATKYLQSKS

IHVAQAKTGVKYCHEKALQFDMAVYFEANGHGTVVFKDELIEKLHKWENTLHDERKKLAL

SQLLAASQLVNQATGDAMCNLLFVEALLIQKNWNIDEWDAIYQDLPSRQTKVKVTDRTLV

KSDEEDDTKVLAPESLRVALDAALLEFADKHGRAFVRPSGTENFVRVYAEADTQQDADAL

ALQFAKLAHQHCDGVGNEPASFVA

>contig22979 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61788.1|) 1e-32

MMEPSVSSTATPAPASTDRIASSSPTEAHGGASGAKSAKAPAAEMLRQFSSQFKNHVSQV

QMPPAIKDRTDELERRISATDIARINGYMRLVNLFFACGLWITCFFRMFQAPSYSHFLVC

IYIMF

>contig23998 Frame-0R

MLQDWDKVQEKLEKVENHEQLITARSAIPNALSNEADKAAEAFNIIQMREDTSANLLVGT

QTPATPATPATTATATIASATMADGSKVAEAEFSSKKAWQGDENYELNSAAFRSAMESSI

AQANDTKKNESSVSADVLKKNLKQLDKNTPSEVNTGGKNSTSVDEDHGIGKPQDNDLSDQ

DTIDEGSSVNDSSDDVSSDEDSSDEDSSDDKSNSKAKVLKSPLLGDEKLSNISSNSADSE

PAD

>contig24106 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61173.1|) 0.0

MMTAGHELLLYHQSLWAAIRENEPNVSSKTPLMEPSIVGTLMSKMTRARKYEQVLDLATA

YLNHFEFIAERDFQQQGFLALFKASVKTRRRPHKIVHTFLNYVEESVRARGEALDRIQNL

SLERGFGAAIQCCVAQEEFSLALHCYATMESTRTRLLRDTIDSNIEIQKAEEKAFTVDAV

LPADENIYVNVMKACLAVKDFVLLKEVFQAMTARGVARSAGFGSAIRYCHEHLDANFLEE

VLEKVFETEANVAGAWMLQINHYNDALGCFAATGRSEQAKELFTRLWSNSSIVPDHITML

EMVENYRNASIEEVFALMDAFLERQLAPNLQVLTSLLSICMRQRIVGDAVALINGMEKYG

IVLDFKAFTSIAFIHASHGDIKAIVSVLRDMTTNCIPFDSVFFKYVMNALYESSGIDLCF

ELLRELNHENRAIPEGLYISLIDLGTRIGLIERTLHVAYNMECEGYHVSTQQLHNLLMRC

QSKAEIVEYLRTFSLLHQGRQLGMPRFEMELYKDLCSRLTRFNCKDHVEKVQMLARSAGH

DDVIV

>contig24692 Frame-2F

MPRYTSRVSSSVPVHLPLIEPTPIEVRSMCNHQFSCFATMTLSSVA

>contig24876 Frame-2F|Blast-nicotinate phosphoribosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62006.1|) 0.0

MQSNMNLVPTNSLVGPMLTDLYQITMVYAYWKVGRHNDHAVFDLFFRKNPFHGEYTVFAG

LEEALAMINTFQFTTSDIAYLREVLPHAPDEFFAWLSSIDCSTIKVYAIKEGSIVFPRIP

LVRIEGSLAVGQLLETPLLNLLNFASLITTNATRFKRAAGADTKLLEFGLRRAQGPDGGL

SASRYSYMAGFTGTSNVLAGKLHKIPIMGTHAHAFVQAHTTLEDIRGTMLDGRDFLGIVL

KFRNELDFEHTNDGELAAFIAYAIAFPDAFLALVDTYDTLSSGVPNFICVALALHELGHR

PVGIRLDSGDLSYLSKRCRAAFVAASDRYQIDYFKELNITASNDINEAVLNSLNEQRHEI

NSYGIGTHLVTCQAQPALGMVYKLVEIHGEPRIKLSQDVSKVTIPGRKEAYRLIGMNGKP

LLDLMTGCNEKAPEVGKKMLCRHPFDELRRAFVTPSQVIPLHGLYWDGPQGGLVGELPSL

EKRRQYVTEQFELIREDVVRSLNPTPYKVSVSNELYEFIHELWMKEYPVLELD

>contig25372 Frame-1F

MFIRIPINGWVLNQLKIAIASLRQAQHFTLLPMLSLNIFSYVNQYP

>contig25404 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63974.1|) 4e-42

MLGNLYGVTPYEICWKSRMPSDLLKCCSGKEYYYPSMTEPSVVAIVHAKLLDVEKTLSNY

VLVAAGQKYLLVTHRGKKYSVIRTSTPIATLTSFSFKKEDVVLAAGEEGVIYRLVNNMSS

VSKEMIDFQFYTERWAQVSFPIVKLVTIETHASSLEMKPSTFAWMCLGFEGEVALFHGRE

CVKEWNTASFGYNRKVDSGMPVDLAVVGHTDAKSTQHSGVIVFPERMLEFSLD

>contig25822 Frame-0F|Blast-hypothetical protein PITG\_01583 [Phytophthora infestans T30-4](gb|EEY61306.1|) 2e-11

MVERAQKVMDYVKRGEPIPTRQMFEGPSPEEQLSAFFASIDDWHAAGDDMVSKFLTMARV

GTQ

>contig26089 Frame-1F|Blast-mitochondrial 2-oxoglutarate/malate carrier protein, putative [Phytophthora infestans T30-4](gb|EEY67904.1|) 1e-154

MASSSKSSIASTAQPYICGGSSAVFAAVAIHPIDLVKVHLQLAGQTGSNVTGLGVARSVV

AKEGLTGLYAGLSAAVARQMVYGTARLGMHRAFSDKMIARRVANGESASLPLAVKSASAI

VTGGIAATLGCPMDVALVRMQADTLAHAGDKRGYKNVFDAIINIGRSEGVTTLWRGSIPL

VVRGAAMNLGMMASYDQAKEMLSARYGPGFVTNMGASAVSGFACAFTSLPFDLIKSRLMN

MKVDPVTKRNPYTGVIDCFRQIVTKEGPTKLWRGYWTYYTRCAPNAMIVLLVVEQLNAVY

KKVLLD

>contig26180 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63116.1|) 2e-40

MSTKPQSQMSVEEMQQHQRKQQEQEQMRQSMIQQVMLPDARERLARIAMVKPEKARAIED

MVIQMAQRGQLAAKIDEEKLIDLLNQVGVNEEKQRTKVTH

>contig26724 Frame-2F

MFRSFDIKILAVTYSHFEELMLLDADVLFFENPMTLWETDKYRDTGTLLFHDRLCQKTMF

LDRPVRGNNRLSHLNMYIAQFQVAPFALLKNIKRSNASSENMIAVKLNNYIPSEHLLTSH

SWNRRSGHEMDSSVVLWSKKRQPRATAILAAFLARNGIRRPPSYGDKEFYFIAAELAETQ

YAFSDFGVGGAGWEFLDNGPEKSIICGQASHNFPVKPSNASAVANTSLLYLNSEDILKYD

VKNRPVYYSQARLYEVHPGSFKDRG

>contig27297 Frame-2R|Blast-14-3-3-like protein [Phytophthora infestans]gb|EEY68701.1| 14-3-3 protein epsilon [Phytophthora infestans T30-4](gb|AAN31465.1|) 1e-136

MDRDSLVFLAKLAEQAERYDEMVDHMKAVANNHNVELTVEERNLLSVAYKNVIGSRRASW

RVISSIENKGDSERSEHIKAYRQKIEGELVDICNDILTIIENNLIPNSSSEEGKVFHYKM

KGDYHRYLAEFQVDDERKESSDKALESYKQASTIAMAELPPTHPIRLGLALNFSVFYYEI

LNSPDRACNLAKQAFDDAIAELDTLSEESYKDSTLIMQLLRDNLTLWTSDQEPDTADANQ

GDMNVQDVE

>contig27749 Frame-0R

MSGSNTRRWLQPGELDGERVAIVSYPRCGNSLMRGLLEDITGVYTGCDTRPDRSLSKDLQ

QYGMKGEGVVDDSVWFVKTHFPERVGYKEFSAKKAILVVRNPWDAIDSYFNMTLTNTHNK

SLHESQYQRFADRWDNMLRNEIDVWMKFYRYWTTKVEIPIIVVRYEDLMVHRAETLRRVF

LFLTDSKTLEGTEWEKRIQNVMATGGQKTGPYKPRSGKIGGSFGHYSREQFRNILKTANL

PLRGFGYDPETQNFPNEILLPKRQVKPGKEGAKLLISIDHAMEIRKKNDTFGRRSTYFRR

ALTKPVIANDGTALNMEEVLAARRQMEAKTEEDGATLTRQEPTREDTGLIK

>contig28429 Frame-2F

MYHGVNRPDWQQPGYAVHSSMQSQTGWFPLQDSAQQQQTWNGWLHDAPITNELSQSHQID

SSTSMHTTMPAPPYIWTGEPLLQPLQIRGV

>contig29758 Frame-1R

MGASVDAGTVPKNGSTSNPQRGFSNSWSNLQQLQQYQQLDQHQQQQQYLQPMVLHSRPTL

STPEFATSVPGTASREPSNILVTAPLNGEAMAVSTVITDGRSQGLDSGLAADSKSDDDGI

DLYRWDRIDLNVGLDDDDLFGFLKS

>contig29949 Frame-1F

MADHVEVVIDGDSTEDEDEVTIVTPESRKRRRRSNILLDQDEEDDDTKTTSDSAPRLQQQ

LSLNTDGLSLTNMKLRQPSTMPRSRRHMHQLSIAAAVELGKRGHGQQTHETHEREEDDVR

IIQPPSGISVEGEDQKHQDFIIEVSNEEKMKQRDEHNDLNGDQNKQEVSRVPQDASASRR

SSRIECKRQEKRRQREGAPNLNSAVPTNCLASLQSLGPHYNGDVDDDHASESSDSGKQVL

PPTKRRQSIPRLGERDHQEKGCVDAGDDVDDFICGDDEVEYMNDDEEAVISVESSDDDVC

GDDPVELTAILAARRSREVHEWFEIYMEYLEECIIDPNFEMAMRHKRSKAKHHLYDQSIS

RIERKLCSCRDTVRSGVAWPEEMVEALKHASVFRSSQASAEQDCDACNRRQHVATHRIEL

AGYAFDATKLYSAQWMHYLKKAVKEAAAVNISFEMGSICHA

>contig30055 Frame-0R|Blast-prenyltransferase-like protein, putative [Phytophthora infestans T30-4](gb|EEY64646.1|) 6e-47

MSTMLATERYRYKNDGVMTRTSIDQEECESSCSLFFYPILELPLDQQLELQQLSFVNTEL

EPLLMREKHVAYLRRGLTRLSASFVALDASRPWIIYWILHALDLLNALPKEETSRVIS

>contig31863 Frame-0R

MVSFYSQSSVTFTVDISIGHYFLILLYGPATNSSRRICHSITMRVYHFALLAAAIFITNT

LASTADELTTHNEGTNFVTRLRVPSDKSITHNDEERVLGRLKGFLQEMGSANTPSHSFKN

AYVALPGKNDDVATKTLEKWVNSNLEHVIPTSANLKKLL

>contig31939 Frame-0F

MDAARRLWGQQKAILTSDSVMFKMNTADLYLSARSSRYEAETLADLHVPPVVLCARNDDT

YGTMQVWKITKSNLPFDPEWNRERSYLTGKALLQPRSKRPYAAGDGNLSLSPLSTFPPSV

QESIIMDDLLYVFLGVEGRYIQLSATETRGMKTGRSTLSFTFGLNQPGMDPSLLALASRC

LPLGEYYLKLTVYIEQFARYEYGQVNHALCAALKTLMKEYTIMVGQLEHQVRSANGTFTI

QQLWYNVQPSLRTLEMLSLLVDGCRTSIGGGSLLSKVQRIMSSLAGDSNARMVFSFLMEH

ASVPYLKMVERWIYHGDLVDPYDEFMIQRDDQVSKEDVQDNPYSTYWQNRYTTRASQVPL

FLSRVARKILLAGKYLNVFRTCNRQVDCPFAGEIHYSSSELVYEELIDKAHSYASRVLLD

LFVRENDLQTRLISLKHYFLMDQGDFFVDFMDVAEVELKLRADKLSLPRLESLLHLSLQT

STCSSDPYKDDLQCFLSPHNLISHMEAIHQRAQKGPRDSLTTFESSSIGHPGYKVIDAFT

LDYKVKWPLSLVVSCGALTKYQMIFRHIFFCKHVERQLCDAWLNHQATKE

>contig32264 Frame-1F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 0.0

MCVNIWNRKAAQITNYSIEEVMGENLVETFISPEFRPIVAEVLSQALTGVETANFEFPLI

TRPGTRIEILLNATPRYDLNGNIVGVVGIGQDITDRIAQEHEYFRLIDTANAPIFGIDTN

GRINEWNQKIEEITGYHKSSVLGLSLVHTFVTPDCRQQVRQLLNQALIGIDVGEMELPMT

TKRGVFLLLLVNASSKKDMHGNIRGVIGVGQDYTARKHMEAAKVNFLASFSHELRTPLNG

VLGMLELLKEQPLDKSIERYVHMAYVSGSLLLNLINDILDLSKIEAGHLEISTAPFQMHD

LLDYSIEIFKFKARERGLKLELRCGDNVPKAVIGDVVRLRQVLLNLLSNAIKFTNDGSIT

VGCSVVHSPELPSQFKKLLFQVIDTGIGMDAEEKMRLFSLFTKLERTRQNNPTGSGLGLA

ICKQLAELMDGSIDVDSELGVGSNFFFTVVVRLIDDVDPKHAFYSSEDFLSPSVALLSPS

GALRSGENGESAPSRIEVPKHARILVVEDNEFNWEVVKCFLQQDDHLLQWEVNGRDAVKA

YSENHAEFDLVFMDCEMPIMDGYAATAAIRKFEQQRSLSRIPILGLTAYAMSGDRQKCLD

CGMDEFMVKPISKLSLRKAIRQWMRIRYLGQQNSALGAVIHEPAAEKSFEQQPVTLRSAP

RLTSKSPTRIAMRSSSPLTPMPSFENDLEDVALMDVASTVRLAPASRHMQQLDLAQAISN

LELDDPMSIGLQSSRAVRTATPTTSIFSLGPSVNNTSRQTSTNDLSDVLRLSRNTSGAST

SGPREPEVSYSETSTTLPYTKTPFNGLSCQAYYEVSPSLPANPTLWSHPPFNLIDLPTGQ

QHGWSAFVPKKKVSFHEEPGYESTNPSRSDHYGSSSGMPSVSERMEASSSPMEENLPIVT

TANAFQETLSFSHSIHPHTIEIPTGDPINYTLGVDQCGGQEELFLTLLKKFTTTSEAITS

RIEKAHEIRDFPTARREAHSLKGSSAYVAALRMSKCAFRVQVAYENLMAQQATGEGLDTL

AAKQIVDDSVRLLLKEQRLLRGYIQRNFDFETEARQHEVVIDQEIEYEDRSNCGVM

>contig32358 Frame-2F

MVAALIDLMSSKVIADDASKNLQKKILRFLVFHAFFSVSKEAASKKKSKKAKRNDESEVD

ELAHEAAAVTPPVSNNVANYTKTRLFSLLSFGLAGAEGDRASVSVLSQIFALAQELHLNS

S

>contig32790 Frame-1F|Blast-AP-3 complex subunit delta, putative [Phytophthora infestans T30-4](gb|EEY62953.1|) 1e-170

MFEKNLQDLVKGIRSTKGDVTVYISQALQEIKAELRNTDPFIKAQAVRKLTYLHMLGYDM

CWAAFHVVEVMSYERFAHKRIGYNAACQSFTQSTDVVLLCTNLLKKEFGSTSEYEVGLAI

NVLANIVTTDLARDLLGDVLAMMSAPKPYIRKKATLVLYKMFLRYPQGLRLSFDLLKERM

EEPDVTVVSCAVNVICELANKKPKNYLGLAPQFFRLLTTSSNNWMLIKVVKLLASLVPEE

PRLARKLLDPLATVIQNTPAKSLLYECISTVTTALLYTKKNDGSQPRNVAAVVQLCTEHL

RRYIEDQDQNLRYLGLVGLS

>contig32897 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53024.1|) 0.0

MTQMPRTLQQKKKTTFLPGFGAPDQDYDSDDNDGVEIDDRVANKKTEEELKKDREERAEK

QAALMCELSNFEIKSGDYNVQVHIIEARDLVPKDSSGTSDPVVYVEVFGKKQQTAVKKQV

LSCFWDDLLIFSFRNLDKSQVEMGYVRLSVMDANTFQRAELIGAAQFDVSYIYSQANHQL

ANVWIGLTDTTNTRNQGIQGYLRASVSIIGPGDKLVPPPSPFSEGGTSAMNNVIMPPSVT

QNVRFLGAVIHVAEHLPPMDVAVVGKGGLDAYVKGSIGGGDAIRTRVRTKKGRRDELCPS

FNEELLLVIREPSMADSIQLAVYDWDQVGSDELVGYVYQSVKVVKAMYGKIGPFWANLYG

APLRLKSVGIGDSMKKQMNTYPDIASTYRGRLLLTLRIVDNDDNRFDETNQKRNIKRIPR

DLYPRERIYRLRAHFVWGSQIPSFMSSKRPGQKARMQLVVSCGLNEIASSRTRNINGTVE

WNTMEESEKMLLPEDLSQVPDIFLYLCRGDG

>contig33241 Frame-0R

MRMEYCDGGDLEGFISLHENKTLPLNSVAVPFFFQMVFGLYCAREKYNLRHCDIKLLNFF

LKTASRSKLCKTSGADVVLHYMLEDVCFVLQMPASYSFWIKLADYGAAVSNPESLGSPVT

MDQFATLENSPVEYLLYGDAAKQSYAADTFSLGLCLLHLFTGSAPYEEVLEDVICPTDLL

KDLKALWMSPRKKSRFSVIKSVARGDDEDTLCHTLYRYIVLFDLPNTNPNESCGMDKVWQ

LLLKHLRPEDLAVTRPQLRRKQAAIANDARTASEQFKYDQSLYSIAKGSNGIIDRCRQGL

MAIPGAMDLLKNMVEFDPSKRLTLKQILFHSMFLNLRSSSLQEQVPADYVISYYKRHNKS

SRILLDV

>contig33511 Frame-1F

MVSLTPNAVSMLYHNQAPDGFEPWLQIIDIKKIKPASGAVGDRYRIMLSDGTSYISGMLA

TQLAPLMENESLKTNYVLQLKDYIGNDVQGRRIIIVLKIGDIMPAFDCIGSPGNIESSKG

FAVSSAPMTSAPSSVGLGARPAVSSYQQPQASGSQHNRPTAVTSSYAPPAQPKPSAYNRG

PVVRQDPSIRLTDIQSLNPYAGGRWTIKARVTTRAPIKNWTNPRGSGKLFSVDLLDAKGG

EIRATFFNDGVDKFYELLRPGDVFFFAGGKVKMANRRFSSVDNDYEVTFDQHSDISPAPE

DGHISQMHYAFKKIAEIENVPADSNVDIIGIVRDVGQVNELTSKAGKQLFKRDISLIDDS

SAEIKCTMWNEHAQEDTSSWLNQVVAIKGCRVSEFNGRSISTSSSSSFTINPKIPETGHL

ATWFSNGGSATQTKSLSSGGGGFGGGSLGSFAERAVISDIKTKQLGFGQKPDYITVKGIV

NFIKHDSGMYYQACPKCQKKVVADVAQNYTCEKCQMSYPNCENRYILAVVMLDHTGSTWT

TCFNDQGKVLMGGRTADEVGELRDTNSALFESIFREALFKQYVCRLRVKAENVQEELRVK

AGVVSLEPLNFVQESKDLLEAIAKYN

>contig34262 Frame-2F|Blast-inorganic phosphate transporter, putative [Phytophthora infestans T30-4](gb|EEY59876.1|) 1e-153

MIVTCGLLIIGGILCTAAYGGSAQATLWFLFVARLILGVGIGGEYPLAASSTAEDATSVS

DRNQRVALTFSLQGLGSLTAAIMGNLLIQALANGDKGQNSDSRLETVWRLLFGIGVIPAI

VVCYWRVTAVETDAYKATEERRNAATEADSMATRARFVFIIRHYGVSLLGTAGTWFLFDI

VFYAQNLFSASILAVIGVENASLQVLSAQNAFVALLALPGYYVAVYYINRLGRKLMMLQG

FAVMTVLFFVLAIFWHRIQEKAVLFILLYGLALFFSNFGPNTSTFVMPTEMFPTPIGQRV

MVFRQLLGKLEPRLVPLGFPSGSNMTALATMVPFTRLLRS

>contig34600 Frame-2R

MAGRGRGRANTLPAWMTKQGQTEPPAPSPASHPSPSVAVPPQRSGQFDDAPEPNIAPRHD

AGAALSENKQRSRSRNREIERSSGPVFIKDRNRSRSRDRGGYGHSNDVRSSVRPQERFHS

GSRDRGNVQLRGPTKDADRRYDDSNRRGPPRNRSRSRDRRDYRADQYRRSGTDRNEDRGY

GPRRHEGRPKHRDEEAMERGYRRSGPNGHDDRTSRRYTSDYQP

>contig34709 Frame-0F|Blast-N(2),N(2)-dimethylguanosine tRNA methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56619.1|) 1e-42

MDSAAVDNIRRNIAFNELPLDQVVPNEADATDVMYNHRKPADQFDVIDLDPYGSASIFLD

SAVQSITNGGLLCVTCTNMPVLSGKQPEVCF

>contig35034 Frame-0F|Blast-oligopeptidase A, putative [Phytophthora infestans T30-4](gb|EEY64174.1|) 1e-69

MNTCLDRSYHLGPEDQQGLRIPVAYIICNQSPPVEKNTPSLMTFREVETMFHEFGHALQH

MLTQMEYRDVAGINGIEWDAIELPSQMMENFCYDKG

>contig35290 Frame-0R

MTALSAFCEARPQLLTHHLETIRVYLNEKDIRIPNLCVSMISKILGIKRVSYTIAIKLED

DLKFLVRRSSPSVVGLSIECLAMLSAARNHEPVLLLELLEQFYLCICKYKQRTSLAGLSD

QEDYVLQRALYVAGKIVSSTDVDKCPALSKKFKVLKIGMVASSLYELYRNFVRMPGNDAC

AAKAVQGMGFLFLNQPRLFLSAQQDGLLTFLLTADTRKAKLQCLVSMKELLLFEEVRLEK

GLASKSLNQSKSTEQQVQGDQEADASLIGNVMQAELVNILQLSLHKVPQIRKEAIACIKA

LLRQGLINPLQCIPNLVALETDRVPYVRDAAYSILLALHERYRSQLHSPLIKGFRDSYYF

QLSVYGDATALGIDEKEKAFCLFGRLFINCIKPSRSHEMRLLRALINQFTDQWSVPQPFK

GKSPMPNSNIFTSSLKYMCYVAQVLSSLPYDVEDEPLYVIYLISRYVSLRFSPLMDDLKK

AFVEAGVLSTQLEEDNANLSTLTLDEYSLHLEPDCMLSLQMNGLHVFAIALMLRLKFALK

RNYQLDDEKCATFVPAITDFSVEAKGRAYKKLLLPSVDDLCQPEDPILVSWNLYMVARFA

AREDQMQLNFDLKKSELSAVKGQSRSRRMSASSKQKLVTKDSNDEFADTLA

>contig35566 Frame-2R

MCLKYCCRATATACRLFREKQVQKEYLALVRGHLPLNPAESVNQSANACTFSKLGLFIQD

TEDLERMRNQQRGSKAHFKMPGYPRGVRHGPNIFAMEQAELLRKSNKRLKEDNLCSKAKS

LTAEELAFTQLTWHGLSNEEKHLFSEKSNADKQRYAREFNEFLRLETLRLAHLHKYESLA

ADKSENDNEPLAYIFDAPIIEPH

>contig36079 Frame-1F

MKRDAEFQRLGQELQHSQERVAYQTNDIVRLQSENKVLKRAVAIQNQQKEEVLSENNALK

ELATQAAEHMRRLEQANFTLRVHLQTSTNAGFGHQYQPPDVY

>contig36310 Frame-1R

MRLGLLFTIAFATSLAMPTNALAVSDDVYKDRALTFDSPLTEEREHEDDDSTEPAKPVVH

HPKKKRKGFFAKLVEKLKL

>contig36365 Frame-2F

MTLSMTTKSNDVKTKICDRFLNQSILFLVILDDFLLRESIVV

>contig36422 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66336.1|) 1e-124

MTPSADTILGLLGTGKIGSAIMTGFCSENGWRPKHAFVSARTMAKAETLVAKFPDRVSIG

ASNQEIVDKSDVIFIGLLPNVAREVLPKISFVGKKVISMMATIPYDELLQLVKLPSESVV

RSVPLPVTAKRSGPILAYPDNTYARDLFAQIGTPVMLAEEAEITKLAGITALISYFYATC

NITQQWCVNNGVAVKLHATLFRLSYKRWPQLGQSLMKILARWQMKLRPRAV

>contig36893 Frame-0F

MMFIAVFLDRQCKMLLITLFSDGTLLCSKNDYQLRTGWCICFRSRRFKFLPKCLVPMDFN

GWTLQYPSSDPDDLRDGSTRTTIPLVREDSLSMEPFQVVQSVNPMYPCAASGLQWPPTAP

LHPLNPMRPSLTNAANTTGQLDDGEVLRAQRGESILHVFHPSANVCNVQVCRSVSMWSAG

VPTEASIQAAYMDVIANSKHFLYIENQFFISGMDGNGIVRNRILQALVDRIERAVQRDEK

FRVYVVMPLLPAFEGNIRSHELTNLHAVMHWQFATICRGRYSLFEALKGVTTHPEDYVAF

FGLRKYGIMPNGCVSTEQIYIHSKLMIADDRCAIIGSANINDRSMNGDRDSEIALVIEDM

QYEDGVMNEKPYRRGVSASKLRLQLFREHIGLIDDDLSVVDPTSDNTWKLIKSVASSNTK

IFDTVFDCAPSNRMRAFVNFQSIDVTQIFENQRMNVLKVPGRSHVWDAQNLKEGDYAPWT

DVNGVPIAADRLDLSDFEVDNYRDRKKKLFSMDHDGWCYARNFSIFQEVRTMKTDYKKRE

KLQHLVADRLMAQVRRRRWVKKGLLPPRNDPRDSSFSIESDDEERGRFFSIWRRLQQGDF

SRSNSISMTPTNFSQMNSGGEIASSVRVGSTTAGRRLYHSNSMPSSAPLVVPLRPAIGGT

TPSCPNSPGGASSHHTPESPALTAGARSARTSSLLGIGGNTGSRDATRSARGSFYGMFSV

ANGTRLFDTDDESSEADSDYGGGHGIRASVKRWYNTVDVLDFGRRSKFNAEYFDTDEDHV

HSDDPLLEDGRGSYHAPIRDCLLTEEEAEESGDEDADCQIGHVQTAATVRKEDETRARGK

LSEIRGHLVDFPLDFLVEEILKPSVLPADIHI

>contig37317 Frame-1R|Blast-mannose-6-phosphate isomerase, putative [Phytophthora infestans T30-4](gb|EEY53727.1|) 1e-97

MFLGANEPHAYLFGDCIECMTCSDNVVRAGLTPKFVDKETLHSMLTYHTGKPRIFKGDIQ

CDGVTRLYSSPVPEFEVEAIQLKPNQRYTLSTRRGDSIVIVIEGSGMAEGPFGFTDGRMV

SKGHVYFLPMGELLSIQGGEDGVLLFRASPNETHRG

>contig37506 Frame-2F

MMSPREAVIVEFLEQKAAVDGSKSSSVGSFEELETQSALLPPSREELERLCAQKLMREVF

THIMKHM

>contig37825 Frame-1R|Blast-phosphoserine aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY57574.1|) 9e-16

MLKFVLECRATINLSASLSSLSNKKQLQWIADRLSVRFAKDLSQGNSFLEVENMVKMLDQ

ETRSEESSVVKDIGTLDLQYDGDQGSGKDTTGEFKQVLTE

>contig37991 Frame-2R

MLKEKIYRRLIECQKLTASICCHLIYAELPLNAGCLSY

>contig38011 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61155.1|) 1e-80

MESLFVQSLAVGVPADESQTLASASRTTSDGIFAVASGREGLIRVYAASCSALLHEFATI

HGHVYTLHYTSFSDSLVTLESDCKGNENDDEDVETFLCVYHDWRERTMVRGYTLPLGRLE

SPSSNRKADCVAVCSFTGRVLVAMGTVLNIWQCSHGFFEHVMELKVDMAQQHSFLQV

>contig38741 Frame-1F

MLIGRQHSIGSTMNQQKKRPNTEPSGDLKRRTAKQRNEDSDLIFEDPFGDDMEDEEMIDS

EGDDEVVDGAAANTDHDIDMDGDETSGSKAKKVFMPGVDKLEDDEVLDYDSSAYDMYYAM

TAEWPALSIDVVRDKLGMVRSRFPLTVYMVAGTQATQSDDNQITVMKMSELYKTKHSEAS

DSEDEDSDDDTEGEPVLETRSISHPSAVNRIRCMPQSSNIVATWSDRKKVHIWDISKQLD

SLDGKGGAILPAKQSPVYTFSGHADEGFAMDWSSVQTGRLVTGDCSKFIYVWSNSEGAFN

VDKVPFTGHKSSVEDLQWSPTEASVFASCSSDQTVRIWDIRRKAGSMLDVAAHDDEVNVI

SWNRNVAYLLASGSDDGSFKIWDLRNFKADHPVAHFRYHTAPVTSIEWHPTDESVLAVSG

ADNQISVWDMSVEEDAEAAKPVQSVDGETTLDLPPQLLFIHQGQTDIKELHFHPQCPGVL

ISTAGDGFNVFKPANIS

>contig39030 Frame-2R

MCSFTPVSDSVILSELAVQRTPRHSACMERVGRCLTMINFSP

>contig39548 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53367.1|) 3e-32

MPLLFLLRDELGNDKVNAVWEHTLGLKDTKPTPLTQREEKARFIKAKYHFRKFVEPLQNL

DENDHVCQVQLLERFFAGAACGVVTELMWCVAHGVDVNERV

>contig39759 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY56109.1|) 1e-29

MGTKWKQQFGRKSFVRKHIVEVTDETVVKIDEMIEKADIIVTTPVKWDEVTRMKAIGRTV

MAHMALVIIDEVHLVSEAPHGAVLEVLLSRLRRFQSAHRSMRIIALATTLANAS

>contig40566 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61935.1|) 2e-06

MSTCGVVKLQAQFRGNKSRRVHVKRVRKNLR

>contig40658 Frame-0R

MAFDPRCVAYEGRLQADHCTAEYIGRGNHDADAACFRSRHPVGFSASSRMFYFETRILAT

LPPSSVPPQRASSALALRATTDHAIHDETTPNVQEDLDPEVRNTNLVHHPLVSHEGRAHT

MFSQNPRLRHFTRHRTLRPSEKKRFHHQVAVGFIIDEIEQMSHVTTPIGTNGTRKP

>contig40935 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63639.1|) 1e-87

MRSRGVLSYYTDTIYTIDKREFRPMRGLKQCTVYGFGRRKLFEIVRVSRKLWSVRHVEYG

EIYTLVVKKYAGGVHHMVAVRRMVPDVKNGGLRQENVCYVKKFKGQQYRCILNSEVISQG

KVTMSISIQKPQSPPGDPHFHYMTMSEVSGPSRASICSST

>contig41033 Frame-0F

MEATLLSNQNRSLGNGRKRSRERNLRNRNSRILLSRSINNRLKDKEVNHEYEPCNHQGAC

NSTDCSCMTRDHTCDKACSCSRDCLNRFPGCKCSLGNCRTKACPCLVAARECNPDTCFTC

GASEVPAIVFDEKRRNMSALDLGICCNVNVLRGLHKKVGVAYSTTHGWGAFALQPIKRGE

FIYEYHGALLSQDEAERRGSIYDKMTISFLFDVDDDSVVDAIRKGNKSKFANHSTENKNC

KGKILTVKGEHRISIWAQQDIAKDEELFFDYGYHGETAPDWSQLRIQGSARLPS

>contig41396 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55317.1|) 5e-20

MFLQEIVATYPQITKLEELGHSVEGRIIHALCMGACTPPDNRTIPQVLYTGLHHAREPLS

M

>contig41943 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56595.1|) 1e-128

MVHVTKPVVIIGISTVAAVTLLIFAFTRKVNSTDAKKKSQQDEGVREVPNLHKEQLLSIL

ETICTQMGQVVMQLAKLEAKIRQESSQNGRSLPEDQLASYLMGQFEEAMKAIESQVYAKF

QTTEDEVKLATEYFEEEDDKEVANAVSKLQELYRVMTGGGYSDVEVPAELTLTKFIEIMQ

ETMESLNVAMEEVCLEVKELDPDNKEEAINQRYVKRADNLSAEIHAKHGLTREVLQAAMM

KYQQEPAFLMSMTELQQQQAERFAAAAAIFNGEVNMGLTE

>contig42292 Frame-1R|Blast-putative chitin synthase (Chitin-UDP-GlcNac-transferase) [Phytophthora infestans T30-4](gb|EEY61714.1|) 4e-42

MLEYLEAIGLYDEDLLTISSAGIGAQCHLFEHTLQLSENKKSLLPIQTIFALKETKSGKL

DSHYWYFNAFAE

>contig42388 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59543.1|) 1e-12

MCMYFGRQYKEIFNPPVSEAYELELLHVFNRHLQSDGVAPLGSIDCNISSETIGKNLRFL

TSRREG

>contig42685 Frame-0F

MAWSECESIFSRLEKARGLESYLKWIIIPRTLALGECRNGYSFYRFFSDRDRLFVMSPEK

KWSICATRKHLMQLVGYLEQSSNDFIIATRIRQCLHWMFCDNDVKFQQGLAYCDHTGKCL

SYKKMFGVEEEMLLVMDEEIEKYTSHVSYNGRKFFLGSFHTQQEAENALYRAVTSISRTE

LHVVVAADVSTL

>contig42825 Frame-1F

MSHSVLETAASSSNSDSSPVLIERHRVRVRRVASEEENMDSDATNETKKEEEKVTRRYSH

RLQSSLNSISLGSMANHKDASSALRTSSSRYSLRTRHSNSKRFDESMYNDVFTTSRSRYA

ESTPESLIENKRRRRRKRNRRETRQRREDEDEDGEDQYSGDSSSVQEIEVRQV

>contig42850 Frame-2F

MTLFLTDDFPLEIRALVWKELQEAHLLHLLEPFQESS

>contig43365-0 Frame-0F0

MIWYVWHIGHLHRLRVNVCVYSTAPQMAARLG

>contig43365-1 Frame-2R1

MKVANMPNVPYHCVDRKPQSANSMRCLPVT

>contig43422 Frame-0R

MGRNRNSTNIQVGLSHAGHSVHRTFSQDFVNVVRAMRDCLGHNCRYNDYCVITRSKAQKR

KRTLVFDAINMYGFDP

>contig43804 Frame-1R|Blast-hypothetical protein TcasGA2\_TC013916 [Tribolium castaneum](gb|EFA03803.1|) 6e-21

MAIELWDLLLCGHFPWRRHWLQYVRENSRSVVSKDLWLQVLDFGQQIQPDLKNYDENGAW

PVLLDDFAAYMQERISKRGISMVTQDEELLFRNHGKSPESMNVDA

>contig43893 Frame-0F|Blast-cell division cycle protein 48 [Phytophthora infestans T30-4](gb|EEY70132.1|) 2e-50

MDGVGSQRVAASYTSTTKKLLTTNSGRILVVAATNRGSSLDAALVRPGRIDKTIEMGYPT

QQDIQEILALYTKTMPLGDKIDFRDLAARSS

>contig44131 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57123.1|) 0.0 NOT\_ORF

MVCEPSFRERFDDTMDGRNHALSEESELEDEMMRVNDFDIEWRRQISIGDHVDARNVFGN

WCPARVLEIADGDLLLQFLNMHNSWHQWLPIDSGRLSHPGTKAPTDCVPIRQAQQIEVRP

GGNHSSLWKEALAVKAGGESLLVRYAGRDDRFDEWIQFTPEKVAPVGEHLGHSNHGSMLE

QRKTVVGAPSVTHCRVIQAHNPRFAHYRDSLLSTLGLRVFDIAGDGNCLFRSVSHQVYGD

DSHHALIRAACMNYMESEKEYFEPYVVGDMTAFMRYLRIKRRDGVWGDDPELQALCELYD

RPAEVFAYDFQHGFRKLRCFHENSSLARSRPPIRLSYYGGGHYDSLVGPDHRENLINETP

GRWEQRHIGYSHRINSREMSHDIVRVEQGIQSQSDIEHTEVTQLEQVLVV\*NFLYLSLFN

ARVFAANVGIKII\*QSRNDFNSMDRSLEETLNAS

>contig44698 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56167.1|) 1e-139

MIPESSKSHRPWEDECVVAARIPRDQVVIVHVLSRGGFGVVYSGLYLGHHVAIKMLLPET

RRSLLHVVDLLAEVKLMASMEHPHIVKFIGVAWDSLANMCLVSEFVAGGDLKALLRDYEE

QQYLKGFNFDKLKIALHIAYALTYMHSMDPPIIHRDLKSKNILLHENLDAKLTDFGTSRE

RVNESMTGGVGTCLWMAPEVMLGDRYDDKADMFSFGVVLSELDTHLIPYWHAKDPNDLSR

KMPEPAILQLVASGKLQVEFSKDTMQAVKELGHACVSLDATKRPTASQALYKLHTIRAKA

VEQVGNRIT

>contig44863 Frame-2F

MFQPNAKKWFAFTHPSAIGGILFIIPKIKRQVEHPSDLEKTCCGRLNAFLIRCPGHGIFI

QNPKSASPGPSHKMGIVLPLYLHIPLFISLSIYP

>contig45169 Frame-1F|Blast-peroxisomal targeting signal 1 receptor, putative [Phytophthora infestans T30-4](gb|EEY59541.1|) 1e-114

MDEVMQLMLQARAHDQNDSDVQVVLGVLYNVSKDFDAAVESFKAAKDSRPDEYALWNKIG

ATLANSARSSEAIPAYHRALELKPRYARGWLNLGISHANLGNYEEAAKCYLQALSLNSRA

DHIWSFLRICFTCMERYELVKIADMRD

>contig45705 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65743.1|) 1e-25

MDYGLELAEAFELFTKNIPPSLLSIPCNRDEAIAPSTEAGSDVSSAIPLPESIEFTRQLA

QLS

>contig45899 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70466.1|) 4e-29

MCRGDELLVSCFSGWRGIAFSWAPLLARMLPVSLYDIVIRFGGGLHGMDTFVGKGETRED

TIIE

>contig46753 Frame-0F

MDLVLPPDEWDILESRLRKVNENIERCHRGLSNVVVNVSSNHKQSLEADLRFYSAIKQRL

QEQLLVVMQSGY

>contig47808 Frame-1R

MEGKTTEEVIAAGSEKLAKFGSGTASAAPTAGGGAGGEETKDSKADDLAEEEEVDMGAGN

MFGDDDDY

>contig48243 Frame-1R

MLLLRMILPANTRDILPSTRKSLADVNTSAFSPIRQQHRKNVSSSCDIFAMLVDKPLSQY

RVTSPSDE

>contig48401 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67447.1|) 8e-83

MDECVRAWNNQDLAYLESAIISLGTFSALIPAEQNDLRAINVRSLRSALFSWMNENETES

VKSSKPLLPPLVIKRVFEALGAMWPAQGATTQVLSDSKSAAGITTETILWLCSSVQSPHM

TAWSVQKAIFQMLAKVTARAPVTELLQDRQVVERIIVTCCGPFGVANGKYSVVRVAAAEA

LAALFRRANDNSELALRLIVEQERVVLAIQTLQTSEEASEQQTAIDLKSQMLQAS

>contig48636 Frame-1R|Blast-cAMP-specific 3',5'-cyclic phosphodiesterase, putative [Phytophthora infestans T30-4](gb|EEY57607.1|) 1e-94

MSRRIDHFLTRKPQAVVITHPSFTSSPVASSSSILSTASNGNPCYLFEARPVDMSFTVGG

MESCRRELKIGGEMHIPVNKTTADVRVSPVVENDYAYEKHSTSPVASSSRFPTTGAIEAK

IKSLASYLKSVSAGIRRRIIAFDRTRLTQAYYRKSVPTPATMRTKLNVIVCRYSSSEHHT

TLSWDDIDENECLSFRDVNELISTTPRSRKRSHPSAIFCEAEIRQICACCDIPDQYIEQV

LHIIKSSFGTPGLDVIALEELMPGNVVLFVGS

>contig48896 Frame-1F

MAPQKKPWLLAKNNLFFWSGMTIDRFMIPFYDLSRLHKPVRTHTSNSSMLLFDINGSLAS

TPSM

>contig49774 Frame-0F

MLPIRGTLTVVKGSLCTYGHCSRPSVTLNWRHNICRRSSTLSHFASLSRCEFVHFFHLVP

RGCFSTLLRNGTAPQPDAASESIITLPPQYLLGSKDVHCFVGLNGSGKSQFLTRLQDHVK

TQQANGHLPSSCRLASLSLDAHRDTVTKNGHRVVADVLGGIG

>contig49806 Frame-2F

MNPSYPGSAGDHHGPPSLNSASSSNMRGKGGPPSQQTHQYHTQPSLAQLNHLHPLHGGSQ

QQPQHSMMHPGGAVLPPPPMPGSLGGGGSNSSRSPHPLSGSILHPPRGNMGGGSSNPPPV

LGKPVGSQSSHTASTSRIMGHSVRMQAPAMSQSMGHLPQSMVSSSGTLKPPAPNYNVRPP

SPPHRTQDTQQQQPPPQQVPIQQHYGLDGRMIPNDQVESE

>contig50035 Frame-2F

MARLRDEMAMQYDAVANEPLFQVKYGRKKRLLDLSNDTGVHTSPVEPLVRLPTVLETTNS

MAMDETRAISGRTTSVRTMSPRGFGTSGTLAASRLSRDLSNVTMITLPQEDSSQEVDVPG

EIVHIQTLTTARRCGCTVFMGEQKLQYTLQDASFFRRIWVTPRSLQDHMVHHYDRKIRHL

VTHCMDVEAVDRKSASSRLSWVDDTEGLDRKDKTSTFVTEYQDLEDVV

>contig50040 Frame-0F|Blast-DNA polymerase epsilon catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY63268.1|) 3e-36

MDGESPAKLGWLLNQRSCTMADPIEGKNEVSGLELYFLEQDGKAFKTRIIYQPYFYVRLE

VNRSQEVLAYCLRQFEG

>contig50286 Frame-1F

MFREEKGKRCELQLDEFQSCDESTNDLLVSASASCQEPQEPRILPKTSSSIPPTECSPPD

VVLHSDGCAVALHLSVLKLRCPWFYKQLRQLRHLSAQKEGSYTLKVLQPEELCVLQEYQN

DDSKCPLRNFRALRLDYVRCVAHKFHNKSKLSDTSGGSSIYQPDSSVSVQ

>contig50497 Frame-2F

MIIPFSINAPSTLSSQDFDALLVLGVRGTIGVIDPTCHLTIEALPIELKTLRLGHTVESF

VFLRTLHVFVFTCDGSAFACRVPDVLATAQFADSLISTTLQSDCVLSSEKVPFQPGVMRL

ATHGL

>contig50512 Frame-1R

MTLLRLLTALVLLSTTMIEAGNLRSQHDDDGLIQSHSGSSSVGIVEQIRDEDAILDSALS

QDSSAINDAVLRDKTDDVRAWAQCGGLYYLGETKCQQHTSCKQLSDFISICFPKSRPTEN

IVRLEL

>contig50703 Frame-0R

MLLQNEMQLIAEGMSRPTQLIAHRPFARLAAIGGVD

>contig50934 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66749.1|) 2e-31

MMRWPFAILLSSLATFGVAATTTGQMVQLLVGAGCKFSSYSTLPNATATKPSYRLQLDPG

LGKGIYVLQFTDFNLPEADVLIVRASGTGKSVPPAATLSGKNATGS

>contig51111 Frame-0R

MGAMSPIRRTGAALLFCIAKFVRSAHESILPSFISCFFMRSKSVWGFLTAGPRRAGRQSH

AALELLEKFRHGPETHSEWNLLLWRATFPLVSLVLLTLLCIAGQFGHAAYSLVVNPVWYL

CNFALVTTPFLLVFRFSSLDENEATDPQANICTQHRTSRSQYEALVMQENEQDFMQNVAE

ERKNVFEESWRSRHELNETVTMTRLLYGCGFCALVLWLVMFMSYSSAQEGGAATSTWFPL

YLLSPFLCIVLFYSRGSKLRFSYEHAVAYSTLVVHIPLFLG

>contig52352 Frame-2F|Blast-Dicer-like 1 (DCL1) [Phytophthora infestans T30-4](gb|EEY55353.1|) 2e-55

MKELASATSLRIFATSRLPASKMDWEPVTNPLLKHIHVFNMLPILPSFSMEPSFPP

>contig52730 Frame-2F

MLAMEFVRKDDPEGDRAHLVEALAKLETRKVLVSIASLSPTSPRVEAADGTMLSLLNTLI

GPFIDSYWVAITSLFALRPKGEVTTEDLLKRLQWLAETMYHEKLIHFYESCSRETLQNAL

ALLQRWGILSSCQLPDSSKAKRIKRKPLKLLRLSQPYALDKKLEKLAMRVFKFRKLPLGS

MIGETEILARLPALSRI

>contig53805 Frame-0F

MHRLSKAIGLQAFTITKRALAQSLQRFVDRLECKSTKDEWQRAALQQ

>contig54299 Frame-2F|Blast-urease, putative [Phytophthora infestans T30-4](gb|EEY58029.1|) 3e-47

MDMLMVCHHLDPTIAEDVAFAESRIRGETIAAEDILHDLGAISIISSDAQAMGRSGEVIT

RTWQTADKMKKQRGLLLPDVHSK

>contig54383 Frame-2F

MENNCFPRPRNLASQHLKLTDRRKCVSKISCYCFRSL

>contig54938 Frame-1F

MWHGNCNILSMVMLVAHRRWFLFMWLLALVLYINTTTATNAAIRAVENVDASRFKMRTNA

TM

>contig55032 Frame-2F

MNADGAGDSGVRQKRAAESYSEERMEKLLRTEMAPALNVESTMAGTQTMFARPQQQSNLF

FMGSQSQSQL

>contig55807 Frame-1R|Blast-spastin and Fidgetin-like protein [Phytophthora infestans T30-4](gb|EEY65751.1|) 1e-10

MHLWPGRRPEDAIQKTIMEAVAADKLENYADAVDLYASGIEKMMTHLA

>contig56091 Frame-0R

MIGILPGSYKKCFVSPILFTYRLA

>contig57001 Frame-2F

MQRFAGNGQSRGAVSGTTCLNWSKCGTVVFVEIDVLLRDYASCPKVFAKPKETALCGDHV

AIGGKDVAKTGDARTPS

>contig57382 Frame-1R

MRDEYPTNTSQFNFSVLDNFYYKQQPCAVGLWFVHRLASSLNRLTKATRFRCSSTQLDGN

GCTSSLAQRVFEELRDFTGQMNSRIF

>contig57557 Frame-0R

MRAADHAPFPNVIIEVAFKNESLTVLRAKLVRWMDPTYSSVQVAIGIKIFPANLRRVAIL

HQRGQPIEEVEFGQNR

>contig57975 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY70392.1|) 2e-34

MTAILNALQHEVRQELLDMNSTDVISDKRRMVLMQQHQRLNRRGLQDLLRAHDTDEH

>contig59212-0 Frame-2F0

MTELRVGRTQEISSATVVLVEDIKALKQLVHEEMEQIG

>contig59308 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65987.1|) 4e-30

MAWSFGRILYSVMTLLTFTKGWFNVHREDAS

>contig03641 Frame-0F

MKTHTVFYVGRLKRYVDPNEVTYFHPSKETDGDANCESSVVRVRGGGEGETLLTNRLLPT

RTRTGLGERGT

>contig06527 Frame-2F|Blast-autophagy-related protein 7 [Phytophthora infestans T30-4](gb|EEY60210.1|) 5e-13

MTDTKWQMLKFQPWNSAPDVSFWQTLASLKLDKFQLDDQA

>contig06798 Frame-0F

MSARQANRLAKERKAESSERDVELEDDHELQEKRATNVGFAFLADSDASEDSGEEEEDEV

FNEPTTVVVSVPMTRTKTQKKKSKRKLNRNEKEETESVDDLLKALAIETRESMLNKPTSL

SIDKEPSLFGVDLKCANADTEMKRLFG

>contig07195 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY62639.1|) 0.0

MIKVKWDARPPPHGATPTVKGPNASNTERPTLTALMDGIVLSSTSSASSNPATSRRPPLP

KWDMGTISEDTMPTAFTAASAAWANERFELTESGDVRNKATHARISKLEIREYGEDVLRG

LIGHVHTRMLQELLFLEQAIPPLEFERGSVGSGFSPASSTVGSRVSAGSSVRSSSSSICS

TKDGFRMMIDTDEPRCIFHTSKNFSVAEKLLVFVCSFRGLSCGIWSRSVLLKDGVQVGSM

LPYFQKAIEAGYGVLVMNPNMNTQLMVTPEGTVEKMPIRGSSNAEEHCDHVWRNYIFPSA

AHKVHFIAYGYGGVLVTQLIAKYRYELKSRLGNVAFIESSHKLDPSWNSGFKRFFSQHSI

SWSRSEYPLNTELSRDATAFGATPGVPTPSSTDETYSINLSSPLSRSSTSPNGPNAAHFS

AFGCICLSAGPCEGANESPAYTTKQVLDTVFMFLTSPTPYEFQRRATRELQVNTLLGDQH

QARADQIDESRHGQKPVKLATGSP

>contig07230 Frame-1F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY66029.1|) 0.0

MDIICQAKSGMGKTAVFVLATLHQIEPVDGQISVVVMCHTRELAFQIAHEYERFSKYLVD

VKTGVFYGGVPISQNRDALKNNTPHILVGTPGRILGLVREKTLKLDKVKHFVMDECDKML

EAIDMRRDIQEIFKATPHDKQVMMFSATLSKEIRPVCRKFCQDPMEIYVDDETKLTLHGL

QQYYIKLEESEKNRKLNDLLDALEFNQVVIFVSKKNRGRELNRLLNECNFPSICITADLT

QEERIKRYKSFKDFQKRILVTTDLFGRGMDIERVNIVVNYDFPNDSDQYLHRVGRAGRFG

TKGLSISFISSEEDTEMLAKVQSRFEVNIPELPDQIDISTYMTT

>contig07476 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61679.1|) 4e-09

MPLALHLGFAPHKWLRLLLKLR

>contig09496 Frame-1F

MQLRHGVMLVGASGTGKSSAWRVLLSAMEVVDGVKGEAHVIDPKALSKEHLYGVLDNTTL

EWSDGVFTHLLRQILNSVRGESSKRHWIIFDGDVDPEWAENLNSVLDDNRLLTLPSGERL

EIPPNVWIMMETETLRYATLATVSRCGMVWFSHDTVKTCHIVEHYLLKMRDDVSVISSFS

LQPSESELAKKTAHAYVALLRDLIGRGDDMPSLIEICLEQAMGQVHIMEVTALRLLMSMF

TLLGRGLSRINEYNEGHSDFPMSIEQTSRFVSKWFVFSIMWGFGGSMDSSNRMILCDFVV

QTLESRLVFPVTGSSDSDNSLLEFEVNIEDGEWRPWVRSIPQLDLESFQVLSTDVVVTTV

DTMRHVEVLRGWLSQHRPLILCGPPGSGKTMTLTSTINSLPEFEFASLNFSSGTSPDLIL

KTFSQYCEYKRTPSGMMLAPNAPEKWLVVFCDEINLPEADAYGTQRVITFLRELIEQGGF

WLGGKNTWVRLERIQFVGACNPPTDPGRVPISLRLLRHAPVLLVDFPSYPSLKQIYGTFN

RALLKLTPSLRSYVQALTDAMVDVYDSNQRKFTAEMQPHYIYSPRELSRWMRALYEAIEP

LDYEIDVEMLVKLVFHEALRLFMDRLVTSDEQKWCFHMVKETLRNHFPQSATALEVVEHG

GQHPILFSTWLSKNYTEVTTTDLRKHIEARLRVFYEEELNVQLVVFDSVIDHVLRIDRVL

RQPLGHLLLVGESGAGKTVLSRFVSWMNGMSVFQIKLTSNYTLDNFDDDLRVVLKRCGCE

AEKICFIFDESNVLDSAFLERMNALLASGEVPGLFEDDEYTSLMHACREAVQRDGVIVEN

TEDELFRYFTKQVQRNLHVVFTMNPASGGFQNRTNTSPALFNRCVVDWFGTWNDHALAQV

AYEFTNTLDLAGSTEFLIPDDTAEILAKLIPHINTGTFHDVLVGSIVQFHHAVLLHMRRL

QKRHMRYNHISPRDYLEFIRHFVSLYSEKRAQLEDQQLHLNVGVQKLQATHEQVAELQGQ

LSVKEKELKKKDVEANEKLQQMVQEQNEAQTKKKDTEALAADLASKDEEIRSRKIVVEAD

LAQAEPALLDAQASVNSIRKAQLDEIRALARPPAAVRMTMEAVAVMLGESSLEWADLRRF

IRKDDFISQVVHFDSEKLTARQRHTIQTNYVDKVDEFDYEKVNRASKACGPLYKWIVSQL

SYTNILHKIQPLRAEVQTLMDKSSDLRERYEQAKTTIDALEIRIDNFKHEYAALINEAQI

ITNDMTSVTKKVKRSVALLQSLLQESERWEAGSNEFDTQMKTLVGDTLLSSAFLTYIGFL

DFQQRKILVQDWRDILDSMAISTKPQLSFVDYLSRPNEQLEWQTSDLPSDELCYENAIIL

QRFHRFPLIIDPSGQANNFIMKYYSLKSSAKIAQTSFLDSSFMKVLASAIRFGTALLVHE

VENIDPILNPVLNRELYKTGGRVLIRLAGEEIDYSPDFRLFLITRDPSCRFSPDICSRVT

FVNFTVTPSSLESQGLSILLKSEQPEAEEKRNNLLKLQGEFQAKLRELEDSLLQQINNVQ

GNILDDDRVINALESMKAEAAQISQQVAETETTMAIVEKATSRYRPLAKASSRLFFALDN

LSAVHFLYQYSLDFFLSLLSKVLAQPSQGGDSERLASISTGLFVQLARRVSRGLAENDKL

MFALRLSQIYLELEHHSVTSEATESINNKNAFDGPTDEDMDLLLGNASVFLNADGSARRS

EFEQLLPAFAKAELDQLLKLMKLSTFSHLETHVRGHAAAWNNFIKAPLAEDALPENWDME

SVEVSASPRRAAFRNMILIHFLRPDRITFASERYIELIFTASFPWRGEIELSKNIKEDTQ

ATRGVLLCSTTGFDPSAQIDELAVVSQKKYNSVSMGSAEGFDAAEKGLNTALKHGTWLLL

RNVHLCPSWLVSIEKKLYNARESVHANFRLFLTSEINPNLPVNLVRMCDIFVFEPPSGMK

LSIVRSLDTVAADRMNRSPTERARLYLLLAWFHALVHERLRFVPIGWSKTYEFSQSDFRG

ACDVIDRWVDSVANDRAHVAPDNIPWTAIRTTLKESVYGGRVDNTFDQELMDTLLEHVFT

PASYEHTFELVVPDQDNDTTGLVIAEGKTKAQFMDWVLALPTTNPPSWMGLPRSAETMVL

INQGARMMRNLQVMQDFYGSEGGEDSAAADDENKMVLGAAAADGEDVRPKWVQDLDRRVC

AWLELFPTEGLSVSSDRDPVHFSNPVYRCMFRELELGATYLNEVVNLLRTVQQVCAYKAK

PSNEIREAMRTLYRDHVPKQWMQLYRVSKELSLSEWLSDFARRVHQLTALSAVAPTQIMQ

QPNGIWLGGFFSPEAFVTAARQSVAADLGCSLDELHLLANVEESSAGGFTARGLLLEGAT

WNFTGFAPSNEIRNSLSALHFRWAPRRDDSVNLRLLPVYLNSKRETLLFSVAVHVEETAF

LKTQWVQRSVALVLWELEGLFYY

>contig10292 Frame-2F|Blast-NADH ubiquinone oxidoreductase subunit, putative [Phytophthora infestans T30-4]gb|EEY55113.1| NADH ubiquinone oxidoreductase subunit, putative [Phytophthora infestans T30-4](gb|EEY54257.1|) 1e-109

MALSYGRQSTLAFGGRLIQRQLPEFTKKRQTRSFFTVFEKYLEAKKRYGWKGTLWKLYNP

GDVKFGRLVGKDENGYKYYEDPTEVYGQHRWTEFNVDSWDEVEGTLIPPPWHLWMHHVTD

SVPGEGRQLPENWEKHETVDHTDTPYANHLGPNVPYYPNKTLYRSRGYNVGSLALQPDEP

DQYYLQPGHLRRSRQRKAHFFADVDYNNPENSDESRQVTLRPADIN

>contig15989 Frame-1F

MKFYVLTTIALMACTSVTGEMRISFDKNIKDVFQLSDDGNGGIKISKKPQMSYEDTGSNK

EEETNDDQENNDDEDNNNDGDTIDGDKRKCRPFGLNEGVQQSSTYGGPHGNEFSDKKMVM

PGQNVTSVTLWAGERLDGLQVVTAPPRGVSLTLKHGGQGGKDST

>contig16320 Frame-0F

MMNHYGPSALAIAIEKALADVSSKSAVTRSSKRQAVGLASALSESWSLRKLSPR

>contig16863 Frame-2F

MDVRVRLVFADEVGRHLQRRCGFTSCWYLIPSDLKLVGDLSLTVLREFELRKRCPNGLEL

RLENSPLLATQSIRIVRDSDTISIHCSLCEHDKTRAACFSKCGVKTSRKQKKTEGVKRKS

KHRQQRNVLAKVVDSNCMNFGESREVATVKGMRVPRSSSSSDSDSSSGCSSESTNSNGCS

>contig17275 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64688.1|) 2e-35

MVLMLSDKQFEVAIAQTPSFCEEVFAINTVEKRLSILGNVKRHLVVTPDFEVLLH

>contig17477 Frame-2R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY69433.1|) 3e-30

MTLIPHIKAALAANFTDRQKLLLDEFDRVLRDYAEHNEKIFSKFTSIVEDQIMKRFLENV

AT

>contig18278 Frame-1R

MTRFYRAFSFEEEAVAVEKATLKSFLFRYIEVWARDIDKEITMTAQYDIVELWSLLQFFF

LIAIRTHPTVPHLTAKRQMLTKSRLECKGDALDFRMYQMS

>contig18784 Frame-1R

MAETLRYELETPEAVLEHFHVTEERGLSTFEVEKRRVQCGFNELDKEEGTPLWKLVLEQF

DDALVKILLGAAVVSFVLAVFEGSGEEGIGAFVEPLVILVILVLNAIVGVWQESNAEAAL

EALKDLQSENARVMRDGAMVTLPARELVPGDVVEIRVGDKIPADMRLLSMKTTAIRVEQA

QMTGESTSVNKGIDALPSGTENLIQAKTNMLFATTVVVNGLGSGVVTNVGMTTEIGKIQQ

SVQEASKDEERTPLTKKLDEFGELLSKVIAIVCLVVWMINYKNFFDPMHGSVFKGCIYYF

KIAVALAVAAIPEGLPAVITTCLALGTRKMAKKNAIVRKLPSVETLGCTTVICSDKTGTL

TTNEMSCVTFSHLGKTETELVTYDVEGHSYAPIGKITGAAMAQYKAVLSLQQVCALCNES

AIEYRDDKYVRIGEPTEAALKVLVEKIGFPHDAVKDAEMQTLRASYPDQAAQFCNEMLAE

QNKKLAVLEFSRDRKSMSVICSKSNVLPHRATRSATNVLLVKGAPEGLIDRCTHVEVGDG

SVKLLTDAGRHVLLSHVSSLARKSLRCLALAKKEVTGELGSYDGDRHHPAHKQLEQTEHF

AAIESELTFIGLVSMLDPPRPEVRPMIAMCQTAGIRVICITGDNKLTAESICAKIGIFNE

GDDLSMRSFTGGEFFALPVDTRNKHLSNGYGMVFSRTEPKHKQQLVKMLKQLGEVTAMTG

DGVNDAPALKQADIGIAMGITGTEVAKEAADMVLADDNFATIVAAVEEGRAIYNNMQAFI

RYLISSNIGEVAAIFLTAALGLPEGLIPVQLLWVNLVTDGPPATALGFNPPDADIMKKPP

RRSDDALITRWVFFRYMVVGIYVG

>contig20080 Frame-1F|Blast-exportin-like protein [Phytophthora infestans T30-4](gb|EEY68235.1|) 0.0

MDANQLRELETLCRVLYESTNEVERAHAQQAVLILQSSAEYIPQCQYVLDNSSSPYALLV

ASNSLTKLITTHWNNFTPPQRVDIRNYVLGYLAQHGPTLEKFVTTSLIQMVCRLTKYGWF

DDEQHREIVTEVTKFLQATVDHCVIGLQILSELVTEINLPVPGRTVTYHRKIAVSFREDV

LFRIFQVALTSIKQLQLHNLRGATPQQEARMGEQALAVLLKCLSFDFIGTNPDESTDETG

SLQVPTSWRPVFQDPETIPLLFDFYKTTSPPNTSKCLESLMLFASVRRNLFTPDKERSVF

LAQLLHGICAILRAQDGLSDPQNYHEFCRLLGRLKSNYQLSELMKTDAFQEWMDLTPDFT

IKSFRQWQWSVNSTHYLLALWSRLVAALPYVRADMTPSSVEAGAITFLDTRVPQIIQAYV

QSRLESAEQCAVDETLENPLDDEGGLYEQLEKLPTLCHFNYRHSGEYIVSILDPLLTKYA

EMCSLVDQSAGAAILLPQQQQFKSMEAQIAWLVYMIGAIIGGQAYSSTSTEGDELVDADL

SQRVFRAMQLTEHRIIASGGQTKPSVHFELALLYYFSSFRKSYIGEQHGMPSAPTPSSLM

QPVSASGPSSPLLAPSVSVISFKHKTYVRMFERLGLGDHTVVVNMMITKVGNNLKFWGHV

EVVIHKTLALFFEVASGYSSGKLLLGLETVQYLIGHHTSSEFPFLAVPANTRHRTTFHST

IARLLFTTAFDESSERFERFMEPIENVLNQLLQTPTYRLPEVREAIIGVCRDLRGIVQQT

HNRRTYSCMFDVLYPAYFPVFVRAADELYDSPAVTTALLKFLQEMAYNKAQRLIFDQSSA

SGILLFRELSRVVVAYGRRIQPMSVGKDPYGDKYKGIALCLGILYRALGGNYVNFGVFQL

YQDQSLENALEIALQLTLSIPHEDLMQYPKVKNAYFFFLEILFRNQLASVVALDDQIFRQ

LIESLHEGMNSFEPAIAAQCATAVDHLASLYFHEMKKKRETPVKQALRAHVLNSPNAWST

LLAALLDTLVYGEVNSQWALSRPILSLTLCSEEALTKYQQQLSATQPPENRALIEEAFAA

LFADVRPNLEAANRDKFTQRLGQFRNTLRSFLTIQ

>contig20923 Frame-2R

MLLVFKLVRRSIVGHQNFVSTIEELLNAAQIAVNIKRHNIDVQRDVITGESEKLLIMGET

ACKKYKPYALSAENFFFNHQSELYCDVWSDIIQDAYY

>contig21599 Frame-1F

MAYPTRSPSSPSTTPKQRYNYCLNDAQSVHSEEWRIGDVLSPVYTPHFHEEEQDINKSSQ

HGSFAHSHFRKRNKQEAR

>contig22363 Frame-0F

MDSPRRAAFLCTSTASFQPPDWACMPADSNLHARLEAFRDGRQCATYMVATQRVNLFGRD

QESCDHVLGNPSVSRKHAAVIHDDEGGIYMVDLMSRHGTYVGRKKIPPHDPYLLHDGDVI

RFGQSVRLYILKGASSNGSSAPVKKSWGHRLRVPHVNISAVVTKKSPGKPKASSAVIKLV

NAVCYGSLKDEKVGTFLSGVLELGVKDRHGVADVLVERLQAKYEFYASHVHRNAFVATMA

LLKQNLCVQELEDNLDVFTHISQQRNDNIYRADARKLLQAIAAVRLDPDNPQFADPDTTE

EDVGSACPPTANNREGRERSISEEGKKLSAHGMQLPYRAESVGTSSDLNSNHRERFGDSD

IRHQTSNYKISNQHNDHDGDSDIIASCAPLSAIRCGMKSISVSSLDESVVNRIELPSSES

TDPTGSAFTFISDSNPVNDDDSCASSTGQPFEHLSTEVISGSSTNAAEEFLLERPTVSGS

EFALMWESANEELEEWSVEFGCVDAHELDPRDLESFLQSYRLVCVSSEKLAGQQQGAFIA

EQKSEGTMFLVQISVMPGLTDMFVTLKWIVNSLLYRNGHIIFMKILKHALYQFAGQVQTR

GTKLYTYSPAVSQKRLQSRSGREPDAMKAQSITYSVIHSASRTVSHATSLDDEEKVDDGD

SGDEGTMLARNHLVESPSIDAGKFEEVWATAIK

>contig22529 Frame-0F

MASVECLSSPSSIPPNVTSSPVITTTSTPASSSSIVRPHQALSTLEAMPRSLEPTTPGGP

ESMDYKTVTFTVPPRPMERRGSRELNRPLFSERQRFTPTADKLVLVMVGLPARGKSFIAK

KLCKYFCWKGLQCQVFNVGQLRRATSCQSKQDHSFFDPKNTKAKEERERLALKTLIHVQQ

WLQGENGSKGGDVAVFDATNTTKARRKVLTDTFRSFAQLHQISVHVVFIESICTSDAVIH

ANVKQKVASSPDYQHVPVDEAFADLKQRLKNYEAAYEALEDDEAGSYIKLFDMQSKVHAK

GIYGHVAKSILPYMMSFHIAHRPIWLVRAGHCTEVRRDFQAIIKNPCVAPRSAHLSPLGV

AFAYRLCEFVKQRTSKWMENEGMTSEDDPTECLVMTSTLPRAVQTANFLPYGKRLQMATL

NPLDKGECYGLTMDQMKDQMPDAFAAYESDPWRTRFPGGESYQDLMLRLEPVLIDIEQHT

GPVLVVSHISTLQVLYSYFLGAPIERCPDLEIPFHSVLELVPNQDDWTKTVFN

>contig23074 Frame-1R

MAVDLSKQKPADRDSVKFDEQSMNMEIYAVVSSFLEALKQLHHLRPLLGSSSLECTTYFS

GEVFIRVCHTLMQREKNSAQKNNENLSRREVAQATDLFDEITDKNSFRSHFTYVCATMQR

MKALILLPVDVVHINVHSKSAASAALEHAMQSKGYNLSSTNNPKLLPVTAKAPPAATLPQ

PP

>contig24691 Frame-2F

MLVRLRGWGDDDILMLLTLLRRHLQYYVYASDSRFADIVRAGLPEKATAEILEMVRALME

QFGLRLSTKNFRTDVIVKNRQELYVYEHLYESIYQLPENKAGGVWLPDELSRFFQKAKQY

RGQFTHSEEKYFQQVQLWGKSIAETKSKFYALREIFMTENRRLSQRSEVEEMRLKLLKDI

FTNVPPKRLTEKKIVVASKKPQIWSSADMATLIDFVVRITTQIQTTGSSDLVKDVAVALN

RSEGSCVNKLLDMKNKFLKRASTTRAANLPDSISDPNSEAYKIFSADWADINDPYAFGFF

ALKSLSHRLSSIRSKQRKSKTTRTHLSQTRKATPTIHDTACTSSASSIPTISVVSKHSGI

TATAVTPSSSCKLLSASELPASQFDSFIQEMVGQCPWKETVLLHVIRCMQYSIGLYRSNK

IVHFFSVVASATPGFKFFELFANAQHILTRYKQRFGTLDGFENMTSGNKSSELLSDQGIK

EQYLAAVNEGSEAKSAGN

>contig24714-0 Frame-0F0

MYRENVEKDKNWYQQVLVRELSMPDTIRDRRRRCCWCHRKDVKSRKFINLFLFKK

>contig24714-1 Frame-1R1

MNQANTKKPAHINPYKTKALSAFKICSTCANYTSMITHVHWLYNEKKG

>contig25663 Frame-1R

MQLLPCISAKTKNHSYPEDQSYCWLRSIDILSIEFKSYKLLEVESAKHWMGFVKQLRSCS

CSEVQSCILAAFKRHFNLRI

>contig25821 Frame-2F|Blast-MutS protein homolog 5 [Ectocarpus siliculosus](emb|CBJ29342.1|) 3e-08

MQRELLEELTMAVLEYESSIHEMTWMMAYLDCLVSFASTAKSFNFS

>contig26183 Frame-1F

MAAKLDGIEQLPNVPEGAFLRQIVRPLYSVVAKMRNVKSQKNGASVDHKNVTNYDDVNEF

FWKDTCLAFDEFNVAEAMNVRDFKTFKERRSFCNPVLAFFRIYYFLLVMLHVLVVIAYVA

YRTDPDETDGFKFYNNFFTSEIADVRNHAFYSIFITVSGLLVLKVVLDVWIDGTHLFSST

LYTATVFLRLVWHTVFFGLFVAVNAAPYETFIGSSDLLSMAPGFIGLYMAPIVAVSIVQM

CFHGVIWKSTLLSSMDGTHEQYIGRSMGQKWGDFISYGTFWTIIFVCKFLFNLQLMVKPL

IGPSVEIYNLDVSSTQNGIIESKHNIAFLGAMWAPVLLVYIYDSQ

>contig26727 Frame-1F|Blast-calcium-dependent protein 4 [Phytophthora sojae](gb|ACH68461.1|) 2e-30

MVHNLFDNDQTGKISLRNLKRVAKELNETMTDTELLEMIERADTDQDGEINGEEFYAIMT

KETFT

>contig26950 Frame-1F

MLCRKFGADCCYTPMLHSRLFAENAEYREKMFERHMQDRPLVVQFCGNDPKTVLQAAKMV

ENHCDAVDLNLGCPQGIARKGHYGSFLMHDKDLVKSIVETLSAELNIAVTVKIRVFSDDN

ETLEFAAMLQKAGCDMLTVHGRTKEMNKTAVREVNWDIIRRIKEQLTIPVIANGGIETYE

DIARCVNATGCDGVMSSEGLLENPALFATTRNAPGVNTSFMELARQYLTYVKLYPPATGK

IVRAHLFKILFQDLCVHSDLRDALAAAKSQVEMVEIVNELALRLEEGGKKAGIETQYGAE

TSWYRRHRKGQVKLRRLDSYDKCLDSGFANLFA

>contig27100 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59864.1|) 0.0

MTRGRHPLLLLLAVACLVALSMAGKDYYEILGISRDASSAEIKRAFRKLSLKHHPDKNPG

DESAAQKFAEVAGAYDVLSNEEKKSQYDRYGEEGLQNAGGGGNHDPFDIFSQFFGRGGRN

RREQEPSRGPDIVMPLRVSLAHLYNGKSLQFSIRRETLCHHCHGKGAAHEEDIHVCTECH

GHGVKTATRRIGPGFIQQYQTTCEKCHGKGKIYTSTCPICGGRKVEMADLNFDVDLDRGT

NDGFEIEFEHYADEIDGHPAGHVRLQVVTAPHPAFTREGDNLWMDMDITLRESLIGFRKT

FTHLDGRQVDVVRTDVTPPRFVTVLKDEGMPKHHSSKVKGELYIKYHVKFPDSLSEEQKV

GFRDFFAKVK

>contig27197 Frame-0R|Blast-bloom syndrome protein, DEAD/DEAH box helicase [Phytophthora infestans T30-4](gb|EEY65064.1|) 2e-82

MEALYTVISSSFAPEAVGIVYCMTKQDCEDVADYLFDRGLSADFYHAGQSATDRHMVQEA

WQKGQLSIVCATIAYGMGIDKLNVRYVIHFSIAKSIEGYYQEAGRAGRDGNTSQCILFYS

AGDVCKLRNILSMPQKGLTKKSRAIHMEK

>contig27438 Frame-0F

MRESLPLTRVSMSLLNQGDPNGRDLRLWLLSATTHHGVTYYRIAGRFTSSGQTWEVSHRY

SEFLELRDQLVKFLSSTPDKCPGCRNYLHSIQRFAFPKKHLFASRAPPVVNYRVKALRSF

INLLASWAFSKTPKCPTCGGYAFEVVRNFVLEGGELSADVDMDSIRESMAVEAFAEPNLS

SSRGKPFMRKSSWMKPSLSTYPDLTQSMYTPHSSASTLSTAPYSGEMLEATAQPSSSRLT

HQHSQPVNQLQSSTARRHQHDEDPYDAFNDYLPERQTKVKKPSQQTMEQKSRSGKFSSRP

LHESLEMKKERSHREHEDDNATQQKLVKHRSEPRLSAHCSLVETPRASKEEADHSSLHID

ELRLDGLVDGELDAKSTTSSVYSGDEELELTGVAMASPSQLSKKSSTDNLWQPWELARVA

>contig27485 Frame-2R|Blast-glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY54864.1|) 1e-156 NOT\_ORF

MRLLLLLALRVFPILSHRSLLTKELERHVHALDLVHVSTLSPEASTTRVLCWVNTFHGNH

DTRLQAIKQTWGRKCDKLLFMSDTEDLQYPTIAITAPPLHSMLWQKHREIVRLLLREVTE

DQYDWIFKCDDDTFVVMENLKTYLSSPAIQAAARAGPVLLGHRMTLPWWEMQRVFEPFEN

FHPDHVKIMLKVKEETQSHGGLLYTPGGAGYAMNWAYLKQLVAALDQPFCLPYEVVPDDW

AISFCMRHLGIIPLDTRDIEKRERFHQYDPKELYTKSHDAEAYDHNVFTSIYQEMNWFSD

HNGIGWQNGTNCCAPDSISFHYVKPPLMELFYEYYYGE\*NFADCVSILRSFDILILL

>contig28134 Frame-2F|Blast-Glycogen Synthase Kinase 3 beta [Phytophthora infestans T30-4](gb|EEY57178.1|) 7e-15

MSDASIPPKSAPKDPTLDLKVDEEITTVQTTMSITKSKEDMRNESTGISVGDSSHTLSDG

K

>contig28710 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63888.1|) 3e-55

MMDTKIEWLRTLGLSDDKVNNVILRHPVILGFACEKLNALVQWYQFQGVPKSRICYIFSV

FPEGVSFSLDNLNTKVNFLNQFGCSENQISRILTTAPQTLGYSVEKLRVNTEYLKNLGVR

LEDLPAITARVPQYLGLKTSRIKETVDAIEEMFGTGAGLRAL

>contig28787 Frame-0R

MDEQYSTDKARETLRYGRVIVMTDQDHDGSHIKGLLINLFHTFWPELLKQPGFLCAFITP

LIKVRPTFKQTILETRQFFS

>contig29519 Frame-1F

MGAAIMKSCLAGDPAEAPNRHRERLLHYDARCRYKQSRMRSLAKTMPPSFAASVPRVNRR

SAIGLKVPNSELFAKTFATRCPLQTQDHEVAKLRKSPPCSLSSEAATMSESSFVADSPSH

DRRSHRTPVAGFRALLPDDYVLEGEIGKGITSVCHKCVRRSDGRHFACKIVDKKKLAPSF

RKRLEVAAQLRREVDVLRRVNHPHVAKLEQSFEDSNYLILIMELLEGGELFDAIVNKGCF

SEREAVYVARCLLSAIQHMHARGVVHRDLKPENMLLTRNPDGISPLTVKIIDFGFAKILK

EGSKSTSFLGTGGYLAPEILLRQAYDTSVDMWSFGVLVYLLLCGRLPFAATTQLQPAQSI

QKLYKLTFPSRYWLGVSPVAIDFLRRVLVVNPSMRLTATEALKHPWLRA

>contig30539 Frame-0F

MCRLFTAASAFLGASASAHILHHEVHQPHGLRELQVNLDLASTSASTTDYTCPVCGMSTL

DSGYDNTNYVSMINGQRIYSCGMSPRSFDSYNFEVTDTAYLAANMAEFIVNQTDADAYAQ

CTNNCAECFDGINDPVTGGAVSTENYVYVCLKNGQKIYFASQSNKNSYLSSVNTEPRHLV

DSVICNGAMCSDATNITTLSPAAQSFVADYSTAIAAIGTITDTGTSSISSDFCSGQGSVM

FNGFQTSIHGSCVMLLFQPWVLNSGVKYAFGFIGCFLIALLNESLVKGREIVRRHLLASR

KLRLNDNFHKMQCKALLAVLYMIQMTIAYFAMLVVMIYETGLFVALIAGFGVGFLLYKNL

DQDITKDRGAWRFTNPSTVKIQVKGMSCMKNCGITVENALKNISGVTDAIVEFDERAAYV

AGSAQYSDLVAAIEAVGFTAEVSDSVGRNPSPRA

>contig30773 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57863.1|) 8e-38

MQEAEILLSDLGFDISCQDVTASISGSQSFYDRLQEKVAKEVRKSNYEDYLDEFTQTQLF

CQYYESLLKVEAQKEQHD

>contig31132 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69735.1|) 3e-47

MPSAVNLGEEVLSGIVQVAEHLQGSIIAADTGCIESLRWSGAMPLLLRDFNVSNIVSASD

LLTCASPQDLRRFLLVQEDEKIDHVVFFLSGFLWDYETAFKKLLTLNIINRVTICSSLSE

SAHECYDFYKLRPSTALDATEKVEEMHFD

>contig31279 Frame-0R|Blast-N-acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62018.1|) 2e-56

MAGDVNLFFNDYDDPCACEVEIMIAESKYRRKGFAEEAVMLMMAYATSTLNVTRFFCKIL

ETNDASIQLFEKLGFVKYNYVAAFKQIEMELITKDKHVQLVDAVIKSADIQIPQKSSQ

>contig31604 Frame-1F

MGQKWGDFISYGTFWTIIFVCKFLFNLQLMVKPLIGPSVEIYNLDVSSTQNGIIESKHNI

AFLGAMWAPVLLVYIYDSQIWLAIAQAIVGAWIGFRLKIGHSARIREFVLRLQQAPRLFD

KKVVSAAARGQLAISNNNPLSSNSIAPNANSRLRFAVVWNEIVSSFRLSDLLDDRETAIL

QYQISDTGAVEEPVFLIAGEAQAAADIAARSKTKRMSDAQLLKELTKAGVLGCAKNCIDI

MFQILRQLLGPQDAELVGVIHQILAGGRVSGVVSLTHVGLLRENFVDLLASILELPEPTV

IPPGSMFGFPHEQVVAVVQCVDALLKSMELMLEDEWMAEKFRKSVFATTTPDLLYQKEQL

VSIFADRISQRDSNSPTRTTSPSSNESIVSLSTRLFFLLTLDAADALPRCHEAQRRMSFF

LNSLHMEIPSIDSIAAMKSFSVVTPYYNETVLFSVDELNGRVDSNPLFRKVEQKGRDLSI

LKYLVTFHDDEWGNFLERVGVSSMDEALAETPTQVRLWASMRGQTLARTVHGMMMYEDAL

KMLRWLEIGSDEKISHLDKIKHMDRIAGLKFSYVTSCQIYSDQLAAGDPRAADIDLLMRK

YPNWRVSYVDTICPPQGSGTECRYDCVLVKSDGDEIVEVYRYELPGDPLVGEGKPENQNI

ALPFTRGEYVQTIDMNQEHYFEEALKIPNFLATATRKGQNVTIIGMKEHIFTGRASSLAH

FMTLQELVFVSLTQRVLANPLQSRMHYGHPDVFEKSFVMSNGGVSKASKGINLSEDVFAG

YNVALRGEKVTHIEFMQCGKGRDVTLSQINAFEAKLSTGSAESSLSRESHRMGAGMDFFP

>contig31860 Frame-1R|Blast-eukaryotic translation initiation factor 2-alpha kinase, putative [Phytophthora infestans T30-4](gb|EEY69961.1|) 1e-66

MGRKKKGKKKDTQIVALTNPPTTYDAATLGKARELQAQEVEVLEAIFDQDLIIQSSTPLY

SHIFAIRLLCETTPSSATTAEVLLHFDFPKAYPLTQPPNITVEPKHGLSNTETLKLECNM

VRIALEKIGDAMVYDLVVFATDFIQDHLKDQSSFFDQMMTRQQDKKNQEKMAEVAFSQLE

QD

>contig32894 Frame-1F

MVGNKHKNGIICTFPDCNKPMRTQKFKMHFTRAHLKEGEVYSVDHRRQFEVAREESSCSH

IKSELSPLIATVTEAPLKTPAPKNSSNNLCKETVATVHDDILTAQARQVPTQQIPVPPQP

NDPVIPAVKSKTTATATRALPNSINITTVVPASAATSPPSQYSSGSKRPVTAIESSSVDV

VDSTNALLMQFIALMDQRFQELVGKMGEMIDVQKDLIDALQSSNPNGQAPASAFSQAVEV

VMKRRKKDLSPRGDSISGSNDADGEDQGIVL

>contig32911 Frame-2F

MAKTFENDLSSMLSKVLGIYKVSISNTTQSGVSDQNVRMCVIVMENLMYGRDVDFSFDLK

GKMEGRYKGDNCNSHSVLWDRNFVELAGGIPLPLQESALSLLLSAIINDTTFLASVQATD

YSMLVGYDVNKQELVACIIDYIHKYDFMKMMEHAGKRLIQEEGEITVLNPKHYRKRFCVA

MNKYFVTIPSRYTKVTTVKRNTACKNSTVGSFGSATKEEDKDCV

>contig33624 Frame-1R

MPLVRNKLAWGMDSDGSDWSDEDDGIKEAAPTADLVDLEVLLQKRDDAMKISKTTIKSNG

PVKKFEAAEAIALKSHQNVFPVLAIKVMDEPYEDYSAEHDFAHENRLFEDYMLQEEEAKS

SDLGDLQMVITNSKKRRGTARNSGSGHGESYEKTPAKQRHLLRFQKRINRCPLQCLRYDY

GGEPLWPVTIPQNLNVPSCPGCGEKRLFEMQLTPTINYFLKVDEHVPADKAFLKKPAVPG

VGVALLNTPTGGMDWLSLIVYSCSASCSHSREEFVYVVP

>contig34478 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65868.1|) 3e-85

MSSAQQQQEAQSIGAVENPSEALASQNDGKKAWHMRRCDGRDICSCELRLASACFQKNLV

EKAAKKRRENPSLGPLLVKSNSYLYRKVTNIQQLELELKLCIAAFLAPTTLGRLGLTNKT

FKRDVDIMAKQVTCNFLAKTSLTNLLKQMEPKAMESWSQLMHKQMTCIQKIFVFYTAYKT

GGMRQQNPQWAFGAIDVNPNEPQRVILPNTWTFHGHNPWLRRRGNGKDGEWLLTKKYKPS

KAPKDFLEHVKTWASSLQPGSMLAIA

>contig34676 Frame-2R|Blast-3-hydroxyisobutyrate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY58268.1|) 1e-67

MASVAEAMNLGTTLGIDPKILKNIMDTSTSSCWSSLVNHPYPGLMENVPSSNNYEGGFVV

GLHRKDLGLAIDCAKQAEVSIPLTCQVHQLYNMMVAGGHGKKDFSYMLQYLKNGK

>contig35565 Frame-1R

MEIKVRRHQHHLPHEAKVHITETSEVNRKRGGPMELAQLQLRVLHKDDDFVVLDKGPDER

MDGAFDVTLEKA

>contig35943 Frame-0F|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY57356.1|) 2e-28

MENYNIYDEIGHGTHSFVYKARRKRSIEYVAVKSTAKSRMDKILNEVPFLHKLDSPRVLK

FFDWYE

>contig36120 Frame-0R

MQSEAMNTQGVAAHDSVPAAVPDVVVSCVADATGAESPATPMEVTLLPHTPDAPGSPPLI

RQETIILTVAQLQIEQRRERHGRRKVYSELRDRLVTAMMEQLQRVTGDSDIRHLRLCASR

YESFVWKKSANQVQYKQKLEHRIESLRRQPSHEDNHGVVITVRLVDGHRLNLIRSSDPTL

VTCPYRRYPVQEQRVQSSHLQSSSKRVGKRKNALTTLLLETASLRRDELYFEKLRAMKTQ

YRDEVALVFRELCRVNTVIQHSTSLRRHDSNYLGDFLASLKKIICLLEQQPGEVGGMIPA

RKRTVEYLDVVESHIQRKVLPILHRLRRTYSTILRPIVLNYMKNSFFNRRF

>contig36568 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69071.1|) 2e-25

MPQSRELANKKNDHKDRHSRGPMGLSAAGPKKGGAGAHNWGVSTAEEDAIVAVDRKDPNY

DSSEEQKVKI

>contig36744 Frame-1F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY54087.1|) 6e-97 NOT\_ORF

MNCLDRKVVLHYARCALSSSFGSICIGSLLGPLAHLLWNALRWARRDESTISRRFVSLRS

ERVEHFIRTYHKYSFVHIAGYNKPFHVAAHDAWDLIEHHGVEAIVDDDLTSRILLFGCNG

WAGIMSALTASALAHASSHAIFFTVVAFALCYTSISMATQVVTAVTKTLFVCFAENPARL

SQLHPIIYHRFVRLSELKSFRDLGKPTD\*RLV

>contig37291 Frame-2F

MSSGSSSSSDEELSQLLSMDPLFGVEKADNRVASKLAKEEIYRQILQGDCGLSSSPDFQC

LSPMAEVKGLPIEVRYQLPLALGTANEISKECTICQHCYGIGDHIVTLPCQHFFHACCVD

KWLWNHTSCPLCRAEVYMDQETETQSTKHNFTECSLVDQERIRRQMRSSSQLGDFRPVVP

>contig37686 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63850.1|) 1e-141

MPAATPRRRERVSVVYKSVHLVGVMVLTLASMDPSIVVRTVRWFLFLYFALSSLDLVLTR

YHLWKFEPTIPQPKRYALITGASSGIGREMSYLLSEQKYSLVLAARSGTVLDRMRAEMEL

VNRPTEVLVCVCDLATIEGINKLIRYVKNEGLIIDILINNAGASLSKDFMELLDQEIDEL

MTLDMQALVKLTRSIVPQMVERRIGRVLNISSIAGAAVVPTAALYGSSKAFVTSFSQALS

YELRSTGVTVTCICPGPVHTNFSKVAKMDGALCMKVPGMTVDAKDTAKVALNAMFNGEIL

VYDTWFAFLAANLVQMVIPGRLAAFIAGACMNELKNFWNLLKR

>contig37772 Frame-0F

MDEERLKFQLLLEQKTQDHANSVQQCESLETQFLASEDGYKLTEMDAFSNPPEAFYSLSE

SAIHASSFYKSWAHWRLKIDEMHDFFPQFQNLIAAVHGTLELCGSHVNELHVLCDRLEGK

ETCDISILTLLRKILQFAVTWKTRIEHEKAFVTFDAVQTLRRRLVDALAQWVECDADNGV

QIETNSIPVPTFTITSRETALILQNWTSDRTMQLRVRRWLARMEAYPGVPPLRGASPNHA

LELPSEGCTLDLEEMTLEVKDAFLLLLIPILKQNRALHVRVFTRFIADYETAIIKCNDRA

NDDFDNTKKQWAMRIHVQSAVKKQTTHPVLQKLNFHGPPSPLAPTSPASSVSSSSSSARS

RRQIIQE

>contig37992 Frame-0F

MAALHWLSIRFDIAFLYGSIKRNRENCLLRLALSCEPDSQVWSFQFIFCCSSVAMLKGKI

YRRLIECQKLTASICCDLIYAELPWMLVVLVM

>contig38012 Frame-0F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY70514.1|) 1e-49

MDVNLLYGRGYRAGVDMREQRKKNSFLEQLSHKRQKEQQRADASDTTLTSDQIVARQHER

ERALRNMHARERGLMQEMASR

>contig38250 Frame-0R

MLASSCTWARKECHTDSPNGYESFFRAREKRHTTPECDHGMASYFYQR

>contig38324 Frame-1F

MPAPSASTSLSLLLVALGVLLYFRKHPTTLFNFDVAAALLNRKKTKEPPEQFKRRGSLEF

KPVTVRILYGTQTGTSKKLAEALERTLFALNISGFHFQTSVVSMKDYDQDNLEQEAIVVA

ILSTWTHGQPPEDAKMLCSWITDMTQDFRVSKSWLNNVQHAVFGLGNAEYDEDYGRAAKN

LDRGLCDLGSSSLVTLGLGDDNVDQLKQFDIWMDNLIAAMCEYSSKIAEAALKKTRSFMK

PGKDEWLTQTEFRRQKRAKKTEVAAGNGEILKPNEEDLMNEQFLVDEFSDDEEHTKKMTE

ENNGMVDVEDIGNSMKESEAASLSREMVTPMQRKALTKEGYKIIGTHSAVKLCRWTKHQI

RGRGGCYKHTFYGITSYQCMETTPSLACANKCVFCWRHHKNPVGRVWRWKTDDAETLVKG

SIERHQNMIKELKGLPGLIPERWKEAFTVRHCALSLVGEAIMYPQINEFCKQLHDRHISS

FLVTNAQFPEKIAALNPITQLYVSVDAATKESLRAVDRPLFKDFWERFLACLEELKHKGQ

RTVYRLTLVKSYNMEGLNNYAELINIGQPDFIEVKAVTYCGKSDGSDLTMKNVPWHEEVR

AFCLALCDRVSGAYALASEHAHSNCVLIAKKKFCRDGVWHTWIDYQRFHDLIAKYYEDGT

AFTADDYTAPTPHWAAYDSKEQGFDPVETRFRRSKDGKVVEFAYQSTESGCG

>contig38548 Frame-0F|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY57167.1|) 4e-51

MSFAINAPFVLMAARAHQENFVASFPFGIVLMCSMMHFLGSFGSSWVLGEVSELTFSIMS

TMKRVVVIFSAILFFGNPVKYQSILGMALAVGGVGAYQLVKIYEKPAKLLPLSSID

>contig38742 Frame-2R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY64280.1|) 0.0

MLQLAEPVCKALEKCYNIHQLYSHQFEAIDAICRGENAVLSTATASGKSLAYNVPMLDML

LKDPNATFIYMFPTKALAQDQLKSLRRFLKAADLPLYVAATFDGDTPMKSRSMVIRETRV

FLTNPDMLHLTILPHHRQWIKVLKNMRLLVVDEAHMYRGVFGSHVSCVFRRLFRLCALYG

SNPQVICCSATIQNPKAHFNQLLPTLPQQLAFSTNDCTDADTKAQSNACPPSMDFFHQRP

LKVITNDGAPSVRKLFCIWNPKNVKPAKCTRKSQSVDAFNNNSSGKTIKKRKRLDNTTLS

NCDSKEPNEKVSFSTSAIYHGSRLLARFVEAEIATLLFCRGRKLTELVLMNVHSILDAKA

DTRHLRDRVTSYRGGYTLETRRRIEQRLFSGDLLGVVATNALELGIDIGELDCTIHLGFP

SSVASLWQQAGRAGRRHEQAKTKHSVAVIVCFDAPLDQHFAQKQNAMELFQLEPEAVSLN

PMNHRILEQHLLCAARESALYSPQSG

>contig39301 Frame-1R

MPLVRFNEHLAAVKAIGWSALAWLMDRCWWCSGPPLTLGPGGSGLDTRGRQILQSIMGGG

LVLCTKMVFIIRNTKTKQSSIDGQVRCVPLAWARGFGRWYSKSMCQLVQHALADSIA

>contig39657 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65704.1|) 9e-67

MRKIQNMTLSAYVRAYNDVDSAAFETSARDIWNDQAEILYGSRGACVAGLSDIIAAKTAS

ASVFSKYEIKQYAVQWKHSSMDKCLVTWEIEVCVKKDAPTNVPLTTPFAELAMYHEDRCE

PFSFQMTSHISFKHGKIVEEIRQLNLCRISEKVLEQFAVDPQKATDMLRCLIVNA

>contig39958 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61270.1|) 1e-24

MLVTCEWPKEEPLQLKGMVKDLLRIVSEWIATKPIRFWTFQPWLAAMLSSKAKALAQAYV

DVLFTTGLSQP

>contig40293 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57629.1|) 4e-25

MFISSGTGIAPFRAFLQDLKHEVDASVPKLRSAYLFYGCREASRDFLYGEELQSALNSKV

LDQLHVEFSDESGHRKRYVQDALLDRSELVARHLLIDEGYIYICGSIAMGLAVRKAIITA

IIQHSQFSKGAIATEADAKRFVMLKLEEKIIVTELW

>contig40565 Frame-0F

MEKVFTPRYQSTDQKMRGTERVAARQSFSSKVATIFVIPVAAATLCVVATLSTLAIYEMR

RSSRI

>contig40936 Frame-2F

MNLYLGFMRFNIALNICALSSSSACTRECHSSPLTQ

>contig41261 Frame-2R

MITYQLRQYVYCTARSIFNSLPACFFSKEIWVCLY

>contig41395 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55317.1|) 1e-47

MARVWEQNQVGQRKSGASTCTSSPPDAGVDLNRNYDVCFARDQNGSSNNPCGDDYNGVKA

FSEPE

>contig41940 Frame-2R|Blast-ATP-binding Cassette (ABC) superfamily [Phytophthora infestans T30-4](gb|EEY54021.1|) 3e-09 NOT\_ORF

MFYRRFDRVYSVWKVTRSLCPANSSVLSGVIRAFELGKSNPLGFA\*SLVFSSILYWMCGY

VSTVEVYLLFELIWQYWMNSAYLFA

>contig42505 Frame-1F|Blast-60S ribosomal protein L5 [Phytophthora infestans T30-4](gb|EEY55132.1|) 1e-166

MPFVKVLKNKAYFKRYQVKYRRRREGKTDYRARKRLITQDKNKYNSPKYRLVVRITNRQV

ICQIAYAEIDGDKILCQASSAELPRYGLSVGLKNYAAAYATGLLVGRRVLAKLGLDEDYQ

GNTEVDGEIVKTESNGRTYFVDEIADEKRPFRCYLDCGLRSTTTGNRVFGALKGASDAGL

DIPHSEKRFPGYSRDDKSYDAEVHRDRIFAVHISDHMKELEEDDPEMLASHYAEYVKAGI

NPDNLEDIITKVHEAIRADPSPAPKKSHTFDKKYKRTAKRSRQQRQARVAQKKAHAASKK

A

>contig42686 Frame-0R

MLEEEREIGEVAIYDLAPVRLRAWVSFRWRKPLGHERKRGETDNGKEYNRIPYSSASDFL

FDSTRLLSITDCS

>contig42826 Frame-0F

MNPWARTSNVKESTKANATDITGENRFDIFDKSHDVDFVSMTSSMDMNKSDQERDSDDEQ

VDLTTFNDEYVSFEIQTSLNVKRVNESTEMSKKLALIERQDSFQDSSVDETLKLGKYTSS

LIPLLRTASIDRNDKDAEVNVSG

>contig42992 Frame-2F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72305.1|) 4e-07 NOT\_ORF

MDESHDARICGYRGRDETYFTISRDFCCQGQHGSSASTYVLTKFVNG

>contig43120 Frame-1F

MKLFLSITTAAIAHGHARGDDSLHYNKIVNQTSGAPDPVKVLDFNWDAPCSAEASGIGDS

DVCDKICSRDYNPVCGSDGVTYSNECAFSIAQCKIVSLRLVEAGECAGASSSKSLESDNT

DASCPDACLDVYDPVSDETGAIFPNECYMRMAKCTASMKKLPIVEKSTAAQDQSSYASNK

VEDSAVDSARKEDAVKLSNGIPKAANTTKGVSNGTEKELLATDSTWSGVEDDCMDNLAGK

NTSLKACNNSCLDLYSPVCGSNGVMYSNVCQLELAACKEPDTG

>contig43568 Frame-2R

MNKQVPNLKQTKCVLIGSSTFASCYRHDYYNIVSRRIYHTKRVPLTGRPPPRCCEFL

>contig43744 Frame-2F|Blast-L-aminoadipate-semialdehyde dehydrogenase large subunit, putative [Phytophthora infestans T30-4](gb|EEY68241.1|) 2e-76

MDLRVSTTCFREADEAPLRVLVLPHAGGLSHTLALKWKESFQNAGLSIELWGVDWTWETN

LLEQKSSDRALDLVAAICRQLCFGFFGKPFVLVGHSLGALVALALTHYLEERKLSTPRHV

FFSGSGGPSCWLLFDNVSVLQRDEELIKLLQQWGDTDKQLLDIPEQSQKLLTALRVNLIL

HNDLVQWYKQQHGVKIHSDVTVLGGSED

>contig44279 Frame-2F|Blast-peptidyl-tRNA hydrolase, putative [Phytophthora infestans T30-4](gb|EEY66544.1|) 5e-61

MDKYVLERFNGNEQEVLQSLLDYTTELMRLYLHRGVAQATTYANSMDLQQYLIQYMNDRH

G

>contig45247 Frame-1R

MDESEDAESVEDSERLSVGTHRTMSEKVTATTESESCVETTDSTAAAGESEEPQGDANVA

AQPSAMNDAKTKLASPSPSTEDDASEKLGKEDANSSSSSEGDGLRKSNYFKNVLQSPVFK

TPMRLGSVIKPPVAPSPSDSQSNGGNNPRNTFGWNSVFKRLRKSLVTTPHDKIDKKVLAL

SNEAYAAPNVAPRQTDVLVVDTSRGEDITNFVMRDAGVVVTDVPSASSKSSESASNVITV

GYMFKNKYP

>contig45773 Frame-2F

MAVSLRLYVGGLPSDITKQELLERFGRFVNAAANCHLEDVELPMPKPLGAIVLSRGFAYL

TLQGTDAALQSEKLQKTFHRTKWRGSMLKVQLAKPHYKLQLEAEWAQMKAMRAANKCNKP

LVADADTIQPLNVALPFQGRKTTEFDEVEEVAQNENILYEEDVEAFVRQVEQDMPRAVEI

TAKLTKEEVNARRLAAIEAKQQRKLADKAVLGNFKIGHGNTKKVWSDASDTDHEGKSDGA

VVSNWLDSSDDEVDVEGKTYTFMNPEEVDAAFAIRPELMGEKGKQLFEMQKRFQGDARFR

FDARFVEDDADEFKGNDEVDAEQSDGLTALSAELKVVEDDMEYALEMQEDDATVARVVAT

LFPGLDVTRRLDKQRGGKDPLKEAAWMGQLQRYDPRDVPACHEFEVAMTNNVVKDDATTT

GRRDDYPTGGDRFFSTTGALSTLFSRVRANSEDGEAGEAALDGVVGRSLAAGATDGTNGF

KLSSLFAFPEGEDEALLSTKSE

>contig45980 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64829.1|) 3e-67

MDCVLDPLLLRFRFHFERISSATNRLAKPEWYLHYVLDQTKAHTRFFAQVLTPVLHRHRE

QIHCWDAQILVLRGFVRAACRKLTQDLPTLLA

>contig46048 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY64036.1|) 4e-20

MGAPRSWQYLVDCLRDPPRSDFAFVPHQYILAPLELSQASNHSVDDASTPIHSRPEYYPK

KRPRQRNS

>contig46242 Frame-2R

MAILRYSFLKRLFIQHTPFVRLITMPLLISFVLFFLAFARTAHGIDCPMEFLMKFAASPD

LALCTADTGFSLETIPTMTVDKMINVCKTMPCMKLMDELAAAKLGNCTVPGTNVSIQQDV

LGKFATACQETDSMSSTGSMGSAGSMGSMNGSVPLVDDESKADIADEEQSSERSPPSSST

SGAESLKVKFASAIVLLVVILA

>contig46624 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69160.1|) 6e-82

MEAAEMQLARALAALTECELPQSRSLESRLDAYFQLEDLFHLEDSEASVLELQRHVPLLL

SEMRIDLQQNGLSEILHAALRCLSYLMHHRSLNVGFSDDEISYFLGKLVRLLFSTQDIST

YKLCLWGITVQNFSPDRHILLPRMVEALVQAVVNPFNSRVIEVQALKGLHLLLVKYPEQL

GCSAAVLNLYVRPIASRLTSSEVVTRTQARVVLEEVSKHRTAL

>contig47065 Frame-2F

MWQYPPSLPLERMAAKSIVTKKCVRNIHHRRGNITRRYKFAMHTHDKKQIDLLKQLA

>contig47537 Frame-0R

MLQVAQETLAAQKKLLEQVRAMEQRLARMQ

>contig47793 Frame-0F|Blast-lysosomal alpha-glucosidase, putative [Phytophthora infestans T30-4](gb|EEY58718.1|) 6e-41

MPYDGLWLNMNEPSSSCDCALAAEDD

>contig47911 Frame-2F

MIMMPSTTPAVGSLIVSPAPTTPITRGLWSEQEHEQFLHAMKMFPTGPWRSIAAFIGTRS

IKQVQTHAQKYQQKINRRRRGLRKQKKKFVRPEHRVDAHATGCIQRVKNFTVQGSPRSPS

AFPVDDVLPLSSFETLLMGDCSPKASDVGSNCGSFSPVASDDGSITSSLGPDSLEVLDLD

FDMDSLLFELDPLPYMPEVSFEQALTDDTYRQDVQDSIDLLLA

>contig48240 Frame-2F|Blast-arginyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY69203.1|) 0.0

MSRILEFQGHDVRRINHIGDWGTQFGMLICHLTETYPNWETEMPNVTDLTKLYKSAKERF

DADTAFHERSKAQVVLLQSGDKNSRKVWETLCEISRREFQKVYDRLGVSLNEMGESFYNS

IIPSVLDLLRGKGLVETSNGAEVVFTKAFKQPFMLVKSDGSYLYDTTDIAALWYRLHEIK

AERIIYYTDYTQKDHFSLLFEVGRLSGIYEPSKQRVDHVGFGTVNDESGKRFKTRSGETV

RLVELLDEAKVRMKAQLIERIEAGQTSLPMDQVDAAAEKLGYGAVKYFDLRQSPTSNYIF

SFDRMLSTNGDTAVYLMFAYARLSSIIRKSGVDMAALVTQQQKQGDVLNPEHPTEQALVI

ELLQLQDVIDFINKDLSSNRLCNYLYTISEKVQTFVTACRVLGSEAQSSRLLLCDATVKV

MKTCFSLLGIDPLDQI

>contig48635 Frame-1R

MSATHNIEKRVIRNCSHLALMALIEGFSSCLKKVPKISTPLPKGRSKLLKTIEFQINQ

>contig48688 Frame-1F

MFPPSFQYTSKLYLAKNLSNKPYAGKRGDSWRRFAMQYAPHRSRTTFAEHLHTYSDQSVK

HNPRFLVMIRVFFSTDLISCDRKFTMHS

>contig48828 Frame-2R|Blast-hypothetical protein TRIADDRAFT\_26233 [Trichoplax adhaerens]gb|EDV24170.1| hypothetical protein TRIADDRAFT\_26233 [Trichoplax adhaerens](ref|XP\_002113696.1|) 1e-39

MVWSHNDNWLVTADHGGVIKYWQSSMTNVQLLQGHS

>contig48895 Frame-0F|Blast-DNA-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY69219.1|) 2e-52

MNVFLHDPLLDWQQSTAMHQKVLFESVTEGDTSTFHDSDAEMEDVQESADFRSNKNGTAS

TARGIANAAWLPDIKIAIARRKLDGVSPALLLKEELSQNSHLTHHLSKFYALVDAASFGD

IDERDNEVTTLSSLGQAQQLLAIATAPDLLGRTFQG

>contig49175 Frame-0F|Blast-dipeptidyl peptidase, putative [Phytophthora infestans T30-4](gb|EEY57124.1|) 6e-83

MATHELIALEDVAKMPAPGLCMPVNITFSPDGRIVAFLHAPGSQSGLSRQLYALDVGSRL

VYLLAAPPNQGNTEGNLSLEEKLRRERQRQMGVGITSYAWNPSTLSQHLLYSIQGDIYLQ

EQPGAELKLLFDKKSTGAAGSAIDPQFSPDGRWVAFVQDKELYVIPTYVVEGGQKPV

>contig49553 Frame-2R|Blast-tRNA-dihydrouridine synthase, putative [Phytophthora infestans T30-4](gb|EEY53001.1|) 9e-19

MSELYENKVCLSPMVRSGTLPLRLLSLRYGADLVYGEEIVDKRIISAVRVR

>contig50036 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58324.1|) 3e-56

MNNDKLVFAAITADNYPIRLAFQLISAVQTEIVSKFRSKALSCPENGLKKDCAKIFAAIA

AEYDDRTKVDILSDVMNQVDVVKTVMHNSIQVVLSNTEKMEVVEQKTNDLNEQAKVFRNT

GR

>contig50043 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68849.1|) 1e-51

MGHEAINCMRSGTCVRVVQDTSKIDGLGGEVWAGALILCNYLEMHGQKVVQGRDVIELGA

GCGLCGLVAASLGANLAVITDEYPDLLQTNIDKNQHIWSERQATAQHPIASSGRLKWGAP

ESVAPFAHKFDTMIGSEITQLGRDLHISLLEAIRTVLRPGPKSVALLSMDLCRPSCKGTC

DVSKCTLSHFVTVAKETRFIIYKHPSVSLASHAAVTSMIGALGRRLQVDVDDWSVVFELR

LEDSGLHANIY

>contig50238 Frame-1F

MFALVTETSFVGVSTPIATVPSPDVNPPTEAITLRPRSNRKKADAFWSSESESSVAEVSV

DGGNDDVLSSGRKGNNWPADEIWRLIQAWEEAAATTRGTKLTSALHETWALFVKHEGSSQ

RNRTLTSVKNRMIALNSSFLGISAYIVERGSSSAWFDLTADQRQVEIRSWG

>contig50285 Frame-1F

MLKPHQVDGVKFLYSHVAAGHGCILADYMGLGKTLQVITVIYSFIVDEIEARQRHDQTCD

DSKTIPKEEEEHNKNSNVENAMPTVLVLCPAICLPNWTSEFEKWLTAESRVRCPILTLDT

YTTKSSAAGRLRLLQRWKRTGGVLLMGYEMFRGMLNPTTTPISCFEERDASIHVCLRMTS

AKKEITSTLAQKAADIQRTAREYRQLLCNPGANLVVMDEGHRMKDPSSLLCQSVAQIQTS

RRIVLTGYPV

>contig50494 Frame-1F

MDKCQKENFTSCIEIQCQFSVSNFLST

>contig50700 Frame-1F|Blast-MMP37-like protein [Phytophthora infestans T30-4](gb|EEY55529.1|) 4e-32

MSLSTSLKQALNATFPRVAFTLAYGSGVFQQKNHDASASMVDLVFAVDDAQAWHEQNIAL

NPQHYSLLEYLGAAHIAAFQEKFGAGVYYNTLV

>contig51909 Frame-2F

MASLFDQFKSLIGQPAQIRLRDGTFTCGVLYCIDPYTNHVALLCPSGREESKYSAKVLLA

HTVHDIKLLEQESTDLPTLATLQQ

>contig52157 Frame-1R

MPQELDKKDLICARISTATLYRPISCQESGTESCNAYMQFIDFNVVLELAIASVRLPQLL

KSNTRA

>contig52508 Frame-2R

MVRVMERVCPIGTNKFLWKTMNLLAYGGEGSEDLMNSSADAATLTYSNGINGSGAKDSEK

LNWDPTSSAA

>contig52733 Frame-1F

MQSMASFDTSIAADASDELSILFIARRLHVDVKTMQINYNNTNKIRF

>contig53222 Frame-1R

MYCQFILNLLVRVDVSRARRAATYALAHLTHLTPFLKVPQLLTTIL

>contig54155 Frame-2F

MKGVAPFTPTLVTPDQALRYERQAQELLGDTLREFDAHVAACKSGENPLHDKWHWKALKM

HESLDVYKERQPTHPALNVIPSKMSFETMSSHSFDSVIDQP

>contig54317 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58240.1|) 1e-18

MDLYNAVWRFSFGKDKHVAYGRKALDSIYSLLVKAITKHEGAPHALTPDEIAPIKAICDQ

LVPA

>contig54722 Frame-1F

MLLFETCSCTRLNAISSRLADVGSTSDSYMSTLAVASSAGCIGSLSVVRGV

>contig54847 Frame-0F|Blast-dynein heavy chain [Phytophthora infestans T30-4](gb|EEY64009.1|) 4e-65

MQEINFWCDLNRALLAVQEKLKSPEVEITLAVLQRAKRYLATVSFSTDHGLGPALQHVSS

VMILMKDFPMNSILSATDMSQLYQGVTLVFTHLKKIRVADSYNLPRLLHLVEVVSSDLSQ

QVISLL

>contig55589 Frame-1F

MHDAVSSDDYASSVTLSIPKTAKLRLVSRVKTFFGRLSRKEQIAVLDLGCLAILHEWIRV

PKQSGNEPLNFVCNPQVLETIICILETLPVRKEDLVEEDKLQGTMDSLAELSGIGVESRQ

QMIKLGEKWRDLNPPMPREVPRPPVVPQVPLQVSSAHELPIIEAFTTAKGAAQASGKRKR

KHE

>contig56092 Frame-2R

MKPTNHELVGKRITPFPFERVRLLFDNIDFIASRRGYERIEIPGISNDTAVFKYRFQARV

GDRVVSFLQHLITRRYTEADRVVLIWRKFAEEEGTLAGKHVDETGWNIIRQSVDGTGTLM

ESTSRYVPMSFGSVTTDASELKEFTDTIRSVGEEECQKCVRKLEALLLDDALGVC

>contig56126 Frame-0F|Blast-structural maintenance of chromosomes protein 6, putative [Phytophthora infestans T30-4](gb|EEY55333.1|) 7e-87

MDLAELRDDLEAKTIKYQQKKKNFDKFRDNLVRIRTMLEERKRVWQILRKEIAHRTSMEF

NKYMCLNNFAGKLKFRHDDQRLEIAVLQNEAGASRASQVTDMKELSGGERSYTQVSFAAS

SW

>contig56575 Frame-1F

MCRNSVAIHTMCISRHSVPRVYWYYRAIQARATRTEHGPNHLVSMRYLVLDRTFHGCFSS

KVCTCDFQKVFLLDET

>contig57002 Frame-0R|Blast-AhpC/TSA family Redoxin, putative [Phytophthora infestans T30-4](gb|EEY56677.1|) 1e-123

MYPRANTPGCTKQACGFRDNIQAIKDAGFTVYGLSGDSPKALRNWKTKESLPFDLLSDPD

HQLISYFGSSLPGNKVQRSHIVVLQGGVIGDVAAKVSPADSVRRAVEFVTKTSVVDSPKK

DEEVVENVELTTGDECIVGKSVTFDAELLTEASTTVKVQELFQTRGVIFFMYPKADTPGC

TIQACGFNSNLNEINAAGFDVYGLGADTPADLLAWKGVAKVHVHVSVGSKARADWLFWQL

>contig57235 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57829.1|) 2e-09

MSVSHHLATSVVMASTEAIANTSRSVARRLSSNAVSTVSFTALFVSG

>contig57381 Frame-2R|Blast-mannitol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY56075.1|) 8e-47

MPTTCRICSFLSFVAVRGSCIMVGLPNDEIKFHAFGVVAKGLKFVGSNIGSIQNIKDMLQ

LASEKNVRPVIQKMPMDKVNDGVKLMRDGTVRFRVVLEN

>contig57554-0 Frame-0F0

MLFDREYNTKSSGFQSDVTSTMSAGIHIFVCSTQLYFRFKTKEQLRI

>contig57903 Frame-1R

MLRYKNLPVLILERAKVPFEKLALKKTIDIAVDRKHRALCNQRRLELFFERHLVKLLLSA

SDVIFIK

>contig57976 Frame-2R

MSIVVDIAPGVDQIMMILICIGLLDEGVEDDSSLG

>contig58072 Frame-0R

MTSSSYNNQHTHTHMYTYIHTYIHTYIHIYTNNFIHNH

>contig58186 Frame-0F

MPCLKKCQMAYSNSIECVWSVLSEMYTSNLPFTNKP

>contig59097 Frame-1R

MIQAAREADPRIASIVTIAYDEYWKTRTLKAAFNDLNL

>contig59211-0 Frame-1F0

MTELRVGRTQETSTATVVLVEDIKALKQLVHEEMEQIG

>contig59585-0 Frame-0F0

MHIHYNDRVVLIYSKISQRKRQVRQVLITGMIRPIRVDYEF

>contig04238 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55957.1|) 2e-33

MPYEKRILDMIKSGGSSAEKRIYKFSKKRLGTHRRALRKREEMKAYYAALRAKAVHHA

>contig06382 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY54628.1|) 0.0

MTKKQGSRQKVAIDRKFYYRFLRLFKVIVPGPFTAEIGFAALVACMLVARTSFDIVLLHA

FTAVEKAIISRSQTEFMVHLRRFVAIMLPMSCVNSLLKYGHTELCLRFRTRLTQHLYGQY

VKGFVYYKVSNLDNRISNADQLLTVDVERFSNSVADLYSNMSKPILDIAIYAIKLSSTIG

VEGPIVMLSYLLASGFFLTYLRQPTSQFTIVEQQMEGTFRYMNSRLITHSEEIAFYNGNV

REKRILEQSFYRLINLVRSSQQFRFSLSVIDNVVAKYLATLVGCAVLARPYMDISNKRLG

NSSYADRMEDYFRSGKMLLKMSEAMGRLVLSGRELTRLAGFTARITEMMDVLTDLDEGKY

QRTMIQGREEDTLEESKTQTISAECLGLYPNKGDICYRDYVIQFENVPLVTPNGDVLVPS

LDIKVKSGMNVVVAGPNGCGKSSLFRILGELWPLFGGTLTKPERNGLFYIPQRPYLTLGT

LRDQIVYPQSLKDMQVSGKTDDDLMVFLEKVQLGHLVEREGGWDIIRDWADVLSGGEKQR

VAMARLFYHKPQFAILDECTSAVSVDVEGAMYSYCREQNITLFTVSHRKSLWIHHEYVLR

FDGRGHYEFKKINEADEAFGS

>contig06526 Frame-1R|Blast-autophagy-related protein 7 [Phytophthora infestans T30-4](gb|EEY60210.1|) 4e-62

MANNRSRESVKIVGWESNLRGQLGPREMQLQRFLDPIRLMETSVDLNLKLMRWRQVPSLN

LNILAQTKCLLLGAGTLGCYTARSLLSWGFRHITLVDQSIVSYSNPIRQPLFEFQDIGKP

KAICAANALQRIYPLVKAHGVVLTIPMAGHASTNLPDMTTTLKT

>contig06799 Frame-1R|Blast-Endonuclease/exonuclease/phosphatase [Thermomonospora curvata DSM 43183]gb|ACY98716.1| Endonuclease/exonuclease/phosphatase [Thermomonospora curvata DSM 43183](ref|YP\_003300754.1|) 5e-20

MKLPLLLALATLYHATNADENDGCKYWNSEERTRVTTAYGGNGGTPYTDLYDASPGLRMK

SVTINSGDRINGVTFNVQLSYGAPVVLKHGGNGGSKKEITFSQDEYIKSFVLQTGEKDGK

NRIRYLKFVTSKNQVIEGGTRGNDPKNQLVQEVAPASYQLAGMHGNAGKEMDKLGFVYTK

LAANNCPAS

>contig07231 Frame-0F

MLVRRKVPQKGTQLLSPRFMMAMGMTAHQIAGASGKDSGKVYAMKVIRKAAVFAKNQVEH

TKTERRILQGVDHPFMVKLRYAFQSDAKLYFVMDYYNGGTLHFHLHRAMHFDEVRTRFYA

AQLVLAISHLHTYNIVYRDLKPENILLDDRGFIALTDFGLSHDRFDSKDGMQTFCGTPEY

IAPELIRRIPYGKAVDYWSMGVLIFEMLAGYTPFYHANRKRNFQNIVKLPLRFPLEFSEE

ARSLLRGLICRNPAKRLGSGPCGAQEIMDHPFFAKVDWERLYKRDVSVPFRPVVTSDGEV

TNVPEFFKRQEVVDSVVSEAPLLGQSHVFQGFSYTDPYNL

>contig07477 Frame-0F

MSMKSRWNLLEQSALSEQCLEMALLSIIETTQKNESKATASLLAATKTSDISMAADTMLM

QLSAYNASPVSICASDTLKELSEWLQKWTGSSKLMKTDEEEKEKLLLAEGFSFFKIDDSR

NLFTSKLNYAEPTAVFNKIAKLKRKGGLQSDLTILQDAYSGFPVFLHIRDNEFATFDRSS

LIQGIKHEENQFFTAVALPDTIIAEDSLYAASRDEVRSCSNNYDSSWCSTATMWTLHMSL

LHFAGVSCKYNAAAAQLAETFLVLVNHLPTCACEEHRKNCSSFVRRALDNLGECISGSYS

ASISFIQHLAQASMSEGFYVLNNATIAIDVRIVLNQLVQFIDRTIAQWKYRGVLLRFDAM

TLHSLVLLVKEVEVLWRLENLEKFETCCAADLLTRIAHDQFDDKTMINILDPIMSADLHL

GSLGDVVVIHEDVKRELITALYFQKPKLVAGLLDILDPDWEVLVNFDLRADLRHKLVIQD

DRVLSQVDDILRDLTHGGCEVVEQFRGLTRRHPMLVLSRFPRQLTRHIGTVSLSQLYLNT

TFFQNILNAMQIMQPHLRHQQTVLEPFCYFLFEILRVIADHHAVEFHHFVSHIWEFFYDV

VEADVGVAYELIFLSPRVVVMENIVNMYDSQPATVAFGKVLGQRHNEQGLLEIVKSIRNG

RNMHHTAASQQQHIEQLLTQIECEALPLGKVGKLLIERKDINAVVLGLQAIDSLCAKTDQ

GTSAVALLRRCAAPLASLLLADTVSKAVMLTLCQTLLNLMKFDSICVDYVMRQYVQCLRI

LRPGLKEAAVNTVLDFLIFADTRQRRQILQQLFDDPSEIAKTKLGAYLKSSAFRKTHLIA

SKA

>contig08542 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57888.1|) 2e-21

MNPLLGELRMVKVRHLQSGVCLFTHQWKWNAEAHAEGVDALVMSFTQFAREIDGGG

>contig08964 Frame-0F|Blast-ATP-dependent DNA helicase, putative [Phytophthora infestans T30-4](gb|EEY60960.1|) 9e-23

MTTGCRKELLYSHFGFRFDSSRCVRNCNCNVLLDFNASLNERNDRKECHTSIETRLKETQ

VIKQWPIEYQYQKVLAECKRLKLSKRETLSRRQIR

>contig09134 Frame-2F

MSDHDVPMDINASGNSDSSLLLDPKEMASFVNDYLFKFLQDKSDGDFKTNRPPNVLEKLK

FVDPFYFEGFAVDARDLHTCESELKVALKVAVWKPFRKLIIESKVRILLETAMEDVITAL

MNQFGQKPTVAPQDAELERRLRFGFMETKYFGEAHNKFCEY

>contig09541 Frame-1F|Blast-alcohol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY68781.1|) 1e-90

MMGNVPGVQAEYVRVPFGDVNCYPLPSGVSDDKAVLGVEITVTALHAVDVSHVKEGDSVV

IWGLGPIGFQAAKWCKLRGAKTVVGVEQCVERVKFARDHMNIEVVDRHEFSPAQVVANLQ

QVLPPAGADVVIDTSSCSTSTG

>contig09655 Frame-0F

MDLLGFLLCWGDQTLVDQHLKLSSCYTKWKVSEFARNDSKTGQEGVFHVENGAKL

>contig11355 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68486.1|) 4e-76

MVSSTSLFALIAVVAPGANYVKAHGFITDPKPTWKDKESSEWVVQIPPFWKGPWDEAKGD

DGLLALFKELAPANNFKDLRSLFDGNPEFGEECGYTDPKGTPVDPPSNGAATLSRGIVHA

GSCEIWLDDKLVLRNDDCQSAYGDGTKQTPTVFKPVDYSSCAAGGCLLRFYWLALQNLDG

>contig12901 Frame-0R|Blast-V-type proton ATPase 16 kDa proteolipid subunit, putative [Phytophthora infestans T30-4]gb|EEY61710.1| V-type proton ATPase 16 kDa proteolipid subunit, putative [Phytophthora infestans T30-4](gb|EEY61709.1|) 2e-07

MLAQLVADVCPSSASFFGFMGVASALVFA

>contig13649 Frame-2R|Blast-hypothetical protein SORBIDRAFT\_10g021845 [Sorghum bicolor]gb|EER88504.1| hypothetical protein SORBIDRAFT\_10g021845 [Sorghum bicolor](ref|XP\_002437137.1|) 2e-07

MEEKEEDGGRRWRMGPTTSWVFFSNFASSRRRVRLFLRG

>contig13982 Frame-2F

MALVHQCESTCLRNGAPLLTAPNTTKAFETPVPSSDDDDDEGNYHNS

>contig14709 Frame-1F

MTHEAYDVLRYWFDGDQAETYRYKWFPSDGSDNQMNTDIEVAARFRALLTQAEDGKLENW

RDESPNTCVALILVLDQFSRHVYRDRNSAYNQAQIARNDIHAVSIVEQTLLPNCWHKELP

MPHFVFALMALRHSPTPERLQYVLEAIEAKRQLHMQHGDLLEKFRRTTTGRLQHLRESKL

LDELSDMDILERGFFETDESDMPKNRLYRIMDEYLNQMRACEHTHLAVSLSGGVDSMVVA

YLMHKLKAKHGNYTVVAVHLNYGNRTESDAESHYVQHWCERFGMVFYARRIDEVKRATTR

RDDYEKISREIRYAMYADVMEKYKIPGMCFGHHRGDVQENVISNMMKGLSLLNLSGMQTS

SIVNGVRIWRPLLDVEKDVIFEYAHRYGVPYFKDTTPKWSTRGKLRNHLVPLLRDMYGDG

VLNNLSALGAESSQCAEVVESQVLASIMRSVGESQVAVWIDCALLMDQPFFVWKEVFRHI

CHAMMGNSMVREKPLRELIVKVQRLNVNPAGKADHKNKDAETGSWVTLKKGNRSFLTKDK

HLIIFRSHFFPRIPYVAFQFPIVGGEIYEFGPWKVTSKVLAATHATVQNLRNCKPLTIWD

LIQANGVSYVFPNAPQLVIDCTRRLNVLRAIEKVITDSMPIVSSVGAFDAVPTTWVHVTL

TYSQ

>contig14886 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61913.1|) 2e-87

MIDNLASGDWAHGSINDFLKAGHQILALANTKTQAAYNMHDMCHTEKYLAVDFINDFPDA

NHQINNIALYNTSNWIRTWSEQIRYLSLSSSWIYTRKQSVFLEPSNIPNYLRWNVNIIAL

DSVDVAKMAAQVWTWA

>contig14965 Frame-1R|Blast-hypothetical protein PITG\_13295 [Phytophthora infestans T30-4](gb|EEY60570.1|) 2e-58

MCSRLPRPVSIPKVVRDLLWTITSPPILSKDQFPVLPAEFGVKALNLEVVVDWLNALILD

PSPLFAFLQDTTSNGRSVALGVYFSTLLEFWLRFCPHLQMEKFDIGKQIVSSTNRTVGQL

KFLFRCCIQNESENCEKQQDFHVESSIKFFLLNPVKNS

>contig15078 Frame-2R

MRHPKAFLAFQYPQIQKVFEEIGPLLDSFKKSANSFVVEKETVTLSRVNDGDGEMHFHDA

NDVLPEFQDMPPILVKPRDTREHINLINGNKKLTATVVQEPPTTSKNVQKQPIPVEVIKQ

SPSVEIIKQPDLEKIQELPDSNNILHSDQARTPIGPQLRGTEVDDSLTDGHFVAVTSSPT

KPRLKWKQYGKRISVLIGLLIVLSLAFAIGKN

>contig15333 Frame-0F

MLIGMRTKGIAKKQRREELLKESDVVTGRRKINRKPRDQHKRKMVDYGVQATKGKFKDGV

LDVRGL

>contig15405 Frame-2F

MARSFPNGIARSFSASWRRYPGARFDNAVLRDLPIDKEPNNYIRNAVSGACYSRVDPTPL

PSPELVITSPSALLLAGIEVNESGRHHYDDDNVENKDIDTKYQPMETLVPILAGNKLLPG

SETAAQCYCGHQFGYFSGQLGDGAALYLGEVVSDTERWELQLKGSGLTPYSRTADGRKVL

RSTLREFLCSEHMHALGVPTTRAGSVVMSRELQVLRDVFYNGNATYEPTAVVTRIAKTFL

RFGSFEIFKMTDQFTGATGPSATLPNKKEMLQQMLQFTIRQYFPEITGETMLATFFNEVV

RRTATLVAKWQSIGFCHGVLNTDNMSIIGDTLDYGPFGFLEHFDRQYICNTSDESGRYRY

EAQPAICKWNCGILANELQLVIDRASLQASLETFDTIYQDEYMRLMREKLGLKVPVAQDS

TLVNTLFDVLTHTGADFTCTFRYFSELDAFDTGTSRTQLVLKLAAISETVSELKRKVA

>contig15988 Frame-2F

MSFLLASVRAIFRFVSHPKSSKHVDFFITTSVKPPEVVVSGSMLNMQLAGIFTGGSTFN

>contig16112 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67581.1|) 0.0

MFAADVQPNTRTYGAMILAYARMGCWDETLNLVNSISYTNDAHKKEIFTCAIISCSRNFQ

HFYALKLFELLLDDGIYPGDNVCNAALSSCARTTDMKQLRRIFKLVERHATPSTYSYNSM

IVACGNARNMKKALEVLNKMQIDVSISPDVVTFNSLLLAAVRSRRVDEFPFILSRMAEAG

INWDACTLNTLLEGCALNGDTRMAKQYWSQVSRRKKSDAVASRTNKQYLRLDRGHYETLM

TVYYAAKDYQAIIDLWQKDMICRRRAKSSKTLNFLVCACKGLKNITIAEALMAEFAGRGQ

PISAITHHHMLEVFLAAGKPNAASAYLHKYMESNGLVSTFSFTVIMKYLYKDNYHSDVLA

TFGLYLEARGLSSKNQNPLLHYPTDAIYVLAMRSAIKLQDHETVLAIYGGLPATTSMVVR

SVLLVHAVSSCENEGDWRTAVKMYDEMTGKLDEDTSVDLYKHIVKIVARTGEFDCALDVG

GGKWYRNNRPDKGWGLSN

>contig17476 Frame-0R

MEKRHKKPLETLSPRKHGWIGFTSPIDALKAPPSSAVASRSKVSNPSGRMTSPSPNEYPS

LFDVRGGPSSTRSVDGMSARECTSKGSGGSSGWSDRIWFDKRLGVAKGGEEQAHRSVYHH

NLHSVLTNPKASNWGGTLLDAFYPMLDVDVALASPPGLTDVTMRDFQPYLREFGTNATKY

EKNHLKPVSKQLSSSNVPPIFVADEDVLKCLKDVPYFFFRPDFDLADPSTFEKIMNLPKA

LSLEDELTAYLDGVEIALLRQVASRSDQFFEASADQEVMKQSIQSASEQVANLRKTMKRL

RHLVADKTLDIVNLHRRQKRMKDLHRLVTMVEEVKSAEAAVEALVQCQDYTNALNLIESS

QTILKVYLQGIHGLSSLNEKFKGYLSFMSAQISRQFISVITSPEWTFQDEGDSNHIDKNK

ANSLRYKEDNLLQESKHLVDLLFRLDALDSTVKTYLDQLNEEIRMVVKTVVTETIAVSKC

SVNSCDSDIGALSGNESKISNQLRALTSDDFFQCVQMLFEHLLLILKRAVVVQGILVESM

QKRVNEATDEENRLEVATFGKIYSYGTDHSKASKLALSEGWPSFENVINEDKRHGDRNIK

IRCAKVIRDIDEVIRNTCELSQRNVSNLFAVRKEIQAIYTLPQLRKLYDTTMDFVISIEK

LTGKTDYTLRGALFSQLKLFLETYHKTQVTKLVATLDRETWKSTEISEMRHKALDDLSSG

RGVALVLTDDRTTASESATPLKMVSICGKSFRVVWSVLLMLEIAMNYMSCAANFPVLATD

VLQRSIEMFRLYNSRTTQLVLGAGAMQMAHLKSISARHL

>contig17887 Frame-1F

MKMRPSWRLTRTELLGPDFQPSEAEIHVLVEPPSAAANIATKQGPAQAEGAELVEAISFL

VEKRFKSMEEK

>contig18460 Frame-2F

MAENKRLKRQNDDDTIKRKRHKRNCNDVKKKRHKQHKQHKYNTLKIHRRHRESAHGSEND

GENEYAPVPDFIRARKVLCELLTETPELVNDLLTLMQMLDDGEIAVIGGIKNRRIRHKLK

DLFPLLGLIKLKEPKGAFAKKKNEKEPSLMNVLKHMLTADSDKLGAKEYENTKLKQAEAA

EDTSTIHRPIKRDLPIGPALPSALVRISNTGVQSDDEEDFMGPALPGMKGFRAADESTEL

KMAQQANLLETEQWKLARAGDRGLAVKEAGNTPMRREAWMTMMFENSTLQDALGPQSKLL

TGKSVAFRSKDPAAVDKTWFDLPEERERANRAKLDMELLGYVRQENASSDSAARSIGTSA

TAQSIVNESILPVANPKQDEEMRKQMEQLLKSRGPSLLEQHQRKQAEQAKLEAGRSQIIN

GWNRERDLTARRGMSQDDAERMISAAKQINSKF

>contig18594 Frame-2R|Blast-WD domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY66713.1|) 0.0

MNILVSGSSDSTARIWSLPDKVEDCKSLVSKVLHHGAGPHKDVTTLEWNHDGSLLASGTY

NGKTRIWNAQGEIKHVFQNHNGPVFATRWSKTSLFLLSASFDKTVVIWDTSTETKKQQVK

LHDDPILDASWKDDSTFATCSSDMSICVARVGEMKADVVLRGHKDAINSVKWDPAGRYLA

SCSDDYTVKIWDPAKAINKQVIAESKDMEIESTETSEKESTLDAATSAALVYTLQEHKKE

VYTFRWSCTGPGTSLPDHPLTLASASFDGTVKLWDADSGSCRRTFDHQVSRIWCRV

>contig20081 Frame-2R

MSVLAIDRYKDSRDLTVSLEQSMDMDILLFGHILYEMATGREFMATQPDKSVLQMLAPEI

AEVLCAIFYEPHLLTSPKENSNAEGDSHCTDRKRQYTNFFIVDVEKMVANFALLTLAINV

PPIQSLFAGFRLDSSMKSTIKHSMQINASRTQAHLVHFQDQQLLLRARQRAERRIYEEKE

KQHQKRQHFTLQKALTSQGNACTRNTTLSRRKSYRNTRFLDLVARNSVKKRVPEVRTETL

EL

>contig20548 Frame-0F

MSPPESELEPESERDPSGLSLDRYRQSSDGIEQ

>contig21165 Frame-0F

MEGVEVPVLSLCSTAMDGARMMLILKTSAVMICDESYRTVGIFTSKDLMRRVVALSLKPS

QCMLSDVMTPNPQTATLRTTILETLHSMHNGNFLHVPVFDNNKNLVGIVDVLQVTHGVIQ

QMGSFQKVKGDCVQPLWDQFRSTLDCSNDFIEHENEVEVDELSIGVADCDADTRNKSPLA

GRQSRIELQASTREIATSNVANFNENPLTELETTPDAFVFKLADSYGNNHRFTSSAVSMN

QLRVDVQNRLGDNTIHRIFYVDDEGDHVLLSKNSDLMDAVNRARTWGNKYIRLMIPQYRF

VRRALAHNSETAIGVVVYAAAVAALAGVSYYFSRRK

>contig21253 Frame-0R|Blast-Rab18 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY61856.1|) 1e-55

MLFVESSAKTKIGIQQVFNEVVQKILENPALLSITAPRGRGRKLDGKAEKSGSSGGSGCC

>contig22317 Frame-1R

MRRPGVAAASTSLSLTSTPLAINSNIRRINPSVGSLTSYNASLADSGRWSLPPLNHYMTL

PRNLMPSRFINVVDNFTSSSSNESNSQNENRTEPTFSSVMNNLLNNEDAEFAHDHFLLPP

LAHWQNMVDTNDTASEPVDRPEEIDLTLLSSDEDEDGVQNITDGGDIFEILDASDTPGIS

LPVPFCRKRRRPGSSELKVLVPKRQRMADKMRSAESTNINIQNSEVVEEFKRRLKCSICL

DVLQDMTSTICGHIFCAGCIDQAVRANGKCPLCQRHVHPKDTHRLYF

>contig22362 Frame-0R

MLMDAVEVKRNGNKGRALKLWHVVGDSLWRMGPQRLPNAGFLGVKVVPIREDENAAVALK

AVTFEEEKATTGFQAVIKQDMDKYYVEALLQALRTGKIRDKDLPILASSFHANVLLPCRR

AGVSLNIKQSSFKKVLFFLKAMEAHGLLVVADRNGVQTITSIARSHRDVQSHEPYSTIKD

LKS

>contig22528 Frame-2F|Blast-histidine acid phosphatase, putative [Phytophthora infestans T30-4](gb|EEY67495.1|) 1e-171

MATPSSNGRNVILRHVLIFHRHGDRTPVLTFIGSKMEPTPEENDFWASKVATPEQIELLQ

QTAKVVGPDKTQPPFISPSKDSQHPYGLLTQKGVKHMTNKGRALREKYGHLLDHDVKVED

IYILSSSVPRTIESVQCLLRGFFSRHDDQQSRIPQFYVHTYKHNVLAPVHPLQVFNEIEL

IVHDDVLGLRSEVERDAMKKLSLHLRECLGVPSDQPLSWTALRDALTCRRAHDWPYPEGV

TYEIFKQIEAYDTWLWQRLYHRKAFCYQAFKSGVKEVYEFVKSVVENKQVAKISFFSAHD

NSIVALLGALQIDVGLRLPEYGTTLELNIYEDPATHDFYITPHYEDEEMAFAGHTQDLFC

PFQRFESLALDFLSCEEIVS

>contig23075 Frame-0R|Blast-lipoic acid synthetase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY62412.1|) 1e-179

MLMGDTCTRGCSFCAVKTSKKPKPIDPEEPYKVAEAIAAWGLDYIVFTSVDRDDYEDFGA

SHFAKTVSTLRAKLPEILIECLTPDFQGHDELINQVATSGLNVFAHNLETVERLQRRVRD

YRANYKQSLHVLEQAKVAAPLMVTKTSLMLGVGERNEDLFQTLRDLRDSGVDVVTFGQYL

RPSTKHMPVKAYVTPEVFAEWQKVAEQMGFLYVASGPMVRSSYKAGEFFMKNLLNTRKVE

SVA

>contig23905 Frame-1F

MGKPIKHDGRMNVRGSTYERRAWTRKEDDAIIRLVEEYGTKRWSVISDHLNSENHGTERT

GKQCRTRWLNHLDPTIKKDPWTTEEEQIIEDAQTRLGNKWAEISKLLPGRTDNAIKNHWY

SSMRRTMRRMAKQQHKTIGQSIRSGPGSSKVAKFSADASPNSMVELTRDAMNSGDNFRQS

PCASQALVYKDCYPALVHPEEERALQNGDKKVNSKRKRKDLRICTGGMAAGDNNGMFLPD

TPRRVLHTQLLLQLFNTGDEECGTYITVASATNKNNSRNDHNKKKRLNGPGLGESDAFMD

MDQPCHAFEHLDIDF

>contig24715 Frame-1R|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY60954.1|) 1e-08

MVDNSISSIGFERIEDASIGVKNQHVDLAILSIETSFRGINDANYDLGLQCNLHFLSEYA

QQATGRPSNSWTNTSTIASSCCLIHMA

>contig25028 Frame-0F

MASVARAVERLACAAATMPAAFSSAVLGRAREPSPYLFHWLRAKCIYVLNM

>contig25662 Frame-0F

MNERVMLSYFLTRVQMEDPDVIVGHNLHKYVLEVLLSRIDHFKLGGVWSKLTRLRRGRLH

PSNEGVGWNEYRMDDMVNGRLFCDTYVSSKELLGSQNNYTLSYLVERLLLKQRLNIEMTE

IPQLLLNGPEFFVKFLRHTLDDAMFVLHLMHKLEIVPLSKQLANLCGYLWTRTLEGNKRA

ERIEYLLLHEFTRSKHKFIVPEKYKTRHEADKSSTKREASYAGGMVFAPKKGLYDNFVVL

LDFMSLYPSIIREYNICFTTVERQFTKDATGGSLKRKKTTISAIEDKEALNGKDATFEGA

AFSDDSEIPSLPSSASEPGILPAVIKRLLDSRKQVKQQLRIELQAGNVEKAALLDVRQRA

IKLTANSMYGCLGFRYSRLYAKPIAALITSTGRQTLQRAKEVAEHECGYDVIYGDTDSIM

VDSRTENLDEAKRIGSEIQTQCNKHFKLLELEVDAIFKRLLLLNKKKYAALVLKEQPQCE

PLFEKEVKGLDLVRRDWCVLSKAVGNAILDFILSGNSREEVVESIHEHLEQVAERMRSNI

EPLEQYVITKSLNKQPEQYPDRAKQYHVQVALALRSMGKPVGAGTHIPYVLCKEEEPGSK

RRAYDPDEVQRANGKLSIDIEWYLESQIHPPVNRLCAHIEGTSSPQLAHCLGLDTTRFSH

ATSPFGDEKDPNDAIPSVLQNDTDRFQQCVPLEITCDQCKISSAFPGVFCSYEKDGMVLS

SGLFCPVCKADFWGFDQEGINGNRGDDFEAILSNRLHLATRQATKKYYEAWTICTDVTCK

TRTQKQSLRGNGNICSAVGCRAPITLEYPDSALYTQLKYFESLFNVERARKKIQARVSGL

SETIDVPRFSERHDAVLQKLLTQAEETVERNEYNWVKPSIWQTLFT

>contig25969 Frame-0R

MSPNNENDVLLFADACFLNQEFHRAIHSLKKARLANVEGSKIDFVAPSHVMLRACLLLGK

CMLAIKQKEECLELLGSVLPDSEQDVVQLAKKMQLEHENAEGMNVVSSLALLLGETFEAV

GNRENATVYYRIALRCDVHCSEAFFHLFDKQMLTMKEEKELMASLDFSGDEMHLLQLLYQ

THVGKYDTITPIEERFAEVEHRYGLTDNLDLSITRAEAHYYQHDIQQAHKICESVRERDP

FNFRVIAVYVGTIVELGKKRELYYYAHQLVEVYPTKAAAWYTVGCYYLLTQKYEAAQRYF

HKATSLEPSYAPAWIGFGNTFAAQDESDQAMSSYRTALSLFPGSHLPPLYIGMEHLRTNN

LSQAQDYFQQANKICPTDPLVYNEMGSVYYKQKKYFQAINLFTEALQQCKGLP

>contig26458 Frame-1R

MGLFSYWSRLPALFQAQDNIICKILDLEALVNSLGKTKVLNIRGDYIRERYKAKLCCKNK

DIHYTDKTHAQLFRVKVPFASTSECNNNNQGLDHRWRFDLYDYGSDAKSRVFSTKTLMGS

SYLLLSQMNNQAEADLTLPVLSSTMSVVGQLTLSYLKLTPFIHPKNTIASVWRKYWRVRP

PLTIGHRGMGRSYYQVDGHRLALTRENTLASLIMAGRSGADYVEFDVQLTKDRVPVVYHD

FFVNVGLEDKNARWFGTKHETYEVGLHNVSFRQLTQCYTAPVPHKKENSQLLQNRVKKHW

VRLQGNKEVPSRRRAPRAGDDCDANVEDHLVETFPRLQDLLKHVPAEVGLNIEVKYPDDY

FHSAMRKLSCFDINAYVDRILQCVFDFAGSRRIFFSCFDPSVCIALRAKQAKYPVLFLTY

GSMAPDAIDARMTLQFAINFVKMEKLQGIVSNSESLLETPELVSLVKKIRDMVLVTWGDL

NTKHEMVQLQKRHAIDGIISDNVIDLINQDKR

>contig26825 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53885.1|) 7e-44

MVSSDVIQKEVMMSGRSEKVKSNSFVPKRFASPFSPLHLSSTTTMDLEVLEHRLVARNIG

AYESFLEEHHGIVDEDQWKLVSSKDELKAYAEHQRASDAPRVYQHETPAVHVPIILITGT

IKGNLDDLMYGLACTTTEQGRINFSYVNDDVPRSCVLATLTP

>contig26951 Frame-2R

MIGGDFECLQQRVALRVDVMQRHVIGVAEVVLAPRSAGLRVLRLHARQLKVKIVSINGVQ

TNFEQLNFLGEIVDENYRDLATFDLFYRGAIVASKEGELIVKIPREITFQEDDEDTEDSS

IFRDQQVEKGASDDRANFGGLNEQQLVLDAWDVDRFPKSSTGLKPIVVRIEYEIDEPAGG

LRFVLPDEQYQPKRSPHMYTYCGPFGGLCDGARSWMPCRDTLRDACSVRIELTVPDWCVA

VCSGQMVQQMLNPDFDADGRQWRTFRYVVNPKTNCSSIGFAVGPFRLYVPPEMPRMTHFA

LPECFEDLVHCTSKLASAMTYFEGALGASYPFKTYQQVFVEDLPDQLQYIAGGAILDQNL

LHGSRIIDRELPSHLTQVKALVGSWIGGAVGIQSTKDAWVLIGVIGHLVNTYVRSIYGEE

EYGYRIQLAMDALTTMELTTDQQSPALLSSEVDVYSEYEPLSLTLLEVKAPLVLHMIEQR

VGPKHLSIAIQRAAAGGGAGGSSVSNDAAANGDGNKDDEYGKSNEDKKIADDVGGEGVGG

ESTNAAGKAGISSEPLTTLLFLKTVKSIAGAAGQDLTKSFLLSWIIEPGLPFFTVGYWYN

RKQTQAEVVLQQEIPPGGKLYTGPITITIVEDTSEYTYQKRIEHKRHKFDFPCHSKVRKK

RRKRQGLADPDDSVSVGGPGMGLNDTPVFWVKIDTGCAWLRHVVMHQPDFNWMEQLLSDK

KVGSRVHAARALALFHRPHEKPNVMSCRVLTECMSGLTTHSRRLRAEAAHALGIWQSIHA

PLTNANTQLPIWKAMHNLVRIFKEHFFDRVTDMPLPNYFLPSGGRVILESLGAQQASISS

KQIQVQDYAAGEYEIKKSIPKALAMVRAQNGKTPPEIETFLLQLLTENDNSKNYVEMDDQ

SQVADDCYYVGNLMLSLSVLTLDRPARSADGDAIVVREILRYLHYDQIQPSYNKTITVCC

LEALCNFVLAGRCEEKLVNFYSFASPKHSNLVRKAAIESILRLYFAEDPNGPNANENKYV

ASHTSTTQPRASRRKTTSLLANNYGATAAIWWLCELLTAEKSPGIRLFAVQVCLNCMRGF

PPGVGKEVLATWDHSYTLGLMDYIEMKEPTSFVLKSPEKDKIFGLFDRPNLTKLRDDSNS

AKCIAEKLWNLMNTAAAMDQRLRVALIVLYRKIWGDTTPIAVAHIVQDKPANWAGGFESL

RLMMEESKNRMLMNGGRAGTIPPDDDRKRAFSSTANSPADATLEQFRGKKFKFKMGDTTL

RSHKV

>contig27101 Frame-1F

MVTSFRAEPSGNHAGGSIKRFNAVSKEIPAATRLDTAENTKILAVIKEAEVLHAVTGLSR

HKAKGPDRLNNEFYKDTQALMVPAW

>contig28135 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56726.1|) 5e-85

MDMGIDLEIDESKLWEPTKRQAYMDALPDMTLFEDHVVEGDEMAEAIKVLIEDGETAESL

ALHWKNQGNDMFSDGKKAHRGYFQTAINYYSDALTYAYKSLALPYAERDLSYDINKLTSQ

ILCNRAAVQLELKNYASCRSDAAKAINFDPTNIKAYYRGAKASRLLRKPSDTLRYCEEGL

>contig28553 Frame-0F

MARNKKHEVNIQEWSCPLCTLLNAAKEKRCAACDNERPPNIQLQASQPSEPSIAAAKASE

VQFQYRPSAGVFFSSFPQDKSSPGTFIPWRQERRLEVNNCRQRWRQNVMALPETLENKEL

VETGTPGRKHNNLRSTQRDSNYSNSIEPTSYNNKNVLEEPLSIDTGPERQEEIDMDVDEP

CFNLLGLETPVFATPAAENNLKIQSTSDRQKNDTFMADTRVSSSSEFVPFVPANKLCTDE

LKIEEKLKSAGLDCSTSEDEQETWTCFSCTNVNPFKVTQCVMCSRKVADQSTFNEGWRCS

LCATINALCSTHCEVCNREQRCRESTEVMKPSFQCPVCTNINAFGSSRCELCDTILPAGT

FKSNTNKLLHVSLLIHSLLPSSKLSMKTLLICQVVLPLYSVN

>contig29837 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY57756.1|) 7e-97

MASAVDYQLALTPKGSVHHTFEPAKKDTLHLIKEYCKTRLTTLKPPLKKTDNPLKVLALL

DRMQWLQFLVSFIAWTWDAFDFFTVSMTVSELAETFDRTKTDITWGITLVLMLRSVGSII

FGLASDRWGRKWPFVVNNVLFIVLELATGFCETYSQFLWIRAFFGIAMGGLYGNVTATAL

EDCPLAARGVISGMLQQGYAFGYLLAV

>contig31133 Frame-2R

MKTVLLQMDVLEYSSKNKKRTKVDTIGPEVFGDVIVLETVWEYVKRQDLGVYNRLRALIM

NADRRFVVFANEHHRACYVQKKTLLPRGYTDTQRGDTPLETEAERNERAVAAAWKWYASH

LVALQQKGTRILFLANDGEDLKQAEMLGVQGGITIADFVKPMAEQHPELQDLLSASAVEE

KELMTEGVSGMKKRGKKALYSEHWGTTELLAGIKNQRLFKGTIRCNRDHWLECHVLIHGT

NGVKVPVLVQGREHINRAIDGDIVVIQLLPKNEWTQPSDAFAVNESAAQEAEDEAMESAQ

IGVAEPTVSLAQVELVQSDDILSLKPAGRVVGILERNWRKFCGSLEPPRDKVMRSGSGSC

LVVPVDRKMPKIKIQTRQQEALMDKRILVAIDSWPVDSAFPLGHYVRTLGVIGDKETETT

VLLIEHDIPCDQFSDDVMRCLPPEDWTITQENAAGRRDLRDLPVCSIDPPNCKDIDDALH

AKLLPNGNVQVGVHIADV

>contig31278 Frame-0F

MAFDLISEICVRLFLSGALNDSECSRNSYRTMATVLSSLLN

>contig32064 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70415.1|) 1e-62

MAISRHHLTILEKNQLRAHHRERPDLTQEQLREWIHGNFGKWIGRSTIGKLVSTPDEVCA

NPLAKRVQSGRYPEMEAELFNYIMTMQSEEPGDEPLRDDHSICSEGPLWIKANEILKRTK

GSNQSVSLGWVQRFKKRHGLHRSQRIVKKHRTMENALKGDSASDPILNTALEPKYEDASL

FNCTHEDRRIEDEAIHDNVAMIPLAPKSGTMGPNVKRKHFVAANDILLLSHVLDTKPWTF

ANFMDGWQQVCDQLRQHV

>contig32536 Frame-1R

MSQQVKDVYSGIKKIFPSARRSESFSLSSRFNAVESAPTAPRSGQKKTRPSSFTFTSWKE

KHRTSSEPTPSVVMSLPYGATAATPKGKKAPHDVHRLSLSQTLSHAFHASPLFHSHTPNA

TVASPNSNDDKTVLSYVTPPQLGRRSVSAEVTTLPSLDTRPLQDRSVRHGLNTLPGSPKP

ITNRVNQDTIHPRASPSPDTSRKQLVASDSSAQGAIVSPLASTNVRKPRRLSMSFSSSMR

RQREQIHAFESLEVSSDTVTRLQSPDSDEFDASSRPTRGFDRRAQSLDAMEHTPTHVISK

WWRKLPL

>contig33049 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69370.1|) 7e-28

MEESKPDTEKIFDGSHVVCNLCLGYLAQNSLG

>contig33625 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68622.1|) 6e-27

MNFADNIGSKARVIVHLDLDCFYAQVEQRRLNIADGQPVAVQQWGYLLAVNYEARKFGVA

RGDLVDGAKKKCPKIHL

>contig34394 Frame-2F

MVSVYSQSSVTFMVGISQLATNSFVTCTALQQYNSAYMPLKIGMRICHFALLSVAISITN

TLASTVDESAALNEGSNFVTRLRVHSDAPIGTDDEERFFGHLG

>contig34677 Frame-1F

MWIRSGILSSHRLDLSSTNGRTRSTLGNFRVLMSARMVLQAAVAPSAPVSNAGYGHSFIH

GGYGHGLGPIGLTPPSNDQQAAYSDFLPIIPSECLRVRPVQQTDGRCATVGPSSFTSMFR

DMSPYINFHRGTTMVIHLPGQLVESNLFGAIMHDIAL

>contig35292 Frame-0F|Blast-hypothetical protein PITG\_08664 [Phytophthora infestans T30-4](gb|EEY55920.1|) 2e-06 NOT\_ORF

MNY\*IRDSDGNMLSSKKYNWIEGCPSFVCTSCVRTPAEFVLRIPRPQV\*CYTHAD\*KLLR

WVTALLLYCPSSSIEAGLSSPPSLCLRHAAPFFSSYCWGLMWAGVIEDHLFGVDQSTAQD

VILHHGDNGIHS

>contig35418 Frame-1F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 1e-127

MQYTNEDVLGKDLVAEFISEEYKVPVRSVLEKAFEGVETANFEFPLITKAGRRVEILLNA

TPRYNERGEVMGMVGIGQDITERIAQEQEHSRMIDTANAPIFGVDTDGRVNIWNRKAAHI

MQYTNEDVLGKKLVEQFISEEYRVAVRSVLEKAFKGIDTANFEFPLITKAGRRVEILLNA

TPRYNERGEVMGMVGIGQDITERIAQEQEYSRLIDTANAPIFGV

>contig35937 Frame-2R|Blast-unknown protein [Phytophthora infestans](gb|AAY43427.1|) 2e-12

MGVGACVGNYFQKKYYRDLEEVEELRMYLERRENMKKHS

>contig35942 Frame-1F

MILGILGDKSPANYDAMWNAVLTFLQAFPGVWHSSISYSKFVTTAVYPRLFAQIRHGFYG

SGRSSFPTLLPFVSLIPIRVALDPATGCSALYTGILEHCWKYIESKDSRFGESPPIAAYF

ECIFGYFSVFLTHANDTEFIEENAEVLQRNYVKQFESIFVSSLKTALSSLEFPNEKVSFF

AKNLLTLSLRLRSVSMDSAVLNTLKDDFTERIHTWTRSAISLMVAEVSFVPSRVKILTRT

CFDGAQKVSVEDQAAQWLTTSKELYQHCLDQVDKVVGDPVISLANNASTAKLLEAIYDVC

STHPLDLVIDTPSDVHYDNHYRPVLRMLYKWKQSFEVTNISATIRVALKLTQPFFLAAKE

KKKFVLQLFQDCDVQFGDMAEASDIIQYGLRFPITEKGTMLWLSCGSWQRPYESGIVLGD

QFEPELRTLETIWRGKLFDELLINCLKERLDDLDATAFITLVKACLGSLTDLPVVSSDAV

AILCHFVISNNVDDTNAIVVQLLTQLCELFYKLRGKLPRELEAVEDQLYKQLFHLSARGS

YRVEASALWARTVRFSLKTWSLARADKLVDDFAEVINTFLLTDSPQGTVLFNSKQFAAYI

KSYVTLGADQRACSVSQLVAKLDAINLRCNEGCSKSLFYSRVLPGLSEVCEDKQVIDAFL

AFFVSQASDNVEKAVDLIARLVDLDVIHALTSVVFHSDNQIQRGADVVEILERYLLMDNL

YEALKLSSSIFDNALIAAIASCQSKHKREIEDIRNVVLVSKDQRASEMTQSVRLLTPEQH

RRLDELSVTMLSSNSSVAARKRFIMKLNDDNGDWKAKSTQIVALSLFNAIDLEKKECDEA

ISAVNDFFALCGRDVTAKSKAEMFKYIQLVTLGAKKKVKLSGVCSITKLNIIDISTQPFI

IQQLLELLGTSSPGVVEVDEWIDITRYVVALAEYLPRASSNLCEAWKSLVRMVVTHAIAG

KAETAKVAALKIHKRWSNFGDRRICKGDEERIVLGYPNKLATARQAFMDLVSAVYASSVD

VFQELAVHYREAVLSAVLCTLSESAEMKASIATTYVAVTSPFQCFQLVSLWFSVENVLAT

VHSALRSTLSSLHDVAHVKRLVLESFGGIETLASLFNGNRYPLQPVVRVLLYILVSYSGA

FQVCNYDASVIDVNAEDEAATESALAKVLIPKAMRSALRAVYTDKIGESSVRNIHIRSCK

QGLPDIVGKLLLWDLFLQFFPSSGKDSSKDSEGPSAALIASSLSFYIARYGILTNFLNFA

SALLSQDQQLVSKYSAVELQDTALFDISDLVKNEFDETWILQKTSVFQLGARVFFRTVVR

LPAMVRSWWNDQCSRSTRSWAAKYFEDHITPSVLAAELELIQKASESTTVAGTTWNDDEM

TVRGSRVSREITTTYIKDECALEMVVRVPSSYPLRCVEVECTKRIGISEDRWRRWVLQII

RVTSYRDGSLLDAVLLWKHNVDQEFDGVEPCPICYSILNPKNMSLPSLPCKTCNNKYHNS

CLYKWFNQSGKNKCPICQQPFR

>contig36121 Frame-1R|Blast-arginase [Phytophthora infestans T30-4](gb|EEY68395.1|) 1e-177

MRRPSSSFIRYLQQRNISLSSSRQWDQNRPHLHAESRHNAHLSLPQTVSVIGAPMTYGQP

LLGTDGGPNIMREAGLHKTLNNLGWSVEENGNLTFEAPTSSDPILDSRYGKAKQCFPVGN

GLKRLYELFKEKAGEGKFCLVLGGDHTIGTGSLAGVLSVYPDAGVIWVDAHADINTPADS

ESGNMHGMPVAFLMDGMIDSSKVPGFEWLVNGPTMKPEQLVYVGLRDIDMFERRVMREKG

IKAFTMQDVDRFGIGKTMEMALDHLCSKKQRPLHMSYDIDAVDPLVAPSTGTRVRGGLTW

REAHYVAEAVAETNLLVGLDMVEVNPSLAPGDGARITVDMALLLISSALGNRIL

>contig36367 Frame-0F

MANENKANTNHSQFFFTLDACEFLNKKYTIFGKIAGNTIFNLLSVSDLDTDALDRPINPP

KLLSAEVLWNPFEDIIPRTVNLKASSSVEDASRKKKRERKAIKDLKLLSFGDEEEAYREE

TDRKSKSKKAKTMISSHDLLDDRILKSKVDAKVLQRINSSGREAKKEELRNQARLYLKAA

VAAASAASKDVEPADKQIDCAKLLPQLTKPETLDTDFNRTINEQIEYRRLRDELRKSKKA

VPLLLGEEAKQLEKNRASQDMLTPFQQKRQNYLQRKRVSNRTAREQDTLSKLKKFQAALF

DVNSANAFSKENANEIKVEKESYHGQILGDDNDDDDTNHNKSWMTAKLKFKKHID

>contig36420 Frame-1R

MTLTRQQEKKLCVQIVLYKCQNLVDADMDIVDSLSNTFVNFSLSGVTKKSSCIKNSLNPQ

WSPPEVFEFELEEWKNNFLIANVFDKDLLKDNLVGSAVIPLSLYVENRHCEMYSY

>contig36569 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64789.1|) 6e-85

MHPSLPISKPVEIPAEAKRGSPGNKNPAVLSYDPTGTRSAMSTTHEARDKLILQQVSTHN

VRFEWEGDAEKEILDDLDSKNLPPTPGRPYVWDFPSQSRVMRW

>contig37290 Frame-0R

MESGGADGIKSSELEAGLWWRWTHGTSGLTASSSQISSLHDLNHHTCVNTTKIAAKTAPG

SAVRCPKRSSRVLSMDNSANDLTWSRSSDAASLFSVSTATHSSQTKAVCIKKKTMLSSSV

SSRGLLNHSSNQASLKESLSSSPCMPSEREEKHANGSESSWSVTKRPIFHQKKRNAKSSS

SQVTHGRAPRSAGPRTARFLHTTDIKAPNPEASVFAFSDLPLS

>contig38325 Frame-1R

MTTTTFENEFIDRLRTVTISLNEIHSILSIFQNMMPVFEQYFLMHKHCNSDVSKLIQLSC

LSRYEWSRVRYLMVILKPFAEATTKLDDEQYVVSSLIVPSVYTLIEKLRGLPFMHLELNA

SRMTNTLAKTRASDVLEEVPEDIEAFHDLAVKNLAVRFGYLFSYPDACWSIEKRQTFNWL

WCATILDPRTRSFIIKGSLPEQEFWNLIKVEAATIASRKIKDKEHKGDVVDDSIHANKNY

KVNSTDLWDDLQATLASCAQDEMLLSSTKSSDALPSKSLEMEVTFFQDEERLVLRANPLK

WWQNQRLKYPFLAQIARYVLSIPCTEKVAPNPVQYDKGLVKQGLSQIGMAELCELLAASI

NLHTEEKAAQLKLQA

>contig38549 Frame-2R|Blast-putative tyrosine-protein phosphatase OCA1, putative [Phytophthora infestans T30-4](gb|EEY55694.1|) 1e-57

MSYFIPPVNYGMIEEDLYRSGQPNELNFPFLERLNLRTIIYLALEDPNPQFQSFVEEQEI

QLVFLGGNTRMESRRKAWEPLSEETVLAALEIILDRSNHPLYITCHLGRDRTG

>contig38808 Frame-1F

MLPLREYSGKRAVATHRQVNYNPRKVSFLVLGLLFFVYMYFNVRFLATSTNLTNSVEAPG

QEWSFRSTNRGGEEEKTLVDRFATRQVKHLVFTSTCRDLDFVHAEVLAFTLRRTGYDGNI

THLLYGCTDIEASELTRKKNSQHSVQTRCYPEIS

>contig39300 Frame-0F|Blast-hypothetical protein TRIADDRAFT\_5525 [Trichoplax adhaerens]gb|EDV20601.1| hypothetical protein TRIADDRAFT\_5525 [Trichoplax adhaerens](ref|XP\_002117027.1|) 4e-18 NOT\_ORF

MAGVFFQE\*LKRLDADMRAANRNILLLMDDTPLHILDVSHSEC

>contig39959 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61270.1|) 5e-73 NOT\_ORF

MFVKLANLTQTSQLHDWNLESLQRALEWASAAEAVTCCDKTQQKIETSLRRWFPVATIPT

LPVQGILTVDTLSDARIHLLRSILQSPYLASHPTRSELLIAVLQKLQSLREATPSPATDD

VENDQSNRLHSRAIANQTDLILCML\*SALLTEAFLRAEQTVAFLAIIQRMSDKCNHIRVQ

VLSGWVLILPSRSYTLLPRTLQLKAMAKTLQRNAVDARAAVKQEVYSCFIEDLRSCFEAP

ESKDV

>contig40564 Frame-2R

MLQMLLSPRNVKIDSKISNNLMHFASSMEQQSSSPRVPVAYNSTFKVHEKASMSEQGMVK

SNMEQQKVDDTSPFASRMKLKITNTIYDSPERKRGEMFQPLPRAMTSTAESKSFKSRLSA

ANSPLQKEGWFNGYRVTKPCNSPISPVQRNQSNLFRMPRMNESQNLKAALASNIRGVATE

HPKVCIFQYARGDNVMRLSSDRRRWSHLFPESDQNTPRVFKDGEEDFVTLGEPRFRGPNW

QSLTLPAILPLTTDHFPSTQELNQGYTEAFYTLTIPTTATQSPKIDCVPRYRNHNELLLE

IICQRLARDFQLVSTCDSTADLMASDTPLEGRTRVYRLSMGHRIHQLIYDAERQTVEVKR

FVQREPHNPKAAFIIYNYSLWVGLTQSFQPHQQTFHRYPQPEDNWNALDNLLCGYLDDMA

DSMKCRRIRFAIVPPDFSP

>contig41185 Frame-0F

MGVLKYSKNTQELLLQKHYLALEKSRAFLNEILRDYHDLLRHLRSLTTECVTLVDDAFTE

SESGSNEINAIAYPIKLQEWMETVLAMVEHELLRKIRLVAD

>contig41260 Frame-1F|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY69560.1|) 0.0

MVPMLGSLDTMQFPDDEIPEKERVKESLSHYRGVHVSFPLRLDTVKKLINQFRNGILLHR

VFVRHILDESEKLFRTLHRSPMNKIEIPEGVQLVVVGDLHGQLEDLLTIMDKNGVPNSKM

WYLFNGDFVDRGSHGIEVMLLLLIFKLLYPDYVFLNRGNHEERMINEVFGFEDEIYTKYG

TDNDEVAGWNGLGTSINYSPMKLFQMFETVFSLFPIFALLNKRVFIVHGGLSNHENVTIE

ELLQLDHKREIPTQGTSRADEIFTHLLWSDPRDEAGWKPSNRGAGVEFGPDITKDFCSRN

KLSLIIRSHECREEGFDIAHDGLLLTVFSASSYCGSQTNKGAYVQLELGEDNQVKPHVVQ

FSSQPLQKLKDAGRNEWRKKAQRLERRTLMSLVEMICEKKTPLLSAFNEQDVIKSGHVTK

VEWKAILQKVLG

>contig41394 Frame-2F

MTRSRRESRGANFDERWKLTPNKAALLRMQKRPRLVDSSSCDEASGLDGLEGHTIASAAS

IWRDDKVFDVINSDVKLNVTRRYLRAARALYEVQSQLKRPAAILKMKPNLFGMKTCSTFD

ALAALMSPLRAHQVFDDWTGLEIGLFEEAYERFGKDFYAIAEQIPEKGVRDTIEFYYIWK

KRGPHARNREDGNLSDDFLPEPEPDVSSETLKLMDRL

>contig41479 Frame-1F

MNDLKVALLSSSAAEASTHPHVSVVSSPAHRFSRFRDLKGRGSHAYSKWMYPPEGEFRRL

VVPPHSIQATRDRLQISKDHLGEWPSTAICGNDILASVLYSSGIVSAKAGKLTPLAQTLV

AFVLYLFRSIYEEAVTAIPLNGGSYNILLNTTSKRTAAVAATLGIISYLATGVVSGTSAL

RYLDTQVNVSVVPGTIGLLFLFAILSIIGIAESASVALVIFIVHVATLTLLSGFSLLYAV

QNPAIFWQNIKTDFPDVNVAGDVIKGNLLTGIFYGYSSAMLGITGFETSAQFVEEQAPGV

FRKTLRNMWVFATFYNLLLSFLTLAVLPLEGPDGIYSDKDVVLASMGRVAAGKWLESWVS

IDAFVVLAGGVLTSYVGITGLVRRLAFDRVLPAFLTQTNKWRGTNHYIILLFFVLQSSLV

LLLRADASVLAGVFTFAFLGVMALFAFGCILLKLKRDDIPRDVRAPWWSCIFGLVMVLLG

LLGNLLGDPAIFTYFALYFVVFSFTMFVMLERVFILRIVLYIMKQLFPSRSDSCKDNEAA

TSQGSYKKESRTGAKGGRTITAVLQDIHLPQIVFFLKAPDLSVLNKAILYVRKNEQTHNL

LIVYVSEDANLEKDFNAEVTEADVQRRQMEREKVKDMGAMTSMFDITYPKLKIDFVHACG

SAFDASFVHWLSKELHVPPNMMFIRQPSTKHIHRVTALGVRVITS

>contig41602 Frame-2F

MTEGGSSDPVPPLPTSSLSMRGDRSKQPCRELNSLFEIKQLMISAPFPSYEAADKQDAPS

NCPKERRFRRSFASRLLRLVFKQEHVRQAGSWPKRANSTSVPTLSANRSYSSVNIAIPSH

VSSPVPSYSP

>contig41941 Frame-0F|Blast-glycosyl hydrolase, putative [Phytophthora infestans T30-4](gb|EEY61621.1|) 2e-62

MIWPTNYFKMACATMFSLFWGGATCAPTCIVDGMSVQEYLQSHYLNAMAQLALVLKGLSN

VVGFGT

>contig42290 Frame-0R

MRVRLVWVLLLSLATHEAVDANDNPTASTSRASTRDQDAVIQKIRGLRNEGMKLNDAHNF

RGAIEKLRDAIAALHDRVFGEARQTITDASEISQDAALYAQILNDYGSVLIRAKQYDEAI

EVLEDSIAMVQKIYGDSHPSLSLSLRSLAEAYMAKKEYKMAIKRYKTLRKHVKRGLGATH

EAYIEASLKIAEGYKKLHKNEKTLEVLENAVKAQGSEPNGLTTGVAELYMELSTAYVAMN

DIEKALRAAGTANVIFLQRDGKDSLSYAFSLNALAGVKMRQKEVDEAIQLLEQAHRIAVS

IYGEKDAITIASAKTLREVKEHKMDLQTSKDEL

>contig42773 Frame-0F

MSDSGWNDAMATSANAASQFLNSMDPLAACTTQAASPFLPKAMPQDSPKFEDDNGQTVGP

VTMAEMEEHSQSTSDGSNVYNPNLVDKSTKSDKVRRAMLERERQVQRDVDRARENLRKRE

EAVLNMAAMKDTANSVIGPRLKVWAEDNGRVKNIRTLLSTMHQVMWDDCKWTEVNMGKLL

QPNDVKKHYR

>contig42993 Frame-2R|Blast-mRNA cap guanine-N7 methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY68229.1|) 1e-87

MKFYQGLQPPEKEREDQKVHKPDVRIVDEHDREVCCIRFDAATRAKLSGPTIAEEGTFGL

RYNFTLRDRVEEDAEGGGCQAVDLPEYLVPDDLLAKLLREHGFELLLKQNFHRYIQQRKD

QDRNRTLLEKMHVTNIRGSISDAEWEIAGLYQVLAFKKVY

>contig43367 Frame-2F

MYHAFIVVLSTGVVAVLVASSPFHVGSQGRVMWQNNCDLYGNDIKSISGIPDVCGDYCTD

TADCTHWTWTQANGGTCWLKNGQTASTSQSWGANCGYIIGRFSDSNFDSTAKHLMQFIDQ

NVNQEKKENFELLSDKQNYKSGYVKTGPNFSSSWSSYSSFGSVNKSPQTDLTFQLPTVTA

PAPVAPAPVARVDQAPVALAPVPSPFSPPPQKSGLMSSNYGLTEVETSEMLSSINAYRSQ

NGRASLTIDSRLMSAAYVHSQDQASQCKMSHDG

>contig43806 Frame-1F|Blast-small nuclear ribonucleoprotein Sm D3 [Phytophthora infestans T30-4](gb|EEY55559.1|) 4e-47

MSKTAGVPISLLHEGEGRTVTIELRNGEVYRGHLIESEDSMNCQLSDVVLTQRDGQKSKL

EQVYVRGSQIKLVILPDILKNSPLLGKVQTLSKKKEESMKKKSNKMQSRRRAGPGARK

>contig43891 Frame-2F

MASTWTLQLIERRRKRSPVPNPDIISIHSLEAPQRQKLKNFGGMATSLSLAEVRQIAAHL

CGALAFLHDLGLIHADIKPENVVRSNAEAFVGSCASLPLCSSPIKLVDFGNCLTANELEA

YNGKHTSGGFDVQTVTYRAPEVAAGLLLCSAMDMWSLGCLLLECVSGKPLFTTLALAQER

DDFSIVENAHLLVQIEGVVTNKTPLHIVCAPYRSAATNGENAEMADFRAKQVTSTSLQAH

LDAAAPDSDHFHNFIYRLLDVNPATRATAREALFHPFLQAFFPFKTLFDPINDSQKTKEH

KAVTGIARSVFIAGRKHEMKRSRSCESEIRGLQKIKSAAKEASARNVDLRHVLKIIPRDV

SNRTSLSPRKNL

>contig44133 Frame-0F

MTVFSQEKLALSVSRGPKHLSGDGSPFMRIILSERRSSFSFLPVPATVHNLCKLSRNE

>contig44278 Frame-0F|Blast-DNA-directed RNA polymerase III largest subunit [Phytophthora infestans T30-4](gb|EEY54825.1|) 1e-97

MEPGEAVGAVGAQSISEPGTQMTLKTFHFAGVASMNVTLGVPRLKEIINASKVISTPIIT

AALVCKTDERSARIVKGQIEKTTLGEIAVHIKQVFARDQAYLSVKLDLHAIEQLHLNITA

SSVRTSILNAVGIGPRSALRLLKEQHVLLNARCPDKLR

>contig44414 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66719.1|) 1e-39

MRTFFCSNSSRVLDKKAMRLCYIQFLQEMEKQLNAVVLAASSFRNLSLITEQIIAAVYRH

KCLHSRRPQVRQILTGHEFAGWTMFVAQLRDTYINAAPFQLNERIA

>contig45022 Frame-2F

MTLVSSQSEAPGSTTESSATCSLQGTSQATPVVTGVAVLLYEWLRDGWWRNGRKNTTFAM

SYVPAALLKALIIHSGDSLQQRMAALPNGFVSCSSLASDAADVTYPDVYQGYGKPNLTNI

VDFTGNRSDLPSLYFLPNSTENSEGL

>contig45057 Frame-1F

MLFQIRLARQYTMSGELFKLPEPSSFPLQTALLKFEENCQKHDSKHSVKKDRIKFLR

>contig45246 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66368.1|) 0.0

MDPSEVTVLVVEDDEFTRMATIDILKSCRYTVFAVENGQQALNLLVTNHAKFDLVLCDVM

LPVMTGIQLLDEIQKHSATMGHIPIVMTSSNEEMDVVTSCLSKGAKDYLIKPIQVNTAKT

LVRHVWLSRRLERTSNKSMWQDIEVIRTIGKGTHGTVVLARRKMDGAVVAVKRVRISQIS

ENGRKQADNEVILLKSLYHVNIVRFYDHFLADDELNIVMEYSDGGNLRQLVKLRSREKMG

PFPEPVIMSWFAQLVLAVAYIHGKNVLHRDLKAQNIFLTHKNVVKLGDFGISKALAGDDT

ANTACGTPESMSPEICRGEPYGKKSDIWSLGCILYEMIVLRRPFEASTLPEIFTKICKGE

FPPILPSFSRELRLLVQLMLQQDASKRPSIEDICRFPFVQAPIQAFLSEHVAEFQEALEL

EAKLHQPSLYSMGAGNPPVSPVSPSLRRRNYHANGETPTSGFSDSALESGSPHSNRSDVS

SNAGHANNGNLRTSAIASVAIGLATEAMPSSGGRPQQKSHFAKGLADSSEFVEDTIADKL

RAQVTIGDIRVGLFTTYTACTSADELVHILKTKFDKTHEEAATILSDFLSHSVLSVVFAE

NALHPDLGAKDTYLRFQVDELFVPLNMKYVCVDNFQHGPMEICLRVREAIAELHAFKSFP

RGIATGFNQPNHVSASCNSATEYFDAPLSQKYRRFLKLGSKLQKIDVGSLPKHERQPFFI

NIYNAMVLHGLIEFGVPQNIGQYKAFERDVAYTIGGMEFTLGDIKHGILRCNRKPPSNYW

ERQLQAHDPKLQFRLHIRDPRSILVLIDCAEPLPNAKDVTILKPGRTDTDLEEQAEKFCE

RFIEVDERVGEIVLPRVLRIFRDDFGSSEAEMVSWLAQYMNKAPADLVNYRV

>contig45538 Frame-2R

MVCDAASRTVTSEQEMANRGGAWNVPTNQIYSKTTGINPEETAMILASLSKGFSSTGAIA

VSRPSDSDEETMESSDPDDSISHGRQVSVTSGTGRVHRVQEIHFDGPKGSKLDFTDDAGF

SHCFQNESNRVKSLVTKHISIEELRAHFDRPIIDVAKDFGICITLMKKICRRNGIKRWPH

RQIRSLSKSIASMEAAMLSSHGNEREKYRDQISNLRLKRESVIADPNKELLMHSKPSPTT

LMHCDSSNQSVGPSCHLP

>contig45772 Frame-0F|Blast-histone-lysine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY55136.1|) 2e-84

MDIEHLPITMQYRELRRRPFDERMLVRKSSIHGYGLFMKEAVSEGQMIVEYQGQIIDQSV

ADERERRYEEQGVGSCYMFRVDDKTIIDATRCGNLARFINHSCDPKAFARIVAVDGGEKK

IVIFAKRAIAVGDEVTYDYKFPIEDEAIRCDCMAMNCIGRMN

>contig45916 Frame-1F|Blast-Mitochondrial Tricarboxylate Carrier (MTC) Family [Phytophthora infestans T30-4](gb|EEY57963.1|) 3e-20 NOT\_ORF

MPALDKPRFDTSTYRGRWRTFAELVSPKYVKVLLRDST\*QKQLLTHRNRWLFLSSKQIQH

ATKTLDDYRSGKLAPGQVTPAELWNLRQGTSCI

>contig45981 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69160.1|) 3e-10

MEKLTKTKDSASAVKLDTFISFFKQLWRLKQRTRFGNKCKKTQHKCSSSNATRGISANEI

FGKRALRTRDKEHSAFARFLR

>contig46513 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70409.1|) 1e-168

MAANTAEQLAKEKEEGASEFQKQKKVVSDLLFNAENGDLEQLQQTLKSLQVMGVTDVKEA

LVDFKDAHKRTALHFAAAKGRRKVISFILDRAPKCVECVDEEGATPLLYAVKENEYAAIK

LLLAYFSDPNTAMQNGTTALHEAAANGSIRTVKLLVEHKAQLDASTKNGTALHFAVSENR

EKTVAELLRLGAKVDITNAGGVTPLMLACLMNKRAVVKVLLESDANVAVTIEGNLTALHM

AAETGFTEVVREFLNCRLDDTKVIANVVSNAGATPLQLAAGMGHHEIMTLLQPITKGFEN

VDMDTLMAQEKSKLDAFYNQAEKDKHSGATFKTHAPQTAEEKLEAQNQKQLAEIGNENDI

VVPDAVEATEEQKTRATSLKNEGNTA

>contig47064 Frame-0F

MDHQNNNHWVQKHNYRQTAALPPSSPLQLSPVQLCLPYTWEDANKAGNPMLQQNLRSWQL

QLKSRGESSFSQSRSPDSSNGRAVHSDSNSSDRNYRQSNLVPAKVWEAAMEDVAIHGMSL

RNAAKVHGVHFAALHRRLKKRQQYKLNTPCEPDYIPFEDEAGIVRVIHARADMGVLLTFT

ELVDLLKRTALKHRSSLSEDVGIALVRKFQSRVEQSIRHLILDWPTVANNVLYLLRDMSD

SEIAHRDDMAASSNATTNNVPATSSGPRGQCGSESSSGSLSSLSSWAASLPMMQKSKSAQ

ANSIVYSKNPSSASSEETDNSSSS

>contig47266 Frame-1F

MTPPDHSLAQQNGVASSPFDDSVAAAKLPLEQSIPDSPGAEVTPILSSPIVEEMVSPQLE

VTPSPSRSSSGKSASPKTPCPALPQPSLDTTTSTEEIGQISSSVDPPGDGTKLTTPDEYI

STDDVTPAPSTLSGEDTSTVSGKAPCPSLPVAGSSSLPTPAPSSIHDIDETSLSKTGKPP

CPPLPQPSAGSDTLESAG

>contig47536 Frame-1R

MQYDDSVSKLSACFASQEEAVICRSSSILEKVRVLAAFHIIIKCVFLRSAQNLPSGKKPA

RNT

>contig47910 Frame-2F

MLHSQNLFRAKTQLQDFSTMNVLKERQMNPTLNETESGADAEAIGLIICGGGVPGVALDA

ERVELPEFTSIHDGGHRSCNGR

>contig48155 Frame-1R

MRRLSLTKWRLKTLVSSLLLSVSSCDASSRSMRSANPVISSRSYTSCVDLALSSALTSSS

SPLRLLAFRDQFVL

>contig48397 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67848.1|) 1e-24

MGKMVPDLEPSNLSQLVALLGEQGVAWYDAEPKLKPKLKYKEDHEPLKATDELVLTLKQQ

AQQLLEREVTRFET

>contig48403 Frame-1R

MRLLDVFLTSVSAMQRAHEGLYVLFLRPSCEYALRKAFVALPPGQMEILWKQIVEKLKSR

ALRDDNVVSAREVAVTRLVFSIFLQEIHVLPQNRSKVVELVLFTYKRLLSSCVDDLNEVA

VPFTSYQRELFCIFGELLVFDSILDENIRNQTFNLLFAILRGSRFVSVMTQLLNYGSFET

TEKKRKHTKVISYSAGHELCSTGIIKLCLFWLRRAEESGDTVNCGTNLSRKGRENVARLV

LKYVVKWKCWEAVSFHLPELMANASSDECDQTFREILSSYICEAAVGDLNGPATRLLHDA

AFYEIENLRDVAPKSLSIIANQFVHEIQHESVTCMMRPHCFFKLLVEVPSDYLKLKDCSN

LFAAVFSFYEAITAAKYYLRDLKSEVCQTLLSWTHMHLSLIRRNDHKTQSQLTEQLRFGA

RIIFSQLLAG

>contig48780 Frame-0R

MDCESGSWPILGPSCWSRHTTRMFNFISCLPNYISSMENISSCYIYQGPVQNESIRLNNV

FGIDHKYSLYVKWLQKNSWHLHAKK

>contig48829 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66267.1|) 5e-78

MTSRTDEEVYLVENATLSTCEVRIMTDEERKFSIMQRSMDEILYIASMVAQHQIPMDVVN

TILELAGVLIAFQAETWEFCHGRSNMNEKYLQLKLPKIAELKLPPGVDVSECSLLVVDVA

SKDQGWATDRREHNGTYCASSSWCELVLTSTNSIGDSEETDRVVIWPNLRAGSTFRHHRK

YFDKSTKLLTNIKLGDCASIVLRSQYPGWTNSAKYGWLAICFGVKLNDNFLFANIPFPES

AARREESANSSISCCIQ

>contig48894 Frame-0R

MLSRWLCSLLLAQLCGHFAFSQPLHEAPASASIKLSLSSSPYDHQTQDLCTKFALICDFV

VQSCSFKEKNQLWLKNATNLDTNFKCVNNFSLLDQHNATLTKCIEEYSKDDSDRKHQAMV

CQELYSTWHQQNTCNQFHATEAKAATECSGFYSHRPWTQETLPLFCQDAFTMYKTMRHDL

DRFCERTSNSDAFWEGYVNYVASDTCKHYYDMMREANEQECGKSDREECQTKYQWYVDNQ

KVVETECYEIRASKAFYHGFYTWKKQQS

>contig48960 Frame-0F|Blast-isocitrate lyase [Phytophthora infestans T30-4](gb|EEY53375.1|) 0.0

MSASNVRISQIASHLSSHDPRAEENEYMQRIKQTEAFLRSERFQYIKRPYGAADVVKLQG

TIPASNAGVAMSRKLYKMLRELHDAKKTSHTFGALDTIQVTQMAKHLTSVYVSGWQSSST

ASTSNEPGPDVADYPMDTVPNKVDQLFRAQLFHDRKQYEARRRMTAEERIRCPPTDFMRP

IVADADTGHGGLTAVMKLTKMFIERGAAGIHLEDQKPGTKKCGHMGGKVLVSVQEHIQRL

IAARLQADMMGSPLVIVARTDAEAATLLDNNIDARDHPFILGATNCTVESYREATLNGRG

SEWDKRACVMTFPEAVREALKISGPPGALTKWNAQCLELSLPEQQTLAKSLGVKITFDWD

LARTVEGYYRVRGGVEYCIARGRAYGEYADLIWMETAKPGVALARRFAEGVKAKIPHQML

AYNLSPSFNWDAAGLSDKEMETFVTDLARLGFCWMFITLAGFHCDSLGVTRFARDYAKRG

MLAYVEGVQRAERHENVETLKHQGWSGTELVDAMQNTITGGLSSTNTMGHGVTESQF

>contig49174 Frame-1F

MPMQQRPENTRNTSYTRMEDLLQPFEVSRTSMTSRHEVVQPRSKWKWYPCCCSRRH

>contig49493 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58133.1|) 1e-108

MVAEGGLASKLITCMKKMCISYGIFAQLLEEQLLAQAEPYSELSCILEVLAIKVGNEMSH

EYVKNDLNKLLATLCNVLALLCDSKHESVVSEYILQVLFGCLRRICEISSSSRNHEKKGE

IKATKYAATLNPDLLVKHTLACLSRSSSSQTRNEALLFMSSLVDLHPASVLTSLDKILGF

VSADSMRHEDEYSFYVLETIIKAVVPHIVASESKQSAALITPQRFVGLFVAAFDQISKMR

VEPLFRVVVKTLGSNLLPYCAVELLQCASLDKDSDVQRERIQFAHNLCYNFDCVE

>contig49552 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69008.1|) 2e-43

MLLCHSFRSLVRQFGALSVARPLATQMPRFRTTAPVSCAPLLFVSTLAMRTGMCFPQLQA

RAMGYKLKTKSAVKKRFKVNRNGLVKRAQANKRHIATKKTRERIRRLGKPVFVQGKIRKN

ILRMLGKK

>contig49776 Frame-2F|Blast-alpha-soluble NSF attachment protein, putative [Phytophthora infestans T30-4](gb|EEY65730.1|) 1e-147

MSAEAKAKDFLAQGDKALKKTSFFSFGSSSQRNDDASDLFEKAANQFKIAKNWQKAAEAY

EKCARCQTRMNENSCAAQFYQQAADALAKVNLMDAMVHYKTAISMLCDAGRFSNAAKLQK

RIGEIYEQQENKEEALDAYRQAADYFSGENQESSANNMMLKVAQFSAELGKYDAALEIYE

NTAKSSMESNLLKFNAKNHLLNAGICALATKDMVLVQMKWDQFQDIDYTFADSREGKFLQ

AMTQSYEEFNADAFADAVFQFDKISKIEPWKITLLLRIKEGIAGEVDVAQDLT

>contig50037 Frame-0F

MQWNVTPPRLIEVEKPGIWGYDLYTPCSTKDDYDDDTDVSVSYLNDGSDTEDEDEWSCSG

SEAESDGFAFGRVDNVEL

>contig50042-0 Frame-0F0

MRQAGKSDADEFSELDAEQKTGKRWIEACLNPALQLTKILSFLFLQCLGHF

>contig50796 Frame-2R

MVIPTAVVVNSSKHKVMSVKKCSVCRTEAALYTAECSVCHGKTHYNCAIPKLQTAPSTPW

FCEKCLTGQANRIREFLQQTRRVLVERIEETSRKEMQVKATEAAILEDSRAEIEHEALNK

VPLETVGIDEKDLAVMADACDKS

>contig50936 Frame-0F|Blast-CDP-alcohol phosphatidyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64290.1|) 7e-37

MMPAISDKLDTAVETSQVDVLKQRVRHHSTGDRKSTYFGKYVSQEGSENLRTYEYHGADN

SLVYKHVLTPMNNFLVELLPLWVAPNLITLVGLILVAA

>contig51225 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57113.1|) 1e-15

MLTSNGILEALNRYQYPLDGKNIDVIFAKTTENERQILCNFFAQNAFDSLSNDVLPILFE

LPIFAVYTK

>contig51351 Frame-2R

MPQTHRPTEFNQTKWRCSLTLVKISLSSCEWVEHNYMASICRHNEGTL

>contig51449-1 Frame-2R1

MKMNTSSTATTCSRLVVESPSRVKSDWSTRERR

>contig51643 Frame-0R

MGTWLGSEDSSVSGRKAHNQVSSSTSSSSDPRSSIGGAIKSVGAADVSNSTAVHLHRRDD

NLNTLAASFSTYLRPESEPRGSSRVASAHVGGRPRAETDSQMRSSLPPTLSSDVVLDRRL

LHKYEQVNQEIERIVRASQMDFAGAGDAASVKQVKHELRQAKKSSAQ

>contig51908 Frame-2F

MANTTVDEGDAVPRSDSSDTEKKVYKKIQLILQGDFIVEMHCSMRTVIARPYSALLAIVR

PDWDLRMLVLEFKQGELLVLDVDGRDQLVIMLLLVCREAGQHNVVLNSSRFNYCRFYYPH

TADSATDDSNTAGVTMTTFLLRRLSHTGRGEDSYGEKGRSSSVWSFRRRQGGLRASLGNN

DTARSDTSQRGGWFQRRINSNKRATEPSFDMRHSIDSGLFMYEGVSITVAMEELNANLPL

DELMHSGPGQADEVNKSIRLVFEHFIMLVATHRRYGDTTRSEITTTIQALLRLYHHP

>contig52156 Frame-1F

MRIVYATTVCFCPRMPLDVYIVKFPSRTSMMNISSPSSFSASDSIRVALSPTVVASISTA

PDAQTPIRP

>contig52400 Frame-0F|Blast-gag-pol polyprotein [Phaseolus vulgaris](gb|AAR13298.1|) 6e-10 NOT\_ORF

MGTEIEALKDSNTWEVILKPR\*AKLLHVKRVYKVKMLTDGTIERYKAMLLPCGDNKFMIF

IIPTLYQL

>contig52509 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63287.1|) 2e-22

MRVQSAAAASAQALLQNNANCVAHVLQSNYFSRAASPSISASWERAASRPPINVDPYVHT

R

>contig52732 Frame-0F

MYPGQQNLEKIMAASRADTLPPPHDVAQAPPYRKYAQPLKKARLNAERKRRVAPRMRTVR

FTTNVHPTTLVPYLFSERRG

>contig53223 Frame-0F

MASDKRPHLQGKRTRNRRKRAAFRNSNRVSASITPNSDIDGDKQQPQQALVESCSDFSSY

DKIMSQSDTEDELDSGLVIVCCQTLPDFCSVFQPRHEMQSRLVGSKVFTVHIPT

>contig53348 Frame-2F

MDSALAAADALDEAMQVEKARDLERSAALSTALIVSPGTLSTETPRYSAYLSEAIAQQSW

LLTAPLNV

>contig53454 Frame-2F

MLRIEMSSSKLLLYLRSRSEFRIRTICHSLPIDRFWVHDPSNPGADNVHIEKDDPRVVSC

VCYPGSVSAPLPCESWSCVLPHAIIVSIAVRKIHLDDTAPSSAVKQDMAQELA

>contig53616 Frame-0R

MKLNRRLERKRGSRLCDPCARNYMPTDGSGEDTTPPDSSPLLTAMHSDSALIHKEGTPIS

LPRPISVPSAVLVPAPDKAPSLKAIAAVQTVPNHR

>contig53681 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67876.1|) 5e-26

MTHAEAVRYPKLKPTLEKYQQQIANVTVETITDIAIAGFASKIYAVRHSKFENVLFLDAD

SVPVRDPTFLFESQEFQEHGA

>contig53807 Frame-1F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65628.1|) 8e-11

MYVVAIEPDMQCNVYYGAIINPLCAAITINLSGAHGRYH

>contig53872 Frame-0F

MQIWLMLRDFMPFDNSQQRDLRANLFLLIFTEKSNFG

>contig54154 Frame-2F

MDMDMQVQRVTELEGLLHENQIDTPQIRKLQEKNDELWLQLQQWERVYHKEKILAASELK

TQQDELLNELEYLLAVSEDEIIQRQEVIYCSKGNLLAKAN

>contig54381 Frame-2R

MSVGHYVGRGNGHVVHTWRHGLRHASGRDNVRMASERGQYLTARERRRDGHYRQGTRVRR

LRK

>contig54723 Frame-2R

MTTRVFRLMHWRVLQDGSIIVVTAHSKGDHSVKNFEPQIFRVNAWMAGSVLIPNANYTGV

NFTYINTMTLNAPSLQFSMLRMQASLTG

>contig55030 Frame-0F|Blast-MMP37-like protein [Phytophthora infestans T30-4](gb|EEY55529.1|) 4e-21

MSRSTSLKQALNATFPRVAFTLAYGSGVFQQKNHDASASMVDLVFAVDDAQAWHEQNIAR

NP

>contig55319 Frame-0F

MAVHTLPRAYQLDAHLKENPLSYSLCSSNFAHKSVLNIVVSLHGISRVSWETLLSNKNYR

IVFRSSTRVFYLRMYSAEYYPHVGVDQWNSWENWKSF

>contig56093 Frame-0F

MKNLFIPIAAALVALPSFGEATTYACERGVNEKQSFNITNTVTSEKNRMCSAVKGSSENS

IEWTSNYEIVEIDPYHQPSTGVAQYKFESLPLQDVSQVPVSFTYNFFNTSAISSAVIMTM

NTRRGAGGSASFNHLVVLASYNGARTVTS

>contig56574-0 Frame-1R0

MPPFQIVPHDYEWTNSLVFQVQS

>contig57003 Frame-1R|Blast-60S ribosomal protein L8, putative [Phytophthora infestans T30-4](gb|EEY69751.1|) 1e-23

MNPVEHPHGGGNHQHIGHPSTVRRDAPAGKKVGLIAARRTGRLRGIKKIEKDT

>contig57555-0 Frame-1F0

MLFDREYNTKSSGFQSDVTSTMSAGIHIFVCSTQLYFRFKTKEHLRI

>contig58204 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65892.1|) 2e-08

MREKTMEEAPETPGGVTEIPNDGSFLEKMLALQQEKEKIN

>contig58590 Frame-2R

MQQNTLHCVRNGCSRTESFLPAHAACQLVRGVLTAFLLYPHARKQCRQPPLV

>contig59210 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54488.1|) 4e-22

MTDVRRTYGRVAPHKRATDYEDQDATEDLTTQLSAILHALAGRFPTVGYCQGMDYIAAL

>contig59539 Frame-1F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY67640.1|) 5e-11

MEKLMEGETTALVEALTSQDKKLRGSDLVEDVLIGMERPSAR

>contig59584-0 Frame-0F0

MHIHYNDRVVLIYSKFSQRKRQVRQVLTTGMIHPIRVDYEIRCGNAGEVTVAV

>contig06738 Frame-0R

MQAMLGDHAREPPFYLQRSTSLQPHHHDATSHANLPTGAIANLAPGADINSNASVVSRRM

GTSRRAAPSEDRPFSCPVPSCGGRFHRKFTLHEHLKTHTGEQPHQCPVAECGKRFSTSGN

LARHRKLHAMRKISCPAAHCTRVFTSREKLVPHLKVHLARTPHTCDFDGCGKTFSTAGNL

TRHRRTQHRAGPSTRQDEVSTLVSTLPRPKFEFPGRAPPPTGSLPMRGLLWPSHPPVEQH

HPPQQRILESDVQDLFDCLFVENAQAAAAAQANGHHNVAIFRDRLPKLEHPREHRAPYHH

TQAPYLSATYEF

>contig06969 Frame-2F

MVRQSSIMGGIGRLTFEDASQLDAAETIGGYKLTARELELLDRVSRLPFPKKYAWFLERM

SALLRPWEEGRIKLRVKRDHILVESMEQLLGIQPEHIHFPLRIEFIGEAGIDAGGLQREW

FSILFGRLLDDELGLFMTCHRHTQAVAINPNSEDCTADHLLYFRGIGRLLGRALLEGQTM

QARLCLPILKHFLGTPITFSDLQYVDPEVYSSMVWIRENDGVDALELTFCVTELRADDEV

FTIDLIPEGREKPVTDANKLEFLHLKLRYLMLDRYAPQLQALSLGLFEIIPQEALLVFDY

QELELVLCGLPEIDLNDWKNNTVVAPSFSDAPRVVDWFWEILQRFTEDERARFLQFSTGS

SRVPVQGFTRFNKL

>contig08361 Frame-2F

MLRRSKIKVAQDVLGTLRESALLPVELNFSRTEPGKEYFFPRVHFGLVAQKIFKKTFEHT

FFQVSDGYLHLKKSIKVLVSTLFDPIAPETYSVFA

>contig09465 Frame-0F|Blast-double-strand break repair protein, putative [Phytophthora infestans T30-4](gb|EEY59993.1|) 3e-31

MPERKLVLLPDAQLGIALEKFTRKNNSSAIQEFVDNVLHETQHELGSKSSA

>contig09843 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58827.1|) 2e-17

MAPRDNSFSVVHQQPLVQEQYHVYLQPFHRSPHNTFPSHGRVHRLPNMATLLRHHHATQH

RESITSARDFSSNFVRHRTPVLKYLFQCPQFATPMKKPRNGVSHCEVEPIGQDLDCSMGD

RTSTLGIRNQGQSKASRYLREIDRRHILLRIAQGEKQSALAKEYHVSRAAICNLNKHRAE

VLSRKHEHPLAK

>contig10166 Frame-0R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY57969.1|) 3e-23

MSSERFLFKIMVDRMESYRYFLCQLITFLYIPPLFCLVSYKATHK

>contig14221 Frame-1F

MEALAAYASSDDEMAPRRASMLSLPTVNSAPLMNVIDKQEQKNKSAFLVAATKAHLALNL

PIESTLAPFVGPHSADLNKLARSHPLRAGSGKEIVTGIVEPAFLEDYTFDAQYHTYNHTE

TRNVTRMRVKGAPPSAPALPGETVPEHTKPLDTEDVFTKRNAKKRTHQHIGAVKATMGHV

ISDSIWAPCHEKGTFLTDAEKGILTDDQKALRDEHEELKRRKAQALAEINEELEFDRIVE

KKTSHVLPARLKAGQTALPGKSTFLGDHEYDYQGRAWVAAPRTLKPDDGDHQVFVPKKCV

HKWTGHTKGVQAIELFPRYGHLLLSGSMDHSVRIWDVYKERKCQRVYEGHSGAVRGINFN

ANGTQFLSCSYDRFIQLWDTETGQTVQSFTTRRVPYCVEFYPLDNTQFIVGDSNKMVVQF

DTRSGEIVQEYNHHLQAVNSVTFVDDNKRFVSTSDDKKLLVWEWGIPVPIKYISEPSMHA

MPAVTLHPSGNYFAGQSLNNQIDVYTARDKFKMNRKKVFRGHQNAGYACQIGFSPNGQYI

VSGDGEGKLVVWDWKTTKVVKKFRAHDRGPTMGAIWHPLEPSKVVTCGWDGL

>contig15158 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63766.1|) 0.0

MMVEHTTQQKPDPIAININGASHSIKQELNVKHDGSADTIKEEPHLISPPSAYSNALNYT

SGANDLPVKSESEANAMKTKPVPSLPREVLNYAPLLVGKYFIQDKRAVWSGMWGMSEAAF

NPDGMVSTFHMKSQENVAIPICRGSTESVHPAMLGLALARSSKLSNASAGELSPIYLGYE

TNASTFTAMPFDGKYSGSFQIQAVKGKHRTVSETDVGIRFVHDASTPSQYVVSGFGENRF

GLFTLHGFLDKKTNELRLFKVYKPKEPVKRTMPRRARSSRATIPAVKREVKSLPISAPGL

AAITASVDVVKVLTPLAHPTIVAPKSISTPVAENLSPSLVLGRSERKRSIPAHLREDNIL

ELDQAPISMKKCLSVLKGIMANPKSSPFLAPVDPVALGIPDYYQVIKEPMDLGTIRNNLE

SGLYVSPAAFAEHVRLTFQNAMLYNAAHSQVHIYARKLVDDFEKRFKSLNLKFSTKNKLS

DLKLKTERKAEGIHSSKRVRGGKGTKGNSKRQISGEDTGLIMSLKEDIERLKATLEQLQP

SMTKAASSKSAKAAK

>contig15349 Frame-1F

MNFLDLPEPLHWLHSKMLQTWARNDLSPSALAFQMSPNEGTRDHKDFLTFPKLLFKNYLH

LRNPNSITARELEYSAAMLECYGNPFPDYLGKVLPEKASSNIYSAVAADLDVIIDDSVDF

LNQRN

>contig16753 Frame-2F

MRWFALLVLIASTLGVCAEKNASAQSVFKQDALLLYQKTPVSQQFHEFVENASFSAAFSG

CGLCQQTGQCDHAFRGQPGQFCLSMASGAPCCCPLDAQCVANRYECRCRRVVPTYGNNGG

EYHPPHAHSSGMSGIFIFFALMLLCCICCCYLPTRRARQEREQVAYAQPVGPYQYGTNGG

QEQVPYAYPSGPPRYETPSYCEGGGGTNPMAAGALGALGGLGVGAALGSMYGGRDHDNDG

YRGNVGGVSDNTYTFSGDTGGGDFEGSCDDGGTFAGDSY

>contig18085 Frame-2F

MNTSMPSSAPSAWHKRVGRQKQQAHSKLGSWFVSKFTSKGKLLREHDEETAQNLRRRPVG

KLSAVTNQQQANAARREELGNPKPMRQKSYLRLQLQEMKRQSAETLQRVQKRMDGEVVRE

EHELEAKSLSDEDEDGHVIDGPEDVQRESVSSNPASSMGSSTCLRRRSAAEEKQERDDEI

LAHETQRHEYSEEVNRRMSQATQLYAEAISALDYALHPERQSEVGGSSKPLFLGVKTGST

QMPKSEWI

>contig19226 Frame-2R

MLAVILGALLFVICKASGQHPTSSRYRYIPKYFSQRDPSQSPPASYPPHMGLQDGYTWHD

VHAEVAAGRLEGRNVKLLVFLRHGEGIHNVATNKYGMFAWDGYYSKLPEYLDSPLTKTGV

IQAGKASKMLDGEISMGLHLDNVLVSPLERTLHTYSVAYQNQQNIKSTVVELAREILGVS

TCDQRRSISEKRLEYPHLDFSKIKSDADPWWTSDHRETDAEIKIRATKFLNFIFSNTSSQ

SVGVVSHSIFAAALLGVINHPVYKIATAEFLPLLIEAFPPAN

>contig20248 Frame-0F

MERRKASLSPPKCSPETDPDVSLLLDHNLNDSELVILTPPRPCCKHIQTTKRLQEAVMQL

LLWGRRNIAKVFLTYCGIWILFSLCWIRWPIYERQVVPVLKTRLGDTLEVEPFVVSVALV

FPFFLAGLVFYWQQDIAGTITRWEHELKVVEWIRSHLNIGKRFGFDAIDVVFVGGFLLLQ

LNLVVGKLLIDNENGKLAKSGIVVRTARALGMNGLYAILLSVLLVAKQSFLHKVFGLSGE

KAARYHTLCGHFGFLMLVIHGGLYTVVWYMQEKVEQMLFPCISASCSPKQRYGSIRNFCG

AVAMLFFSIVAISSINWARRRFYRYFIVLHWFNAGFVVLTVLHYYAACFWLIPAIILYGM

YCAVSNFGRGKASVVSATAISNKYVALELRRAPTNKSDFLPGQYVYIKI

>contig21607 Frame-1F

MDFKDLYVFVGPPMTRGPPQVSPLPSLPFHPPPSAAPVSSLPPKLPRPPLKAMKQQERLR

PYHRQNPNQRRKGCRPRRDMQAFGCCEG

>contig21852 Frame-2F

MGKRRRAPSDVSDDVQTTQRTVVAENVKEIEASTPHSQQRIVPPGRKRKGFLANSKLTEK

DRRHVRYKERELLLSIKENANDLAKISSDTFDTHTQELDQMYDSVCYPREANLDASNLDE

LNVAVARQSQAPG

>contig23047 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58727.1|) 2e-33

MGKLVSAVSKSRALIQRTLKRTKYKEMHELQLKKLRLKSSPFNIEFHLVDMEGCGLIRRT

KVTGNVLVALADN

>contig23982 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY57646.1|) 0.0

MDAYEQVRIIGKGSFGVVTQIVRKSDRKMLVWKEVNYGAMSEKEKQLIVSEVNILRELRH

PHIVRYLDRVIDKQATRIYIVMEYCEGGDLGQFIKRKKREGSYIEEGFIWHIFTHIFLAL

KECHRHREGNVIRPILHRDIKPGNIFLDSNNNAKLGDFGLAKELSSESRFAQTNVGTPYY

MSPEMVNEMTYDDRSDIWALGCLLYEMATLGPPFDATNQLALAKKINAGKFNRIPSQYSE

GLFQVIRWMLHRQRSRRPRIEDLERVPQLQQRLRAYTAANVPQPGSDQNLQTSYNQKMKE

LLGIEEDLRRQEAALMAREKKLKELEVDYMRREGELKKREQMVEMMTRKLSYNANKDGSP

TTSDDSISSADVNINH

>contig24118 Frame-1F

MLMSQETIKNQVEVTESSLVNVSSSCMKSHESISPRTFPKKNNTGGGTMFTASSKKRTSH

RAAGDTRAAANKVKNSFLQRKIDFVLNKLRLLEEDIVAEPGQVRYSVENDQKEILCQAIR

VMPNRGAFGISDSIPQTPLPTLTPVPAVPLSTVETTARPGPLVRRNVSFGIAIKQPSAEK

QEVISIDSSFSSSDECDECMVGYQGKAYTERKDNIKVMMERNGQGCRAKYRKLNSLIGPC

NEGNEHKAQHPDARMAEAETAHIVHAKA

>contig24275 Frame-0R

MLITPILFTYCMSLYFDASM

>contig25562 Frame-2F|Blast-phospho-2-dehydro-3-deoxyheptonate aldolase [Phytophthora infestans T30-4](gb|EEY69972.1|) 1e-115

MTRNIKGKYYNVGTEFLWIGDRTRQLDHAHVEYFRGIENPIGIKVSSSMAVDDLVPLIRL

LWKNPDANPGKITLITRYGCKKVAEWLPKHIEVVKAAHLNVIWSCDPCHGNTIVADNGYK

TRRFDEIFKELEQTLAIHREAGSILGGVHFELTGENVTECIGGPQGLDEQDLPLRYTSYC

DPRLNYSQSMELAFLLAKNLSTHYDLAPLNENSRNRKRLMEIGDPSKRLRAYHKN

>contig26817 Frame-0F

MVNRGTSASQDGRYFAQEKKLMAKMTFPKCFEQRVDMRKVQREVINQWVTERITQLLGFE

DDIVVSMAINLLEPKVDEKLDPKQLQVALTGFLEKQASTFTEELWQLLLSAQSNATGIPT

AILDKKKMEMQSIAKEKEALKIVLNTKRKEVERQDRQVQEAKEKRPSPSHAEKRRSRSIQ

RRPPRRSPSRQRRSRSPLHRRPRSRRSPWRSFSPRRRSFSPPRRSYTLRHGRSRRKRSRS

PSVKRRPRD

>contig27186 Frame-2R|Blast-cell division protease ftsH [Phytophthora infestans T30-4](gb|EEY63068.1|) 1e-151

MKVPSARRLVTALCVLLLVGRGARKLRLFILSRLTRSRASSALKTIPTPSWRLLSVFLSD

LKTHSLGKVLLAGDHCVVQTKDTATTYKVLMPPRTDLTYLLDALVHSGVEFGSTAPSRVR

QFAPVALVLFPFLYLGLTYKMLSQMFSTDNHSVGKDGCQNVRRPEASPRIFFRDVAGIDD

ARQELEEIVDFLRFPAKYEAIGAKVPKGVLLCGPSGTGKTLLARAVASEAKVAFLFCSAS

DFVEMLVGRGAARVRDLFTQASQSSQCIIFIDEIDALAKSRGGVNSNDEREQTLNQLLTE

MDGFEGKGNGIIVLAATNRPEVLDPALCRPGRFDRHVYVGYPDVHGREAILKVHCRHVR

>contig28657 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63166.1|) 4e-30

MAAKFSMVNTSGLFDSAAHVEASDRMQSAMEELKLKNDHQETTRMKEQKEHERVEKQHAR

RIEEGLAAKAAYEKEDRSYIGHTNNEIASESDDDTRLDELEEDPELE

>contig29315 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65987.1|) 3e-10

MLLVAVFFAAELAPIYLTLDKRLLAMLSVENYEPLLDH

>contig29478 Frame-0F

MFMHSQSFSSTTVCYVGASIFHLKAQQAKRWRLGSAPRKLPRVFDPKTKE

>contig29504 Frame-1F

MAMIFRAKHEAGMVREKSFHSTPTYFVEIFFFFCV

>contig30111 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62051.1|) 2e-95

MMTEDKKPEDELQFISVESDAQTINVSSAAREKPTGTQMSVAHTASDKKTILTSMHKTVT

SAKHPVAAFFHLFFKGLAVLLYLFGSIFISNFVLIFVVCVLLLAFDFWTVKNITGRLLVG

LRWWNKINDDSTSEWVFESHEDMAEIDPLDSRVFWAGLYGAPVLWIMLLIIAILKFNVEW

ALIVMVAVALSGANIIGYTRCKKDAKQKMQLLMSNGAMGALSSSAGSSLLSTLGGLALGG

GLGGLSGAPKRPPQREDV

>contig30322 Frame-2R

MRLGKRVQILLLLFFSNNNSWIAVGGQYQSHKGSEPKRLVYPSATTFTKASYNAKGSQVS

DVDSIESTANDTDEEQEQDEKYYFKLSGATSRLLVPIKASKTQKMRKGKDFAVSQVQNFK

NTLYAYYQDVFTVKSSS

>contig30397 Frame-0F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY54597.1|) 0.0

MENTMAKEGSTVRLGDIDFDELDDYLEQFQQDEVIKEALSQGVDIREYAQQIEQELRAAE

AAAVSQYVMKSADIVELHEEVQECDNLLAKMQEMLLGFQADLGGIGDEIRHLQNESIGMN

VKFKNRRETEEKLQTYLDQVAVSPSFVKSIDEGEVDEAYLHALVTLNGKLRYAALKAPDP

SGPILDLIPSQTVAFNDVKAQLQKLKGRAVAKIREFLLDKMNEIKKPKTNVQMLQQNTLL

PMKYLMTFLVNNAPEVEAEFRDFYAEAMSKTLVNVFKSYYAGLMKFHEEVASHADFIVVD

EQTLKGIFSYRVNLSKRKDTFSVTERENILEFASAPPLILHVAQQERSKLPYEAIYRNVQ

QHLMDSATSEYLFLINFFKPHNQQETSFRSRDLFMRVFAKTLSLCLENLENYLFTCYDAI

GLLLMIRITYAQRLVMEKRSITCLGAYFDHVALLLWPRFKAVFELNLMSVKGANVKKLSP

IDLHPHLVIRRYAEFASSILSLSLHTKHNQLKHGAVDSKISNAQMHENGAKDMVLTNLAI

LCDEILSLLSRLSNQHTTAKDKCIFLINNYDLVLSHFEERRVNTEESSKFEKLLATQRDK

FVEEELMTFHVKLIQFVRQHEQVTLDNGERLSTESNQQVDTSQIEAIVREYAATWKAGIE

KMNGNVMTYFSNFRNGMEILKQVLTQLLLYYTRFVEIVKRSFQQPPSFYSEIVTTQEILN

EIKKYSRSF

>contig30524 Frame-0F

MSRLLSLVLALLSAVTSALVIE

>contig32078 Frame-2F

MTAKKHSVPHTNVSALIADTGYTLKEFTKRIKAQLAYSRVNNKQAAAYKRDASMTV

>contig32481 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54348.1|) 1e-100

MVNGMVREVDRAIGALSTVALGIGLLVLREVYRSVRDNQSKWECWVLEDSGKDTYYQKKY

GMPKLPLFQHQGGCDCGSLRFMVLAPKRVEAFDDSNTFSCKKGRFPFLIIPTSCFEMVGS

SDLSLYESQATSCQHVFCTKCGIHIFQFDHTQPDSIAVNVYCVEDNTFENVKIIFIPKGS

RPLFGRANRVPLSMELPYHRPSQPTRIDTVREDSEEST

>contig33455 Frame-2R

MSDAVKPLQSLLDAFEERLARIEAKLGVPAASARTLPTDVSFTVSEELSHLLEAYDEYVA

QCLPPFIKVANMLGEDTQKLGEVTEKAFAAQRAYLLMASQCKKPAAPNSDHLKDLQGCIK

EINALRDNRSEFAFHQNMVNEGIQALGWLCVEPAPKPFIESYVGGSDFWGNKIRVQHKAT

NPDQIAFVTSFKNLLTELMVYVKAHHTTGVAWNPKGGDVANYTASNSQDSSGGIASVFAG

IKSIDQNGNSTAGLNKVTKDMQTWRKDYKSDRTAPTPAAAASKKPVIQAKVAKPALCVER

NGNWQIEYQTGPEPLTVSSINMKQQVYIFGCDSATILLEGKAKNIVLDSCKKTKLIFDNA

VSSIEIVNCKGVQVQCKGMVPSVAIDKTDGCLVYVSWEGREVQFVTSKSSEMNVAFPQGA

GSDDYVEKPIPEQFVHKIMDDLTISSDVSDLYSH

>contig34313 Frame-1F

MAEYGVLCRYFFQQMLVEGNGARPEVLGSSFLLSSHPTLAEMRCKFPFRGLYHFRLKVVQ

SDASLRYLWKDLIDEEQALPVTEAGEICVKVLQVAPSDERDRAHAIHRNFIDVAEDRQYH

AFFNWQSKLHAEGYSMPQPQHFMHQDVGRVFIEVKKALTSKMKGSTMAQTLQKHSAHMWE

KVAAATGVSGGPSDAPPTAEALAHLAKLIGAMKTPLHPGNHEHVNLLRRLWTSCFDAQPF

RLTSLEWNRLGFQHGDPMREMQFLLPLQSLVFFHEAYRTVALPILNDQSGPEAFAYVLVG

SEITQVLAEILQLRDGGCLGLERPFWRLFEDPMAFYELYCLAFRSFNASWKQNSTTSLDI

NGHINNVANFAQKLLGRGPINIPSLVEQAKQMQNW

>contig34443 Frame-0R

MALHAGWSSALKLCRKTSVEGYFPTIYSESNKLIVTNAKRQFGVRLVPQMFGLLPQTKSL

>contig34810 Frame-2R

MPSRVKKRNLEKKDVPVDDHETLRRSQRKRVCQ

>contig35181 Frame-2R

MNRSASGLGREVGRKMNRSASGREVERIERTVETLNASKPIVIPIAPKGSYRAHKLKLRL

SGHMDGVRAVAFHATEALLVSGSEDCTVKVWNLSSVANGPPTQRAIEVDSIVTMRTHTDS

VLALAVFGSENCECPPGRVGTFASAGRDGTLQLYQLPSPEVDKPEPYTYQEYGDMKIYSR

KDAHSDAIWDLHAHPFSNTLFSAGADGFVRTWGVTSELTLKGNLRCTSKTNTCGTGPSLS

GFLVPTSVHSLLADPKTCVVGYTNGSIAQFDYAAERVIQLVRAVDVDTMGRRGQINKLSV

YPTM

>contig35260 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60556.1|) 1e-87

MAPNLKMLGVTLTLAMITRSVLDTESSFQTGIVRSLYGLSQLFCYAMLLFLYNKSQNNTE

PGVVIVKEDLGFGQTGDRDEKITVAEHDQRAAKKELQRHVLGSAMTLLMHWKWGFFPPLV

IQTVTQPFNLLKAPIVKVTLLGERAWGELRRPWMDQNDMGKSMRSWNETIMSAMGEAPVK

VSKKASKKAAKQRKKNK

>contig35642 Frame-0F

MTLKPTLKACQCTFFLLWGVASLLCIETATVNATAPSTEGHRRLRQLVNPTLNETNYRSE

DRVFPSGVGLKRTAGIPFETRPFKMSKSEADAVIKRIYHHANEHIDIALKNSNILSSNIL

AKKHIERIIAEKVVALKSQPQSLPFGLAFQENVFKDWERRGITIEAAYEKLSLEHEINLG

VGDSVMEVWFSFACHLKKEKYSTQFLLSKLLEHFLFEPFALFNFLVRLHSN

>contig37150 Frame-2R

MAVMAVHPLLRRGAFALLVFIALSALIHPTALAADNSNSANDEPSLSNIDTYDVIAIALV

FAGLTVSSAGGMGGGVFIVPALVLIIGFDLKRATPISNVAILGGAAANAWFNLRKRHPFA

DRPLIDSEIALGMIPVVIGGTVLGALINKLVPEYVLSLLFVVVLATGASRTMKKGIRLHK

KE

>contig37518 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55408.1|) 1e-121

METLPSQINLKHINKKQRVSIRPLPLDQQAIDSFIRDGFVLLREAFAPSTAQQCRDLIWL

RLAVDGITQDSSTWVEKHGIAELYTPADNPLWGDVMTPRLKRAIDQICGQGRWADFGLGW

WMITFPDQCQPPWDAAGKWHVDGASYQHHVDSNESGLLAIFLFSDIGPGEGGTALSVGSH

KQIARILEKNEPRGMKGGAVSYEARKYSRQEVVEVNGLAGDVMLVHPFLLHARSKNLGQK

GVHSVRIMCNPNVRLHQRMNLQRSNGDYSPVEQAIVDALNEAII

>contig37675 Frame-0F

MAMAMGMKSIAGDAHFFEESMNLDRIRKLLDNKLGVAGHSEKLEAMKALLASISKGEDVS

PFFADVVKNVIVASVEVKKLVYMYLVHYADANAQCRELALLSINSFQKDLADPNQLIRAL

ALRVMTSIRVRDIVQIQLIAIRKCAADSSAYVRKCATNAISKVFVLDPEQKDVLAEIIGE

LLNDPSTMVLGSAVQALNEVCPDRLDLLHRPFRKLCHLLADVDEWGQTVMLHVLLRYCRQ

QFQAPVYEKKEVESSKKSKKGFYADEGSGSEDESKPRRNKQAPFMLGKRDALPSVGSVFS

NSFANSIGDELEEDHRLVLRSSIPLLKSRNSAVVLAVATLHYYCGTHSLATSTLIGKSLV

RIMRNQREIQYVVLTVISSMATSRPG

>contig37709 Frame-2F

MENDFYHRTAAIQGFTDRVEVEHKLMRTRMLNAHADVSESLLDALTDLMVQEGGIEMEKI

VCDINVDGNGGGTFTQDDQI

>contig38573 Frame-2F

MQNAENELMELEESRALEVKAIKKVVDSIEQYSNDLIKCDQQVYLNEALLESIHHRRSFI

RSTNMNDRFIPAYRYSTKLMTTSSDQLLLTVLLDKLREMTELVNEWTKMECHYEKMTLSL

KASLTTVGIKRKRVNSFVKLHSKPFAKIEIPPSRRLIERQIENYNVNVKVIRKNRARMRK

TMSGIIKIAREEHLNPEVVQMTDILYQKCRDLKAEEEEMHLRMKEEAMIREKGEKQAGPY

QVAMDNDETRFDESEAKKPCHSFFSSEISNLSSEMALPVKATSMGDMKGISSLLGSEDLH

VHDRESEGDLAEASLAIADIASSVLPEVTKENSSRVDFRDTPLMTAKAPSDVLQSQYSLY

SESEDIDKTGAINQSLVEISNRSWTKRLKF

>contig38739 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65759.1|) 4e-67

MEHLPDGLLAHLFSLLPSRDVLQIACTCQALSPSSPCVQLALERVITRCSRLSSVTSFLQ

ASSTHWPRSPSVLRGAEVLYIKNLLACSTIRSFEDKDLCSPRSVVVSRAWLTAFKKRSQD

FEQYLLQFRQTKRQQRRQNAAKKKDKTMYDRLGIATNSSLIEAGAMIVCAHNVLLPAVQC

VGRNRRT

>contig39646 Frame-1F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY57593.1|) 0.0

MADDDAASVRVAVRIRPLIDREKVERCDECISVLKDENQIVMGKNRAFTYDYVFGQFAQQ

SDIWGCVDPLIRATFEGYNSTIFAYGQTGSGKTYTMGSGSSVHFSPEDYGIIPRVITYMF

DQIKAKKQNNTHYAAKLSIRFLEIYGEEIHDLLMTLEDSSGDSKVSLREAENGEVQVTGA

SEIEVLDSVECMRLLEGGTLCRTTGSTLMNAHSSRSHAIFTVSMVQHIPIGDPHITGQPM

DEGGYETRSSYFNFVDLAGSERQKRTQAEGKRLKEGIDINKGLLALGNVISALGDDKKRG

KVHIPYRDSKLTRMLQDSLGGNSRTLMLTCVSPADVNFEETLNALKYANRARNIQNKPIV

NRDEASAMTIELRRQVQSLQMEVHRLRNPG

>contig40260 Frame-1F

MSSRRSSRSPPQTDVIKSERSPLLPPKNISFNYNSDSAVYHRKEDESGNGSRHFFGADND

GSSSENDEDDDLSDLDRQFSPNSYRQQTSDAFRLIPRANWKKSRFKRGPPKPLPAPGTVS

HTTRRSRIRTINKQLREPPSAPKLRVSAYCTCEQLQLFKLLKWLERVETGQLPGGELHSD

GWTHKMYMGAIHSSCAPAIDHEGGLPYQQKDAFYFATGCAVFWGLTRAEEQAHLVALSSF

SVGPVKQVEVEDMDYTYGDASSICNDAITLRSNRASEKLAISFAMAQSSKLDVFEERVEE

TIRETKHVPQNLAATGSIQYSQSDISKLIGRLFIERSDVNLNSDMLDEPDFFWEDDEYEP

LYKKVMKYLSVDNRVQILNTRLDILRELLDVLSQQLAHQHDTKLEMIVIWLIVAEVAVQV

VWNILIKDILGFFPHSDTSD

>contig40642 Frame-2R

MGGFVLLVLLQSLVLERFVAEIAPQKLLTDRTWFSQVANVPVVVDALACMAVSDPLHPGV

AVEGYELVERLGLLGVCKHQQTPQMQWPVPDRNMVQIIPWTLLSSNVDRRHLTVCPLPGA

AKASQQFSAPPLPLPELVKKDADIRIPPNSPEGPMLEYHYATEEAERIYVNAHYRLKKKF

DA

>contig41443 Frame-1F

MAKPCGSLKKRRRRNDKKHSGTNKDAVVQQSRAVKSQAKAILTMTASSNPNPRNLGPFSD

RQRILVVGDGDFSFSLSLAVYLGWQKCGCYVLRLQSGPKEQIPRCFA

>contig42125 Frame-0F|Blast-inorganic phosphate transporter, putative [Phytophthora infestans T30-4](gb|EEY59876.1|) 7e-16

MNQFLVRGLGFFNDAYDLFVMNIVNVVLTEQYGKDVYTSSMKSW

>contig42583 Frame-2R|Blast-electron transfer flavoprotein-ubiquinone oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY63626.1|) 3e-67

MNEPREAMDYDVLLIGAGPASLAAAIRMKQLSAEKGTDLSVCVVEKGAEVGSHIVSGNVL

EPRALNELLPNWKELGAPLDTPVTKDKFLLLTPKKSLSLPHFLLPREEHNDGNYVISLSK

FVRWMGEQAEAAGVE

>contig42709 Frame-2F|Blast-eukaryotic translation initiation factor 3 subunit, putative [Phytophthora infestans T30-4](gb|EEY59042.1|) 0.0

MGDAASKLVYGSVDHGKTIAANSTMHKLILEAGKKLHIAERCIQPLGKSEQDVNFELEQK

SLGLSPVSAGEAGTSVVNICGAVEAKGIQGSDGRLYVLDLVRITPKDWTFYKKREGALGS

ANENEDVAANEDGLCFKRNDEGYIALLRPELVQLYSLWKQNQLRRSNLKACNSALEKKEA

DEKYDRMANEAGENSGFSKESIDENKQDGEAKSEIAPVLLNPNVFMDYAASTDKEQLEAD

ETAAKDAAEYLQRIVLPAFVADVRRGAIAPADGCALTQLMHSCGINMRYLGRLASLAKKL

EAISGISKYLLELLEVEMISRVAKHILADLLNSNDSIRAAPGMVIVKLLNNILISSSAGM

DKTDSEKALGENALITGLMDATTLWKRIDDEIKARYDYKLTLWGPGRDGFHKGEHGFPAG

RANKPVMLRRLCLRLGLRVASRNYNFSSSSPIRLDDITGVVPVVKSSLPAHPFAQAKQLL

ERGRIDLS

>contig43395 Frame-2F

MASVVTEMVMTRSSTRLLEQPMNTITPSPTKATIHIQLESKSSPLLVNRLAESRSVLTRS

KPSDTRPLPSPVKDSSSTESPSPAKRKTLAASNQRKKIPLSTKELRSKTRRKLTSFANEA

VDKKALSPIKSRKNGRTTVGPSDDLMT

>contig44637 Frame-2F

MVKPIFIRPEMTRLYALVSTMMFSRPPKSESYRSLLASRRCSSKRSKPCAKDASDSCRWL

IGSI

>contig44941 Frame-2F

MIFHGEVQQIPECDDTLCDIAEFFEAFAFARNPRTELDCQLPKKKDKSRIYSSNLIITMS

GDDAGAGASYYVGGYLLLGLVGGSALLALRAKARSYQQRGDGEFASLIT

>contig45111 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58050.1|) 1e-156

MGEIEVFLRNLAALEPDSMLQRSLLTEFQFELCSVEFVSSLEKIDTTGEPIEPKWLTYDL

FRRLNCDGAVEGSTCYQFLHAFRNRVVTIENAVCPGGNESEGIALAAAAAVKDLRNTITS

IEKYILEHLDPQYVDTLSLLDQSVNVTSVVEDCVFHAVEDTISVPLENQVTFLVGTTVNK

EAEKRLARNIERLKCRSQIESGIPEHLQSDEDWGLSCHHLSMIDERTLPMDKIQELLRAA

LEIFKSCGEKNLDWHENSALTADDYLPIHIYVVVKSGLKRPLATKELLGAMIHPSLMLGE

VGYFLTMFEVALQYIADM

>contig45524 Frame-1R

MFSGFGGGGSKHSAPASQEPAQNTLSQPKSNGGGSGVNNYSFDPSGLERAAKAARELENS

RHASEAFKLAKETEHTKQLENQVKIKENEALYKQYEIVRVQKEGEERRKTLEEETRQHQQ

RAQYQDQLKRKQYADQLAAQKYMKEQELKKQEEILARQEASRRKTLDYEAELRQKTELAR

VAAETEGRIKQERLNHDLHLEEDRVRAKEHRETVLEAIKLAGNTVGSGIMTFVGDSEKLT

ATVVSLTALAVGIYTAKVSTNIAGKYVEARMGKPSLVRETSRRSVAQVVANPIPSIKRSL

RLQKATNALEGVVLEPKLDERLRSVALSTFNTKKNRAPFRHLLLHGPPGTGKTLFAKALA

RHSGLEYAILTGGDVSPLGREGVTEIHKLFDWASHSRRGLLLFVDEADAFLQKRSNTVMS

EDMRNALNAFLYRTGEASDKFMIVFASNQPEQFDWAINDRIDEMVEFRLPGFDERVRMLK

QYFENYIRAPKNSRAKKIYVEDIENSDFEDLAGQTDGFSGREISKLVIAFQAAAYGSPTS

IFDKNMMRQVLDHHITAHSQKEAWKNYIAPSQRRDTIKKIIES

>contig45689 Frame-2F

MVSFFYQIMATVVLLSGSSNAENIRNLATTGQVAYQFGLTHGSQAGGVPFSVQPAQNEQI

ATIRLNTGRR

>contig45780 Frame-2R

MYTTALTYNKRSSFYTRHTPLLTASQNEKLRVLASPTSSVGSIGRSKIVTQCRRAGCEND

ARRKGLCMEHGGRHFCKKDGCHKCAHRGGFCISHGGGRRCAVAKCTKSAQSGGICYSHGG

GKRCATEGCTHAARSGGFCIKHGKVQQAIHQHPGQS

>contig46239 Frame-1R

MYTRSSIKCDIWVKMVQHAVQNARNQQPNESLSNTSNGTPRLDV

>contig46455 Frame-1R

MMQHIAVESLDVKAKQPNLIKVISDIDDTLFPGWVDARYPLHVPYPGVSNLFARLSRGLA

RDANGDNLRPSITFLTARPRGWLSVGRYLTLQHLKSLGIPNVTVLNGSVKGLMSIEKIAN

LKLDNFIRFAALFPEFKFIFFGDSGQGDALLASRLLKSCSEQVLSTFIHDVNPNSARAGD

GGLKLEYAS

>contig47078 Frame-2R

MAVDTTETNALRRRFVQGESELTEEAPTPHRVPRPRKGFVELLMSPLSFVVGDGEPEDPQ

VAARRFAHSLMRRYGENVTPHFEHLSFQDAVSTARTASKFLLVFLHSNIHDDADSFCRNE

LCTERMSAYLNNSDCIVSWAGCVQHAEGFNVSLSLGCATFPYLALLSCISRGVSVVEKIT

AKLPVDEIIDTLNAAVDRNNHVLATSRHVRQQQTEAQILREQQDREYQESLAADRRREQE

AREEAEREEQEREQREAEARRLEDEKVREEEDVKAVIALKRARIADGPKVRTPPSNANYN

TAVIKFHLHNGTRLHHIFYAHDTLQTVRDFVDVEFYDRHIPIRNYELATNFPKKVYGPDL

LDVTLAEA

>contig47104 Frame-0R

MKKEVNAMLSRAMHVIAETQKDLNGGGPLASIGSSGHGKLNAMGARGLVFSDVETSRFGL

LHSQSAGETATNPVTLASPTDGTRSQVIMRNLKHRRRGGHKLRTRSQVNATTVLESQGSP

SMNVVSNTRETQSPSTPSLGTSASTRLGTLFYLDSSNPTNSGTNNS

>contig47481 Frame-0F

MYREACELDVKTIDPAMRKALGTIEYGEAYVVRISTGGALGTKRHWVQWSNQ

>contig48310 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53264.1|) 1e-41

MKLLPIRLGTVRTSVKPSVNVSVSHLPAECPSISNASLVRVCRVCTTREARYTCPRCNIP

YCSVGCYAPHGQDCTEQFYENHVRNEMQLSSKAREKDTGKQEKNIQELLKRVQEFHNKHQ

QLTNG

>contig48365 Frame-2R

MYRNLALPVIAVQEHRQSVENQSSHHRLKLLALDN

>contig48479 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58515.1|) 1e-71

MKREVLTKPLEEMTTTYKERVATMLSEGDKLDAMLFLSQKNVAVAFSKFNELYDQMESKD

ESYAMTSAAKREDLWLAEMSYCVYVQKLQQCRVEYVTKMASLFHQYKTMELWRASVIQTA

LDTYIRKQKLTYSEMAGAMSESQAAVQ

>contig49072 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55648.1|) 4e-80

MGRARKRTMAMIRLVKGLSRNGGMRRPSWVSMVERFPPPPIPRQDRDKLPVITFPQDRLA

ALYMKERDGMVDGQTAFEFADEQLTLIEQGIPEEDAYNMLIEKYDQVESHRFLEKFSKMR

GIEFADPAEYDDIEKAWVDAESRAIKEAMRLEHEEEEALRNM

>contig49274 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60002.1|) 1e-31

MSLQPSGYNDQNISEMIGAIAFVHSWHCFGMKLSNDAGYKIGKLSAEERLLR

>contig49883 Frame-1R

MSQAKRVTALGVRIARYSGPHCRGSGSCLIRDATGLARHKIKLHLRWQAPSDVSNAFG

>contig50131 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56934.1|) 4e-83

MTSQGNSKGLDALGQEVLWSSSGQQVMMQWEKRYMETCVEALAIQPTDRVLEIGFGLAYS

GSCIQRFRPRSHTIIECDRETLERTRKFAAKYNGVEVMAGTWQCILPTLDKFDCVFFDDY

PLPELQQKKTSANVTAVPRQQSRWHDFLDVALKHCQDGARISGYLARSLDLERPGCSVKV

SRVQVDVPEHCNYFPYKTALVPVITVMDPLAAARLPIAETGSFHSLPHFFMQFERACQYL

SSSDRAKFSQWRERFCGIRKSLLEHKVDAHLHKDTNVKEECDAIDDDEKSSYYSSEAIRR

EFLRTLRSKAKSSITSA

>contig50881 Frame-0F

MSTYLPFADATPMLRTTGVLTCMPISSISSLTPTSPRHQRSRHKLGFCSR

>contig51055 Frame-0R

MLATILASRKTYRLQRAMRHAVVVTSFYSNSALRCGIRYNCSVSNCNL

>contig51169 Frame-2F|Blast-inactive ubiquitin carboxyl-terminal hydrolase, putative [Phytophthora infestans T30-4](gb|EEY64894.1|) 1e-53

METQDLYDWMELLAAQRSLDHASQQALDLGRIFRLDLSSKETSVYAFRGLVCYYGCHYVG

FFASRSIDDGVERERWFLFDDTRVKLVGTWADVRSRIERGAYQPTLLFYERKSIQLAMLE

EIATEIHTWWAAAVHECKG

>contig51914 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68405.1|) 3e-65

MASIFHGQKFFLTRTLSSNVAFRLRCLIEEHGGIVSSSPAGATELVDYDKLDSRRPDWIS

ADFIDDSVASGILQDPAKYSGVVFSLTSSKAHQNGRVQYSVEDDARLLHFAKLRGWESIK

SVPASTWKLAESNRVTDHSWQSMHEHFRKKLQKKTPAEQRIIMARASEIIRGKSAKFIP

>contig52146 Frame-1F

MSISVSRESISKLMGELVESFPIEGDGRSSISDFGKLLFTEGQSNNNAAKIGQLMSSSLK

ATAATPPASAIHSETMPARTGMKRVFTEIKGVPRQKQHDIMKTKDKAIPKRWTP

>contig52829 Frame-1F|Blast-pre-mRNA-splicing factor ISY1 [Phytophthora infestans T30-4](gb|EEY70156.1|) 2e-27

MARNEEKAQSLLNRWTSMKQDFAGTFKNRRPYLASQCDNLKDAERWRRQIVREISKKVAD

IQN

>contig53606 Frame-1R

MTLEDSALTKRPKLCTRRRNEVDEARNHSFNSPHADRPAKRRRQTSMQIKHIKHEEQEED

EMEEVDEDATEDYVDHV

>contig54856 Frame-2R

MVHVLSIAMPLVVRYRAKRISCIQVTRVD

>contig56472 Frame-0F|Blast-SWI4 1, Peter Pan-like protein suppressor [Phytophthora infestans T30-4](gb|EEY58369.1|) 2e-42

MSFVFKMGKVPNAVSTLVQDVRHVMAPYTADKLREKRKNSLKDFVHVGAPLGITHFIFFT

HTEAGTNLKIARIPRGP

>contig59312 Frame-2F

MAGALDTHYGTKMLATHLIEVEYNNNYFSPNIVPHLKNAIFFHWKQTNSVENFRLKLNFN

TEKQMVSSTIDCGG

>contig02209 Frame-0R

MAVLWYPIWALASTLIVAKRNPMYPTRSGIKPWVDPDTPTSKHVHMTSRGRRWDLVMSDE

FNVANRSFRPGDDHMWTSLDKPDGVNGAMQIYSSNMTSTKCDDDGTCYFYIESIDEVTIL

RVYNMYLHPPAFVDAYFFYRAAMVQSWNKFCYQGGMLEVRTQLPGAVTNRSGNPDLRKGK

NALVQAGGFYPTWPGIWMLGNLGRAIFSASTNRMWPFSYNECAPDKFDPIHQRISACDDN

PGYGLHPNQGRGAPEIDILEGAASLISSSIQLGPGMPDEYRLSGADYDGCFYTSNCQNPG

ANHIDVPSPVMERMRGHKSWYQGLRYAANNRCVPPVSVKQDYASIAASLQSGVKANACSQ

TTCPASNDIHADLSRIDGVREDHWGINSNGTCFPLFNVYLGSYLCDPDNTYFKCAAPRNE

TTTPPSNAMDHFNYQMDAISSNWPVHLEAYVTYLVYQVEWVTGKNGYVRWMLEGEPLFEI

PSSAVLEVPQNVNKSNPQKLMVEEPLYIIMNVALSRTWGSSPPNPGKPCRGDGSDPVVNR

ICDAFPMYMKVDYVRLYQDLANDLDDDNYMYVGCDPETHPTKEWIDGHIDEYEDNNNKAI

EVNGKAFCRTHDDCTIGGLMGRTNIETGRCVNRRCECLYKFWGGPRCTTAVSGTTKSGSS

SYGPPVWASIAVSTLVAGLVTFSIYASSIRASQKEKEATKIAKTKGESSSDPLYLTKNDN

RT

>contig06371 Frame-0R

MLRNGTGQSVELVDCEMRRPNKIAFSPSNHIMYITNSQKGDSYIKSYVLADDGTVTNSSI

FFNFTAHPELETSEGSARGIKVDINGFVYVVCYKGVYVFSPEAELAGAIMSSEILDSVTL

GLGRLFITGSFGIVAHTSGVASQTIPQAQVTCSA

>contig07484 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61679.1|) 2e-14

MPVVAAIVCELLVLDLIIFRATRQSIFRQIAAGVVGLVLGSIGFHVIIVLFGAPILE

>contig15159 Frame-1R

MGTKSLGFVHRVTEFAQGEGLSSIAPVRWGATVGNVHTGAIPPWMVETEDEYKQCNQREQ

AWTVSSTTNIKTDKKQRGVLTGLRSKSEYTSDWLPNFGGVWQEGSRSKTKQAFQKPTTVA

KFSRSHVLTRPTEAPSCNFFQTTQSQAVPPLPSSSFDSFLIPTMTNEESQAPITIPLETI

STQ

>contig15348 Frame-1F

MNFLDLPEPLHWLHSKMLQTWARNDLSPSALAFQMSPNEGTRDHKDFLAFPKLLFKNYLH

LRNPNSITARELEYSAAMLECYGNPFPDYSGKVLPEKASSNIYSAVAADLDVIIDDSVDF

LNQRN

>contig15692 Frame-2F|Blast-eukaryotic initiation factor 4E, putative [Phytophthora infestans T30-4](gb|EEY66427.1|) 3e-76

MSEQRIPVEVEKKVAEENIFAGLSNEATKHPLQNRWVLWYDNPKKRHSTDSWEENLKNVY

TFNTVEDFWCLYNNILVPTKLSIGSNYHLFKEGIRPMWEDPINAKGGKWIFTNPRSRKAR

LDECWLYVMLSLIGETLQDEDDVCGAVVSVRKPQDRI

>contig18084 Frame-2R

MLLNRCRVYFFAGHLCNRAPFASTDNSGRQPTLITVTMGWLGYFTYTTWRGRLQVTK

>contig19902 Frame-0F|Blast-lysophospholipid acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61085.1|) 0.0

MNQLVSWLTNAATPLQFTMINYQLTQLATIVGIPVDQLRCVSCLLAVYPLAIVVRKLPFV

AAKHWLHICAGVSIAQFVYGTGWLHSLFSSLVTYTLVCILPPKHAPFIVFVANMLFVAML

HLHRMRVNYMGWSMDSTASQMLLLIKLTSFAFNYHDGVVPSATTIQDGDSDHTKKVKQSR

KQLAIPEIPSLVEFLGFVYCFTTFVAGPAFEYKEYHDAIYETRLIDNNNVRRQVSPVRAA

LSKLMLGLGLMGLFVQCGNLINLNDILNDQQQSIGTKWGRLFLALFLTRTKYYVAWKLAE

GATVLSGIGFQGFNEQNQPIGWDGVSNVDIVGFELGANVREISRAWNKGTQNWLERYAYT

RTGNSLLATYLVAALWHGFYPGYYLFFLTMPLATSVNRLARRHVRPYMVDSLMKPLYDVV

GVVSTAIIVNYLAVSFVVLSWEDAVAGFRSMHFAGHVGLGLCYLLLTFVPIKKIRVS

>contig20249 Frame-0R

MGAVNSVRKLTIDSIALLEQLEPNATELAAKHAVQRRVQQLLQQEWPTCRVLAFGSSESR

LGFGGCDVDLGIYFEDVHVDAQGQFSPQERVTLLATACERLASAFQVQNFVRNARVPVIK

LWDPERQVACDICVGGINVLLNTALLKYYGQVDLRVRPLVFAVKYWAKQRGINDSLNGTL

SSYGYTLLLIFYLQSHYAEMQFPAILALFQNLQSQTKVSVLLQRLRSFPTMEIPSPFGTS

EFNSVGALLAGFFDFFACRFNMEDEVVSVRTGRALSKTTKWSHPLSWRLSIEDPFELAHD

VGRVIFHRKGQNLIRAEFKRANNLLIREHRLRDICEPDQSSWNNMSSCYICLCRDHITRD

CGQLVIQRLKLGNPGSKARLLFSDCWYCGEYGHYKAECPMLFFRDIPCPLKVTDNILPAE

SATALSSIPLFKFAPPSTPTVPSAPESIPFSIYKERIWERGLIPLDSPMLRLSKKKKRAR

HGATSSLSSPPSFCHLPSNGLSQSEKRQQQCYQQQRQEQRHELHKRNFEMMVLKRKCGGN

ARSGRSHTGK

>contig20555 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55200.1|) 1e-27

MHSNETGWGILRPMTANAATGTVFDTCSRHVMMHFTSSSTRPRIVNDFTDLILNTGDEET

TIAIQNLEKMLLDAALEQIRL

>contig22063 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57790.1|) 1e-09

MMLPTRRRKLLDAALLCNVVLSCSPELATVFQPKTPFLIFNDAVTTICYMIFPFVAFALL

HKTPSDFS

>contig28106 Frame-1R|Blast-nicotinate-nucleotide pyrophosphorylase, putative [Phytophthora infestans T30-4](gb|EEY55072.1|) 1e-149

MVDQTNNFANLLPPSWTKHVQLWLEDDIPSFDVGGFVVGEEHETALLLGKSEGVLAGVPF

FTEVFRSLDCTVEWLLQEGEEVKPSSVLGGKVPVAIVKGKCRQLLLGERTALNIITRASG

IATQARKSVKQARALGWNGHVAGTRKTTPGFRLVEKYALLVAGASTHRHDLSQMVMLKDN

HVWAAGSITKAVQRAKIAAGFSMKIEVECRRIEEAEEAAKAGADIIMLDNFEPEHLKATA

AELKKQFTHLLIEASGGITPTTLSQYLSPDVDIISQGLLTQGYSCLDFSLKIQKSEGVLK

L

>contig28656 Frame-2F

MLLAKGHGEYREISQDEFLKEVTTSPLVAVHFYHRDFDRCKIMDMHLKKLAQNHIECKFL

TLNAEKAPFFVEKLLIRVLPTIVCFQNGLAFPERVIGFDGLKDDDDEMTASDKFPTIALA

RKMVRIGALRENFEIDTE

>contig29505 Frame-0F

MRMLATSSPMHETDHLRLDHSSHVVRIPSVSSDPDKGDDDLDDNIDELDPVDGFPSPPTR

MRPRRRFVKSGVTTYELSFSRRHARRVPNSNDDGSDDFEPDEYHPALPGIPRPSPVVSSL

SSVLTEVMTGKTQALNNIVDTTPPQSNVTYVVEHAPDGTPYVAASDGNKYFENSTIGQIF

LKSKGVKVKAQDSDVNFSQSGGWSSQQQSTRRPDIVDEATTLNEEATLTDVDAKKGSKLR

LGFKGFHISKKKKGAASEVPAGHEKDAAVLNTFNGFSSLDIDKNSTDLSPAATEMNVPHE

PLEQHPMAIRLLDSCGMQSAQQARHALLVDAEMTNPSVFNSSSTSSIKALPRLQPKADLS

QSALPVMNDVNDDDDNLLCRSFQNVRYVDFKRSSLISDEDQEENGHDDEHLNDHEEHRDP

DEHDNYDEQDDVAAQDGRIRVSSSATSVAEFIGGFKGQLSRRSGANGLINRKRAVRHARL

TAAEQKAADFARKIREARNRIPPEFRVELQKKNKWQTATRHVHFNTDVLVREFEFESEDE

DDGYNSPDEIVDAVQLVSKRDAVHAEDVVAVVPMEQLELPVELLQTVGNGFPSPPASDST

DEATENVQDNPLTFSQLKNDMRMSFSDL

>contig29743 Frame-0F

MDGVHRFFDASIFETEKLGSNKIGPVSKDEECFASDRRSVLSLLKRISCGCCRQGIYKRL

PSVTTIEEAIQSESFILPVHVIDSGNVDKGFSDSGGWHPFLRSIRLGLRKMKPYWHKMYI

SSIMQGIR

>contig29930 Frame-0R|Blast-mitochondrial 2-oxoglutarate/malate carrier protein, putative [Phytophthora infestans T30-4](gb|EEY67662.1|) 7e-16

MKSYCHSTFAVYHFLKDEAVRRNDGRPVPTGYNVILGMIGGILGGACGNPADIVISGCKR

TVYTA

>contig30688 Frame-0R|Blast-F-actin-capping protein subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY62586.1|) 1e-66

MHGGTAGVYIVGTTLVVHLCTERINLRNYWGGRWKSRWQVDLATNVRALKGNIQLHVHYF

ENGNLQLQHTKDVDEDVSIQTPGTLGDAILRVMKDAEDAVQRNLEDMYINMSEETFKEMR

RVMPVTQTKMEWSVHAHRTAKDLGRK

>contig31636 Frame-2F

MFYPGSPHSQSIKKHELRNEILQLQKAGYIPVGITNASEDVKKAAAALNLPYVIGTRLQQ

QKEMEAAVGEESSNNETVVSHNADFTNDDKAVPSTSSLTSAKPLSPMVITHSVRSGQQIF

AQNRSLVILGNVNSGAEVMADEDVVVLGALKGRALAGIGGNVHARVLCHSFDAELISIAH

CFTTYDDLDESGSLQQHKPTAISLENHRLHFESSSVGPKS

>contig31940 Frame-2F

MYVFIKSLTSVVLAHPGCGDKLNISNPQNGECEDEVNNLSLYSECECGPLPLSLENIPSS

GILWALHSDSQQFLWEHCTKPQMQWDDFRPLWLGLWIKDVKNLHRIVDRFAKSSYARTKN

AMDVCLLYVALGKKKMLSALANMTQSESNKTLASFLVNDFSENRWSNAAIRNAYSLLSKK

RYDVAAAFFLLCEPPRIQDAIRVIAVRLEDPGLALIIARLAEYQAGDKLKHDFTTSQATI

TPAGNITKQLLKQDIIPIFRQKHDIWLESCALWWLEDFEQAWTVLLPRNQDVDVFVGNKV

TALSQNDLLSSVLQATHFYVNLTSLAIYSQYLYSNINSSLLTWAKEKIHAKQFLNDSESA

TLTKKRLQLVSMADIEHAFSFAAYVCKRNGLSDTALVEMLQARHLVNVHARFEISTVEAG

DLKIDRSIKETRCFAANVSTSPRFASSVKSWRQENKLECTISP

>contig32343 Frame-1F

MDDSPRSNNIWHVDYNATVAKDAAMGWQGMGSVLVFNCVMFLVALAIFQAGARSTRFSLF

RFGASSMLSDRAQKAAHLTLQKWGDLLWRTPIRGTNVELRLGPEGTYYLLYQIYTARFLG

VLSVFAMLVLLPLYLTVGADTIQQVEKAAKAAVEGIESIASGPTQGIISFDILGQNVPIA

SVTRQSNVSAADKDGMDTKWWSFAHATIRVMPQESPYLWVPVLTCYFTTLVFVVYYRRLS

ALATIPTLDTQPTQEPAQRSSSMMSNATSVTTVDPTAGQDDKREVISDEASSPDVIVVPM

AETECAEKEFLTATGVTTKAADLPDTKPSMATRAHLIGMQPSLLSNRSLFVDRGLPKNLR

EQRVLHLLDEVFPGYVEDVSVVLNLAEFHRLQARRRYEEIRLARMKILHKLALNGEKPSW

SIRLLPGTVMIPSLRLLLGHIFCCIRRCFKPVPMEEQIEYQSNEIKSLRDQEKQSLSRIL

HENKGAGRAFVIFKSARLRARFVRRVRNQSITSILARFPDSSQPRLVRYVRELGLTRWHL

EAAPEPDDIDWQSVSFPFAKRTVMVLLVNICILGVLLLFTSPIAVTSAISSSSSYSTGAA

QSLSDLVAQLGDLLQKVSPRMAKLLAQYIPTLILVMINAVLLNVLQIAGRIQPIATDSAK

ERLILRTASVYLIFNTIFVPSLAFMSIDAVLLYLEDDGEVLGMLGTLFLHNSGIFYVDYI

LQRCFLGTALVLLRATEYVKFSWATSRALTPREQVQAVEADPFYTGTQSAMQISTLTIVL

MFSTVVPLILPLGTLYFVMQHGVDKYSLLNVRRRIKGRGSIARTATHATCVSLLLYQGAM

SGFILERGTTSQSAAVLVLLMVTYIVVLWGYVRDKEQQQDMIARGHKYPTPLQSTDMPSE

ATEFPLGLLNVSLQPLDACKLKEGNKDNEPEDLAAAEKEVSAAVLQRSLEMLNDESSALL

INREVEEPKTLDADSVDFVSRTSSTYIHAHELWSTRSWRLWYLASSVACSYLLND

>contig32480 Frame-1R

MMWARMDNHIKYREPSSDDTQSSTSSTSQNFASSDDSTTVTKDQLEFYLKVCRPFVVGKR

FPFYRVRLIISCLSATWNNPRSKIVAFSLMLLIT

>contig32761 Frame-0R

MCHRRILYKHDVGDREQFYSFILSRY

>contig34442 Frame-2F|Blast-tRNA (guanine-N(1)-)-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61696.1|) 1e-49

MNEKEIRSLANQLKHCYAAIKRMSDPFQFVYCNPSEQLEHSLTRFGAENWYIQWRRGAES

VADHFSPKDLVYLSPDSPHVLSTLDRTKIYVIGGIVDKSRKK

>contig34811 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59543.1|) 1e-117

MPYFLEAVLLCALASLHRAVPKKTNAPGLTNSNPFLDSCRAMHVVQNAVNVFAHAEICGF

NLPLRTNVVVLRKATFATRTAQSIIIKCIAWRVEQSVTDKFGALTHLSILFGAANAMKAT

METLLSVFQERVLLKMQLNVNSRRKRGWANPLLAKTYGKKFITRQCISKAEAKLLPFLSH

AVQELHDFLQNQSTVNNINLKVAKADWKCAASVWSEYKHHEVMLSDVKLVAACRSLQEEE

LTTTLLKDWRTALPFDTDDIASDFDDDEEVDELNEESLSEDEDDGFAVKSYASSIREKSA

AGLELNESEQRVIKLHDNEDLGFPTIVVNYKKQKTTRS

>contig34864 Frame-0R

METGTVVLVTHSASGGSFRALLACYSSTFPFKLSFCSLERPYEKLKVALNGQASWTLAAA

KYATFLVEPDASDEVKGVELLVHFKAVAYQKKISRTKSIGWYLGMTSSGLIGDAGKGNGS

LFRMAIVSTQASFVLDASRSVMTRHPLILSDSQRRLFIQNGYLQIRGVVPMHLVNTALRT

INHKLGVAKNLSNGGAEGAVKLAGNTSNSKSILDLFYLSDVGKYVEALVGAGQVVPPVGA

QIALRFPEIGEPQEPLGTEWHTDGMRQGCIHPFTLLVGIALSNVSEPLSGNLTVFPGSHK

LLQNRFTSDGKLNGYDDECIKAESIWGDGTLPDLGTPVQLLASRGDLVLAHPNLAHRGGL

NFSP

>contig35643 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67877.1|) 6e-65

MHLNGYNNTMAVLHWALANYQNLDQIVIGGYSAGSLGAQLWSTYVA

>contig35830 Frame-2F|Blast-prolyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY65796.1|) 1e-148

MELQEVAGTQGFSIKFVYEQKQFDLKNGKYEANPIPRMALCFARHDREVNPLAAKPYIGG

DEGEIIENKVKIVELLSNCDPASKLSLLLDDSLKHQLHASLAVKALCAVAELLSKQKKHT

CIVWGNFRLAQAGDWCPRCNGGSGAVLEDKRGIEVGHVFYLGQKYSKPFCATHNDAKNKS

HPLEMGCYGLGVSRLIAAAVEASHDEYGIVWPTEIAPYKVLVMSIGGKKRDDPVCQAAWN

IAERLASGNVAGLVRDDVLLDDRLRESPGSKLAESELIGYPFRVVLGKRFIKEGLVEVQI

RATMEKKFMKPEELPSFFVGVENFK

>contig36394 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63987.1|) 1e-89

MTDGDVIVPYSSASIRSYSPYTSTFLTERFLEWRWHIRHSGFAEGNKCGHNHSAYASFLE

QLNSKVDTSITVDEQDRGLDASGGPRLPSIDGFDCDNKQEVEFSHEMLCSLQQVLPWRRI

DVTVEPSGVKGKLRLHDWPINKMQPSDCQANEFIDLLCNMVGADHELCPLAVPDGVDQKD

IRTLRRT

>contig37124 Frame-2R

MNQFDAPSEHFLATPTDHVSKPQSPTKGNCNEIDELQMHQETEWDNQFGTKDVLQPIGKF

ATASRRYDEDTVSIRSPIICKATSLKAPSATRSPTCVSALAYNHVATHDQDVLEPSWTIQ

EFQEYLSMLELLQDVCQDGGHTNGEIQLSAGSLGQMERLLLSLLPQRGE

>contig37151 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57882.1|) 9e-37

MILYSSAAATAQFAVFKMITWDWALLLCGVAFAVTSLSQIVILGFVRRTGRQSIIVLCLA

SAVMLGCVTMTYQAIKTTIEDAGDPVTIDICS

>contig37582 Frame-1R

MSLASERTVSSELTTQDLVSELRDVMASSEMPVGAFRTSFTRSLSPPSPRMKTKSWTNSS

SSPVSLSLRQYKIVDCLVMPGQLASNLHESLQDTKKSVGSGHYRPSDLQPLGTTGSTYGD

DEDYASVSSKGDSDEDLSNDTCLFQTHFESFSMEKDRGALLQKRKIFEAKPSQLDSPLLR

FSPSTDKEERDEVRERMAGLVRPRSASAPFQSSQRSTTSSDDILPKASRSDDAAHRVPTA

YHVEEIVREIRASLLRCRWECPSETERVQKLMSISKVMRSLHREGVRSKFRSLQYDDIGY

SKLLQTSPSIIKLLKLAGYVSFKEKLTIRQVKPDYLAMFLRELDQEMNTFGTV

>contig37708 Frame-1R

MEILSMHPPKSQKHWVCSPLQLVFPVASASASTLGTPMVVAMDMDQAWDTTNTTHTTHTT

VVMLPRSATAAIRTQPLLRLPPAICAHKWRDNPSTILVTSNTTFQSRNKCCIL

>contig38068 Frame-1F

MRCYAYVLPPLMMVRIYLHEEIMQMPSPKELPFTIRTGCSFFYHGTVGIANLILLSLSGF

TTIHCCR

>contig38121 Frame-1F

MTRRAKERRVERVHAKLEQHEQRIQRINRLNSRPVWSKLLEDLDRPFTNKISSNVHVSST

ESPKHKPLIVDELQWKSSQVPIAASGGFQLPIKLDAEKGELHYTFSTRNYDVNFGVQMIC

ADGSLIELLSSQRYESQKQLVEGQLSLTGPGMALLLWDNSFSWLNTKQLAYHVELKQEAL

SLSEAEKTQLASQARLERERKLEQTEAVYDGLETQLQTENQTINFLHYQIKELQLQLKQH

EEERELINEKRLVVEDQIEELCWELRALSWRCLDQTSLYRIFDFLSKEDLLAWSLSSKKW

YYHGRAFQGQRVEAT

>contig38815 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58861.1|) 1e-117

MEYYVNATDERKYAIENCPFNPMDGGQCGPVKDGVFPSTCNQYIGANGEPDLGFCIGGTL

LDEDPIAPYPHNYWFSYPNSCPEKLWSNKTEACRKKYAGGMCPFGKEPDGETCTFSYEIL

GYILLDDVVGITLMLNPATGKPYADYSEFCMAGGVEFNVAVKSSVVTFVDGLDFWKKPGD

PKANSERIAKLM

>contig39885 Frame-2F

MTSLLSSAPPSCVAMRSGPSGIAMSSGRTRQLSRRFSKDRQACPT

>contig39962 Frame-1R|Blast-transcription initiation factor TFIID subunit 6, putative [Phytophthora infestans T30-4](gb|EEY66408.1|) 0.0

MSQLRSEMLQVVAQSLGLDDISDEAVRELLPEIEFRVREIVQDALKFQRHSRRPQLDPTH

VNQALQARNLESLYGFSAPGTIKYKPCKDNETLYFAEEEELALSELLNAPLGQIPLQPVL

NIHWLAVDGVQPLIPENESVEDDSTCHTSIKDEAFVNNVDRKPRIKHVLTEEMQLYYTKV

TEAIKSDDFELQRAALTSLAKDPGIHQLLPYFSRFIYEEVKHSNHDLSLLFSLMRACRCL

LVNQSLHVELYLHQLIPAILTCVLGMQLCENPADDHWALRKYAAKLVAQICKRYGEKYPN

IQARVSKTYHKAITDPMCPFTTQFGALHGMLFLGPLVMENLLFPNLERYYRRLEPALLSS

NPNLVERLEAQNCLGILVHASGTYFSMAKSFESTASMSLPPTAMGDTNSLLLDAFGESLL

PYLRP

>contig40180 Frame-0R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY59960.1|) 1e-168

MYQLALLGLMYGGLVGYSQVFVNTFLTQIDKIGHWNVSSVHGAIAFGCIVLPLSCSDLTE

QIYIQLLMSVVRFAALLIMIFSAAFAIYTDPYDSGVPANSSSEAPYISDYSLVDWTGFSV

MFSTSVFSQLFQHSVPGLLAPLGHQNQEKAAGIFSSTLLTTMLFYIALGSICSLYFGPKV

STSVNLNWAEFTWGLNESMELVPLWAKFLSMVVVVFPALDTLSVFPLISVTLGDNMAAIL

PSHWTQGHRSSTWKLLCRFGAAVPPLLISMFVSDLSLTLQISGLLGIYVAFFAPALLQLQ

ARQDMTKSHIYSGMFSGLAYVYGVFMFGTVALLILLYQVMLQILS

>contig40405 Frame-0R

METTNAALLRLLDRKTYNQSDTQSRVLKDKSTRTRQSKPNVTSLFQVIQEGNTEKVKRLW

LSGMEVNVTDALGRTSLHVAVETKQVNMIELLLSAGVKTNVVDSFGRSPMSIALENNHVL

IAEMLRAYQVTATASRMETSHATPSQIAMAFQATKRGEVETLKQFVPAFVPVDVQDYDHR

TLLHVASAEGQWFLVKYLIECGANVNVMDRWGSSPLSDAIDFAHNDVANLLIANQANESG

SRVTIAVDSIDSATLAKALEYTLRVLTR

>contig40579 Frame-1F

MLRDDPCASEAFSELLISLFVDFLRYFVLQFDHFATDGLTLLLLRLVQSTRSFH

>contig40830 Frame-2F|Blast-DNA excision repair protein ERCC-1 [Phytophthora infestans T30-4](gb|EEY61779.1|) 1e-129

MDSSEASASNVGDDKVGAVVRETLPLRSNPDTLNIISVPSLLDSRTQLKPPGSDGIDNDA

APRYLPREDGSAQTSLKFSEAFAQLRKTSSYVAPPLLENTNSVRDASATVYVNRRQRGNP

MLKAVRNVGLEFRDGLIPDYVISEHSCCILFLSVRYHLLHNSYLEERVQSVRKDDPTRYK

SKIVLCFVDVDDNEVALREINRVALFSEFTLVLAWSWLEAARYLETIKAYENKSATIIKE

KVEAEFLPKANDVLTSIRSVNKTDVITLLSTFGTVKGLMNASMEELALCPGLGAKKVRQL

LETFHVPFTKQ

>contig41864 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65173.1|) 1e-80

MTDNDSILLRVAHEHSKQFIAGTLKSPWDYFEYSVKLVLARWTALRMAIEGEWGGGDTRR

KYEILLEEILNVFKYHRTVYADAMSDNITGYVEAEFGLICEDGSVEEIATLLTVLSDECK

NAQYSRVKTMHEQVQSLFSIDLKASKIKVQEEQVGFIEGRAKPLSAISEEPHQSEELSVD

EDGFTTVRRSGRRKMPTKFYDPMAEFPGAA

>contig42090 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY62237.1|) 2e-51

MDTCEIPFSDVKSTKGGRLPGMQLAQLVRLGKIRVSLRDDCPSSLRELIMDCTQLDTEAR

PSSMQVAFTLKSIIAPMLRLSVSTATTSFPDSDPSSDATTFADCQS

>contig42151 Frame-2R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60832.1|) 4e-39 NOT\_ORF

MNLVHETLDLL\*STAMSGTLVESSSVIQKKRVKAGVNVVANPSILFLD\*QMSGLNGGVCV

NCHAWHPVDCPYGTYRTVYDSSAEYCYL

>contig42582 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65169.1|) 0.0

MSAPSRGIISSRGRRRAGSGSNIGTASAASSASSLSSASVPSAPKMLVMDADLSIFFNSV

DQIYTLNQQLLDHLSRHVEDISATSLQTENGERVHKNCESTEFSGVQVHRAGAIFHAYAP

LMQLYTSYASRHSAALTALDSPQFAGFLSELPHEADVNRLRRYLNMPVERIPRYKLLLQE

LLESTPPEHIDFVPLQSAIHSVNRVASKIEDISERRENARIVAAVSAKVGIDLTGRYFVR

DGSLRKVCRSKVHTYYFVLLEDAMVYGRQGGIYKKKFRLIDLWECKVAEDTETMPGFMTT

VVSSNNAFCFYSPLKSFILLTESKEDKNRWTSDICDCIDRNLRGKTHPRRPSVRTELLTD

NEDDSSSGYELEGGFVIKNGWLNVTEGAVESINGGSGTYASPSPTTNSSISKKSRRLWIT

LTLQTVSMGSTFKAAQPEETIPIELCEVASQNNEKCFRLQLLR

>contig42674 Frame-0R

MKGETECYECAPKVTQKQYPICTIRSTPEKMVHCIVWAKECYKLLFGKIEDSMLWEDPNN

EDNNTFIRLCVRAPNMNFDDVKKLEEYACGVFRGLFDLEIKKKLEMKTYKAAAKCPQPLL

LEEIVGSNVVQAISFNDEAEAKKKGDGEIWNARNVWNVSECATRFISCIVRMLKSEHSRA

SLGSYEFDKDDAIAMEFVTAAANLRASVFSIQMESLYCCKGIAGNIIPAIATTNAIVAGF

QVLQAFRILQAAQPVGKACKYTNCNRSWNARGVLLQPSDLEKPNSQCYVCSKHTVELAVD

TNHMLLRDLVEQVLKKKLGVNEPTISIGSNTIYEEGEDAETSLAVNLDKKLVNLPGKGIC

HETTVSIEDFSQEFCCNIRVLHRDEAQFEEDSMELFALGGDIAELVYPKENENKLATLKG

SVRAQKLHEDGDEDFEMVESVNASVHKRRDTD

>contig42708 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63599.1|) 2e-17

MVQARRKQRFPLGTRVSKYFNGFAEPFEGSVDQHSDVTNFYHISYDDGDSE

>contig43394 Frame-2F

MFSIRNFVSRVSLLGVLFMALLSGFGAVNCPYEYMTFFWQKVVDEDIEFLEKRLRHNLDI

VIAKKKRLTLERRASVRRQEDSIASKTTKTFVLLWINRFFTSNDTTYMKSLEADIRTLES

LGRELFLEVNDLRNAQARSFGARTIRGRVLNCFGYVMSAFCMYKMGMSTVNVIFRRNRDK

DPITDVVEKLLYIWPSLAEQLNLRFLSEIASLSFVGILVFTQTRGFLVTLLKFFRTYSNT

VSSNSVVLWLAHLMGMYFVSSFVLMRMNLSPLH

>contig43776 Frame-0F|Blast-isovaleryl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY63767.1|) 9e-37

MAKRVADRAIQTLGGYGYVGEYNVERLWRDSKLLEIGGGTNESHHKNMVQDLARSDL

>contig43963 Frame-2F

MPPKSKLSRSSKAVSKGSSKRAKVLPSTYGEEFALNRIVANVRRATEHAQLPENVVTELF

EQKATVSYLTADCKSWVYHVPRWYWHIFQYATLEQVSFDDKGTSILPTTWSTLFKQAWDA

HPKDYDTIMMFGKPVKLPRFQQLCGDIRSYRYSGKTYQAQKTFPPGLWHAVQHMERIVKD

PATERTRLTGGLVNWY

>contig44683 Frame-2F

MTGNDASSSVRQRNSRGRAKPTSPKALANEAVAKAMTSSKDEQSETKETFHEAAHALGRT

PSWQARAANHVVKKRIYSILAGIIIGILAVTSFQRFYLEKPLISEDSLLMVREMYDNFNW

STLDTRPTILGAVEKRPGLQLFQEENVTAYSPVVLIPGFTSTGLEIWNGSACSKAYFRQR

MWGTSRMLQQFMLNQKCWLQHMMLNRSTGMDP

>contig45110 Frame-1F|Blast-ATP-dependent helicase, putative [Phytophthora infestans T30-4](gb|EEY57215.1|) 2e-67

MLWMDHLYNTVVRPNNVESLVDLAAETTALVLSRHLQLARDVVYTYIVANAGDGIVSLEV

FTKGRPIITDLLKNLCSWNSVTTIPIQVHGALFESIGGVSELLNCVEAQTTSSRQLQPLL

DLLQKYEAHSQQYLQQMCDEVLSKGLANPFRYPIVCQHISTCYLSPTNFVSQ

>contig45323 Frame-0F

MAIPEAMLDNALRILSMCSLQDSLQGTHSVAEINSEAVVGIFFIQFKSIACRTLTKKLLK

LTEELHAKGKKLSVIVVPADQQQFEIVDSLLDQTWLVVPYAEIEARKQLIETFNVTNVPT

L

>contig45396 Frame-2R|Blast-secreted RxLR effector peptide protein, putative [Phytophthora infestans T30-4](gb|EEY70235.1|) 4e-08

MRFILVIFMTAATICASWETISVEKDGEHDKLLVITSTTRYLKEDYGAVSNSRLLRVSVG

SNQSGTMQDEADIGEDSYMDTVYFKLWRLIGKTPGEVYTDSFGTMDPASAAQNPSYNRYI

RYKRYYNNHH

>contig45688 Frame-2F

MFMLKKKRPQVDSAKQMKAIGLELAKIVLVMLSIRAASVQLNRNN

>contig46072 Frame-2R

MTLVFPQLDNFAQSQNSDKFRMLISATLARKYAFIYEFVFDVKNGYKPIHEPSSSSGSSH

ERSRHVVLRHAPDDVRTVLELDVEVKA

>contig46238 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY64219.1|) 1e-08

MWLTQFLEQTDVDDAAANHSAFSHLLARDGRICQLPV

>contig47079 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67399.1|) 1e-171

MARLLKADADGFAFAARQLQLGQLVSFPTETVYGLGANALDPNAIMAIFEAKARPLTDPL

IVHVPTLEDALKLVDMTPTGRQAFECLGKAFWPGPLTLVAKAVPELPLSLSANTGFVGLR

CPKHPIAQALLKEAKIPVAAPSANRFGHVSPTTAKHVMDDLGACKNLSVIDAAGEGSCEI

GIESTVIKIVPEERKVILFRRGGVSEQALKKVLEEHAEMLGVRYELVTIRNEAKMQTNEG

QQAPGQMITHYAPDVDTYLYVTDATKTMNASENENVSGWVVIDFHGKLVRLKNRVRAYLD

LSPTGDVAEASQRIFDSLRWAENVQGVERVIITGVIMEPHEQAAALHDRMFRAASGKQCA

LQLQD

>contig47714 Frame-0R

MNSVVQRKLNHRALNSNASASPHTRCAIDAIYRRRFKCLLEHPILVVLCPHRNSSVGYIQ

QSIK

>contig47761-1 Frame-0R1

MLCIEHKRSASNHHWDHHDLVPEPNSPYAAQSLSSFYLSRALSTRAFISFIMMIQGKINC

GH

>contig48311 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65162.1|) 3e-53

MSSRSDQTLPYDCNLNEPIRVYPPNPSHNGRLSAMLSLQKKNVAVVGILSTSSSSCSSAF

TFANRIIGRYAFKDDDMLSAMTVNDTRLPATIHLYYDDVARCIYLLGVAVPDSLCYNSHG

MIITKAELPSKNSKHKSSVRRQPTIEKEAEDLPELSWAQRIRNVVDNCTREKLKMQVLLY

SSCNMLIVLKESARVTTNALK

>contig48629 Frame-1F

MSEEMCQSQMVLARKITEFELQTPWEMVFANLSTPFHEKDHPVLAQKLHSFWSRHARAVW

ERNFWAPVSRKLNLIEFNKRNNRQLAAKNAFESLIVSAYKELGAVFFFMLDSQEPRHPGW

WYRGPVVALFAFQMNMGEDAMWKYVKNEAFKRFPDCKQPLPLTASNSGAMRIRHERQSAS

MWMNNHHQTAAFLQAIAAHEAKNDARTELMEPP

>contig48812 Frame-1R|Blast-enoyl-CoA hydratase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY66838.1|) 1e-130

MVKAEYENILTEVHGKVAVITLHRPKALNALCSPLIEELNAAAHGFDADKNIGAIIITGS

DKAFAAGADIKEMANKSFVEAYNSNMFANWGDITKVSKPVIAAVNGYALGGGCELAMLCD

FIIAGDSAKFGQPEITLGTIPGCGGTQRLIRAIGKAKAMEMVLTGNMIDAREAQKSGLVA

RVVPSDQLLDEALKTANKIASFSQPVVKMAKEAVNAAHEQTLQEGLKFESRLFWSSFATK

DQKEGMAAFVNKRKAEFKNE

>contig49169 Frame-0F

MIGSPIVSIGSSSQTICRDAPPPLVDASGARRWIVDHIVGHQGRISQVPKSDSVHTKPRA

KRIVFFVWWDIRWLRNIPTWWL

>contig49275 Frame-0F

MRRIDWNGAHETEVIEGEGSIEPDNGCLLVWQGIVARKAFNNFRFQECRTSVTARKVMEA

KNVVHYWDLVEKSTETIAVAL

>contig49882 Frame-0R

MLDSLLTRSANSPRPDVDSPINQTSAKSAAITSGRAKQSQAATRQHSNGLDTDWSIVPDS

KEHLPKAIIYAINFIFDSTPGIETEKFYEVDADATKLKTALNFLNEFANPSVTRKPTKEE

LEKLLDATTAGAIVLLWLKQLKEPLIPYTMYDDFVSSARAAKSTSFDLRKNLRALLGALP

EKNLTMLACLLYHLNDVNVYSSKNKMDAAKLALHFTEYIIRPQEISPQDDNSKSDGELVR

HLVEELITNVDTFIDEKEAQLLEDNCLL

>contig51054 Frame-2F

MLLVSRHIQISKMLRRSTLARRALSIHATRLPYSVQAARIFETNTWQYRVSSSPKWQTWA

IALAAAGAALTAAGSADTA

>contig51472 Frame-1F|Blast-peroxisomal 2,4-dienoyl-CoA reductase, putative [Phytophthora infestans T30-4](gb|EEY64424.1|) 2e-82

MDSASIAQVFRRGACAGRVALVTGGGSGIGQEIALKLAEYGAKVAIFGRRASTLQSTVVI

MRERGVADEACMFVQGDVRSTERAEEAVKQVVNRFGKLDVLVNCAAGNFLALAEKLSTNA

FRTVMEIDAIGTFNMSRAAFESLKRSGDGRVINITATLQRPATWYQVHASAAKAAVDSIT

RSLALEWG

>contig51638 Frame-1F

MIHDLTHCPSLTDEKYNNQCENAARLHLKELTELAPLLSFVSLYLKNDPEFIPFLTRSIK

RSMTKIYTYAVSAQHSTKDQLFQQVITSLDAICKALKEISLAAASLDIKIMDSLTLEQIR

LHRMTVILSARSNLEISTKRIESLMPMISRHVAAVQKLLDNATQGVKFCKSLLLEVLADL

NYIARECYSFAAYCYK

>contig52532 Frame-2R

MRIRAFFVHVPGTRAKIGVHDHGLWLLATMHCVMHVTDLAQYKITFVIHTEHIRVRKNAW

WPPIGLTFRHGSIE

>contig54857 Frame-0F|Blast-phosphatidylinositol kinase [Phytophthora infestans T30-4](gb|EEY59985.1|) 2e-50

MRTSSNIEEAAPDAAVAHFNPLVLLQSLLSADLVSIKQRIKAAQQLEEYFRLLPGTPGLL

LSYEPYLPLLMDVMVSPLQGSHELQSSVIAMLQTLSTHNPTGFGDWIARNLHQGNEPWLV

QWSYALLLQTEKMVP

>contig55322 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66899.1|) 9e-16

MADSDASSGSSSSSSSDSVLIRVPLDQNRRQKLRAQLQEDQRRQLERQLSAA

>contig56851 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59940.1|) 5e-49

MASRGWEGNADLAPRDTSTASAFGPSSSTQNAGDGAAISKAPGTKQKKRRNLLRESHLVS

AEGFKKVHRTFPYQVSADVSGREAQALASLIRMYKQWAYDLYPGLNFEDFVERTEMLSKG

HQVQGLMTELREKERL

>contig57229 Frame-1F

MDHAIVDAAKAWNELNRSVKTFDTWSSRSNAMHWIATRSSWLAHKNRSAFGNPASAIDDL

CFGSPACASAGENGTALTCCSTLPGCCPSALGCCPLEDPALLPNNACL

>contig57711-1 Frame-1R1

MSRSETSAKAITIGKRTTFLSTTILYGHTSKRN

>contig06307 Frame-2R|Blast-cysteine protease family C15, putative [Phytophthora infestans T30-4](gb|EEY68028.1|) 5e-38

MTNNSQLAVPPVNANTEAAKNSTQKRDVYLTGFGKFGDILENPTTSLAKKLAEHPKVTES

HVLEVSKTGSAEVLKKLHARAEEGGRLCILLHFGVSANSRTLKLEQVGYNVADFRVPDER

GYVAKDEIIREGEPDKIYTNVPLDDLQKMLQPICSHISISTDPGRYICNYVYFRSLVWII

HRKAMGFPEPLALFVHVPKFSCMSFEDQVAVASKIVDIVAEM

>contig10164 Frame-2F|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY57969.1|) 2e-06

MTFSTPPFIHLGIDARTGKSYHVCSHK

>contig14050 Frame-2R

MTKKNVIETGSNAISEESRTKTSCVDSLKLTKKSEAKASSDNFRKLLLIVSLAVVATAVG

FTKYANVSLQLDGFHSLKDRFLGLVDSNPEMVLDKYKTELTVIQVRHLVSDLQCSDLDYA

PKTLYDGKVISVLQAMEAKEPMGSDRVFFMLNGANEGVYVSWNGNFECMGQAAEFAAAWL

GADRDVMANGVRLYNQLGWPVRNAKELLEAKQRVHILLDFQLWQWPGITKGHTYVLENGV

TLTTLGISPKVFDVAFFFNQEEADKIIEIGLPQLNRSKVDSSNSSSIVSETRTSHTSFLP

DSLFTRDFRKRSALVARLPSPSYTERMQLVRYGAGEFYRQHFDTFHSRDFVPKKKNPFVY

DDYVVWTTWAADKLRSLDQEKVPEMFQEGGPLFPDANDTKIFPSALLGLFCDYMNKTNRF

QALYDPLQEEWIRTSLNNGTENIMEELMEETRRPTYLPQIIQTWEAKLGLGELHYTIPKF

DMNAISLFFYWVRWAKERVEYLGDKVPAIARRGGTLYPKFTIAFQETLLGFILDDYSQGF

IVRLTNVEWYDWMVFNRGRNNVLSKVLQVWPQFAELVIRTWETRVGIVPELRFSLPRYVQ

HFQPQRLVTLFLYLNNQTKAGGETVFPFSVDRFSNETIKRDGMTECSRGLAVPPIALHAS

LFYVQTPEGIPDTMSRHGGCPPQEGVKWGANSFMWDSDAEEGANLWTTK

>contig14955 Frame-2F

MVQLIYPIILTVALLIRSSDQRAPTPGTLYGDFEGGSTNFWIGEDAPNKKTISGIRIYSG

ERINQVGLFFNKKATPEMSGGKGGKSTDLILEDGEFIKSVQVSPIKLPSQGRFRISYIKF

VTNKGRFLEGGKKTQSGRILAGGTDGPHHGQKLVGFAGRRGAEVDAFYAIWGNVY

>contig16319 Frame-1R

MSLNRVKGGIASPDDFPMKLLSHYI

>contig18087 Frame-0F

MSGYESGASLPSRAVPDFGNYSQLETPRNSSRLFALSPHHVVDVPNRTQSFSAADIYKAN

AQKERNTDLQRGSNTPLPDHRSRFLSDSELLLAADPMHTRESFATLNEKDAKTWHQRSTE

IILKMLNTNLERGLNGMDVERRILRYGLNALEEEAKTPVSVIFLLQFYNLIIAMLLFAAL

ASLALQEWVEGIAILVIITLNAAVATYQEYSASNALAALASLSSPQSLIIRDGMQQVVDS

KFLVPGDIVILVTGDVVPADIRLITSVDLKCNEMLLTGESEDVAKRFNAQICSSKGGKSA

KLTANNMVFSSTTITTGNARGIVVETGMNTRVGSIAALLQAKSGKGAKAERKWIRNPLED

CIAKHQPRLTPLQHALHHMGYVMGLIAVAVSLLVFLVGMIRGTKDPRHPNQPTFLTMIMT

AVSVAVSAVPEGLPMVVTICLSSGTADMVKKNVLVRKLASVETLGAASVICTDKTGTLTE

GKMTAVKLWGDFCEYTITGKGFAPNGVIISPDGTNQADLTAGNVQVRATLMASVLCSNTQ

LKQVEGDDGEARWIPFGNSSEAPLVVAAAKAGIWEDNLMRDYPRIVEVPFSSSRKMMITV

NAMPVVNGAAMFDTLTFSGDRPPSLVASVKGAPNYILRNCTTYCQKDGTLTSLTSVQRDE

MLKAVDALSSQALRVLAVAIQPLNQLPFSKDCDDVDEKFKALSTPLIFLGLVASIDPERD

GVREAIATARAASIRTVMITGDYLATAVAIAKNIDLLQLGADFDAQATDCTQLRPHGDVY

LPPAEIDEITSRTLVFARAKPEDKIEIVKSLQRQGLIAAMTGDGVNDAPALKEADIGVAM

GISGTEVAKGASDMILTDDNFCSIVSAVEKGRVIYANIQKFVMFLLSTNIGEILLIFISV

AGGFPLPLEALHILLLNLFTDGMPAVALSLEKGDPNIMAEKPRNKKSSLIQGRLWLLVLF

NAILLLVGAMITFLLGLYWNFGEVLTKDIYNAGGGSTGTDYTDVTCQRWEGISDGWRVYG

NCAAQNKDDSFIFGEEVAGMNLFENSTVHCEGGDFVCVPTGLGRAQTMVFLGLAFTEVLR

AYTVRHFTEPVYVRMFSNGYMQLAACMSVLLTVLVSTVPVIMDDIFGFEYIPWFQWLVIG

AVAVSNAFWGEVLKAILRRNDRIQARWDHLKSGFENILLEIRHVRHHVERLEAESLKRE

>contig19901 Frame-1F

MRLLNIALATVAVATAGPGFSVSADSQTLSSFQTGVATVDRARRILLSSRSEEGTYLVSQ

PSSIPDEERFWGSKKKHKKHKKHKHHEESGSQSSSLDSSDAPDSSDAPDSSDSSELRVKN

EERQF

>contig22060 Frame-1F

MQQVKKTRMSSATGCSINTAASWKEHILDPIPVAAEDVGDAVTCLLHTILFTRAPGPVRP

SEATCQAFPNITYALCAVGDVSRKVDHSVRSFEELVVLGGSNFVMGVSSGMIPAYGQTPL

TSSKVRGATSGYMVVTFFERKVKKALFGLMSNEEKTIFEKWVIPVTVTSSPAASQ

>contig22536 Frame-0F|Blast-ATP-binding Cassette (ABC) superfamily [Phytophthora infestans T30-4](gb|EEY54021.1|) 0.0

MAQGPLAMHEHVSFRMERALGRALPQMEVRFKDISISADITVKDEDDIKVELPTLPNVIM

KGIRGLGAKKHTVKKQILKNVSGIFKPGTITLVLGQPGSGKSSLMKLLSGRFPTQENVTI

EGEVTYNGAPANQLIRRLPQFVSYVTQKDKHYPSLTVKETLEFAHACCGGGLPEREAQHF

SNGTSEENQAALDAARAMYKHYPDIVIQQLGLDNCQNTVVGDAMTRGVSGGERKRVTTGE

MAFGNKYIMMMDEISTGLDSAATFDIITTQRSIAKKFRKTIVISLLQPSPEVFQLFDDIV

ILNEGHIMYHGPQADALAYFESLGFKCPPRRDVADFLLDLGTDKQSQYEVSTMPSSSIPR

SASQYADVFTRSQTYGQMMDELHSPVDEKLIEDRVKHIDSIPEFHLNFWQSTLGVVRRQI

TLTKRDTGFLVGRSIMVILMGLLYSSVFYQFDETNAQLVMGLIFNAVMFVSLGQQAQIPM

FMAARAVFYKQRRSNFFRTSSFVLSNSVSQIPLGLAECLVFGTMLYWMCGYVSTVEAFLL

FEVMLFVTNLAMSAWFFFLSCVSPDLNVANPISLVSILFFILYAGFVITEEQIPSFLIWL

YWINPFAWSIRALAVNQYTDSSFDTCVYNGIDYCADYGMNMGDYSLSTFNVPTEKFWLWY

GIVFMGAAYFCFMFLSFIVLEYHRYESPENVTLDSDDRGNTSDSYGLVQTPRSTPINGDA

VVSVTPDSQKNFIPVTLAFKDLWYTVPNPSNPNETIDLLKGISGYALPGTITALMGSSGA

GKTTLMDVIAGRKTGGKIGGQILLNGYPATDLAIRRSTGYCEQMDIHSDSATFREALTFS

AFLRQGADVSDNNKYDSVNECLDLLDLHPIANQIIRGSSVEQMKRLTIGVELAAQPSVLF

LDEPTSGLDARSAKLIMDGVRKVANTGRTVVCTIHQPSTEVFNIFDNLLLLKRGGETVFN

GELGKKASAMIAYFESIDGTAKLEDDYNPATWMLEVIGAGVGNSNGDKTDFVKVFQSSRN

YEVVLSNLNREGVTSPSKEFAELIYGDKRAATEMTQAKFLLQRFFRMYWRTASYNLTRFI

LYLILGLVFGITYINAEYTSFAGINSGMGMLFCSTAFIGFISFSSVMPTASEDRLAFYRE

RASQTYNTLWYFVAATVVEIPYVFFATMLFVGPYFPMVGFTGAATFFAYWFHLSLFNLWQ

AYFGQMLSYLMPTVEVATIFGVLLQLIFFLFGGFNPPGSSIPSGYKWLYHITPHNYALAL

SAALVFGDCPNDGDGSDTGCQIVSGTPPQLSANQTVKDYISDNFLINHSEIYKNFGIMCA

FIVGFRILAVLSLRFVNHQKK

>contig22785 Frame-1R

MIASCRIYRRAPCVAVLHMAPLRRRADPSGGPFCEFLHLNSKHLLVSASSHSLKPLVGPS

TSVCSFSASWVCNTSHALRLELTGTISESGEQLARLSKVVTFCRFRLSIRIPRISPPLPT

LSCTNVRHAVLISEFARRLGHVPTSVQPLNVVFINGLDDVVSG

>contig24202 Frame-2F

MLTTNAKEPKTSPLTRFISKLACIYYLERTLFPSTSASGIAFVRQFASASASSCRRAPTF

VIKTNLAQAASKKNKLKG

>contig24493 Frame-2F

MGNANPFWSARISLGEGLPDGYCSEMGIRYVR

>contig25678-0 Frame-2F0

MGGIEGESSGVVIEADSGVNKALVTRVCVGNGLFNHVLGRTLGAIVSSMGVVKGMG

>contig25678-1 Frame-2R1

MPFTTPMEETMAPSVRPKTWLNKPLPTQTLVTSALLTPESASMTTPLLSPSIPPIQTPTG

ASLPDTMAPTPVPVLVDTQAPTTIALPTMAPTTVVLPTNSSP

>contig27401 Frame-2F

MQIEATNETFRRRSPELAAFCDDHELMLKRIAFAGIIYRDKLTSGPTGEVWRGEYEGRHV

AIKCTVAAAVAVAHRGSFGMIAPVATSDFEIKTLVAFTKEIRMAARLDHVNIVGFIGFSW

RTLPDLCIVSEYIALGDLAHFVAQPESNYLTWKEDKLAIAADVANALVYLHSLSPSRIHC

NLTSRT

>contig28105 Frame-2F

MSPVIKRKFCTVCMCPLIGHFIHQQTLPPGWDNRKFYLKWVNLFCPNVNI

>contig29740 Frame-0F

MQALEEQAQFDDDRLQWDACASHKDCETCLNASVACHFCKRDFQCHAIGSPFGCPIGVSV

CHHLEDCERTKPQHVGYGPPPSVVIAVLCLIVTLTCCICGISAICTFFFRAKKSKSFRSN

NGVAVKADKWMKKQAII

>contig30038 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY65916.1|) 1e-110

MYLIVADFALQSCIINQLPRPKSIRKTKYQRNRELVMKSARSSALSSQQAPIELYSNDSC

SWMMTDSPHDDFSIPMVYEGRKMRYVYDDYIEGGALRSGKSPELFSRSYAGLLAQYAAVG

FIDGVLPNVIYPYLQSYLNLPGEQTATALMLVQMPWSFKVFCGIISDCFPIWGYRRRPYI

LFGWIFALCMLVALSFTPESGPYFTNSKYRDVKPVDYTPEIIATINYDAANQGGKHIVLM

MGCTFGYLMSDVCADGIVVEVAQREPYEVRGNTQTVILHHAHSFQSTGLRSFGFKF

>contig31680 Frame-1R

MPSCAVSTQTFLFSMPSETNIWNPKRHFCK

>contig31943 Frame-2R

MHDVQADGSWKCGKCGTLNRHASKCSHCHLVFYSLVTTTAPAEIFCSRCGFLNDGDNLSC

VQCDNTIRSTLDKISTDLKDSTNFLARDMGVNIHVKCPGCFIVCYVPPATACLRCGACHT

YFASPSVGEVTNFHMSRLASSISSSFLGFFGKKRGEQKESNATKRCPDEAQEAPLGKLIA

TGQGVVSSPRDSLNSSDSMELSTGSQLLNSSEMSDEEKEDRADSSHIDERPAEPKTPLTA

ESVNFVSLTQQALAREDHASFLHTDPLQTREKNRNIASFNSSNGFQKSLPMLARQIPMQT

ALPLPRQELIEVEGDILEL

>contig32340 Frame-0R

MKTKIALQVAQSTQEQDDNADETSSFYRGITWLLSALDSNLGGPGSGAMSPTKCLSRELE

HPQTSVDFEWNADDLLIEQQCLSIDDSTTTKEGKWIREMLQPYRIEFLLQDVSNLPPRAL

REVIQALQDEILSVLRGLDDEAVRSDRKRSKLLLSQGGSVFLAHLLSQVVATSPSLYTTC

ENKDYGIRALLNAHYCQLVTYVRPVLLATTPSPSNLTYDKACFLMYKSIHGLFAWVLRAP

SDANGYLLITFLTTLMEKSDNDDVLSPFLTPILCGLNRYVASKAPTWVQYTHKEWLLLCH

LIQSSVNRSYAASHGFRLLERFVTTQIWTTDGHAMYLRDCFTIMMRFAMKSREPHDAWTV

SRPLELLVLMFDSLGRDTMEFRNERLRFLGGMALVSRRLLGPSMDSIVATELKSVAIDGF

QHMLRAHAG

>contig32483 Frame-1R

MKLPLPLFFKHYRTVDVPFILKDLTLYIKHGRYYLGG

>contig32762 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66796.1|) 1e-100

MKLFVPLFASSAMLAAQVSANGVCYDPDHSAISGGMTAASVIEDIKMIKSHGFTSVRTYI

SKFGDTNLGLLLSNCNLTVALGVPYPHDDYEEQLDAAITAANNGDVSYIFLGNENLASAT

SVPEEMISIIEQTKLLVPDTVKVGTVQRNTEFLQNSAISGWSDLVCASDVLGVNIHPYFL

PETIAQNAIDVVKNQWAAMEDEDFSDKLMITEVGWPSSGTLSNCVGSLAGLQTFYDDYMS

WSSSMDESFYFQMFDTPYKTSLYEKSFGLLTSDALSKINFNPASQSGP

>contig35217 Frame-1F

MQGTGLGNRKIMPQNVETGEDRRPEDSDGLVQLAVKDLFDEMARRPDVEYFMRVSYLEVY

NETVKDLLASGSAATGRRRGSIVHIREHPVTGVFTDNSERVVTDARGVLQALRDGEKQRA

VGV

>contig35288 Frame-0F

MLGVTPTTAEEKLPPATAGWKIYATLFKFAWTAALWEKKCRPLDWERVTRHATLPCAVSK

FSVYP

>contig35406 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61504.1|) 1e-171

MLAVFRSMRMVHEEPDDLAVSYYLSTLELIARDSFGPASFFDLNGDVSGLLLPVLPAFPN

NGYTFCAWMKFELLPEDVAPLFTFCGKTGVGIMCSFLRSSLILTSFDKRKNDGHVEVPDL

VTPGRWHFLCITHTHRQFRGSKVDVYLNAELRQSVRLAYPNTALMVPVVNAFLAMRESTN

ANALRILLGPTALFGQALPASIINNIRSVDEYDALVFQFNSYISSSTTSSTGGVNTTSGT

TGSANVAGNSTDGLLWAYDARHCDRLKGVCYDSSG

>contig35640 Frame-1F

MRPLQHLVAFVVLLLSVLYSLPFMLRAIWWIITRLVEIVVLFVGSGSFWWFLRSYQLQKE

QEHLDQVLLKLQYYTRYRVGSGNSSSGIGSNIPSRNVPDDVVSSNNSMTEAGFQLRVLKR

LPIGAHLRTSWNLPPELCEELANFIQSIGKDYVLEWFHDISSNKDFLSDVHFLLAEVLGA

LASRVLEIDSSQAMALVAKSLELLRLHLGWFREAYADLAKEYPNVFDEEDENDSNLYKRQ

EYVIAFVQQSPFLHPGCKHLPKTTKTSAEASYLRHLATQLLTHLRPQLEHQYHTNLFVSI

ARNLLREITAFKILQPLTQYAHAQYANALILSCLQSFSSTKARVPNLPSASHGVNLVPTV

S

>contig35958 Frame-0F

MDPLDTYMASLKLPSGQNLETVTREGGLHGARSLTIHKGSSAVVKNRRYRRLKQLLKSTT

EDDHYFSDRMMQQRNPALFHFYLGQYLGLHEDTTSAMEREGQQFSSFLLDTCQRKEMEVR

RLKEQKTWESFNAVNERQEQKRIEKLYEDDIVEEEEEEDTTLLSVDERRQQLIDIMSLNF

LAGNDSCYVSYEAIDADESLDDYDEINRDAEDKYFAEDNVY

>contig36003 Frame-2F

MMSHMMSVTRDISALPHESYNQEEDTPTSWWTPNKALALKGLIWLSMGYIFYLSASLIAE

TTAALYSLSWEVKFEPLLVLMVASCIAGHNTGIRHDMHVILDTAAPYMFLPFFVMTGAAL

KLDEVVDAIPLMSVYVGLRYVAIFIACYISGRFLLKLKPQQYNNLWLTLTPQAGVALGLA

SEVQAMSDEPWAAEFAATILAAVVVNQIVGPVLCAIGLSRAGETLKDRTTEEEIHRSDGH

SNHKSIHSRPSPIRGNSASIFYDGASSTFSVVEPSQRMLKHKDAHLPFYKVKSAVVIGDD

EVALEVAFNLSLYGAKVNVPLLDKERALKWQKMNRAILTRTNHGDLISYENTLKDRDAAK

AMSSADVIILTGDVDRTRENVKLLKSLLGENHPRVIALVPDSSFSKEMRDLNVLAIQPSI

ALANIATRMALLDKTLAEALSNELSTTSDFSTASYFLQPDQHNPVESLHLEGRAIRLGRS

VVNHHSVDYDRLAEVLAAEHLPMPPPPSRVSMFGTSSAEFDPFDSYRKRRPALFGKHHDY

EKTTTALYPCTPGINHSPSPRSNEFNVLNTP

>contig36308 Frame-2R

MARLLPRNFRSPPIVAAFAAATGLSTITSNSSTRLESIPASKPTFTERTIGNYENRLRKF

SSPERVFEYFSSVEI

>contig38269 Frame-1R

MARVYVGNLPENVRERDLTDRFERFGALVSINIKFPVRPPPFAFLTYEHEKDASDAVRSM

NNSTFAGSRIRVEISRGTTEPRPRGTQYRVKITGLPDAMSWQDLKDFLRKGGDVVHSDVD

HRGSGTASFATPDEMRRAIRKLDGADVNGERVRIRQADVGRHSRSPSHSKSRSPPRRSSR

HPSRSRSRSLSRSPRRYSSRLRRRDHLRSRSR

>contig38571 Frame-1R|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 7e-10 NOT\_ORF

MWISDAMSMGFVTVTKPDVLLDVVAHRRLPLSHAIHFEATHRPRARRFSSAKINFLAIFT

ERVRKDANFCLHGAG\*DRLLLNQKVREVEIAIDSRLIEPPKAKVIFFLS\*LSQNAKEWTL

EK

>contig39961 Frame-0R

MLDTITSRSQYKYILKKQMYLEYVFLRITGYSS

>contig40262 Frame-0R

MNDRSMIRPLFGGALSCDVPESFADVSTFRQVPDNQEVFANAATDQCVIVELLQYEDIVQ

DAQSALYFFNEIAQSNGCGPDEVTVLFEETSNAEYTGINVPHATQIIVGDQCVAKFKEGD

HAKNVVRVYLGNIRLPTVTTDVVLSVSTPIRINPASSSREAFQSQQDQESASLIFKQALH

SFAVKDWSLFT

>contig40288 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57563.1|) 6e-32

MEIRNLMGYGARWDTEIFKFRGFLEPPMLNGHAIKWRHL

>contig40406 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54446.1|) 1e-114

MLGTQASGSGNWGSSFGQRTDMDSVPLFEREHRNDSQLVQRLQNELADAKRFVEAQARRQ

NDLEYVNEDLERRLEQEAFDRITLDAQKAEDEKRWQQEKALLQEQLKQWEARFEEETRRR

VMAEERLRRAEKELYRMHQKKYDIEKQVRREENEKRKHEAVIVRSLQSDSQRAQQIAANG

FLDPTVNPRDVKPATVRTRQALSSAMDFLGV

>contig40640 Frame-0F

MVANPLIDSTLPSGSFSGGDTVIAQYLATKESWWVTYPRILVVTASTLSTYNPETFLCTN

QWNIIDIEAVKLFPTKNDFVLRLETSRFRSARLKFNCP

>contig41009 Frame-1R|Blast-Rab1 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY58069.1|) 9e-18

MASELITIREKVGDSNRPSGSKLMENTKAGGKSNGCSCN

>contig41812 Frame-1R

MTEQQTLIPPSFNAPPFSQVRTYVAPQVHNEQPNDDRGTSSASYANTTKTAASPQVTLVA

PPQGYPSSAPPPYGVAYTIQKPSYSSEVQDRSYVSNNVSVLPPSGSGYQLYGEQPSSGAK

VLADDDEVDTAEPEFTLEYDDDD

>contig41867 Frame-1R

MCSYRMTRELLKKYGFILRSFLNFCPCFRRDVSEIQPPIISARPGRSALCLSPAGMYQND

YSSRQRCGTPSESRP

>contig42093 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63221.1|) 4e-07

MANTDLTGLYISCLLLLASVDSAILSKRAIPFVCYTEKDAVKNAAGINYFSRLKKTKAMM

LNAKLRRLDVAT

>contig42127 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57156.1|) 2e-68

MGDFPPPERTSVIASELVHRAVDKSYEDFRTLMHQLPMMRENERREPLLAHLQSSRKRFA

QILAVLKWSVQSPLMQQCDMLLQQTESYRNNVNETNDRLFFMHADLNRAKERRYDLSTAV

DILFGGSYLRLPSIIKNAMYP

>contig42581 Frame-0F

MTLSLEERDDTCAPVALIALKQNKRVKRLKSWKLANQKISCI

>contig42848 Frame-1R

MSAIAAWLREGFVVKQKVPIVDAETKTDTVNSYIGLMMGFVESIVGLGVEEIFPVFLVYL

HNLRWYPSDDPATKKQSKFKKFALTIFIPTVMMAVGSSLSAVQANQREDKATSSRHMAAT

TRLLMQNVPNFGDDGLGGTILKTALTRMVVPMQPLDMSTCDSSGNDLFEADMLLAAAPKA

LFGFPLREWGAEFGKEKQFIEAFKRYDVTHNGAREAAGDEKLGGVMSLAMAQDLWKQGNS

IFMQSIRATSEEKKSSPPLRISEFFDDVLKSLLDTGVPLAVNAAVDASFEFRELSSLMDL

HVMTLRLPLRSHANTSVVCGVTSCALLEPQLNFGQRLPRKQIGMAPMNMSDAAFLYAFTT

VSSYNRDTDAISQSLVLSFGRISWRFIQSTTKCKSTTSKEGCQVLYHQLDSDYRHLVLPK

QWLPTQFQIANHGQTVSLVQLLEPKLRLHSGQASPFAILQHLESWSRISTHSCSAVVETF

LQYIQSNHFYFAGDIVEIMAASALFYIFQNAELVDTSSVDTATAIQRRLDGTTTRRVRVF

LTNTRVGIICTWTACGVLLLLTVLVIVLPNERARLAPPRGGNARAERFVLVQTEQIYPNL

IYKKRFLIGKTGEEIKFGEFAVESVGLHHKMEED

>contig43308 Frame-0F

MNNCKPAATLSSSCCFEVTDHCFLIVNPFTLVLTQNPFVISRCFCRAGKMCRQSGRVEC

>contig43397 Frame-0F

MMLQALMRTTSKYAARVNCSSQLQLVRRFSFRKHRNDNDDEFRGSRRRDPKDIGEEDSSD

LYDPYREYMETTGERGYREFNPDHVEEYEHEWEEPAAMMEDKSWPATTGSDLFTDMLNIP

SEPPSGEKLDKILEEAFARMGHTGNIDDIKLPQMDVEIPVDHPDKEALEIMKLSMMNNGR

LKMDDKNDLLKSIIDELNHLRNDKTTLFQGLDLSEEIDAKEKIKASKK

>contig43775 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55071.1|) 9e-47

MISFPIDLELPHDTVMKLHSTRNWAIQTLLEAQKTQSHNFRELILQPHMLSNSLRQMQTK

LFKSAPCRPIDVQIEIYQSLLAAVRIADEKSKLSDVMEMCASMLHIDEYFLQFAESALNG

RLKILSFGPTFLQRLFSRSFMQLQVDEGTMVTKNRLSMLYR

>contig44680 Frame-2R

MQEEDEEEENFLDYRCASVTGYSRDTDGVVYYEVIVRSTAHGPLSAYKVRRRYSEFRDLH

AALSKVMHVSHQKLASVTALANISDEHNDEHSSVGLCFSVNEWNRALEPALPPLPDKGGV

WSYLQFDSIPLLERRAQYFHAMLVAAQRHAIARSSRLLHDFVGTPPDLVSQHSSVENSYV

SLNRFAAPKLSFDIEIQERKEKAKSIRRRRQTFLESGEASCASLTP

>contig45038 Frame-2R

MSHSPWNADPVTGQKTKINTPAPQMKTEEHAVWNAAPKPNVSTSEKVKDKTRNMLEDAKD

IKAKVTSTVEGYKNDSVAKVKKMKQERKLNQEVKKAEKEKKAEESAGACGLCGCTVM

>contig45320 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54011.1|) 0.0

MLIGNHDGELRQFNIESDQVVEEWLCHSPSSAIVSLETNEVTLMGLQSRLILTGAVALSE

LSANEIALWDANDTSSLVERWRFQGGLRPQFNHYGDRIVTLDARSNNDDDGYGLSVKGAL

VLDIATGDVLCELKDTSRSNDYGAETNCCFSPCDGTILTDGMLWDARIPTRALYKFDKLS

NVGCGIFHPSGNEVIVNSAVWDLRTYRLLRMVPALDKCNIKFNTSGSVLFAYYPYAGGDY

LERRKSKLKSWFRVLDARDYRDITTIDLGHPVFDLSLNNTSTLLSVVEGRYVEAGDVNDD

DSVCRLYDIGRKRAAEDDSDAEDGEEESDTLDDDEYDDENSNDEDDDMVGDDDTDESEED

TSESSSMEGGSSEEDDGTEENSEDTAAHILGFGGDSGEEDGDGSILSTHDLGYVFELPDT

TYYEVHGQYSSDEDEADEDE

>contig45768 Frame-1F

MTTGLPTSPYPPLPRTPHSLSPYNSSPIPGDGKISLRVDQPVEGCLMMTHAFFRSREGDI

DDKDVKMQYDWFKSSLRRACANHACLRHTSDEAGNVLLLTANLECVQCCRLGIARDQSCF

CSLECFRMSWHTHKDLHDTQALVDAQRRDALKFTWKSQLYAMER

>contig45782 Frame-1F

MSTLTRQSRPNRQSSHNRAFAKSIALKDLSYSDNEDNSDDNKKTKDPMAIDSAVEAPRSP

QNDVTLPPLAPLRAIGFPDAKIRRTGLQIKDGLNHRTSGPGGLARRTSGRRWRAHPSDYD

EVVARAQFFKPRIPPTH

>contig46457 Frame-1F|Blast-serine/threonine-protein phosphatase ppe1 [Phytophthora infestans T30-4](gb|EEY53386.1|) 1e-174

MNMYSQHIRIFTTDHHSCIFCIFVYTSCINRSSPRSMTSVDDVMLEEIKPSSSRGGPDEW

IENLRNGKVLSEIELKQVCEIVKLLLIEESNVQPVSSPVTVCGDIHGQFFDLLELFRCGG

DIETTNYVFMGDFVDRGHNSVETFELLLCLKARYPDRITLLRGNHECRQITQVYGFYEEC

VRKYGNANPWKYCTDVFDYLNLAAIIDGRVLCVHGGLSPEIRMLDQIRTIERQQEIPHEG

SFCDLMWSDPEDIETWAMSPRGAGYLFGTKVTQEFNQINGLDLICRAHQLVQEGYKYMFD

NSLVTVWSAPNYCYRCGNVAAILSFAIISSGISNCFARLLNPRKILTSVL

>contig46769 Frame-2F

MQVPLDQNDLVLSEFRAWTLYNTRDIAASKCVFEAAVARQTKVFAPFLKKLKGFEAAVNG

VDDLEQKWLQYLNFVKHRVAPLLSSDGTELVVCLYERAVARLCLSMKLWVTYLDFIESKG

LQSKLKVAQRAVRNVPFDSFSWTEALIAMEQQSMDVTAISRYLRTELIERASVPMGELHL

LNTLLTWCDVARRQAFTTVNIGSEMEAVETMLEEIFHECHQLLAKAYPNYVEGALRLAEY

HAQCCWTLVIPGRSLDARVAKVKDLWQQTLSTLLGDYAATWIAYYNALQQMNVLSVENVR

SSVFDEAVKRVKDMPLALADAWLVFERQYGDLTHYLCARRFHSKHSAFIVTPVDNMVFEG

DTKPLKAKKRKAIAVEQLAKQCRTQRPKMQNVALLQSNETTA

>contig47340 Frame-0R

MLFLCISSNLSIAVYVVYFSSSSALNSCCLDVLPTAFTSTLLICVMANLTRFKYLWYRLL

AGNLVNAA

>contig47717 Frame-1F|Blast-L-gulonolactone oxidase, putative [Phytophthora infestans T30-4](gb|EEY69252.1|) 2e-75

MEKLLRRIDEEDIPAHSPIEQRWTARSTSFMSPASSSNPDQIFSWVGVILYLPTTNKDAR

KAIQDRFMDYYAMYRDFMEPFGATEHWAKIEWPEDAVERQKLRSRLKTRYPLDKFKKARD

ELDP

>contig47762 Frame-2R

MTIKTRAQPGAVIDSGTAARCTILLNLSTKIRIPLFLSSSSGNEVRFACRLKGMNLRAST

AGSWRFEVAYSPCSIIGKLRIDRCC

>contig48312 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55096.1|) 2e-19

MPFFSCYLLTPKQSPQRLRCTYIGFTVSPTRRIRQHNGELVSGAMRTRKHQP

>contig49070 Frame-1F

MTLRDAPPYHAKEGMQPGYVPGKSPSAVHVAFHRKGVFLCIEGRRDQQDELVSIAHDPIS

TTALSVQSILTARKTTIRESVFLDTCMGKVVDIQELDPYSSEGPESTWKDETQASATAKE

ISSGSKRSFDEMDTGISAFSAADNVIVFGEMSLMYSQPSRHFLCLTSSGIQVFKKIRPLD

QLHRVLLLARGHELKAQLAPFVRYFGEIQVICMLFALACGVQTDPLVTEMSTAISLIAPR

PGGLSTMKSEDYLYTAAVQSIFELAQGPPDNVPSEPATYASNGTAVSSTNTRVVLTTEFA

MSYQHDGLVAFASRVLRPLWIPKTLGRQITSRVADGATSTTTSANYVTRFEYVQPPEKLD

EIRELLFQLRQLMETAGPFAVSIKCGAALENNPSLDGVLGENVEAGLSRVSELVMRHQKA

LSEDQLKRETRFKAEQRSVYYLHQLVLRSIEAISLLRIAQEYKVS

>contig50058 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55988.1|) 9e-41

MEGDALSKQYVVKVLLQMAWKFDLNVSGCLEWFRHWQNTMRWRMRCTIWTER

>contig50883 Frame-0R

MDSKKLLGDKLLSMAFRAVNSDFMVVKSISMQLSVVAAFAPVASTAATIMARFI

>contig52144 Frame-2F

MLLQEEGVLAAKLDHITYLLDGLLLDSYKAPRAHVAHNRSILELTQLIQEPQILQAITLS

SQRCRVKQ

>contig55659 Frame-0F

MDLAVENLMGVKPEKLRFSLLLANKVSRSEGGRCWVGGFHLLAWDILYKSNRWTF

>contig59163 Frame-1F

MLINDLEKRQRTSRLGTGVTPPVSLSLSAAHTEAKMRKRK

>contig59310-0 Frame-0F0

MPAPQPDQIHVLVVLPNEVPLTISPNSGEARFVEGYESLSKTLARHEQVESLSKAIRV

>contig59310-1 Frame-0R1

MPRKCLGERLIPFHKSSFAAIRRNGEWDLIWKHHQHVNLVWLRRGHLVF

>contig05945 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57196.1|) 3e-73

MIILPRLPILISMNITSDSHDEQLTLSGATLAALHEFAIEQGISIEDCSSDVRLDIQRAL

DIEPKEDSFEFKFCKNGDKADAEIIIRLNGLRRDIGQTLQSTGLTLWRAGDFMSEFMYQD

RSRFTGKSIIELGSGLGLISILASHLTNKQVVATDGDDDTIELLRANCKLNGVEGRVQCR

KLLWG

>contig06306 Frame-0F|Blast-30S ribosomal protein S16, putative [Phytophthora infestans T30-4](gb|EEY63084.1|) 1e-08

MVVRLRLARWGRKDVPFYRIVAADARAPRDG

>contig08559 Frame-1R

MGGCYSKSDTNNYAVNRNHIKSSGGNRGSNRGSTKSECGRQRHGAQSNTEPVPHRRPSNV

TVHFQEFKDQEKDVVETMLESNKGLRMAEISFNDLKLQKIIGAGAFGEVIKGTYCGTPVV

VKRMLRNKITEDNLRMFGDEIQLMMNLRHPNIVQFIGASWNSYSNICFVTELLERGDMFA

VLRNPINKMTWAKPILRMTIDASRGMAYLHSMKPPIIHRDLKSMNILVSSTWGAKVSDFG

LSREKSVDETMSVTGTPLWLPPEMIRGERYTEKADVYSFGIVLAELDTRKIPYHDIKAKG

ARNKKVSGSTLMHMVAYENLRPSLSKTCMNSVRDLYKRCTSDDQSERPTFEEIVQLLEND

VRKETLLHTYGAMILAQEDEVDSEASPEELGVYHATRYVE

>contig09466 Frame-2F|Blast-double-strand break repair protein, putative [Phytophthora infestans T30-4](gb|EEY59993.1|) 1e-138

MRDERLNRMFAQGKVVFRRPAEHAEEWFSIFVVHQNRDDKGRGSKNCVPESVIPNFIDLV

VWGHEHESQIDVQESVKGDFFITQPGSSVATSLVEGEAKPKSVAVVEIHGRSFRMTTSEL

QTVRPFKISEVILSEIENLEPNDPDVAEHISEYLEGRVIELLHEAELERQDRAKERAKAR

DKRQHESPFPLPEDASGDNIKELVLIRLRVEHTGFPVIVNQR

>contig16448 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58267.1|) 2e-61

MYYTKKEEVSMDPATTFDLLEQWDAEWEKKRGDEAESKEDKTVEEEEENVDQPRRKSRVR

DPPRRRFDELNMFSIVDLVGILMLASRVLNLGLLPSDFAEWVATGVIPYHNSLATCCANA

PDVRESVKFIVSFFQSFMR

>contig18701 Frame-0F|Blast-triosephosphate isomerase/glyceraldehyde-3-phosphate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY64623.1|) 1e-175

MVNVAINGFGRIGRLVLRAAAKNPNIKVVAVNDPFITTKYMEYMLKYDTVHGRFAGELDH

DENHIYVNGESIRVFTEMKPENIKWGEKQVQYVVESTGAFTTLEAASAHMKNGVEKVVIS

APSNDAPMFVMGVNHELYEKKMHVVSNASCTTNCLAPLAKVVNDKFGIKEGLMTTVHAVT

ATQKTVDSPSKKDWRGGRGACFNIIPSSTGAAKAVGKVIPSLNGKLTGMSFRVPTADVSV

VDLTARLVNPASYDEIKKAIKNASENEMKGILGYTEEAVVSSDFIGDSRSSIFDADAGIA

LTDDFVKLVSWYDNEWGYSSRVLDLIEHMVKNE

>contig19298 Frame-1F

MGKKNFRWNTTIKKLMKIEFKSWFDAGKIPEMPNVYHATEEPYIKKVLKAYRMYTKKKG

>contig20557 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59506.1|) 7e-18

MVVGLIKDRKRGELENRACRVRMKKLEREFKEARRDLVQLDSARIRAARSHAKMVEQQQI

SKQLQRDLDSAKAALALAEREKQELQAKRKCDKTTRLGYEA

>contig20733 Frame-1R|Blast-Sulfate Permease (SulP) Family [Phytophthora infestans T30-4](gb|EEY55880.1|) 0.0

MAPSTSASTLDSDELSLSCLSAMISSLWMSACEFWHNITRQRLVFFLKQHVPILDWLPSY

NIQEDLQFDVVSGITVGLMLVPQEVSLSAIMGVPPIYGLYTAAVVPMIYSLFGTSRVLSV

ANGAEVSLLVGSAIKKVESEEERIATGILLSFLSGVILLFMGMFRLGVIADFFSRPVMGG

FLSAGGVLIMLSQVASWLGLEVKSRDLPVLTVLDLFQHFPELNGLSFAVGLVSITVLVSM

HELKRRVVKELARVENEFEDQFAIETSRALTQLSISMEPSSDDQVKASDDDEDQEAKVVC

QAAANTEITVESEGNLKPLKRQARKKEKQMDSNAISRSVSPRGTRWANLPAVFTTGALQR

RDYVLSSPWGSLSRKSQEPSSNEADLARSCRQKDLAAITRNNLHGRMDDEGVGFSLSDED

FITIERPLDFGTRQDTATGTGMFETQNIASDTAVASMKSSMSNGEILDTKTPQAKAKTEL

KRRVQELVSPTKSDTESELADPSSALTGRMLAASSLSIRLLRSKMAVLVSLRLLCDLGAF

MVCLLGGIVGYLAPTGSLNLAGDIPG

>contig21604 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69376.1|) 2e-80 NOT\_ORF

MTRYSLVFAIVAIAVASSLCRGTELKELSSPRVEDLKQPLQRVAFGSCNDQSFPQPLWST

IAAHKPELWIWMGDNIYADMKELDEPHPFSISPRKMFVEASADVLIRRYNKLMANEDYAA

FVNRTPIIGIWDDHDYGINDGGKFYSYREQSQQLFLDFIGEPIDSLRRKQEVRCSISSYG

QFKKST\*\*FCYILLWRP\*QGIYTSYTIGSRDQTIKFILVDN

>contig22061 Frame-1R

MSGFPAFQCNRRNLICCKNNPNSAE

>contig23981 Frame-2R

MKQRLQLRILNAKQKRRLEKGIKILLKVPSALSAIVDSAILRFYPVDICAFVPSALMYCA

KAPPYVQFAEQVLNHCLLFVFATKTAATINIEANYCK

>contig24180 Frame-0F|Blast-NADH-cytochrome b5 reductase, putative [Phytophthora infestans T30-4](gb|EEY68703.1|) 1e-131

MFTSSMHSAFRQPLRSAASVTAMVSALGLANISSTARNSEEPKRALSPKEFRPFKVTKVE

DVTHDTKRLVFALPSQDDEMGLTAASCLVAKADVNGENVVRPYTPTNTNAEKGHVELVVK

GYPDGKMSKHIANLKVGDELAMKGPLIKFVYTPNQYARMGFICGGSGLTPALQVIKEICR

NPDDSTQVVLIYCNKSEQDIILRDELDAMQYMYPQLQVIHVLSQASPNWEGYTGYVTREL

VQKLLPEPSDKCWIGVCGPPPMMNAISGDKNPDKSQGELKGVLKEVGYSNEQVFKF

>contig24203 Frame-0F|Blast-nuclear transcription factor Y subunit B-3 [Phytophthora infestans T30-4](gb|EEY58732.1|) 9e-63

MASKEEHNDDEIREQDRFLPTANISRIMKVSLPSTAKIAKDGKETVQECVSEFISFITSE

ASDKCQQEKRKTINGDDIIWAMSTLGFDSYVEPLKLYLQKYRESVKVEKNDKKDNVGSFG

A

>contig24276 Frame-0R

MSTASSFWLSKLKGLDANPKTIDEFKVRTLQGGFFSLLAFFCISFLLVSELGYYLTTDTV

DKMMVDGGRNTLVSINFDIEFPHMSCAAVAIESADMAGNAQHDIVHNIQKISLDLSGQAL

AEGMQGSIGGALTNHSDLHEEIEKPKCGSCYSAGEPEECCNTCESVKAAYVRKSWLMPSL

HTVAQCQEIEIEKVLRGEVKEGCRIKGALTVSKVYLNGHALYV

>contig24492 Frame-1F

MYVSRLDVTQFDSWPRSSYTPVLPAQRPIAAVASLPFKAGHFHFLSENTQSIPYLSSSVQ

IKSVYMP

>contig24553 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66492.1|) 1e-113

MPLESVCLATIEKAIGEDIKLDEIEQYFPDNTVKQAHQKTRLENPQTPDEFAPSSKKKRS

ASGAASSSPQGSGTGVCYDFQNKGVCQRGRFCHFSHCACNSTCSCTPAKNTYGQRPAYRR

NDYDAPPSPEAAPSIIADEAALPDKATVVRHVNSLERDSSTKVEGDHGEEEEAGELTDTS

HLHINSIFTPLESFDKESIATKRAQLTALGNRRIWASLGLEDKPQRTRPCGLIISKSGEM

VYVRPPDK

>contig25037 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67964.1|) 2e-26

MEAMRFCCSSELHRARRHRKYRYQQLTTLSDLDDQLLTVTTEKVRSKVRWCLY

>contig25679-0 Frame-1F0

MGGIKGESSGVVIEAGSGVNKALVTRVCVGNGWINHVLGRKLGAIVSSMGVVKGMGV

>contig25679-1 Frame-0R1

MPLTTPMEETMAPNLRPKTWLIQPLPTQTLVTSALLTPEPASMTTPLLSPLIPPIQTPTG

ASLPDTMAPTPVPVLVDTQAPTTIALPTMAPTTVVLPTNSSP

>contig25693 Frame-2F|Blast-coatomer subunit epsilon, putative [Phytophthora infestans T30-4](gb|EEY54897.1|) 1e-121

MAEPDELFMLKNQLWVGNYQNVISEGSMLNHMNQTLRNERDVYVYRAHVALGNTSFVLQS

IPDTGNVPIALSALKLWATYLSGQIDPEMMALTLKEWLADPTSSDNGHLLLLAGQIFARE

GKFSDALTAWTRGNSLEHMLYMVHLYLEINRADFARTTVATMKSLEEDSTLTQLAQAWCL

TLQGRDKADEATLHFQELADRFGSTSLLLNGTAVAFMAMENYVEAERLLLDALAKEPSKE

DTLVNLIAVSAHLQKPLEAYLCQLQQVAPLNVWLQKYELLEHEFARMAGT

>contig26735 Frame-1F

MLRAGDSAASSASNSSALTFSDSDAEFDRALKSYDVPAVTKALHQYLVAETQASISAGLT

AKRQPAQLRSVFYVRFNQILDRIFGLDLNSKQKSGGLLDYSIGVGMLTTPGSVAILSVKR

RAEQRRDRAMAGVATNEGEIDEHLINLTVSGRAIVKLLGGGVRSEDGSLFQFLFRLHHPV

EFKLALDLLPEKSKMTIVSGQGVNLLFTQLMHKPLAKQRLDLRNPELLVTITELYMFYFL

RHPTGSSHQTQLSTSITVEPLKSSPESFNSSILSSAAKLPQSSWRKYEKDGIVALTKGSP

YNVLLLQYLRAFLPDSNYGTRSRFHGRLLKESNLFLHILIEFWLQQNLVTFSDESLEAST

PARCAIRPPLAGSMHIVSPFASVFTSTSYVAPSDDLLSSLSLTIIHLLADSFFPAALTED

SASGSHGNAGVYLSRSVTMLRPPLYAFFRLVFSRAPIGLSSTAFLAIADVWLAFIQPWCC

RSWIDSKDQLVGDTTAEQNTVFEYTSAWESYVLANYHFYTVLLGVFVKRANEFDFSTGDK

RNLQTVVRVMKVFNTDLLAILRRASLYLEKSQQLAMLSNYQRGANKTLMVSDSLSSSSKR

KSTLMGDAFTTSQVHVLTFYCKSLGIDCTPVPLHGSFHRDAERLFDKLWAAVATSNSDAS

ASTTIIYQNVSAVFRTSHKKSVNMMAEQAEHLSRRLRVIFEISDAYVASTAHSRSSISTK

GDMKSFAPGREKFSPHLLTREGIFQLQHGMRLCSSDTANYVGDPMLSPICSYEVVWLVRL

SYRVSTWLNAHFGFVNPYQGKHIESNLAVNSARSFSCFRFDFRFLASKINLSFLSAVVLL

LYALYIR

>contig28452 Frame-1F

MFLFESESPDAEKDKVLEIDRFIQLYDIISCAEFELESILESEAENIAVLGSQDDVFDPV

DELIVDLTVENVEEAFDCGNFHFRDKKESCDDNSKSFKFNGISKIEWANYAVSILKNFGV

IKYCEQKQALSSAEDNLSQALFIADDADLVLEVLVGSDPLSDEWFQDIAATESSQLFSRD

KWNDTYKLIMDNAAPDEILESQLFGDDGNYDLTCSFKYPLTRHRYCQTNNKSSSSRYLLK

SRPSQDQYACNENFTELGEKLLTPSQNQSVVPVSKPAAPSCLAEEKSTGILGSVSKPSKS

LVRSRPSVHAPAASSKRLTKSASLLSFQPKGDMLSMSSIPKPRGSLLKSKDRSSTTARQR

>contig28654 Frame-1F

MHFAPKHECIPQKWGRFVALTGEICIEKPDNIKRFRHLLT

>contig29316 Frame-1F

MNPEYLNLIFQSTEASSRCTLNHP

>contig29507 Frame-0F

MREDLAQVTCDPNDLSAVCDSFVETGYVP

>contig30112 Frame-0F|Blast-RNA polymerase-associated protein RTF1 [Phytophthora infestans T30-4](gb|EEY59894.1|) 0.0

MLVRGVYVRVPIEMVDGEMVYRFCEVVNVCKLPRGYTFCGETTHMGIICAFGKSRREWKL

NGVSGHSLREREFLLWRAVMNKERLHFPTYGQVKRLYSKKERLITQHNYTDAEVDEMVKR

KQAVGLSSVSLGVQRVRLERDLRAAQDMKNFEKAVMLEERLQKLLAKNEERKNQNSDDVL

RINEINRRNREANIQQDLHAQELNDAMNQKMTSAERLQFVRANQTTMYMSRDKLDKNLVE

GKLIQLPDGRVMTSNKLHVVEALPDDLLDKVKGAGEKKTTDGLEIDIDLLLAKQQERKQK

DAERMEAKRKEREGQVEYVGGAPTNVQERANATIRIKDDDGSWMTLRSPAEIILEKKNKT

VVSDKVKASRKGITVKEYFDRVKKARLK

>contig30769 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56802.1|) 9e-89

MFSMLWPLMPFACFLINSIKGRTDGYRLCKTLKRPIPRRANGIGAWKGILTTFAYIAVIV

NVLLICISTGVLEFFQDNCVRDIQNQLEKQGKSLDDFIFGPDFGCLHFAWRLVIILLLEH

FLIAIAYVGMQRIPHVP

>contig30783 Frame-0R

MGLLLRQSVKINTRVVVFNQILKLKRIFVWQIVHELLAESLQVAEYQ

>contig31634 Frame-2F

MRTRQHESALQHKNINSLEADEALKSPELVPATSEPTSPVASLVFPPKPEKLPVRQRIAI

TKQSQSSTKVLPGLAFAYQHEELEVTEEQKRRFQVENVQLHRHFQENLEDVKKMELKMTE

ISSLMGQFADKIMEQHSDIQLIHRHAQETKSNVTQSNRILEHAQSIGKGYGFIIFCFYVT

FALILHVLHFFNS

>contig32716 Frame-0R

MFDDVDLVEQSPRLLRRFSDYGANEEQGTYTAWVCRILSRPVQVMILFGCNGWWCTRKTS

TLCTIPNVVRRH

>contig33768 Frame-0R|Blast-APS kinase/ATP sulfurlyase/pyrophosphatase fusion protein [Phytophthora infestans T30-4](gb|EEY66435.1|) 0.0

MKDLKILSFPKVYYDIQDHKMKPMDSKRKQDFLSISGSRMRLMASQGLQKCEGDSVPFGS

KDVPTCVPQGFMVKSGWDIMTDYYQNMKNSRWIPFAMQFSKPVIDTSRLFSSEGTFGRTD

YKLYFMNEKGENISPWHEIPLHPADAKDNSSYNFVVEIPKGIAHKMEVSKEERYNPIVQD

TTHNGTRGRNFLYGVPFFNYGLFPQTWEDPSLKDKDGHGGDNDPMDVIEIGVNQLAMGSV

IPVKILGSLELIDQGEVDHKILVISLADKDADKINSVSDLQSEKPGLLDAVVDWVRNYKI

SEGKSENIFSREVPASVEAATQIVAQAHERWQKLKAGAIAAKNEFWLSQDSLNN

>contig34310 Frame-1R

MHRAAQKRQLDAPLLGLLFFSVCLKLLLLPSYTSTDFEVHRNWLSLTHELPRHLWYHENT

SKWTLDYPPFFAYFEYVLSFVAAAVDKSMLTISATPVFSPSILLFQRLSVIASDLVLFYA

LHAFCSSWPTVTTTEWAFSTAKRVAIMLITVLDAGLLFVDHIHFQYNGMLLGLLILSATK

FRLQQDFHGAILYAILLMFKHIYLYAAPLYFIYLLGHYCYVKKIPEHEPFNRNHDSQEKM

QRTRSISSTDIHETIQFIHDGNVVFSWTNFFKVGGTVLAIFLFAFGSILWNHDDPVAGFI

QILSRLFPVQRGLCHAYWAPNVWALYALLDKVLVILGFPASTGVALMSSGLVQETRFAVL

PSVSPLMCAFLTFAMMTPVLRSIWKYPDPSIFTSALAYCMLCSFLLGYHVHEKAILQVTL

PLALMAGDSVASMRLYRFASGVATISLFPLLFTPAEHGTKVLLGACHAVLAKVVLVPLLK

HSLKERHIKVTAVGMSLFERGFLTGLTGLALFAAVFPYLPQVGARFPFLPLMLISIGCAL

GNIYVWGFTLTQHFRKLDAVKTYLDARKHN

>contig34866 Frame-2F

MVRIYLWRSRTLKRYTPRPSLPSLIKHHTKISKSTKASFILEAAEAMPNDKKTELLGVLP

DSLTSSRRQTTMSTA

>contig35216 Frame-1R

MIHAHFLQPFPVSLKKLSPSDESTHIDTILQAIESCASAPELALLYTKMTGSKTHRTKTD

VLTAIAKVVKTQRRIDGSRIPL

>contig35263 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY53362.1|) 9e-71

MGHVELAAYLTISSPFLQRDTILHAFGINGVYEHGCFLLLGGSVDQVAITSTVAVPILQG

WNAGRMEIKGFRAMIEPLSRMQARTCIVANIDPKCAIPKPMLNYGIKKMAGILLYLIRKE

AD

>contig35289 Frame-2F

MRAAHQRQLQKAPPATAGWRLYANYVGIVPAPQRSGTQTVGHWTEERVTCQAKQRFMGAC

ASRQVCSIPVNQRNILEDRFQDDVDEAIRG

>contig35641 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60292.1|) 2e-48

MKDGKPALIEVLAPNLIDSSKYFRFNRKRSIIQPSVWYNADTEPGSSGSPVISQRDNTVV

ALHRAGNAETSQSSSAELFNMGVRIDLIARDLQRRKLLPRNSVAL

>contig35959 Frame-1F

MPSYPSWFRILSEESGIAGAAIAKLPLASYVLVRSHFRDAFETFYPKPAIAAKSLLGLCR

ASNARFVSTQAEGEPPVKSEYLLVETLLVAALEEDAKAKLAYYCSVLYHLVKTDARVVSP

ALAVVVELLFREVPTMRAAASRSFVLLLSHFLSNFDFKWRWAAWSYVLEASEDDPQRLFV

SAVIERCVRLSYLQHMQSALPAEFHVLLPPAPKPRIRLKSMKENDTIDNDSSPVSEFYES

VTTKLKGHPPALALRSWLNEVLPRLEFSRAEAVEVVWTCILEAGAATFTHMRLLLEKYGK

RNELFGNEDQSTHEKESDELVVVKTVASVWLKSPQHIGLILNAMLRQGLLCPSTIVTWVF

TPDAVQQYSWPYVWEILNDTLLFVQDGLQTKTQQLNKALKPRISDGRDNEDMPDVAALED

ASKRLQEELRQLLVLLFRGFNRVMIQHKAECDLEGANPHDNWFCSVLAQMQAVGHRFRVI

MEDALDELQLDVFSSNASADSDATRIFQLVRNTYRSAETEA

>contig37153 Frame-0R

MVNCGGVAYWGLVLAQIPWIAMFVILSSRYLHKVYLLKKAVKYPYLDGDIQWTKTMVIFF

PLGCAAAGIVAGLFGVGGAIVASPILLELGSVPEVAS

>contig37676 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66740.1|) 1e-11 NOT\_ORF

MMMLVILETVDAESELEALRSRRVLLLYFR\*AYDTVSRDFLF

>contig38268 Frame-2F

MGAGTVTLLEINNVPNQTRIACCLPSGEFVFVADTCAPELGATNAADLYGGNLFQYLVQS

DAENLEEFLQRADYSMSHMHALEQKHIMVRLINKPNIQLHIQLSTAPLTLRMKRCIDTIQ

SLSSSFNLFADSSSFVLSQDEFRSVLKTPLESDESPHLFAPLPTEDDDELVFLKTENGCF

SPTCLTCVVPLELKHRHSSFEDSGTEETDDDLRKSLSNLAFEADWTSEACS

>contig38570 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53229.1|) 0.0

MLRVLAVLLLECVLAFAQQPETKRFTSLTPPISLPQGKVSNTFHRLAIPKGPIAVYRFEA

DVVEKDANNEIVPVPSFDAYLHHHVFGSTHQHYDAMKTRWAPMKPKTFSRSVAFGAGTEC

RGTPQEFYFPYAFMTVEGEDEWLANVHVINTRQMAPEKAHHCLECPCTSEDVFTNTSVNN

LIFHKNSCNRQLLFENNTVCLAETYRGGLRCCENKESCLELDELERTRASDAVYYLRYSL

EYAVIVPENRPLYLAACCDASGDLQHSGNIEYDVPICDPSTHPGCIHTLSTRQRLNNGST

PLGTNAPHQFEQARDVELVYAVGHQHRGGLGIQLYDDATGELLCASVPEYGSGTEAGNED

GYIIAMSTCTFDPPRRMRTTDIVRIVALYNNTVPHTGVMSLMYVALSDFPLLNTANLSGG

IDTLTTATMTSTGSSDVLKLGIVAGAIACVLLITILARRKLRSGYAPLTSQNN

>contig39645 Frame-2F

MKRFALSLAYQQKNLAKQRPAFQSQEAFVNFVGAWNSLENAPTEENYNAQLEETRVNLPG

DTMQYLASAWLIYKVMRSSKNVDPTMRN

>contig39887 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54116.1|) 0.0

MMTVVDVSDATLLLDRVLHLIPPSTVSALTPSMHLSLTEGMLQLVELWIDSAIGIQRTRP

SVLQQISPSTVLALFGEWILPACELEATDFQSSRCIAIVALCKLCSVRCINTLTRSHLTI

VARVLFKGITSFSGVVVSTVLQKSSVLFSMNLEGLNILVPAYLYAVDEIIIGNIWSRAEH

SKAKSSEWNNELIAALDVVFALLVLPKRFPNQDFVRWKQKIMGVCRLDELSLMQDIIGEI

PETLDGFHVIVGRILMRIAQLPFTDVVDIKKRALWGLYCLVVMNLEAENTGEHVVEAIQL

SEWVVHLVDVCQSEDFSISMAALTILQDMSDYHEEINAFESSLVARIVMTLAVFAQQQVE

EASIEVQAA

>contig39960 Frame-2F|Blast-tafazzin-like protein [Phytophthora infestans T30-4](gb|EEY53093.1|) 5e-73

MLWRGSRLVSSFSRSVFTFGSLSVSAGTVALYVDAPVADLGDGKYDGGRRSEIFPEWLHD

MARVPLFGAVTLGSKVYLQHFNRSTIKGVEILVQQLDQRPKGTSVITVSNHSATVDDPAI

FANMMPWRYMWPRNSRWSLASQEYCYTKGKLASAFFFGAKSLPIKRGAGIDHP

>contig40289 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66295.1|) 6e-62

MESSDRLLIRKLEDNEPHAKAKRKGESNEEENEKESQRRRNLIRQSRRHNWQPKYEMEFG

LLAIEKDPASEAVLLAMCGFCKTFGREGKYDRLVQQDHESGNDSKKRRRRSLTTTKFFRA

FRVDNIRSHLQGAHPRRWAEYEMLPKQEDIRNRFLNLQGELRPYEDLPIMDDVVLENSFL

TAGSDMAYTQTQLQAQTSALSKTQQAAIQAKQNRHVSAVLGDSSKSNLYMSASLTRN

>contig40959 Frame-2F

MATGFNDCRGSSIAADVDACIERMLDHFESCEQALRIDVLRALSTQAKLAYETERIREHL

TKHPVSQDLINGITSQSIIYKMLAQRLTVDSCSCNYDVKSNVVMTTSVRWTLEPTSGTKI

TKKRKKLTSVVTKKKAMLTKYRFERVRHTKGEHEEKDEEETRINFSIVVAFGDDDANPQE

LLRFEMVCEHAYPTRYYEVRQISEPESEELLTKEEHIENAENEENQTANRDGGVKKELNT

FGEELRAFYLSDEVLDNMVGWTGSGDEELNAVDVIGFFMALPVHEDEWLIDERVCEILF

>contig41008 Frame-1R|Blast-Rab1 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY58069.1|) 2e-18

MASELITIREMVGDSNRPSGSKLMENTKAGGKSNGCSCN

>contig41813 Frame-0R

MEGSGVVLIPPSNAAETHCSFNQTPSVPVLLLERIYDGCISGTLADKGRVLLRIMSDGTL

QGEARRPVEPVSREVMSSRKRSRRVIAEHPDGVVVAHISGYAHVVPLKEAVLSPCSSTES

CNGTSPAEYCCVFEVTKRLHHVDRHSLSCH

>contig42153 Frame-2F

MPRNAHSCSPDAHFFSRRLFSVALCLLTPPFQAPITLFFNNAVAVRVVCTTV

>contig42603 Frame-1R|Blast-hypothetical protein PITG\_10029 [Phytophthora infestans T30-4](gb|EEY56491.1|) 4e-31

MTTELRNRATGVPKQVQRGFDVALGPTIYSGERYSKMSERLKRQNKKPSEVADMNTRRIL

QSQLIAFVVAFVFIVSLVILMMYQAHVRRFNRKPFDA

>contig42849 Frame-0R

MVFEVLAAVLHLGNLQFAMDNDTCVPVGDESVKGLRLVATLLKVSEDALNKALLTRQLYV

GGKVIVQQQNAEQVSDKRDALAKAIYSSLFLWLVSELNRTISRTQDKWGFIGVLDIYGFE

KFEWNTFEQLCINYANEKLQRHFNQHMLEVEQNDYAKEGIDWKHIDFDDNQECLDLIESK

VNGTPGIFISLDDGWRLKGEEANKKFVSNLHNSFGRTSSGQSSSKHKFYVHPKMDADLHF

GIKHYAGEVIYDASGFNDKNNETMNDDMKELIRQSESPWLRGMFDLNMQSIEAIPSNKTQ

PHTISRRPNEGKKGTQGNKSRHIREISVSAQFRYQLQELMNKISLANPRYVRCIKPNELK

HSSEFNDADCARQLKYSGMMEAIQIRQRGFALREDHDVFFYDYQSLAPDAENIKELVVKI

SSMLGAGKEEW

>contig43002 Frame-1R

MGATFARFITKFQRDRKLPPSSVGLVKANSNKSKHLEVATIAIQGFTVDFVHLRAEAYSL

NSRIPNVTFASPQDDANRRDLTINALFYNLHTREIEDFTGQGVLDLNQRLIRTPRDPERT

FLDDPLRVLRALRFACDLQFTLDKTLETALLSQREIVHAMTRKVSRERIGIEVRKMLAGE

DPARAFDFLRTFKLLDVVFGTPPCHSSEGSREALKYPPRPWTDLIQQRASHILKYLQQSR

WALAKYKISNVESMAA

>contig43774 Frame-1F

MSTAEPWDFAWIKVTVQSLETYKSALETAE

>contig43961 Frame-0R

MLRRVASSSLRRASRNASKTCCNATSYRLYQQRLNVPTVEPQWCPIQTAQFSTDVPA

>contig44681 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56888.1|) 2e-48

MNGNLNMGMMEYGMDTASMMQGGDLNAGFMKQLQDGSKEMVEMDATDYDHDLAMKAQNRN

RGNYRCSKCGEPKKGHVCPLVPSNYKCNRCGLTKKSCSCSAPTTRSIGVQAEMDEDMTTR

VLDLSVQG

>contig45112 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61205.1|) 3e-58

MFFSKIALHAPETVKVNDIVRLDTAVLAEAMSPLGPNSVLTISDIHLNVSLIGAGKSLGT

LSTLSADIRNGSLVGRSNISVDCLTELRLADNGKAFGRFIRASVIKKEIMLTLHGSIEVA

CHGALGTLKLYGLPLHTHTLLQGMNHFQNVTVKSFTLPGTGSAS

>contig45394 Frame-1F

MWASVVVMRIDLRINTRMFPY

>contig46070 Frame-2F|Blast-conserved oligomeric Golgi complex subunit 6, putative [Phytophthora infestans T30-4](gb|EEY58675.1|) 2e-43

MDASGASTLATLRRSLRSSLEHQQLALAELALDNLNATIERISKLASEVDALDMKCDQVH

KYLETTKRDTEQVQTEAATLATERYGLRFVLLLLSICA

>contig46456 Frame-2F|Blast-diphosphomevalonate decarboxylase [Phytophthora infestans T30-4](gb|EEY64532.1|) 2e-07

MIYVTRVGGGTQVLSTEEALVDISTGEPLP

>contig46768 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67198.1|) 8e-08 NOT\_ORF

MKADVYACMMVNLRADVERE\*VDPIAECCCISLRQDKHHSIEAASAGLFTHYAR

>contig47482 Frame-0R|Blast-5-methylthioadenosine/S-adenosylhomocysteine deaminase, putative [Phytophthora infestans T30-4](gb|EEY54489.1|) 1e-104

MSCHQSAYKLRPLANLKRMGLLSEHLICAHMTQLTAGEIEDISQAGVHVAHCPSSNLKLA

SGLAPITAMLERGVNVGIGTDSAASNNSLDMFSEMKLAAILAKAETKKCSSVPAAEALQM

ATLNGARALGLENDIGSIEVGKRADVIAVECDNIEMLPMYNPINHIVYVAGREHVSDVWI

NGKHLLANHKLMTIDEKALKMSVRKWAFDISAYRKQHKVEQ

>contig48278 Frame-2F

MELLKDTKPEPATAESASTEALTVGSASTSGRPLFDEMYDDWSSFDAAIARATAAYHPIR

KRSSLTFEVYNRTVSKGKHDRKNIAEFLSKTFKCTHGIKFRSRGNGKRLRHRLRDIGCPF

HVYASAVEYGPNTYRVRVRTHEKHNHPIGPDSMKMMSGALHESDYELAPQGGSNDSTSER

KLTGSTTASTHIQHTETVVSPENAADVAQTAYERQIKEQLEEADAHVCAQVRTQTEAQTQ

ANDQSQAYQYTNSQEFLKLEGMQAMIDAQRTLRTQQNFLHVQPQPPPVDATHILNTSSHD

SELLEEEIDSTMSDDIFESSSTSQTATTDVKVAINSNVQAYSCNGFDAPGKFEATMTFES

LRKRIANFADERDWNQFHTPRNLLLALNGEVGELCEIFQWKGEVKNTADWTAREKEHLGE

EISDVLIYLVRLADKCDVNLPAALNDKIAKNARKYPADMVRGSSK

>contig49071 Frame-2R

MSRAAASTVLTNSSLFRHIMRFIDGVPGRILSCVTSFQAAHCSDPWSVAGALPKDAIQRG

DFDTLRHLWRLSRSKSFLAGAELSFRDTILYAIQNGRLAIVQYLASIKLLPFKFSLMRSE

EDTLMGWAIRYSDVPTLQDP

>contig49549 Frame-1F

MRAKRPFPPMTSFVHSRPCVCDHVCDALDAR

>contig50132 Frame-1F

MYHAPTMARASRLEVCHIKFLLDLTAGPTTNFRMSSQFFLSKVSIIE

>contig50882 Frame-1F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY61535.1|) 2e-34

MRLERSTENPIQTLALKKCAHKCDFLMRASHCRCLSDSFAQPMIEIRHFSESSLSLPAGA

NKCARRCPSNGACSVSEWREDDTSLHLHNARFSGSCNASARSREWYIWDFVSA

>contig52145 Frame-1F

MTSQEQKAFLAIVAGTKRTVCWENDSSRPKDEAALRFQASLLWPSYLSASALPS

>contig52530 Frame-0F|Blast-U2-associated splicing factor, putative [Phytophthora infestans T30-4](gb|EEY54549.1|) 1e-13

MTPTDVSRVEEDGAPTAAAQSNLPWGMETTEMQPSSLTKLTDDKLARFVLGHQQKTKFQK

DREDREAK

>contig53605 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54557.1|) 5e-26

MAIPNRLLTFKGHRDSVNTLLCEEGVHPNLLASGGDDGTCRLWDLRTAKVTKCFNVKKAL

GTEDVSES

>contig57713 Frame-0R

MTRDEAAWREKSIAVLPSQVTTPYFTTSKSKKSLAMANKAYFETTKKSAMRTNRVQCDNP

TNSLLSLPAEEPTQVRMKLA

>contig57766 Frame-2F

MAQLRKIFKQRVHWPAHPCCEAFFLF

>contig58491 Frame-0F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY65440.1|) 8e-12

MVTLLCVIVGVAGKAFPVDINTSQFVGHLKDKIKEKKFNTIKGEARTLQLFLANS

>contig02297 Frame-0F

MNGFSHANTYFVYTSCMSKRLQLRFLSKL

>contig02631 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55164.1|) 1e-40

MSTKFAVPPEAPYPRAAWGVNLGGALWHIRNGDSYVNCQEKARELQALGILPLQAVVEED

ICDPVRVVVR

>contig06749 Frame-0R

MVSEKRSNLECFLDSTTPVVPSQFLSKSEIRNLNKLWHPWERERVEFFTLGDLWNCFDEW

SAYGAGVPINVDDAGDETIVQYYVPYLSAIQIFTSNSSLNCQREETDSETRDSFSDSLSE

ESESEKVSRWDGCSSDECVFDQETSSHLNDRLGHLYFQYFDRSTPYGRVPLMDKVCALSK

RYPGLMSLRSVDLSPATWMAVAWYPIYHIPMGRTIKDLSTCFLTYHTLSSSFQELDENGL

SKRKRKEGICVPAFGLATYKMQGDVWISSKQDQEKVVSFVSVADSWLRQLGVQHHDFNHF

MGNRRG

>contig07481 Frame-2R|Blast-hypothetical protein PITG\_02018 [Phytophthora infestans T30-4](gb|EEY61680.1|) 1e-26

MAFTNEKKPSASVTPKNLERMISTKALRSAWPSSSAANFSRISQEPGIKMIVTPKPYHAT

HDTMPPMNQGLFIALVLGR

>contig08435 Frame-2F

MSFSFGTTTAAPAAPSSSFSFGATPAIPVSSSGLSFGATASASAPPAGNSFGGGFSVPST

SSGFNFGPRPSATPSPSLSFNASAVSSSTVPSYFGGTGPSTFGNGSFTTSAIPQTATWGG

IGSFGSGGAAAQPVATVQSVGPPITLETAFEALPENVMRNIAQFYVFLKEQDQIDTFLKT

VSPGQLEVLRDSMARLEQEVLARQNRQDRQTFSVQHLRQDVRHLLHQVDAATLTRRSLDS

SSKSGPLNMYNVTHRVEMPSPYYWDLVDHYEQKMAVIKTQIQDVEALLQPLLDGRDESAK

AREAPATRQLQQILLVQNAALMQAAARVAEVHEKAEEMRRLCLAKMREDFARQGDKHPAA

FQNPFIKRKMNSETERRQAIDKMRFRTSVAPTIVTPQPAAPAATPLGFGFGNATSNSLTS

GGGYNFGVSAPAKAVSFNLTSTAATSATPFATTTSVTATPISTNSAVGFLAPTVATSGFG

NNTSSFTTPDAVATVGTKRGGRAQKMRR

>contig09414 Frame-1F|Blast-hypothetical protein PITG\_11438 [Phytophthora infestans T30-4](gb|EEY59408.1|) 1e-91

MEKHGSSTCASFLSNDGSDDLVVRFKWEGEAIGLELMRETSPATVHTVHWGANPLGVTLG

VEETSRRVIVTRSTRSDVSVGDVLITARGESITEENFVTRMAELKLEHEYSPGIPFVFAP

PPTPVHVKKCEGALKEAGVNSTFELRFVDGRVVRYLEMKELHVLIRNSHKPCTMAFVQSH

EKQFYGILQKQEQHRRKLHHANQAAATSAGLALAAAVVVNLT

>contig10896 Frame-1R|Blast-60S ribosomal protein L3 [Phytophthora infestans T30-4](gb|EEY67987.1|) 0.0

MGHRKFEAPRHGHLGFLPKKRTKHHRGRVRKFPRDDASKAPHLTAFMGFKAGMTHIMREV

DRPGSKVHKKEIVEPVSIVETPPMVVIGVVGYLETPRGLRTLTTVFAEHLSEEVKRRFYK

NWYKSKRKAFTKYAKKYQTAPDDIENELNRIKKYCQVVRVLAHTQVRKVKLRQKKAHILE

IQVNGGSVADKVDFAKSLFEKQVPVTAVFAKDEMIDVIGVTKGHGVEGVITRWGVTRLPR

KTHRGLRKVACIGAWHPSRVRFTVPRAGQHGYHHRTEINKKIYRIGAAGDKKSCMTQQDL

TEKDITPLGGFPHYGIINEDWLMIKGAIVGTKKRVLTLRKSLLVHTKRSALEEIHLKFID

TSSKFGHGRFQTAEEKAKWLGPLARQHRA

>contig12722 Frame-0R

MVLHTELRHPHVLRVERVFDDARNYYMVLEYCAQRSLAAFVKTLPSRQMNEKTTKKLFRQ

IVAGVVYLHASNVIHRDLKLANLLLNAQGEIKISDFGLATRLGAEAHVTMCGTPNFIAPE

VLLAEYHPYTEAVDMWSLGCILYCLLLGKPPFEGRKVSETLENVANAGQTPLIFPHGFSF

SASDLIQRLLTSDPSSRPSAQQILLHPWLRDQSQKRLIPLSNSRQPNALLNVPQPVPLHP

RARALIKSRESRSRSMQEEESMLPSFNSSIPAIGKQRFTQKKSSGQRLRRDAAVRTNTHQ

STSSDSSRDSSAEDHLSSNGNSDSSDCTLSTPMDEFNQENDALNIVEMATRMKAVVSVVI

HFEVQNLTWFEPFQKAGSNSKLSLQWSCKEPDEIGQSPKYKLKISNGWEVDYNPIHGVVT

AKSVEGEFLRYEIPGMTGMQSFTQAATVERPSMPLLIRFCHCLQLRTMQLRRFALRGQAS

KLPLIQYDTLPESLLASFHERLNLFKTSYHAGFKNTEGESNMSAIKQIELPGIGCGSIDS

TGDLRVVFLDGAQLTLTASGHELKFRPAWVTKKDGEDEKAHEDVFELLSNSSFKASYLPS

VVKQKFECIPEFIRRLKASI

>contig15231 Frame-1R|Blast-hypothetical protein PITG\_05283 [Phytophthora infestans T30-4](gb|EEY69099.1|) 3e-21

MESGLLWYHPEIVSSCKRNWVFKKLRMRDGDIERFKARLVAYGNEQVFDMDYGLTFAAVM

GMSTVKFILALALRWGGYLLDRAISLTRMLKPKRNNTWKFI

>contig17462-0 Frame-1R0

MHDSNWFVQAERERRCAKGNFTIPVPPQTLPLVGSTLRPSPQVSWW

>contig17462-1 Frame-2R1

MILTGLSKPKGKGGVQRGTLQYRYHHKHFRLSALLCVRHLRCHGG

>contig20239 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57863.1|) 1e-45

MGEARYFELINDGKNPMQDGDMVLVLRDSAAKTQLPTVESNFFASLLPMLQSSKQPIEPC

ALEIIGGSNQHPHAQLPLIYPG

>contig21603 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69376.1|) 1e-118

MTHSWMEFHVPSIRYIMALAFTYANLLLPWEFRPTQKSFYGHLNWGSIDFDWNAKPNPVA

IVKTRGADDQVKLQFDFQSKPFYSNSPEKDASECQGPRSIPRWQRLLWDGLYVSTLGGFL

LLIPVNAFIGVWLGWFLVKKAFCLFAAKKQPIETKKSV

>contig22066 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64903.1|) 6e-11

MYDFEIATYSSSEGVQSGNIGGSVRLMP

>contig24204 Frame-1R

MLFGTFHQKLKVSAIDNIYCATCPKTYFVGFSETSTMTIKETAAVILSITRYSSSSIDAI

HVFLTIHAHRIIKSSNILQQ

>contig24554 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66492.1|) 1e-169

MVRGNEQLIGEHPYFVCEKSVGVRYLALLVQGRCYLISQNYEFREVTLFCPVRPDRLQPG

VDRNTVVPHQWTILDGLMVCEKDGSKSVLTLLLYDILALNGSPVMTSKLQDRLKLIQNDV

VGPRKQLPPPKGQPADMFQLILQSMYPINRVSHVIRSILPRVSQTRQNAGLLFTPVLLPY

TPGQSKGLFHWTPTSMLSADFQLGVEWRGRPPKPGFKLMIHDKRTPIYHDWITFTPDEFE

AFRQDKKASSRIIECVYDPEWLTFIPSHDKSTWEAGNPDFNATELGLGWRKG

>contig25030 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58708.1|) 1e-31

MTSVGVAPKRPVLNTRRCSQQGIAMSVETRPPRELLEKIGISGKEVVKIIKDRNWNIEEP

HGLQQQNIYHLPGRIDKNEEAIQNQDFFVGEGELYAFILKKVKSVV

>contig25236 Frame-0F|Blast-CRM1 C terminal Exportin 1-like protein [Phytophthora infestans T30-4](gb|EEY58164.1|) 0.0

MEAVGQKLLNFSQPFDVAALDQVVLCMNDPKSPHQRVANQIMVALQEHQDSWTRASDILE

QSSSIQTKFFGLQILEDAIRYRWKILPKDQREGIKSYIVSKLLMMSSNESTLHSQRLFVN

KMDLVLVQVLKHEWPQNWPSFITDIVNSSKTSEIMCENNMTILKLLSEEVFDFSKDQLTE

QKTKTLKESLNHEFTQIFQLCEFVLNKSTHVPLLQITLQTLLRFLSWIPFGFIFETDLIQ

ILVTKFLATNVFRNDTISCLSEIAQLRDVPEQYSSIYIQMYMGVLNEVGKILPPGSSLTP

FWEQDEIFVQRLSLFFTSLFRYHIQVLERPIAVPGDEAHQALLAGFTYLVCIAEVDDDGI

FKICLDYWHFFTRDLYTVDQNQMNPLAGFPNQLRSRRQLVAPVMNRVRHVMISKMVKPSE

VLIVEDENGEIVRETTKDTEALSQYKTMHETLVYLTHLNYDDTETIMLEKLTAQVEGTEW

SWNNLNTLCWAIGSISGA

>contig25283 Frame-1R|Blast-cleavage induced serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY65993.1|) 3e-96

MFVLVFAIVSNSIGVLSQHLVLASPAGVPRPPPPLDPKSEEGKARNRSWLRWMVYLAWKN

GMTPLSIARFVGPYGPKLVQNVVHRRTSFMFENSAMRDGRVDLKELGKYLYHNWALKPSG

ERAMTTHLAPGAHAVRPLVDMLLPHRVKMPLTFIYGENDWMDYHSGQEIVKHFRNMGQAA

DLYRVPNSGHQMFMENPDEFSRTLIDSLTKDELTNMHSIP

>contig27182 Frame-1R|Blast-glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY54864.1|) 1e-148

MLLILLLALRIFPIVSHRPDLLKALSNHVPAMELVHVSTLSPEAAKTRVLCWIFTYHENH

DTRLPAIKQTWGRKCDKLLFMSDTEDLQYPTIAITAPPLHSTLWQKHREIVRLLIREITE

DQYDWIFKCDDDTFVLMENLKTYLSSLDMQAAARAGPVLLGHRMTLPWWKMQKAFEPFED

FHPNHVAAVLKTVNETRKQGGLFYTAGGAGYAMNWAYLKQLKTILDEPFCLPYERIGEDW

AMSFCMRHFGVIPLDTRDAEKRERFHQYDPQYALYEAA

>contig29409 Frame-1F|Blast-divalent anion:Na symporter (DASS) family protein [Phytophthora infestans T30-4](gb|EEY54598.1|) 1e-97

MKFGKQLEISANPEWRDNYVQYKRLKRLIKRVAFEEEKKQTKQKKLQQKLEHNIDDEELQ

VIVDENHPLLKPVVDDVQDAKDQFWEVLDANLKIVNDFYIGKVVTLKRSVGEFEVMLEND

KRPTGHVHTRTRTHSQAEHGFAALQEIYDTLVDLRAFVQINFSGFRKIVKKFDKTIKAHQ

QEAFLERLNHEQFYESASIDALLKRVFCLTS

>contig29935 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67822.1|) 1e-130

MASAHVVGKRPILVDAVQMNRRIYTVVSVKLLKRGSDNEQTIDGDDSLTLRNYSYIKEFG

EWKTLKLSEKRFLQFAEINSRQSRFDLVTQDSSMSLELEVPIGTDAQTNYYLVNQATVSI

HLQELLQLHFQSLRPIHSLPEPSMREVCMIRIAFRSLAGHLHSRWLVPGNIMVESQEGDT

RITRQQTGFEHFDIVTCRAHASSMKVILPEDPGYAWIEVRGTSETALSRRSCLYFYAVVL

HYGERQITKHGGVRALHLHWLPGVLESRPTLRSRKRRYLKGNLSIATSSYESTLQDLTLT

AQMLSSNRLERYAARIESYTR

>contig31686 Frame-2R

MLRRGSRAALCRSVLSSRRRSSIAASKAISENHSVDAEKWIGLMHQTSQLETQVLLPLNE

KLLGPLDRKHREEKLPSLPFVFLLGNHSSGKSSFINYLLDRDVQSTGVAPTDDGFTIIAP

GHDDLDQDGPALVGDPDLGFSGLRVYGPALIQRTQLKVRKGIQANYMLVDSPGMIDSPHR

LPVETPAFRAHNIIQSQTTGRDSDRGYDFPEVVRWYAERADVVLLFFDPDKPGTTGETLS

ILTRSLVGMDHKLHLVLNKVDQFRKIHDFARAYGSLCWNLSKVIPLKDLPRIYTMCIPTR

DNQMQPAEGLGASMKDLNAMREEVVSEVQRA

>contig32485 Frame-1F

MARGEEKSKAESVINAISVAKNDDTKVKLPEIFFREVPSEWREWIFCESFVRLDQIISHV

AYRDLPLLLTIFASLNSFACAEENTRSSFFARREAAAKSDLPNISETSGKFLEYEDNVGG

SGLRITQIDGQENVAAVHYDLHLRT

>contig33451 Frame-1F|Blast-vacuolar protein sorting-associated protein 41 [Phytophthora infestans T30-4](gb|EEY55617.1|) 0.0 NOT\_ORF

MSLPSSENNDQDTKSIIFFL\*EPHEPLLKYERVSGHFHAIFKDDSLSCIALHVNFVCAGT

YGGNVLLLELDGRFLRRLHQHYKKVNQVCIDETGQYIASCSDDGTVAVYSLLLTANVSST

TELKGHKHVNNQSLDIVRSTSVSSTGGEVNIYNYFSAVYAVQLEDRYAMKRDKCFACGGV

SGQLVINKKGWILDKENTIHEGEGPVQLIRWKEGLVAWANDWGVKVYDSEKDQRVTFIER

PPNCPPMELCKCHLEWQGTNILLIAWAHTLRVVTFKKEESKEPVSPTSTAALNTVDQPMG

ILTAEVVALLTFDFFIAGISPWGGSSVVSVLAYRPVGSRTLSNKSLITNDPSKKIDGEGE

STVMPYPEVHVVRLDGKQVSADLLHLKGYQHLRASNYMMPTLRYAPAQEFPLKSLSASSI

YDAGYGQLAYVCTPKDVVICRLRDVDDRIQWALARNEYAQALDVALHDPRALRQVKLLDV

IETYLGELLRQKQYQFLC

>contig34278 Frame-2R

MLPMSRTTDSWGEDISIPQIDEDENRHGPELEQLSSSTEISRQTAENSLSKCRSQESPEL

YTIREISHPFSKNYASRCLETANKSSSSKMTHHCKGGRDAMQARFEDKVQNCDSSSGKHC

NDTNVKRFDDKQCSKITSDSFDQSTEKIAASQSSSCNEFFYLEPECFQDGDAAGSDYLND

TETESIGPERVQMCYEDDKKKRKSRIPFTKLQRCGLDDVMSENTLAQKGSNSLNCLGDV

>contig34447 Frame-2F

MIMSLGYTYPRRIFGSTHETVAVAITTLQS

>contig34814 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59542.1|) 0.0

MASDSSEEDEPIAAPQVASTPPKAWMDEDADEEEEDADLSQLQRQRSPKFKRCLAAIETD

QWNTDAWIALLNEVQLLPIAEAREHYETFLKQFPTSGRWWKLYAEHELREKQYDRVQDII

KKSLMQLRCPHVDLWRFYLDFTKVVKVDVAVDSKDASAIAAAKQLMVDAFELALERVGGS

IHAASIWQMYLGFLLEEQDLQAFLNVRKLYHRMVMVPLVGMETIWREYEKFERAIPNNEV

LALNFFKVFRPKFDAARAVLRDRKSFYDAVNTNILAVPATTSRADLMDMANWQKIIAFEM

SNPERLGALRLKSRMRYTLELFLSVKRHFPEAWYQYTSYENQANDPDAASSVFERAIEVI

PDSSYLRFAYADHCELRGDIPAAKAIYERLITDRGSALAYVTYQRFARRAYGAKGLAEAR

AIFKRARKDEREGACTYHVFAASALLEFYSDNSEAGKDIAFKIFELGLKKCIQEPAYVLC

YLDFLGHLNDDNNMRSLFEKVLSVMPSEVSRSIWDRYVEFEHTMVASGGDLATVAKVEAR

RAMAFPDEPFVEMKGLLSIIQRYSFLDLRPPTTCDQTFLDMYRTSFRDESSRADIADSGE

DREVIGGAGLLGGFGGNS

>contig35835 Frame-1F

MRASCTTKRCVKKVAGSCRRGTRRERRKLGIACSR

>contig36005 Frame-2F

MAPATLENDHEMVITFGDFSLEETKKALEDAATDLQTPPKPNETSKTWADALSVSQTQPK

PACIAPKAPWAATAEYNGSATIKNTPREPMKPLPFEKAIQETLKILDVSAPAKEMKK

>contig36773 Frame-1F

MIVSLAISSYDFYKPKDMMASILLFDEGSTTLFDIKQN

>contig37604 Frame-1F|Blast-serine/threonine-protein phosphatase 2A regulatory subunit B', putative [Phytophthora infestans T30-4](gb|EEY66161.1|) 1e-167

MSSLEVGGSYKDPARAIFVQRDLNHFLGSPAQQMILVFVRHLNESVKGKKISSDYEYSPN

VQKSVELLDEINSWIDEIPPIQQPMRFGNKAFRTFFDRVAEKTPAMQENMLPSALRGSII

ELMAYFGDSFGNRVRIDYGTGHETSFIVWMFCLHKLGYFTESDFSALVLRVFTTYLALMR

RLQRLYTLEPAGSHGVWGLDDYHCLPFYFGSAQLIGHHEIVPESVHDDDILLANHTEYLY

LDAIKFIKEVKAGSPFAETSPMLNDISALPSWTKTNGGMLKLYEGEVLKKLPVIQHLRFG

SLLPCTWNPSHIPGDSLAHVPVTTHPRTSVGAPNIHLDSAPAKVPRDAVETVLDTKDDSS

TALQHTKKTQEE

>contig39318 Frame-0R

MGHLYQVVPPAAFVYVMDQYLLTGDSLVGLFIVIAALIRREDVLVACTSTEDVQDEIRAT

FDVAAFADSETVRFLCLLAARLRSQTPKTYKCLQREGTGAIRCSSRQAIEIAFGSGARVV

TKKTWTRPSSGSIGSASSSVVAAPFSTDRKSTAEAAVDMSQWVMKESRSIAGKIFWYHTQ

TGKTQWEHPADKHDPPLAYFALPVSVEEVGAQLMGSGEFSSGLTSNLRYFVVDCRGLRSS

EELKSGRIPVAYTLDPSVFDSPELIAKSLAAFNPMKSQVHLVLVGHGVGIPPELVTSEDA

KTSIRDAVRLDTDCLNQAALFFQKRGFRFVSTLDGGYASWHAFMRDRVGSSPQELLNHVA

AECVYCRYDAIVRTGVDPSKKNIKPKFRRKKTMPTTTSMPVNGGQGDGSIVSTSNANAST

SQNSSGSSRAPRRQLSLSRNSLSSMRNKLSEVSMPKKWTWKRRSLRDTRTINQNHSGSSS

ETATVDDGGSEHDSFTDEQEEKSEEITHEMLRAALEDAEDAMTSVEGTNENQFVGVFTID

YSEDEDEDSKLHETQGREKEECSSAFSMKAVVGAETESKSSE

>contig39448 Frame-2F|Blast-AP-1 complex subunit mu, putative [Phytophthora infestans T30-4](gb|EEY62681.1|) 1e-133

MVLSAVFITDLKGKVIISRNYRGDIPMSASSKFTRYVQDKDDSEQRPVFTEDGFTFVYLK

HNNLYLLTVTKVNSNVALMLMYLTRICQVFRDYFGELEEESIRDNFVIIFELLDETMDHG

YPQTTEARILREYITQEGHRLEAAPRPPTALTNAVSWRSEGIKHRKNEIFLDVVEKLNLL

VSSNGTVLHSEIIGAVKMKSFLSGMPELKLGLNDKALFEATGRSSSKGKAVEMEDIKFHQ

CVRLARFESDRTISFIPPDGEFDLMT

>contig39642 Frame-1R

MEWLHDEERQPLLSPSGRSPRRNTPPHVPSRMVFEPPPLRRDAGGTSLHFTTQPSPKNVS

LPIQTRATPHCYSSISSRHMPQTLTGFNRFKITEALQSVPCIAIAVLVNLMICVPFGLSF

FPLNWHDMPVPHALGIQMFLLSSTICQFTFVWQSHFDGAICQMMVENVPFMHTIAVAIIQ

ELGPKNPSVLPTILVTYACSSIVCGTLFFVLGYWKLGNLVYLFPKHIIVGAVGGIGAFVM

QSGLENATGRGFNWSWVAIKGLLDLEIRWLWITAALLAILLWILTHRIKSPLFPPLYFVS

IPPLFYLGLCISGVFPWNPLENMAGSLVARPRCHSTRSGSNTMCL

>contig39967 Frame-1F|Blast-vacuolar sorting protein SNF8 [Phytophthora infestans T30-4]gb|EEY63604.1| vacuolar sorting protein SNF8 [Phytophthora infestans T30-4](gb|EEY57535.1|) 1e-125

MRRRGVGIGAVRKKQEQNKQFSEIGDQMVEENLSHVASQLELFRTNLQAFAGKYKNNIKK

DPDFRRKFQVMCAKIGVDPLASKKGFWLELLDVGDFYYELAVQIIEVCIITRPKNGGLIG

MNDLLRLLEKKRGAGMQMVTDDDVKRAVKKLSVLGEGFQLIDMEERTMVVTVPMVLSQDH

STILALAQTTGGMVNISILARELQWDKKRSMLALNVLLREGMTWLDEQTSEPSYFFPSIT

LSGTYT

>contig39989 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61852.1|) 1e-47

MDGPLGLTLVEDAISGAAVVNRLTGKGSSANLELLRYGFELMSINGKRFESLALNDLCRD

LLALPKPVILVFRSHECDDISGKDEVFERCSSLYQENPSDSGGALKRNAHYDSAATSALQ

RICPQQASSLRNQHEYEVIWTSSQLGLQLEIFHDKSGRTATARRQYPIVHKILKNSTLDL

PSHAVGHFFVSINNWDTLGLNSTELRTLLRLASRPVVLRFRTQGNSSDHKQTLLATTFHE

KDEESVYGRNETITSTYSILWSGGRLGV

>contig40264 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54170.1|) 6e-39

MTRQGYLIVYDKRDHPTVRFMSLEDGYFRQYASADCLKCLSEVRLSGCKITVKAQKRKDG

VPNSFYLETRKVFVKERSYTLGNAARIELSACSNEDRHGWGKALFSWHRYYWRDPVAATS

ETHASSYETLLQLEQVIAKSTLQKSSSSRSISFVAATQPISFLRRNAHTLRRSLLLTVTS

NSKPESETEPTDCVKDKVVLEKVECQETTESHNPCDMKADRSTRLGCGNN

>contig40835 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59543.1|) 5e-78

MLSLLIFCDHRVLLIHHLPKLTYQSKECVKLVVQSYMELLATDRSLLVPVLGSLSEMPLD

ISEKNTVVEATEALLDAVVEEDIPSVVQNLLSIVTKKSAPKALARLRIECNRIQSGTLSL

TMEVIGRYATTGLVVLAALLRLIRLVDPLTRFDVVFLTFVMGKVAENELV

>contig41278 Frame-1R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY53382.1|) 7e-81

MLQQAETQRGFSPLHLAIRSGNFEMVSLFFRPEVLPRLDLSFSDRDGNTALHLATQLEVK

FASRVLELLLCFGADSNAVNFLKQTPLHLCSMIKRSESASCFIMETLLRHKADPQKVDFL

KRSPLHYCMGRDMMDEAILLVKHGADLNIPDVDGMRVVSNFKAIELLRHLRVTPSWIPDT

DVTNCMVCLQPFPFFFSGKGHCLRCGRVCCSDCAPSSPSWNGRYCFDCKHYAHYS

>contig41447 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61892.1|) 1e-40

MDRKAANLAKQNEKPMTFNGTSYGHSDRAFRMKEKDRKERELKNDMAIRIQSRERGRLAR

KAYSERLEASGKIAVRIQANFRRRQAQKHFQIHLQRRQREEACAVVIQKHVRCRAQRTRF

QAKLVERNDAAVYLQCLIRTRQAQAAYRNQIKAVCNIQNFIARMLAGQKAKNEVSYLRKE

RSAAILIQSVLRSKAAKSRVLARHTAIVRLQCAWRGFKAR

>contig41814 Frame-2F

MGGHEHHREGQKSSRSGPWEGSEKLKQALGGLSTAKGVSQSRIGAVAKLAAHYSKHYKHV

VHDIETFLWKAEIEHRLAGLYAIDAIIRQSHAKNPKDAYIKRFLIRMSDTIAAVKKVPNQ

FQPKVYHVIDEWQKRGLYTSKQIEDAGGRDYLSSRHENRSENGTPRTSPGKLASLLSIIK

QKKELAGEQQEQQRYNDSFDEGIDPKDNASAYNHQQYDEQRREDPQLDCRGVVGIMGDAP

TNPIGSNRVQRDLNDRADILNDRDFKKARGSRWGPPKLDNMHPNDRPAPIVTSFDKDENH

RQDSSSAFVLPPESIRQTAILQSSHGGPSRHEEWNRNIPSNGSGLSWPRESVRSPQSRGL

GRQTANPYEQANMQRAPFISSDDRRSPGNRVPGTSGEVCRNYLAGRCTFGDRCWHIHDSQ

AAIVGGSRSEIAESKRKTVLCNNFPMGMCRFGDK

>contig41861 Frame-2R

MYSAALLYLVQRGVPASLPDAISRRRLSEMALTEVGNFAAATADIEVNVPTATAMVTVAG

SIFIVLLMLCVIFLPTSRVKLSPDTTPAAQYVQILTDDLYPDLVHKKRLRFSNGDCLLFN

EYVVDTIGLHAKRDQSKKIYL

>contig42095 Frame-2F

MTKDKREEYSDEIDQVESVPTFHTPWDVTETASGLLIPSYVLTQLLPHQRECLEWLHKLH

ERGVGGIVGDDMGLGKTVQLASFISSLYGARRLRTVLLLCPASVLLQWVRELHKWCPWMR

VVLLHASGTGVNTQSSKDQYEQLIEEIFSYEEDDDEARGLEENMPRSGGVVISTYENVRQ

YQSLFLTREWDYAVLDEGHRIRNPDAETTLACKQLRTVHRIILSGTPIQNRLRELWSLFD

FVYPGRLGTLPTFEDEFVLPIRAGGYATATKMQVFMAYKCALALKDLIQPYLLRRTKQEI

RIGHTASSMGPLLPEKQEQIIFCRLTKRQRALYKRYLASSEVALILRREMRPFRAISVLR

HICNHPDLLSTFGDGGLADKKHHINDEEDALSKMLKGEDSDSGEVECVEPFGAASSSGKM

IVLQKVLSMWKDQGHRVLIFTQMRSMLDILESFMSRNGYACTRLDGTTSVTERQQRLDAF

NSPV

>contig42154 Frame-0F

MRYLLSKTYLLAYIGSNKFKNLSLRIQATKLR

>contig43773 Frame-2R

MVMTSRGKPSVFAAFSQLRVNGNFDSGDESAEERQHERKNKQKERKKSRNKKTSSDLAQL

KDLAFVSKSKSKKSKSKKSKPMANCDPCSPSEFCIEAPATDCNSKENDVRKFPMSSLSSI

IEPQKTLGLIGVEKTLMPSSAEKKQDRAPLQQQDRQKKQQEQHNKLLTLNQIAAPPAVSR

PKSSSETELGAVYTPSHITITRMDGQMQRTLSVTEVMDQLLRCTQQNTQLLLVQEKLGVR

NSLRE

>contig44686 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59936.1|) 3e-17

MINKPELLVTVLFGKQSTCFSVPADDPRALDIVKLHIFNEFQLESKFQRLVLRGRDVNSA

TALTNNCKLLVLRNRAYHENNSASKQDKTTFTDSS

>contig44945 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57628.1|) 1e-153

MMRSIMLIAALARTSFASTGPYDGWAPHRYCNSMDGIEATRIPQLTSQQVKRVESLEQVQ

IIARHGARVPYAKLFCWDSNIHNPMGAQWNCTTTSVSSHDINLNENTAGFGRLYRKSYMK

GHNILNGDCVVGGLLPLGRLQHKSNGEFLCDSYVGDGPLKLFPTANLSHLELSKIYLRSD

DQERTLGSGQALIDGLFPVDSTRSFEMQRMLSWDVSDIAMDYISPNENICPYIGHISELS

SKSVEMEKHLQDTATVKIDKHFSNIVGEFSWSTVLECLSTARCNNLELPSGIDEETFAKT

YHEVEVRQGYYLLYNNSWYAKLAMQPLAHDMIRRLDDALTGNPDAFKLSVTM

>contig45326 Frame-2F

MLPLLMQFWSMTATELNDVLQTQGQAATQTNNEKVATIALSLLTKGVIQLNVLSTATKLI

STMLLNAFRDLAALQSGEVMRSVFIEFYNQLERLVRFRQALSVLIENPSGFALTSDSKII

VLALDKCMHRIAVTILGVQKAYPIEFREHLQPYLSFFWNVCHVFAMAPAHASPRQLQIDA

LQYFANVLACRLYKIRDMSGPRCSTQIISKVITATGDVALTNAILFEAQTEINAFFTQVD

NRFASLLKMMVMPYMVLNDKDLAEWRSEPEAFYTVMESLTAQESVRACAENVFLTLVQNY

SEQTISALIQMTSDASTYLVDLGRERPMYANTDRRVLDIDAVLVAIGLSCYDLHDCFEFE

PWFLTNLVPILVHPDTTVGSFEGLPILRFRIVWLVSCWLAQLSASVRPPIYDALLNLTTF

MHEANADVALKLRI

>contig45393 Frame-2F|Blast-ribosomal protein L31 [Phytophthora infestans]gb|EEY60634.1| 60S ribosomal protein L31, putative [Phytophthora infestans T30-4](gb|AAY43425.1|) 4e-08

MVKEMKPRNTKRAPDVVARDYTINLHKRLHG

>contig46451 Frame-2R|Blast-hook domain-containing protein [Phytophthora infestans T30-4](gb|EEY55947.1|) 1e-149

MEREKRELTERFERTLTENRELAEKYTILEFERDQLRSERQNTLTRDNKKIQQIVDNEVH

ALQLQMEEKDLELNRVKRESGERLMMLENEVRRQADEIDISRSKLGTLNKLEASVSKYKK

KLEEMNSLRAQVRELEMLNAQYLDKVVDLESTIKTMPGLKNLVEKYKNQVVELETANVQA

SSNVSVKELKIRRLQEELENALGGKEFLESQVEELRTQLSNMQYGESTDDGMAAGESSAV

NGGGLSADMLLGRDSVSGFRERVARLERENAELKSGNADAGL

>contig47346 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63236.1|) 2e-14

MNRRRSTLNTNFDSSRKPCSTTIDSFETQHDKSKHGSIMTNTELLHLAREARASVKFESL

ASKLVEEKDWKFVKDVGEFSVFRRYESKKNNSKRQRSLEVMCVGKLNSSLEEIASILHPS

SEAEHNTVMSA

>contig47485 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57840.1|) 9e-13

MKGLIDRLRHLEYSIRLMKGGSAYPPNFVMESV

>contig47764 Frame-2R

MRSSFSSFIWVLHAIREGGEGRKNLFVYRLALSVSWRVYYNRRGTQRTHCAY

>contig47816 Frame-0F|Blast-Zinc (Zn2 )-Iron (Fe2 ) Permease (ZIP) Family [Phytophthora infestans T30-4](gb|EEY57839.1|) 6e-29

MVVQASLRLGPRLAMTLLSIALLSAFEEAVLPVPLDAQENQRFEIKSFTQHKAHDNKYDH

VHDGSADEEKIATKLKSARFTPIIWGHALLATALVGSAPVLILFILPLGVSSLEKQQPLL

RVFLSFAAGGLLGDALLHLLPHSLPEHLLHARKPTLHNHSHGHKSHEHSVA

>contig48314 Frame-0F

MGSLAIHQSHASRRTSPVASAVSDPTSPTTMASPAVFPPLHVHIPSTSRPHRLMPFAPFP

QSTDDAERRNVTALTIVDLLASTTYGTCLKQQSPQPQSSLPSLRPLPSTSTESSFLPFLP

KIRISSLDRRYAFPSTSSNRMIQATYVSPKASSSHNSPRGEATTTQPKAAADEFVMTPIA

PKRGRGACATGTVNNSRKRQKDELTRLRAHVQELQRELEHVRFNFPSSQLRSVAVGQPV

>contig48361 Frame-0F

MKKKSSLDTTASCEISALTSSVKAIDVSNERENLMTPNSVISEVDQEQFATSDLLNKSEV

VNDQDKRNIQAEIIKMAATEASTDSEVEETMVIDPVVAAEETTAPVSSFSYVSEQICKNG

YAVSSVAVAVTTAILATLIARR

>contig48978 Frame-0F|Blast-inorganic phosphate transporter, putative [Phytophthora infestans T30-4](gb|EEY53220.1|) 2e-90

MLDSRGMKAELLLNQVALHERASNDGRNAKTSSSSGVLEHLPVNDPQTMRPGYGSTALEA

TQRGTDDETVSNQIIVSAVANLSTAYNLAVINYALMMLERSYPDSSPELRSTVDACSLLG

AVAGQLTFGYVGAVLGRRQGMILTLLLSILGAASSALLPWGSDSVYYVLAACRFVLGVGV

GGVYPLSAASALESNPTQNEYHKSKIVAAVFSFQGIGQLLAPLMAYIMLALKLQHSIGW

>contig49076 Frame-2F

MKIEVESELPQLSRCVAWSCLFRIQDASDTTSFHEFRVDAFWCLTRDGMAPEEFPKSRSI

VVSQCGSVGMEKLEIEVRNLHKSAMTFFCIESAYDHWKLVRQLVRYSDKRKHNSRALVLK

ILPECPYNMYVIPPGASINSEQNNYWPEKALQSVAIDRKCVVGFLTKRKI

>contig49869 Frame-1R

MSTCPHCFTGTCRRHKQQDNGRSMVKTANAESTLKKLYDQLVGSKLQKLQAEAEKDPTRQ

HAKDFRKQLDLSRGKSLRKSHKSSLKSKTSAATSSGLNSQALAAINDSDSDLEIERHKRK

KHKHSTSSRKRRRKFKGDGDGESIASDDSYRSNYSHDPHKILRHSHKKNKRKKRSRTDDK

KAFG

>contig49887-1 Frame-2R1

MGRCSSLSMYSSSSVARSMFQFLLRSLVYETNEA

>contig50416 Frame-1F|Blast-3-deoxy-manno-octulosonate cytidylyltransferase, putative [Phytophthora infestans T30-4](gb|EEY53560.1|) 2e-63

MECINIVVLNFNYTMKALGVIPVRMESTRFPGKPLAVFFGKTMIEHTYAAVRSSKLLSKV

VVASDSERLLRVIKEVGGDTVLTGACNTGTDRVVQALHLMDPKEMSGFDVVVNVQGDEPG

VDPRHIDKCIEALRGAGPNSVMSTLATPLYDEQGAHSRNVVKCVADCN

>contig50885 Frame-0F

MEPLDATTHNYARMNVGVPSNGNVRMHPLALAMGVVVVFVVAFLVAASSHQKQKLQVMAR

KLLRKKRTEESKDSGGSVNKVADLPEFARQAAESGNARVVKRWVHSTDRNLDARSTENLT

ALHYAVRGGHNECTKLLLMASADPNATDERSITPLHLSALGGHALCVKLLLDHHADPFLE

D

>contig51051 Frame-0F

MPSSVATENKAPDITTSSSSSTTLPTKSSSSLTMQAFAKPVQPKQLKVIKKRAIKRLERL

PFGGGSAVSKSSDLIGNLMLRKSAKDAAAKTTSKSLERTDVVSSDAKVEVSLSPTIHKET

AATISSHADPLSIPLPTIQSFKVATTSSTALSGERKRIRWADEKGKELVQVKLIESWRDL

VPFDPRHDDQSFKDAKLREHANERHALLAQHHKVPPAVAIAQSREWTTPVFIRLPQAVAT

RVYATTVTDEMRVQESRRRHVDEYEVLVGEMPIQSPKEWERLNEPLRGPPLEIPLCDAVE

TEASNPPPLVSAPVSAPLNSVVPNHNGREAFSAGRFGQSMPGYTMIDSNAYTNRPSLEAD

R

>contig51477 Frame-0R

MAKSNKACYSLLNFQYCRPTGREFSNTCDALTDLLSPPFLRRFCAMSGCHVVTSDH

>contig52142 Frame-1F

MPIGGNVDEDKVELDIDVIHDYDELQRKTLSDCSDMSDDDEFGSANVAARYDGSSTVAAD

ELNNIMPVASEMESETAQTTSNLALEASVVDRYYRGVDERTRQRAQGRNIREALLLAPDQ

SRIKYLEQLLSESVARELQLEAELDSVVHHAAKAISNDTNGTTSGAIA

>contig52418 Frame-0F

MFLVSRRWLLRWREYIRNLEGGVPAPLSPLSITCSHHKLVLPPGLIAAQLGQLFNASSLE

VELVTIEAMQALADRYG

>contig54852 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62219.1|) 6e-35

MESTVSYGPAVVMRHGDQVVHTCSLTHARQVYEHILSFQAAKADSDAYIEDHGFCTGPGT

TMLNGFSPSGHSTPCILLWFPGWVLD

>contig55028 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64249.1|) 3e-46

MQISTFTEEIVLCVGTSSTRDAWMRGILQHCDSKTNFERAQQGEMYIGFAAITALRPANR

VELNSRLLFPRLRQQRMWTEDARHHANDDFLGVSDIPSALKLVDRTLASALHILNNTQQL

SVTDVMAFLDDASALR

>contig56821 Frame-1F

MSLNRRADPPSLSSIRVLKRDQTVKILGIIFGLDSVDEATVEFWT

>contig56854 Frame-1F|Blast-aldehyde dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY57483.1|) 0.0

MLRSSSLRAISTIASRQNLGAARTISSLPSFATVDLNFSGTKPTDGFNLVNGEWTKTSKT

ETIVDPLNGEEFMTMPLTQKNELAPFVASMTSCPKHGLHNPLKNVERYLLYGQVSAKAGA

LMREEKVADYFAKLVQRTSPKSYFQARNEVRVTGKFLENFSGDQVRFLARSFGIPGDHRG

QASYGHRWPYGPVALITPFNFPIEIPVLQLMGALYMGNKVLLKVDSKVSIVMQETLRMLH

QCGMPMTDVDFINSDGVVMNDLLMQVKPRNTLFTGSQAVAEKLAMDLRGRIKLEDAGFDW

KVLGPDVRDFDYVAWTCDQDAYACSGQKCSAQSVLFVHSNWAKAGLEKKLASLASRRKLS

DLTVGPVLTVTTKRMLDHVAALLKIPGARVVFGAEELENHSIPKIYGAIKPTAVFVPLQE

FIKPENFELVTTEIFGPFQVLTEYNDNELPQVLQALESMDAHLTAAVVSNDQDFTNEVLA

NTVNGTTYSGIRARTTGAPQNHWFGPAGDPCAGGIGTPEAIKLVWSCHREIINDIGPIPK

NWTIPEAS

>contig56995 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63492.1|) 8e-09

MSQSMEYARSVRSALSPQTLFVSAFPILISVSLLHRSHNISFLQLDVVA

>contig57259 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60938.1|) 3e-12

MGNTVTLLSACEYGDLAEVHRLLKTSTAENLEAKDDSRRTPLL

>contig02296 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53257.1|) 5e-14

MIHLIHGGIHSIGKTCNVCMREFYVLRKRHTCRICRGPICRRCSIFRQVPKQSMENKLRI

CYCCYIASRTKDLKNRINQSNGDSENCESSNNL

>contig07574 Frame-2F

MNPPAGGPSVVGGDYEQQHPQNPNPNGNVPVNPPASGPGVVGGDNEQQHEKKEEVGNKSE

KNEEEKKKNEEEKKM

>contig09158 Frame-2R

MTRENQKVVAPPSLYFWPPSAQATPGAERPHFSSVSMDSSSNLAHLGPHKTRELLVSAPK

VAQQSVFQSMWIGATAGMGGIIAVYPVDVIKTRMQNSLVATSAAQTLTTIFRNEGVGSFY

KGLGPQLLGTIPDKAVSLATREFVKSFFDKPNAFKASLTSAAVSGCMQSIVMNPVEVVKV

RMQLDRTLKPIGIIRELGMQGLYRGYTACLARDVMFASTYFTLYDMAKSQLGVQDGTSLG

WSMIAASTAGIPAAFLTTPLDLLKTRMQARNATVCGFRETYRLVTARGGISALFSGYGPR

VSRIAPQFGIVLVSFDWLTHRFNPAVERLPEPADVDAYADY

>contig10163 Frame-0F|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY57969.1|) 4e-22

MLFMAGGRTDPTQTLLFMQASIPVSACMSFMIYGVRYTQLQVAGMLIITAGLVLSVIPCI

E

>contig15245 Frame-1F

MTSDSLALHRQRKRKFFAELAQLFDEDPPEIRPLEGAFFGPELPLIAPSLVSSSQESNSV

TPTLSLPFDCISADSIESVDLNATRSLSSGFSVFQASQQSSIFNESTVDSPLLLPNEINS

SFDSIIGKIQKRKDQHVHFDLKPDTKRNSTLHGRHHNCTLLPATTLANTDLMSDKLLETV

HQELADYYDSDRMCELLPCWLQNSEASCAIHQDHVRRPMLLFSLQALDESIARSKWLGQH

SWRVQVCKLARRVLSAMWEADVLDTTSPGQDIALPDNSSQKSAVAGVAMDVWRIIARYWD

KYKHNYLHQQEPFFHDAAESRPTNTGSKWDQVRALLHVYGMKLSEASSLVKQRGSDHFFV

SECATIFFPLNHGLSFIEQFRDNLNYRKVDINRGLTKIAQRPTISQQDGKTAFNAILIHL

SNWNEHVQVFPCGSFSRGAAYISVLDILVAVSSSHGDTTNPKANAEWFDKVAEALIAANV

VVEGAMRRLSPSRGVCPIPFKNNCVLLDLKVYCPPKSWIALVYFTGPECYVLSFFASLLR

RSLIELPNTSFECIFNGVAETLGEKVLSEVASEKDLFDLTGRDYLQPTDRM

>contig15696 Frame-1F

MVKLLCALVGEGNVFSVDIDGKELVGDLQYVIRKNTPNKIKCSSAQLKLYLARRGDAWLS

DSEPSAQQLIEGNVDDDIEIMLSCKPIKTSWPIQHCLDEKQLPAPQLKQIHVLVVVPIRP

LQSVPQIFFIILTNNSAVKTVERYEAVAKTLARTEEVESLSKTIRTILEGNFKVTPFVVL

ENSSGTGKTQMAFNLDATGRFDVFYIWCAKLGDSAQS

>contig16756 Frame-0R

MPLDSIREVHASFSFGISEQQSGNSSSAVIKINTGRSTDGSATFVHIIRLAFYNGPVAAT

SSEESTVLVNGNQFYVITNKVNDVTTFTYIPFKNAMEFVGNLLDFPKSLPKDSITLPLDL

LSIEAGSEVFRGKVSFNAYLEVNVVKL

>contig18080 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY54360.1|) 1e-148

MIGKEKLRRPHERQSIEKEIETMRVAVEQFENGHPHIVRLLCTKESQQHIFIVQEYCAGG

DIAQLMKTTDGLTETQARLYMSQLASGLQFLRSQNVVHRDLKPANLLLSSRNPATAKLKI

ADFGFARELESEMMAESVVGSPLYMAPELLEYKCYDAKADLWSVGIILYEMLANEHPFLV

VDKVHATNHLALRRNIYRYYECFGHVRFPKKIKVSLECEQLVAALLQVDPRKRISFEDYF

RAPFLLPPAPSDTDLPFDTAGLDSSETKQPLVAEKQTEYEDWATFSDEYVMVESEYEDVG

RKVLNSQDLNVDLDAKPKHHTKEYIPERDSGSTLCDGGIEIRDIVIDTSSPRHGGPEAET

ARSPVLNTLEVKAGMIERNANATMPKDHWLIGERRQWVTDDNRLEELLGICYKSFTCGSV

ALFVPTPFGDYIAFHEGCPHYYLSEESIVASKKHDRNPPYVLGHIVYIEDHETSDEKNPY

CLREGTKYHVASVTPLATSSHNANGSVETADSSDASHELPLSQVLTGKAVVTGYEDAGLH

QAEND

>contig18707 Frame-1R

MEKCLMSNHEKLRKKTEMRVLHHPFVAPLRFLYQSHSRVFLSMDFYSRTDFSRI

>contig19573 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY70392.1|) 8e-33

MTAILNALQHEVRQELLEMNSTDGISEKRRMVLMQQHQRLNRRGLQDLLRAHDTDEH

>contig20238 Frame-1R

MNRDVLLLKKEHKALNDEASMTSSEQSYEYEDMDIDIVARDVVLGDMDTRVDSASMTRQT

LISESKRLEDVSTRQTLISETKRLEDVSTTPSLEAHQLEDSHSSITTKARTVSIASNPSV

PSSQLYRMNSFASHTSSTLGPPHGSPHGNVLLFVPMAGSSLTASASRMNQAHCELVDLMA

NGHKVPSRGMQRLENIEWRYGVPEYVLTDLAYVRGRTREPDTTPLASYVEECCQTFIMEA

THKARYDQWESVNHAHFYLQVNDSKRIQGSSILENDMFGLLYLGDTEASIGTRSDTSRES

QDLRVEVAKAFPDGFPMEVLEVFTQPPQCYFSWRHWGSFTGKYKGIQGNGSNVEVRGFGE

MTVDASRMRSLRLFFKLNDLISALQHVTDLVPRARRDSIPKKRLHVPNGRMARAASATVA

SVTRIPELKTSEIIEGLANFTIEAKEQRRKQTQ

>contig20735 Frame-1R

MIAQVLILLAVLLALRVWLVIIPRRIKVPISSYLNPLFHQLHVDNRKKRRRIRVMAVLGS

GGHTTELLKLMKNLKRAVYTPITFVVAKTDNTSQAKTELDWKP

>contig22737 Frame-2R|Blast-bifunctional purine biosynthesis protein PURH, putative [Phytophthora infestans T30-4](gb|EEY57972.1|) 0.0

MSHILHAVSTGSQASLVPIKRALLSVSDKTGIVELATYLSQHGVELLSTGGTAKALRDAK

LHVVDVSTYTGSPEIMDGRVKTLHPKIHGGLLGVRGNAQHEADMAANGIQNIDLVVLNLY

AFDAAVANGGDFDTCIENIDIGGPSMLRSSAKNHKAVVICSSPSQYPTLKQELETNLDSF

STSIEFRRGCAAAAFALAASYDSSISSWLNGQLGTSVPIVTRVYQNEFPLKYGCNPHQTP

AGILSQMGSKLPFTVRNGTPGYINLLDAINAYQLVRELRESLNLPAAASFKHVSPAGAAV

AVALDERLHAAYEVGNGTLTPLSLAYLRARNADPLSSFGDFVAVSDIVDEATAKILKREV

SDGIIAPGYEPAAFEILKAKKKGQFIVLEANERTYSQPEMEYREIAGVTFAQKRNNVLFS

PEKHLADVQTTGAGPLTNAKKRDLTLAAITLKYTQSNSVGYAKDGQMIGVGAGQQSRVDC

VKLAGRKVAIWHLRQHPKVQHLDFHDHVKRQERVNARVRYIEGDMAPAELATFRTLFKTI

PDPFTTVEKDDFLQELTDVSLASDAFFPFRDSIDHASKLGVKFITQPGGSTRDSDVKLAC

DEFGITMAFSNLRLFHH

>contig22782 Frame-0R

MAKIFRSPLAMITLASCFFQHAFASEKLCSIAPTTYTMAKTKYPNLVNALTTLEQYPIVA

WYTDRQSEVDRKGMLSRITSECSDNSRMTIAVYGLPNKDCNTKLSSSGTVHSTSDYESFL

STLTTAVGDRKVLYIVEPDAVGLLANNGCGQSAGYLKNLKIAIAALSANPNAELYVDVGY

WLLGNSTKASEVATIVKELSFSGVLKGIAINTSNYRSTDECMSYCDTFQAAMGMTTLSCI

VDTSRNYHGSPTTDWCNIKSAGIGKPPTSKTNISNVDYFLWVKPPGESDGICVTSTQSLT

GVTAGTFYAEGFQSLWDQGYFIDEKTKATIGGSTSDHVTSNDASVQFGAGSDVKDTSAND

SVIQTIGTVAPADTDSSDDSAVTTPATVATPIVTTLPPTTISPNATDFGLLQQTSACKPK

RRMREL

>contig24205 Frame-2F

MLRVGHFKTSFPMDGGQLDRDHLRRQKSGINRQ

>contig24270 Frame-2F

MGFAFCLNSLDCTTFPLLHKEFAQSFVSSIGSRLNRIAYVDNDLRHRPNQKCRTRGDVIL

LKAMQDEKLRAIALDGLDMFRD

>contig24494 Frame-0R

MVVHRDVKSRNVLLSASLNAKKLCDFSISRRNQSGNNTSSNVIAAAGTLSWTAPALLLGE

ACREKSDIYSLGILFSELDTCILPYYDPINQSKQLTRHPLRLMRRIVHDGLRPQLSANCP

LPSTHISAACVPNARPSAADVGAWLASARDEQLLRKPSNVV

>contig24555 Frame-1F

MNVIYSVKDYVSNVFYQDSNSGAIDVVAVQQPDGTLRCSPFHVRFDEAKPMEKQQVRLEV

NGKVVESVSMKLGSNGEAYFARHVELEKDELASPTTSPSSHRIHQDTYAASDALKPQDES

ESNDRSALEPDAFFSKLRNHDFADEYSSVTKSCTVMDIATNNASAWDDNLDCSHPSMSLC

GHLLDQAKTKSDVHRIFFAHLVAFDNFRNHPEILKNSNLRFFVGDNIVPYDAAIQAYLVS

RVLFPYSQHLRVDTSAANRMIHSSDSYSDHIPNQTSNSSIAHSVSCGSTPSLEAAYENCS

DDDNSTQDTASVTSEEYVEKSFVPSEDEMRDMSLRIGMNEIAFVLQSHNQDEVARVSAKL

YLWPVTAKLVIVQIDGAILSSAAYGRMFQRRDAAAMHPGAVEFYSKLARNGYHIVYVTYF

GLSQATLLPTLMPQNTGDFGEPALPMGPVLLSPDRCPVNDRTEAQDFQKTALRDLSALFP

REVNPFYAAFGTSSIHSTIFSQVGVFSGKVFLVDPSNGSLRHWTLMAFRESYASFLARLD

TIFPPIQSLMPQDSDSCSSKQQQVVPHERIPRCIKATSCRFYNKIDLLPLVPSCSLSDEA

YNDMNFWRLEPGQV

>contig24977 Frame-0F|Blast-ferredoxin-dependent glutamate synthase, putative [Phytophthora infestans T30-4](gb|EEY58996.1|) 0.0

MAEMALNKMNDEGLLRAHSKKELASFEVFDKYREAVGKGILKVMSKMGISTLQSYKGAQV

FEAVGLGDDIISMCFEGTNSRIQGTDFEALYTDISRFHEAGYPLHSDMLPLIRNPGSYHF

RNDSEIHYNSPKNIVALQRAARENSREAYAQYVEETDALCKRVNLRGLLDFKFVEEDKMP

KIEEMESIADIVKRFNTGAMSLGSISQETHEALAIAMNTIGGRSNTGEGGEDVKRFTKPG

GPPNLRRSAIKQVASGRFGVTMNYLTNADQLQIKMAQGAKPGEGGELPGHKVSDYIGSMR

HTTPGVGLISPPPHHDIYSIEDLAQLIHDLKHSNPSAEVSVKLVSEVGVGVVAAGVAKAK

SDHITVSGHDGGTGASSWTGVKNGGLPWELGLAETQQTLVLNDLRSRVKLQTDGQLKTGR

DVMVAALLGAEEFGFATGPLIALGCIMMRKCHLNTCPVGVATQDPELRKKFQGQPEHVVN

FMFMLAEEVQDYMRRLGFRKLDDLIGRADLLKVNQDALHYKSRKLDLSPLLINASTLNEG

AGVKKETEQKHEVEKCFDMGLIEKAKAALESKTRVVIEDTVTNLNRTLGATLSHEICKRY

GEEGLPDGTIHLKLKGHGGQSLAFGLAKGVRLDLEGDSNDYVGKALSGGEVSVFPSVDFS

ERANPENVIVGNAVLYGATSGEAFFLGKAGERFCVRNSGVKAVVEGVGDHGCEYMTGGRV

IVLGSTGRNFAAGMSGGIAYIFDEDNSFEKKCNMGMVRVGPLVETAADYEIEEVKALITK

HLERTQSPKAQYVLDNWDSSAHKFMRVMPSDYERVLLHSAVVVEETRKLVSDSI

>contig25031 Frame-2R

MNNTITLKAMESGVTAFGPPPASTYRFVILHLAEKLKLTLEDRTTKKQWSSGFLDEKEYV

TSTNRIPNASLLEYIKVFKDTLEYLVRDEKTALKNDVMTQATNLVDSSKIRRKLTLLGDD

AVQLELTVKIRIFQSAWTAKYVFYLKPVALERIDILEAKFRDLQDELEMTKNTLDKEKQK

RVDVMEALSEVKNKLVAAETELASMNKAQAVVRLNAASDNIAELNDKGQVLWSTVIGIGF

ASTKNGYGVRFLVAGWYVVNATIYLAPQTNGTDIKIEVNGKYLRSQPAPCTLKQNASVTF

AITTYFRKDNELSIVISKFPKNVGANLDAFRVGK

>contig25695 Frame-2F

MVRVYVAALTGFLALSASASATLQLTSVNESLADAYDSTAPARGKLRAYAATNVESDERA

FSNLLEHLKTLNVLFSPLSKERMEAAISKSDSSVVKHLSEDGAVNEKKLGIGRDGVKAFE

PAKVSKVKMILEDIFRKPYNKILLKVLSKANGGERNLVRNLAQAEMLGYKVFFLKSTLAS

KWERDGVSLMDVWSYICKDVKAPTEEEMKIFSHWCGYAFVLSAKGKFSAEETVIEKTLLK

VHNDNKNKKGKLAINMLAQIHLSRKFKVDANFFELYDPSPSSLKKLLLELEKSPRACDLD

VELYRLLKQAVTDDKFMKGIWDRSTKKPEQPNAKRN

>contig26733 Frame-0R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY60539.1|) 1e-128

MSFSNSGLSPWTKSVLAGSVSGMASVAVCHPFDTIRTRLQVSPAHFRGFFHCVQQTVQQE

SMRGLYKGFLPPFFSQGVFKAVIFTTSSTLRHDVLPFIPLLQPVLTPTVLSLTAGAIAGG

ANACLVAPVELVRNRLQMQYENQLETRYYRGAYHCVIQVIRKEGKLALWKGLSTTIIRDS

LGVAFYFLGNDVAKHFLAKKERFGETSTLLTAGAFGGICYWAAALPFDTIKSLIQADGQS

GKYTSTVSSIKRLIHEQGVLQLFRGWQAAFSRGIPSAAITFWTFERAKARLDRL

>contig29365 Frame-1F

MLNHMTGDKPHQGVVLDAAPIQLNEFVPGAPSDFTKSEKSPVILVLDEIHDPQNFGAILR

SAHFLGSFALVVSDQNSAPLSPAVSRASVGALEVLIANNKLFKARDLHEMLAISRDFGWH

IVGASTGSNSITSTKLSGRCQPTILVM

>contig29408 Frame-1F|Blast-divalent anion:Na symporter (DASS) family protein [Phytophthora infestans T30-4](gb|EEY54598.1|) 0.0

MERRMRRMQGDQHSLLRKVKLLPFGISLALFAILMIVRITPKGEDVQQRCLALLVFVTAL

WVTEALPYFATALLVPPLVVFLHILNDKAHPENLLTAKQSAKEVMSMLVNHTTILIMGGY

SISAAFAKCQIELYIAAFLQRRFKKSPNLFLLAIMLMGLFLSMWISNHTAPVLCVSVLLP

IIRDFPTNSTYVKTLLIGLAFACNLGGMMTPISSLQNTLAVSFLEKAGYTVTFGQWMAIA

VPFCTVGTILCWAFLLWVMEPSDATYIPQIVYDQKQTISSLHVVVVSMTLMTIFLWASFS

VTSASFGDLGIISMMFMFIMFGTGMLSQFDFNSFSWHILFLIGGGNVLGD

>contig29747 Frame-0F

MNFNSTPLPVIDTSAKEALVPTSVAAEERNGQTETSFVVDHIKNMRTSKNFFSDLFPKVD

KQLWSGNPFTNHEWKDWANEMISTNLDTKDIDALIAQHMMKLLGPEGFFRALDKAAKDTS

TKALAKKLEETQFKIWDTLNPGGKMTSSVYTALQLGNLDVNTFNKRLPILFRYYRHFMDK

HFPRSAELPLDIKDSIDKETVKRFGPYWADTTAIAALLGLNFESPNLFKHPAINIWLDVM

KMCTTRQKLVDPLIIRTFQWLGARADMENHALDHAILDFADRWNRENVQPFEVLTILGL

>contig30327 Frame-1R

MGIMPDMSAKLPMNLPLENIADYQYAQENTTSIAPSMFQDKTLPDLPTIANFEVGPMAME

PSMQTLTVGLVDNTPPPPPPALNVDFTTMKEDTPPPPPPPPLASQDKDVVPPPPSMVYEE

DDAPPPPPPQEDVPPPPPAPEQVDSLPTAISFLDQIRNPNIKLRKVDASVEKADPIMKAG

DSATKPLTIAEEMQQRMLRRQAAISGKQDQMEQRREREKAAAKPVTVLTAKEVTAPAQPP

PPPLSHDGQQNQLPTLAMSDDGSDDGHGHLPDDNKSNDGDDFLAQIQNIKKKQKGGSIRS

KQVLPRRMEEVKNPIENFESQMIGLRNREDSLSMSEASDWSDN

>contig30392 Frame-2F|Blast-notchless family protein [Phytophthora infestans T30-4](gb|EEY68294.1|) 0.0

MEIIGWFVSVTALIHSYNRTERVELQLQKNIMIGQNLILLMTNNFIIIFLVKQMKLDLIS

GSAGDDMVVMSCVSQDEKGLNYAKGSSAIAQFQSEDGTNVGPQLEIPLSSNIRQMEELLN

ELLQNGKNRVPYSLFLGETEVTTSLKATVEELNLSTETALTITFQPLAAFRVRPVTRCSD

TLQGHSEAVLHVSFSPDGKKLASGGGDATVRFWDTNTCMPKHTGRAHKNHVLCTAWSPDG

AQFASADRNGEICLWDPLTGKQIGQPMNGHKQWVNSLTWEPMHRNATCERFASSSKDGSI

KVWNARTGRSIASLSGHTDSVECVKWGGEGFLYSASRDRTIKVWRMEGEHVGMLVRTLLG

HGHRINTLALNVDYVCRSGPFSHNITSFESREEMQQAALKRYQEARMGQPERLVSGSDDF

TLFLWEPSENRKSLARLTGHQQPVNHLSFSPNGRYFASASFDKKVKIWNGQTGKFVATLT

GHVAAVYQVCWSSDSRLIVTASKDSTVKIWELAELKNAKTTLSGHADEVYALDWSPNGDI

VASGSKDRTIKIWKH

>contig30785 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53648.1|) 3e-42

MDFSNVNELQAQQKLELIEDDTGNLYYPLQMRKFQGVSSLTLFVESNYGGDKTKIYYIGI

KGESKQWRHGIVECVYEARPQPADHKIKDINGSTSLF

>contig32008 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69237.1|) 1e-169

MLQQLQKEAKKNEKANFDTYDSLSSSPSDSEEELGEVASKKEPVVEFSDGTSTFKVFKNI

LSGVGEKTFNPHTSLQKVCLSKFRWAVLLLRSGRFAGAVFDKEKALCHKTFQRYTTRRKQ

GGAQSASDANRKVKSAGATLRRYNEVALKQDVAALLLEWKNVLDDAELIFISSGKTERAT

FFPEKSNVLQPGDKRLKRIPFTTFRPTFEEVCRVYSELRTVRFAPLASKEKPLPGSIKML

KKKNSKKSCAPAPETVQKAEATVVVKKEELPLIIQLVISDDMIRLKELLSNADEGDVSVN

AADANLMTALHHAAANNLVLMVEYLLQHGADPALLDLHNRPPYYLCSIKETRNTFRRYMG

KHPDAWDYKMAQIPEGLTAEMEQRKSEKEAEKRKRAKDRKKQQKKEAAEQRRIEAERQEE

LDRKIAMGMSCGFCSKYAGKSPLTRLEYKYCSTDCVNSHKRQLMSEAALRRFTG

>contig32347 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59500.1|) 3e-52

MVYTIVVHLYAKEGKEVEEKLRNKLSEASQVYSKDTETIGWHVMQDHQDPRKWCIVERYE

QESSQKYHLDNPYWKTFDPYVIPLLEEPMDLRRFHELDTSKPVQVD

>contig32484 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54348.1|) 2e-11

MMWARMDNHIKYREPSSDDTQSSTSSTSQNVGLPVYFCL

>contig33076 Frame-0F|Blast-trafficking protein particle complex subunit 3 [Phytophthora infestans T30-4](gb|EEY62001.1|) 1e-42 NOT\_ORF

MSSVSRCQDFKETCDVVVKVAF\*MFLGINVDVTQWNAENTACSLLIYDKSLTGKVRVFFF

LS\*KILP\*FSL\*I\*KIVELPPSAYGVLWYTHILCGMLRGALEMVQMQVETQFVKNVLQRD

EFLEIRLSF\*ICCVCWSEKVSMDPCALYEMDRKELKGRIEETMGT

>contig33098 Frame-0F|Blast-F-box protein, putative [Phytophthora infestans T30-4](gb|EEY63750.1|) 1e-19

MVASVIQAAIIVWARGRFVDANVSTELELLLRFVYSFSSGLRSFLKYAKYLSITHFASAK

KLLRHEYLQCVG

>contig33450 Frame-0R

MATTGIDRRRASTQAMLAFHACVTPMLVLVCYELAYLVHKHKAVTFCGIPFERDCSSGVA

VNRVERRWWLSTCLRFIVWLLGCALLVLNLLVAYHWTANRTFGVSSFYELQGDTSTHAIC

AILPAIALVAWALYIGIRLWNYGTNYSYMVHATCFNPWVWMLVGALALLLGYLMPSPIYA

LSSNAGEMIMMATIIRMFREVHHDMQQGLKFGEFIDPERAAVRKQRPLSPNSRSNSLNKS

ASCTTMSSGQQNGYIAVTTPKGSD

>contig34279 Frame-1F

MYSHPGRSEGVQLRLKRAKVALMLTVPVK

>contig35210 Frame-1R|Blast-pyruvate kinase [Phytophthora infestans T30-4](gb|EEY55428.1|) 0.0

MSGAIGLSRQGVELENIMRSVEGVERKTKIFCTLGPACWSQDGIGELIDAGMNVARFNFS

HGDHASHAETLNRLRGALASRPHKNIAILLDTKGPEIRTGFLANKDKVTIQKDAILELTT

DYDFLGDETKIACSYPELPQSVQVGGSILVADGSLVLTVLEIKDDSVMCRANNSATLGER

KNMNLPGCKVMLPTLTTKDEDDLVNFGLVYGVDYIAASFVRTGQDIDNIRQVLGPRGRAI

KIIAKIESQEGLENFDEILTKADGIMVARGDLGMEIPPEKVFLAQKMMIRKANIAGKPVV

TATQMLESMIKAPRPTRAECTDVANAVLDGTDAVMLSGETANGDYPTDAVAMMAKICVQA

EGAIHYDDVYQSLRNAVLETYGPLSTQEAIASSAVKTAIDIKAKMIVVLSESGSTACLVA

KFRPSMPVLVLTAMAGSARQAEGFYKGVRARCMGSMIGTDSILYRATDLGKQYGWVKPGD

NVVALHGMVEARSGSTNMLKVLTVD

>contig35508 Frame-0F

MGSNDLSNDLLVVKGASKPLHSSPLKRRTVQLKVNQKFAQAFEERKRKEEISALEKRGLG

TDDDESSSETEDEDGEELTKDLDADIRTTLKLIRKKDPSIYDPSITFFQNSEKVESGSDE

GQAKKVSKKKVSAPIYYKDLVRQQAIAGV

>contig36004 Frame-2F

MLASTSTFKAWRHMVAFTREFEEPTLAQLQLDEHSLHDVHRKIPQAIRISGYFMDVLSAF

QKMRGEQEDALEFLEFFLEYLHTEYDQSGLVLPTSCEHQTRRKAVQNETNESIEMAQTNE

DGWAEVGKKGKSSLLRQNLVDSFRSPINWLFKGTLRSEIKHSGKRQSSITVEPFHCLHLN

LVFKSHDSRSFLSAVNSSTQSSPLTIEDMIRESFAVEVIEDIHATSRMTKVTTVESLPVV

LTLTVKRFSYHPEQGPVKLQRFVKYSPLLEFPVHFLSTPCRAENRIPSALSVNTL

>contig37094 Frame-2R

MIVALQIALNRGYPEHLGPSWHRTMHLTPVLNPCRAESCLYHQCFQFEQVHSPLRTIRDI

QNFVKTFYYDFDYAAASPSGLLLAMFLSSFEIQVGNSVLSNSFQVNLKLQ

>contig37670 Frame-2R|Blast-CorA Metal Ion Transporter (MIT) Family [Phytophthora infestans T30-4](gb|EEY67748.1|) 2e-86

MRLTAMEVRSPRTDYHRNDLRLSYPTEMSSVSSPEASPQKRFACQFDPGSRNGRVLVLFF

DRKGDSELKELSRLDVLRMTHQAAISEQEERQEYTEAEDDAGLQLRRLGSRGAKSRRPTL

SMMRGDGIGMDGPNFATICDVQRVHARDIRRMENAFSVSNEPAIIIRKQAILMSADPLRA

IVMRDGCLVYVPDGADSLLSILKNQFRETARENAEDPYEF

>contig38125 Frame-0F|Blast-pol-like protein [Danio rerio](dbj|BAC82617.1|) 5e-27 NOT\_ORF

MFKLLERMGFGSRFIRWIKLLYTDPLAHLLINAEIQSALHPTRGGKQGDPMSALLFFTMS

HLETFSDPMRNKEYA

>contig38150 Frame-0F

MEGDDRELLREWLIRNLEPVCDADPEVLSKYVLALVQNDPLKPGLQDTCISKLEEFLGDE

TSGFVSKLFQALMDGSYKSNNTIHNGEDQSRDVNHFDDDFTPWRERHRLDEEDEQLRYNK

RRRDEDFTRDDHIKRHQGSPRRDMGGQRHPYPLREAGMRGGSIGGRGRPYGMGRRDFPPE

WSMPPQVMWPPHFPLSHGANYPPEFDPNIYVPENGAMMPPPHLMMPHPMGGRGQFYSVGG

RGGRGGRGNYYSGHHENENTEALSAKTTLYVRHVDPKYVNMTMLSLHFSKFGNVVNVQMR

PSAKCAFVQYATEEDAKKAFHSPLPVCNNRFISVKWAKHDAQSLEEPAGEASSSATTGPE

VTRVAGGGKEKEEGDGEMVNALPEMNMTAEELQAAALEKGRKVLEEKRELLEKQRALKKQ

KEALMRRQLAQHKELLERMSSNSSQFSIADKRDLLDKITALSADLKVVTPRQSTVSPRTA

TLSGEADDLNGLKAELSALEAEAGDRGGRGGRFSAVRGYRGGRGGRGRRGYGRGSHTLDN

RTTIVKVANLPEEACDPVVLTQHFGNFGAVERVVMDEAAPGQGFIKFQDRYAGQAALTHG

NVFGDKQL

>contig38576 Frame-2F|Blast-structural maintenance of chromosomes protein, putative [Phytophthora infestans T30-4](gb|EEY68020.1|) 9e-95

MYIEEIILDGFKSYATRTVVSGFDPRFNAITGLNGSGKSNVLDAICFVLGITNLSQVRAN

NLQDLVYKQGQAGVTKASVTIVFNNQDAKASPVGYEQYEQISVARQVVIGGRNKYLINGH

TAQVSQVQNLFHSVQLNVNNPHFLIMQGRITKVLNMKPPEILGMIEEAAGTRMYENKKI

>contig38598 Frame-1R

MAPTFESVQSTTPTLSTSASTSGEKNTTVLTTKTSEHTQTSTFAQQLTNSLANVSLKDDI

QPLNNSIECRQMEERCNGRPSNCSNDWDCSYNFLTASSKIVSETASSNNDWNCSYYNLKP

HLLRATFSASSSSSTLLSDAEVNPLRHSMEDLMVHEETLEEEIEEDRDHAVTRSIFDIIR

VIGSGSYGTVLLCCLRDSPCRLFAVKVVYKSKLSTIYSLDGKSNASREAQRLLTEKNVLV

AVNHPFITKLYCSFETQEALHFVLEYCPGGDLYSLLGKFEKNRLPEDYAQFYAASIALAL

RYLHKRGIMYRDLKPENILIDEAGFVRLADFGFAHEQMKRFENKCTSFCGSADYIAPEVL

RGDGYGLAADLWSFGCVVYEMLTGYPPFYSPRDRAKLFRKIERDTPNYLSHFSPHLCDFL

SGLLHKNADHRLGNGPNGMQEIFDHPFLATICWPRLKAKLVVPPIIPNLNSELDTCNFEE

QFTSQQVQGHFEFKERERQSALADEDDNSFYFGDFDWCADELHLHDDDRILC

>contig38811 Frame-0F

MSVLLEWIENYVLSFEYPITQAPRRLQLAIVPLRSTTLANWLTAPCFNHAYDAKQGVQED

LAWARGVLGLTYALQFNQRLRHATMVAGSKLESLVSTPSVASSASIAAVGTGVDICLHYD

LHSYPLGNIVSEVMAHGDQGGAFEFVAPTLIKLIFEEFPHLFDAATPSMSSGSTLQVIPL

ACGPQDLRERDLAVSWFRCRRRQGRNLPIVSVVSSPVSWTAVQILLASLQQAPIQVVLRE

LVVLINGFLPYAMLSSLQASTFSRQVSAFCAQLVSLYETRARRERGPSRTLLMRFVHALC

FPDILWRHQQLQTPPWKALQLLTYMQILEEPFRLIQDAHEGVTREPAVLRLLLGLVRDVR

VAANVYITKCDPAVLGPVGDLSAMTTSVQQHLLVQDCLLMHELLKRLVSLRLSSCSHEVV

EENRIFLCQFVNELVVADTERLASSSPRLLL

>contig39881 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53024.1|) 2e-81

MKKDSKGELHLILERLAPQEYMAGRGTGVNIDPELESKLTSVSTEPPNLLYVTLKSGNRL

LGMDNNGTTSDPIVFLTFDGQKHESTKKEKTLKPQWNEKFGFYALDVKKNLSILVEDYDV

TINDFMGKADVPLKDLKPNIEKSISVDLG

>contig39988 Frame-2F

MATAGADESRMRANSVLIHFREVCCDKSAQLKIKVEQCEQNID

>contig40184 Frame-1R

MDWSSVYDNSGEEAGNWEGYGETRSSRNAYRLLHQQTSLQPVHDQEPSVQYSPLVAYAFT

VNYILGVGSLGIPYAFYRAGILMGNAMIILVTLLSYITVMWVCESVARAREASLLSNETT

ALKATITTSTTFSKFDHFP

>contig40834 Frame-2F

MYLLDRAHRLFGIYEEESTDLKRPSALKNESLEFAKTLDVTTECVQVTLRFPMITSDLIR

FGVSSKRGLCEDRLVVMLGSLKMASLSPLAVGDDDEIRTPMLPRYRKATLLPWLDEYAAS

FDKMQVSLLTPEDSNQRSENLEKVVLFTSYSDERLGDGCTIRLRLQNPSREEMKEAIRSK

QLLSQDGSENPDVSSMNCSMDEVSGDDNDGGRVGLNGWDLEALGRTEAYEKAAAAASLYS

VEINLHRATAVLLKSSLDRLMVLCDALLMINPIDVDSYNQMFAAAVLRNRLMPSYMSLNL

TVDEGTVQLCDYLVLPPAQALQRTNSNSSHVTQSNSSSEPEKVLFKYHFVFETLKVFQVS

QWMGQLVSRVHVVAQNATFLEECDFLDSVAPILYRTPFGASKAPIVFMGVDIADQTNVMR

DMKVDFHLSHVSLRYDVRSKWLFHLLEMVLMDYPVPIIPLDSATMSDDESRELLETMKRD

SEYEAVPLAIAPKTVFTKLFVNCYDVLVDYAPVSLTSRTILVFGKINMSSNVVTGAVLQG

YKVSVGDLEMFLAPSHAGYGEIDQVLLGNELLPRPNNNFKKKALKFAATYAGSRATLDAE

YPSLLIFLETFGFLQLVTMDFVDVFLRVLIPPTALEVAQKNRDKKTSAASAAPELSVELN

LGTANIYACYDSFNTLLELLSVWTDQLASKQDLRDSTAYVGLDGKSDSVSVVTNLSPVPA

SGMRSLGTTASEPSVSSLHSCRSPRLVSEAPSNDNQQSV

>contig41815 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY69207.1|) 2e-82

MRGRSADFSGTGVAAGAAGVVAGAVVGVAGVVASPATGGLSLPISLAGKSLFFSGIAALT

PSTIMLSRQSQQLNGLSLLVVNLKACLEIMNQKREEMAVSFAAVEGLHLDIKQATDFCQD

AIELESSIYENAWGFIEDISVKLAALKQSAELFQVSPSLWHFCKSEDAMYQYLLAEEED

>contig42289 Frame-1F

MLNQELATFEAEYQHIEILLRRISFQSTTEELRTLVIFWSTSPFLDPVQTHAFR

>contig42605 Frame-2R

MSSTVTRPTTRRKTSEKNALKRAWRWKDSVAISEEMRAVVHSETELLNASVLCAALSVTQ

SEPTDSDQEAIDRIARKLKIYLLRSPLPHTLQPPTLKITFDYVLVHSDVAMFCAVRATKP

ADILLAVVGSAASISHSSMHRFGGARIHVPFWNRVQRLDLQDVYHQAQQAKKMLLLCGHS

IGGSIAQLGYCELVYQRLPRKTRLRLEKRDNELLKQREKNNLAGGGVSFELMLDEDERAE

ILRRAPHMLAIGFGSPYAGSTGLNLFLKSLQLDRHVITFVNEFDCIPSILNTAQSAALIA

KTTERLLAIAKATKALLHLLPIQMQQRFVGLADTGTAVTASSAYLSMSLGILQKSFDRFR

DFCILKEIGYDYSPCGTYIILSKSSAEYKIYVDSSAISKTLHDENAGSSLTGNAILQHMM

SAYVNAIARRSISIQINASMDFYERLGVPRNATERQIRSAYKRLALKWHPDRWATNIATL

EEQATAEEVFKLLAESYEVLSDLKTRKTYDAHLNNSPGLREEFMRDGTVNGMTIDEAIIT

FRDVINNFV

>contig44687 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59936.1|) 3e-63

MALLQAHQHVLQEKQEELRELLNDLASAQVALQRIQRQMARNFSSKDEILFELSRILGEG

QQIESNLDLIKQHLATAKCSRLRTSEDRLATVTHAIHESKTMQEVVQRLLETQMSL

>contig45327 Frame-1R

MEKNQPLVDALVKYGEKELHKRHTGRGTAFLRAARRLRDADTVVSSGEEAKQLGQIGDKV

AEFLSNNFGS

>contig46076 Frame-1F

MYRSIEWNTPGCPIINGVMVSQSAYLPAGSGGLLSGALDCHQRSSAWAFSLSRYRSRERS

ANIPCSKSIASRTRDTPAISPG

>contig46450 Frame-1F|Blast-phosphatidylinositol-4-phosphate-5-kinase (Pi-PIPKD10) [Phytophthora infestans T30-4](gb|EEY64054.1|) 0.0

MGRLPPATESDGLLHGRDLDAAVEQLARSRYKPRKSRFCTRWLLYVCGCSQALIAGPCSG

LVAAIAGLLVLVGIACSMIALLGSYSADEYLFLGAIVSAAFTLVIIVAFLASPAVRAHPN

PLIFSKSLVDLLLALIYIAEYCLTEFSDSVALPFRIAAITQALLVAGEFWFFAIPIDMVQ

SITNPFTSYAHNFRVYWFYSVLSGIVCGLVLWSLGDTVSNCIKTNDATVECEKIADASEQ

RFIWFHHNTDQPGFFWHQWILYHTCVVVYLLFGIACMIYVRSRLRRGLEETFEVRRRVLS

NGMLTCAVFISWSFLMICLFAMTNTVTVKRELGKLLFTELIDLSAFMHASRGSVNIIVWI

VVNSPYFPSFYSKEATSSSLELLEKNELLTRKSLSPSGDSSGGTDTSDGMREDHHKHEDK

MMNPQLNVALRKQMIHMATNGIIESIQHHHRMRRENGNNHTFQMDWQRSPQRRIRQLMSS

WSINDSVCSQTIPPRSMPILRAMRNSSIRVVEEPRDNPSNLRFSFLPMALTEMQFYDFQP

RVFASIRQLYGVNDAEYIFAFRSTINERISEGRSGAFVFNTCDRKYLVKSTTSKEKNVLL

RLLPSYLRYLKWNPETLLPRFFGFHAMKMYGQIFYFIVMGNVLSTTEVIHRRYDIKGSWV

DRNAPACVLGEKYRCSKCNKFFVFGGTQHTPCFLPEEEHYPDITLRDNDLKKRLKLNPET

ATKLMKQLTRDSDYLASAGIMDYSLLIGTHYSQFTITSECRRELSRWK

>contig47101 Frame-0F

MAQSLTVPHAPVGEEDDFSFVEEATEYSKQRHGFGGVYGLTSLTIRPLPLLSDWCSSLCL

TKL

>contig47347 Frame-1R|Blast-Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily [Phytophthora infestans T30-4](gb|EEY64401.1|) 1e-126

MIAARLGTRVIAANAVISGLWGLLWALFWGYGCATQVRVANYLGAGKPYLARRITVLGFA

CTMVVVLFIVTATSIMEQHIIALYTTDVKLLQTCKTVTPIFIVACAFEAIEIIGAGALIG

MR

>contig47484 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57840.1|) 2e-41

MENKDGQQMLSHLLAIAYHVLEETKYMNLKPPLRPISKLFAVDASASGSPPPSPSETEAR

FDEMHFDANGTPTSTLGAAHTNVGETSHAVVLSYPFEEIQDTYTKIATLKMQYMKISTDL

LEAVKTVEVKSEPQQGEK

>contig47710 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67126.1|) 5e-56

MKTRLGLTQEVVRCIEALNFPCPVLIQPHQLLLQDFGDILVVEKLVLWLINAKREARHLD

KIRQNRAYLQAQSPWIDKQVATPLKKEVAYILDAFAPTRRWQFVRGDGNWEEDEDSLIQR

CLLEYG

>contig47765 Frame-1F|Blast-CDK5 regulatory subunit-associated protein 1 [Phytophthora infestans T30-4](gb|EEY55916.1|) 2e-93

MRSRIPGVAISSDFIAGFCGETEEEHLDTINLMRKVCYDQAFMFAYSVRARTHAAHHMED

NVPQEIKLRRLREIIHTFGEVITRKNHIEESDRLHVVLVQGPSRRSTIDDPKHTGLTDTS

KRCVFPSQEMPGSLRSYIEQAGLAAHDFQPLSKVNSAAVYAAPGDYVLVRIREAGRYTLH

GIPLARTTLQEVVEIVPPEILGPRPYSCSELRL

>contig47817 Frame-1F

MDLCKRLQSGSRPNQVFSRIWIVRHARQIRVRKYGNFWIYGTSYVDDILIGANSVEAIKL

VAADISRRCKLKVLGSVRFILGIEVGHKQSQRKLMISQRTCINGWWKV

>contig48360 Frame-0R

MTKLIPRNTTVPAKKSQSFSTYADNQPSVLIQVFEGERTMTRDNHLLGKFNLDGIPPMPR

GVPQIDVTFDVDVNGILNVSAVEKSTGKEQKITITNDKGRLSQEEIERMVADADKYKDQD

ERNKIRIEAKNALENYAFSVRSSVKDEKVASKLSRDDQKVIEDKVGETLQWLDANQAAEK

DEFDAKQQELSGVANPILQKLYASEGSGGTSGNGGMGNMGGMDGSGFGNYNSAASGKEGP

TIEEVD

>contig48799 Frame-0R|Blast-nucleolar complex protein, putative [Phytophthora infestans T30-4](gb|EEY59969.1|) 1e-159

MKILNDVCRSSDAADSNKEGDFTFDVQSNAVYNRLMINVFSRTHETLAALVALAPLSEEN

SKFKIDDKKWKKHALVIRRFFSCAWYLLEHTSGQDVQLFVLRELRHYLPYVVPCPKTSRR

LLKALLQIWTKSLNANACMLAFVRIRDMALAVPFPFLELCLKGIYVSYMRNTKFTNEMTL

PHHVLMGNCVVELFGLDLSSSYQHAFVYIRVLAIAVRKTITSPGSDSFKAVLNWQFLNQL

RVWTAVLCAYPAENQLRALVYPLSQLLFAVIRLSSTLRFTPLRFHCVKLLQQLALATNAF

IP

>contig48816 Frame-1F|Blast-acyl-CoA synthetase, putative [Phytophthora infestans T30-4](gb|EEY63260.1|) 1e-13

MLHIFEKLLEHEGLIALTSTTNNQTIEWTYADLLTRALTLCDSIQEKLPTNVEQPRVALL

GARGAS

>contig48979 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57172.1|) 9e-37

MRRVGTMAMLPLHQRGQIISLANASYRLKSTHVSVIGLHWKTDETRLRDIFAKFGSLESA

RLVKSDPSLSHLWACLVYSTFDEALEAAIEMNGQELDGRLLRVSIIDPPLVENNSDT

>contig49868 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62986.1|) 1e-46

MQKANEVYVPEELRANSLSGIRLTAAGASNRGIMQPRAFENVFKSLEAQEKKIAADKAKQ

AEQEADDGEIDDAEEDMGD

>contig49886 Frame-0F

MCRHHRAVYDPSTALRQVLDAMIVVAL

>contig50417 Frame-1F|Blast-3-deoxy-manno-octulosonate cytidylyltransferase, putative [Phytophthora infestans T30-4](gb|EEY53560.1|) 2e-32

MYAFRKNFLFEFPMLSRSSLEESEDLEQLRVLYSGYQIKLVTVNSTLPGVDSPTDLASLM

ALWPKRT

>contig51025 Frame-1R

MTSNALARFLHLLRRRIVARVSLLRRFSRGRISVPDLHFREETLYGATYHCGLRKSIFDN

ETAMNNYADEVNLNRIRNSSCHDRQTFINRHSN

>contig52143 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65899.1|) 8e-08

MLAHAQSDLPAREHLILKLIHRNDQVLPHSRRMKPISSTFQRKPLVKSRLAMEAKSKHAE

>contig52419 Frame-2F|Blast-GPN-loop GTPase, putative [Phytophthora infestans T30-4](gb|EEY65657.1|) 8e-36

MVAFVPMNINREESIETVLMHVDHAINYGDDLEPHEPKNLDAEE

>contig52536 Frame-0F|Blast-regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4](gb|EEY65901.1|) 4e-21

MLMTLVGLPLVKRPRICSQDLGSECSTAALYHSVCCQKGIAMATEVEIANMQQLELEKTH

IADAKAAEIVALLR

>contig54303 Frame-1R|Blast-type I inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY60218.1|) 8e-28

MDDDINDEKEVIPSSPSDESPVEPVEALRRRMISFDSAETIVSKSAAGQNIGIPSEQRKL

AETIVAMGITEDEFQ

>contig55029 Frame-0F

MVKKRNFVLVKKSHPLLRKLSSVILYLCIHCMSNSGLHIAKVPCRNADVALHHMVKALCS

RRGDVSKMRIPISIRVHKMHFVHKPGILKMLLRRFLSTLSKIHPNPLPVQSICDSLQVRY

LGCARYREDEQN

>contig55326 Frame-0R|Blast-phosphatidylinositol kinase (PIK-L4) [Phytophthora infestans T30-4](gb|EEY63983.1|) 5e-16

MLPSIQVTSYSMVLRLRQSILALVDQMIRKHSSILEGDRSFNKLCQLVEYFIGRNGHIMD

YAVIKCA

>contig55591 Frame-0F|Blast-polyketide hydroxylase, putative [Phytophthora infestans T30-4](gb|EEY56473.1|) 5e-17

MHKRSRVLVVGGGPVGLSTALLLEKVFNVPTRIVERKRSPTQHPQAHFMNLRTMEVFYAT

IPAFHDRLLAQAASSKL

>contig56994 Frame-0R

MSENMLMKADEELLQKYSAAPRCHRSLGTLLQVSSTELNRSASGRNLRSKHLPSSAYPLT

PSAPTPRAPPLDSKQRLCIADSTKNGPVSENNCTFQRRSSFSISAHVLKDLKRVRSSTDP

KIKVKEICEQRER

>contig57258 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60938.1|) 3e-12

MGNTVTLLSACEYGDLAEVHRLLKTSTAENLEAKDDSRRTPLLL

>contig14227 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62016.1|) 2e-84

MANLILAGAIANGKATIDPSTAWVATSAPMEGSMGSNYIQSWCGDDISMAEAKVIDLLGN

CPTNAGEMSLAYQNSSLASHLLNDAYVAAQQAYASNVTAVMCSNNYMGLATVKAAIYALA

GELVPHHSSENDGIVEYSSCAMGFPLESFGTSYKSERYVTELNHVDTSFRNGDGVFGDSR

KPLKWFECLL

>contig15992 Frame-1F

MPKETTSRGEHYSLCIIKAARSHPYSSNNSSTQRLPSPAAVSCVGIPRRASPDLLRKQIR

VSLGP

>contig16755 Frame-2R|Blast-protein arginine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY60167.1|) 1e-119

MDRLGCKYTKHTAKCREVFKQEVAWASHLSVRAVMLPTPRHTHCSANYARVLNQSLTQAQ

YLHFWVRIPLTLQPQESKATLPMEIDPVIGLCRTEMIERNEEANENQIDPWTIWDSLRAR

CEYHPKLHVALEITADLPSDEAIQRWFGEPLKAAIISTTIFLTNRKGFPTLSQRHQKLMA

QFFQHNVQFYLSGRPRHRGKLSLYVQYLHFLYSKRPNQDRKALFEAPYLDYLQAP

>contig16939 Frame-1F

MFVFSFLHKREELDDDEDESAERLVTTELFYQAMENMPHLTTPQRLEMRRFWRNLVNKNL

QKRPSSDMNDALNDDETRNPELRIRDVQVFAQEYKRVFPDIFPEKHVLDAAEQAAALMPS

AWRDLVGSTSSMIVSTGKRLNHIAKDTKDEVQLAMQRSVRTVLERALHIVASRLKEKLKD

PDMPKYLKMNIDIGIEQFMPDVEMEILRKSRDLFRNESLKSDMENMAHPTTQDECCASSL

NSQSDAPSFSIATRRFSVFRAVRGHILHHLFPHNKTIWRSFKDPWWGLYTSVGLLPVVGQ

LWWIFLFLIKDKTNEHQLCQFIVGFKAAQFITLGLIHMMLGVLLYVKCIVLGSMLACQGN

MGPALTEGSACFFALQILLVWAAFFRLPYTARPPEAVRLRLKDIENEDCRVFRDAFGNIV

HLDRGGYLLKFCGYETLIFIITMALASLVLWLPLDSWQRQALFYWIRTAYGLFSFPFLIF

KIPVLTNVLMHTRPMGYNEQGETVRFIIKQRNE

>contig19905 Frame-2R

MKDPPSACSLLSKSRGRGQSLCHAEQFAVNRARSKTNKAGTETRKVWLKCAHARVHKDEG

SGLRRTSTIK

>contig20736 Frame-1F|Blast-eukaryotic translation initiation factor 3 subunit C, putative [Phytophthora infestans T30-4](gb|EEY57814.1|) 1e-174

MMAQLGLCAFRCGLIWEAHACLSEICTGSRTKELLAQGLQSFRYGERDLEQERLERRRQV

PYHMHINLDLLETCHLVSAMLLEVPNMVNPNVTDRKRIVSKAFRKLLEFHERLVFEGPPE

NPRDHVVAAVKHLAQGSWRQSAELLVSLPVWDLFPGLNVAERVKAMVQHKIQIEGLRTYL

LAYSAEYDSVCLDRLMEMFELDEKTVHSVVSKMMINEELQAAWDQSSQAILMYKTERSSL

QTMALQYSDKLAQIVENNERMMDLRSGTSKEEWNNRRGGNDGRRGGNGRIGFSAGSNRRN

ETSNSRDGFRPRRGGGGGGGRGPRQQR

>contig22468 Frame-0F

MKRKLSEVADGKTALDETHQTVAALVAQQVASLIIEPIRGSFLGRFGCVAFGDQEKQSVN

TFLHQKLGKDSLSRRLGPGGRKLTYIESCKAIELANRAFGFNGWSCRIVECKEE

>contig22532 Frame-1F|Blast-translation elongation factor 1-alpha, putative [Phytophthora infestans T30-4]gb|EEY68224.1| translation elongation factor 1-alpha, putative [Phytophthora infestans T30-4](gb|EEY53099.1|) 0.0

MGKEKVHISLVVIGHVDAGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKQSFKYAWVL

DNLKAERERGITIDIALWKFESPKYFFTVIDAPGHRDFIKNMITGTSQADCAVLVVASGV

GEFEAGISKEGQTREHALLAFTLGVKQMVVAINKMDDSSVMYGQARYEEIKAEVSTYLKK

VGYKPAKIPCVPISGWEGDNMIERSPNMPWYKGPYLLEALDLLNAPKRPSDKPLRLPLQD

VYKIGGIGTVPVGRVETGVIKPGMVATFWPCWTVD

>contig22907 Frame-2F

MDSSNDTNRICYGSGRVIQGFVHRRPPRVIYQFDKGTRGKTHHSLSHRVVCLSF

>contig23647 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63876.1|) 0.0

MESGTRARIGHFALGPASHMMQKPLQFRIRFGLSNATINRIRQLLLVTFLLLCASDARRA

VAEPSHPYRRVEVRVEDYSFTDRPGEKQQVAVEAYDIQGSDFVPWPDVDVHVVTWETTDK

PFKKTVETKEHKMKQQTERLPAVVDLNEIIEDLESDDANNKDNDAVLKQYVSFRRAMWWW

SEDKTELNSQEQAAVLAVVVAVVTVFGLCGVLLWNVSWFLWRLLREKRTLNQLFFEDDPI

VIEQHLGKFSEKILSLRIKQIACVRLRHLQVYLDARNLMQQLESVTFLELAMKLEKLPLH

PSTRKEMTFAEINTAVEEITCRGEQIAVEMMQLEVPSRWKRYADAELWLRVQDNSLQSLH

IANARVQQIAEQISELIMEKINSSEPLSKPVFISLLASLRQTSGTPHQNGAMGKATINEM

DAFNRCWSGSMSISGSVGHLGGGIKEKDEFSFLLKAFDEKSEQHKIQAELHRAIECFQSA

HEPEHEQLLLLENADNSRSNQAIQRTNQLGVNSAANSGVTTGSMRRLERWVDQAEVMEMT

FIEEVENAQFLLEDARRDSFCAAVVSNEGKGLDSVQTLATNFVALGAKREDAILKAGEIL

ANRSNMMLLVNSLRTMFDQLRKRDVMKMNERRNRDRVKAQEKRDRIVQKFVNKKRIMAEK

IDRTREAQRQREEEARLRRQMEEWKDARAQDAQDRASFVWKITKADVLVVLVIMAIVFFE

NVREVALVKPLCQPDEEHHWWMVSWWAPASFQVFGCEVAYGIKILGVLAVLGVVFFLLSQ

LNLVAVMLPMFGAIALYFVRNEWLNMLLRLPLLLVIYAFNLGILHLYNRYEDRCKDDQNF

QREDKDSIVHAAKQRRILLYVVFPIVSLVLTVVTGVGVACDYPEQCVGFAYAAAMPVLEG

LWKLARGAYRL

>contig23931 Frame-2F

MDTFHHASQLIAQLESDAYDASDSMDRGKREHYDSDRDDADETQKLFRFQEAREKANALA

STALAASVQPQRMTPRVVNESDVLDDNVALERAIHASLARARDVKTTEMPIATSEERIAE

FVRRTVPYETTSLLDVERSHDTAKNGHVPACVGQVFRTAHNVSNPVVFNEATDFETRLRE

AMETRAAQFQETVKGRTVSREKHDETEVNEAEIGIDARMCDTKEKEDDGMEKEVWGEEEP

LVGTGMGATLALLRKTGDLRQTRVERQAGRANDVRDCAFEDDLRIKNGVKLDYRDEFGRL

LTKKEAFRLLSYKFHGHEPGKKRKEKRLRQLKEELQAQKMLSGEGSMKMMKVLETKQKHT

KEAHVVLSSGS

>contig24398 Frame-0R

MNLDGRPPLLNLLPIKHLILSFVSFNFTLRPMHCPVTSTMSTLCSVSSAHVLGHKRRRTA

EVASMKSEDACHYNLNESGCATSGESSGDESDCCYELDDDCYLEDENFVAPKRRRDLDYM

TKSVRLMKAQVDNASAQLKELAALVAVVAAGAKN

>contig24556 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54895.1|) 1e-150

MGGVYTRVRTISSLRPGDHICIWDYSRWPFSYQHHGIVWASSDQLQDIRVCHVWSPLAGY

KEAQADSYFRISTLEEFLYHRSQKHLRLVEYHTSAFRDFLSKWGEVHRGKSDLPEVVLAR

CKFLLGLGKGDFNIFTQNCEHAAHWCKTGQQWSKQLLTAASGRVPFEKRLAKEDVIALET

EINEIKAVSRLVVNNVLGLSESKVYLRVQGNKYIRIKEDGRHVHVVPEGDRPETCGRTAF

RLECYSKQYNCVKVAFYHEDSDRYMFSRSTFSCFRDLRMKKATCWRGTSGMRWAYALSGY

LNSMNQHRRYIGTRDDGLLIDVSLREDASFVEFIPCRPSEAVAPTEKEESHVPPDITLVK

QAYNHAKSVKETRSQSMLEFHEEECGLQGASFL

>contig25696 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55915.1|) 4e-46

MPGQKEQVEEDMARYRGLQEEVQELAKQRQMYAQQANENEMVKVELDLLNDEAKVFKLVG

PILLKQEVDEAKSNVNKRLEFISQKLSEVNIKIEDKEKKAVGIRTKISDMQMEMQKRAVE

AATGAVVAH

>contig26019 Frame-2F|Blast-DNA mismatch repair protein mutS, putative [Phytophthora infestans T30-4](gb|EEY69245.1|) 1e-39

MAQMGCYIPAAEATIPIRDRICTRFGTSDDMEENASSFAVEMTETAFIVETCTSRSLVLL

DELGRGTANDEG

>contig26811 Frame-2F

MKGNTRVDNKKYGLADNSTVWCATHPVLRHKLTKLRDERTDGRLFRHLLREVTYYLGYDA

SDDLETIPKDIKTPMGDHQGAELSTTVALVPILRAGLGMV

>contig27870 Frame-0F

MVSPAQVEEMLKPLGVSLYGLNSDEKARLNERMIQFFQYVRDVHKAEEQASNAFWAGFDH

YRVLDDSLFQLKALLDIVSFMLAPIQRSFLALGSNQDDEMLKFCLHRRRPETESSGALEL

KDLGGDDTIEKTRKTLLEVQKLLRPALNLAKQVAYPACFLQTLIFCSEVWVWLERIASYK

SEKHLKEATAFWEEAVRVIKGVFFRRVAFHDIANAHTLHLSGFGTDVSMPFGRNKGRFCV

VPILNFSEGFIRRLKAMTLQLILAACQLQQFQRVPEYIEQTVLAHLDELLSARMCLSSIV

HQLQTFRTLQKSCKRLPPSGSASNLAAAGLPSGSSVSSVGSSNNSRSSSFSAVITALSPQ

RSAIGKQTMPNSSPSSAGIVGIKRGGHKKNQSMSSISELLASNVPSRYQEAAALYGVSAS

LKSSSTPRTGLASLSERPNAPPPAGKVGATIHGSKKSNERKSQRYTR

>contig28101 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56120.1|) 2e-64

MSVSFLSVATVLTTVHARTDIVAQLYGNTAITAPMPPQSLNSALQELVVSVANFTQYPAA

LQRAMLWSAGWVRAQPEAAILDESSSAATYVQVYVLCDRTMSDVFQSPHAFDDPTRCGIK

ECKSTLISFTKSTCDPDYVRSRALCAINPDATTFEFVPSLQTKNGPLWAMDGQIDATFDP

QLFQYANASSNTSTPLFLLTQKSAWTTMKDDDTCPNSAQFIAP

>contig28457 Frame-1R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY62207.1|) 0.0

MMDKKILSFDTQSKASPLSMCWCGEDSVLLYWPSAGLVMVGPYGSWLRFPYSESIVLAQE

VDCCRVYSASSHDIVLRVPTCVENIKGMGSTAPAAMLYQALDAFDSGDAKADEHVRYILS

QNALEDAIKDCVNAAGSEFDYAAQTTLMRAASYGKCFVDSALDATAALPGGSNPESGNTM

MDTEMFVDMCRKIRVLNALRQQEIGFPLTVTQFDRLTAEVVVSRLVAMHHHFLALKICEY

LKIPTDRVLVHWACEKVKAATSSDVADEELVALVRKKLKKATLVSYADIANCAERANRRR

LATMFLDLEENASDQVPLLLSMGEFELALRKSLESNNTDLVYMTLFHLERTLPSMDEFRY

VLNREPMYAEAVNLMLLYYRETKSPSSTALWTDIASAENDLLLSFKSTDVEEKSTALKDA

MTKYTNAKLPSHAKLTEEQIELLQEQGKLEEKPENIKRRKLVGLSISETMKLLLCDSKYE

PKLLPVVAAFAKKFKVPDKRLYRVKIKALAETRQWDALLKFSMEKKNPPCGFKAFAIACL

EEGEKQQAENYTGRITSVDEKFETFIRLDMYSDALQLAIKLKDPEKLTNVRNLCNDDNLC

KQADKAAMDLGFVS

>contig29313 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65987.1|) 8e-38

MPLFLANLAMTSYFLALCYVLITAMTVNKYMEVRGVLKRHQHTTWSTVQLLILSIALGSF

FRSATFSTLCILDSQAAADLSIGSPSSHSWTRGKFPPRMIKVDPEG

>contig29366 Frame-1R|Blast-cell division protein kinase 2 [Phytophthora infestans T30-4](gb|EEY70261.1|) 1e-171

MENYQKVEKVGEGTYGIVYKARNLTTGRIVALKKIRLESDEDGIPSTAMREISLLKELSS

HPNVVYLYDAVYQKNKLYLVFEFVEQDLKRCLEKLPARMEVFQVKSYLYQLLAGIAYCHA

NRVLHRDLKPQNLLIDQYGNLKLGDFGLAREYGVPLRRYTHEVVTLWYRAPEVLLGAKHY

STPVDSWSIGCIFAEMVNKQPLFPGDSEIDELFRIFRVLGTPNETQWPGVSTLPDYKTSF

PQWRPQLLSKVVPQLDRVGVDLLSRLLMYDPSNRISARAAMAHPWFANLHPQYASFRNNG

SSNGTQTYF

>contig29502 Frame-1F

MVSALRRMAPSVSPLWLFAALVVVAMSIYVHDLNVMLAVRRALLYTSLSSAFYPNDPVKP

VDCADAHRFLTDVMQVKGYHVLCIESTANDLLRVTGFKDGMHANSSVTTTMDLQTFQRAI

EVDMLQIPEPTDDNARKYKQLPAYFSPEGEKLKKDTLTFLQYRVVFLFEGGQFFWPGIKI

GHKTVVKNTFGRGDLVLETISMTPLVFSVEEFLRDDEIDIILELSMPHLATSGVSLQDGH

ENRPATDWRTSTMYWLDSSLHPVVKDIDKRTADLVKVPISHQEPVQVLRYERTQHYDQHV

DYFSPDRLRNSPDLIKKIEHGYKNRMITVFWYMSNVTKGGHTNFARSGGLPAPSSNKECS

SGISVAPKKRKVVVFYNLLPNGEGDPMSLHAGCAVEEGTKLSGNKWVWNKPRYNND

>contig30391 Frame-2F

MDNFVLHGKAAVPNEAPVSKPKRKRQTTIHNGEKVVSVDHVQYLKEELDDVKSVDNMLSI

LDALERLFMSLEMLEKTRIGISLTRLLRRSDSKEVQYRATKLLVVWK

>contig30618 Frame-2F

MVTSVKCATSNVNYVVVGGRDSSGDPSGDGELRYIKNYTIHPSWKADESHYDVAVLQLEK

EVSKPYARLPKSEKTDYGDVPSIVFGWGSLDRAKPEEIADSLHYLELTKFSYDTCKSKVK

VDYFDTSFSCAGGSDENGVSLYDLGGPLITKSEDKNVLIGILTYVDASDDFRNPSIFTRT

MYLVSWFREMLLVHNDGYNGIW

>contig31631 Frame-2R

MANNATLEEQDPEIFHLIEDEKNRQWKCLELIASENFTSRAVMDCLGSCLTNKYAEGLPN

ARYYGGNEIIDKIEILCQQRALAAYSLDANTWGVNVQPYSGSPANFAVYTALLRPHDRIM

GLDLPSGGHLTHGFYTYSKAENTRKAVSATSVYFESLPYRVSADTGLIDFEKLAETAALF

KPAMIVCGGSAYPRDWDYSAFRKIADDNGALLMCDMAHYSGLVATKEHNSPFEYCDIVTT

TTHKSLRGPRAGMIFFRRDERKFESRINNAVFPALQGGPHEHQIAGIAAQLKEVQTPAFK

TYVQQLKANAKVLAKTLMERGYTMCTGGTDNHLILWDLRPQGVTGSKLEKLCDMVCITLN

KNAVLGDRSALTPGGVRVGTPALTSRGFKEAEFVQVAAFLDRALKLCVEIQSTSGKKLVD

FIQAAEVHEGVKQLRCDVNALATSFEMPGFKVSEMRNKRIEE

>contig31947 Frame-2F

MKKDKKIVFKGTPGVGKSMLVVVFAFYMALIQGKRVLLFRRERGKQYSLLYLDAQKRIFW

RVHHTKYQELKLYEEYLNDAELCLDGFEEDEIRSYEGLLGVFRLLATSAQYKLRSGEAHL

YSECLVPFWSLSDMNAFGERFGWPEQEIKERYFYSGGNLRDFTAPREELY

>contig32102 Frame-2F

MASLTSNDYYENLGVARSATAKEIKTAYRKLAIKYHPDKNPADKLTAEANFKIVGEAYNV

LSDNDTRKIYDIYGKEGLEDGAQPMTKERAMEIFENFFRYGEAMDPDAPNRSKGLKRAAG

GAVYAPAKGILYGGKSIVGGVLLSAASVVAGAGAMVFNVASGIKEMSEAGVNAARKHKDH

KRGNEREGDVVVAPIVDGPGDHGDQKAAIVAVNQKPTPTFIGGLRKATIGAVAAPVAAIV

TGGGVLLASGVAASGYVVGGFAGAASNVASGVREVKAANKLEKKRRASSVTSTRDSTTST

KSSPGMSEPSIKSTSSTNTTASAAQTA

>contig32344 Frame-1F

MRKAVTELNRHKAVGPDGLNNAFYKDSQLMMVPTLVTMRNAIVAGVDIPPSFQQALIILL

RKKEDSADTMDYRHISLCRRVANFCESIASRLQRIIRKLIRSAQEGFIKGHQMRKTVMMM

LTQLTIATCDPG

>contig32713 Frame-1F

MKCWSTHSPVLALLLLAQAALIDLCITAITRSAARFFLPEEAQQQKLKPVLEHLEAFGIL

QYQPADHQASWGTLLSDSAHFDLVWSVGISPPLAQLELPYQFNAKVNHLPGAERLTSLDA

LGQHLAAQQHHVKFFFYFVPAHYELPRDQALLTSAYTKVLKKNMYSPKRSRDKNVFRRFL

LRERDANDNNDVTQRAEVFVSDEELKLKLQSSAYKGKSVVVDQYVEPLLLDNHKFRVGFY

VAVMSVDPLRVYVYNHALIQIAKSEYPSELMVDTDPSTYNYDHHIAPWDFPDLQAYFHEL

PSASREGTNAWQVVKKYLRKQGIDTKHLQNEVDSSIAKVVLSSRGYFQGGLAKVKRANAH

KGDGGTPSDLSDSFFDFWRFEFEFDDVAKPWLVRVVPNPSLKGVSSVLGTDEAVKKGLIH

DLLNLVGVYPQTRRPFGKIHRPPTNSTFCMDKCHDQNRAWDTSCWSCPGWFLPHVTRKLY

DATSEYDRRGNFNLVFPSFDQELSTFLDTELSEYDIAFSRYLKSLSSSYSNLVDFPASDR

AVMCVYREHCNHHGDCVNGMCSCDSNFEGRTCYIPKDINQEGYSQRKYGDVILQGAELSK

DKVENLTEIHQDRKPPRIDGISGVGLGFLTILLCTLVIFIYRFLFSRKSSGCSDLPHDGK

AI

>contig33426 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67179.1|) 2e-53

MMWLLVRLKVGGRKYENVQGQFVTSPVYQRLKRILIVYALFSLQFQLASIVMYASRDDEA

RLLDFISVSLLVYHLSGLALAVTTMCSQACVLNLCRSCLPEDMEAQVQSRFLQRGDLLSP

RDTQVVMESAEPPLVNPV

>contig34315 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57246.1|) 1e-138

MGQGPSAIPTSEVKALVDLYDALNGDRWRRRDGWKQPTRDPKHWFGVEVVMGHVVALELP

TNELSGCLPSTSLARLPHLCVLDLSKNQLRGSIPAELGKLSALKRLDLSCNDLTGAIPSS

IGNCHQLEELNLYQNSLSGTINKELGKLLNLRTLQLQHNSLCGAVPAALCELVHLVTLSL

RGNCLIGHIPAEIGRLESLVFLSLRNNELTGVIPSSLGCCKVLEFINLSSNQLRGDIPAT

IGDLECLEYLYLFDNALEGRVPGSIARLKLLKESDFRDNRLHGELPNLLDGCSSLEAVMT

KWKGRKASYRHAMFGDPMPSPDIPLTSSHQFLQTLEDLPATLSNTFFGLSFVHKSEWDRA

SKDDRVDNFSSCCRIFTQL

>contig34445 Frame-0R

MKIFNVAAAIAIAIASVGVNADQTSRRLIVGGESVIEGQFNYTVGIRAYANGRSNCGGVL

IHEFLVLTSVGCATNVSKELQPRFAAINQKIVDGTDSKTGEVIEVKRVIFHPMYDDIKVT

NEIALLVLENKSRIKPAKLGSDPKPGSKVWAFGWGRTDSSHDYPSRTLQRVQLEVKANDL

CDMYEMLTATNLCVGGEEGKDVCNNDYGGPLIAEGADKNSNDDDRVVGIIGLGSGNYGEG

CAIGVPSLSTRTSFALNWI

>contig35402 Frame-1F|Blast-plasma membrane H+-ATPase 1a [Phytophthora nicotianae]gb|ABF85691.1| plasma membrane H+-ATPase 1b [Phytophthora nicotianae](gb|ABF85690.1|) 0.0 NOT\_ORF

MKLRSDWRSMVQTNSPKRRLIN\*HCFLSFMWNPLSWAMEVAAVLSIVLLDYPDFALILFL

LLLNACIGYFEEMQAGDAVSALMGELAPEAKVFRDGEIRNIPADLLVPGDVLRVRLGDVI

PADLKFLEGDSVKVDQSSLTGESLPVTKREGDEGYSGSVVKQGEIEAVVTSTGVNTFLGR

AAEKIASADSHGRLQMVLTTVGNFCMVSILFWCVVELLVQMAGRSSQNPCVIVTDGCLGV

ANILVLIVGGIPVAMPTVLSVTLAIGSSALAKENAIVTRLTCIEEMASMEVLCSDKTGTL

TLNQLSVDMDNLIPYNNFTGGDILKYGALSARTENNEAIDIVCHNSYPGKDTMWEEYTLL

HYTPFDPTTKRTIAKLKDNRTGEIFRAVKGAPQVVLDMDVNAESLRTEVEERINEFASRG

YRGLGVGISHCGDVPVEECEWQMIGLLPLFDPPRHDTADTVKQAIALGIAVKMVTGDQKA

IAVETCRQLGMPTNILDTSFFNTAPPPGLNLAQDDL

>contig35644 Frame-1F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY56966.1|) 1e-110

MELKFEDEKNRREQFQVNLEQLTVENTALYAQMVAQQTTYEAKMEELQARFEKRNVSLVD

EVKLLQDQNRLMRKSEPRNEPKLNGNGGTSTLAYNHSSNVAMHDENENNARHIQELTDHL

LQTRRELLEKSNFIAELELKAAESEAIRRKLHNTIQELRGNIRVHVRLRPFLRSDGPEAL

AENPESAIMCDTFASTITTNVDNPHTFAFDKIYGQSDSQEFVFKDVSDFIQSAMDGYNVC

IFAYGQTGSGKTHTMQGSGKAQMRGIIPRSIGLIINCCEELTAMGWNFSLMVTFYEIYNE

TIRDLLTVNSGSDAKHNIRTDNRGRNYVDGLTEVFIDFDQADEQVDEIVNLAACNRSVDR

TDMNALSSRSHSIFALKIRGYNEAQNTEVEGTLSLVDLAGSERLSRSRATGDRLKEAQAI

NKSLSALADVFQALAKKSSHVPYRNSKLTFALQPALSGEGKTLMMANLSPTFASLDESLC

SMRFAHKVSRCELGTPLRQIKTTRRQSLGTGDLARNGVQSTTSRESRRSTLTPGMLRKLV

>contig36771 Frame-2F

MEMGSCWAISGSSGRLSVKFAQQIVADAITIDHIPAQTASDISSAPNEFRILGISGHPLR

ETVEVTPFGNFSYANTGPASQTFKLKLPL

>contig37123 Frame-2F

MATKEELWQQMLHDCSVRSRLPVANLLVVGDIESGKSALLERLDEVKSMHSNSAIETHAV

DTLMAFKILDVLDPRAKEDGDGSSEDVIAHIGTWILNDLGLKDLIKIALKPQSLQN

>contig37156 Frame-2R

MTSSEVALEKSMTGDEVDLSWPLVEMLEREKHFAWGTHSIIMICYLGVVAASIGDALVSC

GSLAYWVILLAQIPWIAMFVILSSRYLHKIYLCKKAVNYQYLDGDIQWTKKMVIFFPLGC

AAAGIVAGLFGVGGGIVAGPIMIELGIVPEVSS

>contig38575 Frame-0F|Blast-succinate dehydrogenase iron-sulfur protein, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57141.1|) 2e-29

MQAFRWIEDSRDDRTEERLRALDDSFKLYKCHTIMNCTRTCPKGLNPAQAIGKIKARLAS

MH

>contig38812 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56616.1|) 5e-58

MVVQEQYGYMLALHRSDKSVSAALEAVRKMATLHDSSYNGIIELFGLPQIILEALQLISD

SNGSDFNGLRFLAGAEEGTSVLYRKSEFPQGAITPVKFMWRPLKEDYKTGKFQLHEDWQ

>contig39235 Frame-0R

MLLFIDFTMRTIHNIISPKWLNTYQLVQFGVRIGASCHFLDIADFIFTNRFLFDSARSVV

NHTSMADTQRKMIIPRSTESEYVTDIKVDHGTFECETWRHH

>contig39965 Frame-0R|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY68210.1|) 1e-138

MEVRSIEVAVKTFKYANIECLEHVKEEAYLSSKLVHPCVMMTYGCYTSDCNLYIVYEYLG

GGTLQKMIDLNQNTPFSYERGLRYALMIAVGMRFLHGLPVPIVHRDLKPLNCIFDSKQEM

LKVADFGESRLLRTCSVDGCRPTSFRSADVTAQMTTNIGSACWAAPEVLKDEATSEYSVK

IDVYSFGIICWQLFTCGSPYADIPGSNLAVAEAVLSGVRPTIPRGCPRLFAKIMQRCWDD

SPIRRPNFEDIVQLLEIEIVEERRQQLMRTHGWGSDTIIAPLTLDSRNFVAWEIA

>contig40338 Frame-0F

MESAMLRVQLLLGLMALGYATIFVLCVVLVIYMRHHRSGALRGDTRAVRRALLPAFQPLI

WLLTTVSLVYTICLTLLLVLGSDSGRVRTEAFYSGRLFMMALPVLYLQQRAVTTRALTRA

SLISFCLAAYNIPIVWLMDISVTQMTAHYVTMFTGSFPLFIMGWVCLRPSERANKTTRRE

YGAFVGVYYILRLSYGQLFYKGDNYTNATFTLIVASIFWGSFIPVVVWRVLKADTAHWRG

LGRRAVHLQSMFRQKYNCLHERVSSRGLHVLIEMHRKQIIDFAYLELHQKIGAGANAVVF

RGTLHCKTPVAVKVYTPHVLTEDVVAEFSHEAALCGAFHHPNVVHFYGMCVSPPTICLVS

ELCRASLEDITRISARLRLPQNSRQEERKQVSTLQHRQRQRQRFLVDLNYMIDATRAVVY

MHSFTPAFLHRDLKPSNFLVDEYGICKLTDFGESRSVPAEHKGNKLASITANDSSKPIDS

TRSITAFYGDSYQRVQTPVSPYVMPPMPLRPSMRDRGRSAMTVRGTADYMAPELIEGKAG

TAVYGEAADIYSLAITLWDIANPLVPKYPEAAQSHLHVFDSVLNGERPSLSPSLHPELIR

LFTDAWHQQPERRPSATYILRALEDLQQQTSAQTALQLAMELERSE

>contig40402 Frame-2R

MLNAKALSAKNPTTDDYLEQLKNIYGDLNQDAIGYMWKKYVTNLCLSGQINFDEFAKEYA

KG

>contig41445 Frame-1F

MCTFRLRSDDHILWSVFMICLMAMKLLKVLTSRHCIYIINSASSHSTPAIFCHLLSRWSR

CTRQSSDCAEKFKTIDIAMCTKTVIAW

>contig41799 Frame-1R

MRTTFVQSVVIAVFFASATAIDTLIIPTTKGLEDATRSGVARALRGALSFSEKQYELEKQ

KHTSSYTDVVARPFHEEHSELIRTAKALTP

>contig41816 Frame-2R

MGSPLFALERLGAFPRGWNASTSTGNSTSKIPPSRLLAQMPMSAPHQKLVPQRGSIVMNP

LKLKYEFRAVKGPRTGTSTDFSSALTKQDENIRGNSKPFTPGGDSLTELKTEKKEADLPR

MQQLLLLEEERARNAIVLGESDVAKTAVESLVFNVPGLHGCITAEDVAKMATFKVEENTK

AEEQM

>contig41863 Frame-2F

MPLVPTDLARKLRAAGQGHVLKFDDADKLSALEAQELTKELETLDFDLLQNIFQASTSAK

TSETGTIEPLDSFDLLEQCHIQEKLRWKKLGFEAIAHGQVCALVLSGGQGTRMGYAGPKG

MYDIGLPSEKSLFQLFAERLLALENLATKYGSAQPRAKVQISFCVMTSKMNHSTIVNFFK

EHEFFGLKESQMLFFSQDKLPCFSTEGKLILENAYKLACAPDGNGGIFNSMKTSGALAEL

QARGVKYLHVFSVDNALCKVADPTFIGYCIYKQADCGNKVVWKARPDERVGVVAKRNGAY

CVVEYSELDQVSSEQIDPSTGKLSFGAANICNHFFMMYVNNYVSNVNTCQHFELT

>contig42123 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55342.1|) 1e-15

MEATTEHHPSSEEMSPSQGATSNPFKSALHKFGPKKKERALSTNLSNAPTSSFFTRGHKK

TAAQHKLQAPPVATNQLTTGQLPPVWATPSPAPSSVPAAALMDSVSP

>contig42978 Frame-2R|Blast-predicted protein [Micromonas sp. RCC299]gb|ACO67200.1| predicted protein [Micromonas sp. RCC299](ref|XP\_002505942.1|) 3e-07

MMTTITRPRTEGLKWTLDEDSLLRDGVCKYGGKKWKTIAEHLERRSPEECSKRWNKLQSL

DTVVKRPW

>contig43393 Frame-2F|Blast-snRNA-activating protein complex subunit 3, putative [Phytophthora infestans T30-4](gb|EEY54329.1|) 1e-128

MAKTITAMSFEFARPMPALDEEEASQDAIKSTEKKHVLNENDPILWFEVLHPSKDPARTQ

SFLVRQSQKLTDLVDLIVCANDERLAEYAKASKLLYFGKKMFVDRRVPGSLDYSNEIIQW

IQAKPERQEKFGAFPIDGPPRPSLHLSTFADLDLLIDVPGVYIHQGECEHLIRLKDARLP

HEYDASTSSGIFPLRLPNALNHPLRNCLICQNYSAKYVCYGDRLAVVDPMFFCHRCYRAA

HYDVNGNLIYNDFLSFPFVQD

>contig44684 Frame-1F

MPMNPTHSESGNLYVNTNYGIVSASNNVDCENSTTNVGMDSIMTPLGFNSDGSFETQGFL

IGNMPNLSTHQRQMMGLMNGGNYGAQGAPLMPNSFGYGGMPPSSNMMLESLPTSAFQPPS

YPYQQTHQLAHHPHLQETGLGFINMTPDLAMYGDTNVNIFEGLTDDAFFPMQ

>contig44947 Frame-0F

MQSQNIAIVNKLVIKYPPANSYASYACSPRLNHYATLGCITERKLGPS

>contig45324 Frame-1R|Blast-N-terminal acetyltransferase complex ARD1 subunit [Phytophthora infestans T30-4](gb|EEY69831.1|) 8e-96

MVSIRNATANDLLQVQNSNLWCLPENYQMKYYYYHIMTWPQLLYVAEERGGKIVGYVLAK

MEEEASVPHGHITSLAVLRTHRKCGLATKLMLAAQRAMVESFGAEYVSLHVREGNVAAIH

LYRKTLKYQVYDIEKGYYADGEDAYDMRMPFTDKCNQAFASQVNRFKKILEVKDAEIAAK

K

>contig45618 Frame-0F|Blast-ATP-binding cassette sub-family E member 1 [Phytophthora infestans T30-4](gb|EEY69572.1|) 1e-147

MPFSVREGINIFLSGFVPTENLRFRTEELTFKVSQNADEFGTGEGDANSFNYPAMTKTML

KKKNDTAFKLHVEAGDFTNSEIICMLGENGTGKTTFIRMLAGLHKSDEMEAAEKIGDYDA

MSKCALRYDASTVSYKPQKIAPKFQGTVRELLHRRIREAIVHPQFATDVTKPLALDNIID

QAVPHLSGGELQRVAIILCLGKPADIYLIDEPSAYLDSEQRIIAAKVIKRFIIHSKKTAF

VVEHDFIMATYLAD

>contig45786 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59354.1|) 4e-88

MAEEVVEALQTTSVAEYAASLNLASLPTRLMLSMPTPYDVNTMCLVVYLAYMIDFYSSRF

PLRKTAEVFSEEKGIPLSIVRHLFKLFTDMSEDNNGYPTYLQSKMMKDKLSLHLLVVALT

VNGFALDLAEVGNDLKRSPVHIQAYARQLGCLVEKLKTDAGVYAGAGSLASKKPTLRAVL

SVPLHFPQPKRGNPSRR

>contig47344 Frame-0R

MCRLEQASCKMAKYRCWLLPALPLKHCVHCNVTGNMRGRFLIRGDERRIMFVCLGDSYDQ

TASEWQNERYSTKLHRQLRLPQYA

>contig47487 Frame-0R

MYILYGLSHMPHMANTAVLWISSYSASIQKNSPPATIPTPNAPHLSQTRQ

>contig47638 Frame-0F|Blast-ribosomal RNA large subunit methyltransferase N, putative [Phytophthora infestans T30-4](gb|EEY64253.1|) 1e-101

MVKNRTLSPLSAFDQNALPTFLQNQGFKELHALTIWRYLAQNSDALFSDIPAIPKTLRVE

LSEHFAPFTTSVIEEQRSTDGTVKLLLKLQDGHEIEAVIMRHKGRNTLCVSSQVGCQMGC

TFCATGTLGIIADLCSGEILEQLAHANRVARIRNVVFMGMGEPLNNYDAVLAAIRAMTRV

FEIAPKFITLSTVGVIHRIRQLSRDAPLVRLALSLHAPTQEMRCQIVPTSTAYPLEKLMA

AIDEHLAMK

>contig47713 Frame-2F|Blast-trehalose-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY58496.1|) 0.0 NOT\_ORF

MLASDMGQELGESSLLDQLHDLHRRLAAVRHDSQRHTSLSRNLGPIPMANDNNKIIVCSL

RRCVRMLKTERGDSWQYIASSTGLKSAIDYLGRSNTVRWVSWPGATVDESSQDGVRRRLE

TEFACHPVFLNNEILDLYQNQFCDVVLWPLFHSLPQHSDSRLLENFGEKYDAYCLANQKF

LEAVSEIYKDGDLVLVCDYQLMALPGLLRRRYPDITCGFYFHCPFPSSEFFQMLPVREAL

LHGVLGADLVVFNHFDYVRHFLNVCTRMLGLESSPSRVEYNGRLI\*LGICPMGIDPVKYA

LTPKVEACGKMIKRQQDCMKIIVGVSKLDFCKGIPEMLEAMEYLLQHYPEYRENVVLYLI

VRDAGRTASLQYRVLSRQINEFVGRVNGKFGTAEYCPVRYLKQSVDHSQLVALYNCADVA

IVSSIKEGINLQAMEFVAAQKTSCHGVLVYSEFAGCASSFQGALLVNPMHIEHVAASIDT

ALRMNTTTKRIRHHQLSRYVNTYTSMLWAQRIMSALNEAAATAQEYNRLDKLDTVQLLGY

YERSQRRLFLLDYDGTLVNFQSMEELAEPSPSLMSCLEDLTADPQNTVYIISGRNKSRLQ

EWFGHLTRVGLAAEHGYWFRPASKHPSALHVDEKWCNYGEGLPGRISQDTPHAAEAGSIA

LVNEDTPLALSSSTKGVTDTERAILEKAPWQCMFSDVELEWRDEVESILEHFTERTPGSL

LDIKDCCYTWHFRDADPTFGLKQAKDMQLHFDQMLRDLPVGVVMCRIKKYVMIRPWRVNK

GRAVSRILEYESETPYFTALDFDFILALGDERTDEDMFDVVQGSNCYTCTVGMKVSRAQY

YLDDPDEVLRVLAACTSLVAVERQPL\*GDKRAVSLIAAINN

>contig47814 Frame-0F

MVDFAVDKSFLFSAWRSVDGDEVYVHSNPMALTGPKQIGGVRVSSYDVLMQKYAKEDRDW

LFDLKEEGVLTIIDTFYVERILIPGRFSRQNLSNAIVEIQQEAGLGCTTFTLSSMDYKEL

LIRLVSSRLFKEAIVRTKADPCLVRIKIWKELIALCTKHWRCENVPIGFAITTNALLPGS

PVLLRRNRVSLLFPSAASIATALPSEERRSSSIECVTEVTSDVLPIFDAFSSQSFQSLIH

REVADVASAWKVESFVALARHCVRLGVHPSTAPGQDFTLRWF

>contig48815 Frame-1R|Blast-integrase [Beta vulgaris](gb|ABM55238.1|) 9e-08 NOT\_ORF

MYCEFKIMRADVLTRAFAAPHLRELRELTCLV

>contig49074 Frame-1R

MPATGHSNSWQISAGYNHEREQEKESKRQHVMLRHALQIQASSLNSSTSCGCKTGCLKMY

CTCFSSRGFCHTGCACDDCKNGRNYQVERVQAIQNYMDNNPRAFSYASLPPDTNASGFLH

LLPQKSSAVVMRGCRCKRSKCLKKYCECFQNNIACTSHCRCMDCFNHFKSSAAHHHCHLH

KQSIITVYSIPPADHPPRLFHPVHVTVTKQPRRNCVAKTVRLNL

>contig50667 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69521.1|) 6e-59

MIGQEVCYPIRDTFFFASNMRVIKYMCDVAFADALLPVAGDYETVVFLMSP

>contig51053 Frame-0F

MTYVEMNVIYHDKVLGAPFTMPSARLVAYDTTLYCDDRSRADEQRSVIDFVTSTYPAASI

KLCLQKSVFEMDENRTTGANNEAE

>contig52140 Frame-1R

MKNSGHVLASTHVSCGAAMSRAGPVQANLRLCAKHAPTITTVDLVGEEDVSVVKKRRKSY

I

>contig53600 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53281.1|) 2e-10

MNQSCNATVIKHESAAFGLPAGLDRSPLQRFDISDFESHHLNETIEALAPVLALDASDVA

MFAEPADISLPATPNYSSTDSADSIFYSNRAIPHRKTRPRRQRLSTASAASPMLHQHH

>contig54300 Frame-1F

MESLRTDGTNPYNVTTGTNLWLSAMENKENDSYLSAHESLGSSQNSSRNSYEGSGHNIDS

DQSSQISGHSNRSEEFPDHNEDNDSARGSYEL

>contig54559 Frame-0R|Blast-fatty acid synthase subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY67793.1|) 3e-25

MGSVSFLPISAPFHTPLLLEAKHKLVLDVQRIQCEIKGSQLLVPVYATDPEAT

>contig54850 Frame-2R|Blast-hypothetical protein PITG\_14851 [Phytophthora infestans T30-4](gb|EEY62411.1|) 8e-14

MLRYTTSGLCQSIRQVRREAARKQQKQQRLQTVLKRSKGTKSTVCGPAREQSIITNQQKQ

TFGRIRHTETVGRDLQLAPS

>contig55325 Frame-1F

MRRVRYDEADLRTLRELEQPLQLDTIGITGAYRMYQARQSRLSLRLASWREDVKQSGGND

DHLHHKLAQIRAVQFWCRQTQLSDNSPANRAVLTPNVP

>contig55488 Frame-1R

MNPKDTEGQEQAANLPYAASAQVPHSATTTMAASLNTQEDERFINVPYAAAQATPSASEK

QASTLPPIAMAQPLGKNMQNQPHSQSGSNIPPRNYQNGLGGANLSHHLVTVVPIASSGDD

AEDDNMRFKYLQKNRWMAILMMTYYAMTFLILQPIFLGVMGLLTAFAGQHGSRAPVNVTR

FNWLRHYMWANYVILILNIWLLVVTLVFSGSVFGVAKNKSNESTDTTFSFTSSKELFIGL

LVAANTLIHLRCLRTVQLLIAELINAGRDRPAPVASAVPTSTE

>contig56078 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61055.1|) 1e-115

MDTKEMEDGTENMLTDVGFMFDACLEKVTCQFEYGDDAEVSVLLTYAKEDPGVVQSGHYV

WPAAPALCEYLTKHRDIIPSGNVVELGAGCGLTGLAIAQLRPEATVIFTDHDPGVLKVIA

YNAGQQKRKQASCLTQSLRWGPDGAKEIEALEKLQTGPINRTRVTDLIVGSDVIYAREVV

PLLFWTVDRLLSSNGVYLMCSSFKYDDEIEKEIDVQSAKCKLKREIIACSLDEGGTRIQC

FTRLVTS

>contig56672 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY61622.1|) 0.0

MSSPDGYHGLKFVGIMGHDNVSHNGSKTTVYFVQVQVPEGMFMVKHRYHEFKEFHDKLSS

DGYRCPALPPKKFLGSLNKEFIEKRQQELSNWLHLLCQFDPASGHSDPRASELFQDFMLS

NKEPLDKYQGARTISYDATPPTSQSSEDETSIYNTPKTTLDDFELLKVIGKGSYGKVTLV

RKKEGQRLFAMKSLNKSNVKRRNQVEHTRTERRVLGRAKHPFIVHLHYAFQTSQKLYFVL

DYCPGGELFFHLSRMEKFTPVMARYYCAEITLALEHLHDLGVVYRDLKPENILFDPVGHV

LLADFGLAKEGITDGAEGTNSMCGTPEYLPPEILDRVGHGTAVDWWAMGMVLYEMLTGLP

PWYTRNRQKLFDRVRNAPLTFPDDVDPAARDFIGGLLRRDPNTRLGSKSADEVKTHAYFS

GMNWQDLYDRKIPPPFNPCAAAGKAEETKNFEAEFTKMQINSVENSALGSLRVSDASRPS

MTFQGFTYNTPNDLSMSSSAGRG

>contig56823 Frame-1F

MLRTSIKKTLVKPPAFGHLATTRGFAIQSSRPLEGVANSSLTSKYTVVDHEYDAVIVGAG

GAGLRAAMGCAEAGLKTACISKLFPTRSHTVAAQGGINAALGNMSKDDWRWHMYDTVKGS

DWLGDQDAIHYMCREAPEAVRELEAFGLPFSRTEDGKIYQRPFGGQSLEFGKGGQARRTA

CAADRTGHAMLHTLYGRSLAFDTSYFIEYFAIDLIMNDAHECVGVMALNMEDGSFHRFHT

NNTVLATGGYGRAYFSCTSAHTCTGDGTAMALRAGIPLEDPEFIQFHPTGIYGAGCLITE

GSRGEGGILRNAEGERFMERYAPTAKDLASRDVVSRAMTMEIREGRGVGKYHDHIYLHLD

HLPAEILHERLPGISETAAIFAGVDVTKEPIPVLPTVHYNMGGIATNYMGEVVMPDVSGL

PDPHRVYPDKIIHGLFAAGEVACASVHGANRLGANSLLDLVVFGRACAKRIATLTTRNEA

KRPMPRDGGLQAIADVDTLRYANGSIPTATLRLTMQKTMQADAGVYRTAKSLATGKEKID

EVVPQFQDVKVTDRSLIWNTDLVETLELKNLLACAACTMHAAEARKESRGAHAHEDYTTR

DDVHWMKHTMAYHDEHGETHIAYRGVQDQTLDEKECQHVPPFARVY

>contig56856 Frame-0R

MPPTSVVSLKRHHLLHIHSINPHSTRS

>contig57899 Frame-1R

MDKVRLLCAVYGEGTLFFVKIARDADVVALQTAIVNAKKGV

>contig59167 Frame-1F

MLTSLPLPLPMPKLGMERSASFHDYCESSGCNPVSIRQRSRIQATTPISVMKNRTSP

>contig59314 Frame-2F

MVCDQAYEATVIPCAHDTIYHIDPKW

>contig02647 Frame-1F

MGAGPSLCTFLKSINDDDLAKLIESVRESVFIDVSNTDTCLYCRIQAYKLEPQRIEKMFS

LARQHYFEEISRQLPSDFSTIGTVVTLSTSVVHQPPQVANMPSASPLLNELFPPPNLSAM

TTASISADMHSVSMMSSTDVMETVSPYDEHLGVARGKYLMNALWTFEGHRLCKLQTATKM

SQKKTQRHELENDSNHSSGSLTEAIIPSKNKVDTNGQVVMYGSCGRDKRYARCSVCYFRG

LRCNTAHYCACCLKAVCIRPRVYPGEEHSKICWNVLHMDNEIINRVMKTKKRKLNSDAGV

AKGLEASGSATHLRSLETEDSGYRHQKSNQGTLCMLEKPLASSFEADENGAVNL

>contig04858 Frame-1F

MIARLRGFVQSAVTYGENLHETSPSVSNQYQIKRCEQIDLNLLTMLFKTRAQVDEALLDD

FDTPRALILVLNLISDSNLYLVAHRHNVTKAPDEVLGSVLNFLLEMLDLFGLEGLYAEFS

EIMHRRFPSRNAKQIRKTTELFSHSHEYDSLLRSLVQFRASVRAEALQNPKEPSTARILE

LCDAVRNTELPRLGIQIEDLAPGRSVYKLLSRVERQAAAVDKKTGLKPLEQKQRKFQTQM

QISPTDFFKKTPEFIGRFDSFDANNFPTHENQLPLTKSQRKKLIKKLTKYQQSYTKYWTD

QRND

>contig06113 Frame-1R

MRPCPHPGSVITTNPTHPLQILTINLTRKLRYTDVYRKGRTGKAAKFAEKVQIPPTCTQF

CFDGCTR

>contig12071 Frame-1R

MIRVERSTPPLAVALLQLCVAFVIGNDSENSSTSAMDGSIDDTSNSFEGAAELLSSAKDI

RVGAAIVAAIAILGGGVICLAGYRLFRPTVFFCAFMVGGFFIAGIIETAFASMTWMPTAS

WIGFGVGGVIAGVVVLMLYSASIFMAGAVGGIMLAFTINTSVGTQIYPNNPGVIFIILAV

LLGILGGLLALKLERPVLIVTTAIVGSTTCIAGLGYFIGDYPNGADLKEFGFKNMKGDWV

YDLPDAWWGYLAAMIVLFLVGLTVQLRKTAWGYDHSGNRGSQGLSKGNA

>contig12668 Frame-2R

MSPVVMMPGYTKRFLEGSITVESQLRKIQSCFDRIMATNEFTVVEGTGHTGVGSIVGCNN

AQIASELGIDMILIANGGLGSAFDDLALNYAMCQAHNVKIRGVILNKVRPDRIAMVKEYF

PKALKHWKVPLVGVVPNLSSLSHPSMLDFEGLFQTRILSSRARRFQQYNKTTLVTAGLRR

FLTKLSAPEYDHTMFVTHVSRNDIILGLLSHAQNFELTEKRPYGGGLILTGSPARDQPQD

>contig12981 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67499.1|) 1e-150

MMRLLSLLATLLLVVSWSNVDVEAKKSRKEKIVPLKGSEKLVQLQSHKLHGVVPFTNDMF

LKYVSRPDRPYHLVLLLTAMTEKYKCEACKHVAPEFELLGTSYEAAKQLQVDTRDGLDVF

FGVVDVENNGIAFKMYDLTSAPHILYVAPDRSIDAANPIPKTLKTEPQNMYNIYSQGVLA

EPIADFVKQRTGFEIEVQRSKIVRHALILLALVSVVVTAKLVLVHLDFVMAKIRRKQLWM

SVSLLFYGLSVSGMVYCIIRNPAPYSADRAGNIQYFHPQGRQQFVYEGLIVGGYDIASAV

FIILLSQWALYVHNPTVRYVSIVGCALGFFVMYRQMTNAYKYKNRWYTGWMGI

>contig15993 Frame-0F|Blast-ankyrin-like protein [Phytophthora infestans T30-4](gb|EEY59188.1|) 3e-27

MGDVGLHRRTRMHWTAINGSVNAVEGLLQETSTKFLYALKNGLRGVNAMS

>contig16938 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66866.1|) 7e-39

MHQSSDTFVAEKQQVSRGKTKGDEIEDLFTLLKEKKQRKSIAVAHQKRMEEEEKHSQKKE

KERLQQQIQQLEAQNTNSTVAGVNPDPRPVRYDEDGLPIYTEAALQIGKGGNTTDCPFDC

WCCF

>contig19368 Frame-1F

MNLLAALSKKMSTDHQEMPSAKLNACLFENFCLCGQSKAIGPPIC

>contig20553 Frame-0R

MASTSTVRCVVYGVHGDVEFCELLGFLHGAAVAQGSKLEISSEILSSAAEMKALATEELE

KDIVNVPYIVQQNATDHLSSLFARISVSQKVYIVFGKMAILQWIKQHLLESSATLASITL

EHHPLRLFISGDRAHVGKSTVCLGLIGSLLQRGYAAKDIAYMKPATQCQKPQLVTKFCRQ

QGIACCDVGPILFYKGFTREFLKGETETSIQLLEKAETKLKEISRGTKIVIIDGVGYPAV

GSICGVSNAHVAKKLKSPVVLVGTKGVGDAVDSFNLNATYFMSHNVKVLGSIFNRLPEDG

FYSLEHCRDNVLLYFKQFQVEKRVYGFLPELQDGDVNVPIAAIVHETTQKESVSGVLLTS

FEEAFVKKVVEAFHRSIDVTTLLADVQANQGLN

>contig20737 Frame-1F

MMLWLLLVLSAVHSASISASVDVSICHDATYSLSVDASTLCAGSGTPTGIQCPRAGAIAT

SDCFPYLPSYRDGHCVAPEDAVCQLVHENTWGCVLPSVGCRGIKTSKCPTWDYDMNTTIA

LDTSGSFDGNQVYNQSWFVQTTPLRDLTKCGDVPTPAPTVPQVTVATPAPDPTPLPTTIT

PEPTPAPTTKTPTPAPTTITLEPTTSPLTPTPAPTTRKPKPAPETTPAPTTTITEVTPAP

TALNTKPLPVSITTAPSPLASMGPQPTPFVKSTASLLSKSTAPLSSKSSSNDDVSNADTE

STKDTAVNTMSEATTLPSPALVQLSSEFDESNDGMSATVIISVIAAFAVAAIGAAAVVYV

KKQRGTTAHMRFSSEYEMAFTPPHATMSPLTVTSPRS

>contig22469 Frame-0R

MQQKQVNSGGSATLSDICTMQTAASIMSVRHGVPAAAMASPYPQHRVNSNAPPPPRLTTH

KYSPSSVKSENVVEVQAQSDAQYNMEDLSLSQFDFDPFTEKSNPV

>contig23985 Frame-0F|Blast-protein tyrosine phosphatase type IVA protein 1 [Phytophthora infestans T30-4](gb|EEY69073.1|) 1e-53

MIAPTNKPTMVKWEHLFFVIMDAPTDSNLHVYLKELKKHNVTDLVRACEVTYSSESVKAA

GIHVHELEFPDGESPDPKILDQWLDLVEICYKDNVCSSNNNRSIAVHCVAGLG

>contig24207 Frame-2F

MTADVNSAAAACPHLPQKTSTKAHGCPVDQANTEASSEHSEITRFGLNAELLRVANHAAG

FAVHGSEGSHLSKSRVVSSIPKGEVTPEHQTGSEEKWEYPSEDMYFKAMHRKGWAPEAQQ

MKTIVAIHNAVNEQSWREVLKWESFHTTKEPVKLKKFLGKPTEYSPKAKMMNLLGWSVLP

FDRHDWIVDRDGKEVRYVIDFYSGAATPGKPLSVYLDVRPALDSVEGVVDRLRWQFYDKI

APYLPFNGAIVGSRTKPAAISQTDDQERHSEVTPKTN

>contig24272 Frame-0F|Blast-tubulin-specific chaperone C, putative [Phytophthora infestans T30-4](gb|EEY62994.1|) 1e-114

MRDAAASASSLYLSPYDTRQTQHIVAKLLELIDTTRTTFAPRKKFTFRAHAAQQAKMTEK

RQNVLQEASTDLNKNQQPSSVAVKTIDELVYANKKNEVIIIDHSSFADTDNLSRLDLNFS

QLSNCVVFVCVETSAIRGDTLTNCVFYTGAIFGSLWLEKSNNCDFFVACRQLRVHLSSAT

QFHLRISSHPIIEDCEQMQFGPYCLQFPGLKDQLEQLGVAKDSGLWAKVNDFKWHKKQQS

PNWSLLDSKQLLPVIPVDLESRVSYT

>contig24557 Frame-2F

MKRDFKMSQTLMNQAEKAQQEA

>contig25169 Frame-2R

MRELHLTINSGYNHFMGPSIMQSQANDSLEAVARLPPPSFNKWLDMAFAEEKAATKIQFF

FRDCLNQRHLSDPSVQRRATKILNFDSASVPEELDEDHQYDVLLLYGSSLGTVILKSCEI

TGYPCVKVAEGNDYLPGMWNLRKGDFLISVNDQSVKRSKVPFCKVLQILDSGVRPAVLRF

RRPVSHELQCHTKRPRHLS

>contig26731 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63937.1|) 1e-55

MRLITHNLLMCNKKGVENGFPLTIEADEIEVVTCDFQADFVRKMLTKLDWDAFLMGAKAL

KLADGLPETLPSAETNCTDEETLRTIHHVLLEVHVKQGKLVCPESHRVFPIIDGIPNMLL

NEDEV

>contig26810 Frame-2F|Blast-predicted protein [Thalassiosira pseudonana CCMP1335]gb|EED89479.1| predicted protein [Thalassiosira pseudonana CCMP1335](ref|XP\_002293018.1|) 2e-28

MQGLQEVCAENPGVEIFLAAIDDGLSEDGYILPGLGDAGDREFQTGAQAEKVEIAYKKQK

L

>contig28100 Frame-2F|Blast-Poly(A)-specific ribonuclease PARN-like protein [Phytophthora infestans T30-4](gb|EEY53399.1|) 0.0

MVFIWCVLNIDHRMLRISKSSLRSLLFIHPRYFSAVPLDTPSSAGEMNVTRQNFASHFSD

LQKDLQLPTCRFVAIDTEFTGLSPNELEREQYLDTLEERYRKVKLAGESFLISQFGLSTV

HVDRKDNIQIRTWNFYIFPRPYSSLDERFLCQASSLQFLSEHGFDFNKFIGDGIPFVNLS

KTSVMKKRLQRRINGLTKVNKNLHLSDDGVVFQQEVNQQLDQWIAGGAKKGEKLLVPTRN

SFYSMIVHETVRVKASFLYAESVDSGVEVSYVSIKKKEELIAAKIWQMRKEMDEAIGFSK

VIEVLSESKLPVVGHNALLDFVYVFHQFYQPLPETLAEFKTQLLELFPTIYDTKLITLRS

PLSEKLKSTSLSSLFEYMRTNVKPEPKSLIPIEKQFDTYREALKTDATDNSKMLCHEAGF

DAFMTAVCFLGILAHDAEGELSDQLVPKEGIAARMKVRLEELESVKNQLNLMISDQSVLD

LKDAGQVINRDRVFHVSSTTKRRIQHVRMEDVFKSSKVQRIVRESDHDAFVVLREPTEVD

EEIKTKLGLDIITYDEHVAAEAEKSRLKKVKDDHMLFNTISASQPSRSGVEIAAKEETTA

WPSCIIS

>contig28650 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59357.1|) 4e-78 NOT\_ORF

MPHLEDFFSHRDGPSLCVGSRGKDDKTLNNSHGDGNLADSGVLYLHGPEASGQTSLLLQF

GFTQVRAGRNVVLIICGDAGASQQRTVSDIVPLSACSKCQRPVQTGEDPGIWSRIRIKYT

R\*IPFCELFL\*K\*CIFCTCSCRYLHNSVELQHFLCSLHVIDNETSVLLIDRFELFFESQS

DMEKVYQTLAFLLETKEYMKMATGVGMTFVTGSTDAFLLRGRALLRRWCRFVEILSPSEN

VPECILREEVENGIANEKDMARIQIKYEFAPPDTDSAGTFQLVGIERRFFLKP

>contig29745 Frame-1R|Blast-ATPase [Phytophthora infestans T30-4](gb|EEY61047.1|) 5e-88

MVHAGSKTHAASVIFIDEVDALCPKREAAGELTSSIHNRVVAQLLTLLDGIDSGFSRANV

VVIAATNRPNAIDPALRRPGRLDREVYVAPPNTATRKKIFQVHLCQTPVAVSNKLPQEAE

KQRNWFLETMAAKAVGYVGADIAALCREATMIASTR

>contig30390 Frame-1F|Blast-protein pelota [Phytophthora infestans T30-4](gb|EEY68290.1|) 0.0

MKLIKKQIGAKDGAGSVILRAEEPEDMWHIYNLIHASDSVKTATIRKVVKEGVTGSTSSQ

RVRMTLQIEVEQVNFDPALCVLRIKGKNILESPQVRLGAYHTLDLEMNRDFTLTKNCWDI

ISLERIETACDITKQAELAAVVMQVGLAHLCLIKGDMTIIRAKIEISIPKKRPGNSAHAR

GIDKFYENIVRAIRQHIDFKLVKCVLLASPGFVKDDFFKFLIEQAVRQDDKLILENKLKF

VSCHASSGHKHALDEVLCDPKIQSQVADTKAATDVKCLDCFFSMLHTDQDRAYYGYKHIM

HANANMAIETLMITDALFRSQDIAARRKYVDLVESVRNNGGTVRLFSSLHVSGEKLSQVS

GIAAILRYPMPDIDDDDVEDESDFEEDKEKENIAGDIGLDDLLVEALTM

>contig30787 Frame-2F

MQDNHDQSHDHDHDQSHDHDHDHNHGGGVEHATGDSLYPFIDTSKLWVLNALDPRAASHP

FKPFHERQNHSCFLASNYDDPELILFIPFTEAVSIKSICISGSA

>contig32486 Frame-1R

MKSSKESKQAVQKAKSTTNATVTSLSQRLTLLKMAARDAVSSTSNVIKTTSNYASAVQME

FVDKKRSASDGGWVDVRLQRSASLISFIGKSTDVELQPGPIGIVFQKSRLIKQFQAVVDS

VVPDTQASATGMITTGDVLVAINDESLERVAFLTVIERIILAPRPVVLRFLTPSKMQREL

ITSSLCSQPHATSL

>contig32639 Frame-0R

MPAQGLITVAQELIPFQNPDDIIFEVISWGFAILYILHFFVGKAQNRKIANKWLKEAEPV

LRTQFSFLGSSVDDSLGLIEESYNTYKYFCTGRRFLTHFVASLE

>contig32767 Frame-0F|Blast-importin-like protein [Phytophthora infestans T30-4](gb|EEY66017.1|) 0.0

MADYTPEQLEACLLQLTHPDTEQIKQAEVVLKAYTKKIASVGGLLLQLQLSTKPEVRQLA

ALMLRKKIFKHWPKLEATAQAQTKQVLLSRAAEDPVHVVRSTVASLISALALHEVPLGKW

PELMIFINTSASSANVDQREMSMKLLQLLGESMGTSLQPHFNDLKQLYAKALQDPENLKV

RVGAMRAACSLVEFLEESDLRGFRDLVPLMITVLQQCVANGAEAEAVEFMDVFSEIASHP

FPILDQAFPQFIELLLQIILANQLESSTRASASYAMGEFIKKKPKTIGKKSLVAKIFTTM

LDIVAADEAVSCGLISNLLEREGKTGGEDEDEDDDSPGHMAQQTLDSLALSVPAKYLNPV

VFGICNEYITAQDARKRKAGVLTLGILSEGCCEFMCQNLNELLPAVYRVAQDPDQHVREA

ACFALGQFAEFLQPLITDHYTDILPIGLTLLDDASKVIKATALYVLDEITQSMESDQVLP

YLDTLVTKLVAVLRTGSPQLQKMALDALGSIAIGAKDAFLPYFPSVAELIQPFWGIIDPK

FYFLRGAAIECLGYLATALGKEPFRPYFAPSMPFVFSSFELDDSELKEQAFVYFINVSSI

FKEEFAPFLEQAAMHVLQAIVSDEGLRVMDDDEDVLGGVDSDDEENEDDNVLRHISIRTD

ALNSKVRAVAAVEELALNCGGAVFEPYIPKFLEALAPLTEYIHEDVRGAVAEALAALVIC

SFEASHAMSSDVQVWNKGDFNKNILSPNNAVIASAVMKSLVEELLEDPEEVVVEKAFNAI

KAMSARVGPVVTMDHMNELMRITKTVLSHEHICQTTHEEDEDDDEEEGGSVLESASELIG

VLAKCYGEHFLSAFQELFPALLAFATGLRAVRDRAAAVGCFAEVLRELGPGALGLVESVY

PVVLQGLTSDNYVLKANSAFCMGVLAEISGEKLTSAYEQMLQALRPLFETSGNDEVVTDN

ACAAVARMIMVGSAKMPLEAVLPVFLSALPLKADMDESPVCFRCLNGLVTSQNHVVLNLM

PQVLDVYAKALASTSSVEEETQAEVKVCVRGLLQAYEAQMKEIIAQMSPEAQAALSTAIM

>contig34444 Frame-2F

MSSKKLVIESMMGLVFLLLYSATAFSLFNHDSSPLFTQSFQVHSFSEKDYDTMLKGHDTV

WLVDYYAPWCPHCRHFAPMWEQVAKFYASTDKVQVGAVDCTKNSGICSNESITGYPSVKI

HHVPKDAAKAAMMPHSMQSVKAVINWTENLLISQGVKSGVDVKDVTAHLKNLRNDFFVTD

GEDGHISYSELTRETKYRRLHDAGIAAISTFQDGFFIGANVLNGERYEVALMWVEALAAA

FPLEKNRMVIAELVKAIKTSNYWTFADWEVMLNNWQERNRETTFPVNLFFSSENGRWKFC

KVYTCSMWTLFHILTVNTVVNSTKSETQSWKSSRVISAIRLYIKNFFGCEECREHFMLSN

PASVIDDLAMKDEEGLNAGITWMWKQHDTVNKALLKERWPSKNACPVCYVKYNQSLALSF

EQLHENEIVAFAINAYGYDEEEVYDLEAAFQGTLVAAWSKMQIFSAMLMVIGFFALLVLA

YKTRRYRGWDRKVQMVRDHTA

>contig35267 Frame-1F

MRELPPSLTHGEWQCQRDIDLLKRAHAAHQQLTMRVMATMHELRGERYYPLHTQTKQLRV

RVYHSYIPAVQATPGRWTLKIEGIDATAGEPTIVKFSSYFRKASIELDPHSYSDHMIEWT

SFQKTSHEVDGLEITRVGSTAHTVKIKLLPAQTPERFTISSELEAAIGQYLGPAKAYTKQ

DIVLAMWEYIKVRNLIKPDDCRVVFCDDRLLQILACVSLPFTSIIVALKKHLTPIGMIRL

EYTLSLSTACNAKILDEKFFDVSVAATSELDEVRARALKECEEMQQDQEKEMTLLKKQEV

DLFERLQMYTRKKKWMTEFAQDPCGFMADVKTSQLADEEILVAETELDECTVPRSMQFQQ

PWTREVVRELLTTRSTN

>contig35339 Frame-1F

MLFDALVWQKPKRSVYYLPITSNVGPEHTDKHCVVDLLLKTYFYCYDRRNPDHSVRCKSL

RSPSQANSSESGLLSLEPVSVLCAPHTF

>contig35645 Frame-1R|Blast-50S ribosomal protein L11 [Phytophthora infestans T30-4](gb|EEY63376.1|) 1e-67

MSAAVKGVVRLRVLAGKASPSPAIGQALGPLGVNMMEFCKAFNERTSQITENIPVPVVLT

ALSDRTFTFITKTPPASWFLKKAAGITSGSATPGQQVIGTVHLRQIYEIALVKQQDEMVD

YIDLESICKTLIGSAKSMGLEVVP

>contig36006 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67658.1|) 4e-82

MNDDTHPLPPPPLHVAVWDGDIDRVRSIINAVCPEEEKLRSAAQSEALKTLLETKDVRGN

SALHLAVRIVQPSQLAIVKLLLGRDASVASRNIDGWSCAHDAALCDDEFLLAQLYLRGEK

QVIKSVEATQETFMLALEKLPDFEAEIFAEAHSWVPIVSSVLPSDTIRIRKRGSQLRIDS

ALKGLEGLKWKKGSMSQVYMGRNGGERAGHAVVLNHDNKVFYDVFTAMYNSSVGNIDMAL

QVSLTTAMSSSSMDATKLEFVKLKSAKTEGLKDGESYIHKEEANTKSRSRQRKCPWPGTT

YKMQNFSIEAQLRPIVNSNRKMKQLTAGKETPFDEVQQLVEHFQTSLPYSKDSKGSKSRS

CSINDNSLSNDNAGRVMQLEKGQKVEMHLDVIAGDTIRWEYLAKSSNFCFVATCFHDDNK

QVICRADGIKGKAIVGA

>contig36770 Frame-1F

MANCNTYSRGLRSRSRSDSTSSEEEEIYDDMNIGDRENGDTTPPKLVQRTLLLCSDGVRD

EDDDEDSDFEELDDFSEPLYRGTFYSCRQIDLDNARRLQIFQEERGKKHKNEMQRLELKL

KADGAAAYFNMPTNAAVVIEKVAQLKAVKTLHNFLRRSWRYVLRNSFMTVNVLWLLAPLC

CFVIAIAAPHYLNSVILYADNITSKVVGIGGADAGFDAGAVRSVVKEILDMKLVTLNEEL

GVLRQTVQSQELEIEAMKLLHDTVRRSHDEELRKLSSTELDSVIYVHVKTVVAKHTKELW

DKSMNSTSRLQQDVRAAAKERSLISTTLKHQAEHLDSLRSNVDRLAISERGSDSLVRKDL

>contig38127 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65801.1|) 2e-85

MTGEAPLSVSEVNELRLKREKIATERYLMSLEPHKAMLEPSLYPHIWSDKECFLICKEVK

RTAAEQGWCKERHAAYQTTDMPCHQVAVLYSWVRSTLTDRLFPRIAKGYNISKKQQLLFR

DLFFVKYEARGTERSELALHRDGSVLSFNILLNLSSEFTGGGTYFDTTQRTIHVNQGDAL

VHSGKVIHGGSPILTGTRLILVGFLDIVDCAFE

>contig38574 Frame-2F|Blast-succinate dehydrogenase iron-sulfur protein, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57141.1|) 4e-66

MNIDGGNTLACLSPIKKNKDVTSIHPLPHMYVIRDLVPDMNNFYDQYTSIKPWLHSDKPQ

SVNHEHLQSVEERKKLDGMYECILCACCSTSCPSYWWNPEKYLGPA

>contig38813 Frame-0R

MPLLAKLQRYSRRQFVVALICIVSCLGIIGQIQVLPVLAVLFLPVFIFFRWVSRQQQHHG

ATDREIEQIFQIFLGGALVFWVLALLSQLLMFLILVSISASNNWNSVENEGQKHSANGRP

ELVTGLKLGTAIFNLSIDKPVGYFTIVFATYFIVKAFVEEYLKYWIVQGSCCYEISKGSC

WKRQICRYCSTNSESKPAFSVLKQRQQRHGALQGMMCHPSRLLFYRRPHANHAFVVFLAV

MAGALGFSFMENTLVALFASTFHDQIKIAILRSLSNAPLHCICGGITGVRMAERLLAHRH

GSSEFSGANAAKKDLGRWCTKIRVIFPAVLVHTIYDTQLFVLMTLVPEQVKAANWIVYHV

VVPSVLISIVLVSSFIQLRRKLHMMENKMNETHYMHVAVDLESGELLGAVNGDFDEDMNI

FRNENDVTDSEAESSGPNSSRKVRSVFTK

>contig38909 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69730.1|) 5e-33

MSSSPLWHESRPSSPFSAAGMVDLALDSLGLMTGQISTRSSVPSPLQADLFTHSEMYALI

LLDETHSFFSMEAVNAALDGTQAFHK

>contig39234 Frame-2R

MKGLIKVKGTMGLGFKLNVVLAATRNYIKNKNVQKKLAVSAAAPAAPIKLNSKTIFRLLE

DVVVKDGREMTKKVKGSIQFDINGAGKWHLDLKSTSPALTEGSKQADVTITVADADFVEI

AMGKLNAQQAFVKGKLKIKGNMMLAMKLPIVFSAIKPQSKL

>contig39964 Frame-0F

MMKIHNVAAVIAIAIASIGVNADQTSRRLIVGGESVIEGQYNYTVGIRAYANGCTNCVGI

LIHEFLVLTSAACATNVSDEVQPRFAAINQKIVDGTDIETGEVIEVNRVIFHPTYDEKKV

TNDVALLVLKNKSRIKPAKLGCDPEPGSKVWAFGWGKTNSSHDFPSHTLQRVQFEVKTND

FCDMYEMLTPTNLCVGGEEGKDICDNDYGGPLIAEGADKNSNDDDRVIGIIGLGIGNFGE

AC

>contig40212 Frame-0F

MATTALADHVLLLGSSQENQLLVADAATGAQLYCFKNCRSALKGVLVVPRTDHFVAVQDG

RLALNLWNWGKDMPVWKCHVAEKMGPVASSRCGNFLFVGAESGKVYIWDVKTGELVTVFD

AHYKRVSDLSLTSDDSHLITAGEDALVHAWRLVDLLDEPDAASSFQQGATPVVSFTDHVL

PITSVHVGLGGVNARIFTSSLDRMCKIWSLNSSQCLFSVSCPSYVTTCIADPMEQRLFMG

CGNGQIYTVDLNAAATSVTAANARVASTSTDSAPWGPALLPDSFEGHECSITTLQIHASG

VFLVSGDEAGVVHVWDSLSRQSLRNIKLFKGKVTALVLLPRPRNLYYQAKTPVGPENDDI

DNIMATSLPVAPLKKYMNATNDN

>contig40339 Frame-0F|Blast-MtN3-like protein [Phytophthora infestans T30-4](gb|EEY60773.1|) 2e-83

MTESPCVLVIRVCASMAAIILFVSLSPSIRVVHQQKSTTTMPSALPMLSMLANCVSWGLY

GLLIQDYFPLVATNAVGLVLSLCYLVVYYFHEAKKQKLLLECLATALLLVALVLVPIVAS

HVDMKETVVENIIGFSAVACSAVMFGSPLVLVKKVIKERNTKLLPFSMIIAGAVNCILWL

GYGLLLANAFIIVPNAANLLLGVIQLALYCIVPRVSTYNTIEVTTTVAGESVYDTVDLKE

KKMEKNNNDAETATKTEQASMIVINKEAMGKNQLKSSDSNRQESAKMNTAARVEANRVV

>contig41444 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68700.1|) 5e-51

MGAFLSMQKFLATPLVAQWKFPFMVNPRFCRRRTTTFELKDNFWTHTINVNGYAVREVNS

GRTLFRVMPTIEGQALNDRTKWLFDEYKIPVAHLTRIDDPNAAIYDVCLGKRQLPQPTVL

TTL

>contig41798 Frame-2F|Blast-vacuolar protein sorting-associating protein, putative [Phytophthora infestans T30-4](gb|EEY66878.1|) 8e-06 NOT\_ORF

MLEKKKAPEAVAAAVDVDKQNLSGIAYGMVSLNL\*LNFAFHRGGKEDDTETTAETAKLCG

LLASVAVSEK

>contig42584 Frame-0F

MRLQRDDAVADAKRADAKSVQLACSNNPQQKIRYLQQIKSDNQALRQKNCMLNVRVAKQA

AKLAQLKKGCSLLDEHCETPIDTSLESLMLDEMLRETRDESDVRPVEIFLHNTRHRSELL

EQRLESLRFARQQLSANITNLESAMSASQNQRVTTNVSPNINLST

>contig42799 Frame-2F

MILKTDFEAKCSATIFYCIASLMPYCKLFPARKSP

>contig43006 Frame-1F

MVRDHDSKSLIKSMHVSEPAREYSVGSNLQLYNMTQRTNDEMDANKSIYENVTSHFVTSS

SGRSRKLRMPTPISRIPTPGKRPSASPKALWSSLSTDSGLGLAGRSPGIANELTPRSSIE

NKRLTDSRRAFSASMRVSSASDGNSGLNRTNSNSSLSSVASSVASVSSLLRDRSKPPT

>contig43392 Frame-0R

MSVQTFEKASVGASFLPLAFRWTMADPATSINVLLGKPILLARVLAFVGSADTRLMVCLN

QVWAREMMKPSVWEISADVPYEPLLINCFRRAANYCYREVDAPSPNVNRRGSPPAIRACL

LNERTSMREYVHDLKLMTAENEWFDRPPRTLKLEDVLEIKNEMHKNSRKAFENPVLLNNR

FSRNHELVSGCIDQERANFYSWSLEKQRLRASMTQSNASCYDISEEALAVGCTDGSVKIW

SFASLESRNIDTTTLVNASPTTSISHRSSLGMVPFIRTRAKDKVVNVRIDHNDGTFLHLA

TSTEKGEANVWDVSKGEIILSIPSSKIHKSMLPRSQRETCPQITSLMLLRNTLVCGTSCG

LIRVFDMRSCRLTHRLAGHPGAVVKADTKGRVLWSAGDEGTVRWWGGKSARILSKSALCE

GSISALEMDETVVVAGYSEQGMEAWDVRTQQSLCTFSNREHGGVKALQFDNRKLVSVSST

GKAALWRWYEPNPVRWFETQSTSARIISARFNDRHLVFGTDCGEVVDYDRLAPIF

>contig44685-1 Frame-1F1

MSQSMYMTPQVPTLVSTNPMAMT

>contig44946 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57628.1|) 3e-13

MPLLAASLKENWDRLWTPYAGMLVIEMYKMKSGS

>contig45523 Frame-0F

MLFDKLQFICGPLTIYLLQRHNEQRINRKGHLACFHAQGIPLLHFSKAPTHWRQGSPI

>contig47639 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64254.1|) 3e-38

MVEYCMLKGVNDSLETAHLLGKLLQKRSVHVNLIPYNTTDVGDQFESPSPQDICAFHAVL

RKTYHLKSTIRENHGMDIDGACGQLALKNKSEGNRDIEDLG

>contig47712 Frame-2F

MVQPISSLTLVVMAMCLVSVAPLENQLWLSQFKSKINILPKTSGNCFVCFYQQIKYAGPK

FCIGKRIKSCTKANPITAPGTIGSIKFGKGCNLVVNMRVTVVPFEERVDVIFKDVANTGY

NASADQQSTQELYVEEAGRACSLGFPASGEGYGVCYSKNVRAIDLKYLNSITELMLFKSV

AEKFDVILYEHQDYNNCTKSSIRRNGSQAMFHRFSENSKTLETNNFIGKLGMTTSLQNKV

RSVK

>contig49075 Frame-0F|Blast-phosphatidylinositol 4-phosphate 5-kinase (PIPK-D3/GPCR-PIPK) [Phytophthora infestans T30-4](gb|EEY69389.1|) 1e-108

MTLNEDYVLANVRPDSLPTQVGALISVISCSVIILSFLWRRKWRRHPNPIIYWKAVVDLL

YALRFQYNWDVYTNPLGCRALAILTQFCIFSSECWFLCMSFNLYQCSTNPFTNLKHNLQW

YHSFSWSVGIIFAALLWLSSVHFDPKIHPSCFVDETVDNELIVYYVVVILAVLCAAIFAV

LETQTHPFKGMKEALKAKKDVIRSARIFT

>contig49884 Frame-1F

MLLLNWRHTSVKARAFFASCVASNGKIMQCFHILPRGCFSTLLRNGTAPQPVAASESISR

FTLSVHLG

>contig50136 Frame-0R|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72305.1|) 6e-14

MTLDAAAFPSAHGVQGSTPD

>contig50349 Frame-0F

MWKHQQLKPKALWLRLDIKDMDEAFGSGKLNLFYKYVAADKSFG

>contig50666 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66784.1|) 8e-25

MDLVELKGYLRKKSRHDRWQRRYFEATTHYLTYYKNQESEKLLACIDLWRTQTIDFLPM

>contig51027 Frame-0R|Blast-peptide chain release factor 1 [Phytophthora infestans T30-4](gb|EEY67853.1|) 0.0

MLLRHPRRVLASVLYPWLPRQLDRAQPIANVWKHNQTRGFAMPAVILSQMSLLTRRYDEL

THELSHNDGSYSSEKITNLSIEMAELEPKVMAVQELQRQEKAVKELGGMIAEQLESDEPD

SIELRHMAEEERRELLEATQKLEADVVRLMLPRDEADDKSSILEIRAGSGGDEACLFASD

ILKMYQKVALAKGWKFEIMSISETDLKGVKECVCSLTGRGAYGRMKFESGVHRVQRVPVN

DVRVHTSAVAVVVLPEAEEVEVEIDPKDLRIDVYRSSGAGGQHVNTTESAVRITHIPTGI

VAAVQDERSQHQNKAKALKIMRARVFDGIRRKRDAERQSLRSSQVLSGDRSERVRTYNFP

QSRVSDHRVNVTVYGIERMLNGELLDEIVDTLVVNEQNQLLQQLETSF

>contig51913 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57277.1|) 3e-39 NOT\_ORF

MMSRVRENEAKLAQMQGKIAS\*RALGASANAQKIEGKVVEIEAHLKEDQTCLSALRSRDN

ELLNATRRLLMEPSFQEALVTSTKKSNTILSA

>contig52141 Frame-1F

MASLGSEAAHEDHLLLMDIDKSRHELDNVFKANGLGHLETA

>contig53058 Frame-2R

MLAEYFDTGTRLISAEHVDQQKILLDLIRKVVREQCRRQDNRIRGQDRRQRFHSIFLVEV

LA

>contig53708 Frame-2R

MMSAKPSAWEHIFSTSCHAVPNTSLRRQNAAAYRAVKNSFVSSLTSTNLKKGETPQCDSQ

K

>contig54208 Frame-0F

MADPAWGTTSLLEEESTHALCTFQPTDPLSKHHKVSLEQQLAAPLSQPHSVGRGTFPQHA

REAPPADGYAYCVPYMHHITP

>contig54301 Frame-2F

MSTGAVVGIVVGIVAAVAIIATIIMCIIRRRREGDDDPLSPFELSMDKTYNPTPNNGYGA

QNAYNSRATGAAASGSVPNT

>contig54558 Frame-0R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY68001.1|) 4e-68

MESYISINGVPVVSNTRILQDLVRHDMRFDGLIVTDYAEIQNLHVWHRVAKTDQAAVEMV

LTKAPLDMSMVSFNTTFIQLARQAIHQKPALLERIKESTRRILTTKAKLGLFENALPGTE

AD

>contig54851 Frame-0F

MTNPFGKAFQAADHEWTTELCQADSDGDGATNGQELGDPCCTWTPSANFDDSASWAKPTH

PGVFNSFSKEELAAMGCSGEADLSGTSLSGASTSMSSSSSTFGSQSSSSNDGSFNMMTPK

IKPRFSHGSKVNEVSPTPAVSQAENLKTSIVAIYCFSAFVLIA

>contig56079 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70543.1|) 2e-20

MYKPPNKFRYVFPMWSRLSEGIADIVAPEKGDKQECESHEQLQDRLSAVEAPSQHVSSNI

LQSDNEDDEQEQYICELERALLQRKKQNETLEAKVSQQELT

>contig56673 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59538.1|) 2e-08

MLLGKLSEITRQVSLSFPVLNRLHPFEREVVLLTLGQG

>contig56857 Frame-2F|Blast-2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative [Phytophthora infestans T30-4](gb|EEY66237.1|) 3e-12

MDPVEPGYACGSDTAHMSILGYNPIVNY

>contig56996 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63492.1|) 8e-09

MSQSMEYARSVRSALSPQTLFVSAFPILISVSLLHRSHNISFLQLDVVA

>contig57717 Frame-1R

MSNECKYESISGSWCLQFCTRFSNNHRPYLNQLSALPTSCPTRTFVSITKLSEIQ

>contig57762 Frame-1F|Blast-hypothetical protein PITG\_01286 [Phytophthora infestans T30-4](gb|EEY61042.1|) 1e-11

MAKKRRNVASPVTQRASLHASSRETQVDQKYAEKSLDTLRSYYDQLGGEVAGVPTSLERT

LLFQSVVVLGVQNGLMVV

>contig57898 Frame-0F|Blast-hypothetical protein [Vitis vinifera](emb|CAN79872.1|) 4e-13

MQYVIRQFDAETAFLNGDLEEDV

>contig59166 Frame-2F

MHTYKRKPAKVARSSTVSDREVELDCVVVCSNLNETLTDTIRNLSC

>contig02275 Frame-0R

MEDDNATPEVTPTPNYGLSSRRSERKLSASVIKVALHGDQSTSQSPVSTQPGQSLVVSPG

NYRYLKGVELENATYDFAIVTRRTSSKKNERGLNASINVVSDISAEVEGTLIEKLVVSGL

DVDVLEGDFSCVKIDGKKASKHFVLLIRGNDEALAIYGRRLRFQTWLRSGNSREVDSVVQ

SSPIVTPAERIQVIDHIIRETAKITQDHPNVQSIFPVHDPATNRYLLKTFIGTQRLEFLS

ENFLTKVRAHFGEKVGYYFAFMDFYNKSLVPIALLGVLLTCLRSVIGTPIYMRVLVGWAL

LISVVWSYGFLKAWSRRNNELNHKWANNIETKSTVYPNPKFCGDAIVNPVTGLPDQSYSS

WKRYPKYLAVAIFMMVQISIMMFIIAIWITAFEVLKVRYPDRGIFSVQWFYILGGGVLYG

LFVDIIQWSVIVTRAARMFTDWENWKTIEQFEKSMIRKLFLMDFLNYYTWFFLLAFVYVI

PGVGDTITNFLNTIIWKDPSNCCFGPYLNRSGSYCDSCPPAWIKMAQHETHCIPCRGWVT

FDVNHLDLETLFLTPIIITQLLNLLIAVAVPWIHRKHYEQRLRGTDRKVMAMVKAQGERH

VLAEMSCRHEDSNNANGLHGDSLLHRSSARYLENSESEVELLNAKARAVLFEGEQENYDP

YNDYHHMIVQFGFVVMFSMLWPLMPAACMIVNALKTRGDGFRLCRTNRRPFPRKASSIGE

WHNMLHFVALTGVIVNIGLIFISTGTMEFFSPTCTEQISYAMGSDLSHYRFGPDFACFSL

TTRMIMILVSEHLLLLLIWSFWKIIPSVPASVQINLLRQEYAFKSKLYQRAAKEANLIAS

SLSTSAALPARGGDNTHSLTVVSEPTTPTAVLQRGGVANGYKDEMEPLLSTQRLAQAYAA

ETSFKFQTKHNAA

>contig06730 Frame-1F

MYHNNGCSNPLHPTQRPTLHSIIAGLEIIKCGYQVPDDPVLKDQHLINHGKGSWV

>contig06961 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69724.1|) 1e-07

MVHCVTRLNVTFWVPMEQYLLQLPKRLAQQMRAGIANGDAANVDMVAG

>contig12793 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53427.1|) 2e-21

MENVIDDLAEKADDEDAPIAKITSKISSWLK

>contig13817 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60200.1|) 4e-60

MSALNGGGGFDMNQMMAAQNAAGMMDEGSDSDEDEMPDLDAESKSE

>contig15811 Frame-0R

MRARARFSQADKDAYNEMVSNVLLIHFEKSTEAHELAAVLLKSRDSNTKKVALQVLMRRL

SDENGNDNVCKIIAKDPDAFFG

>contig15886 Frame-2F

MFKEKESEAEAASKQFGEESIDQILSRSTTIVHDPTRDVEGNEKKSVMSSFSKATFVSST

NPDEEVDVDDPNFWTKVIGLNGVEEQKTTEPSPLQKRRCRRKVKSYVMDDDKAESGEEST

NSRKKLFPELGVQKDEEFVVSEDNDDDSSDAAMEVGAESVNSRGKRSKQPVLPIYHYGDQ

IADLLGCFGYGRWGDMKQYARDLEIYSDSELSKFAQEYVVGMIRVTTAIATFGRIGLELR

PSQVYMISFADAGLTSPLEKYAFELSLSVRHYPFLTPMLKDMRLANLLAVGVPIQMWISD

YKVQTARNLRAKLHQIDTMFRLNEFVRLKCANMPALVSVIEGLQKVGSEAEVNKLIETGT

LPSSLDTSHSDKTGEAATVMETGEAVAKLLSKQTTAVINNESEGTKGADQSHVVTSAASA

NSKIMTSSECEDSFAKPVEAKIISQDGHAKSALSTGSAPNEKLTMTLTEDTLVTNCTSKS

SNNSVASIVTNAGDSMCKTDAINLLIPSGGKVEIVAAARGEITSFGEDEKVVSKEHGLKS

NAPSKALTSHELEQKRTEDRKQALQILRSLVPLNAPEPVAPWWIYRVDDVMLMIHVHREG

WLRGRLP

>contig20240 Frame-1R

MEDLILAIGSTSGGDVDKFDHFDVATCAPGGGKLKKVGTVPDKTEGQMKKHKTSKKESAM

QEVASAAAQSIALRDCVAHVLCRVNDLTEEHGHLLLRCTQLAGWTRRTYWDGRNFIPQVG

TDAKPYLTFLGSRTFAYVLPSGSANLPPTGPADV

>contig20932 Frame-0R|Blast-enolase [Phytophthora infestans T30-4](gb|EEY62269.1|) 0.0

MLARPSILRSCFATSATARSIRNASTIQSIHAREIIDSRGNPTVEVDLTLSDRMEIFRAS

VPSGASTGIHEAVELRDGGKRYAGKGVRQAVDNVTSVLAPKLLGRDPTCQRELDKLMQDL

DGTNNKGKLGANAILGVSLAVAKAGAAAKGVPLYQHFADLLGNKHLVLPVPSFNVINGGS

HAGNKLAFQEFMILPIGAESFSEAMVMGCEIYHELKRVIQTKYGQDATNVGDEGGFAPNI

QSNREGVELLMTAIHRAGYDGKIGIGMDVASSEFCTSEGNYDLDFKTKTSTDILSGDELG

ALYQNLVTEFPIVSIEDPFDQDDWRHYASFTATIGDRVQIVGDDLLCTNPTRIATALEHK

ACNALLLKVNQIGTVTESVDAVALAQRNGWGVMTSHRSGETEDSYIADLAVGLATGQIKT

GAPCRSERLAKYNQLLRIEEALGHDAKYAGKHFRNPSKM

>contig22466 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63146.1|) 2e-17

MIVTYCLVFAPAAFFVIDDVLFGIKVALVVSICVTSLSFTMVACSDPGIVFQDLEVA

>contig23649 Frame-2F|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY57700.1|) 1e-145

MAEKAEIYSVLTDLTAGTIGGIAGVIVGQPFDTVKVRLQTYSKFYDGAIDCASQTLKNEG

FAGFFKGMTSPVIGSAATNAVMFAVYERMLKAIDDDPANAKLESVFYAGAIGGFWQTVPL

APAELIKCRLQVQNGRRSSHYQGPMDCIRHIYKARGTPGLFLGFTCTLWREVPSFAVYFW

LYEYTKRFMVDSGINPATSMLTAGGIAGVASWVVSYPFDVIKSAIQTLPVNYKPGEHKIA

YQSRQLYRLGGWRIFFSGLGTACIRAFPCNAVTFYGYEKSSELLKNVIRD

>contig24110 Frame-2F

MKIFFTTFAASVALLLNSCSDALNVKLSGVNYGAHPDGTICQSAEQVEQAMVALQKVADT

VRIQSLSNCNQAELVLPAAKKAGLKVQLGVATGPDPSLLNTEKEKLRSLIQSGLVDENVI

GMSVGHNGISRKEVTAAQAIANMNDIRSVFTEVGRNMSLTISDTIESYVDNPIMYRDVDF

MSITYLYNIENTDVDEAVATALDRIYSVRLAAVNKQVEVAEIGWSSGIGVTTGSATPANQ

SKFLSDLVKAFTALRLNLFWSSGFDEPWHSNAIERYFGLHTANGTLKSHIDQLVITFLDP

RVINIHGLFLSVSSFSFGSNKLTMERLTNYLPSRDEQTFFIDYNTNQVRSLSSDRCLTCQ

EPVNGNLPVILTCKTDDNRQKWTYNTRTRQIQLVSNPGICLDVDRNQNNLIQVWDCATDN

PNQMFNLSPPVLRLVWSHQRQNSDTFSSSTYGFSVPLIMIIR

>contig24208 Frame-0F|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64361.1|) 1e-134

MGCCCESRAPKPLRYVLPCIIVWIIVYLYISFVIFAHSRVIEAGASYWELLLFHVMTFLL

SWSLAQTLRSSESFLPRHTLTKEKLNEFKRKRFDAFTLQTETKMNGGVRICRKCRAFKPD

RTHHCSTCRRCVLKLDHHCMFINKCIGYYNYKFFVLFLGWSATTCLYQSCLIFRYLLANS

LDRAGKLYVFGKLEMLNPHLQIASVFFGSTCLGLALLCFYIMHMYFVINNYSTLEYCEKR

DNPDFINYFNVGIVRNVQEIFGTPRELLYWFVPVHCPSMRKRDGKTFPGNRKVNKPD

>contig24558 Frame-2F

MRLLQVTNAFESHFKRPPTGVTCAPGRVNLIGEHVDYEGYAVLPMAIDHSIYVAFNKTVS

GSSKTGVMAVNVANAKQQYKSVRISLDEQKCDHGGLTWVSYILCGVLGLRDAWPESFKGE

ESELQLLVDGDIPAGCGLSSSSALVVAVALATSCALEIPLARSELAELCRQAEHRVGTIG

GGMDQAVACLAQRGTALHLDFAKVPARSEPVVVPYETGEVTFVIANSMVVAKKAVDAATR

YNKRVVECALASKLIAKKVNLDAWRQFTRLVDVQIALEEAIGEFAFPELIALAITSCPLS

EYLLADIEAEVGEPILNLFEGSFMEAAVKEVLKSVSTFKLQQRAQHVWGEADRVKQFVRL

CDSLATEDQTDCLLLQKHVHCLGEIMNASHHSCKTLYECSCLELDNLVNAAKSAGAIGAR

LTGAGWGGCIVALVQKSEVNDFMSKLYLSYYRQLGMSPSDAMDAMFESTPAPGAEIYTYS

SPNQFTNLVIREAFPDARPLTAAQHL

>contig24684 Frame-2R

MTSGTLIFLPCREPLRVPFGHGGPRGAYRPRGNSRDSSLEYIQCFQHHLIQTRGERLELH

GACESFHDSDKAPPCHPQLQDEQHHVGSAGAAYSR

>contig24860 Frame-2F

MGFEARYVLDVTDHVWTEVYSNHFKRWLHCDACEDQLDCPLTYEVGWGKKLSYIFSFAYD

EVVDTARRYTQNWPEMCARRQDVSELWLRTTIMQINNELREQQSPERKRILTNRAKSESE

ELLRGRVIQKSEIKGRVSGSADWRSQRKEDGTEMNANLETSRTDTLAHPSLPFEAADLLQ

QIFKNMVVGCQSSKCFNPYCYSNQTGFRIVEASSDINYRAATAIKLVNDLDSYNFPIESL

ELWQCSSRSNVLLNVVWSKQPVLYLPLQDSPSKKGSVPLIDISGHGQHVQNSQHCALRKP

FRISQTGQTIDTDNDAREDEAYGMQLQGGKFLAITAQTIPRVGGFALSFLIRFDLNEGLL

GKNWGIRNILIVRLGPVKSSCSMEFCVNWDQATNVYSYSLKANKTSSSATLPLAFGHYAH

IALLRNDDGVVAFLNRTKLEILVANGKISGQDHDITIQGPPSNVNCVAAVISHVAIIPAN

SLDEIQAFCVAMHRNFVSAPPLKAFGPNGKCSEARCSDIAAGMQSKYRVARIFIWGHDFF

DGIQFIYEKVQESSDTTSTVTYTFWLIGGK

>contig26783 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56190.1|) 4e-07

MRVKVKRRYLLKVTPIEAWDLVP

>contig27133 Frame-1F

MSSTTSGSTPKSRDTWSSTRPIVVTNKHAGTAAAIHHANPVKFNGTETDHLKRLEAIKEL

TFEWIRNRSCVCFQNIFNTYFVGIYSCITKLSKFWYVWSNKMRDFVDS

>contig29236 Frame-1F

MSSSNDDEFVTISTKHRKKQPPAASSEVISKKSTSVTNGESSSSNNNSNISLRPRTMFAM

KGRGRTESESSAYRPQWSKDGEGFVSASAGVSSSMKDPATGNDENRGDRRKNKVMRYTKE

ELLALYTASSEVPDFPPETTVASEQSLPPVSTLPFDYEDVYKQWSLNRTRGRGRGRVNPP

VGGQPNARGQQDRAHEVDGSKSQRDEHHRHNERDPTWERGAKITEGLLGDDAWDDVLESG

ADINEMDLSSMAEAAEKFRHEMNAMREELEGPKVDPNEIKDDMDAFDKKLEDAAATGQFD

DSDHEDVQWDDVNSEGEDKVARNMKDSVKDHTENLLAHHSSQNQLFDDAQETSSKELVFE

KNRNSSLALMAVGTEFADISPLHPEVVDEWFYLDPQGLQQGPFKTAEMREWFEAGYFKPH

LPIRFGRKSVFIALASQFVHGQMPFTAPPGHINDLGKVHTELLQHEQLFLDVQLQQQREQ

QQQQQQQQLIQHQQQQQQRIRQQNQEEKVHVEMQRLEIARQQQQTQLYQQQQILQRQQEQ

QRQQQLQMLLQQQSSWQSGQRESIMSALSIFGGNPESVLETNNNSSSDSMQDRYQLKNRS

QTRLDQLSLQNTQTLGPGAMLNLNEGQRRDQAFWPNIGPEMGGIVNSTGSLGNVKSSSAA

HNSTRQSILSSPTADLVADAWLTNANSPDRQPPMFDDIQNEEKRRAALETRKYGDRVNIH

NTNKDSSPDNFAMELNADKIHERKMLKSPYRKDRGSAKSENNVWATESVSGPSSTSSKSL

KDIQREEQLVMLQKKQNANLTQMGVQLKMMLGVNSVASKSNDGATQVSFHTLDRTESAVT

ARSPPTSVASPWGAPATVNKSNYLKSMRDIFAEEERLAQERAEANENAPVSSHWMNVVAG

NKVAAAAIPKPARSVLGPVPASVLKSRQQKRVVNGVGKSSVSKAESDSSFWNFGAARPAD

MAFESSIAHGDAHNAFGSSKVSSEFMGWALKQLLTIDSKANVTLLEYVASVEDPGEIREY

LAAYLGSTPRVSAFATEFIQRKKSQDCGNRSPGHHDAQQRASEAGTSNKRGKRRVKSEKI

DTSSLINYSVGS

>contig29368 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55310.1|) 2e-59

MCDSQYGAKQWFSSETLSCHCSLNDLKRAFVACVFKTWPTALVTAAIGRCTPASDTECFH

YRCIAAAHASIIEPTSHRLLKPKCRKITAHVPFKQRIQFVLTNMRNSFQIYVKSVLSNGD

VAYHHVPLANVEYQGPRKHLVDYTITLTVSSFSDPTTFTMTVCLGHPRLPGMDDPSTLDS

KDSGAQMYTAISASVLVSITQTLR

>contig29939 Frame-0R

MSPNTRPFDKFRLRIKRPCTEALRWSSSPSSAGKSFSDLICVSVIYSIIYKWGNLHPTKL

STLNVTT

>contig31949 Frame-2R

MRVSKKPRVNFWRWLLQFHIAEASLFHPWGLLAALIRSPSRLLDGVTASHHRFLDRAAAS

VTQNPMLFPNGFFSDGWGDLNTPTRILELVQSRRMSDVVELQEEHLMWDSVQKLSVAKVA

LRVGKFQSTLDNAQQLLPKASLDAFCELVTPLEWEGQAKG

>contig32005 Frame-1F|Blast-phosphatidylinositol kinase (PIK-L1) [Phytophthora infestans T30-4](gb|EEY63188.1|) 0.0

MLSVTPSNSGESTSFGFGEKDRHRVAFAYLKHLWAAGQKQDALVDLHRLVARISSMARHR

AQGSGGINTMASPAFEAIPVRTDEKELLVKCHLKMAEWQLAVHDQQIENVPVENVLSSLR

LCTELEPRSYKAWHAWALMNFQVVEHSTHSQHISAHATTSAVAASSSVAPFIAPAIEGFF

RSVALGRSRWAANVQQDILRVLTLWFAHGHCSDVHTALEKGFRSVSIETWLIVIPQLIAR

IHTPYPRIQKQLHRLLVAVGQQHPHALIYPLSVALKSSVPERQQAAEAIMSTMRTNYVEL

VDEALLVSRELIRVAILWHEMWHEGLEEASRLYFGEHNVDGMAEVLRPLHAMMERG

>contig32636 Frame-1R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY61176.1|) 1e-163

MVLDEADRMLDEGFEKDIRGIISHTHPERQIAMFSATWPQSIQKLAYEFLNDPVKVTIGS

DELAASQNVTQIVEVIDDRARDARAHALLQKYHSSRKNRVLLFVLYKKEADRVERMLHQR

GWHCVAIHGDRSQQQRSEAVEQFKSGEVPLLIATDVAARGLDIPDVEYVINYSFPLTIED

YVHRIGRTGRGGKKGTAHTFFTANDKPRAGELVNLLREGNQEVPKDLTKFGTHVKKKEHK

LYGAFAKNIDSAKKATKITFDSDDE

>contig32768 Frame-1F

MLIGLIGGGCVLAVIGIISIVWRCKKDEHLLLTKLDSFIQDCGDTRDEDDNRVQVNPVFL

NDPVIITNRLEYKLIKMGQCVSTGGFGVVFMGVYRGRRVAIKKIRPDRSVTTAEVEMFLK

EIILMAVLYHPRIVEFIGVAWDDLRHLSAVTEYMDNGDLCQVLHNYKLKGERLSWKSHKA

TIALHIAEALSYLHSRRPTIVHRDLKSKNVLLNMHFEAKLSDFGISRMRYLVETHMTAGV

GTAFWIAPEVLLGRDYDEAADIYSFGVVLSEIDTDDYPYWNNTNASNRGKIQEAEILSLV

AEGTLRPQFSVDCPKAIQDLADCCLLQDPKTRPTADEIIDTLQHIKIQVGCRVSLGV

>contig33095 Frame-1R

MSQLGKSGQAAGEAELERIFGHIDDLRVSEAALASVSISEDEEDEEDSSAFDDDDDEDND

VEGSGEEETSWVAWFCSLRENSFLCEVDEDYIEDDFNLTGLGNIVPYYDYALDIILDIDT

PNDSSLTQIQQEMIESAAEMLYGLIHARYILTTKGMGAMLDKYQNVAFGRCHRVYCQGQP

VLPVGQSDVPRHTTVNVFCPKCRDIFFPKSQRAG

>contig33763 Frame-0F

MVLKSLFVFATSASLALAQGSGSNNLAMAVGTNGDTVQATGGTTVFMDTEYNPNKCVLQF

LSLECDDNCANLNGYELECVSQGRQNGKEKKLCQCKPDEAEMCQNSVSSNVTSGTVAQFG

ECSNENQCADVYGYITTSTEGGPICAEKIHCVQEVNTTATQPASICHTCMSCIAQNDAAE

NQLANVKRFNCSAICPQEILDTVAERNAAGVGIADSYSLTSSDSGSVEPD

>contig34003 Frame-1F|Blast-SCP-like extracellular protein [Phytophthora infestans T30-4](gb|EEY56881.1|) 3e-48 NOT\_ORF

MVFRQSSIALLLLIASSSNDATTAAHVRQRNLQTTLSDVATYTSYEQYASSMLLAVNAQR

ATRGLPPLCLNNKLRIASQSHSDDMATYDYMAHAGSNGSTMSERITEAGYQWTTVAENVA

AGQPTVSAVMEAWINSIEHLKHIMGDYTMFAPTYAFNKNG\*FRHYWTQDFGSSDVESCDH

LVDNIS

>contig34973 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66901.1|) 3e-28

MASTSARWLVGCRHAIVSVKILPETLIVRLERDDLDRPVLERFAQVPPTDLLQPEAMDGV

PVGSLLVKVNEHDFIKSNLSFEAVQRIMRETIYLPRTLTFYVFATEESTMPPSEQVVFRD

FRPREVDKLAKGNAALIFEEDEEKTGVNEKDKSEDEKVLGDVNDDVMSSDGETFHDIYKV

EEVEVLLATQKQNDDRSSSFSLNASNVSDSLRSQMTSLESLKIDEQAIHNGRDKFSLKLV

ESPIKPRNHLALPINSVPVMVQKELSFGTMAKLAETRHFDSDDSSDESNGSEKDLDEELS

PVLSSKAFNYTADLAKSSADFVTVTAPPGLLGLHFDASILNRAVVMGFVRLQDGSKSALE

RAGSVVPGSVIVRIDGEDVSNMTLYEVGLKLTALSHQSRTIVFRVPPVATQETPHSKMLH

PHINHHL

>contig35189 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61806.1|) 1e-112

MLCVRALVLRASAVAALPARNQVSRAFSGNWEYPKVEGSVVDVTKALTTIGARLSIPTAP

LYFTRLKVDYIVREMKGKEELQKVHETLLLCDAKMAYPSTLAAGSFISACIKQDAADTAL

NFLRHAENIRCYLKNQSFVRLAEYYAELNDQDTVDEIVNIMAAKGVPLTYKMYTFRVLNA

KKQGKWDEAIALAREAAAELQINSHLIIELLRDQNGNIYKEHVQLAKYLADKGDVFVNER

LADIFAGGDGNLPEVKVEETKQAGKEPEKNERTAKEHKKN

>contig35505 Frame-2F

MVHISETRHVYPFNWDVVTRAFWNKYPNEHLSHIERVDVLDRYLDAQGCLVTTRLAKVTQ

RNLPGWVRSAIGDSTYVLEETTCDPQRKHLVLKSTNLSLRSVATVEETCVYSVHPDDSQK

TLYEAEAKVTAFVPIFGRKLEKFSINRGSDTAARGIRVVEEICNEIFQGTYQPAYCKIAD

AAEG

>contig36302 Frame-2R

MTYSRPLRDSNRLPIKSVIRAVAHQ

>contig37284 Frame-2F

MDRTSQFSYVLRQAVSFSVLNK

>contig37608 Frame-1F|Blast-fatty acid synthase subunit alpha, putative [Phytophthora infestans T30-4](gb|EEY67793.1|) 0.0

MEEVLEPLVELHSEFLIRGSFNDFESTFSTDKSTDEFVLSRQEDVEIFKTKSWLKLDADA

TVTVGDHLVMKLTTKKQYASINLLMSVEVSGTLFREEAGSNVELGSIEFESCNVNESPVA

DFIHQVQPHHAKDSGLFATGGFYLLEKPLVIDVPTDALAYALASRDLNPIHRSKYAAILG

HLPEGKPIMHGMWTATKVRDLVIRSFGLGLDSNVVDYDVNFDGMVYPGDKLFMQARHVGL

VNGKKVLSIEVVNDCGERVVSARAVVKQAPMAFVFTGQGSAAVGMGMDRYRESSVARDIW

NRGDTHLRKTFGFSILEMVRNNPKSVTVHFGGKKGRKIREKYMSLSCEDPVTGEVAPLLP

EINARTQSFSFSAPEGLLFATQFSQPALVLLEKAMFSEIEAAQLIPDDAHFAGHSLGEYA

GLSSFAGALAVEDVVEVVFLRGLIMQKAVKRDAEGRSDYGMVATNPTRVGPHFTEEVMHQ

IVDGIEAASGKLLQVVNFNIQQRQYVVAGENVNLETLSLALSAYKTLNATATVDVSKVIT

EALTQARARKEKCDQSGRPFTLARGLATIPLVGIDVPFHSRELLGGVPSFRALLRTKFDP

QVLERQLPLLVNRYIPNLVATPFSLKRSYFEEVYAATKSP

>contig37701 Frame-1R

MDVGTPLSQDVYQQLQTSRGPHTPSSSGTSDTGPRTMAPRDSDPSGSGKSDESREYRVVS

LPATQRMQNQLHDFCSNVVITSKYTTWSFLPLFMLESFRKLANAYFLLVSIMQCIRTISN

TNGVPTTLPVLTFILTVDGVLAVIEDRRRHVADKKANMAQCQVLKETYTGTKEMLHHAGG

TEDPDIALMHWAALTVGSVVKLYNRETAPADLLILAVAEPNP

>contig37796 Frame-0R

MWSRRSWMTTFDPLFVFDVPQTVVDLSVPLVSYPAGTHDPWFDRVHPQHSKPSAELAREL

ADMVRKFKGKEQQSQRETARRERKSHYYMENSRFDQHSDKENQQSAALHELMTQLKQLKQ

LYERSETLP

>contig38061 Frame-0F|Blast-alkaline phosphatase, putative [Phytophthora infestans T30-4](gb|EEY68014.1|) 1e-161

MLRRQSVRTSRPLHWKGPFVFQDHIISDHFKICTVLLFQYHGMCTLTRVLAFSTAAAMLT

NASTRFKYKTIDVDYNFDENEDFPRSVIMMIPDGTGPNVFTLARTVLDPTLKTRLHIDSH

LMGTVQTHSSTSYITDSASSATAYSTGYKTYDSAIAVDTYKQPLGTVLEAAKAREMVTGM

IVTSRVTHATPASFAAHVHNRDLEDDIAAQYVANKNLDFLLGGGRRHFNHSMCEDLKSNG

YTLANNYQDLLDYQLANEDTGALRLFGLFNDNHLSHEVDRARKLVSNNSTAREPSLPEMV

DIVLALLRKNEQAKKHGYFIMIEGSRIDHAGHANDPGTMAKEAIAFDESVAIVLHHVEQT

PNTAMLSAADHGTGG

>contig38128 Frame-0F

MRWKVLKYIMDRAKLNIQIIYKMQLITRTSEMARLFGIDFYSVLSRGSQYRVEAVMLRVT

KRKNYLLISPSKTQVAGQAPMECIPLVMEPHSSFYSDPVVVLDFRSLYPSLVIGYNMCYS

TILGRFKDGQDSELETSLG

>contig38906 Frame-2R

MQGTKLLLVGIKELQGDKQNLAQQAVTTTVAEFVAELVKNKQAVAAQIMTGTFPTILQQT

AALSRNRKLVTNDEEVEEEENSGDEDEDGTADSGSESLDGSKSNLTNTSTLSGAVSMADI

AEFQIILWTSVLLVAILLMAIMAMANMDVGRDSLLYAKFITDVSDRKMK

>contig39985 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69263.1|) 2e-86

MCSIQCAPIIENEAAVARELEEAYLQLCPPVSSNNDISLYPLNIGPARQPRTFQVMRAPQ

DMTANSVRHEIADNSSLAVAASVEFALSLKQGDVVDVLDRSGCWNYGEVVDIFPKDRLGI

AKLILLRFSLWFEDTVEWIAASEGRILPQGVAAGLRSCSVGPTRAHRVRVQHDHSLAKDL

ERLFSKRQCNQAASTSQFLAHWKHNIVARSSTIQHNALQKRKRKRPSKSGAVVVSTC

>contig40282 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60956.1|) 5e-07 NOT\_ORF

MHLLWECPSAAA\*WASLEVHWTCEQWPQKRLREMKTCCASRHGPARSSRTRWTQLHERYP

DTNYRGVVLTAKGDVDFRI

>contig40505 Frame-2F|Blast-diaminopimelate decarboxylase [Phytophthora infestans](gb|AAN31485.1|) 0.0

MPLPLPKSALQNLEVLAGKYGTPLQLYDEQMIRENARRLLTAFRAHFPDFQQFFAVKALP

NPAILKLLHQEGCGMDCSSSAELHIVNELGVKGEDIIFTSNFTSHKDLATAFDQGVIINL

DDVSLVDSLVAVRGKCSELISFRLNPGVGRTDSETKSNVLGGPDAKFGVPPYQIVEAYRS

AQQAGSTRFGIHMMTGSCVMNQEYWRETVTVLFNTIMQLKRELGIDFEFMNIGGGLGIPY

REDEEPANVESIAKMLRTVFDEAMKEHGLKTLPRLCMENGRFMTGPFGWLITRCEAIKAT

YGRYYGVDACMAHLMRPGMYGAYHHISIPARTNEEQSPSNVVGTLCENNDWFAKDRMLPS

AQVGDLFVIYDTGAHSHSMGFQYNGKLRAPEILLRSDGKDSLIRERETYESLYGS

>contig40839 Frame-1R

MTEMENQRRMNEWRMKENALNGMHTTLAGNMAVATSAALNTPSQVNSSAISRTSMLLAPR

VTSSAASSFDDVDDADAEDDDDEEDDDDDTASGIVV

>contig41003 Frame-0R|Blast-hypothetical protein PITG\_18705 [Phytophthora infestans T30-4](gb|EEY68804.1|) 6e-37 NOT\_ORF

MGISFVLRPLTYSSFLSVSCPLAPLLFLLVVEILGIAVQQSPVLTGLLVPGCGTVRHAFS

AFVEDSTIFLEKGRQLGPALYLVSRFGALSGLQAQPAKSKLIFLNSAVRGKDFNGISVLQ

PADTVRYLGYEVGTNN\*QHRNWALRIRKLQRRLFTAVKVSTSVEHRVLILNSIILPSVLF

TAAVFDIPEWARKAIQNLYNQFLWARATSTEASRHKVNPGLLFTPKKAG

>contig41274 Frame-0R

MATNRTKFKSHLTSRLLVVSSHQCPT

>contig41973-0 Frame-0R0

MPTHEWLRWFAYPHEAVAAYKLTGEKLPLTKITGPCQPHRYVDGSVHKVWEGVPSMSETQ

KSFVGRYVLKMF

>contig41973-1 Frame-2R1

MVALVRVSARGSRRLQANGRKVATYKDHGAVSTTPLRGRIGSQGVGRRAINERDAKKLCW

TVCVENVY

>contig42284 Frame-2F

MEYLSGGSVLDIMRKGPLNEAFIAIILRELLKGLEYLHSENKIHRDVKAANVLLSGNGHV

KLADFGVTGQITETMTKRNTAVGTPFWMAPEVIQEYGYDCKADIWSLGITAIEMAKGSPP

LSDIHPMKVLFMIPTLGPPVLDGNFSPQFIDFASRCLQKAPQDRPTASELLLHPFIRSAA

HVTHLTELLDRNQLDDQHLNREEDGRTQSKIRFYNNGDADDGFGHLDNSYLPSLCVNCDD

NLPMYGQSNKGKCHARSTSIGSGWDFNTVRLSSTALQHEAKAQSQAVAAALTKITHLDRT

SSEVFKNVNKHSAALHLGPNIIEKASFEAKSTSAVAASRNLMENDDRSDESDDTFSIVVK

PAISDVLERVMNTSKTELMSTTHYDAIQAAAEVQEDLLFELLHVFDNISQQKGLLRQVLC

CLADYTHASISTKYM

>contig42701 Frame-2F

MVKHIAVLRMSKDPGAWASSASKCVLVMYHYHRHGRSVNTSRISNWLYGVTALKSRLKVG

FAAAVVDLVTDSFVSKMLCVLSRTLDGVSISIHCNEK

>contig43009 Frame-2R

MRRCAEDKRRLEAERTDHKGLVILRGQYGVHPTNGDVVNAQEKDQDALQEVESDYRTNEA

IQCVDVTIPLQFLVKNGELALNSSSKASLLGFYNPCVAESDTIADTRASVSAPKPLLYVR

YAYDTQVFEATFEDDQAVLLPSKYAQIIGPLGRVY

>contig44747 Frame-0F|Blast-isocitrate dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY53404.1|) 0.0

MFSKTIRSMAAPARRGFATSQKIKVHKPIVELDGDEMTRVIWSQIKDKYIHPYLDLNIEY

FDLGLPNRDATDDKVTVDAAHAIQEHHVGIKCATITPDEQRVEEFKLKKMWRSPNGTIRN

ILNGTVFREPIVISNVPRVVPGWKKPIVVGRHAFGDQYKSTDFIASGPGKFEVVYTPANG

SPKQTFEVYNFEGPGVGLAMYNNDESIYGFAKSCLSFALSKNQDLFLSTKNTILKKYDGR

FKDIFEEVYQSEFKAKYDAAGISYTHRLIDDMVAQALKSDGGFVWACKNYDGDVQSDIVA

QGYGSLGLMTSVLVAPDGKTVEAEAAHGTVTRHWRQYQQGKKTSTNPIASIYAWTRGLSH

RGKLDGNQELIDFSQGLENAVIKTVEAGHMTKDLAICIHGSNVTPDHFLYTEDFMDKVKE

TFDVMRQ

>contig45119 Frame-2F

MNSKSTVKRIRMTLDELLPRLIGARDYAGASKVLEVIYHQFTLNPALCIEASLEILRRQQ

DYYIDLLSFYKAALGVERIDKLLILKEMWLLHIVHGEFYEAYHLYEDKIQQIEEAENDAR

LLANFGILSYWLMLIESKELRNMLKLDNTDCEVDDGEDDFLSSGIYLDENIESMIESNYQ

FKTPIGVHILYQHASNALRRAVALCPNSAMFVEYYVQLLLLVG

>contig45681-0 Frame-1F0

MRQKLLAFITSFVFLMIRAVLDAP

>contig45762 Frame-0F

MEVTVIPRRNSIDALHRNESSRKSSNDISYAAANDPKNLTQGEVLKGNDEREADIDGKEC

RVEVASSEKAHKKDVHDTKDLTDMTCPAWTTKSILRKVSYLAPCSRPTQNVSFAPNTVID

LIAESSPT

>contig46428 Frame-1F

MSKLSIMSREGSITQQKLQVVCLLCGDARYAIHLSIQKSRASSAKEAVALSMHFPCRRRS

VHHGDERPISRQPCPFAPLGVIGGIHLKIEIYQ

>contig46763 Frame-1F

MAHSEFDELEADMDVKELIKLRQAVRHDIIEKENLARKLQRDKAESSPSKQKPEIPASSR

IWSYATWLAGTSGAAQSGHYLPSRQGGGIGVEDVKWSDQDTKDLYEAIDYHPENDRNKSQ

VSENGNLEITERLLSEHQHILYRLQLTLAKASFGLSLEDIPANLG

>contig47636 Frame-0R

MSADVTTVDMSAIDTKNQRQRERKAALTDTYSSISHGIRLNDIDGSNDCGKVLGRYSSHE

CALLCKTILNHLEMQTLEPTVLEKAKSPAFIEWKSVASTMMAAHNVQLKPQECQLLWKCL

AYGKIPVVRNDEMLLDSDDEDFCKTPAMINAEVVSRRNIAASKQDQGDASAVSSDMQREL

LDGEIDAKYVKKSEASEKHVENKFDLKMDAQNASLRLYPTYLLPTGTPDSWHRPFGPKNA

MPLTFVASRFLRRKLSVPAKPNENSSATPE

>contig47782 Frame-1F

MTRLIILNIQLYRILAKPIQPLGYCEKPRSDGQKRFKCKP

>contig48318 Frame-1R

MSSVTEQLIACADASAIISTLKSFLTESTDIQDLQASINEIVTFLMASKERKVLIRTLMS

DYSETNVEHDVQLELLETLLRSMMQESIKNDYTILEILLSFFQLAVARLSAIGSGKRWIK

WGECVLTVVYQK

>contig48620 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60956.1|) 6e-25 NOT\_ORF

MPTLL\*PIMEQLRRDHPNEAAAYESI\*KRI\*FIVSSICITTLGVQQIRVTFQHAVVPINS

SVAKFWETNMRQLRAIRKRESWRADSQLHGTRLIECQRQLARHPREPSRTVSSSVQQPDS

TEE\*AFLPI

>contig48794 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65049.1|) 1e-25

MEIRDMLIKYNIKDFNIADAKSAFRLMSHILTQVSQPTAFNDAMLLSDVFKNLRCDRALV

RFTENLFTHNIDETNSLWNEVARRVAQAMEAFAELKKRFDLKSNLTLFVSLMEEIVSFGV

TLLEVEIEDRSEAQSIGMCKQPRSFSLCMLKSLAAAYLPELKSLLDLSADD

>contig48974 Frame-1F

MVEDKSRSGTAPINGARAMYASKAKVANTLSVFMRLKRKRTDDPLACLLVESEPDSKRSK

TNLVEALAQLSITEKCFVFKHIDTLESIDSGHVNWTQRLKRKARSLKDEHAEMMAKKHTN

AVFQSGPMSSKQTEQRAKQQQSCFKSRRNEEIFKSRGLQHVLEIKEKQTMELHGIRLVDL

HMSTKSTLALNEKMEDRLTKSSRSAVTVNGIRMKSKRVLNPYERELDEAIWTAFRANDFA

PFFRIYYTRRQDGLVDPVAFQRTADGSNILMAAALHGRSDVIEVLLRSGTTSVLQQDFVG

VTAAILRDVEGMPMWKKHFLLVNKQSMRRTTFMTSIVLTCRQAAMPKAQQ

>contig49115 Frame-2R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY55432.1|) 4e-80

MSGKPRVEMAPSSALPSYDRFQRYTAAPVDEAHLSIAQRLVLENKKRAQISARRRNTTEV

VASLQHTPVELGAHIWVPDRERVWRVVEIVRYEPSEDPEKGMILTLNGKFGQEKLDMRDI

GDLYKVNPRVVDDMTGLYYIHEAGILENLCVRSKMDNLRPYTLMANVLI

>contig49160 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65174.1|) 1e-45

MIKRLRELKPSASEDTKVDILDGIIVALDLLFRRTDGKKYDKRLMI

>contig49326 Frame-0F

MRRLRLILLIYALKAAAATSVRTQKSYQLAMLSLKTRTQQLGPPRTSDKTRAEALAETTR

VVDKANAAHAAGKTKYFMTYNELSDLTDEQYQGFLTSKPDQESPRRKQKHTTLWTQGIHR

KKISRSFDLDSQDRIKDEVKVPIALDWTTKDGGKYMTPIKNQGTCGSCWAFAGVAAVESR

YAIENQVRASALSVEQVLSCSGALDHIQSKYDDNMTSSSDGCLGGMAFLTYAFMERVKPH

GIACERDYSYAMATNESNLQCLAVFGAKVVVSWTANVSDYQVVASNENALLQAVTHGPVT

ATLDASGKGFRHYGGGIYDAMDCVNDGNEVNHAVVIVGFGETESGDKYWILRNTWGTMWG

ENGYMRIARGTKVGPVGPCNLYLYADYPVNLTLGSAVTSCNVSSLKYEPLPLIQLLRLST

SQLTILVLCTLLSVIAGVSLYHGTEYIQRRKEATNNLRYQDSCDRWVLPSRDQIAAVLAQ

RKRRPGAQMVNT

>contig49476 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY54758.1|) 2e-63

MRGVAATNEEMLKKARASLLEANVELKEARANTLKWKNSAQAAKTLMNAKIADFESARKQ

LKKARAEATSSSLARSQVSLSLEAKKKRLAQTKQELATVRAELARAREAIVADRKQLGET

HEAHVAQLRDSFEQEIATLESQVQSYSMALVILLPLVIAVVVFALAR

>contig49542 Frame-1R

MLLRYTGQSGITRCTSTALSQQKALYYCYLDVELIVDAPGVLACKVRSSDCRDCLLPLQN

SCLSLRSSRIRKAVEFFLSQLRAHILTWQLLALKLFMRYDKKHTYI

>contig49810 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58305.1|) 1e-102

MSAKSPEVVDSMIDDSLLGILVILLVVMLSTGYVYIQQLRQGDIPLAGAAAANLARMAPS

TAAALSLSSKRTAISTTGLNDRQARLHFTLPIRNGARCITVSGDALVKTENPESLAWTDD

EVPHLLADLSYVADLHLLFVVKDAGDTASMQRIRDFVATHPELKSSNSTLGGVKAHKILF

CTTAIGKIAFVRQIEPQIHVEVDAGIARDLERHVPRIVHIPKSSQDTATSTMPNVIHVAD

TFTSYFLLISAKV

>contig50052 Frame-2F

MPQQNKLQAEDAAAADASSFLNDAQRSVDFLFAPTVVLPGDDVTDTLTNTNRRVKLGSGL

KQVTNERIVCTTAGVLRYRPANRYWVDFYHKRYVVSIDDSVIGIVTDRNAEFYRVNIGAA

>contig50139 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61308.1|) 7e-75

MVKVAVKTLTLNVLRVNDARVRSFVLQLDNLNYFRDIVEIANDLTLKLQGILNQWPSAQN

ATERTAITETMEEA

>contig50669 Frame-2R|Blast-sporangia induced myosin-like protein [Phytophthora infestans T30-4](gb|EEY59554.1|) 1e-26

MGYFIWREEDGPLKISLKAEAGKCYPVIMDMDKSGAVGRTGNHNKVRIGDQLLTINHCDV

FRLGFD

>contig51028 Frame-2R|Blast-gag protein [Phytophthora infestans](emb|CAI72293.1|) 3e-15

MLFAWPHQPRSIQIDPPKFDGTVAHTIVHWLLAVEQCGVAQLIEDDSRMVSYAMSHLRGK

ASEWAYSALMADRKAFPTWAISKEKIRAMYQPPNNEVLLQARFFGARQAKRSLQEYVQEM

RSLSASITVGPI

>contig51891 Frame-2R

MEKLHDALFAGLVDSCHAQDTKLQEMIYRFRHYTPEDFGLKKGFQVWPTLLNTGLSLSCL

VLVASVNSVILWKRAIPFVELH

>contig52344 Frame-0F|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY64227.1|) 5e-29 NOT\_ORF

MCHVFGDRCIESFSGKTMAPLHRMVGSGVYEVDDAELFCSQMCEQGLLEHDDGRVYIHNS

TIMHFDNLFDAERRVDNET\*TVKTHDCLAEVSGVLVIYYI

>contig52414 Frame-0F

MKVAKLSPFYAARLRAKLQSQTTSLQCTAVNFELLTMCVNAKEKMVGLYTWLKQDQSKSS

ALRTYIQLSGHDVTLKTSKFQLEAVRYSKHIQELAFETLDRTDVSSYELTIALSVCVAYQ

VRGSFRLTDEERIRFLQCLEKIASQSVSTRAIRLAFLVIVFLWYPLASALSKQLSQRDDH

LKTAVTLSQQVILSLFQARATGAGPL

>contig56560 Frame-2F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY68963.1|) 0.0

MTFKEYREVDARVASRGYEISDQDLEILEQVAALPFKDKYAWFLEQTSALIKPWEDGHLK

MRVHRENILVESMEQLLGVQMEHIHMPLRIEFIGEVAIDAGGLEREWFSLVTERLFDETI

GLFMCAHVDSLAYVINPNSVEASADHLLYFRGAGRLLGRALLEGQLMKAHLALPVLKHLL

GVPISFSDLEFFDQEVYNSLKWMKEHDEVATLGLDFTVTNRKLSGDVETIELKEGGKDVD

LTDANKLEYIYLRLRYIMLDSYAEQLQHLMAGVFEVIPQELILVFDYQELELVLCGVPLI

DVDDWKAHTQVSDELPEELLAWFWETGRSIYGRRTRGYCSLQRGRRVYLSRVSRP

>contig56858 Frame-1R|Blast-ubiquitin-conjugating enzyme E2, putative [Phytophthora infestans T30-4](gb|EEY61803.1|) 2e-64

MSRNPPEGVSVGLGDDDNIFNWDILLVGPPDTLYEGGFFRAVLEFPADFPNMPPKMTFKS

EMWHPNVYPNGVVCISILHPPGEDHLNQQETADERWRPILGVESILVSVISMLSDPNDES

>contig57071 Frame-2F

MFQFHAPDGSHDDQVGEIEMYRARHRLICRGHQSSASPSTQVEDLDIEDGRARKISTKWR

RQQLQQLPVTNQLSNSVETLVGFNAFDFSASPEAFHETQQLNSRKLVSPSNKSNQEDQHT

NNNHSSLWERRVSVSQQSKIPARHVPTLGKDALWGGQVHYSTQDAQRQALYHRP

>contig57394-1 Frame-1R1

MTADVPLDPVTDRHHLQNPI

>contig57673-0 Frame-1F0

MIVMLSQCLKKRGVLQNASLSISFVAARTTISPDEVRTRNALTYASPFGPDERHYHFATR

YLRFRRR

>contig57673-1 Frame-0R1

MATHKLMRFWFAPHQEISWFGPLQTKWTTTHFARPHAFSGIATA

>contig58777 Frame-2F

MQNAVTGVVAPLDAADVDKNSDFEHQVCEGVLSSEKKLAFSQAELPTGQSTTGSSEFSVE

SSPIELEKASHVVIKRTSLNRKRNRKMRIPRRLPPVQEKATENSVTCRCSHDDP

>contig02649 Frame-2F

MVSQKRQAFVQLPDIVSASNLVTFYQTREAQIRGKKIFFDFSTRGEIIERDIPSTYQQHQ

PSRASPYHQLQPMHYPSQQDMLMDTGGGLIQHEGPRRGIGPPNQILMVSVSKIEYDVTVD

VLQQVFQKFGNVQKIVTFWKDNEFKALVQMESVDQAQAAQSALDGRDIYTGCNQLSIVFS

RHPELRVRYNDDRSRDYTNPNLPPGPGGRPESHNENEPIISISSDQRDAPRERGYSNLPL

RIDELNYRGVMNAPGVGHGDEYAPDPRSNRNAVSRYDERLNMDRPSDTRNGRDLPQHSTG

RAIRGDTRPSPALICSNIDRELVSPHRLFTLFGCFGDVLRIKIMFRKRDTA

>contig07413 Frame-2F

MARSMVTLSRFISMIQNVYSRGINYVQDLWKVLSQDISVGRARCISRLVNVETGDPQGSR

SSNSMQAFNIVPRVAVATLR

>contig08553 Frame-0R|Blast-choline dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY54332.1|) 0.0

MKNWTWEKALSIYMAIEDFDGPNSSFHGVGGSVRTSPPALASDGSKEFIEACTEVGIPRT

MDFNGPNGRFGVGYYHFNTRNGVRDSAAKTFLGPILNSKTFKSKRDNFQLMLDTTVTKIG

INNENVTQGVEVRFFDGTTQLIRLAKHGEVILTAGAINTPKILMLSGLGNHATLRNAGLQ

TKKHLPRVGMNLQDHPVVGMVFEYKAGRNVDLKAHLASYLKATNDKSSNTSSYGLFGSVG

ISAGAFLIPPGATQPEIQLTLFPQKSEPHMSNSAGLDHMAEALITIALLRPLARNRVVLL

RDEDDSVDDNDSDDHLIPRVVSEVPDFEPEHLRPGDIWKITWGIRVVREIAARLGEKKVI

GCEISPGADVTSTKDLNDWVLENVFRNSHWVGSASMATTANEGVVDNHLRVFGIQNLRIA

DASVIPFIPNGNVHSTVVMVAKYAAEILREDEAEYRQNYDKK

>contig12886 Frame-0R

MNEGRRKLQTVQVDHYDGQAIYTGNELLYELGGYLGGGAAGVVYEAFSTRTKQHVAMKIL

NPVGYKLFSSSLLARCIVAVKGKPLLLLPSDETKRGEDSGRRLPRRAYESHRMRTPRMRT

ERIR

>contig13816 Frame-2R

MFFRCHFAAHRFKDCQEKDCANISENRSRKPVASVIHGDMILHVLIILPDGKDICDFIAL

KYKSHLNWKV

>contig14228 Frame-2F

MQLLLFLLLIIVLTAVYCDYILKERRHLNQNDGHASLRANFANGIEKDKEERGFNIFRKK

NPVDKAARWLLEGYKPLLKQQNPIQRGIEIQTWLSVIETEPIMPKDVITNMESYFNNEES

LELCLWLVHAKNLKLKNWGIHARDKLNAAVIDEESFPTIFKKNPTV

>contig15151 Frame-1F

MATVSVFITGFGVVHNIAQPDGVVFMGTVQQGGGSSWTVYRPFEAFQRLGQQLSMIFGQT

VPACPPRMFDVRFSDSLEKARVDLSMWIMQLLQHAPIYKSHVFVDFVSADANVPPTGMQD

AAQMAARNIGDLDMDEMFGSNIDDDPRSHEELNDDDMFQFDYNTDMSGAGLDQQTLLEET

QMQHKKQVEEQKKRSEKVTLEDFLMIKVIGKGSFGKVLLVRKRDNGLIYAMKVLRKENII

KRNQVEHTRTERHVLGYVRHPFIVGLNYAFQTSEKLYFVLDYCAGGELFFHLGKVQRFPE

HRARFYAAEITLAIEYVHNLDVIYRDLKPENVLLDENGHIRLTDFGLSKEGIQDDFTGAN

SFCGTPEYLAPEILNRSGHGRAVDWWSLGALLYEMLTGLPPFYCRDRDRLFEKIRKGDLS

FPKYLSPNAKQLLKKLLERDPTRRLGTGPTDAREIKDHPFFAEIKWDALATGQVPPPWRP

TFSGALDTSQFDREFTDMPVVSPDNHVRGMAMVVGRRPANGNAYGSSLTGNDPFKGFTYT

EDSYLQDGLPGRSPGRSRLRHPNM

>contig15249 Frame-2F

MEDLRQEHLVRLGQNLVRSIDRSRWIYNRVSDWERDQHVTTILQQHGPAFTRNMSIADKF

VSEWAPVFGVIHRKQPLHSLNAAIQQFVHIPTERVISKAANADLLAEFSEAEVLTAIAGL

SRRKSAGPDGLNNDFFKDTTALMVPALVRVSNEIMTGAEPPPSFLEALIIPLRKKGDLAD

AMDYRPIALLQSSYKIFTKVLATRFQRVLPTIIGDSQQGFVHGRQMHKLVMMMLSQLATA

TTDDTLTAMNSRVILLLDFRKAYDTVDREFLYEALTTFGFFERYVQLIRRLHTGTTATFL

VNGEQSESFSVVSGIRQGCPLAPLLFLIVVELLGIAIQQSPVLRGLPVPGGSGGLHTFSA

FVDDSAIFLDKACQLDQALRIVSHFGNLAGLVAQPAKSKLIFLNKGVRVQTFCGISVLQP

VDTVRYLGY

>contig15810 Frame-0R

MPAEFRPLPSDFFEEEVLPYNVLHYVETYSILSKEELNEWFLEPVAGAVPGEIVEKLHGT

FVNDLLNLERFSKAKLEPHLYLNKLISENTDQILDPETLLQWLRYYNLYWKELLEKASGG

TAQDIAIREEVLRVLKEVKTDPPGQDLVESLRRILDMQAFVDMVTSKPVGNKDAVTEALH

KA

>contig18013 Frame-2F|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY57374.1|) 0.0

MIAANLDATLVLAGCQSLVQIDGKMVGDPVEEASLRAIDFSYDAATRHCQAKKDLERASE

RRWGQDINQKDVFVQIMHRNHFASKLQRMSVVAKVHLGTKGVRVRSLVKGSPEAIALLIS

SKNIPPWFWPTYQSLARRGMRVLALAYKDIDGRPSEAEVAQQPRAWAENDLTFAGFAVFQ

CLVRKDSGDILKMLKDSSHLVSMITGDATLTAVHVSKEVGIVTRSALILSESSSLNDPLK

WTSAVDDSVLAPYKSGDIKVLVKKYDLCVNGKTLVAAGEVDEEIWKNLHHIRVYARMTPE

LKEKVLTLLKTHGHYTLMCGDGGNDVGALKQAHIGVALLGGFGSANADKSVTGLAKYQKG

NVATVSTRDELMKLHVSALKKRLMQHNIKPTHCKEKQDYVELILNEQKKKSMELIKKKQQ

ALAKKNPKLKILTKEEQRVDMKRKQEKLEADVQARQARGESFARMKAIAAFAKREAEEKR

KQQGERTGAKGFANFANNAAMAQYMDDFEDGELPMVKLGDASIASPFTSRAPSIKGCVDI

IRQGRCALVTTMQMYQILAVNCLISSYSLSVLYLDKVKWANSQMMALGMISTVASITLSR

ATPLDKLSPVRPLTSIFQPALFLSLAGQFALHLGCMIYLTNLAKEYTLQEETIVSKPGEY

QPTVMSTVIFLINGVQTVSVCAVNYKGRPFMKPMTENPGLLYSLGISIVGVFLLCTERMP

LFNKVLQIVPMPDAGFTRLLTGLLTLEVLGAFAWDQFCLLMFAPTIFVASMRAITFKDVR

QLLKMTVVSLVIIYVLANIDYDEIERQQQLLEASRVDADIEDSSS

>contig20234 Frame-2F

MENGPNDYTTMRSTRDSDLSALTMHTDEKNDLVEKQKKR

>contig20241 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58034.1|) 7e-61 NOT\_ORF

MERGDLRDVTRRFKRRGYALTWATYKTAIALQIAEALMYLHGLSPTVIHRDLKSKNVLLN

AEMEAKLSDFGIARNGVSTTGVNI\*RLGLARLFGWLPRSLLAGIMTNERIFTRLESFCQK

LIRTIIRTGTRSTRHREKLKRMRFTPCCTRK

>contig21358 Frame-0F|Blast-ATP-binding cassette sub-family F member 2 [Phytophthora infestans T30-4](gb|EEY61242.1|) 0.0

MARETKEPRVKKERKGKKESRKKASDEKKAAEKAEALENMSNADRLAEDGIIATCSHNVR

GVHKNFKDINVLNFSITYYGKVLMEECDISLNYGRRYGLIGRNGSGKSTFMNVLGARGIP

IPDSIDIYHLKHEIEASDMTALEAVLSVDEERNKLQAEADQLSEKMTDELISEEDSESIS

DRLTDLYERLDDMDAATAEVRARQILSGLTFSDAMMSKKTKEFSGGWRMRIALARALFIQ

PTLLLLDEPTNHLDMEAVVWLEDYLSKWKKILLMISHSQEFMNEVCTNIIDLTNKKLEYY

NGNYDTYVRTKAEKEENQMKRYHWEQDQIKHMKEYIAKFGHGSAKLARQAQSKEKTLAKM

VREGLTEKVESEATGDFKFPNPEPLPPPVLMFQNVAFGYPNCPLLYSGVEMGLDLDSRVA

LVGANGTGKTTLLKLITGDLVPVAGNVRPHSKLRIARFSQHFVDVLDLTKSPLEYFRSLF

QTKSVEEVRTYLGRYGITGEVQTQIMGQLSDGQKSRVVFAYMAQQNAHMLLLDEPTNHLD

MESIDALARAINNFEGGMLLVSHDMRLISQVAKEIWLVENQSIQVYQGEISDFKMRVRKQ

LKLADKETVKLADV

>contig22908 Frame-2F|Blast-protein phosphatase 2C, putative [Phytophthora infestans T30-4](gb|EEY57130.1|) 1e-138

MGNFLATPNTEKQTDGGEGNGLLFGLATMQGWRTGMEDAHVAEINPKGLPPGCSLFAVFD

GHGGRLAADLAAEGILKELVATMKDDVFPGVQADDADPNKIGKAMRDAFMNLDQHIFKTF

HSSYSSDHSGCTAITALITPTHIIVANSGDSRSVMAKNGRIVEMSYDHKPTNAGERKRIQ

DAGGMVRSNRVNGDLAVSRALGDFSYKARADLPAEQQQVSAEPEIIVQKIEKTEEFLVLA

CDGIWDVMSNDEICAFIRQLLSNGETDLRLIAEEVLDKCLS

>contig24209 Frame-0F|Blast-hypothetical protein PITG\_16467 [Phytophthora infestans T30-4](gb|EEY65012.1|) 3e-08

MSSEANAHECGAEHSFGSFGLKKRKKKGQMKRLFVAQQTGKNVQMGWVTLQWLLEAHGWK

VLSLTILIYVARQRYNEVVSRRHHDQTLAAAN

>contig24861 Frame-0R|Blast-peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase, putative [Phytophthora infestans T30-4](gb|EEY63832.1|) 3e-25

MHELEQIFAASDILSRQNAISAALRYLGNIAQQPEDPKCQRIRASNNFFSSKVGTLGKAV

AESFMCWCGFKENIEQDEVFYVYKPCELHGKGSMQRLPAETQKRVHFLSSFKTQ

>contig27086 Frame-2F|Blast-heat shock 70 kDa protein, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY64540.1|) 0.0

MLRLTVARSAAPAVGKRMFSAAAGSEVIGIDLGTTNSCVAVMEGKTARVIENSEGARTTP

SVVAILDNDERLVGMPAKRQAVTNPENTFYAVKRLIGRKFDDKETQEVSKVVSYKIVKGN

NGKDAWVEAKGKKYSPSQIGSMVLTKMKETADGFLGKPITQAVVTVPAYFNDSQRQATKD

AGKIAGLDVLRIINEPTAAALAYGMDKADGKIIAVFDLGGGTFDVSILEISGGVFEVKST

NGDTLLGGEDFDEELLRYLVGEFKKETSIDLSNDNLAMQRLREAAEKAKRELDGLAQTDI

SLPFITADASGPKHLNMKITRATFEKLVGKLIERTMGPCKKCVKDAGVAKSEINEVILVG

GMSRMPKVQATVEEFFGRKPSKGVNPDEVVAMGAAIQGGVLRGDVKDILLLDVTPLSLGI

ETLGGVFTKLIPRNTTIPTKKSQVFSTAADSQTQVGIKVLQGEREMAADNKLLGNFDLVG

IPPAPRGVPQIEVSFDIDANGIVNVGARDKATGKEQNIVIQSSGGLSEAEIEKMVADAEA

NAAADQQRKELIEAKNDADSTLYTTEKTLKDHEDKIDAETLEKVKTALADLRTKSESDDT

EAIKAAIQEVQTLSMKVGEAVYKTQQSESAATNDKPDENVHDAEFKDKKE

>contig28458 Frame-1F

MESVCESRQVVLVTRPSQRDIEMWTERATSTMVKSTGSSARPLPSQAQRLCQSRRWVLEY

KPVVRHSGWLMKRGHGLRNFKRRLFCIVDNELIYHDAHDATEVRGRLDLTRKSTVQCMLH

SGFKFAQGSYTMVLYALDNHDRDVWIRKLQEHNVHVLPQGAKTAKLKKQHSDNADKGELI

LVSGWLRKRGRMVKSTKRRWFELSNTTLSYFAHPQSGSRKGSIDVSQARVSPVDTLKTGE

RHSFQICTPTRILSLHADSQEERSLWLAALASVGASHGPTNAISATALDVHEFAIPLRAS

DIGRLCKCGALSQGGEAIDGVCRRCMSSFISNTDDEMVDVAREVQLLLASPYSPEGSTSA

AFLKEHANHPVANTTVRKFMNGLSNYLLHTRLKELQLLAGIAQPPSGSTSETEDEEVKDI

MKRTTSSTRNHDSEMISEMTDQIQTIVHEQVEERILFPLYRAILTNVRAQTREDAKVLKG

KIEILRSKSQAFFGIGPGSESSSRWFSACVKLREVDKVSLPYMKRDQMLTACKEIYAIFH

TEHPTEAPMSADAFIPAFIYVLIHSHLRDPVALKELITYFDSGGLHGEIAYFVTCLEIAL

EYIRSLLTACTVVLSSKRRLGIEFAKHPESDVVIVRRLVSGEQAQQSGAITVGDVLVAVN

GLPVYDMELAEVAKLWRGVDGEAEFCFLPMNEYQRKYGCCAR

>contig29383 Frame-2F

MSSTVLEQLRAEQEEIEALERAIVATLGDKPRNHRSRVLHGHKVSNLLTEVTKHSKHTKE

LYDDEDGIFTEETTNMRGRAVFTSFYEHLKAIRSFHRKYPNSVVSHELDFAEALHPNVQF

SGEERLGKYVDLNQFYTRFLNISELKWQARKTQEALNSSARNKGKKQTVGSSIDYLAYLA

SFSDFSAIPPAQKTQSVPYQQYLKDLKEYLLDFYRRTQPLVDLDDMIDETSAKFEKQWAS

REVVGWDFKRQSDQMNVNKRLEHYCELCDKHFSSIGVYNSHLTGKKHKKYAASASEAPSD

SRKSVTSSTGAEPSKGSNEDVKGKQKAIAFDEVLIRRMYELLTEVVQGTISYLELKQTRT

HEELQAEIEEEEEGTFSDVDVENENEEEDEEEQLYNPLNLPLGWDGKPIPYWLYKLHGLG

VEYKCEICGNHSYWGRRAFDRHFQEWRHAFGMRCLKIPNTKHFHDITLMRDVIQRKCCVC

GTLWLTYWWFVVIV

>contig29471 Frame-1F

MEPSDDGLLGELTSQMATTLQMKPCSTSVWTPLDAYDASASVSRPFRKGRSYPRVKASTS

QCNGTTHVALDALDGLVDASFQDRFLNSGCSWASWVWTDILKAQPLTNTCERRFCKARLF

VKMCDVLWQREAKWRNLLQRYEARATQSAQALLLREQATEEEEKHERGLSLSTATARLDH

AARNDDVRSRSDDEIEEFDDGDWDAGTEQEERSVLSLDTTGMATNEPSLPSRTYEEICRE

HLATFMAGTETYMRESDLSKKVNEWQEKL

>contig29853 Frame-0F

MFDVFSFSARTATGALFLLLLLVFFFFATVEADSGAALLESTLAVRPTAAAIIAPPTAMP

VVGFCSSKAIIESAILLLNEVSDAVVL

>contig30118 Frame-1F

MRLTKAEKHREKALHQTHLLLLLATRIKWTQLSRSHLLQGLLLSLLTTSALDLHATLREQ

PLSYSLMLLIRWFHQEFQVIKEDSFQGEKMTDNGLLNVFFTRKGHARELTVLFAALCGAF

QLRYRLTSALNPVLIQRSQVDSKTTTSDNELQHKGEKTKTNVNVKTN

>contig30617 Frame-0R

MKIITIAAILSLAVGSVGAIFGGGVAERDTYTFMGSLRETEAGKTKCSA

>contig30680-0 Frame-2F0

MIEARRCGSLHLFPLMISKCFSCFRWALC

>contig31948 Frame-0R

MEKLSMTPNSYPVGTKSIAAGNYMSDSSTKRQSNDDVSVVPAISIFPKKLTAGTNGGDDF

RLYTDDIIQVESIRKRAYLGIISRDVRFDVAGKAIYLQSWPYIEQHLFYSEERGISEACL

RELSAATTLSSLLPDRFMQLYGIVFPADRKGRQMSDPAGLSTSNADELDLLAAAVDDDGN

LLPEGLDCLGRQKHYLAFEQPLHMFSGIFEAHVSLAPELRKKAIFDMLQSLSAVHDQCYV

HRFVAPSHLLV

>contig32637 Frame-0F

MADELKDEKKAKKAARKAAKAAKTVIDSSAKVKKLKRSRDKTETTVESPQKLAKLHKKEQ

KSDKKSLQSVEHAKKNGDRNTDFSNGPYQQPAAKDGSFTKSFYNEGKNTANMTDEEVSAF

HEANQMILSGNNCLYRPVLSFKDISFEPKFMKTTKGFDKPTPIQSQCWPILASGRDIIGI

AETGSGKTLAFAIPGLIHIAAQSGVSPKHPGPLMLVVAPTRELAMQSSAVISEAGKKCGL

KSICIYGGV

>contig32769 Frame-2F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY66954.1|) 2e-44

MTCSPKLTLWTFLVVFRARAIGGQTSSPSNAAVSGLTLAESLAQEWFTDNFNDNETQLAV

GVNSALKNLTSKDMICNGSPSIQRRTDKMTPNGGCPAIFTSMNGSCSCLTTGYSDTNTFE

FYVRLRGDEGMEYYPKSLDSSTILAIDSIRTLLVPSDLTTL

>contig33094 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56370.1|) 2e-99

MTDRLKVIKDHWNKIAVRFTETANKHVTLQCSQHLHSHMQLSSAHNVLEVAAGAGLGSLD

VVRYLLNDPSTLSNDTKRTYTVTDLSPVMVNLAEKNLSGVAMDIVEIKCKVANGQDLNEV

ATGSVDRYIASLCLQLTADPDALLREASRTLASNGIAGFTIWGSPDRSGLFVISSASNKE

LGIEENAGEHSNFSLGKDLLALRQRFEAAGFKRMQIWPFQCVVELWSGENFAKFLQEMYP

LENEELEAKRFAIIKRMADEWLAKGFPLGLETYMILARK

>contig33429 Frame-2R|Blast-electron transfer flavoprotein-ubiquinone oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY63626.1|) 0.0

MELRARVTLFGEGCRGSCSEEVMEKFHLREGVQPQTYGIGIKEVWRIPKEKHQAGLVQHT

LGWPLQRSLMDKTFGGSFMYHMEDDLVQIGLVVGLDYENPYINPYEEFQQFKTHPAIRKF

LDGGECVQYGARCLNEGGYHAIPKLTFPGGGLIGCSAGFLNGVKIKGTHTAMKSGMLGAE

AAFEALTASNTTPVAETGEINADEPPIDITSYEFAVENSWIAEELKAVRNVHAGFHKGFL

PGLLHAGVATHVLRGTEPWTIPNIKTDSAKTRPAKDFKPIEYPKPDGQLTFDLLSNLQRS

GTNHNHDQPAHLRIKPELSEIPAKESLPVYAGPEQRFCPARVYEYTDGSEANGIPQLVIN

AQNCVHCKCCAIKMPKDYIKWTVPEGGGGPAYELM

>contig33762 Frame-2F

MWIHSSWVIFLLTRHRIFVHPIDGSLTPNR

>contig34002 Frame-2R

MRVKDFLILVFIACIATCSSFSNAKNLAKVSEERGGKRLLKGSGLSITSNTRVNSEERGI

GDAYKSSSSKLASTLESRSWNWFKLNFVAGIGSAIGFILIYSLFSLTCKDNILK

>contig34381 Frame-2R

MMSEPIPTLSDMGTSLLPSEELLPFVADSNTLPACTTDTACLSTSSLLDYSLHNRSCGHL

SIQHGNHRDYVVQNHLVCQDSVTKLAHRTAAERTVSFDHCTMAQDTHRPGCGHLPVRHKN

HIDYVVEDSLICQQDSWLEDDNLELLGDDF

>contig34796 Frame-2R|Blast-UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase, putative [Phytophthora infestans T30-4](gb|EEY58960.1|) 1e-106

MAALVASRISNALIEVEECSQVSRVELPILDGSSLEYIKGIRRVGIKQQKGAILKHLRIK

RPVQVLQHDKAAWFLPFPKDLSTSASCLQAPTLQMSVQVNFAHMQLGTTFCYFSLGYDSA

KTLDAFHDEIAPARTFTFEQEIDWMRSNGLARGGSLSNAVVFTSNGPSSTLNDDRLRFTN

EWTRHKMLDCIGDIGLAGLPLHGYFFATSPGHALTHDLLRELFKDPENYEYSTQEMI

>contig35504 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69065.1|) 5e-98

MGRIRLVPAFQRLAKDDIWGVRKACAECLVNVALALAPADRGPLLVPLFESFINDSSRWV

RMAAYQSLGPFLAALETNHVTDELVGHFTSMATTAASQLGGSGEVDIKFHCAFNFPAVVS

IVGITGWRKLSPTFELLHNDTYWKIRRSFAYSLHEMAQILGQGITETQLATAFDSYLHDV

QDVRLGAMLHFADFLENVSPSFRESYLPVLAEFESFDNSTKWRFREVLSGQLAQLCRTFT

PEATFSVVHPLVFKLISDPVSVVREQSYHACPLLVARLSSNPEWLTAVVEKFKTLAISTH

YQDRQCFIKVCASFLSTTFPDLGKMELEKLSRHFFSSRLATVFFALALDLVSNVRVVFSG

VAIKHQQLCREHAECPKILREILTATTFNCVDKLVAALSEQVNVRLKAQVNEAKGTKTEG

DLNLMEFADKECDSSAENKMDAFEPIENAPGVKMMTF

>contig35571 Frame-2R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY56172.1|) 1e-87

MENSFSDTAVEDKREESPQYHEAHAQASFLAHFPHLREFVCGGSAAAINIIVTFPPNKVM

FRQQLFGLNTWQAFDNVRSEGWLMLYRGVKPPLLQAMVSKSIMFGLYNYYDELLVEKFGD

HQGLSMMAAGMAGTSEAVLAPFERAQTLLQTPKFNQKIAGAYDAMLHINKYGLREHYRGL

SAILCRNGPGNILFFGL

>contig36008 Frame-1F

MTEHEEFEAPHASHQRPERLRPRRLEPDTLSYLKEVTEMLTQQKDTTTTEDVHLMLWNVL

EELAPRAASAASDRHAGELLEVFLPLMSDAQLRFLLHKMNGYVSHLWTNRYSSHVLQHIL

SRASLVMAKEVNGDDDDIESVENEDDRMKEIPPMSDVIINMVKEVKNEWISLMNDVSASH

VMRSVLAVLAGKPLVSEKRGKKAKHRVVTFVEARTDKNGVQVSFAVPNSCEKLLKELLAV

LIESSTHELQNLVYNQNSGPLIASALKLAPHKSQKILMKRILQWDDKDSCESGFYQLAAD

AVTSHLLESLFESASDKFFTKVYERCMRGKLLQLAEHNIANYVVQDTIKLVRTEAGALKV

LEELETVLWTLLSMGRPGVIWRVVGMCVKFKVHQKEVFNALVSAVAKQESKKPETVRKNL

VASLLNVQLSTSATSAKVQLNCMGAKIIEQLQQFEAGEYLAPLYEGILAFNSVQLMALAK

DSTGSRCLVEPIWESKELSTAWVREQLYERFVGKFGTLAMDRLGAFSVIKCYETVPLDKK

EAIVRELLAVETQLSGSHFSQLVMNTCHLFEYKRSREKWEAIYTKQQKIADLFKDVVEAD

ECSKALQVHKKSKKRKVASVVEAEQRHEEVAKSADVAMILDTLRSSAVEKDQRRKTSKKS

KKR

>contig37159 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66417.1|) 1e-60

MICEYNALSSKIFDIDQVADRVKKKTKELSGAKPINMQEVQKALAMTQQFRKDKTNIEKI

RDGVVANIVVYLKTESNEIKAFLKTCTADVPTAQTAIHRKCATYEASILSNLKNIQRVQR

NMEDLMRLKKDAFAEVTRLGAEIAQSEEEVRRLDKERREEFLNAMSV

>contig37700 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY68024.1|) 5e-45

MYGFISLTGIEFSPEFALAFAASRPFRRFRLPLDLVVAAGVTKVFPSFSRVHLSDLANAL

PRRSNLSESNIVSTPSFFSKSMEKATKVIDDYGAAYMVGSRLAGVAVVCP

>contig38594 Frame-0F|Blast-N-acetyltransferase 10 [Phytophthora infestans T30-4](gb|EEY52909.1|) 1e-112

MGYGSRAVELLTKYYQGDIANNTADATDDKKLKSEKSLSDANLGNEDENAKESKLRKEKL

KPRKILPPLLLPLDERPCERLHWFGSSFGMTLPLHNFWSRAKFCTVYIRQTANDLTGEHT

AIMLRSLRCNDLPTAPAEGWLDEFVGDFRRRFTSLLSFDFSVFPCVLALSLLSDESTTST

AVSNEDPKSFALHRSATSEISPVELAMALTPYDVKRLKSYSKNMVDYHMIVDL

>contig38730 Frame-1F

MSVTGIVRSHFVHPGAGYTLQFPLDCSTGYVSDPTSQAVKLDDRQLDAYFVAPASHIGRV

VTGVVFVAEQSRTIRSIITRAGTYERYGITAISFADKLAEQGYKVLVLDLYQLDSATQEH

AAVLHQAALYLKKKQDVQRVGLIGVGAGADLSIKVAMERSAGMDCVIAMCPKGHISWESY

ENSDELDRADSPVVPILLQIGAKSPYAASKAYKALSSSCAANPLTAATFKTSLFDNQRSG

FAFSNITDEDAATQAIAEILDWLVQHLHRFQMAAATSNTDSWWPQGRNGPFFNVGLRAWQ

ESRGNWLRATQT

>contig39445 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69830.1|) 7e-89

MAIKEVSGSAVHFTDGTLESSMDQQDTYDKVDALSKKRKGQHVVRSFPTPKLHEKTISVL

SSLYAIIERGGSAAGSDGMIASYLEKTLGVLRCNCTSLEEFQALWACPVFSRCRQLYQPM

LVKCPHVQKELFSLLPSDIEAEFNTEHNNESSAIIVDVKNAPFTPYQNST

>contig40188 Frame-2R|Blast-pre-mRNA-splicing factor ini1 [Phytophthora infestans T30-4](gb|EEY55429.1|) 3e-63

MAKHHPDLVMCRKQPGVAIGRLCEKDDGKCVICDSYVRPCTLVRICDECNYGSYQGRCVI

CGGPGISDAYYCRECTQLEKDRDGCPKIVNLGSSKTDLFYERKKYGFKKR

>contig40571 Frame-0F

MCDGKTARKSERQDQVAIHLLHVMVLYRDILFSDLE

>contig40838 Frame-1F

MSEKWFKYDDEDVTPFDPANIEAECFGGVQRRSWHGSNNSMEMEVFSNALMLFYEKVIPV

EPEMAFDATTEADSESSMRVVAVPDEERCEYEAEVWKSNEAFLQTSYLFDVEFHEFLREM

VQSQDMKEKLASALRDDSPMVPLPSAGSVLVPTAAPTTLRVSTVQNDEEILMTLTEIGIE

FVLSVLLHSREKHGIARWITVLAAKFTRSKTICVRFFSALSTSKRLLWLRGLLFECPDSI

ARQSFVHLISRALTAYEAHRKIEYSTLNESKVKAAAAADTSIIRAFLETIAIFLDQTSIM

QQSHLEECFMLVRNCAEASEMARIQLQQLDMIARLINFFLCDRGPSALKDAFPSSKLQPT

ASRYASPDYQYLLEAITAMLGLPRRTSEPLLTESSTQYPHRTVLSEKADHALTEIFKDYE

KPNVTDGNSGLGLEDLKRFFSVTLSSATNSPAVEQQAQHMLIKYGLPADVAAKDDTKPIA

SRVELDGFLLYYTDMAATSPKSVLQNLRAFCFSEDLQRHSVSTGTLLTGAQILENLSPLS

RDALLSDIFFDSALEEEAETTCELLLRLSLGDNSTSSRLLRALLHCLQSTETGWKGQPVV

DACALALQRLLSYESDYQMKLVELALIHSDYGLLSTSRNRENLRSRYVNTAHVPLFIYRQ

LVLVLELRARVSAVSAWLAEHRNKWEWLYEWLRIESLQPSLGGRLPLLRREPAKFEMLWR

LGEALGIPYQEEQRRYVVEGAGYNAVNGVYASTSHVHDNCLTYASVKSKIEYTLFRCCMP

SKARRWYISYSPNKNLLGTMSDEDFYFVQSHTEDEAPPVDGWKVWVKNDKAKAPVPTVRL

FSSTVAALDGEGDSVDVPDSVGGLMTEDGFSAQDDGSIIPGAPSSVMVEETVDVDADAET

VEYDDSEDELRDSNERFQAVHLDTQEDGSSTDGFM

>contig41796-0 Frame-1F0

MTNIKGTCCQGTTGQLALYNPHSVPAE

>contig42285 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63752.1|) 1e-112

MPPGKNKQREKLEQSRASSSSRAHQSLLASAGSNSALPFAFIGFANFAQSASNTVQATSK

TNTLNTKPIIQSIYDGSDHEIALALKMLAKKGAVTKIKALQCFLTDVLPPRQPAEIRPML

GHFTQLYTFEMRDQNDRKIRQLLNEVLAALATKMRPRAFKPHLQRLLPYWLLAMHDSNVD

VAAVANKAFRTLFVKEEMRKTVLEENVPGMMEEFHNFFTKTPDTFEGIPLQPDEKEERYE

RCISAAVLTVNAL

>contig42511 Frame-2F

MLSPRKQASKMPRSGGYGAPSFGASVLGGPPPGGRMNNLNGNGYQPAPVAAGTGPALYDR

PSEAPQDPRRRQAAPQDPHMFNAVPQGISSVNEGRAPMAMQSFTALPISVQNHIHSLVAN

QTLLSLEELGGKCYEVLGQLSEPLANQVLTRFAGANLSNVRNKSGFLIGVVKRARQEYGF

N

>contig42609 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY55432.1|) 0.0

MSADDENLINPVEKIQDFPTGPPIPYKGGILTCTMLGHRKQQDQNWGDEYTEYVLRVTWG

RDILEQSKTAWLVGGRYNDFNALHQELKAAASGRRGKRAPWFPRFPKRHPFSSMMGKNQE

EKFIIKREKEMNRYMTQVLTQMPDALLNIHLDRFLNLTLRTQDICEREAYAEARKRWEEE

EREALANAADAEPLNDADLQEVEQLVHQLLQKIIYAAGDVRQDTELQEMIHAVKVLQPRV

AASAQIGGKVNVELIPLAMQLQDDIQDAFAQYNDTLLALRLGQDLN

>contig42977 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61613.1|) 7e-75

MERLTDAGIVSLTESLPDLQEISIARCSQLSNVAVKGILDACRGLKVLNVSDLPLLTDEC

FESVRTHEHALRHVNMRCCIGVTDVGIQHICFGAKNYLQQLDMSSVSEATDAAMMALLKH

CATSLSTLDMSFCRKISENAWDCLLIMRANCNRSCYGAARRSRLAFSRATLVTS

>contig43008 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63366.1|) 3e-66

MTSKKLVAVQKAQLMRHQIDARGLFGVINALLLLMVLYTSNRYPHKFVRVDGDCDSNWLA

VDAPEGSEVICCNKEAGGYANAPCYTGMDLMPILSSLQGAWAIPLSGLVFNYGSMMLGPR

VTMPRVRVYVRRGLLYAGIMALRTLVLYQGLGALEQQFWNLFTGHSRAACWYAAQRHSKR

CPAGFDHSDHIVLLVSHYLSISMFEWFALNVESTGPSLKRTCLRLWLLVVGGIATYLLFY

TASYFHTTAENLLGLVIAQGCIMVPLVLLTQDYFTSIPWLRLTNFILLP

>contig45033 Frame-0R|Blast-ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY54221.1|) 6e-66

MGVRGLTSYCRQNEAKTSAEVPDLYDVTLAVDFVGYLYHLCKELFKESTASSSWLLLGGC

TLRLERYVDAWIECLYERKIRLIFITDPPLCFGGDNHRKGYCLADRALQKAEQIKQLAQK

LEETLSLESDESSRVIAQNSMENTARRSFQRNSIIAKTLLQTNGRFPFAREKLRGVLRKH

GI

>contig46230 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53721.1|) 2e-46

MGSRALIGAFRGGLSVNVCRQALTTRGGHAHRPPPPPFARIKVPENPLHEEAELVWNDGV

APETLIDFDAPHIPKYQALQHWLLGLSALATLMGVVTVYNPDSWRQA

>contig46560 Frame-2R

MDMEPELRKLLALWKQELLQQ

>contig47004 Frame-2R

MARCYRDRRKRIRSPACSAAVITYAMWATWKSCEKLSFVSVASVVFLVERVR

>contig47071 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57951.1|) 3e-22

MFLKQGMVPDVSAAQIGCRYCGSSTQKNEGAKIATALLKCVCNVTFYCCKEHQVEDWRNH

KSSCTKATRVKE

>contig47488 Frame-2F

MLFISSLSYGLSADQQSIGRFVSSDVERQFYTLNHEADAIKSSTFPGAAALDRLSGFTRS

QDKNVEINRAQMVFTTLACY

>contig47637 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68493.1|) 7e-08

MASGIVLLGEQYDVHRYNCRKSYVETM

>contig48654 Frame-0R

MMATNDAGMPVFGCTCDVGYSGEKCDTITSSFTFSNNTPSNGNTGSLSGGQDNEFSVGFL

HFGSDDSQSDNSLSGGSDSSSLDALKRSNADSNTTHNSSLLRSDQSDQNASDKSSLGKAK

GDDPSNSTAASSSSTEETTDSASTSSQNGLQSGVVVLIVLLSTFFLVGTVIMLVQLRRKK

RKVEEEYANALAFTHENDGSRDPAFGLTTLSSISL

>contig48795 Frame-1R

MEARQSVQDAVVERILASSAIVAGCEAITTIRATINTRGPLRSKSQLQVNASAKVSEMFR

PRSHHLRTPASTKKFTCVSNIFKDPKGGRYSGADIAIGGIYDTNIRMCGNLQLRSIRNPN

AGTMPSILSVNETMRKTHLDKPPDGGPDGVHLLISAASGTQGLRVLIGSGRGGSAACALF

VARKKFL

>contig48881 Frame-2R

MFLLKGHEDLRQDERVTQLFGLVNALLINDRHTSKKDLKIHRYPVIPLSDNAGIVGWVPH

CDTLHQLIRDYREARKILLNIEHRLMLQMAPDYDALTLLEKVEVFQYALENTAGQDLYKV

LWLKSENSEVWLDRRTNYTRSLAVMSMVGYVLGLGDRHPSNLMLHRFTGTIVHIDFGDCF

EVAMDREKYPEKIPFRLTRMLTNAMEVSGIEGNFRFSCESVMAVLRENRHSLMAMLEAFV

HDPLINWRLLSSTNVLRPSHASNSVASSVTSSSIGSSAISMESKSDDESSNASFHPSENA

AHEQAFAHESTESSNREEQFVHHRSSSISVPGSIPKFGTTQFASCKMQAAQEGGGMEDTN

NASMMSENQDKRLDDGAGDDVNSETFEAQTLLQTQQEHQGTNAPVPRELSIRLATSRPLC

LDSQETEAPPLPSSLSSRPMSLSKSIPLPVRKLPPRVPAVYRLRDATIDENEESNTVEKI

NHTTTNLHAEISSLAASVSSVGHSSLSRSFSVTQAQLHVQPRGPAKQPQSNVPLLSSSSG

PVPRMAPAASTSFVSVTATRIPPSSEAVPPSVSSNDLHASRSVRERELLNALGPEGIAAP

RVALNEKAVAVIRRVQAKLSGRDFEGDAGEPLDVSAQVQRLISQATSHENLCQCYIGWCP

FW

>contig49114 Frame-0R

MTPAPKMEVLMRPMDMLQRPLRVISDSSMTMRFSLPSSFLQSHPVQSSAALVKSKMVENV

IDDISESWEERDWDTEVMPTLTPASKFQELDEWEQKSMPDLPDDFPRLIVNLTRIQRQHF

PVSKEEKKIDMMEVFRTIETALHQHYTQLVEVLFEQNTCFHCTYGNSHAMINNLHAAYPE

DSFAMVDYPTMIDNVPLHEFLYHLSCPSKWKSVEYLKDCLRQCSRDIRWKRSVITELEVL

AELESQQSNQKMKRLSDDIDELSRLRDSFRAKLEKIAKVDCKRSGQYLMLRKLEDIENRL

GQLLNKYFTEPVLENRECYGAFGHSGNENGIQVGMNVLDMVIAMVFSRLPRDLSQQTTTQ

EHYQMLFDHHIHILRLWKKDFGRLPPQSRAAPVINGSESDTRDVFNSKDEHCVSKISDQT

DIEKQAEAFSVYCQIDDSESDNRESEHFVTNDAGYNVEDKTCQDNDMDGYNADFDSDHSE

EEQTITMQV

>contig49811 Frame-0R

MESMRLITLYKVVNKHAIGCELVALRDEKYTVD

>contig50053 Frame-1F|Blast-fimbrin-like protein [Phytophthora infestans T30-4](gb|EEY59946.1|) 2e-12

MSYQVSSVFLQKFSPKEIHELKRVFKEHDHDYAAAVAVS

>contig50138 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60981.1|) 4e-52

MRLTRALLLRHRHFNLLRSFPCAHSHVLSTRRTFSFSATYPTSSESAAMDDTEDKSTSRL

VCGKCTTTLSDTKNLVFFKWRNGIHVSSASVNH

>contig50347-0 Frame-2F0

MFVRSLRNASKTVGVISRMLQ

>contig50668 Frame-1F

MGRVGQSQSAAKYELHFADRRQLEQDRMSSYTDDAFECESPNAILAGSGIGPTEERCDQH

ATESAGSSPYLV

>contig50888 Frame-2F

MGLDKKVLPCNLAVTCTRAKKSVDSDDDFFDCDDTNSESTVESSCPSPHRSSPLSSNSYP

SRLEHEMETYEDDECLQRLLHGRDEDDEAYMLLDRINNLSEEFSAHRE

>contig51807 Frame-1F

MKFFTTILFTAAIATKYVLANEANTTTSAPATEMMADSPVTTATTDSKHVIGSILDEISQ

TFGSNALAYSSASGSESGSRFGIAYVGDNSTSTNDGASIQMTSLAMLTILATIAADLL

>contig52345 Frame-0R|Blast-exportin-T, putative [Phytophthora infestans T30-4](gb|EEY56559.1|) 1e-110

MTPEKKLALLQQLQILDMLASLPIREDEAFAEEIGEVINAAGVELVTCMDAFRQTNRIDL

VHVTGSMLCQLMPLVWDLFAHESKDVSEEVFEIVNTVGGAMLRTEMNMADSPTRKQEVFQ

PSKYIPQILHGVYRQTRFSLELDSDAAEFEEYRRSLYTIYLNIVRQCPHDTLTFLTNLAQ

GLPIQFAEIDPRDLESFMSLVYRFKEGIAPLRTVAVPFNEPTSPLSLFAV

>contig54206 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53647.1|) 2e-16

MLSAKQSSASLSSQHPVSGSNGDSNIISFSGDNALYIDGALYDDHQLECIKARSSLSESQ

ILIAHES

>contig55410 Frame-2F

MAERHYAEAQAAAHQAQRYQRAGQWNEALSLFEKALHIFKRLAVVESAVQREHLQLTIA

>contig56077 Frame-2F|Blast-flagellar peptidyl-prolyl cis-trans isomerase [Phytophthora infestans T30-4](gb|EEY59582.1|) 2e-22

MDAALNEAWRRGNPVVFFDISIGGAPVGRLRLELFKKHCPRTVENFRQFCTGEYR

>contig56727 Frame-0F|Blast-hypothetical protein PITG\_15639 [Phytophthora infestans T30-4](gb|EEY64423.1|) 9e-11

MTDAVAKKAVKWHKLPYTKFLLHESKRAHFQPFLIAGV

>contig57896 Frame-1R|Blast-folylpolyglutamate synthase, putative [Phytophthora infestans T30-4](gb|EEY58400.1|) 5e-30

MLSISKGLETALARSRASKDKEVVVVCGSAFLMAEARQALGYKEPIDSVALNDGNSVDRS

TFQNQLSVAQHKATIAAVL

>contig58776 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65949.1|) 1e-51

MSGSGRKSAYRKGVTKRVLYGDPEPQENQIIVRVTGMRGTNLFEVVDAVGVESVTMLPTK

FRKLIWVKRGDFLIVGEGDGGEATTATGKKGAVTSIVEHILYKDQIQNLKRKEL

>contig02202 Frame-1R

MVDEVVPNSVGWYILEGYPWWPVYICDVFKLRPTLHLLGSGHKTILKKARDFPKDFIVVY

YFGSHDFSLVGLKNGVLRPWECAQKEQFLKGHPKHLTKKKGTMDELLVAIQEAEDYLSQP

EDMRLPQHMVPSDLDPTLEPPPPELMSVDMATDYEVDDDEHMDDDERTLFNEKEIERKLK

KKKKEKVKKDDKKRNNDGSTKKTSPKVFKTVDTDVKSQILDRKKSSRRPPTNLSPVELSI

ILEKEIRWILVNCPFEEMTTKTVRKLLEDRLHLDLRHHKASIKEGVARVIASMEEEDGAE

STILEEPRETKTNKGLNVDNPVHVKEEAGLENLNPVVKMEGKEEAMELERTRMELEAVSK

NLSLALELEPKILDALESLRSLESVNRNVLAASTLRSRLVKLRAHKSSKIANLVTLLVKM

WKVEDLIPAPKSITKEEILKVKAKLERELSHDDLLGCLDQLAE

>contig02299 Frame-1R

MTLPAAPPAAVAPRVLNSDNCATLDSSGPSRRLSLSQQVQSAVERLLSVSSAFKDLQPGK

DTQVSTREETITMMQHYLKRLHLDDVVDSNSPRSLSVVHVAGTKGKGSTCAMVERILREA

GYKTGLFTSPHLVSPCERFRINGKKIEDDVFLRHFEAVWDGLECTQDESGPFPPMAWFFR

FLTLMALHIFAHEKVDVVVLEVGLGGRLDATNVFRKPVVCGISTLDLDHTRVLGETLDQI

AFAKAGIFKPGVPAFTTEQEPLAMQMLEKCAYETATPLLCVPALDKFGPDGANCQLGLQG

DFQRTNASLAVALASTWLRSKRGQGATPQVDWTTALEPVVRRGLKNAFWPGRAQLWEDKE

HKTRFYIDGAHTLRSLECCADWFSHSQITQPSAHVLIFAIHHERNVAQLFEPLLKLRFDR

VYFCSTRSSRPSIAKVHTFSEALAIAGYQNVIAKYTSEEVAALDNVSTQDHPWQVTLSRI

WFGLMTHVVKKDRKKCLISVKNSVVDCINELRALNIGATVCLKNGRVTTGYAQRDEHLSV

LVTGSLYLGGEALDFLGWQE

>contig05687 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69713.1|) 2e-39

MMKSFFSVKSTTPKSSLSNSSRTYTMDFLNKAVGTFSADKSTGKSKKKDSILNKALDAAD

KYHAKEKASEFAQKRVAKRESEKQTPNYVEKKDKSKIDKAVEAAEDFLAKQGQSKPQHTK

GKKDNQMDDVFGKAKGFLSKNF

>contig08972 Frame-0F|Blast-ATP-dependent DNA helicase, putative [Phytophthora infestans T30-4](gb|EEY60960.1|) 2e-19

MGIDRSDVRFIIHHSLPLSLSSYFQQIGRSGRDGNSSVCVLLYSKADTDRAAYVSTNSHL

LDGRNTDEISYGSSRNEL

>contig09373 Frame-2R

MCSCILEMRMLQRLDFTVLFCNLPSGSICNTMLMSSKKEMTLSTHEEMTLSSHNFFSIVN

QLPN

>contig12791-1 Frame-1R1

MKVQRTWSRVNARHGNLLGKKHISRKHGKKK

>contig15127 Frame-1F

MNASSSPWNMAPKASNSETASPWAVSPIQKSNPFASRNTASQSAESDSELSIDGLSMKED

LPNLSAFSSAFEPKVEKAGELIAGSKAELGLHAGHFPQNSTWTSIVTEQVQVQKTEELIA

YDKLAQQIPGFVPAKISAVAEDKVVEKSLLMGVQPQVENNEMRFTQAEASESAWTEHVDR

DAYANVANKFSSKKVPSEEVADILKDQAIEEVTPFEELKKPSDKAPFEKAPAGLIAIKSL

PRKDVIKATSDIRNTPLVQKAPLQEKNSIDAGETEEVINKAAEEIKGHLFKALSADKETE

AAFCKDMTSLPTEDGACPWTNPPMQEEESNAAFSLTNFAQNAEESAPVVANIPEITEPPT

NWVHNLVPGDIAVEGITNGEAVGPIEKLIFDGNLSSKIPILEDPELEKRPTDSLSWNTVP

DQKCVKEIVTPVREVVVGPIKEDVAEPVQEPILFNQTSENFKDTMLLTQKISEAAAHEAE

KASVGSETSERKATAEAFDCYIANSIVKVDKLSEVEAITANSTNAPEFCGISSCSIM

>contig15343 Frame-0F

MYYHGMSDAKPLGTVNLRRVTVEMCEGYEVNARNKSLSFFKVIPPSASERTYYFGAESER

ELVNWVHALGAQSAYGLIDSRRPYGQSNSRHDRFSYQQDYSTYNFGTERQRHQSYHMGDY

SRESGNMATSGFRSRPDPRSSQLGATELAFEVSKDDVEPNDARGATRPRRGTMNGFPGAV

QRALARRSISLREKEDNEGYRFTLTGASAARECVRAEPVADLTNTLSAVEQASLLQEVNG

FETGIYIYSADELQEAAVLQKYMRETPGALNPTILRTTSTLPPESLSAQLSQYVEQKQMD

EAEQLLTELVLLKFPRLVDAMDYDPLAFTRLIAGGDIATATKKDEIASLVKRSRSQRKSR

KANCE

>contig15677 Frame-1F

MQIMRDLLWSDPKASKGYEENKRGAGTMYGPDLVQKFMTKNKLALIVRSHECVPRGFDWP

YKEKGMLVTLFSASNYCGRANNLGCFMRVPSGVDKPAFFQYMASAESRDMAVSNLDALFS

LIIQYRADLIVEFERLDPEKSNQITVQMWSSVMEDVLDLSLDWKALQPLLTALDDEKLVP

YHDFLDRYNAEGAISHTKNNGIADPEREKQRSAFNSMYRHRSRLEALFRVLDRDGNGTIS

VDELEKGIKLLNEHLPPGAKPFSTNGKDYMRMMDFSYDNELNINEFMEGFRINAKLTVHA

KWKRARKKIKALSAIGALRGFTLPCSASAAAAGGSSIVAMVDNDDEEV

>contig15699 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69573.1|) 3e-25

MLLRKAGKAIRSLGQTIDRVGVSLEGKLTYTEHLNPSTRAIKNLGRSPKFGDGVFVAPNA

SVIGDVKV

>contig16759 Frame-0F|Blast-lysophospholipid acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY53424.1|) 1e-123

MCFRVVLFRFRYYLAWSLAEAASATAGVGYVQATGKWNGIRNNDIMCVEIPTNFRVAINN

WNIGVARWINTYIYQRVGLSKSGRSGLLSTMASFFVSALWHGLSPGYYLFFLLGGIYIEV

GKHLRRRLRSYFHYDEDRSAHPHDIFLSYFRGNSHPLAFLYDSMGVIFTWVAMQYAGIAF

EILDVRRCIAIWGSWFYLPHVVCISLLLFFNLFPRRSAHGQKSKDPVKEM

>contig19992 Frame-0R|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY70055.1|) 2e-21 NOT\_ORF

MVGVRIKKVQANKQDHEKAILARKKGKLL

>contig22738 Frame-0F

MEILRMGNAETQWDTARDSTGKKALKSRQQRIERPPQWPANGAPTYTRQQQQRSSISKKA

QFQQQTQYDSRYSSQRDSQYQPQLSLPPPPPPPPEVPMLEPKEYHGPSLSMLELQQSQVE

FMQSNVDVVHRHTDPEVIARTQETVEKVMAELEEDPEFEESWIPYTSLYFTRAISKGAFG

EVWLAQLENTQVAVKKILDERKHDVKEIECFGAEIKLMALLKHPKIVSFIGISWSDKQDL

CAVTEFMAKGDLCGYLERRKGKLNWPDHKSWLTEDIAEALVYLHSLNPKVIHRDLKSKNI

LLDNKYRAKLSDFGISRKRSVEQTMTAGVGTIYWTAPEVLMGKKYTEKADIYSFGIVMSE

MDMCEVPYSDKRDSSGKKLQSMKVIQLVIRSALRPSFRKDCPVLIKALADRCLDANPDVR

PDAPELLSILRDIQKEL

>contig24686 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60238.1|) 2e-88

MTANYDDVHEGLPCETSEAEIALVLEELKYVPNNLVKVSAFVDSNGHISHTRESRDYRPA

ALLLYPLRNAEDAYKRKQRAKVEPFPTIYWLASSKLKAKVSTLEDQHYVLTLQHRLDTDQ

VAKEKMVQSHREYAEQRWQMLTRHDRDLLKRRQWEFFLRDVGIAGIRDFTNVKCLHTHYA

HYLSTGNNQIGEWVQELLDNPANNIPMDTKN

>contig25164 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54879.1|) 2e-86

MRLDSFTNTVIGVGGKECDLKLWSLETEQVLFRAKNVTHDKLDMRVPVWIKDLRFLATPG

TSNGHRVLVGTGYRHVRIYDSNTKRRPVQEVHLPGENPIQSLCISSNEMQVFIGDTAGNL

DVLDVRTLTSMGRCTGPVGSIRDLACHPTLPFVAAVGLDRMVHVFDTLTRKLRYTIYAKQ

RLNAVLFTTEGIHATKHDDDDEE

>contig27306 Frame-1R

MQFQSEMCATKIDIKHAGDIKSFFENKQEKQEPIDSSDTLTTKRKTKESTFANTASNLSP

KEEDTKSDTSINKQVKHQHIEYIPASSLLNKCLSDKKSTT

>contig27492 Frame-1F|Blast-mitogen-activated protein kinase organizer, putative [Phytophthora infestans T30-4](gb|EEY69177.1|) 2e-30

MAAEEVPTVCIRELHGHHGPINSIRFNSKGTYVMTCGQDKTIKLWNPHRDCEEKPKQALL

VKTYEGRHGYDVQDVT

>contig29380 Frame-1F

MLDYKPLRAIWPIQDCLNENQMPTPQPDQIHVLVQMTSHSPFRRTATKPDL

>contig29407 Frame-2R|Blast-divalent anion:Na symporter (DASS) family protein [Phytophthora infestans T30-4](gb|EEY54598.1|) 5e-71

MVTVSLCTMVICLTTFVSHTVASIILLPIIVQMAIQIGDPHIPVICCALAISAAMALPFS

SFPNINSLLVLDDHGQPYLEVRDFLRVGVTFSLVTMALIITLGYGLIVLVLGFNIEPSRM

IIGV

>contig29472 Frame-1R

MSFLFSLTLVSLRVSSSLKPVFGKMCNEALIISSGQNAWSANYFC

>contig30328 Frame-1F|Blast-carbon catabolite repressor protein, putative [Phytophthora infestans T30-4](gb|EEY61326.1|) 1e-37

MEKEGLGRLPEYIASVGSVLLFNSGENPYQKYTSWDNLLGTDYEEEEEKRKELAKAPRTI

EYGDE

>contig32780 Frame-0F|Blast-glutathione S-transferase C-terminal domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY67023.1|) 1e-138 NOT\_ORF

MQVYFARQKEAFACNRWEYLLFACIVVDRFFPAKERIAAAQLTNVDVFCGFVDDYHSHFN

VGVALHACGEATDMVMRKCLAERAAYVLAPCCVGKIKSSGLTYPRSVTLANEVSRVEYEV

LAKAADFGHSINTEVAHADINRRRRRCKTLLESDRNMYAEEAQYITFMFVMYPSTATPKN

DVLVGIPRNPAVEATEQRNADVMFHLMCKSPL\*TN

>contig33233 Frame-1R

MSGQCLDKNKQSSVRIRIAEVSKNHVNQRFRVKISVPKCNGSCNYDNFVVSDPILVLSKK

KKRLGIQHIEATTNHIMAKKLKRSSISKLEGLKDLGNALKSTPIPNLSNKVVDFAKIESP

MRTGVATAPFTPETPNLCLWANAAFDLLSKLQWQRALADNSNNLGRSFDAILALPLPKVY

ECPSCHETYGETPMHRNHCDLMLLLERDGNNETGTKYKNHNEVASFPLQWSSDKHVEWRG

QAQSMFTNHASTLKAEASSIDSIVQDTRKTLKLERDDMQALLDASKSAPPTTISSWKDYA

SISQLLFSTSFEFSKIPQLSTSLPSTVQSTGMLPPVGTLSRSILSNSGAVNISEEDQVGE

KRHRIPSQRYPSLLAAKCSFSTDAANLFQETELALHGNGRIVSSMNLMNITDYYLRPNVG

NIGNDDVFHGHVSSAAPLPSDSFDKRENQVKKIMANDFQGCGFPALDDLSNLVGFYQVLT

DTNNNLAELQFAPHLFPLPEEMLLELKTTIAEWGRNLSICWQRQSIEGKNEETLVGLKKA

VLEHILR

>contig34001 Frame-1R

MDGSYIPPPFPFPEAWPKVFASQILCQDSMWLTPPAFITSREWKVSMSADFSKTSDTADS

ISTAPSMQDKDDDDDDCDIAYVLSEEWKKHFQLSSRLQKLQKQTQKSGTKSKMRKQQQRQ

NNQHKLIKTKAAGACANRSSHLQREVQAAKLRDEERKRTRRSGESGDAPPGPQIVRLEGL

LNARFDEFCDKFQPAMWPYDSLPC

>contig34382 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58205.1|) 1e-108 NOT\_ORF

MSIVGTKSWLADRNDQLEWLKVDLQSVDRSVTPWVVVMKHNPFYNTWDIHDCQCSPTIFD

IDSADAAKCWNGQYYSGIVYWEPQCGLMAKLEDVFSANRVNVVISGHVHAYERTAKIYKN

KEDAEKGVYYVTTGSGGNYEGHAGPRIPSSKIPSWSLAANNVTFGGSRIIATRDSFRFLW

FANDLDTKEAVPTDNFTIVANGLASITWPLTSLHSDDSP\*LTKSSSCTLLAFKVDRIGLK

IREMLFAPHPFGYFHPSLY

>contig35507 Frame-0F

MGRYADNTYDFRRISGVYREDLVDCAVLGIIHNRSPDDPFFLSCFKWMTVQSPGKGLVKQ

RDVCFYEQMGITRDHNGKEIGYTLTESVDLPNCPPFPNCVRAKLSVCYLYRHNKSGGVAV

YMRGKNDAGGKVIDWVADLKSAELWLRIDRARPVAHAVIATVLIEAGKSFRRPVNVHGKC

ELCFTKASTFLSSSKTCAVCHRLTCSNCGLKVRVLSTQHFTGPEFTHFCKKCVRLIHQVD

LRAPESVQNLVEYAARSLSEAAPSGVRITAVSNTSSGGEVATTPTFAPPLDEPEQYAVRA

DVQDAMQRRQSLYPPTGYDEIDFKRRDSEIPLRNSIGV

>contig35572 Frame-1R

MTDRLVHNRAFRVSKERNQLDLLCEQRRRQLSHRKDLPDQERLATPAGKANNHHERTPAF

FAWNEEAAFSRSRPTWQAETPQKIARTLHLTPPRECQPAPERSPDGSRYDERALLLHENE

DICTIQDHDIVTSNPVERVITVTPTREDILDRVRPSGSTIRSHDSSSHAHLSTPRPLTPL

>contig37512 Frame-2F|Blast-hydroxymethylglutaryl-CoA lyase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY58132.1|) 6e-41

MLQAAKQHVPVQHLAVHFHDTYGQALSNLLIALQEGISIVDSSVAGLGGCPYASGASGNV

ATEDVLYMLHGLGISTGVNLHKMIETGNFISKLLGHSNHSKVAQALSSNTTSRL

>contig37703 Frame-1R|Blast-4-nitrophenylphosphatase, putative [Phytophthora infestans T30-4](gb|EEY62530.1|) 2e-08

MAHATACVRQIPDCHFIGTNP

>contig38063 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64662.1|) 7e-58

MASGRDKFLKAKSLEILARLSSVDSIFSELEPLEDSLTPKTGDLVQELQERVVAMAYFPV

LIASACSSAESEVRSNAIKCLSCGVNGDKELVGRMLEEEMLRAFYTGLRRWM

>contig38597 Frame-1R

MTPYSPPEWSSSGRNVFGIYVEVIKCGVVIETIQLPCTKEQSYTMAGRTEGVCDLVLAHP

SISRTHAVLQFDEQGTLFLYDMHSTHGCFVNKKRIPAEEFVRLHIGDVVGFGESMRLYAI

CGPPELLPVEYESLNLVKFRERLETKVEETGASWGFGNDAEDEESEEEILDDKMEELPDY

LRNVRIKFGSMCLRTGC

>contig39446 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69765.1|) 6e-64

MSSDDFKAMLEVAAPQEEKLSTKTIRKRLGLLDRSGAQPSASETVVREEQESIKSEMMSL

AKQLKQKTQTINQSLTEDVKILDAVGQSAESNSALLDRENAKLKQQLASSIGLWTSLWLV

AMLIVVFIATYFYLKLFSRRW

>contig40280 Frame-0F|Blast-asparaginase, putative [Phytophthora infestans T30-4](gb|EEY56768.1|) 4e-35

MVTRTKLKTRDPSNSFSASFDGANEGVSPFIVPFGASEAHVCASSGSMHAPTPTTVDADD

VGLKTKRSHCLVIYTGGTFGMVPDNNGVLHPSSGFLAKKIREK

>contig40572 Frame-1F|Blast-secreted RxLR effector peptide protein, putative [Phytophthora infestans T30-4](gb|EEY65643.1|) 6e-72

MLTGTSLNVLVDPTRSVGAANAVTSSQTDTQSRQPDSITNDTNASAPPASSHISISGMGF

PLVSSVVFPFSLAAGLGGSHATTTWNLADFVRRLTSELPISTLYGVVAGDATQLYRLLAH

IGFALLSGVDVPRATRPNFRSWAQEFENELRALLCSRVLPRGVLDQVFGPEERRVDFGNE

FMRIIEPSIPELIDLFFRATSASRAAAFGTSSAMFLRSIAQQIIDQIRAYARGDSMEDER

DSNE

>contig41001 Frame-1R

MMFGSDAALPFSRHSDVLQGAVPTNPVELENLVSEIRRRGNAAFQQKALEEAEVLYSRAL

AVDESNLLQNRHLFFANRSAARCSMGKIEQALEDADACVALDSTYAKGFFRKAQALVKLG

RYKEAQSVLDQAKALEPTNSSVDTLYAKVEEMANEEKVLPATRIPKKVTKTRVNVTQSRS

PSMAKATTTAASTVVDEDAEISGQVRGYKKLADGRVTTYFNNELTEEAKQLIGDIAPKKV

EHPHKVQIKSVDGGSAWNQGNTFEEKDMTSWAKSKLETLLSGVSAPLGTGEGVVSSLDVT

NLEGDASIAVVRGAKRYIFDFTLTLTCTLKQSDGSVTGELKFLDLSSDCGGDYDVEPIVP

TRYQSESGKALHAALNSSTSPFRKSLAAQLVLFVKDYHTF

>contig41795 Frame-0F

MKLALPDELLSRLVSFLYIDDLLSLERASHSWRRTLAIACFWTYAKFDHQWSRSECASTL

VNLLAMRHGPHVKMLTLIGCAIPEGSLVKTAKYFTSLTHLTVSGCLTLADIDFSAIIQAS

SQQLIEVRAVKCLRLTDHALQAIDGYHSQSLDLLDFSYCRQISSNGLEAVICRCKNLRSI

RLKGSPAVTSSVVTCIAKSCPKVETLLVGGATNLNDDCLLALGTHCPNLTALDISRSNPF

GCSRGGISDYALEYLVLRCPRLQHLAMGGQGRLKLSVINSLAKFCPKLETLDIGGCRNIV

SNPIELGAELKRLRGLNELSVALIRELKEAQVHFIASQCPQLKLVEFTLPRPELVKMQYL

SCVCLNPQHTRN

>contig41971 Frame-1R|Blast-small nuclear ribonucleoprotein Sm D1 [Phytophthora infestans T30-4](gb|EEY58508.1|) 8e-52

MKLVRFLMKLSNETVTIELKNGTIVHGTITGVDISMNTHLKAVKMTVKGKNPVNMDSLSI

RGNNIRYYILPDSLNLDTLLIDDTPREKVKSGAPVGSGRGRGRGRGRGRGRP

>contig42286-0 Frame-2F0

MKDFSPLLTVSTLLRIKLGAQVIDILQI

>contig42286-1 Frame-0R1

MSMTCAPSLILNKVDTVRSGLKSFISH

>contig42512 Frame-2F|Blast-polysaccharide lyase, putative [Phytophthora infestans T30-4](gb|EEY68248.1|) 5e-73

MVNSGRLFESCGTCGPVKRAVIVDGIVNVNPTAELIRMNANYNDRGVISKAIITTSMANY

PVCTCFEGGATPLMLGKGALALVCPNSSAAVTFKS

>contig42567 Frame-0F

MLRRLINDILETHRECMELSLIKLALPPNLRCFGIYSCTSYISNAKSFAPQEFFFRCNVT

RLGKSHGVKQRF

>contig42589 Frame-2F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72305.1|) 4e-26

MHKFQVGDRVLLSTEGLRDLAFTNLGASKLAPRFIGPFNFLKTTGDAYALEISSSLRLHS

TFYVGRLKNITGYSP

>contig42974 Frame-2R

MEPRPALALFPKRQREDIMSLFTAPSPQSCEQLPQFLPSHELKFGLAPVARDKATSHITL

VLCRFCLHFGRNRQPNTQHGFNQTIQFFRSVCWTNQYVQHHRMNHSKIWKRYERCFDHEK

EHFFPVSNIAANKALIVQEIQLLPNELWAFGDSQDKTQLDLNPAIIKLVAMLPIDHNMTP

MLQHTSLTPRKEHDTQEGMHTTRWVPSEGTFQSCTLILDSKNSFYQVVVHSRSELDCIVE

LLATGLSFEQLPSVIQSYQFHSSILFKTITFL

>contig43968 Frame-0F

MLSCKKTFALCATAALIMSGFSEVESSIASYRRGLREGAVSGEGYSDKMDYKRKHYEHTD

SDGDVGHNGDDTVLYQDSQLHDGLIDIDLVAKLELALGLLREDGVDLLSHHNGALQHQNG

ESPLHLDDLLEIGVGLEIAIDLLREKGVGLLNHHGAEQHQNAETPLHLDNIVDIDADVGV

DLLSV

>contig44688 Frame-0F

MNMLHMAAPTLFPEPPSPTVDFTSTSLNMFLPTGPMNLMQACNSFNPSTSIPGDSTSNYV

ISSEMPTFTPDAYMASSSSSLNSSTSFMSEPNFIMNCGLTTASEPHYMR

>contig45328 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY69921.1|) 0.0

MTAVGITAEEQRDIFQQLSAILWLGNVQFKQTTDEAHNPRAAIEDLEARAALAKGASLMG

IDKDKLESLLTFRIVNICREDQKVLFDARQAKKVCDSIMRSLYEKIFDWIVARINQNVTC

PKRNISNSIGILDIYGFEIFEVNAFEQLCINYVNEKLQQLFISQTLESEQEGYRREGLSW

QNISFFNNQVVCDLIEDPKGHGIFPLLDEQCAIARLSDLELIERYNSEHSKNPHYIASRV

RGPTFGILHYAGKVEYDVTLFFDANLDTFFNDLQDGMEHSSNAFVRDIFLDKRSKETKLK

RPPSTSQQFRTQVADLLKKLDGCNPHYIRCIKPNEHKRPLAVNKELVTEQVKYLGLVENL

SVRRQGFCYSQPYAPFIKRYSFLSESTWPTPVA

>contig45614 Frame-0F|Blast-polyprotein of retroviral origin, putative [Ixodes scapularis]gb|EEC04541.1| polyprotein of retroviral origin, putative [Ixodes scapularis](ref|XP\_002410644.1|) 1e-09 NOT\_ORF

MEALRQLPAPSTGQELQQFICALNWMRSSLPAYNRLVHLLSIFTEKVYASAGGRKKTKVR

RVILTDIGWSNAELTAF\*RCKNALKHALTLANPDPESVCALYADPVTSIGDRPSPRCQRN

ICSVALQISIMNL

>contig46761 Frame-0F

MLKRQVHFLMNPRSVRHSSICHRRAMSHCRIRNSPSWYHTRSSSTKRSLSFSSPPVTLVS

LPPRLSPTHGKPTTDRVLTFLQSARDRNVPVRSGKWSMAEDAYLAKLIWLFENGLLAEME

PKTSLRSYLALMLNCCPMRISKKQMHGHSFMGKVKYVPQASNMTQQEYDALCHDVWALRN

RFLQTWVKDEYTRRNATFKPHDTSFQEWYEKVVALVPTPRLIKRSSLKSCKKKRRIEVLD

EITLPIQQNIEKEQVKKMAKILPCEVQNLEHECLRGTSRIEMLEPEDIMLLDPAEPISEL

AFDNKRLAFPTAYCGESLSIEDLDWLTTTDRGHVFAQWTNSPGGNYTGEALAKVNEDQVQ

VSMHLSDTEPTDLSMIRRSSELIIDFGAPSCWYVGDEPKHTPFFDVSQWADSDLTEALAT

EPSIFNWDDSVHILNSPAIEFP

>contig47007 Frame-1F

MLTAAQKREARRARVLQSSESRLNMLKGSIASQEPPSAINEPSSLEQRVDEGVEELLASC

GEAAVPQSELQFPPRVDPLQRRRDAANRRLQKEKMVTEMLNNKALNTEGEEHEWPTKLAT

TSSCVAKPTFNRHAIALKLRVLEERVIIYLLVAAAAFIAMSMDIRSIIANLAGPDHLVVT

YQDLLSKGMSIASIRQHIEREQVDPDTRRNLEHFVTQQEGVHAMETTKTSSFTWLPGMTD

LGTFFTALVDHPPILLGVVLVRVLIEAAVKGLESALDLPDVKNPQEENLGFVANMVFISH

PTLKGA

>contig47818 Frame-0F

MDRIDYRWIQRFMEATNIVGRAQTGKLMVSEQRIEHIEKEIACHLGVVARKLFVILLFIL

>contig48473 Frame-2F

MATTMESLRAEGNQYFSAKEYQSALEKYTEALSAAPSGQTGESLKNVVAQRVLLHSNRAA

CYLQLENFVAAEN

>contig48796 Frame-2R|Blast-guanine deaminase, putative [Phytophthora infestans T30-4](gb|EEY69083.1|) 1e-101

MAHCIWCNQHERALLREKQAAVIHCPSSNFSLSSGVLNVRRLLHEGIKVGLGTDVSGGYS

PSMLDAIRQAIIASKLVANGNGSANDDDEGGILYEPLTYAEAFYLATTGSAEALGLSDQV

GNFQVGKFFDALVINPYTSNSPIDETIDTVEAPDVLHTFQKFLFLGDDRNIVAVFVSGRR

VIGSPC

>contig48882 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64057.1|) 6e-46

MGRQHISVAVVALSAVTGTTAAAVSMMAYFRFQHPQEFADATIRLSHPELSDDINRKWGL

FGTGIFDSVPQRVNDFFSVPDMAERFELQKKKRDEQIRQTIEDLRPKGK

>contig48976 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63049.1|) 4e-19 NOT\_ORF

MLNASPGHLIFGQDMISRQLHQANWSYLS\*CRFDAILADNDRKNKKHLEHFYQPGDHVMI

LVPKQFRAKTKHVAAGPYPILTIHTSGTVTVDKDSTKQQISIRRIYPC

>contig49162 Frame-2F|Blast-nardilysin-like protein [Phytophthora infestans T30-4](gb|EEY65469.1|) 2e-07 NOT\_ORF

MVPSILLLRLLRGNWSQISKESIGMSP\*PLPNPFMPHDF\*ILPFDPANWPAAL

>contig49324 Frame-1R

MMVDPRYASVMRSTRSGNYYKVPLSANATKHAPDMARSANYDRYEHKGVTAAWGTSTMRR

LPAVAKRRDLNSSLDGIMLSKDAHTFQPAFAFDLNMLVASLTKTSTSSSNSSSSGEPASE

PMPEYSRIPEATTPEQRGRRGALSGEDELARSFSPSATTPPKNSIISYSLNKRKQRRLAA

KALAAASADGPTFEVALADAGNEHNLQCVPRFVPEYQSDAIASRNRELSLDQQSYAL

>contig49540 Frame-1R

MHPTVVEAEGYSLHIRCVAGIESCCYVNSIDVAFDLGCIMGRVVNKSHIFITHGHIDHIG

AIVIHAARRVLLKLKPAHYYVLASIVPHLKNLFESSAEMQDGPLPATIVPLQAFDEVHIS

AKYVVRAVPTKHRVPSLGFILYEKKNRLKPEYKQFLSADIAALKRAGHKITNCELTPEVA

YTGDTTIEVFTAASDDDRSKDLLYVRVLITEATYVDSKMTVDDAIARGHTHLDQLAAHHQ

LFQNVGTLVLVHFSPRYQAKELIKCIQARLPPTLQHKTILGC

>contig50050 Frame-2F|Blast-PREDICTED: LReO\_3-like [Danio rerio](ref|XP\_002662897.1|) 2e-06 NOT\_ORF

MASSVIFVTKPNGSARLLVDYSLLNR\*LRRSPYFVPRISEILLRLAKVRYDDTGCQHGIL

RMTCGEAKSTADRLLL

>contig50344 Frame-1F

MGARGQVGPASSQLLPDEGKMAKYYVVHAASYMNLAHSVHYKRWAVPSTVLQQFKMALEG

SYDVFLVFTIRSSKQYQGLARVLTEACSTINPSLGTDLSINSVPYEVDGKCEWTGAFPIE

WLHSCECPWERLAQCENKQLAVMECENGHEMDAETGHAMVRLLLNQPETVLDYQSVEDEA

TLSGGSEALALRRREAAEASHNASKGPELNNLGPSIWKASKPGFVFTCTTQTIDECFGRM

LFGLAIEFEGLAQQHVTPGTPLFLLNLSDHHLLGIFEAISPAIVNLLPGAFCRGPSMSSP

FPVQTRFVIMLNAPALPISDPQIQQVIGDNGINVGPLSV

>contig51163 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57727.1|) 2e-90

MAVRGNYRASLQFPNAHSDGIWSTFWTSNNKILTGSVDEVAKSWDVTNDAVSISHQYPGH

VLGTISIVGNKGGTHAVTSSLDCQIRVLNLISGAVEKTIDAGPGELWQVAYSPDETKLVS

GSQQGKINFFDIKAEKIVQEISTQAKFVLSVAYSPDGSHVACGGFDGFVGVYDVETGSLV

HKYDDR

>contig51361 Frame-2R

MTSMPRPRDVFTSPSVLIQHNQHDNPNPLSRPH

>contig51479 Frame-1F

MQALGKYLGTDEAEDAIAGQQASSRQSCAATRPDLLERRAASVLHGVKASRQTLSSGQRL

TLKKAGTKRSSKIRSRRVESIRVAKALAAMNVDGLLSSSRSSKSKTSPLNAASVRSIGTT

RSQRCDDSSPLRMGCSGCRNLRRRCTGCSGCCLHCVCVRCGCRMCCSSRLAAVQKTMAQM

LDLIESKEGCVSEGIGTEYCGMVVYCQ

>contig51804-1 Frame-0R1

MLVLVCVPREQLHIVGTFGSCLSSIRQPARTKSHSPL

>contig51804-2 Frame-2R2

MSNVCCDACARLRSTRTASHSRHVRILSLEYSSARKNEIALPVT

>contig51893 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68017.1|) 2e-19

MKALLLLADNYEYRAKMARARNSSPKGTEEIINETQDRQSEDKRGRSSEQNKNLEVARLD

TLDTEKAETQLNVAAAEMEELWRRLNEIGL

>contig52346 Frame-0R

MYPHTVACRNDLYRTVLHQVALCTKECTDVRSSLDTC

>contig54205 Frame-2F|Blast-choline/Carnitine O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY67951.1|) 5e-21

MAEAHQAIGVFDEHKRGVELLYSEEGIRVSFTIPPLHEIRRSVVREFFHLQRAIK

>contig55026 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59932.1|) 9e-32

MQFRIARTENEINLLCLAKKTGSHVPSTTTAHRQLELNHGALECIKMTEEDWRRRKSGES

GRCFLRQLSSEIQHLLNSLLALGDHLRAATDELRWRLKEETVGVWV

>contig57073 Frame-0F

MQAQLSKDRGNLEGAFPFTNKWLNMEGRAYCLRNDIAKTEVDLLRQADGKALKRLLRACI

WTLVIKHIDGLAERVWPETFALDIARIRACRDTIDRIAIVSSLVAVVQDVGAFHGFKMKF

LNVLGRKLNVLLCSNGVSKAQVVAQVVTDLQQFRNEKLTKEWQNLEKRLLGSFAVDDVVR

QLFFARVARAIESALLPVFEKRA

>contig57396 Frame-0F

MSLIGSNFVPWIPPFYPPMYSASQFFALGVSMAICIAAVLYADYFAQLLPKHEATLSIPE

QHQMLASLAFHASKSGNAAASGVDSHDPPRVAFCCSADLDVAVPAVELMQSVQDLERQQL

QPSSELAEELTKNHHERIGSLKQLQESFAYYFSSGAAAEQSTVSPEQFREIVTLADAL

>contig57895 Frame-2F

MSWYVNLNTPLQLALSWITLASRRHSS

>contig59318 Frame-2R|Blast-glucose regulated protein /BiP [Phytophthora cinnamomi](emb|CAA53369.1|) 9e-24

MNLSKVILIAAAALATAVVAEDSKGPRGPVIGIDLGTTYSCVGIYKDQKVEIIANDQGNR

IT

>contig06962 Frame-1R

MGQDLCNRSYRQVVNHTDLCRVLFPIHVHCKMLVIRYHTQPRTQCQYS

>contig08645 Frame-2F

MTVNLLRVVTSNWSGRIWQVFILPQHFHYRIVSTVILSQFEQFQHFYLNRNEQPRTTRQT

CRL

>contig10899 Frame-1F

MANLSSGINSVGNGGHECWYWDTE

>contig13814 Frame-0F

MSKNWQITKPVELSAPLCLTFELYSMSEVLRTGVLFKKGSGTGPFGRKNWKPRYFVLTPA

RLQYFTFEDGELKGELSLQGCDEGVLEVMPADSMKTGSSASTIWRVAINAPERRLLVAAS

TEMEMNDWVDKLVMAFRMNSGQPSSYRSSMPAPSSTYGTMPGTNMKYSNPKVRDFQNFSV

PRRTNQRHSTGAADMRPTFQEQEFLLAQLESMETHQSEEKRRVEVEQEQEAQLRRQDILD

AEMRDDLVLEQQREQEEAALAAADALQRLEEQQKQEQLKLQKENERQQVIELQRVRRLEE

VARLQHEKEQEKIQSRQLADEVLQKATLKNQQGEDALERQRREKREQHARQRAQHEKALQ

LQKEQEDLVFRMSQQLQTDLSEENTEQFLPEPQASTLRSSVIGNVKRELIQKQKQEHQRR

REAALQQKQRNQEVKPRRHQVEGAKVEMTPFEMEVAPREIEVVRRAPIKKPVSPTAVPMG

SVEF

>contig14521 Frame-1R|Blast-2-oxoglutarate dehydrogenase E1 component, putative [Phytophthora infestans T30-4](gb|EEY65322.1|) 0.0

MIDRGTELGMEHLVIGMPHRGRLNVLSNVIRKPIQQIFKEFQGTHIDVESYNERDVEDWS

NAGDVKYHLGTSYDRTYPDGRQVHLSLVANPSHLEAVDPVVVGKVRAKQFYLGNNADAEK

KVMPLLLHGDAAFSGQGVVYETMHLSGLDNYHTGGTVHVVVNNQIGFTTDPKNSRSSQYC

TDLGKAMDVPILHVNGDDPVSVVKVFEFAAEWRQKWRSDVIINLTCYRRFGHNEVDNPFF

TQPLMYKRIGQMQSVLDKYLEDLVRAGTATKDECDAIVSKVWAFFQRTFDETEKWEDVKQ

SDWLANRWESFKSPNQQSRIRPTGVHMNVLKHVGEKISTVTPGFQVNRQLDRIMTAKQNA

IKTGEGIDWGTAEALAWGTLLLEGNHVRISGQDVERGTFSHRHAVLHEQETNDVYVPLNH

LATKTLPSAPLEYKTPGDDAVPDTQAEFVASNSSLSEFGVLGFELGYSLENPNALVMWEA

QFGDFANGAQIMIDQFLSAGEDKWMRQSGLVMLLPHGYEGQGAEHSSCRIERYLQNTDDD

PNVVPLMDEENRMQIQHTNWQVVYCSTPAQYFHVLRRQIHRDFRKPLISVQPKHLLRLRQ

ASSKLDDMVTGTQFQRLIPEVLSNELVEEDEMKRVVFCSGKIYYELMQARQEKGIQHVAI

VRVEQIAPFPFDKVAEQAARYPNADIKWVQEEPLNMGFWTYVSPRIETALTQLNSDSRRP

AYIGRAPAAAPATGYNAVHQIEQDRIIKKALDV

>contig15812-0 Frame-2F0

MNLLLGAIGACSVLFVSNGQFLRPDDGALSRPFAASNATGFVPASVDKSATSPRQSDSTV

AEE

>contig15812-2 Frame-1R2

MAPRSRFMRAFRVSACLTAIVNV

>contig16758 Frame-2F

MFKGRHCRQELSHFLLSLSNLPRSAYSPTNHDELFHSYCHGPRRCGGN

>contig17524 Frame-1F|Blast-aspartyl protease family A01B, putative [Phytophthora infestans T30-4](gb|EEY59472.1|) 1e-07

MALIAIVSYGLFSYFARCSECMTTSSLASIQGISASQYTNFQLFKQFNQTRLFSRDKTNE

THAKSHTILVSISKQPTERNFDKKSRKTTFHCGKGHKCGNKQKYLAFAFSDNTTSTSGNS

SMIVPFDKDNAPRVDCLTGK

>contig20243 Frame-0F

MFKTTQMMHRTKYQIKEVATSRHIDFRYHSPSFQHLHSAHFP

>contig20452 Frame-1F

MPVHGLGASNNGSMVAESTVIPNLASYVAVNPDLPLRNVNLRRLVPLAVDRAIREVISPV

VERSVTIACITTREVILKDFATECDDTKMRKAAHLMVASMSGSLALITAKEPLRNAIGIH

LRALLPVAAGDAQQLEHVIQVCSNENTDLGCMLIEKASSEKAMRDIDEALANAYASRRRF

QQQQTQSEKNSDRIHFFESSASSSVGAPCDQWPAALPEIFRLKSGGVPPLLFVVYETFQR

IPRPTSMPLSTRPNSGAYSVNSADKVGDVAGVSVAAALDRFAGLLERFELYVQKVVRQAS

TTQRELPSLLTTSAESEVFAVLREVRALGGSVRPAMRDEVCLKIANRIVKFMYELGNGSR

GNELFLEILVSSLEALTCCCDKLRKEIVGWVVRAPVDDKLKLHCGIIVALIRFKVVDARD

FDIYLARNMERNSIAIEFAAHVVRQCVTMDHVSVAAQLSNTIEALARIVERHGVATTNKN

VQILAALLEQARVQKVQNCLAPPAPSKNMGAIGSGSAAKTASERPLVQEHAAFRHTVSNA

LEHWIAIYNDPIGNSKMHAQYLQMLKQYGLLADDESVSLFFKFGTELCVDACLKSSVSAS

VTLKAGVKVSLNYAVLDALTHLMALLVKYLDPLPASKLQVLNHAVGAIANVLVATHDLSR

KKKAPFDQRVFFRMFVNLMKELTAREPTLDSIHLPVLNTFASALNTLQPAGLPGFVFAWT

ELISHRCFMPLLLRAKQQRGWQILHRLLMNLLTFMEPFLRCANLAAPLPDSITALYNGVL

RIILVLLHDYPDFLSDFYTSFCDVLPAACVQLRNVILSAFSRSIRVPDPLTQGLQVSQLP

EVSVAPRLMPTWGAALTHNGIKDYVDEFLHATANRASVFPADLISKLMRPASLSERDLMA

CKYALPALNALILHLGKEGIANMTDGGLMPTSALPPLTRADSANSPTSKFEQTAAMDLFR

YLADELDAEGRYWYFSALANHLRYPNSHTHYFSCVILYLFSYSSNKLVKEQITRVLIERL

IANRPHPWGLLVTFIELIRNKSYKFWEQEYLVCSNEIKEVFDDVARTCLATASGASGASP

LSALGGNAASSSASL

>contig24687 Frame-1F|Blast-Rab2 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY60239.1|) 3e-81

MVFVTLKYIIIGDSEVGKSSLLLRFTEQHFQPVHDLTIGVEFGAKLLEVDDRKVKLEIWD

TAGQETFLSITRSYYRGADGALLVYDVGRRESFEHLGRWLQECHQNCHNDDVEIMVVGMK

CDVSDEERQVTEEEGRNWAKAHDLYFIEASAKTARNVE

>contig26014 Frame-2F|Blast-S-phase kinase-associated protein 1A [Phytophthora infestans T30-4](gb|EEY61016.1|) 1e-91

MSDAAAPALDTPKQEEDSRKVNLVSMDGDSFEVSRSVASMSELVKTLLSDDADDEEVQEI

PLPNVKSPILSKVIEFCSHHNNNPMREIEKPLKSADMHDVVSEWDANFVNIEQEILFELI

LAANYMDIKSLLDLACAKVASMIKGKTPHEIRETFNIVNDFTPEEEAQIREENKWCEEA

>contig30615 Frame-1F

MKIISIAAILSLAVGSVGAIFGGGVVERDTYTFMGSLRETEAGKTKCSA

>contig30761 Frame-1F|Blast-DNA polymerase lambda-like protein [Phytophthora infestans T30-4](gb|EEY65984.1|) 1e-105

MMEFLDVERDVWRQYMYKKVVSSLKAMRHRVCSVKDFKDMHWVKGRLRDKVIEILETGRL

AKLDAKKSNPRLGALVKIARIWGVGPVTAAKLYGQGFKSVADLRKPGAAAGLTTQQQIGV

KHYEDFLTKIPRDEVHEIEQIVVNEVHKMIPNAIALACGSYRRGKLSSGDCDVLITDLDA

DACTILQELLQRLHASGFLTDDLTHFQKQKSGGCDTYMGVCRVS

>contig32635 Frame-0F

MDLITTSLNMAPIRNSFEVGIADKEASMRKMRQWRSNSWDADGQEPVANEGGLNHMVLTV

QDRDSNVDTGKSTEVRIALVLQQQRSVGDAAKQGGVVLDIPLIIAAFEARQKRLTQSRKL

HLSPPLENHLKVDQNEQAKLSELDKFEEFDVSLIRSGLVGRKNHLPILSIRGCTPAEYSS

LENTRYLIDAGQHTVRNGGEVEWEITIESIYSAVDLAIIESVEYRLMLVDKNARSWLQLS

RERGTLDRAHSYQSVVLYFLRGVVGVYSTFLVLQNLVNPSDLKVIHVRLEVIADLNSLRG

MSSGLDPGKNLFRVLVSNHSSPKRSRRSSIVIFPEKSVAGASRLNIDIGEVYYHKVYQNH

SIMIENSSGLSLDFILSTNAKPQEVSFSASPMSLNEINTVTLGSHAS

>contig32819 Frame-0F

MRVPTYLSLRRLRTQAAHKKTLNFILRAFGDSADPAKRSLTGTLVPLADLEFAMPHINGT

TNGLHDDTDNKLQFDKQKRLINNYEAPKLQDVEFTAQRIGFPISEAELKERTEFVDDDSI

REESRAEATAKAERIMAVLRHSMSELEIGKVIHRIAQYATLPRVTGLSRKQFLRSLDSRF

GENNTKEYFYMLAFLQGKDDIIDQLEIDSRIGSVTSEDKNKIVSMESEVIQFINDEFVVP

QIMGLHPDMVADPKFVSIVFCYCRLACLNSLKLMQRPAAGFNRGSKSSLWQVKADFRKVL

DIEGYSHYADMLGLDKLSGKEENEDTDAVDAEWEEFNLENDRIDFRMLLSQTQGIVDIMK

SELSNETISKMLVAMLASVKTSKLHRKIFQEMVCNIQTAFPDVYH

>contig33078 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64106.1|) 1e-101

MMNLFKHGETKATEDHAKRGDHVYSTADDVDFEAYGKESVQVLLNRHTGADKVTTWELVD

DTNEVKVWRGAVKDCDWAPFRAARRIHANKRLITQVLLDPNRLLELDEMMEKIETLRDIE

KSGHLAFRQITSKGQFPIHGREFVVVTYATTLEDGRVIIATRSLNVANVTPLDGYVRAHN

FISGYIIEEQKNDDDSVYCDVTLLAHADLAGYIPPSIINMLGTSSTIKVLANLATIVTAK

>contig34318 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57255.1|) 2e-41

MTKVQPSDARDMPLEERLHEKKTGFSVLNKTATDSRSSLHRTNKNQPLELSSKRAVGRFR

QVVKIKKRRVLDPRFEAQSGRLNEDLFNKSYGFLDEYKQRELKELKQQLQKCNSATEKDE

LK

>contig34448 Frame-2R|Blast-ribosomal protein L18 [Phytophthora infestans]gb|EEY64878.1| 60S ribosomal protein L18a [Phytophthora infestans T30-4](gb|AAY43426.1|) 4e-29

MPIRQFQVVGRKAPTEKEPNPPAYRMKLFAPNPVLAQSRFWYFLHQVKKMKKTTGEILDI

NE

>contig34970 Frame-0R

MYRNCVVSIISDFFNLEASSFLENRSRTRWMHIKARINIDL

>contig35281 Frame-0R

MSEEKVHWQNYVDVVSSLKKPATALYFDYAVTDFDDTAAYISFLEVLEDVDLETQIKDII

NAGHFWGKHSIGKEWGLSKIVNYLDVQHVLYNNNPAKIIQSFTFPCTKIHLILRTFQ

>contig35573 Frame-2R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY56172.1|) 3e-17

MLYINKYGLREHYRGLSAILCRNGPGNMLFFGL

>contig35649 Frame-2R

MYMWYFPKVGTRQRVVGKRHNFEYVVIFLNNPAVSNPEILGCSASNIAKRAPCPASCLDG

KSLKVVSKEISGLYNVNITSEKDDSQKPSIPLVMWETLSPMARKGLSSYNFDEDVPIIDK

HFYSKIRQSW

>contig35951 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56246.1|) 2e-52

MKQLRDESHHLSTVEIVHRFLQKSGKLEAVLCPSSVAQEHESSCLADFLRELEMAQSIVK

SEQLTFVVPYLQHLRETALTSSTSREDTLEHNQMNNEMGRGCIRVLPLTKHALESAMASK

GEEEDSHHVLIFMSMRDSKFPGRMKRLTLPLPYELLRKPFPVQTRSHYLEQCERLVYEAS

NAS

>contig36969 Frame-1R

MDTVQQNAQAKHYELVEQHEEKDKGVYTRQIDSKKEAMEPQAAKGQYEKQRSARRHQTQA

YCENRQQGRCSQRRHANDGAKGEQNVDYKRTKEVEDMKQDQWARKQQKKVAAERGRRALE

SLMSKQQGQKALEWLVLMDKIERRAHGYERVGDMNGGFDLREMGDKKDVERRVEQTFARV

FGLEGDSVELSVFSIDTEENQSIGQGCTDRELWEGETSVADCKGFCQGGTNARDDSKEVH

SDATIKGEQFDSTLKTTRLRKDLQRDQLDKKAGQKLKKRVLTQGLPNSFDSKDERETGEG

CLPGNCGHLSCQRQKFGTIKANYNLPGNRDRRGYLDEYLEGTDRENDDCYDASERHHGDE

EYIQHLE

>contig37566 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66993.1|) 1e-103

MRLKIGKEAILGEQREKQQIKDQMREMLQRNANEQEIAQFLNMYKVTYSDYGPNRREKLH

FHLSRIRELLLPTQVTKLSLYSVEQGVDMLRRDHTIKDDLMSAPGCDLSTTSLWGILASD

LDLTAEQQRQILKHRVAIKKVRDDLNHTLSIVKKLEEVTNEKNTALEAQVAELQQILTPS

QATKFIIWVKENPAVMYMLDKLVDSTLQKNTCCR

>contig37841 Frame-1F

MPKDSAGVHKSHGHDRCLPVLVGSRSTDFREVSKPPSRSLPCFVRIGSRSRVSSKLTKQL

NIAKQGTYRIRANDMFIHFARDFQHANFIQIVKLYVHASSK

>contig38260 Frame-0F

MSAMVEATNELVLSAETHDTEDVPAQSHSGGMIAPSQLKIEHAEKRSSRLEEGIDSIESK

RAIETVGRTEDSRRVRVVYDPSPRVRKVSMEEIMCLEDFKVPKARVGDLEHFYSDDESNG

GLSDTDVVLVSENRLIKPRVQGDYHKQRFQHSDSSESDGNEVAAKQRLRKQH

>contig38578 Frame-2F

MLAALRSIHKPVVSGLRSFSVPAFSPDLKAQINKP

>contig38596 Frame-2R

MMVRRVEELQDWICSVTAASNDHGEHLSDMLRDGQLLCQLANRIEPAAALKVNKLNTVFH

SKANIRLFVDWCQKKGLKEGEIFQPDDLLDSDANFNSVLETLSILFDRFGTIGYTGEFEE

DPASDVESMTSTGSSLDSSPVKKVNSNNNKISNFMKGGFLSRKKKKVVDELSDHTPPSTP

PPASPQVGGGMLSPNTGSNQSTNANRLNAFLSQVPASHGSPSSNEPRAKKLPTSKPPSVR

RPPSPKQQPRSQPTTSDTRNKLTAFIKTNPSAVESPIRSNNQSAPTKAPPAVRAMDKSNL

SAPLSKPGGNRLNNIMNQQTSASPESSKPRSQSKLAAFLATTSPTPSASSTPHQPFATRN

LSKKPLVAKPAPKVHTSPVPHKPRHVIERSSGHCNFVRKRQTYWVPLKRRRNIFSLEKKR

NAFMQEQLTIKEEQLRQQAAGASNKQNLIVPGVQCYI

>contig39238 Frame-2R|Blast-1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase, putative [Phytophthora infestans T30-4](gb|EEY63008.1|) 1e-127

MRFRPCIDIHAGEVKQIVGSTLMDNGIEGPVTNFVATQKAGEFARMYKNDGLVGGHVIML

GVSEANTNAALDALQNYPGGLQVGGGINADNCRFFVDHGASHVIVTSYVFRDGQIDYERL

EKLVQLIGKNHLVLDLSCRKKASDNNFYVMTDRWQKFTSTAIDEALFHRLSKYCDEFLVH

AVDVEGKRCGIQQELVKLLAKWSPLRVTYAGGASSLDDLEIVKDIGNGKVDLSIGSALDI

FGGNVRYEDVVMWDKKLAGNDKSTLSSP

>contig40281 Frame-1F

MYNGIGLRTVRGSGTNGYVQRNLSFIDASRARQTLARNKGGDVSGVFGSRGGGGNNLAPN

PKILLHERKRKVELHLMELSLAMEARGCESEEIHSKIERERGRLLSRLDEVKVDEILDND

SSRAGQRRNEEKDTKIKEAFGIAADYEAGESFDAAIKERRRQGRQEKRDRELKGRAKAPL

QSVLFEKMLPARADRFSSHCRSRSRSRNSSCRNLSSRGHNSRDRVNIKASHESKTRSHYR

EKARHMRSSLSAEMRQRRSKSCSASDFSSSRSSSASSNSNFHSHSVGIRNDCRSGKGTSA

KMQVSRRSSVLSPGSSKLSPSSHACPKAGGYRDTQSNIIKEKVKEGKPPICQSSVRSAVN

EGEQNENISTIGSVTNSDPDKKEELGALSLSTSTIDETKLGMMTEICRDKNEPIPTPRVQ

EQEDLPAAQAVRKKIRENRESREPSATDKLAKSRKRKPRSAHYESCESVASTDSRVPRHQ

KLRSRRSHLILTKRSRSKDSASSRFSLYSRSRSRSRSRSRSRSYYKSSRSLRRRRSLSRR

RHFNDDRSCSR

>contig40649 Frame-2F

MEVLGQLLDGSLAAATDVRAQSEVRLTELLRTRGFALQLSEFLFSIEATEPQRQLSALLL

KKLITSYWAPTDDHTYVVAEEEKLQVKHTLVLALQPQVLALFTGRKLQTALCLLLTAIFE

RDWPDQWPEIMPMILSMIAHQHTLQMDVAVRFLSLSDGHFSSDNCLELVTSVFPHLYRAF

QSPTDLSSATKCRIARIVQSLLLMVSMEANVENLKARHVLQEYTTQWFALFFNQLAHPVN

NYAMKIQVLTIFTSFVREWPVEMTEVLPQLLSHVQNLLLQEASTYEQRVVLSPSCEEEDY

DSDYDGALMNQSALIITALDLMRGVLHAPTKTTRHVLVTQLSAFVYTMIGYMQISVSQMK

AWLDNPNQYVADEDDASLALNVRNVATDLLSELETVLGRKAVIAALNAAQRRLKTDDLMH

WRLQEAALLVVGSLASSTLKIMETNATDMNRVLDISAFLQTLFQVMNAESQEIYLRARAL

WCASRFVTVMHPEMLDAFFKIAISGLAQEQMVPVRLYACRAIGAILRTNTGQTRVMEASQ

VVLDRLVTLAEHSTHETLHIALETIVIVLQEATNLPFEPTQRVLTCFLHHWRSQLNDPLI

SELIDSA

>contig40951 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65080.1|) 1e-106

MLPIRGIIYGDADSLLRLLRRLPPNMPTRVTVEAELSKTTVESAAARVSWEKPVDNQVPI

VCYTVRWTRTKIEEVKWLKLLTLPLPTTVIVDKLHHGETYKFVVQATNQFGFVTCSSRST

YMVPVPELKGKLRPRHRPAETRALRSQCHVCHDPRYKKKVPFTATLDRRILHYCCVCDRE

>contig41000 Frame-2R

MDRNDVQNLVCGGIAGCMSRTAVAPLERLKILLQVQDYIKKGGPETGASPAKYRTMWQSL

RQIHMEEGVHGYFKGNGANCIRVFPYVAIQFATFEKIKVLISDNTNPLSSLQKLIGGAVA

GVVSVCVTYPLDAARARLTVQGGLAETRHTGLFNVLSTVLRVEGLRGMYRGVLPTIWGIA

PYAGLNFTVYDTLRTSVPRDAKNEPDAMYLLACGALAGTCGQTAAYPLDV

>contig41277 Frame-2R

MMLARMCIKAGHGVFLFAKFRHLYGRYLDWPLFPDSLVQPCNKFESLQ

>contig42287 Frame-2F

MAVLTTQTSDELEYAEPVKTITDENQLFDEPQVAHTDEDALLRTTRDSSATAISSDGEAL

TEEERDRIRETRERVLHEAASCATPSSAQHFRRATTVDVPVLPRRRAESDDLSSPEANVP

VSRLRLMRSKSWSGGNQRDAALEAIANQQVRFRFATAASAREVVREMYSYR

>contig42513 Frame-0R

MAFFFTSAGLSLRHGVSDLSHYVLLSVLEDHLNPSAKLYSQSLLCPQNSRIKTAWTR

>contig42841 Frame-0R|Blast-exopolysaccharide phosphotransferase, putative [Phytophthora infestans T30-4](gb|EEY53591.1|) 1e-31

MPLPIKDDAATQWAPSLTVTRFRSENELAFAGMTPSFGWTLASKIGYALGLAIATVTSVY

IFRFTSEGIYGMHLSKQT

>contig42975 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54483.1|) 1e-55

MSNAAIDPEQFYLVRGAQNIKTDEVDYRNLMVHYKLEPQLIKLAEATLPSTYHHLLRGVG

DARDSLTPGECKSDLLSLLDGVPFDRPIEPLPESVVKSALQLPAGSKSGPVMHPLSSRRA

QGLIHAPPFTGT

>contig44689 Frame-0R

MAVASKSVLLHLDDLVHSNSYLEWAPIIVSNCLHGMDKRAAPCVKEAHKTNLVEAQELMY

PPFRLKLPSFSNLLMKAEWVSRCLHYDDTHITKNEEWAEYPSFTGQNMVFLNAPYQGEPR

PDVWSPYACMGQNVSYASFLRNMTSNVTNTANKTSVETLVVATSPDSWSFQHFLDRVAVV

WSQAQLVIPTIEKNDTIIVTGSEPRDKIVNDIYTLMVGQHLHDSKLVFAKRLVFSCRAPL

IHPFTTQRITETIFQALPPTSGASDRNVILFLSRSIGGVMRNGGRQILNEFEVYDAISAE

LNATDRPERLQYFHLDKFDGLDDIASFIRDNVKMMIGPHGAAFYNSRFALPRTALIEIIP

DPKLFFRQCFWEQARL

>contig45031 Frame-0F

MDKPLFVASNPFPCMADLVEADAVGSFDPNATGKAEQLRQDGNEAFRRREFLKAKDLYTE

AILLQSGHSVLYGNRSAANH

>contig45329 Frame-0R

MQWVQIYQPKSSSIRSRSKLHFRNRSSRFFNHSQAEDDIDDTVLVTADEQGFLTLWWMGR

VLLTRIDTQKLVEKIENQQDDTIGFRIEQVHLAPDMSALLVLLTFPSKSRQHVDFTKPDH

LDTKLQRLLTLDLTAIQYMHEDVALVVTIFDRTHIIVNQITSFGRQMAAEWKNAMRPFEL

KMGLIGSLYEKYACEDLPQVDMLSVAVTGITAPALAQYFAQDIQATSVYRMQKALFSGCE

VLKRLVGEKLKRELVNFLFLVSELRGHIKWKPQTYSTRMGISADALDDLVAITQDALVAT

EKLTLAIYETRQDFALFFQWLLERIRVHTNSPVSGKVAGASSRDSGHAANSSQSLLNLRR

LCEFLKCAAKCATNVRHEQSKTSVYTVDNDFWK

>contig45615 Frame-1F

MPVDVLGFFNAGSASNPTRRCVGIEHILLEATIKSYRRFYSNACSCRMPVVFFEQVDVAH

DNRLSL

>contig45682 Frame-0R|Blast-50S ribosomal protein L3-2 [Phytophthora infestans T30-4](gb|EEY59241.1|) 1e-131

MMPVWDHFGYRHNCSVLQVEACQVTQVKTADRHGFNALQLGVGLRKPNNVSKPVLGHLAK

AGAPAKRQLQEFRVSEDALLPLGMTLSALHFTAGQYVDVCGISKGKGFQGVMKLHNFAGQ

PASHGNSKTQRHMGSTGQCQDPGKVFKGKKMPGRMGGKRVTRDNLWIAKIDVDRNLLYVK

GSVPGNNGGIVRVTDARKKIAETPLPYPTFMAVDDEALPSEVLAPHGDVDPYYFDEK

>contig46232 Frame-0R

MERDSIDHATLLPYTNMQQTSLTNR

>contig47006 Frame-0F|Blast-pre-mRNA-splicing factor ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY62021.1|) 1e-155

MATSRRSVIQNDTELHEEDEFLFDDQIEFISQQMLAGRHVSEKEVQEARTKMERAKHMSL

QEGRKQLPVYPYRESLLEAIRNYPILIIEGETGSGKTTQIPQYLHEVGYSEIGMIGCTQP

RRVAAMSVAARVAQEMNVKLGNEVGYSIRFEDCTSEKTVIKYMTDGMLLREFLTEPDLKS

YSVMIIDEAHERTLSTDILFGLIKDIARFRDDIKIIVASATLDAAKFSAYFDDAPIFKIP

GRMFPVDILYTKAPEADYLDAAIVTVLQIHIT

>contig47073 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68162.1|) 1e-104

MVVCHVKRGVSIEFLFETSVETNNDSLIRSLCHVHNLRLRLAALADALNDLASHGMANLP

QDQRLNTCQEGVSNKRRENVFQNDPLGYPTGKHISSQLKYMLVRVAADAKMILDSKAQIA

RRICIQESELIEKLENIRKAVATAFPMGLSVHDPIKIMLDADNSKQVLAYSSAVSEVMSE

DTAELWWAGKQFFRDQHVRDLTGTNEKTMLVVKLQKRGGGGPGQELGVREEESKAMMAFC

SKKQQEQQQAAEDDATDYMMSSWADPKALKNALRANGNIRPF

>contig47349 Frame-0F

MKISIVNDTTISCTLRDHSAKDRQERSGIFKSNTEGNSDGYQTNLTTAAASGGVPCIRLE

VFGVSEAGEEVTHELCRLLERKLDEGTQVVLMKLLARNIKFQLSLKDLAFLCPPAAEPSS

VVDYILPFDEAGCFTLLHYLSQTLRLTPYIRPVTIGESFSSRNLRDSTNTALRGAHRENF

VATSNFNNSFNEEASTPLSQFSNGKASFDSDGKINDIKDCVRMHPACFGGYQNKLWKSQN

IRLPLFDASTHSPVFFSLRMHEMIIESTAGSSFVSPEILAQA

>contig47781 Frame-0R|Blast-imidazoleglycerol-phosphate dehydratase [Phytophthora infestans T30-4](gb|EEY58663.1|) 3e-82

MLTALAKHSRFDMELECKGDTWIDDHHTTEDCALTLGEAFDVALGDRAGINRFGSTCVPL

DEALSRAIVDISSRPHSEINLHLIRPSVGDLSCEMITHFFESFASAARITLHVDVLRGRN

DHHRAEASFKALAIALRTAVQRDGTAGVPSTKGVLA

>contig48472 Frame-0F

MNVSPYDSEAPSAENLEAYLDQQHHSGPVKLFVGQVPRTMEEEDLRPVLEVFGPLEDLVI

IRDKITGAHRGCAFASYFTRAAAEKAVQELHNKVTLPQSINPLQVRPAEGQAGASQEHKL

FIGMIPKTADENAIREVFELFGTIDEVYILRHPATGQSKGC

>contig48656 Frame-0F

MPQEGKYASFSSSLIATVRINALATTLQLRFSHVDVDYKNADSNVLVSRARPNRRQCHSC

FCARNLPAIALVMQNSPDFTYWGN

>contig48797 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68251.1|) 7e-24

MQREAESISTTTAAKKTKVSRERQLKINAASRRCRKRQKLELQFLRTHVLELHAALKDQI

NYLQSQLSQQQRAARLSHFVDDSMRKVEEVSSGSRPSPAVAPSAPLVSFSSDLLPFKMYE

NSGEETDGMLSNDSVNHIETDDASSVHTIDPATGYSLSEK

>contig49079 Frame-1F

MTLVPEEQQDATVQGRVTGIIYPPPDIRAVVDKTAQFVASNGRAFENRIVGERMSAKFSF

LRESDPYHIYYEHKVSELIAKKDEVSSLVESQQQEKTQNIVKAAETSGDVVVEKKAVQDV

TAQVAKKIKEKKLEPPREEKYIIKHPTLSALDQEIMYLTAQYTALSGSSFLSGLATREQR

NPQFDFLKPTHPLFAYFTALVENYTLVMSKQEAEIKWIEDGMERMKVLDRCVHRIEWQRS

IQERKDKEVAESDAERRALAQIDWHDFVVVETINFENDDDLNASATFNTDEGKGSDDDMD

MDEDEEDEPKPQIKVVEDHVPQVTAATTQQPLLSVDGKTISSAEANEHMRILLMNPKWRE

ETQRHLEKQKESSYA

>contig49325 Frame-2F

MFAAGKATATQGVDADSKDDACDWLSVGKSFAQGKMDDMFTVKHNFTDSSASTMQVYRHQ

HDKHGSIRKKRCKRQNRPSDDSTTVSSHGSYLLAKHKKKRKDKKRDRSRYQMNSSDDGKL

GHCSSVLSARSSYLVQSRFDHHIDEERTERKPVKDNISCIEKADCSVATIFEFDRIGDRD

NQFFGSSYLYDQPLYVLASRRNSCNGVWISQAQLSYGRSDTTVKEKRVN

>contig49475 Frame-2F|Blast-methylenetetrahydrofolate reductase, putative [Phytophthora infestans T30-4](gb|EEY69178.1|) 5e-93

MKVIDKINASIDRHEIFYSFEFFPPKTPAGVDNLYARMDRMAALNPLFCDMTWGAGGSSA

QLTLELSANAQKLSGLEMLMHMTCTNMAEADIKKSLDQAKDAGIQNVLALRGDPARGATS

FDECDRGFSHAIDLVRCIRQNYGNYFCIGVAGYPEGHVESKNKKADIQCLKEKIDAGADF

VITQL

>contig49541 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60121.1|) 1e-83

MQGENRGSNCMEMAEASSPRSRISATQEIRQLRAQVKAMEDVLETLQFKWIEQLPDSRSL

QEAHHLARIKYRLIQTQNEHSELENAFVRQQLMYASLQTTILQAPLYSNSEELMMMLQFQ

TRLGRESKERQIKLLAHFNRSLATIPSSVNKITQTAIDKALGHRKEGDTKEPLTPLSQIN

ITGLVNSTLISSVFMLEIPNATLKEVYEAILVSYIEAIPALMQRHFGIHATRKMLDSADS

PAIYYRLDLHGNDITSSMNHVICSELTSSYGMVHVDSIIDDALHPVSRTNSLQYIVSGIT

ITPRIEAATGKTLSVRLQRVLVYHYNLLPGDSALMKDLAIIRPV

>contig50051 Frame-1F|Blast-exosome complex exonuclease RRP40, putative [Phytophthora infestans T30-4](gb|EEY58507.1|) 9e-64

MTGLAIYGELNDGCVFKTSINLAKSLLKENCSVLASLGKKLSFEVAVGVNGVVWVNANST

KNITIISNAIMNSETMPTNAIDAMVSRLVEDTDVA

>contig51360 Frame-1F

MVFVSGRIPCQHMYMCIDHDRIVTLWVKTNISACSKHEEITYRSILTDNDCLSKDLMDAL

HNEDDRCDRHERKLLQDFRVAHIVYVKPWQRYKLAKLSAFACLDSNVPMPSHGGHTSS

>contig51478 Frame-1F

MVLILHLRRVKCWSRVHRDDHPPYLFGGARDAKFANGLNPRRML

>contig51496 Frame-0R

MNKDTRPIINAAANFSTSRWTEAERVQNIRNIVHALKQHAQRTQGPVTRVLKAAGTQYQA

NWISNTIDVLDCPPHLVQEVTELLMVKEVIYDAILDTDFAESEIDLTNNQSAPVGWGPTR

INAPDVWAT

>contig51805 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56478.1|) 1e-123

MFRKRPDALLSRYASIGARCKYTSDSMQMRELVRKLDYDGYLCGLLLPVETRPSYFSIRA

LNAEVATIKDSTFSNLVMGRIRMQWWRERIFNLYDYSVKEGNSRPTQSTALLRGLDKAIH

EHNLTRRWFERLLDARDLDLNREEVLSMQELKTYAEQTASSLLYLTLECLGVRDETADCV

AEHAGVAIGLTTLLRGTPYHSLRKETYLPQALLDKHDLSIMDVLGASEKPSNGDKLAPVV

FEVACCAMDHLRQARSLRKNIPKEARSAFLPLISSSLYLKDLEAANFNVFAPELQQRNMF

QLHLQVLKHYFWR

>contig51892 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68017.1|) 7e-08

MGWKTEESEEYESSAPAVQAQFHACRHEQAFRRDD

>contig52347 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57619.1|) 2e-06

MAGFWRLNVAIVRTLQCHETSLRQNRAVAVLLTSKLRHFTSIRPKDALYEGQDFARQVEK

KF

>contig52417 Frame-2F

MDEVKSRTPSGNGFDMSIVLILTYQLQQFPWEGMDVMSLCSGVTRMPSLDLLLQNASTHA

SIRRSQVRYLVNPAGDLKSTQTQVGSILESGAATYGWNGIVGNVPDPDTLRDYLIDADLY

IYCGHGAGEAYLHRDKVLSLESNCSAALLFGCSSG

>contig52538 Frame-0F

MHDELPLASPTAISPITVCASRVTWAAISYKKNNFASTQSHSVSKLRVGICVPAEQLPRP

THQFFSPLGTVPIKKNDWYDESLKHIELSSAIECKIDWEMNTQLK

>contig52822 Frame-0R

MIQTIPRAHRLITDRGRLSSIYSNVVNFSTNNERLPRLSDLVLIRHGESEGNVARQRSLA

GDHSLFSGEFKHRHSSNWRLTDRGRRQAAAAGDWLKRNNLAHFDRYLVSEYLRAMETAGR

MGLPNARWYAEMLIRERDWGAMDLMSEQERFVKMQDELKRRELNRFYYAPPGGESLAAVA

QR

>contig53054 Frame-2R

MLKLVPMPLVVVTGANRSLEQELMSCHQIRNWYQVTLRTLT

>contig54554 Frame-1R

MYESSWQAKGWRAQLLQEIDVHMLRSVAAADRKQRASEALNEGQKRFKRPIEGIGPHVQD

TAEILQEINRLMHSIRASQDDLSSMIEAIILKAEQLPYPDRIDPTGCIGIPAFISTGTDM

LLRMRDIERYLLLVVAAVRRYKRVRILNC

>contig55027-0 Frame-2F0

METNARYALHDCEAAPPVWAARVRLTPELLQKLRQKPEHVALRLNVPVCDGASTTRGSNR

KTSV

>contig56075 Frame-2F

MMFWGRSNSSTTTSATEHDPSSRPSSSNAAIVANIAVPIAPSYVLSEQRRNELLLAARSN

RMSWVDNVDPQDPHSHRHCPLSTDQTTSILPSHCRAAFDNIQVEIATFWTQFDEFTHKLL

PNRLHHFHQAFTAPRTTLESNKPYQTLFYELQAQKHELEHWQQSPPPRKTFSSCDHEMLF

LSGFQQFLSILKNIQAAELVYRIQSFVKRAETWQLSIMLQARALQDRPGGRIQHFIHLLI

QQIQQCPTLRALFQGNNVLTVEDSEGINLLEEVVEAFVLEKLYGTILSPSLESIQEDTSF

YNRVKLLQFVTFQHLDVPVPITQEQERTWQGLIEQLQTMTRCPSPRRKMDRILCLCQDLT

VFLKHQNHGRFPSA

>contig57072 Frame-0R|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ32239.1|) 4e-19

MLAYFAVAENESMGRLRYNMLEKLLQPCGPPPQKEEE

>contig57397 Frame-1R

MRTPDEDLQTQQRRQTARVIAHLLIAQ

>contig57894 Frame-2R

MNCVRVYGNLQGQGSSNNLDERSLYEGISICVLAVVLTLNTNFHFEH

>contig07489 Frame-2R

MKFFFCSAIALAATASAEDTSKPLCIPSETEKGPYYFGNFNPDPPGYSCLSVTSNDSSAI

SWKVDFSFPGVLVDDRYWYDSYLSLNTHTVTMARLHSIPVVFNYISFVNQDLSAIAHITM

HVQPDNIYNLGSMVRLKLCQSGPDPSWLGQYQKEVQVGNVPYSLFQGNIGTMALFTFVPK

KCTTSFEGDMKGFLSPLELQSSYRLLTVRAGFMIRTGVDAVLSVDKQYMTYIAAVDPSP

>contig12883 Frame-0R

MLRRVIQRTRLHLPAPIGHDNGAGDASDGEDFPGSPSIAYTCLRDDASVHDYFRQRPENT

SDTRVIVAENSAKTRKRHVAELSLEEQKRAADAWARLQTIYGLFRELEASASGDTEFSDA

KTLDNINCGRRPAQQSLRRNICDDGLRSLLQQVQLRPGVIFRDLQTLSMADAREENAMPL

GFTASMFAALGNAMYNEMLVAAEQNRICPDAFEKLGEKLYAEATSVVVSTA

>contig13813 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60200.1|) 1e-14

MSEHSKALWAPVKWAQRKDALYVTVDLPDVKDEKVTLDGKNLTFK

>contig15815 Frame-2F

MPEEFRPLRSDFFEEEVLPYNVLHYVETYSLLSKEELGEWLLRFNADAVFEDIEMKFHTA

SINDEANEIALFEQNLTPQEYLDTFLLKSTVQSLKPKKLLRWLRYCNLWTRYSEKLEFTV

RQKAIRKKVLSVLQNVETSQPKQNLVESLRRIVDMQGFADMVIPEPLEINAVVTEALRKL

>contig16317 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53711.1|) 6e-38

MVRDLETMQKMHEAKSIRANIDESETRRLRGEVSELKRQNLEQQDKLIVLEHAQNEAMTQ

KSVLNTQVADLEAAMQREVINRTELLETLALTIKAAEEKEIELNKKINDLQLEVEKKTFR

VESELLDLTQQVRKTN

>contig16630 Frame-1F

MRFQNLQGAPVSTTARICYAALCSSAFLTSYQTLVKLVVCTARNSFHRDFAATSLVAG

>contig19297 Frame-1R

MRLSVFLAVGVALVSSRLDTTVQAADAQVKERRLNIVQAAQEAAEKGAASFQWGVNKVLR

KTDDTYGEAIATALAKKKELVDPTNLRAAGGPHVDDIAKNVDGVVPPVNVVNKEVDEVAK

NVDNVAKNDDVVKSLTKKEDEVIPNNKLDDVLNPTPKALPGTLEHVFESVKALANAKAVG

EMPNKFTDEALMKITKKLVKETYKNPSMGAKFKKVLLWLFGGTLVGLGFYGAHQLSQQVF

PSPPEKVTTKVHN

>contig19994 Frame-1F|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY70055.1|) 1e-123

MSIQVAPTRMALTTFKGKRVGAKKGFELLKKKADALKMRFQTMLRDIQKTKMAMSTEAAE

AFFSLTQAQYAAGDFRNKVIESVSTAEIRTQNRIDNVAGVKLPVFTEVEVSREKNENIGL

AGGGGKIQNCREKFRVLLRALIKLASLQTSFVTLDEALKVTNRRVNALDNVTIPRIEKTI

SYITRELDELEREDFVRIKKVQANKQDHEKAILASKRRSRVKSIERRGLGRRPFCGRCGI

GS

>contig20558 Frame-1F

MWSSSFTDSLAENVQLPGIVVCPHCSQGYGRASLSIHVRRCRTLLSPTAQEAAEHKRLSN

SMQNKPPPSLVDLCLRHITKHFDSICMDKIMAFPK

>contig23843 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64117.1|) 6e-18 NOT\_ORF

MMKEWNDAKIKTSAV\*MDFDTETERQRTSYYDKAKSVLGCSHY

>contig24279 Frame-2F

MNLGRVYSHPSSSWLSLFCLRSIGVLDRWLKLIYVTSSTFALVLFFVHKCLTKYPGQTR

>contig24680 Frame-0R

MHESAITGSQRSMTSVSNAYYSRVTV

>contig25038 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67964.1|) 2e-22

MSWCGASNRNCSVCLSCSSYLLILLALAELALAVMILI

>contig27083 Frame-0R|Blast-Holliday junction ATP-dependent DNA helicase ruvB [Phytophthora infestans T30-4](gb|EEY65914.1|) 0.0

MAGRALLLAGAPGTGKTALALGISQELGPKVPFCPMVGSEVYSSEVKKTEILMENFRRAI

GLRMKESKEVYEGEVTEMTPEETENPLGGYGKTISHVIVGLKTTKGSKQLRLDPSIYESL

QKERVSVGDIIYIEANNGSIKRVGRSDAYATEYDLEAEEYVPIPKGDVHKKKELIQDVTL

HDLDIANARPQGGQDIMSMMGQMMKPKKTEITEKLRTEINKVVNKYIDQGVAELVPGVLF

VDEVHMLDIECFTYLNRALESTLAPIVIFATNRGVCQIRGTDISSPHGIPLDLLDRMLII

RTMPYSVEEMVQIIKIRAEAENIKLQDDATVRLGEIGSETSLRYSVQLLTPSRILAETQG

RTEVAVDDIEETNGLFNDAKRSAHALAQTEGYLM

>contig27300 Frame-1R

MLTERVYGCVSNTECPTDSTNHSVPDNCEVTTYPPAPPVSNVTEEVPYQPMSNETATLPS

PDYTQETKTFPPSPGMATISPENNTKMNNTVPPMVVSPENATFPPYTQTNNTVPPMVVSP

ENATFPPYTQTNNTVPPMVVSPENATFPPYTQPSTEQPSEATPAYETTQPPTDAPEQQTE

GSAAYNTLEPYTEGSEQQSEDSSAYDATDLPTVVPVQQGETPAYGSTEPLTDPPVQQTEE

TLAYGPSEAPTNAAGQQTKTMITSQQPAMTNSSRRSLRTKQ

>contig27494 Frame-1R|Blast-mitogen-activated protein kinase organizer, putative [Phytophthora infestans T30-4](gb|EEY69177.1|) 6e-09

MSTCFSDFPANFFSVTRARNAYMPIQILDDFRDSVTSLVVTDHEIVAGLVGKIREAKQY

>contig29232 Frame-2F

MMCWSRAVVARTAWSSSIAAVPRKSIEVRGKIHLKPTIASFVVKSTAISPALPSAATIAC

RSKRGRGSRFRLGASVQLGRHQVDKVLRLKQRN

>contig29386 Frame-0F

MAMTSVWSAHVTKEGQTYYYNRCTKQSAWKKPAEFDAEEPRSTEAILFSSKKAEWEELWD

PKNERPYYYNHATRKTQWQRPKGVEIKPFVGFPDKRHHGSKTKKTEDAAMKYESGQTNTV

ETNTGHGNNTNQSQHEAT

>contig29401 Frame-0R|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY66090.1|) 2e-23

MASKGTSLWRMAGVSYLEYVNKSANVLRAALKDPVKSTVEARSNVEFAAFKWNNGDRGGR

VDVDSIKKIAEVFKHS

>contig29508 Frame-0F

MSAKFTSQMSTLLLTRRRASRVAFASNGPLCAVAGVYSQSVRWMGRGPTIQGKKNATDA

>contig29856 Frame-2F

MINIAWVSTAISWTLAILILIYSSIQTSHEVLQDYPKVLLMYCGAAMIEALAEPMYVLAH

ASVLVSWQVAAQSAAFLVRAAVQYIGVVVLEWSLTAYGVAELSYAVTLLIVFAFFFWRRI

KQSKRGMYPFALTSMGQLLPGVPEGGMEWYHPDLMTLFLPLSVQSGVKYLLAEGDKWVLT

SVASLQHMGVYGLVSNLGSLVPRILFLPVEEATKTIFSKFALDEHVNREKKLQNLADGQT

LLLVMLKMLNLVGLVFVCFGTSYAHTLALLLYGAEKVNEGVGAALAAYCVYIPFLGHGVC

EAVVHAIGKDYELIRLNKFLGVFFLVYALSAFFFMQVLDWGTLGLILANCVNMACRIIYC

LTFLASYFHLVSHRASIMGHGLWNGIAFWRQSLPHQVVLIALVASLVVTAISQRIFLSSE

TIKSISWVQHTLHVAVGTL

>contig30612 Frame-0F|Blast-ADP-ribosylation factor family [Phytophthora infestans T30-4](gb|EEY54603.1|) 6e-12

MGLSDIRNRQWSIKETTATQGSGLFEGFDW

>contig30685 Frame-1R

MRAPTEERICESLIDEQYMERPEMGSSHVRNELLSNTFKPVSALENHVVARNSFDTKEGF

HRR

>contig31743 Frame-2F|Blast-eukaryotic translation initiation factor 2 subunit alpha [Phytophthora infestans T30-4](gb|EEY54277.1|) 1e-174

MAETTPAVVTGEETSQAQEILHLQCRFYEQKFPEIDELVMVNVRSIAEMGAYVSLLEYNN

IEGMILLSELSRRRIRSINKLIRVGKNEVVMVLRVDKEKGYIDLSKRRVSPEDIAKCEER

YNKAKTVHGVLRQVAQENHLKIEELYAKVAWPLHKKFKIETISDDEKKIEYVHCYDVFKM

GITDDTVFEGMDISLEVLTALKAQIRRRLTPQPIKIRADIEVTCFTYEGIEAIRSALQAA

QDLGTEDVPVKVKLIAPPMYVMTTSTLDKQKGIQKLQEAIEAVREHITAKKGTMSVKMEP

KVVSVNEEREFLQMIEKLENESRMVDGDAPED

>contig34270 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65784.1|) 1e-167

MVDKQLLGLAFVQSLLWEYMCNAEHDDVMQMVANVRDASLALLATRNGARVVNKCLSFGA

AKDRKRVIKALKDKILEACNHPSGYLVIMRILDVVDDSILVQKSVLVEMKDELLSIALHP

SGRKILLQLLSPMNKKYLSADDLELLKPPMLPSSEDSTVLVVNYKKDPESRREELLMGLL

PKLEEMCADNAGDLMRSKEGRDVIVEVAKHSENSKLVRSIVAAVVAQPSEEQEEPLYSDA

NGHYALRRLIKESALVESLLIAVKEQLSKWATSNRGSFVVLAFLEAEHAPKKILDEVKEA

>contig34869 Frame-1R

MLEYDNSAFYYFSVSLCALYVVPVTFLSLRRILYGVFLKDRLLDKSHVRCERELRKVKQL

QAEKTAFRNVFSLPFVLNLLVLGTVWYALVRMMLLLKDDSEIKSFDPFAILGIAAGTTER

EIKRAYRKMSLLYHPDKNQGDPVAEQKFMLVAKAYEALTDEVAKANYEKYGNPDGRQALQ

LSIGLPTFLLDPANHNLVLFLYLLILVVAIPSCVALWYSHSKKYGDSMIMYDTYGLYNFA

MSQNSHPRMLPEILAGSAEFREIPSRSTDEAELAALSKAMKQADVMAKPKFNHPAITKAN

LLLHAHFLREKLSPSLQSDVNAMLKKSIQLVDGMLEISVMKSWLQTSLNLMEMQQYLTQG

LWFKDAPFLQLPHITEVEVKHIVSGKHPVRSMHQYIAMKPEDRKGLSGLSEANCKEVTAV

LDMMPHMELQISVGVEDEDMIAEGDIMTVTVTLTRQNVKEGDTCDLVYAPRFPYPKMERW

YCVVGDSKMNHLHAFAKITSQERVVEKKLQLQAPPKAGTYQLDIFVKSDSYIGMDLRAVA

KFNVASASSLPVYQPHPEDLELDNEPTLFEQVMNAADSSDSEEENLEPEEVKEAKKDK

>contig35574 Frame-0R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY56172.1|) 8e-49

MMTNDFLCGAMLGAVISTFTFPINVARTRMQSVYGQPFIGPWEALQLTYKERGCSVKRLY

RGVQMNFFRSLVSWGIINSTYEKLKAIT

>contig37561 Frame-1F

MDSQARGGGLQQTQKLFHSLYARFLSQGLDPNDAVARALLEMQEVAAGATASTSVSTVTP

TQKDVKMEDATHLHVQKGSPSMAAKTELASTSASATGSLFALVNATAASSLTTTKSDLTT

RVDENEGSLQACEALLGLLLERTLTLAIETDDFRVAKRLVYQVFSDPNALSAAFLKENLE

KAENEVNAQWWGIDREQMLRVFTLLHTAMAGSDREAMQNTFRNALERLVTQP

>contig37705 Frame-1F|Blast-4-nitrophenylphosphatase, putative [Phytophthora infestans T30-4](gb|EEY62530.1|) 4e-33

MTKRLSRELYKQWIQGLDAFLFDCDGVLWRGATPIEGSATIIDLLRSLNKRVVFVTNNAT

NCRATYVKKLASQGISAVEADIVT

>contig37792 Frame-1F

MSIVSARPESCTFVDANTTATFIGLQDGAVIMRSQAILY

>contig37972-0 Frame-2F0

MKDDGNIDVDVEFSPPWKAFKSSALSNTKIGGQRAAPPD

>contig38065 Frame-0R

MGSSTMTCIIDTSRNYNGSPTSDWCNVKTAGIGKPPTSETGISNIDYFMWVKPPGESDGI

CTNTMYSTASLTGVEAGAFYEEGFKALWDQGYFAREQSMAGNSTDNANQSSSQAGAEVVG

SDLNQTSIGQNSDFAQYVGTVAPVDIDSPDNTTTTPPLPILTPNAT

>contig38735 Frame-2F|Blast-3-ketoacyl-CoA thiolase, mitochondrial [Phytophthora infestans T30-4](gb|EEY53526.1|) 0.0

MTLQNVYIVAAKRTPFGSFGGKLKDISATDLCAHAAKATLEAAKLDPALVDMVQVGNVAP

TSPDGAYIARHVQLKAGIPQEKPALTINRLCGSGFQSVVGGMHEIILGDAKIALCGGAEN

MSQSPLAVYGHQARFGVALGAGLNLQDTLWSALTDSYAKTPMGMTAENLADEYNITREEC

DAFGLRSQKRWVEAHKAGWFDAELAPLEVKAGRKTEMFSVDESPRTVDIDKLAKLKPVFK

KDGVVTAGNASGITDGAGTLLLASEDAVKEHNLTPLARLASYQVSGVDPRIMGIGPVPAI

TGALKRAGLKKSDIAIYDINEAFAAQWLACVKVLEIDPDIVNQCGGAIALGHPLGASGSR

ITAHLAHALKRTGKKYAVGSACIGGGQGIALVLENVV

>contig38902 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56708.1|) 3e-26

MDPSGVDMFECAGMLNLVTVAPQSWRAIQ

>contig39440 Frame-0F

MKHKNWRAREQSLHAVWRCLEKHNLFEERHEELLDDVLKLLEDSSKDVRDASVSALEKFY

AFLGSSLLRNLEHKKIRTAHMKTLTDRFRQIQSNSLTMPLSGAASTRSDIFPQKLSSIVS

SPELQASSSSSMARYLASVRTRKMKEAKTVDANASEAQSLSHKSSTSSQVVNSEVLRHLS

GNDISEKEITRELNAIFDKLELENSWDIRVIGLKLLQELASRCSKASNSGCALSILTQGL

CPIRERLCLQVSDLRSSVSREACETIQTLANTLRDEFNAHAETCLENLLKATCVSIQVVS

TSADTTIKIIITSTSYGFPRVIPKLIECVKSRNQVLRCNAVSYLTLTLQKWSISFLSKHS

ELFVPIMPAILQDALGDVRAQSRKCYWSFHYLFREEAKNIFHRLDRSTQKNLSDDPSRLT

AKMTRPKEFSSMNSLLDFSSQNTYCLAIREPLLAPSSKSVPVAVNSVVFCDEGQHTCKSD

EATNEKLPRRVLGEIPASIGKENNAQLCRMLPQGPMRIGPTVRADSPLSKNNIDMVDEVK

SYAASGPLRVWSAPRTSQLMNATAENMNALRQAPSKSGSQTSSQHQSSKAQRVQLTAESY

DPALMEINEVEVGPKRLPILSMPPPTASSASSSKANIPHEEFRDRAKTNTTLKKSERPRA

MSWPETDLLENAIRNIEDKTWSTRLEAAECIGKFLQERVNQRQSDGSEDDKFYGQIFHAF

IEHLSDSHHRVSQEVLKNLPQLLKLSHDSQRLLPQLKLILPKLFQKFIDTKESTRAAAKE

SLEYIAIMVDSSTLAAILISMLGYGSNMKVKAAMCHFLREVLPGAEGYMKAGTNGSHMKA

FLLKIAQLMNTDVPVSVSSACGELVSAAAQLYGSEMEEALGLLSPNKRSTVIKVLKSKNI

VFKPERLESSLATASHYTQLQEADKNIEDVAPPAINLEKSRKRAEAPSVNSSSSTRQTNQ

KRINTLPEKNAPHSARSPLRSIKSEVINRVNASLIEKVSLSSPVEASMDKHGLQLEEILC

LLEQNDLSAMDLKRTLFKTLHLIEAGVPETWDRCYGRLLLLLLDTSTEENLSALQVLHRL

VICQPTRAQLFFDLLLQRLTDAMVDQGDEACHLMERILFKVVTSSSDYEQTLLTLLSLDS

CEEPPQMQVVLRLIKGCLRTSECGNPRNMAFMRNNKVTSRLFSVITRCLGHTSSSVRKCT

VDCLVAFYFATKDDSSIVSKFLAELNNTQRRLVEIFIERAKLCS

>contig39888 Frame-0F

MEHRDRKRKALEISESPKFVSETINELTTVLVASDAILRMEISELRDEVSKLEKKLTEKE

EECVRLESEVAFFHPDAIIERIRTKLWYHGDLTMLRRVIELRPRMLRSAETRGDRSLYLC

DTPTKKSKQTVNGARVLDFSPCNEKDKSTAHSSPAVGLDDVIDHGAAEDKDHEDEVGVTQ

KEDNELAAVSPAPDAGVQVHSTPQDGVATEINHANMNDDGREVAGIVSQQENTELAIVLR

APELDVQVNLSVKPRMTLLSVRKAGGCSINENN

>contig39981 Frame-2R

MFDGATQAVTREEESLSAGLADLAKPPRTLWAVTSLARGFTHMSVFYTLRTTGGWTIDYR

IATLHGRTIFMSSGSRDFSFLAH

>contig40219 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64637.1|) 1e-167

MISTDMISKVQQRDAGFNNDASIAASSLRSLAKFVYYRLFASLYSLVGKLCTNVVMVNST

WTYNHIKQLWGKTPTIVYPPCGAMQEYVEFSLENRELIALSVSQFRPEKNQLLQLQAFQV

LLTKYTEPMTTTFKDFRLVLVGSCRNTDDSARVETLKRQARELGIADRVEFVVNASFTEL

KRYLSRSSIGIHTMFNEHFGISNVEMMAAGILVIANNSGGPKADIVKPETGYLALTADEY

ATKMMLLLNKSPAESIQMRKAARQSSLRYSDKAFGEQFLAEMNDFF

>contig40332 Frame-1F

MVVQASLRLGPRLAMTLLSIALLSAFEEAVLPVPLDAQENQRFEIKSFTQHKAHDNKNDH

VHDGSADEEKI

>contig40501 Frame-1F

MKTKKKFGMSNLTGGANSWMFGLQLHDPCVYGSYEVFKTRFQRTFEPPHAECGARAELLD

LKMDKRDIHVCAQHTR

>contig40574 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59896.1|) 3e-16

MLTSRQNDRILLRQRFYKIAEAWMR

>contig40956 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66981.1|) 5e-67

MVNAELIVFLRTACPLGASLTILITLVSCLIIVKVDGIWVSGLTWPFLSDMGRDYPAYYV

FAAGLTIVAFLLVITWTFNWFYHMSALPANAKGFRVLAAITFVAGSTANLGLPILAFFDT

SKYAEIHVLGAEWFFYIETIAVFLNTLVSYKLYTLLIALQADLENAISTEGSKLQRRKKT

LLIQFIFFSLFFVAFLIYMPIGTSLATPAPRLSVDDCIDKGLGDTYCEVTMRLNLTSTSL

YDNEKTYGTSQMRAIAQLSCILTLVGYSTSFITNDYDDSEGQNFKTMGL

>contig41007 Frame-2R|Blast-Rab1 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY58069.1|) 6e-50

MVYDVTSQESFDHVNDWLTEVNRYANDGTCKLLVGNKSDVKDNKAVPYETAKVFADSLSI

PFLET

>contig41793 Frame-0R

MLEVNSRVCKVSQPSPKFEGLIFHEQTPAQISV

>contig41869 Frame-1F

MKLSVQHPHHTLVQLIALKNSGDVEGKGALQFRANVGDAKAEGAKVYLSELMKTEQHDLL

ESLDTVASAYVQLALFNTSEYHNQKIKIPLSVVTISGIHSGRSGATTFDQCLRVRARRGG

SASMPAVLTTNIAPQADMDYSTIARMLSFEPKFSITDSGIHRPKIIYCYGSDGNRYKQLV

KGQDDTRQDLVIEQVFETMNQFLMEDKATRNRKLRLRTYRVVPLSPIAGVLEWVENTVPW

GSYLVNRTSKRLSAHERYHPHEWKHMKCRQFLKNAPDKLSAYLEIQKNFTPVFHHFFLEM

FPDAAVWYRRRSAYVQSAAVTSIVGYILGIGDRHSQNILIHEVTGELVHIDFGVVFDQGM

ALFTPETVPFRLTRDMVDGMGISGVDGVFTRCCEVTLQLLRKKSASVVTILEVFVHDPLY

RWTLSPLKALRIQGGGEKETRTRSLSRSSSSLTEAGSPEDADVLHAEPGSTDAAARALIR

VKQKLEGYEDPNGSALSIEGQVKQLISIAQDPQNLCKLFPGWAPWL

>contig41977 Frame-1R

MEDSKTLGHTVVQAATIINVPGALKDSNAEKKAVVDCLSRCTECEQVESATHGDLLRTCI

GCNITVHANCYADALPLAQAMERKVSNIIEKSGDSLAWKCECCRRGVDRRVIKCVYCGIE

GEHHAIKSVECGIDRAFWSQYLQLDAHNVDGLEKFGHVLCINWDPRRLAVHIAKERKIKY

AKNACKKELTIETAKDTQSKNGAASEDFKEMDISSAEVSEVTVSDANEVSVQDPVSPGEC

CFCHSKAGVRIQCRRVQCAQFFHVMCAHKGKGHVELRTGHILQFQAYCERHCSSFEDIGD

LLAKLITRPIRLLVGRDDMRRFGTIAKHLPNYTSGAQVMRDLATLIVGYCDKGLRGSKSD

PPDYNVKHLQMLQFFLSHVPQLEKVYALPETPLQDYVNDKKLFRRLEKMFNPLRYLAKYP

GPYSQQYNCEVCQDPFHERQHLFYCTVEDTPHVQHWRCTKRRSNLHDSEVRGGCGAKKKT

ILMKIVR

>contig42129 Frame-1F

MLGRRPLFPGHGYLHQLKIIMDVVGSPSEESLDFITNPKAKRFILRQPKKPKVPLSSVYP

RATPQCLDLLEKMLVFDPRKRITIQEALAHPYLSLVRDRSVEKVCPMPFDFAFENSDLTK

QKLQELIFEDVCAFHPDARIPDPMTSASAAVNDRFGAESTLALSLRRTSVSAAGASTLAV

LPATAPSVVVPPTPVTLTASVILRNSLQQDAIDESSRAGKSVCQAQTSPVVLLPSEACAV

HENRAFESALNLMSPAASISGIATASSQTSGIMELVKTESLASPAVMHERSAQAEELAIK

IVQSPAHISDIEDSEGMVVASPDDNLSAPLNNVFVTKSATSIDGCSLSGDDSTRTKRKVG

YGGEGLDNTSESEQAIGLSISSQQEKQHFKLPISPSSVV

>contig42280 Frame-1F

MLEQINSSRFSIFLIIKCFIGSCAGRLLKGYNNDACPTSTPPEGSKHEIFPVTDLTRKEI

QWFHPFSHNSTFLRHLRHHWLSSGHCKQDLFAPLISFFYPLRKIRDHLLRQQFAL

>contig42514 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54931.1|) 1e-52

MPALALHWDQNALLRFVAAANKVNTSIAMPEWLSQPRGNITSDSIVEDMMAFLATKASGR

FGYVLLVSDSVMQFGQLCCMFAYVENDAFVRAAAEAADNRNEITLAKIYCITSGSAFAAV

PMEFPSRESQCRRLFA

>contig42561 Frame-2F

MPTLGVTLSDIDEQSKSAVQSPTETFTSEVGDSSDCVAIADNFVPTRGLFRALVLPTRDR

ARKVAQKVFMDMYAYPTILEDQLHFIRARTLVVWGENDDVLDVSCSQVIDDKLRVTRKHI

LVLQCGHFVPKDKPAECLDAINKFLADNELRALTACTAQKACMDIS

>contig42679 Frame-0R

MIITSPYVAACFNVACSDKLPTMRSYTNLILDALLFGDDKASENNAISQSPYESTTSHST

NQDRLRFSRRTSPVSELSNPHPVSSKLFKLFRPNGLHSKRNMTNTHLQVLNLDIASFNKL

QGHMPLTLKEIVKDPKKLPYLLQWLLVDTEALNESTHSNYHHV

>contig42792 Frame-1F|Blast-cleavage induced hypothetical protein [Phytophthora infestans T30-4](gb|EEY56378.1|) 8e-27

MLKIDDVQGQHQEASRHQSQAMSSCPMRRRMRTREKEEVGAPAVWIAPDWRTHPVIENFY

GHARRARASSFDEVMHSPMNAAEATTLGASCCSYKAA

>contig42972 Frame-1R

MLKMNQLDSFPELRKVKAWATMVYEERDGNVEEIIPSLRKYMTRDQLDALLKKSTDDDLY

HDELVERLKTKLESS

>contig43306 Frame-0F

MFKSSTPTGQRVALVLLVMVSMSVVV

>contig45612 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61250.1|) 9e-10

MLMEGESDSRVHFSDVSDPWSSSRHVAVLQTLNAVEK

>contig45685 Frame-2F

MAGSAMAMVKSSKIIRVGLDAPHQ

>contig46235 Frame-1F

MRANRHGVRCLLPIRVARVFLANHNLVGAAVDAFYYREPKHASLICSKMATFMPLKDAVI

EQRVTFSRAQFAQLKQQQFFPPKPFMRQSARYKALEDNETHPDFQAANLGVKLACGLELL

YASESMDQLGRPWREIMDEILQTQGEQELSSLPIDPDDDDSWLYMPPNTLERELERISGA

KSPAANTGGTDELQHMANVFSTFVNKESGLDGVEGVEPVEFDMTFFLDILKGANVTRKED

FEDFIEENESSEEDEDNEYALDEAVDQMEAELANTTLAKSFSHLNEAHDDTAQKSRSNET

TKGGSTSFSSAQPLDLDYNLLSNLLESFASQSGHAGPVSNILSEIQYPRTAMQ

>contig46767 Frame-1F

MSCVTLQRNACANRHQITLLERNSCSVLEPMKYRATRGVANGWSGKIFDIVSFLQCRR

>contig47074 Frame-0F

MDKPPQGTSAATFGSMNDFNLSILSAGAAFALACIKRVCGSRVSFDTGLILRLAGEYSQP

LRTWILHSWGIILQSVISTGGDYEHFVSSTISLLEAQIMAGFVYSKMNKHGMRWNIGTKV

ATGRIINNMVAALGPELDGSSARLSQLFSYWAFLRQDGDTRLELEYLRFLEQVVVFAPSR

FQAADLRYILRIVSDTALLNSADISLQTAQQLAGSASLPPSGSNTVMDMNTEPFERIGLV

NVGAISFAGMSRSILQNVGLSCIRTLVERDPTLIRRQNLFCLLLTALHVEYNALAWTYLP

KLHGMWDALSLAFADFTTIQRNSIDTLQSTALALLDVEGRDHESAEPCIWALLCRGIAIG

ESASSSANPEDFKTNLKAINLDILATTSIDDDNSSKLSNHALKNVSQVDANLLSSAAIAT

QVHTWRA

>contig47108 Frame-0F|Blast-Phosphatidylinositol kinase (PIK-L2) [Phytophthora infestans T30-4](gb|EEY59643.1|) 6e-83

MEKYFDFIWSAFWDSKLVVRVSASESLQSCFRLIQQRESNRKTSWYNRALEEAENAFKRN

SSDATHGALLILNELLRNTGDFMHSHYARACRLVFSHQDYKSATVRSAVISLFPRLAKFN

TSVFVEKCYRPCMNHLLEVLFSATTTTRPDALLSIGKL

>contig47632 Frame-2R|Blast-Mitochondrial Protein Translocase (MPT) Family [Phytophthora infestans T30-4](gb|EEY57510.1|) 6e-46

MNFGGLMGGNAHAGMPQQPSKQSQLMMAKVEMASYADLFERLSRVCFQKCKFKYTDGQLN

VGEMSCIDRCAGKYMEAYSSLGVKMAQVEKEIMDQAGASAGVPQ

>contig47719 Frame-0F

MANPPLNRQPHHSSSRVSSQEAAFATHKRTSSTALSPTAVLLDQLTLRVSSLRLSKRDVR

YELHVEHASSKLRWRMSRSFDEYKAFQRQLLAALRLGHFCQGECPWLYSFLKSYFPKSLS

FLGFGCQNDCAVEKRRVGLEHVLTSLQNFVVNPENAAMCSIVAISVTQLVANFVFRDSSA

KHHLLHDLRVSGSNNSNLNKPRDSAYSPVSVTSDEGDEMPDETEDAAALCMLCSSSLRCD

ASGAQVCSKDFPNSSLKHRSNAFSYTTQLACGHQFHDECIVPKLNEELRCPMCRVKVNAF

>contig48369 Frame-1R

MKLVEAANWFNLLVTERTMSELRQKQELANSASKTFLFKDRVIQQI

>contig48475 Frame-1F

MSLFLALRMLLRQLLPVLPASASFNFFSTEANQEEYNAQPVDVSSEPAYKAHFLESKNVR

PMAPINNCRSHKNAEEHPVYDMDKFSDIEQTHHPADTMSARVAYYAIKILQMGFETISGH

SGPGGEMTEKDWLHWCLFMESVAGVPGMVAGMLRHLRSLRRMKSDYGWIHTLLEEAANER

MHLLIFMNLKQPNWCLRALVCLAQGIFFSCFLLAYLISPKTCHHFVGYLEEEAIKTYTSL

LLDIETGHLESWKRKPAPLIAQTYYKLPEGSSVYDTIKCIRMDECHHRD

>contig48651 Frame-1F|Blast-vacuolar protein sorting-associated protein 8 [Phytophthora infestans T30-4](gb|EEY56484.1|) 1e-14

MSGVESLLLESDEEDLGELDLSTITLEEILREEELANNSVEDTDGSTQ

>contig49546 Frame-0F

MPNHTKSSCSNRTKRSLLSLSSSIESPRA

>contig51059 Frame-1F

MPVETSNIDVPMGDHKNTRRTLQAIFSTQPSSMFLTSSVSLTYRINSICMQQTMEKIRSG

THLPYPAV

>contig51367 Frame-2R|Blast-aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY67916.1|) 2e-90

MDGDLAPLDAMAMLCQQMNAFLIVDEAHSTGVYGPHGAGIVCELKLEHKYPNVFVSRIHT

FGKALGCHGAVVCGSQVLIDYLVNYARSFIYTTAFPFDQLVSVICAHEYSKSSDAAVLRR

GVMALVRYFKDEIHRAPSIPSDALLASESPIQSLVLKGNHRVLWASQHMMAMGIRVVPIR

SPTVPKGAERFRIVLHAHNTREQVDQLVRALNTI

>contig51491 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69265.1|) 2e-42

MEQQDALVDAIRAIIGPRDISSERILSLLALADNNPNKVVDLFFHTETENGAIQTTNDVE

GSDEEDGDGMNWTESPVLSNNPLTEETDTTGANRAKWTSQAEELSGLLGGEVDREIILSL

LSSAGNDLNKAVEIYFSEAGAEAR

>contig51895 Frame-2R

MSNLVDNKVNMGSSGWTKSMPQRKTKSARFHAR

>contig51918 Frame-1F|Blast-histone-lysine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY67226.1|) 6e-14

MNCLDGTGGGLPGEFHSKELLEDAI

>contig53703 Frame-0F

MLRASKLSCALRAVVKKQHNKRYLLSDPQSSTMAISNNQRLLSTAIAQENHKRLPNRTDK

FIGKTGAEIFHETLAEMDVKCIFGYPGGAILPVFDAIHESKHFDFILTRHEQGAGHMA

>contig54203 Frame-2R

MSSEQSPPNFQQIIDEDILVTSPTSYALRESFRRSSFSASAETNPMLLRSSQSADQMPLP

RTSSRGSVLNRAPPPPPPHLPPQISSVPLNGGAIDELPRPLSNSNLDILHEQNHGDNDPF

GHSTG

>contig56072-0 Frame-2F0

MTPGSEICSGNPPQPEDWLLHGRFVSESL

>contig56678 Frame-0R

MFLEKHNKTYKVVRDKLMEAYIGDRGALIQLLKDGGDIGAEVFKIMPKGWENITDNQP

>contig56722 Frame-1R

MVLHFRSPEIQREDSSMDLVHPRSRSRTSSAIQFKPSLGVQEYNELESHVQVDHHRTTEM

QK

>contig56829-0 Frame-0F0

MNVMRLRQSAAALSAKQILSRTVPAAMKDCVRNFANIPP

>contig56829-1 Frame-2R1

MFAKLRTQSFIAAGTVRLRICLALKAAADWRSRITFMAKQENLSLCGPLVLKTDS

>contig57075 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY60261.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60174.1|) 4e-19

MDSLLARVRPSCTKLVAREDSSVRINIDKARSFVKDLDVNEFDQLAEPVSFPLNFSSQQD

ELNFL

>contig57224 Frame-1F|Blast-adenylate kinase, putative [Phytophthora infestans T30-4](gb|EEY60144.1|) 4e-61

MEDRMTEGGQVVDFHSCDFFPERWFDLVVVLRVDNTTLFDRLQKRGYSDKKVAENVECEI

MEVVLQEARDSYAPEIVQELPSRTVEDMESNIERVLI

>contig57390 Frame-2F|Blast-general transcription factor IIH subunit, putative [Phytophthora infestans T30-4](gb|EEY65991.1|) 1e-09

MSEVLVAVVRVKKRDGRAEFSPNGLRWTADASPEVPDGQCLPIVVP

>contig57769 Frame-1R|Blast-structural maintenance of chromosomes protein 5, putative [Phytophthora infestans T30-4](gb|EEY64212.1|) 2e-37

MEAASIQIDNLCQFLPQDKVGEFSRMNAVQL

>contig05226 Frame-2R

MSDKESADTSGDISEPSEHEVELPDIGSPNLSDRESMEIETKPILPRLRSNSSRTNEEKK

QEENAPPSPIRSDVSFDFNGSLHGSVDSTKIDTNVTMRDLRKKSTEKDVKEKPRRRGLVS

DRGFDEDATSPFSINEDHVTPLSNG

>contig06397 Frame-1F

MSEVEKKEETTPKVEEAEASKDLESEESQAYFEPVVKLDEVEVTTGEEEEEVLFKQRAKV

FCYRESLLDKGTGKKTWCERGVGDVRFLKHKEHQKVRMLMRQEKTHKILVNHLVESRTEL

TPNMGSDRAWVFSCYDFAEGVVETQVFALRFGNAENAQKFKEAHDAAKANNKKLESGADD

ADTSAGDEAAKALESLDVKKEE

>contig08643 Frame-0R

MSFNLFNFSISYLFCAFENKNIAFLWCIDINCCLCLFQ

>contig12796 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53427.1|) 2e-47

MTRIRDYANAGAKFTHDANAVLRSTLDLALSELPSDDNAVVTTPRGYKVDGVLLEDNVKV

CGISIAAKPEAQICLSRVLRTCLPFEAKFGEILVQEVANGGNTRI

>contig14453 Frame-2R

MENGIWVFYHLQGEEGEDRAHPNAFRLTAVSSSDVTLADVLRGFPLRNLTAFHFRFRLNS

SKGNTFYWLDITQSSQKVPLAGGRVICKLLRLERPKKLGIVFRRRPVFKWASGSPLSKLH

GSSSSVGDGLSNSQTVNSLGESSSYHRSSSLPAYEQNRPAKYSDQTQNSEGGYESRRSMS

PNRTEGVKEPVLEDFLSGDRQAP

>contig15344 Frame-0R

MKDSKSLERNQAVAMFNANKGSNSSNLLTRAFSRALSNALLPPLITTNVSQSSGFTSIDD

QSRVSGGNLNGSKDSMVTIESSLSSLDNTRLSSIPRESISGLRRKSGWLHKEGACVRSLK

RRYFMADGPKLYYFEQIGELPRGHGIVTSAFLSDAYPNCLELILTTKRTLRVVAESLDEI

RSWLEHFEASVSGKETTFDDHRSANNRFSLGTDEFASNETEMDSGWLLKKGQNFRTWKRR

YFKLDGKQFSYSSAPDAPPLGRGVVEQVTIGNARPFCLDVCFQNGRIMQLVASNEKDLMA

WNRRLQAAVLSESIESDFKQETQFDFDDADEDAQLNTMRTVVTAASAFKRGFSKTTSTDS

TVSSSDSMTPRDWQLDCMIESTETVNALLNERAEAAGIAVAAAVERAEVQKSTRLETEEP

VVCSGWLRKEGGTVKNWKRRYFTLHGPILCYFKSDNGALLRSFTVCHVVTLRSKRLCLEI

TTEEGRKLLVASETQVDLDRWLDHLHRAIAAEKRIKVSMEKQAEEAIFCTSPRALPNEKK

ECGCRTDKVL

>contig15670 Frame-0R

MKFGKVLQQSTQMSPCAWEPFWADYKLLKKIIKDCAQIKKEEKLQGDRLVKIKIKPSAKE

DNDSIRQSQDEMNFFRTLRMEIKKIADFFMKEQAKHTSQVAAIDASFQQVKTNPESTDAK

TALMKNCVALYKKLLLLENFAVMNFCGISKILKKHDKWTGYATRNKFMHTILMKQPFATY

EPLLQMIDRLEHIFMQATGSSIEQHDAQKTSSRRSEESRSSSSSPSSNAPGTSNPATAIR

DSHRVSSDARSHSNPSPSDKPRGATGNGHDKRRYQEVTDESSLRMEESVTLVRVNALRDD

VRELKKIESAYDGDEEYEDNLDDTSFPEDDGDVPPLRFNGQLQDEKHLVMPPLPKHIALT

DSQSDSDAAAIAMLSMKDSTELHSSGISSDGGNSATDSCRSRRAKRKACAPLYIEGKRKM

SVTAILN

>contig15814-0 Frame-0F0

MNETRGVAGRKGTRESAVVWAQELPIAYRKHAASPNGTEKQIHEGVSSVRVPHRNCEC

>contig15814-1 Frame-0R1

MNLLLGAIGACSVLSVSNGQFLRPDDGALSRPFAASNATGFVHAFVDKSVTSPRQSDSTA

AEE

>contig16631 Frame-2F

MAVHPNGDHLLVGSYDRRLCWFDLDLSSRPFKTLKYHEKAVRDVSFHAKYPLMASASDDG

TIHIFHAMVYSDLMKNPLIVPLKILRGHKVSGGLGVMALAFHPTLPWVVTGGADGSIRLF

QNIH

>contig18017 Frame-1R

MGDLQLGKINLKRPANVLLESMACDTNGETTPWISRNLLQKVCRVRGTNRFVRSNRQEGI

IVGWEVDRLTLGKMGGGKKRRKDH

>contig20559 Frame-1F

MMSHLRESSLELRVGKKFRLGRKIGSGSFGDIYLGTNMTSGEEVGIKLESVKSKHPQLLY

ESKIYKILSGGLGVPSLRWFGVEGEYNVMVIDLLGPSLEDLFNYCGRRFQLKTVLMIADQ

LLCRLEYCHSKNFIHRDVKPDNFLIGLGKRAQIIHVIDFGLAKKFRDPKTHQHIPYRENK

NLTGTARYASINTHVGIEQSRRDDLESLGYVYMYFIRGSLPWQGLKANTKKQKYEKIMEK

KMNTPIEVLCKGYPAEFRAYFEYCRALRFDDKPDYAYLKRLFKELFFRKGFQFDAMFDWT

VLNLRSGRRERGTSGEGERSARAEPRQEAARDGRQIASQGRVYVRDEAKDGDTQQQTQQS

YRSAGYRDDRQAATDQSYLATDASRDALGEAKPMSRQRY

>contig24115 Frame-0F|Blast-DNA2-like helicase [Phytophthora infestans T30-4](gb|EEY60610.1|) 0.0

MFGSGTLLNETTLNNVSKKIHVSRVISTEEMMWSIKWGLKGATDASIEGNIVSLGKRRSE

ETESVIFPLELKTGSKKFAALEHQGQVILYTLLLNERYRQRCQDGLLVYVPPIETNRISV

NSSHVRGLVMARNNFASAMAKVKSFSGSASAQVYPPMIRKRRECERCFQVDECVLHHAAT

ENGTEESSGLGDFFTLMTNHLKEADFNYFKHWTRLVDLEQQYAEKNLRALWLQVGWQREQ

ALESSTCIANLKLVSDAPAPSKSGAKRILRFVRDRRR

>contig24304 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70127.1|) 3e-07

MDVGPMASTKLYVGNLFYELTQNDVEAEFG

>contig24528 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61532.1|) 7e-10

MAEDDAPYSTVEPGVEHYYLEICT

>contig24810 Frame-1R|Blast-calcium/calmodulin-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY69769.1|) 1e-72

MAAFIQANGMLKGRCGTPGFVAPEILCAGKGEAYPSGVDMFSAGVVAYTMLCGYEPFFGV

NDSDLIQMNKLVEYEFEEPEWASISEEAKDMITRMMEKDPYKRITPKEVLQHPFLREATV

ALEDLFIRL

>contig27082 Frame-1F

MSSSDSSKTTNANPAPNADAQDLSVFVQTLLEQM

>contig27301 Frame-2R

MPTLVRVTIFGVLLQMIIFLFAGFNLPGNSISSGDEWSAIPLISY

>contig27495 Frame-1F|Blast-mitogen-activated protein kinase organizer, putative [Phytophthora infestans T30-4](gb|EEY69177.1|) 2e-25

MWDVQTAKVIRKFEGHEHSVNCVQFNAYSSVLLSGSYDKTVRAWDIR

>contig29233 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54983.1|) 9e-53

MLNPLTPMVYREAEEMDPFVYARFDWGEEKKVSVPDKSDKEILAVLKGLVDHGLGLPKSP

ESDIIVAAPIIEAFKGEDAYEPLNLTWDGKSVRRNPAFDIPIEEALKA

>contig32109 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64456.1|) 1e-136

MNDDFSGALRRLQSDTHDYWAPIHSVCRVDASRLTPFQFYRDYVSRNVPVVLLNAMTSPT

WQRAMANWQNDDYLVAKSSNLPVTVDVTPNGLGDAVITLSDHDEGTFVMPEERSMSMLEF

LKNLKNRPNFDGVPYLSHQNDSLRTEFPKLFEDVPSAIELAVLAFGNEPEAVNLWIGDER

AVSSMHKDHYEVKNLIYIASRSNNIIGIRIFIAL

>contig32633 Frame-1R

MKVLTNSHSVASASSDGSVHVFRVDKVNSVGGNVQATGIKELRANNSAVMAIDYFNNVTE

ALLLYATRDGKIHAWDLRMRREAWTLSISPELGYVTCMTHSLDVSWLAVGTSRGFLCLWD

LRFLVLIRIWRHSSHRAIHRIQPCLGLPNTLPLDETSVPLVFVAAGDGEVAVFDLSIGAC

RAVFRSLEALASESEACKCPTLLHVPIPHRSRSVLGSFLGILGITMSFDEISTTPLSEEP

SVRAIFCPSLHVRGIGDALITGGEDRQLRYWDIRNGKQSYTICGNGEAKSFYSIQAPPND

WWRMNSDSGNATSQRFDDIPAAPISTTATITKPELAWSKLSPPLITVCQDSSPYSNSADV

AAPNYGSVETAISMERRGLVPPSPAHTDCILDLTLVGLNSGQYSSPMLVSSGRDALIKVW

K

>contig32787 Frame-1R

MLTFPRVFSRCCNGRLFHKIFVIVLIKRQRAQACRCLETVIAVTPSCTMLITRKRSKHIR

CAISLQIPTNVDFSSRNFLGSISLLLARGARYLRYTYDVQLFKLVLILIF

>contig33090 Frame-0F

MATWPEPPHSPKPNNDDTANIPIFGTFSHDAFFSGSGSLGLGLAPPTFCNTMDLQPPLLS

LAPPLPPSSLEFDDIGRAFYHLQQQQQIHHQQELRIGSSASSLASLGGVALNQHDTSRLN

SFGPFMGHTIPDSQHHNLSDSMLHLNLGSNNERRVFKGTEAWSDPNVSTASLRDQMNAQM

AALYQHPKPEPCDQSRHAQSSERHSSNLQTSHVLNRQVKQLSKPSTESPSTVLNRHQLAP

SMSPTRRSQSRSSTPLRTHSSSSHSSQLYHEKNNSLQSNAIV

>contig34385 Frame-1F

MHRQEQAPLRRHPSEGSDFSGSDHLKFSQSPQKFLERRNSTGVGSGNPLLMKKSTSAQRD

EPIDASSLLSSSLQNEMQTNSDASLGLRLRHNTSRPSTQHQKGDLPVVTLESLLTELYKN

HQPDKLKNVSTVAKQYAGKERELIKLLRGKYGALSVKRLEENLETLELAHRAHTKGKRAG

RKRGCFIRTISLMFSLSLLLYFSFGAVFISFVVLDAWECHTFDNDEKEPESAEECGLFRK

ELKSFTYHRVADYVSQSYSNACFCAEWNERKSMMLSSFSFDEVVNMAKLIPFSPDSFGRP

WIASVKKQILSQE

>contig34868 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65536.1|) 1e-142

MQLLQGAAASFASLDEKKEVNAFAKNVPMKENNSLLLRSRVKTEKVRLSFDGRIIVAKEL

VRQLFKLRVFSKTQLVVEKVIKKYERYHRYISANRIEELPKELQLIVRTDGVGIDKVTTL

AADVRAFKQLFHLRQKQIETEKQVKTLMKEAKEAGLMQTCVRTGRNQVSLLQRREISWQQ

NSQLPPAYVYSRIRRLKTLSGHLQIQAYCLAYDKVGKVVITGSDDRLVKIWSLQTGDLLF

TLRGHVGNITDLAVNDANSLLASSSDDKTVRVWEITTGAPVAVLIGHSGVVNAVRFHPMR

NIIVTASDDGRCFCYKLPEIPRTEQPETKLETARRLYSLHAYMLSLHPIYAMKHARREGI

RSCKVHCVTFSRCGDFVASGGHDGIARVWDISMASALNAPTVVPR

>contig35287 Frame-0F

MSVKALGWLIPNRSQGWTMDTNCERSPATIMAHKGCFRPLELLNQPQKTAELIQWKCAFC

QKVWFGNQDTILVYHELAVTLENTNVDKAPIVVLCEGTTVDRLLRLASENYMRLTLTEKR

EKLHQVVGKTFRFVLSRCEPRDVYIPTGMSLASARNCTTFEKIRFRMDWVHPVDKHAHAP

LIS

>contig35957 Frame-0F

MYGPSHKRSLDDNDRDGGNYKRSRLDDRYGGGNRRNDRRGEGDGEFSNESDRARAWRLAK

KAIVELGDGAEHDQLTRTSELLLRELEQDEQGVKLSHLACVVLRGASRLAHKTALYATLI

GLVNARKPAFGREIVANALKLLQKDVNFFSLEKIEEAEDTPDTDVYRQSGDVNAIATRVR

LTVRLLAELVAAKVCNDEDVLVMLDSIQGLCTPDNWDVDDETHVFLRAKEDTAAWKDFFA

LVVLDALLHSGKALVASENLFDSLLSRCREYVSNRKEASHLRGESLHSLSWCTRRLQLTL

LWGPEKEDDDMSVRCASSDALSLLYDALHAIRNGDDKAWIVPGMRHPQESFALEFEHATP

HALTLSLSIDVT

>contig36307 Frame-1R

MAYPYQYPTQMAALPSPRNAAYAATGASQQRFTYLFNLAHQQYVAGNYAEALRLCEQLYE

SDAYRTDNLLLLGALHFQLGNLSESIFYNQQCIRVAPNFAEAYGNLGNALKELGDVAGAV

QFYIRAIKLNPRFGDAYNNLANC

>contig37128 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69701.1|) 3e-31

MEVDYDIGSSTVASGILKLLMGYARELVIDLAFVIEAQSVMELPERVLGTVRLDCIDLQH

AVPYPRMDSKKENENRVVY

>contig37515 Frame-1R|Blast-vesicle-trafficking protein SEC22b, putative [Phytophthora infestans T30-4](gb|EEY54389.1|) 1e-110

MESIGDANGNLDTYKQQAKQIMKRFDQRSPTKCSIESGAYTFHYLIQEGVCYLTLADRGF

PKRLAFLYLEEVHAGFVEELERDSGKNWRDMVTTVARPYAFIKFDKFIQKKRKEYADPSS

SQNMHRLNDDLADIHNIMRKNIQEVLNRGERVEHVSRISSNLADRSKDLKWGAKKLRMQA

IYRQYGPIVAIVLFLLLVVYIKFF

>contig37704 Frame-1F

MVKTIHNWDDSVLDMVFSTSRNVVLEVQEKARRLTYVGLVLALQLLQTSEAGHEFNTLRL

ETTDFFLAEWGQDTELNDVISPVPGV

>contig37793 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58401.1|) 5e-19

MLQNEPVIITGGMEFWPALGRVAGPARAWKDVAYLRRVAGFRTVP

>contig37973 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58880.1|) 3e-47

MQHELNQRRLPCCQFCYLPLLGDAYRQWHDIVTRYNQNLKETSPGDKSTKPVKANA

>contig38819 Frame-0R

MRRSRNSAKLSIKGKLYHKNEW

>contig38903 Frame-0R

MVAEFPGVVSFLSKLLANEQISILNMSTYDTDVIFVQAQHLEAAIMCLQSKLSRGLHGLK

EAKEAENALVPKLPSHASESSEEMVDLRSASRVGDGQYLTVYPESLVLVRLQKDTLRSSA

YGLTQLVLLSTKLASIEESDGEALGEMSFWCFCETAEEVSLIMDQRCLPSFEESPLIISP

DRWRAIKLSGRSYGFDETGVVAVMSGCSTDAQVLNVSCFGSNVAFVLDYMLADAIEALCS

SLDISRVER

>contig40333 Frame-1F|Blast-ATP-citrate synthase [Phytophthora infestans T30-4](gb|EEY68820.1|) 0.0

MSAKAIREFDGKRMLSTNLPAFSLNKRFAQVAISKSFANQSRKDFFSAIETNSPWLVALG

ETKLVVKPDQLIKRRGKANLLLLNATWFEVQDWIWERINKPIQVETVTGVLTHFIVEPFL

KHSAADEHYLCIVSNRDGEEILFHHEGGVDVGDVDVKAKRLQVPIESIASDVEVTTALLS

SVEEVRRPILAKFIVGMLATFRELHFVYMEINPIVLLGDQISVLDMAAKVDETANFLVGD

RWGDIEFPPAFGRAKFPEEEFIQDLDSKTGASLKLTILNHTGRIWTMVAGGGASVVYADT

IADLGYGHELANYGEYSGAPSETHTYLYAKTILDLMTRNFDERGKVLIIGGGIANFTDVA

LTFKGIIRAIHEYQQKLMDNKVHIWVRRGGPNCQEGLTVMREVGEATGVPIEVFGPETHI

TAIVPMALGIVEMQTSVTAQPSAKVIGGTKPVVSKLASTEGSAVYSDNDESESIEETECK

DVARKEIPAVIQDESIVRMNDKTRCIVYGLQQRAVQGMLDFDYLCNRKTPSVAALIFPFS

PNHYLKFYWGTSERLIPVYQKLSHAVKKFPDVSVLINFSSFRSVYQSTMEGFEHSDTIKT

HAIIAEGVPEQQSRLISRKARELNVGIIGPATVGGIKPGCLRIGNTGGMLDNIVQSKLYR

PGSVAYVSKSGGMSNELNNIVLQTTDGVYEGVAIGGDKYPGSTFIQHLLRYEANPEVKMM

VLLGEVGGTDEFSVCRAIQSGAITKPVIAWCIGTCAKIFPFEVQFGHAGACATGESETAL

AKNAALAAAGAIVPENFDQFGNAIRKQFDLMVASGAIALRPEVPVPRVPMDYAWAKNLGL

IRKPANFISSISDDRGEELRYSGTPISKVFEQDLGVGGVIGLLWFKRNLPPYASKFIEMV

LMVTADHGPAVSGAHNTIVTARAGKDLISSLISGLVTIGPRFGGALDKAAEMFARAHDSG

LSAADFVVDMRRQNKLIMGIGHRIKSLSNPDKRVTIIKDFAKANFPSTDVLNFALEVEQV

TTKKRSNLILNVDGCIAVCFVDLLRNCGVFTLEEANEQIENGCLNGLFVLGRSIGFIGHF

LDQKRLKQPLYRHPWDDISYLDEEI

>contig40500 Frame-0F|Blast-neurobeachin-like protein [Phytophthora infestans T30-4](gb|EEY55313.1|) 3e-70

MNGHWVTLESTVGTCAAIQQYTARLDTYTTKRMFPDYQTAWSRLVGISSLPVLLEYVLTA

YEKTVRVSQSSAFEDGSTRSLGEVMESLVIDFVWLFKGLLLCNRPNQDEVLQQYSFHLLA

HVLLRHPDALSVIWTPGSLIVCVEMVKSLAHMIPAPRTNVDGGINHPFHASIWATNPLFA

TGIHALLLDYRLWSHTDYKTQSIYN

>contig41271 Frame-1F

MRHPCWRTRVLRLACCYSWHRPLLQVSTVISTCTST

>contig41792 Frame-0R

MESVESWVQDTFAPIVLTCTTLEADRIAQKNNLSVANLLNGFARIDDADAPLRSVTHPIQ

LARFNFRFLAASQFHTLGINDATEHLNASVKRYPPQPNASAVSAVELNIPRVANVEDVPA

YLRIIGADAEDDPDPMPWYKSFKHTLMDTFRCEEFSLLCHPVAMLVIVSSTDPNPRHSFE

ELTAPENLPLPFQEGIYDINSIPKYYVILHDVLETMGTSIDPDAILTSLDIATGNGTVIR

INSLLDASFSSHSATIWTENPFVRPPLFPQMIQTFPQVNETVGTSLSRDDVDQLKAFVRD

FGLRFLVSSLEKRIAKLNEVVSAMKKGVKNVFKSWLRKPKDLRPSHASASGRIIYKCDAI

ESQTRLLADTAFLVRDYELALQMYRLVREDYKSDKSMLHCANANEMIALCLLMTKGSPIQ

ITNALDSANAIYAKTPSL

>contig41868 Frame-0R

MEATALSPSLQDTEMTLATVLMPHVSMMEATKVPDMLLDCVETPSTASTFELPPGAMPMS

LLRSEEENSTASSKAKRKNLTDQQRVTIVHYLLANSAGGRLKHGDIKAAATHFGVHRATV

RRLWKLHVASSDTHEGLAGNVASRIKGHSGRKPKVPDDELKARIAAVPVDRRMTGRGLST

ALNVSNSVIVRH

>contig42560 Frame-0R

MRPWPKFLAIKAIIFFTYWQSILISMLVSVGVISAKWHIGCPDCWDAQKIASALNDFVIC

VEMLGFAIAHHYAFAIEDFLSPSGVSLPTSNVKAPLLANFMDAINVTDVSTDLKNSRHEI

LTKKQALAARFERFHVLSPSNNSVF

>contig42678 Frame-0F

MRIKVVNQLGVDVWYRQEGTFECLHLKPNTTAAYSWLSLASIPFYQLSFALNDPRKKISQ

ESSENYPWCDPCRIKDNDVTGRYFGGHGFIWVCVELMDLQTLVTLRSSLTFSNYCDFSVS

VKVNEEAYTYNCEKRDEFYREHAPATHHLHCISLDGSACTLLAKPQSERSV

>contig42704 Frame-2F|Blast-Ammonium Transporter (Amt) Family [Phytophthora infestans T30-4](gb|EEY56738.1|) 3e-55

MRGGRRDPTFVVIATAIVALSALAAVSAQSTTGTCNVSQYLDASSNQCVNYTSRGEKAGN

AYDTVLDSGNTAWMLMSSALVMLMTPGVAFFYAGLAGEDMASNTMMMSFMSMALVSIQFF

AFGYSASFSSDGIFAWAGYNNIRA

>contig42973 Frame-2F|Blast-cleavage induced hypothetical protein [Phytophthora infestans T30-4](gb|EEY65820.1|) 1e-06

MLRFFEDNVKKEDEEEKNCLVSSSAASSQAPKHQKEQLSSDSNSLLVSEIKSAGTAFKFA

NDKDFDEPNERT

>contig43307 Frame-2R|Blast-Voltage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4](gb|EEY55981.1|) 5e-88

MGFVDMCALVPSYLGFILPDARPLLHLAVLRIFRVMRVFRLLRLARFVDAGAALSDNIES

NKRRIAVFLVALFTMILVIGCAMYLIEGDSHDFSNIPISLYWTVVTMTTVGYGDISPQTI

IGRILATVVMFVGYGIIACPLILNQTGSQDILTEVVECPRCFRRLHQEDASFCRVCGTSL

RQPRAKYLKARRDRRLRLAKLQLPTAKDRMPTSASSTMRSNMHLLSEDLNSTRTIDSSMG

>contig45613 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61250.1|) 3e-39

MSLVAPRVTSDESSSLAFSTACTEFLQLVKEIHTELGNKIHLVSNYRTFARSTYGTEKDM

EICIEKVKIVFEQLQSLSRYLEDHYAPEECLRGLSE

>contig45684 Frame-0F

MKSGSVPLKTDLSENEHLVLINLARVLWKEDMNDDWASGYLLAARLSASAEVTLKFRAIL

DPTLHDWELLG

>contig45767 Frame-2R|Blast-methyltransferase domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY63625.1|) 2e-71

MRDVQLHSCDFSWEDLAKECETHVESSSVVKDTDSIVDFVAPQQLIAKAKAKWDVFHARN

NGKVYKPRNYLVKEFPELSSSEFKAIEVLELGCGYGSAIFPILAECSNVHAQVCDFSAHA

ISILERNPAYDPLRCRAFVCDIAQEAFKEIAPGSIDIVLMIFVLSALLPESFARTLDKIF

AALQPGGLVCFRDYG

>contig46766 Frame-2F|Blast-3-isopropylmalate dehydrogenase [Phytophthora infestans T30-4](gb|EEY67409.1|) 1e-174

MPGKTYKIAVLPGDGIGPEVCDQAVQVLQTICELYQHQFEFLPALCGGAAYEHHKTHLPQ

STIDTVAASDAVLFGSVGGPTDAQEDPKWKDAEKNCLLGLRKNFQLAVNIRPAKIYSMLP

DLSPLRPNIVVNGVDMVIIRELVSGIYFGEHETNGDTATDVMKYTKAEITKPMRFAFETA

MKRSKKVVVVDKANVLDCSRLWRKVAKEVATEYPDVHLDYM

>contig47000 Frame-0F

MNKREVFILAWRIMCCWIKSKFANKLQLRSPLGIFVMTNFQTFLIDRNTDVNFVKC

>contig47633 Frame-0F

MASWRLRTSILIEWRSSISIRAFRIECVHRAGQNSTRILAGVCKQIQVLRAYYQCLTHKS

VLGDAHVLNIPLAFKSMGG

>contig47718 Frame-1R|Blast-L-gulonolactone oxidase, putative [Phytophthora infestans T30-4](gb|EEY69252.1|) 7e-63

MENLLRRIDEEDIPAHSPIEQRWTARSTSFMSPASSSNPDQIFSWVGVILYLPTTNKDAR

KAIQDCFMDYYAMYRDFMEPFGATEHWAKIEWPEDAVERQKLRSR

>contig47787 Frame-0F

MVFICQDIPAFVRNYKLSFEKSCGISFMFASNLSDDAVVEVAIFGCINLFSIVILPYILA

LVLDVSMHGNGRTQSLY

>contig48276 Frame-0R

MIDEAPCGSLNVDLETDLMAQVTATVAKEAGNVSPKFQHHEVPLFQLQLEKPSKKPRPVI

QELK

>contig48650 Frame-0F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY61687.1|) 2e-21

MCAFWWQDCARAFNPRIKTAFVMLLCIGVSASRKLDGMRVVNHHMRRLSQASDSYNFMFY

FVIGAMMVTCLIYNIFFKHKIEANFLRHQAL

>contig48971 Frame-0F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72292.1|) 1e-26

MLKDFGHEQVGVTWVGKDNQGAIGLANNAGYNARTKHVESPLHPG

>contig49110-1 Frame-1R1

MLAELDELLTLTPEVSLTLAQLPFDAGIDLNAVAFPETKISLGQLNEGLNPASFEALQPE

PRGKSTKILKTKL

>contig49165 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61423.1|) 4e-31

MEVVALNQRLRGSFSTLLKLLPPPFAVSAFAQSATSVSTKHRASSDFKMDGYTQHCRLML

WRLNSYQYGSLSAYLEDLEQLERVCESPDTRKQVKQLLDETRVSESEQQAPKSTLNATKS

SEASVPLDSTSGIPGIQEIVFNTQTRPL

>contig49279 Frame-0F

MSSKEEKIPIAWSYSAFEDAIISSSSDTSSACSSACSSACSSACCTYARFSSSANSELPH

PFQWD

>contig49323 Frame-2F

MLGDRTDQDLSTSFSSSDGQNFDYRTVCGDTNGSETFVSGSNHESESQPSAAMAVLEAIE

RESALYQQRASSLSSFLDSSMPFTQNEGQTPLPPRIPKRPPPGFAVDSMSTQQHQHTSNS

>contig49473 Frame-1F

MHVAQTNGVAKTAFDAPTNSVARRARMGVSETPEATSTLSGIASPLQNGFLVSNKNSLTV

AHAKSSKKLPNPVIHSTAWRRLLFKIAPANILDVSIIPYAADFDRPLWDYDRSKKLRTKC

SLVDTKCVDF

>contig49547 Frame-0R|Blast-nuclear transcription factor Y subunit, putative [Phytophthora infestans T30-4](gb|EEY57166.1|) 1e-128

MSNDGDANATNANLQMQLQLQNQRAQMQQQQLALHAFWQHQIQDISQIDTNTYDFKTHQL

PLARIKKIMKTDEDVRMISAEAPVLFAKACEMFILELSLRAWIHTEENKRRTLQRNDIAM

AITKTDVFDFLIDIVPRDDIKPAKKGPVDPQTVYQQQLQQQQAVMLQQLLQTQQNGAAAG

NVTWPNHQLQQQMIQQYQRMQQNAVMSVGGAALSSNGVLPNLSPSASDMVGQVSANTTPG

GNVSASDQLSLNQRSVDV

>contig50057 Frame-0R|Blast-anaphase-promoting complex subunit 10 [Phytophthora infestans T30-4](gb|EEY65500.1|) 3e-34

MDTYWQSDGLQPHLINIHFSRKTTIKEVALYLDYKLDESYTPKKIAIRSGSTAHDLKEIH

VQHIVEPNGWVSIPLYMDDGL

>contig51490 Frame-2F

MAQETKLHEHALSNQSLLENKVRELEKQLEELQERLNQKCEELVEFQSEVGSHVVVDDVT

PGDKFVVTSSDNDAISVLTEQVASAQRELTEAMELNLHLNNRNAWLEEQYMMLSSVQSEG

DEEHEDEGVAKVSPEKRIIVLEQQLQEAHRAVNEKAEHVSNLEQNHSALSTEFDRLHSSH

NELIESKQSDNATLDALR

>contig51634 Frame-2R

MDRDLSRTGQGIVMLTAGCSIFSVNRKLAEITEQRMMDNGVGMDMISLSTPPLHVVPLFI

YSNLTPEVKTATSVENNISDFIVGDVAVASEVSRSLDNPSFLNRTSSLLSQPKSSEGVQS

GVYSLNRSSTSAMHETNKTIAGDNPTYDVPHWVNITFLDFGCNCGTPTISLPHETVLSGI

SHNLQKGLPECVCQVKLSHHFTPLPLFRMFDADLPYRKIAFPVTLRNLMLKDLSIGKTDK

FTDSHAGKEMCINSKSSTIAGNLLLFNDNIESLLRQRAKNNGLSDLTSSILPLEPYRQSL

TSGLNALSQIRTATHLSASL

>contig51803 Frame-0R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY53246.1|) 1e-75

MLIDAGANVHTINKRGLTPLAVHLLTLTMDNPTLVNKLLEAGADPDSELEGVTLLHVAAR

RNLPMIAGVLVSYGATMQSLNTDGLMCYEVASSRVQQSMVRHITHMPAFVPATQRRTCMR

CKSPTLVPMKRTIRNRMKKVFGLHVRAHEC

>contig51894 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68017.1|) 7e-08

MGWKTEESEEYESSAPAVQAQFHACRHEQAFRRDDVRVS

>contig51919 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56527.1|) 1e-43

MSANTSEVLNNLIILQLEGVKRLATEYHQQTEAYVQQFGIMPFAQEPADPAHEARITLRS

LASASPSLAEGCAVSEVILDATKKHCGANMCATSPDNLDKFLFISKNDVKTAV

>contig52411 Frame-0F

MAEAAHPCMPPPGIEPGTFCLQDRCSATEPHRLHRYVIHLATNHVYFISLPYLPDHVEHP

FKKGLLNGIILRMSATLMQYNIAVKK

>contig53052 Frame-0F

MLNQIDDSLCLARSTPCIYVCGGSKVQMKASHSWVKNNKLML

>contig55021 Frame-2R

MLQHNTSALVSAEIVTRLLSRCVQQQRPLCYESWSVLLRKVTSVLVQWSATNCMAQQQQA

RLNLEQLKAILDEIPSLKQRLLPIAADSRMVCVPAIL

>contig55483 Frame-2F

MYFPTTLAPSIELNMPMSTRQAPRMRSSSAILALQQFHLLHALAHAAQ

>contig56073 Frame-2F|Blast-beta-galactosidase, putative [Phytophthora infestans T30-4](gb|EEY58470.1|) 0.0

MGLFLHVRFGPYVCAEWHNGGLPVWLNLIPGMKVRSSNIPWQREMERFLRYMVELSRPFL

AINGGPIILAQIENEFTAQDPEYVQWCGDLVTRLNTSIPWIMCYANAAENTILSCNDNDC

VDFAVKLVKERPSDPLVWTEDEGWFQTWQKDKLRPLPNDERSPKDVAYAVARWFAVGGAV

HNYYMYHGGNNYGRAAAAGVTTKYADGVNLHFDGLSNEPKRSHLRYLHEALIKCNSILLH

NDRQVLKPHDLPLVDGNRLQISSLQRAFIYGPTEGSNQVAFLENMANQSVRVKYAGNIFT

LAALSMIILKDGVPLFDTANVHESFRGQQHRLYSSIVSPEALDWQFWSELNVSSTVPRRR

VVADRPIEQLQLTVDQSDYMTYKTRFTMNGTSDSNEKASIVNVISCEGSSIIAFLDGWRL

GERNFAYPGGNCSKEFDFHLPASMDLNRSHDLKLISVCLGIDSLGKNHKKGLTGSVRIGD

TDLAHGYRWEMFPSLIGEQLQIYRPQWFDSVYWTPLPTKTRAGVASGRQMMCWFATSFSY

PAPQVLGNGLQSSILLDFIGLTRGRAYVNGYDLGRYWLINDQGDFVQRYYHLPRDWLFQN

QKNLLVVFDELGGSVASVRLVSSRMVLDDEKAFKDFDRSVEANFATNKIFSHVEVSRA

>contig56147 Frame-2F

MSHLPPTLPVAIKKEKEEISVVAAAVSISGGNSSIPRKDSIGWGADDFLGMISHTPPAFS

PGSLTMPMTKRGRSGSISSRLLSASDLEERGYIDRFQKGVLKDLIISGDEALQKALEKFD

AGDPTTLEAMLDSGVLNRNASSIDLLDDLDLGFLNVGSLGDTPKDEFPSGTRNQSLDEWD

ELGFDSSFTDVSARDILDGEFYSASLGASLPNSLPSMGLGITPPAGFSFAEDFLEKQVKT

EPGVKRGKNEGNKSNNGIASTLTSLPGASNMSTSRPIGIPGAARPYGGNDKCKEGQNQNF

VGAYSPDSRRKRIDKFLDKRQKRVWRKEVKYDVRKNFADSRLRVKGRFVKKEDEQLLREL

LSFT

>contig56723 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63687.1|) 1e-29

MARLLKPHAPTDATPLQDYLINWNAGPLGVVLQPELGADMPPVVVQLLPQPSVLKMAGVR

IGDLLISINGKKTTR

>contig56828 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60162.1|) 4e-39

MPVLIDSLSKCVTVCLSCILHSRNNPDEIRRGELGISTRRRDIINATFIIYDE

>contig58772 Frame-2F

MGWLAPEDEEYAQKFIDELVAMADNPTQLADAVVAATTLDKRIEDDINTMLAQDEELKAT

APTFIPRKLLSPEVAEFVPTRSPETPCRGNLNHFQTASTSCV

>contig03652 Frame-2R

MSDEFNTPKRSFRPGHDHIWTSLEKPDGVNGALELYSHNMTSTACDSDGTCYFYIKSVDE

VNIIHVYNMYTHPPGFVDAYFFYRAAMVQSWNKFCYQGGMIEVRVQLPGVVTPDSGNPDI

ATGPSTRVSAGDYYPTWPGVWMMGNLGRAIFSASTNRMWPFSYDECEPDLFEPTYQRISA

CNDNPGYGLNPNQGRGAPEIDVLEGAAGLVSSSLQIGPGMPDEFRIKGINYGIDGEGCIY

SGACKTPGANLPDVPTALYKKERGHKTWYQGLRYSANNFCKSNGKEKQTYQTVAASVKAG

IVENTCSSDTCPASKDVNGDISLIDGMGDDYWGINSNGTCFPLINVYTGAYLCDPDNTFW

KCAMPRDENKTAKSNAMSSFNYQMDAISSNWPVHVGAYLGFVTYQLEWVTGKNGYVRWNL

EGSPLFEVPSEAIWDAPQNA

>contig04558-1 Frame-2R1

MRTKQLGLTLRKYSTTCCRGCRSRNA

>contig05027 Frame-0F

MVLGDKCLEDLPTTLQSGEVLCDLVNILYKALGMKSQICPVRGRHTDKDAEKNVHVYLRA

CEVLGVARVDLFQPQDLLDCKRMDKVYRNILALQSVAVLLSNRRSIDERSVMVTFPVTWS

PQSNLANPDDRDAKELEPLTPESIQMRQQSRWLRLLFEYEYQQQRHEKRDISGESATITG

LGPVAHGIWRTEERIRAILLRNDREYGAVPEELHGKLWMLASGAQIEMRKNKGQFTRLLA

TEVENTEASRQIDVDLHRTVAEEDKQHWTDEKTQMLRRILVAYSLYNPSLGYCQGLNYIV

ARSLHYLNEEEAFYLLVAMLQLVPEDYYTTMLGLAVDQHVFADLVRIQYPEIIQHLIELG

GSGMELSLACTEWFLTLFASPCQRIVTFPIWDAIFFQGDEVLFKVALAFLQQAKKDLLES

RNYGDMLNHLNELGRGNIDALSLMKVSRDQTCVLRSRLEDFRAHHRLQLASGIVASSVDA

EDPRNSHHGRRSSEARADSKLRLFGRKKQGVSRHMDRIPPRFARTFDRVPSVEYIESIRR

DHLNLAQYYQGFPPQIKEEYWGSAERSSQWSTRRVSTVCIDKLNDKTTHEQPNVLSCLNN

EMHCINRRTAPDGSNDCELDATRDCRSKSSGVVHEQASSCKLGTRNAINVRLTRMRDEEA

GRSPLAWIQRFEEWHKELKIQKEKKKHAKRRRWHQRSDSLFNESNGWNTTISTELMTSQL

MIPSPEVEIDSLERKSEDSESFNKEEIALLEEPLLARSSIDAFPSLPGIVGQRLSRPTRE

NLLSDTNRVMLLPSNGESRIAQGLSDQNPLSRSPHSYVNTASFTQEETHVHAFLETEDAK

EQGQGVSPTLTQLSIPPVHEFLYSPVQCQLVPSDFITRQSSASSVPPRGRQNVLLSNENS

LSLLKPPCNSKRECLQVLRERANVLQYMHRKASDASSLAGSIPRSPAGISERSSDSFRVA

DQSQSGKSMPYRNSSFSFFDKLSSDLENSTHGLDSLVDESDFQGESSGRGSMSSVATG

>contig06736 Frame-0R

MTHRAALLRSALCLTTAKPRPSPTLFYFPGLESAPWHDTSKFEWIKHIEANREVITKEFL

ALKAQRANRKSPGTDYNTSDHEHQLHQGQWDWLSYVTQGRRQADFAVYCPKTVELLETIP

GFLSGLPFAYCFFSVLKPKSSIKAHSGPCNIRLRCHFPVFVPKGCGIRVGSESRQWEEGK

ALVFDDAYDHEVWHTGLKKDRVLLLFDIWHPDLIQEERDAIT

>contig10829 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70657.1|) 2e-24

MNQLAEQQVAVQRKLAEAQVKAAQTARAQALAQAEAAEFAVKNIEAQVAAKKVAGEKVRK

RK

>contig12795 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53427.1|) 4e-07

MTRIRDYANAGSCIAKLSNNVLVEL

>contig12935 Frame-0R|Blast-large subunit GTPase 1 [Phytophthora infestans T30-4](gb|EEY67589.1|) 1e-19

MGRKGTKLKKGELGNALMRTQKTTSSITTKDVASSAGKNVSERDGGDASTALASYLEGSS

L

>contig15123 Frame-0F|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY69640.1|) 4e-50

MYQILKGVDYMHDAWVMHRDMKPQNILVVGHGRKRGQVKLA

>contig15347 Frame-1R|Blast-methylmalonate-semialdehyde dehydrogenase, putative [Ricinus communis]gb|EEF29994.1| methylmalonate-semialdehyde dehydrogenase, putative [Ricinus communis](ref|XP\_002532382.1|) 1e-11 NOT\_ORF

MACPFSAAN\*RIATADDEWQVVFNCSDHHHGQVQALLYYPAARKLKPREQETIKALSEVA

ATPKLFLQHCV

>contig15606 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60002.1|) 2e-21

MGEKLVLSDPTGEHYPWAEENFTLPRPKITVSEMKCIAMGMKQLGLKTLKQYEMKFIQPH

GL

>contig16445 Frame-0R

MSIEAPLSDSDSKDIAPLRKEAAFFIEHSCTQQRRHTPCRPRSGYTHPPWSATVHYTAFA

SPRRRPLRRVRVTRHPPCRPPTRRTRRRIGLAVARARALRTTCP

>contig16632 Frame-2R

MHVDPRWKYALETVGEKKQAYAEYCTSAKNRETIEKRRGMKKAREEFVVLLRLFETTLVP

RSPRRVVTWNEVNESTDFYALRNDPRWATIDDSREKQQLFTTFLHDVEREDNTRREEQRK

ALQRGFLKLLQQRVETNDVVLPKRLDREFKRRVLEVLQDVTIATNNARIGDEALRMVDRQ

DVYDWTDAFLREQRELTHVERKRERLERASRLDRFKTAWRVHLDELIQGNHVTAASSYES

CRVDYSFDVWDVKRVEKGWIQDDDDMTLYRKEQRRIFDKTVRRLRRALEPTAYVIRKFLD

RSGPSILHVDESTTFGAYETALEKGVRMVMKTNALEEGEEETDVDIAMDTKMQRFKVTRA

LETAVMETKVVFPSFVRHVFDMWVAMAKEGKSRTKDDKRRKRCRQASVEHDRRHRTRRAC

IVTDDDEDESTRRRGLRKHHRSVSKSRSRSKSRRCLSPRHGTHSRTRMEDTVCLETTCDG

TTSVVRYKPLSEAEEAAKVEEIIRQARVKFQGKEKNGMDCELEEGEEIEEGEA

>contig17468 Frame-1F

MRAFVEEASEYPLRDIANVWPWLAS

>contig19578 Frame-2F|Blast-predicted protein [Physcomitrella patens subsp. patens]gb|EDQ61794.1| predicted protein [Physcomitrella patens subsp. patens](ref|XP\_001773421.1|) 3e-72

MELAIVRRESVGSGTQRHSASETVTKFELLDGAPVKGESVPVRLYLAPYALTLTYRNVEN

RFSVRYFLNLVLVDEEDRRYFKQQEIILWRKSSG

>contig20934 Frame-0F

MARAELAKYNAIMFQDKKLEEKGIQKGRLTPELRATYETKIKNLEDALDKFHLSVAGYNR

TKALLSFVLLVAFALLMFFQPWAKHFENPQDLTYDEYVTLDEELTEPRKQKLLESSDEL

>contig24682 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65824.1|) 2e-52

MGANRLRNDGAAAIFRSVVKRARIKPMILVDLSGNLLTLSGLVLIAEILEAAAVANAPYC

GSNEQVDALRHRKRRRTNDLVSQTSPRSCSTGNKFIEELWLLNNEFLESDEIKSNSSSLI

ASIRNCVGHLRSNEWASFPQVYDDEV

>contig24813 Frame-1F

MEESTLARPRRGVSRATRSAVKPSKGGISDVLNTGGSSADEEDEDEEEEEEEEIEEEDDE

SVHGVDESELDVIDAGFRTSPTARELHTLEKGTLVRILKTPDVDQRVPHTAFKMGVVDEV

PQHPNTWFKVRILDGDVVYKYRPSALEVLDEGDDSGSPGASPPYSLIAHQDEYSHYDDAE

ADKDEESKEKRVIDHHELGNRVKLKLGALNAAEKRYLKNYDGREGTITGRWKAGVTVQLD

GSKDIKLKLRQKHLVLLLNTRHAEDEEEKDEETKEGKKAAVILKKRRGKGKLLSTLDPDM

WIERKCRINVGKFKGQHGRVLRSGNGWVQLRLENSSENTAKRAYELTLLEDLQTIKMLHV

KTLEKENKRRGENGVTVVGDDREDEEDDDEANQSGADELQAAEHTDDSQGEDNGKRLCRV

STRGNYGMSWIGKKVNLPNRKGFGIVKKADRETCTVEIQTTQVLQIYKKKDLQLASDVYA

KTARQNSRNRNNAKAREKLGLEDDVILMGTTPSRYIAFQDLVKRFAMRRREKLKKRPNLI

EWEARLNLNYLENGSSDKNNLSVVDLVLVPQCEICGLEKEEKDGNCWNNKCPRSPAFDVD

SYDPKSEDAFMRVPDVPFFNNNMTISLCLDKEDSSRKRKLGSLHTTPTEICQPNLVMNPF

STTKPEPKAEDTQTKNSRIYVYKNNVGAMLGHTSTDENDLDNTSNAIANNARAQMGSIEE

VTNGLNGGAMSEEMLSTSAFRPHYDSVFSR

>contig25160 Frame-0F

MIDGIEAIAGNRRALANSQSALEFGVLNVLLSFLEKLKSSHQKIFVLGTTSRAEDVDSAI

ISNRRLDQVVYIAPPTQIERFEILQILTNAWKGGLDIKFLNQLSERTGGFVGADLLSLCQ

KAFQVCLNESTKSKAEDNFTVCPRHFEQALAVTFPSVLQAHYLLQKQQQPISTSLQNYGD

AVSEGVFSCVYGMNDAVQNLRVSLIDPLVDCSRFLKFGTMPPKGVLLIGPPGSGKTYLAN

AVAKEVRRLGLASFVSVQCSDLLTKIVGDTEKALHDLFVTARNAAPCVLYFDHIESIAPL

RGFDTSTEQTFDRMLSMLLVEMDGFNSSRLELQRSLASDEARTAFLKEHVVILASTTNRK

SLDPSILRPG

>contig26738 Frame-2R

MEQLDTYSTRRVMYPRVKEAESKDCRLEQFSLSGAIYKIFLNFLPLLRSTRHPRLHLLNL

LCFALPDLPEKSFKDLISESNMQELNNLRLEHILDMLSGICRPVMQDQSRWIMVDKELEL

TVSMIWKLVELVLRLLRLYPPSQYYVEGIETKAESSKKGMKTREKG

>contig26785 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69848.1|) 3e-14

MKTLVSVVLSLVLLLLDAIQGAFEASSATSSSECCHTCIGKASSVPYTYDPGRFCGLHQS

NRRGLLL

>contig27188 Frame-0R

MDMRGLKLGEVTMRTAYLMGSCEKDSAVVTYLFMYISNHLK

>contig27302 Frame-1F

MAEISCTHLHALRLLSLRNPSIMSITERAFRPLVGSSRNRTFG

>contig27878 Frame-2R

MVLFPINSTTASPIQSGPVAIIESKVAEEAVKALVKQPASSKIGKRRDRGFKPKLKPKKT

QIAKCVGFYVDALDKKLMWGEARIIQCNLDSHKIKVHFVGWSKNYDLWTDPISITAHGRY

ARSTNKSEKSWDGDMRLFDDVLGTIVEANFNPVPAPTHSEPQSASVSGLKRMASTSKVTL

GEKGAQSLRLPNEFQKKKSHSKSKNHVTSIENANLKKNAIASKAAGSKKHGVDSLRGTNG

LVGGATNKENAQVKRDPFRKLKSRKREAEESVPTNDFETHSFNKVRAYSFNQLPLIRDLE

LDDGTVLDFSEQREKARVQREAMQSFLSKCALLWKQQLSV

>contig30610 Frame-0F|Blast-ADP-ribosylation factor family [Phytophthora infestans T30-4](gb|EEY54603.1|) 9e-10

MGIAMSKVFAALFGSKEVRILILGLDNAGKTTIL

>contig30764 Frame-1R

MRLFANKNGWSLSDRALTRVMRVNGKRVRLSDSVICESEVDVFIALGLIYKDPTERNCFD

IKFIEEDEAHAKKRLSIEDRI

>contig31639 Frame-1R|Blast-histone acetyltransferase ESA1 [Phytophthora infestans T30-4](gb|EEY61204.1|) 1e-108

MELTRLTSIKNEDIIATLQHLNMIKYLGGQYVYVVPTQIADAHLAKLSAKGPQVFPEKLH

WAPLHLDIKRDKWSLKAMTADKEE

>contig31741 Frame-1R

MLIYTFTAMTVITDRFYPTFSFYYTSDDPKFLRQWFQLACLASTFWVVLELWLKWLHMAT

FALIVLWSTMLPLYLFVVRHPTLRHSQAWVYYFCSEFSIRLYFGWLSADVIFSIAGVLQE

LHGAFFGFGVYASLLGALLVLMFSTYVHGHDPVVGLVVTWVLFGLIFKQSSYPGDTQEVF

NELRAVAVVVAPVFPVLVFIDSVRYVYTAHWQASRILRGSNEFKSFMYETTSEYGTV

>contig32784 Frame-2F|Blast-inorganic phosphate transporter, putative [Phytophthora infestans T30-4](gb|EEY53220.1|) 2e-97

MDTKGVGRFKLLNKVRNSTSLQRKLFGASASWFLFDVTFYGNIIFTPIILRDTYGLDKHH

FGDIALCSLIVAIIALPGNLLAVCVVGKVSFRTIQIVGFLVMSLLFLALGGFYEQLLNYR

GLLLNMYALTFFFSNFGPNVGTFCLPAEIFSDDVRVELNGIAAAAGKLGAAIGAASFGII

EARFGVSYLLALSATVSLLGALITYTFIPTKHYKLLKTARHA

>contig35576 Frame-2F

MASSRWAIEHDELLLSVAGRYGTWPERMHVFTQELHSRRDFLLLPEPAFTLPEIQSHLKK

LCNNVPNEPIQSLSNGWYPKRTTLLQQIDANTKDESYEVKTVVFNHAVKEKGWSFRATLD

QVKWKLLRIATTE

>contig37516 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64310.1|) 3e-50

MDYFEGELRKGILKALVHRHMSLFLHWNADVRTKYHHILVYRLVRVNRFVLDSPVDQLLI

GHCAISTFEFSRAHDDEFDDDYVLSHRKHKEDSRFHDAVQHPSNLSMTTADISV

>contig37970 Frame-1R|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY66120.1|) 1e-103 NOT\_ORF

MKTWKRTRNKRATTHIKTGASGQYLTSIMRKSFEKPPEVWDAFRNSIFGYSRMNVVNASH

LHW\*RVEADPENPAARGLYGQVVDDVWLVQEKHGSFRQL

>contig38265 Frame-1R|Blast-nucleolar protein, putative [Phytophthora infestans T30-4](gb|EEY63521.1|) 4e-82

MLCWVTPHLSNLRHNLKIHRFQSSRIYTMADNHPINNTCSPQGVATFAAGCFWGVQLAFD

RLPGVIKSSVGYTQGNVDSPTYRQVCSGTTNHAEAIRIEFDESQTSYKSLLQEFWAIHDP

TTLNRQKNDKGTQYRSGIYYMSEEQRKLAFASKEEHQKKLSKPIVTEIVEAKTFWVAEDY

HQKYLEKGGQCADKGCKNPIRCYG

>contig38900 Frame-0R

MWRGAPSPQDSIGRRSTPNAATTPSSQRSGTTKHGTVLVNLDVFIHRANIGRDISPNDDT

LVVLFRRNSKEVTSEPARWNAEHCAVWNQHVGIQTSLLRQKLQMQGGSATSMGFLKKEYE

IVLVALPSHSAVALFSVDFASLVQQNTQDLHKSFHISPLKCRDLAATLEFDISWELEDNT

GANTMMRPSTPKLVGRSPSSTILSKSSQPPKPQTPKAQTPRSRQASKSRRSANDTMSLSS

RRTTTSSSSAGSERELLEELSSSNCS

>contig39312 Frame-1R|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 5e-13 NOT\_ORF

MDRELASSHRRLITSL\*SSRNEFAKMEIF

>contig40330 Frame-2R

MCIRCFTCNLFGGAGTRHDSMSVVAKVFSRLFYGNPDLVISDIVAGFILLAAVQAYEEHQ

EVLATSLHDEEEESKKHRASFQASASKPKTLHDAVTINTGIVNTSNIDQSSHVVSIDVPS

LNDADARFQHANKTFYYHPADPHLRDVELIEKLQEMAHYSKYAIGIYGWMLYVWSHPWSG

TFRLAFSCLRRHVSYVHGDNWFHLSQTALQLETKLHRDDIVYASFQNSVYQPAFAV

>contig41791 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60890.1|) 2e-76

MHVRVCRLRKSLHLFGPPHLVSPLRFSLQHLSSSSNAKPSILDGPDGVNQLARRIVERFT

TQMERYRKHSVFLPSNWWLKDFILFTKLQVPTHTEIDAVDFLHGAQFACDLVIQTMYSKE

FLNYATGAISESAAAEKMKLGMSANCFDAFVFAMKQTHKSGNQFTLRQLDINGIHLFDVE

WQRMSLAEYKQEQAQEATNRAKIAAMEKDGIAEENEKESLADIHVEDHAVLIERLQLDVV

FNAVEHLTIETLEAPDRVTAKKSSATWRFESLVTQPEDLDWRIVSVS

>contig41975 Frame-0F

MAPLQDTDSIRSDNNPVIDCPLKKKAKICHRSASESDKSLQNRFKHPLGVKPIGNLFEDT

ANGLVECRTSGLGHLALLQDSLLLSLLNYCSALDLATLAACSRSAYVYGTHDELWRVLVL

QEMDGSFIAESTWKLSYLKTKYSNTVSYLPSIHVNGVYSDLLFQSFYCSVAPIEKSWLVV

ENIERRSAKTMTMADFKANFEGPNKPVIITDAIENWPAMKNWTDEYFIRVCKGKTFYAGG

FQFSMDKYLSYCRALRDDQPLFIFDKDFAAKVPQLANDYSV

>contig42563 Frame-1F

MSPFEHGEVFVLNDGGEGDLDLGNYERFLNITLTRDHNITTGKIYTHVLEKERRGDYLGK

TVQVVPHVTDAIQEWIERVAQINVNGTHASGVDDDAVDVCLIEVGGTVGDIESMVFLEAL

RQFQFRVGPENFCLVHVSLVPVLGSVGEQKTKPTQHAIKELRSAGLTPDVIICRSSKELE

P

>contig42970 Frame-0F

MPINTFADDEDGEALLQRQIAMLRLCGGLSLLFYGALSLAIIWRTSLHFLYSSNGAKKAF

HVTLLISTLLLLPHAIEWIWFPTPQAWMVMYVCRLYSLLLFSICKSYLAVCWAGVVSAGQ

QLARHRVTNFVTGLNILLILWGLVIPILLFKFSDNTRGRNRFMRSTLRYAMTYSGFVVVF

TYCVLLGYQGFRLRRRLLLARGAVPTESLTRSLNQLILAISIFLVSDVVRMLALLLNESE

AAMPIVVYLILYSVIPHIFPTICMLYLMRRLTGRSGSEVNVVQLKVNRSKGSMSKYMTEH

DSDGSTGSDGASRETVVIRVQGGKLQAQRHCIDLQVKSEQEYFEYS

>contig43304 Frame-1R

MKAVGPKDMTDYVAVLRVNMDSTENSIMFYDSEITILCGLMCSVSQINAALPALILLLLY

RGQALSPNRAMLC

>contig43779 Frame-1F

MRRQLRQPLLPIRCAYNAKRDLSRPMSSIKELDLFTPTEEHGALRQMLANFVKTKVDPQA

LEHDRKEKFNIKLFRELGDLGLLGITAPEKYGGSGMDALAAVIAHEELSSSDPAFCLSFL

AHSMLFVNNVARNASDSQCQKYLPDACSGAKICGMAMSEPSVGTDVLGMRTTATKADCGK

FYLLNGTKMWITNGALNDTELGDTFLVYARTGNSGKAKQDFSSFIVEKGYEGFSLGQRIK

DKCGMRASNTAELVFENCKVPVENVVGAEGSAVLCMMRNLEIERVTLAAMSLGIARRSLE

VMNNYAKEREAFGRILNSFGQIQKNIAESYAEFMAGRAYVYNTAR

>contig45687 Frame-2F

MGSEDECEDGEILQEGEAIAQVATMNQFSVSVALSTLNVPRTHQGIGHPSKSVASLTPTR

QTPRKRTHLALDHAATLKTASSIYDTRVPLSQRQRTTNHHNTDRRRDDAGYEPLDDRMYA

ENMIIQHPRQQPSSNVLLDFAMWMSAVRSRTRLNLDDVQTLVLNVLRGDKLNEDGLVSPF

LLPYLFPGAPLPTKVCIIMLKNMHPSVVQKFRPTLRFFDQCSSMPVVVAKAELTQIRRSE

APIAELMYRFTKPRVDLTILSVALSTLNVPRTHQGI

>contig46237 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY64219.1|) 5e-57

MYTRSSIECDIWVKMVQQAVQNARNQKPNESFSNTSNGRDSDPQAGRVSTWNPLSSGNHP

FSTSSILSQTVRSSGDWKARNLATIK

>contig48477 Frame-2R

MLPSPIASPLLVRCGFLKNQVNGSLFSSWKDVLCALTQDGCLHLLDLKENTTRAILESTE

AFLSAIATNEQTIEVNCQSICLTNCRIEILGKSVTPNFEITEVTTPSGLLGSMLRVGISR

TLTFQCPSQSDLIDWVVAAKQFISVGSSMINR

>contig50340 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58053.1|) 1e-69

MAHDGSNLFQIRRIFGFSTSTPISNGSIAALHIASMAVHTLEKKQLLALAICENIAKPVF

HSKSESSSTPSASPADAKTTFLLVRTIEEDQRTRFWRIPVCSTPKQQKAGKAERLFALEF

SPEGDWLAALSQRKNRLHLVPILKIVSMQRRAMLDAAYQPTSHHR

>contig51167 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60205.1|) 1e-15

MIRQRRKWRQHERDKAVRNVFEAQMHATMRRQSLKKASSRLVQEIEGDCLTLDLGR

>contig51365 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64236.1|) 3e-18

MCEQNDRVKCEVVAVVFSVFARVVSPALRCIANGLIPACYERLFFCSQASYEAEIAILKH

VSIDAALSGNTSIMYAPSGAIVQKLASTDCFEPLTSVQLLGLLVVLRSSDSHARADGSLL

PLLVQSALFCLKKASAEKAEHDSKGISSDIRA

>contig51637 Frame-1F

MKVPRKRRIYDVLHVLEGIGVIKRVRYDEKRKVSGGYFLYYGKASVVQHLVQLKSKSAQI

MTEFRQSRQSQNHSIVEEDSALVKVFEDQAA

>contig51897 Frame-0F

MFERGGIDTNSSNNAGSGGSHTFSIETHRDAPHSQESVSFLSSMPIEEFVAKYQVIKISW

RGKYDRILAMAPTRFCTIDPRDFEVTNSWLLTAIISISLDPSDAQCFTVTLKGTKKEEQL

KLRCLYRSRLLMDLYRLKEQYQQRNVRSETGIQCAKWSRRRYLINCTLFVGMDGITLLQQ

GRIRSKYLYTEIEHLSLLTDSQDGFAVGYTGRSRLLFSKLRTQIYQRIQTTAEAIGRNFD

VRRKVTPKYSEAQARTLSLHNKGLLELDSEDQVVAYFNYLDLYVLVREPTNIDHFRIQLR

NGQVRLYLSTDRDGVLSAIYDICVTCQENVELFISGAVSPRGLRLLPFSAVEDAAETQPI

LNEKSIGNWYLQRLGSLGKLANPSKIGDRRI

>contig52412 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68516.1|) 3e-46

MFADDSVVVVPNQYALRVATASDFGKPVDLMCYCLQRHAMVELQLRRMIGVFNKTEEKRI

VKVSVAAFAARLDALG

>contig53051 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64099.1|) 4e-07

MQRFWWILTALKGPFQAKIQPVRWQYLTQPLLFQILEFVATTTYVSNEKTLPAFDSESH

>contig53701 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61322.1|) 4e-90

MVNLIKLLSHPAAQPFADDVTDILIAVGASQRAFAAISKSKEQRRRYTNAPTEASLRRAR

IGKRTAAQSITEQVENANANAHGKRRRVNLSESSGGLIPCEAATHDGIVNMQAVDVANLV

LESFASEMPSPAPLHIELELVPSALKARMSLLLSKLATPSSALAIEKSTKRMRDPRLRRD

QRLQTQNKEQPALVTIFDDVVAD

>contig54308 Frame-1R

MRDENHRLAMNYGGNATLEYLDLFDMGVDGLFSDNCKVSVLARDAWLALQ

>contig54551 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67255.1|) 3e-26

MIFSMLYATGALLILRLNGRKHEHLHGIVMASPLYRRLKLLMLVCAVFTLPYS

>contig54858 Frame-2R

MTPNEQQQRAQAFAHSTAYVLSYQIAQSLENQIS

>contig55022 Frame-1R

MPKAKLKILNGDNVEIHETGGLLLMCLEISPRADTLCKCFIDVCEGPFSEFFPA

>contig56070 Frame-1F|Blast-PREDICTED: histone cluster 1, H2ag-like [Oryctolagus cuniculus](ref|XP\_002721657.1|) 6e-52

MSGRGKGGKGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLK

VFLENVIRDSVTYTEHARRKTVTAMDVVYALKRQGRTLYGFGG

>contig56566 Frame-1F|Blast-phosphoenolpyruvate carboxykinase [Phytophthora infestans T30-4](gb|EEY56657.1|) 1e-165

MAMHCSANKGKHGDTALFFGLSGTGKTTLSADPQRYLIGDDEHGWDDDGIFNFEGGCYAK

TINLSAANEPEIYKAIQRNALLENTFVDPMTKEPDYSNTLKTENGRVSYPMAHIANHEPT

SSGGHPSNVVFLTCDAYGVLPPVSKLSIGQAMYHFLSGYTAKVAGTERGVTEPTATFSAC

FGAAFLPLHPTKYADLLQTKLKKHHTSVYLVNTGWTRGSYGTGKRMSIQDTRACIDAILD

GSIKTSEFTTDPIFGFDVPTKLGDIAANVLNPREAWSDKAAYDATAIKLAGMFQQNFQNY

VSPGVTDYSKFGPTISA

>contig56720 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55812.1|) 2e-67

MFRAKLTSMGATARSRSRLQRLLATSAGSDVENQLFLKSISEDQAKQALERSAAIRADHL

AIKSEFPTSSQGDHVVSTDEANRKRIIYRSKQRGWLEVDLLLGRWASENVMKLTSDELQQ

YEEILNEETIDIFNYISGKNPVPSKLDTSMMKRLQEYCLTSPLGKASIDGFAENKKFMSN

>contig57077 Frame-2R

MATDNTSSNADWMKTVQDTHPRQSFNELKREGRMANKNTEAPLKGVYYGKCQYKTGKCYN

ERTFKRNGEVHTLCEEHRTKQNSIQRRSDRKYQTVHAVRRRERSQRRAVLKRQASMAVAQ

QLFFEHQHQKTMGIPLPSYHPLHLLTVNPNDGQNMSPIRIPPPIGTFNDQNEMGSPLVLS

ILPQNNCITHANNKSGHAPIKDESTPTGIDDLTPSAFLTIPMYGGDLCMPTLRDDEILVS

STSSDSFGYMPITLSSGEKKESWSEDDIEFLQTILL

>contig57253 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55633.1|) 8e-09

MDDGEFLRLLERYPVVRKKTHCRVQWND

>contig57675 Frame-2F

MANLQVFTKMAHQVGGHSTSNTS

>contig57891 Frame-2R

MIQAAREADPRIASIVTIAYDEYWKTYKLEVAFNDLKL

>contig58429 Frame-1R

MPTLEPLSDLDLSKSPALAAMTAIRAREAPVARQGNASNESSRYAMSAELLKRLNITSEE

DEEDVADREE

>contig58771 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61143.1|) 2e-07

MQLLETWSTPRLEALGVDGVFAPYIVGMLPP

>contig03059 Frame-1R

MLAKRSNNRTHSRPYFTHCNNGQLLHRAVTFLSYSCQWLVWIWRCHKNIYRAII

>contig05224 Frame-2F

MVYERTFVGVGTVMPTVVGVERLGHDSPSSKRTKAKPPSKKTNSSRPLALKELPKVVQKQ

IVESEWASLYDSQAGCMNDLNIICRSSEIRVRKLPTKERGGAVVHAYAGQSFNLFSPSPF

SRWISGRVVLPPGAWKEPEGVGQAVQLFYVTGCQPKSLEVALAPETDDDFFTSKFTTHFL

LSPGDEFYVPPGNVYYVKNHSTSADCDLRFTILKPEELQMADNNESDVEKEKGKEEPLVT

TELLQEAAKIVNSPLKGEKAADIDVDSDTV

>contig08902 Frame-1R

MIDIIKIFQDQMKENKNTLFVGTPGTVLPLITCSFLF

>contig09127 Frame-2F|Blast-Amino Acid-Polyamine-Organocation (APC) Family [Phytophthora infestans T30-4](gb|EEY62249.1|) 0.0

MSNSSDCRVIRTRFDSCEESHRVHLVPPSSADRSPLKSWRNLPSPIDHHTPRSLQYEAGA

TETQAWKLKRTKKRTINHVTLGFIAYFAVAAGPFGIEDAVRAAGAYPVLLAVVILPFTWG

LPQALMTAELSSMIDENGGYILWVRRGLGQYAGWVNAFNSIASNVCDLPTYPVLFCSYVE

AFLASGYGYTLSSIEQWLVKCVALLLVFTSNVVGMRVVALASVLMSLFVLAPFLLEPLSI

KTFNFATWGSVSPHLDWSLFLSTILWNYQGWDSLGCVAGEVKDGGRTYPIAIVIAMGLIT

INYAFPVGAGIMVQSDYSQWHEGSLETIAMTVAPYLGVWVGMAAVVATLGEFNVVMACSS

RALWATADYKMLPAFLTYEWKRFGTPVAAVAIQTLTTGVLMNFSFEFLVVLDTFFNNLTL

LLEFSAFLRLKYVEKNTLRPFEVPFGNTGAWGITVPKILVLVGVLVAQKRHVWLACGLFN

VAVSGAYLVWRHFQPSPRATCESSSTAYGTGQLS

>contig09574 Frame-1F

MGALVSGQDRETGSKKRYTVFQIFVHFQSGAVRFLEKRYSHFRELHKNLRRLYVMVGKLY

FPPKKFFMSLSLRVIEQRREAIETYMNAVLALQPRPIEVVDFLSAGSSSVESEEEDGSST

DREARGVDSINEPKHVQSTSKALASSTHFSENNNFAPNDAKECMVSMQDFEILKMLGKGS

FGKVYMARERGTDGKIYAMKVLRKSELIKRNQVGHTVMERKIMSSIDHPFIVGLKYSFQT

ASKLVMISDYCCGGEIFFHLKKFRSFSEAMVRFYAAELVAAIGHLHERNIIYRDLKPENI

LLDGTGHVRLTDFGLSKTHCTDLSGARTFCGTPEYLAPEMLISRKKKTEYGKAIDWWSLG

TLMYEMLTGWPPFFDRNIEQMCTKIMKSPLKFPSHFGLSFEVKSLISALLERDPTYRIGS

RPGAGVEDIKNHVFFASIDWSQLEMRSIKPPFKPRVRSPTDIQNFDREFTKELPDHGFLQ

QDKRLRVSPKNEFKGFSYTRTEESMTLSRDTCSKRGKRRLEPRHSDGVEHRIQLVTDTQN

VDHGLIGRDRADFDTGCI

>contig12794 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53427.1|) 2e-12

MINHDTFFYRHYSNYNYSFYSTTMFLRAGRKYAKLGAVALVSTPLFLSPKQTHAEQRVYT

SGEALGRGVRRELWKAQ

>contig15672 Frame-1R

MCSKMRARDSCCFCIESERTCSAALMSLMFHVLRRLINHQLLCLPHYV

>contig16930 Frame-1F

MNPVASEELMKLRHHASPGLRPQHSPGVKSRSNTFVGSTPSSILRPSHHQPQETEDAEYG

IEVKERPASSHGNRPRAGTLTRSKSEELLSVAASSTNVVAAEVATPKYTNYMDDAITNSV

LLAATTQHFGGDLVTHEHNSRAQLGGHRSLLVRGPRTVMQHGSGGKLMIFLVGLPGRGKT

YIGHILARHLTWMGHHSRTFNTGEYRRKLVGSNVNHAFWDPMNEESVQIRNDLSRKCLED

SIAALESNDCDCVIFDATNVTRERRDMLLSEVRQRYKCEMMFIESVCDDPELIASSINEM

KLNSADYAGQTMEEAAADYNNRIQHYQFLYEPLEAEFESAPFIKIIDVGRQIFCNQVYGY

LQSRIMFLMANLNLKPRPIWLSRHGESMYNKQKRIGGDAPLSPLGVQYAVQLDRFIDAYY

PSHDTELAVWTSTMLRTGMTVERIAARGRSIVKWKQLDEIDAGICDGMTYKQVAEEMPEE

YLARKNNKLHYRYPRGESYQDVIHRLEPVITELMRMNQPVLIVAHQAILRVLYAYLTNKS

PEECPTLNIPLHAVIQVTPKAYKCEEVWHRPM

>contig17520 Frame-0F

MQIQLLEQQHCGGNSLNRSMQQKYADQNADKPASKKGKIVRRRVKTNDLIENTSDESRGF

VVERPSTRYCDIGGIQAILQEVRELIEYPLTHPEVYAHLGVEPPRGVLLHGPPGTGKSML

AHAIAGECGATFLRISAPEIVSGMSGESEQKLRELFDEAISRAPSIIFIDEIDAITPKRE

SSARGMEKRIVAQLLTSTDSLNLDNTGGKPVILIGATNRPDALDSALRRAGRFDREICLG

I

>contig18015 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY58585.1|) 5e-26

MITLRQILLFCVFFSLFPLVALCLCFIENPDPPAIPSAHPSA

>contig19579 Frame-1R

MDLPLFVSSRRGSLNFTRSSSPFKTKLSSADGTPNPNRSYFMRHRSIRTVEPREGQTCHD

TVRRRAQNNAI

>contig21158 Frame-1R

MASSREDEYDYLFKIVLIGDSGVGKSNLLSRFTRNEFHLESKSTIGVEFATKSIVAEGKT

IKAQIWDTAGQERYRAITSAYYRGAVGALLVYDITKHGTFENVERWLKELRDHADAHTVI

MLVGNKSDLRHLRAVSTEEAMAFAEKQTLAFIETSALEATGVDTAFQRLLTEIYKLMSRK

TMQAETNPTTSLPAGNSIAITTDNTSEKKKKKNNGCC

>contig23048 Frame-0F

MNSSISVKLKAMAAYRQALPKLASLSTVPMDVFISIMNEGVDGANLLQSHSLI

>contig24683 Frame-0F

MGRKKIQIKRIEDDRNRQVTFAKRKNGIFKKAMELSKLCDCEIALVVFDSNEKLYQYSST

GVDQILLKYTEYGEPYETKDNTDYEIMFGEKKKQLQQAAKEAAAAMAAGINSEASSSYNM

VHGCVPNGAPVQSLQNMHGGMNGASLGLTNDPDQYMLNSRSRPPQAQKKRVHRSFQQLLK

KEHAGFIPPSLPPYQHGMGMLGGLSGHHMLSALPSPPNLAGIIPSPTTGMLLHDFSPQNA

GFFGHHSMLGGGLPGEFHDNKSSVLGLNLVPSDFSNSSASSVHPQQPQQSKDVYYVQSKQ

MDSPKKFSEECAVSPVENSEPYSDKQLNEVAYKIENYSAEDSSQPQSAEASSNSKDFQSP

MENEAANEITSELAISPDRQLKDVQLKDERAPSNLSKSDDILNASPTKSESISQSLATAS

ETQEASSVEFEKRPRPEVLVTASTSPNKRQRLAV

>contig25675 Frame-2F

MQPSILLSLAALSAQLTNALDVSVCGDATYALQPVRGAVCSGNGPVPEGTACPLRGDVAV

ADCHFDLSSYQSGRCKAYEDAECRVVTASTWGCVLPSIGCNDTATVPYETDTNCPTWSWN

EATTLANSMDLSVALSSQLEYNASWFVQTTPLAELNHCGEPPPVTPTLTKELPSLAPEKK

TNVPPWELITKAMPSTDSFQSAAPVSAYVPTIPDALATTLEPLESKSATL

>contig26784-0 Frame-0F0

MTTFVDFMTTKRVQSDWECHDGSCGIVQVVRAWSMEKKCGREVQLLKTCTIWC

>contig26818-1 Frame-2R1

MSCHLTVFHDDLTIDVDEAKASEKKTATDYMIVTTNETTNDALGD

>contig27497 Frame-1F|Blast-multicopper oxidase, putative [Phytophthora infestans T30-4](gb|EEY66763.1|) 4e-85

MAIDGGDFHHFQHPPEAPLFSIASGMKTEELPIEANARKIKYGDHIEVVLVNARNEQHPF

HMHTHSPWVVRSGVASLKQIQDNQLPPLQLENPMTRDVYTVPPCTSDGKDGCLNVGYVVL

RFTADNPGVWIFHCHIDWHVEAGLSMILVEGEKELQELGVTSFSNTILSVCGSTSKFSMS

NASCK

>contig29477 Frame-0F

MRRGYGRSISLTSHQVASTNRYMLPMTLYFVVCSLIHSRFFLLSMLAGRGILQ

>contig30035 Frame-1F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY65916.1|) 3e-85

MVCFVALDVFVKLLTIWDIIRSPYFWLGIATLEQIPLGVNFIVSSFIIVELATEGHEGAM

YGLLTTVHNLAIPFATTITRNVDSFFHTSTEQIQNDTTGVRNEITASVVVMWTINLCSLG

FLAMLPRQKEETRAMKKLGGSSHIMGVVTVGYLASALFWTTTTSLLSLFPSTSCLVIAGG

NGCSNHIVDLH

>contig30611 Frame-2F|Blast-ADP-ribosylation factor family [Phytophthora infestans T30-4](gb|EEY54603.1|) 6e-38

METLQYKNVKFQVWDLGGQTSIRPYWRCYYPNTDAIIYVVDSADVDRLNIAKQELHAML

>contig31638 Frame-0R

MRMTKSSSVAEAKPLSDDHVDRQMWVPSIETAFSLLLIPRMISALVNPIADCDETYNYWE

PLHYLLYRFGFQTWEYSPIYALRSYVYLLLHYIIVKLLAFGSIYGLVADEKFVLFYGLRA

TFGLLSAYAEAHFYNSTIQCFNRRTARYLLYVLVLNAGIFHASTAFLPSSFTMMLVLLFT

SAWMDRKHYQAMVLGILAVLCGWPYVAVLFLPFAVDMLYTRGLVPSILVGAAIGGAVAAM

ELCVNYYYYHKWVLPAWNLVVYNVLSSETDSTLYGTEPLRYYLFNLVLQFNVVALLAVPA

MLLIVVLPTSNETSKTKLVAYISPMYLWVAILFVQPHKEERFLAPVYPLFCLAAAITLSA

MATFSSQFVARFGGGRNVSKTVITCLLGLYAVLSLSRVVSNVVNYSAPLRVYQHLSTNVL

PQRETSRDLQKTHSIHLCLLKEWHRFPTSFFLPSNATQVAFVKTLFSGQLPKAFETHENG

TWTIPRAMNNKIKKK

>contig31740 Frame-2F

MGVIASGTVCPFGNVKCTSLTGEKKPRAPAVDWQVIKLAKERAAN

>contig32077 Frame-0R|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY62010.1|) 2e-88

MIDGKSKEIKFPFNLFADSTYEVTCELAVDVGIREPDLEDIADSIRFLVTEGKINNLSDV

QEDVWEEAPEPYSFSSKPFPNVLKMTFVHMPPGAYQPQQPFLLNSSGLDHAQSVLTASTS

SLSTSGLPSGLISSNATTSTTTIGAPMSIQDVVLPGLQDSLNTTNLSDPSSTLMVLDSTF

PLLSSSGSSTGALSAQSSNDVARSPPRPGLAQTASDSMLTKETLLNILEMRARGVSMGSM

ADPAYVQQIQQLEDCLKLAR

>contig32631 Frame-0F|Blast-autophagy-related protein, putative [Phytophthora infestans T30-4](gb|EEY54259.1|) 5e-38 NOT\_ORF

MQFLKQLTDPALKRLYKFVLKRMIGRFLAADELDLDQLNVHLRSGRLELCDLLLNAEVLN

AELCEAQRLPFKVKKGYLGSVRVAISYADIMSESCLIEIDDIEIILVPLEKHETFSRFNK

ATDEKNKKRSH

>contig32785 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66327.1|) 3e-49

MRQRITPSESGTEMQYQQYHHREDTQTRYNNAAQVESTIVEITGMYTRMATMVSEQGEII

SRIDDDMNLAQTNVESAHNELLKLFTMVQGNRSLILKIFLV

>contig33092 Frame-2F|Blast-Ras-related C3 botulinum toxin substrate 1 precursor [Salmo salar]gb|ACM08920.1| Ras-related C3 botulinum toxin substrate 1 precursor [Salmo salar]gb|ACN10463.1| Ras-related C3 botulinum toxin substrate 1 precursor [Salmo salar](gb|ACI33791.1|) 4e-80

MSTMQNMKCVVVGDGAVGKTCVLISYTTNTFPGEYIPTVFDNYSANVMVDNCPINLGLWD

TAGQEDYDRLRPLSYPQTDVFLVCFSVVSRASFENVKSKWLPEIRHHSPGVPFILVGTKS

DLRDDEETLEKLKEKKLIPISIEQGEALKVELGAYKYIECSALTQKGLKSVFDDAIRCVI

SHQQIPKTKHRSFNCSIL

>contig34004 Frame-0R|Blast-peroxiredoxin-2 [Phytophthora infestans T30-4](gb|EEY63257.1|) 2e-98

MAPKIRHDAPPFTAEAVVNGEFQTVSLSNYKGKYVVLFFYPLDFTFVCPTEIIAFSEKAA

EFRKLGCEVLACSVDSKFSHLAWINTPRKQGGLGGLDIPLLADFDKSIATAYDVLIDVGG

EIGAAFRGLFIIDGEGKLRQSTINDCPVGRNVEEVLRLVEAFQYTDEHGEVCPAGWKKGH

KTIKPTVHGSKEYFEAAH

>contig34273 Frame-2F

MSTVVKTFDAESPQAAQPLQQIITVLEKLEPLALFSKWSPPCQLSREKLLPKKVYASSYF

DENHKVTKIFESNFGFWRSSCKVDRQLPKEDEWIVLEFDPAVTLSTIELQWREGYIPKHY

SVSASRDGTLFETVAIVMRPTKEDRMLIPKGFNVMAIKIVMFSSGKGETFGLISIVCKEA

IFCYVHTPTVVVLQMVRQWLFNGAVSSLPEVRNLALQALQKLLLASGSLCGLLQLATSLV

LNTRSTNVATFDRQTWDCFDQLSEDGSRSAQVFIIKLVTSIQRFVVKNRSDSVTLTNCLN

DQEHVAINNGTSNTLMASSIEQQSFLKAIERRSHLGMIILHILSELSTWQMKRIQKAEEF

KTEQELESLQLEEPYSMEICSDFFDISHRLIVSVLSRWLPRAGEKIQNNSRPEEGNKEGS

NIVSSEIGSSQDVYDALASSFAQFRFNADMQGNLNGVDACIHQCNGDQSGKPMFLPEELC

VAVLKIVTANLRRLVFSKIDPIEVGIAPARVQSEDDLLSAPPALAPTVCLLEQLISLGAM

RNDSLFPVSLNAAVAMEVGTEAFYPSAYQRTKILTSRMGKGATLEVQMRWPVKERGQEDP

RYERLLLMLQVECIKLRIRHAIRGSWYFFLHLMVEIPSSQETEEMLTRCFAPCIKSAGFL

SWQVAAGAQELPINLQRHLYWNRKEKMSQDSGVGWIRVYPKSVAAYDDVLQDVEGFLAKH

GNNDGSMLRP

>contig35955 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54106.1|) 2e-09 NOT\_ORF

MESACKHGDIPNAYVKADKEENLDIHIRVLLGIQVDEVTKKL\*VCQE\*\*GRIGAEKSTVG

LKQTGRLWSKLLLKKLVEIGFIQYINDMCVYYRWTSDHILIIGIYVDGLLVT

>contig37706 Frame-1F|Blast-4-nitrophenylphosphatase, putative [Phytophthora infestans T30-4](gb|EEY62530.1|) 2e-27

MKQHNIKGKVYMVGEAGLKTELELEGYQVSGMEHSDIKGLPHAPAIDMETKAVVCGLDR

>contig38066 Frame-1F

MKFATGLILAAVAVTEATAGNSEYLRSKDSDTLNAGNNFPSSSKNENTTDNDDSNKLPHL

DAAFVDNLSKLNVSEFKHLLTSMIEGDGSGLSDDELLDALKNIYDDEDDGPQTHYSSNRK

VSLTDLNPSSSVSSQYESTTTTKDSSSPIQSNPSYSDADSDEEPSLSKRSTNDVNKNGME

YYNDIDDSEASPGTKSFSKSGKEGIESNSVGSTYNDPMYGTTGEDEDVPSQTSSKAWIDD

SGSEEYPLTTKDNNPSKKYAYSDNPGSLDEVDLTSPLDPTSYPILDDQLPRRDVSPGSHK

FRENLDHATKSIIDSPPTNAAYGSKSWLDDEDDDALTKNGKYDSVDDDDSLDATPYTATK

PVFTKSSKGGIDNNSVGTTYNDTNYGTIGDDDDVATDKTLKAWIDDDASVNSPASPSYGS

KSWLDDEDDDALTKNGKYDSADDDDSLDATPYTATKSAFTKSSKGGIDNNSVGTTYNDTN

YGTIEDDDDVATDKTSKSWINDDAVVDPPNSPSKGFFVSKKSWYEEDDDVLAKNGRHDLN

DDNDSIDVSPHAASKYVDAKASKTGIDNNSAGTSYENFADDKTDDAFASKTKMPKDEILY

LDDNLQMDNKKSDAL

>contig38736 Frame-0R|Blast-AP-4 complex subunit sigma, putative [Phytophthora infestans T30-4](gb|EEY53525.1|) 1e-17

MIKFVLMVNKQGQTRLAQYYDFLSIQERVALEAEIIRKCLGRNETQ

>contig38996 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66913.1|) 1e-45

MVYSTCSLSVKQNEEIVSAFLQDEPLATLDPIVADKAVPC

>contig39313 Frame-2F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 1e-15 NOT\_ORF

MRAKFPDLRPEKMSMRDNVQKT\*YLASCIVMKLNNISIRSTSLCWTCVRF

>contig39649 Frame-2F

MACLSAHAGRNRSPSFSTDIFLKVYAYVSGLEAPLTVGSGRCNNQC

>contig39982 Frame-0R

MGSAGIAKFCSAFVTIDSLREEYWRVEAPIGLMSPRQGHKRCVSESEDAKPCVTLMRRRG

DSVGGESIVECLLLTGRTHQLRVHLQHVGFPIVNDPLYGIPNEDKGMRLAIRQVQNVLFD

AVPISYYQKFHHEDDKLRCTRVCEVCIAKTQGIFEVENKDVIMWLHSYRYETPSWSFEVP

LPSWATLPTALPI

>contig40285 Frame-1F|Blast-protein phosphatase 2C, putative [Phytophthora infestans T30-4](gb|EEY61469.1|) 1e-111

MAVDEMLKEDPEFATSCDEVGSTGLFAIITPTDIVCGNVGDSRCIMSNSNIVEVLQLSVD

HKPDLDFEKSRILAAGGTVFRGRVCGGVAVSRSFGDLWFKRNTELKAHQQLVTSEPCVRV

QRRDPADEFLALCCDGIYDVMSNDQLRKFIRSKLKSGNRNPKEIAEMLLDECLAKGSRDN

MSAVLVLFETASKK

>contig40577 Frame-1F

MFRARKFAEVPSKREGAELLLNDSRKRQRLEHWNALYAPRSGGEDDLGEGASLLVDTNSH

TIMESASLPPQVLQELRMEWPQLPSHQHHQVCCCSVSVPSARYRSGRQWIRYFFFPLRTK

ILLWQQDRDKVVLLQLPKHLEPSEVLYPFLFAQCAQSLSLMIVGKSGIVLLWGDIELPYE

SVPLSVQIPLAAKEFVSTHFSAAMMSTQESLDTDDTYDDAAGLMCWSNQGSIWEIAIEDR

RIRVRAFEKQNDGFFSGITKTVSQFFFNSSASQTGSNVGEVDVNQPIKCLRVLSSSVGDE

SLLRKSGRDAEETADMLVLFQDGILERRTFSIEDVMNCSCESQWHLNMSGVAMRYFRDTF

SDAPVAQVCIVSMPYVQEMCFSLLVAFVCSHTNTNATVKYAFFNFSLTSDTSPELKWASM

LDYEPYFDDQSANSFFEVDTFVITRGALYLVWTQMKPIQFSTIILPQAGQSSIQSSFFSL

QGVKGRTALAFGARVDQSSFNNDSVIGSVSFLLIEEDSKSLRGSVCVATASSMQKLERLA

ASIRSKASIQPTRRKHEAHFYTGESSPSSSENSSVEAYARFLLTRFYENPDSTSAMRVSS

KIVELAAQAALAADDQILDAKASSGLRWEKKTGDASLQANMLKSDMDVFSVTPKLVRYQL

EEKCACHVAFIQFLQHCCASVWKYIEDSDELKRHLTENEEKLQAAIALSKFQASILPLSS

AEGKTTTSDAQNNEHSLNGKFLLHAIEKTVQERGYPMEQLRLAGYNSFDVFYCEVSKIAE

LIQNLGDEVAILAASIG

>contig42283 Frame-1F

MLHAMKQTRGRPLHGEQELIDHLEVIVEQIADEKEVRARQLEKANRIAILEAIPRKRSLR

LQVKQLEKVEKHQQHDKELSMEEIAEMKRAEFLAKVEREAAKEARDAERESRRLHREQME

REEAQTERERRRIRRIENEMKEDQGEVLVETERRKEEVARESQQDNATL

>contig42517 Frame-1R

MILGRYAASALVLVSTAKHVQVEANKCKASDSFFSFLVDDLPTNHGFNTCVANNAGTIAK

ALAKTLFSGCNPSDVYDLVKNEDLRNFYRLFRSIAQTPAAISKLVYKYMAAQTDESVDSL

CDAFGGTLGPCAGHVIPKLLPG

>contig42562 Frame-1F

MDHIIATTTRSTPMKVSLYAQKNQESSTTILIAPKSLVKKQDAESFSMHGVTSARKMRRA

LQSIDNNLPSQGSARAMCLPKHAHAVDDSKPYRPVHAYDRVLIKANQATKASITGHKRRA

AQAISKVMAPAHFRGYPNEQDRINLAWMDMILALLEKRYGLDTSLPVSITDLEAA

>contig42706 Frame-0R

MTPPDFLLRMPPLKLHVRNATQTSGEPAVFELFCRLDETRNKQEEPVGVVQWSLWKTYEE

FQAFDNQMRAVRKSTFAKMMVTVAFAPGHRVRAFFHQDQTSSFLEKRRAELDFYIQRVML

FPDVLDFSKRGSCKVLADFIGAEQFMDCSGLLPSCISRSSSLKDVLRDSASSYSRASLVS

SSGVGNKISSRRKMWRMEIEMEIARRCGAHELKRFKKCARAFRKENDPVAAASMFVEFSK

EFEPEFAFWILRCFLRSVKSCEKREALCVSGGISSTSIDAEEMKDMQHQSLRTHLTEEEE

EAKRLSKKFADQEVQSFSNHHRGSSDIACPRRVSRKKVNRQILERVGRLSKANSDIVREF

KQAAKALGNQDMSGQAFVDYLRLTFGNNEAEKLLHMVVDVIPQPQVQQELRVALAR

>contig43778 Frame-2R

MTGSYRTAKRERQRVFMQIGGVYILIYIKQ

>contig44638 Frame-2R|Blast-26S protease regulatory subunit 6B [Phytophthora infestans T30-4](gb|EEY67608.1|) 0.0

MEEIGLPPLPSDEEPLVPVTIESKTDLYTKFKSLERHLEFLDIQEGYIKDEMKNLKRELI

RAKEEVKRIQSVPLVIGQFLEMVDANYGIVGSTAGSNYYVRILSTLDRERLKPNSSVALH

RHSHAVVDVLPPESDSSIQMMQMSERPDVSYSDIGGMDIQKQEVREAVELPLTHFDLYKQ

IGVDPPRGVLMYGPPGTGKTMLAKAVATATTAAFISVVGSEFVQKYLGEGPRMVRDVFRL

AKENSPAIVFIDEVDAIATKRFDAQTGADREVQRILLELLNQMDGFDQATNVKVIMATNR

ADTLDPALLRPGRLDRKIEFPLPDRRQKRLIYQACTAKMNLGDEVDLEDYINRPEKISSA

DIASICQEAGLQAVRKNRYVVLPKDFDKGYKNAIKQAETTFEFYH

>contig44740-1 Frame-2F1

MSLGEGVICSDLNRPMTPKDRAVIGYLFNFIDHRTNGCGVSLAKKAKDVAAQKFNYFYGF

VRATFTVESRPQNRLRRRV

>contig45398 Frame-1F|Blast-ribosomal protein L31 [Phytophthora infestans]gb|EEY60634.1| 60S ribosomal protein L31, putative [Phytophthora infestans T30-4](gb|AAY43425.1|) 4e-39

MKTQDVRIDSKLNKFIWSKGVRNVPYRVRVRLSRKRNDDDDAKEKLYTLVQHVQVATFKG

LQND

>contig45686 Frame-0F|Blast-DNA-directed RNA polymerase I and III subunit RPAC1, putative [Phytophthora infestans T30-4](gb|EEY69491.1|) 1e-154

MAIEHIYIWNNSSIIQDEVLAHRLGLVPLEIDPREFQAFPENEEAEATDENTIVFKLDVT

CKLDPEHAKDPSKAIHSSVYSRDLEWVPQGNQEERFGSIRPVLEDILIAKLRPGQSVALE

AHCRKGVGKDHAKFSPVSTASYRLMPQVELTEKINGADALRLVEDCQVGVFDIEDLGGIS

TAVVKDQRACTMCRNCIREPGREKKILLGRQSDHFIFTVESVGMIKPEELLLEALNVLAE

KCNLALESFAHV

>contig46236 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY64219.1|) 2e-31

MTTRQPNVMLALAAGIIWNKSLKREFTFTTRDEIQLSPG

>contig46764 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64663.1|) 5e-50

MLQDGEKEDIVWTLVKELPLNDFSFEFGTGNSAKRVRQPSNLQLFACSTL

>contig47002 Frame-0F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY57525.1|) 1e-30

MRTSHGGGSFRHFFLRRHDKSSTNWSQGASSDEAAVGGATAQQSLITRTRLLDSWSLSEL

FALRELVHLAINNSMQLPDLCVSSSALQRVGHSDEPTRSGTCSSTSSSATFTSATPPSVA

SVDELKCQEKELQMHLDLMLGQSKRFYFSRPIDTRLRLDSRRQFVR

>contig47077-1 Frame-2R1

MCCVFDRRLLHRRSYMSRIWTLDYV

>contig47631 Frame-0F|Blast-Voltage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4](gb|EEY65674.1|) 4e-39

MAVFFLPNKYSDDANKEDAATVLRVLSVSQQKQEHTQLFALLVNSDNRILLEATGLRKEN

LVCADEIRLGLMGLSCRCPGLSTVV

>contig48274 Frame-2R|Blast-ATP-dependent Clp protease proteolytic subunit, putative [Phytophthora infestans T30-4](gb|EEY53720.1|) 1e-102

MLSGGFKMAGGRRRLHSIINSLVPMVLEQSSRGERVFDIYSRLLKERIVFVHGLVTDDMA

SLVTAQLLFLESENPEKDVYMYINSPGGIVSSGLAIYDTMQYIQSRVNTVCMGQAASMGS

LLLAGGSPGCRSALPNARIMIHQPSGGAQGMASDIAIQAEEIIKLRARLNGLYASHTGKP

IKVIEQAMDRDLFMDPREAQEFGIVDSIISSRATMQSREA

>contig49321 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66901.1|) 4e-67

MLHPHINHHLTTLPKLIVDMERRRKLELELIVHYDRQVLRRRDCWFCIDTKWMARWINFV

CHGGPEPGPISNETLLHKNWRKMLSQDAPGRPGKVREGLVLMKDYRVVVPIVWCLFAELH

GLSDAPSLARYLMDIHAEALCDSDLSKVLDFWQPKAAGLANEVKDKCLVRSSNKR

>contig49817 Frame-0F|Blast-amino acid/auxin permease-like protein [Phytophthora infestans T30-4](gb|EEY64738.1|) 5e-73

MAMPPIEGSPFYTLEDAKISFNIFCCFCGIGSLSMPSNYARAGPIYATIALLLMAFANIY

ATIALSKVIYASPPSVKTFSDVGGWVFGSTGRYVVMTSQLLICLLLPCAFLVLGSILLDV

LFPNAFSQTFWMIFMAITVIPVCLIPTLKEAASIAL

>contig50055 Frame-2R

MTLSPKVIHWREARSYLLATTATCVPGTEVQNEKGEQLSDVQVNGYIRGKPLSVNQLIHI

TDVGTFQMSCITRGAVRQVQCGKMDADMNSKPPVVPAASNHDEVLVLARVDPALQEDLRF

EAEYNPFASEQTWPTKEEIDDAEAKAKKQHENDIAVVKGASSYQAVWLDGDNETDDMKDD

EDEEEAAVNQDFCKTGDDENDEDNDLFMVDDDDVVQAQKRQDDEENMTFPDEVDIPTDQP

ARVRFARYRGMKSLRTSAWDPEESLPSDYARLFQFKDFAMVQRLALLRGKVAERAMKDQL

RRKSKTQHSRSR

>contig51166 Frame-1R

MASHLHGDSSTDIETLRAAIALNTLPEQRLHDESEFADSEVASFIAFSSCCVEDIAKDTV

HNLDVAISRHKHFVKQMTISKSCGSRGYGFKDEGFYNILHFLAGLMAGFAIGFALTKQWQ

LHVLHTQAKAPTLYAKLANFCRRIPATHTPWHLISLRTENIHFLTIIGIA

>contig51364 Frame-2R

MVDTYKSTFDAVDEIIEKHEKEHDGQKPKEVMMYCTGGIRCEKVGAYLTQYKGISNIQKL

HGGIINYMQFLNEQRHAHHQSDHGVQKFSLFKGKNFVFDQRCVDRFSESEKVTDDILGKC

FQCGEPCNHHTNCSNVMCHGLVLQCSKCAVAMLGACGESCKHEVLKMRSMTIEEQRSYRK

VNALKWKPKNPNSASVKFIKIRPASPELLQKSEMLDHSIRQKSDR

>contig51636 Frame-2F|Blast-Amino Acid-Polyamine-Organocation (APC) Family [Phytophthora infestans T30-4](gb|EEY66603.1|) 4e-94

MPSSSVNGDLQLNLLSPAIQDGGPTSGASIPVAWESEMNFICAETASQLRQRFIQVQVTD

RRYKEPSWMHPNIGGDAQFVQGKKEEIDAIREELEIRKTSNKLGEWTATSISGNAILSSV

LFSSGQTIAKAGKLAPVTQIVVIIVIYCLRCVFEEVMSAVPLNGGFYTAMLNSASKKVAA

VFAIFSMLSYLSTAVVNGVSAINYVNVSLLEIPVMGCTIALLVVFALLCLLGIAESAFVA

LIFFA

>contig51801 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66652.1|) 2e-35

MRFKDAIACEKFMIAVSCAKAQVLVQASKSYERQKPAILFDQVAIGMADAIPLTFGDVAG

VMLRKWQGSMEQRASFFSANPLDIMNQEPT

>contig52413 Frame-0F

MLLGGFISDNLAHPALETRSNSSAKYRLSRALKKATLQMQQGFYCQNPK

>contig53050 Frame-2R

MVVTFAACLYDLYFLLLVYTLQCASIRASFSFGVDVTFTLLFVSAGCALAASDYLRYCSA

LDLKVHCALLASGTALCFMAFGSFLLCVAWGAWMWNTRIQPSEKDQLVYRRGSLSSSVHF

GVGLEFETA

>contig54550 Frame-1F|Blast-phosphatidylinositol kinase (PIK-L4) [Phytophthora infestans T30-4](gb|EEY63983.1|) 3e-15

MTTRLSAEDVEQSDVSSLLQLVRVHQRQHEERAYDSSASEAIHRCKIMLTKLRKLLP

>contig54859 Frame-0F

MHEYQQDKERCARVGGSTTGRDQKRALPLIYTEVATQPA

>contig56721 Frame-1R

MVLHFRSPEIQREDSSMDLIHPRSRSRTSSAIQFKPSLGIQEYNELKSQIDQNSTTEVQK

>contig57076 Frame-1F|Blast-lysocardiolipin acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY70071.1|) 1e-15

MHVTVVGVMFLLSLVITGWASVIWVLTPCFFIAALPLPSFIQSKCFYRRVTRF

>contig57227 Frame-0F|Blast-bloom syndrome protein, DEAD/DEAH box helicase [Phytophthora infestans T30-4](gb|EEY65064.1|) 6e-67

MHVRAATKKIDAIDLTLDNAPLSKSIRPKRQRSFYEDSDDDIENREPNTALQLIQQSRRR

PVASKKAPQVNKRTKVTSGSVSDILAQANQVIFGNVGFRKNQKEVIEATLRGEDCFVLMP

TGGGKSLCYQLPAVLSQGVTIVVSPLLSLIQDQVTALVQNSNCGIPAAFLTSHTSLTLKR

SIMAELRRAIPSLKLLYVTPEKVIKSPEMIEVFKLLDQNQMLARFVIDEAHCVSMWGHDF

RPDYSQLGLLKRTFPSVPL

>contig57252-0 Frame-0F0

MLLDPPCHSKWPPILLPLTSECHSPHAVG

>contig58770 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60283.1|) 1e-20

MKKYLNEYKQRREAIDSLRTRFNMYASKSVETSDGRCVKVMTCTDFLHSFVLPQFHFRSP

>contig04057 Frame-0F|Blast-hypothetical protein [Monosiga brevicollis MX1]gb|EDQ88626.1| predicted protein [Monosiga brevicollis MX1](ref|XP\_001746730.1|) 5e-08

MKSRIILAAATAFASIASAQEQTTQDSSSPAQVTSRSSEMTSSTAELPSSSSENAGSMTD

DTTLNEKNSNNSTSSTSTNSASSPTSNTMTSATPSAVEDVFKDLKTTKTPSDSYHMPAVR

AVHARVQS

>contig05344 Frame-0R

MCLNDVLCFVCGACCASCCINAENQGRQDAYLHRIPPKAKTKVVYVAPVSLTRGPPRNFI

RPSRRRSTYARHPQCGNVI

>contig13376 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54408.1|) 6e-67

MASSAFKFSVQRFDCQGQDKAIAGTVTALESANLALWMFVKILRGKIFPNAPNVLSDDPE

SRHLISFVGDGPMGVARWKPKIFQSGIHDAIIERFGIVQSKRRQGNAKRFLRVVVEDIWT

FYAQKPTHPQALIAYVPQNDSFAAMKLFQSVGFQATSQAEMVVDNTLLQMQMAWGCCNPQ

VNE

>contig13615 Frame-2F|Blast-retinol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY55158.1|) 3e-47

MQHAIETNQDSWKWWVFIRTVSLAPQQSSETGGLSILYAATGDNVQGGDFFGPKYLGYYG

FPSREDTSALSKSETAALKLWDFSENLTQIKFELK

>contig14669 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY55699.1|) 2e-30

MVSYIGALSLQPTVTSFILKGGSSLDGSVKSKVGTVNFRSNVISTQLSVTHVVLNNVDLS

SFATLDQLPVILPSIVQHLSLVNTLLAAFPTLVANFSSLQTL

>contig14755 Frame-1F

MTSAALIEHFDASIDSQETFDVLLPQLETIITQKSTSDLARILKVKDTDTANRFQEPNGR

ALILFVRLKTENLNAFEMLGRVRSLYHDKKLKSFPAFFWTTLKDVDIGLKIDNFVENVLP

ITVHGKLRNFFRRMWFKLISIFKKKQYSEEVVSNLERPRRNAFKTPVNNIVDASPDIPET

FPRSAFGNAAYGFGASTSSAFKNIQINPLDGVLKSLKAFRYENKELQLPIQFKVFSIEFA

GLRNKLRNTIDIADKHLVKVKEIFENERVKDLPEQPVKANAVDGTRSTVNDGFNQPYRRN

TNAFSKYEEALISSSVSAEVIAKKLAQIADHVRQLVFKHEKPAEKAEKDVLLAAHPRLFK

SQDKNSQQHTYGEALLKILDQEITNYMQKSESLNLDLKHLGSRKMNLISNEVEKALSKLT

KDSHKWTA

>contig14838 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY64219.1|) 1e-140

MRATCSYRDLKPDNIMIDIDGNIALVDFGLSKTNVNQMSGARTMAGSPAYTAPELLKPKR

SRDYGKAVDWWCLGILLYEMLLAKRPFHHLNVSVLYKLIEKEPVKFPSQCGLHPDTRSLI

LGLLEKEPNKRLGARQTSDILTHPFFKGVRWDLALRKKITPPWIPPPMSMEDERMKSPDI

NFDKYLASKTASTGNIFSLIFPWKHPHTRHRRARSEMDYDSFGKFSYVSDTSNSFLVDED

EMLDAAFTGRRSIQMHTLAGEA

>contig16847 Frame-0R

MPKRSTSWNFHVVLKELQRAMSIERRPARSHLYCQPLNIPPILLQRPL

>contig17101 Frame-2F

MGKKPKAIEVAPVPGFFGHVVKSGCPLRWSNEVNDFCMQLNSAALGADATKGRSTLSVVA

KSSKIALCTLMPEVTEQWNLTQTFTPIDGAIEFTVTGPNAIHLTGFIEVHDEEDSGNEND

FDDLVADDEGDWSSDVDEDNKEEPTHEDRFEVLEERLNNEAESKKMLPEGEVKKSDEKVS

KKRKKKENKNLIKAEVGDKDNVAADEAAKEILEKDASKKQIKIAKQAEKEKKIAEKIAEV

TASHPQTKKRAAP

>contig17862 Frame-2F

MAITGVIDGSRFLLVCNCASHQKASREMYFKTLKRFELPATDHVLVGGDFNCTMEISDRC

YQPSAANHALPGLESLLATWALVDSIASPDGMPKEIIRAWCRETYMYCNPLPSEDEASAR

LERWYG

>contig18225 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54116.1|) 0.0

MLFAKLLKRDNHAMIKKYAFRCLALYTDATRNLQQLAAMLSTSTSSYQASRAGSIRLLND

GVEIDIDDVEDDRSAVVLAHSMPTRKNMHLELLRESVDFSPYGGGSIILPDKFLNEGVHV

EGWMRPMPTQAEEPVDMLKFVMDLSLEREDLHAKLSSMGTRPNGGSDRFIFWAELIMKFY

MPLLYPKVCLKVKIKEEGDTLGFFHHCPGSFQRVVARWVYKLRSKDDLMEVLWSRREFSE

VIMETIRQRFAYRDTELVVDAIKFYSGICTNAQYVPTGMKSQMDESSRAMISHVSQLFHP

SVQLEDSKILLHCIDLLELISQRRLDDYTSTYLRKFVLSTIDNCIMLREPGNRPVLTAML

SIVLHVWMHSAVVTKGIGAQVWM

>contig19671 Frame-0R

MPPTSVVSLKRHRSLHIHSINPHSFKTLYTLVYGRFFISLANIH

>contig21236 Frame-2F

MKLQFKSGDNTLTGAFVETYLLEKFRVVAQIPGERNFHIFYFLLSGANQALAKELKLESV

NNFAYLNQSGCVSDPNVDDEILFDEVASALGSVNIDAALQKQVWTVLSGLLHLGNIRLIN

RETAEGDAGEVTLEAKKYVASCGELLGVDSANLLHVITTREISTRTENFTIKRTAKEGSY

VRDAIAKSIYNHLFKWILVKINSSLGHGDNSLPFIGVLDIFGFESFEENDFEQLLINYAN

EALQATFNQQVFIAEQELFAAEGIEVGKIIWPDNRECIDLISQKPNGILPLLDQEARMPN

PTDAKWNATLHKTHAAHSHFLPPHEKDKKYEFIVKHFATRVPYTIGNFIDKNNDTIPKDL

EDFVTSSKSSLIKELFSANLDRGAMNQHKQSVSAKFCDQMRELTDTLNATRCNFIRCIKP

NPTMSPGVFDHGYVVDQLRCSGMLATCELLKVGLPTRVAYEEICRIYKPVLPPSVTPMFN

AYNDRTFTEAVLWSFRVENDAYRLGRTKVFFKTGKIALLDALLKVDMKKMGPWIVARLRK

WLARRRWRYALAKVLAQRAFLWLLEDTRRRKAAVVKMQAVMRMYAVRKHFVRQRNAHRHR

MRRKFLAQKHWKMAIGGVLASNAFKKLLEQTRERMSAKNAEQNVAAVKIQSIVRGKFGRK

LAEKRRAQVEDEKMRKRLMEEAARIQAEKKNSAKKRWLTAYYTIQAQRHFVQRLHHIRKA

RLAVEEARRLAAEQEKLRIQREEEERQRRIQEEEDERERQRQLELRRAAAATAIQHAYRR

SVGREEAKRQAAVERAQAASLA

>contig21405 Frame-0R

MASRWLLKASSRRSLVSLRTPSCRYLNQQQSYAVSSRSKDIESDMLHITSTPRAPLVDDL

AEFDDDDAEEMVTIGPVGAEYGGPTRGGKFKEPTRFGDWERNGRCSDF

>contig21799 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58040.1|) 0.0

MLECNTTSMMELYELVALEMMEAQERDVAMEMLRTTPALVAMKQTQPERYLRLETLVERA

DFDSSKVYANRSKQKRRDDVAQLFRNEVATVAPSRLLVLIGQALKWQQLQGLVPPGGNLD

MFQGREKENVVDRTEKLVRKPAGKIKFSKTSMPFCAQFTRNGRMLVTGSKDGFIEVWDFE

TCKLRKDLEYQAKDELMMHANSVTAIACSLDGELLATASDDGQVKVWKLATGSCLRRFDS

AHHEGIQSITFSRDGSQLLTASFDHLVRIHGLKSGNTLKEFRGHQSYVHVAFFVSNGNKV

LSVSSDGTLKLWDAKTTECLKTMPVRTVSFPTDVEIVNAVVVPSVSGSGEDVIICTRTSS

MLRVSMEGKVLLTYKGDPLNENKSGHFVACTLSMHGKWLYGVTDKGFVVSFATKTGEHEM

AMQICNADAFGIAHHPHCNIVATFGSDRYVRLWKA

>contig23159 Frame-1R|Blast-importin alpha-2 subunit [Phytophthora infestans T30-4](gb|EEY66875.1|) 0.0

MMEHLSELPQMVVGVNSGDPALQIDAVTKFRKILSIERNPPIKEVIETGVVPIFVQFLQR

EDFPTLQFEAAWALTNIASGTSADTAVVINHGAVPIFCQLLLSTNDDVREQAVWALGNIA

GDSVVCRDMVLRCGALRPLMQQLTENSKSTMLRNATWTLSNFCRGKPQPMFDLVAPALPT

LGQLIYTHDEEVLTDACWALSYLSDGSNKKIQAVIESGVCRRIVELLMHHSASVQTPALR

TVGNIVTGDDLQTQVIINLHALPCLRALLESPKKGIRKEACWTLSNITAGNQEQIQLIIE

ADIFPSLINFLSTAEFDIRKEAAWAVSNATSGGSAEQIMHLVNLGCIKPLCDLLEVKDTK

VVIVALEGLENILRVGGLKKTNDINDVATLIDEADGVVKIQALQYHANEDIYVKSMKIVE

TYFNGEEDAEDSLAPDTNANAQQFQFGTTSDQPTMFQFGQN

>contig23230 Frame-1F

MGSASIQEGVADSAPEAESTIAGVQNPQKLNKSPTDHHSDENLGMWDKLRKQHWTQGDSK

QERPGNIKAAGFKMQKISCEEKLEILKRRRPLQNNKKSQHTETSETVQSATANKQLHVQQ

QNNKKAVNDLRPTGDDVEGQAVYASCTTDMKTSLPALRPLSIPLCSVDIVHQDEVPIELC

PFSSDGSAEESQPEHPPRITDNLQNALNELTTAAFAAATSDLSTPRNITPTLTSVTAREP

TTNTTSRTMGKRKRRKKLSYSAPRNKLAAKMKQEMPL

>contig25940 Frame-0F

MSAPIDDLLYGGDDSGDEDEMNTTMRSFSGIPLTAAVAPPGGLLAPLPKPLTPPANATPI

RPHPQPLAPSPPAIAPSPKQSPGSGQQMFQQMFALLKQMLPVEHYATLHSEMRKGNGNDI

KSIVDIIKRIAGDAIFSSVIQKMNLSRTFPPTNAS

>contig28855 Frame-1F

MSLWHAEDMLELVGPSLRQLNPDAPLVAWKLVIADLLDEASSSFGLWCGVRAGAQGVSTP

ERDCLRTYHTSTGTAQGVALCSRYLDSTFAQRNTREKQVEKLAATSAILLPVDLGLLQEA

NTCIKWERQVVDILSLLDSGCRATLLAVGFASAELKLSQALVLSTLERCIERVQRQCAAQ

VAYVDVELVNAGITLPVTFGQVLKKIAELSPPVRHCKSVELKELLESNVRAMMDCFESSI

GMQRSICTTFAKLRDEILSSGVLDLVYLPPELQFAIVDSPRDWNSKERKHEIQNVMTSLE

VTCIVLETSSINRGLTCDVYFKKLENFIDRLFLSHAARVAVSTYELKRRIYGALLPIHKK

LTQDGKTELVTPEDADVLLPWRSIYKEIYETFFETLEDIMIYYPTNWRIPLSFVNDVHPP

AAKQPQTSVRSIKLDRHIVMQPVQVSAQSVRKSFGPLSLIDETIQQYKAVGEIKRLRVEI

AKERAATSQFQHNLRQAVNRWND

>contig28969 Frame-2F

MDSVRAKHAAELEAKRKKLEDIRKRKAAIRAAENSSAASESVIPAIGQQENKFDDFIQNI

LKTSDKEERIKADEHTSRQDHGTMHSLSLAEKLSSLSTVLNVAEMHIQPTLVETYTKHTE

TDITLEHEIFLKQDGVAFMDLDKPHTSPERLGNVNVSSSPQNRTFKGNTEISSTGSKTLT

ALTEEVKTDLMESNAMDAFLNKASRVIERALNTTSKFDIMIDYGADVERDNAMEETVESL

KPHCVFADPQWSTHRAVTDVDVSPFYPELTLVAYSARGFVEDEAKDDSRSSQWDTMGNSA

TVALTDVASTMEGVVLLWSTALPSRPEYRFTCHSQVTSACFNPFDRHIIIGGTYSGQIVV

WDTRAKSAPVQKTPLSTLSHTHPIYAMAVAGTKTSYTLISASTDGRVCIWDLDHLQKPLN

LLDLRLSLSVLSNYTSTKASDKKMEVSVTCFAVLGKEIQQLFIGTEAGKVHTTKVDQPKI

KPGATDDISSINADKKSLKIQFGSSTEDLVREVIVDTMSEDGSHFGPITAMHLNPLLPMH

HDNLLLTSSLDSTVKLWSLEHPELPVLSFEPSSEYISDVRWSPVHPALFAVADSSGRVSL

WNVLKDVEVAAVSDKISEHSLNKIRWSLDGKNIIFGDASGKSYIYEVPSDIAFPSPNDLS

LLESKVAKFVAATALIKP

>contig29188 Frame-0R

MLGNCVFFKKDWCSTGILLSEQQKGLDDRCVFQEWLLNVETDVQVSLRSMLRSWMRRRQR

RGNGRYFKGREASGICNFSSALDIIKH

>contig30429 Frame-0R

MTRGFGKENRALMLPSITLILEKIEAFGLTLLEPDVEENLRFHKKINNLLITCGTCQLDV

LLLENPGDIEVTLLRRFLTLLCRLFAHPSLLVTEAQILLWLTILKNPRILQYGQPFLPEI

LSQLRHVSFDKYFKLSSPEREPSGSQELACQCSIIEFDDHREYVAFYGNFRGRLYALLRV

LVQFNPTIVLQSLQERLVAVLTHYAAGTDHLKSPHGFCSDLSITYLYHEGMTSLLDCILK

QLPAQALTNSINQQIIQQMVQAILSYASPDPLLKFRQLLVLASFATYYALDTSTLTSVFD

LLFANINYVMPDEEVHGQMSSSTLNVRRRALSSLVSICQAIPAHILPVLPVLCAKAQELF

AADRVTDTEGVMLYEMLVLVSNSMETQDERVQFIQLIVQDPLTQWTSPDMTALVSSPETI

VVAIEAANTDEKAKKLLGMVLKSLTTLYSIAKRAGATFSSKKIHATDAFEGAWPHVLPNL

LALVRSLHGLHRPAIKDQILKSSTACWVLSVSMDEVAQLLGGKNELEDHQVAQLPVASKW

SKWHKNVRDIAYHLLGVAVGRSHFYQNSQVLSVLENSLLSDLDLMEHRHLKGALAYVFLP

LLKKCPTELYASLLDPVLTTLLTHFAQRAKSMFNPATEGTTRWSALIVGVDNAKQEVARE

KMVMELTRQVMDFLEYAVDPKTVIGVDTDHPKHVTKPADAYQRDYMLIHSATLPLAIGAV

VMEVIRWKDTLSCRKAVLLGDILVNVLHENTRYHLLLGRDLFTAALEGILKEHIGHVKDD

GLKWEIINLLRNIYCRLTLGLSPVEECIGIDPCHQPLRPTSSLCSIPRELLLSLPNVTLG

EIEALETLLREKHSVKTQKNAFKELLEVPILAIRSQQPLVSGSALPATGNALKKTSIVGK

GIADLPEPLQLSSKDDSKRKMWKEAQNLALDTQFLFQ

>contig30933 Frame-1F

MGGKAKFKKHTAADLERRQKQVNKGGGKAGASTRGVAKLNFTCDICMSASPDIKSYELHY

ASKHPKSTFNREAMIEKAEALRQLQRGETANGSHHKKE

>contig31097 Frame-2F|Blast-peroxisome assembly factor, putative [Phytophthora infestans T30-4](gb|EEY67451.1|) 0.0

MEILDVVQLPIKHPELFAKGVRQRSGILLYGPPGTGKTLLAKAIATECNLNFLSVKGPEL

LNMYIGESEKNVRQIFAKARSCRPCILFFDELDSLAPKRGRGSDSGGVMDRVVSQLLTEI

DGLCSGGNDQVYVIGATNRPDLLESSLLRPGRFDRLLYLGICNEKLAQMKVLKAQTRKFT

MAENTDLNAVVDLCPPNFTGADFYALSSSALATALKRRVEALDKQLAKINAEDCYSSSPM

TIRQLLNQLTPAELSVPVCQDDFLEALSQVVPSVSPTEMQHYENLQKQYS

>contig31156 Frame-1F

MKNFAVNTLETRKQELLQLGGLDFFMQDLVQHVYRLESGFLLSFSDGLTVECTRLLHLLS

LSLRVLDQATFRMIPVQHYVCKHETVLTGVLTLIRMLSELSWGIDARRKWKTAPVQMFLC

VDVLMLALRVALNLTHQNGHAAEQVHAQKGMQLLVQAFLKLSSLEKNSLQSWLRKKWQFD

AELLLLTVMVNSIECSEDNRIALAEASVRQVEVLMAHDRVCDYFVQYFLSKVQSYKHLID

GTEADLISANDEWNPEDVILGGCTSLLLGYLMIDSMSNRAVVLKLLPDHTPRLLLRALAV

FVAFYSQIGALTSDVAASALLVEKILKTCGESGIRDEDNEVLGVTAMKSNVTEIVPCFVK

HSTCKALKPPALRNRVLKNVCSRLDDSDEENEVNMEAQQNGRSSRIDSEFESLTRDHSLL

GWEQCRITPSVQTSVRTGSSEPRTRISSPVAVMPDGSMSSPVITRLLHQTRQLVREFDLN

FATSSRLAYAKKADEITEREAVGKDNSSSYLCMVMTMDVTCRDSGHDSLDLKQDMGSAYT

NDGQTNSRLQEMKPVTQTKRRKKVTDNCKVSAIKLQLSQDEISSSPFPLTPQRDNKSKVL

LQTPPRAGRTPDMYRQSPLLHLTPTKSSPSTPLWIEKTSRLLQTPPKTKQASLVKESLLS

HGRNRRKMKMVRAPTCARAASIFDFTD

>contig31211 Frame-2F|Blast-anoctamin-like protein [Phytophthora infestans T30-4](gb|EEY59667.1|) 0.0

MTDPYPQPQTAELRVRVPLHYGTSLVETGGRWDYVIVFPNPPKHVIEVSDERDTIIKRLR

AAGLRLRLFFSVGKELVFCKIRAPEELMRREAEVLKLHLQLDPTELRHASFNGIPEYGIA

PFPIRDVKQIYRYSPFDYIFAPYFQARDLQHFYTRKGPNGSIFSSTDRIGLIEHIITNHQ

TGAGQDIDRLIYEETIVDTYPLHEEQEKMDLKDNWIVWNMSPMNQPFDRICQYFGVKVAL

YFLYLGHYTKWLLYPTLVGIVTGIISYSIPRDDYNAVFAYISPLFGAFMTIWMTIYLENW

KRLSSRETLRWGTAHYSETVNLRPQFYGERIPSPINGKSTRYYSPREKLKRVAYSWVVIS

FLILIVFVLVSSIFMLTYDLTKGNDSNFLVLDNFKYGSIVSSLANVVQITVMTKIYNYVS

IVLVDQENHRTDMEYENSLIIKTVIFQFVNNYAGLFYVAFLKEGLEGCDISCIHELEYML

AIVFCSRLFVGNITEVAIPRFFVYLSKYRLLGHIDDYKKSDAERELFMAQYDWHGTFDDY

TEMALQFGFTTMFVVAFPFAPLLSYVNNYFEIRLDAYRLIFESRRPRPRNVRSMGYWYLV

LQAFAAISVCTNGAVVIFTGNFFNHLAMATRVWMFTMFICFMFLFKYFLEVCIDDIPEDV

VVQKYRQEFLISKCLYHMPDDDVNWTFGADYDDIEIMLNIDDEDSS

>contig31480 Frame-2F|Blast-propionyl coenzyme A carboxylase (Pi-PCC1) [Phytophthora infestans T30-4](gb|EEY56094.1|) 0.0

MRLARLRHQLPIKSARPALAALRQLHAISREKLFDKILVANRGEIAVRVMRTCKKLGIKT

VAVYSEPDVNSVAVRMADEAICVGPAPSSQSYLNLPQILKAVQFTGAEAVHPGYGFLSEN

KDFCEALDAMGVKFIGPGHEAIQAMGDKITSKQLALDAGVNTIPGFLGEIHTSDEAIQVA

QEIGYPVMIKASAGGGGKGMRVAYNDEDVRIGYRLSKEEAAHSFGDDRMFIEKFIEDPRH

IEIQLLADAHGNVVALPERECSIQRRNQKVIEEAPSMLLDPDTRIAMGQQAMMLAKKVGY

VSAGTVEFLCDKDKNFYFLEMNTRLQVEHPVTELIANVDLVEQMIRVAAGYELPRTLVDR

PLKIHGWAMESRVYAEDPRRGFLPSIGRLLQYKEPTNVPGVRVDSGVVEGSDISMFYDPM

ISKLITYGKDRAECLERMETALDNYVIRGPGNNVSFLQDVYRHPRFVSGKFTTKFIDEEY

PDGFVGVKLTVPETKILCIVGALMHVKKALASSQLSSRLQSNSAENSGLYDALNANEVEL

VSEQAGIVPRLRATAPGVLSSRELIAIAKRNNFQDLGVPLSVSIDGPFGEATPVIVLQVE

VEKKRHRSEIMTLALVDDAWHVIGKVHWSLNGPLFKASFIKENEAVDYPLVSQMVQTLPE

GFRLQFHGAVHDVVVRNELEAKYAQYMQPKPEVDTSNLLLCPMPGMLISVAVEVGQHVEF

GQELAVVEAMKMQNVLRAEKRGVIQNIVRTAGDSLKVDEIILEYD

>contig31848 Frame-0R

MEKMGWAAGKGLGKNEQGVKSHIKVKRREVLQGVGAEKQEVEDQANQWWYNVYDRMASKI

VIDASSSDEEKSAPKKKKKKKRKRDEKNTNERKLRIPTDEELFAATGGKLFGRRAYGSCN

GKLKRDEMQLKRAKKPKMSRHESLKTSDHTDIDLQKKLG

>contig32243 Frame-0F|Blast-NAD-dependent histone deacetylase sir2-like protein [Phytophthora infestans T30-4](gb|EEY56617.1|) 1e-158

MFDIEFFRSNPKPFFAFAKELFPKSSGFTFVPSPSHYFLKMLEEKGKLLRIYSQNIDMLE

HAAGISQEHAVLCHGSFASATCLACKRIYPNEAIREDVFNQRVPMCLSCNSPDGIVKPDI

VFFGESLPKRFHDSVKSDEGEADLVLVMGSSLKVNPVRSIVGRFKKDTPMVLINREPVGR

PHKFDVELLGYSDDIVHELCRLLGWEIPQPDPVRLGQSNLSLSVVAPTTTLMPLSFEFVP

PSRHLFNGSKSTYCSSSDDESSSSSCEDDTGERVALDADSDTIAVPIDADDQNLTRPTGT

KPKEYQDERLESGDELLGMLSFVHN

>contig33604 Frame-0F|Blast-proteasome subunit [Phytophthora infestans]gb|EEY57611.1| proteasome subunit alpha, putative [Phytophthora infestans T30-4](gb|AAN31468.1|) 1e-120

MEAINNAGSAVGILAKDGIVIAAEKKTISKLLTPSKTSEKTIKLDDHLICAVAGLTADAN

ILVSFARLSAQRYELAYQEKEPCEQLVQTICNYKQAYTQFGGQRPFGVSFLYAGWDRHHG

FQLYHSDPSGNYGGWKATAIGANNRAAKSMLKNEYEEGMTVDEALAFLVKVMNKTMDSTS

SSAEKLEFTTVTRSVDGKVVHRQLTEKETNELLQKVAVDMATFGDM

>contig33998 Frame-1F|Blast-peptidyl-prolyl cis-trans isomerase 10 [Phytophthora infestans T30-4](gb|EEY58162.1|) 1e-21

MALCASGAYDCTTFHRNMKGFMVQGGDPTGTGKGGESIWGGAFDDEFHPQN

>contig35088 Frame-1R|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72331.1|) 5e-07

MWGKPKKQLSHVYAPPCQIFAYGRKLCLPVRVKDPL

>contig35743 Frame-0F

MLSKLLRFIFGLRRAMRSQAQWLLMSLMLLTSLVDSNKWFTAERVIRKNESGTRQLQTLT

KINKAKVGSKTFALVDHYDCDNKMLVTVRRFFKVNSVLFDKCVAETGYKLYPFTGIIPNE

SILSELLKSSACMGIITAVVLVRMPPCLLDELGMRAACETILYYSEAMKHGVEIPTSTQF

EELMTWRRDVNLAKAAGKPYDGKSITYSEFTKYMGKAVTNTNVSVTETLTVLINDQVVEA

NDSIKPLITTSIDNYIVGRVSAAKNESSDSLNATAYKTGVNLQSSVGAALSVALTTFVTL

LFVTVLVI

>contig36108 Frame-1F

MLQKVIKSVDWKERYYCLALTKSKCCCESLDVDLSRGMLLA

>contig36449 Frame-0R

MLSVIGDNLLSYWLDAVRGDNPLQYLFMGQKCTRSRMHLDPGGLDITIAPILGTKRVTML

HRAAAKLESVHEKVNFHDVDLDKIPQLAFIPAWRVDVKPGQILYLPEGTMHACENVTACL

SYHSFHADSGNLPGFLRSFLAQDSLTINHAEILWNAAHDVMSALEDIYHANNQVLGDQVS

TLRKLDTLRGLRHACRILSLEQVLPTEDSWDWKELLDDIDHLLVRVDSSAKLYKKKNSTH

ESTLTKAVAALNGDEAGEAKQILETAATHKKVVKHKEQATAASTHWDSLNLKVGDIIGVQ

VFEKRNRAEVLQVVLDKILVQIHYSDWESIYDEFLPVSCLYQRKKGKKVALKKTPEVHET

VMASWGSKGDLY

>contig37334 Frame-0F

MGSKLSTSRSIEAMQHQTLLYRLQKRAYSVLLLWVRFWIVASGVEQYEELVRRIVKLVKN

RLYHSVAEKHASLHELIMTLAELWLKTLRLLLVPDVFARYLCATFMLHIIYELQSIAQQV

LGNAGLRLTFNGRHKLRLRLQLKHAKSFQERQSIAGELDKLENKDKWRKNPASGFFLYKR

VMDKTQMYKKLKTENDIMGLMFALRAGLLRKHWGLGNPKLYSVSNVGTKHVIEEYLDTIV

QSMNTVLRANEKIEGNSDKLSIDNKLAFFSETRHAYGRSALLLSGGGAHGFYHAGVIKAL

VENNLMPNVIAGSSAGSILAGALAVRNDEEVLRFLTGANVNMTFLKFNISEQDVADYGPS

FLSPTQALLSSGGLSSCEMPSSY

>contig38304 Frame-0R

MRRGSSITGRLRNSDTIKLLSLTVVFDASAWYTSCSLRSLTSTGRAR

>contig40013 Frame-0F

MAKLIEIRVSEAIEKAGQDEAVRMGSMGNSDSIGFSNGIKESTSDTQNGITIREVLSIDK

QVQVKPRMGKLLTSKYQELKKNEGSSKSLKRPRSSSVADKKAAASALSLQLTYRSRCICV

FQELDGVDVLIFTLYVQEYGPDALAPNAGRVYVSYLDSVNYFQPKKLRTLMHQQVMLGFL

EDCKNRGFHTCHIWSCPPLKGDDYIFFCKPENQKIPKSARLRQWYQKLLEQAKHDGLVAN

ISNLYAEYYMKKKAAHELPYFEGDYWPRLAEDLSKQLEEKDQNNRNKAGGANDGAETGGM

KAMPLDLKAPT

>contig40088 Frame-2F

MTPHSRTCLTGIEKANTQGIERDKMKTEGSAVTPHNVFAKLPSYNPYVGTFHHAPSAGNR

GAIYFSSDIVDMAELEERKKFRHHPLTGIFHSLPGYYDPLHKLASCRRVMTAEGIYSDTE

SLRSFVAMDITDSDDFASLQQPMHLNRMYSDTRCIPDADLLSRPRRFSDGDADPFFCGNK

TGSPIKNKEIYQDESTDSDGDEELAASEHPAPRSLPMNILSVTSKFDVPPPVGTMPPRRT

PYKKARMSSGTLFTSSVTEGLSPVRLYNSSNYDRSELGNSVGCAELTDGFISTGKGIFRK

VGFRSSLHEHPLDTMKCKLRTSATVKDERSLSEEASEDDIRNEYTQAAPRIPANPFVARR

LTDGEELRIMAIHRTGCRDAMALKNDHCGTDSEEELNYPKPYFIHEKAVTEQYELVGEDQ

LGDGSYAVVKPAIRRDNGNEVAIKQIHKRFLRDEAAKNAVSREIEIHLRLRHKHIVRLYE

VYETPEFLYLVMAKATKGNLTSLMQRKRMLPEALGGKISQQIVRAVLFLHDMGVLHCDLK

PDNILLSDAKTVSFDNSDNSPNFRRSSPPRSTLDPHADVKVNDYHIELCDFGLSVKVPDV

RFFKLTGDVHKVPFTGVTGSAGYIAPELLQQQSYGKPVDMWSVGIIIFEILTGYQPFYPP

HACIEEDANFSDRVWETISADAKDLVQRLLERDPAKRITAAEALAHSWFESAMFAI

>contig40743 Frame-1R

MELQTMQTLCKAAKRRPRGIMTHLIANLPGLKRLNTWVKTLLKHAKISRNAISRHHCASV

HRRYRSKMLHRALWTELDDAYHGYVQKLALSKDILHPKLSLHNAKPLAISYKLPQPNFTP

VRRDRFANLLLKEGIPFDNLK

>contig41692 Frame-1F

MRSFNSGGICSLNSNPSHLFERSQNSLRQRSFGRARGITGSPLKRPRNHDSESDEDNQRY

PGRRTERRSVFDGFKRMRVSSPSESPRTDVDSAMTDEEAATPRTTWRANKAIVPAAPQAG

KKRPLLYNASASDKLPWKTMRQAEYMGFESSIEIPSGASCRTMVVFDPYRSITLKPTPRV

DLVDDEKASASEAGSTECDDEPFLRFEELPEDNDEPVDMDID

>contig42334 Frame-2F

MKTFWRQTPRSQLAGRLQARMLQSSYTAATSTPDDAIRFLVIDGYVKAGRKGLKARGATT

AGQLYANMLVKATKYSIGRSATYDVIYPVDSGFKPPDLTK

>contig43193 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67069.1|) 8e-89

MASLVKGLAGDLTGSADICKIVADFSKCLACGYVLPNETIAFSMSSVKEEFTFTNMALIV

LKGENATTTRKLVERYDFKEHVIKDIIFECAGHVDRDCEIKFRIGDKSFSIDIAKSEQTS

AQGLYKVLELLGRAQAENARLWDMSILGMKHASEALYLTENNGATLQMQSDEATAWLNEA

YKRTHPHCYRTVIQKAFSDLCLVDASKH

>contig43449 Frame-0R

MIGNFKKGLFVAAVAVALATSVEGYTGAASYESKRMLRQQTQAIAEESVADDPECGSLEM

AEIDDPECGSLEMAEENNDNNDNNDNTNDNNNNYSSGNNGNNGNFWTPPDNGNNGNSGNY

WTPPDGKKNLHTGQEGTPSGQDTKGNTVIQTD

>contig43535-0 Frame-0F0

MRFLDAKASPTNASDARMPRKRYMATWRGCQMATQQSECVQTSGNKHHLAGNTE

>contig43535-1 Frame-1F1

MTSRGFLGRTCDFSTLKRRRRMLLTHECQERGTWLHGEAVKWLRSSPNACKRPATNTISL

EIPN

>contig43535-2 Frame-2R2

MVFVAGRLHAFGLLRSHLTASPCSHVPLSWHSCVRSIRRRRFSVEKSHVLPRKPLDVMSE

PE

>contig43823 Frame-0F

MHGVLRLAQLRSTRWFSSASTFTKLALTQQNRVTFQAGDAMRTDLVIVPVVISDDFALSI

SDKTTDVHNLVTIKQDNAALHIVKHSVSDCKLELRLPQTVSLNVTVANGSVTLKDKMEGD

IKVVMGRGDIKVDKVRGSDVSFKTNGGQIHVFTLMEGETVRLEASESINCKRLMARKAEV

RLGNGEALSSSFGAIYAETCNIMSANQSGQSKLCVGNVHGYLRVSSEGLDSIEIGSVSGT

LEMEDSGPACRVNAHFDSWTNEASSSVLVSGDVRVSLEPAAAINVELHGKEITISKDCVF

TSSEREQLEEDFAVFTGKLCAQEKAILASSDSTGKINVKCAKEDAMRTSFFMKDSVADDT

KDDKTPRLLVHSLRGNVMLDQLNWMDNIKRH

>contig44480 Frame-0F

MLDQSSDGNSDITTEDYGNVVLLYAKLVAQVLSTIMSAFVGTRHLLQVLALRKEVLARRQ

LQTPILALAGNSDGSIPTPPSLLIVTNGVPTTTSQPSGHTSGTDDSRRNRQASLLFHERE

NALYAPIGGLDFMTNENDDDRPRVSAASRILRVMCITDFVFSLSGLVVTAVELWRPSAGG

SFQLLFWAQAPHWCSQIASFCWVATLALYIAKHRNRASFDVAIAHAIIWMVVVFYWILEL

YSSYYKTKGFVHAAIIIWKVMAVGCFLITTISWLHFAIRWRKQERHKGAYVVSKLASYTM

AFFIFVGPIVLTDLVL

>contig45933 Frame-2F

MASPRDATPIETPALEMAQQEQDFRSRVQAVSLRRRQSDDTDGNESHRSSLVSHRSLVSA

KTASAAESSHRTRQAAGNMSNVRLVKQSSFRAHYDDDRCSLPAQNATQNDDSSGKPHAFW

QRINKKRKEPVPLRPQSPV

>contig46604 Frame-0F|Blast-hypothetical protein B14911\_09737 [Bacillus sp. NRRL B-14911]gb|EAR65846.1| hypothetical protein B14911\_09737 [Bacillus sp. NRRL B-14911](ref|ZP\_01171366.1|) 1e-19

MSKYSAHWDVIGDIVTLVKSTGSPALILGNGDVTSLVDAQQKVDMYGVDGVMLGRALLGN

PWLFQGYPDTSHVPLRAKLKVVRRHTQLFQELLLDPGLIGFSRMKKFYGSYLKGMPNAGQ

LRDHMARAQIPQDVFTIIDEFLEQLEHTRNT

>contig46998 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53361.1|) 4e-79

MVEKEERKGSLGTKLSPVRLMQLAFAVTIVFSMIYMYQFVSISITLHSAKTSEDSDERGV

VRNRVLGHSVLHLQGFEAGHKFISEYDVETQGPLYILVMSDANEDGQYWCPDCERAKKPV

MDAFNRAPRGSRLVEIRVGSHSYWADYMNDFRQNQLFYLDHIPTLLRYDGGGNSSSLLTE

EFCTDL

>contig47243 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56765.1|) 2e-62 NOT\_ORF

MATELAKSDKIAIDATHATVAARLVELRTTLTSYEIDVYRALVKDCGEIIGEVALRVCLF

TTEWAIAGQVSAKLRARAITPVVVLVAADERLDTI\*HPLPTTKRVLHKAMLVICGQRAGL

IASVTHLVYFTTKASPLIPIDHLRRHEHEAITYVVLLGNSKTIGQTAHKMLQRAQKAYAD

KGFPNEWLHHHKGGG

>contig47513 Frame-2F|Blast-DNA repair protein, putative [Phytophthora infestans T30-4](gb|EEY61644.1|) 3e-72

MKKNKGAIAPAVAPGFTLPEALSTKNRTVEEDQEINVERESIQHVEENQEEENKSIDWEE

ADHKQEILEADQNEQELSVDNIELDTSRMSQIDLSAVFSLPPHVQKDMLHKILRDRRQEV

RNQFIPLAGNPEKYSHAQISAFLQTSKLNRRIEVAKRQKRQEETAHEGGCGPGHRIDSNS

NRFYIYESTSKQSEGNDEDNYDRVADVKQISKAIQPYEDHNAAFKSDEKLRVATSFTPDA

AAKEVIAAWIARHQVRVKQEPVLAIELLRNAQLEKEKEKTFIGNSLDVEGKQLPMHDAKA

MLELQDLLNVDAKDEDDDVEWEDVAAPLTKSNLPSSLNVELQVNDPSVENLTTAKTIKYV

RRAIAPIIDIKRPAVDNEVAIVPSSSAVAADSLMSGVFCTDDISNVDDKLDFSSSPLDAK

NEQCLAQDEEESEKFLTLRNELEDIKAHEDLNLLKNDALQSAMATASNLTQWAAGAVRRA

LQAHSLQHAENIGIDKWQNGKAIDSIVALPPRTNGMSKTSLELSNRENKSNANHLSIEMN

SIEVEMRKEITAAPKFEDTKEELQAALNASIACDRLEVEETEGARVRYLPYTQSNDSHQP

NDATNEKYTEMDAVALRN

>contig48174 Frame-2F

MQHQRELDKLRHQSQQPRDDEPPSSHHFLINSQFSAAAKERYLDQQRQLHLGIATESNKE

TRLNSKKTLDQTAGEDAELMETSQGEWVPITEAFARKVNFNLTLESSPLHNA

>contig50265 Frame-1R

MPRLDHCSKMRDRTQLRPQHPLDLKHEYSWYKVLPGWLVVTMLTRTGISRTR

>contig50579 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62016.1|) 1e-61

MSCEEGLVNVRPLNEAQSKYRLCTAWRLGAIAAFGSLLFVTQGTNYTHHLHAHIAKHQIL

RNLQEQPALRLTFELKRKAMYVHGASTFDVIATPAPKRSINDKRMAFNGIASFVKEGNVH

EYSLVDGMSYYTHRPSGLAASVAQSTCLPAGTIPPIGSALDAIKNARTFVQTSADNRKCP

DSSVM

>contig50988 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65045.1|) 7e-24

MSSENAVLSRAVHGGSYRFVQRLLTFSANSFVLRKLHLNVTGAVTVRLELTLASIFFLRD

GFRLAFLRMP

>contig51204 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY55712.1|) 1e-108 NOT\_ORF

MRQGLVCVECGASVEELVRDYGKGNLRLSICSICNSIADKYVEYETILLFLEVLLLKPQV

YRHVLYNLPTPVTIRTTLKLFIVLVMLDMNVKAYLVDRDAGVTFRSESMYKTFDGVTSGA

RIGQYSLHLVCLALVENMVYFGAIFAAVWCDLWHRKWREKLQSSGNLKVIWTKYASAMCI

SSFGKLFALLTVIWEFHWSFVHVIGALVFVSNVLALQLLLKEGDPAQAKSPYIVALVVLG

IIVRGVTQFVL\*AIGNSVIFYVL

>contig53152 Frame-2F

MHLAALRDIVTLPLDAEDSCSSNQQNATAERKGEGSI

>contig53246 Frame-1R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY69816.1|) 1e-120

MSDPSRTVARLRPAKAITVNEATTVLEAARLMKSHRASAVLVTNWEGALSGIFSNTDVAC

RVVSKKLDPARVTIGSVMTPNPTCVSLEDSAVDAMDIMLSGKFRHLPVVSSPSGNIVGVL

SVAKCLHDAIRRVENMSTSLQQELGANKDNAMLRGMLEKMLSPSLHDVVSKPREKMPPLV

YGHMTVYEATVYMAETKRPALVVSSNPDAPDLIGIFTSKDVLLRVVVEDLDATTTSVSEV

MTPNPEFAAPETSVLDAFHIM

>contig54621 Frame-2R

MSPPPRPTCKPQPILMLMDTFATITTKKKRTRDDVDCSSMLTKHAHINLTASRRR

>contig54984 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69290.1|) 4e-28

MVQEIECRCDNPLACHSLVTHMCELYAACGDKRKREWSKAGQCQEYFHGK

>contig58016 Frame-1F|Blast-Poly(A) polymerase, putative [Phytophthora infestans T30-4](gb|EEY62302.1|) 1e-21

MIAEAKILSWDELPEFVFPSGRKSAEAERAEFTSNLQKMGFTFGNTSLFQPLCDVNRCTS

SGKWRGGYGPRKYAGGPRKQRRDYQNTQQSQGG

>contig58162 Frame-2R

MFPADVLKSRMQTASSVGSLSLNKAFHAVYSELGIHGFYRGWSAAVLRAFPANG

>contig59279 Frame-1F|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY66202.1|) 5e-09

MLWLPTHAKDHFVLRPEVLEVHCAKDPGMSSVREKNC

>contig00791 Frame-2F

MDWEAQCLECDEVLDDEDLLDSQESVGLVVSEAPWTAELSYEEQNVVALEDRDVDSVYRA

MLRQELLRSDFSKPYEYLKYRRVLVDWMGEVGETHLRMRKEYVHAAVGYLETYLARDTPL

PRKDRFQLLALSCLRMALNSKVWKTSCHHWPIFGN

>contig07282 Frame-1R

MKSVQDVIRIYVNLREKKTPRTPAKFIYYASIADEYANSGYDSGRTKECVREQTAKLGFT

FCFNSLGCDTYPFLTQKLAQCLANFIESRWNPIALWTAI

>contig11919 Frame-2F|Blast-ubiquitin-conjugating enzyme E2, putative [Phytophthora infestans T30-4](gb|EEY62974.1|) 3e-85

MSTAARRRLMRDFRKLQNDPPSGVSGAPMDNNIMLWQAVIFGPDDTPWEGGTFNLTLEFS

EDYPNKAPTVKFITKMFHPNIYNDGQICLDILQNQWSPIYDISAILTSVQSLLCDPNPNS

PANSEAARLFQENRREYNRRVREIVEQSWQAIA

>contig12370 Frame-2F

MDFIRTRAKNLLSFYRFAPQQRVSLDDFEEQGQRRVKLLSRMSAKWSPSLIQHPPDDLLN

EIAEYSEGPDADLLSHYALRLAFCRITSEWDWFVATESKLFAIRLGKLPPLAAIELLASE

GIQHEFLSEGDITDKGIFRVPFAEAPQLVKHREVVIRDGFCLIPLRKMNNVAIYHFRRCL

LKQMRELQSALPAQGPEVERLTPILDKFVQEAKVLTGTANLLRKTTNKPTLKVEAIDLIA

EKHFPLCMVQLHRKLRANHHLKYDGRVQYRLFLKGAGISVHDCIQFFRSEFIKSIPATKF

DKEYTYHIRHSYGLEGSRIDYAPLDCERIISQSPPRHGQYHGCPFRHWDRSVLQDELRRR

GLSLESAMEVTQQASAGNCQHACSIFFEKTHSSTIKNVHAGTQDAFAGLKRTPSLMHPNT

YLNASLATII

>contig12503 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57791.1|) 1e-16

MKLQLLLALATLYHAANAVDDIGCKSWGSEERTRVSTAYGGNGGTAYNDISLVAPGQRMK

SVTINSGDRINGVTFNVQLPSGATAAFKHGGDGGSKKEISFSEDEYIISFVLQTGEKDGK

SRIRYLKFVTSKNQIIEGGTIGN

>contig15425 Frame-1F

MRSSDTSCASKSPKRSTVSTICSQDEGLRSSLFSFNSYDFENPQCDVRTSKTIPTLLRQC

SVSARNLLSRSHSIDAQTSSQRLHYGLATSLKARKRQTSLKYKVEPQLHSISVRDSRENL

LLVRDDAEYSDYFVAHVTNALDRQHDGVVFYEIEVHLSKQQWRVNHRFSEFRVLRQQLLQ

LLSQRHRRQEFRCPICENVLASIIESPFPSRRIWKSPCVSSASRRTRDATMINDRKVRLQ

AFVRWCLFTVRSLRQHVRIRADRMGCELTVVLQCIEEFFSVTFARYLEFLVERGIVDQVA

ESSLYGRSHRFNRAMSDGFPRTGD

>contig16183 Frame-2F|Blast-endothelin-converting enzyme, metalloprotease family M13, putative [Phytophthora infestans T30-4](gb|EEY56805.1|) 1e-16

MGSLKSLNSTKKYENDNAKNEAFKTHQSDKLQPGIVAFPSLRLKRTVATWAIVGFGAQLS

IAVASGMQSDNGTSPSHLQATSPSHDWIDELPTSVLTHINRNVDPCVDLYEFSCGAWIEQ

VKIPEDKASVTLAFSTVR

>contig18224 Frame-2F

MEKEEMLEKVVSGRAGWVAAFSGTQHEQKVLAMKTRMQTLRHHTEEPLSIVTTPRGLDPF

LHSAESTPIGKRRDSSESMAMTPLEATPVSYTRVEAGYLTASKVIKAPVLTTPSLPTRSN

FKSQTTSRKTQLLPLRFQHAGPPLRVIAINENQSDDDEDDDALMGSQATPIKPEKADTSI

KKPAIKSPRVMTNFSKKLTFDVGDINHILKWNPHKEKANKLMKKENLPSIPATDLKSIEF

DFNHSAKPTVSEVLLKIPETYKLPEKATGNLPELPSRERTESELPLNSRDVSPVLTSAPV

TVNSSYVPENPSPRVHRPFPWELKTDAVRTEPLEWTSYNMPYDVEENRSPKRQHMDPAVA

VATKIAVSSSPGSVSSLSSPLVSSMSNTTPQDALMSLTGKVMVNGQKYIKLEQIGSGGSS

KVYRMLGPDLKIYALKKIKLKRLDAKTVAQFTNEIELLKLLQGNPYIIKLIAAEQDLQQR

QINLIMEHGEIDLSERLRDLKGGMDENMIRVIWTQMLKAVNAIHQKRIIHGDLKPANFLF

VNGALKLIDFGIAKTISNDTTNIERDSQVGTVNFMSPEAIQGNSASNGQRNPKGKMKVGR

ASDIWSLGCILYQIVYSKPPFGDVQNIIEKFRCIIDPAVPINFPALQNKDLEDVIRSCLQ

RDHRLRPPIVGENGLLQHLFLRVGGASAASTPMTMTNAPQVLSQLGDFMRSQGVAASRVN

MFVAIGQDCLQTVSNGIPLPSSYVSNNTQERRTDI

>contig18251 Frame-2F|Blast-ubiquitin fusion degradation protein, putative [Phytophthora infestans T30-4](gb|EEY58728.1|) 2e-82

MLFKVTNEGVERFSHCGVLEFSAPEGSCYMPYWMMQNLFVKEGGILNIRNVSLPKATFVK

LRPQSQDFLDVSNPRAVLEGSLRKFSCLTVGDTICLMYNNKNFMLDVREVKPAPAACIIE

TDCEVDFEPPADYVPPKPSPAAAGVATTVPSDLPYG

>contig18619 Frame-1F|Blast-spermidine synthase, putative [Phytophthora infestans T30-4](gb|EEY58737.1|) 1e-113

MSITTTNDKQWFSETEAMWPGQKFSLQVEEVLFRGKSEYQDVLVFRSATYGHVLVLDGVI

QLTERDEFAYQEMITHLPMFAHKLPKRVLVVGGGDGGVLREVVKHDCVEEIVMCEIDSMV

CDVSKTYFKETVATAFEDPRVTLLHADAALYLRENTTNKFDVIIVDSSDPVGPAEVLYRA

EFYENMKNALSLDGTICTQGECLWLHLDLIVDVMQAAKISFPLSTILTRL

>contig19670 Frame-1F|Blast-elongation of very long chain fatty acids protein, putative [Phytophthora infestans T30-4](gb|EEY65470.1|) 1e-154

MSSELLQRYYEWANTTELKLLDWVDPEGGWKVHPLANYPLANFASVYAICIGYLVFVIFG

TALMKMGIPAIKTSPLQFVYNPVQVIACSYMCVEAAIQAYRNGYSPSPCNAFKADAPVMG

NVLYLFYLSKMLDMCDTVFIILGKKWKQLSILHVYHHVTVLFVYYVTFRAAQDGDSYATI

VLNGFVHTIMYTYYFVSAHTRNIWWKKYLTRIQLIQFVTMNVQGYLTYSRQCPGMPPKVP

LMYLVYVQSLFWLFMNFYIRAYVFGPKKPTIEELKKKL

>contig21471 Frame-0F|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY57809.1|) 1e-122 NOT\_ORF

MVFLLTLVFDTIRFVSGFSAKNASVDKYTWSYIERKGKDKKDADVVVFLHGFSSTKEAWV

RVARGIDKRYKIIIPDLPGQGRTTPVDTLTDYSMPNQAKRLHDFLEQEVPADKNIHLVGC

SMGGMLAGVYTGLYPERVKSLTMVCPAGISMPSKSTLLKMLEETGRNLLLAHTVEDLGEM

NSYLSYEPLKVPYVILKILALERTKQLPVLQKIIHDSLQNPTVLEDLLPQIRQKMLVMWG

KSDQILDVSSVDVLKSKWSFEAQGQILLFDQCGHTLHHEKYVECTAAINKFLLEL\*IKVK

SQG

>contig22809 Frame-1F

MKALITLANFSGRLRWRVCNRTSCNCGATRELEAMMAPGMPWTIPHPKFQIVSSCIQKKA

VNKDVDFHRKSQ

>contig23231 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57876.1|) 1e-131 NOT\_ORF

MRASEALQWTSESFRDTTLDLYAASKVFGIHLITFEGLFVVLFSMMTTSLYYFLGKSSTG

ASSRAKMSWTIVSFAVISPMIMQITQAFSRREQALDILAESRSLILNILLANAL\*NWGDN

GRKQLPQDHVQKTKILLQGVLQHIMALLIMPTVTRGRHRLTSHGRILASQSIAPVKHLQL

QVIQTIRQLHDQVEVMKACGMPANEASRVNQYHWLLLARLERLQNIKFYRTPQATRSFTR

LFILVLPVFYGPYYVFIARGNENQATNFAFCLLLSVSTSLLMIGIFNVERTMEDPFAGGG

LERNHVHAIFT\*TQHLHDACMNEKEMPCQS

>contig23507 Frame-1F

MRSNESCPFSDGRNTNVYASTYAVDCKACPFSESTEPLWLLFHLVLSFVLVAHVRWSQVV

RHNHVCKQATCYQQQQVQNYAAQAVEKVAKVLQEETKYKVLDLKEDLVLPPTPALSVIEE

ASTARLTALRIEYTTYLQMIKVGLPRVVVNHKMRAENKDPNVLDELLSTTLSKAKKPAPI

EIPPRIDSKWDKNQNYTQKVEAFQRMLKVGVPRHLVESKAKQEGIDPADFDKMPIDAMDF

VSASFTYRSRRSSISSIISTAPSTPDALAMSGRTERPLPSRSLNTGMRKKLHWSTTLHSD

TLAQPRDSFWSHLHTKTQQDRVCISHESRQWMEKLFVQNDVKARVSRRRCFNRDETNQVL

VDLNHELQWNNGGDEVEVEPGPESDALITTKHLRSALVFRKRYIMLLDFKKSQNIAIVLA

RVKRSFEELTFDILTLNCNVLTSPALQSLIDMWPDNAEQEAIDEYHGDVTSLATAEQFLI

VACKIPNVLQKLRCLQFKLDFATRVKELCDNLKMLTRGIRQVCASDRFGGVLEYIFHLGN

LLNFGEGVEYTEWIKSISISSLAKLSFTKAYDGRISFLQYVIQSIERDEPHLALFCDQLP

LITRCSKLSFQSLIAEHQSLKIGLRMLINETQKSADFTTENASLRVALAESHNSMKLYAM

EVEQELQDVHELVNALEN

>contig25848 Frame-0F

MEKAPSEVPALDNVSDVLAMWKAQKKKDAFPKQQIVFEQVDKDNFTRRRTKSRSERGPTT

SPETIVNSQHKSFQKRRGSDRASEEDTVSLDSCDDCIPGEKLPPGWTKHESRGYPGTYYF

AHESGKVSWDVPTDDMVDSEQISDDCHSDHGEQNAKDDKVVTDEYEDTQHCEEAEILPDT

IKSAETSPEYFSEYETEAATAGATTSAAYRKNKPKPKSTWAFKLPKLLPTTTTQTLPTEP

VVV

>contig25934-0 Frame-1F0

MHQVAVHFWLANRINSLFLHLYMCLIENRYVNHTVFTSS

>contig25941 Frame-1F

MPATLARPTMLSLPATASVKPEPEITVTTNATLPAPTVANQQSRNEALEKILFAKRLLAH

AATCILGHGMCQVKKCDDVRRVFKHSLSCGGTNGCSHCEQLKGLVKYHAKECAVSRSDHC

SIPFCDGLRLTYAQNSSVGSNGRQSGGSEDEDDNTPLSSSVIKSKKPVSGKSPQNRSPTI

LPLKRKNSTATLIRPASASASPAPLLSPNFGASMAFPTPSVAKPQQKNVTANMTQEYGRL

LQLILHVEKCTTSTCIIGEECVEAKTIMKQMSTPNPP

>contig26360 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64602.1|) 1e-127

MTDQITSMEGAIRAAEQTLENLFNPTLDQDKRIPIDLLHEAKGLAFLTVIKVGFIWTGKV

GTGVVISKLPDSRWSAPSAIGTAGMGFGAEVGAQMIEFMIILNSDVAVKSFMQKGQLSAG

ASLEFAAGPYGRAAGANANFSASGIAPNYTYSHAKGLFGGVGLQGSGIMARADINKRFYG

REISPTEILTGAVDQPAAASQLYDALQRLMSIPPSGSVQNLKQKLWSPFMDRMPAAAVGP

DVQVAYDR

>contig28739 Frame-2R

MPGTGSLNASHRHFAGRPHEIEHYFHQKVVALARRSASLSCWQRPSIFGERTKGQMILPP

GGIKKKTACLQFLRRPVIAVCMQAAPNVRCVRMTPFNLSI

>contig28821 Frame-0R

MHNNFTQVALSATMNKMLSKNLGAKSRICRSICETMRLIWCERSIVRHYKPFSEACCSAG

LPLSPKILLASSKFGKSYRSDR

>contig29642 Frame-2R

MHKKTNCKNSQTKRQRLEPRSALSDIVALLPRNLTSFLSPEDALNLLLHCASLLSQDVRD

AVATQGLRNFHDRGKAHFGKGCIRDWHYLVPSKAAAGCGDCCGCCRSPVPSDLPLPRVSN

ARYSLLEAMCLIDKGIQQHCDQVLQLDRSFERRQYGVLQPVVFSLATALEENFHDKRGSV

ESLNSINVKDVANLKSLMNRVETNFGKRFFDLPVERHCSSMVEAHWTNISVDLATNTTSC

HFCDTKTLSMIEGPLNPQFREAEYEFLMRQHCKDIYQPLKKFMLRHLHHVRYVHPPHGWN

DAGDNFQGNEWLDLIGGVTPGGVLCGVYLTDIRIPRAWIIDRLAPGAYPFHESAVDLTLL

RIAN

>contig30428 Frame-0R|Blast-peptidyl-prolyl cis-trans isomerase-like protein [Phytophthora infestans T30-4](gb|EEY54813.1|) 1e-71

MAFCRFGPCKSDVIRDHKTGDSLCFAFVEFTDRRHCEEAYFKMNNVLLDDRRIKVDFSQS

VSKLWNKVQRRPWEKTTKRDGDAFAGNEKGSRHFGKKTGAEGCQREGGLLEFKSRETDKF

QLVEEEEAALSLRRHKPRSDHQE

>contig31096 Frame-2R|Blast-protoplast secreted protein 2 precursor [Phytophthora infestans T30-4](gb|EEY61795.1|) 6e-97

MTKIAIVYYSTYGHIAKMAESVKKGVESVDGVTAEMYQVEETLTEETLSKMHAPPKKDHP

VATPDTLKEADGILFGFPTRFGSMPAQVKALFDACGGLWAAGALVGKPAGIFFSTSTLGG

GQETTAFTTLTFLAHQGMTYVPLGYRSKLLFNMDEIHGGSPWGAGTFAGPTGARQPSQLE

LDVAEAQGESFAGVAKKLCA

>contig31849 Frame-0F

MLYLRALDETELQVHTGSQSGYTIKKASMIICFRWKYYSVPKFPHSMSL

>contig32512 Frame-2R

MSMKKMDRTSQFSYVLRLAVSFSVLNKDTTQTK

>contig33902 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66138.1|) 9e-70

MKQNVMIAPTAAVCTAAQLQGAITIGNNCAVHPGASVRSPGGIIVMGERCLVEDGTILAN

DTLNVMEIGSNNLFESGCEVRSHSVGNGNWFEPKSLALEGSIIGNNCIIGSGVVVAAGEL

VPDNSILVAVQTPGGDMRRIVREQKDYFVKAHSTMIQKYVDIFSRGSKSIYALEKHHDMR

ELSEQ

>contig34626 Frame-0R|Blast-mismatch repair endonuclease pms1, putative [Phytophthora infestans T30-4](gb|EEY70560.1|) 1e-51

MSENVADVFGTKFFRTLMPVKFKLKDWSSGLKDSDTIEKNAVETPLRVITRKVEGYVSKV

GAGVGRSDNDRQFFFINGRPFDLPKMAKTLNEVWRQYEMKQKPACVLNFHLPMNDYDVNV

TPDKRETFLK

>contig36192 Frame-1F

MEVKVSSPDTKLTGTVLQHKAMDLACKIVQERYAALPEKVQQALQKFTGSNGWLDGYRTR

FGSFSSKQLGDQSVIKNVDIQTKLRELHHAFSNVDLEDIWTGSEFAVMFKPEGATGGGDN

NGRFTASLFISAAGEAFDMQVIGTDRNPLLLRGIDTKETYNIQYGYSKTGWQVAQTTVSM

LKSLNVLAKARKRTYRVILDSAVPHVKAALILDSQGDHRTFFVYDHLQIFFLPPNFKALR

FHPCHLGVIQAFKSHFRSEMVETLFSIYRQSLMTQDHRGYRPQRHLHTRNIFHWFCVALH

SLDKHLIQSAWARSGLLPTQAIASLDLRVIVTNGSTPVTTNQSSVGTNCSNGCAYIERNG

LHGPELVDGSGSPQLLNGGVLSFGQPYSELQDQLTRIAQVAPGFLRTIGVPDPPNAQSFV

EFEGDASVTDPGIDEVQIIRGVLQKHGYLSTKQLDDESCKDDTCESLDDVVDEPCPRPEE

IIASVGILKRYLRLSRNAVPSRVAAIIQLNSVKRAVDAA

>contig36534 Frame-2F

MNGYLATESSEKGVDLIYLSVKNRGVAAVATLKRSPKYLAHVKRIQDFVDADDATASGCA

HRLRSLEENSVEYELVVTSNDLMVQIDDEIEAVHRFIADIYVAKFPELDSLVPNALDYAR

VVKAIGNEMDLTVVEDLPKLLPSSAVIGISVTGSGTSGKPLSSEALTMCMHGCEELLSLE

KDKIMILRFVESRMKFLAPNVSQLVGTRIAAQLIGLAGGVAQLARIPSCNLQVLGQEKKV

LSGFSSAAALKHTGVVFFSDLVQSVPPYLRMKACRAVAAKLALMARVDSQPHQKDPQGLI

GARFRTELVGKMEKWQEPQKAKSKKALPIPDQKPCRKRGGKRYRKMKERLQMTDVRREMN

RQSFATADEEYGDNAMGITVGRLGQEGSGRLRIIRKEQKQSSKKLRAAKFAAFSAGKPPL

SGLASSLAFTPVQGIELMNPEAAKARVAQANKKYFSAASGFVSVVKDP

>contig36541 Frame-0F|Blast-6,7-dimethyl-8-ribityllumazine synthase [Phytophthora infestans T30-4](gb|EEY66511.1|) 1e-70

MHFEYICEAVSQGIMRVQLDTGVPVIFGVLAVLSEGQAKDRAGLSSKGHNHGTEWAQTAV

EMARFREATLQGGCPMRMHESLPYNSLQDCPFFSVSTWLHIAALGVLGFVAASVVKKLA

>contig40012 Frame-1F

MGTSIVEQMLQVNPSEHALVVTSPPLAPVIINETMDQVVFEELGFTSYARVSAAESCVLS

YSMHCEREKKSPSMGLKPINNSPGRTLLNPPSPLSLVDVEDPLQFSMSSCHLVVDSGFSF

THVVPMINGRMCLPGLKRINVGGKMLTNYLKEIVSFRQWNVMDDTRVINELKEALCYCSL

DFKGDLTRYHLNRYERKHWVLPDFVHTFQGRCRDEDFTVDGDKAQINDQQPTIPCDGEQA

LEMSLEMVTVPEVLFNPSDIGINQAGIAETIVQAVKACPIELSGAFYANILLVGGNTKFQ

NFRQRLERDLRPLVPDEFDIGFHQPPDPILAAWQGCCSLAKSDILSERIVSKQEYDEYGS

NICFQRF

>contig40089 Frame-1F|Blast-integrator complex subunit 3, putative [Phytophthora infestans T30-4](gb|EEY54602.1|) 1e-27

MGPPPPPPSAPPPPSSPTSTPISAPPPPPGIPPSPPSVDDMPPKSRSSHSSPTTSTPSVG

NAAPTPHSKLLNHLPLDAPDEMDRKWYAHFYHMQKNIQGEDEATALAILKQQSAEGVAPL

PFQPDIALLYAVVTDSTLAKQHLRYLTAVAASDNYKNCMGWL

>contig41693 Frame-1R

MLSVTKASFNLRSRIQDSSNGLQCVDIVECSASGRLFIDKHTFMTSSTLEGRNASATALQ

ELDLHLSIKNTANIVKLESYALIGDQLHLLYEYCGRGDLLDLMTQELRLRKAGVFPRKAS

LTTLTNSGRRHIFTSILQGVNALHSMEIVHMDLSLENIFITDSGIVKVGDLGHAQRFQHD

RPNLPILQVAKEAYAAPELLRHTEIEDARSADAWSLGVILWTLCTKRALIHCASSERDNL

FRRMAECGTAVALQETGFLSNVPQLCFDLVVGLLDVNPKLRLSVEAALQHPWVKELAANR

ASRRLMKITDKVLNKDSEKKTILSSEIALDTTRVPLI

>contig42335 Frame-2F

MGAALCSCGGLDDQGLNNFGYERISSVKNSRLPVIGRKYGAFPQRHRHLQHAEHGSVFLS

RGETFSVSADANEEASDRTYKLLHGSAQAYADAFRAKLQEPPLSPRSKFYLLTTRLALGS

SLTTTESSGESGSEEDAVKRRKERACNSYLIPEEDDESVTDEDWQKRANPLITIIVPPGP

CGLVLQVGIGASDVPIVDGFVRKFDGRKSTIENSGLVHKGSELCAINDIDVTRMALKEVI

HTLNLSSHLERTFSFRNNISHH

>contig43109 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53705.1|) 1e-154

MLQSLDNGRRTMILIANYRDSTRCSETLRSIFLNAVAPNNLKISIHDQIYPAENERSCVD

VFCELVGEKDCHRAQIVSSQIDAANATGPTAARYETEKAIMDEDFCMTIDSHLMFVPNWD

EKIIAQWDSLGNPNAIITVYPKDMHLMSIYDVDEFLHLMCVSRIETNETDSMVQYDGPKL

IKKKNTPKPRLMSQLAEGFNFGECKQLKEVRSDPYTPFLFHGEEYSRAARLWTAGYDFYV

PSDDIAYHWYEKRKVVWERDWKERYVIQQISRRRIRHILGLSVSKEDFDRTNLAMFTLGT

KRTFEQWKNFSGIDPSAEFIAHNASQFDNCRELQYVSY

>contig44023 Frame-2F|Blast-SUMO-activating enzyme (SAE), putative [Phytophthora infestans T30-4](gb|EEY58879.1|) 1e-119

MLQGMAWGPIGHEMNFLEAIENAYKVYTRPEVPDEVVVVCNAAASHTVSLEALDKMKDTK

NFWLQAHALAEFVKQNEGLLPVTGVVPDMTASTESYVALQELYVNKGNEDARKVHEILRS

HLRDLKLPEDCISFDDVVAFCKNAPNIGMLETRTIAEEYQRIDLSSVDLEDENKEQSPLI

WYVMLRAVAAFVSEFARYPGSEDAATIQDGTWLVLKAKKLAAGTDVADWITDNHALEMTR

SCQ

>contig44588 Frame-0R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68035.1|) 2e-83

MVWAFSPRDGGCIQEWVIDREELVYIPLQLVHPQSKISIRPSPYVQYAPLTTSLEELGDE

VRTAKAINTKRFVRAGSCVCNFETLATMDESESAARSLELVASCSMSSAIPLTGYVVRDL

PTWKCAYEVEAYYLMRATFSCADEPQLP

>contig44849 Frame-1R

MTGMHMSTKQVFSNFTLRQLSEEVQATRRQHVTRRRSRKPSAEDYEGKETSDLSG

>contig45262 Frame-1F

MRFCADGVWQNLKRSLFLVVFLNKGYVKCAQAASAPVCKRQRGNGQDTRDRYSTERSGR

>contig45428 Frame-1F

MLRPSSSPSLITDTLLIVSQLARASKSNYDLILKANLLPHFCDLVQHPEATVRAKALNCI

GNLCRHAATFYSHFATPWDGQIAHTIVAGMIFGLRDNDQYVRRFACFAVGNAAFHSGELY

DALRPAIPPLIQNLGNDDEKTRSNAGGALGNLVRNSDELCRELCAHAAPWALFKLAMTET

SVACRCVVLFSLGNFCTYEECFNHLVEAESDFISELETLYNEAADDVSRRNIRRIFAKCE

ALGNEEDHDTR

>contig45932 Frame-2F

MRQLRAVGKREFRRSETMIKGASLLLCSSKLEREPSPHVSSHYNHWTRT

>contig46902 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65497.1|) 2e-76

MEEHGGRKSDGTKFSKGASMDASGSGYGQSSAYLQQKHEYTRVLVTSELHTEMWSIENKK

LLRSLLRMQHKWGTVSSEFDILNAKRMELRKENEHLKQDKEKYQVMMKNLKLQATYAMEN

PELVKANELAKRNSELNDDISKMSAGNKRLRKERDTLQAHLDEVEKQLAKVEQKDSKG

>contig47242 Frame-1R

MASAMRIERIWPRLMTTLCCGHHFPDGCVVTKQDTIPCQVGHMSHVSPILATYGD

>contig47589 Frame-2F

MRMYIARKRPSIRRRAYIKFGHRLQSASESGGLF

>contig47978 Frame-0R

MRDTIPVAPVARYLKAGELRKSAKSEERMFSSSKLFKFSKEDEKLFQEAAKEITDTASTA

KGATSKSETVKREIDPVEKTMAAKRRKRADARKRIDLENGMEKLNTDDN

>contig49752 Frame-0R|Blast-para-hydroxybenzoate-polyprenyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64293.1|) 1e-94

MGASSLALVSTYPIMKRYTYWPQAVLGLTFNYGALLGWAAVHGSCEWPVVLPLYAGGMAW

TLVYDTLYAHQDKEDDIKIGIRSTALLFGHNTKPVLNLFSAAAIAGFGTAGYMAGLHWPY

FFGLGGGAAHLAWQVNSADLNDPKNLQARFASNKWFGALIFASILMGNNV

>contig50211 Frame-2R

MQNHQATSMMATLMLAGATQATTCGQHKKLSWLLSSKGAAEEFRQMQPKSEASLKCCGIC

ERKFGILSSVASCNLCLVSICSRCRISRDLCFVKRPSNITQHRNQSEDQDATIQVQRRVA

VFCKNCKVTASNLDARVMVRRQVEAGKKQRDDNSKVCRISGGKTTFLDTPGDLKLESSDP

LIALSLSSFQDRDSINEETRLELTSYKHRLQHQHQYAGEEPELSCIRLSAPDMESSQAEL

VR

>contig50578-0 Frame-0F0

MNLKLLCSFEELYKYVIGLVNCVGD

>contig50578-1 Frame-0R1

MSISNTVHQTYNIFIELFKAA

>contig50729 Frame-0R|Blast-phosphoinositide 3-kinase regulatory subunit [Phytophthora infestans T30-4](gb|EEY53006.1|) 3e-55

MDIFSAGCVIAELFLGGKPLFDLPSLLKYRTGDSEPLRQQLKKVGDSNLEELLIHMLQLD

PSARNSASGYLAKYTSSNGLFPPYFDHFLFRFLVLVLSRGGKV

>contig52716 Frame-2F|Blast-ATP-dependent helicase, putative [Phytophthora infestans T30-4](gb|EEY61840.1|) 3e-55

MGLGKTVQTIAFLLLLKSLEQSGKSAVGPHLVVVPASVLNNWTREFAWIAPKLRLVTYHG

SKNHRREM

>contig53247 Frame-2F

MLQEPNSRFSPISASKNVSACLQPSSLSDTPCFPIHSNHGPVQSTSNGNERQCQLDQGQP

GVSLALVCGTSSTIRFETIQQDHGKNHNLVVRNISNNQQQQVHRPPKFSAAIVPHRMTPD

MGEERFHSNKPGGDDELRAIWVNDYDNSNALVMQLDMEIAKRMEEGHEFVHKMNN

>contig53997 Frame-2F

MIVQGFPCGKSQWSQFLTRSCYALGHGRDGEQVSLSLAEIEHVILRARLPRAELPYMKVA

SVVMISNGLGSRLHNLGIRHPDFRLSLALVLNHMNGEGIVIYDARKVHEQLNATLRSLLK

CSSAQGGLTMNEDSNTLMLPRVCKWYGLDFGGAAGQQNGDLAAIYCARKLLGFMDGTLQM

QVIHALSVDDASLRIKFRSFEYTPKTTLVQDTSDQIGEAELKN

>contig54747 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53445.1|) 7e-64

MVLVRRRDNRRGKETEEITVASDASIVANKGVRSLGVARTGRFAADMRVSMGGYGRADKT

WGVDHPWHSTEAGDLFAQMCAKDCMEEGTLDDDAMHEEPLRGLSRAQLKKRKAKLKKQGL

SAQQAAKEALKEAEASRLYADKEKRMLEEQEIKRREEIKKNRQQKK

>contig55155 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61737.1|) 6e-28

MEAKSKHAEKLHRLPSDETVFYSNIWSLPEIVHDVSAAKISMQLVDISQVAYVLTSIDYK

SGYEGATATETINIWASVDSQQNAAATKTVYKSKTQQVTG

>contig55825 Frame-2F

MRPTVYRMLWRTRRSLLSKEFNIQIGQLNVGLKKIHANQHNFV

>contig00330 Frame-2F

MRFAIRRHLKKKNSELDLPHTPKIAVGHSIDEETLKELNQTMTPLDKKTFLKGILHYENT

DFNIYFLIMKSSKEVINTVVGVIKNTVLNNSGHIASVYEFYEIANVYVYTVAQMKGEIGY

DDVLNQIKKSILRYNPRLLISLAKRLLIDPTISVTKAKEFLMNTTITNPIETLKNQKLEM

SQEDLTDVDIVLDSLNLKTDDQLETNKDEFLKQVEDKTGVNLKKKLKILGIGLLIQIAFV

SLGVPFGSAASKIFAKFANNNE

>contig00792 Frame-0R

MKDLRKSHDSLNNEAQVIEQIERLKVALLRKHEEAKQIARQLETCSEQLLALRGGVILEE

FSSRQLNQEPSRLRSRRVVATLSSTNETKVRLTSEVLKAMDQNVGLSRRRAYASSNTSSV

SAYSARSMPVARSTTVHTRSARATTLADNVSVSSNASNSSTTSAHQLSPRNTALRNRTKR

YNYMPQKYSATTSNALDNTSTSLSSRGAVMSRARISRDSFITRSESPGVGYYDVQVKDRV

KGGEIGDSDRSLVWT

>contig12218 Frame-2F|Blast-protein arginine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY60167.1|) 1e-172

MDNLESQTYETFEQDAFKYNQYEKAITKALSATVEEKVSVVMIVGAGRGPLVRCALRAAM

TANRKTRMFAVEKNPNAVITLRNLKFSEKWDTVTIIASDMRSWETTERADIMVSELLGSF

GDNELSPECLDGAQKFLHEQGISIPQQYSSFIAPIMSSKLWNEVKAQDSLKSFETPYVVR

LHNFYALASTQQCFCFTHPQLNATIDNRRQAELRFLAAESAVVHGLAGYFDAVLYEDVML

SIEPGTHSDGMFSWFPIYFPLRQPLRLEKGEEIVVNFWRLESNNRVWYEWSISSGNGKCH

VPIHNPNGRSYWIGL

>contig13240-0 Frame-1F0

MTLLGAKSATACTYSASALEESYWALFALAKLQTIPAKLSPPGMCGFGFKGRLSLKCCAR

LHYVS

>contig13240-1 Frame-2F1

MFHDKLPRIYGGHTRSVFIKKIWAITRGRSRHRRVRSIWCSLQWLILDPIAAIRASLIFV

LN

>contig13662 Frame-0F

MELMACIYSKSSEQEFIQVVAEIVSDMYDLVEIDTSTMPQDETENQLLHHDIATTETSAQ

RFGPQLHKLSEETREAAEIKFEELEKSLETLEIDSQQYNDIRIEMAALEALLQDPRVLHW

LRCLEIVAQLLKLTSHTLSDPIISGMGRYILPAIDSDVPALREAGLENLGLYCLLDKRLA

ERYLVVFWRALNNPEEESEVKHTCVQAILDMAFSFTNLLPHIFGTTRTEEKRKVNEKTCS

SERNERGRIEPTNEQSGHEEVTKDHENQDESDVVPGLEMLDLDTIFINLGQLVTVDDVDL

QSTVVEGFCRLFMMNRLDNITVLAILLETYFSPKLQKLQQQSDYGFQSRSLQLLSMFFPA

FVMATSVNCMLLEEAATHLIQKSMEKLMLEHDTMLDLGACAKYVMQLLSHRAQEPATSVQ

MSDTKHQKVPPRRHCAHHNRIGITICLELLALEKVAAMAGIRQELVTKRKRLF

>contig14722 Frame-1F

MKCGRYEYVTAGSHPGAEVKDHMSTQRSRVQTSLIESSKYSRLSDTPGTLGLELEKSE

>contig16566 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67619.1|) 1e-46

MGLLSLFQDSLLLMEAENIIRLLHNFPKTTSTQKVFEAIASVKLSCDEINELLAGGNLWS

PDENRQVPIKFPDTYE

>contig18227-0 Frame-0F0

MCLDVLCKNAVGDTKTDVSLWFGRERRGKDRRQA

>contig18252 Frame-1F

MKAEDIKPARVGGAGFGSGLRLKKNDEKCLTDPAALRATRLRKYEAFHGTGHSLSGKTSA

FSSVSTGDSSPKRSSNGKNIHSNSSSSIHGNTNGKSSTTPQTKKVSMSYRLNGEVVNVAD

KGEANDEEKKENEEHEGVVPFQGKGRRLR

>contig18964 Frame-1F

MYLDIADEHIMCQKPHVRLK

>contig21234 Frame-2R

MVLTDKQRHDLHQAMLDYLVGMGERFAAAAAAFENEADISKSSDGKHAGLLEKKWTSVIR

LQRKVMELETKLAQFEENAKVGGVLSRRDMLGARQRTEFLPRAPAKLSLTGHRSPITCVL

FHPVFSVLVSGSEDASVKVWDFETGEYERTLKGHTNPVQALAFNVPGSLLASTSTDLSIK

IWDFSSDGDYECLRTLRGHDHNVCGIVFGPDLASDRLYSCSRDNTIKVWELSTGYCVNTL

NTGHTDWVRDVAVSHDGLYLASCGNDRSILFWDLPHMRILQSIREHEHVVESVVFAKAGQ

EQVIEKIYAKKLAATGHFSPANGSSFAEVNNRVTDSTAGEPSGVAVVSKPTIRRMKILLS

GSRDRTVRLWEAFTGTQLIVFASHENWVREVRFHPSGKYALSAGEDKTIRVFDIESGRCV

RTLDEAHSHFVTCLDVHPSLPLIVSGGIDKIINVWECI

>contig21289 Frame-0F

MADPSKMSAKSGGDVYYDDGSDKDLAATLDALLLSAGGTLSRSPPLSSSSSGMPNGEIPL

SGDPLPKLLQTPGSEMTLATLMAMLEDPKTQNEISKKDPLEEAFPDTPSGSKAQLDLFDL

FDKNAVTPGLDDKKGLIGGEEDTTMVKGASKSNNFAAQNEEEVDVDQDDPVQLQDHPLQF

DPQA

>contig22891 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62288.1|) 2e-62

MASDDPTVTGHCERCRVPYDTLSGSRCAYCRMHVLLCDACRDKAQARGETADDVFCSDHV

ALIAGSLQDLQSRVQTLQEALAMAHGRNQKGRRRSLRKQLATVERRIQRLSCA

>contig23232 Frame-2F

MSGTEARQWTIAETHCLVKTKTENGSKLVNNYLLLHTLGQGRFGNVKLCERIANDGSSSS

TTETGQSVSNATIPKDNVTSASTPLPAFAPQKTRLFAMKIFSKKKLRRLKDYRIKKQVNE

SALKADLAIMRMHSVTTALDRVYEEIKIMRSLYHRNIVLLFEVIDAADESDKLYMVLEYM

AAGPCMVYRPSSKDFVSRVTGGVLGEDLARSYLSDILYGLQYLHQRHICHRDIKPENILL

CGSGRCHITDFGCAKQCFNDRKASDAILEFTDPRSLKRILLSDTVGTYQFFAPECCYGEP

YDPFKVDIWAVGIVFFLFLFGKLPYASENIQQLFDEISRSTLTLP

>contig23504 Frame-0F|Blast-phenol acid carboxylase, putative [Phytophthora infestans T30-4](gb|EEY63169.1|) 5e-93

MPIKVPGYHSNTPLHPSFDEDIRDVHLLYDYDAEDSNGQPEKWRYELWFFSENRIVYSIH

GGPMAGRLNYQTVAFQCIRPGELWQCNWLEETGTIVSLVYDLKEQKITSMAGFSKGHWEH

PKEAHGDKRNPEDYARWRKLAEHGNQRDRLILCEQATILEKFKGAGNLVPIAVNAETL

>contig24736 Frame-1R

MTSFRTTDFIRGSSRSTFHSVRDELNSSMANSTNCANLKHGYNSSAAGYIPGKLPLPNDF

FPVPKLSAKEKRYLLGLAKHACKEVVYYSRHKDGPMNWLHLSSADGVDVFQGVDNMDSSN

APQDGKALMYLRGSCKIRATIDEISDFFKLDTPEKMSGYTQTIGKDVLDHKTLLTLATPT

HDNPKHYIAINWTAMESPSKLARNRDFCYIECHDEFIDANTKRRGWVQSM

>contig25421 Frame-1F

MKFYQRPLTATYLSQIMPALVETLNSDQVIMPESIYSSMVRAEAHAAKESCEKEISAYCE

AAGLEEMVSCDAFETMLHNDVNLMIQDAFERMTSFPMAVRKEIQSSLRAFAEKEITIALH

ANSDKIAAHVSKQVDQAFQTLKNECQVMEQTKLPMENAILRQECARFLDREIQCIKRLPT

GLQGSRGVEIECSRIRQNASLLFDKLGVANDKAIHQSTAVLNDVVRGAKTRMTSEMHENL

DKRFAVKCPVTVTKLQTELETIFNMGMADVIQKAGHVSDFGVFDYKADLEHHKAQLLNEM

NRRYMIEMRQILNEVCYEAREDLGKQVTYRLEGKLPMLEEDIKVAIDSAAIHVMKAMSDK

LQGWTILKSDLEMKSKELEKLGDELADKYLHRNQQLEKDAGLRQEMEHYEKLRVEVTQAF

EQKLKQIGLPTTDDEIDSVFRHALQEHAAKFLSSVADVETSQFTAKGLREILTSDCRPAV

ENQKMLNQLAIEKKEALDLAEKERRARERERQAAEQKEAEINRLKSDHSKWLGEKNNESK

CLRDKLQEEEGRARELQQRVREMKLQTARMERLKHEEQLKSMEESRRDAMSKEMEATRLK

KELEEMKQVTADVEAQKRQLMLQVSLDAKGKDEADELKRQLEEMKHMIAQKEQERASMLQ

QIQREQASREQAEIAAQQAANAAEVAARAAISVSRYQQQPIETKEIGRKRPVTRSGSEDI

EMEDASHSRLRTAGRAAAAKPSPVAKKPRGPNKAKIINTQGNKRKMSLAEARKAAQEEVA

KRVQERATLLSSKKKR

>contig25937 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55034.1|) 2e-47

MRNPVPTMPGGGTVVFVTEKAHRYLTDNVEREEGGTPDILGSIRLGLAFRLKQLVGTQRI

MKLEQQHVTHVRHSLMRNKHIVLLGRQDHDNDQLPIFSMLIRFGDRFLHHNFV

>contig25942-0 Frame-2F0

MVTDSLVPMATQITAVPTHSWVEKSGTSSFFELRWKKSRRLQC

>contig26239 Frame-2F|Blast-S-adenosyl methionine synthetase [Phytophthora infestans]gb|EEY67024.1| S-adenosylmethionine synthetase 2 [Phytophthora infestans T30-4](gb|AAN31489.1|) 0.0

MTLSLASKDRTFLFTSESVNEGHPDKLCDQISDAVLDACVSEDPNSRVACETCAKTGMVM

IFGEISTKAVVNYEKVIRDTIKEIGYDDPAKGLDYKTVNVIVAIEQQSPDIAQSVDSVTD

EDVGAGDQGIMFGYATDETPELMPLSHVLATKLGSKLTDVRKNGTLDWIRPDGKTQVTVE

YKQEDGRLIPQRVHTVVISTQHNDDVTNEQITADLIKHVIQAVIPEKYLDENTVYHLNPS

GRFVIGGPHGDAGLTGRKIIIDTYGGWGAHGGGAFSGKDTTKVDRSAAYAARWVAKSIVA

QGLAHRVIVQLSYAIGVPYPLSVHVDTYGTVKEGLTDDELVDIIKKNFDLRPGMIQKTLQ

LKRPVMQKTAAYGHFGRDDADFTWESVKALEL

>contig28857 Frame-0F

MFEMQSKCNKQAINSEFYYSPFEKQKCIEKANDRGRKEERNDRNDAPSRYERGFPVNDRI

ELQLILSNPTGIHINLLEVKAWVTFENGGIANKATKDVYVKCYSCTFSLDPYQKRKSV

>contig29641 Frame-0F

MVRKNILCLMAALPFVLHVNSAETAVQEKGQSSDLSNHHGDLSRRFLQSTAFKNDPESLD

PESRNLWNSVWRLFRFMPRSTAKLAESNEKGVARSLGKVREVVGDNPSGVTKVSKDQVRT

LSKYASTHRTDWNSMLVYLYYTLGIGLFIYAAYGAFFLGFHPYGMGGSPRAN

>contig30931 Frame-1F

MILKWPLGKAMRRYCHAARLEHVFEFAEALCGEQARDLQLVTTYPRRVFRVDSALKTLQE

LALIQRQEVLFIEKGRIEDTNGMDEHQENDEIVTWDQVEGEWKEAREVMEKMLDQRIDGR

MEAGIHAMEPILPVVESANYEQKWEVQLKELDDMGFRNRVLNIQALERYQGRLLRV

>contig31468 Frame-2F

MQRLGRRVVASSLTSNSRRLVPIRVRSFINAHFSNSACVRPFSSIASEKEAFKAFEKAKA

LLDSDDIPQAMECLSIAACANIADAQYMLGFLLLNENDVEDESDTQQQNKQLIQDAEAHR

QHVRRVDDAHNIKEIRKSARAAYKQYLSNEKHKKHAKYNDAIVIEHASTQHLDRAFGKTM

ELFLNPNSKLELLLENHKDHDSEDAIDTTKAVEWLRRAADNHNRDAHVKLGNLCLRHDPP

MALEASAWYTRVTKDKNPHPDALYNLGVMLYEGVEHAEPPFPGNKLASIPFFTRAAEKGD

ISAQFFMGVLLHQGEKDLGIEPNFKSGWMLLEMAATNGHPAALYYLAQLYRSGDEKHAFA

ADRTKFLEFLDKAMESGDPDAFFCMADIYYHGSDGFDQDYEQAHNFYMAAAEQGHANAFC

CLGALYYNGVGVQQDFEKAFLYYQEAADRDSMEAWKNLAEMYTTGCGVPRNEATANAIMK

MLEKVQADGV

>contig31482 Frame-0R

MTKEGIDSPAQHDRIISDYELAREGQPPFENLPSLSPEPPFFSEHHLQIPN

>contig32511 Frame-2F|Blast-nuclear pore complex protein Nup155 [Phytophthora infestans T30-4](gb|EEY53449.1|) 0.0

MIMLDDDSRTKYIEELFHYALTSEDESFHNLLYTWLYERGHTNLLTAIRSPYIEDFLKTK

DQDLLIKLYMDQQKYLVAAKIWWARAHEDTLGDDEYTNSFAVVVAKNPDIVKRQYYVSKA

LNCLKSLENVGEASEAIQEVRDVLDVLQLQVRVLKALEQQVIELETSSLSSEENLQNRKT

DLQLLTFRLFDATTLYNRFAHKFDMWTECLHIIHVCKSEEGDVIATLWRKIIFSMLPQSS

NNAAFNAWRLDQCEKAGLLATSTSSTMNSSFESGNWIGQMQCKLLRLGKSLYWEGDDRRG

GSAVGTGDIVFPVGFLADTLEWVSLWYIRSTGMGAFTGSIASAAAIDATTFNWVLKLFLD

VDVPHRVLLSHYDQVYHEQPDHLYREGWTLHLLQSILAIINIWKKHAMSPRAEKDQLADF

AAYCPNIVDLCDGFITDLRATSLDEDGEATTLLVQFRRVKSELVNIRTFM

>contig33606 Frame-0R

MSSYLRGLGVVVLSLRSLYQVLDLMLIQLERVPIHDDFFAATSCNRFAFFLKILTAVISL

FEAAVTMH

>contig33901 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53142.1|) 2e-28

MTNLCFGGWIYMSLALTRKNLADFG

>contig34625 Frame-1F

MAKKRRNSAVLANKASPAAIAMSSSPLPNSLPTTPTRPRRLNLSSMYASRSGVAASTRSQ

LTTTQLPVLSPPLKKRVTSRRMGKAVKLQLPDDDVAESHGPKRGIRSGDTESAHNEEKLY

PIKPDSYLPEAYQHRSTVLQHAGSYYDAMLIRASVTQHHSEFIALQALKFDEQFYLYTRA

GSIGCPGKTTLAGPFSSTEKVTLQFCTLFATNTHCEWEDRHALRYQEGSYTWIELDHSNG

PPFSESLSSAVADNQGELHNANSFQNMEIALTSPAPSPAQISSRKRRRASMWTTTQATTV

TTSKRVRRGLHTQCEWLYASGEETIVNAESTDQLTCAPVSELPVEVQDFLSLIADQADPP

GMATGTKEVVDET

>contig39169 Frame-1R

MLLSAAEGPSGSGGPAKKGDSFEQMIDVVLANCGGLTLAGGLGFCSGYALKQVGKAAALA

VGIFFIVGQAAAYSGYIEINWGKVQKDMNKQVDHNGDGKIDSKDVKLWYRKLYTILKKNL

SSSAGFSTGFALGIYCS

>contig41625 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66214.1|) 0.0

MVLELKQSLDSQMDDSTFKDMLHNRSRVLMDKNYKNWNWDIISEMLEGPLTNPQRLSEAM

KTKFFKRLSGFFRCDQGNKGYFSNLYWIPDHVPYLRPACQMYTLLLNHPEGLLFLKTDRR

GQLLTEISTALELEARPEAAIVESHIGVLKARMFSPDYVSRRMLREYFTLLGLMSSSKEG

LKMMEQSNLFQRLYVMGTTKGHDFLCRLILANLDYSVDGSSRKLLQSWMTEGSKALRLYA

TCLLRALLRSEVADFDKWGIDALVTQLAQEEEVARAALSVLEEAAETPACLLAMILKRPV

KLIQLKDQRAESLLLKSLSLAEGLNFLRDTGDWIPCTLAAWRREKHISYVHAVEHALFRG

LHRDAAGRERGQSSSSTTNYQTCAPTPIPINVPTKRSGSVGLKPTSGGSSQRSLWGLDWL

YRMPWNMEVKIVGPPGSGPPSNLILETYIDGAMRDADEASAMDDELRINSIRVKGIVVDA

RNMAQPVVVNSQQTLQACLFLGTQPVDRRGFTKPPPQSNGGFVSTSGSANSGSSALSSDA

QQKLLRARSASNSGGGSMDRNSETIMSTSLDFADTGISSADSVKDENKDWSSCQPEQRSS

QYLTAPHCSLCAPGERAVWNFRVEMDSVAGTITSNGNVKRLLLKSVEFTLQLLPIRPRTV

PLPVHLYGELAKTSAGCQILQATGHLPEFLFCLSDAASVPLEKRAALWALGHVSATPRGY

DLLNHYAHDFVEMIVKLATDSPLVSIRGTCFFVLGLLARSSAGHRHLARLGWDAPRDTSR

TSIAVPQNCTSLFMWPSSGPSMRCSLTQTPRASPLQRLLSHRRDKMPNGWREVLRLIADL

SNHITQKEAHASLNKLRSSKPELFEEPVLLLCAHALLEKYSYRLALRQFVLNAFDRAMLT

DEVLDALRIEDDDELGNQSHQCVPIGRQLRRRQSSPSIPSFTSSVQSLNAAMQATSSVSR

LSFMQNVLNTGSTMGDQRPTMRSNTQNDP

>contig42336 Frame-0F

MTMSNILLPIFVGFLVESFVSNAKTVESATSYVNSAHEMAVNDEEDRMTLLETRQLQEED

DLESASVALASTAKRVPPSPCSVSSSSASEVHFKYKRRGSGVHDQMFDAVKLSDVSRLTL

QVEQKEEELAQQDMEIRKLESNVLSMKNRLKQSQHVILAYESKMEELSRALRVAQDRQLE

IETGHPSSFQQSNSENSLSSHNRTRRDRSSSWKIWTAHV

>contig43821 Frame-0R

MTRGRVTGSPSGYTRGSSEPRRLLPGEFLGLTASAVSMDVEVLLGNLLPDPIFASSSASW

ININALTLNTNGIKRNGRPLVDIVSPTTLSHVYKKVSLPTSNTSPTSNTILTRFHSPIF

>contig45261 Frame-0R|Blast-phosphopantothenoylcysteine decarboxylase, putative [Phytophthora infestans T30-4](gb|EEY65968.1|) 4e-23

MNTDMWNHPITAKQLCVLNEFGYKMISPVEKKLACGVIG

>contig45931 Frame-1R

MFIPFLTFRRHHRPRVKEAGRKVCKESVCP

>contig47241-0 Frame-2F0

MNGTRMYTPRKRSCGLNMFDCCCSTAGCVRRNMAIRHEGHTKMGHARRLLLSIPRGRHHE

GLSKKQTRDGCTEYFRV

>contig47241-1 Frame-1R1

MLRLTQPAVEQQQSNMFKPQDRFRGVYMRVPFINKSTNKSTNLASVKSTSSAHAKATTLL

MNRNTRLITSRTTSALVS

>contig47511 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67968.1|) 9e-45

MKDVQIRDKQLQEAKEAAIYEKQKVADRLKKMTREELMSREHLINEYGFTVMSEFDELGN

IVKIKGSEVATEDVGPVNTNRQRVQQAQNSMREKMKTEHDKKVKYEKELLAKDKARKDKT

KKRTMKKEKQRGCG

>contig49751 Frame-0F

MQWELTSKAQLAHLLVVELLAYQFASPVQWIKTQALLFSEGGARRFVEIGPAPTLTNMAI

RTLQVGDFPNVSREILWYQRDREAVHFEEETSNISASEYARGLAAEAEAAVANAFAPKMS

AAPLKPTASTPAQILATPVQYTQAAPVASAPAVAVADAPVSPLHILRVLLAVKLNKDLGE

IKEDTDVKALCAGKSAVQNEILGDLEKEFGGGVPDGAGEIPLKELAAKFSGYTTLGKVTN

GLINKVVASKMPGGFTMSSVKEYLGVDKGLGAGRTESILAHSLLLAPQARLKSDTDARKW

LDESLSGYASFAGISLDRPSINAASGSAGMAFNSASFSVPTVVDKPVEAKHALLVMLAVK

LGKIFSEISETTTIKELAAGKSAVQNEIVGDLEKEFGSGPDDAAEMKLSELANKFSNYAS

PGKVTSALIAKLLASKMPGGFTLSVIKEYLSSERCLPRSRTESVLLHALTQNPQHRLSDD

TSAKQWLDGVVDDYAKYAAIDIPYLSKLGGVTTGSSIGQQAMLSSALPSDFEKRLKSMIA

DQVEALNSYLGDDQLDWHRKIETEVDMREDLESSVSQWVTEHGEFYGAGIAGKFDAKKER

QYDSYWNWAKQDAMELYYRTAAAASGLAISPKLTVNKGLSAHFEAMTRFINKNVDTITDE

LALPPLEWFKPYLCNRATPELLRCTQFFVSRALKESSPELAQAVQLLVEQIEEWLNTNPV

NMQIFKPTQPLLRILDNGVLEYAEVPRDGVTDSINYVDEVARGLEYNDAIETGKVAGSDV

TAGMTSAVGFETTLNDNGSMNSDEVDSYDEEDYKDEKSAITNKQTSNTSEASKAKGAKLN

ALRDSLRKRSKRETEKSLVARSSSLRFGLNENLKKIVLPHVHIRKPSNVDPTIRLYDVES

TCVLLSCMREMASTGISFTGKVALLTGCGKNSIGAEIVKALLEGGATVFVTTSSFSMKTA

GLFREIYEQHGSRGSRLFVLPFNQASKVDVHSLVAHIYNVHKLDLDFVIPFAALSEVGRT

ITDIDSRSELAHRIMLTNTVRLLGEVVVAKKSRDITTRPALVILPMSPNHGNFGGDGLYA

ESKLGVESLMRKWYSEGWDDQVSIVGAIIGWTRGTGLMSGNNMVAAGVEKMGMRTFSTTE

MGFNLSALMHPSIVDRAAESPIFADLTGGMAQISDLKDQVDAIRADINKKSKVQASIYAA

QENDKKMSVLPLFKQVAAFNSKTFAPRANISSYYCNGFPKLSGVTGLSASTEQALLRGML

DMRQIVVVTGFGEVSPWGNSRTRWEMESYGEFSLEGCIELAWLTGRIVFDKGNWVDAETK

EIVPDHQVKSRYEEDILKHSGIRIVEPELFDGYDPKNKMVLHQVAIDKKMSPIEVADRDE

AFQFRKELGKENVDIFQHSSGAWMIRLRKGSVLNIPRALNFDRFVAGQIPTGWSAERLGL

SKDLAASVDPVTLYALAATMDTFVAAGVTDPYEFYQYVHVSEVGNTSGGGMGGMRGFSQI

YKYRLLGKAAPSDALQECFINTPPAWVNMLLLSSSGPIKTPVGACATAAESVDIGAETIK

SGKARVCIVGGYDDFGEEGAYEFAQMKATSDSVKEVGMGREPKEMCRPCSTTRGGFMESH

GAGMQLLMDAQLALEMGLPIYGIVALTNTATDKNGRSVPAPGQGILTTARETSSDTSKPS

PLLDVMYRRRQFDDELDSIEKWFAREKALNNEDESRVAFLDEMKARKVQSAQAMWGDSFY

HGRIDIAPLRGALSVWNLSIDDLGAASFHGTGTTANDKNESEVTHKQMAHLGRSLGNPLP

VICQKHLTGHPKGAAAAWMLNGLLQVLNTGLIPGNRQLDNTCETLRKYDHLMYPNRSFQT

VGVKAVLMKSFGFGQAGGEVLLVHPDYLLSTLPADDFQQYSARRTQRMVKMNLHSQNVIT

GKLLHIQVKNEAPYSSAQESNVYLDPTARAEYDVTSKTWRFGGADSLTANENRRLRAEKR

AKKAKAAAEIASLSRKTSNAPFEDSSSTLLTAINQAALDLGLLSKNMGMGVDVEPVATFK

NLNGREDFIRRNFTDKEMAYCYSSPYPAASFAGRWAAKEAVIKAISSSAPTEPNLWKGAG

APLREIEIYMTASGAPSVLLSGYPLQVYNRLGLSKLSVSMSHSGDFAVSQAVALFQQE

>contig50212 Frame-1F

MKMDRYMFARAKMLDIVRLYIRNLLAWKDNTAQSFEDAKNLQMIVEECLNGLSSVCSTEA

FALRELLVHDNFIGYLDILQCLVDENEKKNGNYHPSIFMTALEILQKCCMKLRWSGKSQH

KHQVNDTVRNFK

>contig50267 Frame-0R|Blast-AP-1 complex subunit gamma-1 [Phytophthora infestans T30-4](gb|EEY57305.1|) 1e-61

MSQKLRDLIRGVRACKTAAEERAVIAKESALIRTAYKDQDKQYRHRNVAKLLFIHMLGYP

SHFGQMECVKLIASPYFAEKRMGYLGLILLLTDQEDVLTLVTNSVKNDLNNQNQFTVALA

LTAVG

>contig53150 Frame-0F

MQQDIPLSGANSGQSHYSNEAPCDANLSSIANGKTKWCQDEHKRFMQALELYGSRQTGNE

WGLIAAYVKTRTVEEVRLHGQTYLKRLVQQIPYTVEGSRHVFSAATWNDPCRPSYQISRD

LVDFRGCGGQAKIANGGSKGLSSAASECAQL

>contig53244 Frame-0R

MNYTISRANYQHSLSGSFHDPLIRSTSMMSDFADGGSNNSLLSGGSESNISPRSADATVF

EELGTASHPGALARPVPSLLREAMSFRRNSLMSDSPYFTTYGEGNVEVYRPLPIDTTNVE

LPLRLLRLVDLLAENAHEVWAKGRMDEGWTYGPQRDDGSKKHPCLVPYVFLSDDEKEYDI

NIAKETLKTLIAMKFTILDHSGKY

>contig53323 Frame-0F

MASVDRNALYGLDLSAALSQESCRKLQLYQMSLAALIYWQTLPRQDGQLAIVFQTFTGTR

RQADSSQAR

>contig53428 Frame-2F

MAEPRAACGESGSSNDFHLGDQILSQDNFMQHQVNT

>contig53994 Frame-1F

MLALHRRVTVAEQQVRKHHY

>contig54450 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53546.1|) 2e-19

MAVKCSMPQFVARCLEEIGLEGRCGMPLRELFDAMNPENDVAYRSYTWYVLRGMED

>contig54623 Frame-0F

MLRTKLSLKAVLLKAAEQEHQQLAAS

>contig54744-0 Frame-1F0

MANGEYQLLYLASNKKFDALLAEHGNKPIAMTGKLIGVHFQFAHESNSNAQDDKIVAVAI

GHDL

>contig54986 Frame-1R|Blast-N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase, putative [Phytophthora infestans T30-4](gb|EEY53387.1|) 8e-25

MMRFLPSYFAVQEMSKGTHPRIACERALNQIAAIYPL

>contig58278 Frame-0R

MSASFFEPPSGPIGESSSSACFVSYAV

>contig59512 Frame-0R

MIISSSPVMVLHYNASFASMTVGSSIKSPLTINPSYCNNFKNNIYEPSRSIN

>contig00779 Frame-0F

MQVVEDQPAVASFSLPASPACSPVGSNSILLWKEDASITLPVPDNALDFPLVLWESSDPR

DPHSELSCTSSALVPFQKLQLDTNLNQTTLPYSRSRTSSFPSRDSSSNGSNSPKYQTSTK

QLASGFRGIIEHDNTSQISQEFRTAMRLGDSTQQEEPQLSVKLRGDRVELASASEEQHVD

FLGPAENIKRLFKLPYSHSRVSLAVHRVGKTLIVDGELHESDIPVGFENLPQEMLQLPSE

SEKKTQQLLYEKFIYESTVSQISASEGQKLENLETKQTLKKHHKTIKKSKNEKREKRSKV

RNESGKLLVGVNQDERKEIVPTVLTVERKVVTTALKKNQESSTRTQDRVTPPNRSTKTNW

FTSPQYASAFRSESQTFQRILKWKFNDLKMILGSQVLLFENHEHPAVSLKLHDMDKDLSV

CTVLDYYLDNVIANIPELALCMHSKGVVRGYKLVETRQIPYMSGTGRPLFDVHDVSMNAS

MLLKFLQENCSRENGTYWLHRNEGENSLRLYDVDVLSQGNQLKWKYMMAMLCYRFAARAS

RLLSSLAAGTPQLQHQLQQRQRELLSTCMTLLNEIAAEKGGIAHRSICSSVSEQLADTYL

RECSQLLSLEARYSTTADSMKAMRFLEKAKDYLLASIQLLKECIRDENSVALRHHTDRLD

ALSLEKEMELAPENERDDMASFLTEELHRLELKFSSTCLELSQIHAGSQKWSKAVETLVE

ACQFLTFAPFQRVFCRLNGHHKRVMQKSKLCLKSWILKALDTVIFHVRSYSCAPQKQSFD

ARCLA

>contig03428 Frame-1R

MKIITLWTCGYREVADWDRNEVKKKNCIYVVYMKRV

>contig07176 Frame-1R|Blast-pre-mRNA-splicing factor 38B, putative [Phytophthora infestans T30-4](gb|EEY62272.1|) 1e-104

MSRSALTRHALQKSLRNLNVPDDPPEEIERRVKQDELSIYGNDTTYNLNTLLHQNILQSA

YFHELYKFRTYHEVVDEIYYRVDHAEPWSPGTARIPSSCFCLLLKFFLMRLTRKQMLGLL

RHKDSTYIRVVGFLYLRYTCEPEDLWTWFEPYLEDPEEFNASANPSVKTTIGEWLIRLLE

ENNYFSTILPRIPKKIEDGIKV

>contig10248 Frame-0R|Blast-ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY65798.1|) 6e-41

MDKGTAAGGALEDVRNGAFFSFPYEPYSIQLDLMRQIYLTLEQGHCGIFESPTGTGKSIS

LICGALTWLTMHTDAYGLLERFANDEKNTTIPENSKLGAEPSWLDEFGQKSVDEDIKHHQ

QMVKEALADIEMLRLDPEAITKKKRKMRIAYAYNERKR

>contig10518 Frame-2F

MDTVLTATAVPYPCRSFLSVTASKVDTKQAMQVPATAILHSPPQRLSQLKMVATLAPALF

GEVFLCRDTKTGRQVAVKRVDLSCAKAQVTRSKHIRVVESLKQERDVHRRLVATETRNLV

LLEEEVQYGGSLYLIFPFCAGGDLFDVVRHSPLDGRLPETTARRFLYDVVQGLLCLKQNG

LAHRDISLENVLLDVHGICHVCDFGLAIEAENVVAPGRVGKSWYMAPEVFAVQESYDPLA

ADIWSLGVLLAIMLTGAPLIEKPSMGDYRFCVLSQGGGVRQLSHIFPSKLSEDVWDLMEK

VLSIDPIQRPTLEQVATHPFLS

>contig10796 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62995.1|) 5e-74

MYPGGGQPPNGYPQQPGHPPQQGYPPQQYPPQQAYPPQQGYPPQQYPPQQGYPPQQGYPP

QQGYPPQQGYPPQQFPSQQYPPQPAPYGAQPGYPARGLHAPQPGFAYAQPAYVAQPGIMM

AGGMMKHGKLKHGKHKGLKFKGHKYKGHKGKNFKKMGKKMKKMFK

>contig12372 Frame-1F

MDKAIQSAQLASSGCRSMKQMLLMYE

>contig13663 Frame-0F

MSDSNDDDFSLNDSEDERFHETEEEEDDYAAVSDVSDTHEFESKLQSAHKTPLLKKKAIR

LATKTIASKTGPSASNQSTSFSSKTSLKSAYLNAEDAETAVLDYMR

>contig14723 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65154.1|) 8e-20

MEGTWFTLINAVLFAVQAVVNIVYAKQLVTVARDYETLITPASYALVLWVLVYAWEAILV

IVEVVA

>contig15427 Frame-1R

MEVSRYRPRRRRYGVSRRKLTSIWTLLGGAFFIVYLLFLLYWRFGNFATLDASMTFNNLR

KSRHSIQIHPDDLLLDDTNTIQRQRKEHTHQLPIKAVIATSSPPILPVAITSVPIKSLRV

SKNFIHSSTLEKNATLSVQEAERITNTSKNQANFQPQAAPIQSLSNPITAIPATFTRREQ

FSSLRNETISGYTATLEFLNAYQFNASESLYLFFVCSDALFQAHDWSEECRQSKKHVYNI

FSHSSRRNRLVTIYAGSEKYWTHQNAFYNNFNLKVKSVPSILKWEGQKNRTSGMLVQTSL

YDEPFLSYLFQTTDERKLLFPANAIQHKQLITIRGYDAYVDTMTQFENENHPVTTFVLMV

SGRFPNNKRPWCPYCRYSELPVEFAFFSYAPKNARIYRVEVTDSYTEWMDRTEFTNDPNL

QLKIVPLMYKIDQVPPTTSNGSTSIHFSAHKFRYDRLAPLR

>contig16134 Frame-1R

MTRKHKRLASLCCLVLLSCYHIAICVQNVALTEAPVLNKSRRLRSGVGLEERVVPTSEGL

TNSFGTLSQGLTHFFRTLTPRMKDYVASWKWIIKYFPHLHVRFAKDKVAAAARVFPDDLA

NSMTKNLFEVNAFIEWDKLIRRSIKRTTEEVDAIITAALVAKFGNARAIQLFTEATFEAG

LVNAKWLPLLHNHYVQAKADLYELFKDILKIKNLNGVDQKSVEFFIKVGSVKQNNEDDAF

EVMNRVLIENEEVLVDMHKLGGDVAAYRDKWHLLKFAYYTIVFDSIPNADAIPIKRLKNL

ADKRKYGSNTAASWIADSYAQSAEGFNVLRIAKQTLQKEDGLNSIFDKAFAKKILKQIGL

KWDRNNYDIGNVLKHFVAEKGIADNFLQSPEGLAVLHAVTASMEVKAKGTEEVVLVFRKA

FGDDLVAKMIRNADQKDLNLVKFKSVFEKMVVVA

>contig16567 Frame-2R

MSDFELHNFFLPPFLATVDAGALTVMLNYSSTNAQPVISSSRILETCFVRILALMVFWYR

TGLKLRTSETGTELWELTKKLWP

>contig16844 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68165.1|) 0.0

MMQYVRSDPPRYNVTVEKVKQFERLLVSLDQTIMSAQVFQSCIEQDFEIFSGGDIVDVEE

NPDGSDSEQDGRRTSSSDGELRIDIQTNRVFLDEFVHCISFRLGIAEGAISSATETFERN

NLVGLTGLYVLLRRLQPSNVPADPILYKRLWEIQTKAPCVTICGKIMWYMPEFLLKYSPM

TSKKLVPTNYEEFRREYLHSLDDAFPADITTAKLELSAWLVRMESFFQPTTRGMGDASRT

LSIRGNLILKGLILAKRVQTMMHTLVNLHLSLQIPMPKRVVRPLYTCIEILKAVEFMLAR

KNPILAESSSHLLRQVAHSLFSLFRPLKAHLEASKKFDDTKLDVLAAVTVLENILNSGES

FSYTRITVLDLAAQIAMISSPDNGTTNFNEKESDVDTSVPLGLKDAGEPFKLIWKLRLLS

DFQRKIKSACDCSFFYWSRELLHPFLSDLYDQPEQANRIQYIVGGFLDGIKLLRGAQHET

DNEPYVKAFAEFIESVLEEEIVDSLCKDVENDLRLHVHSVHLDHLDAPNPKSADFKVLHY

YLNLRPIRLHGKMLDLRQHVTHYLESTFYNLTTVALHDWKTYGEMRNLANDKYGLSLSDN

HLPMGSLDQGLDVLQIMRNIQIFVARYNYNLNQQFFLERRSDKGSRHLNSINIHSIASSI

RTHGMGIMNTTVNFTYQFLTKKFDIFSQFLFDEYIKSYLQREKRWYKKHRDDKEVDNKYP

FDRAFQFNKDIRKLGVSDSGKTFLDQYRMLITEIGNALGYVRMVRSAGMNYCSNAIKFVP

DLNRTHFKFEVYAGTGAAEEKNVESGQVTQDKVLGANLSRETVEAARNLDSVISTLAKNF

SENNDYFKVLVKVFHDVTASDEQKHLVNFYMIIPALTVNYVETTVQAKDLMYKNTRRRES

YFSDDGFAIGVAYILAILDQGEQFDALHWFEEVVRKYQAEEEAYNEKQLEREARKREQAS

RKQKETTAELIDDEEEVHTLQLNAKRIELNRREFDLLDWSLNGARIFFKD

>contig17915 Frame-1R|Blast-ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY54768.1|) 1e-114

MESIVELQQQYLQQLATIGFYDATSANQLNENATAPRIIKAALCAGLYANVAQVVYPEQK

YFQAAHGVIEKDYNAQAIRYFVPSGSDPRHRERVFLHPSSCNFTQNKYDSPWLVYTELVQ

TSKVFIRESTMVNSYALLLFGGQLEVLHEKNLLVLDDMIHFHAVARIGVLIKSIRQHLDH

LLMEKIANPTVDIAQSELVTAISILLKSEGMYAAA

>contig18503 Frame-0R

MAFCIESCSARLHERGPGNHIEKSYAKNVAVNGAPKWNFHAKSKQSRAFSPLETDAASAI

MSNLAVRIDGSSARTRERGPGTQIVKSHTKSLL

>contig19672 Frame-2F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56110.1|) 1e-79

MTAGVGTSLWIAPEVMMGERYDDKADVFSFGVVLSELDSHETPYAHVKDKSPMGRKMPET

AILQLVAMGKLRVEFSPKALQTMVQLGTACTAIDPTERPLAVEALEQL

>contig21288 Frame-1R

MYKSDEACHILECKLWAMSSK

>contig22120 Frame-2F

MVDRYKDYLNKAFYFPEGRKKSPGTSRIEKNSDGPAFSNLYSRKVLQVLATAIINIDNFE

KLASLASGPV

>contig23246 Frame-0F|Blast-DNA repair protein RAD51 [Phytophthora infestans T30-4](gb|EEY63552.1|) 7e-29

MDVQYQEEEQELGLETHEMQGPRLVNILEQAGINASDVNKLKEAGMHTVDAVAMATKKQL

VGIKGISEVKADKM

>contig26432 Frame-1R

MASTRPASAQCLSEATAGHTLAADCHALPESSVSETKLISNASNPTASTPNDPRPVTSDM

ISFKATVVLNTNEDWAPRPSNVPPPVRRKRRFLWLCQKEPIVDETKRRSHPFGEMKIEST

IERRSSDFSRNGYMYSRGSLANDALVTDIREVRPSALSRGSSLRAWSQALSVTHEGDEDV

TAITALVNTTPMTVWSAFLQTANKYPNEVAVRGWEHIIAPVDGTYTWAQQAIRVQRIARA

FVHTGFCAGEGVVISASMSPLLQAVNLAAIALGGIVAHVRNSWSTRELCDAIFPTANATI

LILDAIYDNFYQALATLANQPVSFQIRAVIVLGEITNSDRAVADLGTHIPVFSAHSFLSI

PSLES

>contig27578 Frame-2F

MQRSRRNALWEDAKILAVTRYVTSLLAFGLWHLLVYAQISIIGKRLFESKKAERIERQKK

REEAEERARHIFLTSGLEYFIEEALQKIKTHVEVVVKDNKQLQAWKVSQKTAVTADELNE

LLQDLFLAVLPTPDAVSAAGKQESSAELRKWQEFLIYPEKRNGEDEHVISLLNDLWDLLE

SNLFLPALQHSLGFLCGNSFQDLDDVVYGQGKFESQTVDSSTAKPFHKNLAPPLAKLIPC

LQAEMNKLLLSFGPNTYAAKYSQGLNEIEAFQNFYEAVFFEQSAQDPYIGPAII

>contig28306 Frame-0F

MSRKVIVDSQVAQLWSKDAHQSFEMGLLLGYVSSSNIEDFVLAVTAVPPESESNEAPTCL

RDVSVEWVQEVAQQVDRLLPGGIDIMGLYLNSIQDVSNQLVPYLRATAAAVAQPLDVCGS

ESIHYLAMVSTNGDVCFQSFTNLKDVKSTRMLPAKVETATKEIEFKQYRTLIDLDELIPG

TDVAPCAAIPASKVAEKFMNELEKHLEPLIRRVEASIAVSKSKEVSDVQHIKLLEIPAWE

SQSHIEAPLGGIHGAINCIAFVPESELNAYEMAVKYLKRDFVKSLLIRVDMARERWGEND

EVKPNTVFQKGGVIQFAQRGLVPWRSAAALNTQFMASVHVFADEDAEIAVKNAFEILGDL

SKSNGANWSPIETTIQLRKDSTCVMITTEPSKFIYYLLPLLLVLLLLG

>contig28399 Frame-0F

MIRGVDPFVPSLGVFLPSTATKSLSNRPHDCQ

>contig28535 Frame-2F

MKNPRAAAHRTLRFVCGSTTAERESQQKSVAGIAPKLKRQRVNKPLLVEVRLVEFIGDIS

EASDNNDKYYGLFLW

>contig31155 Frame-2F

MASSCFIWYSVARKASLKLLESVSFLPTAPSRIPTSSGTFKKIPPMFQCRQFTTHFFHVQ

NVPGKTWTLLK

>contig31483 Frame-1F

MMPLRFATALLNTVARPSMRLRRCKYLSFRTLQQLGCFNAEDTSWEWLKDQKNSRLQRFL

KLEQNYLANQLSKPKFRKVERTFNIELRNRLARDDFSIPECIGKYEYFMRQAPGENFPVY

YRRLRNGVSDPSATLTPEEIVLNQNAEPALNHEFHFVTAMKVSPDARQLLLVVENDREQC

QVVLKDLESGKLQFLANVPNIKNVEWSSAPEPHRVFYFTKVDAHGRPFAVYSFDVATHAQ

RLIYEEQDKAF

>contig33607 Frame-0F

MLYLNIGYSVRTGRLFQVEYAMEAINNAGSAVGILA

>contig33900 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53142.1|) 2e-27

MITEGAIYANVVSVPWTYLWIVSAASRQTFFGVLLVAVYLWRPTKHGLLYSQMDQLPSRE

PVMTHSIAHGIEQISRVTSAADDDNSPPSSRTPVTVLSTKGSASSTIE

>contig34691 Frame-0R

MAAGWNSVPSRKRLTVATLTVRLIYCLIRRFSCGLREMSSFFAFARFFLVL

>contig35010 Frame-1R|Blast-amidophosphoribosyltransferase [Phytophthora infestans T30-4](gb|EEY65962.1|) 1e-128

MGAKLAEKIRRERPKHGIDVVIPIPDTSRTSALEASQSLNIPYREGFVKNRYIARTFIMP

GQVARKKTVRMKLNAIRSEFQGKVVLLVDDSIVRGTTSRQIVQIARENGAKAVYFASAAP

AIRHPNVYGIDMPTTDELIAFNKTEAQVAKVIGCEWMIFQDLHDLEDSVRQENVALVQFD

SSCFNGKYITGDVNQAYFERLHAERCDARMEAKNMGFTPFDRTISAPQSDESIDMYNAPQ

>contig36543 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61826.1|) 1e-87

MTATTERLLLTIALGAVIAVCGFFGIKVVKLLRRKSMSSLRLATAPRVSLSKLQTSGCWV

ALCGTAFDVTGDPFFEPKYGGIYSKWVGHDVTSLLLQLGLVLDAADDAKAVESYLDHEWP

LDELQGDGEAVKRRFELIQEWFMRLYSRYKVVAQLSDHYVGKKWDLFRAELLPKDAGQNA

GGKCPLGFVSKTVSKAITYEKEDFKNMRTITFQGRCYDVKNSTLFRPDGGKLAHFVGHDI

TYALATQSLSKEHMDVEPKRAYTYSEQVLLERYRKYFARELLLVELKREQRKNGNCMGPI

NLHQIIENSDSVAQKTCLLDLKRALGNARLEQVNAVCTRTTMTPLHKAVEKNRLDLVEEL

VQAGADLMARAALYDDATPFEMAQRFRFKDIAAYLNNRV

>contig38307 Frame-0R

MHAVTEHYLYRFSTIPFRQCE

>contig39168 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53074.1|) 5e-52

MLLSRTDRDMRIICNTWGLRGRVPDERHDSGPFKNVPLFVYRSLGGELHSSRCLSTPKQP

QFIASKDSKDRQL

>contig40010 Frame-2R|Blast-actin-like protein [Phytophthora infestans T30-4](gb|EEY62680.1|) 1e-23

MRVVALDAGGATLKASVVISGETSTVSILPNHVASTSVNPSTIYMGQKLQELEQQRAKLR

YLRPVQR

>contig43190 Frame-1F

MMSSDNFLKDMASRGIKDLGIVNKCLGLRVKLDDNEDYVLDQEVTIDSLLKEFGLATANG

ARSPIGDECNDVDETNAESLKPTTKVGDASVKAFQSLVGSLLWIPRCTHPDIYFAVHRAT

RQTHKPTTSD

>contig43820 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66229.1|) 3e-82

MAPSPTSEQHSNKVIDSAPTRSYSKRGDGFSVQETEGLLQEVRNRWQDGWDIIAEVHNAQ

FPGHKRTAGSLKRKFAKLYRTKSNTTVKPKHARIAAMAKKVREEMRGQRRGLAASSRMLG

DDLASETDAGVGVQDVHPDLNEVEIITYQSVTQPHSVPEDTITATEHELRQTLTQSVPMS

QESVDAWQAAIDRWPVASEQLRRMRSR

>contig44021 Frame-0R

MSAVRRFEGGAIIKSVNVGSLMLLLGGIAAVLSALLARHGFTGRDHVVGIDLGTTYSVVA

ILQKNEITPIADKDGHVLVPSTVAFLPDGGLLVGREARAYRTTDPQHTIFNAKRFIGQSY

TDVMGSEANESGVVPYEFSVKKLENNDHDGVCFKLNLHNQPECVAPLEIGTAIVRHLRSM

ACQFVGHEQITKAVIAVPVDFNAKQRNATKAAFEAAGLVVSRILEEPTAAAIAYGLHQDP

NVSFLLVFDFGGGTLDVSLLFARNDAITVLDTVGDNHLGGEDLDVQLSAWLVQQFEAQIG

TAITSRGGTETYRTELAHGLNEPPCTLAGVRQVAELAKRQLSDETVTTAACAWSDRGQVV

RPVVEITRSQFESLCLPLLERTMIPVLDILEA

>contig44155 Frame-1R|Blast-deoxycytidylate deaminase [Phytophthora infestans T30-4](gb|EEY53332.1|) 6e-39

MNAILNKNSTDIKGCTIYVALFPCNECAKLII

>contig44212 Frame-2F|Blast-guanylate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY53008.1|) 0.0

MWGNPIPLDNGTSVVFLDTEGLGSVDREQTHDSRIFALALLLASSFVYNSRGVIDGNAIE

DLSLVVNLSKHIQTSSSAKDGISNADKLHEFFPSFMWVLRDFTLQLLENGQLISSKQYLE

NALEPTGGYNDDAVEKDQIRALLCDYFRHRNCVTLVRPIDEEHKLRNLSKVPYDELRDEF

RKGFENLSKQLFGKAKPKSMFGKPINGAMFVNLARSYVEALNSGKAPVISSAWSRVVQAQ

CHDALEDALARYKAELNVRVRRYISPQQYVDDASFEGNAENNLDGEFVRVNNNLDRNDML

HECGNLRSVALLSGALTNASIDEEEPLMPENETIEIMEKDDSMKTRSSIQMVRLPCSVDK

LRSVHYLCKRLAKKKIARDC

>contig45930 Frame-2F

MPVCSHSPPLATALLLPQQSEATNPRYNNIHGPMNLPTKKLVKGSSFTLATLLEELNSST

IAAAHVP

>contig46900 Frame-0F

MAPHGYCVALKGATRPELCDQNFIAATSGATMCTPCQRPLFSFLPGGTVCSAAKPGEIYN

HVEWPRLALELASLELQDLVLESKYHESPIQALLQAWTEILTSYFGSECVLHVLQVVQLE

NPFQLVRILVAVDMTEIPDTAFTTNTDHVIQKEVIATRKILDELRGKLSGSRPGNGSDNE

DVEHLADLIESMSFREALVRRLNRTNQTWALAYEMVNISMVKPLFHSTRALACERGTFFS

ITESWNGNDRVCVPCPAGSFSNVRGALKCKPSPRGTFVYKQGMATFESCPLGADAKSGAT

SCVQCSWLTYECNGFWQDLIITACAVAVLLRMFYQKCRALCVGDKAAQQQDESVALMTTV

RTHGRSLEGVRYSPMGIISADAMFGSSSETNCQL

>contig47240 Frame-0R

MNVMSNCSGELSSESVSDAGAGAACCLNGTNKSIERLSLDLIS

>contig47510 Frame-0F

MKHKRTLVKAIQSSSWSSGNLS

>contig50213 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63729.1|) 1e-103 NOT\_ORF

MLRLTRTLHVHCANIVRDDCFSQRQRASMNEEIFQIYFRTSSHPAMHELKHKMMEY\*GTL

ERWKFRDEDINSPKVLLTAKNLSKHPLLFVKLLAAVLRYLLILPSRLFVSSICDLIYRFP

PRQALNRSLTLVTAASEAALVCSACIVMAYVISPSKIFFYCCC

>contig53854 Frame-1R

MELMFSSEDEGDSPPSLPEFISHQKPSQLPASQDSIDEELLNSTSRVQVQNRQISPNAMS

HKPVISARQLLMSSSNLTVNKVSTGNEKLSSQAIKSGLLVAPKKPLASLTPE

>contig54451 Frame-1R

MCGEYHKQFESWTLSLTRFECLR

>contig54745 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53342.1|) 9e-11

MNERRWSNGDGDHGKAMKTEHRGGALARASARKVKKQLDAKWVQ

>contig54987 Frame-0F

MQRLYFAIRFAQLHIYSFRVRVSTISKLPRIVVLLIV

>contig57991 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67964.1|) 3e-23

MSWCGASNRNCSVCLSCSSYLLILLALAELALAVVILT

>contig58918 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57031.1|) 2e-12

MANAFAVGDVDGDGASELVFGSLTGKVTIFK

>contig03755 Frame-0R

MTSIEAKYNSKAAQMYKIALAKKIKASNVQVVAPVLVEKPRDNDIDGLEALVKHVEIKSE

LCHSTAVHGHLKREVPVVAFVGKHSSQAEPMTQPSGLLTGHRPMVLLGTKNGDAAMPLKT

SSAQLNTRSKATRLGASKLSTSSKATRLGATKLSASASDFDFDDIPFENPPPPASTKLKL

SAEKQIKDDEALARALQEAENERESASASPAPATYQPIPIQAQTLEKYKNAKSISSDNFF

GSEAKELDSAQLARFQGSQSISSDAFYGNETRGRTPSSDLTNEAR

>contig05340 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69169.1|) 2e-19

MRRRYHRHFGLPNANQILLCMCVCTLLFFALLRRHWLHFGEDPDIYASLKRIYV

>contig06208 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53321.1|) 2e-84

MQSTNGIVRYRYFSLRHVAKYLLGHEIQEADHDPVIDAQYAMKVFKKFRYLHENPSRRDA

VLQTLLKTPRTPSFAERYPVIDGVSMRAPRKQSTFPH

>contig07287 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65955.1|) 8e-25

MSFANLKKTERDEYAASLAVLALYDAGVEITADALNETFKASGNDVAAYVAPLFADLLSR

GLDIEKF

>contig08761 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56828.1|) 0.0

MHVSDRPRQRASYSGPPRPLTIEAMNQLSMRSLGELNQLSQATREFGEVYSGSPDTSRRS

PKFLQRVFDPMEKKSDEECLFRVRISGIQCRNLQGRRFSGKSDPYVEFYWDDPNETAPYA

TPVIKSDLNPNYKGLLIAFEYKAPLRELPDRNLLVKVFSTRKFNAKYLIGETKVNLWSIA

TGPVHHDHHLIGCDNGRVVFNCYMEQCSEWNISVSEVGLMMPAIANELDRPEGHDFQEDA

SLPLKKFGVSYKCTIGTDEKFYMSNKLKHAFKRELGEINEVSFQSLARLAVLSSRVPRPN

SQPKGESKTEDEHVADTLVAQDPIGVEWTTATDYLPSISRYSTFDELMSATLTLEVRQVL

VGRGQMSNDPDGGFLSLLEKYECETAALPNVIVHFDAEIKNSILFGQTWLSLEKIFEDAI

QERMKKRLDADPNFGMDGLGFSEQYVTSKFEHSLTLKGHQVGVIYGTILFKRIPDVRQLR

CGVNSENGISSSSSVIVGVVPAGNKKHPRNFKVVIPFEAQRLLEKMQDLVELMTTRQKDD

KEGKVRKATKILKMLQVSHKVSMLSWVYVSAEALEETKHILLRLWHFLLDNIRVRHYTLR

NVIYELLFYLVKRAELSDLPLLGFDSAVAITMFGAKHTHKISRKDLEFGLKLRAMLVETK

YCVLQTVSVRGVMNNNLMFFVARMLSVLCFRLPSFGVELYQLWSESYIEPVPELAGEFRM

NADANLFAMDGLEAHLDWRRFHKAIYDEYGEKALRFQEEEAEDKYEVTSEAWRSRFRRLV

GEANTLNILLVDQWLWYVLDTLAVLNKKIGWIHLPGYTQVLMVFFLELKTQKSGWLPPTL

YKLSCTMLSNPSLINPMTKFLLSSTNVHDVTAVIGSVELLGVWMYMIRSWRVRLSSYRLS

HLENNDRWNFHQDDQYSIPAGDEVSLLPPSFDFRFLCSALRILLDSEHTQVVLTTLEFLY

NCWDCFPERHADKLRFELLRSFIRLFLHWHSEVRSFFQTLIALRAMKPHGWTQKGASFVN

TPPHSRRQIDAVAADFNMSLGSEEPIDSVRRSRSHSSNSLVETVHKRMGSSSPWSSPRTS

PVASPRNSGTPLSITISSPSSRPYSSGHNTPTSDYKSANSLPAKIRSISEEYIKHTSLQP

QMDIHIQMRLNRLLESIYVAAKKYIDHQSETGNLLGKQMTQATWKKKGMLMKQGFIYKTT

WKHKFFSLQNNKLGYADIENGPIKRELNIIGSVVTELSNQLDHSQGSRVVLFNCFSVDSG

YQKLVLCAPTFEEQREWIEVLTQNATAKTAVRKDNETLSPVDLADVSDQLESLAGKYSTT

DKVSDNLLPYSVLAVKEWLDLRVTAMELESKIAAGQPIQMPVLLSKSSLYADDD

>contig10791 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69420.1|) 5e-11 NOT\_ORF

MVTFKKRQDAARETERKQQKTPSKPQIYNAAVSKQLLQLYHLLLIFQANRVKIHVGNFSS

PQCYLASMNLCSITIL

>contig11987 Frame-1F

MRNNSHQVSRLVLSKGRRWLLLYCCTGIMVTFTLHGVLLEKITTHRVLGEFSMTFVFCAL

NAVVAFGLSHARKEKPSAMPSSFLAIVGALAFGSTIASMMALRYVTYITRILGKSCKSIP

VMIMGVLLGKKYAIKKYVSVFILSIGVAIFLLGTPHEHKRMHQDASHHHLPEHERTPNIA

LGFSLLALSLVLDGATGALEDKFMESYDIGAFDLMFHVNIYKAFFAAAGLVVNDEVPVFL

QYIVPLLPSLLMLSFTGAFGQAFIFFAIYKFGALTTTIIGTCRKVLSIVLSVIYFGHVLS

IEQTTGLVLFFFGLGLSWVSIKNCFGSLSSTSAAANCSINQTELSKEGLLETCSDMATDS

GSDEQDSPIYHKTKALGDMSVETVRQFELINAWYRQTACKDAKLMDEVAVFDANDVAGQV

I

>contig13372 Frame-2R

MSEQKTPRTRSVGELVSLALIASSWLVYLGKTCDKSHDVFPLATYLRERIRDDVVIQMSQ

TFVKIHKTALWNIGGHLSTYPLTQNGHENFNRRHNTRHHLQYNHKNNFGRLTSKTEACII

LKKV

>contig13664 Frame-1R

MFRSFRKFRNANLIAMHYVLLKRYFVRAKVIIRCNSLKPVFRNTNIAGTTFNMSTKFDNA

VRTCILLSIKLVPLIPLCHDALLLSVQECTKLQKESLNCLIR

>contig14724 Frame-1F

MGGASTKEAFTQPESPPAKAGDNSLTQQKPSFRTLSANQRATTFDERVHLRASEASRGNR

VMLGLGATSEFRPLQRAATFDPRLRSQNQVFMASDVMHRRFFNVRERRVSTSTDRILFRI

AESDTERQEAIVIVDPYSSGMSMAEKVLQRGFLCVCVYSDTLEVTQERIAHVPSDLASKF

LAIIYHDGEVERKDERKALQYTVAALNRLKNIDVVGVFAGAETGVLLADKLSEHLNLITN

GTNGSAARRNKYLMGEVVRSAGLRAVAQVQATKWSQVEKFIAEELEPVFKINGGNFKVIV

KPVESAGSDDVMLCHSMDEVKAAFGNIQGKINALGLENQATLVQEYLEGTEYVVDTVSRN

GVTKVVALWEYDKRAVNGASFVYYGVLLRAAPDGSVLAKVADYVLKVVRALGIAHGPAHA

EVIVERGEACLVEIGARCHGGSGSYLPIVMPCLGYNHVDAALDSYLDAEAFERLPERPKE

LKLHGCEAMLVSHEAGKLAGYPGHEDLANLSSTASIIWYTHVGEELSITIDMFSTPGSVI

MVHADEDQLNCDYARIRELEKKGLFALEPPTKDYTKEKVAGGVVVVVDPFSTGAVLAHEL

MARGYDCICVYSDRLENIESVASLIPEGLTLEFAATVAFEGNLEETVNAIRKAAERIANK

QPQNVAQQIEVKTCATICAVFAGAELGVKLSDALTDSFGLAGNIMTHVNARRDKYLMGET

LRSSGVRAAKQVKAKTWTEAEAFITHDLKPEPFEVVLKPLESAGTEDVILCLSIEEAERT

FNGILGKINGLGIENDAVLLQEYLEGDEYVVDTVSRWGKHKVTAIWKYDKRRVNDAAFVY

FGLSLVPAEGIVNDMIDYQFQVLDALGIRNGPAHGEVKFCHGSPVLIEVGSRCHGGEGAW

VPIADICVGYNQVIAAIDCVLDEKAFELLSDRPQKLLAYGCEAMLVSYKNGVLKRMPGIA

EIERMPAFLKKELFVAPGDNMRQTVDMFTTPGSIMLSHEDRDVLENNLARIRELELEGLF

EVE

>contig17866 Frame-1F

MLQRLRHAVGWGLPAPPPGTRVDFQVCAALGHGQSLWLIGELPVLGGSVDIQPNPSGTCP

ENGLQLVTTPELYPIWYNLEPVVAPAGSVMRYRYAVCSGSQFLRYEGASTSDPVTRELLV

GTGYIQTQDTLDGRVGQKVLLTKNDNGTNATTKSVTSALKQEVADNETSDDDQPPPAVWG

VIPRLSSGQAFVDRRANGNDDGSGTLYRTTTRWINNPRPETLPDTTPSPTSLRLDQVDVT

GSQPTKEIASPTSPRPLTTPVTMEATDGVIIAVHRLPVLVHRTHEGRYQIEWEDDNLICP

SGLMKESYQEANWDRMSSMRLTWVGTVHCAEAIPKEDEDLLAKQLADFHCVPVFLSEPLA

ATFHNFCYETLWPVFHNIVDVYGALPTRWWNPSQQRNAWASYKTVNRIFVNKVIEVYNEG

DLVWVHGLHLLIAPSFLTRRLPCVNVGLFLHTPFPSSEIFRTLSMRADLLRGVLAADHIG

FHLYEHARHFLTSCRRILGLKYSTQPGGYIGVEYNGRMVMLTISHIGIEPTFMNRISASD

QVEVDTSVLAAKYASTKRKIFVSVDRVERLKGILLKL

>contig18254 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57929.1|) 2e-72

MDPVVGALWTCSVCSNYNLCSECYDLGTHGMENTEQMQALTEAIVQFKLQKRCKYFTPEF

LLSLRRDICKGRPDKFEYLGEWIANIVVGTSVAKITVRGIEIPTLLPMARQRFVSYLMPL

VSNRTD

>contig18669 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60336.1|) 2e-58

MRSFIAMNSVANTLKRKRWIPHPIIPSEFSIFETEATDPILRGVYSIRKDRRGSFVGNWG

FSDKAFQSVDGVSPFHYTSRTRALQSRRQEHWGPISGQYVGFFQLRQHNGTLVKIRENQL

EIQFVPMPSSDNEEEEEEINNDESDEIDNICETVATRYVVLGKGKNRFGRFLIRGYLNPE

SGR

>contig18962 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66834.1|) 2e-44

MTHEAAILKTTLETKVIEPTCMNAGKTLVLGLSQLQQRLHLREGENRLLKQQLEALEARQ

KETTDEIVRLSTRNALLESVEAQREQALVELAKLQKHQVVLLELFGEKEEQVEELQTEVA

ELKAFYRKQLDTL

>contig22127 Frame-1F|Blast-ribosomal protein L28 [Phytophthora infestans]gb|EEY66351.1| ribosomal protein L28, putative [Phytophthora infestans T30-4](gb|AAY43419.1|) 9e-61

MSSDTLTWLLTKKTSSFLVKRNGNDFAREKFNLMNLNCRKYSGLASNKGVDILLSDKKLS

LTTKIQKASKKPLKAMQVVPLRKGARGGANTIRANISRNFYRRDLKKAALAKWSRLSTVA

KVEKGVLQKKAIRSRRIKA

>contig22228 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64603.1|) 9e-37

MDTGDDPLVWQREGALTQFALFYAPVLCVFVFNVNMYHSILKYLHMDPMASRFRRKVTLY

LGILLLCSSWGFVNRLLQFLRADHSPNAFCGFLESFFDPVQPFLNALAYGTTKHSIEAFK

ERCCQNWRWFSSSDDDESSSIDDTPLLPHRLVSDPLDQEFGHYFDQRKTTTHHSS

>contig25427 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60943.1|) 0.0

MARQAVQIMTQRLLQVSEIFAKIEPAQVVKELEPILFSTIHTVVEDMALKYSPDLWAVLP

TRVKEEIVEKVKEESPAHIEALMDELRNNIEDVFDLEDMVVTNMCKDKQLLVNMFITCGY

SELAFIRNSGAYMGGLFGLMQMGIWFVYSDRIVVFPVIGLLVGTMTNWLALKMIFEPVNP

KKYCGVTFHGLFLRRQNEVAEVYGKLVARDVLNSRNIFEAILKGPYSDRLFELVYDNVQE

AVNAATRTTQKIIHFSIGEELYANIKEDVTNHIVEIFPESLRQIESYATVAMDLEVTLRE

KMKLLSSEQFENLLHPIFEEDEWKLVVMGGVLGVVIGVMQAFLISH

>contig28532 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55784.1|) 1e-114

MKYSPRTMSLVFLFTLQQLVTLVIASDSASDTVESLFNSTKGIKVSGSILAIAAMAVGAV

MLVMGYRIFRATLFSIGFVAGGVTVAMVVEKAFEDESWMITASWISFVVGGLICGILVVW

LYSLGIFIVGASAGVVLAMMIHNSVGYEIYPNHPQVVLIVLCIALGIICGLVALKLEKPA

LIIATCLFGAAILVWGIGYFAGDFPTTNDLKEYGSQDNNGDWVYSIPDAWWGYLAGILVL

FVLGMCIQFRKTGRGGVYHQSRALGHQP

>contig29117 Frame-2F

MDIRATRLSPYRFHADKPSKYTTKR

>contig30937 Frame-2F|Blast-pyruvate dehydrogenase [Phytophthora infestans T30-4](gb|EEY61206.1|) 2e-83

MRGSNLVPLICYGLQQLKATDLGHSALQIKSAQEDVKDRLDKFFLGRIGIRMLIGQHVES

LEHPGGRVHLLNVEDIVREACGRASELCIKYCGVAPPVEIHATASASTSLMYVRSHLHHM

VFELVKNAMRATSENHKRRTQKDSGAVNYFKQVMNPNSPSLGFFLPS

>contig31026 Frame-1F

MDVSYERPMSTSSYFARSTPPIRLLLRINAAEGLQHLSSHGTYCKVYVGSSDMVHGSGVF

ARRSNKLAASTSSLGNLLGSSRIKAAPRSTLAHSSASFSAGDSIDSRNKMRVLKTNVQKG

KRTDPVWNEKFDIPVLNINEDVLSIRVKSARLMSSLSIGACSIPLKHFVVQEATTIDRWF

DLSVGKKDAGRIRLQLRIIDPSVSKLKDTNLTTLSIRQRNSQNSDTYLSLPVEESPREIA

ARTLKKMSRRDHKYHRFARHFDGRSVTSNSGGSSKGSSKSKHSDLKRALPLSSTGRDNSE

CATSNESIGDSESASDVSISPVASNPASTSETAPFENSDTFRARESSLNTVYARDKSMRI

SELEQSKAQARKVSPLCL

>contig32247 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54799.1|) 1e-20 NOT\_ORF

MAERLYNRQVEG\*\*DEQPTLEHAMQRLLHTFATKNTQAPTMKIFTAPKSQKRSWTDHYLY

LVAVSEACGGADNLVQLNIVHYADTSMRVSILESPNLMLIDYLR

>contig33907 Frame-1R

MNGKPYLLSSLSRIERATQIAKLRYAGNQFLNWHSRLIHVC

>contig36179 Frame-2R

MDSGVCVTSPECGSSQGRSPYDHDFDHDVKIHGKGSYESPRETAHVPATHASSMDSFPIV

NDSSSADKL

>contig40017 Frame-2F|Blast-ferredoxin-dependent glutamate synthase, putative [Phytophthora infestans T30-4](gb|EEY58996.1|) 1e-168

MYARGGTLHSSYFGNRTSDLLPVCSDSKSDSGNFDAVLEILTKASSCNRSLPEGMMMMIP

EAWQNDSLIAPHKKDVYKYQSLLMEPWDGPAMMAFTDGKYIGATLDRNGLRPSRYYVTKD

DHVLLSSEIGILENLPEKDIKYKRRLEPGKMFLVDFERGMIVSDDEVKKTVSENRPFKKW

LDENLVSLSELTGTKKEAVPPQGRRRNYAELNRRLNMFGFTTETMDLLMMPMGIHGKEPL

GSMGNDAPLAVLSEQPKLPFEYFKQLFAQVTNPPIDPIREELVMSLMCPVGPAANVLDAT

AEH

>contig41696 Frame-2R|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY60151.1|) 3e-12

MLLCQPQQFHLDSFRMLLSLQANINAQDSEGNTGTKGLTLVSLSNDP

>contig43197 Frame-2F|Blast-lysosomal Pro-X carboxypeptidase, putative [Phytophthora infestans T30-4](gb|EEY65165.1|) 1e-130

MSVLLAFDTLAMGNFPYPSSYLAGGAINLPAWPIREACSHLAGDFSLPPLGQEGKDTTLL

EALRDASNVFYNATNDLKCFKIPTLWNYDGIWDYQYCTEMLPQETYFNTNGETDMFWPRN

ITFENIRAHCQRHWHTTPDPESIRVSYGDELLRSASNIVFSNGLLDPWSCAGVLHAPKDS

KVSIIKIDEGAHHLDLFFSHPEDPPSVIAARFTEVKMIHQWIEEFAAFH

>contig43531 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59398.1|) 2e-33

MGRLHAFGLLRSHLTASPCSHVPLSWHSCVRSIRRRRFSVEKSHVPPRKPLDVMSEPEMM

RHLMRSQRVWWYMGAVVLGSVGLVAFGPELKLGMSKHTAEVASRSLQDETLRGNTRELAS

QIVQTVLNDPKVLTQASEFLQR

>contig43544 Frame-0F

MTEASIQSQRLRRLYEASKISVHISTRMALADDVGGPVTMYHMNICFRSTRNRWSIAKRF

SDFYSLRQQLFKWCQQYKQQRLDSVHFGLVLAVNYALQVDFPRRHFRNDNYKIIERRRVA

FAIFVPSLVKILASTPFAMDSIDYSSFSTMTANIPPLFEQLFTILCDFLEFSDKHFESEI

KLKLTVLSLQDVIESTHSI

>contig43629 Frame-2R|Blast-hypoxanthine-guanine phosphoribosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65230.1|) 2e-64

MDKLKGRHLLLVEDIIDSGKTMTKLVPMLEQYAPASVRVASLLEKRNPASCGFRADFVGF

SIPNKFVIGYCLDYNDIFRDLDHICVINEEGIAKYASSS

>contig44026 Frame-2F

MTSRLKYKLGKQMALADALSCRPDYELAYVMTAIRETYAKDEPCVASLQSLQVTYLKTRK

VNCRHVGASSLLLI

>contig44152 Frame-0R

MKERKLSGRQIMELFYSEIEQPSSLIENSDAPTVFRCKCGKTRAQRLKHGYTNLVQHVLL

KHMDWVAAALHDARMTPNKLKSIKRQKDGKGRDKKEQFNKTAQSSIDPIPNSSVNSETLN

RLTTITPLQTFTSSSVQKRADYLSWDDYFMSVAFLSAMRSKDPSTQVGA

>contig44215 Frame-0F

MVDTNSDAAIATTLPSMNPPLFFEIVEDQVYRSNKCDTSSFSFLGTLQLNTVVYLSYDDF

SRDLTVFFTEKNINVIHLGMKYRTPSSQWKGISEGMAKDAIECILDKKLHPILVMCKTGV

HFAGTMIGCLRRLQNWSLTSTID

>contig45289 Frame-1R|Blast-phosphatidylinositol kinase (PIK-5) [Phytophthora infestans T30-4](gb|EEY58194.1|) 2e-60

MPYSAMQYIEMWVEKQQGGKITSLSTLESNAIETDIRDLLVEAYSFDCDDDGLYGINDGR

TIESQLVKYNREGEYVKVLSLYDVSLQFANQQPQIYKDEMSSHPPPHLVHGMLTSLHALG

YNHLLKGYLQSLQQNDTIEICSSASSQALEHIYNRSWMNMQWDEVLPQLSSPNETWDSPN

TKHQPVA

>contig46600 Frame-0F

MKTHGRRKKRRAAKSTSQTEDVARHNFLQALEAQRANARTKKITPDLSKSAVVTLPGFYY

DETKRRYFRCTP

>contig46907 Frame-0R

MTLRQALRVKFGPHIECPTSAEAEQLLRDSAWVLSVEKMNALLPTIEGKWVVDDFMSDQQ

GSNGTLNAGSVLFRTTNNCFAHEVKALMSDDNLQHKIELTGYLFQQLPEMQVLATRPDSV

KDSVWEFEGFWRQLFDENVLAHSVAPIAAPTWNCRACTMNNEASMVKCTTCGTDRPADVT

VPTIPTSAKGSNPAPFLATFSSDMSFMRIKWSRGEQQGV

>contig47247 Frame-2R

MDIMELPRNKFVLADDIRDSYMEEILAESKQFEKMRNDEESINMNLLPVLKGKSSAAAKA

FSTFIPGSNIFSHLLDTSIIKDPFGHSGAVGMFGSFPEFDNDEIVIDPDPRLFQPNFTHG

RGQRDDSNGYSVLRIAMSTIGEADVSNYDAEVLLEAISMDIWDSSLKYTSNLPFLEQCNL

KNNGQGSNDHMHAIPKDNKIDSYQERAKSNENRVKLRKSRQDANKNPTKLMSNSTAQSFR

ATVTEDDLKRRPTDRLSMSPDAKRAAQRAIQWHFGAIPSCEVKLKCIVGGRIAVSP

>contig50214 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66022.1|) 6e-38

MFTLCTKLSPHQNAPVNLSYGVAEDSSEEERAHLCETSCLVLSGRLILQ

>contig50759 Frame-2R

MTCISRSLSQSVLLIQASDFII

>contig53325 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67447.1|) 3e-46

MMTSRIERLRRVKVPELTREALYTNQLCVLKLVKVLEIPTKLKVVIYLAGSASFDHVVKS

FSDEQLSWVVKYEAKVLEDADFMRFVMALVLGSQVAPKHDDGKKSFDDVMLTNRTRLADA

SILQSLILLSASEAATNVLPTILQLLC

>contig54980 Frame-0R

MRTYVISDKSAYSHSPRKPEEDTAGV

>contig55150 Frame-2F

MVGLLVHPSLLHYCTFEVAASAL

>contig55958 Frame-2F

MLGYCPFDMPYAVASKYLHPISYFIVTDTACTIVTDTTCTLCNFIRCYHTLLFARSCGTE

TARSKRCIYGFKTL

>contig56357 Frame-1F

MPVISVKCLRPDNFAICGYRFVTNA

>contig58294 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65664.1|) 3e-18

MLFGATISGATGATIGAVLAVLRHESIKFYAASMGSNFFLLSSTYIG

>contig58683 Frame-0R

MVCKFIIALLIVAFQKPLVTFAGFLFQPLYKNPDIELTIVMIACPCLMNALQFWIQDNFL

KKDVRDESFIVAQAPLSPTQLFNSNGTLPTLNTPTDEESTESNLEIIASSILQKDTLGNK

NVQTDLHSV

>contig58805 Frame-1F

MYHGVNRPDWQQPGYAVHSSTQSHTGWFPLQDSAQQQQTWNGWLHDAPITNELSPSHQID

SSASMHTTMPAPPYIWTGEPLLQPLQIRGV

>contig59059 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63146.1|) 2e-17

MIVTYCLVFAPAAFFVIDDVLFGIKVALVVSICVTSLSFTMVACSDPGIVFQDLEVA

>contig03181 Frame-1F

MKQRSLLKGRVKRLLKEQKDMGQVSEAAVLACSSLVHFFVKDMATKMQMEAKAGVGLTPI

EL

>contig08258 Frame-2R

MEDSRSRKKAKIVANTLDPILLTELGPYTFELTRTNGVVIVYNVESLVQYILATGDFSEP

ETRIPFSDQELLQMDREASKAGMKYTSVLNAKKNTQKYEILRLQRDKLLGLERCASEYVH

QMLEIIESDDSEDGEVLLVLTVFPSFSDIFEQIRKNDLEHANHCMGHFIQYLKGPTNRPT

VDTSGLLPVILSFLGDVSTGKQDAKTFGF

>contig09671 Frame-2F

MSRATLSIAALASAVAVVSARPEYAQRVPNGLNYLNGVALGHIDPAGGGDLSPFGNDFNR

LGEVWSPELCQLDSDNDGQTNGQELGDPCCLWQPDSTLVELRSLNISHPGLDTSMADPSL

WSNVCGNVTSSASDDGTPVPAPSSNTPVTPTPTVSAATALTSVVYTAVAVSAVVAAYIV

>contig13108 Frame-0F

MKNLSHSRSWKRDQSLNRCGRSQLLTKDWVWLLVKIRKYHGASYSETSSAGKSK

>contig13247 Frame-0F

MSSLQKYRSQTMKDYGLMIEYKHLRQHVPSGIYVLPSFDHSRIWYGAIFIHAGLYRNGIF

KFTIFLPESYNGPGTYPRIVFNTNIFHPYVYEDTKELDLKPKFPEWDPELHYMVAVLTYL

KSVFYMKDFPNLLQVANGVALDIFRHDPENYVNKVEECVDESLTNVYTNEQGSTIRFTKH

NPAHDNLRQELFAQLDGTTPAPQMFEETIATPPSFRSLSIVTAAAAEGSSSQATFAVAAD

EPMPDS

>contig13584 Frame-1R

MIGGALAVATKGLSRVMFDAALLTRYTVRVPIAPAEGLVLLSCSFGGKLHTVSLHEDSNT

HLAKERKDLKHRILLNSSEDDEMRKFREEVIYKQVGSSWKMEDEVIDRWRIYLERCYEAN

KRLDEKELAAMLYELDLEKVATKNKNQAFVKQNRIDLAETGRQGALLPKQFSTQLCLRYS

VAPGIFTADLRRAVTHHLKAGKILLGADEHEIMTYIDNYGPENLAREGRNLRLSIQSSAQ

NRD

>contig13665 Frame-2F|Blast-pairing protein 2 family protein [Phytophthora infestans T30-4](gb|EEY59429.1|) 2e-66

MHKGIAKPTLTRMLDNLVVKQELVSKTYNKATIYYLNQNKLPIPSEEEHKTIEAEIQTLT

AECATYEQELKSAKATLAATMAQLSDIDLESALKELEATAATFEAKVASLDKNTCLLCRL

VLKTHLSAILSSIVQRGWHESELQWMESIKLPMAWKRNQKLYLSS

>contig16132 Frame-0F

MVLSVKTMMAMALCLSTFAASELGQSLALRASTRRKLAGIHHTTQYAPKGAYQPKDTPVQ

EDISESSDSCDSRDSFDLKSTDSADVKLKGSESLDISSSQDLDLDLDGSADVDVNLAENE

VLDYVGEGKQILDLTSSNNLDFVADASLDVSDVVDTDVDFTDGIVAVDLHDDEDYSEELE

LKNNEELDETIDVPEGVKSIHLRMHNGNVDLDIVKDVTKHAKSDTKLEQGKMVLFKTDQK

KEKNAIIPPIKVENVSFAAEAKNWISMKGSTPVLLGGLIGAAVGIVGVAVAAIAKRRNRE

SDSAGDINADADVDLDDISVESESDSDDDGDVETDLTACMDENAEEEKKTHVVEGSV

>contig18220 Frame-0R|Blast-putative GPI-anchored serine-threonine rich hypothetical protein [Phytophthora infestans T30-4](gb|EEY58896.1|) 2e-06

MKLLSTLVFAAAPTAYSTAEFSVSSCTSEASRTSINHLSFIEHVIFKSSGGAIFQNVQMV

TAAEFNSDDPSQFFMQNASSKHTFTCSFAYDESNVPACESARVSSDFLDSSPSDALSAGT

PVSDFEGGDATEAPDKILISDGSSKSLFQGFAAVAAAVMVTATAALL

>contig18255 Frame-1R|Blast-peptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-4](gb|EEY66297.1|) 0.0

MSEASTNKPVDLSGDGGVLKETYVEGTGDFPPAGNEIRAHYTGTLLDGTKFDSSRDRDAE

FKFVLGKGNVIKAWDLAFASMKLGEKAILTCKPEYAYGSSGSPPKIPANATLKFDVELLG

FDPKNKEMWEMDTKEKIAEANKRKAKGTEEFKSKMFDTAAATYSEAASYMEDMYDVADED

KKTMKQLQTTCFLNSAMAYIKAENYAEAVSVASKALSNDSSNVKALYRRGICRMHTNDLE

RAKEDLLAAFKIDPANRDVRRELDNLKKKTKEAREKEKSVFGGLFSKVSMYDDKSTVEGE

PALDPSNPKVFFDIKIGGEDAGKIVMQLYEDVCPKTAENFRALCTGEKGNCSTGQPLHYK

GNAFHRVIKGFMLQGGDFTRGDGTGGESIYGENFPDENFRLKHTDAGLLSMANSGPGTNG

SQFFITTVPTPHLDGKHVVFGKVVEGLDVVKRIEGLETDKGDKPTLPVVIADCGMFEA

>contig18570 Frame-2F

MADDADFKEREAALLRDLSALYTKLNQVREKRVKVEQESGGGGGNDNDTDDESSRGSKRR

RRVLLVTRTLPFGLVSDDAQSQWRAEFTEHASLDGAMEICQSLHENYDCVWIGSVHGEVE

PSEQNTIKEQLRQDRKYYPVFLDKKRERLFYQGFCKTVLWPLFHSCPPTTDDQITQHETM

EGGQEDERSMEKMWQAYVATNQAFADAVQEVYEEGDLVCIQGYHLTLVPQMVQNLFPNEN

ICLGFYMHIPFPSAELFRILNNREEILTGILGADLIGFQTYEYARHFQSACVQLLGLESS

HKGVDSNGHFARVTICPVGIDAEKYTALVQSDAVQDQIKQLESQFAGKKVWLGVDPLDQT

KGLVHKLVAVEDLFAHEPELAKKVVLLQIVTGATVFESALESQVESLVSRINSNLQDIGT

EGPVQYLNKDIAKEALIALYAVADTLVITPVRDGMNLVPFGYIVCREAVNKHARVILSEF

AGCAQSLGGARLVNPWNTEELTDALQASLQESEEVMRAHQHMYSYVSSFTSRHWADNFLE

QLHECSEENAVSVSGRELSRRDMMSAYIRSSRRLIFINYEGVLAAEASIPELAYPPQELI

WQLSMLTKDVRNTVVLVSARSTSVCEQWFAGLSGNLVLAAEYGVYVKWVGKNENWHCTVP

NMDLSWWEHVVPLLEYYTERTPGAYIERKESSVTWHYRDCDLDHGLWQASELLVSLREIT

RSLPVSVCPGNRYLEIRPQKVSKATLFERIWEYMNWSLLNPDDDPVTTDNFGASFFSSSP

SVMKSRDFIDEKEATVMGEDENSGTHPLHFASLNIDPEALDGADEKQAVDFVLVIASGDD

RTDEDLFAVLVPPPIDLEAYCRQLEKDEFDRLSDHKLAPMNINEGSVPLLQRRSLIQDKG

KNDYATGSLSFKGIDDNMSSTAFRRLLGRDSGSGTHQTNDADFLTLGENMTKLTPLAKPS

ISEGAANMFPVAMLNRQSNAVRDEITEKSKFTPRRDFPPSAALFKAMKVKYGANFGIHRL

PDTPAACWALVCPPLTRAKLEDGVGAQIGMDGKISLTGGGASAMGLASPFSSRSISATAL

DVILPTVDSGGLADTLISSAEHVQDETSSLVSTITVANEFLKEKASRTTSISTEDVDENR

YRFPVNTFVCTLGRKLSQAPYYIKNSGDLFQLLQEMGMSSHNRKQRMLSMGSVGDC

>contig19007 Frame-0F

MNASLIENELESISSYRSPSKLSMDGAHESLMLAADAQDGPEEFNFQV

>contig21233 Frame-1R

MGFCVTRLLYQRLSCNCIHWSMSCTKSRNKIASSFAVCGSIERIEIEIAIQRSQI

>contig21475 Frame-2R

MAAHPIAEPSTALDMNASFPTRRPASVFQLAGATTTGSGRFILPDVALRKVVKKPIFENF

NDAAYNIKPPTQMLRFIDGLRYHKPTPEENEALNLSSATERICLHVLNDILMMCGARKGA

RFSSQDVNQFRIIAEGLEARYKAVDETFHLLPTDVLKHRFEGVKKLEDDPSHFTFLSNRR

RDSLVGLEECNPDDQVWRQAFYFQWLARQYVVTFERLKIAMQQICDRVQKDMAILGAISA

PTLADINDAVEAEFEAKTHRPFPTFLFNLIQKYHRERRNKSTAWTTDSSEPPVDSIGQFA

LYISSVVLQPSPMTAAELLSIQVLLQIIKAEYRVDHCLMYVVVTKVAQADGQVYVNTSSC

FNNVVGTKNLSKTYQRDGYIRVLTHDIMGSLLFAFLATVRELRLVPREKRLLSREKKCTK

RADIAIELIE

>contig22229 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64603.1|) 4e-14

MQIMAILQEVVLVAAACASCAGCSFLLLTWKNAEAPNYVSRRIVTSLGFAGLATAVAFA

>contig24469 Frame-0R|Blast-hypothetical protein PITG\_02637 [Phytophthora infestans T30-4](gb|EEY64109.1|) 5e-91

MVSSPVATPTPLESATIKCISRPMSGSHTKPTTRKILTPSKPKANKRKRDLFSPHRVVAK

SGDPQTPCSRVRKSSRSNPSTPLSTPHVRTRTRSLTPVPTQRAYVSRSRTLFKYKFDFCL

TGFVKTGEEALKALIEGHGGNIPDRYENVLHQANKKAIVIATPVSWRKRKFMQAVACGIP

ILHTDWIKDCIDTGTVIPFDGYQVPIGYSVTTRKFECFCPKELYIFQGYSFGLVTDVSHV

SKVEAKNKTDLMAFLLKAWGADAVYE

>contig25945 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58154.1|) 4e-53

MLLNVNGQVFCMDHACYHHGGPLVNGDIEELGGKTTIKCPWHAYHIALETGEGLYKGVDM

IRTSTGKLQPTLPRLQSKGVKQRIHVVELRNQGQDIYVADSSAVP

>contig26283 Frame-0F

MHHERANINMQVRHKVHESLDAFVALQTAHFPIESPHGTDTGMPEPSVHRTGSFESLPVS

LVHATHQNLAETVETNDVKNTCKVYLWGRVPSQETPCSLIVRPQSITIETGQPIVQVACG

GEHLLYLTSTGDVYSYGESDDTTPNTFIQSPPSSSSPLPLPTTTFCTPRLVQALALEKAL

HQTRIVSIACGAHHSIAITHTGQVFTWGRGEDGRLGHGDVRDRIVPRKVMTLLSERVLEA

SCGGAHTAVVTAVGTVYTFGRGRHGRLGLGDLKWRATPHEIQTFPVCTRICRVVCGWNFT

AAIDDQGRVFTWGKTGEGQCGIGYVTDDQVVPRALGGLDDGAVVDVACGYTHTLAVTVTG

VVYSWGLGEYGQLGTGNVYQPVPCRVPMMWPRSCPRWDPVYRVNCGAFHSFATSKARVVF

AWGLNAYGACGVGDTLNRDTPERVDAFAPECDRVLACGHKYTVAIEIPNVLASLNDTMAT

ATVPEPVVQEDMQEKEEELRRIKKLWRTRVLRGWETNRATPLAHALWRQGIPPSIRAQVW

PLAIGNKLKVTPEMFHIYRRRAAAYKRTIATPLDGGREHTVALIDTDLPRTFPTFKLFDA

SGPYYAFLQELLETYAWYRPDLGYIQGMSYLAAMLCLHMPQDRYLAFQCLANLLVNEHLF

TFYLLDVDLARVYYTLFDAFLQTRNARLLTHFRAIGIHSCSMYLMNWLQTLFLQVLPLET

AARVFDNFLLDGTVFLFRTAMAIHELLAPQLLEADMEGVLPLLQHNIMFHDTWHQHVSEQ

ALFATIATIAVPSEIYAALDRVVNDVFFYEKRSELDSEGSAHLMALASGGQSVGIGRVKN

ERRRMYAISDTLNGVLGGF

>contig28533 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58283.1|) 7e-15

MTDRASAGDVPRNVAANIALNGLEACATYLPLVWGDMHLSEAMMTVFQGVHVVLAADCFY

ES

>contig28748 Frame-0R

MIDFLVPLHAADLELVKVGRYHVHTVLSFEDETQADILSRVQQLEDQVLGSEAGLELLQE

EWLDLTYSLVKRLPALSEQSRMRVVEMLSAFVSNVTENVLSRRPNNEAADDVVGYRSAFK

ASVYFLVTALTSVSGLQMEAEKSILKRKGKAKNQNSAINRINWSKIVEGAIKKLNHSVSP

TTFSMWNMNVPEEEFSMLYCKVVFELLGNATFCRGKSLKAQLYHLLAMSLQKTPAIHISV

VASLIDLIYTHEHLSTCIAELIELLYFKYANVSFTADLISEIGKISSRDLSKDVCGTRNI

AMFLSILSTLTPGLLMGNLSFVLALLDSEAYQLRNAAVTCVTQILLWNFHKSDQQESPEA

AKRVTIEAQKEQRQKQNIDDDGKIGYLDSGDSSCDEVGSDAKSNDDELWIKDSIGKVDAP

RTFSRSTRDQLLSVLEDRTHDINSFARGHVLKMWALLCEKGALPLRMLKSVTSMAVGRLQ

DKAAVVRRHSIHLLSLLLERNPYMGNLDREFYETKRNELTEEMRKKRDEVIAGAEKKMGK

AREEAAFKGADESAYTSFHPSLPTEEQAAALEEELQKTVRLLQFYQDAIDFINEIEFQAL

PLMGQLLGSKSMSDVLEAIQFFEKAYRFHLCAAQTGIKKILPLTWRHDVSIQEKLSSTFV

GLFVRIDEHDPERHSPQLVAESLVKFLDECTVAEYTCLEQILGELHRSQKLPMVVITSLW

ELVDVMIYPVSVVSNALALLSMIANIDDSMLFANDRLGQVLLMGFGDVACSPDSRYRILG

AACRLVQCIKLEPKNAIAESGSQTQRRIQRSNLDATERIILRLQRFLALDFVGDDGIEVE

CLQSTWFDTVQQAIDAIFSICEHPEDVCGDVIKHLSLRLFESESDDVSCVELAHFFFVLG

HSAVRVAIHVESLAAKVKKMRGNRSATSRTATTSTTHGEAEDVSAMEDELGVAAEVEAEE

DTFVNNIIQKEIAYRNLLGLYVPLIIRVLVGAEAELKSDELLTECAVVALSKFMAVSEQF

CEKHLQLLFTILQDSPQPSVRGDVIIALGDLSFRFPNLVEPWTSHLYNRLRDVNLNVRKN

TIVVLSHLILNDMIKIKGQISEIAISLVDENDEIRCLAKLFFFELSKKGNNPIYNMLPDA

IGQLSTSELIATSDFQAIARFLIQFITKDKQVESIVEKLAQRFSTSSSIQQQRDVAYCVA

RLPHTEKSLKYLYQYRKLYSDALLDSAVAEYFMTLVAKARRGNSSALLSSAEMKEAIDKI

EQYVTGKKDGKEEVNFFKRINNLFPLPS

>contig28850 Frame-0F

MYHMFSFSSLFCFVKTMFCGEKTSSYSKVSIRSY

>contig29079 Frame-2F|Blast-fatty acyl-CoA reductase, putative [Phytophthora infestans T30-4](gb|EEY56496.1|) 0.0

MELCFAGQNLFITGGTGFLAKAVIEKLLRCMPNIAKIYVLIRSRKGVAPAERLQKEIIES

RIFNRLRAERPNDFISFAKQKLQAVGGDITAPELGLSAEDAQLLRASIHISIHSAAAVQF

DEPLETALEMNCLGALNVANFVRSCPKNLCHLHVSTAYVNSNRRDTRISEELYPLDFDAH

VALKSVTMASSSELERLKVNLMGTYPNTYTLTKSMAEHLLVREIAPTFPLILFRPTIIGA

SWKEPMPGWIDQVAAAGAIFLSAGLGVLTMLPGDPRNIADIVPVDLAVNCMLLSICARIH

EHKSSCIPQEHTSPLAKDIAFNNPMVVHCGTSDPRQNPLRWRVPCVLVPEYFRKNPPLRG

ISPAKFSMIPTHQSFQIQWFLAYALPSSVYSTFANKSGHPGHIKNAAKLWQLTWRARNLV

ELFKPFTENQWIFVADVVENRLKPWATQDFWIDSHEIAWERYVRNFCVGLKKYMLNEDVI

DVDIEGVNQTKLALSTGRILEWDPDHHAISFPGLLSDVAWAYTSSRKPGYTTSGLLGRVM

GITGWKEGMNHEASHVPRLHVESTGGLRNSVLEAEVVRTAISRRVHDHGMDIDDVEREAA

AILNAMASQQNYKVVRKFGWLLRKVCRNMYEQIHVDETGLTCIRDLLAERRGSVVLVPTH

RSYVDFLLMSYVFFAYNIPIPYVAAGEDFLNLGRLTKLLRESGAYFIRRSFADDPLYSAV

FCAYTQYLVARGHTIEFFIEGSRSRSGKQLHPKFGILSTVVDCYLSEKVKNLYIVPVTID

YEKPLEALLHQNELLGEGKIRESISALFKAMPIVRKKFGCISVKFGTPLDVKKHVSAARA

RAQKQNVSVPTSAIVEDLGYAITDALIDSATCSMSHVVATIL

>contig31027 Frame-2R|Blast-5-oxoprolinase [Phytophthora infestans T30-4](gb|EEY63846.1|) 1e-117

MPMIKAVPRGFTTCADAYLTPVIKKYVASFCAGFGDGLDKVKISFMQSDGGLARMKHFYG

HRAILSGPAGGVVGYARTTRPPEALDVFSAVIGFDMGGTSTDVSRFDGTFEHVLESVTAN

VTVRAPQLDIQTVAAGGGSRLFYKNGLFLVGPESVRAHPGPVCYRKNGYLSVTDANLVT

>contig31485 Frame-1R|Blast-PLAC8 family protein [Phytophthora infestans T30-4](gb|EEY54306.1|) 2e-30

MMLFNYIWHLRVKTRRRFQLPGSAVTDCLSSWCCSCCTVDQLRTHVRCYEPGKFTFKAPD

VLQAYPGA

>contig34622 Frame-1R|Blast-predicted protein [Phaeodactylum tricornutum CCAP 1055/1]gb|EEC50081.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1](ref|XP\_002178416.1|) 2e-17

MLLESSRTKPIATATSSPVPTNTTHQKGQSGMNGGRWTDQEHQSFLTGLRLYGREWKKVA

AKIKTRTSAQIRSHAQKYFAKLSRDDKMCKYSGLSTAMFGPVEYFSDGGSSVAQNSSDDD

GCLDGPPQNVRSRFAIQNAAATIAPCRSKASELYNQPKDFAKKRLRTQSEDQLKVGLATA

KKTIKLQKRAHGVSLARVEHLPSQEDLLAKASPNLRHRLSNLIDAELCALQVLLSHAM

>contig36178 Frame-1F

MCRCKRAMATSIRPSPVVNKRPTSSYMQYLIFFSKEIAVSVCIPRLRESRPLVVPRAARV

PP

>contig36196 Frame-1R

MLLKYFIAILAVQHSAGAALDPNEQKLIDPIRRRLEPLLSFPANQLVDESHGALRTSRGL

AQDDDNETRMISTAAIKPPILKSLANSQTGGMRNAVSKIVAEKANQVEHFLADKDTVAAI

AAKGAKDLPDAETSSTARTSRIAERSSDAKASNFVAETSDAVNAKPVVLLLDEVEKKKLT

TTYGTDFAEVLASHLPAAKKLMEKSERYAFEYKVYLDLIDHVPHKQFIVKSLDDYDPEEI

YGFLPHFASMDMRNELAWSNAVLKAKDKPVLFNPIEAFKNVASIDGETKINGIVRKLRFL

VLAKNKHALTNPLVKHVLNNVLRDFEMDTNSLRVILQSFPDFNELLKDFNSLFKKEAKAA

NAKLKKATGISRNGVFHILSLRRLSDNNNCFLL

>contig36530 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70087.1|) 3e-52

MSMTPLPPGWLVRVSRSKSKIYYHNTSTLKTQWSRPTPEEIAVTAPDQSKNAHDNTKRQK

LDLLGDTDDKLSALHARIVASMRVGGSSISRGTKKTVKFDPWPHQVTAVKQVITAIQTKI

FKDDVNSGGTERFLLQHSTGGGKTMTIAALSYQLLYVKDTRLMRFHTVVVMLDRVKLNEL

>contig36545 Frame-1F

MPILTTLSSASTKYYKSLEVRATLKVLP

>contig37069 Frame-0R

MRFECLCISMTFSKKRRRAKLQDASDSIRIQPWISKALHCRLRDSRLACIVARYP

>contig37331 Frame-2R

MLEFTNELKRTPLINVKLKTCGEPLMGPAQNRAVTTSGRTFSCLERW

>contig38301 Frame-1R|Blast-phospholipase, putative [Phytophthora infestans T30-4](gb|EEY68002.1|) 1e-180

MKIFSTETAVKETGSTSISNSTTPPGAHIFKASSTLVRNAWLDVINEQIVKVSSHLVEQL

PAEKLLYDTAKLADLPSGKCIDYFNALRAGFLKEKVVNGWYDSWNDRWLVLQENHLSCYE

NSPKLDYVEQFALWKTKAFCYEREYLIRVVARRGAACEMRVQNQESFNRWLTVFKSIPTV

EIFRHEDLLENSPSSVLITTDSARANFDEVDKADNGGEWIKSKIEGHLIQYDESDQEYVA

FVIQVASSTAGNNIVHRRYSEFTKLHRELRKMFQPEQLPTLPGTRLWNKFDPHYLKQKAI

GLHGYLYEVCKRCANTRAQPLLLEFLELASSTPPELTNTSDEEFIKN

>contig41622 Frame-1R

MTPQAQLTDLKLFLIIGIKSLNI

>contig43178 Frame-0R|Blast-chromatin modification-related protein EAF3, putative [Phytophthora infestans T30-4](gb|EEY58978.1|) 3e-78

MTIQIGDIVLAYHGLMIYDAKVLKVDNGHGVQETTSTGGQPTASTQYYVHYQGWAKKWDE

WVRHDRVLVDTPANRALQKKAKDDVAKTKKNSRSSKRKKISSAGVDTPSARKSPFKRLKR

SAEGEVEEYPDAVEGSEDDGAIPKQISIQMPFSLKKQLVEDWKNVTHAPHKLVPLPR

>contig43545 Frame-0F

MPHCFSQQLHCSAVISFGGGAAVSFMSI

>contig43628 Frame-1R|Blast-hypoxanthine-guanine phosphoribosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65230.1|) 8e-30

MVTQDPQPAIFLEDNAVYEKSQFLIPHHYVDSVESVLLPKGLIDDRVEKLAHDIRYAYEG

QTVHVLCVLKGGSAFFHAL

>contig44027 Frame-0R|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY53271.1|) 1e-122

MCGFLVLPLSLLRSLESLRFSSLFSIACIGFMTLVVVIKYFQFEHEGLAPTMAYQLKHLP

IFDMRLSHLLRAIPLVVFSFTCHPNVLPIYLVLKHRSSKRMYKVMGRSIGIATIIYSLCG

FFVVLTFGEATQSNFLKNNYHQDGAVIAGCLGFSIALILTVPLFVHTLRDNIREAMLANV

RLDLKHHAELSIVLVLAVLLVALGSGDIASVLGVLGATTNPMICFILPTFFIYRLGNEQH

RSQQIIAGLIAILMTVMSALSLLHQMQLLY

>contig44092 Frame-0R

MLQMQCHLRETSQKVEHFDILQNREGVITRIRRKGVKTRQHFPK

>contig44153 Frame-1R

MKIFTPIVAASMAVAGVASDVASPSRQLIVGGRNALPGEHDFVVSVRAVVDEITYCQGCL

ISPNIVVTTQFCGMTEPAEYKLDYAVVGAYNSLGSTNDGKPDGEAFKIIEHIIHPKFSDP

IRSVNLAVLVLDGESKATPMSLPQSSEINLETPLRGFGYGTIYHHDDPDNARQSETLQTS

LLNPISHEDCVKKNKDENITTAFFCATGENNGGFCFGDSGGTVIDEKNELPSAYIAMERV

ATITLSPIWPLR

>contig44214 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58446.1|) 3e-36

MQSVEVGECPPFEQQKVTRSTAAVCYTFRSLPKGRVEVFMMGHHTVGGKSRSWNTDSI

>contig45266 Frame-0F

MMSFLAQPFSPHTSSCPVCGPNEGMGPPPLNLHNFMPVIASTDRPFVCNESGCGRRFNRK

YTLTEHKKTHTGEKPFVCPLLECSRRFSTSGNLARHKRMHASLKPFECDIYGCKRSFSSQ

DKLDHHFKIHTGRKIHMCRVTGCAKTFSTAGNLTRHIKNRHPGLSWSSYYSYPDAWMTYA

QKEFRPAVHKASPKFFAEPLTKIESMPSMFSRGSANISSFHKEMSAFHMAYTFITQSSQD

IARHPINAEFESAVSDVTCCS

>contig45936 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60430.1|) 0.0

MVDSATGDGREALRVGDRILLLLTIFLFLLLSAVSGNILYGRYATKKKRGSSAAATAATE

IPGAVQSNRLPYNAAPQAPLPSLNVVGGSETAQMGEEGAAAASTGSEMRHRLFLLLFVAS

TLRVCSLVTELITIEKVSVLPSTSIYCRLLAIFLWLPSMLFVSMYGLVLLFWAQLCYACW

GKAHPWPRRVFFMFNVLLYVGFALLFTSASSSAELWRGCDLLQGSVYVVGLFGILYYSIR

LINFFRNQSPDEDFFFDLSVAAISNNNGPRSRRGESSLPIAARSSPRQLVLRRITAVCIL

LCVLFAVKAVCLIGMGSGYMESKEAKYRTPLGVHHIVYEFTIHFATEFAPSALLLVLTRH

VTTSSAQRQRLRSSSATSASASLSSGSYGANNPRDKPATPNFAYVPIRGGGHGNAAGQAY

QEDAIPMLSGYQYQATQRVYGSTSTTSAAMTNLRSSNTSGAFLLSNVGRNASGSE

>contig49639 Frame-1F

MSEAAEKEHVAEVEEKEFNDMYSEITSIRDALESSVSNFDTAMAHATTMVPAMYYSSPRA

RSPDSGDTTGPTQDEEMTSDQLNSVARITFAAARATRQAGQAFLAVGERPYDMDTQEIDK

ESDRGVSERSSSVASDPTAYDSDE

>contig49756 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66995.1|) 7e-52

MHELGVAWKALSTIERAVFQGKARDDAKRFRTEMETFLARQQIKERASQDSSTMRARKRK

EYDQGETKYEQLQDMETEGCSGRKENHGPGYKLRKSGLPRRPKSAYNLMFMSKRTELLAT

NQISHNECSALCGRLWRRMSKEDREPYIFMAAEDKRRYNLELEALSIEASQESGT

>contig50699 Frame-0F

MSINERKSKCARQNVDFGLAAWNDQAVTSNNRFHAGTSLKIPRRLTDMHERSSNQFEGRS

ELRAEAFEYHAETKDAFHHGLAKRVQRSGHHTNASIVRESPFKSEVFGHKFDRIRDKQCV

PPATWYTGEKSSRGSTNQSNDFRSDLTAS

>contig50758 Frame-2R

MDDPALLKSDLTPQSSRVLRGFFSVNRNVPIITLC

>contig51201 Frame-1F

MGGFTLDSSTEIAIKMRNNHLLAQYLQQLDQLAMDPAMTENCVILQGQAVLNLSLEEFKE

YSPTLLNFLFSPKFAKFPERKKIIEYLIAACIKSKSQQGDIATPILGSFMEHLSLRSQST

DTMDLLEGLIRNFGEENLAILLHAAKLSTDSNLRTIGTTFEISQFELWRKYGADSNKLHT

LMTANNLSNDFRENILDSYTT

>contig52712 Frame-0R

MYESLQSSSHLLRSRRKAFSLVILLPTPRSRCGAAVYYLSAMNLMSIISELSDFAVAFA

>contig53852 Frame-1F|Blast-dual specificity phosphatase, putative [Phytophthora infestans T30-4](gb|EEY61533.1|) 1e-52

MFSLLEWKHKCSYCRKAFCSKCTNTRLANPERGKNAASIGTTDEQRPRRVCQVCVSRLWQ

INLPRSRKSLQSRLLRCKHLNVNSLSTFGRTVCISYYEGTE

>contig53993 Frame-1F|Blast-WD domain-containing protein [Phytophthora infestans T30-4](gb|EEY57502.1|) 4e-24

MFNPATWSPHQTLPAHTKPISSLSFSSNEELLASSSADSSIKIWRLTASNELETSSKTTL

YGHEAGVSAVCW

>contig54624 Frame-2F|Blast-homoserine O-acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56792.1|) 3e-50

MQTLEWAFQGQEYVKRFIVIACGAQHSAWQIGISELQRQAIYMDPNFCNGYYTLDAPPHE

GLALARQIAMVSYQTHAVYTQKFQRCQDAHLDQRDKLALKYGRYVVQSYLAYQGLKFL

>contig55151-0 Frame-1F0

MFQLRVETAIISLCHTSINPAIRKRMLYLSPSIASSHSVVWYQPLLDLQCPILEEKVIAL

QCPCSITQFHGLHWRLHP

>contig55151-1 Frame-2R1

MGIVKQLLSLPVWDTGDRAAADTKQHYEKMLCLETDKAYACELLDLLTYGTVKLSLSQLE

AETLKEQNKVRLDAV

>contig57997 Frame-0F

MPVAKLIFRTKQSARAQVMRT

>contig59058 Frame-1F

MEGTVADNSMKPSTLVNPPPIVQEVEMQEVET

>contig59560-1 Frame-1R1

MGKILVRGLRGAHKQFLLRNVVTGWLLEDNNGVP

>contig07173 Frame-0F

MKESNHFMEWENPSYLVKDLDTGESYRVEEIDQQFTLVTLDSVAAQHKLKYDDEQHDKDN

TTASTSSYLLSLYTADETADIVIEDDVPQDALLVKPISLLRARSSNMAILDAPQDELPIG

LPVQCHFVGCFETHQRISGYCADHEMIAKEKEDSRAQALYLIPHGARADFVKIGSYGFAY

DVSNRLYTVYAIEMRCVQSGATWVIYRRYQQFKELNDRLRPKGVRVPLLPPKKLLGSFEP

EFLSKRQTELSEWLRYLLNYDRVDQSAKNPHLLDEVRHFLTTQADQPPLLLDRLPLKRSR

FFGASLTGDEEGQHGTTNERPVTLEDFKMIQVIGRGSFGKVVLVLHKETKHLFAMKILSK

DNIVKRKQVEHTRTERRVLGCTRHPFIVGLHYAFQTTQRLYFVLDYCPGGELFYHLSRMK

KLPEHMACFYAAEITLALEHLHGRGVVYRDLKPENILLTIDGHIKLADFGLAKEGIRDGV

NGTNSLCGTPEYLPPEILDRLGHGTAVDWWNLGMVLYEMLTGLPPWYTNDRKKLFERLRS

ARLHFPPYVSRRAEALIRQLLNRNPADRLGSKGAHEVKNHLFFENIEWVTLLKKQVTPPF

RPCHSILNDADAPLNFEAEFTRLPLPSTDAAGSPLTSRGMAGKSDTFKDFTYESPGYLES

VAKKEKL

>contig10968 Frame-1R

MYTAQNQKNGFFTCIAEKAIDLGQFAEEDGSDDAAEDPPLPIVRLKTTRRSLTIAKIETS

GRERTLVISRPCGPDNGK

>contig12283 Frame-1F|Blast-actin A [Phytophthora brassicae](gb|AAO92429.1|) 0.0

MADEDVQALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPKHLGIMVGMDQKDAYVGDEAQ

SKRGVLTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANRERM

TQIMFETFNVPAMYVNIQAVLSLYASGRTTGCVLDSGDGVSHTVPIYEGYALPHAIVRLD

LAGRDLTDYMMKILTERGYSFTTTAEREIVRDIKEKLTYIALDFDQEMKTAAESSGLEKS

YELPDGNVIVIGNERFRTPEVLFQPSLIGKEASGIHDCTFQTIMKCDVDIRKDLYCNIVL

SGGTTMYPGVGERMTKELTALAPSTMKIKVVAPPERKYSVWIGGSILSSLSTFQQMWISK

AEYDESGPSIVHRKCF

>contig13244 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67781.1|) 0.0

MSAMNLSREQQNELLFVGFNQDSGCFACGTDSGFKIFNCDPFKETFHRDFSNGGIGIVEM

LFRCNILAIVGGGRNPRYPPNKVMIWDDHQSRNIGELSFRSEVKAVKLRRDRVVVVLQNK

IYVYNFSDLKLVDHIETIANPKGLCALCPNPSNTVLACPGVTRGTVRIELYDLRKTTLIT

AHEAELSQICLNLDGTRLATASDKGTLIRIFDTQSGQITQELRRGADRAEIYSICFSPTA

PLLACSSDKGTVHVFSLTAEGSGHSFSSDPTTMGNVPSNSLPSHFSAGSAPRSVEEDGTG

NSKSSLSFMRGLLPKYFSSEWSFAQFRVPETRTICAFGTEKNTIVVVGADGSFYRAVFDA

NGECQNTSYSKFVQTDEDE

>contig14375 Frame-1F

MGLSQERKLEYFDKLEKLLENYTKIFLVGVDNVGSAQMQQIRMVLRGRGEVLMGKNTLMR

KVFNNFVKKNPGHPLELFIPLLKGNVGFVFTNDDLSEIRKVLESNRVPAPARVGSISPID

VVVPPGPTGADPGQTSFFQALQIATKIQKGQIEIVSEVLLTRKGEKVGNSEAALLQKLDI

KPFSYGLVIEQVYDNGSIFDPAVLDLTEADLCAKFAAGLRNVAAMSLELGIPTLASIPHS

IANAFKDLVAIAVESEHFSFEKAEPFKAYLADPSAFAAPVPAGGAAAPEVKKDEVPVEEE

EIDMGGGMDMFGGDEEY

>contig14753 Frame-2F

MRTNTSPPLGASVSITEVMPTSASQFRLQYTDDRRTKELRWVLFSASHRGAIGKIIFTLE

KDSAAHVKSVVINKDFRGLGLARVLYIATLATLEEKKVQRLYLEAEEDSSRYGKLVDLYQ

KWGFHELSNAQILVLYNGNDSLRKVPMVSVFQKSFYFPRAPMESVRFCMLALQTPDGSYL

VAEEDGKLTVSAKSYGYMWQTMLGATGEICLRSVHGKFLCVEEDGTILANRRASSTWETF

QVVPHGDKPATDISRGVALRTYHGGFLNLNVTENRAEVSKDPVSWDGSDMMKLICNKNPK

DPLFVKIMRKYQTTAFVQAQYAKYGALQHARMSILKACKCVMELAGDSNRDTSWVMKYML

ASAGAVKQDGHPDWMQLLVFLRALGMVFLCWTDDENAVLRSISAQEWLRNISTWVVGERS

PNSIDFPELTELNADSSRRGKRDNALNQGKVDDFLLTWTPDEYLYRVLSINTTSLPVEAL

DIIRFWSFKAWDSFNKASEPQDVDVMDWIASVGKIARVPEQVVQSICVNEELPYYLLLAE

KYLPDTLQW

>contig15909 Frame-2R

MLNGFLEIFFIKFCVAKSVQSSKAIHRNPLFIHEINKSALT

>contig16049 Frame-0F

MKVAHGLVLAAMLCVARVDAIDFSESSLASEDAGTLSTAEQVDVGAETSTLTDTADTPPV

QSTGDTDASCSKEFELAPETTETVESPTSDSPEILEAPKILGAPETPETPETPTSDTPEV

ESPVPSDESCSKEFDIAGSDDCDQELEIANVDDCSQGMDIAGDDCDDGVDIAGADDCGEE

LDVAGDETTADVSTDSATTSTETTLDTTMPDASTPDISTLDTSTTDTSTVDTSTDTSTPS

TETETSSSGIPEEEPMNPGKSKKEAEPAEPLLPTFSDSPDTETETSVETPTTSSETETVP

ENPIDTSLDTANAPETESGSESLTSDVPVEEPMNPGKSKKEAEPAEPLLPTFSDSPDTAT

ETSVETPIDTSLETPSEKLVDASAEVPVEETPADVSSDTSTVPVPEVLTAASRDGPVPPE

STEESTIDTLTDTATTPDAETPTEEDCLDGLDIADTEDCSKELDIAGSDCEEELNIAGTD

SCSQEFDIPDIPEMPAETPIDTFAESPTDDSCNEELDIAGPSDTPTDASCEDELDIAGND

DIAPLTLSPTASNTMSSSSTTADQSPEQVSAFSAGAVKFMSADDSVDTGTSLVVPIVAAA

AVCAALAIVGMIYIKRRSHKSKKAAGGIFTVDKNSAL

>contig16131 Frame-2F

MKFVFVFGALFALFIRLNCAALVAREANSLELSHDRANFRTITRRLRIDTLNASEERNIF

NFWRRKKHANWEGLLNVDDVPQFTPRQIQENIKWSKKDLKEVLTALNFRKVTSPEVTRQK

MFQLDEYLDSLDLKTEVKTMDEIVAKRLKVLGMLKGNDWEHTKELKRHLAHVWVIKRIPV

RNVYRGLKMNEEESLENLFSIRSGEETLDFFLDFFYATRKYHNDKEELAELFLETYDVAT

VLHLINVGSRLDSAQVFVAQLEHSLHRKWSSMSHNKVFFDILHLDKKGSQVFNTFEMQTW

YRFIKGTDPDEAEAKTLIFLIHSYGTAFLSDELIRGQGQSISSLRPIFRKALLDHWAKQK

TGS

>contig17293 Frame-0F

MFMRAGRHLVALLAIAVVALAIDIEEEDDVIVLTESNFAEAVSTYDALLVEFYAPWCGHC

KSLAPEYATAAKNLKEMDSSTRLGKVDATVETKLAEQFAVRGFPTLKLFKGGVEAVKEYD

GGRTSSEIETWVVKKSGPAVTIIGTIDELEEIKEANDVVVFVVVDSKEGNARSMLEKLAD

DDARAVYVATTNTNVTEDANAVNTVVLYKKFDEGKVIYDGDFDKDALGEFIKGNSLPLVI

TFQQDIAPTIFGGDMTEHVLAFADTSEDYVSGIETALRSPAKLNKGKLLHVIMPSTEKRI

VEYFGLTDEDMPTIMIVNMSGSMKKYVFDHKADDLIAKVTDGLADDLIAFETSYLNGNLT

PQLKSAEPEDDSDEAVKVIVGKDFQKRVIDNDKDILLEFYAPWCGHCKSLAPKYEELAEN

FADVDSIIIAKMDATANEIDHAGVNVRGFPTILFFPAKDKHNPVVYEGPRDVEGLTQFLK

TNAQKFVLDGFEHGAELDQDEDEGEDEEKKEVEHEEL

>contig18397 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY57212.1|) 5e-81

MLTFILNWIPNVGAMIASVAPVCIIAITPSNLMNPMEKFLAMFFPMCFHMFVGNFVEPRV

FGRKLEIDPVIVILSLSAWGLLWGVVGMMLSVPLTAAAKIMLSHLKLWPEFVALVEGTYF

TRFGSKPSRYKKEEDDQKDFETMEVQTESEKERANGSHVRV

>contig23243 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62432.1|) 8e-20

MAVKTAHKPLMSFLRLQVPIYEQLRIEEALFRADSKRNWFLYNDKSFPATIVMGISGKPE

QLLHLDAVKR

>contig25425 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60944.1|) 9e-74

MSQMATDQLPESLAWVERGSVLIRRMNSERIAEDPRVRRLLLKLSLPPSPTEVTAMEAIA

EENAHVCCDDEEIPMVRPSSKSLLLLDAPESFEAIEADIDADDVKQESENTASNTSRVLL

WTYRLHASLQSTVQYALFAKTSEDGCFIQIAPRVYCVAPPHITTFNRLFSAYSSTRNWNA

AVKV

>contig28303 Frame-1F|Blast-mitochondrial import inner membrane translocase subunit TIM50, putative [Phytophthora infestans T30-4]gb|EEY70509.1| mitochondrial import inner membrane translocase subunit, putative [Phytophthora infestans T30-4](gb|EEY55063.1|) 7e-64

MLRLVLRNAQRGVGASAAMAASRQLVHLAEASVPSSVSKASSILSKVGRDIPLTVVPRAE

RRAARQAVKHSSDGGGGHKIVRTSSLPAKISFALLAGSISGSIVWHFVLDDSIKSRVTDT

LGATVFGDIYSFIAKKVETIVKPFTDPSRQKLLPDWPIPQVPAGTP

>contig28376 Frame-0F

MALAREMTRFNKFDYGQSCQSSDLYTVNGETSDWMWQTHGIFALSPEVGPKFDVMPVLGF

WPLPDDVPYLSSELHYSNLYAARIAGPMYTVDVKSVKLTTMDANGSTVSVVAVHVLISNQ

GFRPETAEILGSFFLNGTNASKSVHLHLPSNVPSSGILDMESLTLRIPYSQKIALNDMTE

LYLIIRDALSCHLVRVAVHFSITQDKTFHTSFQTWKALPLPRCGTCSNFGANNDTPTSQE

ASLLCSALDDVAVLKPIEMRPFTSIVFTENNFTTQRLQEWKSKASSLPSLMPWSASVAVV

LILALILLAMCAVFFQQRRRPCSKRTNVKSSSKGSMRRQHAQYSRIQTDVPMSIEAEQTD

DNDGDETSGFEAEFGER

>contig31217 Frame-0F

MTEADQLAAAIAASMQGNDVDETSKQDEDAMKQEEKAQPFVTLAPEPDASAPDVTRVQIR

VPDGSRLTRRFHKTDSIAMVWTFVMEQVPEARARTFELRTAFPPSAVAYSDTLSIEEGKL

ENASLMVKWL

>contig31486 Frame-2F|Blast-PLAC8 family protein [Phytophthora infestans T30-4](gb|EEY54306.1|) 2e-26

MDLQSTRAHFMQVSTSTNSTLNHASEVSHILSPPSALNLSTPRVPDFIAGDGILIGAWAS

GLFDCFGNVMPNCIMVSFCPFVALAQLSTRLG

>contig32199 Frame-2R

MASPDAPETTSFDQLQALRNVQLIERNEYPLKHLPQDKVRRRSRRDDDDDDESSLCFCTY

PDTVERDEASQKAEEVRRCDDVSCLNFATYIECSASCPAGPYCRNQRLQQPEQHPLLEPF

KTENKGYGVRTRQFISQLSIVGEYVGEIIDEKELARRLKSVPRHELNFYYLLLAPGIYID

ARTRGSFTRFVNHSCEPNCKTEKWTVKGETRIAVSAIQDIAPGDELTFDYKWKALGSRQI

TCFCGTKTCKGVIGTQNLTLEKAQLGYFRDPETQETGAILVGRRVRVFLSPEDKTEYDVQ

LIKGYDERNDRYEVEDLLEPSGYETDEQDTEEDEGLEKQYVQLKENEWQLYCPPGEKDVE

QVFAIPKKRLISCGNGSRDPSPKK

>contig35745 Frame-0F

MNLHFLLLSLLLTTANAALNKNASENSAQPPSSLPEHSRPFLPKSPNKDLAIQGPRFNDA

HDMTGSQATSIEERNLLDSIKHTTLDAVYKLAAKLRASPRFMFYAMGIFISRLTKKLHKK

INLYQWLLYVDKHMFQPCKSHDELLAASSTFFSFFQRKFTDVQLAGFFRSLRTYPGLSNL

GDWMQTYMATNVATSSAMREAWSWYGDTIDVVFKTLRVENEADLVGSRVVTAWLEYCHAR

>contig36546 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65607.1|) 9e-08

MKGVKENVEWFSPEEVSAAREEYLQEQEKEQPSH

>contig37332 Frame-1R

MIQQNAAQHIDTTKATEREHSRNDRIQSDHEVELVLRDCVSDVVH

>contig43546 Frame-2F

MSTGDTTDKTPYAEAAAGSHDKNMSLADSTVSFPQIAPLAKYKLVFLGDQGVGKTSMITR

FMYDTFDNAYQATIGIDFLSKTMYMEDRTVRLQLWDTAGQERFRSLIPSYIRDSSVAVVV

YDITNRASFLNTSKWIEDVRTERGQDVVIMLVGNKTDVSDRRQVSVEEGSGKAKEENVMF

IETSAKAGYNIKALFRKLATVLPSMENTMMSGDSN

>contig43825 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57619.1|) 1e-51

MIFHKASRISYSTELWTSWGSMELEAKNLQEAKRIFNVVLATDPGNPMAGLGTALCEAQA

GRLNEARENFQNLVETHPRDVLIMQAYGVFEAQCQHVGLARSIFQSAVSQPRASG

>contig44486 Frame-0R

MPIVVNSTPPLSSADTIVHSSSLSTWEPDSKMRTHQTSALGVRAHDASTAINVSNKENHL

RNDQDNMVQFSGLYVVRGPTESKHVRYTMDVTVDDVQLHTRCIQRFQSFYLLRKRLLAIL

KTCHDQWPSQKSAGVGLHDEPPLSAGAELVSLLTRTRGTQCTVCKSTYHQLAAVKFPHRT

LFPPRLQDIQDRSQMLETFLDYCVRFATTWSACQRSKRMFVATLGTFLGVDLRTHLANQK

EVGVISEARTVVCINKLQDNLSDAFEPQSPSEVACPPFSHEMSNANDSEDDRHTEPNYSF

ISNLANDTSMKKRSQSHR

>contig46369 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66235.1|) 2e-42

MNVVVNETSMKAQDAMLQRYREVYFDFNTEFRRSMSALQEKRSAQQLFGN

>contig47199 Frame-1R

MYVQERTPTLVRLSSAQLLPHARLLLFLFDLLYDLPIK

>contig50216 Frame-0R

MQVCFHVTALVMINALSISSLTSAKFSLGTAAFALEPSHMESHEAMRSLRAQQTSTLDVD

EERLRFKLTRLVGNICEKIVDAFYRVKNRTKVFQGEFFPPDP

>contig50263 Frame-0R

MQTDQSQCVSCRSYLSSVKAPRKI

>contig50915 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62605.1|) 1e-68

MQTDKEDVAARLHSAENVRDFLMEKLKDLEDTLANSMTMTAKKDEQACVDREIIGFLDAK

TQEYEVALKEYAQQNNSLRVELAHVHEEHASKTTIIQDMVELLAEEKKELESQVRAQRKI

LVREVKGLRAQNQQIVAEKEKYFKQLKHLKHALRHLDELT

>contig53240 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63778.1|) 4e-39

MAELVVPPKAFKRAECEYHECVRPNNTSFYRSLNCKALRLLRSVQ

>contig53558 Frame-2F|Blast-vacuolar protein-sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY66104.1|) 1e-100 NOT\_ORF

MLKARDMVCLIERYVDTQRSVESIAEDDTTTSREDEIKKLSSLMLDMGITSPVTRENSGA

AYYVQLARQLAEYLTDHMPKNGGIMTLSDIYCMFNRARGVELVSPDDLYHAAQLQKKLQL

GYSMRKFPSGLIVLQTDSHREDMVAQSLAKMAKKSSSGYITCSDVSVELHTSFPLGWEYL

KIAEELGNLCRDETFEGTNFYPNKFSLFVQDT\*LEKRKLLR

>contig53990 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64078.1|) 3e-08

MASNELATILARRRSKAGGDSKASSLAVDNSALSTSEMDTFTGASSSIAERIARLKQQNA

>contig55509 Frame-1R

MNWQRLIQFRICCCITICQRAKEDSEKFLKDRIESPSNK

>contig56355 Frame-2R

MVNELKGKRHKIMRYHNLPLTLRESLR

>contig58807 Frame-0R|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY60229.1|) 5e-53

MSEDKYTLEDISWDEIDKLKYYIVGPTIFLGVRAAVYPSNLVKTRLQVQSKHKPLYSGTA

NAFATIFRQEGARGLYKGFGASTVNVLTGNVYISIYEKSRKVFRDHTTVG

>contig04050 Frame-0F

MDTVNTASVEGCLMYVQAEGININVRAEEERCLRKSGMSVIVFYEVLIKQTNETLAQFQE

TWGLTPEYGPMLPMDSGRCTPLSGETDFPAGCLQFNGEKDQPNLGPFIGGGTKDDDVRAP

YPDNYWFSFPGTCPLEAWGDKTDSCRKDSRKGLCDYGQGPNGVDCTFAYSVLGWVAIDDI

VGITAIENPETGSTYANFTEWCMADSNNTEFAANAGTGEMEKGLPFWEDPLNSTANAARA

QIVVATYESTLTSGSSQIQSSVIASFRPMPTPEQLATLNPPCYQSVEACGSGNGCKRVGY

SQLCTPCTADEDCPTGGSGFVYPTLAKAFTTLSDSETTTTLGNSSGTNGGAGGNADSSDA

MSLTCTIASIGFGLAITVLAM

>contig07172 Frame-0R|Blast-pre-mRNA-splicing factor 38B, putative [Phytophthora infestans T30-4](gb|EEY62272.1|) 3e-16

MYADEENEPAMYDAIIDSVEEGGQY

>contig14727 Frame-0R

MSRMEHQRVATFQGMNTERWSVLKKAPYDWVSIEDCLWEIDARRAPSCRKSLLLVDSISS

NTTDLLYQLVLKKESLYFECLSYLRVEDLARLSKVNFRLHSHLVDNGPIWKKCIRSGGLL

PSIRSSLWLAVFYEATPWQSKVMTSPYLSATRRSRIYDELLHTVESKAFNGFHGVDHDTQ

WAVWFQEIDVDVVRTCHRNTEVHSTNKSNTASLCQSLVENDKDIHDSVTSILNGIMDTIV

ECQGSVSTTRSIPLLKSRTRSRSFELEAKMRRVLRAYVVYNPRVGYCQGMSFLVRFLADV

ARNEADLFLVVCRVCRPHEGCKFV

>contig16185 Frame-1F

MASLLSAPFVQSDFAFRQKTLYGQKTQAPRWKTCVTRVTDAFPDLVGTYYARVRSDNATI

QLAQEMVTQIQDTFQKNLMELDWLDNSTRKAALDKLGNFTKHIGHSMHEEPYPFQLGRNA

SFVENLEIISNYELTRDIGRIGTPIDPNEWLRSGATVNAFYIPRANRIVLPDGILQSPFF

AQDRHSSRNFGAMGSVIGHELTHGFDSSGRHYAGDGNLRDWWSNATTNEFLKRAEGLVTQ

YNSYEVRSQTGSNKVLGTINGNFTLLENIADNGGVKLAFAAYQKHMADHNLHASSMIRAE

SHLSDTVAEKLFFISFAQTFCAKRSDASIINGLASDSHSVQEWRINGVASNSQDFAQVFK

CPAASAMNPKTKHQLW

>contig18499 Frame-1R

MAKNISFGRGGTSSWADDDDESFQLLPLASKNLPMEIPELIEEDVIGNNEQQHDTLRQGH

NDRYDDRRSGHENRRESYAEHRQDSRDRRPKNSVPNTGPWKLYVGNLPFQSTADDLVDFI

GQEGIKDVRLPRYHDNRPSGFAYVEFFEKEHLLQALELDDQKFNGRHVKMDVALDRGRKT

HDYERTDNRGERVPDNRREKNESIRERQRLTLLPRSTSTEKKELDAQKPSIFGDAKPRDE

NTYLERKKVLDRERKAKAKEVKEAKAKFKEEKIAQTIVKEVKSKPVARKGSHDNSTRGGR

GRGRGSRRRSVGGRGRGALGMEKFQERKPEIRPKQIDPPARISIPDVAKTANVFNVLNNY

DSDSD

>contig18684 Frame-1F

MFSTVLFLVAACAKSSYGHSVSIFTRDSTKYIASNFDEYSTIPEDIDAKRRLREAVGVDG

IARDAEKTFADIRHSLDRLNKDFVRSNSFKNINPLITAEALVKQPSFYQEAFLPLITARG

IKCSKDFEFATMALLGVSPGTLRQKIQVAAQQPSNIWSYQTSEYNEHFVASYKKYLDVVF

MAPTISESSAFVKKHISMSIPEPSEMTYKLLNAAVIQLLQLAIRNVDDVNELAKLATSVT

FKYALEHDEEFSTIMMFGNLEAWISNPVLNKLLMVHQVLLKS

>contig19005 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54323.1|) 0.0

MMGRRLQRRYQGVYQKYSLVTQLVTWIIGIYIVVVFVVLAANNSESASSTEQMSTSNDIF

YFAGVALALYILVQLALIVRWIIYWIVLAELLTFAITNNLYVLFWIENDDVTNTDRQVRY

VMIVVLSSVELITVSTYCFTHYVYPWLVLHRKFDLVKWWNIQPGVETNTLTYRSKARFYT

RKRSMIKYCGGLNAQGQPHGFGMWTDTADHGEKLTGQWRDGVPIGPFRSFEHGSGYSFVN

IRVGFCHNRSEKRPNKVDFLPKHSNNGLHWGVASVECSVSGGFFKYLPTVTHLTSSYANE

APQSVAECLPVLRTPTDGVVFNHKEEEMRTRAQPRKTRVTRRQPFREKSAPILDLSNNDD

DMCKEALILLHGYSCSLDYGMNRLAQLLALGDFPSYIHPFVFSWPSGGVLAYFQARSIGS

ESERTAHDFILFLKSLMDAGYTKLNIIAHSMGARVFFSALNKGLFDEVFLECYYIVLTSS

SFILKC

>contig21402 Frame-2F|Blast-ferric reductase, putative [Phytophthora infestans T30-4](gb|EEY65852.1|) 0.0

MVRESLARASMMSSFANSRYGPQPSGDVMSVPVLGDCNFEQKYTVTMSMDEQGIHPIDSA

YTPLEKLSALREVMSNIPSKNGFIERQTFTQAFEVNSNEFNGYTTNSGAIDGNAILIDAV

MDLEVDVEAKLRFIFETLDPDNSGFVVSDQIVQLLESNFSTASINVVGMDFKTVANLMFR

KAQAQNESMTFDQFKTVFAPYINDSYNSQKQEPMNIAPIPPKSKFNAWYSTNKLRVWWLL

LYFIINNVAFWLKWFAYDVDPAIGWGLRVARANAQIIMVNCVFVLLPMCRSIAQVMKRSR

FLWRYIPFDDSIAFHKIAGTTLLTAALAHTVAHIVNEIYLYRIATPDEIARSIFVTRRVS

AFVNGIRPPFTVMIQSLPMWTGLILFLITCISFPLAAIPKFRQGNFNVFWYSHMLFGPFL

VVLSFHGAASWLARSSSYIWIMPPFIIYLVERRFRYAKMFAAPVRIMEAIELDGTVALFM

EKPRRFVYRPGMYMFVNCPIISSHEWHPFTISSAPGDNYISVHIRACGDWTKALGRVISD

CHERKALYPNIYLDGPVGAPTQDYHRYKTVICVGGGIGVTPFASILKDVVHLWEENRCLN

CNHVRHPGSFKIQKLYFHWVTRGQESLSWFEETMNQIAEMDRDNVIETHQYLSTLKGGEN

TSQLKMFQEFVHEQTGKDFVSGLNTKQLTHFGRPDWDKVFSEARMNHPGEEVGVFYCGPH

ALEEILDTMCKRYSSSDSNGT

>contig21477 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66780.1|) 4e-10

MPVLVLSENPRIIIAGDSFLSSKFDSCLDSAKTAADMLLKTASNEVLDK

>contig22124 Frame-0F

MMDSTINSNTPSPRPDATAQGNDKRSGVVALLNRNLGVRPHRSRRGFASGKARLFLKIDA

DCATTGDGLPLTGQSTPASSSSCCSSDVVPWWEVEYQCPPPGHLGAHVVPVSAEIQVEAV

SAPVDGTTTSIKSDVHASNEHKINAIRTGLVLTETPERARRGTHSKLTAIRTSAPCLLVD

GSPSQKRKMRPDNPTDCEADLFSTPLAKALKRFHASSRYVACIRWLVEVAVKNVCTCNKT

AKIKQCFPTRRPRWCSLLRKSV

>contig23242 Frame-2F|Blast-DNA-directed RNA polymerase II 19 kDa polypeptide [Phytophthora infestans T30-4](gb|EEY62431.1|) 3e-91

MFFLKQLSRDLLLHPMHFGPKLHDIIRLRLIEEVEGTSMGKYGYVITVTEVRDEDIGKGV

IQDNSGFVCFNIRYRAILFRPFKNQVLDAVVTVVNQLGFFADVGPLQVFVSRHAMPTDLN

NGYDHESNAWISDDREVEIRKGCGVRLKIMGVSVDVTEIVSYCRPRVGLAG

>contig23501 Frame-0F

MQAVAAKYAKLYNSYNPPRRVDFVEAWILQLIPSGVNHSNDPTLDSLTLRGTICGVEPFI

AGEYHKHNNNFGFVSDLERNTPQAFSHFTYEASGQEILVVDIQGVGDQYTDPQIHTKRGK

EFGKGNLAVRGFQRFLASHRCNPICRYLKLPLINPKDDESRPVDLQGTIPAQTYMSQPRV

VVDQVDSVLCHYYGDSKAFQKYSAKNRHKKKKNNEESHGRLRTYSISQEIPVSRGCGSGE

SVVELQDAKDRFVAALADQRRSCSMFVCDGISQCNVS

>contig26115 Frame-2F

MPSMPLSVHPLSFSLEFFDIDNLSTEQHTPVSSASSSCSEFDKPSQIRKVKKRCSAAKVL

SAKRLSSEEKQAKNRLFVKRCYYKKREALKNLRDEVNQLESQFAIVLKRWQKCNENFVDA

FRDGIRHITPKDLYAELTITRNFLIEEQQQLSVRLADRHLFRQRLQQLYEPTL

>contig28302 Frame-2F|Blast-mitochondrial import inner membrane translocase subunit TIM50, putative [Phytophthora infestans T30-4]gb|EEY70509.1| mitochondrial import inner membrane translocase subunit, putative [Phytophthora infestans T30-4](gb|EEY55063.1|) 1e-112

MQKQQQKQKGFGGFVRGRLSHHPAPLGGNVAASGFAGAPHV

>contig28377 Frame-0F

MGIDVNLSTITTTTTLTAPESSNLDANAKAFSTQAWAIQLRMSCPTQALYQSISAMQENG

STVILCALQRT

>contig28531 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63747.1|) 5e-96

MVAKQEEVDDLHREVDLLHEEIDRLHAELRSNTLEMDNARSHLHVSELLMRKRENFQDDL

VARGNDIWQRDAEISTKKEELQHAYNSEEKSKCEFEENMLQKSVDFAFLQQQNTKLREYS

EKTTQEMIFSDAANSGARVTANLESKEAYEESNQREQELLKQIDDLKASKLTMLFQFRRE

LRDLNINFGAQGSMIDGSKSDDTAFYNCVMEVSALLKSYKECESRQDALLRRKEEEINEL

KTRINEFEHSIRLRDSRLRKRSEVRDRNSLLSQQSRAMRDEILMLKLQNKELHDKRTFLN

GDGDPKLKKYAKPKSRGRDLKNNDTNLKQSHSKGEMMSLTGKVEERLSKGDVMSLTKKIE

KLTTLVMKKNLQQTLCEASKYKLRSSHSALATKDFNYSRDLLEEKVMVLNGHLTGLMSEN

IQLQHCVEQYAIQFGPLEKVPTQSMIGDPGIRVSIRGNGGSSAIRSQ

>contig29644 Frame-2F

MPRQEEFERYASVSLPKRSDSTFKGQRDHWKDMPLDHIRQRPEFEEYPDDNDNNFVNKTR

AVGGQKSQEMTDIRNVINLDSKTLTVEENSSANFDTNNEINTGSAPNIQHLSQQIEINET

DDDMNDLLSDSCQMAELRHCWRDLSTPHITPPVVRSISQSRLQLYHLFNRLDTSGSGTCI

VSKLIFTAADCHVQSIIELEDIQIGEMLRVQVGLFQFPVISPKDLLSCSAEALEIQLTEI

YDSLKSAPDHVKLSVLAYLFSLSCHARLAHVVVNSSILKLLVHMVTVEARQATPNKSAIS

ILCLVLSILFHFATSMALSSPDQIHLLVASLLRVIHAPLKNHHHNLNASEQEMQPRPLAL

ACLGELLSYMSTQHEWNLPMEGVKTILVCLEDADFAIRLYAVRAFNKMLIHCTDALRVQL

ISQANVLTLMRGLMQYVTNLSSLGSEERSQIIALQTATTE

>contig30934 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61617.1|) 1e-128

MMRKVTFELGRCVRETGQALDRLGLRVLNDNSFKEKFSRHRQVMALYDKRPKIAHDVWVA

PNATIVGDVEICNDASVFYNVVIRGDLNQVRIGNRTNVQDRTVIHTASSTSPGLAPGANI

GNDVTIGHGCTLYSCTIEHNALIGMGAIILDGALVESNTIVAAGSVVPPGRRIPSGQLWA

GNPAKYVRELSDDEVADITKQASEYKRIASTHSDEFLPYGTAYLDAERIKAAGGHL

>contig31025 Frame-2R|Blast-vacuolar protein sorting-associated protein VTA1 [Phytophthora infestans T30-4](gb|EEY66038.1|) 3e-82

MAEPQPVKVPPTFKSLLPFIRRAEELDRDTSRPESKLIAYFCRQYAMELGIKLRENDPSN

ESTDYLLSLMDRLEYEKNKLPEFSQEEGKEICEDFALEIFSKADDEDRTGMANKSTARTF

YAAGTFFDILNQFGEISDDTLEKRRYSRYKAATILKAIKEGIKPTPGPQEELDLKV

>contig32244 Frame-1F

MTGTPVQPPRQAAELSEEDRLKFKEMAMQLLDRTLRDLDEHDVESLAHDKQDPRLWKRIH

HKEHFTTYARCDDAPEAAYVAADGGRSTTSRPSKDVVLGMGYVQCPLSELMYGVFMGNSQ

AMALKSAVVDKNIGNGAVLLQLMGPTEEDPFRFLALKWIEVRPPRGVSGKLVAPREVMFL

GGTGTFKRRDTGEFIGYEVHHSIDHPAFPPVDGLRRTRIVIGSIYRERPNGTVDLFIKSY

SMEADMGSILGALAMAHAAKCIEQVWTVPDFAYAKKLRWCIDHRVHSNSVKALPTKQANC

CATCDKSVTKIWRSRAVHKICNLCKAPLCSNCHVKKELYEIDPHFRARKFPVRICPPCRE

FVKHLDAREVQRQEMLRPQRPEALNPLTPSMLDVLSRNFSLDNSLCMASVESLCLLDSPR

SKSDSVTTDLLH

>contig34578 Frame-2R

MFLKFTEQIALNSTKRNQIRKVKALESRPNFAYYTIKIAGDNFTYK

>contig34695 Frame-0R

MSHGLEREDHSIVDLKQPDFRPVGIPLSPGCYQATAAERLKYATLVRGRVESLLRDEAHY

AERQTRNDSFLHAGEWKQVKKEKELTFYRRFQRGRSLRELALEEELPEIQRAVERGYTSM

ICDGYIKGTIEDFMYGMTASSQDDLMTGFSYKDPPKDCVWLGTKLPPMIDQVDVCYLKAT

GVQLDANGNRYGYLVVHGVHLVQCPVYAAHGISRAKMYFAGLFRESHKGVLKVTVRGIFD

LSKKVRMLKGLVSAATKSIMVGIFNGVGIGEAKKLTLLALRHRSQFQEPVNTQRQSQCYM

CCKRASFLGRANLFGTYVVTCYVCGSTVCSNCTQGIKQRVFLGLASACSKVDCCPSCVHE

AITTIHVSLAEPEFLVVAEYFRKEHSVLSSGMHSDALQNHGLKTNSSAGIPTASTTERSA

GEYQLDFEEDAFSGALSMPMLRKSSAEDSEVEP

>contig35498 Frame-2R

MLTSLELDLLLALLAQDDSQVLQCIYDYKTRTQESAVMLRDSLVAIVDELTLEVGDDEKA

AAAFGHGMDDAVREEDNGPLDGCHDDERDWLGWQRHLTFLLRQWQRQAELSPIAATTLHK

MVAQRHNLLESAYEVFARDADATELLDTLQRVAKLQRQMEQQGARNECPPITTKHLSLEN

VVRQMQRSGTLEDEDAAGLLELFHGGNEALQAANEAFQADRDVRELEETLLLVVKHARFG

KDTVGDAETDEFQVKARLLRTLGQTGRLDIWQVQLLVSLLKSRDSRVLAAVDVYDEENEI

EDFVETLEILAELAAWECHGHAIVQDWIAPLARSNKLPRGGAERLVQLVKSRDDRVVAAL

VVFLSDNNQDDFVDTLVRIACLEAMKLKGMQSDEAREGHVALAMLQELTDYRVVSREERA

QVKALVCAGEARMLAALDVLAATHDAEDFADTARRILALLEVKAVLKDDAAQQLLDISGK

DPTTGRCSIEREHKKSLDETRKKGKEICLCEVTDVTMDLAETIKIDAFEKKQENQAEEGA

KGDN

>contig36532 Frame-1F

MASFPRTPTLTSAAPSPDDTSDMELLAASNRDMFSWLLFNSENMTAPAGASCQLSVDHTH

SLATTVALDDPFRLLGPVDDTSNPHVQHSILTSVPLTHVEALTMATMPATSALLSSQSKP

AQIQRGKKRTTPEAVKDLRVKPLTNTEGLLRHLESANNALVQKRQAVHHTNAVTPATAIS

TSKSLKTERFFATRSSSSDTSNTSGMTSLQRKLKLERNRESAREC

>contig36824 Frame-2F

MARSRSRSLTRSRRHKGSTSSSRRHQHAPASRHHSRNHRDDLASSVDDSKNGEISLSIDE

TNKLRLSLGLKPLVAGPSTKEYAVISVQKTRTQLNAEREQQELQTKLQQSKTRRELTQKV

AGQSLGEQLQAQLIGQRDTLAPSHDALAWVKQSRLKQGLIIEAANDNTKHQHTYEAPALA

GMTVSHSIDHFNEGHEVVLTLKDQHVLKNDGKALNDDEDE

>contig37438 Frame-0F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY64164.1|) 3e-15

MAKWDRVTIHFFLEEVKVALASNSKAIQQLETMMNSVLDNSDEKSSRESHSGAINVQTDP

DQSNFSPD

>contig38303 Frame-0F|Blast-U3 small nucleolar RNA-associated protein, putative [Phytophthora infestans T30-4](gb|EEY64264.1|) 7e-45

MTKEVRGKLVDHLKLFAAFRNMKGAYAQQLLHELFLDLLMKSDEMVSKLALDCLLAFGNK

AVAPYAMQLKRLTDSSSFREELASFKIGDGDRLVLSEHRSELLPLLLRVL

>contig38888 Frame-0F

MECSKVVYWPRHLWASPSVITSGLSVRCVRLSKNALCVVSLGSDPPFDFELLPAKCKESC

RIVLFDAHVAALGNFEKFHSPKLLLQIGDFCRHNEEQQTMASIASDGMDTKLLEAVGYYS

LYLPMTALGNATAAFQNILSEFWILSWLCASVETL

>contig40014 Frame-2F

MASSPLGEIFLVRYEAVRRSQAVVFVFGHFPV

>contig40498 Frame-2R

MELLFQKQPSQGSGLKQGRQILRDRSSGGCSISGSSSGSKENASSLGGNVFFKSHAQLSS

LTQRTLTAPAHVFSTLVITDVLCPILFEMITMSTSVVSLIANMSPLAAFFDYIQCGFYVQ

GICLGRWMVCHFCSARNRQNERVC

>contig41578 Frame-1F

MCEREDNREDALCNDRWGTQNSLSIYLDAEYEPKKLLGAGAFGVVMECVQTQTGRMAAVK

MVQNNAENIIEIKREKLALERLESAGGHVSIVGYEGSYESNDYHYTVLEHVRGASLYSFM

KQHRQLDTTRSLQCISQLASALEFMHQEDIIHRDLKPDNIMVRVHPNRTLNQTNEEVMLK

IIDFGSAGRVSQPESVDTAHTSTLSGTRCYWSPEVLEHHDMTPALDMWALGCILYILIAG

RHPFDLTGASTEDEVLQRVKTEPVSFKLS

>contig41695 Frame-2R|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY60151.1|) 1e-61

MLRLVCASCGITEVGSLCSKCNGELSPPSAYICAKLGMVSELQELVYQDPNFDVNAYDEA

TNATLLHHAAISGKMGVLEFLLETEEIRAKLKKDAVGGETNTTPLFCAASYNQIYAVELL

LRHGADPTFNDEQGFTPFLIAIQRWFPITAAYLIAKGIDINQRLQ

>contig42333 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65936.1|) 1e-41

MIGLARMCFAHGVPQFGSCFGLQLAVVTAGGDVQKICEAMSWASLEKSVLTLQAVHTQCT

RAKRRCLTVLAAIKTRCERFNREGYSLRHMCLLRCKVLVNSVPERRVLGTTVSPRVRSAR

NGAVVALS

>contig43532 Frame-0R

MLESTRKALRSFLLDTLKDPLTQIAVADLTKQTVMAL

>contig43547-0 Frame-1F0

MNRRGLGKHLCIIHIPTDQATAQDLDKGLS

>contig43547-1 Frame-1R1

MTTTCGSRSSMLFAHQTESFQPKRCDALSVKTKQLDANDLCSRRLQEIICVLRVSRIGSG

VSSSLYRGPELLPDP

>contig43824 Frame-1F

MNSRKRSYTGIAEGIGTTHSSPYRKARELVTPQTVPHTSISVRDYSKHRSHEVTNPESEE

VEEEEVFEEELREVP

>contig44090 Frame-2R

MEKQLQLQHQYQQQYYLHHHPPAMPQQQQQHPYPPQPPPAQQQQMFVPQQQIQMQHPSRG

SGGQFAFQHQQYDIPQQQPSSYMHPPPSQFRYLKSMEDKRLTSGGRQPLRRDSGSSWSSF

DASGLPPSEY

>contig44487-0 Frame-2F0

MLRTITEKFVGDAHSNRVHAYTYTGNLSYSLLISTIFFVASSLNLTWSVP

>contig44487-1 Frame-1R1

MGASFGYLLCDNMMTILGLPTRPGFHDVDQTRRLEK

>contig45264 Frame-2F

MTVKSFLPALMSVTSAATTSHVFDTRVTALQPRVFDMYILAQSWQPTFCLGKENLYPGCE

TPQMYWRTHLTLHGLWPELSGSAPPSFCSDEAFDADKIERELGIATLHQYWPDVKFKDAS

PRYAEFWKHEWTRHGTCSGLTQIDYFTHAIDLERNETLAPTPEIIQNHVGGQVDVQKLRT

VFQDAALKCQHVHGQTVVFAQVFTCWQKDAKNVPIRRCACPAHIHAEDTCGHGVVTIPAF

PRDA

>contig46603 Frame-1R

MATKLQFMFAFIVGVAQIFAYISVLVIQVPNVVASPIYSRTAKQLEITDATDNYLDEDED

EDEDSWSFMDNLAALEHLAGLTNKQIMKDKILCVNSMPILFVDDDYCDCQDGSDEPSTSA

CSHVMLVSKTPSLKQHFKCKAGDKLVPSAFVGDGVCDCCDGSDEKATLCTDFCDTEWTQR

LHTLQDRLSVVETGIKIRAGYMVSAIITVHQLSADFERLAETYEARQRTFEDLQQHAQNN

PEMHGQIEQSYNVLRRLQYDMYVQSRVVDRSTFTEATWKSAFVELVGQCFIYTINEKELK

GASPNVIPRTYDITLCPFQNVSQSEPLYVSWKKAELQTKEGLSADSFTEEDTVPRHISMG

VWNKWQDSTDFVRTQNYDHGEPCANSIERNTHVHLLCGAQNRILSVDERRMCEYEIHFET

PAACERAEKDAVLDEMSRVKAFHATYGADKQFKGHNEL

>contig47244 Frame-0R

MLASAVGASLISGLQLRCPMCGTSNDLACVSRCDVCNSRLTIAEELSTTTPRSESSTYSY

SSVSPTRGSFSVAENGRTVIYNGYFSCTMHGTQAVMTADGSTCQVFVLCCTWQPKGLERQ

QTYATWYVSQRFSQFEKLHKALKKKLAHSSMLSLPPFPAKYYLKNRNSKRQQGLGMYMPR

LLEMSTQIPNAQPVPELDEFLDIAHQVQIFQSRLISVADPP

>contig48173 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58148.1|) 2e-93

MGKPKVESVDKLARYSSSTLRAEKVYKTIGYGLGAMGHLMAHVTQQETETSKGLQAIASN

IAMARYVIRITGGFESYVAWKNNSWCYNDDSEHVKRIVSLQALSMMVYYPLDHISYIGFV

APMLLNIDALKLSRQSCQAWGIYILLDIYANTIRIIALNVKEKHVKANEELLVEERTSQL

ATIQARRRELYYVQLRNFLFAGPCLQWSVKKKIISGSRCLFTYFLAKI

>contig49754 Frame-0F

MFDGSFKSARKVNLSGRKKPTAGYSARIASLSSVRKNEVLSGSKEEFLLHNRLAREERQA

LKLRAIASLRIQSQYRRFKAAEQARIDVFTRLAQQVTQTVASQDIQYNAVPTTQLQLYVR

QFLFARAIRNRVGKKTIRRMQDYVVLMLLVNSSRAEDSDSLVNVRKDATWVYQMAR

>contig50217 Frame-0R|Blast-putative chitin synthase (Chitin-UDP-GlcNac-transferase) [Phytophthora infestans T30-4](gb|EEY61714.1|) 3e-13

MFRPSCTQLLRLGSLSWVSTAWRTSSHSYCVTQNNLSWSTKGLHCYPLVIASLENSGMGA

CKGGVAMHCAIEKSCREEIELLEIRKDSFEAFRLGIFLSISCRLCGVFLLFVRV

>contig50262 Frame-0F

MLCEHPNNRTTTFEGTFSAILSSAEAQRLGVAAEDLNSTGHSLQLTTLMQSPSDHYQFDK

TEENHVRVHVPVTAKQMLLRNCVLRNTYSITGMVVFTGHETKVFCSNTEPVVKTSSVERR

LNRLIIGIVFLQQLVCFLGALLGVYWMRDAWASFWYLFSATEREQRTLAGAPALQILTDL

VKLHLRYFIIMQNFIPISLNVSLEFVKYWQAYFIQQDLEMYDEQSDTPAMVRSSALNEDL

GRVHHIFTDKTGTLTMNLMLFRYFMVNGKHYGGRIQENEMEVENSSGNVFNQSGRPQYVD

FDPTELFADILLGGEQSETLCRFLRHLALCHTLIPTKSLAEMCSTSFPEYSASSPDEQAL

VSAAAYCNVRFVHRTPTAMMLLEPGQTVPRTYNLLNVLEFDSDRKRMTVIVE

>contig53155 Frame-0R

MSQTDEQAHIIFQHLQSWRQKLVDLYGVAPWDILPNPTLARVSLDMPVTEQQLLVCGVGN

EQVARFGISLLQELQRHRGRTPSKIPIRSIETKQSHKVGSSKRGPMESLDTRENKNRKNG

EIARSNSAASFKEATPAPLLPAVDSLPTLLPIISDGVASSTSHLLTRKHTPFSATASTRS

PSCERSQQES

>contig53241 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63449.1|) 6e-46

MRINNNKCQDEGAVLLADVLATDNSTLTYLDMGNNGLTCVGMKPLLKAQSLIQLHLFNNK

LGEGLNEL

>contig53850 Frame-0R

MRILSLLASYLVKASIVIFLCESRALLLAGEVSSSVPSCTFRIDNTTKIKDIFECSRIHF

IGSFNEYYVACDLKLPTQPDIALLEIVNVTLDGSVLSPHNGVHVELIIQLNTSLATVSIR

NSQVQASAVHIRAANVSIDEPSSVNVTARGLKFGPGYNSWTSMGGSYGG

>contig54626 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64533.1|) 4e-50

MKLVRSTFSTTLGLSSGLECLDGEQLWQPERIQIMWERRDFYGVLGLPRDATTQQIKRQY

RKLALRLHPDKASDACASLESTV

>contig54983 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65743.1|) 1e-52

MFNLGIRAHSLFAISWNGLNLSSCESPESKIAEIFRP

>contig55153 Frame-2R

MERSSSANWIKFMLNVVDTSAATGLDEMIMREQIRTMWSIQIDDFVSSCLLPLLQHQLYG

LISIEWNFKFFALDEHTLQDEADLQSLSER

>contig55258 Frame-2R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68035.1|) 4e-32 NOT\_ORF

MMHHPEVAELDLVDTSIDGSNGDGGCLMLGNIQLC\*ED\*LVHNFADRTYLSRLVSHIIAN

VHIELSDVQLRYDCDPSSRPPVIATVNV

>contig57128 Frame-1F|Blast-proline oxidase, putative [Phytophthora infestans T30-4](gb|EEY61459.1|) 0.0

MRMSAIIVQAQLLFHTLDGPNFSRAKSRYLERMIDYSTLSAGLRHAGVHATEDEIQTLFN

ELDHSSRDGMIDYIDWVSFLNPFDLTMGSLTQFINETPLSEDEKTQLRNMIKRLESLANE

AAQRGVKLMVDAEQTYMQPAIDHLALNLQRKYNRNGRDVIYNTFQCYLKLASDRIDIDLE

RARREKFRFAAKLVRGAYMVQERKRARELGYADPIHDTIEETHETYDGQVAKLLQHNQLA

SFMVATHNEKSVVKTVQEMQDAGICRTTGGVYFGQLLGMCDHVSYTLGANAYKVFKYVPY

GPIREVLPYLIRRAQENSGLMSGAQLEMRMLKTEIKRRLFGKVS

>contig57573-0 Frame-1R0

MAAFILPIFSAFKPYRIQQRNDMAAFILPIF

>contig58569 Frame-2F

MVKATDKKKTQIAPNKSKKPSHKKQNVKKTIIVPVSKAA

>contig59517-0 Frame-2F0

MLCIALICFMAVDGTQERTFIEIVTKDVRTADIFTFMQ

>contig59517-1 Frame-2R1

MKVKMSAVLTSFVTISIKVRSWVPSTAIKHMRAIHSIASRTEKKSRQRRRLIHNLLQTLK

IVVLLLYFHARIGTFNRRAGGNKLAAHLAVKKHH

>contig59562 Frame-0F

MFDAGSYGTSNGASRHTDVQSSDEHERSHSLQSIKHLNLLKT

>contig04123 Frame-0F|Blast-Monovalent Cation:Proton Antiporter-1 (CPA1) Family [Phytophthora infestans T30-4](gb|EEY64669.1|) 1e-19

MDEKKQRWAGAELLVCAIIQLLLVNLAYRIDRMRGPPLLSTSSWAIFCGLLSGALLALDS

E

>contig04259 Frame-2F

MDKKEASMEAYKGKVVLVVNVSSKCGLTPTNYPELQQLYEKYQDEGLVVLGFPCNQFAGQ

EPGTHEEIKEFVKQYNVTFPLFEKHDVNGSNARPVFTYLKAKLPGTFGNYIKWNFTKFLV

DRNGQPFKRYAPKDLPLSFEDDIKELLAKAAEPDQVEEETKDEVASIESDTATSEKKEAV

EEKETVDEKTEEKVVEKVEEKVVEKKEEP

>contig07001 Frame-0F

MLFSRFRSTMDISSTNMEIIKQLESLSKNI

>contig07096 Frame-2R

MRRENEEECGKKRNKSSKAQESKEIDELLKRGAYDVFRDDDAAGEQFCELDIDQILQRSS

QIVQYTQQAQSSFSKASFVSATTSNDVDLDDPDFWKKAVGLTEPDVVESEDLLPQQRKRT

RVARFGDGGNFSDGISDEEDDKEKLEKEKEERERLEEKTAPREWTQNGRDRLQRALMHYG

FSRWEIIRSQSGGSRSVKDVESFARSFIYVSALACDQRKDDSPFVKASICTAALAQKEDL

IDEEELPSVLKEEDFVLKSKQGGGRRVVVRLDMLQRLQQLICSACDACDELYKNDEGLKS

RPCPTANIDERANYYGVDKLIPHIALIDLGERPAWTQITPWWNEDADRNLLMGVFLHGYG

RCAQILADPRLYFAQSEKFARDQVLTSNVGELNRSNFCLLPAKISKKETTISAEEDDSGD

ISDSESYSSVIAGNSGSSHVKHEGSTAVGSDVTAAIDSFKQPEVQHMNRLLGWLLSAEET

KRRQEKERSKKERVAVEQRRQVRQEVRARTLILRRLELKAMQLAQVDILRHMAILNNARQ

LSDVTLALASTHRIKSTDWTKDERRSFAYMMALYGAPRILAKRVVVASDGRATPSMSPFV

AEKTRDFAWETDSISWRNIVEWGNLNKTAVMTCQFYETKFAPKCREVARMRADLLSSDQR

AVALGDLIGIEFVDAYEGVLAHGLKARNTAWTTMRRTQLLEDVLHILSTKREALEAYVKS

GMSVLMTDMPLWWCPWIHDLGMFYGMARYGVYGWERIMLDRQLPFHRQARAYHFRTGLEE

GKLSFHPLHRHHFESKTAMNDWFKRTVNEFPSFSILERKVEIICAAVLANSEHLAERYLE

PEDRHEFSLSPPNNCFERLIVTHIKQIEELLLTIEPLLEIAPSQWEGNGDRASAALNAYF

AESQRRRDEFLRLAEASSAIDFKSEAKDAYPLVSNGPN

>contig10513 Frame-0F|Blast-calcium/calmodulin dependent protein kinase 3 [Phytophthora sojae](gb|ACH68464.1|) 9e-24

MADQIPPEFLEKYRTGRVIGEGNFSIVKECTNRKTGERFAVKCINKGALNPKDRRNLMQE

IEILKH

>contig10966 Frame-1R

MSTQLIASSSSPELSTYKARCLLIFDVFTCYCLVHKASILQACVHDRSSRSWQLLTSAES

FSNVR

>contig11226 Frame-0F

MIYADIQNLNSHASKDPVNDPGVCEH

>contig18258 Frame-1F

MIQTSTFPRTCVFQRDLHDKDTAQFSSLPDKKLSPTKPLMGRLGAAMSQGALMIGSRWKR

>contig18665 Frame-0F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY55494.1|) 1e-124 NOT\_ORF

MISMEFITAPKISQVKAIKALGLDPPEVAQVLCEVFSKMVFCYGFVHCDPHAGNIFVRRN

PDSSIKRQAQLVLLDHGLYRELDSEFRKTYCDLWRAMLMRDNVLLENCGRRLNIGEVVRY

LPLLFTYRTINHKGRLDVSMSEQERQKLSEDLKNLRFSNVTEFLEQLPRDMLFVLRTNNM

IRALNKDLGGTKRERFSIMGNSAIRGNSAFFSDSSERTCFGVLVLVGL\*WQYANLHLRLR

LADYLMTAMHYIRRESAPKFKRTG

>contig21283 Frame-0F|Blast-P-3 complex subunit mu, putative [Phytophthora infestans T30-4](gb|EEY67762.1|) 8e-26

MEEVNKYREREDVPPIIISNRIYLISVFREDLFVLAVVTNE

>contig21931 Frame-0F

MNVRLFALVGATALAVRTASAVTTCPVSVQSRTTSTLLKPITKVVSSIPATIDSSDSTSS

DVSDPSTPSTDEGSQGLQPDVGSLMNSSLPITSGSADKNNGSGSPSDANTGSDDTGDSGT

TTSTTTPSSPSAPSSSPSSPSSPSSPSSPSSPSSTLTPATPTTDSHITDAPSTTTNSPS

>contig25386 Frame-2F

MIFRSCRVCLLFSLFQCLPCISYQIKDSHISILIFYSACCPYA

>contig25724 Frame-0R

MAEELLRASSFYCVYELQKRTEAFLSGQICVENVVDLLTLSEECNADDLKKNCVPFLMQH

IHEVVRLPAFEEHRVRSSEEVLKALTNLLGPEWTASYAKLKNSIGLNSSDKEDVIKLSAH

ELNDDKRIVALNNEIREKSVSPRFLLSPVPPFSHHKNLSAFATDSPVVSENKHAVKAYGT

EEIRFSTS

>contig26369 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59785.1|) 1e-150

MGNSDSKSKFRESVYKLNNEVISSKNLEFWDKLWRIPTVAEEIFTLIQPDDVRMLRHQQP

ENLGTMLRQAVSQIVQIVDTPVPKYYQQALNCVRVLTRLVPFILEEEVDEFVEQLFWSVE

GDESAKSGDEDEETKDVTYGTDTLAKQLIHAIMGLLFLPEFTVSIHAYKGYGNERRSVTR

SGHSTTEGSLVYPSLLWHSGVGYPDASVANSSTFDRNRKEVLALLLTCFSSILYQTAVKC

NQWKDRFLEVATAPDCPFAPTLFYSLLNIIVSYDPVGWGVPYAGSIVSDDR

>contig26552 Frame-1F

MTSSFRQRPNENYRPSFGQRYPNLDTASVDVDMKDASSTPSSISGQYQRTTPSAVSTSAS

LSTITMGNNRHALHEQNVASYRSTTSSRLMAPTASSLAHRTNSFAYASSLPSYARPTASS

ATGRYQGSIMPSVPSKAAYSTEASRFRPGTSISTVSNRPLYRGAGTSSKFQSNSSSQPRY

GTTRAMNRTPTLTPPGQFASVRSAPPQAPVAEMMDYEDFQTQQKEQDQNQLNQAQKAWSL

SDFEIGRELGAGKFGQVYRAREKNSHMIVALKVLVKEQLKSAGVAHQLRKEVEIHSRIRH

ENILPLYATFQDATRVYLVMKYAGGGDLYKKMRSMAGR

>contig31488 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61685.1|) 1e-122

MLVGTDAVEVASSISAGGLCLLVIDQQIDFHPGGSLAIPTAEADAIRIASFIRQHSTQLQ

QLVFTLDSHQRYHIAHGIFWMDAEGNSPKPFTLISSAEIVAGVWRPRDPTLEKYVATYSK

ALEASGKFTLCIWPEHCIIGSRGHNIVSDVLAAAMEWTKISLKPVQYVTKGSNSFTEHYS

ALKAEFELPSDPSTSLNQDLIDTLKLADKVLICGEAVSHCVNYTVRDLLAAWPNERRNDL

VILTDCMSPVPGYEKDGEKFLQDMAAKGLTLVSSEKFTV

>contig32197 Frame-2R

MALCVSEPVGKIYLVTGELVAVKKFVLGHKKIDDRDQYG

>contig32580 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59644.1|) 1e-152

MSVEEQPNAWPRVPCSSCQRSYKFYCPKCFIPLGVPKNVSVPKLKLPLQVHVWFQDKIKK

STAPHAKVLAPQDVRIVPYPRNENDDAMPIYTQDRSILVYPSYKSEVLDQFSMEELRNVR

TLIFIDCPWQKAPVIMNHPSLANLRHVRLSQPPKESNFWRYHKAGAGCVSTIEAIKLMLE

EYTAVAKTANIETAVGSENTQLSDLLFFFKLQFLRIVDHFNHEADPDRKPPMDAAEKERR

RLMYSQKDMGKKRRLENKLLAWAARSNALQEGKPPPVTTQGKRHHRCYNCKKDDHRSIDC

LQPCRYCKMPGHFSASCSAKQAAYEREMKSQQTPRTKAL

>contig32971 Frame-0F

MANELAEMTWLSAACAAAVTIIASLLLHRICFCDTMPIDNSSGTCSLDEYMIEHSTDELD

AKFQVAVDFISARGQDKLTNEQKLVLYALYKQAKFGSCNVEKPSAIDMVGLAKWESWKAL

GAVNQDVAKQHYLEWVQDSFEEFDVRAPIVGRSLSKAAKMSMSLKGSMGMAGAVSIPKVD

MSTEEWKVKEDVFHYASTGDVDKILAALNQGENVNVQDLEGRTMLHWAVGREHTTVVEEL

LRREASPNIQDSDGMTPLHYAASCEHEALARL

>contig36100 Frame-0F|Blast-lysophospholipid acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61084.1|) 2e-19

MHYFVMPFQAMSWENSLASLKNVYFVGHIAAVVLYLVFSCIPVPKLKKKSE

>contig36441 Frame-0R

MATESSRLNLCLNAERQLLARNAPQRHLPVTIVTGFLGAGKTSLLRHMLQCKLNLNIACA

ISDLAAINVDALLLSNQLEGPGHKLFELSADPNGSVKEFRDAVWQVLKAEDDLGFVDYVV

VETSGTTDPSRLIAAVEETWGSMTRARLDTVVTVV

>contig36625 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56495.1|) 9e-38

MDETWGLVEEQFNATVQQVAKLQKELEYAVESRGNFKRVRYSSRKVARYF

>contig36650 Frame-0R

MWQLQKRGGLPYKCIISRKAALFRTCCESNLRREGLLRKDSLY

>contig37064 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68826.1|) 0.0

MKVVVVGSGIGGSSAAYHLVKDGHEVILIEKNSTLGGHTYGMEIDGEMVDIGFMMFGDSN

PNIKQWFKSLGVTQEDGTTKKRIPMSLTVTSDIKGDLQFSSRAPFNGSARNLFDFRIWRV

LIDIYKFTMDLMSMPVKENITTREWAAKGRYSNVFFRHYFLAFVSILWTIPKHDVLDLPV

SQFLRCLKSHSNSLYIPLWQVILGALGRRTDRPRHLWWYVGSSYVEPFIKLFTEEYNGTI

RYNATVDEVEKGGKAVILKSGERIDCDHVVLATHADESAEMLRWSEKSYRSLMRFHYHKS

LIYVHRDPVMLPFSKKVWSSWNVLITKDDQYILTYWMNRIQRLNTKKDVFVTITPHDYQG

KRPASDTIISTFRWDHPRLLADCIPQNEIIQEDGITLSGAWLGRGFHEDGFVAGRRAAAI

VRDSAHQHTVLYEDPDNIHVPAVPPFGIPFSFHLVGVTIICLMGCGVAKLLSKQA

>contig38887 Frame-2F

MQLGDPMCTRHSFPTQCPYKKTFAPPEVLDRQGTHRHKQKTSVPALQKILLPANHQRKRL

RLSYRKHI

>contig40080 Frame-2R

MPRLSLRTTSSRQHKQQKRASLSLAFCKLTNSLHSSSGNLSMLSSTTTSASSNSLMSLST

ASSSYGGFVEDYEIEDEAVKVKKCSQQGWMYWKQRDDCWLKMYARLYDELLWLSKGSDDA

IAVIQIAVAGVRTTEDGGFIAHGPAGESMELFAYERNRTSGWIDALFVAAQLTESYKRSM

VANPSETEISNRESKVNERVYIGTLVIYNKEQGNSSWKQLLSTKRLRGACRQRLEKILDR

LDTSKR

>contig41577 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66188.1|) 8e-81

MQTTDDEFSSLKCRYASKRCWNLRAIKRNGERHNLCEMHRQKANSNQRRLDKKRKAGHAV

LGLPSPLSSAGFSDLERRMRMRASIAIKLEHELGIVPLTTQYIHRPSLVELQRAAGLLAI

GHSRSTFSTETELWNESPNRLSHAAWMNATYPKSPRAMLRVAKMEPSAEARVWVQHNQLD

VLKADSVVAPKLLPSIATAVARSGEMLVSSVKLKKSRLPDVRRAPSLVTRANV

>contig42064 Frame-1F|Blast-phosphatidylinositol kinase (PIK-5) [Phytophthora infestans T30-4](gb|EEY58194.1|) 2e-47

MKKLIQIATRTDELNHMTTHFNSVREERLGNALGFDDHGIRHLACITDIIFSHDCLVSDL

MQA

>contig43175 Frame-1R|Blast-nuclear prelamin A recognition factor-like protein [Phytophthora infestans T30-4](gb|EEY59676.1|) 1e-179

MASVFLGDLNDFIQPSQACINPLFTSDKPKDDGSTIGTAKITLQTELSAADLVLPQAVKP

NIIRTSTEEKATISLDDCLACSGCVTSAETVLISQQSYKEMLDVVALQNHKFHIVTISPQ

SRASLAAHFSMPVITVHRKLVTMFHNLGVNLVIDSTTSGDFALLESREEFLARYRNQQKT

FWARPPSSVAISSAKTEILETSTAAMPLQDPLVAIPMLASSCPGWICYAEKSQPNAIPFI

DTTKSPQQIAGSIIKRFVSGEHGIKPNDVYHVAVMPCFDKKLEASRKDFQDPEDATKDVD

CVLATTEIIELLEAVNVDFASLELANLSPEEVLLSGISEDGLSVLGSSLKASSGGQLEHI

FRYAAKQLFNVEIKGPLEYVTARNSDFQEVKLVVGGNEVLKFAIAYGFRNIQSIMTKIKR

NRCPYHYVEIMACPSGCLNGGGQIRPKSTLLASELLSNVTKCFEQLHLRDPMANPAVKLV

YDKYLDGMPFSKLAREVLHTRYHAVPKLEQLNPLGIKW

>contig43548 Frame-0R|Blast-ubiquitin-conjugating enzyme E2, putative [Phytophthora infestans T30-4](gb|EEY67396.1|) 9e-86

MQCCKLGGRVRKELEECQKDSHFSGVTAVSVNAATLSELRGSIQGPEATPYEGGHFELEI

VIPTKYPFEPPQMRFLTKIWHPNISSQTGAICLDILKDAWSPALTIKTALLSIQALLSAA

EPTDPQDAEVAKMYLNDHTQFLNTARFWTESYAKQTDAGSDAALLRLIDMGFSADKAKAA

L

>contig43650 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56450.1|) 1e-134

MEARVIDIFSSEGIKLQATHRPDSLSAADTSRKIAENVAQFPYELLQDRPKVFEIAHFKR

QDLFVLDEFVQQSFCRLHYRIKGLGSCAYCEVLPFPQKCGVLVKSLMNSLMREEDKAIQA

ILAESIAQFVVSQAHIQKKCVAKIINNLCHSATALVGVSGDYNDIQNEDNIVQNDQSRRI

PHSLLKPTQVRVVGAEAVLKKICNQYGNILFQKCRTLEAAISKAWEQQGIDELTIKRCMH

LISFLVPHFNSSPMTTCLSWLIPLAKIIQQPRLAHQTRSSVAHGIASICKHAKSNQHRSS

AMLVIYNSVFEAFRNNGDASSNFESLMSAVMVLDRIVHTLGVEIAPYLPSLVHYAMKTMS

SQSKIVRMYAAETFANFIPLIPL

>contig44462 Frame-0F|Blast-signal recognition particle, putative [Phytophthora infestans T30-4](gb|EEY70068.1|) 2e-71

MATADVAIAASFSELEAALQCENFSRAVEICNKIRSKLPDDKDAVKVKCIALIRMSKFDK

ALEIAAKYDFLATEKAYCLYRLKQDAEALQLIQGEDLEAQTDVQLHLAAQLYLRTQDYKS

SINIYEHLLQRAKKGDDLLELQTNLLAAYASANRSQELINREILIEDGYEVAFNKAFVYI

QSGEWDAAEELLLTAD

>contig44488 Frame-1F

MTASPQLHSAIATFCPMIVLDSTISLNLQCYLLHELYFTKRFCSEC

>contig45285 Frame-1F

MFRVLGSSKYQKQAVLQLQSPRNAFQLNQDLLKDTFVCPYSSLEAMEQELKTKHYRLLRC

DLSSHKMPGRSQCVMNNKSLSNLSIEGRHSMYPALDAFIRSQATTGGIQGEIRTVQMRTR

NPLLSNEANTEHKNQEKTPSLIIYHMMHNRWCANIKRPHKSNNIMFIVDIHQHVFYQKCH

DPV

>contig45814 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53153.1|) 2e-26

MGQQDNSMGLPPLGGRQLSFDPTQPQHPQQQQQNNGAFMGGPGEYWR

>contig46367 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66235.1|) 4e-16

MNVVVNETSMKAQDAMLQRYREVYFDFNTEFRRSMV

>contig46990 Frame-1F

MAYRLSCIYDSYIVILEACRIATAAGDSTWSHTIMELLAKGSNDDTIYCENPQGWNEIFF

RFLARQCLELTDPTLACRVIDVIISLVVNTRKSPLISQLCLALLHQIFPSHPTPSKYESD

TRNYYNDIPSRPLPNAVVLPSNGRMSALAKHRCSLLKYRHIA

>contig47580 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68477.1|) 2e-88

MQGVYPKGGCCKLCKSIEHLARDSITATRLATHLILTSLAGTMKTMMEILSRLLNIKA

>contig49634 Frame-1R

MCKESNFEKPGFSSDITSASTASDLGTKSDQTPSSYYPISGASLSNPPDSDFKTAPIPSS

GPSSRQTLTS

>contig50571 Frame-0F|Blast-peptidyl-tRNA hydrolase, putative [Phytophthora infestans T30-4](gb|EEY66544.1|) 1e-40

MQEKPLRLQHEPGNHGNVARFRLPFQQNATDKGYTYPIDDLVNRSSNRAKERTLKEGVLH

QDVNVALLLPTTFMNCSG

>contig50694 Frame-0F|Blast-MMP37-like protein [Phytophthora infestans T30-4](gb|EEY55529.1|) 4e-06

MKFGENPKKVRNIVDGNLNLFQKLYQHKVQVRIATLTNALN

>contig50720 Frame-2F

MITAQAERDYLRLCIEENESEISALPEEKTFKTNVLKDQLRTISDLQEKLRVAEYERDNA

MINYSGKSSVCGTLGFSTSTFASPSLAEVDAKVGNELLERVEKEIERETALLNKLKEEES

GDEIDVDSVEIGADGEVIADGMEIEDDNEEEVDRMRVFQRRQRHLGESVQDLA

>contig50980-0 Frame-0F0

MSNELSKDKNRQRSNKNRSIMKDEEIESVVMTPLSSIWTTGFSSDFLAGSEVQMQLKYKQ

DFVWDDEVFTDEPSIADREKAA

>contig50980-1 Frame-2R1

MLGSSVNTSSSHTKSCLYFSCICTSEPAKKSLENPVVQILDNGVITTLSISSSFMILRFL

LDLCLFLSLLNSFDIESS

>contig51767 Frame-0F|Blast-anoctamin-like protein [Phytophthora infestans T30-4](gb|EEY57355.1|) 1e-170

MDSLLVSRGQEFHPELRKALDLWGHTEEADGLFVEDDSCRRVKGSHWNRFVTSILELPYD

PLTYFAPFAEYRHDEKYQPYYRRYPIKWAMKTEETLFAQKDRIRLAEGIVERHINTDALE

SAGYLAGQMFALHDSKALHELRHSWALHWTMLYQPLHKIRYYFGEKIALYFAWLEFYTKM

LVFPAVAGLVTFVYIEARQAATGTNEQGYILIAFAVFVVLWSSLFSELWKRKNGLLDSLW

GLSGLHESFRYRPQFRGTKSYDPITDAEELTFESKTKRRRAYLVSVF

>contig51987 Frame-0F

MPPVVRYTVMRRYTDFRQLYTYLVETQGSALREALPRFPNGGWISYLRGDDPDLLHHRRA

RLERFLRAVDARPELRWSVAFTTFLRPDLGELSP

>contig53422 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54757.1|) 1e-22

MPKKLPRDRANSFSWYKNVRSKMPTETVPWLVAQIADIECRRWASSAFVGKMIGIRVARE

MISHFRAELDV

>contig53556 Frame-1F

MMLYDHYENSVAAPAVALATSFSSEIAISFLIILTCHFDTLPATKKSSNSKQHS

>contig54122 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67873.1|) 7e-15

MGEVLREHVAYKMRAKARLKKIAELRWQYQREGKQIPVLHELHEMAKISETPSPTVDP

>contig54629 Frame-2F

MPKHHGAFASGDSDGDCEMMDLVRDGVIDTNNRLKDSDSCIHEFYVKSCKYFKATEQKTN

>contig58272 Frame-1R

MTFERVSTVYDITQSSMLAVYGDVNRLFQRKSLKRDFCSFQYQ

>contig58809 Frame-1F

MTVVSLITYVLITQIKSSLKHISMVEYLHKALGRCYRL

>contig59020 Frame-0F

MFIVACIGLCVNLVLMQILGHGHSHGGGGHGHSHG

>contig59055 Frame-0R

MQSLVAYLVSLQAKELLIAKILHNLHS

>contig59194 Frame-0F|Blast-SWI4 1, Peter Pan-like protein suppressor [Phytophthora infestans T30-4](gb|EEY58369.1|) 4e-42

MSFVFKMGKVPNAVSTLVQDMRHVMAPYTADKLREKRKNSLKDFVHVGAPLGITHFIFFT

HTEAGTNLKIARIPRGP

>contig59518 Frame-0R

MVRILESNFKCNNVCSFQVIVCHLYVKD

>contig07000 Frame-2R

MWAVQLSMMSIIFRPATLLQTTWAIPKKILCAVFAAKIVAVDVFEAAWIKELPDYPQGQI

IRATAIAADDGSKAFLALLPSLRLHCRQRVDRMNFPKSGFMFEVRKNS

>contig07585 Frame-0F|Blast-elongation factor 3, putative [Phytophthora infestans T30-4](gb|EEY60196.1|) 0.0

MAAVADIVVAIDILGVASPAGIYVLDLLQTHLNAKPTTAREGALLAYLALCKREELTFVM

EPIIVEQLPSIMQRHADSEHAVKSVAASLATTIAHKINPLALHTLLKQLYHSFQLRQWQS

KVAALKLLKELSLTAKDEVSRWLPELIPIVSEYVWDTKKQVQTASIDALIAVCSTIQNDD

VVPLVPILVGVIARPEDTMEAIDSLLATTFVANVDAPTLALIAPLLHKALRDTSIRSSSL

KRKASKIIDSMCRLVVRPSDVMPFVPLLLPQLDTAIDRLIDAEVVDAAKEARAHLVEAAG

NGQVMEDDPITVRTRLETTIFKAFKEALEPSLSPGCTDFIMAYITDVCTEVATQERGVEW

HAIVMPYLEPYLAFSDAQLVCEALCVAGGGVVETRIRSNDPNDVCDLDFP

>contig09226 Frame-0R

MSGSSASQVSNSQASHSSCQRPLPHDVPLRYHWVGYLQKRSDWLKHWETYFFVLRGCSLY

CYLSEEDARRQNAKSKIKKGKFGFSERVSLVKACDVECTGANTLSHSIISAASPHINSSG

YAGEPGSDVMPSSSSVSSMYRFTLVTQKGHQLHFRTNSEASKHAWLHFVANAFADHDLSG

HLRPPVQRLRTNVEDFYKGYEYFYAALCARVTADERGTDILPNSPFANHTNGPSEEIDRS

NHMPSSSKKPAVSSISVTPNQPLAKTNILAPLDHVLVRFFSFLKSDVILRSNYLPMVPFE

GKYRGFGGILEYFTRLSQAVEVEQYIVESIEIETTTRESHDQYVIVISGREMMHVRYNET

AFMQQWTHKLHLKPKDNGRVSRWEIFGDVVASSVVFKPPGCITTLTLPSLAERIRESVVG

GYVVSILLFHITNVRSRELQGDAFFIRCSLDTNELEGVWHTEAQSIAAAPVKVDTSDSRN

ELSTPSWSYTFDQELFLQFDRLSRDDNTVLLIECCRQSNHEVVAHSHVNLANFLNQNHGK

STNRLLESSRHGVVDRKNTMQEASIRRDIQTYVLSNDHQSFFGKLQLGLTISSMSHRSNS

HPRASMSRYRDSYRETTVNTDLNTTIVATSDSPYRSFRSLTRGIHSHVEENVMHQFVING

VRYQLAEKYRMVKIVGKGTYGEVIAASDFVHGGTFAIKKLGQFLRHPKVALLALREIQLM

REIGTHPCLMGFRELQRPVSFEHFEDLYIIQPLMETDLCRIIHSKESLSDDQVQYFLYQM

LCGIHYLHSANVLHRDLKPSNILVNSDCRIKICDFGLARHANDQDLAEGLSEYVVTRWYR

APELLLANAYTKAIDMWSIGCIFAELLGRRIVFPGTSYVNQLKVIVEIVGTPTTFNFCDN

PIARRYAGRQFLLQNPQVPKIEWGQVFPQANPEGLELLDQLLQFDPSKRITAAEALEHSY

VSQWRNAQLEEPCHADVATKLTQFDYVQMSYDPQTLKELLYQEVMKAQHSLPEHQETIIE

SESN

>contig11577 Frame-2F

MIGIHTSLLKQVKSYQFLGQARGRNLAAGSTLGN

>contig21031 Frame-1F|Blast-eukaryotic translation initiation factor 2 subunit 3 [Phytophthora infestans T30-4](gb|EEY57273.1|) 0.0

MQEQVQKHLAVQDLSKLKIEELTPLTQEVISRQATINIGTIGHVAHGKSTVVKAISGVQT

VRFKNELERNITIKLGYANAKIYRAENGTGIGCYRAFGSSKPDRFVDENDDKTTWILQRH

VSFVDCPGHDILMATMLNGAAVMDAALLLVAGNEVCPQPQTSEHLAAIEIMRLQNIIILQ

NKVDLIKEDAAVAQHEQIKKFVAGTVAHDAPIIPISAVLKYNVDVVCEYICRNIPVPKRD

FTSKPKLIVIRSFDVNKPGEDVENLKGGVAGGSILEGVLRVGDEIEVRPGIVSKDEEGKM

TCVPIFSRIVSLYAEKNDLQYAVPGGLIGVGTHIDPTLTRSDRLVGQVLGLKGSLPHVFT

ELEINFYLLKRLLGVKTQEGSKASKVQKLSKAEVLMVNIGSTATGGKVLAVKQDLAKILL

TVPVCTQEGEKIAISRRIDKHWRLIGWGQIRRGSRIEIADSE

>contig21044 Frame-0F

MQLRDKAVALTQSENISAEVKVTELANNIVQLSEQIELMQKKIGELNAKYTLLKQRKDTV

STKLVKTNNSKAKLEQLCRELQKQNKLIVSESRRIADEEDQKRHDLSAQFKKTIEEVSAK

MDTQGQDYVSSLKENESLQQKLKTFLEQYTAREEHFDRQLEAKDLSVQLAEAKLQHQIQL

TSRESKKVKITLDKAQEFSEREIHLQSQLNSYSKKFDVVQETLTKSNQMFTSFREEMNKM

AKTTKRLEKENVALRKKCAEYDSGAIATIHEKVTAAEETLKLQEKVKKLESLCRHLQAER

NSNRQT

>contig22610 Frame-1F

MAPLPEASALPPPAILLTSMRQQNKVGELQEPESENACNNAQIKELAEAAMDHAMEIAVQ

EDTINMDDHSTLKKSVRFNCAEVVEFEPTMWTATVSSEGVPLGMSVDVRRRTKRQLDTYE

SERNSFRVGRQDFMELGYLEPEERLDILEKAGHSISIISHVERETVRINRERSESNEYDL

MYQYGLGEVPLMVDSNVEMTEQDFGDDGMLVDDNSASAYLYGIGSRNMVVDSFIMEDMKA

NDSINARAYDGLSIVYASDCILGDGESSDESFELPYSIDSFDSPLSCDFLRMSTSPTDVS

STSDCAHVAAKPASCALSVSKSSAN

>contig23150 Frame-1F

MRFAFSCLVVLIAASVVASETTDFTRKALATDEASTILVPKFSAQRRRLKGSLYKVIVGV

GSKVLTNPKVQKFIDLYRRLKKPKRATTATFMPNAKPAATATFKPVF

>contig24036 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68591.1|) 4e-23

MELTKLFKIFFVLRNEALRLNMVSPFLEAYFREVCSFDQLQKLLQWTETHRSIILEEISL

DET

>contig25725 Frame-0F

MAVQGCDFVIHTGTPSSCSVRDPLSELQEPGVHSIGSRMHCIIPMMTNFIQACARARTKR

VVLTSSVAAMADVVTPISIINDACWNVTSSLEKNPHFLSLKLAEEAAWQLVDQLPSDRRI

DLVTINPGTLFGPMLSKSKLAPGNQVIYDLIAGRYSALVDLNWSMVDVRDCASAHVAALE

NNDARGRYICVNRSVWMKDIVEVLSSNGYSGRDLPWKVGLPHWVGRLPAYSVQLGQVGAS

LYAKDPASVRASPYLGDKLLEHLNIRFRPVESTLVESANDLLKWGLIKPWAEDHEALVCG

CCHHSFTFYRRKHHCRECGTIICNDCSMSRAVVEGSTGRARLCDKCVMRSIPDLLGLLRN

KDPDKKRTAVIALESLMENPSNHDYVTRFGGIVLLMNTIHHHDESISSHAAGALCALSCS

VASTLQMVLEGAVLQMLEVEEMLSTWAICLQALRNIWKQINRHDFRRMLYAVARVSADAN

IGELRGNILLTFVHMMDPKEVPTLLSEGLLSVLHHMLLSTAEFPRCAAAHAIKHLVPTRY

DPDVSIEVPPYLVDDHEELFLNSSLSDLQFLVKGHIAPINAHKVVLFFRNSYFKNVVKFG

SASSQTAVIEVDNCRYEVFSIMLRFL

>contig26553 Frame-0R

MLEMVKNDVRSGYHEHVLNGRYAKFNAHAKESQGTSYELWTDETARQQLKVIVQHEYVRT

IESRTNMMERFVVFTEKHASNVGSHPFLAGLRASLQWNLESSTIVAWKLSDSVFVESGDS

EFTHNALALLVRVLNFSHCESTAIQASKASNKAKIRDWYLDPYLSDQDIRQIIRLIPAAK

RLEGNPTGTKLVTRLDRLNVHGQRDERSRFFNRWCVLL

>contig28744 Frame-2R

MRQTLILAMAIVSCRHPCSAIELGHEGALVYEVCVGLKNLPASKRDKSSGMKTKREAHAI

NRLSAAQPLLFAQQVRQITLYKGEPRSKQRLEC

>contig28829 Frame-0R

MLEEHQVFTTVQLLDEVNEVAVSETIVALRNKTRPRLGTLNAVSMSSDRIRSSSSSPSHA

NRLSSFLNKFPSAPIVATKPAKPPRTPRISLTSSGTSTHSSPRDLDEQPVLIDDTNASKS

RLRMPFRAKSPSSPSPLASSPQSSHVSNPSPCSHDDTPSRSWSSKLAALSRSVSSSSSLA

SCVTPLTVEDSNHTPLSSPPASPLNRVSIPSAFLPSKPRESLSRSKLSAFLNTVDTPSVV

LGTEETPPFTSLIQDVETVKDVEEEETMASVQADTKTDSEPIVMARARPSSMKLLAFLQK

VEPVAMPASRDDEDFEKVSAELVTMDEDMATYKAVVCQDKDCSQEVAIPAPLMTANLDMK

QDVGGSN

>contig29075 Frame-2F

MDAISLKRGVDSQNKRRKCTKKEDCLSLKDTSVCAKRTGKKEGYCIPTWFGICHAWAPAA

ILEAEPSCPVERNGTVFEPYDIKALITLAYDGSKIPTVFTGSRFSGNDTIMNGTDEYGRF

LDQRRRDISPGFFHIAVTNIIGRFNSSFVIDITAGNEVWNQPVRSYEILRLSWMSPAAAA

KKYFKVDKYPFNDAATRIAAVTTRFSWIVESGSNEPLVASGLVDKSTTSVDYEYLLETDS

TYLILGGEWINKARANHPDFIWLPTSKPVNNSITSVGLHYEEIESLVIESTSMGTECKLP

ITESSSGKSSSSVDFPSMTPTGASDASTNKDASDDDSGEANLSPSSADEEDIKTTASPAT

ADIIVDATSSASDSSGPSDEQYAATPPADLAAAATNSATPTADTTSSEATVPVTPVTDSA

SPVTDLASPVTDPAP

>contig29596 Frame-0F|Blast-CBL-interacting serine/threonine-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY62050.1|) 0.0

MGAQIKKEISIMKMVRHKHVVVLREVLASRTKIFIVLELITGGELFDKIVSEGRFSEETA

RFYFRQLVDGVQYCHESGVCHRDLKPENLLLDENGDLKISDFGLSALYEGGGPDGPESSR

ASLLHTTCGTPNYVAPEVLADKGYDGRAADVWSMGVILYVLLAGFLPFDEPTMSALFRKI

QKAEFSYPSWFTPRVKALLNRILVPDPETRILIKDILHDEWFITANSADEQVTPIAGPGT

ISDELTEASVPAPLDHITIKPSQADLDAAILEHQDEINSDKKDKLDGGLKVMNAFDLINM

CGGMALNRMFQSNDEKRVKRSSQFTTTIPAASIMTRLTGHLESLHCDITIENSSKVKAVL

QTPKGAVGVVIQIFMLAESLHLVEVRRGKGDIFEYHRFYSQLNEQMKDLITPSHST

>contig31218 Frame-1R

MIIAPLVSGRPKRGFWKALITAGAAKTKTHEAHPLVVHDNLRRKSFNQRWTSFTTSLKSV

LHRDRQSPRLEGGRATI

>contig31333 Frame-2R

MQAQLSKNRGNLESAFPFTNKWLNMEGRAYCLRDDIAKTEVDLLRQADGKALKRLLRACI

WTLVIKHIDGTAERVWPETFALDIARIRACRDTIDRIAIVSSLVAVVQDVGAFPGFKMSK

FLNLLGQKLNVLLCSNGVSKAQVVAQVVTDLQQFRNEKLTKEWQHLEKRLLGSFAVENVV

RQLFFARVARAIESALLPVSEKRADLHFSLAPFATDIYDAGFELRRLVEHNERVYATVYN

AMMKKVVDSALADYKES

>contig31489 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61686.1|) 5e-11

MNGRINSVAALATKAVQVLAPNNVQLSEHEFQRSPKEEQDAAREAAKLVKPG

>contig31841 Frame-0R|Blast-acyl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY63794.1|) 1e-22 NOT\_ORF

MASSLKTAVTRSHFESSNAFLAYNES\*MDKLANNFALSAYLSLTLGSELKFAEMTLSPLP

GLIDYVVFQQ

>contig32581 Frame-0F

MSLEGSHTRAVIEYALDLFSNDLELAKAWICEPSSCIEFERTANAGNKSQSGGSATEWLT

PIKIEEGSKEPKSVNDALEVAEEVAGETLYLLSLLEACSAHGNDDIFLLSVLLGRVENLS

HILVWCYNSNEGLVTPGLSSIAFIELPRLKLKLQPKKELVGERIRLYVMDQNGWFVSNLN

VAIPDSSKYLCKLVKIASNCIVLESDTTDLMLICPNHDLYSPVILGDPFSSVLVSDRSSV

VWQQAMETKFYTYPVHSSHTFLLLPSFSSKLYLILTSMLNHNYAAAMEMITGCNIDVKFT

DE

>contig33366 Frame-2R

MSHKTICPRSTSLLSISASSSSRIESTSSRTHFFDSMIFFHESCKSKFEQGAADCQLSIS

FMKFSP

>contig34576 Frame-0F

MLAIGFKLSDTSAASLRSSLSDFLRREYDENERQVENHEGMLDQFLQLKTNVDLVRTPSS

ISRHVLLRYYAQLDRMVQRFSCDGEGAGFQSLRLQFTWNDSFCPRKKSTQTGLSYEKAAV

MFNVGALESQLGVQIERNTARGLKAACHHFMKAAGAFTEVKDFIVKQTLGTGTADMSAEG

LSLLISLMLAQAQACFYEKAIKDQLKDGIKAKLVHQALEYYVSALEFCRSSGLVGAIDKS

WEAHLQFQAHCMRAATQFWQGKASKAIAVERGEGYGEEIARLGAADAECTKACKVATENK

LPSSLLESAQTLQRVVGERLVLAKKDNVSVYLENVPEVSTLPAVGKAAMVKPLVFTSDEL

LQDLGGVDLFEQYVPKDLLLRADSVKQDIQTLFEETAENVSKSTKAANKQLKDMGLPASI

EAYECDFPKTLWRRILYVKDMTASIDSSAIGANKNPVVAFIQQQLQAVTRISDDAEKQLY

SAEMLLNEEEMEDKVCRQKYGESVWAQPLSSSLNQNFRFDIDRYYRLLKESKKSDATIRE

KIYENENKLEALAQSKSSLKDELPRLSRDKSNSNEEIAEISSFLMRLGQLVEEKDQLLRQ

FKESFDKFSALPVLLGGEKMNAEAALEADKQFFKDHFSGKITLIFKEEQTVLDGLMQANS

RFEANKETDHLLRERQAFLQNLSDAVDVFEQLESHVKEGAKFYSELCIRVAQLHQTVEDH

CSSRALERRELEMNLTASEEMRQREAADAALAQKMMADMRVCNDGGFSSTRDEALARQLA

GSTPQHYPVSCTAPRMYETLQSQPQQTLYTANQQPHYGYVLTSSISAPSYEMNARQHPAQ

QQNYHQFPGQQRQDYDLPFSQGHMGDSV

>contig35496 Frame-1R

MGTAWTDDALQQEVCDRILAVNGASKTREIADTIIIAHSLGNLLLAGAIAKGKCSIASSS

>contig36440 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65080.1|) 2e-66

MTVAEVADWVAYAVQLPQYSDIFRAHFISGYTFPLLMANDGMRLQEIGVSSELHRYQLAM

FLQMKYLGMGRKPEAVGSSVCTTEGTTAQDQKLLQIAWTSTVATPQRYQLQRRSPGQSTW

VTVFTGADTEFLDVVEPPEHVIYRLTTWNSYGRSPRSFVRCEDAFASASASFKSSAESSP

QLLGSRNSRQQSTIELMEANSEHDESSNERDM

>contig36549 Frame-2F

MLRQLITSWLASLLMLWHSHEQYNLFRPLKNLAKR

>contig36624 Frame-1F|Blast-ATP-dependent RNA helicase DHX8 [Phytophthora infestans T30-4](gb|EEY63970.1|) 0.0

MPEAGERHFAQELRGINMSSTFELPEWKQKSVGKNLSYGIVSTKTILEQRESLPVFKLKR

QLMQAIAENQILVVIGETGSGKTTQMTQYMAEMGLTSTGIIGCTQPRRVAASSVAKRVAE

EFGCALGQEVGYSMRFEDVTSPETVIKYMTEGMLLREYLADPTLSKYSALMLDEAHERTI

NTDVLFGLLKDLVRTRKDLKIIVTSATLDAEKFSRYYFDCPIFTIPGRTFPVEILYTKEP

ELDYLDASLLCVMQIHLSEPEGDILLFLTGQEEIDTACEVLYQRVKALQERALAPELIIL

PVYGALPSEMQSRIFEPAPKGSRKCVVATNIAEASLTIDGILLRCRSWILQTEC

>contig36651 Frame-0R

MRASRERWQGGGSASFVRCRVIFPSPSIAPFRAH

>contig37065 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63875.1|) 4e-44

MTRVTTVAAALNEAEPQYDQTAKYADSVLLHLIRHVALYLFVLLSNTTKLAVTEALGALD

AATSDVADEPIKNLQHRLHVALFAWVDREIDSNHFDGLLLEQRAFVVINRLLRQTRANTF

ATCRVLSGLLRWYITKLQMPLVQYEQNSMLSSTLEYLLTKEENAPINGSVSLQILYPLLN

AVDLISIEQRECLDALVNLLRWLKLHDQSQEVLATFIYNYHAKLIGPLAFRESPGLDHDN

RNLEFCNELGVCFVQMLLQHSDHIFRRDLQVVDIIPSLSYSDTEDDDASCENNNAPFSLA

LDDRNHLKGTKTTTSNISCPNASDCTERNQKMELAPMAWV

>contig38666 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55501.1|) 4e-19

MTSPPKTAAQKRLLQRLQITRDNVAFADNSKSFLEDTTVATLEEYAGWRA

>contig40081 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53199.1|) 8e-46

METFANETLKEATKRLLKEYQRLESILAMHKERVEFELLSRKREENLAQVELKTSDRVRC

IQKQHEMEKRLSQLRTEFECRLKQQELEYMRRIESWKKNDEEHSRKIKLELRRREARTHK

NHEKRIRQEYENKVVEQHLAKDEELLNLEATLRAHQRARRSRQVG

>contig40175 Frame-1F

MDWSSVYDNSGEEAGNWEGYGETRSSRNAYRLLHQQMSLQPVHDQEPSVQYSPLVAYAFT

VNYILGVGSLGIPYAFYRAGLLMGNAMIILVTLLSYITVMWVCESVARAREASLHSNEMI

ALKATTTTSTTFSKFDHFP

>contig40496 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63965.1|) 1e-104

MMSAALPVEGAGAVDMEFIRLQMQQGHPPQNVQEYLWRVRLEAENIPDVVVAPDIDPRRF

DVQQTSNMPKLEAFAVDELDASRFPDNEWKRNLLANFAELRQLIACWEAIGPPKAKTAIE

GDVPLEIQRTKVPRMSDEEGWIHFFFWKTRSKQFSHSSSFKTFAAI

>contig41576 Frame-1F

MQASVLTFAARKAHYIECYGSSLTIQ

>contig42436 Frame-2R

MITPSSIAGSFGAINLTACSTAPSWNTQPPASRSATVTLKQLSGFSMRNLSINGTSGDSL

LNVYFKLVVDGQCVYKSEVAQNTLNPVWVPFQSHGDGSDGLQNVETLLSGGTRFHIVVV

>contig43651 Frame-1R

MGHVWRAAVHPSLMMIASGGGDNAVKLWDVSHELMSSSHAAGVSDFCKTVTIPTTFLKKK

EGDFLSQSVRNIVFSAVDNGKAAFVASEHGDIFRLDLLSLKAVLFFTICSIDGGVQAKAG

SLSTFTLDFSGRFLLLGDRLGRVMIVDASIGILLHSWYAQTNVRVMKLWWDQEDAIFVSS

ADGVLAEWKPLVAEATDKSASPSVKTE

>contig44834 Frame-0R

MPNMEDCVLVARLASRHFFPGGVVKGFVQLVSHEDKNNAHAEIAYVVAQAHGHVTVDTNL

LTLPVVHVSSTRTEILKEQTILEERALMKQKVPEDAYQFDKLPDVRNISGDTGTCIFCST

PSLLFSDINIAPTQSEFDAAAAKSHSVDPVIDIENLRKETAERCTREFALALPPTICPSF

RGTSAKVFYVITITAQCAVPGSKPVSVHLPFDVYGSEYFFEAGTAASEYHLAESHSALSN

DSTLPTSDTNHKTTPKSRHVVSGTSQTGRLARSSSSAPAPAGVRIGSEIAFELRPSLMHG

RVETEQIQRAQTSIFTIGKESSHLVRFLLTKQSYQPGDILLGVFDFTRANIPCYKVSATL

CQEETLSSMALDPDRVVQSKVFGSFHEHTLGVLHTNMRLSIPHDALATIKTDLVRIRMAA

PFRVFGWRAADTD

>contig46366 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66235.1|) 7e-42

MDSFLDERRAVDSSRTITSGIIEQAIATKNALESQRRQFTTSHGKVTTLGSSFASINTLV

EEIRRKKMRNNTILAVVIAGCICFTLWWVVLSKV

>contig47196 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59440.1|) 1e-172

MDPAAYDEDGYRDELLRTMRANEALVYQAIFAPENFTHQKSVLVAATSTGLLLIYQLDRL

LKPAYWDLVRRDEESAYPGPNVSIQAHSTQIYSLRFAGNETNPLLISGGDLDFRVWKWKD

ILAAVDDSSNATKLKPVHIDHLKRKTLGFRKALLPASEINEIAVSKTTGHLFLAGGDNEA

HEWDLVTQQFTRQFEGHDDYLHTVRHLQHSEELITGSEDGTIGVWDIRQDRKVEFLRPQP

TTQSNKSSLPYLWVGAIAHDDSEMWLACGGGSKRAYGNPAQITGGFLGMWHLPSRVPVHF

TKTTSDVHDVVFHQMDLLSVGNDANLKKWNRSSGQLLATARSNLPSCHFCVVDDATDIIA

IGGAAPSIDIYTMPGVVSFSLAINDARGL

>contig47581 Frame-2R

MDENKHQKKKPNPTKELFDGLRKVEQELRDKKAKENLDDNVSW

>contig49936 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55929.1|) 0.0

MEQDPEEQDHYKSVLLSFREYESYMMREIYRRKKNMQKMPSEMQWRLPPSSTLRNLHHFV

NATHQNQIVFNRVVQVQLETGPAVDLPNVTPKTPLQSPPRHFSKLKSTLHQFVRDWSDEG

KKEREMCYTPVIKELRRVLTVDADDQTNRPRVLLPGAGLGRLALEIASRGYAVQGNEFSY

QMLFASNFILNWVSQPQQFEIYPWIHNPSNALTVTDLLRPVTIPDVAPAELLGRSHGTTV

APDFSMCAGEFLEAYADDKECWDCIVTCFFIDAAPNVIEYIAAFERMLKPGGYWINLGPL

LYHWQDSSGDDDERYGQSVELSYEEIKHVMTTYNFRIQNESQLECIYTNNVKSMMKTVFD

CVFFTAVKETDQTSEKL

>contig50695 Frame-2R

MSRSLTDSDVLLANSSDGKVRQSIVEALPSNVLQRLAAKSPNYDPQTISKKHLQRVIASI

VFRSSRSQSIKGIATAGGAKAIVYVAQKLKRTYLNQFSRMIK

>contig50721 Frame-2F

MAIVATSLRALGLFDLSTTCNSVLSYTLS

>contig50754 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55414.1|) 4e-27

MVKAYLRYERACSFGVIASVEGNVIYDSSGRLAISPALQDVAVWNIRQGNKVRELLAPET

GSGQVTA

>contig53328 Frame-0R

MVAVVMAFCIAPRIGWRETFYICCAPVIYAVAIRLYIPESPKWLASVGRYDEAVAIVESI

ERAHGMDPYDPKTETESAATERFYQPQLPDSHIKCIAMLFQRQFCVRTTVLWILWLGLSM

SYYAIFIYLPTLISFKGYDMNGHWETILIITASQLPGYFTAAGLVEVIGRKLALVLFLAG

SFLSAIAMGYVNATEMQVMVTGSFTSFFILGAWGCLYAYTPENYPTAIRGIGAAYP

>contig53922 Frame-1R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY57656.1|) 2e-20

MANTQHQQTALKLKKACGEAANQAIAATTLSGQASHIHGKNRKFGSRKEAMAAKIAAAQA

KREAQKSLRSPA

>contig54057 Frame-2R|Blast-putative chitin synthase (Chitin-UDP-GlcNac-transferase) [Phytophthora infestans T30-4](gb|EEY61714.1|) 7e-23

MSGAPPFSSGYQPRNMGLPPLSHGPRSSMMSIEYDGIPLPPPSIRSCGSQQYVTS

>contig54123 Frame-2F

MWRLNITRLPIISSSCFGSTSVNCVFFSRRRTLRHVISFQGF

>contig54628 Frame-2F

MEWRPQAVSVTQSLPFDNKAMERYESDNRSDVSSASGVSSPGFAVQLHLAAGSTQRLKSS

HFRRDVSKHAVNQSNMQPNVSNHDQDRNSIVYEHSFASTLSDSIHAPFNSVVNMTSAVES

AFPGIHYGINDSSCP

>contig55256 Frame-1F|Blast-MMS19 nucleotide excision repair protein [Phytophthora infestans T30-4](gb|EEY67788.1|) 4e-20

MEFCVNASSSASIIFRLLTAIETAAYLA

>contig58273 Frame-1R

MLQFVLLVTRKATKERLQNKT

>contig58808-0 Frame-1F0

MMNRQQSVYAYDPKRTAASLAAKTHGTKTTPKRHLRLAGGQVWEDLTLEEWPENDFRLFC

GDLGNEVSDELLAHSFAKYP

>contig59270 Frame-1F

MGNFGYRASSHPTITHLRCGLAGRPSIGWLLVCFLAYLRRCVIVPP

>contig59519 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70038.1|) 2e-17

MDRNSDSDKLRPLLIEWPARMKLSSQVTQMLPSSRAQSCVELVSSCKKMLLQQWKPRKDF

IANLRQYVI

>contig01351 Frame-0R|Blast-unnamed protein product [Arabidopsis thaliana](dbj|BAA97098.1|) 8e-27

MARKRRRSESFEAGNDDGLKRLAAFNARVFDLPQDNDTFDDLEPPTVMLKSKHKKLKLKR

ADTDGGDLVPVIKLRKKKSTKATKKEIVAAIPVEKTKERARPVVVKASSRTNDDVPQEKM

KTKKEKTNKVKKAVVKDEKEGMEKVRETKAKKEKKEDTEVMANVATIKEKVRAIEEKKKR

KREKKEKKMIKNEGDTKIQEGTKEKLVERKTTKKEKKKTKKEKVEKEAKVRDITEKEKKE

KKEKKNEANTKQTKATKETKKETADLKTIEIKSPKTKEKKKAETKQMQKKSKTTMKSTLS

QSVRSVPKETKIDHEKIKQRTTVENGMPPPETHNVVVESLSSAGILEERADVSTPPLNAV

HLNGLSSGEGRVENKRAKK

>contig04121 Frame-2R

MVFKKCRAPPLLFNLVFGESVLNDAVAIVIFSLFQELVDSGDTDVDAKVCLSMMFRLLCI

FVGSVALSGTICFSSAYFLRHSDPALRQYPIYEMSIILLSCYASYLAADLFELSGLLAVF

FSGVFIRHYHMYNVSKATAFAFKQLLSTIAFLAENFIYLYLGLSVFAYRDSFVWDWRFIF

VNFGVCLLTRALNTFPLCAIANIGRSEQQKIYFKYQIVIWFSGLRGAIAFALVLNMSTKN

PVHAAILKSSTLFLVLFTTIIFGAATGPLLRYLRLLKDLPSRQEIASSNDNNSDEAGERQ

FLLRSSLSPSMPQSVHSRWVDIDEKYLKPIFGGNPRWKRNTNFAEMEMESTIPSA

>contig06509 Frame-2R

MLRLKQTDNNVNTTSLSKAVPYLCTKVYQKCWRLYNWQVFRLIIEDPISERRLRSALCAF

AAHFK

>contig07586 Frame-2F

MWNRPHLLVLDEPTNYLDRAALGALADGIRQYAGGVIMISHSEEFYNSLCTEKWLVESGR

LTIIGEAQEKEYRAGGGRKVIDDEPEDEKKSSNVNTSMKRTKLTNPKTLRPLSKQQIRKL

SKLCKAAGVSFDDFVDSLTRESPEWKWL

>contig08222 Frame-2F

MAHAWTQQSLLLGVLLLAPTCTAFMPISNALQRARWNLTASQTQWIDPDTDPQFYNISVP

NGPYNFGGNASFNSEYTLIFSDEFNSSKRTFDAGFDSKWTAVNIRDTTNMGQHYFLPQAV

QVDKGNLIITTSKPKKRYRGTKYVSGSVQTWNKFCYTGGYVEVRAILPGKWGIPGTWPAI

WIMGNIGRAPFLGSQDGTWPWSFDVCAPYVEKAEKVKQKINACGNITNKHDKESYPENYG

LNPFQGRGATEIDVIEAQIRARDEPAFISTSLQIRPSLYDDMRPASESLPRPGQWYQGLK

FGEFTRINSDYYGEMGLDSISALTGLESNAFKSYHLYRLDWSPGPEGYIRWWMDNAFLFE

IPGSALNRWVGAVPPRLIPVEPSYLILSTAVSEKFSPPCEGQICNSLWPSNFTIDYVRVY

QGNPNRYTSIGCNPEAYPTSEWIYTHPVEYGLPWYVSFRIDIGLLQLFAVVNAIVGLFMA

FRGTYHPKMMSAYASTLWLSASIYGVLTLSAPSDLAWVQTALACLCGVVLGGLSCLLYPI

SLGAMLGLYGGVMISQFVPLLSTRVITAVLVCVGIAMGSTPLLDIKHVVILSTSWLGSLA

FLMSVSLWASKGDIAENAWTLAGFIFSGSTMDDVGFCSEHCLTMYLVLLILSLVSTTYGY

SHMRGVTLHNDMITARKAKFSPVSASSDARSWKSHDEDGSGLDKNRINFFSPSKLPDNMQ

QFSTIFRIAVNVQRSFGFQLDNFRNQTEHIVVLLANNTRNGGNSYRKLHDLIFSNYSNWC

SKLGIKPLHWSEKRTPQGGLTSVDEISVDLCLFFFIWGEASNLRHSPEFLCFLFHKMKEE

FPSARHTEREAGHFLDTVVTPVYGVLEGEMTSQHDHEDRHNYDDFNEFFWTKSCLNYDYK

HEEVIDLSSPSPALIYKQRKNEGKQVLGSNGNRSGPSGLSTGSQLLNKNKSIAEGFTDSA

KTFVEKRTWLLPLRAFNRIFNFHVISFHFLAVLAFANTQEMVFPDSCKIISSTLITPFVL

EILRDGLDIFAVYDVHQKVFSTTRTAMRVLLHLFLAVVTSMLYWRAWTFGGLWWQSYYSI

AVLVNVPGLVNCIMQVMPGFTNWTRRTKFFPVALIRDIVSPMNRLYVGDNVLDPESKSVG

YQLFWTSLLAWKLYFSYKFEIYPLVVPSFLLYADHLENNVSMITTVFLIFLNWMPFFLVF

CVDITIWNSIWMAVTGTFVGFSSRIGEIRNFSRVRSAFSRAVDAFNTKIIARSSKTGLQI

AESSSISYGSTVGHEVLDRVPGGADATSQLLSQRRTSIHDDETPLLSFSRRKQTPMERQA

ARRRKWHSFSVAWDTVIDSMRADDLISNKEKDLLHFHRLDGYHREIYLPQFQLAGSFEKF

TSNILDIYSSNDGKVSERVLQDKLLEILSDNPMIEESLEEIWELANWVLVNVLGPCHAND

VKHITSVLNSWAVRGVFRALNLQKIANCGRALASLVHLLKSNIRVWKSNAKVVPVRKDPS

DYASFEFPQRSSSYRPPPSGLIKSASTTGLSSLGIEPPRRSRGSGVARIARMQQQTHKPA

GKAIHSIPSANIMQIRERVRAFLNLVKEILAHVYEQDPVHAESKEISDRLTWILTQERGF

MWDDSYTSEQITLTAFERHTDVVLSHLHGLLTLQKIDAEPQSYDARRRLLFFVNSLFMDM

PLSPLLEEMKSWSVMTPFYAEDVVYSRKDLESKQDGLDVHTLLFLQTLYKRDWENFLERV

KPKKNIWKDPETAIELRMWASLRGQTLSRTVQGMMYGEAAIRLLAEIEQVPQQKVEELIN

TKFTYVVACQIYGRQKKNNDPKASDIEFLLHRFPNLRVTYIDEVRVNYQKEQSYFSVLIK

GGEELGTVHEIYRVRLPGNPILGEGKPENQNAAVVFTRGENLQTIDMNQDGYLEEGLKMR

NLLEEFDKGTADRPYTIVGIPEHIFTGSVSSLANYMALQETSFVTLSQRTLARPLRMRLH

YGHPDVFNKLFFITRGGISKASKGINLSEDIFAGYNNCMRGGSVVFPEYTKCGKGRDVGM

QQIYKFEAKLAQGAAEQSLSRDVYRISQRLDFFKLLSFYYNHVGFYLSMSVIIWTVFILL

YCNLLRALLSLEGGGGRDPVMLSKLQLMLGSVAFFTTAPLLATISVERGFKSALNEIIVL

FVTGGPLFFLFHIGTKWFYFGQTIFAGGAKYRATGRGFVTKHSSFDELYRFYASSHLYAA

VEIAFGLTLYYKFTIGFQFFELTWSLWLVFISWYWSPFWFNPLAFEWSDVVEDFRLWFKW

MRGDGGNPEQSWAAWFKEENAYFSTLRPWSKACITMKGGLYAFIALSISSTSDEYHSILT

ESTWLPLVICCSLAAVYLSAESVFFTSSRHGENGLVRFLKLLLALMLSSCLIIAFVYVDG

MWQTLLSMGYLAAAVGCWALLVLGSNSPFVGTLYFVHDAVLGLVSLSLVLLLAALYVPGK

IQTWLLYNNALSRGVVIEDILRANSSNDDRDDDLSVQQMRSIIIEQQRFISALTASSSET

DITAADVGKDGDLMHAMSDNALSAVLRNMSESELSALQNSSSRLQAIMSEEERKVAQRLK

QQEEQRLAGASSLSHTRRAFSTNDFSSIASNANPTQDATRNGTSTN

>contig10964 Frame-2F

MSTSAAAATVTATSDDMLPATKRQKNVREVPAFPRIEDGSKDGMVEVHNTEHKGGNDQKM

YPNMALTLQKDSSWILSDVDSFGNLGPIPSINAVLEKRISSQFSISSLLPSSQIALPTEN

LTDYTEATTDNEGQGPAVIKLRSDGPGDTTKYRNLLKGDLMYPDDVKPMSFYEKQRLVQK

ITMLPSQYLRGLMDVISKYQPDTVRQIDDDGYAFDLGQMNENTVWAISDYVKESMIELDG

YIKSLHPSENVNLSIEQARQEGPFMTATTAKDNITISTLAKHSSDSLTLLTPSKLSAITT

NENQNKFLEQVELYSKPKVTKSRVKPSKKHECPTCNKQFRGRSELQNHIRTHTGEKPLKC

SYAGCTKRYAHSSNLRAHERTHAGIKPYTCHYDGCGKSFAHSVSLKEHIWMHAGFQPYVC

P

>contig12210 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60650.1|) 1e-79

MANRNAQELAENVLSLYDVSTDRDATIAKYYMSDAVFTDPIVVVRGIDNIQAQFRILSKF

IKSSKATLVRGSMAGASVLTIDSSMVYRLKPFPSVMKIVLRVFSVLELKNGRIASHTDHY

DFYSVLSNIPFVAFFYGQFRPMFGATSSAVIKRLVPPHTKKAISATSAVASG

>contig14663 Frame-1R

MRVSFKYYNIEACSIAVQVIDCYGLNYLLLN

>contig17868 Frame-1F

MNQSPSRRRSLSRGRRLHSHNRRFIKRSRSLTNRNSRSNSSNCDRCSKSVERHVAKHEKY

VKTKKKEKLHEKRSKRKKQHESAPTVKATVTTMAVQKVSNDVSKQTTSLMPVDARNFFEQ

LQRQEAAKMPVGTVHARGLPAPVSSTALSSLDKWECSKAGCGHLNFKHAPACNKCGAMKR

MTEWR

>contig18403 Frame-2F|Blast-aspartyl protease family A01B, putative [Phytophthora infestans T30-4](gb|EEY59472.1|) 2e-06

MMRVASFSKAPIEIGCIYNQSLLHQQLDGNMGLLQVGSFANVLLTGTLSYHKSQQVTILC

NLWFLLQNEVLISLRSSCCFVAVKNKFYRETKLFSSELKGTVLRASIREGHDIKY

>contig18494 Frame-0F

MKEVLDRQLQQCCETSVTMVTTALLRIVKHCVLLLQTHVVHKDLLTQTGLAYCLLLRILL

ELTARSSYDATQLLLQAAYLEMRSISTACLNNYVQRHVETDMASFGGLSRLAVYRGLLTS

LTNESIAVPAENFGINVNSSSKTSVLNTILSKVQQYCEHESHTTRLFAFQVLEAILRRAV

LILQTKALEYAQDLPLISVSTLTTITTSVLLNWEHPSKKLNQFMATVFAYIVDYQVLSSG

FKDWSNVLLPRVVELPPTSRAKYGSLALLVDQAGAQQVLQACPALLSTLLAAVGQKDYAA

PAAANLFAQILDNLAQHQRNQRDKLTSSITDNDSVAAWRHLWLSDVIQVLFSPDANLRAR

VAMYVIPLLLKKDSACVPILLQRLRNQATNASDRDIALWAELEVLKLARKKMAPEKLLDV

SAHAIELGLCHADGKIRATAFDALCASLKSTSLPTDKELQLIKGYLVINGKEVDPAGRMN

TLIGLKTVLIRINETIRLARKNQTTSVIPYNRSNSRNELETAKSFQHWVELFIVASIYPG

ALPQRITLGLELFLLYVQLFGLMRQTTESSFPSLLYTKHTVTTLFHMLTSAWDSIRSLSF

TILDLFPDDLPGYATRQELSNLLTWTIGLCGSPRQRESDAGAIFIRLLFQKCRVAIHRFQ

LSFQPSFELQNGALKTRSANPDIAFVLQLTDMILYRIKALNPVELQQGASPLVHGFLLAL

HYILDNLAFDPLTTNDASDWPHAIAQVFHAVHESMRVSLAVVGDATCGVGDQELSASFAG

VVGEVSTVAKTTSSALRVDCRGHL

>contig19101 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56930.1|) 5e-54

MEFVVPCCVPPLERTRVLRARSCVVRTIQRFSTTQHYETTGVNFMGWTDKRKYDAHTRCL

QYGFTKKFWYADPQVLLEKTWAIFMDGYKLEKVAFDASVSNRYEVLQQMKDDWRIVRRDH

WIPRIAMTLASVQLIFRLQTHTGYLLGLRTIAVPEIQEALEPHEYFYETFH

>contig19710 Frame-2F

MTRKNKQQQLEATQTLPAVKASSHTSSTSSDSAPEVADTAASLHPPLELKLSSPLNPASK

MSSSNQSPGIQKKVADIMNGTIHIKVLSARNLPTMDFGKRQDPVVLVQLDDSVPKSWAIT

DPAFRGGSNPEWTERNNNELELFYDANLFRDKAATLTFEVYSDESGDTLIGSGRFDANSV

LNIQSGDRKTSTIHLNEPSRTTSNRGELDVEMWFGPPVRKAFRAAGRAYKLLEARDTFVN

TLRSVISTVFVAISNLFQRPKEFARKHRKLSATLTGLLGLMAAGALAVFVVVAVPTTLVA

FFTFPFWIIPFLTTSFFTAPLWVPIFLLIGLFLLVVATFVFGLGITSNVVRRKCAFILNK

IKHSDVGKRVIYEKSL

>contig20116 Frame-0F

MERRVAAFAAVSRASVTLLAVSTSAIVTPYDTSSHLQSNFVLAPFSNWDGVFFSHIALHG

YDFEHFHAFFPLYPLLVRWLARFIPMEDSTAILTSGWLISNASFVLAALFLYRLGCVVLG

DKDTALRAAYLFCVAPSSIFMSALYSESLMCLLSFSGMYFLARHAQATKTSRSFLDLTLC

ALLFGAASATRSNGVLLSLFIAWHRVKNSPSPKALFIFVGFWFRTALLGLLATAPQLIYF

ITSMVSYCPSLAQRFGIKESKSEMADRSWCAGAATNWTAMYTFIQSEYWNVGLFQYYELK

QLPNFILAAPVIILSLHALYGFFRGGVVPNRVLQRENALGGWKRDALSLYYVHWLFLLVN

ALLVVHIQVTTRLLCACPPLFWHPAALMSECNAKIKTSSILTSYGRLVVGYFLLYTVVGS

VLFSSFYPWT

>contig21933-1 Frame-0R1

MDLPYVVKDTVKRTDGYGSNTQSSSMYSFEKEIPA

>contig21933-2 Frame-1R2

MWSKIQLNEQMVMAVIPKAAACTALKKRSQL

>contig22129-2 Frame-1R2

MALTNLFRPSFDGIMGWVVASVAPKRRSTNRSRNPFTLA

>contig22613 Frame-1R

MRCAFRSLGRKKRATYSFIEYATWKPLRSALFLLFVALTANVIIARSCIDRIAFTVLILF

YQKPR

>contig22684 Frame-2F

MISPDSSNLPRVSKRKCHSTQMLQAKAGKRQELEAV

>contig23153 Frame-2F

MADKKQTSLPLPKLSNEPVFVGSSPSNGEYVTVLTPDNKALAPNRMGPDFDPNGLRMNVW

TVNLNDADLRTAYFWWVCCCPCLPLSQLETRLGLNSFCQGFLIDLVAYAGRLVFLLLTVV

ALFKGYLVAFAGFLMLTVVCVIAVGQRVARVRSQIRERLDIGGSRKDDRVTGCVRSASAI

RQMAVQLKCDQLHFSAPATLQAYQV

>contig25384 Frame-1R

MKKMIPNATIASRIASDNYAP

>contig28093 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55912.1|) 4e-75

MTSYGRCIENLTAVELFIYARAFCRFRLLKFEVDEEKEKVKSLAERVLAVESRRSKERKV

AWELTRAFTLFCPEYSILRRGLRFSTTNAVLMDEAQIEDESSFELISILRRLSKCFQKII

VVSLLRNSLEDCTCAKNVIVLCDGEVVRSGAWDEIIKYVQKRGVKCPSQKDLALYLRDKK

AIGALYDPQ

>contig28390 Frame-2R

MQILRFISTLVQNSDSTSPSLNLIFLHDTDYSNTTISRTLIVAQPLPCVDCSPIQTSY

>contig29076 Frame-0F|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY63532.1|) 3e-91

MVETDSGLLEVIGKDFRRLQFVFYGLVSKQTFRKFDRTFALVRMHALGEPEGKVDEFAKF

SLERFDDGNDATAGWWIYDAVEEFQRMGLSSSTCRWRLSYVNDQYNICPTYPSILAVPTS

VSDSV

>contig29595 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61579.1|) 1e-65

MKLRILTYNLFFDEVARSVRMKAVGRLVEHFRPAIVGFQEVTRDALVMLKAQHWTKFYDC

SVDTAPPFQETYFVVLFSALPVLSLETHPFENTGMGRELVLMQVELIPGRTLFVATSHLE

SLPQFAGPRIAQLKESLILLRDRVKIANNDMIETVGDKRRNTDDKGASCLGA

>contig29649 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66740.1|) 4e-21 NOT\_ORF

MKAYDTPSRIVLPHDDELKYRIHYEAHDTIFRYRCQGIFFQVLEQFGFSRAFIVMMRNLY

KATTA\*FLVNGMLSSPMEVKTGIRQGCPLPPLLFILAAETLALAITQDSKLQGIYIPGTQ

GTKHKFLACVVDSTIFRTKHGRWLG

>contig30816 Frame-2R

MAKQEQENEEDHTLDTKHSGEVAPIKAKKKNKKSKKKKSKNIPSSGSKLPPFRGVKGFTD

SYVAVGQTEPPTIPIEKLFPDGKYPEGEIQQHPGDFNTYRTTSEEIRARDREYEDLYQTV

RHAAEVHRHVRKFAQSIMKPGIKLIDMCTQLENKNRELVVEAGFARGIGFPTGCSLNHVA

AHYTPNSGDDTVLLYGDVMKVDFGTHVNGRIIDSAWTVAFNPQFDPLLEAAKAATEAGIA

NAGIDARLGEIGEAIQEVMESFEVTIEGTTYPVKTIRNLNGHSIGPYQIHAGKSVPIVKT

EDQTKMEEGEIFAIETFNTTGRGYVVEDGECSHYAKAFDAPHVPLRLPRAKKLLGHITRT

FGTLPWCRRWIEREDGGSTTINPKGAKQEKYLMALKNLVDNGIVTAYPPLVDVKGSYTAQ

YEHTIILRPTCKEVVSRGDDY

>contig30939 Frame-1F|Blast-pyruvate dehydrogenase [Phytophthora infestans T30-4](gb|EEY61206.1|) 8e-17

MEKARDIAAQEPTPLSLQQMRSFADGGAKLHIISAKFLHKELQSRFAR

>contig31583 Frame-2R

MIARYSEPEEMSRSNPTVPLSSAAFSVFNIRSITRLLNYFAIIVRVCVCVIVRLEAIKAQ

LQFENLRSLKNDGDRITFLKLT

>contig32476 Frame-0R|Blast-4-aminobutyrate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY58016.1|) 1e-85

MGKQHLTKGIGRMSDMIMSQGKGSWIWTSDNRKLLDFTSGIGVTSVGHSHPKVVAAVQKQ

AALLVHAQTNIGYHQPLLDLTDKLLPVLPTSLDSLFFACSGAEAVENAVKLARQATGKQR

IIAFQGGYHGRTMGTMSLTSSKTVYSAGFGPFMPGVTVVPYPYALHGPIYDEEMHAEWCL

EQLQVALLQ

>contig32582 Frame-0F|Blast-UDP-N-acetylglucosamine transporter, putative [Phytophthora infestans T30-4](gb|EEY62540.1|) 1e-158

MGISLKHLSFVMLVLQNSALSIMSKYSRANVGPKYRPSSVVLLVEMLKFLLCTLVLLKAK

RGGLKASVRTLQNEVFADSKGLMKMTVLAFLYAMQNMFALIAYDYVDVATYQIVYQLKII

TTAMFMIVLLQRRFSIVQWCAMVALMSGVAICSYSRLPSGSHPSDEITSSKRFIGVCIML

GLSVNSGFAAAYFERVMKAHKSIQLQQTIDPLWMRNLQLSAISVGVACLDLMRNFSQVRT

NGIFYGFHPAVFVVIFLQAVGGLTIAAVVRYSDNIVKNFGTSFSLILSCIISNIIFEETA

PFSFYCGVFLVFGSVFVYGDSRFAVKPVIDRMDRRSITENLAHKIAIDTKNYTQGA

>contig33909 Frame-1F

MDVMATRQASLAVETEQEQDAPIRREPTPTTKAEISVKRRNVGVPKFLRFLFQILEVEDP

NIIAWSHDGTAFQIIHSENLANQILPRYFKHNKVSSFQRQLNYFGFKKWTKTQTNICTFS

HPFFLRMDKGRMKLIKRKERTNSAAMLGSTIQSHASDVSPPLHGHAQMEDHFDAQDLRSQ

LPTQQALKRQKSNTLSGPTVTFLNSAASGRRHSTGMLPGSEAFGMAAAAAAVAAAQRGQN

RAGTPAEQEFELELEARTEAMAQTSSPQQQFWYLHKLAETKTL

>contig35019 Frame-0F|Blast-CDP-alcohol phosphatidyltransferase, putative [Phytophthora infestans T30-4](gb|EEY67777.1|) 4e-24

MKHTSCHQKTFQLKETTSMKPVAATDDSARPQLKAKPQSYYYVTEEGVKHILEYGYSGSD

ASLLYNYVISPVAQWLVDYVLSPQLAPNAITILALSLVILSHIVMI

>contig36102 Frame-1F

MLRARVLPDILSQIMGEGITAS

>contig36199 Frame-0R

MKRSKSPLESVIHLTTNLNQRRAVLVGLKDRKLRQANNFIRERLKVLPQVTPWCEESKFE

TLDGHYVAEKMDNTLFHGVRSVRQVFEALQISFRNTEASVLENLGDITVRQGDERTASTS

FSNCRLVSMMSHGVKIEQNVVKFFNLVDSDVVADDDEKGPYGVFAINSVDVDDLYPYVPH

ERIRMDIDAAMKLTEHFCRRPPNRKTQTRTRHPLYGNGGFPYPLDPDENKDSELERVVVL

TRYFRVKLHHTEMDIPP

>contig36652 Frame-1F

MLYAANTIRGKDLNGFIKYFFVRAFVPQLLGPLVHTSTRRSINS

>contig37435 Frame-1F|Blast-Phosphatidylinositol kinase (PIK-L2) [Phytophthora infestans T30-4](gb|EEY59643.1|) 0.0

MQLFGVVNTLLANDSDTSKRNLAIQRYSVLPLSHTSGLIGWVPNCDTLHQLIRDYREARK

IQLNVEHRLMVQMAPDYDKLPLMQKVEAFKYALGETTGQDLYRVLWLKSRDSEIWLDRRR

NFTRSLAVMSMAGYILGLGDRHPSNLMLDRVSGKLVHIDFGDCFEVAMERDKYPEKIPFR

LTRMLTQAMEVSGIEGNFRYTCEASMRVLRDNRDSLMAVLEAFVYDPLINWRLLKKDAVP

SHAQPEDDRAGNVERGDGSDANIERSSVRAENEIEREIDAIGEGDATNVGDLEEDKLAAG

IIKSSNSSAPVTPRRRRHSSSEAAMLGYNMDMLDSTIARNSMADVQRDEFGSSVVAAEHP

QLNEKALSVIERVKKKLAGRDFDDGSRVLSVDAQVDRLIHQATSHENLCQLYYGWCPFW

>contig38665 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55501.1|) 3e-74

MDIKTIAAKYGGLPARVVTRAEENWRITTAKNSAVLDFFAGPVACIIVAARALDEPVDKK

RLAKCAGANIKLVEPIVRKVLNAVDIRTVIKTSPSALCIKFGCEALTEIVRHVLEEYRVY

VKQLATANQRKRSRHSLGPVAGIIDDKDPVFAAACLFAVSKKAKVRGARRKRECSC

>contig39815 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55603.1|) 5e-68 NOT\_ORF

MSSQLRFLGLEDNFLSVGGVQLVLETAAVNTTRRANYTMG\*LERGI

>contig40082 Frame-2F

MQGPPSTDSSMSSASVLLPRTMKEASKLEKGLGNVSSMSSSDQSFEDHARGIIANAEENL

SYWQGSRSFDKNVGMADDKAMKVSDTESEISPRHVRTFSQAVNEATQSIQDVSRILTRSD

EKLTTLAASEILQLKLDDPLSSNHIQVLSEDRSEAIDEFGSLNESDHKSSSPRHVSNLSL

LQGQSASTSQITLEHSETKSEGSVSPRAALRSSIQDQDSTSTLLPAAKTLLSVTDPNEEL

NIHSDSDSDQAMDALQQSIAELEKRLGIRFNDLSDDEEEDEIIEDELC

>contig41575 Frame-1F

MTEFVPSGVIEKAFLNDMIYVACPRCFTSVNGQLACNAGTDLRVQCASCQTFMTPKQVLY

KYRLKLQLLYESTVADAMLFDEVAEALLGVSAMTMKNDLLLKYPDLHLVLKELLVGLHVS

FSFQRPLPKRNSKHAHLTRDLKITKIEPLVPQLLPEPAATLAIKLLRQQQEGKHLFLTHD

RIC

>contig43102 Frame-2R

MLSSKEVPSSKEVPSTKLREPYEGFEYEDLRLELSVRNIRLSRSVQRLSNRAGFIQMLRD

WDQKHTSETSGPIHRRTSPRRTQVGMNATRSIRARRGCRFRLINVLLSPEFSKRWPEMGL

RGPRLKVNRLWQDVYAAFKTKNAALSTLQFQDALFIGVTPNVILPHSAEHLMH

>contig43443 Frame-0F

MKAQASAQNPHSTCRPQSLRHHHQCLRLQIRYSCFH

>contig44028 Frame-1R|Blast-cysteine protease family C26, putative [Phytophthora infestans T30-4](gb|EEY65931.1|) 5e-94

MGVARKIELTPEGRAHPMFEGKPSVFDAFTSHSDEITHMPRGGLTLCRNDFTAVQAVAVR

HERGDFWAVQYHPEYDLHELARLTYCRRAKLVELGFFTDFISADRYIDDLENLHIDPCRY

DIAWRLGLDADVMDANIRHCETRNFIKYLAIPYKLTMATK

>contig44514 Frame-2R

MDRLMKEQSDIVRLREELEEKKRKLESEGTKARASESFSDSSLSVTAYKPVQEEPVLSFL

PSPFAVSGASGSTWKPPPSLGSVPSPAFPPAHSTFSSSMTPYPNRSFVSFPSPPGVSRFE

SSLDVEAGISRLQRSSTSIESTLMDLQSKIDRV

>contig45269 Frame-1R

MVAEEASHAVTDAETRSDSNPLTYSSMEQYVRLQEGTRPITSVLIANNGISAVKAIRSIR

SWSYEMFANEHVVTFVVMATPEDLKANAEYIRMAEHVVEVPGGSNNHNYANVSLIIEIAE

RYNVDAVWAGWGHASENPLLPDTLAQTERKIVFIGPPGKPMRALGDKIGSTIIAQSAKVP

TIAWNGDGMEVDYKKHNGIPEQIYNAAMLRDGQHCLDECNRIGFPVMIKASEGGGGKGIR

MVREESQVFGAWEAVRGEVPGSPIFVMKLAPKSRHLEVQLLADSYGNAIALSGRDCSVQR

RHQKIVEEGPVLAPTVDVWEEMMRAATRLAKEVEYVNAGTVEYLFSEVPEENGNSFFFLE

LNPRLQVEHPVTEMITHVNLPAAQLQVAMGIPLHCIPDVRRLYNQDAFQTSAIDFVTAKQ

KPPHGHVIAARITAEDPNAGFQPTSGAIQELNFRSTPDVWGYFSVDSSGQVHEFADSQIG

HLFSWSTTREKARKNMILALKELSIRGDIHTTVEYIINMMESDDFKYNR

>contig46365 Frame-0F

MAAKNSVDLRLLPHLILPMQLRFVHKTPQAHPGSHVLVAIE

>contig47249-1 Frame-0R1

MEPCDSACTLINVSPAKVANSSTFSDREVNLTVYCLL

>contig47476 Frame-1F

MLALQRHAACTFIRRVPLFSTAAAADQEASINVLQLMLRENEGSRASRRLRKHGLLPGVL

YGEGEDGNDERVLVSLPTRSFERMHRKLWTSIENQVFQVQVDDKPPVKAYMRDVQLDPVT

DVPVAVNFLRFKPGCRVSIPITYLNEEGSPGLKRGGFINHIYHSLDCTIFTDDIPTTLQV

DVNGLHVGDRLCLEAINFSDGVVPNIPKGTLIAKIAGRRGLIPRAEAVVEDVLEENEEVV

DEEFDDWNDIF

>contig47519 Frame-2R

MSKAATLLFAHGGGFCKEIWEPIMRHLKNSLPQDVTTQFVSFDFKYHGSNRDESVEAQFD

LLNPSGPRVYHPATQLTAWTSAEVLQQTHCLRSKDVGTPLIGIGHSMGASAMWNTEVQYP

GTFGGLILFEPVYGNLNPA

>contig48525 Frame-0F

MVAKVSRLLVLGPNRDSNEAVTTSLRKLCGNIDASAKDPDATLLRIETKYYQAHVQLHVH

EVRDNAPEPALQHELDDYEAILCVVNAEKYENFLHVQSFAKQIVDILPYDVCLLVSHTSS

ATLESVKKMESWCQENGFELISLDATSDDRSVIDEKRGVSRVLEALQCTMWRSMKRNFPS

KTERGAILCEKEESNRNNVVTKTLANTKLVDDDAFVDTLEQEMSGDGVLKGGEGDDIDLD

QLSAFISEVRTVRDHGAFLSDEKRRERAAEVALKLWNVLGIDDGGDSDDERDTI

>contig50696 Frame-0R|Blast-MMP37-like protein [Phytophthora infestans T30-4](gb|EEY55529.1|) 5e-53

MHKPVKILATNDMIQKASSVNLSHALNYALLCLPEKFSEHDLYMKIAGISYMGDFRMKFG

ENPKKVRNIVDGNLNLFQKLYQHKV

>contig50757 Frame-2F

MFSSSVRAHPIDEVHPLLNTNSPPRTQSISTYRVSQWGVLAIVSILLFSAAYFGVHGPSE

STLRSAKTLSTEAKFDLFQPIFHAEAPPQKLFNHTDAHKNLLPPRFLAPDLVGTRP

>contig50982 Frame-1F

MIPRPYQRTLVAVAILKSTWKLVHAQEIPLEDTIMIDEDEKNSAPALGGAGMLTSADSLV

ENRTAEALVLVLATRSPTITSTPTQAVVSDEIKTMSVSPNVMPTLNSNNATDFKEVATPA

QATTPLNAEPNTADVRIKLPTQQPVDNITMPFLRKNDPAKMSDAAMNGAAEKPITGKMIQ

GSKAIALVAMIAICCIFLLLWRRKRRSSAASSLGALEYSKGSKLRYTQVPDKTPLSNCRV

DDAEFCDVDEEDSFANDCSWDDWEGHSTQTQTSQLNPFASASRAPSLTPLRRAHMSACSS

NLTQTLSSEVASAGERQLLPMNVEFDSSIDSFEVLPAEVHVSPTSDRGDVTVSEKEGDSV

DDLFSQFGMVPTFKTNAVVNASPADRSVTSAHLVDSGATPLSASSLPTAANASVMFAAEM

DDDMNTEDEWGEDDEWVKGI

>contig52661 Frame-2F

MLLSCCLANFTCQPLILPRLMNRSSCRSG

>contig53554 Frame-2R

MKCIQDKSSNSEKDFDRLLKQRENDIQAKEVEIASIIKQLQDVNARAHASESAKITLENE

LATVRVSLQRTQLSLSNTTSLTPSVAHFSAT

>contig54054 Frame-2F

MADMILSMPQPYYDTIKAYADFSPFVCTVYFSLIESFMFMHYTQRMTSLDILFILRKLTR

STPR

>contig54120 Frame-0F

MDELVRELESDAHLRVFLRADCNVSAIASAVIARGSTSEPRTSSLSVDDDIHELRESDEF

VKCLD

>contig55255 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66837.1|) 2e-14

MTSVNGSSIQEAYALMATLLAPRVPVRYLELCSMLLQPRQMQEIFEERASAKRCA

>contig56236 Frame-0F

MRFVTRVSGLLMMLVFALAVVYTYWNELPLVRKTLQLSYEHHVLSPEREALSKNVTVYRN

GYSTGGVEIQLSAQVLASRTKKGELAAYLSQFVEVEGLDETMNDSEEEMERVVFTVVADR

VYNGQGALVHGYTDLQFGDRLYLVAPNLHFMWPFVKLGHRVLVTSTFSPIKEPVIIESMS

ESPRTFRLHNFFTHEEADTLIKQTLLIDDPYDRLQPSSVGATMDRQITSKHRTSENAFDT

MSTTAMSIRKRVFDVLSLGTYQDDMCDGLQLLRYHQKQAYIPHYDYFPINLTENFNFNPH

RGGSNRFATVVLYLSNVPLGGQTV

>contig57998 Frame-1F

MHTIQICRPVSVDSDNTQGCVC

>contig58168 Frame-1F|Blast-nucleolar protein, putative [Phytophthora infestans T30-4](gb|EEY63521.1|) 4e-29

MGVMHSDRQGDSDRQAFADKLKNALKMVLGNAMGMLDAASDQMAKNFLMDRLPPALEDDE

ENCT

>contig58638 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60832.1|) 3e-49

MKAGYKWFTYLMPSSYSLSALVGVLFGEVQDVISVTSNGTTTEMTVAQYIENTYDFRPNR

KYNFMVGLLVIWAFLQLAIYLTFKYVSHLKR

>contig59022 Frame-2F

MDNLLERLFGNKFKKLAHNAITGPTDCPAFEAALDLVVYHWLRRQKSSEITILISDMLQD

DKLSKNFMALIQREKEWLAKLNYYA

>contig59057 Frame-1F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY67180.1|) 3e-25

MAAKYDSKKMHVTETGWPSSGEPYEENSPSIEGMQKFLNDFVNWSFDHPKTYWFMMYDT

>contig06207 Frame-1R

MRALFEPSGAFSGLFYPSAFFKSTLSRVYVVPMTRTESATDLATLLRQKYSKLSHTAIVA

MRQLCLFCSSNHVTKS

>contig08894 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70430.1|) 0.0

MSELYQEAASLLKKLERHQGGLKSLAYSDSTLHKRSSFALVCETLRYKPLLCQLLSAVPD

CRKSLKSAKTSNEPPALVFVTLYDLLFGRQKIQGGGYVKKALVQHQTSLRAALARLKIKR

KVVCNEALLPPGNRQKHLALPRYVRVNTLLALPEEVESFKLEYDAKLDQDVRDLLVLPTG

TELHEHEMVTSGKLILQDKASCFPAFVLHAEHADAEGNQGDVIDACAAPGNKTSHLAMLL

QQLDSNGGDDTIPKRRVFAFDRSAKRLELLKRRMKLAGASNRVQVELRSFLEVHVDDEMF

RNVRSILLDPSCSGSGMTNRPDHLFNVASLHDTVLKPDLAAEYENDSSKRLQLLADFQLK

ALRKAFSFSQVERVVYSTCSIFQKENEEVVAAALRSEENVTATRPFVLRPALTSWPRRGI

QVDGLTAEEAKALLRANGMEDSTNGFFVAYFERSSRKYGDTAESKVKNASRETVVAEALS

QPNSSTLQCENPQLSKKRKILSATQKENRKRRKRGKRKKHGVAKTGTDYGSNLNK

>contig10510 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70673.1|) 4e-76

MFYPGNLNVSSCCSKPICSECYLQIRPPQKPICCPFCNQEAFGVQYAQPPPAEMAFLRLI

KKAKSPRRSSVIGIPKRAVPLPAASSLQSVHYASVEDRDRIRDSLRSQLSISDKPVTDSP

HPNNI

>contig13249 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67780.1|) 2e-21

MTGIERYGSSGAHTVEGNAAGSRAARLTKQREKQQKEYEAKRQDIETTNRRGMRIDANFQ

T

>contig14132 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY61080.1|) 1e-121

MGTPTKRTERVLSDAADKVAKAEESARQYEAQLAEAAAKKQHLEDENEKLRASILNMALQ

NASVDLRREHVQLRQTLDSYQSKIDQMREISLLTAKVVDSRIKTKQGRQYVEYKLQIETD

IRGTLVLWHRYSTFLNLAATLKAKNPSSVHDIPELQTQSLTGFFSDQLIIDRIAKLNEFL

DVVTKADEFQWGIRIDKDTCVYKRKSKRVDRSYSIDSRESISTLTPSMRDSMFMPPSSRA

TTISMDSY

>contig14833 Frame-1F

MVITAYYRRWKTSDEALKDLNLMDINITLGGLNGRWFAHWIEFVFKSEKSLDPINHVIVF

AKTNYSEQEIAVLLQSAIENAPTIIVKEMVEKILVEYIKQTPTNNVLAGLGLDQAGDNLF

STPNILYWI

>contig15557 Frame-2R

MTCLVVSGVKRIFIKYACHPSRSSSAARTNTHYSDYVAACKTSITAVPQLVRLHKKNSF

>contig17740 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57614.1|) 1e-20

MWLLFVIKITVKFVCDTLVNFVI

>contig18187 Frame-2F

MIPHDLNDGALGTVPVYLYYSLSILGG

>contig21280 Frame-0F|Blast-P-3 complex subunit mu, putative [Phytophthora infestans T30-4](gb|EEY67762.1|) 0.0

MKDNFSTVYQLLEEMLDNGYPLTTEPNALKAMVAPPSTTNRIAAMVSGKSRVSNTLPDGA

ISNIPWRKSGVRYTQNEIYFDIVEEIDAIIDVSGRMISCEVNGVIQSNSRLSGVPDLTMV

FTDPSVIDDCSFHPCVRYSRYERERVISFVPPDGQFELMQYRVQIQELVPPVYCQPQITY

KENGCGTLDLVIGTRGTPTLSSNAKKNFVVEDVTVEVSFPKSVRTVDVNTEYGTCLFDEA

SKSVKWNVGKLGKKGLNPSLRGNILLHQSASAPDEKPVVVLGFKVPMATVSGLNVETLLI

TNEKYKPYKGVRTMTKAGRFQIRT

>contig21491 Frame-1R

MDKDVIKEEIEEETKGKENEHSGIKILQETVLEFEFAPNLPILRARELALEWTKDAFGSK

AEDDITGVSIWSAALILSRWILDHRDVFNHKQVCELGSGCGVSGLAIYLYTNASRVVLSD

LFATTVANLKYNVALNSPRFQTTQATTTTQDVRLDCCGRCGAIQRFTVENPNGKLLTCGG

CKAIVYCSRACQKKAWKQHKSECQTIQAQRQVIETCQQGNVHVQAIDWAHRETWSIKCEH

DRYDVLIGSDLVYHQAMVPILVHVVDGMLAKTGQFLHIASQARHSLLEFENAMTARGFLC

HVDQVPEKYKTNPLRGTDAAAELFALHFNEMSDQYCIYTFTRTMEE

>contig21792 Frame-0R

MISALAWVPRGASRRIPEKLKLTDEELRMLHEAAVEEEAEDQSDMATEDVYKLESPLDHH

VDSQDGLPASFKMDEYEQEDDNAAIQNFYGGDATEATEEEEVETDQPDEDGNISMDDDDD

RDDEFDREDVEVRPTDSVILVANTEEDFSTLEVQVYDDENGALYVHHEINLPAFPLCLAW

MDCAPVPLNPVTGPLDGSYVAVGTFKPGIEIWNLDILDVLEPTATLGGEDDRGLRNVAVP

GPMTSLKRNSKLVLKKASHQDSVMSLDWNRNHRNMLVSGSADATVKVWDVTTQKCLYTIT

HHCHKVQSVRWNPIETSVVASASFDRTIVVLDGRQPDAFSTFSLTAEVESIAWAPHCPST

IVAASEDGMVVAYDVRMNHSEPLFRLEAHHGAVSAISFSAQVPGLFATAGVDKCVKLWDV

MENVPKCVASKEMNVGELFALSF

>contig21932 Frame-1F

MQSFLSSDVIEALERRSSTVTSFLSNSTLSESEQCSYSSENSFSSCMCSAMLVDMDSSGS

VADAAKKELRASNEVNGVITKDDTTTTGTVVAATSKSVAGVTVAITGIAAIASTAIGGVS

SAGASVAAAGSTMAITTVEICQFGVLINQLQLEGKSSALAQFGKAMAPAAFTFLPIGKLS

DSNSDSSTSDSKTSTVFDRRLEESDISGSESSRDSAQLTGIETYSRQLNIQEDMLFVVTL

AGVISVMAGVVGLFGVGYMLSGVVMPREEYLTKFFDKMIGFEVLVAILSQYTIGVTATFQ

IYYSTKYESITDPKCLLAIAAILFLAGGILVYGYYVIKKHEADITDVGTLQHTKKTVNMR

YGPLYEEYKFKNRYFFAAKMMLALTTGMVTGYASMSGKAQVAIILALNVLFFFYLEIQSP

HHSKFVQTTTSFVSVMKIAVLVLTFFLVTAASSDGFPTSLQNGISVAIVGLNLFVLALLM

IRSLYMFWQKMKLQRDAAYDHEEQTAQEYFNDESPARQKNIGISNAYPSNQPLQFQHANM

NKINSPYVQGNATGDYNSVDEIRLRSTTHEKDGRQQTYDSSRQSAVNHYNTQDRNIYGHH

RNDVVEL

>contig23152 Frame-1F

MVEIVKEMLLECTTREPESASRTVRQLVALATHSKILVQICDESLQWIITQELVLSLAIK

WQQLPQSSRVTAISGELVGLLTSRSAELLNAGFQLILLLQNLIFAQMSSSFAASVASFHE

QVLAFARSETSKTFVQSMAQYLPYICQHSIQLLHEVTR

>contig24034 Frame-0R

MPPNPQRSNFLSRDVMPSIQQPASPKATTYEQSVKPIRKLTSTPRSGSIHFRSTDLDDAN

AIEKTASEFYSDDLFKDLNITVFPADADGLISKQIFQMLDILDFSPSWDSINGGAKILIC

LAAKLCETLSEKTMAFFVQFGPNRVKAEKITESMLRCTAPESIKIGSVDMFVCIRGKLQE

CIQVSRKKHFTYRSIRQISHSLVSGTAEDKLKFRGEILNFSDDTAPGSAKNGKRSRSPTR

LLQNLIMKQSEGKLLETSRFLSTFVESDLDERQCKIRVVERLSEFHQAVRDKTTEHREKD

YPFSSISTGISGERSIHSKKLVKSAAPKKNSSSNSSTSPTSPESRDQFSLSTKTSALLSS

LEASTILDDCTIEALSDNDLEQLSEKLLERLVCQLVTVAHTSEELLEELNSLDETGLSLL

HYVSFYNYSKLVPVLAAHGAHINQQSTQGQTALHLAAGCGHDKVVNELLQSGADLQVRDF

DGLTAADCAGLSGHIEVAAKLHICIGYDVFGGEPSATD

>contig25312 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57605.1|) 1e-169

MAHGGKVVKNTAGKQSVRANKKVNKQASKQSRKVTSVAKPKRLKAHVQRAIKAKEPKLVE

NTKNLLVMRGNKTSEEVNEMLRDLRMIKAPFAKFMGKKNDIHVFDDENKVEFLTQKNDAS

LFIVGSHTKKRPNNIVLGRTFDGHILDVIELCFSNFKSIRAFKCKSKKAPGSKPSFVFTG

DLWESVNAFSKLKNILLDTFRGTIVQSVNVKGLDHVIICTAWKTKVFFRSYSIDFKKGDE

SHPRVELDEMGPRFDLEFRRTKFASGDLMKVATKKPKGLVPKKIKNITRDDLTSNKLGQI

HMDHQDIYSMQSRRVKALRKTPADLDKANANVAEGGPKNNE

>contig25385-0 Frame-1F0

MANSVAINGITSIQSKYLEHMWGEFSKNLGWVQTFLIKDASN

>contig25727 Frame-2R|Blast-Heat shock protein 70 [Ectocarpus siliculosus](emb|CBJ33898.1|) 4e-20 NOT\_ORF

MTKLFARV\*TISIRKSPRLSTYADNQPGELIQVFEGEHSMTRDNHLMGTFKLDGIPP

>contig26906 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64337.1|) 0.0

MNPSTFGDLRLLPDDYHRQVAKELAAFFHIFYRFGGVSNRFDLNDAVYVDFLKNILVGSM

CIGAVVFLVLCVIVVRRTILHIRSAAAQRTSMTTSSMELLAVGMLTFLAISALGGLLGEG

QVDYSAGVVFDTMMNTSELFKHTRELTEQNLQTSNAVRFHADHLITTFNDTELPADAFKM

SVEAMRLVHASKDLWHQSDTLLPKNYSEIVQDLEFRYFLLKSSTNGAILAVALASLLSIA

SIGWALVSPLRVSMFILLSVIPISHTLVGAYLASTIMTADFCAAPINSTLEIIGTAPLAS

YYVECPANASMPFGNAVVSVGETASRVMVLQRELELNATHQGEIGRRMKIEFLDPIGKQL

NSLDTFLSNFASLQTCTNVSNAFEVATTTFCEFGMLGFFSMWVHQIMLCLILFVSVVVSV

LVYERVHMREVNPDIHYQLIPSYEEDGMEHVYLSSD

>contig28580 Frame-0F

MNAEELAHRVTVDGFVTLPLATYGFSPTVVEKVRCQVLNQFEMFLAEASAQKLDLTLDEN

AERLPGFYVREGGRIDMQLYISDFTKTPSPAQTLQSVDIKLLQNTATAWQSVLQELFCQA

NFHLDYIGCVISRPGDSEQNWHLDGVHYNRHIQEP

>contig28733 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69161.1|) 1e-27

MKKSKQLNESIEGDRNADSKSIAPVRDSASNALDYSKELFSLARHTIGETAELAWGGAKT

FAAPVFDVFNRADGEEGTELRNYIGLARKSLNARVFAAQVQWKNSKEIADAHLVPVKSVL

NAAQQ

>contig29594 Frame-2F

MIDPFRVLNEYVHVRECLLTKKTIRLTVIHESVIQETALMNLSIGRSLSSCTGSMSNIID

QFADMFDGERATSLQMTTLGDEWERPSMDRNSSLPSGIIQQPFTVRVRRVLNIPRTTSVR

KRSSEEAIVSQIPLMSSSVLVRLELYDGGQLLDNAVIDTVDVRLKAQRNDLLHAEWEDPA

WHKFNIDICNVTRTMRVQLTVLGVKKVLGGSLSNLDASEEKMLVTGVNAFEVDNTLVQGL

HYVHMYNNLHSCIEGPVPHVALPSEPMIQIEFTKFDAPIKFDWSDDDDLSATDRAHRRSI

ITNSRSVMLRKEGWLQKVGNFSSLTRWRRRWFVVDQSTCTLSYADDETAPRKLITLRNCS

ITTADDMNQKFTTAPVNKGTRKLRQTWCFKVRPMGSSRDYIISTETKQEREEWMLAIQTV

AKGEAINSDFNSSLGNYDDASLSNPLLECHPAEETSDQLDGRNILESVAQERRDSTSRSS

RHSSYQCELLELRKLILLDPLYRFSPYQKEQLWMHREEFIDIPSALPRILSCVHWDDRDE

CDEALKLLPRWSVPDHQAAYIELLNGEFAHEGVRTFAVKKLSQMADTTFSYFLPQLVQAI

KFENHHVSPLAMLLIERAIKNPNQIGFDLFWSMKVEAHNAQYRERYGTILNAYLDVCSSK

MRAILKLQDKLFSEGGMLERICQSVKAKRRDGAAEMKRAMQQGLEALNELLPGSFQLPLD

PRIEVGKIIVSKCRVMDSAKKPLWLVFENAEEGGDPVTVMFKAGDDVRQDCLTLQLIRLM

DEMWRDEGLDLAMEPYKCVATSPMTGILQMVPNSVTTAEVHRRDGMMGTFKDPSFSDWIR

ANNPDPRSHKAAVDLFSRSCAGYCVATCVLGIGDRHNDNIMIASSGRYFHIDFGHFLGHL

KYYKLGIRRERTPFVFTNEMAYVLGGVEGKDFAKFVDTACTAYCVLRRHMHLLVSLLLLM

VPADMPELTGRDDINHIVTTLAPEVSDERARESFEQTIHFCLDSRFKRFDNYLHNIAHAF

G

>contig29648 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65208.1|) 2e-85

MAIATLFYIDLTRISGMLSEYIETICGPTQLVGEIDDGTVPDTLGLRIVGDIFKGSSTSW

KRKGDGVVVITFVSNDTKNVAVNILSGGDKFDEKDVPAGKIVTWISSVEELGGKTLYLDR

WRAGFLGLPSNNGGSLKLWVPRASEGGHLEITVHLNKS

>contig31331 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53199.1|) 1e-136

MSAIETDLARRDSQLFDHFTRYQVTSETYAWTLLKTVFTEVLSENEWMCVWDHFFAYSDT

PQLIYVAVLAYLSYYRTALLAACDRISIEQFFHQQNAIDIQKFVRLVMKLREKVNLKEFT

LSGGLDQPKSEFKNYRPLPKGLYPAYAHYPQSAVEFLINER

>contig32477 Frame-0F

MSRRFTRKGTNSQAAKRWIADELEIMKAFPTAGGISPIDTMTNKHKMRVLGEIFPSVVTD

VRQDVLVAANYREELAAVMLGDIMREMPTASLHKNMEILYEGLHAEDDGALELVDEEDWS

DIPAFSKGTDTWVYIRDDRKIVNEVGDKVRTFAEVLQMIPLARKE

>contig32972 Frame-2F

MVTTSVVKNRAPAPIQITAEQILLEANQRKDELAQPPRRRIADAAELAEYRMGKRKSFED

ELRRQRHHVGTWMKYATWEESQEEFERARSVFERALDVDYKTPTIWLKYAEMEMRHKFVN

HARNVWDRAVTLLPRVAQFWYKYAYMEEMLGNLNGARQVFERWMAWQPDDQAWYSYIKLE

MRAKDIPRARSLYERYVKCHPGEKAFMKYAKWEEMSQKQFVLARKVYERALEELRSDEKT

ELLYLAFAHFEERCREIERARAVFKYALDTLPKEEARALYSAFITFEKQHGDKDRIEEVV

IAKRRVLYEQQVAANALDYDTWHEYIKLEESEAATSQSFGRVREVYERAIANVPPFQEKK

YWRRYIYLWIKYALFEELLADDDSGTSSERCKQVYQMCLKLVPHNHFTFAKIWVLYAKFL

IRQRDVQGARRTLGEALGRCPKKKLFVKYIELELMMGEIDRCRKIYMRFLEFDPQNCETW

QKYAMLERQVGEIERARAIYELAIKQPVLDTPEIIWKHYIDFEIENNERENTCTLYERLL

ERTKHVKVWISFALFEASSRDETEEQDTKLDAARDVFERALRYMKEQGGEELKEDRVLCM

ETWLEMEKKGGDAKMIQKVCDMLPRKVTKQRMVYSQEGVRNQVFVFEWNVIRIVTVRVFR

IDGAWARRIQ

>contig33908 Frame-0F|Blast-xaa-Pro aminopeptidase, putative [Phytophthora infestans T30-4](gb|EEY60965.1|) 1e-176

MLKTQDKCLYVLFVRPQDPHSEQWDGARIGLDGAKDRYGADDAYQLTELAPVLQKLLSSL

DRVFVLKPAGATYSPAFVEATKQFHTKFISGDILVENLRVLKSESELKRMRLAADIGALG

FIDMMKSTRPGMSELALGSTFEGSIKKNGALWNAFPNVVGSGSNAAIIHYLAKRDMLQKH

DLVLVDSGCEVAGGYVSDITRTWPVGGELSTGKALMYELVLAVQKTCIEHLGNMMKAKEP

ISLNELHDYSVTVMRKRMLEMGILKHSSKTMSHVAMREFQKYNPTHIGHYLGLDTHDTPH

ITRSVPLLPGMVITVEPGIYLPKNDFDLPEEFRGIGVRIEDDVVITESGIEIMTAKVPKE

LKDMEALCYN

>contig35494 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66604.1|) 2e-40

MLPNAFFTAIVVPLVFAIRTQSDGQILANEMTLNWPTLAFHFEIKRSSMAIHGYANFSVL

AFPVLSRTYKGIDSIMYDTVATFTEGSTLSRYMVVEGKAYASHVSLRDNGLNAGVECDDT

GVTPPINAIINAINQAEPVSSNSSNSSGTIECSSETALMISIDGIELGLCFAESSGFTLY

GS

>contig36103 Frame-0F

MGEGITASMYVLSVHDLYSIYYLRLQAGVLSTFNLKTLTCVFVILTSSNSC

>contig38884 Frame-2F

MVIIPSLTDFYIIFICSVHSSTSAAQNDTVVQIFGHIHPQLQ

>contig39160 Frame-1R

MLLRASTLAFVLAVVLVAAGFVDDTDARPMHAAIVSKYNNYLEEKETIILELNNWLDSYG

TQGLKYGYIPSRDSRNSADELEDLLQRFYLTKEQISEARIANPMAEFSTDGPLTLMTMDE

FKEFLLNKHVSDSKGNNGTSKKPIHSFEKENSTLSSGELKDYDPAPAHQHVEKKKILAPS

QEHTKAKPIVRRLEDGGSVASAHSQGDHTSNSELEQFSKPTYQTNSAASANTDGYTRKGW

NFKDLLTDENTYDVKAPNVDNGLSWKRQGVNNWARDYIQVSGNDEWGSGSNVGSQSISKD

LQSDHRFIPAKRHSIASSTMENTHAPGANFPPTFKEEQTTSTQEALDAVIFAARTSAKER

LVNKEPDSAIDIISKDIPGLTDSTTLSVTATKDSKSVDWSLSACVNPPGLQGDQCSSCWA

FASLGALE

>contig40083 Frame-2F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY67267.1|) 4e-51

MGLFSVVMYTLLLSSLCLNFVDSHEAYATKVPNGRNVKGVDAIGHTDPAGGGIRNAFGRD

FRDSGHTWTEALCQKDSDRDGQTNGEELGDPCCEWKPESAQDPLWSTGVSNPGDDASTSM

KSLWPTYECLTTTKGSENSDSGSIGIGNRTIDSDSLTSSASLAWSRLTVATMTTLLILLA

TFAS

>contig43198 Frame-2F

MVVKRVHTWDEGDEPLELDVRESRKKKPKLRVDPEKINASKIVFDEDGNQATVADRFKVR

ASDATEFADVEQHAKNYTEQVAARLAARDAEDRRLEKDRVRTKHNKKRMKLKGAHLEESD

DEGARLGSRSDDEGTSDGIPSSSDDDDENEDELKRNVDRHAVASQEEIALRMLQRR

>contig43442-0 Frame-0F0

MRDTSLTRESCICRCSICHCCLCFSRV

>contig43442-1 Frame-0R1

MEQRQMQLSRVKEVSRMKSFEEDEDEEDESDCDELQGRERESSRMMLSPALAELL

>contig43828 Frame-1R

MIQEFWARKRTITGLTLNDLCAIKAIYWYFSLLPASDLARSAVHLGTSVKCWRSLQVTIL

RMARFSHHERVFVVLGHF

>contig44331 Frame-0F

MTIHYRDMVPNKTALCQILHRLASAKNPFAWLSSGTDALRAMQRAFAEAVLLSFPGFDKS

FHLYAGASGQTCPARTEEYRMLLSYLNQAPDQLYDNGVGIAFESNFFVSIAQFFSEFLSW

FIRITK

>contig45817 Frame-0F

MNRGNRSKSDLADKAHSFLAFWQDYSPNSELLEHDKF

>contig46364 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55937.1|) 1e-39

MVAPPGCCEICQIAEIFANPQLQNRSVRITGKLDSYDAQQRVARVSFQGVSMTVETQQLV

LKNLQLRLGSMYQFLGETHAVKKVA

>contig46908 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY62457.1|) 1e-31

MVFFLFEHSWRPLCFQVPYGLLPLEDLQWMHESQLRKRFRMNITDENAAKTQTAEESDES

RRLLKSNVSTYDQVQLIC

>contig47194 Frame-2R|Blast-DNA-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY69219.1|) 4e-25

MTKLSERLEELAAFLAHEYAVDSVEETLAHLQTEVEEAMALSRASAQQCTILLFQSTDPP

NLLRFLSSSANFADD

>contig47518 Frame-0F

MPYDSNSNLPRLSSPQPSSSADTTALLRPPSQTQLRRSETSGAKAAHNRTHEASDIPVFH

SIQTAKVAATEYFNSLSPHLSRRDVLRDKENGKVAGKSTPYDHWKRLRRARTASGNSCAS

TSSTSSFASYVINSKTLPRDFDLNSDDEVDGDQGRIVNEEKNEVTDGILPYVLQHVIAPV

LPSPPYPVDPYHFYSNLKRKHEGPGTAAAEVTSSLAVLFAASDIAAIFHPLKCKFKCLKY

VHYSHVEFVVRVYKHQEALLIEFQRRSGSILLWDGLYRILYEKLVPIIDLTALPCAQSSG

QKRITKKEAAELSATGIPEP

>contig47583 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57857.1|) 6e-77

MLDNPDVVPQVLEEAQRHGNRIPDARVYEIVEQYRRGGRFQIPPNAGGLPAYSPYGSQQQ

PQFGGFNAGYERQYQQHFPMQQVPPGGPFMPVKRKADAMGSIQSGLLPESFNRPVRKRGT

MPCRFFNSPMGCKNGDLCHYAHVQPAPSNGPELSGIYNNNGRMMVGRGGAGPIMGGRGPP

VHMEPYGAALSHHMRGGR

>contig47972 Frame-1R

MELLPTEPAREAQVLRSKKIETSRATKENFSELPPVSCAQKIVSAANEMPYYEEQTENEL

QSFELLPSLSNGPVMASNLLNVSLRAASPDKKLVRAGIQEDKAHERVDDDLSSVVANESN

FLQASNINSKTRADSDAEDMLAINPMECTPPSKRYLAEYLHGAT

>contig50697 Frame-1R|Blast-hypothetical protein PITG\_17521 [Phytophthora infestans T30-4](gb|EEY67029.1|) 1e-24

MIGLTCPGAEEYLRGLDPRTWALYCVAQQLKLYGWTSTLFAPNETLLSLAPYELMQHYMK

KFMNVTYNQAQHATKWVKEGKCFTEYCDKLLAEQREAAKFQVIQPSNDGAMFVTECRSFP

ARRYRVDLNERVCSCAYLFQMGLPCRHVLAGLIYSKRLKEEATFVDACFSIKTFAEQYDW

QDLNKMELLLNSDL

>contig50756 Frame-0F

MMHSPALTLRFCCIHNDVRHAEHATTISSSRPYGLRQLNPGTGARYLPAASQVAQAAIA

>contig50983 Frame-2R

MTPTSLHDDFLNMMKTQGLEKIATEAGLLRDGALVASQLSVTPSFTTNTLVDIESERKPM

LAPSTLSSPSFTSPPPG

>contig51764 Frame-0R

MFSFGSGLLRIKSLFFVVSRPMDQATSSSEILLSVALRSGIAKPHHVYNHMTRFSDAFNR

RAQQTLHLISCAYQL

>contig51984 Frame-2R

MKELGCFGLQIPEKLQETTCRHGYARACEKITNGSLAVTVMVHLPKLATGKHTAAFALRC

LLNQDSRHIVARWKELFSDICGRQRQGHGFHCGASIRKCNKE

>contig52660 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60396.1|) 4e-13

MAVVGKLLIAVGALLLVHAGYYSVQYEFYVKLTETVDAPMPPYEV

>contig53555-0 Frame-1F0

MVPAIPVAAVVEICSLRAFDEPERMGSVELPEDPEGEKIAADIAAEGTTVSALVVGVEGT

LTEVEGEFVVVEGASVI

>contig53920 Frame-1F|Blast-CASP-like protein [Phytophthora infestans T30-4](gb|EEY57173.1|) 8e-06 NOT\_ORF

MHNAGLNF\*KAFDLDSKRVLLDSQGSTMKSEKEAS

>contig55254 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65766.1|) 2e-30

MIDTSPVPSSDSIDKNLRKYVRFNYDIFTNPRALFA

>contig56967 Frame-1F|Blast-glucanase inhibitor protein 2 [Phytophthora sojae](gb|AAL11721.1|AF406608\_1) 7e-12

MMNVVATIIAAATTFAGVTGNTVHTSRQLILGGHPVTDSSHQYVAGLRDSPYENTFCGGV

LITKLHILTTQTCVEHIQDGMSMYAAIGARYIMGLNFPNGTQEANALKSRRSRSTQSIIT

T

>contig57999 Frame-2F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY59803.1|) 2e-10

MVKLMCALIGEEGVFYVDIDEKEPVGALKKAIKTENPDEIKCDAGDLELYLARKGNAWLS

D

>contig58169 Frame-2F

MMSHVNGALDRETILQAIVVSTMVYCRAFSMDFSRF

>contig59056 Frame-1F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 3e-64

MREHIFTGNASSLAKFKTWQELVFVTLSQRVLADPLYVRMHYGHPDVFDKVLAITRGGVS

KASKGINLSEDVFAGFNCTLRGGVITHVEFMQCGKGRDVALSQISMFE

>contig59272 Frame-1R

MRSRNLSVARRIRKLIDLKKLRAVAC

>contig02150 Frame-1R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60832.1|) 3e-49

MKAGYKWFTYLMPSSYSLSALVGVLFGEVQDVISVTSNGATTEMTVAQYIENTYDFRPNR

KYNFMVGLLVIWAFLQLAIYLTFKYVSHLKR

>contig03852 Frame-1F

MDRYTGILDCIDLDECVIVLKRTKRICSSNEALPFEEGRSLLFRHSQVAHIIAQGGVEYT

DRISPLSTKTHGFCTDSEISNPTHKELYGRELKTAREWLDAAFDTSALEDSNDRRGSSTW

NQFEANEKLFGVVSTFEEELYTTKLDKSKLSLTQVRIAEKLALEMERQCARGNVHLQEER

GQMDTNEGMAWDEEMRYSSVDRGWNEKRLVSQKAEDFKNRMESGEKERELDRGLEKEWQS

TMGIPKLSFSEAVQGRSSLGAKKGRNST

>contig05348 Frame-2R|Blast-3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57732.1|) 1e-167 NOT\_ORF

MMKRLSIVRGFSTLSFHAPPLAPCRRVVVTGLGAVTPFGVGVNRSWNALLDSQCAIKTLD

TLVHTGLSCTIGASVPRKNEDGAFITRNWVNPKNIRAQEPDFIAFALAAADEALKDSGWS

PQSDEERERAGVAIGAGMGNIQEIMDVGQLITEKK\*KRVSPFFITRILINLAAGHVSIEH

GLKGPNHSCVTACATGCHSIGDAANMIRRGIADVMVAGGTEASLNEISICAFVRAQALST

KFNDRPQEASRPFDSQRDGFVMGEGAGVLVLEEYEHAKKRGARIYSELRGYGLSSDSNHI

TAPLENGDGARRAMESAIAQSGLAMSDIGYINAHATSTPLGDRAENAAVNELFGEQAKQL

GMSSTKGAIGHLLGAAGAVEAIFSIKALCH

>contig05418 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58090.1|) 3e-52

MTKEYTLDEIRRLAESNPEKLAQEYQASRAATANLVGRARAGIAARTANPPTNKFNAWAQ

GYGNRFIYNGSVKPLVHMMLILGGAGCAIEWWCHHRHAYAAKEEKHH

>contig07092 Frame-2R

MTWLQYGPRLRDTESFFPPVSTKSVVGVIHKQCLGNFQKKDLQDRRLVLAGFFLLSSTRE

HAKRINVV

>contig07179 Frame-0F

MEEHNGPFVELRSDTSKSSGSARPSYSGSRQSVSRQSVSMSHSRNHARSRVLSHSVKPYT

DADANETILLANAPPKYTGGFNDIMKQIKAKNYYTQQFQRIQQQTNMGRSLYFSNVAPTF

YEDNYLAIAQETSVNRVRACFFIGFVGLTSLYVNEWRSHKWAPSDATGRTAQDERTIIAL

TFGIMLPSLLLGIVATFTNVGRKFLENVTAMVFATVAIMMIAKKPVEKVRGPIIPLLLLL

IPIFGITRMRYIKSCCIGWGIFFTYLIVMMSVRPTLPNPSLFDSYTDISYQAINYGITAI

GGMVSQYRQELLRRRNFCLQLPFSGTMDADAVDEIKTDKFSKKTLLHRVSLKFRHPEVEE

CFYRYWYLIDPFPYENPNSGSLHQGVFRTIRFAIWTLLLNQLVLLLQDIKFLRVNRDALV

DDSDLTYALVLRFGITVPLYLSAALFMYFVGKAFYARWVKEAEEAKHAALTRDSRVTISI

KHHDKSHMRMEDDAYDTPRMKAVVEAAQVQQATKDRLLDLFINKGGYVRSTQIFSSIVIA

CHVCCMGILLLAVSTGAKIDAFENTNFGTSGQPKPVYYMGFLNAVLFAHRSGFRVRFIYA

TSTTFVVALGILIAASSLSPAHYQQYAGYMSVIFLMGMMISYEEECLRRTFFVLKSIRTL

EFEEWFRVVLRIQGWVKARCCKRLQDVRSKGNNDFDANRTIAPAVLVNTSAQMAYASKLG

MYSQMFNILIAIADVITSNL

>contig12407 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66108.1|) 0.0 NOT\_ORF

MDERPMLRGIFAFEDEETPEWRRVVMSETTGGVPKFATKEECEDFIRKHCWRGSNPDFPK

LQHVFSMFVDWQQITEILLPKIDEYDQKFPQEAVPEVSSNNRFVHGEGVAIAQNVDYRVN

MPFHQQTNRESTLNTLQYLFFHMRCGIFVMIRRRRVVLFAPFANKDYENNWGHHVTFDSS

DGTMFTYYREKKHYYRRENIIPDVNKWWANGNIICNEHCRYHNKEDETQYWGDQFLTQLR

DMLENACKHRNIADCEFFINKRDHPHLKENLSEPYGFLFNKDDRNTEDDIPLTKNLYATY

APILSFYVSKRFADIPFPCSEDWEAATGLVFPQSFRHTHCDKCPCRNSVRCENDWECYCD

IGGNGRKRHGIESVRDLFTASNFRKFYKPWSDKVNTAFFRGSATGGGTTIETNQRLHLAH

LSNTWKKDSGMNAEVKSAALNRDGVDKELPLLNAEVTTWNLRDKKIAGKPMTFLRNEDFN

FEAGRQHFIPIYEQSKFKYILYVEGHCAANRYAFLMRLGSVILKVESRCVADEMWYYPIL

KPFQDHVPIQSDLSDLAEKIIWCRENDEKCQQIAARAKELYETFVSKEAIHDYIEVICNR

VAQRFQTAPKWYNRPMDVESMKKPDFGRCRGMCVGGPSARYCKRCLEMKESDDEARAKYD

RDRKRSRDDKLDGSSLNDYGRNRKNRDHDHGRGRYSRGR\*QSRL\*SCRPRLFGNFY\*RR\*

HS

>contig14834 Frame-0R

MIQYLEALSVKRPNKRLRTSAHNP

>contig15550 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60220.1|) 2e-33

MIVEEEWSKEQEANRKPGQKHPTPSPGFADRVFYESLLQQRPESRMAQKWCLEYGVLEWK

EAEKLCKKLGVS

>contig18229 Frame-1F

MMQLLIGKKPGDEELKCFIALSVTDTEFSIGTVDKKHATYSPQLATKPDEELLNTANAVC

RFVALNSGKLYCDDLAVDEWIEWESNTLVPWLRVAKANGNKNGEMAGQLAAILEAKEEAR

SMKSGDLQFLFGSELSLADIVAGVTLRAAFKVVKEEKDEPPLLRKFRKYVAELFVREAIA

KGVLSMKTATQLTKKKEQCAIGASSIAAYNIKRSAFKLDEKLEEGLTYHNILEVVESVFD

AAIKAAYPGLAIPPVEVARTNTKNAMFGDYQCNSAMSIFTVLKNTHNAARSPRDVANTII

AAMPQTDLLDRITVAGAGFINAFLTKKFVTARLLNLLLNGVQPPP

>contig18614 Frame-1F|Blast-NADH dehydrogenase flavoprotein 1, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY53182.1|) 0.0

MKGLVRVAGKTLSQAARGLRTSAAMANSVAEEPVMARVYGGLKDEDRIFTNVYGEDTWRV

DGAQRRGDWYRTKDLLCMGPEWIVQEIKDSGLRGRGGAGFPSGLKWSFMPKQTDGRPSFL

VVNADESEPGTCKDREIMRKDPHKLVEGCLIAGFAMRARAAYIYIRGEFFNEALILQEAI

HEAYEQGFLGRNACGSGYDFDVYLHRGAGAYICGEETGLLESLEGRQGKPRLKPPFPANT

GLYGCPTTVTNVETVAVSPTILRRGGSWFAGLGRKNNHGTKLFCISGHVNNPCTVEEEMS

IPLRELIDRHCGGVRGGWENLQACVPGGSSVPVLDEELCQDIMMDYDDLKQRGGSGLGTA

AVTIFDKSVDMVGAIRRYSHFYTHESCGQCTPCREGTGWMEKVLTRMEKGDADIEEISML

EEISRQIEGHTICALGDAAAWPVQGLIRKFKHKIVERIEDPSSFKPEDHFQNAWSGAPLK

NQAWIDKFADGSTYKSTASV

>contig20110 Frame-0F|Blast-HSF-type DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY59256.1|) 7e-43

MQNPYPIQAKVSTASREVAPFLRSLRRMLFDESNDVLRWTPDGRAFEIHDMQEMTARVLP

KYFKHCKYTSFQRQLNYFNFRKWTKSKAVVCTFSNDYFLRDQPELSWRISRKKTLNSYSL

PKYRPARTHVIPYWKRAPVLTPHTLSFETVPLTGDFRGRFLFPAIASTDLMLKQHENLCA

QPTQQARHYYSFNMAAALPFETYSASKSNETELFDWIDCLLPTMDDSVKSSATPNTVSLR

KGIEFVPSTSL

>contig21287 Frame-2F

MARVKTSSHEALGDEAISSTQSEAHKPKTRIANLVLQSEFQGAKAKSRRTKRHPNDVRTE

QDMDAIAGFDETSESEYNEVVDTFGGAGFVLVDLERELDIVATAKCCAGALCKSKSKRKK

ASKKAGIETKKQQEVDTMKRAHEETKKEKKLRQGEKLLESLEAQDGRVEKTDKVKKTNAV

TEKVSIVSRANGHVEEGEHGKEPVEAMNGTKKKEIKLQKEALKTKKMQNVIQAPSSSNET

DKIKKALASRSLNRNDQMTQFSKYLDRDVVVRGLEKGKLVQGKLRVNANYCMDGYITVDG

LSMDVLIKGMQNRNRALDNDVVAVRLHPESQWKPLNDDGNVKAIKTSVVQSISSNTTDNE

NALHSLWLPSVDTDENFFKHLDKSNDSADLLRQSMKHLNERISRSGRRPTGTVVFVLAQG

NSNGFVGSLEAATKVKDMKTPLSINDNFAYFHADDQRLPRRIRIPKLQLPDEFIRHPLLY

SKTMLCFCRIKTWPTKSQSPTGEFIKTLGEYTGIETGISAIILKHGLQAHTLDFDSTLLN

ELDEKYGLSGEKWEIPDAEVQTRRDFRATQIFSIDPSNARDLDDALHIRALDEARTKFEI

GVHIADVTYFIEPNSRLDHEARSRATSVYLPNRVLPMLPRLLCEKLCSLQPQVDRLAFSV

VWQMNVDGTLVDGVEPWFGKSIIRSCCKLDYSSAQKMLDGVIHCDNVDAWVMDRRPIPDA

NPHITNASVIQSVKDLWSIGATRRAMRFETGAISLDNMKLVFSLNSMGNPTRYGSYEQKD

SNRLVEEYMLLANYLVAQQTLRFHGPLAFLRHHPPPVTRAMDQAIKQLDKSGIQLDGQST

RQLAKSLERVRNDEGETTFLIVQALITKPMKPAEYIVAGNEASVDSWRHYALNIPYYTHF

TSPIRRYADVVVHRLLEKSLTNISIQTKDFESKRLELTSVAQNCNEKNLASKCAEIECDQ

VFLCSYAQHCGDIEATGVVLSVGQKSFTVFILELGLEKRLILQELCLKGTWNGKTSELSI

ELPEIITNRELRMEGTDNCKKGVSKMVLIVKFMKHLRMRVSATKKMPPNLAFSIIG

>contig21795 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58040.1|) 3e-07

MESTSQELDVPSSDAIRLILQFLRENRLFRAMRALQEESQVRL

>contig22220 Frame-0F

MYAVKLHSQHIGTFRDLILKLVLVVDVFKLILRRENMLQNVTN

>contig23155 Frame-2R

MPVPFKLITAVAIAFLLIGSSTSLPMAKTSLTSTTNQGRHYESREEDGRLLRGAERALSV

EQEERGRFNLLNIFRKLFKGKPKTKRTPAFKKIV

>contig23249 Frame-1F

MRNELVRLQWQCVVLAAILDVLSSYAGRFWTHWIQCYTEGMLYGSVANEFCFSRSPIKLR

EAEQLALLTICFVYASAIIGMQIAVKLQ

>contig24033 Frame-1F

MAWSLRIVCGKRVAACAPVNITTHFLNVREFASKKEKLKSKKSGGDANFEQMLRAIKGQY

PD

>contig24460 Frame-0F|Blast-pyruvate dehydrogenase [lipoamide] [Phytophthora infestans T30-4](gb|EEY64114.1|) 1e-170

MAIMTGAKVLAEVYRLHHIPLPKITLQALLKRGPHATPALAASLHNDPESLRKWREVNLP

AIVTSAQQLHHEVPIRIARRIVDLENLPGELPEAEPIVSLREKLLSSFDRLLHCPLPMNL

ASEHDFMELHRQIRNEHASMHGNISKAVQALEYEHQGLTESLDNFYNSRIGIRMLVDQHV

ASQTPLPGFTGIVNHETSPIQIAREIVAKVRPLWLKNRHGDSVPEILVSGNEDATYRYVP

QHIEIILTEVFKSAVLNSIAKAKKTGMLSPPPVKVLISGGSHGVCVKVSDQGGGMTREQA

DGLLKYHQTAPSSISTGYDPVAEVLERRASGLDFSDSFGLRIAQLYAKYFGGELAIMPMD

GHGVDTYIYMNCLTEASQLK

>contig24738 Frame-0R

MASAASDSKSSRMTYRFLGNSGLLVSKLSLGSWMEVSDQYTPEAWYQLMRLAFERGVNFF

DNAEAYGGGLAERNMGAAIKKGIADGVWNREDLVITTKLFYGAKPFMTKVGPNEEGLSRK

HLVEGVKGSLKRMDLEYVDVLFCHRSDPHTPLEETVRAMDFIINQGWAFYWGTSQWSASD

IAEACQIADRLGLIRPVVEQPVYSIMDRNKVDFEFLDLYKKYKIGLTTWSPLAHGALTGK

YSSGAPDGSRMNNELYKSFVPDFPERVVKADKLKPLTEKLGISMAELALAWCVSNPNVST

VMIGARTVAQLEQNLKALDALDKLTPEVKAEIEALIPFVPELPKPDFTATFRNKHL

>contig25382 Frame-0F

MRNQAARNKYELLAKDDETSTSSLPRRTYLFKRAAFLLIIALCGVAIVGVLLITFGRDVV

PLSSR

>contig26556 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY70264.1|) 6e-31

MIRGEKYDESVDIWAVGIIMYELLVGKPPFEAP

>contig28095 Frame-1F

MPSQLQMFSCLDCNVRRLSGMTLPSSGSLAYVNLEGSTVESYEIANSTLPLLTGLTRLKV

AISSRNCPIDAKATIYPIQFVNVCVLPDAIYNRKYVIASDFDTSASVSSTNYLTATSGWM

LVAVIAGAILVLVLLGGVFAYVLFRHRRWNDSMKQYTNETRSDFQSVVEYRTTLKPSTHA

YFERTLDTRNIPYEEPTELESDTRVCSKRQGFGSSLTSSTQSIATVAAVVPLKNDIRTDL

DLRHFQLLHKDVVRGKLIATGGYGAVYKATFRDRIVVTKQILPDRVRDPHMLNSFMDEIR

TCASLDHPKIVTFLGFTFTSLLDLSAV

>contig29070 Frame-0F

MPASVAIRGTAEALMSYRKATYCGQMKKLNWLLTTKKTIMLDEPSGVCIGCHKPVKKTTS

RDRQCQVCMNQVCRSCCQVHRLAFLSSTRRIVYRNLVFCAHCLRVAGSADGLDIALAELR

RRNPLEFFETSSNGSLSVSPSRSTLPDIQQEFFG

>contig31466-0 Frame-2F0

MVVAEPFRNLIHLNEYKTSVMDT

>contig31466-1 Frame-2R1

MWRGKVNGGNEPCTALFRVATDNRKGCVPNMTAPKETFVPF

>contig31585 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62973.1|) 7e-47

MMVSTARRQISQKTFDECVAENVEEFDMSPAEAVAEAIQQFQSQGVDLSNVIKIGMAPAA

GEQETLPMRLKRLIVDLEKHSLDKSEDKNLLFLVGELHRTCEKAPEARVVAGRHNAVNTI

HALLETTNPAVVIASSNLLVLLCASNTENQDFVGSLGMQRLVQTLQHPWE

>contig32584 Frame-0R

MYFYESRLLASFRFCCCSISAACAARRSILRFTRKLKPRVTSTSPKTVTSISPPVTDLCR

ISATLLELAMLLSLGGSHNTLSVVVSDMTGLEFSTDFDDWLNLQKPVALFYFFLRAPAKW

>contig32975 Frame-0F

MWPLKWVCFFKSTTTLVKLTIHKGLHRQFTYRMQFFAQNFTFRRLISECHFMAYFERAKG

ALCYTTPVKNTLNTKEMVNYFK

>contig35493 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66604.1|) 1e-68

MRGSMASNYFQDSCRNSTNYLSDKIAARTGFCPTTKGITSLAYEGTDYSSAKLDAAYLAA

QHIYRRNVDAVMCSNGFSGLPSRRRLWFWTLGILTPHHSLANDGLVEFHSCAGGIPASKF

GNSYEDRFYVTKLNHDDTTFRNGDALFNKAKMPLKWFECLL

>contig36445 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63560.1|) 4e-32

MHTSNTLKRWLKAAVWMTLLGGIAYIFIKIVPMKLFIANSMTWIQTNPTIGAMVLPLVLT

LAVLLCIPSPGVEILAGSMFGLVAGTLLCVLGKTIGQMIAFLTAKHFGKDRISEFLKTNF

PTFATLATVLQSSSWKLLLLIQVANVPHLVKCCGLAIADISAYRFAASSAMGGLPYAILW

SYIGVYGNNLVTADLSGTSFRH

>contig36621 Frame-2R

MIMPPRPNIIFATILVSQMLLFGVYLQYSFTHEDGLIGDYQLNSNSLRR

>contig36654 Frame-2F

MSDSDARRPSASVGSASLTNALTAPVFLQKTYDMIESSASAVACWSDSGSSFIVKLPREF

AKTMLPRYFKHNNFSSFVRQLNFYGFRKHKKDEIKLSVEDDESKNWWEFYHDKFLRGRQE

LMTQIRRKTYTEPTSPDHEEVETLKHSVQGLQCQVFELMGQLSDLTGLVKSLLQGTPSSM

CMPSQLAPKRVKLNDGSAPIRRMAAPPPNMVPKSYMPQLKQKSANSRPDLLMDTKFQDFQ

IPIILSEWTEAYGIENLFNEPRALDAAVYGGYD

>contig37060 Frame-1F|Blast-Phenylalanine--tRNA ligase [Ectocarpus siliculosus](emb|CBN74527.1|) 1e-10

MDRNLTNSEIDDLQKVVRARIVHSLNVVLR

>contig38308 Frame-2F|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY60480.1|) 0.0

MITGDNAMCGCYIARQSGMVASSSRVILGEMVSTIERKKLVWRDVDSDEEYELAAIKYLV

EQGEDVELAVTGVAFDNLMSMGEIKGLLLNIRIFSRMTPDSKVECVKLHMETGAVTGMCG

DGGNDCGALRFAHAGVALSDAEASVVSPFTSKSKTIQSVVDLCREGRCSLATSFASVKFL

IMYGLIGSVLRLFMYFHAINMSQWCWILVEGFMLVGCSYVITLSKPLDDLKIMRPTSSLI

GPSTLSSILGQEAINIIYLGFAIHMLSSQVWYCPFSPDNVDVAKWWLMSDNHLATTLFFT

VIVQQHTSAWVFSFGSTYRQPVWKNVLLIIFFAAVVAFDLYLLLGEPSIVTDRFRIASGT

NVIGLPDIPMPMSFRLKLLALLLGNVLTCILYEYVVVLGPVRSYFRNKYHKDLIPMNK

>contig38663 Frame-0R|Blast-cyclin-like protein [Phytophthora infestans T30-4](gb|EEY66597.1|) 1e-120

MIGEHTDDEPESSTSRTSSLSSGDKQLKGTLKISGETRARSTENDEAKNCISVAMKDIYE

RRWDLLKPSSPEYVCMGSGSGQIVEEVLANTAMPQLSTKVEPKIEAQQNKKQGEIYDSLG

GYSTVDDEEDELLTRNRQTSTSTVPFDWKAEKGESIEITEASEPTKSNYFIKEELLETST

AASKETDSASLLSSSVLVKTNSRNDNEAEDGSSMLEEEDCLIVVVDDSFIGHGSLPRSTA

AEEHASDEVAAEAKIINVAIGFKEAQLNVEVVSREAIVEYIDSATGHKLLSESLKVPAEN

EFREASCTCLDIPFGDKIKLLDQSTPKKLADAETKGPKAFTMDQKVAKVKTEELSQVVKK

GETVAIKFLELGVDECMIRHTVGSPSQSFDMCTKESGVYSPGTTDEYASSIYENLRAREH

RYHVTEDIFAKQQGVHSKMRALLVDWLVEVHQRFELEAQTLFLAVNYLDRYVAQVPVKSQ

RYQLVGVAALLIASKFEEIYPCDMEDLLYICERSYVKADLVDCEMNLLNKLDFNLAVPSV

STFLCFYLEHFDEDKERISQLASYFAECSLLDFIYGSTYEPSVIACACLVAAYCYVENQT

PCRIWNTRFVELTGYQVSTILPCTRDLLSVLNQPSELAAVTTKYSAKEYGEVAQLPLRDL

RALLH

>contig38883 Frame-1R

MKTSLGSMRKDLNCLLSVLHNFHCQTHHLCLYQAISLNLLWNRRLCSRKHCDSCKGLLND

DTSMSRRSYVAATHSLTIIFFVCCAC

>contig39167 Frame-0F

MEGPRPTHFDDESDEEQNPSTYMWIEGDSLAPPCQSDRDIVSKIVEIAHLTPAD

>contig40493 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65068.1|) 3e-09

MDVNPFERLDQLCGQIEHVRRLAIEHHFDLSLSVFEGETPSTIAMSMLDRGLDPISLRNE

IQQHVRKYL

>contig42433 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68225.1|) 1e-107

MKLCLWGNKADGCYKEVKGTMSGVDASLIFDDELLLVDHSDKVIQYLQQKAQEAPVQTLG

IQFINDNSGTELLLDLALADHLLTYQWCVKVTLNVKTEPMYVSDAILADVHEHVVEMQRD

TQTSEVQALGTRLTNYIDSKQLVVCTDLYWNQYTYYWDMPVDLRNGLGTETMMVIIKGDL

NYRRLLGDRLWPPSTPLEEAVPYFPTAFVSFRTMKSNPVVGIPADIVKKLENDDPKWRFN

GKRGTIQSVLKTNSGLK

>contig43104 Frame-1F

MATLGAMAEAASRRLVLERIEYVREQLTKLQDRVDRFDAVADALTELPNEISHKVMVPLG

KRAMIPGKIVHSNEVLANLGDEYFSWRSATQALDIIKRKKEALLKQIQTEENNLQELNSK

KTDVDSVAQLQKMFEDENIVKIQETEEESQLGSIPIALDEDIKEYFELEEEERLKQDRKQ

AAWNWDGMMKRMEDLEKLEAAGARLNEEDNAVKEIKSVEAQIAALKANGNNAFAKRRFKE

AVQYYSQAIELNSTSHILYGNRAAAYHRLKNYKLALEDSDVAISLHEPWVKGHYRKACAL

AALEKYKEAAEAFERAKELSPSDKNLEEKAKQMRDKANDKANRTYAESQEIKRQLSSEPP

KAENAPSMEPTFSANSSTSGVPVPATSASTAFSGSIMEHESYEALETVPVPVTTPFSNTR

TSRFQVSNHSGQIVTLEPVGEAQPVKRVSRFKAARARRD

>contig43171 Frame-1R

MMQLMFIFYQWMITPIGTYNPGTIDCSTTFTLLVLVGDGACFYIQSALAYALMKLVSPVT

HSVANCVKRALIIILSIYRFGERVTSLNWCGIVLVIIGVCLYSGSSRLEREHASNKLTMI

PATLTFVNKTSTIDNLSEIRIEKGL

>contig43621 Frame-2F

MLRNVLIMASSGIVLFSKEYVNAVAQ

>contig44336 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67625.1|) 3e-32

MFMLRMSQNDDLVYAVLANEKAHGLAPSDNGMEGFVEDCSLLECGLDGANILQQVEIYAF

KSDGQF

>contig44466 Frame-2F|Blast-signal recognition particle, putative [Phytophthora infestans T30-4](gb|EEY70068.1|) 0.0

MLDSIKRLKNIDTSVLSEKLLPAQREAILTNRALLLCLMNKTEECRESLSILKAQFPLSK

SVADIIVLLAIKDQSPAAVVAQLENDTSIGGRLGLAHVFLTEGHVLQAAECIRSIEQLAH

SPGTVATLVALYEQGGDSASAQAVLEDSLAYHKARDYTSEHAVKIREGDCWYKIQKQQYR

EAAAAYLELLEGETAGALDRDLRFRLMASLVIALSFCDADAAQARCAMLPAIDESGVDPS

ELEQRAPRSAHFAAKFTDTGDKKSERKRAAKSPEAVARKRAKRREAYLAKLRARPDYNAS

IGLLNPDPERWISRKQRSYGKRGRRGRNRFVGAQGAGMSTEKDAFKLDAAARAARKAEIV

KPAAVVVSSNSGIRNSKKKKKRR

>contig44512 Frame-2F

MLDAISLTEEELGMLFGPAVNGANGSSAVSKPINRKKTRRLMMQNEHSTKINATFRCVVD

DTRCCYRTGKCQNLQALKRNGKLHKLCEFHRERANMNQKKLDRKKRMERSKVPLHMRCGS

ASSVTFEDKGRCLNLKNPSPRTVEAVTSNNFYKTKLKPELDSDLFLPTSLEEAPLGLGCE

ELAIFCSLMTFDINRMPLPIDMPFLRTSSHHPTSIV

>contig44585 Frame-0F

MDAPVPLNSERGTHTKHAIHQIIFHARPTMSALSRNTC

>contig46363 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58410.1|) 2e-27

MTNKLEFALEYGWHTKRIRFRAPDYQTYHQWMNFVKAALESGRRPLASCGFMTTAERQHS

EFDSSSLASTLNSSSQGTSAFTLSNRQSVTEENNDVYQHLKDKVFDNFLRSKNTNYQIDS

NTRDGDASSFFACVSAAIGSCSHENSHQLWLPQRCRIDKFSD

>contig46608 Frame-1R

MLVHSAERVRNYPLNRIFELVVAASCQDISRKIDCGWCKEPFVTSPSQIVPI

>contig46994 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54088.1|) 3e-99

MSKKKHNLNYPLAKSPSRAMSNFDAIDLLLRYETPLVKDMEPDDDVLEWVAAYVGGEEFQ

EAINNFCGLHVNHFSILLTKGGPSAADLDKVESTWKELHEAFIEMANANIEEFLSKRGFT

LDQYNNRCVKEIALAEERQRHSRLSFFVQILLACCEYEQFLNLMKRVADPEYYDKKELQY

EAEVLVLEAEEKGASYAPKAAGAQAFLDFFQANPDLTLDELTQEFETKTHLT

>contig47470 Frame-0R|Blast-oxidoreductase family, putative [Phytophthora infestans T30-4](gb|EEY67891.1|) 0.0

MILARASRSVSCASRLVSAKRHFASKANCVNLAVVGTGRMGCIRLSGMQNDPRVSIAAII

DPNASAKQLQEMSRQYGTECLSTLAEAEDALNRKNETLDGIWISTPTHTHLSLINECAAG

VLGTQLKAIGIEKPVAARVDEIDAAYHVCHTNDIKLFCSFQRRFDPSYEALRVQCVDKKS

IGKLQSIHTVFRDHPCPSMEFLKTGGDPFHDLAVHDIDYVCDLVGEYPTKVYAYGTSLSA

ELRQLNVMDKASVWLEFPTTGVVCTMDLSRSAEYGYDQRIEVSGEHGMLQVLNPSKTAMV

QSITGGITADALLHSFPERFRQAYLLELDSFINVVQGKGTPRIHWRASRMNTIIAEAARI

AAVEKKIVSIKYLESKQIAPDGDPIVECKYEF

>contig47584 Frame-2F

MSLGDESNCNGTSNTGSREDLVKDDAVINVAQTDESEPVPSQRKRHVRRGEVNCRWLYNQ

VQAARGLILIDTRTREEFEEDSIPSAISIPPMQSCQTLQDVEDGLLEEQRHLFTSKKRKL

RDVVLFGYTVKKLTVEDANESASCGWLHRLERLIIEDALVTSVKLLCDGFLTFKYR

>contig49630 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59609.1|) 4e-66

MEGFLLVFSKEQRAKVQYCVLENGMLRCLDRPGGVLHESVGLTRHRIRVEPLFADNAGVC

PNRFAVHALEVKRNDHEGAFVATSKRERIYYFAAVTSKSMIKWADAIHNWRRHAFNDPKV

SVIYAFGTVMDDANRAIDAKHRAFLLETQRLHLVNMANRFDVQLISPNTKTTRRPSGLFR

MSLLCVSSAY

>contig50690 Frame-0F|Blast-hypothetical protein PITG\_05283 [Phytophthora infestans T30-4](gb|EEY69099.1|) 5e-14

MDMSTVKVLLALAATWGVPAKLFISRQLSWTESSYNPLHRPQ

>contig51208 Frame-2F|Blast-FAD synthetase, putative [Phytophthora infestans T30-4](gb|EEY63991.1|) 1e-38

MISTLKIKGIYMGVRGGDPYTDDMEHFAPSSPGWPPFLRVNPILKWTYADVWSFLRDCSL

SYCTLYDHGYTSLGTVFD

>contig51763 Frame-0F

MLRPLSCASSMQSGTPPCGCIPMRARLHQILVHSVRNSDAGSSLSSYERDYLMQSPLFSP

AKATETAGSLWLLLHAAQCDCGCDIAGCSVMRRVLNHCLGCELVVGKCKQICNDAKAMLL

HYGSCNSKGSLHGRSCSVCWNLLEIDYSHQALSNCHGSGHPNSHTPSTTSSSFLLTSPAP

RRDTPPFVPMSMSPCMSCSPATHSPLKSATNASKHVPIQPNPLPTASNPMGVRSALPPHF

DTSLSLHLEQMSALFRAEVKSRVEKRVTAAAGQDLLQHMQKKTRLRSLDDLRSEARGIVL

EEMERELRLHGQAYNWANSTHNDNIMEDALQISPYLRHVLMDGFRAVQSQYVASQPTESS

QPAALNARQSGPLEK

>contig53552 Frame-1F

MVLAWMIKKFHVSFNLSGHAVTCVMQSYGMLRTSARDSTVAFICMSLDVTYTRAKMKIFK

SARTTYHETG

>contig53927 Frame-0R|Blast-H - or Na -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY67420.1|) 1e-45

MLDFMKLAEDEHSPLPTDDVLLNTQAELPISGVIIGVQNGLARVSGLRHATIGSVVNVSD

ASGHSISQGLVLFMEEKVVHIALLSARGTEPVMKNMDVTLHCKQLEIPGSVAAFAGAVID

PIGRPHQF

>contig54126 Frame-1F|Blast-urease, putative [Phytophthora infestans T30-4](gb|EEY58029.1|) 2e-25

MRLSPREEDHLWLHMAGSVAQKRLARGLRLNYTETVALLATQVLEFIRDGKTVAELMTLG

AQMLGRRQ

>contig54988-1 Frame-0R1

MSAKPRVREEWRDSAVVLLDVWHTLRAVTLHFLWADRNRCLFDRRQPTPALP

>contig57123 Frame-2F

MVSLLEFSEIMMPRNCWLVSLEPAFQLLLRKGVGPKGTPTLSRQLAVDWEGSCYVCV

>contig57578 Frame-0F

MESDGTILLIKPEIEMGPRRVSLLALQSKSEEFEESTSLRLIEAPVFSRKTVLRDSISTT

FLPHLISRQIKSEPTIKQRKAFPLREKEEIHQYCYADKIISTQ

>contig03426 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58341.1|) 3e-14

MSLISKVASLYQKTISKSFGMYGLKYDDALVDTAAVQTALHWIN

>contig05349 Frame-0R|Blast-3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57732.1|) 6e-20

MPPTINLTETTEEFTLNYVPNQPQEKKLRAVLTNSFGFGGTNACLVFAK

>contig09679 Frame-1R

MWLLVMLLLGGCNGEKSFLDFSVPDLQGHPVSMREFNAFPVILVVNVASECGYTDRNYLE

LQELYEKYHDEGLMVLGFPCNQFGGQEPGTAEDILKFTKEKYHVTFPLFSKLDVNGESAH

PLFVYLKKKLSGFVTDDIKWNFTKFLVVNHKPFKRYGTTTSPLEIENDVMQALHNSRHVD

EFDDGGAADGDDDGRDEL

>contig11447 Frame-1F

MLAITSFPRRFPTTSKRPLLPSARWIGALAMRDSSLDFVTSSMSTSSSLAVSSSHTPLSS

RASTVSTLVKNQSIIKSTNVLRVSTFATSADIVHEEDQQLQHQIDYDDTFLFGERADNWF

TTARNPRTDSSFPGRNRATGRLNALKAPNLLSCSRDEMLDYFDNSWAITDALFSSLQGAR

AFITPPPHYLRHPLIFYYGHPTCFYVNKFLVAGLIQEPVNPFFEQVFEVGVDEMRWDDMS

KNEMHWPPVADVLTYRRQVYHLIRNVIITHPGLEPGHKQITETSPLWALLMAIEHERIHH

ETSSMLMLEHPLEFFHSTSLLPSYHESLIINNDDVSRQPLAGVDYPRNDFVAIPAAKVQI

GKPRGFPSFGWDNEFGQREVSVPACRVTKCLVSNGEFAEFVRDGGYLEPSFWSSVGWEWR

CFRNTKWPAFWVQDGPSGSQRFKLRALFDVVPMQWTWPAQVNRHEAQAFCMWKQTKQTDK

KVVYHLTTEPIHQLLRDAKDRSENVSIDDVSMTLESTNTTNNLNWAHLSFSPVNASPLTG

QGFHDVFGNAWEWCEDMFSALPGFRVHPYYDDFSEPCFDGEHNIIMGGSFASAGANGASK

FSRFHFRPHFFQHASFRVVEQRMDNEGLITLATTDVNAPPPYVNGNSFRSTEQVVVSKAG

FEAREGKGLSCRSLFEDLQQKSERALESFVASLTYDGIAKPIVVDGGLIVASNMRHIVDC

GEVIVVMPSDEANYAVLKGNYELIRTAEVPVFTQESATKASLVAATVSAWKKL

>contig13733 Frame-0F

MRAVRRRKVPLSRDDSTAMSRPQLVKTISPSIKTFEVSNDSSLTFPHTKSPSFMKAVHDK

RALAEKKRLVADT

>contig15429 Frame-2R

MSDQDSPLPRRSRSPSVRAENNEEKKSVSESFDMDEPRRSRSRSPTARAPAVSVEVNNPG

NNLYVANLSARTGQQELEELFSKFGRVEKCEVIVDPVTRESRGFGFVTYEDVRDAEDAVK

ELNNQDIQGRKIRVEHAKRKRGHEKTPGQYLGPRLASAKYGGRNNRDRGRDQGRRSRSRD

RGGFSRRNDDRDRGRHDDRDRGRGRYDDRDRGRGGFDRDMHDDRRRR

>contig17746 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57614.1|) 6e-15

MVYDHKNARQIHGNETRIIKL

>contig18228 Frame-0F

MNQLINRCVTTMILTTHLKQLTRASKTLNGNTLFRVHPLAQSLFPRDRTASLQEWKEIPL

PTDEKLQKHGIINASVRADFSCTNCRYFCATFNHEAIQVSAIVKIA

>contig19106 Frame-0F

MKIFVPSFIASVALVLFPSAGALNVQLPGVNYEMMYGDNKCKSAAEVEADMMLIKKVADK

IRIHSLIPCQHGEVVLPAAKKVGLKVELGIQTCSNYYQEKKLLSRLVEVGLFDSNIVTFH

VGSNEVSNGEVQPDVALTHLIEIQSIIRSCGKSTAVTVSDSIDTYMQNPSIFEKVDFVSI

SSMPIRNGIAISDAVSITLEQVQKLLKKATELDKKVAFSEVGWSSDAVGSDQALYMKRVF

QMAKAYDFEFYWFTAFDSKGGNGNQLAANFGIFDKNNKMKAHLQELKIELLEPRILQNLG

TKLVLAESKSAVVMHKHEAAEGANAV

>contig20641 Frame-2R

MISRLQEQVKVLQEESSSYLESEKKEIVAAAVKVHELELVAVKAENDCLQNQLLTVQDGG

IDDMRKKLVAEVEVLKKLNSQLIVELESKQQTEPLIVKPWKVVLMRRQSRHYAPK

>contig22683 Frame-0R|Blast-predicted protein [Laccaria bicolor S238N-H82]gb|EDR04366.1| predicted protein [Laccaria bicolor S238N-H82](ref|XP\_001884885.1|) 4e-09 NOT\_ORF

MPECEGDNMDQELGPRLDEGERLHVLVTHEASTFLAYDGACYVWAPAGKQPERKAKDVQS

TSMTLFATQLGGCASRMLASGRRSEEVSIL

>contig22870 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60284.1|) 7e-28

MRRHASKERLFFLLVLTGALLLLSVTMLRNSNAIPATRTFRDGFTVAEDMVRRTQTLNST

DRSPKKAVLPEESTLNHSENSVRMTTIKTEDGDEITIKRAATSKGNNIMTISRDDRGKLT

IEDTTTTNEKTLTGFPNITFYEGEKVKAFINLETTEDDEGFGSNSGKVAVVRMGPVISRD

AGT

>contig23730 Frame-0F

MDPTPKQQLPPRGMEILSYASNAIEKLLQGVILRPSIQSVTIRPGNLYPQRESMPCCSER

DLAWLQSVPEELESNEWRSQRRTFALPAEPRRPLEGVPLRSVVP

>contig25314 Frame-1F

MDFHRDVLTIFVRSFHFKDESIITALRMFLASFRLPGEAQQIDRILNTFSLQVYEQCRER

FLMASVDVAYLLSFSLIMLNTDLHNPNIRLEKKMKLEDFIKNNKNYGNEVSKGLDLPDEF

LTELYTTISTHEIKTLEDGGKHGQVTRDRWKDLLYQAEKNPRNSCFIVHDSSAVDSTFAH

TFNASSEGINKEIKRNTESASTGAPCLVRKASKEQENGMKAACNALRGNQYNRHIFELIQ

QSLVRAFSSVFQQFVVDSLAKDAARGADFVVGSSYVMHYVPQKSALRLACNGLVLCTAVA

SHVSLLEPCNALFIRLCKYTGLVSSDIYPLGYHGRNNGMAVYCENTSAPIATAAVLKLV

>contig25383 Frame-1F

MTADNESSKSKNQVGFRLKSDPVLLEDGSDLFVSWEGEAAVALTDRDFLTLSCGPTNNYQ

DFIAMKNATDSDNHSIRFYNLYMLRCNYTVIYFNYDKQTNMASPIAKLEVGMKEPFETPK

HGHLSLTDDDNAMAIMFNSGSKKTPMVKYGENPKDLKFHATGTTTTYRADDLCQAPANVT

GQQSYRDPGYMHTVIMTDLKPETLYYYQYGLEDVNAMSQVRSFKSKAHTNSRHAKFIAYA

DMGSWGATTAGRVYKDVTERGYDTFLLHFGDI

>contig27576 Frame-0R|Blast-carbohydrate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY62983.1|) 2e-64

MDKQTRATEEKLEKCRHKHVQLFHALVKAMKDIEFLQNYGKPLQREEMELATALKKLQTL

LDSPGQYKARLADAVSMQQMQKEIQPPLTSQLSPQDLEQVY

>contig28003 Frame-2R

MRREEWKCPVAVTAVGRMECSLDDVLFSLMVPNSASQRLRSFLMDRRPERNCQLVPLVTP

TPERPFEFLAISRFVNAQYSEWPLIFQTMKEMVVVIATGKINAMHGKRCGYELVQSISLN

HASSMPRARVVQTRVFWEQSDGSIAIYTKLIVDAKHRIADSVTQLLMGRELLGFWKYVPR

SLETKKLWWCVKNKKALIHTLRTFSVSYDNDESMICKLRPKTLPSKKAVARRQCEFCDTR

LCHGSKCRVTCHLTMVLSSDTGFLEQTLVVCLRCAAFVRSRNSGAIARSLLDDLEQTSFR

SALSYTKVVIRGKERT

>contig28397 Frame-1R

MQHYVYALALSRLEANGAQFIGHVSSYDATHHERMFFKQRGICRLNCCSLKALKALELEL

SIFVVCVDLCDLIIN

>contig28586 Frame-0F|Blast-ribonuclease 3, putative [Phytophthora infestans T30-4](gb|EEY56061.1|) 1e-125

METVMRKLTIVQCRQAIASKSITRAFSTYSSLPDGFQSPEAVADAVAAALANETEAKIAV

KHSKCRALGNATQFSKLERRHLEGEVIATQSITFDQLLYPKLNVGWQLIKPQHFEKVPIP

RGWTNGLEKLQKRIGIKFQDITLLQSALTHHGCLPNNAVPEDVPVVRLSNRSLEFLGDSL

VGVAAAAYLFQVLPRHQEGQLSRAKSALVNNDTLSKISTDLGITDLLLWPPGFREAPGAP

LVVKGHVTIAAGAVESLIAAIYLDQGMEVAMNFVNTHILPRAAGYATREVIWEPTVELQN

LLQGHNYGLPIYKYLPAATNASEFTVELYVKE

>contig28740 Frame-1F|Blast-V-type proton ATPase subunit E, putative [Phytophthora infestans T30-4]gb|EEY56665.1| V-type proton ATPase subunit E, putative [Phytophthora infestans T30-4](gb|EEY55813.1|) 7e-98

MLVHNAKIKIQEEFTRKEKEREINKRIARSAEIGASRRQKMIARDQLLQTLLADGQAQLK

SYTTADDKNTTLLRELIVQGLIKLIETDVVVAVRAQDVPLAETIVQDATEKYIAIMKKEA

DLDVSKVKVSLNKVEEGMLPESKAGGVILYAKQGKIICDNTLDTRLNQIYYDLKPTVRKM

LFPTP

>contig28858 Frame-1R

MVSMTRIQNSVLVVAAAVSHGCSYALALEDYHFAMLAAVNHERAKEGVPPLCMNNKLQQA

AQAHSDNMARNNYMGHEDVDGSTLVDRVTRAGYSFDAIAENVAIDSSDVAAVMIAWMKSE

NHHLNIMNTEYTMIGIGYTSSQESMVKIYWTQDFGTGTTEVCDNTSPTLGNGNVTNPGLV

PTMAPTLVPTSVAPMATPVPATIPPIPEVPETLAPLATLYPTTSGPTEAPVQTTLAPSAP

PTAETPTLTPPMPTTLAPSAPPTPKTPTTPKTPILVPPFVPTTR

>contig31337 Frame-2F

MEANSTDGSTVETNTREALDLNEVLLSDAALVHELIFNPQYQTVRDKDIETSAAMMTSTQ

SVATLAVRVREAMTRAFWDRVVAMNDVATLLARTEELRLSFRKALGGGYNSTLGARSRLL

ANEVDSALEASRLAEMMQDPLRHASLLEARCTTVLDVIERAEAPARLERTRHFRSEWVHQ

IASNKLPPIELLVTFLAFAFDKVDELRTDVLNAH

>contig31467 Frame-0F

MKSMTQASQGTAYGSHGVNSGSFWDSLSNYLWAEEEKIDTSFSLVNQMLREEVLNLGGGI

LEKENWLRLTRKLQERSLTSLLQTLISCRDPFKCIMPPSDSGVDAMMQENAILVLELSID

IILVNSHRILQFNLWDSFHLYAKRILSTPLRELHMQGLVERVVVHILRVSIRLFHDAKVR

PKLMGTLELLLTMDKDMYKALSDRLASGISMLLKANVVYMQDFHDWEVLLGILQHVVEYI

NCRSACWDSVTMLAERGHLTDDNFRPWMAVCCGFVQHPTSYAADALKLLQGLANSDHSYK

MKGSSWLQVMRVMLKYLNDGRPPVAKTAWDCLRNSLLLPGLPIAKDTWKRCFDDIIFAFD

DQVNDITLRMTRDAPLYSVTLLSKTFLHNLNVLMELPDFPELWLKVLRRLAKKLVASGLS

VAMRSQQTSVVFETTLQSLYNLLLVLKAEDVLERASTEGSDETLFDETCAVIDDVCPHLR

EQLGLVPDTVVDESDGQSTLKEPQANLEPPIESESVQATEHQCGREEGTEVIAELADSAS

QNEAETIATDDVQVQDNAEVATVDELKNHYESLPDDALTNSVDLTCKDSPATLETIIIGD

GTIGIKVDEVILDEITEAV

>contig32974 Frame-0R

MRLRLRAPDEADAESGFTFRNSSSSTLYKPEHSSMLPPLDVCSPDYIEERLDNLKRRPNW

RDYLDQYVQDYPDSDSEDERVVCQTFETPGFIHSTFWSLLVALLAPLLILYALCIRHQSY

GFWPLGCRSVKELFGCALINVIFMAFGLML

>contig33609 Frame-2F|Blast-chaperonin CPN60-1, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY58953.1|) 0.0

MNPTLAVAVKKASALSPAGRRLFSSGKDIRFGIEGRAAMLKGADQLANAVQVTMGPKGRN

VVIDQSYGAPKITKDGVTVARAIDFKDKFENMGAQLVRSVASSTNDAAGDGTTSATVLTR

SIFSEGCKSVAAGMNPLDLRRGIQMAVDHVVDGLQKLSMDVADKEKVAQVATISANSEVE

IGNLISDAMERVGKEGVITVQDGKTLFNELEVVEGMKFDRGYISPYFVTDNKTQSCEMEN

PYILLVEKKVSSLQAILPMLETVVKQQRPLLIVAEDVESEALAALVINKIRGGVKVCAVK

APGFGDNRKASLQDMAVLTARQLFLKTWATVSRRPRLKCSVAPRRLQSPRTIRSCLTVLG

HRRL

>contig33995 Frame-0F

MKANGMGRSSPVAKHRFRWEEHRCWQHAQASFEYHGEDAGVASSYFHIVADGVSSPFSRN

SLNAIDATPVSSAILSAEVVRCVQTALQELTSRNTEPIGQLAFEHAIVDAIKMARINCFQ

YRNSRLATTLVVSYFSRWTGKLLTFSLGDSKCVVVRQGKIVYETLAVLREFNVPTVVNLK

EQILAKDYVVQGFALQSGDICLTFSDGLGDNVCKDDLLATVASCELDERGLQSVCQKLLN

MSKMMAAEATEQLFPFATAAVVEYRERTLQETKLALEGDVDTSGADHRAISLELFNRHKG

KETLDRHLMLRRPSRKHHYSLMQLK

>contig35085 Frame-2F|Blast-60S ribosomal protein L8, putative [Phytophthora infestans T30-4](gb|EEY69751.1|) 1e-32

MGRVIRGQRKGAGSIFKSHTHLRKGPAAFRALDYIERTGYIKGVVREIVHDSGRGAPLAR

VTYRDPYRFQIK

>contig35171 Frame-2F

MFPANSDMLATEKDMQVKNEAEYCGKELIKSQIHGTGVKGVHDSDSDDVITLSEEDDEDA

DEVVGEDDVWSTVEDHSTKAVGIIEDETLGVVEINLNFLCKSSRYVTDSWYTLGGTRTGE

VRIRTICSERAKRLLTVQDRTMLFEKYVSHSIAKPMRDFYGFTLPDSARKDWVHLRSYQD

CREERRVEDWTKLYNVQFSERLRRCSYKKVDTAEKAFLMQLTRAGIPRHLRERAYMSLSG

ASEKQTTAGPHYYTDLLKRVTTMETETFGQIELDISRTFGHSGTTICSISGRDQLRRILF

AYSLHNPTVGYCQGLNFIVAFLMLMADEESVFWLLSVFCEDLYPGYYSSTMSGIQRDMLV

LKQLIAEELPQLDQFASQVGLPLELLGSQWLLCMFTTTFPSETVFRIIDCIFIEGSTFVF

SVVIAHLRQLELDLLALADFHEVLSSIKVAESACIDGDQFMKAVFKEAKSITPLRVQTLR

DQKSGSVRSERERVERARAFNQQLAVVYEIPALSKYAVELFCFLHEEAEESSRSDVAFVL

SMLCHGLVWLATHCKQRNR

>contig35492 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57870.1|) 3e-59

MKGLSLLSPKAAREQKLRLSFYLLDPEGTGFITKKMTTELLRSCLAECNELEISLTEAQL

AHIVDNTFTDADLDHNGVIDLNEYQALDASHPGLFDFLTVDAFGVLSHLERVHSMNITVP

Q

>contig36620 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54442.1|) 1e-106

MCIYSSQRLHALQDLVYSVKVMLENADVIYWIDSGTLLGVYRARQLVPWDYNADFGITMT

GLEYLRTTNKEQLEVPDGYELTVFNSSLYEVGDTSPAIPVRFVDMKFGLYANIFAFKEFK

GLFKDNIKPAAALEIEDDTVGDGAIIENLMGPDPSGIWQRCAHCQYVDEDENNVETKASN

ALMLKHFKVPRDWIFPLRTCKLELFEVMCPAQIAPYLMIIFGNRFLTPELWE

>contig36655 Frame-2R|Blast-phosphoserine phosphatase [Phytophthora infestans T30-4](gb|EEY57606.1|) 1e-106

MAMNGNVKFEKALAARLGIIKPSRQDFQSCLKQNPPKFTPGIKKLIKTLQDKGIAVFFVS

GGFRLMIEPIAEEVGIPFSSIYANTIFFDDDGNYSGFDDAELTSRDGGKAQAVRVIKRIH

GFEKIAVVGDGVTDLQARPPADIMVGFGGVVTRDVVKKEADLFITDFDHLSKLLL

>contig38309 Frame-2R

MAFVLCKVRHRVSLSPCHAEDARAGIEQNLNDQLMQYSEPLKGVVLSFSEVQLDKPYGVI

VNEMPYIHCKVLADALVFRPKKGMILRGVVNKIGSNHVGMLIAGVFNGSVAGAELPVGYV

HNYSQDCWLAKDGSSIAVENDVQVKVLRVHVASGMIAIEATMRFDGAGFVKDIPSKKKKS

VSHLNLAEGEPLIQRTKTKKTEKVAEPVETLIKKHKHDKHADREVTKEVAELTRKDKVHL

KKQKKNIYKDVKAKKAKKHKKSKHV

>contig39166 Frame-1F

MTDVETPRVSLTVISAANVGEMRMEGSSTVGLYCQAQCGEVVLRTAAKANTTSPEWMQNF

TFGVKKPLGNTVAFKVYGLNERGGDVFFGGVSLPIDTLVSDAQSTHKMTLVDAAGKSCGE

LTVSARYEPKFVAPPQQVTKETPKLKLASPLKVAAPFSPERNSILPASKEEKSVAGNVSA

NHLIDLAASNTLKSTESSNLYVVTILEAMDLPACDGSGIEATSDPYVRINCTKNSSQRTK

TQQQTLHPSWRQQFYFKIVPGEKQQLELIVEDSNLLTSDFMGRCVIDLDEYKKQYQGTKQ

TFWLALEQQLESKDKNDSSDMSSDCKMNNQNGKLCLAIDMQYIAQDICSLAQGEIDNITK

VPSGHSVSHLGYSVGVDEGKDNIGSHGDEATMAMKMKIMLR

>contig40171 Frame-1R

MDESLLNASEDRITHAEEEDELLWNELKDNHRAPPFGGSRHPGSSVGDHTGNLSSGAHSL

PSLRVNVHLPAISTLIREVLDTARAALSGSGSRGNREEATSSTSHVPDRYGNVANLDAFL

ITLYNYYYHKGFWCIVFVELVSLVTGLFSVMLSSFLIGCVQWGPLLECHRGSRNCAQEME

HYITCRTDTNGRWGLVGAFYFVMFLVYWLARAFQLVKTLRDTREMEVFYHERLHIDARQV

QTIAWDEVVNRVLNLIHGANAPVNMRQLSSYKLQIDPALLSSPHDFARRIMRRENYLIAL

MNHALFQGTNVLPLALQFLSTAHIMCSRNLEANLNICLLDQIFDSELNLEPSVIHNVEML

QKRFVVAGVLNVVLAPFILLYRVSRFFFLAAQEWQLHHVYYLGTRRWSAYAIWQFREYNE

LPHVFDARLARSYSLADRYLGMFPAGSLAIVAGGVSFCASSVMAVLVLVSLLEESVLLQT

TLFGHELLWYLTISTGLFALSRSFTSSASPFLVNGDCEEAMRQVAAETHYFPKEWRSQCH

SFEVYDAFTVLFPYKAVLLMEECLSVLLAPYILCVSLPRLSREILLFLRSHSLVHPSTGA

VCRFAEFDFKEYGHDAKMENSFINFKQNHPKWVGAREGEALMQRLSKLKEEEMEKSMRMG

DTMMYSGHLSMSQQLMQSQAIQSAMGVGRMSGYMPQDNEFYWLEKLHQQGRLNELDVEGM

KGNSKDSISVSSLGSP

>contig43105 Frame-2F

MESVRGAYGFGIFDVHKGFWQIPLHPNSQEVFSYVTEYDFFTQTRVPQGANDSAVYLQVQ

MNLFKDLLYNSVLVWIDDCSSTHNQP

>contig43170 Frame-2R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY61802.1|) 4e-39

MSVFGGLGFELYLVGWTVCKRSMHKVMGDGLKDMVLLASVRILTVLLGLTALKYIAVSFT

>contig43444 Frame-2F

MMNLFGRKSAAPARSPVATADTIRKLREQLESLEKREVHIEKKILLQLAEAKQRSVAKDK

RGAIFALKRKKMYEAEIEKLQGARMTLETQVMTLESAHVNMETFTALRSGAEQMKAIHGQ

MNVDTVDNIMDDIQEETAMADEIGRAISQPFGSQLYDDDELEDELREMEELELEEKVLQP

LVATPAEAATPAKGAKALTAPVAAAPMAQYHLPEVPSHVIESNISVVGTANDDELEALRK

LEASMSDAF

>contig43620 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56054.1|) 4e-23

MLVIDGAMTCATQDVDPIGVLANLQALVNSAFDMMSFSGDGVSSMTIQNGRN

>contig43655 Frame-0F|Blast-dynein heavy chain [Phytophthora infestans T30-4](gb|EEY64009.1|) 1e-138

MDELQDTLWSAVHPRKVRKQLDEFIEVMRRFPARVQQYEAFEYYISLIQSRKAMNSLLSE

LKSDAVRDRHWKQILRLLKIASPLTELSLRNFWESKVSSNDNELKSIMRTAQGEMALDEF

LRQLSDFWTNYQLDLVNYQNRCRVVRGWDEMFAKLDEHLNSLSSMKQSPYYRVFAELATS

WEDKLTKIRSILDFWIDVQRRWVYLEGIFFGSADIKQQLPKEF

>contig44337 Frame-2F

MRLTLQVSLIIHFKVVKGVCESCARCTRPNAQQSTLADQKMSRMLTWLSFLMITKGRKKA

FQSHLSSRKDDHCIRRFVRLKLLHQVLRRRKQQEIRA

>contig44830 Frame-1F

MGSFAMINSADPYKFHGHPNIHLDRDKKLLSASWPRSRDRKQMRCLRLNDIRTRRWVATL

SLESIRGAS

>contig45280 Frame-0F

MPQPEDESFDEIDTFAFRQKVSASRKLERCSRTNITDQVYRLLASARF

>contig45424 Frame-1F

MTAKMKLHDFSNVCSLSWIYFSHH

>contig46609 Frame-1F

MIIGHPRLQVKFFLVDNQSFFLFSEGITQRIALPLHLTDHCHRYRSRYKMIVHYLEPTRV

AVSASVEPVAFSDIYTIALSCCSELDSACQRQLQEGLGL

>contig47471 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62031.1|) 1e-07

MVQFSFDRPWLLCETVIQTLKVPKKYVPNRLIHEETAVGMVFEVLHGVNSLLFEFIAFKP

IPS

>contig48179 Frame-0F

MYHNNESPTDVPHYNKAVDARRKCVQAITRRLIQRRNPFIVKVHTRNCGNVDSRKELIAA

KIDDQREERQIRLGNKMERTSQTLRWNYKQVPDLEQDQQISSIRQTFGPVLASSLNIAGK

VAFKLVTSIRGEPSGNCAGGSIKSINAICGDIKSETSSYS

>contig48522 Frame-0F|Blast-threonine protease family T01A, putative [Phytophthora infestans T30-4](gb|EEY63538.1|) 1e-07

MADSAYSFSLTTFNPSGKLLQIEYALNAV

>contig50574 Frame-1F

MLSPSQAILRLIPEGKIQMTADEFIQRTSKLEIDEQSKALVSGFSQDKKTAANFLLKAED

SAAKQNLLVALIRDTTEKNEMKLPDGATLDQKSYKELLNIMKSMGFVT

>contig50985 Frame-1F|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY69486.1|) 1e-07

MVGGGADAGICDAEAATHFFDQNRTCTEYEKLFTAPKSGSRTSTKHYLYQVAVSEACGGA

DNLVQDNIVPYADPAMRVSMLARLNLLRTDYLRQARELAHQHKSNCVGD

>contig51209 Frame-2F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY59230.1|) 9e-45

MSIKLTVNDGHEKLPITHQELSYRVVSRLGTPWMVETIQAIGDDVWREFLHVMPPLAGER

KYTLSFVFSEAWSVARELTDEEDDIPSVSQFKQALSSCMQWSIKEVD

>contig53427 Frame-2R

MAISRPSAAKVCNSTRRRRSTSLDSSLSEEDTVTLKDTRRSRGKRQKASAILNEFTSLDA

LLSSGLAEKRKRENRERKLKHLREESELKDKDAPIGKLISCMDDTLSALSGDNHLFTSSE

VTITEEKFGYVFMPMTEP

>contig54989 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69069.1|) 8e-41

MRISATEGHLEIIKWLTAFRPELKVSTRVMDAAAYRGRLDVVKWLHENRSEGCSVHAIDS

AAASGHLDV

>contig55159 Frame-2F|Blast-replication protein A 32 kDa subunit, putative [Phytophthora infestans T30-4](gb|EEY53901.1|) 4e-13

MNYGGGDETYDNGGGFMSSHPSGSQQTPTKRSSGAESIFSVTIMQLKSLYASDDDALRLD

GQELSTVQ

>contig55252 Frame-2F

MTDSNTIEPTHLQMEQQPEEETVAIEEVALSILVAPPITEGQAVRLEGLSPSDTVLSLRQ

LI

>contig55829 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64206.1|) 3e-85

MTGKLKYELVQGRTTPTYVYATYPLKFLHPRRSVHQGFDACITYILGYGGGLVGRDCVVV

ECELGPNTSVVLGTQASTKVFKAEHEGDFVSQSFFLKVSSNATLAFVPDPVTCFKSARYR

QTQVFNLEENANLVFVDWMTSGRKRNFLAPGSIRNNRTETLEHWDFEEYDTKSEIFIDGK

RLLTDRVRLA

>contig55951-0 Frame-2F0

MVWTIQDASFLKDLIEVVCIYYGDSILSPEIELLLS

>contig57122 Frame-1R

MTMSEPSPNDRKYKSVYSNNGVWICGSYICSV

>contig58916 Frame-2R

MTGMDKSNGMCYRVALIFLATSSFMETYAYSKPHAW

>contig03425 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58341.1|) 3e-14

MSLISKVASLYQKTISKSFGMYGLKYDDALVDTAAVQTALHWIN

>contig04709 Frame-2F

MQNRRRGRNPCLWVRRHVWAIAVTTLVLFYGVFMVQTTMWVRSFRAIAEEKLIEEAINDE

RTQLLNTAQMIVDEDTTYDINALDRIATEMEAPIGDKEVFISRLNHSLKGLMMENTVENG

SSTAKKSALEDSMEKNKSKLISYPQLNLKRMDTTAVTTLSPKTIHNTTYHLYTDAKKLPM

ADEKRMQLNTQVPDARRSFTNTIVNQTLPFIPLLKSRHFDMSRLVSTRINQLTFEERHDK

VIGYNATLAYLASYTKPVNSSSELFLFFTCSNRNGSINDWNPNCRIAREKVYAIFAKSPS

TNRLVTIYAGPYRDWNHTNAFMEDKDLRLKALPTILRWDGGTPGALRSTWGVLVDTSILF

DPIVRYLFRTLNAQDSLFMKSEVATKEIVTLEGYASFRAFTKGYVMKATMYPLYIMMISG

HYHTIIAFGVHGVDRLNCPWNMRFTRLHHLMQSWSLLKRLTDKVSGTIQRIHLNWTLSLQ

>contig05711 Frame-1F|Blast-ribosomal protein L23 [Phytophthora infestans]gb|EEY61615.1| 60S ribosomal protein L23 [Phytophthora infestans T30-4](gb|AAY43411.1|) 1e-72

MTLGLPVGAVMNCADNSGAKNLYIIAVCGIKGRLNRLPAAGVGDMVLATVKKGKPDLRKK

VMPAVVIRQRKSWRRKDGVFLYFEDNAGVIVNPKGEMKGSAITGPVGKECADLWPRIASN

AGSIV

>contig06202 Frame-1R

MSGFRMSPQSVDYLPSTSPSNAVWTAQELQTLQAGLTQFPADQFDNVTRYIKIAAMLPRK

CVRDVTYKVKALRSSPGEQA

>contig11444 Frame-2F

MSLVTTLVEYVPSMRLLWDYWMATTSSTASSCSSASRLSTFQAKPLMEYIVEGAEKSVVE

WRFRLRVVLSLCGAYLSGTRQSAAMQQALRVVWNKLRNGIGNMGETSPGSLSFLREVLPW

IVDACSCHADLSAELVHFLLKLQRQSGASNDYSTAGKIAGQTQGQLLKQVLHDTYASLLE

QM

>contig11668 Frame-1R

MAVTQFEACDARRAFVCWDEPAMKAKFEISLACDVELMAISNTHVVQTLVRPRVKNAHIR

TRSRPKSASLEKVWKFAETPIMSTYLVGMVVGEFDSVSTVTTEGVLVSVYTPVGRSERGK

FALEVGANALSFYTKKFGIPYPLKKMDMIAIPDFAAGAMENWGVVTYRETRLLIDSQLSS

FHQKMATARTVCHEIAHQWFGNLVTMEWWTGLWLNEGFARFMEFEAVHYLFPEWKVWEIF

VQDITLNVAMGKDCMLTSHPIEVKVNHPDEVDQIFDVISYAKGASIIRMLSEYLGRDVFY

RGIHEYLVKFSYRNTQTQDLWEALEQASNQQITSLASGWTSQTGYPIVTLANDGTLTQKR

FLANQSLESTAREVVAWDVPLTFISSTKPNEVQRLDIWTRDSSKEATAALSSKLLAPINS

SSWIKLNVNQAGFYLVNYSPQAWKSLQVPVREKILGVVDRMSLLNSIFAFARSGELPLTC

ALDFSFAYRDESEHLCWKELSSHLRFYCALYRSDTFYSKLQAYICQLYASIMKKLTWEAQ

EGESLTVASFRCTVIGMLALGDDADVVAKVQDLFQKYFKDNSALSADLRGTVFNVQARRG

SAADYYQLRAQYESSNFIEEKLDCMSALGRFKSLDLKLDVILWSLAKVRSQDIQYVFSGV

AADPSGARFAWKYVQEHWMDLTAQYSPLVVGRIVISVISYFQSDAMAIEVETFMETRKHP

SYSQLLDAALERIRVKSACYQRNRDNLEKWLEAI

>contig13176 Frame-1R|Blast-fructose 1,6 bisphosphatase [Phytophthora infestans T30-4](gb|EEY61702.1|) 1e-173

MTNVIDHSNPITLSRFILAEKEIQCNADLSVLFTSIELACKVIASSVRRAGLTGLYGLDG

SENSTGDQVKKLDVLANDIFINSLKFSTKIEVMVSEEEEKPIIVQSDSSGTKYCIAFDPL

DGSSNIDCNVSTGTIFAIYQRDVTSEGGYKDILQPGSKLVSAGYCMYGSSTQLVMTWGKG

VHCFTLDPTIGAFILSQRDIKIPDEPKTIYSCNEGNYAHWDRATKAFVNECKMKPRPYAA

RYVGSMVSDIHRTMLYGGIYLYPGSEKVKEGKLRLLYECNPMSFIMEQAGGMSTTGTKRI

LDIIPTDIHQRSPIFLGCKRDVERVITLYEEFS

>contig13378 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54407.1|) 8e-20

MSLPDATEVRRISAQLKALEKQRAEGSLTHENIPLRLYSVRSGGFVRVLDKRPEPISQDM

MKSIEAYINKCSATSELEVEETATTQENKEIHEIRQNCEDDGANVVAQHEQQMHKDQKEC

FAIEVGANAVL

>contig14836 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55746.1|) 1e-102

MKLRDEQEEEKRKARGVVTEQGSDADEDESSNEEGEELVAFERVQTKSLFGFHTTANGPT

LQPETKKVGFAAVAKAQNPNSKKTANKVMKAKDMDANAAPQELSRREREALEKERSAAYY

LKKHLAGETEEAKKDLARLAEVKRRRDEAEQRKKEEDGAAAERDMGKKKVTAKNDDEPLD

ARAIKALKPAVLKDKLKERDLSTQGQKKELVQRLIDYENERAL

>contig15552 Frame-2R

MGRRISRKKSVLEFSGGSRSVSGIPSEIGSYDIVWREGDLGLKLKPGYRDVPVLSKLTGK

GTASGLQNAQVGDELLSVNGTAVEGEAYQDTLRMLKHSPKPAVLRFRPGRTRRESMMSAA

SVSSVRSNPSTQREVIKVSSRQHVPLYDSELAPVERPPSSGGMTTERDRFDRDRQKRRRR

IPLDVARELVAASQGSDLDHAIFAGIPITAIEEGSKEAHLLRVQAKLCISNQVKTERVTP

AKEALSRAEQEARVLQEALEKVKSQAKKYEEILEAQSRERVLALAVRHKPEEVVKRQNNV

ISELAGVISGFKRDDYADVNVVPPPLREANVQKIMDDLQTVMSIPVVVPTAKFCAECGTT

ENESKLDMDDDGEFYCKDCWDKFLNHSGLASAATVLTKQAHVVDDEQAVGAEASLMHEMA

MRAATSRMTMEAREAEEVKARMEAERKLLEIHELRRSGSMMPERSHKNTLDRSRRERRGL

EELAQALLEEEERARAEGNLKLAKKLHAQRARTMAESLSPGTALDAGIIGTVPDDMEPLN

GHRSPSTLKLTLPIEETTLVFPELPSSSIPVVVSPAASPELMSSPVSAIDSDMATAVTNT

SLAADTVPLNTSSLPPASTGGNDYADVNSDEEAEDQMHLNDEEDVLREVEEKNFALARQL

DEAHSVIERARMSITMAGEDDDDEVDDGLSEEQISLFKKLTNQAEERMSMVDRLHPQDDS

DSDSDSDEEEEEEEADDGVWI

>contig15901 Frame-2F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY61039.1|) 7e-10

MYCFLARIFSVKFSADANFVLSGSDDTNVRIWKTEASKKLS

>contig17918 Frame-0F

MAGGTPARKSRRSDGFSRRRRSSDSEDNPPPGSQDTNQDLDVEIIPTFRSKHEQAAEDEA

NVSPNERDRLRDREERDAFAERLRQRDEERTKRKRKNVEAEGQQGLTRDEIEQLTKRGTL

DAQQNEKLSELRNFSRQEYLKKREEKELELLE

>contig19714 Frame-1F|Blast-phosphatase PTC7 family protein [Phytophthora infestans T30-4](gb|EEY67257.1|) 0.0

MRRGPLYNHTKLQGSATACIVSLDPTSCELHGINLGDSGFVIIRDKTSDLATARVRGTLD

GSMTRKIRNRDRDLTPAGRRKGAHVTYRSPQQLHYFNCPFQLGFANATVVNDVVKDLTNT

SHAIRRDKALFETPENGVRLRVPVREGDLILLATDGLFDNVDEDVLLDMVRLEPNVAILT

QKLIAKAYDLSLDRTRDSPFARLAKENDLMWGGGMPDDITIIAAR

>contig20642 Frame-1F

MTRPRQLEIALRNRCPKKSAFYNSTHKITALGCAKNGANCPTLRVPTSLQYSAFTLSKRV

KGKSGHFNIKHRTLELINHRRR

>contig21043 Frame-2R

MFETGVIFSARICFAGSTGRSYVFKI

>contig21937 Frame-1R

MSADDRRQVMDTYWTTLSWSQNSLNRDDRGRVLDVKRTTGSRMHHLVFSASDAPEQLNMG

SIFEHGDKRMRKWALIILLASLPIQKKSKRR

>contig23508 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69923.1|) 4e-36

MGNVGSSKQRVYSDNDYQLAIEASKELEHILAQDFKAYGQGLHEMVSSVERAIPTTTVRS

IRYVATLRNRLIHDQEMRMLPDRRVFIQNFDNALVELNVIINKRRLDAGGAQPFTAPQCV

IF

>contig23733 Frame-1F

MQCNFSFEICTCKPFTLTEILGLPSTTLRVFQANPDRSMHLSVFLLSDCQEDQDLIVGNV

RYTTLSDSFGRRLI

>contig24031 Frame-2F

MSLHDKCALSLTISRDSVSCGAHQRDDSVGEKTITSCSSTTRTLMGSEILPESKVGIEAN

LVDGQALLSGAEIGADVQSVIAEDEEGLNKLQAAMELMGPEEKQSLEDEVKILQHGIRVW

LLKRNCKSMRETTKQLREATRSVKNEQGQQELAEPDTHELFERERAAVTVQAATRTMLAR

RSYLQTRHVAIKFQAATRGILCRKNFARMKAHALASLVIQRNVREWWNKQPSANRPNSTL

TSLTTNKASENKSRISI

>contig26288 Frame-2F

MAPTNTGMGVAAKVHPEYFKFFNLLAMGLPAEQVKIKMQASGADPSILDDPDAVIGGNTP

SVGNAKALTDTKAGTLVKDDEQYAKFFKLLKMGMPAEQVKLKMSASGLDSDLLDTPDALL

LGQCSATSPTLTSNKMLSVKEDPAYEKFFKLVKMGMPLEQVKMKMNAVGLNADLLDTPDV

PSPNQTSSGTKGGLLAGMLPPRKAVPTGVSALQTSLTSKLNQKPVSNNQEESQLPKKETV

KPNVELRPLFWTRVPVNVVSSTVWMKLDDSHAELDVDEMEWMFRKNPADTLKKLDEKKTE

KVLTQPKEVLLFDPKRQQNVSIAIARFKMSSEDIKKAIYSLDSQKLGSEVLNVLISISPT

LEEIDMLKNYDGDVKLLGNVERFFLDLLTIPRYTQRIKCFRYKVQFESRILETQAQMDML

VAATDQVTESDKFRRVLENILAIGNYLNGNTPRGGAYGFKLDTLMKLHALKSVDPRVTLM

HFLLRQLEEKAPDVITFAGEVPHIIEAKRLSLDQLRADLSSYNAELAMLKGQVRASQNDH

IEGDKFYEVMSPFAKDAEEVLEELGRDFNGLETSYQELVSSFGEDPRKVGPMEFFSILYE

FVTEFKKAYRQNQTKEYQAIYEEMAAARAVAEVEKAEQLKRDAEKRQRLEEERQQNSLET

KAIYAEIMSIITIWTGKHSPGNEETVIEQFKDTSRKFGTNAITADEFCEQVRQLFGSKCS

CRIIPNSAKLLPDEDKRNGLLEAFARFKEQVKKEKESKKQQRNLLVSSSPAGRERAGSSS

AGRRRNKVAIPQAMKDIEPVVGEEAQLLHKSILESVLAAFNGDAKKMKSFTSHTRKYGNE

QISAHEFYQYLIDSFDPDFVGRLVPDLARLLQDSEKRHALIRALCESAPGWAKFAGL

>contig26554 Frame-1R

MGADGCQCADLEKNEIVRQQRWRELCAKFYYNQDETAKRVLYFFEASKVDEISISAVEET

GVDEQFNEAVKALGLRRCMVPGHDDYFAQT

>contig28000 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53300.1|) 1e-106

MALIELFDGTAEWVSSEILHPQLQAVERAKIITLFIEAADQCYQMNNFNTLFEISTGLLA

PCIRQLNTTWSLISASALEKYQCLQQVCSPEDNYRSYRQAFALAEGHPRLACWFILVKDL

FTYEESMKTMEDGLVNWQKFRKIFRVINDTLDRQNFAFIRSNLGGATGGGTGANTGNVSR

KGRGILRHDRKIQLHIRHRIDT

>contig28097 Frame-0F

MRRSLRRHVGHMALFVLLLERSVRAQVLLTDACEKPAPTLATLRRSETIPSNAEVVYENC

TVVQITSTSSNGSTAVDASNLGIAVISSFPDVTTVILSGNQVTTIYEDSDATVKMLDLSA

NGLSALDALSIPSSVNK

>contig28538 Frame-1R

MVLAIPPTKCSLNVDQLGDLLIDSSLDAALLYTPPRSRSSELTPVLLVIDMPAPFRSRLP

PPCLLTWATFLALEKLLQTAMQAMKITTRKSLTRIATKMFVLQCGMI

>contig28743 Frame-0F

MDPGDSVLHVAANCCNEQDVLTLLQSGSNINALNRRGRTPLHTASMYQNVEVVAILLNWE

ADYLVQDHDGNTPLHLTKDPRIVRMILEAGCTPNIVNADGRTALINSVDHGDGQIVKLLL

HFKADVLFRELKHHQTALHLAVRKGHYQIVMELCKSSDIDKLILLTDRNENNALHFAVSR

DRKNGYRLVDFLIKHGAEVDKVNARFQTPLVVHIMTTRQSDAAIAELLLSRNADPNIQVA

DGSTLLHVAIERELIDIACMLIKHGASLNATDAKGRMVIEVANKKYLKKLLSAITQPPTW

INEKERRACMLCSSTFKFGNRRHHCRHCGRVCCSDCSAFTVEMHRFPKDFSGRTSTNGNQ

VKDPQRVCRTCHVVFKMRSVQKESKSGFMARVLGYEWDEVTAPK

>contig28967 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57761.1|) 7e-65

MDVAMTKAQQHAEAEEKKQFGILLHVGDASTGTVHIVPLTSTHVLVEEVRKDLERLSGVP

TMDQILLGGPPFGRLDPRRIIEYYGIPAEDKEVFLYDRRLLSLDSAMPAPTSAASTPIVI

DLPSQPTTSSEGSKMLSESSHPMMRALAEYEGYFQLQTSQSEALENGT

>contig29072 Frame-0R

MSFSCNDRFDSRRPLWRAKGYIGDKKGKQSY

>contig29186 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66377.1|) 9e-08

MQSKLEKLLACRVITYLYRIPNLPPLEKHFLPVNASVLAEKKAIRGLEADSKKCGMDRAS

AVFPVYVYSFSNPALI

>contig31099 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56648.1|) 1e-26

MLDDVSIQINNTESAVQQQTVAARKVVSAHRKLFCYYVIILLLAAALLIVILV

>contig31334 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65480.1|) 4e-33

MASRTDAQFLRNFFGRKTKFRFYPQCESCSNLQGNVVKHWKSTLKMHLLSFRAYHATGLW

LILLCSGGLYVNGSTFHKTFERIDVVDDAAESCCTSLDRSLLVSLRKREQKLRYMRRNSS

DITQIAVIDKELKAINECKIAIKASIERQMAHA

>contig31510 Frame-1F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY64041.1|) 0.0

MIDLRYTPITSITAVSGSSMDISTPEGYERLNSDLNKERTGAPYVYLCVKRCPEQASTDV

AMEGDGERILPVTELVVKVASSTDIKPSLPGFERVELDLNVGGGSSMGDKKQVYLFFRRE

PNGSPITDLQVVFGNESIPDGFKQIQVDLNQGDGTKVYLCYRCDMPITDLKIVNSGIPGY

RMVDHLLNVCHGDAVKQYLALKVGGNEPCLTDLKLVESHDVAIYEDQGWQSIGSPFSSAL

FPISSPDSSPSAPPQLMVRCGHGNPIFAIDVFRAPRQVPKYNDYEVIELCSAESSAADLD

VRLKGDWMGSEETDRGRRAVRLRSVSKPIANALLLRGSLMEKGVISCIATRVSSWSNSIT

ADTTVSAVPVDPTTAHSTSTCALLKTYHISG

>contig31833 Frame-1R

MEYGRLVVLGYSSYRVDMVQRARSDGLDPAPSFGLAHARDETKFSRKRSLGQLWKPLGDQ

NAHFVLEKRPQANGVRLHRFHHIMPHELAKRVKKKKDLKSITTGMMQRIEATVCKNDQSE

DRNALLRRVPYQLCLPMNDQDAWASVTEFHADPRVDMFQIGRMPCRENDFVIPGPRVGSS

GTISRYAARILCARDPPYECRIYAGGFDANQQMSTAGHALKHCVRCGTWSKRLRLDHTCV

FKTLLQPNLPSKSCQKGKNTVKHYFEKSENDESLEHVEVEVHNVHELPMDGLTKNGVRVW

LPERKQWFEVSVNGRLYVIEARALEARETVESDRLRHLHVAMQSRSGTFNRPITGAEDDL

PPILTNGAVIDLGGVQLQFQTTFRSKIEANDEHQKLLEAPLVYGRATMSSVCTQLERLNV

QCPVQLHSLRFTRTSSEKMVPLDQIPHVFTACGHVFGYEKRIAQSHTCPLCRTPGSLVQL

LLKENSQLQSTEEQHAIPECVFNPCGHAISTKLARRYAALLMPNGRAICPFCAVHLDFRV

PFSRLYLYCDSD

>contig31846 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53527.1|) 8e-06

MTGDATSIASLPLVGKKLMKKLSGMANESAATEISDF

>contig32586 Frame-0R

MSLEAVENEQQARLYGRARAKEIFQPVPWNPLKPVPDDTTQLYEHIDATGYRIRAIKPVQ

ATLAEVEAILTAPTSLGGKDDTIPTLLAQLLPGSYISGGRIARYPVLELSTTEHEHVALQ

YARIKPYVTKPPTPTPHEAIPLVSLDKFVLLSYTLSTRLQRSDKSSLGNSHRSASSVPSL

LHLYRQVQVPSFASRRPNFHPKRLANYDWSITYIIQERASGNTVDRHAFVTVEVVLEWMW

GHVVEVQTLDDACLQRLRSDALSLVRL

>contig34629-1 Frame-1F1

MKLIQADPAANVTELWTSIARL

>contig36106 Frame-0F|Blast-DNA polymerase delta catalytic subunit [Phytophthora infestans T30-4](gb|EEY55821.1|) 0.0

MTGSKRESPPPCSYSEPKKPRTNSNGSRFKPRTFVDDLERMTPISTKASAWPRKPMAPLD

PDVDSLAFQWIDIDMYDGPPLQSNPKNGAAVPGLKASGDSTQSATIIRLYGVTFEGHSVL

MHVHGVLPYFYASCPSSFDESKCGDVRTALDAAVSQRDRDNSSNPRVVGVQVVRDKMSIY

GYQFDRVTPLFKIFLSMPSYVPKLRSVLEAGVTLPGCDFRSYQTYESNVPFILRFMIDED

VRGCNWVEAPKRTYSVRSDALKKSLCQVEIDITYDNLVSHAPEGEWGKVAPFRILSFDIE

CMGRKGHFPEADQDPVIQIANVVQEQGAQSPLIRNVFVLNTCKPIVGAHVMEFEEEGEML

AEWARFVQKVDPDIITGYNIANFDIPYVLNRGKALKVKDYNLLGRLADSVVSMEKKTFSS

AQYGKSENVKTTIHGRCMFDLLPIMRRSQNLSSYSLNAVSAAFLGQQKEDVPHGIISDLQ

RGTDDDRHRLAVYCLKDAYLPLRLLDKLSYFVNFIEMARVSGVPIDFLIERGQQIKVFSM

LLRKCKDANLVVPTLPRSQTNEDTGYEGATVIEPHKAFYSVPIATLDFASLYPSIMQAFN

LCYSTLVAPGDVDKLAPSEYEKSPSGDIFVTSTKKKGILPLILEEVLAARKQAKRDMNAA

TDPMEKAVQNGRQLALKISANSVYGFTGAIVGQMPCIPIASSTTAYGRQLLFRTQEEVER

VYTIANGYKADAQVVYGDTDSVMIKFGVDTVEEAMPLAEEAAKRVSEIFPKPIKLEFEKV

YFPYLLMNKKRYAGLLWTSPDKYDKLDSKGLETVRRDNCLLVRRMVDTVLRKILINRDVP

SAISYTKSVISELLQNRIDISLLVITKGLKKTVDQDDYKVKQAHTELAERMRKRDPGSAP

ALGERIAYVIIDKGKATPLYEKAEDPVFALENSVPIDCDYYMKQQLQNPLERIFEPIIGL

SKVKSDLLNGAHTLKRSKPVLKQNSGGMMNFAVKKLKCLGCKAPLNGKGALCHSCMEREA

EVYSRQLTSVNELEHLFARLWTQCQNCQGSLHQDVLCTSRDCPIFYKRIKVQKDLIEAQG

SLERFQSVDW

>contig36656 Frame-2R

MTFLLFLIRAAMMNYAVGKPSRFFGFKDQGDRILRVSDMRHERMGFMFQLNEDLPSEFLN

APHT

>contig38661 Frame-2R

MELKQAYYSATNKALDVSAESGQAIPSVGTQWEKLATIAFFSLCIDARAKQHVIDESPNA

VRTKALLETLESILKQQKQCCAMEAVKITFKDYLNDPNQDPQSSNNGPSNGFSRIRTLQY

VFRRLRQAGLLFLEDDAVDRHMLLSFEAVLKPALLQILRDSPKGRSIPDIADALLCQELF

KCIPLQWIESGLERLEESQLIVHNKAFKLFYVK

>contig38881 Frame-2R|Blast-phosphatidylinositol N-acetylglucosaminyltransferase subunit Q, putative [Phytophthora infestans T30-4](gb|EEY60249.1|) 4e-81

MLDMVLGRVVLAYVGDITAAHIQVINTSILNFLHQNIKWLMGAPAGFKLNKPLASILGNG

IILWLQLWNFIFERLGHATCSINLEGWIMLFWRYMGLTLQLTLVAEFIRISTWHFRCVYI

YFAKTNRLQFKLFSSLSKLFLGKKINVLRHRVDTCEYDVGQLLLGTLLFTILSFLVTTNL

VFFVFFAGVRGSIELLSLLLWLPVVLLKSLPMASVLYRIWNPNFFIIGMELQTCHDLTDA

ATIEHVGVGRQCLELEDQQREILRNAFASWETSNKIQSKVVTFQLEPVASSFSALFTSLH

AYLQAASARYSLAVIAKACLFGSAEIDRVPLSLLFSYSS

>contig39165 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54716.1|) 1e-105

MKPSLQVALYGLACAAPNVTAETLISHVPLLMWSQRTIFAGSNVYLGYNMDEVSVASAVK

RVLRYNANIDKEGLLSTEALQYQQAELMCLFLLPSLASNQMSQFSSEGNSYVQHAVQSAV

SSVVLPHTTRLKPLLPELSSAEPHVVGAQDLSLFVASTEGKELLVNGKTDLLVVQMPELM

SLPDVDAAILKACSTLEAATGEYVDFAFTGNDASSVQIQDPLARRLAASTKAKHTNITDK

TSMTCEVGYLLGSSAKSNDFCFSHYVSITPDIMAGLLIGLMFVTLSYIGLSVLHQIQIPQ

RYPSRGAPRGKEF

>contig39811 Frame-1F

MHTHTSPTPSGVPLNKRPCHVKASSGSRAIFRIFDVETLLEGLLVMLDLPSSANLLEILA

SNVSWQSVLIQDQFWEKMLITHFGGDLPPVEHFNDVTEQEVESDYEEEDEVQEEEDEVQE

EEDDDDDEMDLLANIEADAMMEEDNSLLGDSEEAEADEDTNSDAGLASTLEAEISAREPS

ATTQMATTVVAETSQMATLKWVNGVPSPMVLDVACPKLTSFLRSAEQLIQFDTLVQILQG

DIGKLETVGDQRVDGLAFPTASHLEDPHTGAASVIFRRAGQKLRDHVADLNIRLNVGDAI

VTAGFDAGVDKLIHCVGP

>contig40086 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63520.1|) 6e-52

MVNVSLHESTQQEEAKDKREPPTNKIQKQQELPLSKGHDTNNDQSLRCHLGRLVIETQQT

IDSHLLLFRVGLIVTVAVSAVASIKLSGVLTRFNSVEDIPPWQFMRRKKLRVRMIRQARE

DPSVFYVYHTPIFRRLMLKDVLPPLPTIASASEETKRAGLLAVRPFGVDVAKSSEEWVWS

NFISSNRYLTIRLLQR

>contig40172 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61387.1|) 1e-151

MESFGAEFKETPYPVIAVIGSRELQDKVLTQVRIINEEIVPKLHYASLPRDHRFPVKKEH

REKHGTFPNQTQRDFDEYNIRGILKTRWMKKHHEVLPAVVVLVNEFDPRWSPLDWQQRET

AMREEVEKFKRMVFARECRVVLMLLQQVDDPGVAPLHTTEERLINLRKRLDTDTKGLVLL

RSRDLVHGSTTLYKFESSVRQMALEYYKVQTKRVKRYQKTLAKSPGSSALHARLSFKIAH

YYEFRRSTTKVLEHYEASYQAILALPLNENEAIDGIAFTQVLTMAEIVNMKLCYHMLFAS

NNSKGAVEQFQRHMGVYARASVVAHRAYEHWKWV

>contig43173 Frame-0F

MAEVAAAVALKRYARQAGGLQIVAYSYAKAVLAGVKVPIAHDAFELHSRVLIQQLRSSRF

MYWIIEA

>contig43623 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53328.1|) 2e-09

MKVKKKTQKMSKQCQTNITDAFDAISNYEEVLIAQGEAMGMERGREHGIEEGYEL

>contig43656 Frame-0F

MPYSALVDFLLAGHIDSSHGHWQQAPLFRWNLSRDDSQSKNQIKSAVQVHPNRFEHSLEL

ASACGIPDFTNYVIKFVGTLDYILITSKVLKVLNVFPLFTEEEVKHEVALPSSTFPSDHI

SLVCDLTW

>contig44099 Frame-2R

MTWLHSLLVMAACAASTAATEISVCRDATYNISVDAASLCAGTGAAPAGWSCPKAGEVAV

ADCVSTLATYTSDHCVTYEDAVCQVIHNNTWGCVLPSVGCNVNAPREVESVCKTWDYSDN

DLIDSSTLFNTKEKYNTSWFMPLTKVRPLYECGRTPTPAPSTTLFEASSIASKTTTTTEQ

LATTSTLNSTNTSSNPLADVSQSEALPTKS

>contig44334 Frame-1F

MAQPFLPITRQLSLIHHNFHRTKVWPAENTDRAQRALYRVISSLENIAGLNMNSSNIKLY

GPWTFT

>contig44464 Frame-2R

MRAGLTRSRTASVQKTARESKAMIFGIT

>contig44510 Frame-2F

MFRKGTRQRGRAQLAEALVLALAAAWVSHVAQYAKSQTINGEVLLQMEQRLLQVATMSHV

LYGFYILCFLAILSSLYRPQASHSLRMSCRNKHDSGLAVGCLLPPLVLLSRLLAEIYQVG

SFSSFTCFYAWVSISIGFSALLKFVVFRSMTSLQINLLVDVVLLPIVFGVLSPTEASQRF

LLATGARIAVAIVLAAGLTLLPRSFTIGEAVLVAQGIGLCAFDLVLVTTHRMRKQQLLQS

VPKLFQAWFIFEIDRPKSVLALEVGMLGSLLVCVASISLLQSNGVSSPTKIAQPLSFHKS

MQFILLATVVVGGVVYPWSCLLLQTWNPFAWLLDFLTEPSISGVMLVPPRLALIVYWISC

LIILVPIVAFASKHFKLRNIVTRKYFHFLVVLMLGPPSFFDAPMLSLSYGVALSVFILVE

CVRAMSLPPFGRSIASFMKSFIDSREAGRVILTHSYLLIGCALPLWLVPPPNPPSPLVMN

AGVVALGIGDAMGAVVGSSVGKRMVFGTKTVEGSVAVFISIMIASGLLQNHRGIIGADYV

QVVKLTCAVFLTTILEAATAQIDNLVLPLFFYSVCNLVECI

>contig44846 Frame-0F|Blast-cysteine desulfurase 1, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63348.1|) 0.0

MFIKWLTKEANMQTLRSLSRSMCIRAKATGSARSFATDKRYTPVNKVPASVLENIKSETI

FSPGFAVRGEQAPVTGAKPAYLDMQATSPVDPRVLDAMMPYMTYAYGNPHSTTHEFGWDA

DKAVELARGSVADLIGANSKEIIFTSGATECNNAIIKGIAHFTKAKKKHIITTQIEHKCV

LDSCRVLETEGFDVTYLPVHANGLIDLEQLKAAIRPDTALVTIIAVHNEIGVLQPLKEIG

QICRDQKIFFHTDAAQMVGKLPIDVDDMNIDVMSMSGHKLYGPKGVGAMYVRRRPRVRLE

PIISGGGQERGLRSGTLATPLVVGFGKACEIAATEMDNDSRWVNYLSNKLYQGITARIEH

VVLNGDLKKRYPGNLNLSFAYVEGESLLMALKNIAVSSGSACTSASLEPSYVLRAIGVGE

DLAHTSIRFGIGRFTTEDEIDYAIDLCVKHVSRLREMSPLWEMVQEGIDPNTIQWSQDAH

>contig46361 Frame-2F

MAAIRPPSIMVQLGAHTFGRVCITELLPRWENNMLERPQFAAGTVVRCLVLSTDNNHIDL

SLREDAIEDPTEYTRKTSKPREHNVGDLVPALVATTTKSGCFVRVDRHTTARVMLRDLSD

DFVTDPQTHFPSGMLVAGRVTKKSDRG

>contig47191 Frame-1R|Blast-DNA-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY69219.1|) 1e-94

MLELIGHLVEKFPRDTSGNVPPLLSWIEIELEKQFSSNGPEMMLISGLLFALARLLECNK

ERYKQDEARKKKIYSYLLTVFATTVSGNLSRFQVTNSAETFLAKHAQIFQQEIGENGELW

FSYVQYCCESENKTIKEHAFACSNAV

>contig47472 Frame-2R

MKPWLLSTRTAATLVYKLAKLMQLSLTGINVFSQYG

>contig47977 Frame-2R|Blast-malonyl CoA-acyl carrier protein transacylase, putative [Phytophthora infestans T30-4](gb|EEY62333.1|) 1e-22

MASRRLALVFPGQGSQRVGMVKDLLADWPRVVGDVLEEASEATGLNLRRRMTEGPADDLT

>contig48521 Frame-0F

MKSQALLSHTIPIAFSIKNTGHLVSPASSSAFKCMSPSLSLSKAVEALRRGLGGFIGAPD

RCVEGLADLSFVCGC

>contig50577 Frame-2F|Blast-Clathrin assembly protein AP19 [Plasmodium knowlesi strain H]emb|CAQ39955.1| Clathrin assembly protein AP19, putative [Plasmodium knowlesi strain H](ref|XP\_002259182.1|) 3e-37

MIETVLLVSRQGKTRLAKWYLNASIKEKTRMIRDITSLVLSRPHKQCNFIEFKEKKIVYK

RYASLYFIACISKDENELITLEAIHLFVEVLDRYFGNVCELDIIFNFH

>contig50726 Frame-2F

MSHYRLQNHFCDDQGVSADHFNYMESMPFPQSSSLARSISTMRPFVASASTSSDAASAPE

SDVTTSPHLPSRPSCEWSEWEETFDSLNPAADDLASANASLDLELDEYLLATAEDFLEPF

ANIDFTPDSPILAADQTLIYDQKHYFQMLQIPSIDTSLGFGAELHNLEACKDNVLLLSTD

HTMHSDRKRKRAKPAGETNAAIKLKRSKQFNANIKSASKVKEAEIRYQRRYNVLHRILEA

WNTGGIEDIEEIANSVYEKDVTLISPDISEGLHGLEAVLSHWNLLLDAFPDGIMEEYVIQ

REGCNEELLATWTFSGTQIYPFLGVQPRHEKICISGKSLFTFEGDKIRQMVLSWNHRETL

LLLMGVQPDKPSSVVFHKSARS

>contig51981 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61691.1|) 2e-50

MCAYEFKPGDIAWNCKACQVDETCVMCNDCFISSDHENHEVFFYYTHSGGCCDCGDTEAW

ASDGF

>contig52665 Frame-1R

MDSTMSSARQVWLFPSTMSNVEFKTPTQPKLEATWRLYANILVAVLQPFQFGWSTSQMNN

YLFHNEADCAARPIAPGTCLMFPGHTQNQWTLAVSSWVLGGMIGSLIMGRVSNK

>contig53248 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66323.1|) 4e-52

MQHVARQGAMIADLEHKACALNGERDKQFIFMFQFSEALRQIVHNEWSAPEKNH

>contig53424 Frame-1F|Blast-cleavage induced hypothetical protein [Phytophthora infestans T30-4](gb|EEY56378.1|) 6e-33

MWSLLCGAQTSEASQSDGLAFLAEKLGVAVSHRALNQLQRYRRHVSGILQIVTAHNP

>contig53550 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59076.1|) 8e-25

MMQQSGATSFVQVLEKESWFWKEHLDKAKNDSNVKVQERHVLTDLLPGLQHIHDVKVGRP

GKPDDSVYRTSEYARKWQP

>contig53925 Frame-1F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY53469.1|) 2e-21

MAPVYDSIYNDHADRQPEVTGLERATSPVTLEKQEKELDCFDEEDTVVDSKNTSPQNIPL

MVADAVCTTCDTLDSALAIAMACETESSMRIKQLEVQLFKLKRQY

>contig56232 Frame-2F|Blast-SNARE associated Golgi protein, putative [Phytophthora infestans T30-4](gb|EEY67395.1|) 5e-66

MLNVLAGAFLPSLLAFPLVCVLTSCGASCCYLLSKRLASEAIVHSLSEQLLPGKLDILRS

KIENARAQGQLLFVLLFLRIFPFTPNWFLNLASPWLSIPLKLFAPSVGLGLLPYNLITVQ

AGAMLSSLRNPSELLDLRTMGWLALLAIGMLLPIVLKNRAKTQILKKE

>contig57121 Frame-2F

MPVCWIFSKLFLAVCVCTSPLRPRSFRECSTLWLALIRADCLNVLATAYTSTQLISVIAC

LDRLKYLLYRLLAGNLVNESKPFCERSLLRLLHLQESDTTAYFHGNCVEK

>contig59053 Frame-0F

MGHRTGQSYELAQFIAATNRNNLTIVCGDFNSSPNCLELRVPKQLLGLRDAYTDTNDEDG

LTFASPENKYSYGEYPMRMDYIMYKINAQHLSLWHLVNSSIFKGFFTDKRGEKTPLSDHF

GVRAEFVFKKAIKSAQSVDQETTSVALVDASDVEK

>contig07091 Frame-2F

MLEAVAHENAMSSIQLRLLKRNKVDHNKANFKLLLEAMEASGPKTGVLRKENPVGELVTT

FQSALNHSTLEQVDVTRGLETVLMIKEPQELENIRWAGALSSKVFKLKFMEDMEQIIDDE

QIRSHEDISMAIEEVFDTPSKIKVTIDPVDIEPCYPPIVQSGGTYDLRPSAQSNQDPLTY

DVIICSLGARYKGYCSNVGRTFFIDPTSSMEKAYELLREAHEVCIKELRPGQSVGKIVEK

VRKFIQSRNATLFGKLTKNLGFGIGLEFRESCNLLTTKNTTIIQEGMAFNVAFGFNEIPI

PESQRKKKKLDSYAVFLADTVVVLANETKCYTKVPKAWGKVRYDIEDDTDVKDEKTARKS

NGNVDTSLSGTRNQVLQSRLRDQQRLLEGKETDQERRDRHQAELMRKKREEAMRRLEEQN

HDLSDDVKKEKRIK

>contig08393 Frame-2F|Blast-actin-like protein [Phytophthora infestans T30-4](gb|EEY68985.1|) 0.0

MASFKPAVVIDNGTGYTKMGYAGNAEPSYIIPSTIAVGGSDSTTVRSRQGIDDLDFYIGH

EAIDHASTHQVNYPIAQGIVQNWDNMEKLWQRCIFQHMRCEPEEHYMLLTEPPLNPPENR

EATAEIMFETFNVPGLYIAVQAVLALYASWPKVKDPSQRSLTGTVIDSGDGVTHVIPVSD

GYVIGSCISHVPLAGRDVTHFIQKTLRDRGEAVPPEESLDVAKRVKEAHSYVCSDLAKEF

AKYDAKPDKFFLKFSDFHPRTKQPWEIDIGYERFLAPEIFFNPEIFSTDFTTPLPNVVDQ

AILKCPIDTRRGLYKNIVLSGGSTMFKDFGRRLQRDIKRLADERQAANLALHSKFQQAHA

EALEVNVLSHRMQRFAVWFGGSMVASTPDFYRVCHTKAQYEEEGPRIARHNPVFNATM

>contig09970 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58032.1|) 2e-71

MQAPGLEERKKALEKKFVEKRPPLAYAKLSGRVEDDTPFEKLITHLPAELGRGPLSPLPD

HRIALGEQKAISRLHARIQWNQSDSCFELQCLGKNGMFVDGKFVTKNQIVKLSSKVPLKI

GHARLYFLCAIRSTISTMSGYKIL

>contig10514 Frame-0F|Blast-calcium/calmodulin dependent protein kinase 3 [Phytophthora sojae](gb|ACH68464.1|) 1e-110

MCHPNIIKLQDVFDEDGRMCYMVMEYAKGGELFDRIIAKEYYSEAEAKKVVKVVAKALRY

CHARGVTHRDLKPENLLYADETDNSVIKVADFGFAKLLKEPSNMFTMCGTPGYYAPEIVR

KLPYNSKCDIWSLGVITYILLCGFPPFYSESHVEEMQNILNGAFEFIAPYFDKVSQQVKD

LICKMLVVQPSKRLTAQEVVDHPWFNDIKEADDDAPMLLVGKAMKETR

>contig11669 Frame-0R

MAGRTEPAAAPVTNNGLNCIKCGRDVSEADAFCIYCGTKVSESLSQRKTTVSPDEQPEPK

PEPKPATSPTPSAAPKQAPSTPDTVKPELKPASKQTNVKQPVAKPATVSRTVTRPPVSNE

SGASPNGSLGISKPVPVQTAT

>contig13379 Frame-2F|Blast-hypothetical protein [Vitis vinifera](emb|CAN82171.1|) 2e-06 NOT\_ORF

MRSAKRKSSEKPMQDKLQAYEENGVWSLIERPTGSNTLHTNLVCKTKRRSPRASKGKTCG

VRQ

>contig15553 Frame-2F

MILALENINDRISEVRKITKSISDSSRIRLREGESESIVKPILSFSPDKAHNQHLITFFE

EQIAQILKEFFPGLAKFEDMASFERYTYQYGVYLKLSEFMPNKQILFELVDKHEIGKEYE

CVRRFALLDQRNEEAWVKATVAANRGSGKKRMADPTEAFKKVEPFKNEANLDTIVRSLRF

VKLVKNEQDSLLAEVIHVLRKIRFNFAHLEEFLTHFPDLEDLGPKLKRVLEKENAKAKAM

EDLSKLKQ

>contig17744 Frame-0R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY67300.1|) 0.0

MVLDDARQDHFVQIETPKCRKATPCNSFTSPRFSLQWRNLSLKAKITNPRTNKTEEKEIL

ANVSGTANPGELLVIMGPSGAGKSSLLDCISGRNKAVMGEITVNGLPWSDATKRLASYVL

QDDLFYQTITVKEHLVFQAKLRMGKLHTKQQYMKRVDEVMEQLGLMKCRDTLIGGSSQRG

ISGGERKRLSFATEILTNPSILFVDEPTSGLDSYMAETVTAQLQQIARDGRTVIATIHQP

SSELFALFDQLYLLSDGSPVYQGKTVDSVEYFASLGYACPSMMNPTDYFMKQLVVMDKAT

DNEGVARIEKFKTEWNIRQPMLSSPSLDEETAVTEYQDTRLNVLGQFSVLVHRNVIRFAR

DRFDLQVSLFQTVFISLIVGLIYLQLDVNQKGVQNFTGAFFFLIVNQTFSAANPVFISVP

LELPIIIREYRGGLYHLFSWYIAKNVSELPMQLLLPVLFFVPAYLLIGIGHGFHVYIYQQ

IIIILVNSCAVGLGYMVSCLVRRIDIAPVIGLVIILPFLLFGGLLINSDDCPDYFVWIQY

LSPIKYGFEAVMKIFWERVPTIACNEVIENCTARSGTDVLRSFSLASRTPFGSGLILLVI

NVGFRTVGFIGLWLSLRKER

>contig18406 Frame-0R|Blast-dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichyl-alpha-1, 6-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58713.1|) 1e-53

MVLNLLLLRHVSFFQMISWGISAGIASLVMTVVVDSYFWQRWLWPEGEVLWLNTVENKSS

EWGVSPPLWYFTSALPRALQMTALLIPFGL

>contig18617 Frame-0F

MRYRMSQASSNIFGLQLPKWSPWTGCVFLHSFATTLRFMTRRNIRTLFLLNLSIESYHSR

RIQLKREGVLVPCLSSSRNNSCRPAGRFAIFNLFSFSLDASTAVRSDYAAVLYRHAFKRG

QASATRSNRIVLDRFVDRYTASFKSHDNPHEWAAVRSALGNLSTPPFEPTTGPRALFKSM

ERSTKGARFFSSYL

>contig18662 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61322.1|) 1e-169

MASDVLVQQILDLYHTHKHIPDSISMLIPILPSLRGDILFPLLPQLLSLPQARLSVAITR

LIEAMPPQAIAPIDLLVALHHVDLKSEPSMQKKVINAINFCVEHRHAFPSDVLLHVCQVL

VQEEKISKLSLRTLILSVTAYPTLQIDVPPLLNILIERKVWEMEDALWKGFMKCSVLIQP

ASFPLLLQKLPVPQLALLLKEEEKLPSLLREFVLTAGPDGQPMEMPSAIDALLEICRNVK

FENAAPDDGGISIKVENTDPVKVEYI

>contig19874 Frame-1R

MRTFILNSKKISQQIHSEQKPTKSET

>contig21796 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58040.1|) 3e-07

MESTSQELDVPSSDAIRLILQFLRENRLFRAMRALQEESQVRL

>contig23509 Frame-1F

MSPTGGTPTVGTPSPPCVTSSQTSMRKKEPRVVSNTTTSGTSVSMSKKAADDAMGSAASL

SSGDLFVRNLSIMSVAHIARGVGFDAIQKSAADVLAEILGKYIQRIGGAAKELAELAGRA

HPKATDVMQAFHDLAPAAVEMNDLIKTLESVKRPFPRDVPRFPARKRDISGNTIEQTTIG

RREGLPPHVPTFLPPLPNRHTYSSESRLVVEREQDLKRQRLGLFSEKAHVRQSLHGLQTV

AAKKPMAMVRQPTWNAFQGATGTNAMDNPFVQAPVVLPSARD

>contig25381 Frame-0F

MSFNFGTSAAPTSGFQFGATTNAPSSSAAPSTSGFSFNASSSAPTASSSFSLNATPT

>contig26289 Frame-0F

MGSGDRLAIPRFLRDSCRERRITDVASTFSPSSPSEGEADSSVVEELQRRKAAFLAHFKS

NSVPMAGGEDTSAPDYSSSRSMDGCFGPHSTDSKCHVCNVPLRLLRLRHRCRNCQQAVCS

VHSKNQVPLPHLGLMKEVRVCDLCTRQLVQRRAGYRSPKRLRSHPSSQSFIERESDVEVS

PLGGESMPKIPSSVPLAGTTVLSGETVPTATELLEGTSRGSFTLHALGSGFTHNSANTMP

GILYSCLLEEQDNTMDEILYLGTFTMGGRSLASRRMSANVALWKWRIFMLTTAEMLCFKA

AGSISDDGTASMSAMALGEVRSTVHLSDILHIEVNDQFPRILTVIRSDGRVFRVRARTPA

QCTEIAVTLRKAMQHFQDALFQLQRGPRPEDNALSCVTLQHESSLPETVVASNLGVGHSF

QVEMYPSSILRFYVTGPAANGTAQVSREMLIRGKKKHVPIVVEAEPFEHGPRDDHVLYVA

IRMENAMKRGSECVQKSTRRFWSLTSLLAIIAAVTNAMDDRSLALLAWVTVLVLFLARFH

EHLRIFITTKRFARPHQYEIECVSVTMGKSEGSVDEQYERFGRRRGAGQSLRSRL

>contig27668 Frame-1R|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ49042.1|) 1e-11

MSAQHNWTSNSATLPFECKMTLRFTDKLDALYVLRTLEVDEELQPKKIIRTLTVKGTELL

VHIAATEIRLLRAAVSSFYDMSMLSARTLLEFK

>contig28395 Frame-2R

MSGKEDDAAFQLVDIDLHKQVKSFEFVYIVTYAAVQTLRATIYIGTTNKTLTNYGDRAHS

YFYTKVFSLVLPMGFFFVPIIDYMVETRGLSKALLFTNVLGVLYNTVELIPILPLQCLAF

ILFTAFRAFLYAIISAFTAKTFGLKSMGSLMGILFSISSVVSLLEYPAVYVTNVLFNGDL

LAVNALSLLWGMLMIPLTLYLRKFEHNQEQKRRSELAHQGNNRPHAYNSRETYSSLMDTP

TFGVTFLRSPSNAPHN

>contig28584-0 Frame-1F0

MMNRQQSVYAYDPKRTAASLAAKTHGTKTTPKRHLRLAGGQVWEDLTLEEWPENDFRLFC

GDLGNEVSDELLAHSFAKYA

>contig29073 Frame-0F

MVTKPKAPKPTTISASTIDSSSAISFASTSSASMAPPTAAVASSITPNTSSASSSSSATA

PAVSTPSAAPATTAASSISRESSEIVTDEHMSASVQQLMDMGFPEDQVRGALRAAFNNPE

RAVEYLMTGIPAQAAVRPQTAAPSAGLGASGEDTTNTLEALRNHPQFDALRQLVQSNPAA

LPAVLQQIGTQSPELLRLIHQNQDRFVQMLNEPISSRETGALPSSGAGAAPFEFGMGNGG

AMPTPQQIQQLVDSLSPEQQTQMAAQMGMTPDQLRGLSQMLSNLPPEAMEQMMASMGGSS

GLEGLGGGTGAGSGSHRIMLTEEEAAAVDRLCEMGFERTDVIQAYLACDKNEALAANFLM

DSGDNFGGMATSDTGGQGDDNDDIYG

>contig29187 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66377.1|) 2e-43

MIAPRKTLYSTPLSIFRQALELVHVDASDVVYDIGCGDGRLLVEAAQSFGVRAVGVEIDS

KRAQQARAAAEAGGVGHLVTVHEANALEFEIPTDATIVFLFLISRGLS

>contig29590 Frame-0F

MRLSVSLVRYTIMYLLIQFNGNDNFV

>contig30813 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67598.1|) 1e-123

MTDAAPSKVEALTWTDTHEQHLVKYFIENCRSRWKIPIPQGLQRDNELVAFRNHKISRTG

FGLVTIARKLGKRKIDVKKRLKEKLLEPTVKLQLEIAKREAEISDNPTGLFDEELAIQES

TRLTALFRRAVTMIVSPREEYYPLVAEELISFWAPHEVRLVWRYLWLKNWIVRASDKERG

RGYCTSKRLQDSLKVTTLSFPLILFQQAAEQESMVSSTIEEVVGDSNDPMKPSTPLGELR

NCDHLFEDDFPTNATPGQCALELG

>contig31098 Frame-1R|Blast-peptidoglycan-associated protein [Erythrobacter litoralis HTCC2594]gb|ABC64882.1| peptidoglycan-associated protein [Erythrobacter litoralis HTCC2594](ref|YP\_459679.1|) 5e-10

MPYCAPTPPLPPPPPPPPPLAPPPPPLPPPPPFLSSNVSDKFLSVAFGESSLTSVSLIAL

PSAIATNAVATISAVRIRRMVNFLKMWAWV

>contig31159 Frame-2F

MASRFCNFAWKAHNLSRIFTISAATTKLTHPIVRMPEKDPSELNLASAAKRDFDRHYQVS

RQLSFLIK

>contig31335 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65480.1|) 2e-93

MSSWINAAVDRLRQHFSGDRSIDVYKTLAAHVVDATTGGALFIGGTSVAQVAQKLLRVGS

ATGFLLPQALGAVAVASSSVLALHFASIPRSIYQEMVAQRRQTSDHRWLVLEARNIQPTT

PWRLLQSEVQERWSILSQSPDLVYMTMGLLCFKLLGGRMSALAPSPLANLGAFHLRKASL

PATIEYATSVERGIIQEFGRLYGCHTCGAKRGVRYHADHMPPK

>contig31586 Frame-1F

MKVPDASPAPATYASPAPAIIVSAGSGGDHKANGAILAPATTASPASATIVSSGSGADLK

GSDSITAPATVASPAPATISIDGGGAVPKADDLKSNTGGNPGVNGKPVDIIAPATGPGAT

ANVKADVVISVKKTIGATPTPCPSSAGIGSVHKTGDSKTTSGGHSVVIVKTGGNIIPAAK

PSSVPAVVKAVGVKENSKVIGSSPLPVVGHNSKTGVYGLTPGGAKANNVVAPVSVQKVGG

SVTVGSTGVVNKTKPTANDAATQKHSQTSTNTMAYHRRLRA

>contig31847 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53527.1|) 8e-06

MTGDATSIASLPLVGKKLMKKLSGMANESAATEISDF

>contig32587 Frame-1F

MCQRKIGPFRRKKQCETCRKWLCIHCVGSKSFSRLRRHKSVSCVRCVEEAQNGSTIQTNE

SATMSVFQFPAVESVVVSSRARDASKRSSSSRLSNRKEIDLGLDPALGIVVATHERRVSQ

DKTELRSSASMRHEQQHENDMARTTLETSIIARNRVPKKLMATHDCTHLCVELGTPKMDY

QVEYMGSCEYPKAPVFQSETEMARAKYVEGTGLYFDARLLRLLRHDPVLEDLAYQVVSIS

SQWHGCSINLVGAYDVYCLVSAYIVPELDVDDADFLELETSPVTFDDIVPREESVSAYAV

YHQSPFFVADLAKDVRFQMHPFHTECGVVSFCSFPLYSTRNDTEDSSVYCVATLDLWKRD

PLLGCSHVSSEWMATIETLRHTISARIEALARESYSFKKPRACAAYSFGSSSDSIGSTRP

ADSMTDLYDIDSESVVDWPTSESGDRYRPLKMRGLGGNGSSWKYDSDNESSTSSTTSSCN

QTPRISSQCYTAAEMHSTIESLLQKASKTSQYLSQTGV

>contig33997 Frame-2F|Blast-peptidyl-prolyl cis-trans isomerase 10 [Phytophthora infestans T30-4](gb|EEY58162.1|) 2e-07

MRWMQNFMALCASGAYDCTTFHRNMKGFMVQGGXXXG

>contig36657 Frame-2R

MVLPGLAELLATQRQRHGNVATEKRSDGPSIASIQNQPEAS

>contig40490 Frame-0F

MEFLNVPTSRGMRLNQRIEDLHEALYEKADYQNELVNLVYRVRWGCQGVRSIGNARSHDA

TLLSESESLELCGCISAIGAAMPTLARQFDVCQLTDSSSSSPLSSDSTSDSINNTIKVDQ

PMHQQVPQAVSEADTQSPFDFVMQLMATNGMNLNTPTSTLFQDDADLTRSPVRQLPPRVQ

KNSFASLTSQDFTNLGSLSAQIGSLSSRSSGLSGLDLNSMNGLHGNQAPSLARLGSIGST

ASTSSRETPPLPFGYNDTYNSVWSQPPLPPSSLSPQKPVMHFPLASYNSDSPLQQPSSVL

SSKSPMKQPPLPSRAITNPHVIQPPTAFPVKQPEAVPTQAILAMVPKFSMYYSRPTELPK

ETDRVRKAMFARMLNHMHELPKATMCPLQPGHDPACPLSHSYLEVMTFNPLYKRLICRQP

SHYWGSQLQEDDNCVCLHIDTGLSWDWMEEHKRLYCARGSKCVNFKCLKSHSFEEMCWYN

PSYKIKRCSVRSHDHIARARGTLAPPLDCSYYHIEEGKNCDKRDFAAEDDHVGLDVPMLF

IERSHKPLADRLEAVRYARTTNL

>contig43107 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53705.1|) 1e-15

MKSIYQPNRPVSSDGYIRRGARWDVRVAILIIFPVGCLIIVLYEFLYLPEYATRGSAVST

PVNDH

>contig43172 Frame-2R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY61802.1|) 1e-32

MSNCVDCIQNVLTKRLLNRSYT

>contig43622 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56054.1|) 1e-42

MFHDTTDSARLSAFIAQELLAAFIVQHGDELGNVGHNLRDFHRFQYRIRSVIRASVEPLV

RM

>contig44098 Frame-2F

MDESVDNDQARGEKKAFDSTTQVMKYNLLN

>contig44335 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67625.1|) 6e-26

MLIDEFLGNLTSHDHLHKPLNNVLALFDKVGLPTSEYSLKHTVLQYVAAYNILRKYEK

>contig44511 Frame-0F

MELQKDALWTQFGEWGEVENINVIQRKSICFIRYRHRISAEFAKEAMSNQSLQCDEVLNV

RWAFDDPNPVAQEAGDRSDRDAIIAMMQAKGAVTTADAAFDYPEHYQMPMTKRQRIEGDT

MASYPDTNLQFSGTEGSAVKTDTEIMAQLSYADPSGEVLAHSDASEDNH

>contig44832 Frame-0R|Blast-N-acetyltransferase 10 [Phytophthora infestans T30-4](gb|EEY52909.1|) 2e-55

MSLAGAVAYGYSNIFVTAPSPENLSTVFDFVFKGFDALKYKEHLDYEIVQSTNPV

>contig44847 Frame-1R|Blast-cytoskeleton-associated protein, putative [Phytophthora infestans T30-4](gb|EEY62663.1|) 2e-72 NOT\_ORF

MHKHKTQKSLLGTVLPKMTDKNWKVRK\*GYEELKTLLERPDVQSSQVREAMELFTNMCED

ANASAMEAGMAAVLAYTRHIEPFEKQIVGPVMARVIDKGFSARPGIVKLCMELTDAFIAA

NAAEAT

>contig45282 Frame-1F

MGPWIERNGPRYGVVLGTSSFLLGHLIVALGVAQKAIAAIYIGYGVFCGFGMGLCYIAPV

STLQKWFPDYRGTAAGFAVAGYGAGAVVWAKVYRPCIEKVGLSSTFFVVGCVMATTMYIC

AIVLRTPHPEFTVGGLNMHGEFVDESASYTDAAVPQYKHRLGSAASENEVDFIISANSQI

RKLALIDAIKSPDFLCMYAMFFANQIYGLVVLSKLSNMCTDIFGKTGDEAANIVSINGLF

NCFGRLFFFAGLRPNGPQLKHGACICSQVCLLYDYDPAANNRGHHAVAHPQNSVHSVRGR

DFYPDSELWWRIWHHPSLSNRYVWRL

>contig45813 Frame-0F

MAVNLGTIYCNTHKSGENEATSYNDVEVPASNISPIPFQLFESLVRNPNCRQQFLKYLLA

EDSKQYAVFLRLMARLLTSFPHTMISISWSAEKSKTIAQYVLDILTDLFESAGIVSNDII

LVQQQLIFRHLMPAVLKHLHGETANNDNILAIACLRLLHVILLDFDYTDNNDEFKFYNQF

IRLCFIPHINALITSRKRITENIWQSMSELLYKLLFFNSSLLREIEEVNLVPTIIILLQI

PADFQSLPSYATKLVQMLLTSNDVRLELLYESGVATSMITSLTFALKHKILDETLLSLMV

ILLTLLDKQYKSTQQPEPTSTPVGYSELVLCGPIMLHICAWSGQEISPESATTDKCRKEE

LADLASRCLMLLSQDFGEEFNKIMFNQHETLTSELGNSIL

>contig47473 Frame-1F

MVHDRTAAGTHASARVVARNLLPTTFSISSVSESITSLNSSSTSASEAGLSAPIVSRRDP

KHAENVTSPSTSTLSTASSPDASCIKTASRRAQRFIQYSQPLATIKSERSFSPTSYNHHS

HLRPRDTSPTDATVGTTH

>contig47976 Frame-2F

MIYIVECTTAVISANADGLIESVNGIGQMEFYQTAVKLREVLLAPECFPMEPSASATLAD

GCGMLSKWHGMNAALAKLACVYLRIPSLLPSLDKETPLKDLLSQRVCSYVVATLTQYKQN

PELRAVVSMQNVLRPLLEVVTLILALASEHIEDIDKKAGERSMLLDAVTQFYVLCTPKSV

SFRSCTAFVVEQLEIVHCGKHRWRYKLAWPMVMQWVVCLADLLGQLDRQHMEMGRRSLLA

LISVLKQLPVGFASGDQMDRVLTSLSAFFDLAALPSSTMTEDEKQRMLARTRFDTINAAD

QLAFAALVYHLPRYPVSLLRALASCCKSSRINTEAKSFLVDIVFQRREVIDLAHLTSFLV

STALAPVETEVVQQRQQLQLVNHVCRTFTAMNLGASLAKILAPTLAKAQAREDLNVTELH

TLVLLYRTCLSSATSAITVQRSDIPIEMEREVENLCLQILTTHTASDFTTTPKEMDTREQ

ERSLVEACVSLLNLSELNIFASFLQQLLAPQQQKSFLARRLLVLQALVRTSSLAETFQRY

LNHVEKLVLAVSDECSGEEDVAQLVRQLRGDLDLIAVGQRGNEG

>contig48520 Frame-0F

MMLISVSRRRKKDGKEQLWSRVKGDEADEDDDDDADEFGLVGMANNNRKNSTKSHQRVRQ

NDDDESYQSSSNDEIDVLERAD

>contig50752 Frame-0F

MELFLFNMSTNNNNTYNNTKLNANITSSLFTNKHLLLSLNY

>contig51980 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60677.1|) 3e-55

MTSIFSAGQSISSIGKSMTAIARIEEHLATFMKKVIYFDKFFQRMRPNLPTCVTDTATLL

FQRCYEYRDEIRDELESSVAYVADAGRWVVGMGDWNSKMEKRLNQISELVLLANSL

>contig52664 Frame-1F|Blast-cAMP-dependent protein kinase regulatory subunit [Phytophthora infestans T30-4](gb|EEY64141.1|) 6e-63

MPDVSPVAMGELTSGAYFGEIALLTTRPRQATVTAKGNVKCLTLDRKTFKRVMGPLEDIL

KRNINKYNSVIANT

>contig53425 Frame-1R

MNFPSSVQSLEEIEKQQEKICRSFYIETYGCQMNSADSEIVRAIFLKDGYTPARTPEGAD

VLMLNTCAIRDNAEAKIWNRLESLRQVRAKHLRLQHKKIQTVGVLGCMAERLKTKLLESD

KMVDLVVGPDAYRDIPNMLRLVLDSGTAAVNVQLSLDETYADIAPVRLNPDSPSAFVSIM

RGCNNMCS

>contig53858 Frame-1F

MSFLSITLNYVLRAYLFRYLAYRMTLAVITDDARRHSS

>contig53924 Frame-0F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY69908.1|) 3e-24

MKAEGFTLTSDSKRLFADRNLEHCVMMPRSFDDLVGQVIQRAEFLCKLAPPSDGAENVNG

DSQIALFNLAEKWS

>contig53999 Frame-2F|Blast-ribosomal protein S6 kinase, putative [Phytophthora infestans T30-4](gb|EEY64993.1|) 5e-17

MIMRRGSVGLASGASAEDSCLFVDNLIRVVQQRLRSELGFREVLVATGEERKDTDTDSSR

LHATPSDSP

>contig54051 Frame-1R|Blast-metalloprotease family M48X, putative [Phytophthora infestans T30-4](gb|EEY59998.1|) 1e-06

MSRAVVRVGCMIEQKSNAPFMKWTSHVIESEEPNA

>contig54749 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69401.1|) 9e-34

MVNMVLTERVHNGADFLRRLSIADAKVLLERTKKEKENKNKDMQKMISVRYRDLIESADK

IINMHSAALRLEMSLKEMPDMWKKMEQNLTGTLAIDDQRGSFNEDETVASFKMPQSSVPG

EVADANGVAYLVEASEEMWQLLDAGELLQALDVYQLAMKVQLMCVAKAAESDYPFLQAQ

>contig56233 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53927.1|) 5e-24

MSVLIRAQPPAAVYVAATRQHVGKTSTCLGLLKGLTSRLDRIGFFKPVGQESIAVEGGTL

HVDKDVAVAKG

>contig59052 Frame-2R

MMFNKPIIALCIASVALFGSTVDASTEVAEAVALRNPTNDNAVYRDGDADGYNDRDGYDD

DDRDDSNDDGNGRRLTGRRSYDRSRYVSSERYNNRYRSRYGGDGYSNRDNRYRSSYRHSY

NSYDRSD

>contig59276 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61989.1|) 1e-11

MSDGNSNVTWKLLGGRVADGNHAKWGLTTPRSGHV

>contig00219 Frame-2F|Blast-cytochrome c oxidase subunit 1 [Phytophthora ramorum]gb|ABG54092.1| cytochrome c oxidase subunit 1 [Phytophthora ramorum]gb|ACD46609.1| cytochrome c oxidase subunit 1 [Phytophthora ramorum](ref|YP\_001165340.1|) 0.0

MNFQRIKQWSTRWLFSTNHKDIGTLYLIFSAFAGVVGTTLSILIRMELAQPGNQIFMGNH

QLYNVVVTAHAFVMVFFLVMPALIGGFGNWFVPLMIGAPDMAFPRMNNISFWLLPPALLL

LISSAIVESGAGTGWTVYPPLSSVQAHSGPSVDLAIFSLHLTGISSLLGAINFISTIYNM

RAPGLSFHRLPLFVWSILITAFLLLLTLPVLAGAITMLLTDRNLNTSFYDPSGGGDPVLY

QHLFWFFGHPEVYVLILPAFGIISQVSSAFAKKNIFGYLGMVYAMLSIGLLGSIVWAHHM

FTVGLDVDTRAYFSAATMIIAVPTGIKIFSWLATLWGGSLKFETPLLFVLGFILLFVVGG

VTGVAMSNSGLDIALHDTYYIVGHFHYVLSMGAIFGIFTGFYFWIGKISGRRYPEILGQI

HFWLFFVGVNITFFPMHFLGLAGMPRRIPDFPDAMSGWNAVSSFGSYISFFSAIFFFYIV

YLTLIYGKKIDD

>contig00840 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55490.1|) 2e-15

MSDDKIPSFSKRKAFMNARLTEVFGDTALSRSGNFISERRDVGKLTHVFSHVKHHMGIEH

IHFKFKPEVLPA

>contig05915 Frame-0F

MADASLPLQSAASRVRVAQASDRVYRDECVFSFDSALFPTGLYTNLATFLSYGAPYLVYD

RSEAPIVYLYQQHKRKPRTSLASATEATPTKLAIGGSGGFAVSVDDKYELEKTFCIVLVD

PNQEVLAREPLDSPTLPLKIKEAAESIINHAGNTVTEEVATWQEERKSTKYAEHLIQVPN

PPHIASNPLVWKCQAPECDKHENLWLNLSDGYIGCGRQNWDGSGGCGAALTHYQETDRKY

PLCVKLGTITAQGGDVYSYASDEDDMVQNPSLAKHLAHFGIHVNNLKKTDKSMNELQVGL

NLSYDFDTVTEAGKSLVPVSGSNCMGFKNLGNSCYMNSVLQLLLALPEIQERYFQASKTI

FSTADTLPVDDFGVQFAKLACATLTDRYKKQFLTPKKSTQPIEEDDRNNVELRPITFRRL

VGKDHPDFSTGQQQDAVEYLQYLLDFMTRAERVYSSRLGPLLSGDTSTSAELPTSNLFKF

KLEDRVQCLVSNKVKYVSRDDMLLQLQISLDDATNTTQVNAYQSLEQKRQRLGDTEKDEY

VQRNERVVPNVPFDACLERTLAPEVIEDFLSSATGVKGQAQKTVRFGSFPRYLLVQMRRF

YVAEDWTPKKLEVEVNVPEKLSLSRFLSKGFVNGEELLPETSGGSTLMESGEIDKADDVL

VAQLVSMGFSENGCKRAAIATGNSNAEAAMEWIFSHMEDPDFNDPPAVTSLSIEAKKGEV

DMTLVSNLMAMGFAEPHAKCALKQTDNNPDRAAEWLFSHMDDLDNAVAQCDPSASVASSV

SVNRLDSETSGEYSLVGFISHVGKNTNSGHYVCHLKKNGRWLLFNDDKVALSENPPLGAG

YLYLFRRIDTE

>contig07801 Frame-1R|Blast-40S ribosomal protein S11 [Phytophthora infestans T30-4](gb|EEY58755.1|) 9e-86

MEHVDQTEKAYQKQEGVFLASKKFAGKKKGPRFYKEVGLGFKTPKSAIEGQYVDKKCPFT

GNISIRGRILKGVVLSTKMKRTIIVRRDYLHFVKKYKRFEKRHKNVAAHLSPAFRVKEGD

VVTIGQCRPLAKTVRFNVLEVEPASETKPINVRKQFRQF

>contig08574 Frame-2R

MARLVPLFLVWAAIFAVNLRSIRATWPPVSTNAVAPERNVAPTRRNSTRDNSISRRQRAF

EERSKISRYVSKLKQMFGVKKQLGLPFDLVAMLKTYHLPTMTPTEVIKKQKLFRNPRNSE

QTRLEVELYDAYVEVWNKHAAYHQSGNAISKCNVLSGLREVVG

>contig08927 Frame-0R

MQRWINRELDPSIAFEMLPTMPVRKWPVFFKVQYLVHYLTHFNAATSKSRLEINNLYEIP

DLKLTRRDSAPSLFLENSMLVVVSHVLGIPKDQIRKWLRYISFLSSENPTFKIEWDSVTV

LRCFFPDDKLKLKLQKVAEDLRYETHAKTLLNDLNQVLFKAHHDKITEYLSSTSNLKVEN

KAFFAQPQMKFLSSDVELFNKLYPETPTTLNAVLKAVLKEDDATFLQRVLSALDNDNSKE

IVLRLYEEELQFWLKKKTPPTDFFNYLEGLNDLKFLIMVQYSFDFIQMIPKDDYAATITK

LGAFEDAWKICTIEALRKEVKFDDAILIDKLEKFIEAKDTWNLKYISGDKLPVKKNKQVT

SALTDTILNEFGVVKDSKKKLFLIWVKYIDALHGETSAFRIKLDSKTLARSFFTPAEEEA

IKAVRRTKTNVSKRLR

>contig11301 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55141.1|) 1e-152

MLVEALRVKRPLSVMTFNLLAPCYFQHGGRLESDDPASFLSRSQASICAIKREQCDIICL

QEFWFESEYQHAFRHAFQPTHLVHTAKRPGDKEDGLAIFVDKRKLEVHSVENVDLIEEAG

DRVALLLHVATKWNSETTPLAQRSFLVVNSHLTFPHSDMYTSLRLNQINRVLSAVRKFVA

RRELRNVPVLLCGDFNDYNDPVYRLVTKHGFASIFAYLHGREAQITHCNHNNMEVSVDFI

FGARLNNAQDDTFVKEKPSLQLHPVDCHLVPRQLPDVARLKRPQFGHDWCKVQSPMLLQD

VDSLIDYWRLVSDHRPLVAKFNILDDR

>contig12050 Frame-2R

MVLNLKTPIDKQSGKTTIVSKSKIYGNVAIRRISSGTDGVFVLGYKKMLRSSRRNWDPTL

SVLCRDCPTF

>contig12609 Frame-2R|Blast-CDP-alcohol phosphatidyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64290.1|) 1e-105

MFLWMLGLLNSKLVLHLMLAHLCGEEYHPFRKTLVPIFYVAGHCAFCMLEGIYDTINEKL

IVREFFFLSLSAYVHIVITVVWEVKNVLGVSVFTIPHKTKDSISLKKSS

>contig15107 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64471.1|) 2e-07 NOT\_ORF

MALILRGSVISLGKTTISRHNASFV

>contig15657 Frame-2R

MAFSFKAKKLLLLAAVTQRLKEISSAS

>contig16289 Frame-2F|Blast-F-actin-capping protein subunit beta, putative [Phytophthora infestans T30-4](gb|EEY59355.1|) 1e-140

MSSDPTTANGGMTTCLNLLRRMPPRQVETDVYNLTRVVPSLAEDLYQLVDHPLQVAVDPA

NGRKYLLCDYNRDGDLYRSPWTNQYNPMSSTSGEAFYPSETLRELEIQANEIFDSYRELY

YQGGLSSVYMWDLESGFAACFLVKKDVENQRFVEKGEWNSIHVIEVQESSTDVLEKGSKK

ATYRLTTSVLLLMKVNRPELGDLTLDGTLTRQAERTMEFEDQFTHVSNMGHMVEDMEIDM

RSSLDGLYISKTREVINGMRKLQQTPALANPFVGELTGAVLKHGQKKHEE

>contig16959 Frame-1R

MGACAGFALRKVSKLGAVAIGALFVLLQCASYSGYVHVDYQKMEHDVKKYLNRHKDETKD

DDSIFTSLMEVLEFNLPAGSGFAIGWIVGFRAG

>contig17435 Frame-0F

MDLFNKAKETLKNGGNSSKSGGIKDIDMVLGKVFNVMDKYQVKEKAAEFAQKQISKREDQ

PRHVGKKDKSIIVKAKEAAEDFLAKQGNKPVASRPVQSNGTNYGPSQSYPVPTSTYESYQ

EYWSRHGSSNNGP

>contig19200 Frame-2F

MLRDTYDTKRLITMLENFAKPFLERDSEANSWRHKLSFKHLLDVVQTNSKKTLYRLFEAW

MNYLAIISNIGVIDGFKGIGDFQ

>contig19275 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56921.1|) 2e-24

MVQSENWLVYSYWNVLTKRTEMVSLSLFDGAIG

>contig19550 Frame-1R|Blast-predicted protein [Phaeodactylum tricornutum CCAP 1055/1]gb|ACI65571.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1](ref|XP\_002186101.1|) 2e-11

MLGYLVNMYDRTLLQRKEEHEVYEVCKSKVRQRLLPMNVIDAEYQFDRHKLTFFFEADRY

VLNFDVWTWL

>contig19972 Frame-2R|Blast-calcium/calmodulin dependent protein kinase 4 [Phytophthora sojae](gb|ACH68465.1|) 0.0

MSTTNANSFEEQYTLGKIIGSGTYSVVRIAVHKPTGQRYAIKCIKREGLVAEDIEALTTE

VAILKQMNHPNIMILHDFFVEDKFYYLVTEFMEGGELFDRIVEKSYYNEREARDLIKLLF

EAIKYCHDANIVHRDLKPENLLLTSKKDDASIKLADFGFAKRIEFDSEGLVTACGTPGYV

APEILEGRAYGKTVDIWSIGVITYILLCGYPPFHDENHNALFKKIKKGKFQFDSPYWDHV

SDDAKDLLTQMLVVEPEKRATVDQLLKHRWVTGTDVATVQLTSALEELRRFNARRKFKAA

VSTVSTTVGFSKKYSKSHSQPQSFLDESGDFDLDNLPEISPVELEAGKK

>contig21131 Frame-1F|Blast-ribosomal protein S6 kinase, putative [Phytophthora infestans T30-4](gb|EEY63375.1|) 0.0

MEALLHQIVLEEQQKMLQLGFVETCIPSAESPARCSIFLSANWHICRRLLLVIVSGNGIQ

PGIWSRSLVLEATNDPHQYRSGSMLPYLHTALSKGYGVVVMNPSTNTVNIGNEKRPIPYS

STPELHVCYVWETFGVRASCSQVYIAAYGRGGSLTKHLVCTQSSLRLKVAAIAFIESSHR

MESEDTPEVRGLLGTRAINWQRSKERPGTQLHDCSQLGCLSLSAGEPTSLGEQKSSNTAW

TIAASMHTVFAFFDSAQGSMPDEGAEDELMDEMSRLSQYAYAGAAALSSVPYQREHIDDA

EFQVEDVTRAHPMGTRTNSARTSRRSMVISTSMSVNDFDLLSVVGKGAYGKVFLAKKKHG

KNAGRVYAMKVLRKHDVFKKKQVEHTKSEQRILKHVEHPFVVRLRYAFQNHQKLYLVMDY

YSGGSLFVHLRKEKRFTEARACFYAAELVLSLAHLHSMHIMYRDLKLENILMDSDGHVAI

TDFGLSKEDDEGSTFVGTPEYLAPELLCSQRTATSYGNTVDWWSYGVLVYEMIRGYTPFW

NKNRRQMFQNILSKEPTYPSELFSPTAIDFLQRLLVKNPRQRLGCTMDGAKEIMSHPWFE

GIQWDALLNRRMEPPFRPVSKDLHGSRARTSSATLNANLHYVPTIFKQQEVADSPVVSIL

GSSTGSGIMAMHFDDFSYMGSDILGSRRTSVFRDSDIKMELGE

>contig23021 Frame-1R

MGQGMNNGSSGMFTRMPQYSSNASGPSLTTRLKDGGVDVSTGASSSGSHLPFMQHHHPGA

KSLELTHPTSIYADVTNPTTSMSMVSLSSDRPGTASVNANALYPPSLVPPSSQHHTSTED

TCGLCSGVHSDRIADHCGHRFHAQCLHSWGGMTTCPICAQASNTITSLPQTSTVVGYGLG

GDNISIAQNSAGEIPMNGGGGISDNTATNNSVTISPNPMDSSQVTTIHTLQANSGGRPPP

IDTRVIDSRVGATSLNGSKRSATSTRSESSNSGRVRKNKKLKDCSVPGCDRTVRSRGLCK

GHGGGRRCGFSGCGLSDQGGGFCISHGGGKRCQHDRCDNSAQSRGLCKLHGGGSRCTVPN

CTKSSQGRGLCRAHGGGRRCMVEGCNKTDRRAGYCVTHGADKKCIIAECSKTGRIDSMCT

KHYFERHPAQPPGMVSTTPPPIITVNANTSAARARAERKRAAEQQAAAAHYTGGAMTKTG

PY

>contig24594 Frame-2F

MRLHLHLVIILVTWIAADYILASSGNNNVALRKTSAANASADKSLSRLQTMAGASEERWF

FDSDCSSHGGDKPCKKKKKNFIYRDWEKVILWIAFIIFTTCFTAILLL

>contig26710 Frame-2F

MRVKFGFQLSTAFLASLKVTTRA

>contig27366 Frame-0F

MLQRLARIQGAAPCLSSQPHLLVRTRNYKSRCRRTLLHFSTLSNSPDHKDQKTTVALVKS

SELKRLLSLYKPEKKPLLLSISALSVSTFITMCVPFGMGKVIDVVSAGTAATMPLSTVVT

LLGGLFATGSIANIIRIDTSNMIGERLTNRLRRDTYASILQQELGFFDATRTGELLNRLS

ADTTLIGKVLSDNVASGLRSTGQALGSITMLFITCPKLAFIMLSIVPLLSLGAVSYGRFV

KALTSQVQTRLSEATEVAEEKLGNIRVVRWFAKETEELETYRHKVDQVLNLARKRSLASA

TFFGGVDLSVKMSMLGVLGYGGQMVAEGALTSGELTSFLLYTLYVGFSFAGLSSFYAELM

KGMGSSSRVFELLNRLPKTRVPEGGWTSLRKPFTGHIQLQDIGFAYPTRPDAMIFNGLNL

EVLPNETLALVGPSGCGKSSITSLLARFYELNGPNCRGQILLDGVDISTLDPAALRGLMG

AVPQEPPLFACSIRDNIAYGCPAVTFDDVIHAAKMANAHEFIRSFPDGYKTIVGERGQAL

SGGQKQRVAIARALIKHPKILILDEATSALDPESERLVQEAVDRAKQGRTVLLVAHRLST

IKSADRIAVLSNGGVVEQGTFDELASRDDSMFAQVVLNRQK

>contig27850 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61044.1|) 8e-49

MQKEGLGRTRRSASETRKIMGDKWRKCSEEVKEYYSQLTEVENEKRRRDYILDVRDREIA

>contig28161 Frame-1R|Blast-ATP-binding Cassette (ABC) superfamily [Phytophthora infestans T30-4](gb|EEY54021.1|) 8e-32

MYWRTASHNRNRFILYLILGIVFGMTCIDTENSFFVGINSGMGMLFCQPLLRIS

>contig28631 Frame-1R|Blast-ornithine aminotransferase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY55334.1|) 8e-36

MNLVQKGLLAKPTHGNIIRLAPPLVMTEKQLDECTSIIKEVLTEAEQ

>contig29218 Frame-0F

MFFLESSQVAQVIENSKPAQEDYIKHLLVAKSKSGESSKVAEMEFDGCLEFGYAIVDASF

CAPSKAQRCLLNCKVILDHLQHHLDLKVCNQPMCEAVEHHFVHLSDCNAIDQSQSCEYCL

LMDERRLIRSAAYMEVEQIEAEATVQKLIHEIAASMVQHTKKHHQEMVQLENELDQAEAR

KEEIIEKLVTKRSELQIVRKNLATRGVATSRRHQLPVHFTKNCRSFKGPENGRKRRLADV

ESESSSP

>contig29283 Frame-0F

MLPLSVSLRRLAGRSATLAMRHAATTSICSSSRRVFTGVRGRASVASFSTAPLDFTSDVM

EEEDVENVVLEPLLKGFVDQKPIEDFALSQETQRNLIRAGVTHLFPVQTESFDLMMKGTD

IMGRSKTGSGKTLAFALPIIETILANRKTSRNPQALVLLPTRELAQQVHDQVQRVAPQLR

VVNVVGGVSYTVQENILRRGVDILVGTPGRIMDLVDKGSLSLEEVDVAVLDEADMMLKFG

FQEAVETILGYVPKGGQTVMWSATFPKWVSSMAHKFLKDPVNIDLVGTDDNHVPATVTHK

AINVPTRDRKQVLENVLRLHAHDGQTLVFTETKQEADEIANALSGQDARALHGDLSQGMR

TSTMNGFRNGHVKTLICTDIAARGLDIANVELVVQYRLPSDKESFVHRAGRTGRAGRSGT

NIVFYDRQDAHDVVDFERRYKFKFTHASAPRPEQMICGALEDVKKQIAALPKANTLLFEE

TAHGLLDEQGPSVLSAALALLCGFDSKKMTTLSMLTGRHHTQTVEVTGISNARELNRLLS

SFLDNHVEIYPV

>contig29791 Frame-2F

MEPPGKKSPGFNCNPLIKSLSSGDLSVAPNRSNGRKANYYNNSHANDLLMDSSAALTSAA

ITHEVHWEGYVRKKGDWLPRWEERYLILDGATLTYYNSKEEARSARNLRGRMIINKVRPE

NYGKAHGFLLEIHGHKHFHLCCTTELEKDMWVEMMQAAIEEGLRHENTRISMEEMETIQM

SPTQVDLRGFYFAFRQLLISHSSSPQFFPKLSRDIVLTSNYAPTVPFWGEYHGLDGVLHF

FSILYETVEITAFFVTDIAQAKEGCTAVVAGRETMKNRDNGRKFTQQWQHTIEFAPDGRV

KSLTISADPIAASAVFGCSATSSLSLPLVAIAGNAIHDNPPGKLHIVVFRGEQISDRGFI

DDDEHTDNLEAD

>contig30638 Frame-0F

MKSYNAFAASAFIVAATIDSGVAMESYLEKLPNGAKFAKELGHVGGDSSKLTDFASNFLA

KSLTWDKSFCGETFPGSTMTNGEAFGDPCCMWTPGGPKTPDFAVAAFTTTPGEPTVCANA

GSSESPPDEKTSASDESAGNNPTQFDPAVPDTTDSTTTESTSYGAPSPDVSTPPAPETID

PLPTSGGGCAVKGARKLRQ

>contig30744 Frame-1R|Blast-medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY56335.1|) 1e-140

MWITNGSVAKWFFVLAKTDPNAPAGSAFTGFIVDADTPGITVGRKEINIGQRCSDTRGIS

FEDVLVPDENVLGDPGYGFKIAMQAFDITRPPVAVGAVGLARRAFDEARKYALERKTMGQ

PIATHQAIQFMLADMATGIEAGRLLTYKAAYEIDCGRKNTIYASMAKRFAGDHANQVATD

AVQIFGGAGFNTEYPVEKLFRDAKIYQIYEGTSQIQRMIIAKEMFSRQNMDP

>contig32391 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63421.1|) 1e-138

MPQCSTCGAVGSGRFCSECGASFVNEIKSSVPQPYYVQHPPQIPPRSQEYASFEEHHQKA

LLYQQPPSNIPPPAIPVVYVGEDYQTDGRNLPLASLNYDNATKSGSRALSTSSSGFFNGR

YSDHPNCDICGLAFDVTKRRHQCRACGRFICGNCSPLMLLIPEGDEIEGARGYDPSIPQR

VCLHCAPRLRPLQADLVSHFAKSNAEAPMHEAKSRLHVPFSCSLEKECTNAADIVGNFFR

TDSGASGDRSIPISMLEKAHGLAIMTIIKAGFFLVGKIGTGIVISRLSDGSWSAPSAIGT

IGLGGGFQVGGEFVEILIILGSPAAVEVFYSPQVNLGAGLDIAVGPYGRSAAAAAAISST

GLNGNYSYSMSKGLYAGISLQGSVIATRDDLNRQFYGQELNASALLGGAVSQPLAARPLY

EALERALRGIQEHKEVLAERSRMMGACNACNCQTFVPHAHQVWNKKCKTCD

>contig33213 Frame-2F|Blast-DNA polymerase epsilon subunit, putative [Phytophthora infestans T30-4](gb|EEY69170.1|) 1e-152

MGFPPPETKEASLEVLGGIDPLGVEVSAQQLEQIRALEENDHFATFIVLSDVHLDDPLVI

RKLDELFQGLESVQPTLFIIMGNFMSTSIGGGTGSDSIQDLREYLEELGNLILKYTGIAE

NSRFLLVPGPNDPGSSRAFPRHPLPDLCTCELLCKVPNVICSTNPCRIRYYTQDIVVFRD

DLQQKMQRHAILPPKPSENEKAVTNNEGETFESVSQTDITKHLAKTLIDQAHLCPMQLMV

NPINWDFDSSLQLFPVPDVLILGDSTEQFQLGYSSVGIFHPGPFHADYSFVLYRPSTNTT

EFSRV

>contig33543 Frame-1F|Blast-pirin, putative [Phytophthora infestans T30-4](gb|EEY56748.1|) 1e-145

MFDPRRIASKFIACEQGEGVGATVRRSLGSQQLRNLDPFLMLDEFSVGLPGGFPDHPHRG

FETVTYMLPTSKGHMRHIDFLGNQGELRPGDLQWMTPGKGIVHAEMPASEEKAHGLQLWI

NLPKEKKNREPRYQEINRETVPHAWDDAKKVEAIVFAGEVFGQKGPIETEAPVTYIHFRM

KSGAMLEYTIPQGHNAFAYTLCGAGKCADEAVTAHNAIVLETEGDGLHVTTEETEGLELI

VISGQPLKEPVVQYGPFVMNSHSEIQQSIRDFQSGANGFENAPTWASEIGNRQKP

>contig34432 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61613.1|) 7e-58 NOT\_ORF

MKRKTRSSSPSPPRAPSRSPSRSPSPTPSLHDESNVVNDA\*GRGRAVVSRERALFFATGE

VAAPPLADEDESWPGYYATIRQLQNNRQAAQDARLQRPPAAEPQPLVWTPKRAARSSVLQ

ADHVVQRLRDLALQTVAQHIEQLPSLEYIDATARHQVARAVVKLRRLTPEVVPLFIFPGV

TEIDLPD

>contig34487 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63236.1|) 8e-47

MAHGVTKLPRLVRRRRFGVQVPIDMNAVQVVNTRCPCCTHSLKPVKMSLAMAASAFTHRS

RGSMKPNTKRCYLCG

>contig35318 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62222.1|) 2e-67

MGALEAVEEMNSKKIKNSMIRVRQMDAHTQQILAMQFQMVRDTWKCTGSQCRADVSIWKA

KCDKCGRTRVYGPSNINIGAESWLCSLCFTANESISSRCHGCMEALPEGDRSMYYKS

>contig35691 Frame-2F

MVQTQTTSCIGLSKTKKLLGEHHSTLGSLWKLTRYQSQVFINTIYLI

>contig37547 Frame-0F

MAFLEDEDSMGAFSAALSFVEQYSIDSPVLRESLSSDTTLSPVDKFVLPSSPTFPVHHTP

SHTVSDLTVSALPSPRFQLSPQSSMRLRSGDFAAASVLNNNKLVRRGRKKTTGGIKKPMT

RGDPNRARNERKIELAFLREKVTQLEVELQAQKLHSRKQTIRLKDEKQHTDLKAHDCTMT

AHETAQIPGTWEEVAYRQRRRREIAERENVRLKLILQDQIRMARNLESLLLKRTKQQVAK

CSTFSQNKVSKYSQGRTLEFRADVNDFQDLLIHLDRAYHEVDAVFAKNGLATMEATHRDA

RMREGADCMYLDIFANKVMPFGMRATAKAVWDHFKGAEKHRGNMYEGKVAKHLESPNMPD

TIMEDFAKEFFADNARADFHAKQVLRRYVEEDREIVIWIASVVPLEFDDQRVKGLAFRHQ

GYALVKRSKSSMPDQEFSLFQLCSLVSPEKENLTVYDPAAVRALTDFMLGTVAGNITASQ

ELIENVLMDQAVNAQNL

>contig37958 Frame-0R|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY66415.1|) 2e-70

MQSSDWSKLINMTAVITGINEDGSLSTTSSVPSGTNVVLMETSAQSLKTAINKMGAQAVE

SNKFYIHETISCLMFMSAGVQALLGHKCMAEMVGAYKDWSGGASLMGMTTFGEIGHLPNS

NDFPHYDSLMFGAVIFSKRKRKEYFCF

>contig38285 Frame-1R

MPPNRILNLYKSLYVALVFPILRCRILSAHDGKHLTQNLQ

>contig38788 Frame-2R

MRSDRKSVCARTRAYRSTPATVPSNACDLMEATGVPYNRCCVNASRILLPTLNQSSDSFF

EPLQPS

>contig38928 Frame-1F

MKKIRPKLAQILFILKALPVNSSSEILTIADRQSTYLLKWRKINRLAIVIFIIISILFLP

TMKLGGRAFNFTKKRSEFTNAGHYPAAYTRRHQSQRHLPTC

>contig39660 Frame-1F

MRDELKNSRLKILQVHCQSFVVKAMSLIVGREACDVLAGNRTSLRRD

>contig40383-1 Frame-2F1

MLLSNLPSPYARQFLCIFTLALRKRFCSFVSPLCLGPVS

>contig40527 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69061.1|) 3e-85

MTMQLDNMVDSNEERGRAIVQTLAVVVESMVHASDRMPLGYYHKTKFEAFRAPGISVCDY

LTRIHKYASCSPECFVLALVYMDRLHQLQGFVLTELNVHRVVITSVVLAAKFFDDHYFNN

AYYAKVGGVPCPEMNELEVEYLLLINFSLHVSSETYARYYNELANHYMYTRVRNSSLTRS

PYYQLRHFVAPDPQHEGQLVYVTESYPKVPPPQEHRRSHPLPLHH

>contig41090 Frame-0R

MGTYQRCCRQLILYMDMHMETSANFLEDMEAFIEPSYHNRPQSELEKLVANQLWAQYNGR

VVEAAHVEVSTTPSTPRSYERVIKTDEVVDGSIIVTPVAVANAIVSGVTQSCSPHVDLTA

VPPSILGSNKKRQLSKERFVPCKSKRARHTVARNLYGAGILNCDEKEDSESDSITGSGTD

AETDVTASDLQLHFNKSSGEVLWPCAGERSFVQNVAYKRRLKAAIQLIDAKNCSPPISMM

CTQECANLRTRMCLMHRIQRGSAKPCHDQFCCVWLEIDTHLVRCQNSQCEFKNMVGLRQT

KYDIQQYALKLEGLRKKLLTIEKQDCSNSTDACSRSKRELEMKIEKLEGKCA

>contig41216 Frame-1R

MPISFRNAVPDCITLTKSQRQSFIHTADAIVAETLQANEHFVARGRKWPLEQWKYVKTKE

QMHVYRSRNPERTMTAFNIMNDEILPSRPRFLSLSAMERAPPGLPYVHEYEAVTPRLYEK

DSTNTHSTSSSNHS

>contig41362 Frame-0F

MHFKVKGTTLFNTCKSPLPPRQVKPARIKVYSAGEWIKIVAQVCTLF

>contig43711 Frame-2F

MLANDFEKRRRTSRLGTSAASSVSTSSSPALTVANMRKSNAIYAEDVVKVKQALQEKLDS

PTGSAPFVDEDGDASWGPVVVS

>contig44651 Frame-2R|Blast-anaphase-promoting complex subunit 10 [Phytophthora infestans T30-4](gb|EEY65500.1|) 5e-19

MHQNGRDTHVRQIKVYAPRESNVFNWAIPNATTPQLAAYSCIR

>contig45638 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68771.1|) 2e-90

MERALGEPALVLCSVCMDSEEHHKRWLPLCIGNDQALLVRDVCVRPLCPRLQLCGHMCVT

HKLEFELSWQGNYSVRACYGCRTSTLQLYSEKREVWFILKASKYVSSAYGVERRVKTPPS

INCEASPTQKRGVKSEMRKCGMRQDLRRKPSRFMNQHVQNEQMLALEWSLGNLPLQKRIY

LWRDNRKRSKIEKEPEACHVDLKLPTTGVSDVNARPEPRDIFCSTSGCRRFAKTGSRCCF

HSSRSILFV

>contig45744 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66652.1|) 7e-24

MAEGGALLHSCAVYLYLYDESNGSYAQQTDAAVGCALLGGEHAAESNSDAFSLLLYDTQK

APLLQLP

>contig46002 Frame-1F|Blast-inositol monophosphatase, putative [Phytophthora infestans T30-4](gb|EEY55619.1|) 1e-130

MAACAFDSADITAMLDVAVKAARSAGAHMKSHVNTSRVEKTKSSKDDLVTVVDKQCQDIV

FATISQTYPSHDFLGEENVAPGSEASTRALDDMMSKEWLWIVDPIDGTTNFVHHRPASVV

SIACAHRGDVLIGVVYDPYRDEIFTAQKGKGAFLNDQPAHVSDETSLSEALVGIGIGTKE

SVRSPMLDCAREFSAKCRGLRLQGAAALELAWTAVGRQTAFYELDLNSWDIAAGALLVME

AGGEASNSDGTPFSLRTRNVLVSNHQGDMHAQMLELIQKADAVSVRK

>contig46213 Frame-1F

MSISSDEDSGMRLLSSSVGRTESTSDAMTAATVAAAQAAQDIIARSGRVCRYANCSNIAR

SRGLCRTHGGGKRCSHPNCNKSAQANRKCIAHGGGTPCAFEDCEKTAQSRGLCKAHGGGA

RCKHPDCPKSSQSKGLCRGHGGGIKCKAEGCEKWVQKNGYCIKHGRECAVTA

>contig46785 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56003.1|) 7e-45

MTHPAILCTIDLNSHSLTAFLINSRARALLPKLTVGSLFANQEHVLVLTYGDKILG

>contig47027 Frame-0R

MADQSMSLMDGTYFVGRKEILDWINTLCGINLSKVEQTCTGAVACQILDAMYPGRVQMSK

VDWAANKDYEYIQNYKVLQKAFMQLKIDKHVEVDRLVRGKYQDNLEFMQWFKAFYERNAS

GQPYDPFAQREKGKGGAQFTQKFGGGVNASASASAASLRRKVGVTTTAKVGRTPLAASMT

ARGGRTSIGASRRPINNTGATATLSEADMEASIAAATAPLEKELEDLTAHNEALTNEGGE

LRAMVESLEKERDFYFNKLREVEIVLQSAEDTEASPLAQSVFKVLYATEEEGGEVEQVAG

EPQDEQM

>contig47092 Frame-0F

MIYQRAALSNLNLQRKQPFSVSSRDCRMDQSKVSPHAIPSQASIARF

>contig47618 Frame-1F

MWSSSFTSLAENVQLPGIVVCPHCNQGYGRASLSIHVRRCRTLLSHTAQEAAEHKRLSKS

MQNKPP

>contig47683 Frame-0F|Blast-cytochrome b5 [Phytophthora infestans T30-4](gb|EEY54438.1|) 2e-56

MGDDETLDAVEKEFTLEEVRLHNTAEDCWMIICNEGVRKVYDVTSFLDDHPGGPEIMVDV

AGQDATDEFEDIGHSNDARAQLKKFAIGKIKGDVKKESTTTTTSTGGSKASASGRQDISG

QNGPVYAVLAAVVAFAALYYKFQ

>contig48295 Frame-2R

MASTAIAPRTRLATKGVTTIYDSYPLSLRTFLAEEGLPPFARSKAHSMEGPAQKLMAVDD

DEYLHNFYDSSSSVDTIDLGNEGITEPTAPVSSSFGKYHNEVFETKERSKVLSALRHRGK

AG

>contig48677 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59893.1|) 2e-17

MPRRKIEEPEHFSLDVRFDLKTAAKLRDIQVAKDEAVANEDYDQAKRLKQVEEHVQSIGL

ELTRLEAQKK

>contig48862 Frame-1R

MVDLRPVSDVPVTLPPPPASESVEDDELECRVCRSEAEPDRRLYAPCKCSGSIRFTHSDC

LEQWLEHSGKTFCELCGHEFTFTPLYDINAPDVLPWTELLSTGLGVVGLKWLPFALRAAL

VCVLWLTVAPWCTSWLYRMWLLRASAMINVNFSERLDASSLQADIYAGVLLTVCIIFSFL

ALMSFADFLRFYMDH

>contig49182 Frame-0F

MGIAPVSVALEAQEIISSVFGIEGHETEFTRYFIVDCRKYEDSQCGRFPKAFHFDPAANS

DAALVDQVIAALGPSKHSGVHVCVMGQGYAHIAEELRRFQLQQGVPAASPFSLSEQLHAK

DQMRVRSSKEFLLKHGYPRVSVINGGYAAAHGFLFRSHDLTVDYLADHNTLNCKLCQHDG

SMNAILPSHFSQVEGSDKKRESDNCRDFGRSKISKMSDELPHTSVEGSKYTDIDLISPSA

DFKILATDSYYSSVAGAFKTGSKTLLNPTVGGTKWLFKKSAARTAEFANAAAYMSNLSSK

NVTGSMQGVTVVDTSSEVLEKKTKQAMPNLSKFRNSLAAIGSESLEMLKKVESVMEHVVE

QVSVVTSSSAARIRVPFPSTSSPSLKDAAAV

>contig49458 Frame-2F

MTYRHAAETVNHANIQTKTAKLAEVKTTLERLSATLNGRSPDFSKLDACVSLVCDGSTLR

ENFFSAVHLLSRWSMQSKSCCPSFLETLTSK

>contig49564 Frame-1R

MQHTKRKYVNEGPMQRQVAQKLQLCADVNDSFSARQHSLAKQYARYQTQKSRANELHRMR

VAVDQILHSQTLLGTEMNRERVLSARLKPIITQTDKVLTRLSRYRTKPAAYCTKKKRAIR

VYAY

>contig51385 Frame-0F|Blast-hypothetical protein PITG\_08386 [Phytophthora infestans T30-4](gb|EEY54827.1|) 1e-38

MAKSDLIQTDTTHTAMEAADERTATIECKKHVRWGSVSVLEFRIGYNASTVPESGGPPVG

LLGRPIRHSYLELSIDDDMARERNNVESALVTTMPPSSSNNRRCRTELWLDPMARVRIVA

EQHALSEDDIALICQDVRVTLDWRALSCMDEVTEKTLGVLRVPLNSRHFRCSAVCNTTRS

KVLLY

>contig51688 Frame-2F

MPQIVQLPCLYIAVAGCFKTLAAFLFITPISQSVARPFLWKPACRDRIHEPLCVQPSSHE

P

>contig52326 Frame-1F|Blast-peptidyl-prolyl cis-trans isomerase-like protein [Phytophthora infestans T30-4](gb|EEY54813.1|) 2e-30

MSVLLETTLGALVLDLYVEECPLACTNFLKLCKIKYYHGCLFFNVQENFMVQAGDPTATG

AGGDSIY

>contig52542 Frame-0F

MDSSIQNLETNNPSPTTSPQIETDVNTQWTNPETSDLSAASNSESDLTPNAPSPNTSEYS

AASSSKPDSGALIQNLKTKSLSPTTDPDTIA

>contig52898 Frame-1F

MALRREVLESVVSSLSIEYPTLTVDELALLKYEDINDDQNGMVIVIACKELRHRALNIPV

KAIAADLGPDHFGILEAVGHARIKGVTVTTLTNHLSGGTVKRLHNCLDTLISCGLVVKRM

MIVAKPTMRRL

>contig53769 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY53382.1|) 2e-58

MQVYVRLHNARDEYKWSRGCVIRRLERDASKVLVQLENRDITVEVDEAQDVRMVNELATA

ETLAEVENLETLTHLHEPAFVDYLAQRYSVDQVYCRSGAVLIAVNPFKDIAGLYNLRKFE

EHITKWTALRPHVFSIAERAYRSLWRTLHEPG

>contig54269 Frame-2R|Blast-60S ribosomal protein L44 [Phytophthora infestans T30-4](gb|EEY69005.1|) 8e-11

MKRTKHFELGEKKKSAGHQY

>contig54539 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69022.1|) 5e-21

MIDANVAGDDLTAENKAQYLFMLYERNFTVFYRDMAEQIQRRILALYSGVDSE

>contig54805 Frame-2F

MIEITFLEWLRDFDRRMTNRKVLLVLNSCSTRVPLADLPQRNTLRNSTIQYLPPNMTSML

QPFDQGIIRNLKAYLSAALTVCSLRISTMVSLSRQRLTSFMLSRCLSQHGLTNFALRPFT

TVSGYSVQSSMSSVLTMKSWWNWNRRLDASGIPTRWTSAICKTILLSGLPRTFQMWMISL

RTTFRLSLKTSRMTARNP

>contig56058-1 Frame-0R1

MSTNLSCDQLGYLNLTNTETGDANGPFNATLL

>contig56894 Frame-2R

MPEPPEAVFDTLQQLRAMLQQLRAPRELVI

>contig57053-0 Frame-0F0

MVATDAPALAARARTFDNGTQSDSPFRCSGFFF

>contig57277 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70357.1|) 6e-91

MFPAPKDGRARECQRFGKRLATLQETTAARMVYERSDTGLFFGMCSADYRLFVWFDSLSS

ITDAREQIQVLLNRLRHDEELMSVTLFRSNTGFPSVRAYGMWP

>contig59468 Frame-2F

MGTWLVKEQDRGQRLNEFPPIFYGAVEQATIFSKQR

>contig01107 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60980.1|) 3e-40

MEEEKLVRLHDMLSKLRPGGKKGGLGFASNRGKKGTKRSDGLPNNGLYSMFVRQGEGTYQ

HKHWTNGMETDAEEEEIEKSVKKAKKEKKRKTKAKKVDDSKSDKEKKRRRKKQGIRRRPR

PRSMNTRKWKPSQKKSSRKRARSGDMRSSSQKAMQLRLKARRLMSTSTECLSLRKTRSAK

SKSLWTTLPSRHDLLTIIALKLTKG

>contig04571 Frame-1F

MRKLNEDRQAIASRKVNNDLVAFFGLYDGHGGSEVAEYLAENLHENVFCQLQKLPIESKM

ATSVQTPSFANALRTAYAATDEAIFNHQLPSGSTAVTVVIRGTTALVSSVGDSQVVLSTN

GHARDMCIAHTPELSSERDRILAAKGQISKGRIYGMLGVSRAFGDNDFKTGRGAFKKRFN

GDLVVATPDVVVHEITSLDEFVVLGCDGLYDVMRPQDVVNFVRMKLGMHNNVQHATEELV

SHAIALGSTDNVSAIIVCFHQHDVVPVTPIEAAKAAEARKRATD

>contig05099 Frame-2R

MCARDRLILHQEPVFKRASVSSGFTPTPRHLQRFLPPASVFYATEYRFNQDFTQVAIKVS

STGFNGWINTSVFKTLLEVDAPTRDSVFHHGPIYMQNIAGQGGKKTGDLPVRALPNLQAP

KLYHVENFRIIQAIERKLIKDQIWVRIVPFKTQKINEQKTDDLIDPQVEDNRDAWIIERN

ANTAQRVLVPWGSHCIKDEPATDDKERYYRTVYSRRPLPLRRTAELEAEIVGHLDPGTVF

SSTHRILNDKGRMWIRVALPMENNSSSTLDVEDTNNGLKDENECVDDFKPSIQYGYAIQS

NAKTNTCMVLEIPAPGKMNPKEYFQVVLPSKGGQMGPESSPSIDTASNRSLTNSLAARVE

ASDSAKIVFYVRNGAIVSAIGTVFDLKQRQMWLQILATELDPTMCLKHDSPLSKIEQNLN

VVYLPHCASNQKYTTILKPLYREVTRIENPQAEQETRRSPSRVVFSGRASKLFSSHLMRP

STISLPSAFQSLRKGRLWGYLLRMENIVASRV

>contig06029 Frame-0F

MQGMNGLAFILLHVLKHDNHDTIVSFLRGIVACILPHVFGICMNPSKFTRCHHFELFHSL

PQVGKVFQDVIQTYLPSFAMRLDHAGLPVCLLAYKWFPTLFSDVTLLASQAQLRFETLLC

CWDVCFLMGIDGLFCVAVALCCVAEKDLKQLERHASAERVSATLGRVWAELTPGELINHV

SHVLDSCAHPVLLKLRKTHLQRLQGDSGTWKEDDVTWKERRELSLMTVTDLDSGNVFQLS

FTGTLGLLTT

>contig06942 Frame-1F|Blast-40S ribosomal protein S3a [Phytophthora infestans T30-4](gb|EEY59262.1|) 1e-114

MDFTRDKLCSLIRKWQTLIEAFVDVKTTDGYLVRLFCIAFTKKRPNQIKKTTYAKTAQIR

AIRKKMTSIMTDEASKCDIKDLFLKFVPEIIGKEIEKATQGIYPLQNVYIRKCKILKKPK

FDLVRLMELHEGGVEEKGAKVAREEDQLVESMAGAGGRL

>contig12051 Frame-1F

MTISRNVYNQLFEQAPDTTEGASKEKVIRLRPTEAKAGAVVMSAKNKIQMWTKEEHERFL

AALEKFPAGPWKKVADFIGTKTPRQTMTHAQKYRQKIHRRQRGLRNQKKATMNALPMNTS

FATVDITADLTNEPKTIVSPYGVADFQLRAGSEAVAAAAAAAGVTNDQLLNILAQQATTI

KKDINPDIRLIEEGVSMKSLELVPAMNQESSSNTNLPSLAKILHLGDAEGHVTMPAELYQ

KGLEMNTTDGELDFDQAAKAKLDNEIGHDGPKKDIDL

>contig12608 Frame-2R

MVFQELFPNESMDTKEKGKDVKVAVGTTPDGFVTIKLRAVPLPFETAKLLEDNAVLLKDL

VTSNKAASIDTNCDKVLGTPEITAMDIQVFKTKLQKSLATSDYSVFQSISLHQIWSCGPR

RMGSNLLLNNIPHYISSTRLFPDITALERPNITQAEQLHKVENSIVTGFQMATSAGPLCD

EPICGVAFIVETVDFHATWSDDVETDTSKYGPLSGQVISMMRTTCLLAFVKQPVRLVEAV

YECTVQCQADHLGKLYSVISKRRGDVIAEELSDGTALFTVKAYLPVVESFGFATNLLIQT

SGAASNPQLVFSHWNRIDMDPFFQPQTEDEREEFGERIYEHNYVRRYIETIRKRKGLSRD

EKIVAHAEKQRTLKR

>contig13878 Frame-0F|Blast-Cullin family protein, putative [Phytophthora infestans T30-4](gb|EEY65576.1|) 3e-85

MEILLIQKLRDICGHDFVSKLQKMMKDKTLSKELIDSFTAWLEERDIELRSEKAANSSAI

DLHHAIKYHCDVLTAGAWPISSTAALHKIVLPPQVLAHTNLFMEFYTGRSTGRKLLWIHN

LSFGMIQSYCFKKRYEFSLSFYQMLILLQFNNAKEISQLQLVQLTNIPEKDCGHHLASLV

>contig15832 Frame-0R

MHPHRVVAMATLFACITSGSPVASEPYVPGLAPVDMAAPKLRGKNAATTNGDTENRINWF

FWKTTDERLKSKIKQQIGLMDQLKLRPYDKKIIQALEKLDPKIEKLLKKYRKKLNEVRE

>contig16381 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53131.1|) 2e-16

MSLLIVRQLRASIVRRNYSTIKRAKPIRVKKSESRRVIPKASKQTDALTEVPTSHPPANP

FTPFEQQTPQPIGGVLK

>contig17548 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58636.1|) 1e-55

MAFGVSGGLLPIPGVTTVPVMAAVFLFRLNPVAAMLTNYLVTPLNIAFIPVFIYYGTVVF

GGGDEEQEFAMVNFMENIKKDTINTLLLFRFKLLHAIYVWLLAMPVVTLIIYGLLTPLLT

RVMPKRNADCKSA

>contig19274 Frame-0F

MIRFKDGNVIKQVLPEDFTAAVVAANTLSYQAKSDNTALYLMAGSRHVLEYELPSLKLIN

RSTLPNNEKTQKPTSVVLRRDTEIGQAVALTLTTDELQLQSLENAEVLSIIALHSLPLNY

DKVVAIDNNIVHTLVLLLSSGKRAILKITSNLTVKVAAIVTATTGVLTESMIEDSVLFHA

AVKDTGKAIQITSYSLDQSPASISYETQFDMTVYGGKIAHAFVNCPTTTRDATLMCQALL

VLEDDALVMTSNDVMNQPSGQIQWLREEALANIKSVRWITPAEMAIEKHALKRIPSFIQE

LALEYKRLQGIVERMSTMSWTLFHESSRQRGVDRSRAARKEPRHAHLFGFSKYIVVLTDS

GKLFALRAEESTIAWSVFVGPKVQLFVTRDHPALGTGAELLLVSNTTKLVWLNGDDGHQV

EATEANTSSEASWVVLLPKRKHLTMDKEPTARRPVAVIGAESLKIALYPKETAALAHLQV

KNFYFYRYDASLNALRGYYLKHDGLEPLGNYRACESWSIVLPREQQVIATSRHHDHSVVD

SAVTITGDDSLLIKYLNP

>contig19524 Frame-0F|Blast-NmrA-like family protein, putative [Phytophthora infestans T30-4]gb|EEY67975.1| NmrA-like family protein, putative [Phytophthora infestans T30-4](gb|EEY62709.1|) 1e-154

MKFVLTGVGGNIGRVAADFALEIKRSDDILVLTSSDVSKLAPERVQSWQAQGAVVAQADY

SDINSLKKVFQGADAVAFISTWLIGDGRRGQMKYCIEAAKASGVKRVCYTSFVEAGSDKP

NNEVPFLPQDHHFTEHLIKTSGLDYNIQRNYLYQDNVPRLFAQSWHYTEDRWLANSHDVP

GAYVAIADCGRVFAALLLGKQEKNTVVEVTGPEAVTDREIFEWVNSISGYKGKFVDLPDE

ELRAYWLERGLPTDVHGDFSNLPMKLCIGDLLCCGEMLANGSMNHVTDTVERLTGRKPLS

YKENLLQYQAIFPK

>contig19973 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56395.1|) 1e-103

MTSKWSKREEQRLLMAWHEVVTVLSNGGFDGSFASRNEGLRLNSLIHQRYVELCGDKNTP

RTNQSTGAKKHAIVMAFRALRNVLRTLASQSDRPNWFGMTPEERMELQKKYGHHNEQAVF

IEKDTYQQLVQIDKAQQIVLTPAGNAPRAPATLNELLGRTKGEVTKKVNRKVSKEKFDSG

PPRGLVIAETISEESDEKEVDDDDASFRTKSSSRRANAEALRHSRYKNLNKKANRNVEPP

DDDKVMNFPPKRRRTNLNDAKWVSRLLDTQTKRFEV

>contig22355 Frame-0R

MYIIFYVITSTRACTQPIFLNGIMFAKPAKLSCNVLLMNKDTKQLRLDVAKNITTSNDID

MKQLIASKAVVKKMSFQRPSRIVVYAAEETKEPLIFDTSGKGDLCFTVYALWRFPSLLPR

LEVHASVSEFVLRGADVMMPG

>contig22449 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61194.1|) 1e-128

MTKHEDIKTMQLYRHLDRIDRRLKDLGYTNKDDPIDPEMLGTLDSLHFFGDEPIRHIVNL

LAETPHKKKVLDIGSGFGGTARLLSHRSGCKVVALELQPDLSEAGRELTRRCGLKSHVTH

LNMDFLELSVQKCDYDAVVGLLCFLHIGHWNQLFQKCYDILKPGGFLYVDDFFRRGKNLT

EEDKLALKNDVYCASVLRKEEIQAVLRSCGFEEIDFQDMTTKWQPYVSDRAHQYRAKLET

HIAQDGEAEARDLDHFYASVACLFEAGNIGGYTLIVRKPQKRFKLKILGLL

>contig23828 Frame-0F|Blast-DNA repair protein RAD50, putative [Phytophthora infestans T30-4](gb|EEY58381.1|) 2e-60

MVLFLNIYKKKGLKDHCCPLCERDMTREEEQAFNSILSEKADDKKVAEKIKKAAEVEASW

LAILTDIKRRMPSWRKWMDLETAIPAKAQELEAIYAAQKALESDVQDKKAAFIRAQ

>contig24595 Frame-2F

MRRFLNDLESKRLALRCASTSSSSQQVGRVVVITSGKGGVGKTTVTASMGYGLAQRGFRT

CLIDFDIGLRNLDLHLGCERRVIFDFIHVIEKNCRLNQALIKDKRLERLSLLAASQTRDK

EALTVEGVEDVLDELKTQFDYILCDSPAGIESGARHAMYFADDAILVTNPEISSCRDSDK

MIGFIASKSLRAEEGREPVKQRLLVNR

>contig26870 Frame-1F

MSPKHCFYFSRHSWSQAPSRYVEGPSLCTIIGDRRDLPTRFNIIVGNAI

>contig27367 Frame-1R

MHPIIVTFGDEVEVRVTNKLTEMTCIHWHGLRQFGTQEMDGISGITQCQIQPNVTAIYHF

TPDKCGSFWFHGHEEVQYAFGLRGPLIVHCPEDQKQSWEKDVEEEYTVMITDWYHDLPAG

GPPIWDTVLINEIGRYDCSAAQSAGFECGPNRPLPRFQFVAGKKYLLRLINTAALAVFNV

SIDDHMFQVVASDSEYLVPSTPINSLTINVGQRYDILVEANPISTTPQLPTQNSDGASVT

SAYWLRVQGQFGIPWTGRPADQVPNGFNPNALAIIDYGSGNTPTSTPWSLNVTIGEFDFN

PVNPLMLPQTPDQRIIVEFNLAVLPPNPTAVLGYVALNGGNFSSLVIPNYPPLYTIAQGA

FTEDLPATANAIRLKYNDHIEFVVVNETPDQHPFHMHAHSLFVTGTGTATLADIRAGNLP

QRLNGPMLHDVFTVPACETDSADACTTKFGYTIFRMNADNPGVWMMHCHIDWHFVLGLGM

LIVEGEDRLHAEGLDAFSPNMLLSVCKGNFSTSNP

>contig28160 Frame-1F

MDVMLLEALQMNNPFTAKHGTRLQMWQNVAEAVGMQVFKNPGAFSWHTCRDRVTALMKMY

TDGKHDKLFKHGTMEENARKETILREINETLLRKNHKMAGQAVVGAVSKETLPGTRNEGN

ELKSGEIISTPVTQKRRKLDNASSGKESAISDEDDSSSDIFRARILELIESKIQFDMDQR

QKETEFREQEFELQKRFLEYLQSK

>contig28630 Frame-2F|Blast-ornithine aminotransferase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY55334.1|) 0.0

MNTVAGMQKSRFIAARMRNCLTRNVWTTQQYIDREEKCGAHNYHPLPVVLNKGRGCKLWD

VEGKEYYDFLSAYSAVNQGHCHPKLVKALTEQAQTLTLTSRAFYNDVLGEYQEYMTNLLG

YDRILPMNTGVEGGETAIKLARRWAYDIKGVPENKAKVIFAKNNFWGRTLSAVSSSNDKE

AYGGYGPFMPGFASIPFNDANALEEVFRNEAKYIAAFMVEPIQGEAGVVVPDDGYLKRVR

DLCTQYNVLWIADEVQTGLARTGKMLAVEYEGVKPDIVILGKALSGGMYPVSAVLTSNEV

MLTIKPGQHGSTYGGNPLGAKVAMAAMKVIEEEHLAENAFKLGNRFRHEMQ

>contig29875 Frame-1F|Blast-helicase [Thalassiosira pseudonana CCMP1335]gb|EED91597.1| helicase [Thalassiosira pseudonana CCMP1335](ref|XP\_002291490.1|) 0.0

MTGDITINPSATCLIMTTEILRSMLYRGSEVMREVAWVIYDEIHYMRDKERGVVWEESII

LLPHKVRFVFLSATIPNSKEFAGWICHIHHQPCHVVYTDYRPTPLQHYLFPAGGSGLHLV

VDEKGKFREDNFQKAIATFVSLFGRGGCI

>contig30639 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69418.1|) 6e-22

MILAMFRALAQELLALFGFLCFLFYILLPVLIFVLRSVAIDMPCEWRKWQLHRAQQHELR

RLRRRIEILTRRKQA

>contig31728 Frame-2R

MESKRCFRRATFATFHARDQTCQVFLNNFEAVSCKLEHIMVLDFSPWSNSEDGNTESKVP

VSTRTRRREKFHGDRLANASSTISDDRYREEKIRVMLTVKSLLYRKEKIISALSTFHKRI

NEQQAQLSEKNATKSSPWTTPTALSPAIVKEFVKNASSDKALVQKQHSWLIANLQDTNAS

LQAALLSLQSFPAQTSLQSGSFITGFDDNILPTETLSEDQMRWAIHFLSASQQKAAAVVA

EAALQIEKEGKALTKHDSFSNVAHSGKILPNFRQLVANCVTLMSVLHHHVAASPDVPHVV

TQKLVERVLELLKPKHESNMDLYTELCAAAKATQDQMALQAA

>contig32026 Frame-1F

MTSRKLQIPVVSIIPGIADAVRQQLAAPTSASSAAKLYNSGVLEIVDLPLPAACTPAVRK

NDHLEDSASHAASEWKLNSAQAQILEDAEIIVMDSHIAAPMLLDPLTNLPHELQHVLKKV

QWVQGTYAGVDSYHRYMATGNNPSFTITRAGGIMPTALAQFVIGWVMALERKFFEAKKFQ

KKRIYGRWELKYRSFQQLTIGILGLGDIGQEIGRMFRALGFHVVGFKRRVSDEDEKTLAT

SADILTTNLHAVLEQSDYLVNVLPSTPATRYLLTENALEVCSKKTPVFINVGRGDIISEQ

TILSALEKGLLSTAILDVFENEPLPKESLLWSHPNVIVTPHIAGTVFPEDVANVIVKNLS

LHFDTKPLLYQMDWSDGY

>contig33212 Frame-2R

MKSVLLGCKTLIISTNFLTIDSTHYRRVPTGATTLAKADGRDFKEIE

>contig34363 Frame-0F

MTDTTKLGKIFIGGLSYETTDEKLRSYFGTYGIVTDAVVMKDPITRRSRGFGFITYADPL

CVDRALAQPNHILDSRRVEAKRAVPRAESLRDIGTGLPSSRPTGSNSLATTGAHGATKKI

FVGGLHYETKDADFKQYFSQYGKVVSAEVMFNRETNKSRGFGFVIFENETSVELVLQEKN

HVIDSKSVEVKRAVPRTDVPPPRSISSRGD

>contig34433 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61931.1|) 2e-52

MDIRTAGQIRCFDSDGEYAVGGGTAGTILMWRLHEPAGMNTVYEIPQAHAASISALTISS

SGSILVSGAIDGSVNIWSLEKKQPLRRTSRSIVSKDLYYSTRIVLFNPIVQLAEADCCL

>contig35975 Frame-2R

MRTGTWAMHGGQNHGRGEVDPFSRSAHASFCLQLTMSSIKVPGAHAKAEWDLTPAPDGEE

HQPALRGQATEPQPK

>contig36710 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67991.1|) 1e-60

MFSSDTMGKLMEDQYVHMHSNRLCVVGLAEAHPALQEELVSVEFAKNVLKSRVTGKKKKG

GQFMQPNTVLCTLKCKSGREYTLYSCIRGSLIEVNERLIKEPNLLNTKHHSDAYLVIIQP

KKVEVAEIQESLLSKEEYKQYRTLLKA

>contig38284 Frame-1F

MRGFLSLTVALILLPGAYASRFQFTLTSRAEECFMEAVHARASDNKVLFRFGILEPKSYD

LVDVVVKNPSQREVMMWKGEQTNFETAKVRESGLYHLCFRKRKGASSTITLFYSFDFISA

GSRSLTLVPHLAVTISKDAPTVSAYSQMALTTVKGQPVRMGIIEFDLVAVSRSILRDSTR

VKLLLTVDRITDGEYVNIALALLPKAVHPVTWEKLEDFATGGYRDYVIDDAITELGSHVA

FDVTELFEEKLNNNEETITFLIFTPGDRDAIVFGTHHVAADYFPQIIVEG

>contig38503 Frame-1F|Blast-3-demethylubiquinone-9 3-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY66460.1|) 4e-73

MLAKRNRFLRPSGRGSIALAHLSTVVDKEVHKFNTAASDWWAPKSTTGVGPLHQINPVRV

QYIRSHVIDHFGHTTDDDPLPLRGLRVADVGCGGGILSEALCRLGGTIVSADPGEQNIAA

AKMHASMSRYTSSIDYRQCTSEDLLLQDEQFDVVCSLEVVEHVCDVPGFLHSLTPLV

>contig38712 Frame-0F

MKGAQDSVRDLEERLTISSLVFMRLKIHAAKSNATASYAHDPVALNANRFRR

>contig39243 Frame-0F

MIKRAFATAIYAVLVACTSASSPHDEIRPFPQPKPTKASEEVALKFKPQLFTSRVVCVPY

PAVDASGTVSGGLKASNGNEDCKFAEKGSQVYGRAMWYQNLYAIMYSWYFPKRFWLGFPT

KRHDWKSVVVWIKDPSEKTRKIVGVSMSKSLDLYNTKTELYPNNFARIQVSASSIVASNT

SLRFEYYEFGMRASYLKLTGHDGQYQDLILWEQLTPAARKALNNDANFYDAIVPFSDKHF

KAQIVAAYPLALESNT

>contig39377 Frame-0R

MNKQSFDLIEQALFCVALDESSASTYDEIARNSLLGDGRNRWYDKPFTLIVHANARGGVN

GQHAWADALVVVRLFDYCIKYVNENFKAKFANRANLEPTLDLKPKLLTWVLDYTAYTAIE

GASVAVEKLIFNSDLATMHFNHYGTTFLKRQKLTPDFFMQIAIQLAHYKMHKRVPAVYET

AHTRLFYHGRTETIRSLSSESLAFVKLMESSVSDGVKWDALQKAISVHMETLKNSLTGNG

IDRHLMGLQIVAEMSGILPKPSLFTDRAFEISKKYLISTSNISGGPQSCPIWGGFSAMYN

EGYGVCYALQPDRIDVSITRYHVCPETSAASFKRFLETALLEMVDLCLTSSLVGLSKI

>contig39614 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54942.1|) 4e-13

MERRIPRFEVIEPGWRDFSLYVHVKSIHVSQGVPLLAAFFKAYYDPKTNPLRPLHT

>contig39661 Frame-0F

MQYLTKLLARSLRYCRGHPAIPISNLFSGQLFSSSPYNAESVAPTLKLLERRKITTLDIG

MFKRTKKPITMVTAYDYPSAIHVDLAGFDILLVGDSLGMVELG

>contig40382 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62938.1|) 3e-41

MSDDILDNMSLSDDEMLDDLAGEMLMEMAERDSTQPALSSNSTVPASWAHGTVVTSNNVA

NPPRMPDLSQMMSQMMPMVSQMFSGNGGSDKLLGCNANSYQQAPVSWQELIKRHVPENEQ

EDWL

>contig40593 Frame-0F

MEMFLLLNLKADKEEDLEIALHGPQEMEFDDAKGLKHYRQQQRGTETLQKSKWAETGWAF

VSTVAA

>contig40975 Frame-2F|Blast-COP9 signalosome complex subunit, putative [Phytophthora infestans T30-4](gb|EEY66768.1|) 0.0

MSDSEEYEYDYDSDEQFASNEQNLNDSGEDDKVVQQRNAAREAQIVLENTFYEAEDFRQR

GDLMQALEYYSRVIALEKETRPVKEQKWAFQALENVVKICLGRRNWDEMLHHYEQMLEHL

EFVTRNESTESISSILDEVSTATGKEAQKECTKYTSKMYELTLDKLKDVSSDRLWFSINV

KLGKLYLDMQEYDQLQRLIYQLYDYCQTPEGVQDLSKATSLLEVYALEIQLCVATKNNAK

MRVIYPETLDLDAAVADPRIMGFIREEGGKMYMEEKEWTLAYNEFFESFRNYQEAGNARA

TQCLKYVVLANMLTSSNINPFDSREAKVYQDVEEIGAMLLLRGAYEANDIVEFEKILKNT

KYKLLSDPIMKRYLNPLLHNIRSNVLTKLVRPYKAIRMESLSRSMNISLNDVENIAVALI

QDRNLDAKIDQTRGLLVLQARQTARDASKTYDALNRWTQA

>contig41091 Frame-0F|Blast-DNA polymerase zeta catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY64210.1|) 2e-19

MDLRNRTTVLGREGDSQKEASIGTTWGVNKAAGLWIHGRYIIN

>contig41433 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70513.1|) 6e-20

MSSRFVFDRRKDKQSLRLMSKYALSETETVSSSIGSDGIF

>contig41486 Frame-1F

MASLDHDHHSSNGNPPSAESALEKVAPRPSEKIRRNRLNMEKMIMKNVAASRNSTKNRAQ

QILEALKKKRQRQEDASYTNADESDHGLKRTKTSPPHDEKTVRTAVAASILSPARRTSGH

NFTSPARRSNPPLPVKSPLPPMVSPARPRSGNMLLLSSPMRPPRNSVVPSPAKQQRSGPT

SSPLTRSEFLTSPLRHRASASPKRPLMFDDNEASTSTRAVGQPPLLASALDQVEGVSSVK

TTKPMKTTKSHFNPFKLKLIRSRLLSLKRRAVQMLMETFLS

>contig42195 Frame-1R

MNLSVLAPSAFVSIICQLHLDLEILDRNRSAFHILSDKVVLNVEMLRSSVVAILLRQGNR

SLVVLLDCSTRFHIL

>contig42865 Frame-0F

MHPDVEALVTYCGRFKDPKLHLVPLLKKDLGLRRLMEMINEAKNSKDNQAIALKMEADLF

KYLHTFPV

>contig43325 Frame-1F

MNFRALFVATVAALMSPTYADLPSLDLCPVTKQIDALASLSSLSEDSYNQCEFDSEFVLR

KAKSLPSPAQYKRMCNSIACQTLMVNIKLLSLPNCVLKLPFSGLKINLFSYAEDFPGNCL

VLQEKESAGSFQHTFSEILQ

>contig44650 Frame-0F

MDEEKVQAYADVAAQMMELHASIALLAQNVEKMARTDEEVTSMTRIFNGV

>contig44728-0 Frame-0F0

MQFTTLRNKLRQSLKSILAASASSSILVGSSSSKLD

>contig44728-1 Frame-2R1

MCCTLRFSSLCTAGRKAVKLFSRQFTTNRTSRSLYKYTTY

>contig46003 Frame-0R

MSGCAEVFYCSRECNMHHASAHRLRCRNLRCSKFNDSESESEDESDEYETDSSAEYETDS

GEDEEEEEEEVETKVKKKKSKKKSR

>contig46212 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59384.1|) 3e-26 NOT\_ORF

MFYVRLCARPSIEATWPPHWRTTFGSKVLTKT\*SHCGGRPEQLCVCKQRPVARPTKGPPA

VGYVHYAIVSVQFW

>contig46784 Frame-2F

MQCKAVLSRGCWFVAKAHAVDKHLMLPRHLSNGSSKDFYASEKFTSNRLKGLQFEEMVVT

LMKSLNCNLRATQQTRDGGIDH

>contig47093 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56110.1|) 1e-51

MALSPVDANNSIPTLEFSINNEPIHAQKLRGPVTADSVCEDDAILSSRIPRDHVLVDELI

GRGGYGEVYKGTYETRAVAIKMLFPETRKSTRHVTEFLTEVKMMTALNHSCVVEFIGVSW

NHLMDLCVVTEYMEGG

>contig47390 Frame-0F|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY65888.1|) 1e-142

MAPEVVGNEETSLHVKREIDPQWSRLIGGGAASATAELLTLPIDITKVRLQTQSSSPVFG

GKPVVHYNGMLHAAQTVVNYEGLGALWNGATPALLRQVSYTSICMVLYEPLRNAFAAKEA

RNHNREVPFRSKFLAGGCAGAIGISFANPMDVIKVRMQADRSGKLYRGVSDALATIYKRE

GLRGFLRGLSPNIQRGFIVNAAELGSYDHSKDLLISSGILKEGVLAHTGASCVAGLAGAS

ASNPIDVVKTRLMSQPIDSSGLGLHYKGMTDCMQKTYREGGFSAFYRGFIPNWMRKAPWC

IVFFVSYEKYRAALMHGDFKV

>contig47619 Frame-0F|Blast-anaphase-promoting complex subunit 7, putative [Phytophthora infestans T30-4](gb|EEY63812.1|) 4e-34

MEKQYPEALNYFHQALRLNPGSSEAVQGLDRLEKLMHGEDPDEMNNSMEQMGQQEHEESM

EANEYLSS

>contig47682 Frame-0F

MTSSYNVHARSPQLQTNLRRAQEGRQTRAYLRIFNDKF

>contig48294 Frame-1R

MYTSTSLFLIRPSCKNTRESVCLGQSLVKSA

>contig48452 Frame-1R

MYTVSYLTKRIAVASGRRALSSAHSHGHNYPHGMHFHVSPVHKNLALAYGTMLWLWVFWR

AKHDGLALLGLEHPWDHHGHHDETHAESVFDKYLLEDGKIKYERSEIGVMPMPVELDEDE

EEDEDSESSTFDVLDDLYDEDEE

>contig48676 Frame-1F

MPIQMNEEAKTTKRNDTSSVQPLLPKAVPPPLPPLPAPLQSTFCDPAPLAPHLGIYYASS

PLLEYKYP

>contig48917 Frame-2R|Blast-acetyltransferase (GNAT) family protein, putative [Phytophthora infestans T30-4](gb|EEY58913.1|) 2e-35

MRDDGCEEVMLETEIANKGAIRLYENLGFVRDERLVRYYLNGGDAYRLKLWLQ

>contig49136 Frame-1R

MEVAQYAKLCSRLSRFLQDYPSDVKLQKNLDKLVKLYDRLDGLEKALPRVEFAAFDELIL

LTLHKLLDAFMRDASKMLQEQFFTVFARVLRRCKSRMQGSSLAHVQRRLHFVQSCVLYLP

PPLELNEEKHTERITLASQSEELRIAVLHSLQELFDENARQDEVIQFQVDQHHFFAYIVS

SLLHIAKQDRCRAAALLAVKVLKCVLFFIRDPSTLRQYLPGVAADLWKCANAPQQASKVT

VAALNCFALALYLCIGDESSL

>contig49183 Frame-2F

MCLNDTKAFSCVPERSFAGPECLADSSRADQSALTLDLSGVGPVSGTLADATVTSHGLKR

SLGAPPTCAPCDKKLKREMERGTFAFHDSKSGNAEGIISRGQRRTSNKRSLTLSPLNTAS

AEQIRRHLHDVRRELFLRPM

>contig49392 Frame-2F

MKVIKNNNDTATRSCEISTEEHVIKASIDHWAKSMIDKDIKPPSLKNFNELYCHRDEIVR

SKCRKFQIYRMETGVINSIIPIKLEGVRAKSEVTNAVEDKAMAANATQLVRQMPVQVTNA

ESAAINIL

>contig50075 Frame-1F

MEIVDDAVKVESDALNKVRNAVVRRNGVRDRKSPSGRSIQDRADHLQVKYNDDAGDVGCI

TVAERSGQSVSCALLGAKYSPFDLPNDIDSAMKPTAGLNCSGLRILIRLNRSSPALSSAA

SSNRFLTLYSCLDQIVLVKEHVQDSGIDNGLVL

>contig50369 Frame-0F

MADELIKLSTVSDVSDSEVSSLCSSELELEMTWGEGPIAPLRAEDDGAAKKNVIPCLERS

GSNGNGSSRARTPQKCSSGSISSRSKRLVNVHPMRSAGYLSKPDELPLSVRKQQRWFNDH

HFGNRAASTRLEDLMEHMEINVEWRSNFQKLAEPQNESLQSSFRKGGGVSDPPAVPRNHR

KDKWNGAEKMFARVDRRARTLMLRSFNSFASFIEAVECVVLHFIQWREVPSELEVARPLL

RMLKHPIEVTNDVGTSVRLILPLLDSAFHRLIIHSVCQFYGVRSRTECDRHIQTKIMVLK

SPKDKHLDIDLISLCDFIVETRVARHVLYDHALELQSKSSECSEDFLIVEAPQV

>contig51142 Frame-2F|Blast-condensin-2 complex subunit G2, putative [Phytophthora infestans T30-4](gb|EEY64046.1|) 3e-80

MLLIFFESKRHAGVDEMLYRICSPILWRGVKAPNDSVRRQATILLFDNFPLRDPAFNNEL

MDLTLQKQLDTFEELLGDFHPALRVAAIEGVSKILSVYWELLPADTIRRFITKLIVDLVN

DVSSSSVRAAVLNGIQFILDNHNSHAILKP

>contig51384 Frame-1F

MGTKRKREVESSRDARLDDPYLLHMPPCLFSNHHRKIGKNVGMVRNCFNNPNCLYGLGEH

YHGIWQSARLIRRLYGSDPRERKRPLNACGKAMPCGLRNLGATCYLNSMLQCLYVNLPFR

QAVYEWEPKEQLVDKALTLQMRALQKLFAQMQLGNESYYDPTVFASTLSLNRGMQQDAQE

FSKLLLAHLRTIFWQSKIPRHWNLVDKLFQGQMCYVTKCLKCQNRSMRPSSYYEISLNIK

GHQSVEDCQCAERFLELKPQALPSTLMLHLMRFVYDAKAGRKKKLTDVIEINKILKMSEL

LRQSGLVEAPGPSEDVIYRL

>contig51829 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69840.1|) 6e-55 NOT\_ORF

MEKTVRMLSRFRNNNFAICDELLLPLGAGCFPLGAMINHSCDPNCAVTFVPKTLNMEFRA

MRSILSGEEVTQSYGSLDEL\*RLVAYC\*HKVRRLIVVDVALPRRERHQRLQDKYHFTCAC

FRCLQPLEERESLDAFLDADVNGVVQAKWTEDRRYEVE

>contig53038 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68367.1|) 2e-17

MNIYPNEVSNAYRSSHMTCGAIPTRTELSALLNLVIPTSEDMLPVETTSRQSSALSFTQQ

ATFDCAFEFRELVDLQVTNNTPTIEPISNWIAPMPSLCQGGSELPLLPFPQTQDPLAFLR

AHELTISCPQTKLKRLGNCQVAGCHTKKQKNGRCIRHGGGRRCTVSGCTRGAQSMGRCKR

HGGGARCTMDGCNTSSQGGGLCR

>contig53621 Frame-2F

MKPAIRRTHDGKEFTSEGRHRLRQNSSPSLCSSDYSSDGFELRAQAAANRREVGLNKGIS

YTCA

>contig53768 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY70130.1|) 1e-43

MTWSMLLLVLIDFAASSASISFLTASATCDPLYEKRNSITGQCDCREGFSGFGCRMCATS

AELTSTSDSDVCSATFGDDYSCVTGLNYDDHAAFKTYGCTLSSDLQTLFPDGAMDVHCDR

DERGIANCSAVVFKATESVRSVHTIECNITHCAFATGNASGECAQ

>contig54268 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68251.1|) 1e-105

MFDFCWETNVAQKISIKHAKKHYVVVTPLDQDVAHVYCKTSGKWSLNVHGVPNVSYNSIV

CRRYITERHRAIICQQSVLEERDFQDESTLPWLFKRWVVFQPQAQNGIEGTFVEAYRTAS

YATGRLIYKENKTYDSFCEHLIRRYAESNALLERMMARDKRFADAFAGCERSGADVEFAS

VSDHVIKDLLLF

>contig54321 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62253.1|) 1e-104

MTSEEIVVEHAMSLKGMYVCAGTAVESDDDYVAVKSNEDVLKDDGGINPGETPLLSIRRL

DVNVKVPPMPRLLNIVECIAPIPLDYRLAHLEVVSSSINNASITREQIIGVLRDLFVPFS

DHQILVKSMRMIEHDEAVLKPISSDDEAFYVVNYEKVNSNKSLSAQEKKDKNEKLQKLEA

SMTLNKILELRSQVTGLSKFYRRNQAELSFADYAAIVRENAAKPSNVIFRAIQV

>contig54354 Frame-2F

MAPANEERQCTCEFSCHLVRLIMSR

>contig56059 Frame-0F

MTALYRNRLRPSRLVLLSWPQAFPHVSTRLVTNLPPISIHRASYHRV

>contig56536-0 Frame-2F0

MTRKVREMSLEISCNVALRTTTRFRINETCLLGPFTI

>contig56536-1 Frame-1R1

MVNGPSRHVSFIRKRVVVRRATLQDISSDISRTLRVIVLKSLEF

>contig57694 Frame-2F|Blast-pol protein [Phytophthora infestans](gb|AAV92918.1|) 2e-12

MRTHPTFYVGRLRPYHQYAVSSEDGSDHPFQESPKDSCDHELVSC

>contig58718 Frame-2F

MHADFMVKKLRVIVYRHGGVHLDRHLDLLRLGKRLAFVFASICLLLYSFMAFYPSKSCDD

SAIVAGQHLSIDGGNLPGNCAAEELDRANSVTWWKTTSVVGVSG

>contig01104 Frame-1R

MGQMVSDKAIFNITEFGPTPLVSFRETALFFMFFSLVPLLALFFFFHEDPDPPPIDDGEY

GGIEFERLELAKPRSSGWTESVLINWERVRQVLAKKSTIRVLFFFIIFIFLSEFTLTYPH

VQLGIWCDFTVKAQSTSDITLEVVYVLAAATWKFCALNWNWRSCILGSLLVITIVPQFVY

FVLAAWIDSLRNQEVFSLIKSLHGYLRASVVIVEVAICAEIAPVGGEGAVVGIIVSMSSI

MRLLSTTFSNALGYAFQTPSLRNTEQESSLVTFGLIICYCVKLMSAVALLFLPKQKEALQ

RLHRTKASSNRDTTWWVLGALGVALVISAVFNMLAVSPSTACLRIVGGGGCSD

>contig04389 Frame-2F

MLLNFTIFGRLALPSQIKKKVTLSYVSNGLKQSLRLKHQARTITTMTVTN

>contig05001 Frame-2F

MKRVLDSTITGVSAVVGLDRQDRIEEGWL

>contig08576 Frame-0R

MSLEMVFHKLEFNDQRHVTQVFHSIHDDSAVIFYHAFFDTFRKSRSQDLELADLFVKTHG

LEFVATMLLSFLPLETIQTFQSYLKRSVFRLWSQVDDQELLFRSIVSQVNFRELSADPVI

HLWYQYLERQNGPSAPVVAIDLLIHVYGYPRILATFSGGSNYKVLRLHQTLQKGLYTKFI

LDNFSAEDVLHDLGLVKGELEKLEKPLLDARAEFWVEYFQMTLKDSSDNLEVPKDSSILY

FFNHMIDISVVEEKSRWEELKRKCQIKKPDEPKTEAIGTLLEQKLKKVTRFKRDDLV

>contig09885 Frame-2F|Blast-pre-mRNA-processing-splicing factor 8 [Phytophthora infestans T30-4](gb|EEY57153.1|) 0.0

MNSSCADVLLFAAYKWQMGRPTLLHDTKDSYDGSTSSKYWIDVQLRWGDFDSHDIERYAR

AKFLDYTTDNMTIYPSPTGVLLAVDLAYNLYSGYGNWFPGCKPLMQQAMAKIMKANPALY

VLRERIRKGLQLFSSEPTEPYLSSQNYGELFSNQIIWFVDDTNVYRVTIHKTFEGNLTTK

PINGAIFIFNPRTGQLFLKIIHTSVWAGQKRLGQLAKWKTAEEVAALIRSLPVEEQPKQI

IVTRKGMLDPLEVHLLDFPNIVIKGSELQLPFQACLKVEKFGDLILKATEPQMVLFNIYD

DWLNTITSYTAFSRLILILRALHVSNDRTKIILRPDSETITQPHHIWPSLTDEQWLKVEV

QLKDLILGDYGKKNNVNVASLTQSEIRDIILGMEISAPSLQRQQVAEIEQQAREQSQLTS

VTTKTVNKHGDEMVVTTTSQYEQHSFASKTDWRVRAISATNLHLRTNHIYVSSDDIKETG

FTYVLPKNVLNKFITIADLRTQICGLMYGVSPSDNPQVKEIRCVVMPPQLGTHQSVTIPL

HLPENTNLEGMEALGWLHTQPNELPSLPPQDVTFHSKIMSENTSWDGEKAIIITCSFTPG

SCSLTAYKLTPAGYEWGRQNKDSGANPAGFFPTHYEKVQMLLSDRFMGFYMVPEEDVWNF

NFMGVKHNTGMKYDLKLGNPKEFYHELHRKTHFMNFSALEATDEDVATVDEEQQNVFA

>contig11303 Frame-1R

MKAKLLKKYYALLAYRTAFRVGRECKT

>contig13073 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53406.1|) 3e-40

MKPGGDERAIALPLSDKRRVTVRYFRNGVLIDLREHYAQDGVFKPGKKGITLSKDQWSAL

QEVSGEISKAAHNL

>contig14083 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55062.1|) 9e-55

MFFFLGAMALILVPIGAKADNFFFAAGAPDHNNKIVGNLLARVSSIRKNGEAYAVFDWDN

TCMFGDISYTSVLYQVENLNFRLNPDNFESFFSLGYNASSSDICLPHGTNSVLGQDVNDN

DVTLAKVLASTAEDYKVLYSAYIAPTYIFKDAT

>contig15105 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64471.1|) 7e-31

MPHNGVASVTLVQGLTSAFYGLRELALVLKHF

>contig15361 Frame-2R

MKKGTLGTEYLNQRKGSLRRPGTTCFKGRRRRRSTIIRQWEMQSCEVIWRRLAGRTVGSR

>contig15729 Frame-2F|Blast-DNA topoisomerase, putative [Phytophthora infestans T30-4](gb|EEY68895.1|) 1e-96

MRISNETFTASGLMVEERNFLDIYKYEKWKGSVIPVYQRGDVFRPSTLVMLLGETNPPPL

LSEADLIAKMDSSGIGTDATIAEHIKTILKRKYAIKVNNNTQ

>contig16654 Frame-2R

MELRDNLDVRLQKGTDESFWWLFDCLLTAVWGALHTVITHQDAAMTNAIVACFPESKHVL

GMWPLPGSLRRSLDRSWGANCT

>contig16720 Frame-2R|Blast-60S ribosomal protein L11, putative [Phytophthora infestans T30-4](gb|EEY64473.1|) 4e-18

MPGDKSNNAMREILVDKLVINCCVGESGDKLTRAARVLEQLTGQKPVYS

>contig17442 Frame-1R|Blast-peptidyl-prolyl cis-trans isomerase CYP19-4 precursor [Phytophthora infestans T30-4](gb|EEY59136.1|) 5e-30

MANSGANTNGSQFFICFKKTSWLDGRHVVFGRALAGYEVLDAIEAVGSESGAPSKEILIT

ESGELFEDDFV

>contig19277 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56921.1|) 2e-44

MLTYNETIENLKAMSTTPTELESTTLVFAYGLDMFYVRMTPAKSFDLLPSDFNHEMLLLL

CFTFLVVTFGTKTLAQRKALQTAWK

>contig19552 Frame-0F

MAESLNESRVQNDENNGENNISDDDSSSTSTGSSSSSSSSDSESDNEAETEKTSFEAAKH

VPSGGIDSRSSYGYANNALGPALSAPRPHGMAANNETLNVNSTRAAARFKAAETEAMMPL

GTRKRDRRTIEEIQRDLRDKRKKPIGKLALKSSPPPPKGSPILSPEADANVGAALASGGS

LNSTFGTAGRLPMKRKPVSAHDRLAMKLNGRKKTNAK

>contig20369 Frame-2F

MLFKSAAGNTDLVVAARGVSVEPPPTGKRRYVTAFLCLWVSMICYAD

>contig20471 Frame-0R

MPDDVDNISDNEPYLSVTTPCPRTVRSDLKEFKHFMCIEDLRGDYGCCISYTQMFAGQRS

KKSYADRLAIRQAQSKQRKRNLANKEAVQSSKSRKTNDAKEDQSGKKKGKATVAPRRGTA

SGGKAIRAKKVKKTPTRRTGTTTKSCTSSNYYDDSAVDLGDEITTMAWEGRGSAG

>contig24596 Frame-2F

MRCWRNNLGTSMMRAILCTLKIHRNEEETKEDEEGRVGDVIGNALEEEEKEDEDVVVNLD

VEETQIEMKIEDENVAPAPCPRINPALMIRGSVLYVYGGVVEDGDREITLDDCWSLDLKR

LDEWKEVLPGTMSLQIWKGEVSETEESSDDDEDEDDEDDDDEDERGAVIRQQLDDAPEEK

KETVERVMLMLTQKGGSEDEVRIQTGKKDKRVKTKKESHRKSLRAEMEHLQEQLGLHDVE

RTPQMGETLRDFFARTDTTWTTEIMRRPSTVEHELNMKEIKREG

>contig26767 Frame-0F

MIEVEPAMWIVVLVMAWSICGMLELFRSIDTNMPVRHELVGVCVMFSWVLLLLHVLVYLY

FRSCIHHLLHAAAFSYNKTTLVANLSVIAHEEAEAWEQEEADKALEIMGRIQEHHEELEL

QRLRTEKRGGIQRRSSYTGVVQDSTSLNIRYFSQRGWHLAVMILLIINGFFITLFIQCAV

YDLTDIYHDFGTLATIMVPLPLLINSIILQRHIFYDFVVVSNTLRIDSHTLSDVIENFRE

VVRLRSEFATAIADQMVQHELAISDLATDLKARDPNGTGFIDVDDLRDVLSKFGYRLTRF

RFNSVVKLLFQLEGTTVPYSHVIRLVLMAHTENFGSTLRSTQAQSRAILQQSQILYSDVG

QPTMDCSQSSYAFFDSTREASVMAPMIEPSGFVQIAMGSRILPQSLHCGVDGNIQQTSLR

SQTMHDLFNLQRLSDQPGMMQL

>contig27148-0 Frame-1R0

MAVLSVYIVLCTSAVFRFSPGDVE

>contig29793 Frame-0F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY62207.1|) 3e-70

MKWTDELRLLCVFASGSCVAFSMMGDEEARFSLLPPGGKDKIATFEAWGGGLVALTEKMA

LVQVLEIDSVRPKVSLLPDCGLSETNPPTCMAVLNPKFLKSSYPEVLLGTSSKSLMIVSK

EGGAQD

>contig31653 Frame-2R

MSEKAPQVLGGTRPNVDERFHLKDVDNNGNDNVPSIYTLQAENDGPEVTTMTSLCMNCHE

DGLTKLLLTVIPYFREVILMSFECEHCGCKNSEVQFGGKVQEQGAKIELELTQIEDLNRQ

LIKADAGVIYFPSLDFEIPRETQRGSINTIEGVLQKAIEDLRENQEHRRETDLETSKKID

DFIAKLALMSAGITLPFTIVLDDPSGNSHIENPHAPTVDPMMKVTHYYRSEQQNLICGLQ

PDMSHDLPSQAPRVLPHRNEGLDKFVEEANIAKKEVIQIPADCFACQAPGVSCMCMTDIP

HFKEVIIMSFNCEACGFKTNEVKAGGAIPPQGERITLKIDQRKEPNVMDRDILKADSACV

NIPEIELEMAHGSLGGLYTTVEGLLDKVRQNIEEGNPFAIGDSDGGRSLLNAWLERLDGL

KRGSEPFTLIMEDPLANSFIYSPYGAAENDPCMTAEKFTRTEFEDDVLGIADMKVENYSD

DTGLSSITEEDANMSTEPIRSDKETMGGGQAIDPSKYHPNPAAVMEVKHQLEQQNERVK

>contig32025 Frame-2F

MVFRKSISLPVAPSVQLRRRQSCRSFSIAKRRGDRQTNRLSPPQSMEQTLLDTVHVEFIK

AVVPGQNKLASPRYIMRVINTALDQTWEMGRTFKEFYELKEAIANVLDYGHFCPSNCPWL

YMYAAHHFPRRRIFRSRSPSVISARLSQLQTYFSTLLQMAKQKRNLACPVSSTKFPELIY

DFLFEGMVFEHSDFMRLSERATIVGGRDTYVAELDPTQDPDDCSICCNALVENNALSIIV

AAVTEKSDIPGSVRAGLTTLDCGHCFHDECILAKLNESLTCPLCVPPSISLELDLVKTL

>contig32090 Frame-2R

MSKVWNKLSDSDKNEWYELAKQDKR

>contig32393 Frame-2R

MASELRISIRCIQVPRCAASKFVKYLNKAGLARSNRQCSEAVDLDGLKARIPLRPVSRRK

HIIVHMATITLQRRRRKSKQVKCFFIQHFESE

>contig34997 Frame-1R

MISNNSSMSKVYLQTHTERT

>contig35590 Frame-2R

MDVSEVEEAFLRGEWTQALRDSHNLLKLHQAKQDQALAASTLLSTDAERLLSVYLQAIFE

LDRSEDVDTATAIVNSFRPLPGGIALYYSRFLVAMNQRAMALESLNDLLASYAVNKATRC

TIEEYIHAVELLALHVLLPGEGQKAAQKFVTKDRVLNDTFKRTFLQEIQNFDGEKKTVIF

GKSPLTGQNSELARNSDFSPKSSGSTEPHNSKIQDDLSSYAMIGGTVVALAVTA

>contig35976 Frame-1F

MVAFAEQSGQLQSFHNHLQPSIGLRCYT

>contig37866 Frame-1F

MSKSTTNIVEKMEFASLGLVLDHTADEAVQCLKVLKQNLAEYDLRHNHNFLNSAKSYMRS

DMRHAKDISSGLKQVAQEITKGEKHSMMEVESARNAMNSTAKAMEILITRSRLYDETNGR

ASGVKGVIQNIVGGKSDTTENSDSLEALIESTLQSNFDCQVLLHQISSAENSLNPAVVKR

ASDAMHDVKDPLTTDKPGPVTEIPRIIHSAYP

>contig38041 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69216.1|) 2e-71 NOT\_ORF

MADYEGYLLLHDFGQRADPLFFQLEGGLLQYYDKKDGRYMGQFLLTRHRVLVQPINGGLT

PNRLSVELCPVRSVYDTERSIKHLPRIRIMLSASTPETQSQWIYALRTWRRRNWKETAVI

AAFDDEVKALRMVMIMHQLELKLLRSTNMSLCKVNMDIYSSDPPYRSSNVMKRDAYPTAL

ESEAIQFTRFSSALTY\*DVYVYAN

>contig38287 Frame-0F

MPVSYGTISISRISLNRMGWTVFGGMINKGRIVWIDDILVHAKTPAAFFDLLERFFEQIR

AHKLKMSVSQEWFVKDSNQMVWSHLQQERIEFTDKPSST

>contig39424 Frame-0R|Blast-phosphatidylinositol kinase (PIK-L3) [Phytophthora infestans T30-4](gb|EEY66032.1|) 1e-92

MSSPYRVPLTRFLNRYASMSVSFFLKREHLVK

>contig39662 Frame-1F

MIHHTKAVKRGASRPLLITDMPFGTCEGAPYEALKNAQILLKEGADCVKIEGGKERADTI

KTIVDAGIAVMGHVGLRPQHISVMGGFRAQGRTAAQARSIVEDALAVQNAGAFAVVLECI

PSAVAKAVTKLLTIPTIGIGAGPETNGQVLVFHDLLGMLQHPHHAQFVPKFCKRYADVGE

QIRIGLERYRDDVETGQFSSEAYSPYKMSKEETQKLTKMMAEEFNA

>contig40381 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62938.1|) 1e-31

MMPSVYMAVETMLATMLSEAVRSANLEHVFRWQELRNMLVLELAQTNMTKVFEAKFKDML

WKRVASDPDYLLEKDSKRYRNIRKTFSAVKS

>contig40590 Frame-2R

MEQGTSKHNLLFLDPNDRKTLLENTLLKDVVVKQDVLSDPSKVAFVRRIFEQGLELCQKL

NEVIQSTLKCLWIGFEAEVIRMTGASSDSVANARLLSQRLAKNSTDNHPDLRVLFAYAKL

ELNVGNERQGYRVCEKALKSLKERNLVGDSNFHRFTFLQARLELWSPFKSRDQKQLRLLR

CLYTLWRAQQPNRVNGKEIEALDTIGKLSKKQFRARLQEQLMSDPSTRSDLIAKYRADLG

SAAQHCALITSRSPEDSTANYIDSNPFGCYVGYCLHNLALIVYAYDGFDAACRVYRQFLT

NSEHQDCKQEVWAWTCFLEFMQQHQLLGLSPRLAPRLWRLTISEAVEYHPYNEVFLRLFA

DSDKGNTISQVHRKYSIWVEKRWRRYYDSPDVIEWLFMLLCEIYRVERAATILELSRNVD

PCIDEHSHPMCCVFHRWGRNTTGITRIRQLFENIVTQFRTKGSALCWELYLRFEVALGKI

DAATKVLYRGIASCPWSKSLYMNGLRILRAYLSEEECYELLEFMESKELSVRADLK

>contig40976 Frame-1F

MPKVLLCGAVQGQWELLFERVRRLNAAAKEKPFEALVCISRCFPLPVDYLAGGDKQTPIP

TYFLPACEAARLWQENAKQMETFDHLSSVTQPSAPVEIGEGFFCLAGAGVATIAGLKIAY

VSGTESPGQKDEKGAVLTYSKASVNTLVQELLNSPEQGDVDFLFTADCPANFQLLLPEQQ

LSPGLQAMRGSEAICELVQQVHPKYHITSRGGDGSRGDVFYQRLPYVSEVTGSKRKQLTR

LINLSGVNTSKDKTRKYLHALQVVPFLQQSPGDRQHVDIPTGTTQNPYLYAKLEQLRSDE

QSILKRRKVEGLSTEQIEQLTAKSRGDAQYFYDEKLAAKGQRKGGLIPGQGKKPRVADRT

ECWFCLSTPSLERHLIVSIGQEAYLAMPKGAICEDHVLIVPIAHEATTLKLQDDTWREME

RFKAALRRYFASQDKELLVIDRNVATLGATHCHLQVVGVPKALAGNACRIFETEGEKYHV

TFKNIGHDGDAQASASTGPLELLCQETNGQSFLYAELPTSDGGTSQLLHRVEGKHYVQFG

RHATACLLGMPRRANWKFCVLP

>contig41078 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53516.1|) 1e-106

MALDQQYVNNTKLRADRLARLAALQTQNPQLANVPDGVAAADEPIEIIETDDDLKKKEEG

NQKLHYPRACYICKKKFRTLHHFYDRLCPSCAELNYIKRLQGANLQGHIAIVSGARVKIG

YEIALKLLRSGATVVATTRFPNDAAFRYAKEKDFKAWKERLSIYGMDFRDLGVIDKFMDH

IKETFGRLDILVNNAAQTIRRPVHYYKHLIDPEVAPVLESMKQINRLPRGHASLIDCART

NLADDDLATNGAAIISPSEDGSTLIKTNFLSVHNSQI

>contig41092 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59354.1|) 1e-89

MSKRVRVHLKHQETFDRTAPIVATFRNGPPPPKDRNDLAFEVFENPAKKQRLVVASSEKV

AYQGANFGYLGSSHDFASYAVGIYDKKTREVRLCNVDQIYVMQQAIKNMSEEIDDNRGSD

KTAIEKRRDLIEAFGSKKSKRMQKNREENMLILKNISGAASISQTLQTKMAAAKQKLAEK

QAQDGSYTKEGAALAATR

>contig41360 Frame-2R

MARRLIKPMPLCAARGGLMYLSISQCSGADASKLSSSIHVRSFCDNCQHRTPRLIIANP

>contig41997 Frame-1F

MSRADYYLVLSVRLSSKAKQSAFCFACDRLKPIIKLLYLSITDYCAAHEIYF

>contig42866 Frame-0F|Blast-integrator complex subunit 3, putative [Phytophthora infestans T30-4](gb|EEY54602.1|) 0.0

MRYLAGGDPSRTTVWLASSILRILIEHEAWLLSCSALIPFVFHTFVRISLDHSALQHAGL

LKQEVELCTTLWNRRQADVAQLGRETVRVLSDAKDIPGMSMLWKQLRNVRDTPEPEKDVN

VFSVAQLMAIPTPPKYLAFRLNPRMEEYLLFMMERVHAGSVTRYQKWFSSQFLSSPGSDA

LVPDLVRYICAVYHPSNQVLSSKITPRYHILGWLYLLCHGSKTPSVLARVQLAMFFDYLY

FKPSDNIMTVEPAILLMVKSLKSHPMVTLSMIQFLVFAVEKFAASAVNRVLMQKGVSTAF

AMILKLGVVSSILPLQSFPMLLSSASELQSELHRIFPEHFPPASTTNQTQTHSNSIMSAG

GSPGRSPNFILSPTLQSPTMHSPVRQSPIQQSPIRSSPNGANSPATSPLGSQSPPHSDVS

MGGGGSTSDTNSLGALSFLPENEQTVEITTEMASAIDATTPLTVNLPKKCAIDIPEIIVT

LGRDDVERFQQTIPDPCTCPSEAFMECLNDVLILWTRQSNGIEIAAPLGTFLHVSLEKLF

VSSHISLTDSPNLTSAGVFVSMLDQVLSDPPELYIPFLKAMYARDVTIAYRLLAFCCSRR

DLKSPDIALEPYALFVEAVGGTLAKNIVKDLNLSQQIDDARVQACALMKKELPLIVSKDE

MNAVNATVVVLCPYLFSNNEHPYLSKLMGRSEALVQLLLELVTPVTLNALCTRVVMREFV

IFKNRLANIVLSSLQWTSWEQYGMWDLVVAELQSGQSATAETTIMEAARKVLACVNPTES

PETMTGLLKCLIHFCPDASILQSIFNLSDAYGNFPFAVLGCWIKKFPAVVISYVRSSLER

HNDLHNDKTLFEVVRKVDHLQHLQSRSSNPNTSRRIAVLRDENIVAALKSIMHRPANAAA

ITGFHALKAIILDVESPNKKPRFNPDP

>contig43713 Frame-2F

MGMRNTSSLRKLHSPQTDGNCGGRHRFQNNSSKHVLRSSSDSTQKHLSSPQPESSNALLK

RRSCHEFTPGERDFPAEALTLESLTHCQRSVHKDGVACHIFSKESRDDHNNMELVKYGSS

VDLCDLNDSSVCSLGKESIRKTTSSSDTSFDSIHLTGMSPVRMGIQELEDIRQSFDSFGD

LLDIHDEDFDAFDDVDETLDTRDMEIIKRTYPLNNELWRQIAELRDAAEDIYQYTKESTA

KHITSGGFLRRHTRLQSF

>contig44653 Frame-2R

MRFIVVDAVMDLILVKSTESNINGRGVPFDGFFEPFIYISTQLFEQ

>contig45016 Frame-0R

MVRKQLDGVFVSCKLVLLFVRHVKIIYVRGSDKCRGIRYQREDCNCIIRNSVLVIFLQRI

EMVSHRNAASSFVLFSTNFRSFIVRWHVRSLLEPIKKYQKLHR

>contig45746 Frame-1R|Blast-bifunctional folD protein [Phytophthora infestans T30-4](gb|EEY66137.1|) 2e-79

MRGRYPYLIPCTAKGIVALLDDQHISLRGKTAVIIGRSNLVGNPVSMLLQKRDATTIVCH

SKTVDLPSYVRQADVVVAACGQPYLVRGDWLKPGATVIDVGINFVRDIAGEFHGIANLDG

LKLVGDVHLPEACKVAKAVTPVPGGVGPMTIAMLLHNVVEAYKRHVGHSF

>contig46211 Frame-1R|Blast-nuclear transcription factor Y subunit, putative [Phytophthora infestans T30-4](gb|EEY58270.1|) 2e-15

MEGQVVELTEAEQAQHQLQMEQQLKAFWAKQLLEMEQLEVGSE

>contig46718 Frame-1F

MRMIEVTILEELKILKRVRSCGLLWASRKNRYANLTLRNSTRKSLRAKHISKFHLL

>contig47393 Frame-2F|Blast-mitogen-activated protein kinase, putative [Phytophthora infestans T30-4](gb|EEY70149.1|) 1e-169

MASFAAMSRATSSRNGIDENSPCLDLDAPTPQVRPSGAVVQSISHRVALARGCSFRDMKR

DNHHFRVGNTNFDVPKRYQMIKAVGQGAYGCVIAASDTETGQALAIKNIPNAFNDLIDAK

RILREIRLMRHLNHPNLVNLLDLLRPPTLQEFNDVYIVTDLMETDLHRVIHSNQSISDDH

VQYFLYQMLVAISYVHSAEVLHRDLKPSNILVNSDCDLK

>contig47681 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54759.1|) 2e-92

MTSGYHMLFTQLFMDSGSLNQVVGTCGAPAWYRKYLLGYENMLRSLDPTFSKLTLPYWDL

FEDAAKRISTRVACNGIEECSSMLVDFGGCNGPEISSGAYIVNGEAIPSGNCANSSIAAH

ACTSRKKCEKCIPRGDWTIGDSSLEVGPTVFIDLIRQARNSTGVSESRATAINSLRTAIQ

NSIQMPLHSILGGLYETRAAAFDPIFLGHYATLDMVYQVYQSCNQSIPLTGS

>contig48675 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59543.1|) 2e-48

MQFGTPLPSFNVNDAHELETIKRLTEEEYLMKICLLQELFYCYLEFALPAEKPRIVDAAF

ALPSIYKAGLNAQTSESVEPFVLNNVIWNLVCGLDIAVTSTNFIAEQCNATIASLKPKHD

SMLQLSRMAAR

>contig48749 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65519.1|) 7e-13

MLEALLKWSKASGKSVELVA

>contig48860 Frame-1R|Blast-DNA-directed RNA polymerase I, II, and III subunit RPABC2, putative [Phytophthora infestans T30-4](gb|EEY60450.1|) 5e-69

MDDMEYDDAGHRDIEDEEIPEDEMEEEMPVEDMFEGGEDVGDQENKLQVLDDSHKQPNAH

RITTRYMTKYERARVLGTRALQISMNAPVMVDIEGETDPLKIAMKELRERKIPIIIRRYL

PDNSFEDWSIDELIIE

>contig49180 Frame-2R

MLFKSQGHANCDGRSGQIWSGRLEGQISWRCGECQRLQSKFHWKIAKVKMTRSVKLDDLV

DRNYGIAERLTT

>contig49391 Frame-2R

MTWRKYERHIGIPGECLGLSLVKATDGYAEVSRIIPGGAAQRANIIIGSFLIGLNNTKNL

KFDEIVNMLRRLPKPMLFHFMFRSQSALEPIVPSIPKPRTEEIKVTLHDKEELGCSLSTN

AFYCIVSSVDDDSIARRHNILVGARVIALNGRKFLKPKETIREICTAKRPIDITLHRM

>contig51318 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54511.1|) 1e-26

MPLVFAGHVNQITWLKPSWARQMPIGAFKQLAVGKRLTNGAMGVTSELPHFVEDDLYCSL

KEMDSSSTKKWDLFAIELNTSHEATAIATEAIKTARQNSRAFLLDIDLDYFSTWNPFR

>contig51400 Frame-0F

MTFEKEFQPSLITQSSMLAVYGDANRFVQRKFFITDFCSFQYQDWQIFVS

>contig51611 Frame-2R

MSRHPMLCEYIHSMLHGCHTWLMRGELEKLCVILLSKEGRAIETLVIEPVWIAPLTEAAG

LNKDHTLPLEQLEESFRAGMVALMTTAVSYEITSIDMKPHTFRILAQTVEDATNRGTAVN

DDTVSNSWVLADVYWCEDQQKQKEIIPVKSIHAETLPIRLNIYMTKQ

>contig52117 Frame-0R

MRHLGLSYCSAYSIAKPVSDRRNQEINKVDVVKRRVARRRSRDILRSNAIRSDLLYIIRF

LFSPACCCRLSKRP

>contig52162 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54343.1|) 1e-20

MACKALTSRILLLFVMLALVVAIVLVSYYKWYPRNRKDYVGILPDMKNSTSGSGTA

>contig52324 Frame-1R

MRYISIHCSPESISQLDQVMRLIIINLIAGSHLLLLACKKQLFMDNWLVVSRNCYPYFNS

IMAV

>contig52801 Frame-1F|Blast-arginine n-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY66512.1|) 1e-148

MAAHGEESETWDDWVDDSLLASFECVFCTCKFSIEELLHTHLREVHDFSLHHEISTRNLD

TYSTIQLINFLRRNTLNGVSAREIQQTLASDGSAAFQKDEYFKPVVADDPLLYCLDCHSD

SSDEDSDMHIEKMRKSKKVLSATIAADDNEDLITKLQLENQELKLQLTKYSKIVRDFMID

QEGTAPIENAADNDTYYFDSYSHANIHREMITDRIRTDGYRNAIINNSKLFEGKVVLDVG

CGTGILSMFAAQAGAARVIGVDRSEMGIVARDIVAANGFSDTITILCGKVEEVNLPVDKV

DIIVSEWMGYCLLYESMLDTVLFARDKWLAPGGHLFPDKCSMFIQAIEDSTKRF

>contig53622 Frame-1F

MRQSHLIGRSFFQRPLHCLAVQSLVDYVSRLPCLQCGQAFAAIANVAPKRVGCGQMQLPL

VCSK

>contig53657 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60744.1|) 9e-18

MTTDGATLQQLQTTCDALKAEITALYEQRGKKHLDELRVKQRRWRVLLLLTAMKSGLRDT

FLES

>contig54807 Frame-2R

MMPKLGSYSRMPCQIGNGGCNLTRQLNTDISTHPR

>contig54898 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53577.1|) 3e-30

MDEDSQQRITYLLQEIDANICAAHCSATQICTTVRRHHQILRQIHEASRVWRPLFDSFTL

QPSSRRATRTPSRFSRPLSPRSRQSSAMKLWKPESHDRSESDDDDEDMDEEASFATREQT

FKTTTLKKPQPLLSDRRNASADEDSLNFSTNSDNLPRMSRTPYMSKSAVSKGAMTQDSTS

TLNSSDRTHWSPPHT

>contig55350 Frame-0F|Blast-exosome complex exonuclease RRP44, putative [Phytophthora infestans T30-4](gb|EEY68068.1|) 1e-24

MTDIETPLLWCIDEQNVATRRGRVVRRVRERYLRDDLSCSLPECALCSTESDVSAASHVL

GTTK

>contig55628 Frame-0R

MWQVKVDCAEHNYGSFEHPSAHPNGRQLTVKDRQTVVALGRSEAPSRIVTALRQQGEGNG

INATAQDIYNLCRAHRANMLAGRSLLHALIWLHDAAYKTNR

>contig57275 Frame-1F|Blast-hypoxanthine-guanine phosphoribosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65230.1|) 6e-30

MVTQDPQPAIFLEDNAVYEKSQFLIPHHYVDSVESVLLPKGLIDDRVEKLAHDIRYAYEG

QTVHILCVLKGGSAFFHAL

>contig57349 Frame-0R

MSKSHRKRLTRWTLSKLQRCTLLSSQLFYQIVKKLSPIAAASLDMFGRNLARSEYCYEAA

QSVAYETCIASRGFV

>contig58443-0 Frame-2F0

MLLSPVSDASTAPTLVCSLSVSLRRRALKTFRHWQQAFPQE

>contig58443-1 Frame-0R1

MDVVVAALCIHSCGKACCQWRNVFNALRRKLTDNEHTSVGAVLASDTGDNNIGWAITYSG

RRA

>contig01105 Frame-2F

MGRRNLFKTTKSDEKSHDVVANDASTIESSTTTNCALEPPYARNTCQYLETTADFTTSFA

TTAPTCESTRRDKKNLLDIPIISSRRSAISSICALVDFDGGLVSAAAVRHNTQGISINAS

CSEPSYDGTIEKGSLNFVTSRHVGLLASTLFAGIL

>contig04388 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63936.1|) 2e-92

MGLWRKALTSMNATILSSKQSLGLQLKLQPEKDIFVFHAVESVANWTASSDRTIGGLSEC

KWGFYNGNQPIEATKDEKSQTTRVLNQVKNQDNVPSAVFAGRLSMDCQPTEVGVVRSGYC

AVRAFVPPGLLLHGYEGVSLRIMTDGREYRMNMQMESWNPFNLFVGFIRTPANEWVDITL

PFRHFLLTAKGFVKLNDETKLDPSKLQS

>contig09831 Frame-2F

MDEKTQIDVEFGMLDTTPLHNSPDLEELGSGAFTALAYARSLDLQSPLLGISVLGALLLL

FGGTFRPIFLVFTLCGYGIVFSLYLSHWVLSKDAGSAEMKAVATPIREGAEGFLKIQYTA

IARIAVGIAGLIFFSYALRPTSTLTSGIEKLGNFTLGVVSSVSFLIGAVCSAAAGYVSMW

VSARSNIRVTSAARRSYGEALLVCFRGGAFSAVLDITLCVGGVSSLYVMLYLIFGSILRP

TEIPLLMVGYGFGASFVALFMQLGGGIYTKAADVGADLVGKVEVGIPEDDPRNPAVIADL

VGDMVGDCVGSSADVFESVAAEIIGAMILGGTLAREAQLPSPVAFVFFPVVVHAFDIAVS

SAGILMVRAPSDVEASRPDHNPMATLQTGYNVSLFLALLAFAGTTRWLLYMPEYPTAWIN

FLLCGVVGMLTAYVFVKSTQYYTDYAHPPVRSIAKASTTGHGTNIITGVAVGMKSTVIPT

LMVSFAVITAYHLGATSGIGGQGIRHAGLFGTAVATMGMLSSAVFVLAMNNYGPIADNAG

GIAEMSRQPEYVRDATDKLDAAGNVTKAITKGYSIGSAALACFVLFGAFMDEFSEFAGRE

FKSVDIATVEVLVGGLLGTMVVFFFTGLAVAAVGETAGEVVNEVRRQFEIYPGIMEYKEK

PDYRTCVALVTKAALKQMRFPGLLAVLMPICVGLVFRVIGEYQGKPMLGAEVLAGYLMFG

TVTGIMMALFLDNVGGAWDNAKKYIELGNFGGKGSEAHKAAVTGDTVGDPFKDTAGPALH

VVIKLLSTTVLVFGPLFVSRE

>contig13072 Frame-1F

MSMMHEVPKPMRKRTAQPKENASKRIKASNSARPSLTQLLSRKAAKGQPLSPSNNSNTSP

ATKLQDTTQSKDPQMHEKGATQITDDSSMAFVLSRKRRVTVRKWKGMKLIDIREFYDDQN

VAKPG

>contig16369 Frame-1F

MPTSAAQIYINDDRPKRLPRLLVPISTSKSLDKASYLDFEMTEIKWTPVRYIAYGVGHVL

NDMCASTWFSYLLVFLLHAVRMSPADSAIVMFCGQLADGFATPLVGVYSDKSPALLWLGL

GRRKTWLAIGSLLVILCFFLVFGACAPRWFSTSPSRMVMLIYYSTAASIFNIGWATVQVS

HMAMVPELSDNDNIRCVLNSTRYGFTILSNVMVFCVFLGLLRVVHPLGVPDAEKFTLLAY

TSIIIGGMCTISFLLGTPENIKKESRTTVATELLKSPVMTDLGKSGAKLDGELPVEGVKS

LEPSGLMTWSCWFKRGMFYEVGLAYMCTRLVVNVTQVFISFYLIVTLEMSATSIAIIPLL

VYVSGFMATFFLRYLNESFGRTGSFALGTGLVAGALALSYFLTPKSATWIYPFSVALGMG

NSIIMVTSVCLTGDLVGNNIESGAFVFGAMSFTDKISNGVAILVIQNMRQHLQNAPDEDG

EFLRQVYCILPSFAAFVGLGTVMFMKFCSGSSNRRQLDGKCVSNSTNEEVETLLVSNKAE

PNEYGSV

>contig16655 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58435.1|) 6e-35

MELFRLYPDALRDTHAAAYALLVMAPLSSIVSHILIYFGRKTPTILVYIVSLAVPALALS

VPMWYWPRERNVYELLSMSRMESNYNWSQKYAFYRKLYQEGSISPEAWREIDMAYDKIYN

AQSRYVYDFWGPDHNDMSLTKMIVHVGLFYVLWIAI

>contig18037 Frame-0F

MKTAAFVPLLEKLSTFKENQYSLVALEARQLLIDNKMPSYRDRLSQVEKILKDYIANGMS

TNLSEACASLLDQSQPLFDLLISLLDHEDQQIRELALELYVQRVYRSYLIESIETMSFND

IFAKTFQFKSPIVDALAVGVAPAESYDDLASLLRRNSSASSLDLGDHNSEGSSEEPEPVE

KPHIKAVESYEKISPTFERHGAITRMQSLAVFQKSFTDVMSLFPLAKKTLSVRKDPLVNV

LHVILLDEHSDETNFLEQTVPYLKSVEQDLRAHNIRRVTFSVRPQNIETVSVYNADMALY

PNIYTFPARLNYSEDKVLRHMEAPLAYKLELRRLQNYSVTPLTSENKNMHLYLAKTKESD

SHIITDRFQRIFVRAVVRQLDHDSSSSRSQYDAYPGPERSLVDALNALEVNLSNPLVKKS

SLPTKNNHVYLNILPQATVDPQYLEGVIRILAYRYADRLEQLRVSTVELKIIARFNSEAP

AIPVRLVAENPTGYVVRVQAYVEAAGHDEPIFTSIGDETHGELDGMPVTTPYAVVFPFDK

KREMAKVMSNTVYVYDFLELIEYNLLRQWRKYVQQRTRGGGSKITIPNLLMETQELILDA

TGKSLMETKRPRGQNDIGMVAWLLTLYTPEFPDGREIVVISNDITFKAGSFGTREDTLFD

LASKFARSKRIPRFFFSANAGARIGMGESIKALYKVCWKDELNPIKGFAYLYLNPEDYEV

ASAEGSVNAELLITTSGEERYVLKDIVGREIDLGVECLRGSGTIAGETSRAYQDIFTLTY

ACGRSVGIGAYLVRLGQRTVQNLTHSPIILTGYQALNKLMGKEVYTSNDQLGGVKIMHTN

GVTHLTAKNHLSGIFSILEWLSFVPAVRRGSLSIRDVTGVDELERSVDFCPKDKSTQYDP

RALLVGKIEESTGKWVSGFLDKDSFRETLDGWAKSVIVGRGRLGGIPCGVVVTEVRTSEK

IIPADPASPASQENLVQQAGQVWFPDSAHKTATAIKDFKGEDLPLFILANWRGFSGGQRD

MFDEVLKFGAAIVDGLVDYEQPVFVYIPPFAELRGGAWAVVDPTINEGIMEMYADPQGRG

GVLEPAGLIEIKYRKQQLLQTMHRLDDKLKQLTTRLAEVSSAEVMSAKISAEIKSREDAL

LPIYVQVATEFGDLHDTPGRMKSVGCIRGVVPWSNSRKFFYWRLKRQLAEFSLRRQVVAA

SAGGPRAATFVGSEQVLKGWFTEAVNGGRVPRQQNVSVSELWSHCDSDVLVWLSSDKDYI

ASRIAELRQEQMASQVVEIGRKDPKAAVAGILEVLNLLSDKDREEAVAALRRGSIFHK

>contig19276 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56921.1|) 4e-24

MVQSENWLVYSYWNVLTKRTEMVSLALFDGAIG

>contig19553 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60201.1|) 1e-47

MLVLSDDPRTTCRASSTLDRNKCLYGAANMLSPNLSSCWNSAQGRPQYVHVYFHRVVSVA

SLDFMFQGGFVGQQVQVHFKQSGENALWEMATIDIDPIDSNDLQTFACALPHIQALAFTF

QRSTDFYGRVVIYRLQVWGTDSQNLDNE

>contig20214 Frame-1R

MSSQAGESEEKNGEGVYVTKNRSIFSMWLHGKAVPSRSHPAVIFRTADVIQEGYLLKQGL

RLKLWSRRYFILRLEERHMTLGYYTSRDSLILCSETPIGPGHLLGHVNTTKYPRRLELRC

GTKFMVLEAETQKAYEGWKSALQEAIRWNHAMVPTKDGSFVTYGKQASEDLKQEERSRAE

AAKKMREKQRADEAAAVANASSKPKYLPASRPGTQCFMTSNARFEIPSHFEYVKTIGSGA

YGVVISATNTRTGTTVAIKNIQRAFDDLTDAKRIVREIKLMRHLNHKCVLGVEDIFEPVA

LSKFEDVYIVSQLMATDLHRVIYSRHALSDEHVAFFMYQMLCAMKYVHSANVIHRDLKPS

NVLVNANCELKICDFGLARGIFPEEELELTEYVVTRWYRAPEIMLGCMKYTREVDVWSMG

CIFAEMMSRKPLFPGQDYIDQLHLIMNALGAPNDNELYFLSNARARKFMNAEFQKRGPYP

TKPLEQLFADSPPEALDLLQKMLVIDPNHRISVDEALAHPYLSSIRTADDETTANTSFDF

DFENEKLTKPVLQKLIWDEMRNFHPQGSDDEAAGTLKNASIISGTIETSSTPAISEEHNP

ASLATLATPVIEEPKHENLPDQHCIQSGIIDKSCASGGKVADAQTRQEAGEPAREVA

>contig23022 Frame-2R

MELLRSLTFAFFVSYSHNAEQFFVRSDGSCPLSALVRSRS

>contig24597 Frame-0F

MKAVMQDERRTFETDIHVPKALLSTMQMSLRYKDERQNILERRCEVLRAAHKIRSRQAML

VKQLGTVYPIEYVGAGEYSIRGIRIANSDLMGGGRNDEEMISTALGYIAHLVFMLSKYLQ

VNLRYRVVPYSSRSYLKDEINDPIGEYPLYKRGVEKERHEKAIRFLRKDVEQLLFARSLD

PTLEAPILARLKELADAECAWLAIDRNLSNNASSSADTGTIVPR

>contig26872 Frame-0R

MQPSLILNYRRFLTQIFLFFKQQTSTVDPGMA

>contig27471 Frame-0F

MDYRQYQAPQPAMLSSSRGMARLNGSNRAAWNAMDLEIGAQMPPANARGATTDGGALSAR

NILLHQKLRERKRYDSADDAMKKAAASRSQTSPPSTQTHVSSTPTPMVSPMSGFSPMGGQ

SAFLTAMQGDGLKRNVPPSTPLYESRGGPEEGRNALIQRKLQSKVSFDSADYQMSKSTLP

AYVNDPLLDLEQAKKASCTSSPINASKLESVTMSPSRASKYGSLLDGKKKPNRRDRLDPQ

YEINPVLEEKLGSTYGKLSAAHVLIRRKLKERKRFDSADYAMEQQGQPTEVPVDLVTGPL

VVAPYGSLRASPIDHQVKHIKLSDNPSKRVASPAKEVVVNAAQAALAARAARYASCHGAE

GTKPMTRHLSQAACDRYGLDKSLVLSGAAIGRNVILQHKLAERKIFDSADHFKKTT

>contig27826 Frame-2R|Blast-AP-1 complex subunit mu, putative [Phytophthora infestans T30-4](gb|EEY62681.1|) 2e-75

MIKAKSQFKSRSIANNVEIVIPVPPDVDTPSFKCSIGSVTYVPDRDAIAWSIKQFNGSRE

YLMRAHFGLPSVDNHEATDDWKAPIQVKFEIPYFTVSGIQVRYLKIIEKSGYQALPWVRY

ITQNGDYQLRMS

>contig29424 Frame-1R|Blast-carbonyl reductase, putative [Phytophthora infestans T30-4](gb|EEY70518.1|) 1e-104

MSLGVALVTGGSRGIGFAVAQQLYQRGWQVALTSRDLTRAQEAAQRISADVLPIAYSCPR

RGEGDASVKAAQVVAQVTDNFSACPSALVNAAGYTKDSLLLRLHEVDLEDLLLTNLVAPV

LMCKAVAKGMIQRRQGSIINIGSVVGAAGNTGQVAYSASKSGLVGVTKTLAKELGTRNIR

VNLIEPGFIQTEMTDTMSNAVRERVLDNISLARFGTADEVAQLVAFLVSDEASYITGQCL

RIDGGLAL

>contig30747 Frame-2F

MRCAALVHSTTILATSVWAYPNDAIRRLICRLKKQFLSFSQSEQFKDAHFSLNLT

>contig32091 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66995.1|) 5e-18

MTDRSEPARYKTAYMHYSGIRRKDVVSKHPAWTVQQVSSELGRQWKALTSNELKPWVELA

QFDKARFCTEAHLRH

>contig32680 Frame-1F

METPSTARLRRRSFFEGTESDDSMTESIVLCESDLLSATALSASRTRPNTLKGAHMSSVD

GNTALQHDVNASLRARAYVLLRDMWTQGILWLQEYNNRKSLYPAWTTRFPTTISNVNACR

PWILTAPLAWIASWKRDAPVKSYVYPTEYLTYASVGLMLLQMLVFYRYQSTFYNLRVDEC

VFHENLLASTELQQPLSSVNESPRDVALQFLERRLEQELNHAIHEPGQARLPWTCAALLH

TKSDRAITQATELAFLWPNSQDVSISSSLKITSRMHVFVSESPLNEAFETQTEGLFAVML

PLNVWRQKWMASRFPELIFVKTEFALQQMLTYRQERQIEFDRNERVRGEAIYTVESTVLD

RRQGFAEGPAVHSFGIYLLKTTVLDSYNRHIRKKWEEFLHVVVVTEADEKHQFTEELLTA

WVAHPTWPMLHVRFKRSLRLCGSFQRLLNSKLKAFDETAEAKDAEGFQKRATKASMRHLN

VDLVCEESANTPQEIGRLQNAIGMHVFPVPPELEEYEDTVLESLAVGAITMTYDTPIMQE

WVPDTCGFRVGSFTYDTSKPLEIEEELEGLSYRGEEGELLHGTTALVKLPKVHATLRDIE

QAIERMLLLDRFRRVAVGRAARKHYLRLRTHYLSAVAAMNSAVCEGDSDEIGETPGEIGL

HRRRRVEIKSLQPFLY

>contig33210 Frame-1F

MAFKIKMPCTIKIRLVEARDMPVVDRTSKLADAYVGITFASFEAKSKVSKKTLNPRWDEE

FRFDVADDSVLQSQPIEFKLMDHDVYTTDATVGIVYVDLNCLLMRDGHVIQGWFPVYDTL

LGVRCELSLVIRLQYFGDVNPFRESSAGVQFFGLSTLDPSLYRIESMLGFVEELVVHADP

EYSWSDSFRTSRRSNEHRQLLLYQLSSQVATLVGKKALELGGNAVLAYKQFFDVEGDSGL

VARACGTACLVIPVEKNDVVEREKCSQTRSRSADGYDCEFGLIGSKDKQSGEGSDALVSP

RMFSRRVLKSFRAPEAFSIYAHDEVQLITLKVFNPATRIQLAGIVSARSVKYLGKLATKL

ADQETRDSWWLELREEIRAHAQSLQCPFVIGYSESCTIYDDVCVISASGTAAVMKNPLKE

RPTKREIPSFHGIDHDGPEIRAITSPKLILTHLESSASFGRRSPSFSDIVHPLLPPSAKT

RSSSHVSNSPCLLCHIPYSRALAPFSNMRMVRCGVCGTKWVPEMIIASIEPPAGLAMMGK

GTFIQARVCRQRRKGAGDVNATIVSDALPFLEYELYRQLIVKMKVLGVNAVFAFDSQIQV

GGSLLIGVITGTGLYLPALPPPPTLRIERNIDVKDDEDRRLVQLQTQIEDLSTLNKDRLH

RDRVCIVQPEHEYSLGGRCGRQQPSTNGSLSSDQSDDIKKEPKRFVQSRSATKRARRRPL

RQASFDEDITIRGAATTETGATVASRTENCSLSTESLETPFASPSQLSLELDSKTRSSSS

ESSSESEEEAFVDGASDSKKTFVLEIDDETDEDLMSVLLEQEVPQGIYLCNTDRLPGDFV

SGENVHLILCMKRVEWEEDRMRDTRLNELLSIVFKELFA

>contig33540 Frame-0F

MLLDIVTVPQSKFILARLFQAVSRDQEL

>contig33878 Frame-0F|Blast-GPN-loop GTPase, putative [Phytophthora infestans T30-4](gb|EEY65657.1|) 1e-75

MRCCQMIMGPAGTGKSTYCYNMHEFCAASGRMTYVVNLDPAADHFEYPVAFDIRDLISVE

DVMEELGYGPNGSLIYCMEYLVQNFDWLQDLLGEYSDEDYFIFDCPGQIELYTHLPVMKQ

LCDSLKDLGFNICCVYL

>contig34361 Frame-0R

MTAPHRHGKLSSPFCHRLHVKKTIKQNGVRSWFRSSLRTDGDKSTSSMAGPETNEHRKIT

EDLASRRRALRVTSSSCDSEVRWTSNAHVEEHYAALGWAVVPTVHDGNSLFRAISDQLYS

NELFHQDIRRRLVAIIENDHHLFQLFVHNTTVQEYCAQMRHDGKQGGRLELYAAAKLFNI

HIVVHAGPTRRLRVASDDLHGPKKQNPLPPYRTLHLLYKDEHYSSLQYPSANKYSSKEAI

KFQKSKELFLKYENIENDAFLYEEDAVPEFGAQLPKQVLFTQGKRRESGATLFTLVHIPP

SVPMRSETSFSSNHVTATASRPALQVPTALFVLERPLPKAPTLRAVPVEFPNKIRFCKGR

VAAT

>contig34996 Frame-1R|Blast-hydroxyacylglutathione hydrolase, putative [Phytophthora infestans T30-4](gb|EEY61393.1|) 8e-98

MIVGPEKEPILARNRSVSGGDEFKIGAANVKVLNVSCHTKAHVAYVVTGDTETPPLLFPG

DTLFVGGCGRFFEGTAEDMYRALYDVILKLPKDTKVYCGHEYTMSNLRFALSVDPSNQAL

RDKIAAVRIRRAKNLPSVPSSLREEMSYNPFLRVHNEIIRNAVGGSDPVSVLGNLRRRKD

TFE

>contig35591 Frame-0F|Blast-cysteinyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY66119.1|) 0.0

MMTDATPENRSVKQPTWYPPRPIEGLTEYWRTHYPLCLYNSMTRSKNAFVPMQGKRVLWY

MCGPTVYDQTHLGHGRTYTCFDYVRRILEEYFGLEVELVMNITDIDDKIILRAAENGWNE

ANLGQDLPADKDVRAKLAMKWASEQPAEDNMRRTRELSMFWEKSFLDDMTALNIKTPTVI

TRVSEYVSEIVEFVEGIIKNGYAYESNGSVYFDTAAFGRSEGKAYGKLLPENVGQSELLA

EGEGALSTGQFDKRNISDFALWKKSKSGEPFWSSPWGEGRPGWHIECSAMASDAVKHLAG

GKIDIHSGGIDLRFPHHDNEIAQSEAFFDFPQWVNYFVHTGHLNIEGLKMSKSLKNFVKI

QEALRDNTARQLRFLFLLHKYNVPMDYNDNSMDEAVGIDRFFTEFFANVKARLRELGVEK

TQKWTPVEKMLHGALLDCKSKVFRALCDDINTPLALLHLQQLAKEVNRYMASGIEIQVSM

VLRASAEYITRILSIFGLVTSATDIGFPLGFGNSAAADQEAVLAPVLNIFAQFRDEVREA

ARLATAEGGDLKSLAGAVLRMCDVVRDEKLPYAGVRLEDRSVGAAVWKLVNQDELIEELE

KKKMEKIKKEEQKRLQLAEETRKKAKLTEKAKVSPNDMFLGMMDKYSKFDKNGLPTHDAT

GEPLSKGQTKKLAKEQVKQKALYEKHNCN

>contig36327 Frame-1F

MENIRKIVSRRSGSSIPHYLNLEWRVDLE

>contig36712 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67991.1|) 2e-15

MSSNATQAPVAKKRRVERRERLRKSALCKHFDKPSGCPFTDCKFAHGP

>contig37258 Frame-2R

MIGTNNLQSIANVHFTSKALLEAARENPAMLYFMFNKKVVGVLIAHDLNKGEWVLQIPYF

PPQESIPWDFSPAQCRDIVHSMLPVNVTVDADDIKILSVGHWHMGLRVAKQYDAGNQRVF

LVGDAAHQFPPAGGFGMNTGLQDAHNLAWKLGLAIQVNDRDSTVGLDAAVFLKSYGRERR

LIAQSNSQLSLCNVARTMKIPRALNLSYDNAQTLSKFINSTPLHFFSLHTQRAIAKQIMQ

VGKLHLGLLDEAKKTGGIGSSLGNWMRASVQDIVTRRQTLSMLFYHFDIGFSYDAISWSA

RAKYLMKDSALDKSAEFDTEVGCGGSIIYSPTFRVGERFPHFWCNYDNAKVSSHDMMRIV

LQTKNVAKDVSNVQFVLVVGRRDAAKIISSCLFPASPAVKKYVSLVVLLSGADTGLEKID

DAVAEAKRVSTFNSILLWQVIEDESDNKAWATFMESKAVALVRPDGHIGALWKSEELDVI

TGELLTQSIHRAVQLT

>contig37544 Frame-0R

MNVANAGGNDAEEERVYRPLLFQSTGYASSELFRDSYEMRSRLSNASTTSSLLTKNAAIV

DVEENQQPRHVFKPQIRLETLSSRAATTVLWITYLAFLLAMILPYFLQSKGYMETEIELS

GALCKDHKRKEPCIHVDTKRNVAQWTAYVSNVSRYTGSISLKLNIQSIMSTSLFGMTFLK

DRSNTIQAPTLANIVWNRDQRPFIMEDSEVDESYYKDEDKEKYHEAGFVLTYDARLYGYD

QEKVPTTNDLIVDDYNQSVWAKCQESGPCDKVVLMEITQDLNQMGDSGYNAYFVNVTYRG

LYPNAFGKDVVYEFAYTKPAIHIGEVIVRGMVLLVSIMAFPYWFIMVFNHHHGSWSNMLT

VQKWLLGLGIGLVLWQNPVYAISELYASTDTRIHLFSILCQSFAEAFFYVFWLSLVDQHA

KDNLSRTSSFATKFVFGLVLFIVDTWMTMLRMFPSIFEDGTKEFARRFHHEEFYALLGFI

RTGLVLFWLGWIIKAGTRSGRHLKTMPYMATRYKQLSYRFLVLETLLIFVYMLLQSVFQI

FFLAQTWYFVGYNAFIQDSVHIFATMFAGHSSLGRFLFLSVYVYLVMFVHLPPLAGDSTG

ILGSTAFHVDEKPRVDSYGFLTPDSNLFCVETAKWLLELAYQAYFDPP

>contig38286 Frame-1F

MYAGVDKYGGTLVGENQPDGTSLSAPASNVGCSLEDAIETASAEETVVVDVPYSYFEDET

DPKSVISGVSKVLLSAQLNPEAGGLMWVEHSNSQKAYKNVVAMSQMTSMLRDHDRNACYG

RGIKHAIQKFKADRGYAPIVLDIGTGTGLLSMFAVTYGAAHVYACEMFEPMAEIAHHVTQ

ANHPDKITVFKLRSTDLKVAPDREEDRDFKMTYHLPRRADLLVSELFDSILLGEAVLPTL

RHAMQHLLIPDAVIVPKRATVFAQVIECAPLYHFNAFDVESTRGPKLARSDLAWQCKGGK

PALPLHFRAFENESKFLTNPTKVLSFDFTKSTSEEATYDEIIVDVIRAGTVQAVLMWWHV

SFDDCDKIVYSTQSRAQNWQDHWVQVVFPVTENIPVQPLERLVLRAHHDDLRIWFDVEST

PSNDTTLTKLKRAIVTEKEPCICGLHLLCNAERISMLTDPFRRESYDASVSLVVADLIKS

EPLRQLSCLDISDGSFGALLAASHPEIRSVTSIESKAVSARIFEQILSYNNCPTEVLHSG

VKGLCPEHLQGDATSVDFLIGEPFYYSMQNLPIWQAFNFWLRRSAVDSLLHPKAR

>contig38408 Frame-0F|Blast-DNA repair endonuclease XPF, putative [Phytophthora infestans T30-4](gb|EEY59646.1|) 1e-112

MDIEVDVVDLVSDDDSNGLISSLSARWLPYERDIVEELYMQDGVLVLGRGLGLSRVLASF

VRLYCSHRSLVLCLNTNDEAATLRRLVLALGLDRSFLPRVVDARTNSTERQQMYKRGGVF

FVTARILVVDLLSNHVDASSISGMLVNDAHHVTETSIEAFILRLYRERNRDGFIKGFCDD

SVALSSGFNRVEQVLKHLYVRDVYLYPRFHIAINSCLKKHQPEVYEIEVTFSTSMKIMQE

ALLVA

>contig39498 Frame-1R|Blast-hypothetical protein PITG\_08664 [Phytophthora infestans T30-4](gb|EEY55920.1|) 1e-08

MVSGAFRAAPWPPALKPEYTAFWSTYFFFGLTILGCVTRLDTSYCSRNTTKVGPVRSRSS

GATGWRDRTYSLIIPAAGETMYRQSKLRRWGIAILLSASRLKVGKRLRAQRLIVPRHPHR

LLRRTTYPQTPPSEVRL

>contig39663 Frame-1F

MLSEPRRMQWDWCEELQMGENSLFKESSRIYKKMVLANTLHNNVVVPNVFDTVWQLDDFS

IFRSSNEEELQQLLLPVDLVRRDDARINEAPSKIVFHATRYLRSLQQSDISLTQASINMP

SVWNLEVTKEKLADLIAEELPTTLLQPPSPVSCSSHHEITAPRNEKVSVPHTKSP

>contig40380 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57021.1|) 2e-07

MSKHESGEGVSGHLSIALEHSSYAPGEVVRGFFTHPTLTIVKLDSINRVKNIRNWRV

>contig40524 Frame-2R|Blast-4-aminobutyrate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY58016.1|) 1e-111

MKGLRQIASDNNILLIADEVQSGVGRTGEYFAIDSHFDTQPDIMTFAKGIADGYPISGIA

SRKELTDTQPPGSMGGTYAGNAVSCAAAIATLEVIAEENLLENTRARGKQLQAGLHKLKA

SGKYPILDVRGLGLMIGLEFDPAKASKGTATKISAACLNHGMMLLTTSIYETLRFIPPLT

VSEDECSLALATFEKALNDVF

>contig40692 Frame-2F|Blast-RNA polymerase-associated protein CTR9 [Phytophthora infestans T30-4](gb|EEY65822.1|) 1e-140

MSDVEMEPSNQRALLIPVKNSEQAVEVFVDELPDDVNDIIDILRAEVAPLTVWLQFAVEY

YNQGHVAQFQEILAVASEPGIEEIYKDNASRMCRIKFFVALASHAVNAMWNEEDEKKRET

ISQRAVGFFQRADRLDHQHPMTLVGKALMFMAKNEDDRADRFIKSVLISNKTNLPAILGK

ALLLYRKKQYKDAKKLYLEAIKLHPRSPQAANMRMCFAYCCYHLGAVEKARAVMRYTASL

DETNVDAVIANALWQLASQ

>contig40977 Frame-0F

MINYTALRLPKAAARCIKSSTPSRLLQQSSASARKTNIPPISEGEKAWCDIYGVDYKKQI

AEALQECP

>contig41093 Frame-2F

MVNSITDTIPSVEKSVVLLVANTTGSIDRAITNVV

>contig41361 Frame-2R|Blast-pyrimidine 5'-nucleotidase (UMPH-1)-like protein [Phytophthora infestans T30-4](gb|EEY54295.1|) 1e-125

MKKFSQDGADHMLVITDFDRTLTPYYKQRKDSKDPLELESSSHGLLMTSTVLQPQVCAGE

QELFAKFYPMEVSPALSAEEKLPFMKQWWKSAHALLVEYKITKSQVVEAVALGSLSFRQG

FHSLFRLLNDQRVPTLIFSAGLYDVIHTALEQEFSKEHQHINVETSLSKLSTPSNVHVVS

NMMRFDDHGVIEGFDGTLIHSLNKTARVLLDSSFWQQCQLEKRRNVLLLGDSQGDVRMAE

GLNADEIIRVGFLNVHVEEALDEYLELYDVVLTCDASLLPVQMLIEQIVKSNKT

>contig41431 Frame-0F

MCLLIFNVTSSRKHLRLIPQFIEGVAVFCQSVKLDGTNLLLTIVGNHSSLREFLSRNEAF

KVTKPSSRR

>contig41484 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66740.1|) 9e-17 NOT\_ORF

MMSTIIMVMMMAQLLTAADQEDMIAGHSRFIILLDFCKDYDTVDR\*ILYETLLQFGFNKC

FGDLIRHFHNGTTASFVVNGCESSAMLVTSNIRQGCPLAPLRFC

>contig41909-1 Frame-2R1

MIADLLTKALAAPRMKNLRAMFNLKNPPDTVEEEC

>contig42258 Frame-1F

MFLAGNVDRQTLAADGTADEATTLQSEGDGNAGDNDAVLKHLFDTGDVRGVFDHSAVEVD

GVQNQEADLVEMEATKIAKGALSALRASGALVRQQRESNYTPTWTGRSGAAGDPSQRRQQ

PANRGRGSSRGRGRSGGVSSRQMLANIKHRQDGVATSASQSVVPASLSASEMTKRLHTFL

VANPAGVTTETLLESFANVVAPKDKLVFRHVLRTMAICRGRRWSLKSGA

>contig42544 Frame-1F|Blast-homoserine O-acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY64849.1|) 1e-155

MPSFSHSSHAASNRDDPRPGWWENMIGPGKAINSSYFRVICPSVLGSPYGATSPRTVNPL

TGEMYKTTFPQLTPADMARCHAKLLDDIGIRSVHTVIGSSMGGIQALEFAAMFPDRLDRL

IGIACTHQTTPGTVAFRRVQRRAILADPEFNGGNYTPEVPLEGMKVARELGLTCYRSREE

FDARFDWNPTGPMHFKEATFEVERYMEYQANKFARSFDPNCYLLLSKAMDLTNLGRNALN

LAEGTSRISCNTLIIGIKQDLLIPINEQRNLISILQSYGRNAKLVEVDSKYGHDAMFHGQ

MQLDMFSPLIRECIEEHLANILPHEQHRYSSL

>contig44652 Frame-0F

MVTTAQERREVGDDATWSLSSAKPGNGID

>contig45017 Frame-0R

MISGSGLALMYWSEAAEYAAYSTNRSPTRANLNRVSPIIVPTGRAPSL

>contig46001 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61336.1|) 2e-19

MGWSSDEEDCAPSLPKLSCTAESVKVLVTLLSCLVHGKRDQRVRCDVDQRGLLFTAHSTG

KSLQIKT

>contig46210 Frame-2R|Blast-nuclear transcription factor Y subunit, putative [Phytophthora infestans T30-4](gb|EEY58270.1|) 1e-40

MKSDEDVRMISAEAPVLFAKACEMFILELTLRSWGYSEKNKRRTLQKEDIQTAIRNTDIF

DFLVDVIN

>contig46540 Frame-0R

MSSATPTHSNGPSFSAVNRALWTHQLAVGRSGLSGESDQKKAMINASSENGCKREEPGVT

ENEDMSGFRRQRQRIHFNVEQLQTVYHLPLKTVRSNGKAFIFLILAKLL

>contig46719 Frame-1R|Blast-dihydroorotate dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY61590.1|) 0.0

MVILSHESLDYQRIEESLIAMDSTAKDWSTLVARLKQYIQSREKRQNAGHRTGVLGVNLG

KNKLTADAAADYVQGVHALGKFADYLVVNVSSPNTPGLRTLQGKIQLRDLLLRVLEARDT

VATTEARRIPLLVKIAPDLTENDKQDIAQVALELKLDGLIVSNTTLSRPNTLKGVEKAEA

GGLSGLPVRDISTKVLSDLYKLTKGKIPLIGVGGVSTGQDAYDKIRAGASLVQMYSCLIY

ESPLAVPRAKKELAALLQRDNFKSVADAIGAAHKENIDLV

>contig46878 Frame-0R|Blast-ras-like protein [Phytophthora infestans T30-4](gb|EEY56377.1|) 1e-145

MSDMRLFIYRNEAASEGKVMNLKSKDSISRLKKVASKKLGVRAKRIFLASGAEISDVDEL

QNNDTLYVSQGEVFYKSLGPANGQETFNMSVLGSGGVGKSALTLRFVRDYFVKDWDPTIE

DAYRKAVTVDDGLCMLEILDTAGQDDFESLRGQWMMDKDGYVFVYSMDSRISLHELQPFF

DLHLQINESRRPLPPIILVANKKDVVDRDPTKCQVSTEEGRRIAHSYNARYIETSALTGA

NVTAVFETFVREVRRKKVPKLKKSTCFIL

>contig47091 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY60970.1|) 4e-48

MVSLMFLPFLPSQRAATQALRCQGRDSKWMAMWTVGILLLAQAWLTMVNILSMDPA

>contig47392 Frame-1R

MLVHSYRKQGLHRHFHARSSRQREISTRSGPRDSLFTPRRPVGAVPELFVTFRHVSLALD

VPT

>contig48018 Frame-0R

MSRRYLDTMAAVRSMVLSDIQSVLSLARQRHGYLLPSNNSDPSNQESSLTLFQGVSQFRE

RLLRCNNMIEFSPVHVVTPFLDVLRHEKTGSKITSAALNAVLHILHSWPWEDIQNQNVAV

EAVSEIVDAVCHCQFQETVLESDQDVRKVVVHVLYAIVRSPYGVNLSDHSMWQLVESLYS

LSRHHHDPL

>contig48450 Frame-2R

MAHVTLNCRLDEAMTMLFNHNALHFDASMRALFGSKKYKSGELLFSHNTCQSDINDPSPP

SLCALQSIVLRSRRSRLHPLTAATQPSRRQRLCFAAYSHYSPNANEAMYTMKTLRQPLHD

HLVGPQHASKSRHTEQIAAGYHLMSSYSDLSGHQTQIVMTAYVLNSAPFTTATP

>contig48748 Frame-0F|Blast-spindle assembly protein, putative [Phytophthora infestans T30-4](gb|EEY70519.1|) 5e-33

MEMLVERYEKELQTLKVAAETSDSHVQDLNKLKYQHEMQIDHLQVQSQDLCHGKSVLLKE

VEELRLQNKEL

>contig48915 Frame-1R

MEKSKHVIDQTTQQISNRSASTKVTTDKMTNESKAVAQTRRSSSTKTAPSPHSPSSEQIH

YKELFAKRQKRDASMPEQMNFST

>contig49181 Frame-2R

MWDILVASKWAKWTYFSPLL

>contig49390 Frame-2F

MDNYNLLIARYQDEVLAMQQTTVAHSTNELFPGYDDGKLTFEEEYRFLCYRHWSLYEAMY

YSDYVA

>contig50077 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70441.1|) 3e-20

MTAPDTLRPMDTIEGPRAKACLFQPPSLKRIVLNPRAYLTPFVLFILFHDLPLFLAFGLI

DK

>contig51319 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61437.1|) 8e-20

MPEDKAIPNHTAHYHLTHLCDYQHLIEDYNGISYRDKITLGSIKF

>contig51401 Frame-0R

MTRRFVCGSCARAFCARHCHHAVRLQHLGLRSTRRCCDHCTQRQEFITYLRTMKRFLEPM

ASRNVSMHVIVASQLNLVGQSTLARTLDKLRYGPMTLNRTIKILYQNRKIPHLFRVACER

LPFYTETCVDRVENLWYQLLHLVQCLDA

>contig51610 Frame-0F

MYNRRQLRAVPDTNYASQADRWKKGFKLQMQESAQQQTDLENALVSELCSSVGSSSFPPR

DVLQKLLRYLHTLDNDYICELLDDKFENPLWQVKAKALSVLSALLSSSDADFYKQYYSGR

LDLFEDLRNARKDMLRKRADKVFVLLRDCIPPDEGTPMKLMQKMQQEEAEEAEAGECTLM

QTSPVVTSQPTPHDLMMGMNSSPRSSSAPLPTPSIHNESFFGFLVQQHQQDAPTLMAAEP

ITPPVSNSAFGFLSENGGEVDLPQTMSLESTNPLPSAPSLSSESSNFSFMNQISPDTSVH

ASTSETSLLSMAATPSAFAFLDGQQRLPQQQKSVFGAAKAQASRR

>contig52189 Frame-2F

MAHDKPSHEASFFADVRSSAEDKRLNSVQCRDISQSSKPFTKSVYKPKSPEALGRIKAMS

VTAAPMAQSITKPSTEGSSEALRLSPDTYRRSQSDGNLRTEVSTIESHQSSKKTAPLTCL

VSPAHSESALINHNGAIGLPSVLMRPMASSKSTGLMALGGTLLAEMADFAGMKSPGGTAQ

QVHVVYSTPGPLFVDLYSRDDGTGARVKGFRRKPDGSMGDSEASKQ

>contig52325-0 Frame-0F0

MLAGSNGLCSHQCESILLEKVGVQRFIDSSPLG

>contig52325-1 Frame-1F1

MAYAATNVSQYCLKRWGYRDLLTHPHWA

>contig52541 Frame-0F

MWRCGAGRRREWRRITRPISLYSAAPTTTSSIRTNSSFRPSNLRFHNTKTVATAAKCSFR

EGNLLPPLA

>contig53656 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64362.1|) 2e-08

MVAIAPNIQRHSAQLDDNLMQLCSYQIATALVITQQPPEIWYKDQYGRKATFELKVERT

>contig54323 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64768.1|) 4e-24

MGWSLPMEHLHLDSKPPTCST

>contig54873 Frame-2F|Blast-histone acetyltransferase, putative [Phytophthora infestans T30-4](gb|EEY53616.1|) 8e-41

MLNHIMRVLQNQRSNAPTNWLQKLPEMAHRLEDECYRIALSREEYANISTLQSRLRTIVR

SAQTHQRNVGATNAMRQSGTSRHASPAISRPAIPTHAATPIP

>contig54899 Frame-1F

MPVSKGTEAANKNSDSDGAPEDLTKESATEHAIAQHHQVKVARAHNGSTSAGGSAP

>contig55629-1 Frame-1F1

MHSLQLHSPLQYAPFCFCSRSTQTQQQRTIFQLR

>contig56897-0 Frame-1F0

MVARMGLSSESASVDGIVPLRVQCSVLVSSVIAARALIGK

>contig57274 Frame-2R

MEICSSNAPCNASTPTVSDLVASLIVTASFWLCQLLQNY

>contig57348 Frame-1F|Blast-ubiquitin-conjugating enzyme E2, putative [Phytophthora infestans T30-4](gb|EEY65550.1|) 1e-11

MDNNLLKTFIMAAMRGRMRKEIAMLESDPPFGVSAWPKDNQIDHLEA

>contig58442 Frame-2F|Blast-reverse transcriptase [Phytophthora ramorum](gb|ABG66535.1|) 1e-19 NOT\_ORF

MRKYKLYANLKKRVFAPSEIPLLGWIVGKHGVRPDSEKIKAITDWPVPVDVKGLRKFLGI

AAYLHKYS

>contig03074 Frame-0R

MKSLHFPLFSKLIKKTIIFLSYPAIKHATPFIFASRKNKS

>contig06763 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63172.1|) 2e-59

MYLLMNLLSPERMIDIYRVCSVLGYCLLPIIGLAAINIVVSVKDLGLIGFLLASVCTLWS

THTASRFFEKALYMTEQKYLIMYPTMLVYACFVLIAVF

>contig07768 Frame-0F|Blast-C2 domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY58868.1|) 3e-18

MDSTRPIFNGLNPVWDETFFFENVRPNSTFKLSLYDVDTDKDDKLGSAFFDMIDAVDDQE

NAFDLPITLKDQRAGVISITV

>contig07805 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67359.1|) 3e-09

MSDPVARAREIAARLAASAIPGSDALGKRKSRWE

>contig12021 Frame-0R

MFSQFYGYAFVLSSKGKLSFETTEIIESSLLKIYKDSASNVALDMLVQIRFARRFRISES

FFKEFARPSDFPLKHFLFNFRKRYLKDSRRYVVDEDFIEVLRQFFPDDRSIARVIVKEDQ

IHRP

>contig15280 Frame-2F

MKDHNESYLNRLFRTFPYDEFNITEGEHVSDQTKESFAYNGKSCHEMDSSLVLIDKSLVS

SRVFDVMFWFFTKERFRIRYSFGDKETFWLSFEIAHEPYFFSPWGVSVVSSTPNEDLEKH

PDTLCGSILQYMPVESRQSEVLYLNGKALIAPYPQGVKLLQMASLTQQYNAFPTHMTPRQ

RRTEIRPTKLKLPIHCLTGLGSTPLPQKFFQLLLRRQLHFLGIMTGVLGPLTLCEL

>contig17431 Frame-1F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY62024.1|) 0.0

MLTVNSMTDKLSTNIAISALGGLVVLPLAWRLLFGTDNGNLSKRGTRNVVRPLTTKPLLG

DTLDVMKNVTNRHDWITSLCLMAKGDPVLLQSWGTPDMLLLSTPEAFEDVLKNQFDNFPK

GPKKTEYLADLLGEGIFAVDHEKWYHQRKTASNLFSMRALRDSMSSTIQRHLVVLNRMFR

HAAETNETLDMFSLLNRFTLEAFTEIGFGVQINCLDTEREHPFQTAFDRVQQSLALRFIR

PSWFWRFQRFFGIGNEGQVKKDMHVINSMLFDIIKKNLDGRAKKALSDEKGDKNIISLFL

DGIDSSSNGVDSVLDPTYIRDVIVNFLIAGRDTTAQALSWFFICLSKHPHVEAKIREELA

AKLPNLLKGQCSPTMDEVSELTYLEAALRETLRLYPSVPMISKDAVHDTVLSDGTFITAK

TMVTLPMYALGRMPHVWGPDAVEFKPERWIESG

>contig18838 Frame-1F

MSDEAMDRKLLSALLVGVNRAFPYADATSATVFKDIDALFQVVHRSHHSTSVQALMLLFQ

VMDRSNSVSDRFYTALYSKLLDSKVRETSKHTLFLNLLFRAMKADVSPARTCAFFKRLLQ

IASVMPPAFACGVLFLLSEVLKVKPHLRTLLDQPEATSMNEHVIEDEHFDDAKTETAEFE

SEDDNAIGNTDESTVDDGLTEAERSAKVLKNMFGNETEDMTASVAVHSSTNNKREEYDAL

KRNPLFAGAETACAWELQLLLRHYHPSVVSFARQLVENKDTGIQYAGDPLVDFTMHAFFE

KFVNKKPRRKDGKKSNDRIGAKAKNWTFAPINTEAVLQANEANVDASDQFFYNFFKERES

RESERKKKRPAMGKNEHNGDALSDVEDEEELDGYAQELAEGMMKDGDLDDEDPDTTGWSD

DSEEEEALEGEIETEVFEDEDPLTEDEDLDGNVGLSVVEADDDDAVLQEEWQGVEAKRKK

RTPPKAGGKRNAMFADADDYDQIVKDAKAQQAKGLKSKKGLMTKKMRRS

>contig20213 Frame-1F

MFCHKITVRIPENTRIETKRMLNFISIDHIILHQFVRMIKTYEIFKPYKVKILVSKYEKY

CS

>contig20499 Frame-0F

MEVISLDSDSNDERDEVAIAEIVVPYTKRVADKGSRITLQLRSNGGAVDEICVHKKETFD

QLHTKFCELHGLPRSAVILSLDGEALRHTETPESVDLESGDIVEAKVDYSKQSEASKKTY

IRLRLVVFGKRSEVFKIDSTATAAKLHWSFCQRHGITNPDDVVMSINDQDLRLNENLKFY

GLIDNDEILVKVKKVEAQPQTIDIQL

>contig23348 Frame-1F

MGSCSGCVSNSVIHYTSSLQS

>contig24590 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55364.1|) 1e-161

MALRPSLQALRSLPVRRVLVQNLSIAPHAADKFVVEFPEEHEGLNIEFNWSLAADDVISH

GDAYRNLRWPKLEELAKREKLTGKKVAIDEVDVSIVFNDFEGLYEKVTEHLSTEPNLYTQ

DGAVGSFKDDRTRVRVISDSALVALFAQTLLVRVPIKDTHAARPIVIYVATSGEFKDQEP

QAQLLFDNDDEGAPFVKVVITGAADLSTIQDAIGLAKKKLLDVAESESLVVPADVLMKED

TTALVFNASGAGRAAAIEQPAL

>contig26398 Frame-0F

MRLLLLALLGAGLHTAAFVEAIVAGVDFGGEFFKIALVKPGTPFEIVTNVHSKRKTETMV

AFDGDERLYGADAATVGVRRPQTAYLQIRRLLGTKLSDPQVSALLEEEYLPYELLQNTTR

GGTISLKHGKEHVFHAEELVAMVFTHARQITDTFAEAPVKDWVVTVPTYFSQAQRQAMLD

AAEISGVRVLSLINENTAAALQLAVHSSYDPDEKPKKILFYNMGSTSLQVSIAEFSSQVV

PDGFKKNKTVSTFQIISNAWDATLGGAKFDLRLAEYLATEFSEKVGEDIRKVPRPMAKIR

AQAKKTKTVLSANEEIPVVMQSLYNDIDFFTSITRSKLEALSSDLFERTLKPVEVALEKA

GLTVADIDEIELVGGGVRMPKIQQQLAEFFGGKDLGVHLNGDEAMALGAAFRAANLSNSF

RVRQVGMTDIATYPIGVRLMDLSAIELAGSNTADIDGETKQWVKRASLFTEAHRLGLRKS

VSFVHSSDLSCTFRYDKPSMLPAGVSVQIATFNITGVDKFVARMAKKDLGEPKITLSFEL

DSNGIARIVKAEATIEEEVEVEVVVKKKKAKKEDASAESSQAGDDVAVEEEEKPETRIEK

QTKTHRERLIVVHAFGTREPEEGYSVLLMSEAIKKDSMRMLKEMELADNKRREDLEAKNS

LETFIYTSHDALLAQKEQIELVTIPEQVESLQTKLSETEEWLYEDGEKVEAAEYKKKMDA

LDSELSAILFRVAELTELPIALNTGKAYAVNTRELMEEWSTSKPQVMEAERNDVLEKLTD

LEAWLTESELSQKATQKHEKPVVTSADVAKKVQSVKKFVSVLAKRPKPQPVKVGENHT

>contig26875 Frame-1F|Blast-augmenter of liver regeneration [Phytophthora infestans T30-4](gb|EEY69279.1|) 1e-22

MEKLDERWRKGNPKCWGQDGDEDSAEEALGHLRDS

>contig27821 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55361.1|) 7e-53

MLTRRSCLVLQSTALRAMQTTTSVAVSKKFQYESLAIHNDTLLPAHKVMRRVLKYLLVDP

KFLKGSILTEEARSLPYKTIFTPQQVMKLTSLVRWGFQQLEGDSLAADAVFKALEPHANM

TRGTVWRQYFQRQFFISNAPLWTYLRVYKTHLDALAAAKDQATAENRKAEVGEDENKEVN

KAAFFTTVQKYTSRREKVFSGKKREVTILDENKNWDWVPLPVAFSIVKEFCFRGRFAEAI

EAYVLLPMTDSMSRDVVAILQAYEQYSSVLCLYEVHRALGSAGNSLDVAPELDALNKVGR

TEEVKMRFQKLSIIEQSRSDIQKIIGN

>contig29496 Frame-0F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY69525.1|) 1e-23

MKTFVHVKDPDTFCLCLRWKYNNNAQLASSFFEITPAID

>contig29795 Frame-0F

MHSDRDGDRSLWTGPHCLPRICRSSTCKEIVI

>contig29870 Frame-0R

MNRRNSSSPASSSASHLYVLAGVKDSSSRANGFTFITEDKKMLQVTAPTAVEKIIWMRLG

LEAIVALPTLPVAPLDMEEFYAMLVVLYTANSENWRTEGDMAVTLPPPSEQVFTRFFRLL

DKNVTFCSNYPPSVPFHGSFRGHSGVVSFMHEFARHTLWTNFKIGGLSIDGSIAVASGKE

ELENRRDARKFIQNWVHKFTFYSDGRLARFEINGDVVAASAVFKVPGAATTLKLPQEFNE

VDAEHGFEGVLLVRVMQGHGLKGGTLVRKMVKEPSIMAQLQYREHPTSKNCMNGSTASSI

LTGPSTLIGGISMPNISRKFSFMTSVASSAASAASSAVGVGTSSLSFSSTPVLDPFRTGT

PRNSGDISYLPTHPVWNCIIELPFSRVIGTCSLVLDVKDNLKNGVEIQLGFATLNVAKYL

MAADGKDRSKIREEAAMAADSKWYSISNAKGEYCGKVQLGITCRRAKLVDEQEDGVLPRL

RKSQSVMIDRNNPPSSTMLQWDTTPAVNSHVLLGAITPSIRKGMTLDEFQMGRSENARRH

GWANVKLSPEDTARSQSAGAIGSSQENDGDSVHKRFPDTFAGFPAATDAIICKENANMHT

FMVCGAPFTIPRHYQLIKVCGRGAYGIVIAATNLRTGGNVAIKKVIDCIWHPHQLKQILR

ECRLIRHMAHENILSLLDLIPPPSYTDFRDVYMTVDLMEMDLHRIIYSKEVLRDDHIRYF

LYQMLSGLHHMHRAGVLHRDLKPSNLLINSDCQLKICDLGLARSKEADDVGMTEYVVTRW

YRAPELLLGSAYGEGVDLWAAGCIFAEMLGRKPLFPGETYVHQLQLIMNVLGVPEEHSFK

ENPLANKLKGRQLLSRTQAVAGIETSLMYPNANPEGLDLLWKMLVFDVEKRITVEEALQH

PYLAMYYNEEREGVPVERFQSFDLDDLDETDLKELMFKEICHFHPEEMVKRAQQQKEHPE

VVEKLPHGWVKRESRSIPGKYYYSNPKRGISTWLKEEMD

>contig32687 Frame-2R

MISRLRLGGAGGGTSNGVASTSSSIFGAAASAMSSISGSGSILPGNSTMESAAAAATADH

VASLAAAGTSGATGLDSANNAKAAGGGFFGVSRMVALVNSANRSLQSLQGAPVIPGSKTG

TQLRGQEVDRDGQVIVEIFENERLEGALQPMDPRRFSDRHAAPGAGQDEKPVGDLPSGHE

WMSDWEIDQNYTAVDRDGWTYAADFVEIVRLLGDDLSHASRHPTDAVRRRRWIRYRQLMD

ENAPQSPTESAGMKSLASSANSTNWADSTNGQGNDYVLDDNDDPFMRTAQKTQTGFRVNV

NFAHRGKKDNTKDYQSISLTDVMWLVNAHDVTNAPTEELMREKTANLEEQIKEATHRSKT

LEKDLRAQHDKQTKELNLQQKKFDALVTQYKKIQAENEKLQISVSGHRVTVDALRKEATE

KDMLA

>contig33006 Frame-1F|Blast-betaine aldehyde dehydrogenase [Phytophthora infestans T30-4](gb|EEY54272.1|) 0.0

MTRVVKSFINGKYVAARAPAPAFTLLNAWASNPETSYKAADTKQVDDAVGAARSAQGQWR

RRSPAERGAILRKAADILTSKTDEIARLETIDTGRPISETTVTDVQSATDCLNYYGGVCP

SIGGQHLELRGGSWAYTRREPLGVTAGIGAWNYPLQSAAWKSAPALAFGNSMVFKPSEET

PLTALKLAEAYIEAGVPEGVFNVVLGAKETGKALVEHEDIAKVSFTGSVGTGRKVYASAA

KNLKKVTMELGGKSPLIVCDDADIEQAVAGAMIGNWYSSGQVCSNGTRVFVHRSVYKEFV

QRIHERTLKLRIGHPLDASTDIGPMVHEKHMKLVQSYIEKGKAEGATLLEGGGERVIPSE

ATKDGCFLSPAIFVNCTDDMTIVREEIFGMVMCVLPFDTEEEVIARANNTKFGLSAGVFT

KDITRGHRMISELQAGTTWINNYNLSPVE

>contig34212 Frame-2F

MHVKRSTSDRRRLSALNDTTSDSDEGATKKLADKPQLHRKKRKIATREPSLAKKTHETSL

NEVPEHPCTSNSTTKESELQLLAIESRRLDFEVVKWKQQQALRRETLMLKSEEISVKETT

TRQKQETRMMELHAKLIIALDKAGKVEQANEYLALLES

>contig34366 Frame-0F|Blast-flagellar peptidyl-prolyl cis-trans isomerase [Phytophthora infestans T30-4](gb|EEY59582.1|) 2e-47

MANSGPGTNGCQFYLTCAPCDWLDNKHVIFGKVLDPASLLLLRKMESVPVGANSKPKLSI

TVIESGEL

>contig34436 Frame-1F

MLKAIEEISRNKISGSNAVAETSRRPDLPKLDDSLPEAVVQYAWGAVVPSPTNDEALNLE

SSPFSSLSIQSPTDVWSSAEGDKTSLRTP

>contig34483 Frame-1F

MKKQMKIAERSGSSHAIILGEQEIEKQVAKIKNLNKREETIVTMQELNNYHFD

>contig35523 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61160.1|) 5e-68

MEEELLLAHFKDCIEFLQKHLIRVGTPTAVLVHCAYGQSRSAAVCVAFLMATQGKTLLEA

YDQVQLSRPCISINPGFFRQLELFERMEFDSNVMGSTSAHAEFRTLMARQDRMKKRKAAI

ANIPQLALPGTSMSCRKCNFALCTARNQLMHSPASGELCSGIFIEPMQWMTNSSVFIQDN

VGKLYCPSCKAKLGSWNWIGV

>contig36258 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66062.1|) 5e-61

MCERIILAGGGSVIPLTKSVDFNSLSKESTSEAPVVALVPPEEPLRDMWMKKFKMHDIEC

IKASFLIDCISKEPVTLLKRENYHII

>contig38959 Frame-1F

MPRNRNAENPVRAAMYRKWYARAWWVGLHAYGYVVLGVQGALSPHALPIYEFVVYLIVAV

ATTSCYVCLQLSSPGHLVKRPMLTPVQAITPLSNSNTLSHMAIQEGDDAELLGDGEHSRN

SVNLHFCHECHVFQPLRTKH

>contig39372 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61708.1|) 2e-61

MAEEYRQRLDNNVEKLVENFKGLIKNSKIRDSANNTRESFQSSIYATTLVQASESLLKLV

SEMKLSLALGDFEGMSQNVDSTSDELIKRCDDVDAHISHLSSDISSALFELENHYYQSKW

RLTPTRDSEETSIEN

>contig39422 Frame-2R

MLSQLVADSNDPPPVMRGARRSSSHSEPRLQGPLLDKDATLRALKDWPSASSGISSGTFS

RHSSPNRDDMLGNTSNVHHDKKVSPVGWKMDFERLENPFKTWSGNSGREAPPPRLTADTF

RPPIHAVNEKSPSPSMTASPRVKAVTPSPLQGSLVLNNKKEEVDANDRVLLQLSVRSMND

EKRLLSSNPEDEARYDVYKEAYADVLYRYGAMNLRSEVLKTKFHGAQDPRGISMGLVCAS

CNTKTIDLVCSGCRDFAMRCSVCQLVVRGQSMFCMTCGHGGHAAHLRGWFEIESTCPTGC

GCWCKQATATMPPYQHEEQEPDTSEAPPRSHSF

>contig39611 Frame-2R

MLKLCVAIKVWNTLSKFWWYYFAFAFNCPPSSESRHINVSTLLRILAVKHQMGFFSSSPL

SARRHRYVRLSDCR

>contig39664 Frame-0R

MKALAHRLRGRRRFDDEVNESGGFRFEEAVMCLEKRRPTLEKAMGDKIRKTQARRDDHWR

KNRELKARACSTSRLTDDGFVSASLAKPPVPARTRVTSIEQQQRLLPRVGSDSSGEKTDT

TSEELLSLDQDYPQSISVCTASPSSVTSRGRPLQSRYEGP

>contig40596 Frame-0R

MSLRFGTFFISICSGDCLPKSDLLGL

>contig40970 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53083.1|) 2e-37

MSEVTGPARATVEETCPKCGNLEMEFYTLQLRSADEGQTVFYECKKCGHKSSVNN

>contig41212 Frame-2F

MADLTQCLVSEAFTESHASDDNEQLPLAVTDPCALTSVATDLAPETRQSALQTTLNVAST

AASLVLYPYVVASKAVVSATSMAVSAPIHLTYLVHAKITQIWEPRSQEQALNDKLDMKEE

RSSTCSSRSDNEMELMLIESKHRSGTVYQLLSLPVRLVH

>contig41436 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY54200.1|) 1e-142

MMTKLQSAELSLSPKEKVIKELEDTITHLTKELADATEHLNCGRQDITTREQKLLKEHKK

MQNEIGNLVYRIESAGIRNVELGEKVIALAKHSKMDQTDLVALSSQVKSYKIQVKSLESQ

LGQVHRRNGQESESICDLQRKLNNITCLKESYQVEISKLRQRIEQLQSEYTAAKQERDDA

VKRVHLLVQCRDDMKVTVEDHTAELVEEIEAIQHQMDSERKRCAVLLANEKTLLRDLYER

NGVVMKLQHTVSVLQRQVQNKSSSSSDRSRSSISGRRRRSEGSSDVNSPVSSSNQSTTPT

ANSFSPPHQRHSQPRLQSN

>contig41483 Frame-2R|Blast-small nuclear ribonucleoprotein sm d2 [Culex quinquefasciatus]gb|EDS31305.1| small nuclear ribonucleoprotein sm d2 [Culex quinquefasciatus](ref|XP\_001843246.1|) 6e-40

MHSVKNNSQVLINVRNNHKLLARVKAFDRHCNMVLENVKEMWTEMPKAGKGKKAAKPVNK

DRFVSKMFLRGDSVIIVLRNPHA

>contig42543 Frame-0F

MLRMLRPAVSLQVRAFAQPLLLYNGARSLRTARGGTRRQKDHIARIAKLEAMAQEREYAQ

QEQRRRVLEARSRPPVIPGFIRVRDLAKALRQPFKDVLKRTVTKAHRRFSLKTKTHPPAE

FRSVKQIVLPYRVAQEVANSFNIQTAYDDVEPRLSDVEADLSKERIGQRQPVIAVMGHVD

HGKTTLMDTLRKQMRMELKLIAPYEKHGITQKINVCEAALTPNVKVTFLDTPGHFHFFRM

RTNAAQVADAVLLIVAADEGVLLQTEESIGALEEAGLPAIICINKVDLLDNKDEQVENII

QELRSFVALQDSPVVRISGKTGAGLDELKHTVSMLVTSLTDNHQLNALAGPDTLAEGLVL

ETVAIKGRGAVLRVLIKNGELVGKQHFVAGMIHGVVREMHDAEGRDVKRALPGTVVDITY

TNKSRNVDAPNEHGFFVLSEDRAKQVIEQRELALEFKDCLVPNEGDLYTHPNAELVTSDK

EVTIKSAQVSPDDAKEPCDRDIIDERELIETKSIIVKADGAGALTSIQDTVDDMAGISTV

RLGIGNISTKDIDVAINGECPIFGFNVKLRNREAKSAAKRGVRVILRATVHELIEEISAF

EELNDKDRKIASE

>contig42929 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54340.1|) 3e-87

MLVFQLHFQLLVPSKLLTVAVDVVKRDDSFSSSDTCIDELGDLRCSWERLVGLPSQKDHS

VVDVWHMEDELVPRIVADKKYSNVLPWFRTVSKRRHKRRMDTNDGSGNEDEVKREEHDDD

ADEEDDDDNTQETEVETDELLRRPVACRVMKAKQKRDS

>contig43320 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64020.1|) 9e-78

MVSAADVDCVSQLPRRRNRRTLHIEYWSRTDECKLRKWDHLDEIRTIYECAEEQIFATIL

KGRNAFLEPNMFPYDTPAGIEHWTLWHVQDLDHKQVKQYVESWIDANAPLVKRWNYDDNP

ERSINIFHVHVYFQVAKGSTVLQGRKVEDLAHDMN

>contig44655-1 Frame-0R1

MPVNFPTDACKGRGIDHRCAIDFHLPKATRSKEVRMLVASVTLVRTKEELRM

>contig45649 Frame-2F

MEDLLDSLGVQFPLLAALSINLNTRPMPQLRCPETPLIPLPSRRVCIRVLHGDKPTYRQL

LVWLDLSYLFHHLPTHDDADPSQKSESIK

>contig45740 Frame-0F

MLKKVVDHSASLSSSLINLYKMIMSAYTKTRQRVLNSRNACRSNQLSSYKVTRRLKENMF

SQTLTAYL

>contig46781 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57999.1|) 1e-158

MQLFAHTQAHFATVSEDGRLKVWDVISGSLQQELKERDHLSYRYTSVAWTQPNNKTKKRS

SANDLGLLALGTSSGTIILWDLATGDVKHTLQANAVHGASVVQALAFNPQGSLLYSSSKE

KYVLEWSISSGSVERKFRVGTTGASALAVSADGEVLAAGGSALRTFDLASGKKRRKLVSG

LSSAVTQLRFATVEHAIESSRFLIAATAGARFVNLYDLGLLDHDAPALTFSLPSSADALF

VRASISEAVIANTSKQGNKTKKKQGVVKPAVDLVVGATATAGAMYLWTHKYQQVNNVSEL

ALASKPLPPTLSTDESAGILSAELCLQTTTDPRMEVLIARGSVMKPVFETVSLVEEDAPS

QWKTQLEFAAISDALLLAAERLDENQSKRPKKEEA

>contig47395 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59159.1|) 0.0 NOT\_ORF

MRIFEMLETPVLRDIEDALFQINRPVTPTQKLQAQARHMAVYICTLYSVLVLLAIGLRVV

VQHRSLEMMLSHILLGPIGIWLCFASLNTPLVLFVAEAAATASILGSFDDILALEESEWQ

EQNAKPRADDFHNKKSNGKSEPRSDPSKVTSRRKDEHMSRIDSAMASILKATALAPLDIY

DVEDREKLRSETAQKLSASMRSIRYFLVVLRFRVMECNLAHVSNQRGISVPFRSFRLLER

LGNITMLCCFDDDILCEQAPSVEEIFLLNDKQSNFSTVLDLHAERNCDTGLQFEDPKWKQ

HLQSLKPIGLAIMVNDDENPSQHYEENIRYLVNEELCPADDDDTRDPYLRNCMQQLSAHI

RMLPFPKHLLNLSREMGFSVAHDLSQFQRRQSIHIICPRLAHYEHTSDHHDQGQEDTRYR

GILKSHLYSTVVLDKRSHRHQLLSRGHPTVVLAHCSEYWDGKSICPLTSEKQRAILDMYN

QWRVEDLDVIAFSYVPVPHKISSHSTRRSSSSNTGTFFESLDAQSIGQQRRLDGTLPPVY

LVDDSTVNELNPPRMCAGRN\*HPIT

>contig47669 Frame-1R

MISTVFLPLPLRQTWRVFHKSQPPNVPKAPIDSLHAPLQALNTRKVLKKFLRSPNDKTSY

>contig48457 Frame-2R

MVAGYNNVSTWLARSQIFHRSLIFIPINK

>contig48912 Frame-0F|Blast-elicitin-like protein INL3B [Phytophthora infestans]gb|EEY69856.1| elicitin-like protein INL3B [Phytophthora infestans T30-4](gb|ABB55937.1|) 8e-30

MNFSTTLVIGILTFVATAYAEECSTTQFLTIAGSVHLEGCTSDIGFRGFEAMSTLSEDQI

VAVCVSPQCLKLMDEMRSMNLGDCIIQGTNVALDKDFLDPFKKRCGGGDVANSSSTDGIG

SSVITSSSVTIKAALELVGLTLLTVLLLSF

>contig49133 Frame-2F|Blast-xaa-Pro aminopeptidase, putative [Phytophthora infestans T30-4](gb|EEY60965.1|) 2e-15

MLRALQARAGSKWSFALRSASSISEASENDSMNPYKAQPGCLQPGLSTTEFQERRQKLFA

SMPNNSALI

>contig49186 Frame-0R

MPQAIISLTKASQHSIISDSNRSDRFNFSPRWWQLASHQCWSKSCTVNGRRNSLNVCRQG

WLTFVVG

>contig49379 Frame-0F|Blast-DNA-directed RNA polymerase I, II, and III subunit rpabc3, putative [Phytophthora infestans T30-4](gb|EEY55741.1|) 4e-63

MYGKVFQYDHEGGNMVAIYASFGGLLMCLRGEQRHLHMIHNDTRIYCLLRKQ

>contig49397 Frame-0F|Blast-cell division cycle protein 20 [Phytophthora infestans T30-4](gb|EEY53557.1|) 5e-54

MLNSVDTGSQVCSLLWSSTEKELLSSHGYSQNELCLWKYPSMTKVKELTGHTSRVLHLAA

SPDGETVVSGAADETLRFWRVFGPNRKARKAGSSTTDLSSSSLSSVMSIR

>contig49429 Frame-1R

MPAGTATITIMWCLFFLLSVASCVKHGPRDATAVNPQNRRHLSMTNNSKLVHESDSSEER

VLPVHRPFSNSMEDSLKTTVAAILKQVDFANPHKTLPFKDYFLTQYRADPKFRHQSLNQL

YEVLKMKLGPNYLLMAGLHFFNSD

>contig49560 Frame-2F

MDIMQNYGRFAFLALVARRHRKNEPCQAIFLRASVPRSQF

>contig51381 Frame-0F|Blast-radixin [Glossina morsitans morsitans](gb|ADD19200.1|) 4e-08

MESSRDQMVFQMKQRQQQIQRHQQESDDLNAKIGSLESDVLAKNSEISTLKKLTRALDSE

KDAVNDQLDALTEKYHEMEEQNNELRK

>contig51617 Frame-0R

MIRFVSMSQFEDSTSADFVGAIPSCLTNLVISILKNPLSTKVSFSWAASRRRTRRNVIFG

SH

>contig51859 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64527.1|) 9e-26

MKVNVYVAAKDGGAAQRVAWYVGTSDAQVEKAIRIQLSMPRNTDFLLRDADGDVVPASST

LPNGQHYTVLMPHE

>contig52164 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59883.1|) 7e-24

MMECAIPREAFRFGKWGRPVRAAW

>contig52472 Frame-0F

MQCKAVLSRGCCFDAKAGKNLMLPRHLSNGSSKDFYALEIFTSNRLKGLQFEEMVVTLMK

SLNCNLRATQ

>contig53624 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66462.1|) 1e-119

MRLSTTGNSSGGEFIIAFASGPIKFKSDEGVLYSRLFQIVDTDMDGYIGGKEGAAFIRRA

NLRNDANREIWRLASGGKSQEKLNKDCWYVAMKLVALVQSTGKCQMQNLHSGDPLPLADF

QLEQPVDNVLPDKTTSDGERSFVVSVSTPIIVGSGYSRYTQYVISTKTNCSYFPCTTAQV

KRRFSDFEWLQQRLLMHFRGTIIPPLPEKRWTGNMDATFVEERRQALEHFINEVCSHV

>contig53651 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64506.1|) 3e-10

MLPVEPASTVAGAVSLHAFSVSFPSQVDMELSKAYGEPKWSNMKRALARP

>contig54324 Frame-2F

MVALKLSLLQQAVHQTKTAFSSNIVHIGDGCARVDDQFFMLQAIIQDSVDLLESKYEVST

LQRHFEIIRYEIDAFVDALNRQTAALYMLPGKETLSQLNLACNYKVTSPRRDNISDSSES

SEK

>contig54874 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65143.1|) 3e-52

MSDKAREATSLYEQKNCERLSKQAELEDLRLRNAQDAELFSMQKRKDVAMRKRLEAEQKA

FEAREKAEAMRR

>contig56533 Frame-0F|Blast-40S ribosomal protein S25, putative [Phytophthora infestans T30-4](gb|EEY60587.1|) 1e-53

MPPKTQQKTKEQKMAAAMAGGKGKGKKKWSKGKVREKVANKVLYDQESYERLLVEVPKMK

LITASAIVERLKVNAALARASIHELEKNGSIAKVLGHHAQLIYTRAVAVEE

>contig56779 Frame-1R|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY70000.1|) 6e-23 NOT\_ORF

MVSSYCNGRNPITWGHDTLAF\*PERMIDPHTKKLCVLSHFAFSTFGAGQHECLGLRFAMM

EMKMTLATLL

>contig57057 Frame-2R

MGWEASMGKRIFKDVLVECLIHLRDLLRLDLAKESSSIQKAKKKNFQSVAHDKLDRLKPI

GIGP

>contig57273 Frame-2F

MNDATKSLTVGVLALQGAFEEHISMLHDLCPLRIRGQIIT

>contig57691 Frame-1R

MVQEMETLALCLSASQRLQELSKCVARFSARFVFYSEAFTRWKARDAQRLTTELLQSYRE

LMRVSNKYERQAKETPSGGDGVHELRRQTQRQLWQVKEALERLGGRKKTMQQLEELTRSM

ADEAEKGHVADY

>contig58445 Frame-0R

MTRKEIEKELKRREREQLRQFDQQQREERQRLAEEKEAAYRIKREEEAKIEAAMEEHELR

VKEDKERKEKKEFDHWKDMFTIEEKGTKLTEDSEESQRLLQQFIEYIVSHKVVLLEDLAN

AFNLATQEVMNRVESLQAANRLSGIVDDRGKFIYITEEEMDNVAKFIERRGRLGLAELSK

ECNKLIGLDGNAQKNKTSTLDWLNTG

>contig06762 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60042.1|) 8e-25

MNMNMDPNTLSPWFTAPEGEYSPANVPNPQFNSNGSGLAFHPSALGSSNGLSGTVGSSSD

FYDDVDNDDEFANEPPLL

>contig07769 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58871.1|) 2e-77

MREVGPVRYSVHTSLSKNVLAFLTPKKAKLASSAYIVQLHNIHHFLPRDLEWSKSYEKIQ

RIFSSKHKESVVLRHGVKAQHALVYEHNSKRTQYGDLSSSDDFFALIKYGRRDDLPVLYT

YVITFNGWYFSETGASVIQDLMSKHMLHSGAADSVKYAGEFRIHRTDNNVYKLVIDNNSG

TYAPPVDILPQLKALFEDNFKGIICEVADYKNETLMKDRMEILAAWE

>contig16653 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58435.1|) 2e-28

MLAIEVTILLNQFDPVIMEVSPYTTPHESVLWCHRFFPIIVFAVVLIKRVFYLDLDKQHQ

RVLIHMLEKNIETMEELQNLTPLLVPKRKNTRGNKITT

>contig17445 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54722.1|) 0.0

MVRGIIFAGLSASKALLSFYGSLLHYWVRRGSYVECPFFSNDLHAKTYLYSIALLNPLWS

QPHYRHPTFYKDLVTNLRNVAIPGTGVPLSLLSYSRLILFPFLLFVYPWLCAIGAFFELP

KEYSNKQGNIIERFLRTFEQIFVCPQNWFAFWRINCHVVSLHSLKTNSPGYIMENKWDFL

LESEKNGIAVTPYLKTPGSLVVKDRNEEGGMGIYIFKNAVNGGDWIIQEKLDNSPFLQKL

LPAVSPLSTFRIITASRHGLGKSEALKGDGNGVKSLSCVFRAGLAGAATDHKSIMFDVDM

ESGKILKGSTTTHWYSVGLQHMFRGKLSVGHDITNHPDTGVSVTGNVIKEIKQMKELAEE

AHFKLMKDVPLCGWDVAITNLGVLLLEVNISCNFFRGSFDQPWYFQFLDDCFCHLETLPM

PVKKTK

>contig19555 Frame-2F

MPMIYRRNRGLSPTRELNDITRGVKSRILDTDASLVGHARRWWIGRGVLLASQKVCQTIW

LAGLVYAFLGLPVLGRVLNFVRFVHRFPVFKIFQGLVVGMLQDVAILLQASTCICLVKIL

FGSDNLTPQGLNYTRNHFYSGFLRDRTGSTRFLPVYMPVLATEYDLRDDSIEALVSGVGT

NHRTLLSLGAAANRPAFVARIRRGLHTLVIVTLLLLILITATIASVADFCLQVTMHPRLN

RAFVTIFFNYMKQFTASLTDEEVMTRTVIGSWVVYVVLMTALTCGIYTGKLPLASDFLRL

SDALCCCVGRPFVTRKDSMGSSGTYAPNLFASNWPYVDKPTRLQRRNSTGCSQMSSGSSH

GSSGGHAAAVVPGPCTFGYGLHTKSSPLMLLSRCLVASLLATGIALSASVFLNGKGGVDM

KLMNNAMFALQAEQFFYHATAIHREEINCTAASSALRSTLGISEKYEVAHLGNDDHCALL

WRKTTAYEGETLFRVNLNESHSHSAELKAMENDSTNAINTKDTARTPNIIVINMESWRHL

DIGVLGGAAKKTLSGKSATPHFDELAKTGVLYTKHYTPCVQTSRTLLTTLFGMLPSCTET

TALKEYSTTLKVRGLPHFLKQRGYFNLFWSAVDLTWEYWDKFLLENGFDKLVDDLKIRTM

LHETRNYKNSPDDHFSWGIHDDLSFEMLLYAIESAHNASKNAPATVLNGTTNMHFSHETD

FVNKTAVKGRHDHGASSNVQNSSTMRVDPLKVALSGWEGLQSPYFIDMYSITSHNPWALP

KFYDVPDLSELYTHSNQKYLDSLYFSDEMLGTFIAALRSKGLMKNTLVIIEGDHGYGRLE

HDNNPSSAESGVWDEASRVPFLLLADDILREEDKGTVVNQLTMQSDLMATIADILGVTPE

QPLYQHGYGHSMMRRRGHSEAGANKAVKGKKVDVKAPNAKANSAQMENLQERRVVLCNPF

DGMSKGVRTEELKYVFHPDGSFNVFELANDTGEKKSLQTGFDVEEMEDGIRDVFEYVTKV

VDLNQFLFEANRFVTILPPAVISAFDDVDALEREVKGSQANNLTIDDEMGHAT

>contig19977 Frame-2F

MIAMKNTPCNSPADSDKPVEVRHQTTSDEVMKSANSEDITSSDESSSLIQRTRAHSRQQA

ASEFESNGVRTRGASKAKLSSATKEKPNKVKQGNAKTASKEKQKDGESDDSNSTGDYVHV

QVGDCVVLDSGDPDDPYVALVSSVQTSQRHDRAVSTFMAQWYYKPYDVKDEVKSLIKGGI

LENEVFLSPHKDRNSIDAVIEVCQVVSPEEYHDIQDEIKRGYREKNKLFFVCRYKYYPNR

SNIKKALEVVENEAIRSGLGRPKPNVGLSYQATIPDYIEPTTSLPRRIDLSVPWKISKEY

AVRPRQLWSPLVATMQSQIFINFRSLVDTLKFAVGNIVKTYRPDARLMGHQRGIILKYLL

SDSIEICVSTGQVITVLKSELCSPLTEDLAMQQLYLSRFNLSQAAYGCSKTIFHAQCKER

KAFQKEVELHAMAKRAAVASLDAE

>contig22351 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69310.1|) 0.0

MNSDTVHSSLGGAMGVLEAPADPIFFSHHASIDLLHSIFYKCVVGNTQPIPIEQKLSDPR

VFTECPRRRPLPRNAIDQNILYPHSNILLRSGEEGMNPTSVFSEFSILEPFFSPLPSSYL

SFSDIRDIGIFSYNYEMTGLLAELFTTCPGAGVGPSSSIFGASVRHLESSNNIMQENTGF

VEAVIVPNNKTEGNWYSKALAAASNSSLVESAMADASQDSLEAIKDVEKMTCVFYDECRG

GVHDLSDEFRKSFHETASSPCTTILADIKSGRDHIRTPNWRSIFLSHMKCGKA

>contig23954 Frame-2F|Blast-splicing factor 3B subunit 1 [Phytophthora infestans T30-4](gb|EEY69696.1|) 0.0

MATPGKSLHMTPGSSMAVDIMNGALTPELAQRLRWEREIEERNRNLTDQELDALFPATGY

KILDPPSSYVPIRTPSRKLLATPTPMGQTPGFAMQATPAREDYGVPIVETPSADGSAMPF

IKPEDYQYFGKLMDEVNEDDLDPEAAMERKIMRLLLKIKNGTPPQRKTALRQLTDKAREF

GAAALFNQILPLLMAPTLEDQERHLLVKVIDRVLYKLDDLVRPYVHKILVVIEPLLIDED

YYARVEGREIISNLAKAAGLATMISTMRPDIDIDDEYVRNTTARAFAVVASALGIPALLP

FLKAVCQSRKSWQARHTGIKIVQQVAILMGCAVLPHLKHLVEIIDHGLEDDQKVRTITAL

ALAALAEAAHPYGIESFDSVLRPLWRGTRKHHGKGLAAFLKAIGFIIPLMDAQYANYYTV

EVMEILIREFQSPDEEMKKIVLKVVKQCVSTDGVEASYVKKKILPEFFRHFWVRRMALDQ

RNYRQLVETTVELANNVGASEIISRVVVDLKDESEPYRRMVMEAIQKIISNLGATDIDTD

LEEKLIDGILYAFQEQTSDDTFVMLNGFGIVVNALGIRAKNYLPQICGTIKWRLNNKPAK

VRMQAADLINRIAVVMKTCDQEPLMGHMGVVLYEYLGEEYPEVLGSILGALKAIVNVIGM

SKMTPPIKDLLPRLTPILKNRHEKVQENCIDLVGRIADRGADLVSAREWMRICFELLDML

KAHKKGIRRAAVNTFGYIAKAIGPQDVLHTLLNNLKVQERQNRVCTTVAIAIVAETCSPF

TVVPALMNEYRVPELNVQNGVLKAFSFMFEYIGEMGKDYIYAVAPLLQDALMDRDLVHRQ

TACTTVKHLALGVAGLGCEDALVHLLNFVWPNIFETSPHVINAVFEAIEGCRVALGPHVI

LQYVLQGLFHPARRVREVYWKIYNSLYMYGQDGLTPAYPVLEDDGVNSYNRTYLELCI

>contig24142 Frame-0F

MRIHFPDGQKLFRCTEEKCSWACDNYKEYAQHQKLHCSVMDEVPNRANENVNPRNGITFD

REQNVRSTRTLLPSSMDILDTDVQVSQSVPSSLVTENGYQHAYRGQLNENGPIGGHRDDL

AFRRGSTLGSQTVTNDRAQVMPLLAFRTRAFPSAAGRIASSLTPLPHLPPTSLHRFYDST

PDVASTHAVANYSNVSSFHVPYSSYLRTAERSELVNSYPS

>contig24887 Frame-2F

MNIQLHFLMLWDYPRRHQKGASEAKLWWACAEYDLREYGIDQYDEFLTNDFGNDEIKMAR

SILLANTYPQDVSLPARLLHTMLLNWGHNVKTLRWFEIRNVLKELIINAQHPPDSPAFAW

YVRYQIDDWWDLLSLRTEQDHIISAVVKDIPLSERLSVEAAVRSYFNGGQFDDVVKALNF

KHSTLEGFLKDKKLELLVRMLDWMKTVDISIVLKLMQLLNEDKFQLMLFDEALWLRCTHV

HATRRKDLMVLYIDNWLVHSIKLRRDDTLKSEVGYNILYNYLVELVDATQHNYHALRSDT

VLRALKERVQAQQQKFLSLPFQQIPRNEQFVAPSIRASKRHKVKGFTES

>contig26874 Frame-2F|Blast-augmenter of liver regeneration [Phytophthora infestans T30-4](gb|EEY69279.1|) 1e-15

MVATKSDPNCVEPACADKMGFLKSAISKKVLVKMTQPEVSNDCPLNRMEIGNATWK

>contig27363 Frame-1F|Blast-mitogen-activated protein kinase 1b [Phytophthora parasitica](gb|ABA40830.1|) 1e-102

MFLRKALFPGHDHVHQLHLILQLLGSPPFDDSGFITNIKAKRWMARQQKHEAKPLRTICP

NATSEALDLMGKLLKFDPRKRISVNDAIAHPFLAPYRADGISMGSERLADSAFDFSFERE

IIGNLEKNTLRRLIFEDVCYFHPEATIELEQFNQEQEQIKRLEEEKRKKEEGGQTKGLLK

GAGKTLMVSV

>contig27855 Frame-1R

MQCERLYPIYIDLIIEGYSLRDQFEWDLLNDYNATETFAAVLCNELKLPKGFEPAIVYSI

YEQVAAYRVALSGYEWIGTVSGKENDTTSCVGYIEIMPCLDDVVRNHEDTQ

>contig30741 Frame-0F

MPGFNTTDLTYLSALCNGDFERYPPRIALLICSSRRHEDTRITFVQMRRWFLGAAVIALA

ISATDALENCTSDVLVKAYKGLNVNQQLVSCMTQNNFGAALDGSVDLSIMSPSSAPDHIK

AICAADSCTTILSALASSPNFELTNCIVGNNVVLKTEVSNLQETCLALSSPASDPSSPTA

VTSLSKPATTTSTPPNGALTDAPTATAPTLPTESVAIT

>contig32668 Frame-0R

MHCATPRIFDLPEGEWFCAYCSAYLNFVENMEKNKLIGLDMMSKPIAVGSEMAIIEASDL

RHKETKSLTASKHASTILMARADGDGKVNKKTSKRSPKGINATKSLALISMEDRAATFFL

VKWVGLSVRFSTWERPEDIGDDEQIQRYFKFSRVPSAKEILDTTCQLPCCAKRHQYALAT

SIVGNRSCEKDRFCTLGYGHNNECSRSIKSLRGAYGSEAHQRIHLQEQIKAQLFAFHCLL

NNHTPDKDVLKQCGMHTNAFVTTKQYMAPRPSTEDDDEEYLDEDGGSSDD

>contig33007 Frame-1F

MKLSHSRLKFYNLLHNSFLGIVKKYAI

>contig34095 Frame-1F

MAHPVVSLSSPAHEPSPLPQSPHSFQSETGEPLVKKRRTKNFQLREDLAKSRGSVTIHMP

AFEPLTFDTWDDFIQTWNNYMTRTKTMYRRRSSSTTTYWNNKQKFKKYPVPEGFKYATMA

YWCTHGCIQPSRGNGVRTHLHNRYTGCSARITADVVFEVVDGEPNRVRWLVRVRNQISQH

NHRISDEIYNCYTNNSSVPDELLLGPEAGKKQELQPMDDSVYDPPARALTELDHIDDSAD

FPKGKSKSASIS

>contig34482 Frame-0F|Blast-histidyl-tRNA synthetase [Gluconacetobacter hansenii ATCC 23769]gb|EFG84023.1| histidyl-tRNA synthetase [Gluconacetobacter hansenii ATCC 23769](ref|ZP\_06834775.1|) 2e-68

MYTFKDISGKSVSLRPEGTAGVIRALVNNNLMFSLPQKVSYSGSMFRYERPQRGRYREFQ

QFGVEFVGSSCPSVDAEVIAMAADALDALGIASRVTLELNSLGDMESRARYRTALEVYFL

KHKNELSSDSIDRLERGSVLRILDSKSERDQRIAADAPQLCDFLSDESKMRFNSTLCSLD

ALNVRYRHNHRLVRGLDYYSNTVFEFVENPYTSDIKQATVGGIAVLAGGCYDELTASFGG

PVASCVGWAAGVDRLNLLRDVRAEATSSSS

>contig35522 Frame-1F

MLAMRSTFNRHSGYGGGIVASPL

>contig36714 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63941.1|) 6e-75

MVSILFVCLGNICRSPAAEAVLKGIVARNAGNEVGSYRIDSCGTGGGSSSWYKAGGWSYH

EGDASDSRMIKEAKKRGYIMTSRSRPLTKQDIYDFDYIVCMDNANKVAVFEAAEAWGGVS

CLDVAKSKISMMTDYCITCKGATRVPDPWYEGGFDRVLDLLEDACQGLYNHLSKK

>contig37726 Frame-1F

MPEVIENQRWYPILGWTARLRAEDPPAWCTTSQESCPNKDEQKDFIWTVYKGADYDEEGW

LYGEQFAETMGPMTRSSVVRTRVWMGSKHHQESEADDDSLMVENDREILKSSEPHTDSLT

LLEEEDQVKGAGSTPGQGIAELPGNQESTSTVHLPSAEVSILSEESLKDGDIVTTPGYFG

RFSSAMASLPSSAMNLAGLSSKQAVYGTVASIKEATLFGLEMAQAATVAAISVEPQPLQQ

GLRPISKNLDDKSNLEVMSMLSKRFPDLSPVERSLVTCCQDNIPKYVSPPELNESKHCKE

CKIEFGMTKFRYQCGYCSESFCRDHLPESATIRAYGHMAPSKLCKNCHFILMEKINEQLV

QWRIERVKDYLEDKLIEYYNTLTDTTVDKIMRAAEGTLVAAKAAPIGAAAKMAVVSADFL

RKYGRAGLIGFILRNEFMQSFSTLKGLLGDLDDLGFQDAAIGTYYFMAMNRGDRGAEPER

EKMHYKGCVPVSDEVLAKLLKYAPLALHGIYEQEVLDIQRISRLQGFTLIYAHVQDQDVQ

HPSFALLGNKESKTALVLIRGSKSVQDALTDIQACPEEIGLSSAGAPDSEATGGFVDAFA

HNGMLKAVMWIKDRIVKSLRVLHHEGYHIVFAGHSLGAGCATLLSVMLQKEFDDLECFAY

AVPACVNYSVAESCSDFVHSVVLRDDIVPRAKASNVMKLVEELKNFKGCWRDTAFEDFEA

FKDRAMTLWAPRKREWAKKVADQRKGKIASRVSASAPLEKLSLAEKKARESGKDEGVSSW

TLTRTNLIDRLDKVGDESREDNVFEPSDETLLDEDKVAAELVTTLIDDPKELYIPGKVTH

IYFYKGIYEAVHVNRQCEELSHIPVQQNMLSDHLGRSYLSALRIVRDARRAKPMLPEWIP

FSTKSRCMCCDSPFTWNSTSSSEAQQNRDQHNCRRCGALICEGCSQKLKSIPEFGINVPV

RVCDRCYYEA

>contig37861 Frame-0R

MVLTFTRTLFCKHQATLNLCHTSSYFCWYWPPQFKRRPCARCHPWCIRKPKSRTQPLHLQ

LKRLNKIISQREDSRLSVVVYGLPEKDCNLKTPTDRTVHTAADYVAFLTKLTTTIGKRKV

LYILEPDAIGLLTDASSCGHKAGYLANLQTAV

>contig37928 Frame-0F

MEMVLVLVFGRDSDGNPLTNSAEMTVRGEKADGSPVQLDFSIVRGNKPIEEITNSTKELS

GGAFTFQNISVRPHHVRLPFGFRQATFHSVLPTRGFDTDMNFLKKNDEPFNHGQKEGVSS

KLSSNMPLVEVFLPLNVTGKELKEGDVFDLAWALDLRLHGDEDIDWSVTSECRFIAPKEF

LNEATMPSITDVSAPETQKNAAFDKSKVYLSASEDGVQEINPSITEAKPKKTQDVKHDDS

IPKCRLAEHDRGIIVTVRIITNHAFDVLSAAGLVDNDKSEEISPDTPKEAPSSAPGASAG

TDKSATVDQLFDEWKRSPQVTDGHICFYDSKRADPWRHRYCFALAMSHYHSQTVEVVHKP

TLWAIEHPPKPQVVYTPYTGNDPALLELLDHCIDTTERFLGLASQTCLSTELPISRPKQE

EKPEVDLQKENEEEGRRLACEAQKQRMKRNEKKASSNFHYLESFSHVLTSIQMALGLGFV

VPATESVEYADVCDPVSPATLKSPSVTLRDAQAHLSTDTFGDSLRYVNKLYNRAFGKPTT

YDRRRVPSHMPFLLQKSIIREIKDHWTHEIDATSSHRFRHPEDMQFSFSYFHYLINRAKI

HPHTLEDIWRDYLDANRNGILDENEVLTAASLARGDAPPEDFVTSVRECIQPKKREKVRE

VTTAEGIVRLHETLMPFITLANLEQCPSIRDALIQNVRYEKMVELMPETEVTFHMLSDDF

NFAWKQMMGTRARRTKFVCINDDMKFPTTRVSQILHELFLSIWPKRSQFELPYHLKNRYA

HRDDYDAANQRLQIALGMLGGVLLVLMAVFRKELREIFRVQTILRASQSSIESNSEPQPQ

ISNLKTHCRREVTSEKL

>contig38046 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69216.1|) 2e-09 NOT\_ORF

MADIKRCLLLHNSGQRRIFYSFSQRANCCSTTTRKTDASWANFLLNRHRVLMQPIDGSLT

PNR\*SVELCPVRSVYHTKRPIKQCRDVIRQRYSKGNHNGWLLVPRLKRGMEVNADTPCQQ

SDEGGLLRLLIR

>contig38958 Frame-1F|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62509.1|) 2e-31

MIDVTSQAFSERDDVKEWLQTNALYIVLWFCLLCVLLMVLPLLCYQIYLISTN

>contig39610 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67876.1|) 2e-59

MFEQESGQILLNRRRAVFALEVLEFFSSHRPNYFDKLMLAHGDKDLFRLAWMKAQTSFYM

MPFPPGIAGGERGSDKKRFCGMTMVQFDFDGNILFMHRNMRKLNGKDDLKFWTHVQMFKW

EQDSEGDGESVSGNASRTAVQRMISYDDIKQKYRIGGLDVGPLFKDFPTCFGAKASVVDN

FKVVRVEDFPFAMLEQQLIDYAREGSLMIS

>contig40522 Frame-0R

MPWSLVMLLLLSLTTFVWANKVLHEAYPDPDYNLTVTEIINARGYDVEVHKVTTVDGYIL

TMYRLPKSYQECQRNTAVVAKKPAVYLIHGLLDSSYTFVCNFRNQSLAYVLADAGYDVWL

GNNRGTTWSNHHVTYTTDNYEYWDFSWQEMALYDMPAMLHYVLNETQHATLSYVGHSEGT

MQAFAGFSINQNLAKKVSFLGALAPVASVGHVSSPIFKLMSIFGVDVIYAILGIHAFGSR

NWLLEQLMGWYKCSTPHECISIVNLITGPSNGINMTRVPVYVSQTPAGTSVKNMAHFAQG

MRANTFRYYDYGCMCLEYLGLAHCPTFMCPNKQIYGTFKPPAFDLSAVQYPRMGFYTGTD

DWLATDADILQIRAGLKNATIVSNLSVKYSHIDFTWGYTANELVYQDLLSQIAKFDSIG

>contig40694 Frame-2R

MIPQLGIRDTVCIYLHATKKIRKLVQAIGNGAPKPMAFRVQQPAERLNRKRNCGKLCKRF

IWV

>contig40971 Frame-0R

MLSFVAALCPLALSLSATAYDTSSRFKRFSSKGYALQGRADPEKEIPLVIGLYPADFGGL

EQEFYQVSDPRSIAYGHYLAQEEIDKLSQPTIGALDAVRQWISGTLPFESVGIFSATSNL

YKISMKVKHAERLLHTQIHHYEAEELESVPAWKRHRMMRALTDISVPEHLQDYVSFVSVN

THPLGLRALRSASSSDTMEFPGTTVNNLAQLRTMYNIPDDLRVTNASNSQCVPSFFEEAY

DPQDLARFFSKFLPGESIPQIIEKGNRINQAERPSLESSLDLQYITGLARNATTYLWSMN

GTNPYSSDDEPFLEFAEDVLAQKNPPLVVSISYSDDEEHIFNVSPGYARTLDTLFIKMGL

RGITVLVASGDDGVTGLRTEFEKIPMEDMCKKSGPQWPSSSPYITSVGATMLLAESQQAA

KMFFRTKEEVVCSTETNGMITSGGGFSNIYSIPEYQRTAVERYMKTWNIPTLPNFFRESG

RAYPDVAALGSNFLIFIKGQISPVSGTSASTPVIGAMVTLWNDVRLNAGKSPLGFINPLL

YHLSETHPDAFHDVVVGNNGAHRRGNTPCDESFSAAAGWDAVSGVGSPNFSVINDIIANL

ENHFNASQLGKMNISGITSVSSDAIIAKSDSGEANTFMMVLFVAAVVANVAIGFVVVVAM

IKRWRNQYTPLNDAVCGLTPSSVSTAIPLKSVKQLKLDAGNVEDVELSEINLN

>contig41213 Frame-1R

MSRSSQVVTTPFSASLCNLLCMEMHITAVAPKTINSKRELPDSCLHLSDFMVDSNHQVAD

VMGWSLATMSTPPAVSKTPSTAASTPDSANMSSFPSKRLSWTRRLVITKQPASEFYKDEG

GKANALEVEVTLVEFNELGEPARSLDKEFIDIPLRILLFFESGKRVDDTDQEIFRFVGND

YDSIVIRASSRKALVQFRLEKVSRRKDGQRFKLRIEVDQEQCTANVADLTPVFTNAICVL

SKRKHPSSYNSDSSIRAKEPPPKLLKRDLTSLEDRMSLKIDGLAAQLHHLNQLVQKQNEL

IAKHQHTAYDPPPINHCSPNDSSILEWLLRSNTAEDGSCLKPALEPHLLPSSVMPFFEIL

DDSYHGIDADFTSVLVPPSAKAITTSSDTQNCSAPSKLLLPFG

>contig41367 Frame-0R

MLSRRYLMSFSVHSFTRPFNVDQVTISISNRYNRSVHPDPTYELQKAQNWTKLQREMPRL

FNASKFRLHKLYEDDAPSRSLHMEWGLTDYASYLGMCCSSERSSQLLKEGEKLQRNPFAF

LSRKIGVAAVLETNDGHIVLIKRSKNVGLYQELYDTPGGHPEPCHILLTEEALETGNERL

KAHFKDATKHEFFQSIRNEVYEEINVSLQQQHPPKLMGVVYQT

>contig41437 Frame-0F

MLDKGMKVTLGMRTLRRFVPIPGKTAQLVQSGPGVPTLKPRFISAVDAASHSTIVNTTDC

RKLICELCRLYYSTEWLTGTGGAMSLRHGERVFVTPSGVPKERLQPEDLFALDLDGNILS

SPDFTAGKKALKLSDCAPLFLHAHKTCNAAVVLHSHGIMCNLVAAICDGKSEFRISHQEM

IKGMTGLTYADTLVVPVIDNALKESDLAEPIARTIEAYPHTSAVLVRRHGLFVWGDSWES

AKRHAECLHYLFKVAIEMYKLGLDYSVPPVSALTTDKDKASDRQLSIAEQHKVVLLDIEG

TTTPITFVHDVLFPYVTNNVVRFLQKTLETPDTKADVAALVAQYKQDRVDGVDSPALGDY

ENREHLIQSLAAYVKWNVKNDRKVGSLKQLQGHMWLQGYQSGELKALVYDDVPPCLDRLR

SRGIRVGIYSSGSRQAQKLLFQYSDKGDLREYVTVYFDTKVGQKRESDSYKEIIQSLGVD

SAKDVLFVTDVIEEAQAAEAAGLDTVLSVRPGNKPLPESHHFHTIRSFSEL

>contig41990 Frame-2F

MHIYYSAHVDLTLPSHSSHSTQ

>contig42542 Frame-1R

MSRLAMMPDDIQGNYLCRISVDDYRLSSKKTEYKVVVQLSFYSTRAHAVGRTSWHIWRSF

SAFRKLDEKLRKRNTALMKGVKFPPLYRRRALFRVDKSPEFLGARMRELDSYINMVSQHP

QLVAFHLAAVSSQTVKSFVGFNVGFGANAEYEQRESQLRPSASILASPAIIQATASVMGD

EDDDFRSVSSCSTVSSFASTTSDYRWSGTGFIGSQSFVRHTVPQGSGSVTSTNSRGSLAH

SMGPGSSSGSWFPASSAHYERGSTSMTALSAPDVIIPELDLQRAKMEDQL

>contig42726 Frame-2F

MAQHGDKGAKGEKSGFFRKMYSSIGSSSRQLAANRHDKAHRSDSTSSCTSSGYNQNSPSD

GATTSSGHSGGGSLQSFVKQHNLNNHLPFSRDDQRINHSEPTQSILSKRPSLIVPFSYHP

HQVSNGTTATSVEGVQIYLDDFQAPISKSGVLIKQANHFKTWKKRLMVLKGHSLFYYVSG

TSGEDSYPRGVIPLQGVRITPVDSARFKRQNCFEICHPGYRPIYLMAKSEADLSVWMSSL

TSAAMPTTADRKMLLVTEPLESLFNTPALEDAVPYKRTYYFRQKVAFCMPRKEDAGYTAV

ELFDLNEKRLTTLCDLNSYCDAYPMILDDPQLFVELLHVVGCYIFRPFARLQSTSPGNIF

>contig42928 Frame-1R

MVGDPTVEVRRACAVGSFYLGEALRDIASQQMPASKSNCQELNQPNPEFADNNSHFLIAA

QFKFVRSILPATYTLSTDVSMAVRLSLARSVGRSLQYVSSVYYDELVPIFTQFLDGSQEA

TVRASLLEEMARYCDSSSDTVIAMIFPAIEALKTSINWRVRVKFVHCVAAWAEREDGATL

PGAFADACLELLGDTVNEVRSVVCEALTPLGKSLGSEWMLEKCVPRVLLCLQSTFRGRLT

GLLAIELIASELQEMDRLRDTIDMVLEQCKSMTANLRFRALRTLGQIVPRLNDPVTTKSI

LEFVRPLTLVDTEADPDVREAAENTQKLLETVLI

>contig43259 Frame-2F

MDVGEQFFEIQAHNLHDSRNVKTLKIHAVTNQEHHREGLSIKEPDGSYLMSGSRLDFGD

>contig43321 Frame-1F

MQVFNQLSEVMKPFYTARGTGSETLVLKRVFLADIGRTIILRETRM

>contig45741 Frame-2F|Blast-bifunctional folD protein [Phytophthora infestans T30-4](gb|EEY66137.1|) 6e-06

MSARILDGKAIAKALREALKNNVAALTAKHGR

>contig46216 Frame-2F|Blast-dihydroxyacetone kinase, putative [Phytophthora infestans T30-4](gb|EEY69770.1|) 2e-83

MELGLGIHGEPGVAKCEQQDVPLLCKTLIEKITEKSSVGLSLAQGSKAVLMVNNLGSTTA

MELYVVAKYAVETLQAKGIELERVIVGSFMTALDMAGFSLSLWNSNGDAEMLALFDEPTT

APAWTYMPFDSSQSSISETFIKVIPPETHKTFERPVAVSNAGRLREKCILAICRTLIQNE

AQLTEW

>contig46546 Frame-0F

MRFDFFFNLHVKYSTCDRRRLSLKFPRWSEIHVKCFAQISKCIQVVAGAIKARHVALQPA

ITLSKHVRRRAYLLNLSRGAWQWRFIRNHVLPRSIRMIHVYVKSPQISHAAVLPAKKVIW

LRFVWTDKAAPLDVDTAV

>contig48672 Frame-2R

MLHKTDRKTNLHLNTAISPVFSIARVLPSDRSTCLNTGWNAHKLPCSIKRQQGWPQRLMP

EAGDGLSFIMPAAAWRLSPINPNTPVSDTCNPRMLPS

>contig48913 Frame-2F

MSYFQLDAVKRLSNMSCVEFTDDDIQKEGWLGVRGNLSRSWKLRYCLLRWDSSSLVCLKD

RVSMVQVSEELIDRHTTLLVEGSAKPHQFPFSICHGERTLRLNAVDGTSRASWISALSEL

IVRSRASFFASEESESGSRSRSFRRLRSSTDEDCLIVSTSTVNEMIRESNGVKKHSRGAW

RPYKFISSTMQSKRKTDLSCRFEYVQQFAG

>contig49132 Frame-2F

MLHESVNTETVQKQPYSSLRFSSHRSRRLPSSSDLSLSSSSSSTASLRRLLKESEEQLAL

ALAQNEEATISTAQLNELNAYVTAYSTASILSRASAFVKANPEAGQATVPIMTMST

>contig49561 Frame-0R

MMTVLTLEAIGRLRFNGYLIPLRGHNGQLG

>contig50071 Frame-1R|Blast-adhesin-like protein [Phytophthora infestans T30-4](gb|EEY64508.1|) 3e-27

MATCSDKSMVACEYSPPGNDGSSAWFIHDSQATQCPSETSADHGLCLVKDDPNNGLIA

>contig50318 Frame-1R

MSSQLLTGHKRRISNSALFQQTPRHSRRRSSTNRDLSFEERNLLYEKTSCSTHVPKSVMR

NQVPGVRIKQTNNSGLEKVYQLATVKENMMKENTLRPTERQRTTPRPPLSRRPVIGRNRA

NSGVGIVRCRSWQLNAEDTETEDECAGSKDSPRTVVQLPAFGRAKVVKMRMATGDCGCSE

VGKSCANENVDDPAGKSALSIDSSRLCFTRHMNEDSWQLHLFSPDALDEV

>contig51146 Frame-0R|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68035.1|) 7e-45 NOT\_ORF

M\*LQLIAEGVLAVGNLLPLFQIDAAELLYISLRLENYSWSIPRPIINPMMPAYTVPYKER

IESIQLLGRAFDRDIIGEQGSVPNLQLQVKLSGL

>contig51407 Frame-1F|Blast-hypothetical protein PITG\_07800 [Phytophthora infestans T30-4](gb|EEY54203.1|) 2e-32

MAESVAGITLAFHGGSSCDIKLDETLPTEFDLVKISDYEAQSLQKSQYQLTILQPQNHEE

PTHYAWTKFARAQCKTVLPNDFDFARPQVSGRYTWMEMSLWPAISVSNMIDTPVELHLSQ

EQIFIDLKLCPTSNKRVSTINPFESIIVILNCEQDPSDTSKSPEAHQFLLQCCSVDDRKD

QVFDFEDCKVVANFHS

>contig52165 Frame-0F

MNLAETLEKDHSFVPSVANSYAQISDQFIQYSFLPAAATIAHYANLPTPDFNRISSFAIT

IANTYARSSDGLKVLGIAKLALPKEDNSKKLSESARF

>contig52323 Frame-0R|Blast-Mitochondrial Protein Translocase (MPT) Family [Phytophthora infestans T30-4](gb|EEY60403.1|) 2e-37

MYELDRGDVTTGKCRYWGNNFLVISSMFSGLECATEKIRARHDVGNELVAGCATGAALAA

GQGFQAQCLGCVGFAAFSYAIHVFTGGQSSTRL

>contig54325 Frame-0R

MQQYAKCDFIRRLFHDFARIINAYDKSDWWLQG

>contig54875 Frame-0F

MAVAGLHTIRAASRGDDAAGSGRKMADRWAGRAPASYTDYRFWQADRLPRDAELSCAPSV

GQGDHRGASLLCGLQLPWLLALASRRWTEYLHLVAQLLQACARLSSYADVGVAENAWAQT

RSRVGPLRTYIPYFSLTCTETNKF

>contig55043 Frame-0R

MQHWRAGIKVVRYLKAIITQGL

>contig55436 Frame-1F

MVPTELYNLLPQSPTAHREESGGVVDA

>contig56778 Frame-2R|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY70000.1|) 6e-27

MVSSYCNGRNPITWGHDALAFQPERMIDPHTKKLRVFSPFAFSTFGAGQHVCLGLRFAMM

EMKMTLATLL

>contig57056 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68096.1|) 9e-29

MDEEWAYEEAADDEKLQIARQFLLASPPGQISEVLRDVAKLVPAHVLTDVALREVLRVYN

VKNCVPVDVPDADYK

>contig57272 Frame-1R

MQRSLPDRLLTETEWRQLGVQQSRGWVHYAIHKPEPHILLFRRPLGTDPTTGRVNLEMEK

QAKEKYANEFN

>contig59418 Frame-2F

MIKTTTRALESSYMATDTMNARCLDHHTALSTHISIETSSL

>contig01009 Frame-1R

MIGRADIEESKSNVAMDAWLPQASYPCGNFSDTSSLKFESTKGSIGHAFTVCIHTENQNQ

VSFYPFVLHEISVLIELTLGHLCYHLTDVPPQPNSP

>contig02390 Frame-0F

MHYELTITKHTIMRLARNGPTTTTNLVFGANQFFQLLVLIGSASSLGAL

>contig09171 Frame-1R

MGYFQGSSQEAHHLAFSLCSDFEGNAYNLFTKNCNTYADYLCQLLLNKSIPAYVNRAAYL

GSFLSCLLPADLMDQAPVGDPYSPSRITSGAPRGFNSAYIPFAG

>contig10133 Frame-0R

MFFAKLLLAQRLVLSFIHQIADIKTTKKRVMRGAGLFVVAVFVCISFSSFTDAQDAAQVD

KHEHKANRRLKPFHANSIVTTENELEERGIGSRISKMFSKKVEKGDNVVLKPKKFSWGKF

FLGTFAGIIVISIAASCYGAYF

>contig11307 Frame-1F

MPSTSTCKTVLRVGRPPDNYNPPQHKEDGYFLPSANGIVLGTGWQATYKLQRSSKADEAH

GTLERTSKRGIWVYSDHSNHGTLVNNKVKVHHDAVVVHHGDQLQLGQMKIFLCLEMGTFL

TPLEAQNIDGIDHVGPVKEIHQTIEEPTRLAQRRASTPSSPAALMSKDQQKKQRLPPIDT

INLTQVV

>contig12878 Frame-1R|Blast-insulin-degrading-like enzyme, metalloprotease family M16A, putative [Phytophthora infestans T30-4](gb|EEY56192.1|) 0.0

MLFLGTAKYPEENSYKKFLSSQSGRSNAFTSQVHTNYYFDVLSDHFHEALDRFSQFFIAP

LFTSAATEREMNAVNSENVKNLQNDHRRLYQLQKSLSNPAHPFHKFGTGNIETLSTIPKA

KGVDVRAALLLFHATYYSASIMKLVICGRESLATLKDWAQQLFAEIKNTGRSVPTFGDAV

PFDESRLARVIHVAPVKDLRIIDISWPLPSLYWDFLTKPTKLLSHLMGHEGPGSILSYLK

AQKWGNGLSAGLFRDNEDWGLFCIKVDGTDAGIEHVDDVVEAVYQYVQTLQQETPFEPWI

FHETQDMALQNFYFKSKENPMAYTSHLANVMHRYPPKYILSGDYILYEYDGDKVQTVLNL

LTPQRMRLRIVSKTFEGTTQSIEKWYQTPYSENPLTSELLNRWTSPPPNPQLKLPHRNEF

ICNDFSIVTPSCSNTITGSERDHTMSPPQLLQQNEQCRLWYKPDVQFRKPKMMLHFLFYS

PSLSISPIHAVLTSLFVRYLKDKLTEVSYDAELAGMKYEIGFTSRAIEFHVGGYSQKLPI

FLTKVLEQMIEMTKTDYMYEQAIFDRVKDRTKRMYENFFLEEPYQHAVHTCSELLEVS

>contig15365 Frame-1F|Blast-acyltransferase family [Phytophthora infestans T30-4](gb|EEY53344.1|) 2e-83

MRCFWWIAALLLSVWIVNEGVFGDRQSHMPLRPHISTFLTGSVAAVVFVKMDTWIKKTEF

VFRYWHIIPIRMIEGVAITMLFSVCFRGLLFHWVHANPAPPPSGFPYISAFLAIIIVIEM

LLPSCVSTLLEWNFLRYCGKISFSIYLLHSFVLYNPALRTQTNYFDRLFSRLFIILAVCT

ATYYLVEYPSMVLAKR

>contig15790 Frame-1F|Blast-translation elongation factor 1-alpha, putative [Phytophthora infestans T30-4](gb|EEY55396.1|) 1e-116

MTVSDVSKSMSLGLTVSGRIYAGAAAIGDSFLLMPVGLLLSIKGMEQDGQRCPLACAGDT

VEIGVSGIDQAAVTIGSILCSIASPVQLATKFEAKIMTMPALEVPLVKGTCVTIHMHNVD

EPAHITRLVSMQRKKEDMEKKRPRCIPRECSGVVHITCDRKVCIEEFAAYRQLGRFTLRD

RGKTLAAGIVTQIIA

>contig17349 Frame-0F

MGTFQELMLLNGLFATMMQSYQHTDNSNVETTKSTCNSAFSQIIQDSLTVSDQEKTCMEH

RSGLIQNEDKVDGKVAWRVYLSYLMSCGSITTIGTLALLLAMQMSSVSTDLWLTKWTSRQ

PTGVALSFYLSIYAYLSLSTIVLGFVGDLYGRYAGLRASKRIHYNLLRHIMKGTMRFFDT

TPVGRILNRFSNDMNIIDQKLNSTILQLSIMLLALGSMLAIQSSTAPILLLLLVPVLMCY

TAYQQYYGKTCRELQRFDNISKSPVYTHLTETLSGLVTIRTFHMVQQHVNIQAKKMNENT

KAFLLLNLCNRWLGVRLEFLGAGITFAVAYFVCRDRAMLSSAMAGLLLSYSQNMTSLLNW

IIRMEIDMENMMNSVERTDEYCRVETEPVTLVAQYYDRYTITKSRPLQVRPHWPEQGKIE

FSNVCVRYDPLSPPVLRNLSFTIHGGEKIGICGRTGAGKSSLLMALFRMVPIQLKGGGEI

FIDEVSTTAVSLTELRSRIAIIPQDPVLFAASVRFNLDPTRQATDKTLWQALRKARLETF

IQGLHGGLDAEILESGDNLSVGERQLFCLARAILRNSKILCLDEATASMDHST

>contig17433 Frame-2F

MPTGAPLSNAIDVEYVRQQRLGSTLNPFEPMLAKENAMTIPDKPLPFVRPQFKSSTIALT

TQPQPEPRLGVEPASSGAIQADDKLAELNAKIQELEQSLDDFAISAARRFAIKKDLAMTR

SQKIRFLRNLGQKP

>contig19206 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY57949.1|) 1e-136

MDSDSSIRRRKCSLRRSVRVAPEHVLSRHQGTMYHLVQDLTKLVHLHEPAILHVLERRFF

HNDIYTSTGQILVAMNPFRRLALYSDAIKDHYYDFGGRSDADAVPPPPHVYSVADQAFRR

MVAPAIGTMKTDQTILVSGESGAGKTETTKLIMNYLAYVSTKRARRAPALESMQEPTIHE

RVLESNPILEAFGNARTTRNNNSSRFGKFIKLGFTPTGEMLGASISTYLLERVRLVSQGF

GERNYHVFYELCRGSSVSERHALRLEDVTTYTYLNQSNCVERLDGVDDSASYLVTRRAMS

SIGMTTEEQLNVMKIVSAVLHLGNVTFKMDTRHGTKDD

>contig19398 Frame-0F

MTAFKSGFCPSQFSPKPPKPLYGLLNICVKKVLLILKLFTEL

>contig22352 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59952.1|) 1e-08

MVINKRILVIGVVVLCAVVGAIIGVLVATSSNSSSTESSEPN

>contig24592 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56344.1|) 1e-100

MVVWRNYLVVFGGFYEAARETKWFNDLYLFNLAELKWQKVVYALHRQVPAERSGCQLAVH

PSKDLVFVYGGYAKVKNVGEKSEGKVYSDLWELNLAPVLKRQSPTWEKLSRKGQAPSPRG

GAAVTVHKQRFILFGGVLDEEKRRHTMQSTFYNDLFVYDMDRRRWFEFKLRGK

>contig26877 Frame-0F

MCNPPFFDHMDEADTNPDSSCMGSANEMVFPGGEIAFIENIIIDSEVLRNRVIWYTSMVG

KKSSLRKLLSLLRGKNVKSTSTTEFFQGRTKRWGIAWSFCNDAIDDLSTKVLGKRKEAHR

RQELRFQVPLESD

>contig27856 Frame-1F

MTTMELICPIRLDIDMDGVRYQDTFLINA

>contig27979 Frame-0R

MAGLVEKLVSLVGRAFYSDEHVVVLSALMREKFMKDDEMGNAVNLQTRQVRKIMNELHQD

HLVCEEVLNDKRAGGSSSTSYWYIDYKYFVDVIQYRLYVMHEQLKDSEQLEIERQTFQCS

DPECGREYTALEAQLLLLPGQYQFRCGHCNAILLECDNNDRLVRIQSLQRKFKDQMNKQQ

GMHDGIYEVLRRIGDFVKQGQVLPTNLPSDNRAAGLGGQHTRTQAGAGSGSRGRHGNTGV

GARGDDRNLTSFLYPYGTQEQEIIVDIASTSTVEDEYLNSRDRHKETETATQPLAAPRAL

PAFLQGSSISGHMAAKHAVETQSGKDSILETTSSSTDTLLVQSEMTEEERQEAFKRAYMA

ELERYNGETDENEVQIQVETQGSWETDMNIDAMEDDELEEIEWEWCVDDNSETNGCLDAT

ILVNGECKRLDGVDDHDLLTMTEDEFLSCYRMCLAENDVIG

>contig29285 Frame-2R

MKDPPSACSLLSKSRGRGQSLCHAEQFAVKRARSKTNKAGTETRKVWLKCAHARVHKDEG

SGLRRTSTIKKIAS

>contig29797 Frame-0F|Blast-eukaryotic translation initiation factor 2-alpha kinase, putative [Phytophthora infestans T30-4](gb|EEY69961.1|) 2e-28

MPRHSEQTYHGVAWTAPLNASMILDGNGVAASLPFDLTERLARFVARHNVSRLKCWQFDR

V

>contig29872 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61038.1|) 1e-113

MRPRAWTASESTEKYHEMQDQQRELASHVQELVLVKTCLEKQLEATTRLALDAKKERHAV

DRNVAQLRQNRVIDINRISLDEDNYDDEEIHEVHGKNSLPEFTRSFMLGKHTQLSLQVEK

SMELIEDMDVNVADTCNSLGQVYLDRCEFPNAVTEFRKSIDANRKDGNVWVNLARALHGA

GDFYDAEIAIHRAMALTSKNYACLSMWGKILHSKGEHDKAVEIFREALSLMEQEEESDED

VGSMTVGW

>contig30012 Frame-2F|Blast-COP9 signalosome complex subunit 2 [Phytophthora infestans T30-4](gb|EEY67722.1|) 0.0

MSDEEEEYDFDYSDEDEDMEDFENADLHVQIENVYYSAKQLLEGEQPQRQEAVNALAQVL

TMQNGETDWGFKALKRIVKLLFDLHHHDEAMRTYEELLGYTKTAVTRNVGEKGINSILDF

VSTSKNWEILQRFYETTLETLKEARNERLWFKTSVKLGNLLYEIGDFSRLSRIIKELLVS

CSEEDADDGVRRNSQLLEVYALQIQMYTAQKDNKKLVSIYEKALRTKSGVAHPKIIGVIH

ECGGKMYMMQRDWDKARSDFFLGFKSYDEAGEARRLQCLKYLVLANMLSESQVNVFDSQE

AKPYENDKDIVAMTILTAAFLHDEIKTFEDVLNRNQEAIMDDPFIKHYIDQLLRTIRSKV

LLKIIRPYRRMDTQYIARELNGISLTEVESLLSALILDKKIEARIDQVHHTLVLSERKPE

EKFQTSVQGWCAALDKFHSLTLARLGTGM

>contig33215 Frame-1R|Blast-DNA polymerase epsilon subunit, putative [Phytophthora infestans T30-4](gb|EEY69170.1|) 1e-84

MTSSVVTLEALESALDTLLVLSTKNEYEKIQVFDAFNTPRLHFNKHNNSYELRVDFHRQL

QAGSESRIQLLRNRFQFIDLRVKRNRMFARPSAAVANTTDYIELSRIESLLGVSGVCRVM

GMLGQDERKRFYLEDFTSRIVIDLSSAAYTDGLFTINCVVLAEGEVVDDVLHI

>contig33783 Frame-2F

MNSSSGSHERMSGLSGFNSSVQCPKPSPRSNQAITRLSSSHGSLSSSRSVKRIEQEQVRL

VGTFYQLGAEIGRGGYGIVYGALDLRNGRSVAIKQVSLRDIDKDELLSIETEISLLRKLK

HKNIVKYHDTIKTQGYLYIVLEYMENGSLAQFMKKFGSLSETLVAMYISQVLRGLAYLHE

QGVLHRDVKGANILTTKDGLVKLADFGVAIKLSDTKKANSVVGSPYWMAPEVIEMAGWSS

ASDIWSVGCTIIELLTTKPPYFDLAPMAALFRIVQEDHPPLPQRMSSALHDFIMKCFMKE

PRLRASAEELLVHPWIAQIPKIKVEESTQLVAESVTSSNDRDAVLNTIRLYETSSSTTDV

APIANAGKVSRILGTATKQLDEDIENWDDVFHMNSKLSMCLLKEQESRISDRAPVGPSLS

LQNFQLSKEDATALFDDNVWNDEALGNDDTSPKSTKKEDFTLWDQSSIIPAQSRLAQLQR

FAEDPDEDLLYDDIDENQLVLAAAKQRQASEMQPLSAVKRLYRKYKEVNDNGLESAEDQD

EGLMFRGGGGLGSHAGSSSGGTRLDQLFDDELDFDYSTARDTNQKATTRVVELLSLLDPS

RDDQVILDACNNLEELFDQNVTLRRDLMSQGGVVPNIMEALEMKKMDVLHAVLRVINIIV

EGNKRFQENLALVGLVPVIIKLTKQQNSCYTLDQREKGCSPKNSYFSTAVRMEAAKFVRQ

CCKTSSLTLQMFIACGGLPVLVDFLSLKEKPPLPGHDVDLVHIALDGIFSVFSIQTIPKN

DICRLFVKAGLLKKFVLVFSVIVSSLLASEKSINEDSVKHVKTDPKAHKAVKSWTMKELH

TTCDIFVLFSRGDTVVKEHMCADAVIKGLLKAIHPTMPHIYEREDALSSRQTSPRLCHSD

EYVSAMIKILKCIRNLSMEPLTLEKLDRAGAISTLVRLLSEQEAKNSYTSDVKRKEVENI

VLQSMFYLCRINRNRQTHAAQAGVIPSLIKVVRNSSPLKQFALPILCDLAHASPTARAHL

WISDSVTLFLALLEDKYWQIDAIKSISVWLIHDTVKMENVLLIPDNLMKLVICFSSALDT

ELENLLEPLLEMLSRSVRLNQALGHSGLFVTEIVKRLQLIPKAIVRKSLLKMLKSLFESH

TSPTQFLIQYNLQPIVYALAQDENSMILVKEIASQLLQAILNAVELLK

>contig34364 Frame-1R

MEDTQAVSSEQELLASLPPPPSAFPDLIASFNTNENVNNESKATPALHQRRNSRSSASTI

GNSVASVAGIVSSNLTSSFASASLSFHSLLSASQNATDSNANDVDEALPIADQTSKEVAS

VATVDALIAAKLLQEVTVQQRMKILEELIQHRRSDWNYLKTMHEGSNYWLNIALLREQQV

LQYIGKKPRSRRSAQFFYLGIGLGKLVEETPHPELLAMDCCQLLEELEFFFASTAVQSRK

>contig34993 Frame-1R|Blast-60S ribosomal protein L24, putative [Phytophthora infestans T30-4](gb|EEY66478.1|) 3e-68

MNKKLKVEEFSRRRARKTLKTQRAIVGVSADDIRKKRNQKPEVRAAARAALKEAKDRSKA

KKSATKVEHTIKGAKGGNAPRAQKKSGNRGAI

>contig35385 Frame-0R|Blast-cell division cycle protein 20 [Phytophthora infestans T30-4](gb|EEY53557.1|) 1e-167

MASPSTVVRRLERESSSSILISPPLIRGGSRKRSHHASESDVHKLSTNRKNSDSNAKKCK

TDPSSGTSFSASNKKNASDRFIPTRSAMNLDLVQCNSPDTAAAIEAAISRSKDSPSHSGG

TSTSTSTVEDEEKQIYKKRLASALLGKEDDSNHKILKFTKAKPAVAPPDSFKSTLQARFS

YNKVSIIPAATAKKLNRHVPSAPIKVLDAPELMNDYYLNLLSWGANNILAVALGQCVYLW

NAVTGDINELMGLDGDEYVSSVQWSDAAGESAHLAIGTSESVVQLWDVTASRQVRSMNGH

ASRVGALAWNSYVLSSGSRDSTIVNHDVRARHHQLSTLTSHEQEVCGLQWSPDGTMLASG

GNDNALCLWKSGNIGATRSMQTPAHRLEQHTAAVKAIAWCPWERNLLATGGGT

>contig36717 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67992.1|) 1e-59

MLLAEKHRNRKQQYERDNEQLLQEMRDLARQEKNSQGKLIEKLKRDITTLSKQTEKERKE

REKDVDRLVSEKMRAYDAAQKRKEDADAEKSALREHIKELESQFASFKRSTGPNDVVTVN

AAAVSAKTAIQNTDAMLQLNQANK

>contig37541 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59939.1|) 8e-57

MEKKAPFQSSGSTYDTPLSEYAAPHSPPRPQEVLQWFEGSDRILLPLTRLDAMMRNFVVP

ILFIFPPPSTSTPFDLHKLHSSFLSLVEEDYPFLTGRFFTDPETGFVNIMQKTGPHQNRP

TDIGFEINPQYVMTTVKAIQIRSWDLMPTARGKSELIRVKGSLLKDGGLCIGIDISHMLF

DAEAIFTFMTVWGQHYSGVKKEQRLKLNHDRHLLNGSGELSTMQHPELRVGVNPKPHFP

>contig37862 Frame-1F|Blast-xaa-Pro aminopeptidase, putative [Phytophthora infestans T30-4](gb|EEY68419.1|) 2e-25

MAPIQQKLIEVSLLTLDEVKWLNAYHEEVHNKLQPFLKDDFEAYAYLVQETKPLSLVD

>contig39244 Frame-1F|Blast-zinc phosphodiesterase ELAC protein 2, putative [Phytophthora infestans T30-4](gb|EEY60856.1|) 5e-43

MVVLVQVLCVDSIETSPSLLLSTESHRFLFNVGDGIQRLCMEHHVRLAKLKHIFLTELRS

STLGGVPGMCLTISDTGKEGVHVHGPPQTNNYLQAMRHFFFRPDFQLQASDVHY

>contig39569 Frame-0R

MLENVTAMTNNTNRASTLGDASDSVKTKMITEGSVSDDNSSRSDENATPYL

>contig40385 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62938.1|) 1e-40

MSDDILDNMSLSDDEMLDDLAGEMLMEMAARDSTQPALSSNSTVPASWAHGTVVTSNNVA

NPPRMPDLSQMMSQMMPMVSQMFSGNGGSDTLLGCNANSYQQAPVSWQELVKRHVPENEQ

EDWL

>contig41434 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70513.1|) 2e-58

MSSSRQLALQAHLQASDALRLTLEAQESATEKPPASFARIGADYKTPHYFAGAKIDAVNG

PTLQATLGGKLGELAIAVLGAYDVGLDHCDRLGRITTLNVATRYCHKDLLALLQV

>contig41993 Frame-1F|Blast-adenylate cyclase, putative [Phytophthora infestans T30-4](gb|EEY56781.1|) 1e-145

MHYFHKVTAVNKPVKICSRRPSYTRHDALLHTRMKQYVSRAVWPYLDVHDEFWGSELRNV

TVLFINLGFSEQDLTNMLGAKDLQRLQDAFAFVQKCVYDYEGTINKFLIDDKGSTVVAAF

GLPPVTHVNDPIRGILASLAICAALGNNGLKASVGITTGTALCGVVGHQGNRREYTVLGD

IVNLSARLMQRAKLEGGGVITDAATKIHAQDVLHFEKRPEIMVKGKNESIKIHRPYPRMS

ILMDFHLSSTLQRPTRQSKINRTISGEEVLGRP

>contig42192 Frame-1R

MARSPSATRSLQRYRSRSRSRSRSPLRSRRRSTHRRRRKVSSGSSYSRSRSASTPPRKKM

RRKSHANKDDKNIEPKNHDTASSDITPPRRFNDDNKEVSPSRGPVKQEDKKDTSVRKRTL

LLDARASGRTGGVYIPPFKLAQLREQQEFDLNVSSEEVQRRTWDALRKSLNGIINKVNVA

NLSNILPELFQENLVRARGLLVRAIMKAQLASPGFTHIYSALVAVVNTKMPEIGELLVKR

VVYRFRRSFKRGDKVVAIALVRFVAHLVNQQVVHELLALEVLTLLLANPTDDSVEVAVNF

TKESGQILAELCPEGLRAIFERFRGILHEGEIDKRVQYTIEGLFAIRKGGFVDYPAVHGQ

LDLVESGDQITHELTLEESIDCEEKLDVFRFDPDYEKNEEMWTAIKKEILGESDSGSESA

SDTDDDGDEEGEPEQVVSADSSMAIQDYTEQDLVNLRRTIYLTIMSSITHEECAHKLMKL

NIRPGQEKEICLMLIECCSQERTYLRYYGLLSERVCVIKREYQDAFDKCFAEQYALIHRL

ETNKLRNVAKLFAHLLFTDALPWTVFEYIHLNEEETTSSSRIFIKILCQELSEHIGMKML

NTRFSDEVMQPTFAGLFSKDNPRNTRFAINFFTSIGLGGLTTDLREYLKNAPKVVMEQTK

GSANQSDSESESDSSDDSSSSSSSSSDSTSDSDSNSDSRSASSSDSSDSK

>contig42725 Frame-1R

MNRSLFLEFCDKNDFAKWVVLKADSSPILFNTDMKTYQEELLKFAGRWPTAALKDVDKRS

IQMAHDHCESDLRDKIATYRTLFASITDALFSVNTTCKPGKRYIAVQTLTKFTVALPLRN

KREMQQLLHLLGQDFKAVWCDSIERVFSMMKECLESSKCDDKARALVRDQVIAKEFQALL

KHWSCRRAACHLTMRPESKNGKIYCEVEQISVKSNAKLIRSTRDRPGLEIVSS

>contig42862 Frame-2R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY67180.1|) 2e-26

MRVKACVGSTPVGSVQRINEWLGAETAHVLYKASDILGVNVHPFFS

>contig43322 Frame-2F

MTYQETTAKALHLSLKRVHSPRIDCHSPSSIYDVDLSRHSSDKVNLSNAESCAMHES

>contig46004 Frame-0R

MSDWDPPTSLKPTATTWTSNNDDDLLVSLERHRIQVASVMTQLPRAQDEEAPAATSPSVQ

STALTTYSSSGFDGLYDSTGYTSNGESNYSSSGAYDRPLKAFTGLSNQGATCYMNSLLQS

MFMTPEFRQGLYKWTSDRANTLMAQDDEQGDDEEADEDNIPLQLQNLFAKLQLTMQDSIS

TKGLTKSFGWTGSDVFQQHDVQELCRVLFDALENTFKNTVNENLVNDLFQGCLKDYVQCY

ECRYESSRIDTFLDLSLVIRPFGSTEMMKSVEEAIELFLRPEVLKEENQWICDRCKVKRN

AIKGLKFSKLPYILMLQLKRFDFDYATMTRIKLHNEVTFSKYLDMNSYVSDEKGGVRGKI

ARKMSMERHELEGKHRPNAQENLASIMSSSPPPGPLSSTKNARIHRMSSMDESHAMAFND

ENSDEDDADGAMPFDTWSPTFDPESIMKRSGPHVYELYSVLIHSGSALGGHYYAYIKSFE

SGKWYNFNDSNVTEISDTELRNAFGGVNGSEYSARYSTCAYMLLYRLVDADKNVNVILPE

SIPQ

>contig46699 Frame-1R|Blast-YIPF6-like protein [Phytophthora infestans T30-4](gb|EEY58321.1|) 1e-34

MLMRVVISHFLLRSFVVSMGFLWSTRASVVFMSKLVPPKRKALTVYPVLLFYFFISWMVL

>contig48293 Frame-2R

MIVEMLDNHDMSNLNSVRAPIGTSDPPNSDVTHPPVSCTKLPIRLPSRNFCH

>contig48671 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55642.1|) 1e-07

METPSQPEFDQDNLNEDIQRMRTLWVNEMVLLIIFYSANKEDNTDVYNNAR

>contig49562 Frame-1R

MALPLDEHLQVDNIDSFLILRSLNTAYSSGYAIYGIWFFPEDDRSKILQLLQRLIQSLKA

PHITRTENSTPTMAQMPIQMLNKKQLTQQEQQERLPSQSRNRSRSRNKRDDSKRSSSTIN

NPITILQRSSKDKRSDSSSSGSSGNGSAKQENTPALGNSIGMVPVSKADGVAAGEAIMGM

ISQNLSQPHKQQPSSRVSKEQLKQALIGLLDDAQFFDQIYLAYVSRAFNRE

>contig49841 Frame-2F

MYGKLFVYAYLDCIRPPSLKKSHADCNQTIASRHLLPTHEGHGNDEKQISVDKSQREWSE

QESLEAATLRASCLSNLAEVCALLQWELQPFLQDVLTCIYGILQLELEVSSSIPKSGTKA

AFENDDQQFAQTRQNKEKQQCVVTARRGSVFVLRYLVEFLGWKMLELMPDQLSPLYRMLK

HVARVDRDRVVQFHASRALCALNEVMRAEIFPECKQQDAAFGISSLR

>contig50072 Frame-0R

MGSQTGLSKHSSSFSSPMKSA

>contig51383 Frame-2R|Blast-diphosphomevalonate decarboxylase [Phytophthora infestans T30-4](gb|EEY64532.1|) 4e-40

MQLTKATSPLLTYRAKTVVPERMKRMEMAILARDFEAFGTLTMQESNQFHAVCLDTLPPI

FI

>contig51404 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69256.1|) 2e-68

MNYGKALLPGEGAAIAQFVQKNMRIPRRGEVGWNGEEIENLENLGYVMSGSRHKRMNAVR

IRKENQVYTAEEKRALALINFEEKQQRENAIMNDFKEMLTARLTKKHGSRLVEDMESAAK

>contig52038 Frame-0F|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY62213.1|) 6e-86

MYNLNDSSTGLCWKDPIEAAKEQVAILQAQNVDFIIALSHQSLTDDNRLSKEVVGIDLIV

GGHDHASMLQTSYGTPYLKSDSNFHSIWTSHVNYYAADDLHDRKALMTHHAIPILENLPT

DKALDAVIATYAALVNELEKQIISSLCEDLDLSQNVVRVQDSKIGHLFADASREFYGNGS

VDIAVMNGG

>contig52113 Frame-0F|Blast-leucyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY66974.1|) 3e-65

MKLSNLLGERRTQLKGSVAYKEALEALVQMLAPLAPHNAAEMFQVLRGGKESADVHAEAW

PAYDISLLDRARVKLVLQVEGKPRDTIMVDHSLLENRDLDGVMLLALASSKIQRRLQGRD

VHKAILVTPKKQGAHGLLNIVTTTV

>contig52166 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68297.1|) 6e-23

MSTERVMARYIVHKVGSFVTKDRVLCLGEYSFSTIDRENQLITNTWPYEDVDGADVLDGE

TDFV

>contig52269 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65370.1|) 2e-82

MRVLEHLLNYSSRLPRGKRTQLRMLLAEDTLKMRMFDTCRHMFMLMEREATAFCDRLQEN

IKGCSGPGSNNGTGPGTSSSGGGRSLGGMGSEARYCFDMSFSLRYMLCRVKMHLELGDFC

NAFAWLSLAHVKVD

>contig52470 Frame-1F

MELHEHDVAEMRIIDMPGTLLDQDYVVQLWLLSNCIFVWMGSATDKPCLG

>contig52544 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63906.1|) 4e-60

MRSRWVDSLKRGISASPRLDERSPQPSRASSTPTSVSTLSSASAPSLRGVENPAYIHNAD

RCDCVGPCSVLRVLENCVLQGGVHHTHLHVLTYLGRPLRSNCCCYPVAVQWFRAVGDEDD

FQVIPGACDE

>contig53626 Frame-2R|Blast-palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58442.1|) 2e-14

MELSQEQYTRYLLQAHTTSLQIAMSTAMHIVFSTILAVGLGVFCLA

>contig54326 Frame-0F

MLKFRIYLSSLSHSLALVMKATSGSLYGALSPPEKKTRSISFRDEFAALFFSAAHSAISA

IKLHRSSPLPRPIHYELRRECWICSERSADLVEAHNVVLSAT

>contig54803 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65850.1|) 3e-96

MDDRANWTSEEHAQHELVVKEFGQMAQDVWNVLTGPNGILEEHAVQTHLALTIAVILLRF

HEPQGKATVIDAVEWLVQNQEHQICDSVTTALTHFAVLHTLKVIPEEVGNKRVKFSKFQR

IQCKDMVQQCAANVVCRVLSSLATAVDANDKQLQLRGLVLQAYASWIEHGTVLPSVIFER

GVVERAFREALVPVSYVYALQLVHEIVCVCHHDEHVQL

>contig55758 Frame-2F|Blast-hypothetical protein PITG\_18705 [Phytophthora infestans T30-4](gb|EEY68804.1|) 2e-11

MVLDSIVLPAILFTAAVFEIPDWAIKD

>contig56162 Frame-2R|Blast-3-phosphoinositide-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58380.1|) 2e-48

MRRTSSLWNRFLLDDELIKMGGLISKRKGLFSKKRQLILTSKPRLIYIDPIRMRQKGEIP

WSDNLYVNSKSATAFDVVT

>contig57693 Frame-2R|Blast-transposase [Phytophthora infestans](gb|AAT40862.1|) 1e-23

MSWGTLAARFRVLMQAEDILQSIVSAPDFLSPELSASESAIRTNLKAFVLNVNWKLTLEK

AVTILTPIELILYKFQDDHASISEVYFESKHLLTDFDAVFGLTTVELEYLKKVITEHWQY

VLSEAHGLAFLLDPRYIGKSMTRDYREQIEELIFTFPETDQDTEVHQERRQAMTEEYTDY

VMYAKNQRNNRTYKWEMLEKGTRTPLQFWQTDADDWPHLKSLALTLFSLAPSSVASEKTL

CKSILTQARRRNKLSFDDMRRLAFICINDSQLTGNRVTGEVPSSTLPDFAMESTALSPDG

MMMWMI

>contig58788 Frame-0F|Blast-cathepsin, cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|EEY57990.1|) 2e-51

MANGGIETTTTYGPYRNAPDYCHFHADNAIGTMKGFVNVTGIDAFNDALATVGPLAVSID

ATLPSFYFYGGGYYEDIQCKSDLDHLDHSVLAVGVTTHN

>contig01008 Frame-1R

MIGRADIEGSKSNVAMNAWLPQASYPCGNFSDTSSFKFRRSKGSLGHAFTVRIRTGNQNQ

TSFYPSVPHEISVLVELILGHLRYLLTDVPPQPNSPPDNVFRPDRPAEAGLGSKKRGIAP

LPIHGISKITLKVVVFHFRPKAPTYTTPLKSFHKVGLESSSTGSSFPADSAKPVPLAVVS

LDSRQGQWESR

>contig01642 Frame-1R

MEEEAAKLSEMQSEVESQMGKNTASSLNEMNGNGGASNSQPAQLDDTSVYIGQVDYGSTP

EELQALFQSCGTINRVTILCDKFTGQPKGYAYIEFASHDAVESALLLNDTMFRGRQLKVT

PKRLNVRGFNMSRGGRGGRGRGRGRGRGRGPPRGGFRGGRGRGFHPYF

>contig03631 Frame-0F|Blast-cGMP-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY54756.1|) 0.0

MEKDKFRRARKTRILDSKKDATTSTFVRFDDEANSELPTSINELEVVGSVMSDLTNTVRL

VEIKGSSPSVYMTLRSVNKQAIVDAGMQKHVSGERDIYVSLYEKNALVPQLFGMNSNDSD

IHMLYETQIVGTFESFLDGEPQGESFVRYYAAQVVMALEFMHAEGIVSRMLDPTNLMIDR

NGNLRVINLRLSKYVGRGRTYTVCGTPEYLAPEQITGEGHNICADYWALGVLMYEMLTGA

TPFARANENDLEILNDIASFQPEQLLWPQTASAELKDIISNLLSPNPAKRLGYSKGHTTA

CEVIMKHSFFAGTSWEATKMGSFSAPLEADAASEFKQIAASGSHDDLVIGSVYKGDSDWL

VDF

>contig05615 Frame-2F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72306.1|) 1e-37

MGKSTILSALDLKDGYYQVLMRESDVAKTALSTPSGMLWEWLVMPQGLKKAPATFNRVVA

HVMRHVRPYAPHYFDDVFVHSRAEDGLSAFDNIKLCYFLYLLKVFFISIL

>contig07806 Frame-1F

MVFADAVNTLESASLLGILITGLLLGLVHVLTGPDHLSALIVLSAGSSWRSCQLGMRWGC

GHSTGLIVVTVCFLALDQHLNMNRFGNYCDFLVGFLMMALGFWSLRYYLQLRRKLQLTNQ

LAQETTPLNMEGEMQLRRSSVESDTEVQKILHFHQLDHQVLSMSTDPLQPSIKTCCFGFV

EADIKNPRTQQLTAFAYGTAHGLAGTGGILGVLPAVFLNDWAKSSVYLGAFCVSSIATMG

GFAALYGEVTGQMSRFSDSSLMRVGIFSSCVSICVGLMWVILVSTGTLDEVFG

>contig08573 Frame-1R

MARLVPLFLVWAAIFAVILRSIRATWPPVSTNAVAPERNVAPTRRNSTRDNSISRRQRAF

EERSTISRYFSKLKQMFGVKKQLGLPFHPVAMLETYHLPTMTPTEVIKKQKLFRNPRNSE

QTRLEVELYDAYVEVWNKRTAYHQSGNAVSKCNVLSGLREVVE

>contig09170 Frame-1R

MLHTLKRYKRSAPLVGTGSTSSGAYDSARAIAAFRQDAGNGSNGAMDGTCGVVAGANARR

REARGPSPEENSTENSETTGEEGSSNTANSNASNSSHDVSMRAALAEQKYFGLLLQNFEV

IFESLHNKKVLLATLRKDSKAPDQLIADLHDDIHVLSALKKDFRMKLRRTIQ

>contig11306 Frame-0R

MQVTQFAAVYSFACSMAIVAALKTMTYPTKSGIGPWIDVDTPSDKYVYQTSRGRRWDLVM

SDEFNVPNRSFRAGDDHMWTSLEKPDGVNGALEVYSHNMTSTACSKDGTCYFYIKTIDEV

TKVQVYNMYTHPPSFEEVKFWYRGAMVQSWNKFCYQGGMLEVRAQLPGAVSAESGNPDRA

RGPSGKTTATRYYPTWPGIWMLGNP

>contig14086 Frame-0R

MKEARCQGNGRRWSPQCEVALIFTRIQTTPQSELLKINEQQIPRRRAHTSVAGGPPQDS

>contig15283 Frame-0F

MENFGYRASSHLTILHLRCGLARAAIHWMVARLLISLSPAMCHRTALRRYRSTYLPVPVP

VLNQSNSHTRR

>contig15364 Frame-2F|Blast-structural maintenance of chromosomes protein, putative [Phytophthora infestans T30-4](gb|EEY70359.1|) 1e-98

MGRIARLELENFKSYGEYHVIGPFHRFTAVVGPNGSGKSNLMDAISFVLGVHSRQLRSSQ

LRDLIHRAPHDVDTNERSAFVTLVYELGADEKPPSKSQAAQTLQKEVKFTRLISEKGVGS

YRLDGHDVSSETYQNQLKEIGILVKARNFLVFQGDVESIASKSPLELTKLFEQISMSDEY

KSSYEKLAIEKDTAEENTIFAYKRKKGLVAEKRLVKE

>contig15650 Frame-2R|Blast-ribonuclease, putative [Phytophthora infestans T30-4](gb|EEY56756.1|) 1e-112

MSTSGYYAVAVGRATGIFRTWDECNQQVERFRGCKYKKFKTQSAAQAYLDAFTRPQRESD

TKRPRSASAEVEDNGTLSPALKRVKIKNLVPIDMATQSWYGVARGRKTGVYQTWNEAKQQ

IDNFQNAKFKKFKTKNEAEEFVAKHGATTRRQEKDPDPQDPTTLVAFCDGSALGNGRRGC

RAGYACIFPHCEAWNVAKKLVEKGVTNNRAEYMGALEALKRANLEDPEQSQVLYIFTDSM

LLIRSMTEFLSAWIKNNWLKSNGSPVLNRDLLELLTAERGNRSIRWIHVKAHTHQEDWQS

LWNDVADHAARSAASSVRSD

>contig16790 Frame-1F

MDAKSNLPLVKRFTGKADYLALERDVSIGDELVYVNHTPTNNYSLIDIINIIKEMPKPIT

LRFRKPLKEELQIELPELGEGEYDFLWEFGSLGLVVGTSAEGMPYVRSFTGKGTSKQLSQ

VQENDEIILVNNRAAEDYGFHEIMRYLMNVPKPAVIRFCRSRANQNHASAHAHYTSRFSL

PTTSMASLSISPLAPSQNGDAPATRSMSVAGVHPQ

>contig17432 Frame-0R

MRNNSLDQLFLGNNLLREIPESVLRVKNSLTVLDVRDNKLQHLYGKIAELYRLKTLDVTN

NDLNDVPPEFGYLKYLNHLLIAGNPLRTIRQTIISGSTETLKKYLRTRGCPPQTVDAMQE

EINEISILRKKMELYEPTDEGEASNLKDEYLYRDASASGKLELIGKSLSQIPKQLCAADK

YRFSETLLHLNLSNNMLVELPAAVGDLKSLQTLAAEQCGLTTIHASIAMMSCLQCLRVSK

NRLTTNAVNYLLCKGAYASISSSLKEFDLRNNILSEIPQTLQRLKTLDTLLLSFNRIRTL

DDFPWSTMHQLSKLSIANNR

>contig17447 Frame-0R

MWRHVRVLCFLVGIPLSAATSAAHLSLKVSKESTDATSLTDSNSSSTSPGTVSAAPTDGS

LSTSAFVNSDTLTASNSSVWHMKPVTSIQARVQGDAPVWNKDAKMWLSMYGKTLNETYES

SLDTANTATVEGVLMYVQAEGINVNEHSVKCERKNKMQYIVFYEITIVQPSYGIKFYEKH

NPPEYGEFVAMDGGKCTDVGDALSEDCKVYYGLDDAMYIGPMVGCGLQTLDPRAPYPGNY

WFSYPGACAQELREDKTEESRALYPSGLCAMGKEPDGETCSFSYKILGYLDLDNLVGITQ

LGYKNYTDFCQDGGVEFKAKNTGSGFTVEESIDFWKNPSDQEANANRTSAMVKMYNDLVI

SGNNSNMEPLPDIKDLTSTNPNCYENSEACATTSYGCNRTLYSQICTVCMSNAKGCVAAP

TSFSFPKLTAVRPASSDSSLNSTETSDSSQLSCLMPMLVGIVAAFVGGVL

>contig22353 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59952.1|) 1e-08

MVINKRILVIGVVVLCAVVGAIIGVLVATSSNSSSTESSEPT

>contig24324 Frame-1F

MLLIILLSTCHRTHLGVKNVRHRDVKSTPALNTSATSVAAFLRHLGQLFPHDEIGALIKL

ARNN

>contig24593 Frame-0R|Blast-septum site-determining protein minD [Phytophthora infestans T30-4](gb|EEY56345.1|) 5e-24

MGQPVITAKNEHAAVAFEDAVARFLGEEREMKFLQPEPPKGLFTRFFS

>contig26717 Frame-0F|Blast-phospholipase, putative [Phytophthora infestans T30-4](gb|EEY68002.1|) 0.0

MSVAVAFASAEALPELTFIPCDSMQIYKQQLSEVTKSLAGLIGGHDDKNNSFQWDKEQIS

ALPREWVWQHICMLQDCGQLLDNALTLLRKKIEESVAVDVETLERKILHSNSSIDCSSSE

DLESEADVNYYDVEPVRGRKEAVALNNDVTERVQKALQDEEEFERFKANALEFGLGHESA

ENFYAYLSKQIPPPMLDAIVVDFARLLPQSSQRVPLLKAHHDHMQRKTARPSITKFRNKS

YSVSMTSKSSASSSVDEAGSDDEKGEEFPSTIRLRSFNHLVFVIHGIGQHIDFRDGEYKS

WNGETGIEGGNHAFRDIFRAMLETTFQNIPLALEMQSIEWHEDLHDPTGLDNIFDLISPE

GSSAIREFNKETLMDVLYYLSPRYGQLIVNSVTQQLNEKYRVFIDEHPGWDGKISIFAHS

LGSMISYDILTHKADEVTSNGIRFSGLNFEIDNFFGVGSPVGVMILARGDLIVEDGEFVP

GIKIPNCRRYFNVYHPIDPVAYRIEPLIKQEMHDRDPVQLMQFSAVKDQTFGQLQDSWKS

LTGPVHGFQYRHDYVTRRRKHEQGMMEVAFAAASHSSYWMSDDVVLFTIMQLCQPVVDTL

HRYMSAR

>contig26876 Frame-1F|Blast-augmenter of liver regeneration [Phytophthora infestans T30-4](gb|EEY69279.1|) 5e-19

MGIYYPDKPSPGYQAKAKTFIEALALMYPCVHCAEDFQEQITKSPP

>contig28636 Frame-2F

MESQSYETFSHYLRVSFKLPAISLRSTRHTHQPSVSDWKLAKRVARYLKTLKDTKLYMRI

ETEDNEMKLTSWNDSYFAANKSDLKSITGGVLTMSGVIVQWICKKQTGVSLSIIEAKNTE

ALHVGRGDAGFTGDDKRDWSSCDGA

>contig29796 Frame-1F

MKRKILREVKTISRMQHRHIVRYFQAWIESKSWWTSDEKEVYHLGDNVLSDDESEQLNVG

INDADGLYEDDSLSSDDLELLASADEDDWLGRIDTSAGLWSASRSVRRTLRSSSHSYQLS

THDHESENCGDNDFEWEALEEASMSSKDELSVTYCNETYRKTSPVLDKRHKFEILYIQME

YCEGNALREVIDKGTLWKNGDKIWTLFRQILEALVYIHQQGIIHRDIKPPNIFLDAEGTV

KLGDFGLAVRPNKVHEDDNNSIDKNTFENSATDAVLSDSTGSLAAELYGKLKVATLESTR

VSRLSKQSNNLMTITSEDVVDIAITAGVGTAFYRAPEQEREGQRYNQKADLFSLGILFFE

MWSPPFSTQMERAQALTGLRENHELPAAFDASDDVKKIILWLCDRNPSKRPDAKELLMST

LLPPKMEVEGTYLREALETLANPQGKFYGQLIDALVAQAPLTHIDYTYDHLESIKMRNYE

VQLRTKTFVRDTLR

>contig32095 Frame-2F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY57494.1|) 7e-76

MEKGVGVWLRDSETDEWHRATVVKLGEPRDQSTARRVTLLLTEGPHIRTEKTLEIDIHAL

EEEKVNDVMLANSNDMDVVEDLIQLPHLHEPGICHTLNERFKINEIYTLTGEILLAINPF

QTLGIYTDKIMRKYIRNGDKCALGHDVPDMPPHVFSIADKAYR

>contig33005 Frame-2R|Blast-betaine aldehyde dehydrogenase [Phytophthora infestans T30-4](gb|EEY54272.1|) 5e-17

MSGVGRENGLAGIESWTQLKSVYVEMNEVWCPYAK

>contig33544 Frame-0R

MERTPSLTEQMRAATRNIHHVSDNLVNLKLLVALTDKQLYGRALMLFYYVYVQLESTIEA

YKDYEAFTGLNELLGTIARADSIAMDLQFYLGEDWSNKYQPTKAVRDYIKHLKKLEEKNP

ILVLPYCFHMYMAMLAGGTMIKN

>contig33698 Frame-0F|Blast-alpha-tubulin, putative [Phytophthora infestans T30-4](gb|EEY54344.1|) 0.0

MREILSIHLGQGGIQVGNSCWELYCLEHGIQPDGQFPSDSTGRSDDSFSTFFSEIGSGKY

VPRAVFVDLEPTVCDEVRTGTYRQLYHPEQIISGKEDAANNYARGHYTIGKEVVDHVLDR

IRKLADSCTGLQGFMVFNAVGGGTGSGFGSLLLERLSVDYGRKSKLGFTIYPSPLLSGAI

VEPYNSVLSTHALLEHTDVAVMLDNEAIYDICRRSLDLERPTYTNLNRLIAQVISSLTTS

LRFDGSLNVDITEFQTNLVPYPRIHFMLSSYAPVISAEKAYHEQLSVAEITNSAFEPASM

MAKCDPRHGKYMATCLMYRGDVVPKDVNAAVASIKTKRTIQFVDWCPTGFKCGINYQPPS

VVPGGDLARVQRAVCMISNTSAIAEVFSRINHKFDLMYAKRAFVHWFVGEGMEEGEFSEA

REDLAALEKDYEEVSAETAEGEDEEIGEEY

>contig34435 Frame-1R

MLHVGQPSRTWTYHMRHSSRVMHQIRRRKSRFSQDVKNNPSRRMAFQRLMSRHHIIATRC

RSMSCLSLCLCLYGILQRVPSRIQVIKVD

>contig34480 Frame-0R

MEPAWWEAQAWYIWRGDGKQYPAVVYDPETEARIEVHPNDLLEYFMAHPLHVIDVTTQSV

CRQCASQNRTFKYCHLDKGH

>contig35384 Frame-2R

MINATRENGEIQLNAALKEMIKRFGVKESTSPKKKDDKINIKTEKKRGRKRKADDENAEA

IEDEEKNKKPRKKVEATCEANQMLADAFSELSGFEFKRGEKFKGGTWSKVAKAIRDCESE

LSCGKEALKLKNVGKSSAALIDEFLETGTLEKLKEYRAGNM

>contig37724 Frame-0F

MTMDCAIIHWACKLQTGVFQSTMEGEFASASYVGRELLRFRKLVRVVGFLRGRPFVHDGI

KPIRQPEPEENILSAKHVDLRVKFIRDYAMKGIIQSKYMES

>contig38282 Frame-2F

MNDDNGIDEHSLVKPRPVRIRYETPARGMGGKREIAYASLGKLIARLTDAHEYDTEFRDV

FLLTYRSFCSPYDFIKKLLKRYKAVLSLSSPVSAETLENTQRLLDQIALDEEENEQRASI

VTSLSTAKSDINTGMEANVSMMRLLSVLKYWIKESTFIEQ

>contig38714 Frame-0F|Blast-structural maintenance of chromosomes protein, putative [Phytophthora infestans T30-4](gb|EEY68020.1|) 0.0

MQQEQRAAKEQEMQIEQEIEQIETEIEVLNEQREKKMGKEFQQLKDNVEKIGKEVIKFTT

KLKHCRASIEQQIIAETSMNEQQTETEQTMAKLANEIEKAKTNVDRVEEAYTAKETAANN

YQHQIQALNAGMEQSGNSDESLSERLSSKQRELQESNTVIKQINLKLKHMEENIKNKRKE

IEQTRTNNRSMDEERKHQVTELEQLKSKVDHLTCSFNPDEERKLHERVQGLQEKMMRAER

EVDEISSGLSSRLDFKFTDPYRNFQRESVMGVLANLLETKNDWSALALEIAAGGKLYQIV

VDNEKTAKDILKFGRLMNRVTIIPLNRISRKTVDSRKMDKARQVAQQQGCKVWEAMELIQ

FKQELLPAMEYAFGSSIICETSELAKNVTFHRDIKIRTVTLDGDSYDPAGTLQGGSAPSS

G

>contig39371 Frame-1F

MKKNVNGIMNKMTREKFDRLAGQLTSINMESLEMLQTVIKIIFDKAVSEPNFCDMYADLC

VHLEANWQVWSFLKIVQNDDDGMFYWTAMSDSDSEVVGPFDDGTSALESASGEEFEPIPA

PINIKLSEVRVRDHKFIKIWVAEDPKAPRYYWSGQDLDDLGDDQVLNGPHESHEVASRVA

IKTSSFKRILLNACQEEFERDNIYEELEQKFTKDKEEGKITPQMEAEYEEKRLIMKLRML

GNIRFIGELYRKGMLQERIMHECIMKLMDVRPNSEGLLACLHPNNPPDEESIESLVKLLT

TMGKDLDKHGAQGCMPSYFRYLEAKLVKDKRLSSRITFMIKDVIELRQHRWEPRRKELKQ

KTLNEIRKEAEREARAPPSSAPSGGGRDRDERDHLRSDRRTNSYRDSYSNSRSTMAPVYQ

QSQ

>contig39667 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66989.1|) 1e-136

MLKPCPRITLQSPFFLISSDFAKLATSLSLPKLALEQLPFMFPQVAVSSLFLQLFGNSHF

PASVRNIRCKAVTVVQLRPLNMSCPTKDEDLPPPSELTCVMVLTGKRFLESEIEFTIQTD

LFDDHGTVWQSVTWFSIPYKQKMLLVPTSQSSFTFNNSVAAHAKANLWKETFKCSERNAT

EFKDVSVVDMTGTRTNEANAAPLLWILARATGMLQQQKRVPAQPLMCSCKFDEDLEVVSL

NENLELQSWTNEEYLKQQTQPECVSFAVDTEGVRVMTGSLRTVGWNFSCDRK

>contig40696 Frame-0R

MTRQVRRLLQLVAERSYRKKLCLIMVIVALSITDLLVFYILFVR

>contig41211 Frame-1F

MANLTQCLVSEAFTESHASDDNKQLPLAVTESCAMTSVATDPAPETRQSALQTTLNVASS

AASLVLYPYVVASKAVVSATSMAVSAPIHLTYLVHAKITQIWEPRSQEQALNDKLDMKEE

RSSTSSNRSDNEMELMLIESKHVLTSKSTVYQLLSLPVRLVHT

>contig41769 Frame-0F

MFCGECGYRWEPDEITNARFCAECGASREDAPGPAPIAPSPLPASTSSFLASPSITFSSH

GTAPTAPGSSSYLFKPSQPSLSASSETYEAPAGAASFNYSTPSARKCTQCGEPFGDSTAL

FCGECGAHRPKENDKDLFGAASSSYTAPAGSNASVGTGNKVSLRDFGERRLQPAEYVSTE

SFRCLYYTQRSVRSASYFRFVRSLYLATDPSSFG

>contig41992 Frame-0R|Blast-3-oxo-5-alpha-steroid 4-dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY67325.1|) 1e-147

MCPGFSCVSREPQIFTTMLVKVIRSGKTAKDYGSVEVAGSDLTVGQLKNAFEKHARVSRF

RQNFKLQQSDKTLTTLSEDTKLLEDYGVKDGSTLIFRDLGPQIGYRTVFVAEYLGPLLFV

LGYLARPAFIYGKQAGAQPLSSTAMLGVAAWSLHFLKREFETFFVHRFSRPTMPLRNLFK

NCSYYWSFGAVVGYPLCHPMYAGPTSTLQITVGLVLMGVSELLNFCVHMQLRNLRPAEGS

KERPIPKGPLFALVSCPNYTFEVLGWVGFSLFTQVAASYVFTLVGFLQMADWALKKHRGY

LTTYGDEYKKLCRKAIIPFIL

>contig42193 Frame-1F

MTRQLIHREISNMSGLEYHENVLRLDEALELVQESKCTTFLVLELAGGGELFDRIKLDCG

INEETARRYFRQLISGVAFCHNSGVCHRDLKPENLLLADNEDHSTLKIADFGLSAIFAVT

ENSANGSTPENGVVEPAIRRLRSVVGSPHYVAPEVLMDAGQGYDGAKADAWSIGIIVYAM

IAGNLPFGKDLLKCVRYDRFRKWSYLTKYSDNEPTKNLEFPTWFFPAHFSIELKSLIAQL

LYPDACTRLSVEGAQCHVWVRGEKLTKSCPVMLENDEQRRNDLDSNTPAVIPPVLYPTHR

NHLSINTLQDNFERGQHMHASQYDSISPQAITSLLAKSPCSHSQAFRCPASPQQAYCVNK

HLAGVVGYMPSVDETSS

>contig42863 Frame-0R

MTQYLEQALATGGALAEEYFGTDSSAFSSVTFRFRPDAPPPSAELSEPPTTNRLAMLRGP

STSIAESEVSECDSITDGNEDSMYQEEELRCVLAVIRHGDRTPKQKMKMNVCHPAFLQFY

DDRLRESQQQYGDGNDTKLKKKLDIKIKAVANLERLLQVSNDLLQKYENRDPTFMNFLEQ

REVEFGEEANDRVKGYRTLRDVLQRWQLVGINRKVQLKPKDFVTVPLEGTDENGESQSTR

RVSKLLLIIKWGGDLTHTGEEQAESLGQKFRRMMYPGGAGGLRRLHSTYRHDLKIYTSDE

GRVQKTAASFAKGLLELEGDIIPILVGLVLKSKDADSMLDQSGSSAQEIIMRVKQRLHSI

IHREDHCSELIASHSRLIRSVALALTKVDQPIRKMGIMHKLLHSLKEQLTRIIQAKAQHK

TEIDRWQQEKADAGRLMTPTISRSASVNELSQPRSRHGHSYTPRQKHSEGSNISSNAANS

SVSLRKFQPQVPLSPEEIQYPEPCGRETLEVMRERWAKLYRDFYVKKRDTYDLSKIPDIH

DCIRYDAVHNAHLNLTDVRELLEISSALSHALVPQEYGINADEKIFIGSAMCRTLLSKIN

TDLDLARDLQPDVLKDHNTHRLNPSYAKKIKSAHRSVRTRLYFTSESHLHSLLNVLRYGR

DECVIKSPIGEESRKWIEDIPELCYMTHFVVRVFERVQYALTDPQRFRVEISVSPGADRD

PLVSDPEKQLEVAPLKIISHEGLTCQELVDYVADCIHYGEQNEINEMISRAVEVKDKAKS

SFDGSSSNDSRDITPVKRSNYSLSNNSNDSNFGSDI

>contig43716 Frame-2R

MWLPICPAMLSQGQLKLSHWRICNANRCVAIAVLELKGQLYCASSRSFINPDASKSDLRR

RKRRSEEKKQHTGCDGLVNIGITCYMSLILQASAHNPMLSLIFLLQRVTACVSHR

>contig44656 Frame-2R

MLEIHGPNGSKGPKDNDVFLRQLSSRNSIDCRHALEEVEKLVASLLNLPLSSSLTKDTET

SSALQTSTYMR

>contig46005 Frame-1R|Blast-40S ribosomal protein S21 [Phytophthora infestans T30-4](gb|EEY55519.1|) 7e-37

MQNEAGQSIDIYIPRKCSWTNRILAAKDHASVQINVGRVNANGIFTGESDTFALAGYIRH

HGEGDIAISDLVRQADAKN

>contig46544 Frame-0F|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY58077.1|) 1e-156

MELKTEDSAKKAVAASSGALITSLFVTPLDVVKVRIQSQMHITSVKPLSDLRITHSSTGT

FVATAVEQCRCRSRCVCNRSITRPVEKLQASRRGCCALASMRSSCTRAVAPPLLQSTSHA

LRHVFQTEGLKGLYAGLSPAMVIAVPSTVLYYMSYDFLLHEGRQHLAQVEGIVPLLAGTT

ARIIAASLTSPIELVRTRMQSDAGGSSILSTFRSAVRRGGYVSLLNGLGATLARDVPFSA

IYWTSYESLQKRLNVAEERLPRAQRAFVCGAVSGAIAATVTTPFDVVKTLQQVSMTGQGS

HPSGMSVLKQVVASNGVSGAFTGLGARLARVAPSCAIMISCYELGKEKLGIA

>contig46698 Frame-0R

MVLPSNCAFIVMMAAPTQITIKTPVNTIADCAAGAVILNMIESVRHSSSGPHRSQSRSAF

KVSSDVLLGIRTTRSLLPTSRKSRRIVVDTGSSRVFSSADGRLILPETSSTSGASLSFNI

AARILRIETRYCHI

>contig47095 Frame-2F|Blast-glutathione reductase [Phytophthora infestans T30-4](gb|EEY60687.1|) 4e-12

MDGTCNNISCDSKLLINTAADMSHRLLYKYLRCGFEDKSRGAFLGKRTHLDLPKPKARRD

DFIGPSTKCM

>contig47684 Frame-0R

MLLLSMRHTGIMAVAINTWSIIDETGSLMYVTRSLRYYRNAQSSSLVCLCTATEIYRLSC

RNFKR

>contig48670 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55642.1|) 2e-07

METPSQPEFDQDNLNEDIQRMRTLWVNE

>contig49185 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64829.1|) 1e-45

MNKLKIMQTSQVSSTPTLSTLSATLLASLPTNTSEKNLCDVDYANFSLALKNLHIRAHEE

IAELVTVLHQIEPSDSIESSADDRDTLAVHDAIKLFQRQLALEGEHFSQLESIVRPRLSK

LQRLQSRAKYLEMAVEVEHLSHEANKQALKATPDALEALMRFVTCAAAISEDYLLIRREA

ARRVEDLYGTFRQHAVEKLQLALVK

>contig50073 Frame-1R

MLWNAEVGFGTGRSLVLVVRVKTLDVKYRIRSSSIVYAMPWRCTTRNGPMFGAHNLVLAT

TFGTLLLRAYTCCCKAQT

>contig52039 Frame-1R|Blast-SpoU rRNA Methylase family [Phytophthora infestans T30-4](gb|EEY65062.1|) 3e-87

MDPLALIPMINVLKLTLSQLAGTLMKAFTDATHVDTLLETVWTAYNDSKAKPDALTRAVI

LCIFQPAFLLQTELNGTMKRWIARFIGFGARHRPNVIFHMACRLCQTWRAHPLMAISFID

EV

>contig52167 Frame-1F

MNCQFGAHVLHVLFTPFGVVSALFDEGTLLREVENTRWKAGDTAYVTSKSWWTQWLLYVQ

SCHYNPDNLHNQSNSNLLGGQETGKQQVHENDLARQQQLPHLVVCHPRP

>contig52471 Frame-2R

MPLVTSVLGAPEMEEQQIAQRLARRTGRQCFVSCQLPDHIPELSAFVEKQIIKRLTDEGI

LTC

>contig52949 Frame-0R|Blast-hypothetical protein PITG\_08805 [Phytophthora infestans T30-4](gb|EEY56044.1|) 3e-31

MVVHEAYAVAKSVNISLDCSQDELVDEIFDVARNTGSNVCSMLADLRHGSRTEIDALNGH

IVAKGERHGIPTPVNRMLMLQIKALETERTRIVKEV

>contig53652 Frame-2R

MIPSARSGTPPIMYNSTLKSVVVDRLCGEAVLRG

>contig54802 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62334.1|) 2e-79

MIEDVYSSLSYCNLHLVADASDTSLNLATKTVSHTSLSNHYIQPVATLDECASKVFPIVN

MIGPQLYSDQFLFVKLLRIASKLVDDQTKKCISLTEKSEKDNACFDKIKLLLATTFLPAM

SLQECNPSTAFLVWDLLKGLQCEERYRIYLQWFEAYDKYPELRLKEAEVVQSTRGVMRRL

TADRAKLSARSLTHVAHSNPLIVFRTM

>contig55041 Frame-1R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY57349.1|) 7e-31

MRKASADTLKSNEHLAVIQSELIQARSDKDAIKIQLSQSQALVQEMQSKIQELEEILNSQ

LKDRKSFEQQLQNLQEMTQENMEASYELQ

>contig55759 Frame-0F

MLPGVYPRILGKNALKESIVRHI

>contig56530 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60832.1|) 2e-08

MSNYYGPSSTVSSSGLPKCRT

>contig56794 Frame-2R|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 2e-19

MYLSNTYRSIQDATYTFVNCMGMQLLGAFFLFFVIDRIDHKRSLCCTLVPVAALIFAFGI

RLAR

>contig57054-0 Frame-1F0

MVATDAPALAARALTFDNGTQSDSPLECSGFFFSSSLF

>contig57054-1 Frame-2R1

MGFNLNSDALDLFLALHLKGSVVS

>contig57270 Frame-2R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY61071.1|) 8e-09

MMRSFYRVFSLPIAPENGEQTLAKCLETFRQSEELTEDNRVFCDVYCQKKT

>contig57692 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69693.1|) 3e-07

MISLLLKKGVQVNLCELRQRTKRYKQNITASTFGGLMHVFGL

>contig03092 Frame-2F|Blast-demethylmenaquinone methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56017.1|) 7e-55

MGQVVVISAPTGITSAVFGGLLATAAKARNVAGIVTDGRVRDVQALCRLNFPAFASGTSV

HGEWGSTAIGEVNCPIVVAGCVVRQNDIIRGDVNGVIVIPAERAQEIVMRAEVIEDQDHE

IVQALNEGLPLQRSLYRVRSSRDI

>contig04383 Frame-1F

MLPGAGQVLRPTSPSQTTSTSRFKTNVRENPVDEGTKTDGNTHDELVLSAKKRRRLAS

>contig04417 Frame-2F|Blast-3-mercaptopyruvate sulfurtransferase, putative [Phytophthora infestans T30-4](gb|EEY54644.1|) 8e-82

MLFHPRRTPQPHIFGRLFSYRLMSSLSPLLSTDEAHSLFKSSKRRVRFLDASWYLDKSRD

AKREFASERLPGAQFFDIDQISDSNSRLPHMLPTQEIFGHAVMHLGVENHDTVIVYGGKH

CFSPARCWWTFKYFGHDSVYILNGGITKWKNEKRDIETGEPHVLVIGAPYNAQPNKALLA

SWKDVLDKVDTETQIIDARGAARFYAQEP

>contig05836 Frame-1R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY64543.1|) 4e-36

MKKMGLKAYRLSIAWPRIIPAGIGKVNEEGVDFYNKLIDELLANDITPLVTLYHWDLPLA

LQIEYDGWLGGK

>contig06473 Frame-2R

MVERKVILLWAAFVVSVLKPLAAEPNSLHGDRNRPDKRPLESTDPLAFEERNLYSWYQKL

LGKTPEVVEASVNIPKKGDLSKVTKVTEQIMNQEHHAPIDSTATGLNKLIVKKTPTRFDD

VSAKVQKMLSIQNVKDTKSVKAVKNGLSAAVTYLTSTISNAKTFAADVSMVLLAQAKGAS

KEKTTADSVGLVEKYLSGPLKRMKLLSWGGETEGKMPPSANLVASVKKSKVTTEPSKKTL

ESTNGGSSLLRGRKDPAELKSEPATGASTSAKPPLVDPESTAKSPPVNLKSSIETPLSKV

VKKPSSWFSTRMKIFYFVGFLAILLVFAAGFAN

>contig13871 Frame-1R

MVYSPRFSLISAAVAVASLKMQQASAGSMYYGAHTVSDATNSIGPNFPGRGGEVDEKYTA

VEVTIDSTLPVLANIPSVPILYPELLSNVTAPPKEPVSNVVGNPVVAEKPEKTPDEYVYT

GSPPVVLGEHASKDCATGWENPLAYPPKHEKSGLTQSRGVSQDRRLNTYSNRDILSLEWY

LQRKLELNWKNLPTEGVMVKAPWPGPYWPDFQDSINVEWARGQPSAAAKYAMAFNYDVPQ

FTDGISRVHGIKSEGFTKQCTRNSDCLSISNRTFCGVPKMETSGWCIDSWLGICHAWAAA

AIAEPEPNCPVTHNGVEFRALDIKGLLSILYADTAVGTVFTGVRFKHGTNSTDTYGRGVD

PIFRDLNPGFFHLAMTNVLGIDKKSFIVDVSADLEVWNQPVRGYKVYEQTEMSLQEAAQT

FYGLKEYPWNVEAKSIVFVTARLSWVDSTYDDGNLVDTGIVDRFTKGEWYYYLLEIDASG

LIIGGEWLFVSNVKHPDFLWLVASKPAPNAVTRTGISYKEVSMLLQKSVECSG

>contig15385 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57933.1|) 1e-139

MEVVVLGCGPSSSVPSMRCIVNKQCDVCQEANANPLSKNRRLNPCLLVRNLKNGTNLLID

CGKTFREAALRFFPTIGVEAVHALVLTHDHADALLGMDDLREVQAMVETIDPLTKEVYKV

PSVAMKVHCSKRTSHDVMAKFPYLIDTKPSTVPIETIPKPFRWTAKLQIDTFCAWKSFQS

CGLTFLPFPVIHGAGYTSFGFEFGHEVSVRFIYISDVSEIPEETQKFLHDVHKPRIDVLL

IDALYLDKYHSTHMSVQQVIQEFASLKPKRILFTGMSHEFDYPKHSVELPQLGTIQGLHL

EMTYDGLSIAFS

>contig16362 Frame-2F

MLRRVLLGRSLQALAIGRRAAPLVRVFFSSLPEGVSPLTMPSLSPTMETGSLSTWLKKEG

EEVNAGDVLCQVETDKAVVDYEMQDDVVIAKIVCPEGSADLPIGTLLAYTVEDLDMYKSL

LDSGDLAKLSVDFNIKPQTDPETASVATTVFPETTHSDRVPLIKFLGKRSLLPEYNHPPP

ESLTKSDPEPPTSQPVAVTTDVAFKDVPLSNMRKIIAKRLAASKQDVPHSYSSIDCEIDR

MLQFRKQLKAKHEVKVGINDFILKAVALALRDVPEANCFFDDKTKRVQPNSSVDVSVAVA

TPSGLITPIVPKVDTLGLSGINKIFLEIVARARQNRLKPEEFQGGSFTVSNLGSFGIDEF

RAVINPPQACILAVGGGRKEVLPPLEIVEGISPEPRIATLMNVTLSSDRRVVDDVIAGQF

LQAFKAYMENPELLVV

>contig16432 Frame-1F

MIQGRGVFRSRSGSTDPPLASTNAVTTREFLPDDPKPKVFVDYAPRAFRAIRLAFGLSDE

KYLASFRTTAKERISAGSSGAFMFYSGDNSLLVKSLKDKECRALVEMAPAYARYVTANRH

SRLIRFFGCHRVRLYGRNFYFAVMSNVLHHEHHTATITEKYDVKGSWVDRRARRPQRGDR

VTCAECDATYLFGIHDESDEFRALADTPRDLTNAFHIHRPDVVLKDLDLCRSFDLRRHVA

EQLHAQLVLDCEFLRDLGIMDYSLLIGIHKCHLRPGEVDGKEFPSRDIGESGMNLAPLGE

HEVYYVGIIDILQQWDW

>contig18364 Frame-0F|Blast-cysteine dioxygenase, putative [Phytophthora infestans T30-4](gb|EEY64224.1|) 6e-07

MDAATMDLAQLVEKLERELEHDPEIAIKHKIKLQKIL

>contig19477 Frame-0F

MSDSQKRLRSTESGKSINAAEMPCRNGYTGFTVPKDNFTIHRIPVSSVTPEEFHSKYVCT

RTPVVLTGALLDEHFTALRKWSLSNDRLKELMGGGDTKLAIERRGDLLDNFGKGIKVEMT

FGDFLQLLEAGNEMHYLTTQEVLNDENGRPEVMTSFMKKLQPDFPLRPKLLGHLIPQNIN

LWMGSSKHATSSGLHHDHHDNLYVLLRGTKHFRLYSPADATNLYPRGQMSQIHFNGLINY

VGKETTPYGADIVAERETLAAFETSAAEWELAEAEKAMEKGVPGAVARLQAAEDRLEKAM

LHVLHIDKNEFDEDENVENGTFYFEESDSEGNDDSEMDEVDTLDIKEHEMKTFKRQVSEV

EVTYPENFSQVDLSRLSGSEEAQQELHAEYPHFCQAKAAFCELEAGEMLYLPASWFHEVK

SLNSTQNHGHMALNYWYHPPDQLTPEFYASPYSSPLWQLDWEERFVSNKEKGYL

>contig19558 Frame-2R|Blast-nucleolar protein 10, putative [Phytophthora infestans T30-4](gb|EEY53610.1|) 5e-75

MFDTRNQQRVGSLDIAAQYATNSNKQFEVTALKFDDDGLTFGVGTTEGQCLLYDLRSSRP

LLEKHHQYGLPIVNLQFHDYARKVVSSDAKVIKIWDRRDGAVFTNVETPAEIKDVCVVEG

SQGKSGVLLVAGEQERIMS

>contig21504 Frame-2R

MLIAMAKISMPAYDNSMQHTSIKTLCLNMPTRSTIGLKSLLGDDDMDTKAEKLVLRTLRR

LYCCEMALLM

>contig21669 Frame-2R|Blast-metalloprotease family M20D, putative [Phytophthora infestans T30-4](gb|EEY53333.1|) 1e-111

MGLYVSEEGLPLMAAEDFSYFLQERKGCFFFLGTKEEGDSDKLRALHSDYFDFNDKALPL

GIRVFMGILQARLKCELYSMEELQAFQMAMERILVNVSVV

>contig24653 Frame-0R

MDNVVVPLAGFPSLFSIPLAGFPSLFSIPLESTRIASVGLNCFGMSSRKASVILQLPASA

KLIDSGIATADEIHPRDLLGTTVLANWPNLHEVLVVGLSTLCGEYRLKASKLLHKNSRRD

ETDIVFTSYGPDEKTAWAYYAQTEVVKFLSGRGLPGSGGIDLGVTGITIVLHVLPLQGMI

SNPRTGAIEKKFGETEALVPAQLTIRNHTLLDARFEEKGTMLLNERFPVDSKALITRGKW

LGCTAIVLNHDEAEHSVSVHVNTIDREPPFGYVIAQKLTDRFFPGYHVAQKLGISASTLG

LLTGSVIIKPKGIDIGLNLRYRKELLLPGYCRLVSRDSVSSSEDAGNVWRKGDIVKIVGT

SSPRALTSDSSYKSPGSTTAWEYTERAVLLIASYQKEFPDVIQRFNHLPFATSYQGKDVF

GIHETERVEVKAEAIKQWIEQQRLGANEHSKHIPITSTYLGVHAISAMEAAGTLRANERL

KAAENHEHAPIVATIRAADLFRPNPLVNQDLTGQEVSLRASLNQGAPVLGDRVINISARG

VPLGHRGTVVATHVSSKCVEVLFDESFTGGEALYGTRSLDRGKIVAWNNLLCVSIPPNKL

HETRNRTATVTKGTTHFHEAMPQRASERMPAISNNRRGLKKGFDKAFVKSMASVVPPPVP

SVTPVPPDVQKIQKLVQKWRYDGEVATLESAQAPAAASSDFMLSKPVTEEPLAPSVEAFF

SAAATPSFTHGTMDPLMHLLPHMNAEIPCQDSSFLPPTPLLTAPNGYLASSSSEYYPTPS

VVPNQQQTQLFQMPDGSYAPMYSLPTQYGFYASSHAQVLIPLSEEYPPEFEPSCAANNAG

KGQHFRTGTGRANARSKDSCNNTPTTRMQNEGHKMWKPKHKNETKALNLLLPSQVLRQQK

P

>contig30630 Frame-1F

MYRQWLFKGPSKRLESLQLLARVIIWLQK

>contig30645 Frame-2F

MSKACTLENGVLNLAVLREDSRRELFSILDSIGKDICLVLDPELNGPLNHVLVDGTAVLK

NHGVKDFHAFGKTVKTSCEFVLFLIRPSVRAVRYVAKYVRDLGADKSASFKKRFHLYYVS

RRTLVCDEVLKKEGVFGSISVGEYKLDLIPFDDDVLTLELDACFKEFYVDGDKTNLHTVA

ASLIKLQTVFGMFAHIKYKGTMAKVIYQMMAHFRREQEVAG

>contig31659 Frame-2F

MRYAHAWLLKNKKVTGEMQDFKKKLELIWFGLYRRGARNDSSGFEHIFVGEQKNGKICGC

HNWLQVYNEERKGLIDYQGYIRPKQRRRNFMESHNKEQLITFQFHWEGKIKLVSTSLVGV

SPEFEMALYTMCFLNGEENNHVHLGPYLVNIKCYAFACGKDTKIGTAYPEALPLTEAQAA

TKIAAILRGHLTRIHNPHIRRQTRPPPSGAAWGPPPGVVRPNDTRSSQKVCTEASRQHAT

ASASIIADSELTGAWAQPHKW

>contig31721 Frame-2R

MLPYERVLGPSWSLVELRKFYVLLKVHGRQWDTIADSLPLRSAAMVRGLFEMHRRYLSLP

EASVEGFCAIMMDHFEMQNELLKRNSMKSSWVKEVIVMNVKQAIGDGLKLTARSRKKRRL

ENLMSTEHLATLQSQKELDQLYCEQRSLSHKKRGRKQRHPMKAIMWLEYGQKLIHGARFR

LPWYHWFHSFSDVDFFQENEFVGCLKSMGLEKTKVATRSIWSSMRASMGRPRRLSPLYFA

QEKQKLQLFRNSNYARDPAQL

>contig32399 Frame-0F

MPNKLFTRHSEDETMAREKFCGPIRIFWYINGV

>contig33103 Frame-2R

MLRRNLPSQAGVFRAISTALTKIRICHTNPVSCTDRHNVRPFSSCFFTRALIRASITTFP

YRWFSSLNA

>contig33712 Frame-2F

MSGGGAWRLKFHSLQSYANKTSAETCCISLVFLCGTIFSFTGFVFL

>contig34098 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64013.1|) 2e-20

MFKEVLANDHKMNMATSEMQPLLEELRNTSSRVIHKRLQDVAEMVAHLQTKWQ

>contig34137 Frame-0R

MRAKYSLLRQNDTNLEGAPIRDILLRTFVANGRTITSNENIRVWAATQFNSFCSKQIGQL

QFDIHGSYSLVNI

>contig36254 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64898.1|) 2e-09

MQVVMFLMRVIMSVTCLLVS

>contig37925 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67222.1|) 2e-19

MDLVSRLLDYIATFPRHEDENELKSQLSGCTQKDLRAACTSLQLPVPKKSSKKSGYITTL

VSYWKGDLKP

>contig38397 Frame-1F

MQNRRRQQLWRQSLSDREKAKILLKQRERQRKRRQTLDEDERKHLRELARLRIGRQRRQL

RRKQLLEDHFALLPVQVPLLPPSVAEGDRLPCLRLAPELPTLRQHQEQQREREILNRLVF

SSSTQTPPPTERVQNFQIEGLPLLPHLSRPNSSALLHPPLPSALFQTSGTLLKTKGALGS

TMSIGLPSVARAVAVVASRPPLSSPIMSSVSLSLPAKALGALPISQQQLLPRMPIVLPPA

HRSLPPLPDFLNSREAFNPATASASTRSRLLSNTNRTLFPSIIDLPSSYTDASDLNLLLN

HEKCEYTDN

>contig38780 Frame-1F

MAKIVVQTAKEEVDLARPNGVFGIPSGELYEDVVVCWAFLYLEGQLDYYHRVHALNSLEG

STMTKIYSIAPMTWYLGDYATSSSDRVDVVSTSKKTMNHWCLEDACAEVLWILLAMQWIH

IDSEYSNSYV

>contig38920 Frame-1F

MTATAFKIKECIVVIAIIDVLLKVAAISARCYV

>contig39682 Frame-2F

MVFFPPVPTIINSIMLRRVVLSSAARVTRRQIRCVSQTPIIYADNKPEENTATKSEEMHP

LSETEVLQQQVEQLTAQNKDMNDRLLRALADAENVRRISRVDVTNAREFAISKFAKALLD

VSDNLKRAHESVDIEALEVKKMLDAIKVLHEGVVMTETQLQKVFREFKISQVGAVGDKFD

PNVHDALFEYEDAKMEAGCIGQIMKTGYLLNERVIRPAQVGVIKAPKTQ

>contig40310 Frame-2F|Blast-regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4](gb|EEY61006.1|) 7e-78

MVVTTSGELYTCGWGEHGNLGTCGYNKSCNFDKTRVFYTFK

>contig41137 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY52901.1|) 3e-08 NOT\_ORF

MSGLVHREIYNKLPTSD\*KTLLSSFTLHLPHIPVEVW\*LNCRYRPNLRLCSLSISTIPTF

WIESLPIFFIILDAHAQKLARFVLGPLSPA

>contig41902 Frame-1R|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY59571.1|) 7e-70

MYGGRMDWMNHEYGEAVVRHLEKTQYAVFLQVPSSGHQVFMDNPKDFNQMLYKAVLDQER

AAA

>contig42253 Frame-0F

MPSRLEQTRSICNDARVTTRDWQTISVHAQIASVIVTLTDKKQGNAGRFESESVARITLT

RIGLEASWALQFTAVKVNLMGLQVEDLLPKSK

>contig42950 Frame-2F

MAPARSVKAFNPAAAFAQRFQASQRPPMPSSNSGSTKSNDTAEEDDDGAHGRTTEPSLKK

VKPRLSIDVARASAARRLRSSGSNETLAGRGSLDVFLNEIGDVGRLSDLKMDGFQTLEEL

WRVSGDMDRLSL

>contig43254 Frame-1F

MSSSCATDCSFSATFTRERHKDQLDQWSIRVIQEEHKHEPFVASTVHPRGRTLMEEPRQA

VLAGGLQAGITAGRFIASLRQSGVAGVIARDVYNIRAHERHRVLGGRYPITVLLDSLAEN

NGTNNNAPYYTPVDAEQQL

>contig43719 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54343.1|) 2e-55

MMEQVRRCRTKWVALKTSLEREILVGDARAGKASESWKDATRDEQIERCVERADRNGRHL

AEAQRTLAQTEAVAENVANNLLQQRNQLEHTGLNVAQIEEDTYE

>contig45630 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54340.1|) 3e-50

MFLVQPLKTHPSLQALQDYVDEEAKALDKRLTASFAEKVMYVPNAESFIPLQLRATMGWL

SIDESIAEQLHRRLYLNRCKYWKSEYTHRHHLKGGRQVKKEQQRRLLLNFDQNAFEEQRR

EESLKMWNSSKRTKLRDDEISLGIQMSASDALVTWRQEPIGISTWSAHTNSH

>contig46103 Frame-1F

MLKILVSRYANKLGTSLAQEYIRAALSGLHRVLQFHRIKLLFAINKTFLETLSLDSSQLG

RLNGMSYEAVLFLLDSCCKMNTDEESHGAQDSCDCKGDGLEAGQLLEILLGIYATIRGRV

LLFTKPLQRDG

>contig46280 Frame-1F|Blast-proteasome subunit beta type-3, putative [Phytophthora infestans T30-4](gb|EEY54548.1|) 5e-50

MQAQTVAMDFQKVFRVTDKTFLGLAGLATDVQSLSQLLKFKINMYKMNEERDIKPKTLSA

LLSNMMYEKRFGPWLVEPVIAGLTEDNKPFLSSMDCL

>contig46712 Frame-1F

MVKKKGKSKRLSLHKKYKIARKVREHKRQERKAEKLGQHKKKKDPGIPNNWPFKEELLLQ

VEEARVAEIDAQREAQQQRKAEKKKAKQLATLQRHNDVTPLTPLNVEMQAKKDLKRAVQE

ADLVLVVLDARDPQGSRSLSLEDGLVAKGRKKLVLILNKIDLVSAETAQKWTMYLRRFHP

TIPVRALNMKVSESTKKTRQEKGHQALYDRQQNLCGMRDNGQVQPLRLFLDELANKSSKP

IRIAVIGYPNVGKSTLLNSIKRRQVADVSSNPQSTKTMQEIRYGEKIVLVDCPALNPDYS

DESSAVLRHGVAGVFVDDPVPVVKQIVERCDASNLMQTLLIPVFRNYEEFLVKLAVKRNM

LRKGGDPDILMVARTFLQNLGKSVYSVSCQPPAKSKSRFEVPAWYKELDLAKLSDAETLL

YSSNPKGHKRVITIKAAPVSHAAGETTEYD

>contig46873 Frame-0F

MKYFSLGLVIWGAILSLTAAKSYYSHLDCLTQGCVGPRIYCDSSTGVCRAATSDTECYNA

TVARFQDECDKGYKCVDKLCRVAAQPVDNRKCKTSCAAGLLCENGHTTCRGPSYKNECFN

LSTGFFQDGCTKGFYCSFNKCVDISLNKERKKHAFR

>contig47610 Frame-2F

MIYPHRYISPINVNLDVPVTPSKCKKVPSQPICSPSANFTTMLQSRSSCSIEPRPSRANS

LLLDLLELPLAAADPNSDMLLKCELDSVLSNEHDTPTGAQQRIFPLPYGREHIPDSNKQS

QDLQLPAEAVSFPAALFTSTTSAATSASRPSST

>contig48013 Frame-1R

MVRSTSKGLTSCTVRRLMLLAVFALSACVATLSTSPNTMTLSSYRHLKELPDTRRALRFP

KTGSIRTTTCSKQWLNSWKLAF

>contig49300 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62398.1|) 1e-103

MEPLSKVHAELVRLIAELKAVFVDHGLTDLK

>contig49425 Frame-0F

MSQRPTVNMEDLQSEIARGSSPILHFPIAPGCFHPTDTMRQKFAQIVRKQVDTMLHFEQQ

HY

>contig50315-0 Frame-0R0

MKCRIKSGMPALESRIELYPSIDLTFNRKNE

>contig51312 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58093.1|) 1e-80

MGVVQSAKCVENPTVQDVLTHIAGYANVPRKKHKFINFVTNSLALRDTKLVEKAWSIYET

SFNALRQEDSATATIEGASIQKKRSSEETTEVPAKKKRKTAEESVKWIQLIKRALKSAGK

EMEMRALRQTLFKQIQAQKLSTMTGKELKKRFKAAITES

>contig51820 Frame-2R

MKALLDAANADGKQTYSSAAEEKRIAQLEQLSLLRESNATLRDESQKYLAKFKEAEAKVR

NLEA

>contig51855 Frame-0F

MLCCARVLHKNISYFEVSTDGCASVGLASISDVFTRMLTAFLAQRTCGLEGRVVRLS

>contig52036 Frame-0R

MRLSTQSNFYHSHCLVIIVTSAYLALCFRTRSMISRVLLLLCQRG

>contig52168 Frame-1F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY69399.1|) 1e-44

MAEKRTVHREGEKMWCPEPRNLWQLGTVVEVVGEKLLVQLPGADAEQQFGTEQVHPYDPT

HSMDLTNVAEMDNLHEAPLLDLLRRRYLEDKIYTYTGDILISINP

>contig52267 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69102.1|) 3e-73

MTFLQVLLSVMAGCAVVIMIWSIHLVTTRHCTIADKYSMHLCVFNCIGCFVSIVVWYIFV

FRLIIDSTFYNDQLNRCSENDSGRTCWQMGLCVYLLIGG

>contig52890 Frame-1R

MSIVAIAATSAWYVALDWIRSTRSAFLPLVRRPNLRQISVSSFTRRFERFIGVGFYCKYR

T

>contig53031 Frame-2F

MPVFKISKNQKDKLQLRLLGLTALAIIERDPVTRKTLASHSLNDMFNVVVYPSVSSFQDD

ASSEGLNGKLALELKHGLTRRYVCLSSRVCRRDKNVSLGLERVSTRHEHELRQSIRNIAG

DIDDPKWLEIAGSASLLSPKEARSLFLSNVIEMCRMNKLHVPWSTEETKIACKEGTWGTE

>contig53628 Frame-1R

MHSFSLQRCRELFTNGCREVKNGIVMVVGHLAHFSTAQQTNFSEEYIASVLSWLMQLISF

KSVDDLIKPEDQLQLVVACSSVCLSVILDHSSKAKLAKRRQVLAKIVQWMDTVPLEQLFD

FPVQFLR

>contig53761 Frame-1R

MQIYKDIHPSPRNILRPPFHLIELSCVSCKMTIFK

>contig54328 Frame-2F

MISHEDLCGAPPIPRVASFNNSSRILQHFGCATSCVIFTLLWGCPYTSEISLRSLSAQRT

YR

>contig54531 Frame-2R

MVQYIVRCIVIRLRQAQNLPALVSTGTHAPC

>contig54917 Frame-0R

MTNQRPETFIVDRRSSFVEQHARGPQWRHPCSERSLASVH

>contig56050 Frame-1F

MTLNKTIAWSFWNFRRVVRNFHAFGLDTHVLVSGPELEILEKDEKDARPKCFQRTTSFGI

NWHELMSENWNRPSEVKSTSGASIPICSGYNGTVDDVHTIHSRTTSTQ

>contig56775 Frame-2F

MGAGGSHSAVLNFSKRPISSDCHWLV

>contig57602 Frame-1R

MRRRCRKLGFQHRNFLRNYCSQSSLPFNRLP

>contig57866 Frame-0R|Blast-predicted protein [Physcomitrella patens subsp. patens]gb|EDQ68719.1| predicted protein [Physcomitrella patens subsp. patens](ref|XP\_001766391.1|) 2e-34

MKAPIYLYYQLENFYQNHRRYVQSRSDAQLRGDAAASTSDCSPLTMSGTGVNKYNSTAES

PIGNNQTDYILMPCGLIANSLFNDIFWVNKLVTNGVTYYQNDTYQDKTLVNLVDQTGIAW

KSDVETKFKNINLQEVAAPDDTMLLWQNPRYRYIIPMFVGQEPIANKTAWTANAPAFGVQ

DEHFIVWMRTAGLPSFRKLYGRIDTDLPEGSELEFLVSSNFVVSTFEGKKSIVMST

>contig58449 Frame-2F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY67640.1|) 8e-14

MEKLMEGETTALVEALTSQDKKIWGFQL

>contig58786 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67964.1|) 2e-11

MFGDSCSECCSGSALFIFNGIDLLCGVALTVYSLFIG

>contig59460 Frame-1F|Blast-eukaryotic initiation factor 4E, putative [Phytophthora infestans T30-4](gb|EEY66244.1|) 5e-30

MDYHLFKTGIKPMWEDTANRRGGKWMVRLRKGIASRYWED

>contig00849 Frame-0F|Blast-DNA repair protein radA [Phytophthora infestans T30-4](gb|EEY54403.1|) 1e-109

MANMLANQPALLERGVLYISGEESVIQVRMRADRLKSLSDNLYVASENNIDSIFGLLERD

DGNFSSSDNYSEFGAVVVDSIQTVYAEDIMSPAGSVSQVRECTLRLLRLAKSRNVTVILI

GHVTKSGDIAGPKVLEHIVDTVIYLEGDPESARRYIRCQKNRFGNTSEVGVYNMTDEGFQ

PLPNPLMAFVSSNDVDGEIETNDNEKRKVEPLDGCSITIAMEGKRPIPLEIQALVNKTRY

NADFGRGGSDQVFSRIRGVGVALDKLQLLLAVLEKRAKVSYRNQSVFVNIAEGYTIQEPA

ADLALAVVLASSLLSRPVLRNAAFLGEVSLSGHVRPVKMLDSRLTAAQKIGLKVCVIPME

HDRLTRRALREKFENTLEVIEVSTLLQALEIALYSRTDT

>contig00940 Frame-0F

MSMQKTCLMEVLKCLWSEDAAAHGCDAEQNGDYSSAMQRLSPHVGLEPTTTGLKGQRSTN

>contig01756-0 Frame-2F0

MVLDGSLVLAIYELPSRTDMRLDESFLQCSIVSMPR

>contig01756-1 Frame-0R1

MSVRLGSSYIASTREPSRTIRYTQLLGGSFRTMNGHRYQIESLTVQ

>contig03093 Frame-1F

MGRKLSNVYDYFFRLESEPGRKGLVRYQCKKCDKQYASNATRLAEHLKMSCAPSFQTNQR

ARAKALLTGPPGPPYDEKLQNEGTMDENEDLSENIMATEASLASQSVSTDAFATAGVETA

QSLALKRADQQLLSSMLESESDPPQDMTEVLLRLAKLSTCVLGDAMAQLKIQGHLVTLEL

LRG

>contig05837 Frame-1R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY64543.1|) 2e-36

MKKMGLKAYRLSIAWPRIIPAGIGKVNEEGVDFYNKLIDELLANDITPLVTLYHWDLPLA

LQIEYDGWLGGK

>contig06472 Frame-2F

MLSIEDRTALSEATTFQLALAGLGFGLLHVLSGPDHLTALATLSAGSSWRSFALGLRWGC

GHSIGLIIMATIFIALDGHFDFSMLNVVTDVLVGVFMIALGVYGVFESVKKWKPRQSKGD

QTDKTSSDYEDDGEASTSEFETEMDTELIASPQRTLLMKTAINSSDQGVITLSDDALAAV

KSLRLETDMESSKTGPDEEITGIEYRDVGSSQLRERSSSMETISLKISPCESGELLGQSS

DKMGTDRIESMHENRYKCCGISIPPIDLQNAQTQKCTALLVGIVHGIAGPGGILGVLPAV

GLHNTLKSCTYLGSFCITTIATMGVFAGAYGEVTGRLGNRSEIIAYRIAIVSSMLSVIVG

ILWLVLAASGTLKEVFC

>contig07808 Frame-2F

MRLAPGMGEKKRKKVFIPVAKYPDINFMGLLIGPRGSNQKRMEDESGARILIRGKGSSKD

PTGDPDENEELHVLITADTDDAVAKAQSAVEDILFNPQQAMKLKQEQLRKVAELNGTLNE

NYSDAYASTGGYAGTSALRSTSDQTSVDMKVPRELVGYIIGRGGETIRDLQLKSGAHIQI

VREEDGVPPTADRFVNITGNQDALDSAQQLIQNLITERQQTHTTGGFRERDDHDRMTRYG

GVNPDGTDSVEILVPNERVGLIIGRGGCTIKAIQQRTGTSVTIPQTPDPVHPEMRLITIR

GTVEAKEAARFEIQSMVSDDPSQRQSYGLSSGQTIYMQVPNDRVGVIIGKRGETIKGIQD

RHAVRIQIPQVPDPGSNPPVRTISIQGPPQNLAIAKEEVDSVIIQGTAGGQGGYGTEYPG

GEGTYAGTSGYTGGYTAYGQDQYAAYYQQQGQQSQYYQQDTATGEASATATADPNDPNAY

WNGYYEYAAYYGVDAANAAWGVTGAAAQASAEAYQQYQQQAGTISTETAVVSASSDAVLA

PSAENDAAVSGTRSVDLVETSQVCALLCVSF

>contig09712 Frame-0F|Blast-hypothetical protein PITG\_05283 [Phytophthora infestans T30-4](gb|EEY69099.1|) 4e-12 NOT\_ORF

MESAQKDKRLLAMDEELQASEENNAWVL\*LPPPRSHVLHTKWLLKTKRDADDEIERFKAR

LIACGNK\*VFVVNYGLIFSAVMELSTV\*IILVLVLCSGNKQNMATFQIYT

>contig10848 Frame-0R

MAQGSGYLKKGKKSVKNMASKPSKKAVRYSHKKSAAKFTKKG

>contig14471 Frame-2F

MQLPRADIIKVADAELHAVKEVRLMAAKRQKKQLNGRMRMRSRLQSPSGCPSSLESSAYG

SS

>contig16433 Frame-2F

MGKDYYAILNVARGATDDELRKAYRKLALKWHPDKNPNDSDTAQKKFQEIGEAYEVLSDK

KKREIYDVYGEEGLKGQPAGPEGPEGGMPGGMPGNMRGMPGGFTYATTSNFPGGGFSFHS

TDPSKIFEQFFGTSNPHEAEGSDPMASMFGDMGFGGMRGMRSGGFGGRDPFGQQRQPRAQ

KLKSVLEVPLEQLYTGCVKKLKITRKVQDHNTNQAREEQKILEINVKPGWKDGTKVTFEG

QGDTLPGRPAQDIVFVVKEKPHSKFKRDGDHLLYHAKLSLRDALLGTGTLTIKSLDGRDV

PIPLGGVIAPGTQLVIAGEGMPQQKQPSQRGQLSGGV

>contig19397 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57741.1|) 2e-72

MNVSNMYMFGVGTKKNEVEALKWLIKAAEVGDPTAKSRMGEYHSLGKGGVQKDLALAVQC

YKEAAAAGVLMAQFNLGVLYLTGEGVPQDAHQAEALFRKAAEKGFVMAMINLAQMYRTGY

GTIPMDLVTA

>contig19559 Frame-0F

MPVKFEEETIRKKKLTSVVWETFTPCSSSGLLDGPIDSAKCMICNKFFSTRHGTSSMMRH

AKRHNDYPNSSSLSKKEKKSAKEIPANSIIGKKIAAQNKNPAMVQFANHTAGSKRQNLTS

PLIEWIIDDQQDLAVVQHEKFLDVLAAAGFKPVIPPVDILQKAMVRKYYKLFTRVGEYIN

RSVVGRVTFSCDTWSGSVCKGYMAIYLHWVNAEWERKTIQVGLEGCPPEFNAYFMSDLLF

NVLQNNWGAGNKLFCGVTPMGNELGVGMGFLREKIKTVVGLDNIAPHWNLTCLGHLIHTG

VRAAIKEIRHEIGKLRSLLSILKSTTESQEHFALRTTEVGLQYPDHLPNLDSPRYWKSSI

TMILESAKIKDTINALYGDATQNMDVYLLEEIEWDLLVWVATFLQKCMQMTTCQNVQQHI

SLSTSTNVCKAIVDLCENTAALASNFTTSAYNKIQAVCLKVKASLDSYHTEHSSPYFRLA

KILDPRFSNECVDKASKKTFLREILRTSAYETPSDTRFDDEQARHDVSAAYTTFEKLLDI

GEGMPDYTIDGDEVDRFFDATLIRDKRSDPFLWWKSNETRFPSLAKLARDILSIPATAVP

SGAVFTQANYARPLNGVISESDKLYKFNELARAWQIERQNFGRKRRRDSFDDLDPPLEVS

VKMAS

>contig22434 Frame-0F

MACATSPLRRSPSNRHSSPSGSFKCSPLMLMPPVSHDGLLIIQDPLQPDNNVGKSCYRVS

QVFRDFSEFLSFVMALIVRGSEMTMNETKKSGKHASPVVSASVNTQEPMCRILKSVFAMK

IRDNRLSLDNTLV

>contig23028 Frame-0R

MLTRRVRSLFLRPQWSRNRIFGESSLHPTLMQIKSSTANDMQRYDRRFHTIVHKSPHRDI

EIPRHTIWEVAAHQASVNGDKTAVICGLTHKIVTYRDLITKARRLAASFVKDGFRKGDVV

VLHSVNCIEYPV

>contig23820 Frame-0F

MKSFNLATAIAIVIASVGVKADQTSRRLIVGGETVEEGQFKYTVGVRATANGCTNCGGTL

IHERLVLTSARCATRDSDDFDPKFAAIGQHLNIGTDIDAGEVIKIEKVAFFPGYNNETNL

NDVALLFLEKKSHQARKIWRRSTAGLKSMGLWLG

>contig25134 Frame-0R

MPMRYSYTSGQTPEDYYASYKFGDDGGDPISSQETDSGHIALNHGAKLDQNGLLQFSEES

FPPPPPMDDSGGFIAKALPSWSPPPARSKKLSAKTTSGATFYNQQTSYYNIASKDELAMA

SDGGANTSYAQDQNAVLAPPPGLTRRPSMTVPWQVAEAVLNTPQTNTGRKKLVESDANTN

LVGLNSSAAEAAAQLTGLSLQSSTPTRGNSSALSSSSMSSSGTLSSSPSSSTTMQVGLSN

AVRRGSFGNAAEFFKFRRRSKSRLELARDLTYGENGEPGGYPCYGTAGAMPGIAERQGDA

EEEIHEDFVSDESLPTSANDESSSQDYTDEDVVQVTDGYDAMTETSSSFVSFINASRQQQ

NGLSALSILPPPPPPPATDDDEDASTSSSTKGNGFPMMSPNGARLRKVAELARQGSLSNE

DKTRAKDEIIQNSLGIGKVLRLVTTKKEDRGDRVSPIAPLMTAPPGFHGVPRLTPKASTK

KIAVPGSGIVRASSLNTFAGAATATAALNVGTVSLGSSAASLEERLATAAQRVAECVGNG

DMVGFQKAMDELDWLRSEANKLMHG

>contig26395 Frame-1R|Blast-F-box protein, putative [Phytophthora infestans T30-4](gb|EEY66921.1|) 1e-23

MSCNVTAAGALIWMTHTILQEHGWMLQGTEIDARRLCLLESYAGDVNFLQTVRYKLSKEA

VDDSIVHMRALLVGSKVFTHFVSSARSVNLRFRISEFVKPREPEEEQQKYAVYIDKWRCN

LEFLRW

>contig26878 Frame-2F|Blast-putative methyltransferase METT10D [Phytophthora infestans T30-4](gb|EEY53163.1|) 2e-13

MRGERRRPTPHLSALTHDRNRYKDKPPDFYALGQIYPEFKQ

>contig27727 Frame-0F

MSGTLKAVRSYQPSRGEQQQSLRRYQSAGSSPIVRAPNLSSLSPLYPLPRSPTSAGSSPG

STRLDDAIGRLFTRYIPTFFDMLEKFQFQKALLIVEDEEETQWKSWHAAKVMLKLGASCE

STYHAMKYLETDLVQTNTIEQMYKKLVVLIKHLMAELRPIAARQSRHNFVDMSDIHENTN

ASRSNVVHERNLQATMALSMCGDMNYYVDLLEQGAEFFSLRAPMIQIYRGLALSTVPRDY

HSILKQLEAIIFRLEIFDHPLLEVMKFSAVEELRTVHAAIQCEIRVAEYDYTRSIVALHR

LKGQLRSWSDHIDASSDYPLFDGNSFEHAGDNGEERMLLDDSDDNNGVTSDSQYSNLSYQ

SSSSVSRNCVIPASLIGESRCVSTGTLRGISSSQAESLVLFRGGRYATMSDNSYEFVDEG

TLLEGHHSGVSLNNSFSPASSETHSTLRRLFSHSNLLRRGSVSASTRRRLVQKAGGPYID

TGGMNLSMPNNTLEQGVLGGRASGTGGGSGTSLGTPGALNNGGIDNGSTNLFATEIMASS

IKRQERDDGFALPVFQWSKRFYRSLVAKFTLYFYRWLEPLEKKSDYLTLELSRFIKTPLG

ISYFELMNVLLSRAQRGDWGKVCVMLILETQALENKGAHYYKSGYRCPSSSYALSTRTNQ

GKGNKKEEKQEESASDDTDNAAGVQSHTQSPASSRGGSGSPANEQNRSIDQEANHALFMR

VDREENEELNDYSELWGLRSWPAVFCYPEGSSLPLDHWPNIVSLIMDHRSTLGSVHPV

>contig30644 Frame-0F

MLYLGSHPRRQIASLTFEFWMVVQDEPVAGRARFFQRGAFVQLFEVMLKQCQFPGSAEEM

DSLELDDLTAFRKGLHGVTEVFISIFSLSKEQYLAHLLSLLVSTRPSNWQSVEVALFAVS

TVADEIKKKLSSHTPELENLMLQIIPTVLSTTINTHLLVIVTASRLLGQFSAWINDKALA

AGVFNLVELCYN

>contig32398 Frame-1R

MRIHRVRQYKRWKRNLNKTSSITSLRVV

>contig33102 Frame-2F

MLRRNLPSQAGVFRAISTARTKTRICHTNPVSCTDRHDVRPFSSCFFTRALIRASITTFP

YRWFSSLNV

>contig33696 Frame-1F

MESVVAPHVEPSCARVDHLAAVKSPLMHSKVEAETETSLVAEPLKLQQPHEDGGESDKAR

TDSDDDDDESSLKPLQDEVLSGTEETVTVPGNEVLTEGDHVTTSREGVEAGTSRSFDAVE

DPL

>contig34073 Frame-0F

MSHIPLLPSKHVAIDLLEMALSFTR

>contig34099 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64194.1|) 1e-165

MDLTAEDDDLLSYFLSADVVAQQMPQMQLDVSNSSTSATEQFTLGRTVPLAIEQTFGSQL

SSDAMPAASSSTTSTFHHSQKEYTERFVTQPVLIDDDTSSNTGTLDSDEKRQRRLARNRE

SARQSRRRKKQYLELLEEKVSQLTESIDATRAAHLEHADEALDQVRSNILKGLVEDSKNG

PSEELFQEKIRQGIALIQERFGPNSVERTAVKEYNFRQLDNLLLPPYCRFLLWLSIQDES

FFEELNGMGSKNASEVPEKKKLPHVVKKDAFMVDFDE

>contig34903 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63606.1|) 3e-36

MEEAECRHWFSQVLAGLSYLQSRYICHRDMSLENVLLDGDTSK

>contig35364 Frame-0F

MCSLSNTSSTKNTPLTSVRLSEEDNALFELTRIAREKVEKARQDFATAGWMERKDGQGVR

TFERKSTPGVVDIAAFLLLPCSVSEIMEVLSNRNSDDFNTTMIALAGDVFSYAVTLREVT

TSSINIHLSTKRMQFSGSIPLLSSAKTFEFLDFVDVDYKTRTAIRLFQTLRQNCASQLVE

GGGTTAGFMLTEQTQLHQTTVFYFGTDTTRSDEVKHRRVIKTRLKAGAVRESSTLTLLKL

AKLIPMIGDIALRRRLGAVKADYSFGFACDGCCSGCGKVVKNFLMRKKYVCVICGYKTCG

PCSLSQDIEGLVGVTERLRVCCMCISAARNRAFGTIDDNDDTSVHLPRPTTFSTLSTTRT

DSMTNSGARHSARGPF

>contig36255 Frame-1R

MDQKLQQVVDHIFPDFQEQEVLLEKEFYAKNNFKLKTEHLDGGNVLILVPKNPSRRNLRS

STLATKSPSGNLEDNIVCSKQLTIEVYPQQTTADAVPMLKFPFMEVDGGLKMLELCMLVK

KRLKLPNNVHLEMACMGTTMGPELSVYFIQRTIWQHKNPKVPLVLHYRRAKNVSRC

>contig37924 Frame-2F

MGTVDCTEDKAFLPIFIGVFDHPPYNLNTLLIVETFCSKRYCTSTSNTYYGSSTFDISAI

HASSAAACTIGIPAFVEYGILISSFHCWMNCPTSIIGDGEATASTFIRFIIWLVPEALPE

VEAAVDRVVPEVEEEVDQQKMSWRQPAGDLG

>contig38781 Frame-1F|Blast-6-phosphofructokinase, putative [Phytophthora infestans T30-4](gb|EEY66056.1|) 0.0

MHSSRRGSIDSSSAAFQAEHTSAPFANKHPKGFGEMVLVDGITIDKTYVLPVPNLREWLP

EKDKNVCNRRKLDSQTEGSVERKSTYNKIMGDSDVILGDIRRNNSQKAVSRAYVRAGPRG

NTYFDPSTVKAAIVTCGGLCPGLNNVVRDVTLALWNLYGVRDIYGIRMGFAGFWNWTSMD

QKEAPILLTPKSVARIHHYGGTILGSNRGGFDEDKIINFLTEYGVSQLYVIGGDGTHRAA

NKISEECRRRKLVVAVAGVPKTIDNDVDLLDRSFGFNTAVEEAQRAIRSASTEAGCVPNG

IGVVKLMGRSAGFIAAHASLSSGDVNLCLIPEIPIELEGPRSCLDHLERVVEEQGHGVVV

VAEGAGEELLGTSAETDVGGNKKLPPIGAFMKDRIQEHFTKKGKACTVKYIDPSYMIRSV

PANAADSLYCMLLGQNAVHGAMAGFTGFTVGLSANRVVYFPIEAVTRNSPRCMDPFGRTW

ERVLCLTRQPNTAREGDIKGAKSSD

>contig38921 Frame-0R

MAHADVLVASPVNEMTGLEMCSATPPDNSKSPHTPRLLQRAGLRALEQIASDKMDVVTTL

CAADTDAVTSSPSAIKRKRLSQSPTTSAGTLDSEGSETSPDELEDLQPSPELTEVKLPTP

TNRSFVAKGNEYKRRKGDVIENALKRFHQDEANVSRCAEFTSICYVRDKTGDDKSKAIKM

RVQVGVSFAQGARAYMEDRYSVVERLSDAEEDADLSLSLLAVYDGHNGAYASEYARRRFK

ELLGENNELRDIGRRAQQSELTEDDVERIRAVLVDAFATVDAETLQRTILLNKRDGSTVL

MGLLVGGKLFVANLGDSRGVLAKETNGTSDSKDEEQVSSVVRLSVDHKPDLKSEMDRVEE

AGGKVIFSGCWRVAHDQVPLRLAISRSLGDHPLKSNLPPSCVAPLVSVIPDVRILNVKAD

GEYLIFASDGLWDRLSDDDAAKIVRAKVAEFHWSKGAPSQKATKEALHFAANALVETALS

KRSMDNITAMVISFSKSFDEDKPTV

>contig38954 Frame-1R

MNWNPELFPYKEVYHEHWPFELGPVNDSFTLGFNPQYTLIFRKNGSLEGALAAATSCTMW

ILLSKHVNVIQHGTDNSNQQCLTLHVYRGTPGKRVFYNHCAVSRGTYSNNLHTLVSLDLD

FASDLNPCFTLVASQYEKVAPLDYTISVFSTRPFSCLPIQQFVTSLPTSVVIAGAWDRAC

AGGRPLYSTFMDNPQFHLQLQQPLRSLHL

>contig39492 Frame-1F|Blast-ATP-binding Cassette (ABC) superfamily [Phytophthora infestans T30-4](gb|EEY54021.1|) 1e-06

MQSSCAGKTTPMDVIAGRKTGKKLVAKFYLMDPLDRSRYPSIHWLLRAV

>contig39566 Frame-2F

MTCLPLALFRDECRLFTAYLQRQISLKEQTLQHGL

>contig40364 Frame-0R

METVENFCHTFSLPYGGAQSGVTPILRIDVLTTDEGKRNYVFDHVTNKYVEVEHDEDEIF

DVPAPQQVVLPTVQERR

>contig41073 Frame-0F

MEDVASGFLRVANEAMCRPIRNLTQNKGFDLSTHVLACFGGAGPQHACSIAKALGMSRIY

IHRYSGILSAYGLSVADSVVDKQSPSSVVLNADSKLAVVRSLTELAQEATMELMNDNFQP

EDVQVQYFLNLRYDGTDNAVMTRGPVCAKGESVATSVAALTAFDFENSFIETYQREFGFV

LQNRAI

>contig41099 Frame-0R

MPSSPNTYLPDVILLSAGLGTAAGAALAQQVQEQQALIQAQAQATQLTETDSESMAMTGS

PPPSASAKAKPRRRRADGSGNLTVEQKRRICEKHRSTPKITQKDLCRWAKLEFNLQRAPT

QPTMSNILKHEHMFKDNVLGVLGSQRKTIRPTRHAHFDQVLANWVMERQNKGNITGDMIK

TKGRELVKQMGLEGKLGFSNGWLASFKARHGLMKRVNNVQSDKITVHTGGVTMKDGGAYG

GILDANNGMLPNGLSVDPNYMLPPVSMDLTLEQIQDLLRDYVPSDVYTVDETGLFYRASP

HKLVQGDEVQSMLSEEARLTVLLAVNADASDLMEPYIIGNVVPPKTIKMASISQLGYHYV

CSSKARMTVFIFQQWLRDFNARMASAHRNVLLLMDNAPSHVLGCVALSNVRVVMFAPHLG

MKVQPMRSGILLAFKGKYRLKHLTLAIDHLEDGLSDIYHVTQVQAMGWIVDAWQQTSREV

IVNAWKPLGVLASLNLDSSMDGADDKNVEEELWGLLYCLQLSGVVNTKVLINSRWENDIH

KRLNEDMIEDPKENDEEFRVPNAPPVERSRVGGAHLSIDEEQQPGIQQISAKEQLKAFRD

VIRYLERTGSADARDPQLMNVIEFLKKKQLSLRFDNASSTTLTI

>contig41136 Frame-1F

MAGQEKISMFYEWLDTVTDIA

>contig41767 Frame-2F|Blast-acetate kinase [Phytophthora infestans T30-4](gb|EEY67850.1|) 0.0

MLRSLFTYSPAARLAAIRSFSSSGSNSRLLVINAGSSSLKYSLFHLHQDGVGSVVFSGIV

ELSTSSHKNGRITHKIIATGQSERIELPLDTHRVALETAVAKFFGSDLDGIQAVGHRVVH

GGEAFTCASLVDTQVIKAIKSNIALAPLHNPGNLLGIEVATKVFGPCPQVVVFDTAFHAT

MPSKAYMYGLPHNLYQNFGVRRYGFHGTSHHYVAKKAATLLGKSLDQCNFITCHLGNGAS

VAAVEKGRCIDTSMGMTPLEGLVMGTRCGDIDPALHAFFCKELNRLFRRWI

>contig41903 Frame-1R|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY59571.1|) 5e-72

MDDFFVEPLELWRREMNLDCFILCGHSMGAMYSTYYAEKYSSCVEHLILVSPAGINSSSL

QQETLPFVLKLTSFFLITP

>contig42252 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54202.1|) 6e-72

MLDLLSPLRGYIAQNLQFYLGKYIEGIQLEGLGLFGGDLVLNDLEIKRHVLRESLEIPSS

FDFSRGFIRELRIHIPWTQLLSQPIEVKVYTIELILTARSSTATPVSVGDSVAIETEIDQ

PKSGWIHDTLQKILANVSIQVNNLVLKYEHDDIVFSIAL

>contig42924 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53590.1|) 1e-180

MDAKPRVMVLGGAGMVGRNLVEYLVDRDLVSGIRVVDKTLPEISYFSAAHMKAFADGRVK

FVQADLTRDPHLDRAFNPEFGPYDFVFNLAGETKCGLSESVYASNCRDLSVLCARRSQEV

GVKCFVEVSTAFVYKSQVKQPAKEDAELQPWTLQAKYKLQGENIIRQLPNMRVVILRLAT

VYGSADLAGLMPRIVCAASYVKLEEKMKLLWDAEMRVNTVHVFDVCQALWHVTSAGKDGE

VYNLVDKNDTNQAKLNAMMEEIFHIKTGFIGKLVSNLARVRLSDVVDDANEKHMQPWADL

CAEYEITNSPLTPYIDKELLQHNHLYADGSKIETTGFKYQYPTLEPKEVRGVLEELIAQK

IFPPILSLN

>contig44720 Frame-2F

MEPVFEIVEDDHEIKVEARVITQEQRGPHGGTILWDYVDDDTLHPLPLDATTRKTIRRNV

CGGMVIRREPGTNMFSVRHTSMKSYSPLPPAHDR

>contig45631 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY63349.1|) 3e-52

MSLLGLVPDLVWYLILKTWGWKDLCPYCTERIKHCDCFNDEVLVLAIEHLGPKWTLIRDL

DRLLAKEAQYESQFTLYTSEQLRERWDVIVERAETHMTKVAKLRMYCHKKQQDACCTSRV

LTRKDHVLSSSHCDLENALAKEG

>contig45644 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59811.1|) 4e-60

MLAKKVDQLLSLVASQGAPIPTLIKARLPINNVVAFSGGIDSSLAAALVYQVFPQTSAAC

IGRSAALPSVQLLQAQNIASHIGIPLWECHTEELKHDGYVANQGQSCYYCKTTLYSTLVQ

VAEFAWREWQQQDQATIEPVLYNGTNADDLLDSTRVG

>contig46102 Frame-1F

MDMGTTVPQMAINRAYPLPQQFQHPQRQPQELKQIGTEQIQAMLDENSSLIVEIIELNTQ

IKHGKGTAQLGEFTEKLDKKRKNLNKNLMTLAKWADESSETSPRQPQALRQSQMTQQQHQ

HYARSEMMQMPMSNQAQLQAQAQAQAQARAQAQAQVQARLQAQAQAQAYAQAQYQARINP

LISQQYAQMNSMTQQQQPQQQQRFANGGMPFGVPESVPHPVRLNNAIPSNYTDSRSAMAS

NMSFQMGPQSYSMMPQTQMQRLSSGTQEMSQQDMLQQALQQQSLSHQSMAMVQQSMGMPQ

PSMATPQQSIQQNMAALQQSMSLSQQGVPHQNVQMPQQGMASIQMNGPMNSGSMADASG

>contig46713 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58482.1|) 4e-53

MGTYLRQSSASLRHSDPRNRDPRVELRHSYVPSSRRSDTHLRFSHQPRYSGKVSRISEPN

AFYRRSSSTPAYVPEAEQSTDVVLAHRVSLDDEQRVSLHAIL

>contig47611 Frame-0F

MAGGVGLISIRSEPRGSQQNKRCCGRTDAWQQLACAVNSTQAERHNVTPSKLTPRKLQQL

LRAASGNACETFLRRSSF

>contig48742 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62344.1|) 1e-49

MNAATDNDIVLGGTDANERAPHLATIGKGGLLAMWEGSSAGGDLTEGGARTVYAQVLDAT

TGQEISSKVTIDKAVVGNRYQALKSFPDGSVAYLSKGTTATSVQVVRFFAC

>contig49374 Frame-2R

MLTNLRLVFQHSEFRPGQEWAISRVFRQKDTLLVLPTGAGKSLCYQFPALFLPGLTLVIS

PLIALMNDQYESLPAP

>contig49451 Frame-2R

MLVLFLTRFSLSSSTESLVPTIEMIIALQTAIRVDKEATVTTKTLQILDALVSGVHGDIL

PIGRVILHCYLPG

>contig51502 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60120.1|) 4e-29

MAVNKVAAFHTQDSTNGFDKMRPISQIDITGCQNYTLVSSVFVTEIPHASLEDVYAAAIA

YHDALPTTLKRHLGIDVTRTR

>contig52037 Frame-2R

MPRVLYLYALINCLKSPRSVFHHRGGEQFHCAHYITLDDMIIRLQSLWCQDAVLWTKHGA

LLNQVVGVIAKNIQRCT

>contig52169 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69217.1|) 1e-54

MCVRPPSAARSARSARGIKAIMTGESRVSITMRPRSCSNVSTASSTWSPTDMNVASRDTV

SGRWVEDVAARTCAKCERFFSLVNRRHHCRVCGEIFCHACSRTRMVLATNSGEIPRRQRV

CDLCASHAHSSAVLYESESSALNQGFRPKAEIAERSAVTGVQPSAPQKEDMAVSK

>contig52266 Frame-2R|Blast-serine palmitoyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56490.1|) 9e-53

MSEWWATIGQPFAEALLSLDTVKIKEAFANAPSSYYEYVRSIYERSPEHVIIETFLIVFV

VYITFVKRDKPKSSAAKFSEREIDELCEEWTPEPIIPSYAIVGADDSKPIGIVEGTPG

>contig52947 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53671.1|) 5e-29

MTTMDERTDRLRDRVPEGELHVWVYEARQLSAQWPLTDAVYNKHGLRVRCTLLGATQQSP

RNNLGSMSNPVWRQSPDEAR

>contig53629 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61157.1|) 1e-30

MSSQRGNVKKRAPKHQNAFAFKHNPKSKKTERILSMPIHGLCEKCRKQIEWRKKYRKYKP

LSQPG

>contig54916 Frame-0F

MLKKEISRMIRVNCVAARTDENILVTIGLQRAHEQHHYFLLSTEDRQPPTKTDAKHGRKL

PTTATAESKKPLPA

>contig56024 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61716.1|) 1e-30

MGRSQVEFRATHGRGRGRGRGDTTGEHRKGHGGGQSSHSRNLGSNAYRFEEHEDKDNNND

AGQEISADRTQFFATEQIHRKKMGVAPGEYFQSRTMKEWEETDEIGDGYGGVIAVL

>contig56051 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58956.1|) 2e-78

MFHKLELSHVIKSQKPHTTDDAINFVTHGYGALVLREAFRSIDWNFTKSKVVMLAPPNRG

IRYYRSMKKHLGVAGFGGVAAEELAQFNAKELDQRLGKLPRRCYPLIIAGNLGLNPFNQH

NYPNDGLIMVEETEL

>contig56701 Frame-0R

MSPNAGETNDVLNMDNYFVWEFSARMKLAKNGLLEHIDATKARVCSGA

>contig01005 Frame-2R

MRHDVAAPYPAPGSSITPPGAGPRSGTSRGFRSC

>contig04415 Frame-0R

MTVDNPTRSNTNGLVRRNDSLLQNPPRFRNNSTSHVIASFGDPIIRHRGKSVPVMPVGKS

RRRRKVTFKNTYTPDVVPPPKVESYDELVFNVAGLFHTLSFLHDPDDWGDAGTGTGSMSS

EDDFYEPEPPLERSVPLMIAEFLYRSAIFLGHPQGDTPWLPGFRLDKKFSGNDVKRWRRL

AHFDWEAEERAFLKNHRKPGQLKALQPRSDRSESVESNGNTSVMSTLGMSFHVRQLENEH

AKATTDTTCPSQKTKFRATMAGWFRKHRTCQEDKELNVVTISEDESAVTTFKPVSWLNPP

PLSSSKDLQLLVAIVNSCVYCGQFQFRQRDIVRLCNVKI

>contig09711 Frame-1F

MCPRFSSHHERKQASPSDSEAFTEVSHIKHLRTFLCCSKVQSSAFLVARVKALRSGLLDE

PDVLEDLVWYQRNQR

>contig12874 Frame-1R

MRVFFHITGASCAKRLRLKSRRYIQLLLLWDLFLNPSSFLRIKVKKKYWNKAGAGTLYDT

QEVGRPIRRR

>contig13873 Frame-1R

MSRHSKNATATTHFTYLERKAAGHGTIKRRYGRDSQLSFGACCLCLASTQSRNPLVSPGG

FVYCKECIYANLLAQKRSIQDNLAEYERYVDTQAQKAQETKLDAERRTFSKALDAANVTK

TGIVDSDPTQQLMTQKLTEKVDRATDDEKRQAMKRTSFWIPDCTPSEEAKVLKPDTKTRD

PMSTDVLKLKHLMPLKLEWDIRSNENNVTVLCAVTKKGISHHQAVLLRPSGQVILESCLK

DMVLPTMTCPVTGLKLRRKDIVRLQAGGTG

>contig16283 Frame-0F

MKDVVILGGGISGLALAYFIRQALPKAAANSTHIRVLDASSILGGWVRTAKLQGYLFEEG

PRGFRPSRNGAEMLRLVEQLKLQDQMEAVDPAAQARYILQNGKIEKVPSSVSEALRWSLS

LPVARAALHELFVKSHSKEDESIYNFIGRRFSPLVAEKLLDPMASGIFGGDVKKLSIRSC

FPMLFDLEKKHGSVVKGMLFGGSSGNDTLLDGTSKSDFVKHYEKSVSVSFTDGMSTLIEA

LGDSTKNDSMSELDLNTQVTQLKVNNLNKSSDEPRFVLEMKDSASGAILEPIQAAHVFST

IPAYCVASLVRDTAPSLAEALDEIQYVDMGMVHVGYNRQVLSIDGFGYLIPSSAREKVLG

VVFDSNTFPSRTLRERFKLD

>contig16728 Frame-0F

MIKFINLNIRSTPSKFRKHYLAPILAGRETNPADRERQVPLLLYPPP

>contig16953 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57474.1|) 6e-49

MRRPVKLACSHIFCEECVTEWFDHERSCPLCRASVGSGTSSEENFRPQFLDGRTSLGPQL

L

>contig19394 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57741.1|) 3e-34 NOT\_ORF

MRYAYVYIYEESVL\*RCQKELQEVVAKLRKLGQRDTLDEFKESPLLAKLKSPVQLHGLGN

MIYRNSGDNDVEVQKALHVWKIAMEKGSDKAKFSYALCKKKGIGF

>contig19475 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61853.1|) 4e-23

MEFAQEGNALFVDEAYAEALHRYTQALEKVPHDAETLCKRSAAYLKLHKYREAEADALQA

SKLDPTLHMAHMRHG

>contig22437 Frame-1F

MALISCLGQIWDRAFWSRVLLLSVHCFSIYFAKGTCVLLLAIDLKQRSAKYKIFFCYCFY

GSFVGVVCTQKIMCKNIPTV

>contig23346 Frame-0F

MESLSPVACSSPKRQRHIWSTRVHREIEKCRVVDALPSGATLHRAQISESRGICESEFYC

FVPFINSSVALSLVPRVDLLVIMPFSEKKLADGHVQYPFQAPKVEIRYGAIYLPVELRER

KALVAEEKEPTFTLKLSLLQKWSPSTTLRMLVHEFFHQIQQRDPSPAKSPSIKKALKGES

DYNGEQSYNRMRRSDARGAIFSCREVDPRTSTLKNTPMLLQSGYIALLASSDAGMEQKDS

DYVYIGELIHLKDIVRITPHGGKSITFFFKDRQLPCRTFLSQHTDEIVRNLRLIIGKPRQ

RGRDQATAGLAAQLLPFLSAEQTEKAKEISMNFMGKLSEVATSVSRMFRGDENKNMEQQQ

VDPLAKAFRDIDAQKEVFYRTPSKARMTEITRRYQHIAEKYVHLNNKEGFVERAISELQI

FIEHPKAQRILVHAHAYEQSNKGIRVG

>contig23416 Frame-1R

MPRTSFSSYQTAFFLLFLTEEHEVNWHRLVSYFVAALAPAEYTGILRAFHRCASLRVSIL

EKMARQLCWSLYVLKRANGLVVSIAFMSSPPE

>contig23823 Frame-0R|Blast-NPP1-like protein [Phytophthora infestans T30-4](gb|EEY65232.1|) 2e-18

MIGYRQYSPPDKKFMDGSSIKLKYTWVGLSHHYLTATKKKGERQELALWDDLTDTVKGAL

QDKDSFGFYTPISDHEFMRNLAKAYDLKRFKD

>contig24329 Frame-0R

MKALAHHYENDEIQIKAVLLPCRCLLFRWLLVMTTSSLGLKLYKNQERYRNHIMSGLHKA

KRMMLLELTIMFWNKATKDLSAMQVNFEQKKLAQTTFPNLTQN

>contig25137 Frame-1F

MPSEQEIHDEKSTNNGHVASVLSLFIKLTAFSLTWLDGRNLDTTTALQEIIAGCLNFLRE

RVTTWRDDKSMHQLVVSQLEALALVLLQGLSMCHLMQVPALMELIALMPWKGARKDVALA

YIRVLLVRHERVYNDEQMSFLLQVLTPLIRDDPTEVQSPSPVVTMSPTQKQNETFEAEQH

ILAKIVHLVMNEDLDVKFRVYSIARRAFLQSGIYRIRFTLVPLIYHSLTLARDLVLYSEV

ATQDQDHAIGSKLNQTKRFTTTPRQVLQFVHEMVTALASKHDAVSVSCVHLFLQCALIAD

GCALESVAYEFITQAFIVYEDQITLARDQWQALELMVASLRATCNLSSANYETLATKTTQ

YAARLLKKKDQALMVLHCAHLF

>contig25142 Frame-0F|Blast-choline/Carnitine O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56514.1|) 0.0

MALLQPGTFGPQGFRECWGDYRAEADLEDSSRPLYQFQRDLPRLPVPSLADSVSMYLETL

KPLVSPTEFARSKDLAIAFLRPGGMGEELQRRLLDRANDRRDSSFLAEWWNTLGYLHVRD

PLVFNVSYFFHFADSVYPTQRSNIGRAAALLRGTVLFARQVADSTLEPERLGKNKTPVCA

TAYKYMFNACRIPRRGQDSYRIYDPKTHTHAVVMRHNKFFQLELLDRCTNQPLGFEALRF

QLARILNVAGAKESAIGVLSSQDRDLWADAREELIRTSSKNEESLRSIESSLLVLNLDDD

DPVSRTEMARGLWHGNGRNRFFDKSVQIIVFENGKAGLLGEHSMLDGMPMARFADNLLSS

LQHGQTDLGPRGQTTQQLERSLIAPKQLTFRFTAQTLRNIVEAEKVFDQTVIDHEVFVQS

FYGYGARLIKNFRCSPDAFVQLAIQLAYKKLFRRNAASYEASQTRLFLHGRTETTRSCSA

ASAKFTEAMEDVSGIVTAEEKKKLLVAAANSHVAYVRKAGAGYGVDRHLFCLKQLMRPGE

RVPFFEDPVMARASHWLISTSHLTNELFDGWGWGEVVPHGLGVAYSIKDQLIQFNIACRQ

HGGWAARMGHLLEESLVEMQQLFVQSKTIAAKL

>contig26073 Frame-0R

MNHALSSKCSRSSAQYGANLKATLSRKLWQTRKRHFSAADKFIYRKVTIILVEQWLQIPK

SISMIRLKMLRVMRKINKLLLL

>contig27975 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61477.1|) 5e-34

MNRLLQHFVDSGTAQPPPVSRPSIPVPPQSSGGSYSAENRGSFHRAASGGPFYYQPPPTP

NVLEEIPLTSQSSGVMYETVDLNADSTYPQWVHQTLNNREESGQKTLSSAVELFDSGPPP

IQELPSSNLYERQSSNPFASSIENVAMLMNTSPRMNDLPAENEGAMSKHDSPKSPLSASC

SQNHTQKLDKGLSMYAVEACQTRSSPRDQQVVQPVDPFASICTHSSNTPFDTPSKTDYQS

SDCLFTSSGSTNKANRALSEPLQYQPTFVQAHELFANEIPSASSLFGGDMSSPSQSPFST

LPAATPSLSSTIQDKASSSRSTPHGNNLSTLLPKPPLKVPCAPMRPPLASSPSHITTTFF

SSTRLPVCLSSTLTRPENHATFALDSLKMDTPMTVSVKSELDARHMRFPHQKKGDDDTMS

NAPSVAPSRMSMLSTLDDSIKLSDMYKHMATRLEGEKDDLLKIVSKQAREMAQMRLHIKS

LELQLKNCRPQDA

>contig28206 Frame-2F

MDSTMTADTSSSVIASMRSAVREREIMAEVVQEVPMKRPRFYIGDISNYSIIDKVGSGTY

GEVFKCQHKVTKDIVALKKLRPDVEKNGFPVTSIREMKILKYLKHPNIVKLNEIVSSS

>contig31723 Frame-0F|Blast-2-oxoisovalerate dehydrogenase subunit beta, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57864.1|) 5e-30

MTVLSSSRNAIKRRLQHAPLLRAFHVATPLAQGLEEVDNLLPVVETQQMNMFTAINDAMR

LAMESDPTAVLFGEDVAFGGVFRCSVDLRE

>contig32098 Frame-0F|Blast-U4/U6.U5 tri-snRNP-associated protein, putative [Phytophthora infestans T30-4](gb|EEY65752.1|) 5e-80

MTSTKRKAEAVQASASSTKRRKCPYLDTVNHQLLDFDFEKVCSISLSDQNVYACLVCGKY

FQGRGRNTHAFTHSVQSSHHVFINLQTDHIYCLPENYEVVDNTLKPVQDALRPTFEASQI

AQLDQNRILAQDAFGVSYLPGFIGLNNLRHTDYIN

>contig32612 Frame-1R|Blast-DNA repair protein RAD50, putative [Phytophthora infestans T30-4](gb|EEY58381.1|) 2e-97

METAYNKIKTIMSDPDEDLQGFLNDYDAIIEQHRDTFTRLQAQEESFKKEQTKAKEEYVA

LRAAKARVETNIDTYEKLVADLIDSASKLSIKYRFHLQPLGSQSDEISSYLTAFQDVVVE

KQNAVNTLDAQQRQEEEKATTELSEVTSQVKQLKNDLAVKGEKLATLNQEKKQIVNRLRE

LGGAGLHSQREADEMSSLVSDAAKTLVNYKAKHDVVALKNEIQGYNVQMNDLNRQVDELR

KNVEQLRLYARENTAIEV

>contig32667 Frame-0F|Blast-arginine biosynthesis bifunctional protein argJ, putative [Phytophthora infestans T30-4](gb|EEY68273.1|) 0.0

MITRLSSFSFPRLLLQTRPISTYGQPFVFESRHEYTDFLKAHQSRLPWGFSIATTNVDFV

PQEAPHLPAKMTMTLIKPVKPTPHFAAVFTQNAFPGAPVLVGRKRLHEPKLGAILINNKI

SNVCASGGGVADAEEVCESLAKQLRLKRGSQVLPCSTGVIGWRIPVDAMVENLPKLVKNL

QSDSVLPAAEGIMTTDLYPKIRSMDVCGGRIVGIAKGAGMIEPNMATMLSFILTDLSISR

DVLRQLLADVVGDTYNSLSVDTDQSTSDTVTLVSSDQIPFDMKQLDRFKKALHDVCLGLS

EDIVRNAEGAHHVMRVRVSGALSKEMAKGVGKSVVNSPLLKCAIAGNDPNVGRLVMAVGK

YMGLHFKDVNIQRRMKIHMGGVLIFENGEMVLNDEIEAKLVAHMRDAMLTEPTRGGLDAS

SHNFPPHGKFVEIKIDLGVGSEESQVLGIDLTHEYVAINADYRS

>contig33101 Frame-0R

MRQFACANNSDDVKRATLTILHHVEPRNDTTSIASLEKNK

>contig33695 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57929.1|) 8e-20

MRNHEVELVLLSPKRPSPLPLVEHDVQYETSDHDDQDDDTN

>contig33710 Frame-0F

MLSILKCHSGEVKKVTHPSLCDDIVHSQTGVIRELRYSEQYARHVERFTSTEMTSYY

>contig34070 Frame-0F

MSFFMLGLSLYKTVTMDPGEVYTSFDEKLHNIRYLVESKLPSATKLCLTCLHKRPLRGKH

CAELNACIAKFDHYCPFVINAIGARNHAAFLSFLFFAVLSISLELVACWTFVRAQPALAV

DIAILWQYGQWNLPGLYNWIWTVIHFHPILFCVVFLNVVQILWIAYLLFFHVYLMCAALT

TNEVLKNENLNHVYSRGIFNNIVDFLGLRGQRPLDWRRIFNYEDFTNQVEDSSQLRKDA

>contig34900 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54978.1|) 2e-67

MPGRPRVIRVQTLGVAEKASQPTQRREAVSYVRKLEIVAHFEAHKNINDTLALFFPDVAA

SEVRAKKQLIMRWRRDRSKIVAICEAGGGRKTNDRKVGMGATLSAEAERRIVDWMHTEKA

SGRFVSAKQLTARAMEAALKDKVHPDSFKASWTWRQSFLRRHGFIKNSQWGAP

>contig35367 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66317.1|) 0.0

MIVDSPGMIDPPGTSLDRTDEDRGYDFKRVVHWFADRADVILVMFDPDKPGTTFETLDVL

TKSLQGMTSKVLLILNKVDDFETVHDFGRAYGALCWNLSKVIRRKDLPTIYTMYVPQEKR

IAPSTSVIEQIPLNVSNMLAHEFDGIRGEVIREVERAPDRATDNILNLLKATTVRLKMHM

TLIEACKKEYLDLCTFWRRAQIASIAAGIGFTTFYLIRTVGYRAPVIPLTTGTMALSGLP

SSPSSQSQLSGAISVQLSGARTSAWEMNWFKQVSRSQSLFKLSTFLKVVLLSCASNFALW

KASILNIEYKRKSVLHWLPLTFNQVYGPFLCKSDRAHDDIMTQWDVVQPGLKFALSSTSI

KNFPTINTTNKTFLEDVLNVHIPRLDRCVRDRSGDDHAYMRFKHHTKSKLDSSPEAGIFS

DTADQL

>contig35598 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66372.1|) 0.0

MTQPAPANWRSISQASPAVTAVKPRSTSGLSRSKSQPKKQCSEKLKPPVKPTPSVFELGI

AHARTFVDSASPEQLEMRLQQLLVSKKFAEAAFIIAASPYLGSRFQKSDVVRLMLEKAKS

PHSLEQAVRLVRILQLQSNAALITLIISEMVRALQFSAAVRLAQEMVPKFEQLSTSAERP

CWTPPALIQAMIRAQKFRAALKFAKQFGLLGMFSAPQLVAGMLETRSWDEAVSSVMEMQL

FQEFPLEALAVEMIRQRQWSQAVKCINKLSNTDDTQANLYEVLVRETARVGDFVTSLRYL

REFKLDEGSKDSSLNLLRYVVDAMIVQKEFYKAIKYAIKFDLAKNPFNMAIAAAEAALTG

ANNEAMPTINDNKVEYLPQYNIELLIRKAMKCGQFHVATTFIKRLRLREKFADDIVFIEN

AQRNCLIEFRQYAQLRLAQFYEAGHQDNLKALLCDQAKDEMIELKPVQVEIVLEEEKEIF

FAQTKKSACQYRERDQGQRD

>contig37251 Frame-0R

MTMLGRALKDSSNLPFPDNFFVKMVTSTQLTDNFHQKATRLLNLTLASEMSASRYHPRQE

PS

>contig37927 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69424.1|) 6e-27

MAAAVAAESNEKIARCMDMLAGHTDEHKFAGLLMVTKMGDLPTDLLQQVRRQVLTTVGVS

FFLRLLHTKGPDDVETLSSFQSLGLNLIA

>contig37952 Frame-1R

MRCLRQATFFKGSVLAANMPIK

>contig38395 Frame-1F|Blast-HSF-type DNA-binding, putative [Phytophthora infestans T30-4](gb|EEY53294.1|) 2e-56

MAMESGTKFEEEAAELPPLRIRASTVASPSPDTLNTPDDSLERSMKRPRREEAALFLEKT

YELLERCPPEVASWTDKGDSFVVKQPTPFAERVIPTYFKHRKFSSFVRQLNLYGFRKVRA

TSVVATVDDGKTGEDASPKDWWEFRHERFVRGRRDLLCEIRRRSPSDTRVLTP

>contig38401 Frame-0F|Blast-elongation factor G, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY55935.1|) 0.0

MLDGVISYLPSPSEIANYALDQSNREARVSVPCSPAAPLLALAFKLEEGKFGQLTYMRVY

SGTLKRGGFIYNMSDMKRIKVPRLVKMHSNEMEEVEEAGAGEVVAMFGVECASMDTFSDT

NQGKFTLTSLHVPEPVMSLAVTPKNKQQVGNFSKALNRFQKEDPTFRVRVDIDSNETIIS

GMGELHLQIYVERMKREYSVDVETGAPQVNYRETIRRRCEFNYLHKKQSGGSGQYARVVG

YIEPITEEELLELEKEGNTSTVLFQNAIIGNAIPPEYIAACEKGVKDAIQKGWLIGHPVQ

RMRVVVNDGQSHSVDSSELAFRTAMVLAIRQAFMKAEPCILEPVMAVEVEVPNEYQGTAI

AEVNRRRGLINSSDADDMHTVIKCDVPLQNMFGFSTDLRSSTQGKGEFTMEYKTHGIVVR

DMQEKLVSAYEKA

>contig39491 Frame-1F

MQPDGWCCIVLVSEKQPRMNEVMVIVAVQLRKVLATTVSHCGTGGDRWEVKTVARLSCSL

NGSPKT

>contig39565 Frame-1F

MKRRNRVLTTATIKSIGLECIHKTCEVSHPLTIFSISCSNTMLPGANMLMSNRKVF

>contig39918 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63168.1|) 1e-08

MAKQPALEHVEQAWLDAGRRGDVLSMQRLRKEHPQWLALNRVRSSF

>contig40598 Frame-0F

MGGTVGGAGSPTNSFMYYNPYGFAANAANPYGFMPAVGPTMESFDMQASGTGLELQGSGG

DAAAKASRATSQLEGPTGANLFIYHLPHDLTDADLATAFAPFGTVISAKVYMDKITGESK

GFGFVSYDSAEAADAAIASMNGFQIGSKRLKVQHKRIHQRMDFMGGDSSDSLIDELASME

YHHGLDDELPSEDGDAPSPHSAEGDPDDINTSLGDAVRNLRLDV

>contig41135 Frame-2R|Blast-hypothetical protein CC1G\_06996 [Coprinopsis cinerea okayama7#130](ref|XP\_001831945.1|) 2e-09

MPVSWVSKKQGGVSLSTMEAGFTAASIMARDLLGIRELLRESDLKFEEPMPLRVDNQAAL

KQLDEASTSAKANNIDVRIKFVGDFKKRG

>contig41900 Frame-2F|Blast-cellulose synthase 4 [Phytophthora infestans]gb|EEY65337.1| cellulose synthase 4 [Phytophthora infestans T30-4](gb|ABP96905.1|) 0.0

MDVQNSINELTKVKGHEQLGSISVHGWMHKQGSRKFKGPVAKSWRKRYFALEGAKMYYFH

SDVDCRKYFNSRNGELVVGAIDLRDAFKLEQSERLDLPARGIVIHTRHRAWLVCPETDQD

FTMWFDALEFTVMSAGSGNVVKRDLPNVRVYEMKGRFSYRFWYLIFIITALIELAGIVLW

FPLGIEPCDVKYRSDTCEEIQLLYADRLQCGNKPFNGMWDPPEWYHWSAGIDTVECFKEP

YIGDWISYFLFYLAEATSISLGFLYYLGMWKPVRRGARYLRDFEPHFPPEKWPTVDILLC

H

>contig42251 Frame-0F

MDAKDVTIFLDRYTSEKNANKLTSQYSFRRKVVGYEVPILSRTSASMRAKVQLFSKAAVS

GPLDQRSNPNSPLRQHHPDVNNCRKSIDLDKSFMHKPSVMYDPFYYYSCYRSSLSPVYEV

DIFIGELVFSISDRQLEMLNQLLRSASYKLLQTHNSSSKIHNCGNNDDKPTAAG

>contig42729 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY66867.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58787.1|) 4e-86

MQQKARNVQELRACGHGEYTTISDTHEFFTSIKTSDKVVVHFFTPANIFCQLVDSHLTRL

APHHMETKFIRINAEKAEYLVDKLGIWMIPCIALVNKQKVAKMVQGLDELGGTDKFSTAF

LAYYLSLHNVLTYDGPEPETSVDDCGRAYATGNDPVSAKQQLEQERIHSIRQSTFYDSDL

EEEN

>contig43256 Frame-2R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65627.1|) 5e-29

MSMVPSDTTFIDYAKNMLVKFPEYEFRLRQSAKRIIKTKLKLGLYNNPVPGKEFLNLVGS

DNDRIVALNMARESIVLLKNAE

>contig44723 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65357.1|) 4e-69

MAILRHYPQTAVLQKTIWTQLPLMCAALGKKVFKGYLELFFDPLIFTLQGSNRLAQFAAR

DCVEQISKQIGPSIFLGRLEGNAEWKTNLGPLVPVQSYMIK

>contig46282 Frame-1F

MVPFHDKSGPFRLSTMIPFMIIKFITIWTALVAAEPPIQLNGWFPCTKSSMQADERDRGH

PDEFYMETSRDLNTQRRAAAQNIEQWQTSSLPFLKQSFDRLYAHQRQWKQRGRLIKTRHR

SRQKALDTSVESDPLYECAEFRVPMCYDGVCTSNKTVDIFVKAVKATNKTNQENKKALWV

LQGGPGASSTGVEELMGTMYLQLEQQVSVYTLDHRGTGRSAKLECRAAQAGAVGSPGGSA

IRLEELPACMDDIRFQLDNQTAAFSVTSAAK

>contig46710 Frame-0F

MRHSDGFADVVATDFSLVFDNNYDANPSLAIDLGAFCARDLVGQYSEQCGILLESSEPLA

IRYTWNYTALTGELKL

>contig47612 Frame-2F

MASKSVLSFKGDRELVTEARAHELVRMYAVAEAKVPPPAFTHITLRNKSYTLEAARVIAA

FLKRLETLGAFEHLTSVDFADMIAGRTEDEALQVLATLCDALGALKTLTCIDLSDNALGE

KGVRACFGLLQHQEHLQHIYFCNNGISAAAASVIVEEVLLFRGPDTPTKLETFHFYNNMS

GDEGAVALAKVLPLAPLLKDLRFSATRAQREGSLTFAQALASLQKLEKLDLSDNTFKAHG

GKAIAAAVKRMPYLVEMNLRDASIEDDGLIAIVTALIEAGAVQILVNFDVSGNDLTIESM

QALGKMLSVSAALRILQLEENEIGSNGAKIIAKALEIGPPLLEQVVANVNAIGASGALAL

IKAVVDKQAFVKLSIDGNQISTSGVAHIKSLLARKNRDYVLGSLEDNDEEEESDKEDMDI

EDITADFGKATLITGASFEFKNKSREVVDTTRAQQLLEEAGIHVNDCTPLHFKSISLRGK

SYTDAGAKIIADSFLSRLQSDLKVVDLADVIAGRPEDEALCVLSILCHALRGHELDAIDL

SDNALGEKGVRACFDLLIPQPKLRRLFFCNNGISAAAASVIAQKIVLQNGLNAPSTLEEF

HFYNNMSGHNGCVAVAKVLEQCKKLTVLRYASARAGPDASKQMARSINKHLYDLKSLDLS

DCSFEGDGATQLAEAISKQRNLQYLKLRDASLCADGAVKVVKAFLRSDIQLLQLDLSGNE

LADEGIEALVPLLQSQSLLKVLCLDENEITSKGLKKVIATLGSNSLLALEELSLCGNEIT

AKGAIAIVDSFVPSKTAFTRLELDANMISDIGIEYIKSSLTKQGMANILGSLEENDADFE

SENE

>contig47667 Frame-0R

MITTRKRGIPFIVINSLLIWFRSTRINAGSYLLLMRCNTINIL

>contig47689 Frame-2R

MDEPMTVAVSLNAVKHHHLGELYIELGVEMVLVRWVFYSYGMGEDTLV

>contig48011 Frame-1R|Blast-DNA replication licensing factor MCM8 [Phytophthora infestans T30-4](gb|EEY69900.1|) 2e-34

MSLAKKVKAYVARLIKAAARRDNSLFTMDDLLEVADSMGLKVDDFRDFVDILRNECYILK

KGPGQFQVQVSSFNMM

>contig48459 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65900.1|) 1e-100

MEGLSNFGSISTMGVSLTHGTWFYEVEVVTSGLIQVGWIDGYFQGNSDQGEGVGDHTHSW

SYDGNRQRRWNSGSSSYGEKWRAGDIIGCLLDLMTQEMTFFRNGVNLGIAYSELHCSIED

ERSGLMPGISLERGEIIRVNLGHRPF

>contig49377 Frame-1F|Blast-GAF domain-containing protein [Phytophthora infestans T30-4](gb|EEY55354.1|) 6e-88

MTLGTYPELDIICSLASKELQCTASMITVVNEAKLHVLASNHPAVPGGVSFPREQSFCAH

TILDTQPLVSRHVQADVRFSAITSVQEMGIKFYCGFPLMGSDGETVIGAVCCVDQQAHDL

TQSQYDTMSSLASTASRVVRRASERRAIP

>contig49399 Frame-2F|Blast-hypothetical protein PITG\_19150 [Phytophthora infestans T30-4](gb|EEY68769.1|) 1e-06

MPFEVVCRLYDIMFVDVCSRYLDSKIIFSTSLSVLLYLSSTLIEIQDVNVVLDVINEFCL

TTLTEYSVAESFLDLVHFMHERIDGG

>contig49452 Frame-1R|Blast-PREDICTED: similar to pol-like protein [Hydra magnipapillata](ref|XP\_002166314.1|) 4e-07

MLHKKGPRDDPGNFRPISLIGVDVKALSKVLTYRLQLFLPNAYPHRPEGVRRGPVYTPPR

EVHG

>contig50317 Frame-0F

MSPNALAPNDILTDDNYFMWEFKARMTLARKDLLNHVMVKPESAVLREIPERKVADMKAL

AVLVKLLSPTYQCMVRECETALEAWEVLQTFFAKKNLHNRVQLRKQLHEFVMETGTSLMD

HLLKFDELCLRLRAAGDSVD

>contig51295 Frame-2R

MILDERRGPVMEVQDAKILPFDVASCAAAVWQCMEADATVMGGTTRDNLWLKLALPLRQH

RGPDAELVLRCVIRRVVTQPVGRVVFVW

>contig51310 Frame-1R

MAGRPYLHSRRFEVYTDNSAFKWVLHHPMLSPEMARMLTFFFQFVFISHYIQGRSNVVAD

ALSCPPVPEAIHQ

>contig52034 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60981.1|) 1e-120

MRLGVGRTSILQPVTVQMLYMLQFGNPRMSAHQACMVVTAVAHLLPRESRRQDWVWRSFQ

AASKMILSEFNGDATTAEVKTRAAEVLVPLAQSFLFVDRFDADLFHRTFNEVNSGGLDKL

DMPPYKLRILKSKLYQVHLDCELQDRSSEFRLNPALMEECKRVFKSQQTRIKNSSFRLHH

LVCTALNELRIENETMYATESGYHLDVVTPKLNIAIELNSSECYQTLEQSDENNDP

>contig52180 Frame-2F

MLVIAPPSGSIRHSSCQAHDASLSISSLWSCSNRDHEKIDNCMQRNLFLIMWTRVRVLQG

R

>contig52265 Frame-1R

MQVRQFNASYTILHHQKSLIPSAGHAALRGMSACLSNHIMCTILP

>contig52548 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66701.1|) 9e-13

MQTDVFGNIPIIMMLFANGSALIKMFAEKDCNSIAFKSVG

>contig52809 Frame-1F

MTILLQTIDKARKRKLVRRGGREKDKKAKALLAAASMPVHDDICDAVASSTNASSDGESS

GSNDELETTVNAAIQAATIASLAE

>contig52892 Frame-2F

MQNKDSMMLPQIELIERVKKLHAEADPLNKTLETAQHSHKNVTFDFHAEMVAALQRNKQL

QLQLEFLAYALHEDRAATDVSGTTDAVPSYLTVCSVKAECESRPVALTMTQQLNNLEREN

FKLRNELEGALASVASALKKCSVGFSSTLSTAPSLTAEISETTSTCSRDDMEEPEHENAV

LFLVFVS

>contig52944 Frame-1F|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY66197.1|) 1e-07

MGVHLSILGMRMYLINGSAFTTIEYENMQVQVGAEHCIVAINGAPPKEN

>contig53033 Frame-2R|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY68210.1|) 8e-25

MHAGDYPIVSSKSSVVPELPAPFDLSDKSNNNTAAINLTTLKSTSGSDSSCGNSWWKRIT

AIRHKRRRTDDRAESRNAAQEMYIRSILESFLSSISSKERNSIGNVHSSVDDSCSNSSKT

SSEQAFNKRRKERDKIETFHTIASIKTIAPAEQTRDSGYTCL

>contig53763 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60956.1|) 6e-10

MNIFLELFTGSSKVDSTCQSLDRRNGHHTESPPVLPSVRHLA

>contig56027 Frame-0F

MAAADASIYAALQQRGWLEGDANWTVADLSSDALIVIVLKFLTQLQDASYHLPRAEAKAP

FGVAARHRVGSQLAKILKVCENL

>contig56052 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54793.1|) 1e-105

MAAVWRRPGVLLSGAALYAGVAFTTYVVLYDPRKREGDGATATVDDARRRKIFDTNAAKY

DKEIDWDERLTGISLMRRFLLRKAHGHVLEVAAGTGRNLAYYSPTSHATLIDFSREMLNQ

ASISQQQRLASCDLQVMKAENLVFNDDQFDTVVDTFGLCSMDDPVRALKEMQRVCKKTSG

RILLLEHGQSSFAWLSGILDKFADLHAQKWGCHWNRDIVALLDQAGLEVETMHRFHFGTT

YFIVAKPQAAGAH

>contig56799 Frame-0R

MDLKKIITQFSLIRSSSYFRDEVFPVPPCGSCVGCVYHL

>contig57059 Frame-0F

MHRIRYEAKKNWYYNALEVDGHMPKKSEVLSHGDLLKHAEVLAKRLVILSNCNFDHELRL

RDTFIY

>contig57341-1 Frame-1R1

MRVLQIFLAHKGAERPQPLALVAATIRNEETFQEFLDQLAAHEIKYKDITATSLEKK

>contig57411 Frame-1F

MVAIHASHKFWDVARHNVNSLIGQLNMWKCTVLVTFDFIC

>contig57600 Frame-1R

MIKNIYFYSGGNLRALLWGKPEAKHLV

>contig57864 Frame-1R

MGGRSPRVKCAKIGHDRRLKTSHSKRITKKANKQKALAL

>contig01004 Frame-0F

MQSTALPDPRVEAPSGRTGVHCHRGTSGRPQR

>contig01754 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68414.1|) 4e-37

MLFSLYIINKAGGLVYQQDLSPLAPKLSSNDHLRLGSTFHSMHAIAALAAPTNSGGIDSL

ETSTFRLQCLQTLTGIKFFITAAL

>contig04414 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54642.1|) 1e-68

MLRNFFFSARNYLDPNCGQVLVSLRNTSFYKRWKIQDQAAASGFQLRRTEEFNAKIYSAY

KPQRTHPAAFRGEPPSTIGALYFIFTLDKTIGAVDTRNWDFQKPILSISFDSSAKAMASA

MAKKIVAPSMERYSFCQLCGLNFSNIKKFNGHINSAKHAKKLKALKKIV

>contig04605 Frame-2F

MPSLKLLVVALAAMQLTFVNATYLAGNRKSSVDAFYSNPNGRRLVEVKPVSWFGTYASNS

GNRRLDQTEEERLFGLGSSKALTHLVET

>contig05835 Frame-1R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY67821.1|) 2e-26

MLISYSLDARPETNYSPNNIAMSKELQFPENFMWGTATASYQVEGAVNEGGRGDCIWDAF

SRTPGKIVNGDTGEKAIDHYHR

>contig12695 Frame-2R

MDKYRRMEKPRREEQKVETDPNEIRITQQGKVRSYISYANGLFVEKNERRVVLKAMGNAI

SKAVTVAEILKHRVANLHQVTRISSIETVDVYEPLEEGLDRIETTRHIPGISIQLSLDAL

ERDDPGYQSPIPLDQVQAGSPSLDRREFKKSRAQHKRSGRRENSHVDAENTATTEETNEE

KDAGEAAPMSRGKRGKGRGRGRNSNGGRVKTVQTTVDGDDAGEAQQPVDGETPRKLGRGQ

RKKTTGSDGGEQAEEGDAVEESRHYRRERYNGRGRGRGRGRGRGRGRGNRDVSHDREGTA

EPVAATVATEATIPTES

>contig18367 Frame-2F

MEADHNRLNAVKALHLWHRCDKMSDFTDDEDRQLVQLAHLFSRKGRQILWGTLTQRMKGT

TKSKEALRQRLKTLKRTYGRNLEDFPEWFFKQSLHAQKSSQLLRKSRHSTIDVKTSNPRK

SESKSIKEARRYKKRQRVKYEP

>contig18837 Frame-2F

MGLQRCIGLGRKVGINGIAHRYRVNHATQSWIGYGMSCFRRRSW

>contig19395 Frame-2R

MCRLRPALAPSPQKLHLLLVQLIPYNDHYRHCDVTYFLKTLQSMGPCKKTYTVLGQSEIN

>contig19687 Frame-1R

MICQRPRRWISKHVLAIARTCYDLCASKDFSFELLVSLSKTRSSLRISLLILLSLIDKAS

LTASWHMHLSKLGF

>contig22436 Frame-1F|Blast-dihydroorotase [Phytophthora infestans T30-4](gb|EEY64470.1|) 5e-48

MWLASTQSSTSRKAASIVAMAFSTDIKWTNARPDDFHHHLRDGDGALSCTVPHVASQFAR

CIVMPNLVPPVTTTEQALSYRERIMFHVPQEKRDPTSPTSFTPLMTLYMTDGTTADEIRR

AAATKQIFAVKLYP

>contig23417 Frame-2F

MACAVQVEVDMLPEPKMEPLRRVLQSPCLLPDIATIQRLVIADSRYYRIKIMTSHVAEER

RPIVTNQIKTANSLRLELLRNKNVVYLKRRHREKSNFLANDTNNSDDNRLGSLFCAYFTP

AGFNDKSVRGESNNEIDQLHRISWGSSWWATHINLWALESVREEPHLLMQPYLNALHALF

RLQQVPQLACAMEVIDLRLFSEQCCHYVPLMESTFKSKGDFKAMEEPKFIDKSLPIFEFG

EWLSIQMEQALGVLWHRTSTCITSFASAQVQLLAEAAPSRLHTKEAQDLMDPFLASVLMR

YFA

>contig24889 Frame-1F|Blast-DNA repair protein, putative [Phytophthora infestans T30-4](gb|EEY68870.1|) 0.0

MKDDLKEPTSQKTKGKSPLHQIQWTRIVLDEAHYIKDRNCNTARGVFELKSTYKWCLSGT

PLQNRIGELFSLIRFLRVNKFAYYHCNKCDCQMLDYNFPDRKCVQCTHSAIQHYSYFNKK

VVIPIQAYGYVGEGKLAMQRLHNDVLQHILLRRTKEGRADDISLPPKLVRIRKDRLDERE

NDFYEAIYTQSQAQFNTYVSSGTLLNNYAHIFDLLIRLRQAVDHPYLVIYSKSNPALQIP

NSAAPLVEEQPFRSNKTVSAEDERMCEICHEYVEDKALANCGHEFCRECVKEYIESLPIG

AEATCPKCSKPLTVDLSSSVEEVRKSIKDEASALTSRSPKTLNLASFHRNSILHRISDVH

AFQSSTKVEALMQELELMRAHDPSGKAIIFSQFVNMLDIIQHRLQLGGVKCVKLSGNMSM

SVRDRTIKEFRDDSNVTAFLISLKAGGVALNLTVASHIFLMDPWWNPAAENQAIDRTHRL

GQFKPIQATRFIIAGTVEERILKLQEKKRLIFEGTVGGSASAICRLTEEDLRFLFAS

>contig25136 Frame-0R|Blast-vacuolar protein sorting-associated protein 35, putative [Phytophthora infestans T30-4](gb|EEY60193.1|) 1e-22

MEHGQMRREGEFRYRAIVRCMDASGFPDDGVSTSSSSSSR

>contig27141 Frame-2F|Blast-Major Facilitator Superfamily (MFS) [Phytophthora infestans T30-4](gb|EEY59855.1|) 3e-81

MLVARTSNRMLILCGFVGMLLSAIGLTVSLVTSFSPLSILFVALYVTTFGASLGPLAWGI

MADMFPDDVRALGCSICVGCSWLCSLLVGLTYPYLADALASFSFVPFMYMISLSFLFFFT

LVPETYNKTIQDIQDEFSAKWQKSKTTTPWRMSGGSQIPVLG

>contig27479 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63833.1|) 0.0

MSAVERAKLLLTKKAGAARTTSSTAIKRTNPLTDILKGGCGSVVGGVHNVKRPRSTKSDK

PGEIKIQGGRTSIQLPLESFLRKEDWDSATGSPLDLVLSEVAFATNNTLIIHATLPARSL

RCCFNVSTQSSMLSGAPYPGTVLYHCNPRRQRGGQVVQNSNIDGRWGCSQPLPRFPLTFG

EPFTLRLTIVPSGFLVFIEEIYQDEFKHRVPIREGENLVLTVPTRDENGNPEGVIVHSVW

WGHAEVPSNLDTRRRGSIGGFRGGDRGGYRSINSGRGKERFQLTPHPYEVYVGNLPHGTS

REELSFLFQYLGTESVRITARGFGFVTLRSAEDMNRAVEDLDGKVLKGMKLRVSCALPPK

>contig28207 Frame-0F

MEHDLSGLLNHPRVKFTRTQIQCYMRQLLTGIAVMHRNKIIHRDIKASNLLLNNQGMLKV

GDFGLSRFWNEVNAKAGRYTNKVVTLWYRPPELLMGSTSYDFSVDLWSIGCIFGELLLGK

PILQGKAETEQLQLIFGLCGMPTEDTWPDFFTLPGAENLRLDDKYICPLRERFTNFPPHA

IDLLEKLLQLDPSKRITAAEAMNHDYFWRVQTCKPRDLPKFCVSSTHEYQSKKRHHEEMA

AAAAINGNSSKANDQNRFLRQRGERSGRRERNEHYGEEYTRSDRSRNYRPQRPNSDYYDR

DRSRSRERYGDRDRFRDRERR

>contig29213 Frame-1R

MLGGITCDKAKLFDTARDLCAPAHIAEVPYQPCLVNSDQ

>contig29499 Frame-2F

MESPRATQFGALVTGRRYRLLTLAATGTAVASAVHRMRLHPPLDSLGLIMQLFGKELLSS

HISATIVLHAFLLSTYSAFLLLARVALGSLRPLELQQTKETILPFVMLRCQLLVSTMKPS

GLEQKMEICVLVVWLTALAVLRALLVLTQARFQYQMTRPMTQFRDLQRLGAVLGGIIVFN

LGLAATCGRLGHFPVHIMHVPWFEASLMLLKTLELGVQVGYQSLDVHASSCSMKEETEMS

ENNELHLLLLQTVLCGCYLVQLVLYYLYVIRVDQFRVSLFDLILILNVKNATMRLLNKVK

HVKLYHYVVLDLDHLFKDATPEELASVADDVCAICLKGMSTQAKKLECGHLYHRLCLRQC

LQKASVSETLVGLDPLTSMVNGLSIEGIGRTTAFRTTATSSTSLRCPICRKQVCGDKSMA

RTVSEEHRRRLVAARPEEPHEAQGIPIGAATGPVVAPEEVIRFSTAFLPRWVPFPHFSFE

IVRHRRGQRIVEVTQAMVQQIYEVFPQYTLDEIRADLVRTHSAERTMERILNGRLEAQRL

ALEQQSPDRSVMDSSGVLGDAVIDLGEDFRWSLSTLASALWGLNPSVPTDSARPRQEDEI

ATDIGTNAPSETTT

>contig30633 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53454.1|) 2e-22

MVEHIQSCIRPVLTSLHNDKCLQSNMHYDDPLPKIIGELEVL

>contig30646 Frame-1R|Blast-vacuolar protein sorting-associated protein 33A, putative [Phytophthora infestans T30-4](gb|EEY56248.1|) 1e-121

MMLVLSNLEKAGLFSRRETLWNEASGFNLARKSFRLLNEDVDPRDPRDCAYVSRSHAAGY

APLSVRIVESAIKPRGWSAVQEGLRQLPGPSGEVSQTFNKNAGDDSTAPAAASKLDNFGS

EDRKVLLVYYLGGVTFMEIAALRHLSRQPDCQYDIIVATTKIINGDTLLKSCFDKEVLRF

LKL

>contig31722 Frame-0F|Blast-2-oxoisovalerate dehydrogenase subunit beta, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57864.1|) 7e-29

MTVLSSSRDAIKRRLQHAPLLRAFHVATPLAQGLEKVDNLLPVVETQQMNMFTAINDAMR

LAMESDPMAVLFGEDVAFGGVFRCSVDLRD

>contig32099 Frame-0F

MDFDEDMSGLQIEDLGEYFLQTDNDDNWKGFLLGYADEELQQDPQPAMNAQIAMNSVASA

HSAAQYSTSPPHASISEIFKYSGQLEIDMGYVSPGKDIAKLLEAELPTASANPDAEVANV

SSKQTSEKAFLCPYGNNRPATSMQCQNINMDSSDEMNNSKTSMKAIRYGYVIVCAFYSRK

KKRCSTLNTISYSYELFVYLT

>contig33009 Frame-1F

MPTACYYLSGEDGEPEVGPFVGGTTKETDPRAPYPNNVWYSYPNSCPLKKWGEKASDCRA

ATRKGLCDIGVMPDGVTCTFAYRVLGFIPIDDLVEITSMESNTTGKTYADFAEFCEDGGI

EFQATADGEWIDGISFWENPQDEEANAERALKLVEAYYNLTNGISTKSRLDSSIIGHMLP

LPSPKELAAENPPCYRNVEICNSRFGCMREFYGSTCTVCNSTSDDCDTPPSDWTFPTLAK

AVGKNGGTGDASADGSLDSTSPVRRS

>contig33100 Frame-0R

MLHTYLSEVQFASINYMSPLKALTGQAPKLTEIVVFGSACTALRELKR

>contig34071 Frame-0F

MTSNGVRIEVEGSAVVKQSTKEAEENTDSVNDEVDGSKLDTSVKISRKKKQEESSQVLPE

AVENRATWEETTARQHRNGAKENGLVSRRMKQIATRDVKKAEESRQQEHQDDSSHIRRIC

IGCDASLLESIEWAVASGSEVDAGQTLGTAGRLEAGSQRLMQAPCKGRFYVLSEAQPCEV

VDKTAGALARTVAFIEYCTHPVRNGRTCLMCLAVVEENEENEGTESVNVVSHGQVMRLNV

EEAKKFDSDNIRRQLGAKKLSLVLDLDHTLLHAVRENDIVGEIMQLDDIHFFFVPGLAQQ

HVVKLRPGLSLFLMTLSEFYDLFIYTHGTRLYAEQIVKIIDPDERFFKNRIVARTDTPDM

FHKSLKLLFPSCDDSMILVVDDRIDVWKENEGNVFLIEPYHFFKCTSEINNASGRGVSGM

EDFETDSREDMHLAQSTLVLKHVHEEFYAGHEQGMQGAIAEEQMAGHGRDVKAILSA

>contig34369 Frame-1F|Blast-ribosome production factor 1, putative [Phytophthora infestans T30-4](gb|EEY60297.1|) 1e-127

MEPRTIDNTREEEVTMVSMEGDEEIDADERDDEFASIFNNEEVPKLMITTRPFPSGDLYH

FIKDLMDLLPNSFYYKRGTFDIKEIVQFASNKKFTHLIVLSEKSKICNGMLVSRLDDGPT

AFFKISNVKLTSSIKERGRRTNHQPELILNNFSTRLGHRVGRFLGSLFEHQPEFEGHQVV

TFHNQRDFIFVRHHRYTFENDKKARLQEIGPRFTMKLRWLQQGTFDTKFGEYEWIHKQHQ

LDTSRRKFHL

>contig34765 Frame-1R

MFVEHFAPSNDFYAAPASPSSVSSRGLWTMLGIVAFVLLVLSFLLANVVAWCLQLRRERR

IQRKTEELFDKSTHIELPFVPVTILTGFLGAGKTTLLNRILLTEEHLPYKIMVLENELGA

VSIDHTLLQAGGKEQDGIYMLNNGCICCTSQGGKGKGGDELERILDYLLQLIKKQNFDYL

VVETTGLADPGPIIETFLQLRASRFRLDAVVTMVDAKATQRYWKPDIQAYKFPIELQRQA

LYADILVINKVDSATKEECERLQQELMGINEEATVFTCVKANIELDKILHINTFDAVRFK

MQSDGTNREKGSIKARGQHTGGISTVHFEVEQDVDVAAFSEWLLDVVKRYVKGVDILRVK

GVLAVAGDAKDRQCVVQGVLDTYTIAPGVPWGDGEQRVSRLVLIGQGFDRLELERSFQKC

LINNCEPKKER

>contig34901 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63606.1|) 1e-69

MQEVSAELHQQLQALGINPSDDVFRTGSEQYDQNGLCSPIPQEVRFLNGELQRCPVEGVG

LVLAIFSGSGAVYEFVRTLRKCIYGKVKHAVRLQMLPNGTFVRTQFEVAIKVMSKSIIEE

GHLQENPLVELAAQQYLSIPGHENVLT

>contig35313 Frame-2R

MTVACIKNWSQPNKLHMFQKISTILKNVTIISKQKNSAECKLSVFSVAKRWLKQEVKGNR

LTHSNAKATAQPCVCRQGF

>contig35366 Frame-0F

MKVDATGVFEVMFFGSMCAKYYLTLHEGDLISFRGYSATNPQELQWTKTTSPLVWYPHDS

SGGAYHVPKKYWKFLEMTKVAPRLLDYTALASQQATTWHLHHLRPSWLECNFVTTLNTKY

LDKKANGHLDSMYFDFVGVVLVVGRICRKKKRKWGGDSSEVTEFRMIKVIDNSSLNELVI

RLSECAQPAVFRALEPGNTLMVTKLQWTHLPDVDAMQYAKTSDFSVLRIDEAVLPFYSLD

ECNSNVSFARKMRKSAVLVSRKTRA

>contig35599 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56597.1|) 4e-47

MWQGFEDPSTYWKGLCHGILFMLPVLAFLFRKWKSAAAQTASQHPVLGMSFLNELFAFEV

VLVAGAELKAVRDQLKSAQEVTPPNDKKVQALRERIVDVATVLQNKLETITPIVSFLLKE

SVGIIKNYQAEKKDDANKTD

>contig37250 Frame-1F|Blast-reverse transcriptase [Phytophthora sojae](gb|ABG66533.1|) 1e-06

MSEFALNNAVHASSGLTLFFVNIARHPRVPFLLLGLASSSTPVGCEKPD

>contig37953 Frame-2F|Blast-delta-1-pyrroline-5-carboxylate synthetase [Phytophthora infestans T30-4](gb|EEY59588.1|) 0.0

MRKETMTHSYTFGGIANKRKITRHDLKHAMRIVVKMGTSVVSTNGEPALGRIASIVEQVC

TLKRQGKEVLLVTSGAVGIGRKRLNKQILLSASLRTHVQGNQQMLALEKKKGAMAAAGQI

GLMSLYETLFSLYDVACSQVLVTASDFKTAQNRANMRDTILNLLELDVVPIVNENDAVSA

SPDGTVFTDNDSLAALVGGEIEADLLMLLTDVKGLYNKPPTLPGAKIISVFRPETSSFKI

GEKSSVGRGGMGAKIDAAQSAISQGVNAVIIASGFENGVVASIMNGASLGTLFVANPGIE

SSDSVSAEKMAIAAREGCHQLRALSSMERTNILFCIADELKSNSKAILEANRKDLLMAQK

SSIDDGLIARLKLSDEKLQTLCDGIRSIAQSEEPIGRLLKRTEIASGLVLHQETASIGVL

LVIFESRPDSLPQIAALALRSGNGLLLKGGKEALHSNALLHKIIVNAVNEASKGKVTKDV

IGLVTSREETFDLLRLNDVIDLCIPRGSSSMVSNIKNSTRIPVLGHAEGVCHMYIHSAAN

ISKAIELAIDAKTDYPAACNALESLLIDEAFVSKNQDKEILTKLEEAGINLHIGPNAAKL

GVATAKSRITNALSAEYGTADLTVEVVHSIGAAIAHINRYSSGHTECIVTEDALAAEQFQ

QMIDSACVFHNASTRFADGYRFGLGAEVGISTGRIHARGPMGVEGLLTTKWKLTSDSGHT

VAQFSSAKTDHPLKYMHKKLNLIKKEAHVARPRSSRL

>contig38048 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69216.1|) 1e-20 NOT\_ORF

MLSVSTAEMQSH\*AYALRTWCRRNWKDTAVIAAFDDKYKASRLIKPCVRWGRNCFAPRIY

HCARP

>contig38211 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56944.1|) 1e-76

MTDGDLWRDRNKVFIAGLPLHVDDDALYEKCKVFGDMHQSKVVYDPKTGRSRGFGFVTFS

DYTNALDAVDQLNQSKWEKRTLNVRFLQPKNGSNPVGKDAIFRANRPTKVIGPRPEGCTT

IYVGNLAYDITEEVLRKVFDHCGSIRAVRFAEHIQTKEFRG

>contig38783 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53849.1|) 6e-56

MGSIQQGVAVSITADALMSFSNIVHCGQMKKLHWLWMTRKTIQLDPPNTQCIICSHVPSR

PQLCGICLNIMCSRCSVTKKLCFLSATTRQVSQRSVVFCVRCLLAGLKADALKVAADEVI

RQNPLDSFDISTNSTPSSRMVSPSSTNPPDATREFFG

>contig39249 Frame-1R|Blast-AP-4 complex subunit epsilon, putative [Phytophthora infestans T30-4](gb|EEY65834.1|) 1e-138

MSGGHLSKEFFELVKSIGESKSKQEEDRIIIHEVAMLKRKLSEVTATSSTSSNLVNKRKR

EFLIRLMYVEMLGHDASFGYIKAVEMTASTNLMQKRVGYLTCSLCLSPTHEFRFMIINQL

QRDLQSSNHLEVCAALMAVCKLVTVEMVPAVQPMILDLLRHDAELVRKKAVMAIHRFHQL

NPDSVKDTGDALRRTLCDRDPSVMGATLCILHDLAEATPTDYKDLVPSFVSILKQITEHR

LPREFDYHRIPAP

>contig39564-0 Frame-1F0

MPMKPEPVAEPTPVPEAGPVQSSALVQASPVSTSTAIEAQGQGQGGLGNMGSMLMNLLAR

TTETQQQLAAQQGVMFETLG

>contig39564-1 Frame-2R1

MSIEPMFPRPPCPCPCASMAVLVETGDAWTRALLWTGPASGTGVGSATGSGFIGIGGCCS

RNAVSPAGCSCDVGGDTTFDWESAALDKSSRLG

>contig41134 Frame-1R

MKLLLYVHHFHVSGSLDDKQRASLTLPAGCPVTLLSGLCLGCLLLFPYSKQAHRSGRCGL

PCHRLLF

>contig41901 Frame-1F

MRLLNLRALVQRIKRIHYLIRARDHRMRMGSLDEPMRHEYRPTPNQVPRQAHAEPNQQHR

KYK

>contig42250 Frame-2R|Blast-heat shock protein 101 [Phytophthora infestans T30-4](gb|EEY64644.1|) 0.0

MNPAEFTDKTNEYLRRAQEMAEEFGHSQLTPLHVAYSLFEDKNGTAKRVADLVHGNVAGF

QQDVMAQLKKLPKQTPAPESVGADSALMKMLKYAHKMRKDMNDTHLAADHLVMALFNNSQ

VASLLKSHQMDENQIKDAVQRIRGGRPVTNASAEENYDALNKYGQNLIELAEAGKIDPVI

GRDEEIRRVIRILSRRTKNNPVLIGEPGVGKTAIVEGLARRIVVGDVPDSLNCKLISLDM

GALIAGAKYRGEFEERLKAVLKEVKDSNGKIILFIDEMHLILGAGQTSGAMDAANLLKPM

LARGELRCIGATTLDEYREHVEKDKAFERRFQQVMVREPSVTDTVSILRGLKERYESHHG

VQIMDAALVAAAKLADRYIKERFMPDKAIDIIDEACANVRVQLDSQPEVIDELERRQLQL

QVEATALGKEKDELSKQRLVKVQEELNKI

>contig42728 Frame-1R

MLVLVGAQMMMNYYCVNAILINVAKTIRYGFLELAGSTVFHNLDVDKGSRGLMPPSPWAS

SKDA

>contig44722 Frame-1F

MTADNAVVQFTFSAWNKFSHVDIRKLLAEGMKDMDKQEIEKLNSIIELYFIIRGPD

>contig46870 Frame-2R

MQMLLAYVAVAMSAVGCIGYYKGRDADEDENVRIYNMAKRAVVKDHRVFDSIGYPKDFER

IAAFNADGSPIQPKSYEGSFRITGDNGTVVVHYRQKRPEEKNDIVTFDQLDVDCENGTQY

SALESFMQNQDVVAHQKAASLGNKMFFPIIGGVLIGGVASFFAIRILRNRPFYVHKLVLD

HINNHDTARQFLGHPIKSDRSKYVGMLTNEIANYTIACSGSKRSGTIIVKADKKATFNVK

GDKSSEAMMTPGTSWKFSTLVLSISRNEKHTTKGAKTINLLSGGNATLAPSKQA

>contig47099 Frame-0R

MNLWKITLELGDMPSSQALNCKLKLSTMPKFLTLSLTKRIITYNDIQISTTQCSDKMVAR

KMSRRLCVSVLEEQPNLTAQSLDK

>contig47613 Frame-1F|Blast-ubiquitin-conjugating enzyme E2, putative [Phytophthora infestans T30-4](gb|EEY56890.1|) 1e-104

MYMRSDFAALRVRKDVNELAKAKFTCAQARTRVEFPDGANNMLQLIFTISIIDLSGPFAN

GDFTFLVDIPKTYPFHAPGVRCLTRVWHPNIDITTGKVMMPIIGKDWRPVLSINTVLLGL

QLIFLEPGIDHALNITAAEQLHQNPESFKKEMQQILCGGRFYGVDFPPHPRQTEMQRHKW

CLRIKRHREDAIPLIDSDWDGMASPDASDNINIEAPVLMDCIGDPARKRSR

>contig47688 Frame-2R

MQGLFLGISPLRLEKNLSIGMNVHSWHSFANLLFVDQPVGTGMSYTQGNDYRSNEEAIAK

DFYEFLTKFLQRHAVYLSDGTGSGKLSREIYIFGESHAGRWIPVFSEYILNRNGELDNQI

DVKLEGIGIGNGWVHPPIQYEYSDFAHGLGLLTFGQVKSLKKSYKECMSALQAKTYYAKS

CFNNLDAITGSVMPGKGGYTLNYYDVRHYVQNVSAYPFEQSTIVQYMNLIDVLKAVHGNE

DRSFRFNICSNKVYGALKKFDGVSTLDKVASLLQKGLQVLFYNGQWDMMCNHYGTEKLLL

NIDWNGSEAYQQSSKYTWRVKGRKEPAGFAQQGGNLTYLVVAGAGHVVPLDVPDVAADMI

YRFIHRIKFKDKEQTVTNARLNATDLSFPYCYSSSKSIAANASVNQAVKISAEADTNNTW

LWMMLLTAVFSSVVIIFATIGCLRRRRQWSHELVSQISDDKRVEQPGNDVLKENLDDSRN

TIEHKASNSESERACSPRMEVTDA

>contig48869 Frame-2R|Blast-Voltage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4](gb|EEY66467.1|) 6e-09

MQNPHEEKQKALLQRIAGSVARLHEVIKEINTQIE

>contig49398 Frame-2F

MFWSAALDLKTQRLPCRSYGSFSRSDVISNSFHIPQSIPEHQPVSQFTSPLPDRRRIEEY

IEHPDTVLARARQVTEHTQTALKLLLQASAQTAPKQNIALEMHSFSKTGTFATLAREVEL

AECTALLKPLHSREVLTTQESRTEQNYWMQELERRRAGLQKSRRRTCTPMSERATTSPLK

VGVVMCSVPLVLVIAFVLYMFIFGDASSDVINVVYQPMSIGEFSIRHT

>contig49426 Frame-2R|Blast-DNA topoisomerase 2-beta, putative [Pediculus humanus corporis]gb|EEB16240.1| DNA topoisomerase 2-beta, putative [Pediculus humanus corporis](ref|XP\_002428978.1|) 7e-18

MYIGSVETTRDTMWMASNDSELSNDKLRMKPQTVEYVPALYKIFDEIIVNAVDNKVRDPS

MR

>contig49453 Frame-2F

MAAVLPFASLSHSDLTMPLTTNALPSSAMKKRPLSPLRSHDDVRNVVVAGRTTSEPSMTE

PAVAFDPRQIKLLKVIGRGTFAHQVALA

>contig50316 Frame-2R

MLQEQLNEQEPLRIIVLQLQFTAAYFITNCTSDLHVTLLDGVAREEAVTIPLAVSCSDHD

PAITSSIGVAQFLELVRQSLLQRFYHQ

>contig51148 Frame-0F

MMAGFTSGRNPRGYQKEAIAPIDEAAEPILADGITSNVEIDSVDVPPKLQMPTPDVEWWD

VEYLPKEKRDMVDKFGFLKVKVLKEGRVASISYADMKLKYCGTAHVVEHPARLNLIVKQN

SMPVGVPLMLTAAERKKIRRQNRADREKEKQDKIALGLLPPPEPKVKLSNMMRVLSEQAV

ADPSAIERKVREQIAQREKNHEMRNLARKLTPEERREKRLRKIKEDAAKDIYVALFKVPD

LSNPQHRFKIDVNAHQFHLTGGVLMCKDSNINMVVA

>contig51409 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61848.1|) 5e-26

MKREQERITTFFQRKQTRRISVGSIDSHEGDDATTVVSISSSNKLYKAQYLLEDARGQDE

PELHMNKRKALICREAREDLVGILQFRELVGCASDQRFISGRQHSRRRRKQQLVRWALSH

FQRLPLKLHLSPHWEQAAGQLSTENFYA

>contig51500 Frame-1F

MDEQRIKKSLVVLKHAIAIGKDEEADSTYARRTLLVLVHQSIRYSDTHPDHVTALCHVLA

DTFQNLHVSPLAVVSGALGIFRTPRSRRFLQESKWGLSWLCSQVLLRLMRRSSQFPALSM

VDDCLLHLQSLLLGERFQLGDSLSSNTSRISRSRQQSHDTVFLSHICALYSYLCKASSQL

ARARVLLFDLVVENPTLRGLYLTMVMLEVYPAMIVREFDHECIERRTLLQDTLLHVLVAI

SDAAAAGHELL

>contig51618 Frame-0F|Blast-reverse transcriptase [Phytophthora ramorum](gb|ABG66535.1|) 3e-23 NOT\_ORF

MARWLSFLAEYSYVVHYKPGSTNIIFNALSRRPDVDPRTNAPVSAATETDDDDCAECVTL

GVNAMAVSAVNPLSVDIPNAYSCSEIYSPIVRY\*CNSSDEALQSLPVRTRAHITRYALNS

YVLTYQIIRFDSPRKVVFLDNDPRGRIFREYHDSASTAL

>contig51683 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54850.1|) 3e-20

MERTPSLTEQMRAATRNIHNVSDNLMNLKLLVALTDKQLYGRALMLFYYVYVQLESTIEA

YKDYEAFPGL

>contig51856 Frame-2R

MLSVNPPRIRNLAKLNNVTMISMANVSFQYENSSAIETSQWRLERLNLSINYGDKVVLVG

RNGAGKTTLMKLFSQILKPNDGSVEYFPGARILAVLQHAVEDFKRQDWSRHLT

>contig52035 Frame-1F

MRKLCLMGINRTVTTISPLFTLREHRNRESIEEHWATVHARLPTSPLVVPANHPWEVHGV

QCFPSPTEIATSTKTACASLEFADKPTYRSHDAYLKLVMSPASTSAYAASPGP

>contig52390 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54036.1|) 1e-28

MSGFERILARVGGDALRSYCSSAIEDELRNLQNCMKTCLESVKQAQKVQEAVAKLDVPLS

RENAATGAEIKRK

>contig53762 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64078.1|) 5e-08

MASNELATILARRRSKAGGDSKASSLGVDNSALSTSEMDTVTGASSSIAERIARLKQQNA

>contig54914 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58190.1|) 3e-46

MILCEWLLAPPGILDASELFMNELYQDHIAAILVHTLANSKLQPRKGSFNPLALKP

>contig55359 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62979.1|) 2e-11

MWNQVLRRIVLAEEKQQSERRRQQLAQATNLVSSSSNAAAASSDITVEVSQLAEIGEQ

>contig56053 Frame-1F

MSFVTLKPATGRCRTVLLVALVLKGCIESSSVIATVSDNETTLSIGSGLGTNEDRSIKIG

HVVPAVLSSNPFAAVYKRYAQMYSAYHKKLNQDEEFEELVRRYTLPHIALMVASAHIYPD

LNTLVLRPLLFKKWGRGNFEGAFKDLNLNDASEALLARWQIWAEFGEWHGRIPIRSSHMD

QVNSAYDA

>contig56703 Frame-0F

MKVKRTWSRVNARHGNLLGKKHISRKHGKKK

>contig57058 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69909.1|) 1e-106

MHAHLVRSKGLLRAAMGIRSASTVGGALDEAVVRMPHKEALRSIKQDVRYSFKELNAAVN

ELANGFLDLQFESGNVVALWLPNSIENVITQLAAARAGLTVAIIEPEVSQAEELAFILQD

SNASGLVFEPKQGGRNQTEIVQGLFPELATFRQRKEVFRPKNFRHLHSIITTSWDPVEGM

LNLNGMMINSPEPYVMKAVSKLLSKQTPLAVTYSKVDGHMPKKSEVLSHGDLLKHAEMLA

K

>contig58712 Frame-0F

MEAYMGDRGALIQLLKDGGKLVPRCSK

>contig03096 Frame-0R

MQNQFNQIFHEGIAGYKLMCFSTNDDEVEQQRHRHGPQSLQQQRLRHFPIQRYRRSSPRR

>contig03395 Frame-1F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY61076.1|) 0.0

MAEDSGMLDNGAMVWVPHQDQVWKKAVVVRRLDDGVSAEVRLQPGDDGEWDTDDGVEQIV

NIRNIARLAGEVSDEAMPICNVFDAAGANDMCTLNHLHEPAVLKNLELRFLKTMPYTYTG

AICIAVNPYQWLDLYGKELYLQYLEEPRESLPPHPFALSAMSYMDMKRTHVDQSILVSGE

SGAGKTETVKIMMNHLASISGGGIHGTKVIDQVLQSNPLLESFGNAKTKRNDNSSRFGKF

AQLQFDTTGSLVGCLCETYLLEKSRVVGQTEGERNYHVFYQIFCLSEARKKALKLRGDVT

SYKYVTEGAEVEVTGIDDKQCLKETQDALDTIGLSIDEQNAIFEIVAAILNLGEVAFEQT

STDNERSHVTNDDIVDNVGALLGTTITALHSTLLERSITAGSESYTIPLNAEQAADLRDA

LAKGMYTQLFDWLVHRINKAICSTNHVKTHIGLLDIFGFESFDTNGFEQLCINYANEKLQ

QKFNSDVFKDVQQEYVDEGIPLILVTFEDNQPILDLIEGRMGIVSLLNEEVLRPQATDMT

FVSKVLDACSTHPSIEKNRINPLVFTIHHYAGDVTYNGTGFLEKNKDTLPTDMVQLLSSS

SNPVIATIFTPTLQNQRNPRGKNGKEGRQKGFLVGNTIAGAFRKQLSELMGTINKTSSQY

VRCIKPNAHKSANEFNRVMIVEQLRCAGVIAAIRISRAAFPNRLPLNEFPTTFSNDLSFG

CT

>contig04387 Frame-0F|Blast-cyclin-dependent kinase, putative [Phytophthora infestans T30-4](gb|EEY63935.1|) 1e-10

MKEVVVSSETDDDDGTYFTFLARSKKEHFTISCVHC

>contig04509 Frame-1F|Blast-hypothetical protein PITG\_22354 [Phytophthora infestans T30-4](gb|EEY59745.1|) 1e-11

MAARAKEVFKRYGRTAFFFHSTVFVSTLAGSYTAINQGVDIQAVAQR

>contig04602 Frame-0F

MRRKLKVYATLAVLRVAASVLLLGMIHPDEYFQSQEIMVRHFLPTDSALRRELFVPWEFQ

LATPNRSVLFPALVVGLPFKVLELVGIKLTGWLMLVTPRLLLCAASFLIDAVLFHVVGKL

SRYDKVEILQEKQEMVLMLFASSWPTLLFLCRPFSNTFELLVFALCFAVLYLIKPTRRVL

FGVLHAQTILLGSLLALGVFTRFTFPVFFFPLGVELVRQQDAFFIHASRKKELATSPSIV

RRIVATIIVVMQGVGAFISWGIIFVLVDTLYYRPELFHGTFDQMFLKNIRKNAIIAPFNN

LLYNTQYDNLKLHGVHPRFTHFAVNMPMLFGPLFVAFVLQRFPNRSVFGTLSVLFPLACL

SLAPHQEPRFLLPIIIPLYIFTVLNGNIGMMRYVTSTKSGQFLWIVFNLTLTLFFGVLHQ

GGIVPMLLSLSSIASTPTKGVIMHLLTSSCHFNGMDDRSRQLVGSVPLVFARTYMPPRFL

LTGMTLTSSFQVLDVAGNDLNNISDWISVHDLLETKTFTVLLVLPASVTV

>contig05256 Frame-2R

MQSASAAPSKWSDLMLQINRMILVLCLGLFVACAMAATCYITWQYDIIENAWYLPLTEAE

RSRPRVLSFLQMMFYYFLLLYQVIPISLYVSMTSVKFLQSRFMSWDLGMYYSETNTPAIV

RTMELNEELGQIAYVFSDKTGTLTCNVMEFRKCSIDGVSYGSGMTEIGRAALVRAGKDVP

MEPTLAYNQTPMPFVNFVDPTFFEAMHNSTDHAKNIYAFFEHLAVCHTVIPEHLESGEVR

FSASSPDEQALVAGAAFVGFQFVSRSVGAATVNVLGTRKTYQVLDVLEFTSTRKRMSVVV

RKPNGILCLFTKGADMMIYPRLQKNAAMERIANVTREHMERYADEGLRTLTLAMKILDET

WFQAWKIRFDAAQGNVKELELRKEGHGNVIDTLMEEMETDLILLGATAIEDKLQDGVPQC

LANLTRAGIKVWMLTGDKEETAINISYACSLLNNSIEQVIVNATICPTEASIISILTTAT

KAFHSKDGNEQVSLIIDGEALEMALRPRVAPYLLAFVQVCRAVICNRVSPAQKAEMVTLI

RTNLPKVRTLAIGDGANDVAMIQAAHVGVGISGQEGMQAVNSSDYAIAQFRFLERLLLVH

GRWNYLRISKLVLYMFYKNITLVLAQYWYGYLSGASGSKMYWEIGVQLYNIAFTGLPIVV

VGVLDKDLPAPFSLEYPDLYRRGPDRFFFNFYTFGRWIAAAVYESLIIFVVMSYGFNASE

NAPGSESRVEFGMVAFSLTVLIVNLKIWMIADQWTCLSFSLWFASVAAWFLLATIGTEVP

FFASFKIGYDEFGAFVPTATTGGYVLIMLMGCALALGRHIAYNLFQRTFYPDLAQLLQEL

IGGKSTYQRRLTLHDVEAESLSMSLDDVETTSYLSEFGHSDAAIRKAQHLQTFDAKASDP

LVKTSATLKIGLDSYAGTSVTSEGQVARCSTSGRTGYAFSCDEETTLAESYMASNSLSRA

DAISTAMRLSSSSLSGRKVVVRQASSDSARLRS

>contig06024 Frame-0F

MQKTEKGQVGNEEGKAHVPVSEKVVLQPKELDRTQFLASLKTTLFPNATSIKKTLMTLIV

KKSHVTQQASILDGNET

>contig07438 Frame-1F

MVMTMESEMVLLAMLPEEDRVLLVQTPGQRTIADLEEFIVDEYTRVFPHLPPLSRNLRIQ

KCVAPELVVDRRVQASVRHRIPHVFVDLAKNVHAANVFENMELIYIVANMPEKLEKLQNK

NSSLDAHHAPISKNALESLKAVTRKGRDSKKKKVEKEASQKSASKTKQPDTTKKVLDKVE

KTTTKIECDDEVKDTQKVACKESADAIQPPTKDAKRIAEKKYLGTGKATARKSIQKIALK

KDSDEENIAIGKIEVSKLRANKKINISKKMSQEPCDSNQIETDEDNSADLKVRKKAIPRK

SENALLKRMLAAKPGATDLGAALIVNLLNEVDRNGIRKELPKSDKASEDDFTEKAVCDTQ

EPPVKKKKTLGEKHTKQKNNATSKAKEKKLDHEKRKPAKKKSVSKPPKKENTLNNSDAAL

TEDVCEDLSTANVVAAPALKPKKKTETLVGTAKQPATKRSRKESTVANKKALEIANPAVR

ASKEIMNGESFEGATLKSISESSDSSAGFPIQAVISVSDDEIEVADSPATKALAECSLKQ

KRQNAPTDETFKSKFESVLKKRKKQILNETSGKDDAAVDGKLKRTSLRSSAIKPSLDSDV

LPAVMKKAKRSSNLAAPVNSSSSTSSDEEKSNYSKSILADLTSHDTGGDVVSSAVVRKGK

MPRKDGTDDFAPAKMLHESSQEASHSSEFSQKSHETNSFLLSTLSKNRFSLGSIPVAKLK

NSSKNPFTSKKTSNKIGNDTNRKRDRD

>contig11730 Frame-2R

MIPAVATIGTASDWHDPTDVQVRKIMMARLRSHPALAQHHPILQTREATGSSPSLLQRLE

WMLYHSAGSLSEYLHQPSLERRVQGLVTHYKRKRSEREPCDGLNGTMRACAKRQRPRLIV

TEDEGDVQSPDARDSVLGSNLDLLHQVCTFLNGLDLVRFRGINKFLYLHAPTFVQSLHID

AGSSRNAATRSSKDALHGLSTFLI

>contig12872 Frame-1F|Blast-actin, putative [Phytophthora infestans T30-4](gb|EEY55345.1|) 0.0

MVAANKIVVCDNGTGFVKAGFAAENFPKAIFPSLVGRPVLRAEEAVQSDILFKDIMFGDE

AAAVRSNLEISYPVENGIVKNWADMEKLWDYTFKERLNIDPKGYRILLTEPPLNPKRNRE

KLVETMFEKYGFEGCNITTQAMLTLYAQGITTGVVIDTGDGVTHVVPVYQGYVPQHLICR

LDVAGRHITNYLIKLMLLRGYPLNRTADFETARQIKEKWCYVAYDTAAERKLALETTVLE

ESYELPDGRIVRLGRERFEAPEALFNPSLIDVEGAGLSDMVFDMCMKADIDLRTDFFKNV

VLSGGSSMYPGLPSRLEKDIKQRYLTDVLKGDKSRLSKFRLRINDPPRRKHLVFQGGSVL

ADVMKDNDAFWLLKKEYDEQGLRILDKLQ

>contig13570 Frame-0F

MAFEGYAHGDENLFAMEMDSYFGLGDSPVLDHNNTNDSTTTEILSPRDLAANINMAMSSS

LPKTPPTLKPEKKNTICYGPINSETPLSVGNGTVLTRKGKKLPKNRRILTPAPPLVKHEV

IEEGSSSGGLASLQFSMQDMYFAVPKEEAGI

>contig16955 Frame-1R

MISRNVLTRNFAGTRALSNTASETYSFVQSRAEYRKEIASLRKVFIGEEQRRKELLARDA

KSQRQKILKLKAARLEIKGQQKIIRAKEVEREKLIHEEKVRNYVKAKAVVRQKRVVEVER

RRESLVASLRQQVAKWTTAENYSEKLKEDVFIYSPHQISFRGSFDPSSTSGSAVSWLEKL

QLMKPAGFNDANEVAASTTKSPSSGIEALELKTEEK

>contig18038 Frame-2F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY56872.1|) 0.0

MWHLVVRNGARLLLGSTAVGVGGVTYTTYTDEGFNRSLYFWRKAFPIYLHYRATQLYIEH

AQLSDKAQQLAYEQLHDKYAPEVFEIVLELKGFYVKLAQTGSTRPDVLPKQYLDRAAKLQ

DDAPSKSLAEISAIIEASYGKPVQELFQSIDPKPLGAASIGQAHRAVLLTGEEVAIKVQH

PDAETFFRWDIKTIQDFCRFFQPAHLPFLLEVEKQFMTEFNYIEEAKYLATVRRNIANSP

YAAKVAIPKPKIALCTKEVLVMEYLQGRKLLDGIQDHFETIAADKRMTVEMLKQDQERKD

KEREAQGFGMETGPSSLQLQLYGLTLGMKRFLRRIRQFSYAYTLGFVAPREWTIQDEKPP

QLLNLPQILKLIMDVHGYEIFINGFFNGDPHPGNILLLDDGRLGLIDYGQVKSISKEHRL

HLAKLIVALSEGSQKDIVDVLTKDMRIRTTKMDPYFLEKQAHLMMDNDDLTVTEGMNPQL

FLEHLDTN

>contig18830 Frame-2R

MVKAIEGLVKIGGLLPKIEDESEIPHCKYGRNEHLCGRVSITGRLIAQLIAFIGSNIPEW

RVVVSATCLVVGLSGFSVGKIVHLVEFVSRQPFLTLTRGEQKRMRDRARALHDEVEKLYL

FTLAMEMKSQSVVLDFHRDIQRIQIDRQKHQDIVTNEMQKFRQRTFGVLQELVIKHRDTI

KTQLLELSKKHKVVTHKHTKHAGDNTSNESCKEIHKAASRNICAEKPTTEHPGEFEIYLK

RDDGPVRPLPIVELSNQQILALAQQNDVTLQSLKQSFDSSYTVPNEIKQKFADALSHSNC

IKYAEDMGPGSICLAYVTTDMVHHKVDLVASLTDDQGESEFDKSFTSVTHADPVLSSLQI

ASKATWNEILLLVVITIIIASVVVRTYNIYHRNKYSGRHRKRKHQRALRRAHQRARAIIE

CNEYSDECDGKVTDLGIEEVFLMSP

>contig20367 Frame-1F

MLCRPYVLGLEEENTVSYKIPFFFLWLLLGV

>contig23825 Frame-1R

MRNYLFKAIALGSLAFVSAQEINIDEIEPLPGLEPNSTMNKIILQFQPQLHVSSGCQPYP

AVDSAGHTSSGLGLWKMGTKCNGSPLGSQVYARTDKFNGYTAIMYAWYFPRDYVVRPTGH

RHGWEHAIVWLGGYG

>contig24598 Frame-1R

MRTMMSCRIGTHVTDDAVNNSLCLDNINIKYVSTQSFNSRDQFFTCIVLL

>contig26390 Frame-2F

MCEYGEEADMEKMREDLNIGLQGGLDDKSKPKEGGHGGCGGLQPKYRKQGIKLLVEFPEQ

MEDVPGSGDRKQNLPAAKVLSIFKNISDEDCHALGLDSRWARPDWLIMTLMPVPPPHVRP

SVAIDGMARGEDDLTHNLASIVKANLALLNCVHKGEPSHIIEQFEQLLQFHLATFLNNEQ

PGLPQAQQRSGKPLKTLRQRLRGKEGRIRGNLMGKRVDFSARTVITADPNLAIDQVGVPR

SIAMNLTVPERVTPFNMNYMHQLIANGPLEHPGAKYIIREDGNRIDLRYIKNKSDLALKC

GWIVERHLRDDDLVLFNRQPSLHKMSIMSHRVKVFDWSTFRLNLSVTSPYNADFDGDEMN

LHVPQSMTARADAQELMMVHKVIITPQSNRPVMGIVQDSLLGAQKFTKRDIFVNKDWVMN

LLMWVSNWDGKVPTPAILVPKKGELGKYDPIWTGKQLFSAIIPAINFTGFSSTHKSNEKF

SDLAPIDSRVIIQQGELLAGIVDKKIIGSSAGGLIHITMLEKGPDETKRLLGAIQQLVNN

WLVGRSFTVGVSDTIADVSTLKTIVDIITQAKVQVHDLVVRGQKGKLETQPGRTMVESFE

GLVNIVLNTARDQAGREAQGSLDETNNIKATVTSGSKGSFINISQIIACVGQQNVEGKRI

PYGFNHRTLPHYGKDDLGPESRGFVENSYLKGLTPQEFFFHAMGGREGLIDTAVKTAETG

YIQRRLVKAMESVMTRYDGTVRNAQGEIIQFLYGEDGMDAVWVEKQRFESHKLNKVQFEK

KYFFDASDEDLGCVPNCPDQLYLEPDIIKDIRTNQRTQQILRDELAQLQKDRVNLRVILA

SRGQGQESDNAAQIPVNIRRLVENAQQLFSIDMLKPSSLHPSRIIQGVNELCKKIIVVQG

EDRLSIEAQENATLFFQILLRSALASKCVTLEHRLTETAFEWLMGEIESKFTSALVSAGE

MAGVVGAQSIGEPATQMTLNTFHYAGVSAKNVTLGVPRLKEIMNIAKEVRTPSLRIFLTP

DCAHDADKAKFIQSQLEYTTLADVTANTSIYYDPDPMNTVVEEDQEFVASYYEMPDEDTP

IARSPWLLRIELNPKMMADKKLTMGEIAAQVEAEYGQDLSCIFTDDNADRLVLRIRIMSD

EEEKLQRSGDTAVGQEDDTFLKRVEHNMLTQMKLRGIEGVKKVYIREGPSTHWFDDVGFK

MMNEWMLDTDGTNLLDVMCYPQVDSTRTISNDIVEIIQVLGIEAVRRALLNEIRQVISFD

GAYVNYRHLACLCDVMTFRGHLMAITRHGINRDDSGPLVRCSFEETVEILMDAAMFSEGD

PLTGVSENIMLGQLAPLGTGIMDLVLDAKKLANAIEYEASEIQQVMQGLDNEWRSPEQGP

GTPMATPFASTPGFSASSPFSPGSFSPAAGAFSPLASPASPNFMAASPAHSPASPLGASS

PAYSPMSPAYSPTSPAYSPTSPAYSPTSPAYSPTSPAYSPTSPAYSPTSPAYSPTSPAYS

PTSPAYSPASPAYSPTSPAYSPTSPAYSPTSPAYSPTSPAYSPTSPAYSPTSPAYSPTSP

AYSPTSPAYSPTSPAYSPTSPAYSPTSPAYTPAYSPTSPAYSPTSPAYSPTSPAYSPTSP

AYSPSSPAYSPTSPAYSPTSPAYSPTSPAYSPTSPSYSPASPEYNPTEGGYNPSVSGYSP

TDADEKKEE

>contig27072 Frame-1R

MAIAQIREFVAKSSEFDNGYIFVGHSQGGIVSRAVIEEMDDHNVKRYISTAGLQNGQFIG

PNKIEVSINDDAAFLAALVPKTMFDYSAYRPED

>contig27722 Frame-0F

MELSYPLVRVPFENASRNFRLYHKQLSRELLQITAQIEALGNSAVHNIDVEAATDKLAEL

AKNLRDLKQKAKDGALKQAFDLQSCATRTRYFKTLKDSETLFTSSFSSFQTPSMTDRLIA

DFLLSQGCLDTAKLIENTREISHLVDHDLHAECQAVLKDLENFHTDQAMTWCSQNGSRLR

RLQSPLEFSLRLQTFIELVRAHKPLDAIQHARAYLTPLAIMQPDNSTLRDAAIHEVQSAM

ATLAFASPQTCGIKAYEQLFAMDRWAALAQMFRQTFRDVYGMHQMPSLSIVLYAGLSTLK

TRACQVTRDAITNAGSATRGKRQRRDSEQGRDNDAEESRHQCDDEPDKSSPDDVIDAAAS

KKRKCHDVEIFVSLCPGCSDVGSQLCAGLPFAYHPHSRLVCRVTRQVMDEHNPPFMLPNG

RVYSKQGIELLKQRSSDGMIQCIDTQGRYSLDDVKPVYIL

>contig27829 Frame-1F|Blast-phosphatidyl inositol kinase (PIK-G1) [Phytophthora infestans T30-4](gb|EEY65922.1|) 1e-140

MWVKRYRIIATSSSTGLIETLINAISLDGLKKFEGYVSLLHHFEKSYGPPDSHRFKEARR

KFIQSMAGYSLVCYFLQIKDRHNGNIMLDNEGHMIHIDYGFLLGIAPGGMLSIETAPFKL

TAEMVETMGGQDSEGFKEYVTLCTRGFLACQQHCDEICDLVDVMSRQSPYPCFLGIDADY

VLLRLRSRFKLTLSKQETVAYALSLIRKSNNNYSTRQYDNFQRMTNGILS

>contig29878 Frame-0F

MTEDDLVGVDTSNIIPRSRRRAAVAADALASEEIAASEGVGPASAAPNDDEEEEGESSDE

AEF

>contig30018 Frame-2R|Blast-dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, putative [Phytophthora infestans T30-4](gb|EEY68135.1|) 5e-56

MPVVRNVEKLSIVDIEKTLTSLGTQARDGTLALEDLAGGTFTISNSGVNGSLLSTSMLTA

PQSAVLGVHGIKMRPTVLAGKVVPRPMMYLSLTYDHRIIDGREGVTLLKSIAEAIADPRR

LLLDM

>contig30634 Frame-1R

MGPKAHFLMDTKAEMRNSGQAQQPLILNRKIKCTILFSDKFMQNSSQSSQPF

>contig30641 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60536.1|) 1e-103

MELPLVLSAVQALYGMEGAVRQREANEFLHTFSSSDAAWSVCFQLLLDESLMLPPETLFF

VANMLHTKVRKEWVRVPVELKVSMTASLQTLIHALRTATRPVFHQEPLLSKLCAIYAVVM

ISSPDDCRGLLSQLLASSSVSGDAGELAFLLIFSRSVCEEIEDAELGFADNDAMEMHLSA

LSGEMVALIGKIVLTHENQNARVASLHGKALLSLKVWIGRAGLSLASLFSKDKAVLYALL

KALQTNSPYLRVCAEILTKLIGVASYPIPA

>contig32614 Frame-2F

MTPRASEANCDGGGDRSLRMKKKRKEDQEQESAMHKSKQLIAESAIGLLSQTGGESTQEK

CRSKQDVHISNLISTSILAFKNPKSSLQPTPAIFAASSSLHAFSRYSATRYVSPETPIAL

SRKKRTYNTLTASSMRPTNSLVRRKESHKAPITLETQETQTP

>contig34076 Frame-0F

MADDLLQQFQSITTSDHDELVDQFAYLLQLDVQTATFFLESCNWNVETAANNYLATMETT

SSPRTNPMDGIDVADDLDMEDEEPQPSQKQPNSALFHAQFVSDLSASQNVLFAPDTPVQ

>contig34133 Frame-2F

MSREALDVMPFRRVLPGVSPNSYFGVHLRGYADAATNAEMAQAHQPALPQHYQPPLAYQP

VKKATAVCTLTSVGACAGYSLTEAKY

>contig36328 Frame-1R

MRIFATASTTCSILSTFHPDAASEYSVDNIVSD

>contig37257 Frame-1R

MEWVRHTKAMRQLIGQIHKTERGYIQPVRLTNEFKEKYLGMQKKYADNPPAMAQFYCRKI

LTMPAFTPRFHQWFYNNFADPTAWFEARLMFSRSAAVWSMVGHIVGLGDRHGENILIDCT

NGECVHVDFDCLFDKGLKLTKPEIVPFRLTPNMIDAFGITGYEGVFRRVSEVTMELLREN

KATLRSVLESFIHDPLVEWGRRGKAIQSSSSSGKSAAELSSERSKQETRRVLKTIDDRLR

GIYNLSNALRPRVLPSHRNSPETDTLPLSVQGQVDKLIHEATSHENLAQMYIGWMPFL

>contig37921 Frame-0R

MQESVFGEILRVSKLMSASAIYQDPAAERNLSEQNYATKSLVKEFWSMVSEIASISELWS

NISSHDFDIICTSFSIVRRDVAVPVLAVLNSYMKLVAAGEAPVEFLSSQCLSDIRTGILR

FLRAKWPHQERDECLLLNFQLLKQLGMSWMVSGTTLRNLVPPDEVCDKKFILILLKLVSI

EIKIMLDEVEYSLIQYDEIAIKLVEETERRNKEIQRVLAVLPICFGIVEMIISALVSDQE

SVSALPFDILLEVKDIFNQIFLVILELLTLVRDYVLTHRYRELRESGAESIRYLDAVICA

SIRVASAWIAEDSDTSVNIVMELVPFMVCYESLHPLVTGHGSLPFQSKRNHNVDSDDDID

SDDEIDAVKKTKHQAAVINEADSSIDQLHFLLPGLLQLSARPDGASIMSENVEVLKRIMH

FCCTTSVSIAYGNTEFANVSTLTLSLGILINLIMTRGNHEDIGASESSDVPNPCEWFRAL

TFLMPVACASGGRLMHDKNLMLEHRGEDDRYVMLLHVVCLVLYIVSHFQDKKHHPCSLPA

AVANLVSPFNDIVSWIISHPPDENIESTVDLFELMRMLSMRLIFTPELLAR

>contig37954 Frame-2F

MLRRTGTSVVSTLQQHAISLTVRALSSKAFFDEYDYVIVGGGSAGCVLANRLSEDPNNKV

LLIEAGPSDRTKWDSWKIHMPAALTYNLCNDKYNWNYYTEAQRHLNGRRLPWPRGRVLGG

SSSLNAMVYMRGHAYDYDDWKESGADGWSYADCLPYFRKAQNHELGSNDYRGGDGPLHVI

RGNQKDQVLFKKFIDAGLQAGYPFTDDMNGYQQEGFGWMDMTVWKGFRWSTASAYLQPVM

KRTNLTVVTDTIVCKVLFQGKKAVGVLTKNHNKKTTTQIYAAKEVILSGGAINSPQLLML

SGIGDADHLKDVGVSLVQHLPAVGQNMEDHLDLYIQYMCTKPITLHNAT

>contig38289 Frame-2F

MSLGSGGRSGRRCSSSFSTCSSTDDDSDDWPVIGVFYAVNKTNRLGDVDAFDAEDEQVLR

AICVELSALVERRAWELVFESPSYDDSDSSDSDGESHVTRTFLSQYTTASPIRRRRRPRS

RLPSVVSDLDHAASVVAATLYHEGCFLGPTSSSNSLLASISSPIQAASGHGSCSPVLQWH

LDPWQFSPAQLIDLSVDMFALHDLVNDFALPEATLRRFLQSVQTQYLDVPYHNTYHAFAT

LHTAFLLVSAQSRTLAPLLVPASTALGVHPTTKAQAMEKNRQKRCGELLLAPRERLAVFI

AAFCHDMGHDARTNDFHVRCSSRMARRYNDHSVLENMHAAACFETMRRPGHDVLAGLEDG

SSAALGNRRAVRKRIIRAILATDMHRHASIVAKLHEAQIRANRNDEEALRELLVNAVVHS

ADLSGPAQTEAQHFNWTARLLQEFNEQHAEEVELGISATAFMDGRPDSAEFARVNLAFVD

SCAFPLWKALSGMLAGLEGCLANVERNRTMWANRLQATEGDGKKEKRSMSELILRKQGRA

GQEEKGLLSVLSPALKFAASLQHKDLQHSNDSRRTSRRSMSTPQQHVR

>contig38784 Frame-1F

MRSSNPENESSTSLLPVLYAKDEALKKLRVQNLALQDEIETLRLEKNTLEHAAEELEFKT

LHTTRRYLYETTTRDVQAQTRDHNVTRFEQHVTTLCTTLQKRLEAHSEAFRIVTDFQATW

RAWLSTHDDLRLIMNDRRTDVMDQEVFVLRSGVVIKAGARFELPVYCDASLDRRVVWNFS

IQEDTADVAFQLTAMRTTTRLSTLVVAKERLHSLSGVFHGTHENVTLSLNGIIRFHG

>contig39563 Frame-0F|Blast-cardiolipin synthetase, putative [Phytophthora infestans T30-4](gb|EEY65382.1|) 6e-06

MSRILATPYLAQLILQEDHVYAIG

>contig39686 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65721.1|) 1e-12 NOT\_ORF

MKGGKKSVNELYSKYLDRWLEVDNLIKLLPNTFAEVRENYICAKCKDRQFT\*LPTTKLLQ

FAIFAASFRLINATTYSPSRSLASRKQQNNMVLNFMQSQLPRHEEVVSAIS

>contig40314 Frame-2F

MSGPQAGSNATESTTISAPASAAGPAGTHALLLSAATVPNSTISTSSAAVSPSTNTALLG

LQQYSSILVPSITSVGSNIKSKPKMESVSATTDFIVVNGNGRKKANVPPSITAALTVSSL

STPVSLCPTQQQKTIGAPSTATSSNCTTSPASTSKATPPLVNSMTATLMGSTERLAALVV

AGGVEQQLTKMKSEHIEASKQVLELQSSLRLSRERLAHAQQSLRELSEVFHARHRLLPYA

QAWVRQAVTLLNTTAILSRPNIDLSTFLPQEFATALFEMAHPNSSSQATPESMGIDQLFP

IVDLFARLLRTVSWSQIVASLLQERPSRCKLNDAIMYAVKYGLWEDKRIVTPLRSLIGRV

DAWVSRAHKCMTKSSNKTQQLSRLKVIMNEYSKLPLTHAETAEPLAVYFEMVMTGGGLKD

KNTEDDEEPTIEAAEAAATKALDEAMVGLSSLVSSTVCASSTNITKKQAPRKRKTYARKD

KAPARSSKKARKLPSASGVGKVAFESIDSSIMTPQTKIE

>contig40361 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65586.1|) 1e-159

MSLNEHDAAMSGLMDVEVTPPPSSLISALGSHQAEVVVKRNQSKYDFVKVRVWVEDHVYV

LSRYLLCRALVSAKINSKDAVQISLDLKRTLVDLNLTDIVQEQFEEFLYKTLSVFGYGEE

HISCHRMMSSFHRNRVPLLIILAGTACIGKSTLATKLADRLNLSSVLQTDLIFELMCNFS

GQEKACYITSKFASSDDLIAEYRKECEVVRKGVNSDIDKCLKDGKSLIIEGFHIDPRLYQ

KTIAVPKQDSKSSCSGIVVPFLLTLDEADHCNFMTNSPDPRYCGDQKAVGFRNLQDVQTY

LVSHTLEADILPFTEVRINIHSFNDTLDHLHDVVLKRIKDVFVSGKATEDK

>contig40978 Frame-2F

MPFYKVLEHLRASRDSERWQQPLYQVMFSWEQSWTQKSPQNSIELAIPSHSAKFDLMLSM

RYRLVKEKSNERVFEGSFEYSTARFTRESVHRFVSYYLHLLEQVLDVPTASVRSPFISML

PRFEQHNLVMWGTPPTLSIHNNDSFLDECLYEQVQKTPE

>contig41999 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68180.1|) 6e-86

MLTSTKQMHSQPKGLRVSKEKECISGNMSDSSEEVAKSLSARSASKKTTNMLKHVTSAKV

MSPLGGKQRAYEDVRSSLSASSSPADGDTFTKRGTPSNSEHLTEVPAAKVSKKASRPSKV

ETGETENFPNFIVNRRTNRLKHSASGSEYSGSPRLGISNNDEVYSPGLRKRPGAFLGRPG

SGVLLEGWLRQKQRRGIKGLKKWNSRYFVLYAKINEVRYYADVVQSAWGPIPLGEIGSIS

LRLIQRIGKRSHPKYNGCRFDITCRNNWGSHFA

>contig42198 Frame-0F|Blast-importin-like protein [Phytophthora infestans T30-4](gb|EEY65606.1|) 0.0

MRSCPRQVQEQAITAVASVAKVIGDEFLRFYDIFIPLAKEVLTNAHGREYALLRGKSMEF

IALIGQAVGKQRFVRDAKSIMEILVRVQTSEELEGPEVQYVAQSCVRIGSILKEEFVPYL

PHVVPSLIKQAMIQPNIQLSDIDDDAVVEDGQTADGKDAMTLEIRGVGKKRLEINTSALE

DKTNACNMLYQLALDLEGWFYQYVAEVAEVMIPLIGFEYVEDIRIVSSLTMAKLLICAVD

GTLNYGHSGADLRFPQQLFEKFFEPLLKGLQEEEDLECLGAYAEAMSAVLEVCKESLEKG

FNVGVPLEHVPRVVEIYKTVASNSAQRLLTQHHENQQDEDYDAEAALQQTENNELEEGVF

RSMVDSIGWIVKIQKEAFFSVFHTQLLAFVTPLLEQKTVPMLRGQAICMIDDIIEHCGAA

AQELLPLFLNQLVQGLEDQSSSVVQASAYGIGISAEKCGMAFDPFRQNALEKLVHLINAS

ANVDDEECGAARDNAVSAVAKICLACEGAVDAAKIWPLWLQWLPLHTDVLEARDVHSRLL

SLVISGNAHVLGAG

>contig42868 Frame-2F

MYRDILYAIESSMRRLIKTLLL

>contig44725 Frame-1F|Blast-Cytochrome Oxidase Biogenesis (Oxa1) Family [Phytophthora infestans T30-4](gb|EEY60615.1|) 1e-25

MQRLMQARPDFIRVYSAYKYARTFTPSSNHKGHIDAVLLGRQGIKAVMK

>contig45634 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56339.1|) 6e-20

MSQGSHGRKDVLKDSLRRRGKGSYDPNEDMSSELSASFFDGTNGSFRTSELSSSHGQTSQ

RNSFVDQAIESFDEPDQSESTSSDSSK

>contig45748 Frame-0F

MDSRRQQTHVAQTNVQKDTVMCHKKELDLARTQQNEGGCGGCLKVKRSQ

>contig46107 Frame-0F|Blast-acetyl-coenzyme A synthetase [Phytophthora infestans T30-4](gb|EEY58107.1|) 1e-23

MDQVYAVPDGFSEAAHVQSMEQYESMYKRSFEDPGGFWGDLGRENLEWFRPFDHAMAGSV

HKGDTAWFLNG

>contig46789 Frame-1R

MKAIRKQVLFDREVAAFRAVARSLATTDRVAEIVGNKNFSSNHRRVHSFQSSETFALAFE

RESNSRCVESSS

>contig47661 Frame-0R|Blast-hypothetical protein MGL\_1762 [Malassezia globosa CBS 7966]gb|EDP43549.1| hypothetical protein MGL\_1762 [Malassezia globosa CBS 7966](ref|XP\_001730763.1|) 4e-10

MQERMTSSIKPAIEYLMSVLCESFPNLALLTPVRRLDESYTLLRLCIEYYFLSKYDSLVT

ERLYGMKRVMHMNVKRDAEPTMRSSTSRVRTFTLLLAV

>contig48299 Frame-2R

MRKYVRTSSRVTAAALMIKTGMRANMLGHLAIFFVEEALQLVIFLYRHFKSRKARIKSPT

KLRSIEEGIQSIESKNESLVSTFVSNTSRNASRSVLAVITGGVGAAMGTVVRPGIGTIIG

GTLGDSIAYVLL

>contig48747 Frame-2R

MPDCLVNRQLFDQLNEARASHQQLEQQSRINDEYRSLLTAIRREREELRRERNEMRREKE

ELRIQRALLQLENEELIGLVDTQRVLNEQYQADLQQTQQAQIAQQQAQLQQYQSVSIQHQ

QSPIQPVAHEMNSISSGFEQFRSQVVVPDKEMYSRLHQIGQSLGDLNIRGVKPKPALLGR

RRKPRSPMSMAEISATPPQQSVTTNVTHPSQFQRLSRYQPIPDQLTDNESVLNQSLDGES

VFVPLSLKSPKPSKQGFMPHPTSSPGRQDHRNRALPFRSSRVIKSRGFYDYDQELNSEDR

QSASGSVNGSNQDSDVGSSFYGDDEGET

>contig49304 Frame-1F

MLGLESAKFNIAATKVTVRNLEKELDTQNVIDLREALSPRYKIKDARGKSDACTKNIVTL

LETKTRLEGNISRMEANIGNESADKKEKLATIKGQLRLELAEVSSTLEKEQVQAQEAMQS

DESNRHLLIELAMAQEEIQSRVGGQISLQIQKLSHERESSLAREEQLKGLFYKLNADVKS

LKSESNGRIGAENSTFVDEMNELTTMLEASQHREQQLQSRLKRVLDKFEHAANTLGGSKN

TEETKSSNDEVVTRECDALYASHERTVRKLNRLQAKYELDIKQATADAVTAQKLDNQIKA

HEIKIEKHESVAKQIHDELKEQYH

>contig49421 Frame-1R

MKESASADRTCKQEVVVHHVGLDFIVKTV

>contig50364 Frame-1R

MPHELRTLVAASFDIFVSIQQTVQHSALNVARASREYREALKTCIFALEDRLESMTNDFA

SSEDESEFLDLLKVSLAIWHLCELLFLRKGARGADRMLAYELARWLQEHYCSTVIEKTEK

ESERLKKLLTPEDDPVFYRTIQSFVMAGNGASAWSLLASHSSYKSLELRHAMSSTGTSTL

TAFHALQKLLLTMPGRADTSWNSADRAEWSHWHTACQYLLYNDSFIKTNAGLKTLVEILS

ANENVLNQCAETWYELMMARLFLDEPKTIAHRFEFLMANCFRVKHSNETIQMGNFECIVL

AILQYDIQSALQDIIALGFSWMAAHLADLLQRNHVIVPLEIMPEGDCTLYERFVLQYAMD

IGASCGMWQVAVRYYECCPQYGAQAIRSTLAREPLETDFKTERLLEYCHGKAFLARTQRE

IMRHRAEECHGKKMYAAAISWLLRGHHFDEIDALCDVLLKECDDRHALTPLHEAVQFLET

RSDLVHPRKLAWVVKYRELVLIQDDLESLRQVLEKDASLDDQEKHQADCKQLRFVALEAA

KRLDWLLRSNDAPKVLRSQILQQTERLLKESPTVFESRHLYSLLTYLQQLDRAFDRHEFY

QVSANQHLKERVESLIGRNLAEAMLQEATASGCGLKLQNGQGKVAGTQPFLIADASMAS

>contig51684 Frame-0R

MSEATAGRGGSLFVRVKCLERNYSHKHVHVALNTDLVF

>contig52032 Frame-0R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY64252.1|) 1e-172

MASRLHLTKCAELMGVGVDQLEILLSCRKIKAGMEVMVLKHNPDQAKEICRSLAKAIYGR

LFTWLVRRLSDEINYFDSANSISDEDDELATIGILDIFGFESLTRNGFEQLCINYANERL

QAQFNEFVFVREQQVYIAEGIDWATITYPSNAACLALFDDKSNGLFSLLDQECLMPKGSN

QALSTKFYRYHGGKGLADSAGPTMRHFPLLMSSASRYLRRNEKHEEHTDQDVKTSPFLAT

QLERVNHQFVVCHFAGRVCYNVEQFVEKNNDTLPADASDILCSSSNEVVAAIGNEDNADI

PGADNRDGARRRYSMLRAPSVSAEFKCQLDRLITQIGRTEAHYVRCLKPNEV

>contig52119 Frame-1F|Blast-charged multivesicular body protein 2a [Phytophthora infestans T30-4](gb|EEY66774.1|) 1e-61

MGNALGTKKTVKEQLRENKREISRAVRQLDRERNNLQLQEKKLIVEIKKMAKQGQIASVK

IMAKDLVRTRQHVAKFYTMRSQLQAVSLRLETAKSAEAMTSALQGTTTAMKSMAATMNLP

RLNQIMMEYAKES

>contig52397 Frame-2R

MRDDPKLRDVPLAVGGLGMISTANYAARKYGIRAAMPGFIGKELCPKLHFVPVNMEKYKA

VAAHIRALFEEYDPDFESFSLDEACLDLTDYVANNWQKYVLIAPDTSKVQEPEERWISTA

TGRAAIAGAVIKELRQKIFDCTQLTASAGIAVNAMLAKVVLLILSLLTP

>contig53035 Frame-1R

MVALGYEFNDFNTIHSIRAKERARVSVHFNNDVSQLAIRQLVISLLMKRLKASSNVIDAL

PKKRLNTAWNKLT

>contig53659 Frame-1F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY54397.1|) 4e-69

MRATNLLKHRDEINARPARTWFMSEKEKKNVSERAEDDRQIRLETASHETNSIDSMSRAK

KLKLISHKKRRLFDIREREERMLADAAQENDASGRSKNQNGPVFTSMQVAGAAKRAKKVQ

QETSRSREDDSIADIHERKRLKRGKALPARCSHGTDAFDTDMTIDGMSASNLKARRDAKP

GLNSFEFKEKITD

>contig53765 Frame-2F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY61039.1|) 2e-35

MDENQKLRAAVKMLHERSSAEKAELSKKLRQAHRENAELVSLREEVEELTIKKSHLESET

EELKEMLDLANAYESMVEDLTDKNLTLG

>contig54809 Frame-0R

MESLRITPLFLQHLRDARGFAIADLLEQAANTQDIKLVQTLASAAYERTWDKLHSGSWKD

VQPVWRQSFGIASILCARCMLHRQQLTECLKTLDLVPHHGRAVCTSRDARTNCKRRIAIA

GNHLGASLIACRLSKKRISC

>contig55752 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54784.1|) 1e-07

MTKYQIVLGCLNQLQSQENCVILKRVLKE

>contig56021 Frame-0F

MRIVCRHPYEVLAEKFGYPFVPFCLPLLSSPVFKLEGFKYVIYVMQRMLLASITSFVSLI

DHHPRRSS

>contig56054 Frame-0R

MWTNTSGVSASAFPSAEIDTVSGVVFAETTRNIQITGFDETEVQKGSLKTVAFDEDTFST

AITLEELILANLDLNPLPD

>contig56771 Frame-2F

MPRTAHNYSMFLLYSALTLQVAPLFVDAAGTSMQNESLTVL

>contig57347 Frame-0F|Blast-hypothetical protein PITG\_14724 [Phytophthora infestans T30-4](gb|EEY63079.1|) 2e-26

MSQCGLRREVLALYRDVLRIARRFPEPSIGRKLRYNAKELLHLRQHEGDAARIRMHLVEG

RDALGVYRVLQNDPELLTAIMRKNVLNMGAAISELTE

>contig57862 Frame-2F

MREELVENGLKFLQHPNVQSTPLSERVSFLEGKGMTKEEIQESIERHQKQGSGTTVAASA

PNAAQQNYLAPPMMMNAAAPMQMMHYQAKYPAYVRVLWTISSLVGAASILTFLWNYAVQS

GYIPWLRPVAPLLEAAKVQKEKEQEAKKDEALLAELSSVSSAIQKQTEELTKISSSLEKK

EHDLQSKLAQVSKSLAEHGNARAIAELKAEVSTLKMLMFSKTSDGVIGIEDIIKTTKIAE

RKAIKAAAMVNPQQPPSVVSQMAMKAEQMEKTLKKFRTENSIEQLQLAAGVLSMYVKNLI

ENPDIPRYRRISPGNANFKQKIEPLKHHEELLKSIGFEMAGLNMEWKWHTASKTTGAMNE

NIALLRALLKALESLTHPQSTSTNLSLEEIVHESLEEFLAEQDKREQSVALEMATKLMTE

TSQENNFADPSSESLFDGSSASAAKSLDAFMTRLEQQNSVSNIANAKTKLSSSSLSEPIE

AAEEEKMPSFEVSSISSNVKGDPSYPESFQEVLKVIQSGET

>contig58782 Frame-2R|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY60147.1|) 1e-141

MASFLIMPSLWTTHMSILSYFSILGILSSFFCLYAIFYVGIAIDTSAPGYVMGSLLYPQS

VQMIGDWDRIPLAIGLTMVAFGGHSVFPSICSSLANKDDYPRVLNVSYLIVGFVYGAIEL

AGYLMFGGFTQKEITLNLIASYPGTLTQMVVWTIALNPMSKIAITLHPIALALEEFLLST

DQKHAVARNDPSKSLAFYRAFLRTLLGSGALCCALYVPHFARVTSFVGAFFAMLVSMFLP

CICYLKLFSHRLSKSEIVLNTALAGLAIIFMIIGTLASFLSPAD

>contig00838 Frame-2F|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ29881.1|) 3e-44

MLHAGAKHVVENFGGVLPSSVKKLLTIPGVGPYTAGAIASIAFGKREPLVDGNVIRVIAR

MLAVGADPKNKQLVNHSWKSANELVSECDHPGILNQALMELGATICTIQNPQCSYCPVKS

TCLAYEEAQKVTVKNRLAFGSSAASCNSCSICDYTRVTEWDETHT

>contig01002 Frame-0R|Blast-CDH1-D [Gallus gallus](gb|AAL31950.1|) 4e-32 NOT\_ORF

MQANDLHLLGIPRSRLKIATVYP\*HDALSEDYPDLSIKVIHSLNASV\*RACGPEHLRASQ

TCYCLQLPLV\*LPKSPSKKSTHLPKMVSGTI\*HAEVSFVNGINQTNHSTN\*ERPCTTTHR

IKKELSICQSLLCLDLVSFP

>contig01648 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64539.1|) 3e-99

MGVPARPMPTKPVCETFDKLRQDAVGLLSLRKHLKSKQNEVQALCDRYHALTGNEYKPIT

TPVLISGTTFHPKQSPCRRLYFMFLASRTTGGCSDQ

>contig04386 Frame-1F|Blast-cyclin-dependent kinase, putative [Phytophthora infestans T30-4](gb|EEY63935.1|) 1e-09

MSLHLPKHQWGTRGMDAYEKLECIGAGTY

>contig04508 Frame-0F

MAAVAAKETLLALQLSCRGDSARECILRDWIKFVESRKEVSLLRSLPKLPSGGAIDWLKL

YEEVVARGGFAIVSQRRQWSDVLGPNGLNIKGLMPYQLAAHYNRYLRAFEEKQLFGRDAP

VSETTMSVLPSKRGAEEEDDAAPVATMQDLQDAQGGMGGTPLPRVNKRFKAQRELQTHLG

TLHNIVLALDSNLPEQELSALNLLTVLSYGDGMEEQHQVTGGTSVNTTALENTLMVDNVP

GLLDALYRQIIACKVLPQFNDWHSPKVRRQLLNLKIDDGERELLDSKALLVLNIVRNLAI

ISANEKPLATNEEWCVFLIVMLRCVNNRGFRNGYRRASVEIGDHVLDTLCAISRRIDFLA

LHPPASLEVWHPQYQLSTQLWQHEQIFPLECLLRELCRILVNRPLQQQRRSILLRACEVL

TNVCRDVALKSFLASSKALKDPALLDRMVALLGCSRQDFLPHKSRFKRQERDSNEAHEDI

NYADSDSDNTTDGDDNSRWPAPWENDGLPSGVGFGVVYVSPEGVRHTTSSPHINGARAAH

AMAFDEELDHEMRDAALEVLFRLSDYDDAMKLRMAQHLTCLRRLAGSLLSCIGRPEAARI

IVATLSNLSMNRATFPFFLAIEKDLILVACSDVSVSDILNNVVADVYGMHSL

>contig08665 Frame-2F

MFFSNVTDTIVVAAGTSRAKQYPVVKMDVIADHHHLWQKHKATLRYVYAHYRHEFDWFYK

ADDDAYVIVENLRQYLRRPEIYQTAPREAMQMGHRFNLTQELVSYYIVDDTIEKRWRDKW

NRWVFNSGGP

>contig09598 Frame-0F

MTNFKHERQYATFSTESQLNFVLNIYDNGNVLSIVNDVGAHGTHVAGIVAAYYPDQIECN

GVAPGAQIVAVKIGDARLGSMETTSALSRAILAVMDANVDIVNMSYGEFASLHNYGRIVG

LSNELVDEHNVTFVVSAGNEGPALGTVGAPGGTTSSMLGVGAYVSPEMMESEYIMRENDL

VGTAYTWSSRGPTFDGDVGVNICAPGAAIASVPNWTLDKKKLMNGTSMSSPNCAGNIALL

VSGLKRLKVDYTPYSIRRALENTAMKIPNVDVYAQGKGLIQVLPAFEYLTRSNAFDGTKQ

FPLYYAIKTSSGDESSRGIYLRDRVDFVHDTNEVTVTVTPVFHKKAAQMDKIHFEQHIRL

VPSTRWIDVGQNMALMHSGRTFKALVTTKHLAPGVHYGEIVAYDTKNASRKALFTIPVTV

IKPEDATMVIKYRTEFHPGHIIRRFVTPPQGATWADIHISRPLQDCNSRVESNASGKLFM

FDALQFQPFVRQSASSFHKAFVLAPGQELGFSMDLVGGLTTEFCLGQFWSALGDSIVHVE

IHFHGIKPDQEKIVIIGGEESHKVVISSTVTHETLAPKISFTKYVQHIRPTTAEISPLSS

SRDEFPDKRQVYQLILTYPFTKSEAGKVVPNLPLLHNRLYESPFEAQLMMIFDHKKQYLG

SSDAYWNDTKLQNGSYLIRAQVRHESVSKLEKLKQMMLELHHEIKEIQASVYGHQDNVAL

GLKPLDKKRLSIEKYVALFLGEPAQDKWPKGSTKGDVLKGSIHFGYQNADLKGSGRRPSG

FEISYVIPSLIPVDKADTKELPDEREEEQITQEAMCDLLLERTNKLAGKKTFLPAWQRLV

AQYPNHLRVLQAKLHHFDSESLRSSNLAEIIEAADAVLALINEDDLARFFGTRSVSSDEP

AKKMKLRKDKDKEKAILADALARKARALGDLAHWKDFETVYAALQKWEDVETVTYLHVSL

LHDRHYDAFGLGLQRLRKAQDMEPADRIKIITEEKLAAEICDTLNALQWPHWTQYERKWA

RRRAPEFYRIF

>contig09716 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66538.1|) 2e-13 NOT\_ORF

MLVGSVAGGPTFFSISRKPSNSCPTSDAEANYASVVDRHTPVCFLQIH\*TIISFMVSTPP

VIDFRSSLFAAKSESLQH

>contig11731 Frame-1R|Blast-C-1-tetrahydrofolate synthase, putative [Phytophthora infestans T30-4](gb|EEY64549.1|) 6e-43

MALYEQQGYGNLPVCCAKTHLSLSTDPTAKGVPMGFAVIVRDIRASVGAGFVYLLCGTIM

TIPGLPTRPSFYDVDLDTETGKVIGLF

>contig12381 Frame-1R|Blast-tRNA (adenine-N(1)-)-methyltransferase non-catalytic subunit trm6, putative [Phytophthora infestans T30-4](gb|EEY56347.1|) 1e-161

MPRVRFLRCTAESLCRTYRLKNPSKICNLREDSLGQMLVYGNVFAGGQVLVVDTCMGLVA

GAIAERQGGSGKHHLFVRGSAACCRYITSI

>contig12604 Frame-2F

MINTDKTIFIEAMHLQPKESSTTSNHSCLSAKILVLCSVPFVASKVLACHTWQNSATYPA

SISTSLMNSSVSLIVVTLANCCSPNVLTSHRHRILVVCLLHALIDCILRFAAAILLYVTS

TTSPSAIQPIKKSNFGRSALRS

>contig13874 Frame-2F

MSLLKTATVNFESEWNAMQPLLASLVTGAPQTLTNEVWLKIYSGIYKICTNPGAPQAEAL

FFRLRGLLVQHVEYVSKELTAVGGEHDFLTKYCTSFETFSTGTCYISELFRYLNRYWISF

SHCRTGQAPVPGVYPVTELSLHIWHDVVFSKLKKRLIKAIIHTYHVARRDNSDYFDDGDC

ITSTIETYYSLGLCRLDQMSLYREELEQPFLDDAAEFYSSKAIQLLSKGTISEYLRETEQ

LCAQEHKRCESRLHRTTVIQVRQVCCRELVAEHADRICEDAENFVINNNKEDLHRMFSLF

SELANENALISFKNILKKIIERSGMEVVKKFQLEETTKNPEGYVEALVQVRNKYFALIKD

SFGYHPLMRTALDQACRAFANSHPRLPELLAKYTHYMMSRDKSRGSKVLVMPGSPQFEAP

ATLDDILEKRIENISVVFCLIDDKDIFKKYYSKFLAKRLI

>contig14400 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56010.1|) 2e-29

MSTTMVATPTSKQTWHSSITLSTRRSVLFHILLLLKSKYGKVDSKISYIGRRAELALYYQ

AYSAWEYHNPPTLCCRLYSLVLKLHLNSLIAKEDAALAVEMVPPAPSRKRKCSSSDETCN

DKRLRFKARDMAMKSLLCCGNEDTLQLVCSFLTAQEILHCSATCSQT

>contig16213 Frame-0F|Blast-molybdenum cofactor biosynthesis protein 1 A [Phytophthora infestans T30-4](gb|EEY57035.1|) 1e-111

MPKDGVTLQPIEDLLSTSEIVRLAKLFASSGVTRIRLTGGEPLLRRDVVDLVAQLREIPG

IESVGITTNGIMLQNKLLALKKAGLDRLNISLDTLKPDIFAHITRRQGFSRVMSSILEAQ

TQGFFPLKINAVVQRNLNLNEVANFVAFTELNAVDVRFIEWMPFDSNRWNDDNFVSYKEM

LESIRKKFPVLEKLVDGPNDTSKAYTVPGFKGRFGFITSMSEHFCSSCNRLRLTADGNLK

VCLFGNTEVSLRDAIRDGVADDDIR

>contig16284 Frame-0F

MNTVDLKSNARSNARKKIKKKGMFKALKKQDKRAVITQTNMTDPHTNKRKSKVAKRPATI

SDEFRNYDERVAASKVRRSGVIPKLSAVASPAFVMAAPIFQFNATSMLKPMPREIEGFSG

FLSALEAPKDATIANSNQHMRHSKNVEYSGNNVFSVLDNGDEEQIKARELSQSLSAFMQP

ATFKFPPAKSNFTMQPSLQSSFQQSTNLVLANAADIDPDL

>contig17544 Frame-2F|Blast-endoribonuclease L-PSP, putative [Phytophthora infestans T30-4](gb|EEY67881.1|) 7e-10

MTAAGELITGKVGKDLTTEEGYIAAKQVVFALLATL

>contig19278 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56921.1|) 3e-44

MLTYNETIENLKAMSTTPTELESTTLVFAYGLDMFYVRMTPAKSFDLLPSDFNHEMLLLL

CFTFLVVTFGTKTLAQRKALQTAWK

>contig19304 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69788.1|) 0.0

MQVKYPIMGLSYARGLFAICGGGGSLKSGIKNTVDIYQLDDTDPTGFSKQITADTGRELA

SGVAFSHDGELLAVSVGAGCWVYHLNFNEKTITLLVKFRTDFHAEESAQSCARFVGNSII

VTGGEDGIVRIWRLSHDPFKPEKEVGTARALAVADEQDVHASGKPVEQPKLGDCVIHGVH

MVTLTREYRNHTKRIRDIDVDLSSRNLVVSSSEDQSCHLWRLTEVTPICKFSKDDALDIA

LQRLRKTPIVGLRKHVFRCVRFSKSGRRLFTLLTPARGDSILIKWKPQTIAQEKADQWLW

EVEHVAIAGDKPVASLCVSPDDRFVCTAAVTGEIKVCLASTLQQYSIQSTGQHSFAITGL

SFAPSADKQTPFYYLVSGGADKNLLSHTIPFEGGLVRSGMENLASGLKRVIRSTIGFWLN

LWMATTLLFILLLFIHAQGALLLDGPLAGFNDLTSLSLESSDFFATILALVISFIVTWLF

ATYSSVTSRFFWNGVLYLLSGLAAFLVAISANHEVIWQTGDAAIDELLEYKIAIIFGILS

TAFFFCHSLLAMIL

>contig22359 Frame-2R

MFAKPVKVSGNVLLKNKDAKKLRRDVTERLIGPCSDSYDDKLKQLLASKASVKKMSFQAP

SKIVVYAAEETKEPLVFDTSGKGDFCFTVYALWRFPSLLPRLEVHAPASEYVLRGADVMM

PGVVFASEEQLQSLQKGGVYAVYVIGNPCAIAVGEMLMDAAEVARNGKKGRALKLWHVAG

DSLWQMGPQTLPNVGFLGDIVVPTGEDENAAMALEAVTLEEEKETTGFQAVTKQEMDRYY

VAALLQVLRTGKIREKDLPILASTFHANVLLPCRRAGVSLNIKQSSFKKLSVFLKAMEAH

GLLTLADNDGVQTITSIGRRHPDVQSHEPYKTEDSVQQEKQTVALKPAGIHSTVPGQHAP

VVEESAGLPPALKTLFLSILPRPSTGQPLQKYWSITEIRELVTRYIEDQALVDPTNKEFV

RLNGPLTDVIYGKKVPAGGYPDRLSRPEMFSLLQSKLTHYHRIKLFPTHAAKFYGGNLQP

ISIHVKRLKQRSNATITTISYYQQFGIDGVTFVKEAQKMWGCSATVQMSEDKSKTEEIQI

HGHMANEVLERLATKYQINAKYCLLTYGKNMKAKKK

>contig23824 Frame-0F

MFNTWDLVRPRFWYPMSSLEQSMMDLEHMYGLMSHSRFPFDMNSEMLAAPSAMEDDDFFK

DLPVLAREQQPATQHREESVQLNDKKATTNDSNQSNKGKPSTSNPNQQNQLGSQSLDNDN

QRRRAFSSYTFSNSSVVDNNGRRVTSMRRRYEDSTGRLKAVHERQVEGKKLRTTWSRMTP

DDKGQHEALCSSGTPDEFEALWQQTPFGEAQKKTIRDQQTNEQQRLEQDKQSNAEASSTP

ITS

>contig25145-0 Frame-0F0

MRLFKTRILAQDFLDTSKYVKSYSRSKISSKTIF

>contig26074 Frame-2F

MSKLLQLVHGKNTVRVLQPKELVMNVRHISKTFRIGRQEDSHEFFRLLLDSMQRSSLRKA

RIKNEHHSVASTTFVHRIFGGKLKNCLQCAKCGYVSERFDDFLDLSLEVAYGVQSVDSAL

RHFTATETLDDRNAWKCSKCGQLSRAEKSLSIAECPNVLTIHLKRFDVVSGKITRHIKFP

PSLDIATGMSQHCDDRRRGRTKYELHAVLVHAGFSTDCGHYYAFVKG

>contig27147 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67982.1|) 1e-96

MTATFMLECIAGVNALKKCAREVKADLAEACAKRPNCELSDSDDSEAQTEYVPLMSQDAL

ERTLRSKNSNHTYSFDLSEKTELAEMAELLFNHRGIVAFYACITVYLYGDLAIYSVAVPK

SLREIVCPRPSADAVVWKCLNNFNSSDIYRLFVVLFGLLLGPFVFGHVNKTRTLQLVSTL

IRHASFGLMIVLAVLGIYHGHGQNVKDVVSYEKPANIAKFCGVCIYSFMCHH

>contig27828 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65923.1|) 2e-26

MDWTLECCNDKQFLSIFLIVCYAVVIFKLWRVPILHPFKILTVFLHELGHATAAWLTCG

>contig30635 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53454.1|) 1e-65

MIRTPLFNLDGIQSSKFQVPLPTSEDNDVSSDEELTGIPGPDIPDPEISFSQEKLGELSV

TENRLDETVGLILCESLARKLTKGERERMKLLNLYSIALTLQSSPIMLGRDQFQDVFGGN

FRGGMLYHLSRRHCLIHVEKVALRDNSGSTGLRVRIEDTSTNGIKINGIQLKNGQSHELE

LYDIITLLRSRRDEVSKCIEL

>contig30749 Frame-1R

MESNQEVLRRYFALVDASYGFVTKHRSSPTVRSVLRVANSFGSSQLTRHHLLDLAAVAPD

LLILKRPESNFRSEFDDLYSPTVVDAESIEIVTFPLAPQPSQRASTKRKALFHVALEKKL

TERNSPRHNQEHQVSES

>contig31724 Frame-0F|Blast-2-oxoisovalerate dehydrogenase subunit beta, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57864.1|) 1e-114

MRVLEEACKYAENVGIQCELIDLQTIFPWDVDTIEHSVRKTGRLVISHEAP

>contig32615 Frame-0F

MKTFTPSQYFSALSPPVDFEMLCESLALWSLELTSELYNYAIASGPTLLIQFKQSKEIKT

TIFDAKFRFWRWLQQLYLHHSATNLWQLAVPQTQEASVSPQFLNEIFERFDDVRTQLQLI

HAAVDDICSKGKQAATKLSCLQEQLRQLSTCHCELKSPSYRSLREPVPTNRSVGDRMIEA

>contig34077 Frame-0F

MEVKQPLEERRMLEVVSVNFIMGYPCRKGMMLFASSKTNCQRNPSMHRRIRLPIRKTTQN

NPSTA

>contig34998 Frame-0F

MVQRIGILRQLYRPVVSFATLQRPQWKSFSQVATAKRKYYNDPSLRVRIVPMLQDNYGYV

VIDEANHTMFAVDPADVGQILPVLREEETTRNREFLGVLTTHKHT

>contig35979 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62683.1|) 7e-23

MPLSPQGRSYSTFGRKSFDDRDNAHTLLRLASHNNGRGIGHSTRATGSSNDCLLDDTEDR

VKRHRQSDPVDKASRTNVWRHPNDDDQSFGGSM

>contig36251 Frame-1R

MKSIELYFDLLSWNTFDVSKGQTMIFDIFNNIFVAHKSGADESVRERKIIHNQYQGSSSN

RKTELIG

>contig36329 Frame-0R

MAHGTSSQSECAPLLFNRVSAMRGRSRIRYPSIIDIIVVHEKYHLAEVRL

>contig37199 Frame-1F

MDSARTPKRKRRRRESSSTKRTNKKSSSLSSVANKNTGSVGNEAKIVWNDSPADKQIKVS

GTGKMAVRREMQGFVGRLARASQQSPPSNSKDDIKLGRKRVCAREKTEPSDDEKASSCCP

YPSEDVNQKAVTSTSKRSREKSDSQDELFHVLDQMEQKYASPDGLTKSKILP

>contig37920 Frame-2F

MDLEPALRRSKREHQPSAKAAASSASVFNCPASPRSSRRSQRRRISSMSPVSTLVPTCHS

SPMLN

>contig38392 Frame-2F|Blast-NhaC Na:H antiporter (NhaC) family protein [Phytophthora infestans T30-4](gb|EEY66397.1|) 0.0

MVQFEKDAAASPIYSGPMTPTYPGPMDSPKPALAPLEPDLSKPLRWQNAVLPFLAIVVLT

FVGMVFDGLNALATQDPNGSSKILNALSHCDSVSSLIRASAAGWIFAVSLLLLQRIITLD

EATKAWMEGIKDILDPTLILTLAWALGSVIGEVSTAPYIASVVGDSISKQYLPAITCILC

YIVSFAVGSAFGTMAIMFPIIAPLSWSISGGDADNLRQCFGSILGGSVFGNTCSPIADTS

ILASLSANVPLENHVRSILPYAILVAVVSVAGGSLPIGLKICSTFTAFGICLAVLLLVVF

FCGTRVNVRHRSLSSCSFLSVSPPMKHEGEQQPLLSG

>contig38785 Frame-1F

MADFSPGGAEPVEEPPTRQTLISDVCSSSLPMPQVMPHSPGSPSLFHLHTSNTNVDVPSS

MLPSISRTAISIPSICLRWLRLNVVQRILSAIVLIPLITVFLWLSPALATATFCTFVTSI

CSYEYAWLQHRIHLRVMTKLSACETELQRSVEVNQTREQNASRYDSSDSIERQSGNSGPR

DQEGVHVTQSMHMDSGRTVVSTSDETVQLSVLPPSSPPRSSIVSSLIDDSIQRQQPGLNN

VDQEEFAYLRDPSFSCSAVSRIADTYFHQNEWVAAVVLSAITTALTTTVFLVYISHIPKL

QQKQLYKLRWFYSIATDFVAAICAFFTPNWKYAFICLLGKTVFTLLTVHSTACPINRFRC

DTSLEPAQVFLSGVVVIVFFRLQTRTSAPATFLHILLDVLGYLYIIGSLSVIVAFVDDER

LESYRKLLIVLLYVVWASDTGAYLTGKLLKRLKYGYYNPLASHVSKNKDYEGTLGAILFG

VAAMFISSDLLNVPGSAVAQTGFTVMAVIVGRLGDLFESLLKRAAGVKDSGKLIPGHGGV

LDRIDALMFASLVFARYYAAIVM

>contig39618 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65743.1|) 0.0

MLAYDFNVASQPTSLHIPLHRFLTAAVRHICFSQSGLGNSIPTDGLLRVFGFDKLPVDMQ

WELLEMPLRCLVMASQIHSNLWRRNGDENMLAQLYNYSALPYCIHYRDADTFMLQLGVLM

TGPDALLARMVDKFQLGSYFLLSNGSNVAELENAITLYGYARLGEGIDAQQRLQMLEEFL

RLVIVLGTSLPSAMGSAYDDEFLAEEMLQQLCTKPQCFSKLFDLAILPSGQDDIPAARLE

SVLADVATFLPPSGLEPGRYELKEGLLQDYNPYFLHLNREAHELARDRWTTYRNACRLKA

KKNTPVAPPKQPLKPAKPPVAFFRPAQAILTCESTVVIVHVILWKILSSADTVPAPASLS

DNTVSDAVISTCLHLLVHGVHTASYASDRRFWARLGKA

>contig39733 Frame-1F

MQVSPEARMTSSLSIDLKRMDLPYKSVIRGFQNMIQQSGYKSLFSGNLVHCLWVVPFVLG

NGFLRPICQQYYWSRTDLDSHKSQFVANVAIGGVAGVALSAILYPLDVIRGRLTVEQYYT

GNRAMSGILKCARFIWDKESIRGFYRGLGPASLGLCTYIGWNVTLYECMRPVFVHYDVDD

TSTHLGHPSVPGQILCATTASLVSQCFSYPFDVIRRRVQLQGAKWHPELVFPSYRNAWHC

VRTSVAKEGGGIRGVRSLYRGLVVNAMKALPATVISFLSYEKLLKSKQDNDHAR

>contig40360 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62194.1|) 7e-26

MREVLILALRWENLVLGPILTLGDKE

>contig40979 Frame-0F

MAWETRQCRDHRQLFKRNARQTQGTPCLATRRHHEARLTELCTPNLSPSFSHI

>contig41998 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70122.1|) 3e-18

MQLMQTVVHNINVKYLGMKREVEKLGNLSEVLQARGNETFLDLSM

>contig42920 Frame-1R|Blast-cysteine desulfurase, putative [Phytophthora infestans T30-4](gb|EEY55031.1|) 2e-34

MASGPFNSNGKQVNYGSARFFCEELEEDLTSLFQEHPSFDQTFEQPLYSLTEKTVDLISR

NIVGRRTLFNSPFGPRALCYADFTASSKPLQCIEDYLNKEVMPLYGNTHTTTSITGLQTT

CFRHEARQIVAQAVNAKITGRGAEDCVIFTGQGTTSAVNKLVQALGLQHPG

>contig43329 Frame-2R|Blast-ubiquitin-conjugating enzyme E2, putative [Phytophthora infestans T30-4](gb|EEY53409.1|) 7e-99

MVAGVRNTAIKRIQGDVREMMTNPSDQYDAAPLETNMFDWHFTLRGPPDSEFEGGIYHGR

IILPSDYPFKPPNIMLLTPNGRFEVKKKICLSISAYHPEEWQPAWGVRLILEALISFMPT

KGEGAIGALDFSAAERRRLAKLSVDFKCETCGRVADLLPELKAGNEEKEVEKKPSKYAEQ

IAQLHLHSLESAPRADTTNGQEETKAVVKNSDSGKQEASDSAEAVVENSSCGKQEKSNSA

EAVVENSSSGKQENSNSAEAEGPVCVAAEADVGADAVISTTNAVEAEASVPGPTVEVIKQ

NGGTSRAASNVVRVREADSVDMFLHYVTIAIVMALFAILYKKLLQMHGVLQ

>contig44724 Frame-0F

MSSHVLVLRTLRRGAIETRRPRLLRHYTLLRLHNSPPTFTPFRATLSLENRHFTTSNGSS

TLQLTMKGGQLTGVAATAVDSSTSHEPWAIVQGVQSILETVHLTTGLPWWTVLL

>contig45635 Frame-2F

MFGFNVNKLKPNLMMAVHRIGIVKNKKANAALAQRQEVARLLMDGKEEKARIRVEGIIRD

DFTIEAYEILELLCELLAERANLIKTEPDCPYEMREAVCTIIWAASRTEIPEFAEVKKQL

TKKYGQDFKAAAIRNLDGCVNERVILKLSVQPPSAYLVVNYMKEIAKKYKVNWEHDDTEV

TDPLAPIPAPTGVTVMNAAVSGSDFAALYKSIPPSYLPKVPTEEKYYSAFSEASLSRRNV

ETYTNQPTHYYTQIDSSAQSDSPSAQIVESAPAPSPCAKDLNVAAAAPTIASTTASDGVV

PDFDELTERFKRLRQNRD

>contig45749 Frame-0R|Blast-M96 mating-specific protein family [Phytophthora infestans T30-4](gb|EEY55176.1|) 1e-43

MWESVAESLNRLPHVNANAKGVEIRDCGWGLVETLQTPAGDHTSILQLCSYLMPRLCGVS

AEQNRQHIHGLAELVAPCYRRLWNQRQRWVENVLMNGAIDAKHEQGYRKTLPR

>contig46285 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67631.1|) 4e-41

MDRASKSSECRAQYRGGLCPMGIEPDGITCTFSYQILGYLNLDDLVG

>contig46692 Frame-1F|Blast-T-complex protein 1 subunit alpha [Phytophthora infestans T30-4](gb|EEY64047.1|) 0.0

METADLVVDGTRTSGRDVRELNVTAAVAIANIVKSSLGPVGLDKMLVDDIGDVTITNDGA

TILKQLEVEQPAGKVLVELACLQDQEVGDGTTSVVIIAAELLKRANELVKNKIHPTSIIA

GYRLAMREAVKYIKENLSVPVDSIGRESLINAAKTSMSSKIIGPESDFFANLVVDAVSSV

KIEQEGTKGKIKLRYPVSSINVLKAHGKSALETELVDGFALNCTKASQQMPTCIKNAKIA

LLDFDLQRHRMQMGVQVIVNDPNELELIRQREIDITKEKIQKMIDAGANVILTTKGIDDL

CLKYFVEAGCMGVRRCKKEDLLRIAKATGGQVVLTLADMEGEETFDPATLGEAQEVSEER

VGDGELIYIKGCKTRQATTVVLRGANENMLDEMDRSMHDALMVVKRMLESNQLVAGGGAV

EAALSIYLENFATTLGSREQLAIAEFADALLVIPKTLAVNAAKDASELVARLRAHHNTSQ

SDLTKRELRFSGLDLLDGTVRNNLEAGVVEPAVSKIKSLRFATEAAITILRIDDLIKLNP

KEEPQQ

>contig46717 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54823.1|) 1e-11

MDSATTFAVPRQLFAGRKRRPFCPLENRSGAFFTIEDYEAHSIRGDVHESRLYESLETSR

QTILTPLNAS

>contig46876 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59083.1|) 1e-138

MSSVTIQDEANVKLHGRMQERDALRRLSVAIMDGDWDLVAKLLGKHLKKFHAAHQGFLYA

VCKQEYLELIDRQEYQKAYTFLTTHLKPLEKVAAATSSSRHEFKELCYLLTCKAVGESDA

FRDWEGVVTSREKLVEQLRATFALDEVFFPQQDGVAVLWTPPSVAMPDNRLVQLLHQSVA

YQMEFSRYHPKTIPKVTTLLRDFECEVLPNAVKSTYVGHSQNVKFVTFVGTDGELLASGS

SDGTIKLWPTEILDTQQV

>contig47615 Frame-0R

MAAPQSPNLMLFNDEPKLIPPTVVTSAHPLESSASSITSLNFAPTSPVEISLNDAEQDRK

VLNFFVSCRGVDGNLIVSPARSAQTLVRGAFNILSSATAMNNTRSPRAKSPTEVNVEVKV

AKEVPIFGFDADVLIHQTAKFSPFPSSKLLVNDKGSPHEANGLLDSESFWSERRKSRNPD

FSVGYQLYCKNPAKF

>contig49370 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62486.1|) 1e-10

MLGRVQRAIHSRLPTSDWLSRTVGPLVSFA

>contig50079 Frame-0F|Blast-M96 mating-specific protein family [Phytophthora infestans T30-4](gb|EEY64931.1|) 6e-79

MVLAINANKLMPFDVRTTGKAVWRHFAHSMDHMPHRTYYQKQPLHVETSDDTVMEQYGVK

ITNGQTNGDFHVKHIIRRYVEHDRILVVWRTITDTVEFSAELTSGIRFLEKGYIVVKPPV

LGQEDCTLMQTCYIIRPEVHHWKESHQARKVGALLDFVQSSVSGSISASHQMIENVLLST

ALR

>contig50310 Frame-1F

MSDAPSDSPASSGGLGTSLMWEKVSLSPLEILSVQLEHDLQLAEEAATSAAHVKQNKYGV

DMDSNTNKATGRMFIEVVAVNNLALDKNATVQAVSGNAQPNLYVSTVVSPLSAFEKTTKK

HLRTSVVQAVDNAKADWEENLVHVGAKTKKFVVKVSLSCKAEVIADVVLGELELRSTDYE

DQMPHEQWLNLKAPALAATSGIIGKIQLRVRFEFSARERYENQVALLRQKKYENDNNIEQ

YKKTARLVKASVQHPAAFGNETAQAALYVPGNKFHMDAHHPAAISIAPLADKTRIVTPFG

RGVVVSFRPLTRMYVVLLDTNAASKNRTIAYLQQDIVKEESDEPDFRMHMKVLTPYGLGV

VKEIRSCDDVIVVETDFAHMFMQRKDIKLPVKELADMSTKDLLQEAAKLADVGNDDFRDS

KLQNAVHNYLRSLGFLQRVDQDEATHKEKATIIQTMIRCHLNIGACKLKLNMFTDAEVAC

TNALGILTVLAENRDGNVVTWMGRLGMSEQLLFEDWPSKARFRRAQACVKLEKYTDAKQD

LLLAVRLNPRDKSCRTLLDKVSKLLEKQKRDEMKAWGGIFDNLEASPSTIKTATKTTTTK

SSGGIFTRKAKKQGERSDAIPSAGKHTAWYLTMPALVSASVVTAGVAAMVLLTLKKTKSS

>contig50365 Frame-1R

MKPSKIRCWRRSNEYETERAFLEGAKYNIADNYCGFTDTINCQSHFST

>contig51317 Frame-1F

MQAKQREFERKVFCQLMKRLEAADAMELASKRTSEWTQIVQELIPLYAHDVNANDIFKDL

FQILEQYRDQKEVRHEIWTAGPFLDLPSHETSLEEIISMVSELEQFLRTSALDAPAIVTI

AKSTGDKFLPPHQVNFVLTCVLEMLAR

>contig51388 Frame-2R

MRHLQSRMLLKKSVACNVFIRASSRSATKTLYSNANIE

>contig51506 Frame-1F|Blast-26S proteasome non-ATPase regulatory subunit, putative [Phytophthora infestans T30-4](gb|EEY55095.1|) 9e-24

MAECEYEAVVKAKHAIEAEIEAIVAELSSGNNPGTDGPLVDAEGFPRADIDVYRVRHLRH

SLACKRTDYQ

>contig51685 Frame-0R

MLSKIDQERGILSLELLIAVLSFSEARSVNTAACHLFLEKKGLSVLADALTCMDAPSFQQ

MLQNKELFDSSNRNMARM

>contig51850-1 Frame-1R1

MLRVYKFIETLTGFNWIGIKSIELRYCDKNGVFAYEKAVEICVG

>contig52033-0 Frame-0R0

MIVLLRRIIIVCAASVLCVRQCRSLCRKVYFTSHILTLTKK

>contig52118 Frame-0F

MGLGKTICCLALICESLRQVRAADVLARSKTGSSIPTLTSPTLIVTPLSILSQWEQEIRA

KTNLSVVTYQGASRQSFQTATQFMGADIVLSTYDTLRLSECKVRDNSNEENDYRHGLGNE

WYEAPRLAPQSKRSVVTSKLHQLKWFRVILDESHLIANANCARARAAFTLSSRRRWCVTG

TPIQNRTADLAALLQFVGLGSRAHALSERELSALVPRVVMRRLKSTIDARSRAP

>contig52187 Frame-2F

MSYPNDSKALSVMLGFQHEIRSFIAPTDQINLSSASWWLYRWIPITRYVFAWPTNQDINA

LAVHLHARLSKGSVSINARKSKRKFKVAPMRLLARDLLLVACGLRPSCLVDCCDLNSEQA

ALLLNSMEHPWLKMKQIRAIHQIIIDVSASLTRPNRMSTMCEFEASHLDLLRVWTVSACK

>contig52262 Frame-0R|Blast-prolyl-tRNA synthetase, putative [Phytophthora infestans T30-4](gb|EEY65796.1|) 1e-105

MWTECARHSSARKWLSTLPSARATPCALRSMIWAPTEKKTPSDAAVPSHQLLLRAGFVRR

SGHGLFALLPLGHRVMGKLEALIDDEMQKIGGNRVDLTILTPNDIWKQSGRWQSRGPELM

TLKDRREDHLILGPTHEESITSLVALHYNAAGETDSSLRLYQIGRKFRDEIRPRFGLLRA

REFIMKDMYSFDVSYEKSMQTYHDVTAAYNAVLISRLRLPVRRVEADSGNIGG

>contig53658 Frame-1F

MTELSRTLAQPTSEEHSPVPQSSTIAKSCIIASCDKKTSAWKERGSRNLTFEERRKMLEF

LLKRR

>contig54358 Frame-1F|Blast-WD domain-containing protein [Phytophthora infestans T30-4](gb|EEY57502.1|) 6e-07

MFNPATWSPHQTLPAHTKPISSLSFSSNEELLASSCVSKVP

>contig54808 Frame-0F

MLRLGGLNAHDYKPSADAIEWRMKYEELEERVIELQDELCHTKSRGASITGYTANSVEAL

NKMLLDLTRQFAVVLHDKHELQDRLNNRQSKKVESIERPFSQDAIDA

>contig55627 Frame-2R

MFLIVKTPTFETGVSIVDRPCLSSMRTVPVKLFAFRKKRFPARMISSSLCAQSAGSRPEI

AQPELKKEISLSKRIEGYTILQEKDS

>contig57346 Frame-2F

MNRIYELITLVQAAFKELDRNKLNKVILTHQS

>contig57607 Frame-2F

MIKKTPQHARHPSGKKRRSGRNSDPPEVRLSKKLAY

>contig57698 Frame-2R

MTTRMLVLRVLANLFLYDKARAVLVAHKTDVLKALPSFLTYPHKLVALSFSTVLLNFARA

IWTCKEAFTIADSIVVMSLAADLLNGSYTVEELGNDTLLRLLVTIGTL

>contig57863 Frame-0R

MVTSAITSTMPIFCAAVFISGLHVIMSAVVEAMSLATTLVIITTIGSWVIMIPASYLIGL

RWHGGLHGLWWGSLVGEAAKCSLLALALWRIDWQHVAQRAVFQSEGNRRTDADFENDLLL

EFALPSTPMVAEATPVLAILLTSRSHQAAVDAAA

>contig58714 Frame-2R

MATRLCLKRFAVYLDYASNERGKGCPSNSLEIGAHNVISISKFPSNRMI

>contig04411 Frame-2F|Blast-acyl-CoA dehydrogenase family member 9, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY56426.1|) 0.0

MQSLLRPSRRLFVQHGLRLLQTAAEAAADVSYTRGLFLGVTNTARAFPYPKLSESETETL

QMLVEPVNKFFSTVDSRAIDETKEIPPKVLNDMKELGLFGLQIPEDLEGLGLSNTGYARV

CEEITDGSLAVTVMAHQSIGLKGILLNGNETQKAKYLPKLATGEHIAAFALTEPSSGSDA

GSIKTRATLSQDRKHFILNGSKIWISNGGWAEVMTVFAQTDVDGKDKVTAFIVERSFGGV

TSGPPEDKLGIRGSNTCQVFFDNCKVPIENVLGGGPDMKTGGAAGVGEGFKVAMNILNNG

RFGLGACAGSSLRRVLGVAAEHANSRKQFGAPLANFGLIQKKFGVMTLEAYAIESMAFMT

TGMIDRGDPSCEIEAAMCKVYGSEVAFTGINECIQVMGGTGFMKEWPFERLMRDCRILSI

FEGTNEILRMLIALSGIRTAGERLSAVGKLLQNPLSDLSGAAREISDRLQRTYSPTPLDG

VHSSLRPSAELLQKRTVEFGDAVEGLLRKHGKKVVHEQMQLERIADSAIALFAMTAT

>contig08666 Frame-2R|Blast-glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY54315.1|) 4e-19

MNRLYLDKIVSILPDGTCMSDKY

>contig08929 Frame-2F|Blast-chaperone protein dnaJ, putative [Phytophthora infestans T30-4](gb|EEY57996.1|) 0.0

MTMRLVLLRSATLRALGAPKLKPATLMYGATALLQQCATFHSTRTTMEPSKRDYYDILGI

SRDASKNDIKKKYYQLAKKYHPDANKADVNAAKKFAEATEAWEVLGDDKKRQKYDNYGHA

GVDEQAGFNGPEGFQGQGFEDIFGEFFSGQGFGGRSNRSSATQPQRGSDIQVDITLSFME

AVKGTTRDLNITANVECDTCDGSGAKPGTKAKTCPTCNGSGVQVMQQGFFAVESPCRRCR

GQGTMIESPCSTCRGQGMVQKPRAVEVKIPEGVDQGMNLRLAHQGEPGQRGGPAGHLYVG

IHVLPDPFFKRRKADVLVDVPISVAQAVLGGAVVVPTLTGEVEMKIPRGTQPDTVLQMRG

KGIKELNSNRRGSQLVNLQVCVPTNLSTRQEELMKEFLKEETDRAEKGEDPDSKPHTFTK

SVRNTVDRIKSFIKGYKSEDS

>contig09889 Frame-2R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY59962.1|) 0.0

MAIKQNSSDTDEKQSIDDVVPDLQAPVATYRLPRFGSRRLSSSSSGIDYNRFPRTKSMFP

EPMELTKDDLSSADALMAAGVFTMNSTLSNVIEKALGQPIPGLEVRFRNLELSAEVPVIK

GGDLEVPTLVNQVSQGFSSLFGQANKLTVEKKILRGITGVVRPGRITLVLGQPGSGKSSF

MKVLANRFHMDKTITLKGDIDYSGKDRSSILDELPRYVAYANQIDEHYPRLTVQETFEFA

HRCCTGTGIEPWGIEALKNCTPEQHEYAVEVLTAHHKFAPNVTIKKLGLDNCKDTVVGNA

MLRGVSGGERKRVTTGEMLFGLKRLQLLDEISTGLDSAATFDICKSMKSAARNFNATVII

SLLQPSPEVFELFDDVLLMHEGTIMYHGRREDAVPYFETMGFYCPPRKDVADFLLDFGTD

KQKAYATEKNVPYLSEEFATRFQESAMYHDTLKYLETKVDDSIIFADFTPFRQTLREDLT

TLLRREMTILSRDTTYLIGRVVMTSVMGLLYGSTYWQIDDSNSQLTLGLLFSVAMFLSMS

QSSQVPTFMDARKIFYKQRGANFFRSSAYVLSMSISLSPFSMVETVVFGAITYWFGGYVD

EVGRFIVFLVTIFLCQMWFASFFFFLSAASPNLTIAQPMKMVAVLFFMLFGGFLIAKGDI

PDYLIWIYWVDPLAWCIRSLSINQYLASKFDVCVYQGIDYCAQYNMTIGEYSLGVFDLQT

TTEWIYYGWCYFIVGYSILVFCAYLMLEYKRYESPENVAIVPHDEHDHPDQTAYNSMPTT

PKSHQNVIQIHNVDNFEGGYPVIRLPTLPTGRGISVPVTLVFHELWYSVPLPGGSNDEQI

DLLQGVSGFALPGTMTALMGSSGAGKTTLMDVIAGRKTGGKIQGKILLNGHAANDLAIRR

CTGYCEQMDIHSDSATVREALLFSAMLRQDASIPTTRKHESVEECIELLELGPIADKIIR

GSSTEQMKRLTIGVELAAQPSILFMDEPTSGLDARSAKLIMNGVRKIADSGRTIICTIHQ

PSTEVFNLFDSLLLLRRGGRMVFFGELGEDSKHLINYFEAFPDVTPIKPGYNPATWMLEC

IGAGVGGGKAAVAADPAQSTDFADRFERSDQKVMMEEDLNQEGVLFPSPDLPELTFSNKR

ASSASSQFGLLSRRFIRMYWRTPTYNLTRMVISIVLACVFAIIYQGTDYTSYSGANAGVG

LIFVSTAFLGIISFNSVMPIAADERTAFYRERASQTYNALWYFIAGTLVEIPYVFISSFL

FSIILYPSVGFDGVTTFFYYWVVVSLNALVFVYLGQLLVYAMPSVAIASTVGALLSSIFM

LYTGFNPPTGNIPQGYMWVHWISPPTYSIAILVALVFADCSDEKIGCSVMSEAPPTIGNM

TIKQYVEDTFDMKQDDIWRNAWILIGLV

>contig12607 Frame-2F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY68890.1|) 0.0

MLEGQVRELRTEHIAVNAQMEAVKAEMKRLQSASVLSKEQHQHQLDLLVAKFQQEKEQFK

IQIDTLQEEKVSLESEVQTLRARVTTARDVDIEELCNVKREADILRRRLGEMTNQGVQSI

AMKDGLILELQEKIKQGDKQRRAMHNTIQELRGNVRVFARTRPFLPSDHCDPTRMIPVIS

CDFDGESLKLLRPGKNASQPDSFAFTFDKVFAPSAGQDAVFEHVCEFVQSSMDGYHVCLF

SYGQTGSGKTHTMQGSGNGQMRGIIPRAIEMILQECEALKNQGWNYTTKVSFLEIYNETL

NDLLVEKHANDEKLCIKKDARGGVYVPGLTMVDVTAVEQVEVLMEQASRVRSVACTDMNA

QSSRSHSVFSLHLQGVKEKDGVVLNGQLNLVDLAGSERASRSNVSGDRLKETQAINKSLS

CLADVFNAIGNKASHHSVSKLKINLFAPKQPFR

>contig13572 Frame-0R

MKNKEITHILRSHFAALSIY

>contig13877 Frame-1R|Blast-Cullin family protein, putative [Phytophthora infestans T30-4](gb|EEY65576.1|) 1e-33

MSLQAAIVRILKTRREIHQAQLVHEVAAMLVNQFVPTTLAIKQNVEILIQKEYLRRHEND

HTRYAYVA

>contig17547 Frame-1R|Blast-endoribonuclease L-PSP, putative [Phytophthora infestans T30-4](gb|EEY67881.1|) 1e-09

MGKIEDRLAELGIELPAAGSPKGNYVNVVRTGSYIHT

>contig18362 Frame-2R|Blast-cysteine dioxygenase, putative [Phytophthora infestans T30-4](gb|EEY64224.1|) 5e-68

MLLCWNPGKYSPVHDHPTNGCWVKVIQGHVNEVRYKEQDNKLVETANIFFTSGVTYMDDS

FGLHKIGNPHAKDSAITMHLYSPPYEKCRIWLDPENVAKSSISVANYYTEYGKKVNFS

>contig18832 Frame-1R

MNFGRRKSDQLMSELNLNGTKAVLNHQIDDLLATSSPSSHPVFASNVKNDATAVLPVTSS

SFYQDATSYPEQTQLQETRQHMNRHGPTYGVKPDISSRYSSSQSTSYQAQAPTPSMMLPY

KFNDSNTSPPFQNCVGSHDFSAQLSAPPKVSQRPPMTSHLYQSHPDRMNLFRQQEQPRPQ

ARNESSQTQPARDYIDVLLESAALDENVTLQTSSSLLSESWQVSNYSQTASNSSGPYPSV

SHQHSGQQHFQLSPMEGVPYTSTSRF

>contig19682 Frame-0F

MWTKDFVRVFQGAGKVAEQALRLQRSEVANQSENLTKHAVELSRLVPFISKQEGSTVADA

QKTEEALLIAAGTPVKTYMEKPIEEFKTQDTKTPNEFKTQDTKASVLHEPILQPQKEFKT

HDTKASVLQEPINLPRKEFETTEFQIKTEPLPIDPKMVENTSSMRPEITIPPVNEPPKRK

WEEKHVPSSPLSRILGFGSLAARLAVGTATEIVRSGGKNGTYNAFVSDANVEKLVETLCT

MRGAALKLGQMLSIQDEAMIPSKLALALDRVRENAHVMPRDQLYQQLEMELGQEWPDRFQ

DFDDIPIAAASIGQVHRGTLLNGDRVAIKIQYPGVAESINSDLLNLKRLVTYTNILPRGL

YIDEIIRVGKEELTAECDYIGEAQNQERFQKLLENQGMTQQYVVPRVYRELSTSRVLTTQ

LISGVAIDKTVHLSQNIRDSIARRILELTIQELFAWRFMQTDPNWSNFHV

>contig23342 Frame-0F|Blast-calpain-like protein [Phytophthora infestans T30-4](gb|EEY63473.1|) 0.0

MLDDDKKLVCSMSIKNAAEAESILEVIRQTPTSIDARFLTIAKEAVTSGVTKRKRDHLLL

LTKNMILHMSEFVQDGLQRFELMWEKSLLDHYQPLVFDSVGNGSAYRVDGSESGVLSRVS

VIVPVYFHAHGTCLFDRSLESRAASRISGVGIDPGNLRMGRLADAYLFGALSILSTSRLA

LSQVFPQLTDDMVRPDRAEVDTAFPKEQQYNEEGVYAVRFWRNNRSRVVVIDDYIPCSQY

GKPVFGSFTGSSGKFEIWSLLVEKAYAKLHGGYEAIVGGQEAYALQDLYGGVPSRYKLQE

RCANEDVAWQTISGALQAGSLVGCSNEEMAVELPTGLRKTDAYGVMKLVELNYQGAHTRL

IQLRNSWGIGTHQQPEKWKGSWSNEDPKWLTFSRMQKVECGFQFREDHTYWMDFSAFYCF

FTTVIESCNLYNFRSVPDGIGNPVSPSLSIHIISGEWNGITSGGRDAMHLNPQVQLFSPA

SNGCNLIVHLEQPSRRMKMETEYTSYIAPVVVKNGERQQRKIDLSQDVVATGTFISNRSC

VLELPLMSADSGKPFVIIPATYDGHLPSQLGFSMTLFTSKPTAVLPVSDTGSLPVCCICQ

RALSGTFRTFTHEQEGLTKVDRVCQGACVDAYRERNTPVCVDCHQRIEVAEGRFSGRMFT

LPDGSSVHAECIDAYQIRTSEKCIHCGHAIAAIPGRFDGKFFQVSGGKCHGECMESYQLA

TAQRCVHCTEPVIKLAGKFDGRFYKIEGEHLVHFECWEQYQQSVAPKCVHCVQPILQIPG

QFDGRFYELASGIGKVHFECWNAYQTLATRA

>contig24839 Frame-1R|Blast-MtN3-like protein [Phytophthora infestans T30-4](gb|EEY67216.1|) 1e-59

MIVLTIAKVVSIITTVMLRMSLMPDFIRWRKNQSTGEMSIMPCVLLFTNCYVLLFYAYAI

NDMIPLFAVAVFGFIVGLFLALFFYKWTAYKKTAMRIFVCSFAFCVLMTIYGLLALTGKT

GQSTDSVKTTLGSILVSTTVILYASPMATIIHVIRTKTASSMPLAMGVVLVVNSMSWIFY

AYLVHDLFIMLPNIAGFILAATQLILTCVYRKPPPKGQVDNSTRVMMPSVVVVSPVQSCE

HAISISPTGSVKSQNFVAALASSKK

>contig27971 Frame-0F

MAALPDLAHTPLYIRQDASKANLATSFELPGWGIVVILNTIAFNGNSLNHDKQVAIATTT

RELQRVMGLFITEFRTLLGVASFRHRQDEKDAAKITNTLDRQLLFLPSSTDGIADWELDL

LMRDRFTKLLQTAIETLQSTVKLVKALPELSVSNRVHSRVEAAVTKLEAILGTNNCHETV

KELHVLLAMARQASELTDAAYSDPTMIRQLYFPQDQMLGVYAPLLAPLLLPFLMGLAREY

KRYQAKCVAKNK

>contig28202 Frame-0F

MEGILWTRDGRSKLLRGWDRHYFVLSEASTLQEYTSDKRKKKELLSRLRRPSFESSSFSD

RNDLILRQEVNIRGAQIEQLPFLRVNRQHAFQVTIIQNEVCLKLVLCARHADDMAHWITA

LKSAALQLEIPRHMSNSSPWRSENDSMVSHEDAFLEVTRP

>contig29216 Frame-2R

MNSESVARQRNAKDGSSYCR

>contig31727 Frame-2F

MIEFRDVSNNRFLDSVSSFRSSREFGGDDFTSEIDGEFHDRSQRSSYQGQRSSFSRVSNI

MKKRNFLQRKALEIQCASAAVRTFFLGSLKTAAHHLKSYGHDDDCSTEATIQSLYDGDET

FFQERFMNGALFPSSVSDDLLIQSFFNPSLNMFIRKILDGKSCFVLYDVPKELRARTLRY

GELFEFMTSGIAHTLPIGLLRAKDGPKGSPYPYIYTCPSSDTIVFPKDKVFVLINVVALN

RLANKLQRRFRKREKPFKSLADLMETNLWLSRS

>contig32663 Frame-2F

MGQTTSIQEDKMKKRIRQVMGSFLDFGTHLQNANEWAQNCATPKNCYLSFRVIINPDVSA

EVLPYLWRIRGNVAVEVRKLRRPIENQPNMGDFRAERSDTIGRAKTLTIAEFYYIYCFLS

DVKACAAHTVCFPEKSISFEETEFDDTECQICMDKKKQVALPCAHSFCLNCFQHWSTQSP

TCPICRAEFNCCEGDDLWQLASVDVDDLGSYATDLVARIYEYLDKRVECKCTEEYMKRSA

VLYSAAVAVKRTPKRNMMRTRLFSSTLPLGLPSALRSRIQLSTVFDPDMMLAVELASGED

QYAAMQHFEQLQQDELLAMAMQSDAEESPDES

>contig33105 Frame-2R

MVACENEQLFGDNCDLTFAPVMDMTTGKMILALARIWSAPATLMLERRQPRLKGQQDILL

RMQQYVPNAYVKARTGQV

>contig33875 Frame-1R|Blast-ribosome biogenesis protein NSA2 [Phytophthora infestans T30-4](gb|EEY60966.1|) 1e-145

MPQHEHMDMHRKRYGVRMDAAEKKRKKEAREVHRRSQFAQKVHGLRAKLYNQKRFKEKAA

MKKTLALHNERTNKHANDDQIPDGAVPSYLLDREGVSRAKVLSNTVKQKRKEKAGKWDVP

IPKVKPIADDEMFKVLRSGKRRNKAWKRMITKATFVGENFTRKPPKYERFIRPSAMRFKK

AHVTHPELKTTFQLAILGVKKNPQSPLYTQLGVMTKGTIIEVNVSELGLVTTSGKVVWGK

YAQITNVPENDGCINAVLLV

>contig34074 Frame-1F

MMSPKNTTAYGTSSIGSSSTRLSGQRKWITWGFVGASACIMTFYLMAGSHLSTLTMAAAI

SHESDVTCVESSSIDGVNAMMQPITGLKWNVGGVKNTKSFITIDVDTKYQEIMGFGGAFT

EAASLQFQKLPPNKQEKVLSLYFDKDAGSGYNFGRVPMGSCDFSVASYNFANTEYDMDMK

DFDMNVSHDTDVMIPFIKRALELCPDMKLFLSPWSPPGWMKRSSPEYTASMVGSAKPLGL

KEDMRAPWALYFSKYITAYKNHGIPFWGLTSQNEPEFAAPWEACVYDPEYQASFIGEFLG

PVLARDHPGMTIMAFDHNRGNAPKWAQVIYNHPTASKYVSGMGFHWYQDGAARKMDGVDY

PEHLSDIHLMDPNRFLLSTESCNCPGVAVGDDAWFRAQRYGHEIMSDLNNFAVGWVDWNL

LLDHMGGPNHKGNLCDAPIILTEDGKDFRLQPMYYFIQHFSKYLLPGSRRVSVQIAAHYA

KPGDAQLVVGYQASLSMCDGSARQLIHRTNDNKLQVTNTPFCLSMVPKTTEGQEIRLVKC

EWTQQEWTFEEDTQRIRIDDECLSLRHGTTEDSVRVIVAKCDANSKLQQQWKFETEDGTM

RSLGSTENQCVTAGYAFLQSTAFVTPEDRTVLVVMNENTEPMEFQVQVGDAVLDTSVLPG

AIRTYKW

>contig34904 Frame-0R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63606.1|) 3e-49

MLFIMVTGAPPFERPDDADPRFQMIAKGLMSDMLDSWGMDHVSASVRDLMSKMLIVDDPS

RRLTVEQIAMHPWIQGG

>contig37549 Frame-0F

MDLVEDYSRSIIFWKKRRAATRAAARVARREGQRLRHFNDEENELEERDSERGNTEERQE

LMPERQLSEMSLCDFPFVLDAASKSKVLQIDSDLEQRARAHDVVLSQSNVVVVGVESPFL

ILKIRRENLVEDAMQQIVHLSTSAETLKKPLKIKFVGEEGIDEGGVRKEFFQLLIRQLLD

PAYGMFTYDEETHTLWFNSDSLEATMEYELIGTLLGLAIYNAVILDVSFPHIVYKKLMNC

TLGLKDLELALPDLGRGLRQLLDFKGDIEEVYQRTFEYSYEIFGEVKTVELKPEGSSIPV

NTENRNEYVALYVDYVLDKSVARQYAAFHHGFHQVCNHEVLSMFRWEELQLLICGSTDLD

FEALEAVTHYEDGFTKVSEIIRDFWVIVHAFPLEDKKKLLRFATGSDRVPIRGLSNLAFV

ISRNGPDSERLPTAHTCFNHLLLPEYSSREKLKERLLLAINQAEGFGLR

>contig38405 Frame-2R

MIIYRPAKRSRKTLPSRLILNNMFKSLLGNINAFKA

>contig38786 Frame-1F

MFLGPSSDDVGKLVPHMPRMISSGGKAIYVSKPKNSDNLMYLSSPFERASEVTDDMDTAS

ESAEAPDVVMSKRKWGGINAAKFIGTMAAGAKQRVAATFKNAKYTHEGTSCQFCKMTPIV

GDRYSCETCVGFDLCENCYSLGGHGLENSDELFYRVQELTLARCPRLAEEADLLELMRFE

ICRSNLRKFSFCLNWLADIVNGKTSKDLQARALEIPSIRRDVRKVFVPLLMRVCSDREDI

EVKTEWELEDDNQAPVRSVGGGISEGDGRFLETLRIWVADQYRTTSPFVERSLLKYREGE

EGDEDVDGSDSDRGHTRVNGDDGVSDSDGVREDPSGFVEEVSSQPGSSDRSRKTSDAF

>contig38953 Frame-1R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY65496.1|) 1e-156

MHPQAAAFESVRDHSTLEMSASEATDFERVPPDSTGSFVKIGGPLPDSSDPRTIKGASSA

PGNGHRLFYLRVIDSRKWHYSETFALFLDFFVQVLAISFTQRASFHDEVTAKASRLFSSG

LMLCYFIDMSIRVLGLRLALIRSHSNIADLVCLVAMVVLLGSRFAMGDREYWFCLAYLTI

VACRLILKPRARTFSKKLHKFRTNGDHIRISIESLRASLARIPGISALSIEMMETDLVII

CGRDEGDMTRDELMNFLERALHYRPPTLSATEFLSHLRDIDASSSTLAYGIMDVVRSTLW

HWSTQITDL

>contig39378 Frame-1F|Blast-choline/Carnitine O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61808.1|) 1e-116 NOT\_ORF

MTKAQITERTMQFQDELPSLPLPSLEQTLNTYVKSCEPLLSSSELDHTMAVCHDFLHGVG

PQLQAILQERADTERNWIEEWWESFAYLQPRYPSAININWYGVLPGNWGPQDMSQCEAAS

IFAVAILKFRNNVLKRSTREAGLK\*LSGDFVL\*REKYPPEKMMGQPLCMYSYSRMFNTCV

IPGERCDKLVSYPHDAKHIIVLKNNCMWALQVLDADGSEISLANILRQFELVRDEATNLS

DLDRYPPVSILTSENRTNWA

>contig39561 Frame-1F|Blast-cardiolipin synthetase, putative [Phytophthora infestans T30-4](gb|EEY65382.1|) 3e-58

MMWTGLLPFPLAALILSRDFLLIGGTFYHRLRTKTISSGFFDTSDSIAFEVKPSMLSKLN

TASQLLVFGSALANTSWQIPSDFILNVLFGAAGMTTVLSGSEYLYGYMTKTAAFKPIGKP

LSKVVQRTELVLKRQEAAIKRTKEALEDRVKRQLRSK

>contig39684 Frame-0F

MQPSLRFLAAVSTLAPYSLAMASQCSNIDTCYEGGATATPCSVSSRGCPPCVTFANDGCY

VLVNGSCPFGVDCSSVWSGASTPSIGDGSLSTTTSSPTDSTPTTPPSTLAPAPSTNTATS

PSTGGTSKSLTSPSTT

>contig39730 Frame-1R

MKYHNEVSELPSLRYAFCTGSWGLRVYNELAAEIVAFKDSVTRLHVPATTQAPSFEGCRD

AKLEQNL

>contig41489 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67373.1|) 8e-25

MPGVAQGFIKRVTATWTPVGTLVTSDQYI

>contig42549 Frame-0F|Blast-mismatch repair endonuclease pms1, putative [Phytophthora infestans T30-4](gb|EEY70560.1|) 4e-61

MASVPATTTLHVLDRRDVHRMCSGQSVVDLATAVKELVENALDAGATHIEVKLKEFGRDA

FDVSDNGTGVAPEDYASLVQKHCTSKIRNFEDIETVGSFELPRRGIELDMRARVDLHGLY

>contig44727 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66319.1|) 1e-59

MRTSHTAFNIEDKELKFKCFKFSSCGRVAILFKEGKTEAYNKICIFPAMECLLEGVVSIS

QKQFGQVVALEWTPPITYERDCELIFLTTTAIGMLKFDCALSTNKWSIIWSSSRLGLRPV

NILSISSYPYGLVQVESSFAHFNLRDIDGNSLSESHPPFQSPIYYHERPLVDQPFTKSFT

AHHP

>contig45636 Frame-1R|Blast-2-dehydro-3-deoxyphosphooctonate aldolase [Phytophthora infestans T30-4](gb|EEY66546.1|) 2e-66

MLQQVKDETGLPVLTDVHETHQVAPVAEVADIIQIPAFLSRQTDLLVAAANSGRLVNLKK

GQMLSADTMLLAAQKIAITQGDADFILTERGSMFGYGDLVVDARNLP

>contig46105 Frame-1F|Blast-pentafunctional AROM polypeptide, putative [Phytophthora infestans T30-4](gb|EEY67699.1|) 0.0

MSATQQVIVPCGSYDIVLGSSLLQSRFVAEDLLHRLSSVSTFVILSDANVGPLYAEPLRV

QLAELLDAESNNKRRVLLYAIPAGEASKCREMKSKIEDEVLFPNRCHRDTCIIAVGGGVV

GDLAGYVAATYMRGVPFVQVPTSLLACVDSSIGGKTGIDVEVGKNLLGAFHMPQRVYIDL

NVLHTLPKRELINGMGEVIKSGAIFSASLFELLENSTETMLSLSDMNVVQRIVALTVQVK

ATVVTEDTQEMGRRAILNFGHSIGHGIEALVQPEYLHGECVAIGCLKEAEIARQMGRCTS

ATVGRLRRCLTAYGLPVRVPDHVTTQDILVKMEVDKKNSQGVKKLVLLEEIGKVAANPYA

HAVTDRQIELVLEKQVQMVPGVKATGQICVP

>contig46286 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63367.1|) 1e-44

MSSLGTQSSDSQTTSLLNKDGSLQDMTSSSMLFDFGGESGSEDPLSDEEEPPSSIRDESD

SWSSGSSSSSFEYGCDCRSVRRVSLMGASDYCLDPNALLSSKCGNIELEENGACPITGAQ

PCSLKGHVLTNDSVCALDRKDETFKCVASENDLEIQKNGKKRKNR

>contig46691 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53261.1|) 6e-94

MWLQEVQKIIHETPMSYQSDKEKLDDMHSRELNAILEAEYAVVAQKLRDAPSHGMCLNAL

YYMMMMCRACRFNRDCFIKDWEVNFERFFAKPPKSERDEVILGAILSTLSVMIGTLTRAE

QLRILVVVKRRVLPLLKRSESICFSLQVARLLLNLSESNIHDLFLSLAADTDIISTICLK

YSTMYATEPSLHGLMLEILLRFARGMNDNAVPCLSPPSRAKICKRLSEMLSPLLTIVCHH

RIPGSFQGRNVFAIASQCMIEILRTL

>contig46714 Frame-0F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY55494.1|) 7e-72

MFTKTSIKTMNKLLAPRARRSVTALALLSAGTYAVDEANANILSRSLRVLVTGGQVLWDY

QIHFKGTSRDDANYRLKLQSLNQRIAQRIYRVCYENGGIYTKVGQQLATFNHGIPKEYTE

TLARLQDQAKPIPFKKIKMSLEAELKQPWRVFFKEFDEKPIASASLAQVHHAVDHQGREV

AVKIQYPHLELQMNTD

>contig46875 Frame-2R

MSENSPSHLTDKRSESMAPYKPEILYIVNTV

>contig49849 Frame-0F

MTMGSHCRQNIEVFQLRLRETLNEGGDDDSVGTIGLNAFSTSEDATATAREPKSSRLQTP

ISQKTIPTVNPRLLITLLETKQNDRVQQNHANDSAMEFVETSQVNEEDIDGREPHEKRRP

CLLASKSGDDG

>contig51826 Frame-0R|Blast-ATP-dependent helicase, putative [Phytophthora infestans T30-4](gb|EEY57215.1|) 5e-41

MQHCRLQSWRVFVTKQFIELLPPLLVAMRPPQASSNASNQSELAFYLKTRHEVLQFLIIE

DLRPKHFDGIAAVALSRAAFTIVM

>contig52030 Frame-0F

MQQQVTGFDKMRQQQECKTKKQKREAIAALMAESTAHVRELLNFAVVLIYTFLRKSGSTK

IQSNDVKKTADAPAELVDPLVPLLMRCVGESKDDRAVINTLKCLGSLLPRQNELPALRFA

QSSLLGRLFKILQQAGAATRNEMVQTCYRTLTALLRQQQGLELAQSKGTSAKNSKCETLR

MTEPQLRVLLSFLRADLDEQDHQNATFALLKAIVNSRLVISEVYDVMLRVGELLVQSDAP

GARLNCATIYLTFLLEYPLGNKRLSHHLKFLVDNLSYGYATGRSAVLEALRSLLLKLPQD

LVNARSQYFFLPLVLRLANDEASECRDLARAALVTLVRRLGNKELNESIMLVVSWWTQAS

KSAAADAVKLLGTAAQVTTLVLETRPEFFEQSALQVLLAARPALELRQRELQTVEDSNQV

RWQPTYHVCAALTAFSDHLAGPYELWLEKPESTDNFLDLVALPLLQYPHAWVRLGVTRLL

TSYLRRRQAKSLSYAAPVKRLSGDALKRLHNGSAYFQRPGRLFAWSSAFCKLLETPVLKE

ELATEVLAALLFLCEALESTDVPQDVTNSAIGSLENVDAIAEDDAAVEEIEDV

>contig52184 Frame-2F|Blast-ATP-dependent helicase, putative [Phytophthora infestans T30-4](gb|EEY57215.1|) 6e-68

MMRVLELYPSSESIVVFYQRMEQQLSACCKCVDIYHASMPSVHVELEFEFTQDSIQAFFI

KLQGLDADRVQRQLTETSMGLASALRENSETIALALYEILTQRRLLSDFRIVRVLSRWVS

SRFSDVKINRKLESLRGCAGLYQLLVSPDSAVREWA

>contig52940 Frame-2F

MANWPVQRWPICSWKPLIPRTGLILCFLRTLHLLQLSIHSLRMKSMWWQRRQSYFRRCRQ

RIRRQIQ

>contig54537 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67166.1|) 1e-21

MQTLEALALVARLHVVAARSSFPELHSNTQTTKEQVLNMTQELKQLAGDWGDRELLASTP

MASARQQFEEMIK

>contig54911 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61695.1|) 1e-34

MFRKKYQCKGCFTYLCKKHVAGKIMLPSYPKKRSVCGDCYRIYRNGPMSASTTSGAINFG

LRANSTSGHHFFGGGASKDKKGS

>contig55048 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57256.1|) 3e-37

MKIMLTSQYLDAMREGCAGLAELTEDVQNCCLVAHADMVAPLIQVAKAMDLNMSRCAVGA

LANIALAIPRFPVNELPLARQTAQELRIQATPVILGQLEHANK

>contig55624 Frame-0R|Blast-3,2-trans-enoyl-CoA isomerase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY64300.1|) 1e-101

MKSALLRSSRLSAFPKRPFSTSSVSLVLVEKKEQYAIVRMNRLPVNSLNTALLQELEATI

KKLEDDKSVRGMILMSSNQKVFSAGLDIMEMYRPQPSKIAKFWTSLQDLYLRLYTTRLAA

VAAIEGHSPAGGCLLAMCCDYRIMTSGKPLIGLNETQLGIVAPTWFRDTFVNTVGHREAQ

KMLCLGLQVDANKAEAIGLVDEAVALEEVLPRAEAAMAKWLA

>contig56023 Frame-0F

MIPMFAFGKRKLQRNFQRYGDTGISAFLKIFLKIITLPLT

>contig57279 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56645.1|) 1e-07

MSITHGTPAESLECMATMDDITIDDGNYCEFQ

>contig57860 Frame-0R

MVELAVKRLRTMTNVHVILVAIGTLIS

>contig58780 Frame-2R

MNHYVLTLLRLEKLARDSQLHTA

>contig01835 Frame-0R

MHILLTLQKNSLGKFFFFFFFLKEKGIQVKTGY

>contig03095-0 Frame-1F0

MSSSPSPSPLPSPLPLPSPLPYPNKARFLPSKDLICIPWDGSCADSTHVKMIDPKTNRKV

FMFV

>contig03095-1 Frame-1R1

MKTFLFVLGSIIFTWVESAQLPSHGMQIKSFDGKNRALFGYGNGDGNGNGDGNGDGDGDD

DMDNGDADDMDEHVVGNLVAGKFSNPENVP

>contig08667 Frame-1F

MSLRALVIYFHLSTLVVVVISNLETLSSPATILSKAELCALDVDRSRIALNL

>contig09178 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65811.1|) 0.0

MNPFIETVFAALGKICRDDEEGVITSVKACSGVIGYYADIRIVLASLLPMVTGRLVGQET

AQYRIIGLTLLGMSIKGMATKTIEAHLEQVTEALCDAHLRESEVADLHDQLASVISSIVF

SAGPLLEQKDEICFRLFWVLNHLLASSSKVSAAHKMASESLEGLAVNMKHPIEMLYVRYM

KRILSNIAPSTLKNTSWQKSKSSRVLFDSLCRRGGRACGENLDKIIPVILVYLEPEHDAD

IRLAFLSLLETMLGMNTISKALMPFNVALLQKAIIPNITCREGRVAATIRKVGVACAYTL

FRQDIADQKCLFETAPQMLLVLKSSIDDSDPKTRQLVCLALQYLFVAFPECLREEPVHQL

NAEILKRLDDSNDTVRRAACETFFTLLKAAPREHFRGTIIDYMLDCLFVHLDDTEP

>contig09888 Frame-2F|Blast-pre-mRNA-processing-splicing factor 8 [Phytophthora infestans T30-4](gb|EEY57153.1|) 0.0

MMHTNSYGLIRGLQFGSFIFQFYGLILDLLLLGLTRATEIAGPPELPNEFLSFRDTTTET

RHPVRLYTRYIDKIYVLFRFDADDSRDLIQRYLTEHPDPNNENVVGYNNKKCWPRDARMR

LMKHDVNLGRATFWDMKNRLPRSMTTFNWDNSFVSVFSKDNPNLLFNMCGFEVRLLPKIR

AVDVEFTHKDGVWILQNETTKERTAQAYLRVDDEALHTFENRIRQILMSSGSTTFTKVAN

KWNSALIGLMTYYRESVVQTQELLDLLVKCENKIQTRIKIGLNSKMPSRFPPVVFYTPKE

LGGLGMLSMGHVLIPQSDLRYSKQTDNGGVTHFRSGMSHEEDQLIPNLFRYLQPWESEFI

DSQRVWAEYALKRQEANAQNRRLTLEDLEDSWDRGIPRINTLFQKDRHTLAYDKGWRVRT

GFKTYQVPRHNPFWWTHQRHDGKLWNLNNYRTDMIQALGGVEGILEHTLFKGTYFPTWEG

LFWEKASGFEESMKYKKLTNAQRSGLNQIPNRRFTLWWSPTINRANVYVGFQVQLDLTGI

FMHGKIPTLKISLIQIFRAHLWQKIHESLVMDLV

>contig10046 Frame-1R

MRQFIFFLQNPIMKSNNLIAPIYLHSLTKTASNSLKVHHLQSLSSVTVTPTRNCNSTALL

NKIDCIEINDTIVRNGVVYYVVNVYLEHNTSRIPTNKTTQSTTRHGFDYQLERRFNDFAN

LRHQVWAYAQRKHRNKRH

>contig12606 Frame-2R

MTPPPRRGSGKGRGRGIRGDRSITTSVSDTEGSKGMPKRRERGSSGSKRGGGGGLSASST

PIVATTRPTRAVTTVLKKVLVRYVQPDVSEMQVRELLKVYGVDEELIWRFVPGCKRNKNR

PPTPSRVYVDMKKTPESARKLIASLHGQLFHPETKDQRDVKPLEVEFAPFQKIPREKQRK

DAKVGTIDRDPEFAAFLEQLATVKDTSPSAEALADLAEGEATEKPVAALVKYLNERKAHS

RDKGKGKSGIKQLDKSGRRQKGKKDGTKQKVPKEKLKSSKDRPKKQSGNVGIS

>contig12691 Frame-0R

MKNPSAAPSLPFADETTLVASGPDLVLKTFSKENPAIASCSVAPGQSLAHKVNIQSKPVA

FLEPAPNRNFEMLPPPSDPRRL

>contig15108-1 Frame-2R1

MRRRRCAKLQHAAPLKLFRMYSLELDDLAFELLNNFAFSRAFA

>contig17340 Frame-0F

MEVKVRKYSGDETTTALDFDAVYGHPLMCANLPFDVFPQHSVPARVAHQLIRDELALDGN

PKMNLASFVTTYMEPEAEDLMVEGLRKNFIDLDQYPQTAEIHNRCVTMLANLYHAPLEPG

QTATGTGCVGSSEAIMLAGLAMKRKWKDRRIAAGLPYDKPNMVFGSNVQVCWHKMCKYFE

IDIREADVSPECLVLTADRARALLDENTIGVSAILGSTFNGEYEDVKAIHDMIDEENEKN

GWAIPLHVDAASGGFIAPFISPDLVWDFRLPNVKSINVSGHKFGLVYAGMGWALWREPED

LPEDLVFHVNYLGGDQASFTLNFSKGAGNVVAQYYNMLRFGFEGYRRIMEASMQNAQLLR

SALVATGHFRVVDKQHMPLVAFALIDSSRYSCFDIQDKLKSRGWIVPAYTCSSGAESLVI

MRVVVKQNFSSHMANMLVQDILKAIETLEKHHLLIDSAMAAPKVEKTHLKDIVHSLTNNA

KHRQSGKTTHGVC

>contig19470 Frame-2F

MDRRSSSRRSESRARRRHSPERDRRRYNYQNSRSRSRSTADRAHRSRKIYKAQTEQRRSR

SPSEYPPNQGSSRVSGSARNRTSKRSRSRSVNYSRRESIRRKYDSPRPNYSHNRVHSPSQ

RSYKKHSWHQNNRGYRRCSSSSRERKSNPRWRSPSYSPSFRRSTSTRRHSPSHSKNYSSP

HGRNAQDHHDSASVRQQSRSRSSRRSRSNSYQRQDEDAISRTDSSHYRSRSPSEKRINFH

PLTARQTSTLSAQVPCQPKVEESAHTKHDVEMVSITPA

>contig20364 Frame-2F

MKVAFIILLAMTSTVFFSGVWPINTGPTNGVVSHGSRILSPYVDWASTPHYSHPALSMFT

TKVTLAKYAKRIGLDLAHYEAAGMAAVENDSALKQLFDRYSAYHNLLLDIERNEHLPDKT

RERAKKLRTK

>contig24654 Frame-1F

MQNEKQEKEYVFVVTQKLSNSSDVRCSQEINASPTVASATTSSSNGSVKFGDSDAEDEDD

SDSVELDQMPLSMPFLPALDASTQITIHEGYSDAIMDAQHALDSRLLAYSQYQQMAQPKQ

SLLTPRRANIERFVFTARPAVVDRPVTVCMGWQRVSNIDSTSRNLLHILEEEGVSYDPHD

IAYSVKYLAPVLPFGDCLFLSIEQLLLYTEECEPLSPEGIREVATKFFFAHYQSSTPEEQ

QKIDKAIQNLYFPTLNGGWGVSPVQTRRFIALRSDKQMLLNKCAELQKLGYSWGKAAEAV

YMDYAQPIVDAHSYCDYMKVGRGANTHFLVGLNYSSRGLISVDNDPDNSRVAWGDDFVLE

ALATAYQRDVFVVLVGCGKMFFLPHRPRGEVGLDQSTICHSKGHAPWFLLMRLIGSDRGG

DHYEPMLCERLRGDGSPEFGSIGDFF

>contig25132 Frame-1F|Blast-lipid-A-disaccharide synthase, putative [Phytophthora infestans T30-4](gb|EEY61944.1|) 3e-70

MSIPLESMQCRDIIKERDALLDYSTYDLSDLKARGKVFHELMARGHQSSTQARIRKGFGI

PLNAFVICALAGSRSNEVKKSLPHILKGIEVFKLNNTQKQQQEIYVVFPTIATMEEQIKT

CVQASGLSLKSQILTNLPAHQRLDLFRSCDVAIAVSGTIVLETTLATLPTIVIYRANWFT

EWIGKQVAAVRFVSIPNLLLGKPLLPELLFRDCTVAKIAETIRSFQQQQRSQKETRELAL

AMSTLTNWRKTAQGRRQFIRASDVVAEHNIKV

>contig26076 Frame-0F

MKALYPAVSLHGIGECVQGVFEKHAFRFDVQEFETQVHSDRQRLLHIES

>contig27071 Frame-1F

MLLILRATLKKNRQPRSELKAFATTPTSYGRRRRKGPERRIFE

>contig27145 Frame-1F|Blast-aconitate hydratase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY67984.1|) 0.0

MFAVNATVRAARPSSLRSTATKAKMSSSCSVPVPLSVLDPKGSPTIDQTYEKIEKNLYTV

RKNNGNKPLTLAEKIIYGHLDDASTKSKRGETYLKLRPDRVAMQDATAQMAVLQFISSGL

PKTAVPTTIHCDHLITAEKGSDTDLGNAKIVNKEVYDFLSSAGAKFGMGFWKPGSGIIHQ

IVLENYAFPGGLMIGTDSHTPNAGGLGMCAVGVGGADAVDVMAGMAWELKAPKVIGVKLT

GKLSGWTSPKDVILKVADILTVKGGTGAIVEYFGSGVESISCTGMGTICNMGAEIGATCS

TFPFTERMGDYLRSTKRSGIASAAESFQVNLRADEGAYYDQIIEINLDELKPMLNGPFTP

DLGHLAGDEMKEASEKNGWPTELSAGLIGSCTNSSYEDMTRCADLAKQAMDAGLNFKVPY

YVTPGSEQVRATIARDGILDTFLKSGATVLANACGPCIGQWNRTDIPMGQKNSILTSYNR

NFAKRADGNPATHSFVTSPEMVTVSSIAGTTTFDPAKDTIKTADGKSFKFTAPFGKELPP

RGFDPGEETFQAPPSSGEGLTVNVDPNSERLALLSAFDEWNGEDLCEMPVLIKAKGKCTT

DHISMAGPWLKYRGHLDNISNNLLIGAENAETGETNRVKNQFTGKFDKVPAVARQYKADG

VSWVVIGDENYGEGSSREHAALEPRHLNGRAVIVKSFARIHETNLKKQGMLPLTFANPAD

YDKVTGNDKVAILGLKTFSPGKPLTLRVTPASGEAPFDITVNHTFNEEQIAWFKNGSALN

LMKKNNA

>contig27970 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60307.1|) 4e-90

MAGTRLQIVGAFVLFVLLAAPVAWHLTLVKRVDLPYLRIQQLSWDASCFGVPDKFEVDVY

SLGSEASLSALSSSASTIVYVPRSIQLNAEQEHLLQEAYKSGLQATDDVLKTLVTRDSKR

FSLVLVCNENAAISASVLAVGKYRHAWSPQCQVSEGDGVHLAMERLLQRYVYPAKDTQNY

NSSTGVKLARRALHYRLQFSLLKENPVTEWKEDLPTLVTQYLGQFIRKVGVLAKFTIETQ

VIQYAKVANEVTPNANETEFYIHADDLKH

>contig30637 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53454.1|) 4e-72

MAEYVALNDLLPIARQPGQICKLLPTSKRHNISIGDQLLESMATDTDIIALIDAALIPVL

TSQFFGRDIQVK

>contig30642 Frame-2F

MAIETRRRVLCHVLPLLTRRYSHTTQSTALATPSSSSFSLNSRGFSNVLEFKTLQPLHSP

LTPRDFGGKAALIVNTASQCIYASQLKQLETIHERYNAKGLVVVAVPSNDFGNTEPGTID

AIVQRYAALNVTFPIAAMAHVRGDNAHPFFRKIADKYSVSVAPTWNFDKFLVDSYGELRA

VFPNDTEPLDAQVVAEIEEVLEDVRKDLEACEERSHVRDEEGRGSDDSRVKMDVEMDTLG

S

>contig32028 Frame-1F

MTSTCSYEYACLANRIRLRILTKLEALECSLLNEAKMCDVSPKIGHRESERDALSVTNSN

SFTNHTVTDPNLDPSEVRRVVGGRLSDDDRTIPTRRTATRLFREEQEARELAQVNTELLP

QAPRLQRCAITDVAAYALKGHEWVAAVIVSALMCSVSSSIFLLAIQDMPVLNTTDFYASR

GFYTVATGFVAAMCACMSPDWQYAVVIFVQNGIFAILTLHSTACPINVLSCHMAIKPAQI

VLAGM

>contig32617 Frame-1R

METSSVVSNNIEHRNLLEIPVDSDTESIKQRVSTATSHSMQNSNLIRTEEAEKPSPGSSL

TIRTVAYALASCIVLITVYSFHMYHRFHIKNAYYVWWCGWLTAIATGLGALPFYWIKDMD

KVWLGICNGLAAGMMIAATGCLFYEGWYLPQATAYSVSVSYRLLLGAFLGVLFIKFTKVF

LEDYDNVSVCGLTGLDARKALLIMAVMTLHSVSEGIGVGVSFGGEGGTRRGHIVTMTMAI

HNIPEGVAISLSLVPRGLSVFYAVLWCILSSAPQPIFAVPAFLFVEQWLPILPCGLGFAG

GAMAYVAVQELLPESLEDTKSVQTTISATAFAFIAFLTIQITLSGSI

>contig33104 Frame-1R|Blast-peptide chain release factor, putative [Phytophthora infestans T30-4](gb|EEY61793.1|) 7e-40

MAAIESRNSRIDHLHSRFSDTKELYELAMEEKDELMVQDCVDAMALIRALAQQLRLEMLL

SHESDARSCFLEIQAGAGGTDS

>contig33690 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55495.1|) 1e-14

MRSFIALTLVAAPALVSVSATLAPCQTNSAHMCPGFYNCNATTISPAIQAAECSHNTRTH

>contig34488 Frame-0F|Blast-trafficking protein particle complex subunit 10, putative [Phytophthora infestans T30-4](gb|EEY55163.1|) 1e-09

MCFQRKETEVYVRMEEKSVQLKEMSSRILEWTHCGVNGGQYMCMEVACSIGGRVFSLLPN

DQLACFDFQIHEVNKSIQVAIVSASVLIPPPFALMEFVLVSIETHEERLEKGRLIVELES

PILRAQSPNELEKLETGVQLMGCGVVHEPWDSTSLSKVVAKLQYNTFQDNSDWNRTSVVV

P

>contig34905 Frame-1F

MPRNQPFLTIGRSTTNNMTLRYRTVSQLHAKVKYHDNHFILYDASSSNGTMLFLSKPLEL

EWGKAMHVKIGRTILTLKAKKKWKWAGSGSGDEEDDEGVSSPRSSAQSGAVGGFDNRLSS

LGLATRWNGFDSNYSNTINDPSAELVATPYLGNLPRTYTAPNVLSSRLNRSVPSYAQHTR

PSRQRSLSSTGLMLHGDDSVDTGLVTSILHMEPIPFATQEPLASAPFSTRFRDIAATNLS

PSLTSQLTVEGTFNADAIISTHIRQEPHIERLGLYGVMTAMPESGATISPTERLMRQE

>contig37922 Frame-1F

MSKKMSVLQCRLLGSFKCQNLVYLAIKFKPRLWKDERVSTSSGPILP

>contig38215 Frame-0R

MFAIDACSSHIVSKRPLRMVFTAISLRVVPCVSRVHCGSRVDRVAPVDVVLGLCLCYETP

RL

>contig38404 Frame-0F|Blast-ATPase [Phytophthora infestans T30-4](gb|EEY68893.1|) 0.0

MGSSGSKCGDASHGKQKKAPESNGVISIKDELMSIILDGLLLYTMFQTSKYLYKQLKPLM

DDWSKGQDSQAKLKTRLQRSGRRVFSTNYYEAIIAGDIVDPHDINVSFEDIGGLERQKRD

IHDLVVLPLKSPEFFVSRGKLLSVPKGILLYGKPGTGKTMLAKAIAKESGAFFIDLKVST

IMSKWFGESQKLVRATFSLARKLAPCIIFIDEVDSFMGKRSGMSDPTLTSMKTEFLALWD

GFTEISNEESEHFSVLIMGATNRPGDVDPAFLRRMPRSFEIGLPDSRQRENILRIQLKTE

RVGDSFDFAMLANDTTYYSGSDLKELCRAALMIPLREHIDNCRASAGDATQKEKPKDEKP

CNHDEVAQAEVFTMRPLSMADFVEAKTMVQPTGVTAYAYEQSQEQTKPLRQVFGGSEVSV

DPDIFTAIIAAGLQNFMHQKQNVFSTSE

>contig39379 Frame-1F|Blast-choline/Carnitine O-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61808.1|) 2e-10

MCRQFELVRDEATNLSDLDRYPPVSILTSENRTNWAKVRC

>contig39560 Frame-0F

MEQRATLDCPNYVAASNRHSLQKNNLNDTLAVKQIEAVAEKLLEKHRFLVESIIDVRLVR

MAETSVALVKFVLCHFATRATHQPHVSPLSHFIERDYNDTQKERLRALNSFLNSYQAITE

SSLEPPSLLFCTGKTIEMPVYAFSNSTSDCTNAAADRLLYQKKLNDVASNGSMRLEYLNS

MKSPSSIRDDKKNTPIKPEPYKSPSEEMLQKVLTQKKKKKCILSLNGESTCRSHVKQQAK

YDLNHAFGPQICKKQNQLSVPAPAKRLSGQISPISIACKETSFLSEMDTENTIRPLLESR

YSFPGTCSSQAFQASFKASGSRTSNECDACIGCNDVCTNEICFSCAEKKYHVCVAFANSL

VTSRATGHQSISNYRMSSSNEHSCNVEREYSSCEMKRHQNQRSCWIRIGDSIADVTSLLV

VHPGGAHVILEAAKHGKDCGPILELHPPAALEKVMQYRLGRYYCCSSS

>contig39731 Frame-1R

MLSGPCYTSIHAAFLIFFKVCHACVSSRSIAATILAWLIMIRSCVADDANIPFACFCHCI

LVQLLTAIRINEFLSSERCFINNRF

>contig41075 Frame-0R

MMLTAEIQSLYQKLTKCCSIAEWSELRTSIFDEEDELMRVCSEHTYALAKAQSTESDVLT

NAEFLNALLVAHSSPADEGNAIDDRWMQKFALITPETVERLRRVESRLRDAVLDLHHSAS

VFHADAIVKDSSDEISAHPPRSQSVAVDDVVIALALEKANEDYFSETSETAHDLDDNDVK

IDGDQPDMEQEFVGNEEGNKP

>contig41488-0 Frame-0F0

MKAYENSATGTIEIKIPKKAWTRMGVGAKRSIALAYNTA

>contig41488-1 Frame-1R1

MSRSGINSSVYDDTSLVLRGNSWFRDRVVKLSNLLSNDKGHCRVGDVSGVRKNLNDVKSS

PPGDSSSMELKAGFTKSSS

>contig41905 Frame-0F|Blast-croquemort-like mating protein, putative [Phytophthora infestans T30-4](gb|EEY64407.1|) 0.0

MPVAESPQSEFVNNAPPKRRCLCCSLELGLIITGALIAVIGLLYGTVVPAVIDNAVKDGV

VTCDASEGNKEEFVDPYGNCDDCAPYYSSVYLMNATNAEAYLAGDADTLEVREIGPYVYR

RREIKADVQFLDGGNRVTYKKYSYHTFDSERSCSGCSDSDEAISLDLGYMSVISNAGGEF

AFLVRLSLGSFARGSNTSAVLELVATNGPQMMRWVNGLNSMDPEAMRAVSLNNTVLNFLA

TGPAAIANMNLTGFAYNGLFAKRTMSQWALGYPSMLAGIGIGSNYVGRCAVNGGLNEQCA

ACTSSTTPECLAIWGECNNCARGARVVAVNEETCAIIQTTYAAAYSEEEAAAFAASTCQL

CSSLGLCAAPLPGIVESSGRDYSETSPDASIMNSYTQRTGCDDDHVINEYEQYDGYTATA

LWVDLGERRNPTLSEMIAFSAYGNCGAPTANLTCSPVMGNDGTSIAPGGVSISGFEEEIS

IAN

>contig42254 Frame-2R

MGLRLKCIFGAVSVLLLLLLLMVATFHLIKLLVQFVTIQYMLVFGTMALIWLFVDRRRRR

YAWGFYSCSCVPQVNPLGKVSQLKGVEEIKAKIKDNGHDKQAHATTSKAPESHEGPLILL

HKVVATLPSETESEDDESEGTRLSNITKTPVRSSSSQSMSLVDVCTNTNGELDWGQTARP

RSLSVEDGTRPSKAFASGTDLRGLSAVSKDRKHRVPPRRRVDSGITVNGKPIVRSRRATF

TSKPDVHSSMSRPSAELLENALHSDGYWIGDFRVQRRLMSHRNNS

>contig42548 Frame-1F

MQHVQAAAAAQLESQLSIKKEKSSKLRVPYKVFWSPSSLLRVNKWDALILDSEILSLLKS

PMKGMFDMFEPGVVVRFQMEIDALLKFMLFLLSIGLGR

>contig42957 Frame-2R

MKVIHMYALISHGRRLYRKLIFTSNSCLSLHSFPLNVSFDQGPVDP

>contig43253 Frame-0R

MDGQLCERQRSISPPIKTSKLSLLDAEMELLRTLEEEVTREDEKSKHDKITALLIRDDDD

DDYDESDDEDT

>contig44726 Frame-0F

MEGIYCQSTEEMLLMNAIKCPRVSESAVLYSVQRQTVCEPYVFTGVKWTTIKTSVASNRD

FCYFDKMGLVRQTSGKRMAYHIMQSVELPEYPHTAAHKRMEASLCYIFEELETNVVGVYM

QGEIENTALSYFATSAILDLLLAFTNALECTRAKKLAEMMVVAPPGRWKRRVSRKFCDVC

RSNRSFFDTLHECASCHLQYVCKKCRVLENVFARDTTVNAQMLRAEFCRICIAKTDTMSI

EDLRAETCGFSVSGLRAADTTKEPEDVDIPGSVRSLTAFTLNITARLQDLGTCSDHHPST

FLSTEQVSMSDDEDELLGEGQ

>contig45637 Frame-1R|Blast-2-dehydro-3-deoxyphosphooctonate aldolase [Phytophthora infestans T30-4](gb|EEY66546.1|) 2e-08

MRRRALVKTLRQASPFFLIAGPCVLEAEEVVMAIATR

>contig46287 Frame-0F

MFMEVGWSQLREEARRLAQEIGESGREHHSLANSCVVRDAIRAHGIPLEHREWVWPILLH

DQRMKVQRYQSDIGATYSQLLHGATEDVYDSDTNSSLGQAQEEAMEKFHHLNPFQERKIR

RILLAYAKSKDAFYYCHGMVESCVVLSTFLVEEDAFWSFRMLLEALLPKYFDESVVDFHT

D

>contig46690 Frame-2F

MSREERKMAQIVATIERMEQETRASEDDSSRTQEAPYSAKQGLRGKKGKKGKLLGGKVKA

GKKTKAAAVVAGARTQFECKMTPQKRWIQLWSAQMEHASNLLEAPCDARKARSHSAAVAE

SGVSVDNATVCASPARTSLVEPEVGILKSFDKTNAMPSVGLIPITMRLGEYEPHSECVRK

VSKLQQPSENREAEVPQANPSTKSVTFSKELIAPKALCATVTSSSELRVKTPKIIELSHL

SPPVERSSPTITSSISPSAKVKDSGLQNSNTASAAATAAKFSPTISEHERFVTTKKDFSR

LTPLLRLEENSSSRSVDRGSESDRMSSSGGTDLVRKRGLERVESSMSEDAKRRAERRRKR

KSNWDVGDPRKGGNPIADPPLSAAAAAANQQSFAKYPSSRPSWRPPLSTLDIK

>contig47028 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67569.1|) 1e-108

MSQSMSPVCRELPSSSRTSSGGKRFRVRRRKWVRYRRVHLNSRNRSVGPSFNAFDDAFLD

SMSGWLRKRGHVRKNWKERYFVLEKSVLRYYTDSCCTKLKGEVLLFHPHARVHYVDVHVA

GGRDASFAIQIGPEYTLLLQAPQLRDRENWMYCIEDALLCRNSYHPQRGACDGPGVYVDL

RESVARRRLLSAEAMALDGRSWRDNLGGISHAHGNAFADVLTDEEDGDVDTSEHSLIQRT

RGRTSSTGSDVLRLWASLHAKPGGV

>contig48678 Frame-2F

MHSTASSSSSSSMKSLSIKSQQTLPSHHPFKESARKNIEMKSIQDPSLELFDIDCNLTHD

DLRDNVIALIEQSVAVGVKEMLVPGSNIEDSQRCIELCRQHPTQLFPTAGVHPYFARTTP

SEVELSALKRLVEIDDVRAVGECGLDYSPGFPERILQMKWFAEQLMMACAIKKPLFLHQR

LAHQDFTSLIDRTIEESNGYFPPAVVHCFTGNEEELKAYIARGDDWYIGITGYICKKEGA

ALKGMVKHVPLDRLLLETDAPYMGFPKCRQAELICAKKQYPNVPSAMPLVAEAVANALGC

STQDIASITRANARRFLRL

>contig48919 Frame-2F

MLHHCPAASLSPSDKSDCWRRSIYSALRMRS

>contig49138 Frame-0F|Blast-hypothetical protein PITG\_05283 [Phytophthora infestans T30-4](gb|EEY69099.1|) 3e-09

MAFFERQFNCRICVLNTNGGGKYQTLDLFCKNTGIVMSQEIRLVVVAERMLRTIVNMVRN

MMFASGLPLSFWGNAGEYAAHILKVQQIPVYSHLCRC

>contig49307 Frame-2F|Blast-peptidase family U48, putative [Phytophthora infestans T30-4](gb|EEY67731.1|) 3e-38

MIAKWKWLSTAPCNGILAAFELPEQCVKASASFEIPIAIRCVVLTMELALVSGGAFLLLL

FSSVVGALARSLVDNNVFADVCETSTFGWGLVMIMAIFLQLPPRVMVRKLKVFGCSGVIT

CVESVLLHAGVVVAINLWSHNQVLISWRNVDIAVHRPDGTFAVANIVQNLLLVPLKEELF

FRGVIVLVAINRLQNIKWSVSIS

>contig49422 Frame-2F

MQTLIQYKSRTYKLQAKLCTFSLEHFCSIVFVVITSYSTHGVFLNAYQEGK

>contig49457 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65900.1|) 6e-25

MEAKDRQQALYNAVCEPIIRRALVLLQLAAVPIQSTSPASSPLKILPGISMASHYDFGKS

PKDESVVIKQEQKRYTRQLDKLMETKSMEMMEEEDVQINSDIFLFLQHSDETSRNVQGST

R

>contig51504 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67509.1|) 7e-40

MVREVCELIVLFRTSFLCASIDLKPSIEMLQLESQIHEFMSRRIAELIVYVMSHGMSSIL

TALMRLVSATSPEKLEWHHFSEVSPCGKEFGSCFEAIDENSNVH

>contig51687 Frame-2F

MGRALQLLVSLIMVMVLHAAADQNLLKTTCPLCNMDVKADINATILGDQYVYACEMAGHI

DSLQNNPAANLGAPKKADISTDEIYKDAKSLRCPVCGKGYDQLTHAVPWISKGAQKIYTC

SEEHAQIVFDNPLSFVAAQASSNDFCTGTGSVMFNGFQLAIGGDASCLMILFQPWVTSSA

VKYAFAFLGVVLLAMSLEGFGELRDYLQARLHRDYGIVSSQTDYVSVSTPLVASGRHSHN

INQNSFTQKTGRVPDAQLSIMRRLPVWCKLLLAVMYMLHLCLGYWIMLIIMTYETLMFVA

VIVGVGLGFIIFKNTDADELRGSVDPCCST

>contig52329 Frame-1F

MGKFVQISTTLVVLVLVLAISASTDDVHRDSPSNSIFKLRSLSTFNMKDAIGLVFIALGL

AISAAGGVGGG

>contig52394 Frame-2R|Blast-hypothetical protein PITG\_10512 [Phytophthora infestans T30-4](gb|EEY56964.1|) 2e-20

MPKSARAVQVATVADHVAMKKQWQTNLEIDLLKSAWIRKDREQYGAHASPPLSAAK

>contig52479 Frame-2R

MEIDDFGSPSDISMRYSRSFSDGLKSCDRGSKSSFALHDIDAFSVQRSKVIRRASEERYQ

RICVFFKSHEPELFMEIY

>contig52897 Frame-2R

MFKKSAAVIHHEAATSEEDHRAKGTHADNERRHSCRVDFAPRWQNSWVC

>contig52941 Frame-0F

MTCLLSAAALDLISPVIKPVHSNTRHCLYLAWPSSRIYTQFAILAQGGPRQQICNHLTRL

HEAWLHNLGASNKADKFKLCLGLCRTLFAFQFLDCRLLVNFICLSLVIPMSSFWSSFRDP

NSSRPACEAALNSASILLSDSPICFLARPCSYSAVHFNNTT

>contig54910 Frame-1F

MIIFDVCLFALATCFLRCRSHCPYRPTLLRIILIALGQRSVESTA

>contig56022 Frame-1F

MSLRKSSTAAALAGILAASLVSANVDVSVNRDATYTLSESCGLPCSGNGLHPAGNACPKA

GDVATAECTPSMMSYNGKDCVAPVDAQCVLMSHKVWGCEFPMSETPLGVNCEVVDAPSEH

MGGKEESGHYYSAQESTPSVEYTHPYSEKHPGEYKSTMHFDSVATGKTEGDFTHYGTPSM

THESKHGHSMGHDYGTTKSALKKYHHSHGYDEHLTMYAPKELQQTNAYHSPMYHGYEAAA

PYGNSVPSAYHNNYDSVYSTPHSSKMESVYTTEKPCDTDVPVYSTLDPISTLPFPITLPP

ITLPPISVPILP

>contig56707-1 Frame-1R1

MPVLESATNLFPIRLQTLEQLTA

>contig58716 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59219.1|) 3e-28

MPSDLPMKYRHPFEFTRTNEAIGTELFESNSWELNMVRECSTKLASYPLKGSAVLFYSQK

PNGEVDPMSLHGGCPV

>contig58781 Frame-1F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY70514.1|) 2e-55

MFREGYCDVLVATDVAGRGLDIPDVTHVVNFDLPSKIQNYSHRIGRTGRAGKDGVAISFL

TDNDEEVMYDLKQYLVS

>contig59467 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65739.1|) 1e-08

MTPEKHVGYAVTWYKKLLFNI

>contig06266 Frame-1R

MEAIRDFIGKNKDKNHQSSDYDDRSQSNSKSSPAYRSSDARGEPDVGTKSYSRGSYGSED

DNVGRRDNKSNSSTRDASSYSSGQGTYKDDDNYRSGSIDTSGSGYVSKEQAHQFVYEGDD

EISSGTRGSPSGMSRGHQSGNYASNDDEIGSGTQGRFRGTSRGHQSGNYASYDD

>contig07908 Frame-1F

MWEKKQSLCFTVRPSPSGHMVVADLGSAKSIKVKMKGAPNNVAAFVSSGDRVLWINDDCV

KDLTFHEALLKLRTAKRPLVIRFKKSSSEDAIAVVSTEVLNTTNFTSSSVLAPTPAISSS

LSSSLNASSSPTTAIPLVEKNAPSAPTPIHLKTLQPSPIPLPTPRSFINPLKKMSVALGN

HTKENVSSAKFQNGLRKQVDRPSHGVLHDSAQINARGHVDQDAKRSGHDTRPLSASNGVR

LSPHGSRGGGNHQHTAAFVTLSNEDSSPSVPTSSDPSRAYRNDSNHRNTDSLTRLRTVEH

GTRKLPLPKSISDPIDDLPLKPLARSGHRHELPLHMSTSDGVRHPDKVVDKDTDVYEVVW

PEGTALGLTLRVHPTTRFPVVARVTGTSNLKNIEHVAPGDVLFAANNMNIVPQAKFKQTL

ENLSRLPKPAVLRFRRTLVSTHATSRTEELDQTLPRGPALKDREYELIWRECANLGLVFS

SDNDVPKVTKVDFDSGGPMLYKVAVGDVLTWIGHMEISGAPFHSSMATLRAVKRPVVLRF

FKRGT

>contig10724 Frame-0F

MSRIIFVSLKAGFAHFLAVAIAGYAAGGCQLSGNLLFSVVDIQDRTSVSALGFMPHRGAI

ITTYVFMHVHIVIAFSTITQPAFYMAERFIFSMHKTVADDVSPASKRMFSKRGLAISKLE

SNYRYSVLSASSIKLMVEQH

>contig13325 Frame-2F|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61866.1|) 9e-85

MGMVFGKLRVETPKFEVVKSTADYEIRQYPPSVVAEITYDPTQFKGDKDAGFSILAKYIG

VFGNPQNTKPEKIAMTSPVITKAEKIGMTSPVVTKGNVGRVTMQFTLPEKYKKEKEYSRL

IDTANAPIFGVDCNCEVIIWNKKAAAITEYTNDDTIGQELFKFISEDYRDAVAKVLSKAL

KGTGTANFDFPLITKSGRRLDILLNATPKYDHFGNICGAVGIGQDITDRRAQEQEYTRLI

DTANAPIFGVDANGCVNIWNRKAANTTQYPNEEVLGA

>contig13718 Frame-0F

MDSTKHELALSREHVNSLANELRDAQSQIESFEKQVLVYDDQINQTRCRHDEVQEALQAA

IVREEATQLKMSELENLFSALSKAYETKEQEVQSQIDFARRMEEKLSQVESGREEINRKY

EAERMELEAQLSNANKKVTQLQAVTDANADLHQGNITQLRNEITKLKQQAEVETKGATAA

RTALGTYKKRAHTALKKASSENKLNIKQAAEYSNKLELEVSVGKRRISALNEELQDTHER

MEAKSMEAARTQSANETLMAEKCAIETALRLEIDSLKAEVTRLETALDNERRPLETQIQI

LTKRNESLEYENHRLEEEAHASIEQAVQAKEDKISDLSKQLQAAVSAVASLANEAVHRSY

SPASSPIEKERRSTASSSRSFDFEGGNGYLHHSTIEAQHEHMTAAVVDSCPIPRASKAGA

GNDSEQLARKLSMDEDEIDRLKAQLQELELSARLYQDKYESTFAKLEAANRQQQVIGDRS

SEAINIEYLKNVIMKYIQSQVSSEKEQLVPVIATLLNFSPQEYQMVATAHRLNEEGSGIF

GTVFSLFGGVTTAPSAPKSLAAPHNFKPSPTTRGNTIGAALGITDKKGVLSFGSDEDEFS

TPLNPFAA

>contig14113 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69767.1|) 0.0

MEQSVIFWQTLVADCLVFIVSSSLTLATEVPKLARLLKTLCGRLKPAVAKVSPHIVNLSS

FAQLFEGGSLAGTSPEGGVRQVSCMLQTITAIQVALFIVLLQKNRKMDRETGDMGNEAAL

SRREHASIVKELHCLFFEEEWEQKGLQSVAMLAWAGFLASNNDGNNNNQNVTFAEVEATT

NVVKKAIEGRAFHTLVEVQLKYLPDRKRDLRLYNIYEQNFELLFQTYSSKMMVDVPTIAD

KAAISAMQSESDDDAAAWNGDCLENIIDFATALGARNATFCSSFWYGTDEELDVHDSDGS

TEPREDDSTRQRNSLLHSANGASCHDFLIACRDAAYKNPGCITAYMRLVGAAASGPGCAP

QAFHHIKKNPQQLSWDQFFAVMAKYQRLLTEAEKPSGYSSLMSGGVPQAIGINGSSFNGN

ISAANPGPRFIRPKELEALEAIQKLIQAVISDPQLALIFFHNHDWSPIPTFVAFLQCRIP

SSLKGSIMKTLAAFARVPDIAPFVWRQVDALQ

>contig14643 Frame-1R

MLIGHSVQTFVSTSARSRPRCSPINLEFPSSPAIPASASNLVFLANMRLSQVFRASLLAA

AAISAISLPGTSALDISAEPNVAHLEASNNEMLTEARRMSTPSTEDDDVEPVKKSPKKKK

KKVAKKASEDDATQEETQPVAPKKKKKAKHAATSAVADDDAAEAPAKHKKAKKAKKNVKK

KKSHNATKKAAATTTDTEDEASETEAATGSGVKDKKVKGNKNEGVIDHSSEGSAEIDKID

LRNEDGWVSVYDDPPLLVIKASLYAFISYNDTEVCDTFNMTMNAVEQKAEENGRFSYHVV

AYINCTKNGEDETQGRFLLNFIPEGKRLLLTECGHREEGEIVNWLRIQDEVPECMTPSQR

KKFLAQPMKHIHATNGVDAEAVNTDFLSRLEDFDKEEVAIVGFSTILLIAIITALVFFVL

RKRKVQKDLERTIAGAKAEHAVEDDDLQTEPEEKATKERKGLMDSAKAKSDDPDMEEGSF

VNSPAVRV

>contig16821 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67747.1|) 0.0 NOT\_ORF

MHKAVSAADIFKHTGVVRDHRDDECSRK\*CCQFFFAFC\*DLTMDDQVEQRLKNNPKVRLQ

GDLYAYQAKYDIKNRLQLLKILDRTPEGMPIEDVIDCYGSVEDDLKELTRTGEIICLKNA

DKGAEVYYSRGTPFLVDLSGVATVEAGSYLAHTSQDVTDEIRRGDAFRLGDNWFRVSAAV

KSSSTTRPAPFAGMTTKSVSSTRDPNVSKKMKFMFKFDKDHLPLDVPFPDAKRRNIASSD

RWDLLPKRGPKFPMVKHGCSNDIRQLWRDTLRMWPSDRAEFEKKLIQAGLTTQAKVDANR

RQMKRRMKDDKKKNRPRKQRDIKITNHHLIGTKLGEILSKGSQEQFTLGAVRFEKK

>contig17945 Frame-1F|Blast-histone H3 [Phytophthora infestans T30-4]gb|EEY69440.1| histone, putative [Phytophthora infestans T30-4](gb|EEY66013.1|) 4e-69

MARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTE

LLIRKLPFQRLVREIAQDFKTDLRFQGSAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI

MPKDIQLARRIRGERS

>contig18294 Frame-0R

MCKKNSQLIHANSRNLVACFQFFFYHCPISFAPTRPLMKPFFILLAVVLAAMSSTGTADD

SKCPSNPTNTTKYAFYTVAKPQDTVCLELTKDGGDTVAWRSTYVVKNTDSSNQESLAVSR

YLLDPWPLNLIGSLILNFHYNYKTSDMTSAVMMRMTIAKTALDPVVIEVRVILAYSGDKT

NLVASAKYLEEVVIGGIPFELYQVVNSHGVVVPTFVSKTLQVSYEGDFMNFIDHLSPKTI

NQQYYLQTLETGLLIHSSAGNSFEVTNLGIAHAYLGPTE

>contig18423 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59893.1|) 2e-24 NOT\_ORF

MDMEHYGVNSRR\*LDVCSHLAQTGAPDCIAQVVVSAFKLIDRMLSIAHLNLVTAWPNRTL

LLCVIFFTKMSL

>contig18647 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54847.1|) 3e-79

MNLAACYLVQGAPDEGDRNDEVLKKAIEKADLALAIDSENKKALYRGGYAALLKGDLKRA

KEMLTKAAKNNPKNRKIRDAMATLKEKLLEHKNEEKERWGGKLLEDKQKDVSTTVVQAKQ

WMKPSEPNYALGTLAIVVLLIVLALGQLRFVE

>contig18935 Frame-2F

MPLLLFLLSFLVKSPQLITLHDWLIPKLISLNSVSYDADVKKRVDMLI

>contig19734 Frame-1F

MIDKDWHLGANASDEDVLRDNLNQQNESVVSVRSESSLFESPNVVLNAHHSVDRNCQSCG

NDPSLYSSKTGSQLVATDHLRKSHIKRLTTTASKWTRVAFEEVSDRTQLPNTGAIQLRRQ

KNRECMRKARHRQQEELHAMKKTVASLEKQYAHLCLRATACTDDVACQTMSNCRTATNYA

QALELVKRLGAENLYLKAEIQQQATWKLHLFRILDSCLTTDTPQWSLQPQQPALSGIEAL

HLHQLDQYEAAQTFGFRPLTELDLTRVILENNQTLSRVQHKLFFPNVDKEGWRIKRRQLF

GWDILQKVEKSVMECVFTKTFTGLRVVPLMQKTWANDMRLDQFQKVKGETCRLEVLQRIN

ANAYVLGRDVTSPTTDISTFRSVFVRFLNETKRMFTSSTENVLTYVDTTAPSVPISFDTD

SKAIQLEVTGYVLGTQSVDSAQRETNDRLEWAHLSLSIEFLNVVNLATGEEYQQLRWTGR

TDYRGEEHAHRNAG

>contig19895 Frame-2F

MGTLSKLGVALGSTSLFCIRSEVFKCQHKVTKDIVALKKLRPDVEK

>contig21210 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68778.1|) 2e-71

MAFLLYLSLVLLVLFINPTKIVSLGHHQPLGNCLENEPFYSLVGMQYHRKKYLCVHDFYA

EFNLCNYPLTQLHYEDSWYMICGRGYENFATYLALSISSFLGINFLLVQVLKRPHPTEKC

LSNKTRYFSFRKCTFKVPV

>contig21913 Frame-2R

MLLNAVRYKTRTGGGLSQASSGGSSGGTKKQRSIHDFFSQSSLGNKHLGVRPRKARRSLE

ASAKTTNRSHPAVEDSEAETISIQKCIDYDVIDDDSSEESMLLTSRGRVSKGRRPRPKKI

DFTACSSQRSEPDYEPTHTPLRFGLPPTSQGYPTPGKATPVHQYSQDDMDFLTPRDQPVL

SLSNPTTPSPLKKRPRLSTEVDIIQEEQVQNLTQDMTYMDVRRNRKGLPIFSSQSSMDVG

SPKVNLELNAKRVRPNSDQAASFLSENIYMNPFAPEPSTELGKKKLSRRKRQSFSSAWIG

VEKDSPVSKYLSNFSELGLIGSGSFSKVFKCMKKIDGWMYAVKKRKRHFRGKADTARALR

EVQALAAMSSSNHIVRYFDAWIEDDLLYIQLENLEGCSLARFVDKYAPQKVPEETLCKLL

CHTAQALYDMHSKKMVHMDVKLQNVLIGPGDVY

>contig23520 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70513.1|) 7e-16

MDLRHYDSDSHHLGVSIEIN

>contig25333 Frame-2R|Blast-mannose-1-phosphate guanyltransferase beta, putative [Phytophthora infestans T30-4](gb|EEY62296.1|) 7e-36

MSRTTLLRGVTVRANSWIQSSIIGWGSTIGRWCRVEGTTVVGEDVQVKDEKFINGGLILP

HKAISTSIPDPGTIVM

>contig25452 Frame-2F

MVGGQAKDREYAVLQHSVKNAVSNYYCAKMTLMPGFPVSQVLKTIMDQSIMWQLILQLEL

FFSSEGEIVQNLTQIGAQPRVVLGAARAQDPTIFSTAQDIYNIN

>contig25863 Frame-0R|Blast-lysyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY55967.1|) 0.0

MSTPTDASPATGDPAAPISKNELKRRLKAEKAAVTKAEKAAKKAAEAASKPTKASATDDD

ELDPTAYFANREKTLGELEKQGFNPYPHKFHVSTSLPEFHALYGNSDAGSHLVDVVVSVA

GRLHSKRISGTKLVFYDLRADGKKVQIMSDIGTYENAEAFAQIHSILRRGDIVGVKGHPG

KSKKGELSIFPQQLVLLSPCMHMLPKTHAGLTLQQDTRYRQRYLDLIMNDDTRTIFQTRA

KIINFIRRFLDQQQFLEVETPMMNMIVGGATAKPFVTYHNDLHMNLFMRVAPELYLKQLV

IGGLDRVYEIGRQFRNEGIDLTHNPEFTSCEFYMAYADYNDLMTLTERLFSEMVKEITGG

YTITIQKEAGEEPVTIDFTPPFKRVSMVSAVEEATGVSIPIEDPEASRVILEELVVKYEL

ECAPPRSIARLLDKLVGHFIEDNQAYWTKPFFIMDQPVYNSPLAKYHREKPALTERFELF

LAGAEICNAYTELNNPKVQRERFIEQMAQAAAGDDESQPHDEAFCTAMEYGLPPTAGWGC

GIDRMTMFLCNRFNIKEVLLFPAMKPDEQTASVASATGIAALVSATGSVALDVLETRLSG

STFVNGSSPSKDDTVVFERVKVVGKDILKKYPNVEKWLNFVTAFPNELRVKW

>contig26574 Frame-2R|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY69813.1|) 1e-30

MSQDFEIVQTYFGNSPHDSPPLANRLLSGRMIVEKLRQ

>contig26927 Frame-2F

MSSGWNINKVTLDSTCSGLAQSDNVCLEGAQCTFTEEKNGISVNSSASTKGLVDNITACP

RTREDDDNIVQEVQRALTILVEQVLVRNVISDATPAVARTHIKTFMPKMPMNRVSSVEPK

LALNTQKMATDEGERKRNAGLQAYPLLCGSNREREDIQTSLERMIGHLSMLKCFKVLVLH

EAENKVARPKRESKHIDVDFEIGQDNSHLAQKHLTALRTKYGRGVSACTEQVITLVNYYR

NFERRTELNEIWKSRITKWKKIEISLSEYVRFLNISAALRQDFIKDLISYLRESWAATKA

RKI

>contig26992 Frame-0F

MQQTSTASFFPTAKELTSGVQWFRDHPVLAAAAAAAVSIITYLNAYDLPEASAMQAGDSL

NAISASHKRPLSTCYKGSPAFVRKESLPLVRKSSSRGESDEKLSAAVSWCDEHGGSLTQV

FEDETLPRIPKGCGLSDRKEDVRDDAGRSCEFALQHHHTCGLCKSGSQQEMDVEAQTASP

QWGWYVPITPPQEQFQSTESECIEKRQFSRAAVPLLPRTTSGQIL

>contig27595 Frame-0F

MAKSAPPVRVETPEIRLHCGPTGLNEAVLSLDFLIQKAGKISPTDKPILATGGADKEIKL

WRMGCLEDTHTKEDVALEFIFSLSGHDRSINCVRFSPNGTYLASASDDTSIILWTKPKTA

GDDWRWGQISSLSALDRTILSLGHRGDITDLSWSPDSAFLASSSVDNRCVIWDVEKGEVA

ERRKDHAQYVQGVAWDPLNEFIVTASNDRTCRVYSLSGFEAATRPNGKKQGRKFMCIQTI

KTREFSEKHVSIIITPIAKDDKVDEAEDAEMAVGDAARKAAAALKHRMFLDDTCPAFARR

LSWTPDGSYVLMPTGLYRSSESASPVNTVYAFSRGNFCQPTLHLPGQEKASLAVRCSPVM

YELRRQSGDYPVNNLFKTKHRSVFVVLTLDAVVIYDTQQPHPICTIKGLHYADLTDAAWT

ADGQTLCVSSTDGYISLIQFEDGFFGTRLLRT

>contig28943 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67876.1|) 7e-47

MVLRHSLLSLSLLLLPIILGQQCAYFSKEDLFSRLEMHIKTCIDPIPSTPALSTLTERFI

ANEFDGRQPLALVFFSNSSHMLRSLAGALASSLFGSSRSPQTVQSVDFQALLEPSPRLSN

YDIKQRLRAAIAAPLNACPERSL

>contig29632 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57383.1|) 2e-41

MTRCIELFLTQFKTSTHINIVSLGAGFDTLFFRLLHQRSFAGHISFTEVDCDAIVCAKTK

LLNDDNVRVGLFPNNLKNLVIATPVHSNVSWQCHVPSASYSLIACDLGDTQLFDTTFTAT

GADRSVPTLILAECVVSYLAPEHGTE

>contig30876 Frame-2F|Blast-pre-mRNA-splicing factor SPF27, putative [Phytophthora infestans T30-4](gb|EEY56354.1|) 7e-83

MAKPLCPLLAQSRALIDSLGYFDTDYSQPESQKKVLAQIVDEMATFSPPQDEYLAYLPPY

SPTFSGKSRLQSEFKRVAARVPLDAIDFNRYQVKEPTGKHAQSLEAWMRAVEQLRVAVEN

QSNRVINLELQQGYGTKLAETRATLLDGINAQYGHAVKTANAVSEKINLARQQEQTRNAA

KLQTYQSRYYELLDKNAAIKRACAVEQGRLQKKSKTA

>contig31105 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54488.1|) 4e-71

MFAPGLQPLQEHCFQTQRLLALTEPALAEHFVSEKVPVEMFAVGWFQTLYLYLNVLPQDT

LNRIWDIFLYEKNWKMMLRVALALLQLSEKYVMGKPIDEIMHFFNTFADSANVVLAEASL

IESALRLKVTKTVLAKLQKQYYKHKRVTLKV

>contig31170 Frame-2R

MKHRRQSVTIIYEYIVYSGQKKDEQTWCGSNSPKRFVQLGLITAVKI

>contig31314 Frame-1F

MIQSNASTVIDKTESTLNEQLGRNSKAPKRVSLASSERCRKRPRSPLVLDEHVSMRKTKK

ILRWSTITIHEFGIGLGRSSVPG

>contig31817 Frame-0R

MVAFCMKYHCAAPSFKIPPKIASIHCINSRFFQFTPKKKYYSVCFLYS

>contig32562 Frame-0R|Blast-SUMO protease, putative [Phytophthora infestans T30-4](gb|EEY68625.1|) 1e-65

MAKQVLNYHDVQLYESDVALFEGQKWLNDNAINFYLQYITQTIAPSDVLLIDPAVVSCLL

YQCEDEEDFKELAAGLCLKSKRICLIPVSDNDRLGGESSHWSLLLYCDENFKHFDSISGC

NKNSARRIARSFMRLLKIIGRYDGVENNFQVKEVLDAPQQQNSYDCGMYVILLAEFLTRQ

YAGEMEKMSMEIFLTPEKVTGMRLRISKLLKKLQE

>contig34519 Frame-1F

MRDNEKLIRAMLLKSIESAETTKVSSGNVSDVVELDNHIEAEVLTLFSSFSDVVVSPAGD

SIDEENLVDLPDFYCEIQEHNVAICPGENSYQSADNGNDNTKNVGAKCGYSLDKNCVISR

EEVRDPPVKQNLTDSLEESKVALFISELEQARTIEATNQSMKLAPANIDSRVFVPTFSVR

IEHSDDLNARPAIGFDSHMLVGPPKINVASREERVRRCKYKRRCRSGSTTKLPNPSLSST

RRASAAKRQRVIGRFVSEAPSFVSITALQK

>contig34641 Frame-0F

MNSHSLGIQGGGMSMPMSMSMGSAPTMGLDANSQNQQQNVMMNTVPMGSVGMTLMNSNVL

NAAQVSDWRIQLTREHRANLIAKIYNEMVRVSADPMPGIKLWMNVSWYELSLYKESLTQE

VYINKIFTRLKSLRVQQSNVSAAMAAQGLPNQGLLSRLDFSYYNTLNLDQRGTGGGNYSG

HNQINGLGPVVATQQQQQLHQQEQQSSASASSTPVKSETSVSGNSVAEYWQQHAALRAKH

QGDVEKVHNAFKKYVDHMNGHDETEQKKKLRYLLSYVELCANILSENKATHQPRKIEELD

KVFKYIVKIVNPYLKKLRTEAGRRGGDSSTLGLSGLPSTSTGPGIAPSMGATPSVGSNKI

PKGVFNGTNAQAQLAEQPHQQNAMNPTTQQKQQQYLIQQRVHQMQHQQQQMQAQVRRQQL

MEHQQLMRQQQIQQQKGPQQQAQLSSEQANLLKYQQQNSQIASKQLSGQQTQQGTTRQQQ

PNFNQPQRLAQSQQAQTTQNQSQNQNLQLPTSRGESPSMSSGSGVGLDDSLYGGMSNDLL

QMPTPSSTLGGLMDFPNELSPTSFGGMDLLDWDDGTSGTAAIGASPGDTSDIMTFVETL

>contig35116 Frame-0F

MGFRVAGAIEATAKQSLSSQNFVRRTSKSNER

>contig36096 Frame-0R

MEPSTLSMVKDHVSDLYAWEKAISKNEKVRKGASTNFAVPPPREATFVTLKFSDETINST

STSTKSLDAHTYDKGYKCQKAKTKEPSVSSPLLENREDFERINGNTYYKQGDYVAAIKSY

TRCLEYNPHNTVVLSNRAMAYLKIHEYINAENDCTEAVKSDPTHVKSYTRRGTARNALGR

HRLALLDFHRAATLDSKNRQIQTQLQSTRELIRTAIKRSPKQTKFSIEIKDNPNLSKQPS

IHKKASFKLHESDEALPSPCSANAISSQSQVTNASKSSGVLLPKLPEKAPATSYEFGRIW

KALALRGSIVEKRRLLTLRANYLRKINPSTLCKIFKSGMESEMLCEIFHALREAVLVSTE

NSVVSKESVTFARFFAVELTKVPRFNMTMMLLSSTEKEDIAYVLKRTEALLPNDKRPEMA

>contig36852 Frame-2R

MRQSHLIGRSFFQRPLHCLAVQSLVDYVSRLPCLQCGQAFAAIANVAPKRVGCGRMQLPL

VCSKECADTLQATKPDKLSMYDSMVEDVKYSATPEASKLFAEVLQPSRRESNNYKGERPL

RSWTDYFKLFRPDNRFLNDVRALRLLSSAYTFVMTISRFFPELIDPDQANNKDKFQIHVI

GARAEATMPHYLWNELSFFHPQQHFWIKLIGDHVPRTANKAQMTNINSSIQLEMINGLYH

TIEATHRENPSAFVLFNPGIGHLHLRANWEPTLLTILSSKRPILITSFSLEDQQRDLAVL

QKI

>contig37006 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55610.1|) 2e-86

MLQLRKQVMCRALQTRAFEWEAISKKLTDPRARAALDSLRDAHGQMAAEARMYVKEPEPI

DFDYYRSVIKNKELVDAMEANYKSISFPVITPEELDISAKSDELPEELRLNEQEVVDKLF

SQLNEKVADSKARIEELKELIGLMEETRTTLDTTMDEMTAMYPEVEEEIDDEIANLEWEK

DTQ

>contig39185 Frame-2R

MMLALQNTIANIVEQQLPADG

>contig40062 Frame-1R

MRALQFLRTWITFTTISCTVFFAYMVFVGLQFYRIMYPTFSDSPNTLDPMWGMGQPLDVK

YYLSTRLKWDAAKDFDDGATPIGDFQQLTFDWNNSNFRHVDVIVSRQTHGEFSNNKSKKT

LNVWDALKGNASVYLHVHVTHAHFSPDPRDENYDQYRTIHQASSLVTYAPKPNAKNASLL

LAPWKPQNRSTLTVGKDEATILYWKPVMSVRLVTDFTRFPVEELPGMVYESLDFVQHPMD

QRWRYMPALYVDELALTSADLVPLNSTLDNGRDGDLVLPLRLSWSPLSFARWQVQLTFAT

VFVSQEQMGVPTSDLNALRSMVTDTHPVLLAVTMSVALLHLLFDWLALRHDVSYWRSKGD

DVVGVSLRAMAAELGSQVVVLMYLVDQDSTLLVTGPQLLSIALLLWKVTKVWRAQRRHLQ

LQYRAVKNDSEDKTKLMDAHSLRLLEETQRADSLATSHMLFVLVPLAAGYAMYSLLYVPH

TGWYAWLLESLTTTVY

>contig40732 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56357.1|) 8e-43

MPSSEDSSTSRYNTWTLEEFGNLVTAWERATSRPRDADAQNLHDAVYKHFVALRGGSTRR

NKAALTSKRSALKFTYLYIRDFDNEQKMKKSALFFELPPQERLDLLSTW

>contig40787 Frame-0R

MTYRFAGSVSFFRCSIAWSALCNVQIIGDER

>contig41519 Frame-0R

MMFANAIGHPMFGCACDNGYSGEKCEIVPGMNTTSTDSKKSKPDLTIDRSSNDREAHGSD

DGTINDVSAKDDVLTDSNALDKSPLLRPSPSRDVDVDSVSSGTPPPAPPASEDKPKGLRP

GGLILIIVLSSFFLVGGIAMLKNRCTAPGHRL

>contig41641 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60022.1|) 3e-38

MCGGAVIGKVTKECVGVVEGIVPIAEQGDEKPLICDNAAHAASQLRQSLAGHVAFIPASD

VRQFIESPDGLLLTGIELPPHFCEA

>contig42006 Frame-1F

MYSLPRCYNVNYGSVSVGSSNLLQGGLKLLIKVFHLQMRLDKCKITWINEGRC

>contig44170 Frame-1R

MEKNNTVVAIFYDERQQVKHYGNNGMCCLVDHTLEQIDAELDATSSSSELTPIASSDNIN

PEAGKSSIESPVTSPTGASSSTTNASNVVSANSPNANVTASSISKPSSPLVQTSTSLSAS

>contig44444 Frame-0F

MATNATSSAVNSDVHSMPTGEHEQPRPIRRLSVTNANALANFSELEAHFRNHRLVVFLDY

DGTLTPIVKDPALALLSPMMKDTLEKLREKFITGVISGRSLRKIQNFVSIPQLYYAGSHG

FDIEGPNGTSIKNQIAEQFVTDLHGVRDELEEHIKGIAGAEVEDNVFSISLHYRNVDPAF

RTQIMNIAHDARDKHPRIRLNDGKMVYEFKPKIDWNKGKALLWLLKALGLDEHDDVYTIY

IGDDVTDEDAFRLFQVQNKHKGVGIIVTEESLPTDALFTLRDTSEVCEFLNRLIACGDNA

RSTRSSPHPTV

>contig44817 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70671.1|) 1e-144

MIRPINMMGNGSSSALPRNLSSSALSERSPLLRVISHGDFTSFDGSYMSMPAPLSDSGRH

PDTGQFQPLVFAEKALAALLNGVLLYALGCVVGVALVSLNFEGVLGERFNWWLVFMPFWL

ANVAMVYAHLASIRHAKTLRHWAEVESMGNEPLLPLLRRIILVYAMSFPMTILLLWSELA

FCASLQHTVATSLYICYAPLMVIQMAFVVRYLLCRSDSTLPGTCWMLMFVFTLLLAYQTD

TQRRYDFLEMPRPLISWWLVFAPLFVFEVLMTGSLLLVLYNEFSGIYRLTRWQLAASVL

>contig45212 Frame-1F

MATNQPREVKGSMLPLKNGLLYPQVASIHCYRKFLPSR

>contig45403 Frame-2F|Blast-L-allo-threonine aldolase [Phytophthora infestans T30-4](gb|EEY64304.1|) 1e-164

MTKVPRALVNFLSDTVTCPSVAMRQVMAAAEVGDAVFNADPSVNRLEKVAAERLGKPAAL

YVPSGTMSNLIAIGVHCRRGDEVICGDKAHIFLYEGAGANAYMGVSLRTIPNKMDGTLDL

KDITSAVRDDDPHYPRTRLVEIENTQNSCGGRVLPLSYIRAIEQMCRKRGLRLHIDGARL

ANASVASGIPMNELVHGADSVSLCLSKGLGAPIGSILAGSEEFIYYATRLRKSLGGGMRQ

AGIVASAGLYALENQFDRLVEDHENAQALAHGLSTISDVVIDPDTVETNIIFFSLTADAK

LEATTLVQKLSSEKGVLVGTYADGNRVRIVTNLHITRHDVEYTVLSIRALLS

>contig45876 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53973.1|) 2e-89

MMDLNSLKIMANRAGNTLYFAGAAAAEIGKEKGTQALAVASGVAAVGRDKMMSSTTFQSA

TVAATAGREKVKTSQAFQVASSAAVVGKEKATVAASTAVTVASAGRLRALSALTLAKNRI

NGMKAGNTTSSPTQAELPSAEKEFYKYEMSEEEKKKMRAQARRRAEKNKQPVSSSSSGSS

KRRDGSSRTAESSRTAESSRSAQSLSSTSAELSKNSSKSSSSSRSNNRSGANSRRPG

>contig45942 Frame-1R

MYVVLASVAVTISCVCVLIWWHKTKKSIKELQKEANHASGYSSTRQATMHSTNSMGGPTL

AVTSPPEGFYVATVLTPRRASNRSGRSRSLTSHTSTVSSSSKSRKAKPVEIPIMAEQKYP

SMSSPRSPMSDTSSIALLSEYASSRGSIDSWRPNAKPADLKDWGPSLKENEF

>contig49722 Frame-0F

MPLIQTMRVCHFALLAAAIFITNMLASTADEVISHNEGTNSVTRLRVPSDKSIANYEEER

LLSRVKG

>contig49797 Frame-0F|Blast-putative GPI-anchored serine-threonine rich hypothetical protein [Phytophthora infestans T30-4](gb|EEY58896.1|) 1e-10

MNLAATLLFAACTAATVNARFTVTSGTTETNTNSSMNSADYVRQWTINSAATGDAVNSID

L

>contig50816 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54807.1|) 1e-71

MKVDDMRETHPKATKEDLRTFMSDSSIVQRDVPNVTNYCMGELLQRKKPYAAYQTRNVLR

KTFGVIIDQLIDRSTTDLGVEMTRQDYWSYASNLGLLALSALDPTGIAFMTYYYVQPLCG

PTEFIGEVDDGSATDALGLATQDDAFHGSHGTWMKKGD

>contig50962 Frame-1F

MTTPIECGDYSSKKLQSSEWFIFSERLFRPHKEQRIARSYRDLNPDCWIQSPKC

>contig53181 Frame-2R

MKEQFMRGEDSAEPSAAVRAAAGDALLSLAVDVPSAVVSSTRTTLDVASARGDSPREYDP

SSEVDYECESDEMADSGRMEQSPDRRQAAVYEPSNEKAHFDRRVNCLFGSDDEVDPSSPV

PSPV

>contig54078 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58133.1|) 5e-45

MAMIIAYHESSWFIRMVRILHIHNTRWEFMLGVKTQGAP

>contig54715 Frame-1F|Blast-small nuclear ribonucleoprotein-associated protein, putative [Phytophthora infestans T30-4](gb|EEY68847.1|) 1e-26

MVMTKSSKMLNYINYRMKVTLQDSRVLIGYFMAFDKHMNLVLGDCEEFRTLKAKIKSAVS

E

>contig55239 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64594.1|) 7e-16

MTSAQLEQQFQARIAQAKEAARLASIAAAARSEQASHAQPFATIPSVPGLPYYPTSSPPV

SSKFTD

>contig56689 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66962.1|) 9e-10

MARDGKKIELQVRAYDQEIVKQHTYVALEFEAKLFCNDGNTATECEVAMKRLASATDDYL

YSSRRCLETIDCVARLSMAGQFNM

>contig56906-0 Frame-1F0

MEQKKLQPNEYIRRMHSDPSGFYTWLRPIVDRFFYEQAQQNLPTMLSMNSKVPRGSDSCR

KRALVHTSAT

>contig56906-1 Frame-1R1

MYKTHLGRYACGECIHLVATFFAPFQSFP

>contig58548 Frame-1R

MAVFQLQNDIETYGLLKTDGWSIPRVMLSC

>contig59077 Frame-1R

MPSVCLLSAINKSARKYVMIQFILMLALALMAAHPFVGVVAGTINEKHQAASFSEARWFP

LETFMELFTRSKKT

>contig05778 Frame-1R

MKEYHVTICQPHTHSIKYPHAKRTKIVVSVSRTKRSPF

>contig10581 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60156.1|) 2e-36 NOT\_ORF

MSVSQCLYELWVESRESNATAFVQAAIDRTQVSYTEVYQWKSSLQQALNGDNQRLVVGIN

LIPFSIEETVAMLLVAEQRRWIYVPIDMEISIDQQLSILQSAGINRLVTTATSQLFRYFS

CAIETKTIVTVSSPFESVEVLDVFKRKPIDRDTPEVGMTQRLYAEENNLPLYVLYTSGTT

GKPRGVVGTRIGAWTRLMWMWKTYPFATLSNSILSSERVLRATKLSFVDSIWEILGAFIK

RVPIVHLQSLQSPPKVESSWYLKSVLLDTSARILDLIHREKVTRLTAVPSVLEMLLVQSI

AKNHVFALSSLCYILSSGEPLRLPFFLQLTKYLPDVVVLNLYGAI\*KLLCLMI\*KRHFFW

TGSTEISGDVTCMKLKGPFTRTQLTLWQQYGIPIGKLDSCGVIGSSTSLLLLPNKLDQNA

LAATDNSHESLWPQQDSSKIFHSTCTSAKGMLYVSGSLVSLGYIADARKEESFVEIHATR

WFCTGDVCCVVNDELFFCGRKDQAVKIHGQRV

>contig11641 Frame-0R

MARFRSMMHVNTLRLNATAKGAFLISSTTLRTFVYILAFVLAVLLASSIVAVEPPPDFLS

NTLWALSSDEINLERAQFKTQVLHIVPDLVPIDVNCDKIERCDKKGVCAIVCKHGSVQMD

HWAQKALKLQRKLAYRRNFCSATLLGSHNSAINIADGYGVEDHVFEGYLHYFKWFKKGMT

IHTNDQLFSLTDQLHMGVRFIELDVHWFDDDLHIAHCGGFKLKLLDGIITVFNDIAKILG

TDIEWDSETIGCKPSMSSIPAKEQRPLKDALNELSMWLHAPENQDEFLIVFFDDETDLMK

WNKVGKLLDYIKEYFAENEILRPLDLAYNTKWPTFEELLSVGKRVVFMSGIDYLASGEEI

LFVKDTVCNWQEPHLPLSLFPDCHFHESATKTPGSPDNKLTIFRPETSEIEYGILNAAGQ

FGINQNLLNEKSLPGVINCGINLPSPDNITPKRVEATIWVVTKGHELQPQKCVALLQQSK

TWQSVDCNTKNLVAACVDVNNPRHWQLGSSSVVEADAVVACAALPFTVMEYSVPACGYEN

ELLYRLLMMQQNGLNSTAGVWLNAKHYVDDVYSTRINDSVVHATTLLVSGVTSIE

>contig11946 Frame-2F

MMQLTSYVVLALICVLSFAIRLFPVVIWGSVIHEFDPQFNFRVTKFLAQHGVYELVNWFD

DRSWYPLGRSVGTTFYPGLMAGAAGFQYFMTTVLRLPISIRDACVFLAPVFAALACVAQF

LLTREVTNNTNTALLSSMLLSVSPAYISRSTAGSFDNEGIAIFLLILTFYLWVKAVKTGS

MLWAALTAISYFGMALSWGGYVFIINIVPIHVLALMLSGYHSAKVYVAYSTFYPLATLGA

MQVPFIGFNAVLQGESVGSHGVFALLQVYALMQWLSVQVPRDHSIRIFRACLYSGCVIMS

SGVLFALLCGKLQWSGRSLTLLDPTYASKYIPIIASVGEHQPTVWSAFYFSLGPSMLFIP

LGLFYSFQKLDAGHLFMILYSTFAFYFSGIMVRLLLTLAPTACYLAAVGASGFMHKIVEV

TRTDSLKASKAETVTRNKSRNEEKENPLKSHAGEVFEAFFAKLHFKSVGLSGGDKGRAPK

ALQLLIVACGVRKN

>contig12235 Frame-2F

MYDKYYVPSEENGENALATTDRKEFAKRPVTSREHSIELTAIIEYKPR

>contig13290 Frame-1R

MLCKLFVFVFKEYVDRCIALDQDTDFFVRSGPPMMLGYTKAHSPSTLLFGHLEPVASSIC

SPVRASAIVQDLVRHTVLFSPALHGKSHIDAASASTNNEQALSL

>contig13474 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64140.1|) 5e-78

MQKKAVKEVPKPWEEALKPATKKNSRGSKKPSAFAAVQMNNSSSEKLTQAEMAALREAEE

ARVAGKPGKKAIKFENSFQANRNRGKDEPSEARSLDAALDLLTTGEKELEKHPERRAKAA

YKAFEETMMPQIKEDFPSLKLSQYKQKLSEMWRRSPENPLNQESLAYNAKKQ

>contig16028 Frame-0R|Blast-presenilin-like protein [Phytophthora infestans T30-4](gb|EEY57615.1|) 5e-32 NOT\_ORF

MESIDQGDVHEHLLPLRANRVLQDELNRNNYTLDELLHSMGSFSAVVWPVAVTMLLASFV

SLNLVDPASAKALAGYKST\*NS\*NVLVHIGNVLNCSAYLVYGPESDEAASTSTKIEDAFI

NALVIVSFFLVATFVIVCCYKFNFNR

>contig17225 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68060.1|) 1e-73

MGQHFLFHRDLVAATAVHHAVNARLSSDLQADLVLVGPQWLRMYRIEPCLRQFTTLESSK

NHVLHLLASFPLAGVAHSLHVLHYNRILYHPKHRFVTGPDVLLLSFPRFKWVLVGYDRRT

FTLVTLAMYTFEEHAMGPGATLKGEPNGREQLLGLATQAAARVDPQTRCGAMLVYGD

>contig21066 Frame-2R

MLPLDAKRSHRRMKAHHDVWVHYRRSLSAQAANALKLSRMVYGVWSIHYRQVVYCDRRSA

TFMWTYGLTLLVLCGTPWLLTPHSFIVAWMPVATLLHRIKFSVRLTVREKCLGREG

>contig21912 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56524.1|) 9e-53

MEITEGDNRYLSRELLEGNRNNLRAGDIFALGAMIYELALGTTLASCGEEWQKIRDGDIV

MFRQYSNSLQHLIASMLHPDALQRPLAEDILQHEVIQPFR

>contig22247 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69891.1|) 0.0

MDVASLHNILLHTFSNDEAARKTAEEAVAGLHTVPGSVQLLIQITVETSVTREIRQAAAV

SLKNLVQKYWEGGDGPEGQLIQVISPADKVLGRQNGLEALLVSQDSSIRSLLAETVAFIA

RFDFPDSWPTLLDEICKNIQSGEASRIINALLALRRVVKNFEYRSEDRLASLFQLVEVVF

PMLENMMVQMQTNHSIEAAHMMHLILKTYWSCVKTSLPPHIAQTEKVVAWMNIFRMVIAK

QLPEANEGGEPTGQPIDEEERGNWPWWKLKKWSLQILCRFYTRYGNPKKAEEEYVSMSTV

YRNQIAPELLPCVLETLALRKNGRFCTDRVVQLALVFLQEAVDSAVTYRLIKPHLGFLLF

EVIHPVLCLTPKDLQLWAEDPHEFVRKTNDVFEDFLDPVYAASNLLADLCTKRGKDCLPN

VLSFYNNILSTYLASPGDKKDYIQKDAALHALFSLDGVLTKSKAHKDQVESMIITHILPE

FKNPHGFLRLRACKIFSRKYIEGIKFQDEQTLISIVNGMLDAMFDPELPVRIEAAKTIRF

VVMYPHSDTVVEVLRPRLPQILEQFFSLMDEIGNDEVVVALEHIIDRFSSEIGPFSLQLV

AKFVEFFGQFTAVAEDDEDASLAAVSCLDAINTILLSIHNHPELYALLISTLAPVIHKIL

TDFDYVEYMESGIDILGSLAFYSQKIGPELWSLFPLIFISFNDWASDYLANFVPVIDNFV

GRDIEGFLAGSVTNPATGANVRYLELVFNMAKTVFDSSSVQEIDLCAACRLLYSLLHNLF

GKVDECIPSITLMVCNKLSEPLVDSTARNLLGVFGSLLHYNPVLTLDSLTQLGAADGILK

IWLVICLASTITWTVSFLFLAQCRSYVRQQTRSQPLCVRI

>contig22632 Frame-0F

MLAPYTSSAAHYSQPPHLHSGERPKIFMHPPSVEYGHLVHQGTPQQHAMTPQHTITPHHA

IGPKYETEPLLMTVQGVQHFYPPPQMNSQLLHVSSDYEYANGAVVTPSGAHSGTKRSRQD

LNLKEKKRMFKLNDRINQLKDMLDEAGVQTKKNKQSILDNAAHYIEMLRSNLLIAKQKAE

RAEKQAEVFRAQAQVASSGMEKVVRGVFQKTTTPRVVLDMDMQTVTFNQAFVHFTGQPEP

LLKKQLSLRSYLCTDQQQLERLMTRVRETKQSTSAVVKTSVADGHFGTVNLVAAVITDDG

GNPTNVEFSLIPIDLPYQPSSVFKPQHDDEAETSAEESVTDGDPKDEIHVDQ

>contig23521 Frame-2F

MPYTTVANGKLSTLLHVNSHCWQALQLHRFF

>contig25332 Frame-0R|Blast-Glycoside-Pentoside-Hexuronide (GPH):Cation Symporter Family [Phytophthora infestans T30-4](gb|EEY58275.1|) 1e-133

MWMLSFTMFICIGIASFFAHETPLDPSTIDAESTWVRIGRAFASVYTGVRTLPRSLAVYS

ICLFFVQYGFTAYNGNKGQFFGLEVYKGTAESADTCNPCTPEQDAYNDGVGIAGGRTDLL

FNILGYVYSWTLPFLVTKVGVKWILTLSTIPQMFLMIMAWTSNVTFNVIIVVITSITQAT

WFALMVPVVVHVFGDGKEIGMYVGAINSANCFGQLLNFAVGSGLVQTSLGYKLPVFLGGV

MSGLGFITALLFFHVEMNSM

>contig25862 Frame-1F

MPWRFGLGLVLNTVMPPLRDRVCLPMSQISYIHRLGPYHVSKSRNICLDNSRTLSKKLKQ

QTSLRIFKYPKVLKVRQR

>contig26575 Frame-1F

MNRVGAERTDTTCRDALVPCNSHRTFDEESWTEVERQDLARATSFVSESMYLVMESPAKD

LYTSETVHFKVHALCDRRVAKRCSKGKVATDADNDEMHGTLFVTNYRLLFRSFHHREEEV

MQIFLHNVAELAEFRITGKLGLMSQLEIACKNFEFLTFKFPNESISGDVYVKISQLLVQK

TLPPAAFACHHEPDTTGWTVFNPMAEFARLQFPTPQKGASIRGFRITHVNSNYKVSPTYP

WSFIVPASVSDGELRKISVFRARGRVPVVTYCHDNKAIIARCAQPLIGLRRNRCSSDEAY

VSALQRECPGNVQFIDCRSQTSAYGNVALGGGFEVLEYYKHTSILFMGIENIHSMRDSIH

KLFELIKHESRGNERPNWLSGLESTRWLEHVRSILVSCFLCVTKLEEGTSLIIHCSDGWD

RTAQLTALVKLCADPFYRTRKGFQVLIEQEWCAFGHQFRARSGRTDTLAGLLGRRQHVSC

VYAICRCRMAIDAPISMLV

>contig26926 Frame-1R

MAPQPVGKWVFPMLRDVILQTSSATSLNAEKKRTDAEMASVFRTPSYLESNVPWQIETQL

RRTTCAFVEHLAQLLDMPEAPSISAQLFIQHFYMMHSFATHDRFLVATAALFLAGKTEEF

PVKVRYVTECSMYLLLCREQAQEKLIKKQKTLTPKRIGTTAIQSSSSPAGPIKKKLKLDI

KGKACELRSMVGNDKKGANSNHLEWLNALLEIVEVGEIEANASKVLLLERILLLTLSFEI

GAPQPFAYVAPHMERIFALEAMHPDISYENIRDVTFMLVADAVKSGLILAFDCIALAAGA

VYLACLYSHQVGPNVATDKNEPWWTVLKLSEQDLENVARGFLWMYEGE

>contig26993 Frame-0F|Blast-5-oxoprolinase [Rattus norvegicus]gb|AAC52955.1| 5-oxo-L-prolinase [Rattus norvegicus](ref|NP\_446356.1|) 1e-55

MTNTRITDPEIFEKRYPVLLRAFHLRSGSGGAGQFRGGDGVVRQIEFLERMTVSILSERR

AFEPYGLEGGAPGARGMNHLQRLGGRTINLGGKNTVDVLPGEILTLQTPGGGGFGATS

>contig28511 Frame-2F|Blast-pre-mRNA-splicing factor RSE1 [Phytophthora infestans T30-4](gb|EEY54384.1|) 0.0

MLVAIPGGGDGPGGVLVLGENTIQYKNEGHSELTCAIPRRAGEDREILIVSAATHKQRDL

FFVLLQSELGDLYKISLEYSGNTVDEIKAQFFDTVPVACSLCITKTGLLFCASEFSNHYL

FQFLSIGEGDDTAKCSSLAMDATNSSTFPLRKLTNLALASSSPSLSPVTQLLVDDLANEQ

TPQMYALCGNSNRSSLRVLRHGLPITEMAASALPGIAKAVWCLKESYSDPYDKYIVVSFE

DATLVLEVGETVEEVAQSGFLRDHGSLLVTLLEDDSKLQIHTNGIRHVPKFQPVTEWKAP

GKKVIQHCAANSRQVVISLAGGEIIYFELGQAGELAEKGKLDLGFEVCSLDLGEVPEGRQ

RFQFMAVGSWDNTVRILSLDPNELFRQKSTLALTSHPHTLCLAQLQNEPSTPDSEYSSEA

LFLSIGLNNGVLQQSQIDPITATLTNSRSRFLGTLPVKLFRVVVEGKRSILALSSRAWIS

YFQQTRRHLTPLSCELLSCASSFDSEQCPGGVVALTNEGMKI

>contig28766 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53789.1|) 1e-167

MKGRFTVNPFNELGLTPSEGADLEALVETIVAASIARYETFVFKEHGRVDADHWKVVKSR

DSIHVYLERTNGPSRIIPQVSAVAPNLSSLLCFGTATGRMEDMMFGVINPTLETMRIKAS

YVDDISGAAVLSTISEPSLEDPFKSLVVKWMEIDLPLQSIGLVHNRDYIYVEATNLVHLS

NGTQVGYHIMHSVSFPETHDLPGRVRANMSVCSIFRQVRPNSCEIYVTGLVDPGGDMIRK

VMVPSMATALLSALKYAHCGQMKKLAWMLEKRYQEAKELGAPNRELICVICASSITSRKL

GDFGKSDDTCKLCFGFVCHTCKISKKLSFVTPDLLLARRKVTFCAVCLSEATKIPAAEAA

RVQILSSGKKEVLQSITDSTTSTASSARATLSD

>contig29017 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70426.1|) 7e-31

MSFFQRLVSYVVNDVAVKSLSNSHTFQRFALKTHYHVEDAKNLASTSANVLKSSLENYAP

KVKEFGEAFREELVRDLKKMK

>contig29686 Frame-1F

MSVHSVGPPHSPLSDDEYHYSDVEEEYQYSEEEDYELTSVRSDESNSVARKQQTSHSLSP

LGSGSAAKKKRLTPSGLGHAGCHKQQDYHVIDEEELLQEQCALISEIAQVLEISEPEASI

LLRYFGWNKEKLFEGYCADPVKTKHEAGVEFAGKLAPIIPAGAKIECLICCDEYAANDTF

GMGCGHVYCLNCWKPYLSLKIQEGPICVTTTCPAHGCKEVVSDLIFKQIVNSKDYCKYTR

YVLRSYVDINRGVKWCPSPGCSKAISSAGGLSSVVCTCGCVFCLRCGEESHAPVTCEQLS

AWQEKCRNESETANWILANTKKCPKCSVRIEKNQGCNHMTCRSCNYEFCWICMEGWAKHG

SGTGGYYKCNRYDSDARTADTDAARAKAELDRYLHYYQRFANHSEAGKFAQRMREGTENR

MIELQASHGDSSWIDVQFLNAATEQLIECRRVLKYTYVFGYYLPPGKEKNLFEYLQENLE

KNAEHLTGLSEMPLEKMNRSEIINYTRVTETFLRNLLTGVEDGLTSNALLV

>contig30499 Frame-1R

MQNHTIVRDRRLAAYDNIDIRKLEEFFGPLVLKWVELPTIGVAASAPWPGPYWPDYQDSI

NVIW

>contig31171-1 Frame-1R1

MPDGPSNCSTSTAPPAATEVIVLGLQGAGAKRTFRLLLDSGATRNIVCASNIYLLSSRVQ

TCMFERYADREPRSVPRHSVSLSYEFDGFASSDEFLVIKLSGSLDCIFKNAWLARYQPDV

EWLNCTMKPRDIDVNAVLAFLNGQSSSGRMLQS

>contig31315 Frame-1F

MAECVEGVHRFTSKERVQLLESAGVSEGMILRFARETSIINSSRKQTLLEVINPNKEAKR

QQREQRCKAESPRHACAPSLVSRHQMIPVNYV

>contig31445 Frame-0F|Blast-Rab5 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY67143.1|) 1e-106

MADAGNSKAREVKVVLLGDTGVGKSSLVLRFVTNNFRPYSESTIGASFMSKMIVVNDTPI

KYQIWDTAGQEKYHSLAPMYYRGAAAAIVVYDITRKQSLTTLKNWVKELKQLGPDNIVIA

IAGNKSDLEEKREVPASQARAYAEEIGALFIETSAKEDTNVSDLFIQISQALPTASAESN

ALPEIVDPYGGGKKKSGGCC

>contig32286 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65817.1|) 3e-44

MTSMWRRLQLRISGTTPARRFQEEADVGVAAVLSCFRSLKLDPQNANRDYEELFNQAVEI

VSPKKFEQQKQYVQDEIAKQVEQGFEAVWKIPLDSKKSTTKMSLSGFVCSTDVEE

>contig36097 Frame-1R|Blast-trans-acting enoyl reductase, putative [Phytophthora infestans T30-4](gb|EEY60654.1|) 2e-85

MNKRFDVIVYGATGFTGSLVARYLISEPESAPHNPSALKWAMAARNTAKLMHLKEQLKEK

LPEVGPNVIDAIPTIVADSHDEDSLTKMVQQTQVVVSLVGPYKLYGELLVKVCAENGVHY

CDLTGEIVWIKEMITKYATVAASSGAILVNCCGFESIPSDLATFLVSDQIQQQYQSTTSQ

IDLYFTAFQGEASGGTLASIFAIFDNVDHRRAPFHASSLFLNRRDDDGGKTAG

>contig36585 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53634.1|) 1e-16

MTSHVSLQDATQRSTATFSAAHNSTIIPCLQKARKTGALNLSSRQLLKFPDEIFRLYDDL

DEDEHSWECAILK

>contig36606 Frame-1F

MFRVTIFAAIALIATNGVPFVQAGGGPTQQISCDDTSGQLKVGDYFKPATSQTSLELNNV

APNSRSPCPGFNSLANGGYLPRDGKNVNKDMIRTAFMNVFNIAEDWINAQFSRLPDVFSL

DFLSTLDRHASFVRDDINLNPNAVEVNTTLAKDFLSRADADGKISLAAVAKARVDRENQC

KAINPVCNYTAPVEMTAFRQAALLLHIMGQIDFITAAHAESFLVQEKIPVDFVKSGVPIT

VAALNMTYTKLVEAAPK

>contig37007 Frame-2F

MNNLWECDVCSFKSYDAHNTCMLCGTDRSFQLIEKSIKTADESASEHSNVASSSAPSSTK

YLLYMEEKDNPFTRSSSMIKANPLKTNASSKMNRDLFKRKLSVLNLRQQSARRRHEWSRE

RNHDGQLIWVRKKNYMDRKALKSLRNLETLRSQSSTSLRDSILSNGSANSVGVVARIVVS

PKNPTGRLSLETAEGARATRCTESSIFSQDELEQVGSLPFQQKHAWFVQHTAAMEVPWDY

GHLLLEIERDNLLHNSCEQLLWATPDQLHQSLRIKFANEPGVDAGGLVREWFTLMTKEVF

DDATGLFYRIGNGDGLMINPASAEASVDHLMYYQAIGRYIGRALFEGILIDAHLAIPICK

HILGIPITFSDLEFVDNDLYKNLKWLRENTGVESLALDFTVNVDHMPDKMKVVELVPNGS

DIAVTDENKMEYISMRFKWIVATSISQQLGSVMQGLFSIIPVELLSVFDHQELELLICGI

PDIDVQDWKTHTIYVGDRDERAIAWFWNCVHGFSNEQKARLLQFTTGSARVPVQGFKALT

MNDGRICPFAIQCVSANECLYPRAHTCFNRIDLPRYGTEKDMRIALSLVIQMEVTGFTIE

>contig37458 Frame-1F

MVKTDRKQHTNASHNIIVAFIVKQHPKRATTLKSTPYASSTFT

>contig40117 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53516.1|) 6e-88

MELVEVFAINTIAPFLLNKRAIPLLENSLNKRRYIINVSAMEGKFYRSKTPNHPHTNMAK

AAVNMMTRTCAADLAERNIFMTSVDTGWINDENPRDIAVRIAETHNFQTPLDEIDAAARV

LDPIFSLYQEGNVEKPLYGQFLKDYAISEW

>contig42007 Frame-1F

MEKAEADVLRKLTQRVCENVAEYVGAQLDGDHNQTQFYPGCS

>contig42458 Frame-2F

MLRNAHRQARQQHLSMQAAQRVGMSTRGSQVLGPEIRRSDEAQRSPSNALGRHLSAPASA

PTFTVGPFRRGTDVAINEQVASLQKQVTMLMEEKQQAEIQLRVQAEMLSGPDRLTNGSRG

SSASGGSTASGLPLPRDRQNSLPMPSGMPKSGLVGPGSNFGRNMFRPMGQQLLSRTKSAG

SFRPTREVDIDSPMFGEAQLQLLQQQSSRSTSMAGNPALQRTTRLQDALNTIAAVESTYD

DIDGSDSDSDIDGRHTDIGDLHDAEAEFEVDDVVHEYLVDAEVCEDVVEDDEDEEAEAFK

ATDEDVLDEIDPDVQSECDFGSDTVPEVDVFVNLGHVMMEKGS

>contig43097 Frame-2F

MPSQGALHNMEPPHTPARSINATTVWLAWRGAADLSPVTSQNKQNNKRMLKADAAYILTP

LVTELCHMLKTYLKM

>contig43462 Frame-2R|Blast-fumarate hydratase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY70044.1|) 0.0

MLSAVMTRSSRMTIKAVRSASSFRIETDSIGEVQVDDTKYWGAQTQRSLDNFPIGGARER

MPMPIIKAFGVVKKCAAKYNLEQGKLDRAVADKIIAAADELIAGKLDDHFPLVVFQTGSG

TQSNMNTNEVISNRAIELAGGKLGTKTPVHPNDHVNMGQSSNDSFPTAMHIAAVQEIHRV

LLPNLQKLHKALDAKVSEFHDIIKIGRTHTQDATPLTLGQEFSGYREQIALSIERVERIL

PNLYKLALGGTAVGTGLNTSKGYDAAIAKIIAKETKLPFVTAPNKFEALAAHDAVVEASG

AMNTIACSLMKIANDIRFLGSGPRSGLGELTLPANEPGSSIMPGKVNPTQCEAITMVCAQ

VMGNHVAVTVGGSNGHFELNVFKPVMISNLLSSIRLIGDSCSAFTDNCIVGIEANREKID

QLMKNSLMLVTALNPHIGYDKASKVAKTAHKNGATLRETVIELGYLTGDEFDRYVRPGDM

VGPE

>contig43585 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57766.1|) 1e-12

MSRAWHAFCMLLSITFLVNAAFTHDSIVRDDDVASSKTAPLSAKTLTTSTQLPVHADTNA

TSSHKPHDSFFSYTKVPLISLNFSLNGSIPPNWVGPSIGDYVDTACYRKQLPLNSHGHCP

QGYRASHNRCWAQCPMAYPVQCFSQCIPH

>contig43606 Frame-2R

MPDNANHFNNVVSVDIKERRLFDVVYGLLQDETEQAQRIHEHFMTDLFLRSFRRVIRWRE

LYKLCAKCSMKPFLTYLRHSSSVIVLSVLETLLLMVSPCPGFEIGDKASNRSEAANRKKF

GEVGGFGVLQSLLVQYGVVVVKQVQTESAVKVVAGVLKLFHVTLTLRRKTTDLLTCTQAV

EALMNARVSLLGLCHCSDGEYEVMRLAVALVKELCRRSNRDQFHKVQESAREYGALLYVL

EMAVGEDEDKKNHDMALVEIRD

>contig44539 Frame-0F|Blast-oxidoreductase family, putative [Phytophthora infestans T30-4](gb|EEY55933.1|) 1e-170

MISLLHRSRNLVRRCSSVRSFATAPFDRPLRVGIVGAGRIGQVHALGVQRTSALVHCIQL

PARDSDPDRAEIIAKKYNIPHWTNNASDVLSHPEIDAVLICSPTDKHAEHIIEAAKFKKH

IFCEKPVDLELDVVNKAIKAADDAGVKLMIGFQRRFDANFLRIKKAIERDEIGTVNMVRI

TSRDPSPPSASYIKSSGGMFRDMTIHDFDMARFLVGDEVDEVYTMARSVHPDVAAAGDID

TAVVLLKFRNGVICYIENNRDSAYGYDQRVEVLGSKGSVACDNQYANQVVVSTNKSVRHD

LPLHFFLERYMDAYVAEMEAFIRACTTDAPVPVGGDAGREALLLAIAANKSLAENRPIKV

DSVRP

>contig45499 Frame-0F

MPIASTFPTPPEGTLDAVRNHRSVSDESSTSAYESALEEDEGETLSGILIEKVKDDRVEF

EIDPEEASETDREDTERWKEKAVTTAEDKTTAIVETIQGEPS

>contig45877 Frame-1F

MDQVVSKKRIDLKPVLSILSTASEGDSVL

>contig45943 Frame-2F|Blast-hypothetical protein PITG\_17492 [Phytophthora infestans T30-4](gb|EEY67002.1|) 2e-30

MARCLNSSCRILDWLFQCCDSQNTKQLINLLIKYTGDFKSSSDWNHARYNNRSLAMHAAR

NNQVKG

>contig46973 Frame-1F|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY53726.1|) 7e-18

MDRFEEIKCIGRGSYGSAHLVRARRPNGMPDRFVVKKIPMELLSAKEKDQSFR

>contig47233 Frame-1R

MCETSDFLAYLGEICVVGSNGNRTVDAVYRSVHSQPKSCENARLVSFKRNSPQSVSLAVE

WDFALDGMPVRYVVGFACTEDGKRLYLGKSFYDVLEVDACDWKQEGKADSSTVSHSSARL

TLELQSISWTGQSGLDVCRLHLKE

>contig47563 Frame-1F|Blast-general transcription factor IIH subunit, putative [Phytophthora infestans T30-4](gb|EEY57658.1|) 1e-132

MSTAESNEGLLVLVLDTNPVNWSKQGGSTTDHTGIQQLISSTLVFVNSYLLLHRSNRIVI

IAAHAGSSVILYPDLEQDNTTGSAEQAAEVDSVVLQRLRQLSEIPLDPLKFNKTAIAASL

SRSLCFINRAMNEDPDLRPRILVIQKSLDVSEHYIAIMNGIFSAQKKNVAVDACILTAEH

SSFLQQAAYLTGGIYYKPSDFSGLLQYLISIYLPDPSLRKLLKLPSQDSVDFRAMCFCHR

EVISTAYVCPVCLSLFCEFRPICSTCGIRSHIQPKRKVLIKKPLIA

>contig48548 Frame-2R|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY53271.1|) 1e-53

MFTMTVAIVGAGVLALPYAVHQAGLALGILLIIKGAIATNFTLRLLVECSDLKQARSYMD

LALLTGGRNLAKFTQLVVCMNLFGTSVGYLVGSAELIQLALRPFVTTTSSSIFYDRQALI

VMLCGFLVLPL

>contig49288 Frame-2F

MAMRSLLRECDHFLASGTMRQHISSFLVHFRQKYERRATSSVTAMGASAWMRLSEPWAPG

TSSYESDSYHEVREGSLEALPQVTALQDARSLLALKNYRFFLERSLELIMEHLCAVAGAS

ALVGDATLNSEFAVSEDEWALVRRAALYKLERRAFISLQEIIYQLLGAGLGSTRSQWQEE

EERFERLRAQVASYPQSFLEIQLSHQSTSEWKIAVAVLDTMDNYSLPSEKAAVLVEVARC

IYETHSREHDVSINSSIQPTPMAADDFLPIFIFVLARCQLRSVIVARHLISETMITALMI

GETGYYATMLEAAIGYIASFDGAAKAGEIESRNSTSGSTILITS

>contig49657 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64257.1|) 2e-85

MKEAIDGGANVTLAHLKELLNEAKEIPVVMDEQRFLEAEIAAREWSSLASLKLASRASIE

EMEELHTDAKAIRERMYLKKQSRWKPQVERDINAAMDQSRKWIAELRDNLGVVAFDKLYA

SLSSYVPLPHLSKSSLSITSVERAKKKSMDAISKLIEKAQALILDVSSYTSPLNDLLLKG

VEAQAEASAILMSIGCLSETSGKNRLVDESSRMDIDT

>contig50817 Frame-0R

MAGVGFDQRVVDYSSLSGVSGRGRRHSASISGNTSILPSCAASSVVYSKLLTHRLLKYLI

AQYEPLDVAQMGLELSNLLFGGSLESGLPCGDGNALGMGIVPKLPSEETLKVALSNLYYS

QREILKEVVADVDVLSLSLNTWTSVFGQNVLTVSGHWISRAFRRRDCVLEVYVLPLDERV

NTIALLRDVMEKWDIPSSKVAALTMRLHAVSTH

>contig52770 Frame-1F

MAAIWFRRVRVAHLSQLLASSSISGDAGKLAFLLICSRSVCKEVDDAFIDKDAMEMHLNA

LSGEMVALIGKIVLTKINQNARVASLHGKASMSLK

>contig53405 Frame-1F

MLFWCLKCTRLSLAIQPHIALQHRTSSPVQLADW

>contig53579 Frame-0R|Blast-translational activator GCN1, putative [Phytophthora infestans T30-4](gb|EEY69168.1|) 5e-28

MNTIVSALSGDNVEKQTVAGRALGEIVRKLGEHVLPEIVPILRAGLLPQLPIGRRQG

>contig54079 Frame-2R

MVATKSELQGISFVVESRCNVASPTLIGCSAQTSCHLCRNNNNEGNQYLIT

>contig54105 Frame-2F

MNDRFFQSFLQSHYTKQAQMCQKLNSNALHLLSQVEEDEVHSFRLAIAQAAAESFEA

>contig54714 Frame-1R

MATDYVSITEMALAKILQRVFRQYTFLVEKHTLSRPMLDDPLVSRQQEMAKHEQYYALER

EECASLDSRQPYLLLCIDQLEAFSQ

>contig55568 Frame-1R

MACRIARVVLLAMLGGLNVRERFLGFGGESFFRVIFSRRWMHAPVSVEVPLMPLDPRVLL

LRQRIFREHCRLLSAVWPR

>contig55937-0 Frame-1F0

MQANRTAPLIDDSIFRCSQFAIARSWQRQ

>contig56257-0 Frame-0F0

MRFAFVWLVVMIAASVAANDTTDSTRKALATKEIATSVVAKPSA

>contig56688 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66962.1|) 7e-10

MARNGKKIELQVRAYDREIVKQHTYVALEFEAKLFRSDGNTVTECDAAMKRLASSTDDYL

YSSRRCLETIDCVARLSMGGQFNM

>contig58031 Frame-0F

MGKTQMAFNLNATGEFDVFYIWCNKVPDKVQDISAAYSSRTDAFSFCLDKDFKNIKDR

>contig58255-0 Frame-0F0

MKAIDLKETQAVAKFVCNKSRKSMLSLVHMRRR

>contig58255-2 Frame-0R2

MRYIPSARPFHCVLLCDCCKKEILSCKIYSICFV

>contig58549 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54775.1|) 3e-17

MMQLARSSHAQLPQSVLDFICEKCGGLVVPSVSADVRVLPQSRKSPLNRRLVKQQR

>contig59076 Frame-0F

MVDFDVATLFSTQYWSNPTRQIDRLRMTGVNASDQRESNWAGELPVKYLSCNEWICVITS

EYALRQLGKIVKTSYYEELYSKGRILGDDGLMGIAF

>contig04158 Frame-0R

MLMMPAPSLALHVPPSLETVFIRMKDRSGTIAIDMTPSVLSSKEMIVRFHELAFGKSFAA

FASNSCLLACRSNKETLVTRLDELQNGEVLVYKPCDELRTLVEQGCITPVFATPVDNCPS

NSPMSLKRKGRAKSVTYNIERVHRYASDLAKMDVSPKERATIEDMLIVGDEQVVDAMEQF

VVHRNSALVQRVLRGPAAKAVESLSMDFSSIHMHSPAVPTSINDVTNPFVSRDSLKRPAA

KPQRPGTINKSTIATERPSLVFESETLPAPPIFLQSIQEKGTLPSGRMALSLSSDLDPIE

NPQTSISVFSVEKLLENVPVGHDFLETYRIGAVLGSGKYSVVKRCTNMVTNDECAVKIID

KRQMLEVRFLKRELEIMYGLQHNGVVRLIELFESNDSLYLVMELCGQELFEFIDRNGPLP

ETTTRLLIRKLVETVAYLHAQCIVHRDIKPENILLPLNSQDLSDIRLSDFGIARKLDGHG

HDKVLTPHKSLSEVANLHDTPATNLTSLPSTTDMVRNRMARAHTKCGTRDYIAPEVMGGK

GYGTEADLWSVGVVTYVLLSGSAPVFLPAANGIKKVFFPDETWNRASDNVKSFIEALLVR

NPDMRSTAADALEHPWLQESPA

>contig07991 Frame-0R

MINIKNSQFLLVIALLASVSAVTPISKIKSFAGPEEETSDLTRQLRASRPVSSKSVPNLL

RSLSSIDSKGVSAGAIVEERNPGIRHSMAWAFSEPINTVLRLKGLTAEEAEAKLRAGKFY

RKFLYGTYPNHFRDYQNNLHPRNRKIGRKPKIVPTNYPQPI

>contig08051 Frame-0F

MSSHDVMIVGVVPSRRASTDARDVLRSYERSLTEAAPASATLLPRPVAHTLAMRSLPTAD

SAVYRHVSPRAVHHSPVAFAEAPPVALTMFSPRRRAHKPSQDAASVRVDLFHEEKSYAED

DDTGEGDRLRPVDLNATKAFGIEVRVDKLVTGKALDEDIMDECDGCLICMDEFSARRKAY

PLPCTGQCTGAFVHYRCIMAWLGQSGSCPLCRGACDPLVLQPMQKLELHDMTKMALQPVP

LDAGIIRCYVKQVYRGMFKQYAYELYLQGQLGTQEEDKFLLAARRQVRSNMTANYTICTD

QDCTDTKRIGRMGSNFLGTCFTLYDNGRDPQKLAKIQDAVSSQDVVVQNVLQIREELGCV

TYEPNRTSVGPRKMRVVIPDVDEDGGLSKIVRPMSRQDRLVTRLATGELKDLMRFSNREP

VFREDLGAYCLDFGGRVSMASVKNFQLISSEDPSMGNILQFGRVADDMFTMDFQWPLSPF

QAFSICLSSCDTKLACV

>contig11945 Frame-1F|Blast-actin-depolymerizing factor, putative [Phytophthora infestans T30-4](gb|EEY55008.1|) 4e-67

MSSGVRVKDEVITQFNDFKLKRAPHDYRYFIYKIEKDSEIVIESTGPSSESYQDMADKLA

QTTDECRYALVDLDLTSKDGRPTSKIVFLSWSPDTARIKSKMLYASSKDAIKRVLVGVGI

HLTATDASELSFESIEEGVSKFL

>contig12478 Frame-2F

MTGALKRIKGGRVLVLVAKLSVIFTSALGLLLALGAILVHRVREHDAALGLTTSKVDSLS

LRSLASFEELTRSHDTFVHVFAVQFPLALTFYASIYVFK

>contig13327 Frame-0F

MEDITMTGEAGAYRTFRSIFGKNSQQHVEKPQLEQKQSDDGANSTLILAIDDEDEAMWSD

EQPLDTNTTEIEPKELFGLQFAQRKSMEEWADDDDEEENWKDALQDRVNQLEIVNQHGTD

ATIAKSSHQVDQQKEAAGSDLPCFDCSQSLPVSPRLIRSRDLVERRPASRHKMQRTSSLD

ACINGDNAISSSSQDFMWSFQRRLTREGKVQASRQQSHSFDLITRNIETIEHHRKGFDSI

KGASSKTRHLISRPNNMDTRRDSPKHKCCYSRHKMKKEVLIETTSSGSTGLSETESIRRF

VLDEIKNMSMERLVSDAQRLASLEEFYRNHQISSSTPSINISTALLSPASQMPES

>contig14111 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69701.1|) 7e-42

MEGGDTRPMGVIPDILLDEDRLNMLLDIVCADYITACYASRENGKRVVLKALEKLYISVY

ARASEIGTDMIPRARPEQDPLFHERAHRFYTDVITEFRVRKQALDAGIDDNPISSVHGLE

DSLVREVMKPKLLH

>contig14209 Frame-2R|Blast-39S ribosomal protein L24, mitochondrial, putative [Phytophthora infestans T30-4](gb|EEY62988.1|) 3e-61

MPLSQSHRYVKSTPAAAGRSYLSPSPIHYSNVNLVDPSIGKPTRIAIRFTDDGEKVRVSK

KTGTIIPKPAVLKERQNPRRTETGPFDTAPQDVLERTVEDWEITRL

>contig17738 Frame-2R

MLLRAFLGSLCVYSLSWRYTVDAFEVITTTEELAAVERSAKVYALLIFGTEAKAQDMSLK

ELALTAYPELSDFETELEGLVTFGVLDIAPHRKDSIGNKWNLKKLPALVIYKGRPKENPY

TGKYYRESKAMDVDVLTNPRKLKKMLKQAILPDYVQELQDDQATLTSVQELISTTAKDES

IALLVSKQKHASPMYRALAAEFYGQGLTFVFLNNDQDGAEEIINRLKIEVLPSFAVLKSL

TDYEVLKAENLDSYAELKKFVEPFAVQKDNAMKNEAVKGTTHSEAVKFFTEKDFDDLVLR

SNVIWIIEFMDAEREETLVEEEWKALLTELHRKAGIVSIGAVSCEKEAELCERHGGPGVR

IYSQGLAESKAPKRGDIATFATLDEAKEAAIAAIPDVTTEVKSAAELNIFVSRAREQRCL

PILFFTAKTSAPPMIKAMVLSVRTQRVMLAVIHDADENLKKQFMIKPSTSTSLIILVPTN

EVSEDGRSAPFGVVAYEKKKMGAYNYPNIMQFLLQVLAQYPHPQTDELDSEELDFSSPEK

SAQSLVPYMTKENMADLCSGNKICAIGFFEDHIETLRDSESRLTKWYTTLVHVAAQSKKK

RNLSISCGLMESVKWLLLKHLALVFIKCRRLLCTLLQSIAMQRT

>contig18296 Frame-2F

MMGLQTLSVVLATLCVLTSALQAAITKASSGSATVEQLLAEVQAAVADDRALANMFNISN

SDQLSERELTALLQDILNVTSSSSFSDASDRMSSDSNADTSASRPELPVSGVATHVLSAV

VAVFAALAALSATL

>contig18421 Frame-2R

MVRAIWLHSTRHLICKFFTDKPPNHEWCNVQTTGIGALPTDQTGYANVDYFVWATPPGTS

DGTCRHRRSNSMAGPPPGEFFPAFFQSLWNQSLLVAEKKYPPISGTLIESDETLADENDA

TDTRPRLHAANDAYIDDDTLHSATALQVSGENSSQNTRGTGVVAIVALVGVAVVAVGAVV

NWRRKEGKLKVARETALSALAPLPN

>contig18942 Frame-2R

MPTSITQVALKREGYGSIARIMKCAIFAVAATLAALNVAANDTPALRALADANIAPTPDD

ESYAEPGEDDSPDDDQEWYGWGRPRPRPRFPKWYWRRPKFVRPKRNW

>contig19178 Frame-0F

MNNSEKPFVDAFIVMREFCSSLALQILASQGKMLMENRWKDRIMIKHYRDQNVLDICYWP

KACTRREVQTLTEQQRLIQQLSNPVATDRKRPALPYPESSLCVRLQVDPNMKRLLSVSLC

PLLPPNLPGIASLIDAMEVPSNMFLLSAENLLIAGMRAHVAAVLFSIGRLLVVDSPDENA

STQLVSGEDVTMICSDTSLRIARADIGGLTQFLEVTFDIRQGHFVVSSVAAARHATLHFT

VKQVERILNTQCKIELGGKVDNLLPNEFALVSGDGKGEKSAEIIHTCIRKVLCEIVADEV

AQIGSSLKGIEVLRNVNLNWERYLAFRQQHSGHTEDLSISDTALYFLLTSSKESSCYLVV

EIDKYSEVDGMNGNGHEALEGEQYVRLPCFSLLQTSVVMPGQQSGVQFIQRFSAIKKEDL

HPSVTRINETSANSLRARSRKRPFNSYELDKKKGMSKKQALLDGGRIQVGTGYWLDESAS

LHFVPHIATVLLHAINICSERIQLQHFVNFARRRKSRIRYSGEAGTSSRDGTGGQVVTLS

FPEKVNADPLKVVAIQGHLKHGEGFELCLQLVSPPFKFILPQKRKEYLLSERSHYVNERG

QLIFRYPTSMVTSELFSENPLELFMVELICVVRPLCELAKKLEKMLTAVERYTWKKTNSG

HFFVERADPFAIILACHAPNPRHCIAAGSSPNGLTTYRVTVQYKQKMGFVVNYSHKTEHP

LMHFIQSALNGHSDPAQFVEALERTCIPMGILASVVESQLLCAKYYRQDPPPSLKDGASS

GDSNAFGRGKINGKGMKLGYKFKLPGEEKGYYAEKSYGGDDKSFVPAELVMIPRSQTQVR

LSYGDRCAVDIYFLE

>contig21212 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68778.1|) 9e-10

MAATSHVVPIALLGLLNENVSLAVVEGATYLSFLLLMLHANSSG

>contig21267 Frame-0F|Blast-beta-mannosidase, putative [Phytophthora infestans T30-4](gb|EEY61220.1|) 1e-111

MRSSFIVMTSLVSSNALVIPLKQWSFSSINGSVYADNVSIPGTSHIHLLEAGIIDDPYYR

FNEREYQWIAYEHWVYKTHVTLSYEEANSDAVLVFENLDGVASVRVNGEKVMTTSNSFVP

YRINATAVLRTGLNQIQVDFPSILQYARHEAVNYPYSVPVSENYNTWSEPTRRSFVRKAG

SDFGWDWGPAFITSGIAGAAFIELNKLAIKVKDLHVVQNFTNGKDDLSKVDVIVRVTLDG

RRINHENVSFNLYVNEKKEFAITRTIPEDWSENGTIDLTFHLKNPKLWWPFGYGKPYLYH

VRVDVSDSSFSSSLSHKFGIRHVELIQEDTNAGNVDGKTFYFKVNNVPIFIKGANWIPTE

SFPTRTKESMVRYLLESIRAANMN

>contig21911 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61931.1|) 0.0

MKTGCVVNRIEPLLKFPGCLMLTTQRLYFQPAPLNNVWDPVLNWEYTAIDQVYKRRYLLQ

QIGLEIYLQSGDSFFFSFQSRNTRNDLYALLVGQPELQRCQRKDLLSMMRKWQRRELSNL

EYLQFLNNASGRTRNDLTQYPVFPWILQDFTSLKLDLNDPSVYRDLSKPIGALNQERLDY

FKARYEEMPCGDEAEGMPPPFLYGTHYSTPGYVLYFLVRKVPEYMLCLQNGKFDAPDRLF

RSIKGTWEGCVSNPTDVKELIPEFYDCALSPTEWLNNTKHLDLGFTQSFERIDDVELPPW

AHDNAEEFVTMNRAALESDYVSEHLHDWIDLIFGYKQQGDEAINANNCTYLL

>contig22631 Frame-1R|Blast-unnamed protein product [Vitis vinifera](emb|CBI30190.3|) 7e-08

MTYHRKPGFPRSLGNIMVEAGSDEELDEQ

>contig23522 Frame-0R

MNMFRRLFSSCRIPASPTDHFKCVDPGTIRHTIVLCDGRIFVLRVYDTQNELLTIGDLEV

QLLHILRHAAYLKSLRLNENESPQFVGALTAMARDQWAEARQTLVEMDPLNERSLDTIES

SLFALCLETSSPKTPSELTLQCAATNAGNRWFDKNLQYLVFTNGMVGANMEHAHADATVM

QSMFRWLGARFLNRKGSYDTFIQSRQHALGFLPPPELLRWHVPDEIVLNTIPKALTEFQL

HGSLFQIEVMRTELFGKTKLLAVNLFSDAFVQMGIQLAGFRLFNRVVPTYESGHTRMFLH

GRTETIQTVTNEVLAWLQIHDRSDAKEADVVDKLKRAMTRHQELSREALSGKGIDRHLFG

LSMAAMQKTGSIPPLFTDPTYGKSGGGGKYVLSTSNVSGCPWLWGGFVPMVAHGIGLCYS

CERDYIAVMITSFDPSSRDTEFPIDSNLPRVTASKFQVALLQAFHDIYDLVERTHKSTDP

FSKL

>contig23557 Frame-0F|Blast-hypothetical protein PITG\_08302 [Phytophthora infestans T30-4](gb|EEY54754.1|) 2e-55

MKLRCLNGDAELVRAAQKINLGILPVQPPASCYRRAESDILGLSWVAVDGEVVIGAAIAD

LEIGRDGLRTVQLRTLAVSAQFRRQGIGRQLVLKVVEQGKKITTAEGKVQGVRLNVHVGN

NEAIAFYKALGFVKLAQIENYYRHLEPRTALMMEYSL

>contig23669 Frame-1F|Blast-RCC1 and BTB domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY57867.1|) 4e-64

MALPTLVKTLSRMRIIQVACGCYHTLTLSDDGKVFPFGRNNHGQLGLETYVDCLCPQFIS

ALRNKRVE

>contig23715 Frame-2F

MSNDAVLVVVIISVFLPSPATETTPASTPSTKTSPPVSAERSSPNPELLLVAITNVSGSS

SCLSWRSCRTQSRLVGSSNICGRNGSSNSKNSGLHNLAFLTDSRPNVVFGLFERS

>contig25861 Frame-0F

MVVHKPHKGQKKIGRRSFILFHLDG

>contig25986 Frame-0R|Blast-inosine triphosphate pyrophosphatase [Phytophthora infestans T30-4](gb|EEY66059.1|) 2e-95

MSSTKPVLTFVTGNANKLKEVVAILGADFPFELHNQAVDLPELQGEPADIAKEKCRLAAE

QVEGAVLVEDTSLCFNALQGLPGPYIKWFLEKTGHEGLINILAAYEDKSAYAQCIFAFSP

VGSEPRVFVGQTHGKIVPARGPKTFGWDPVFQPDGFEQTYAEMEKATKNQISHRYKALES

LKCHLIQSA

>contig27597 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62524.1|) 2e-35

MMFFFRALTASIVPLVSTALQATITSGTSECFYVDVESYKHGISLNYEALRGVADELETE

LMVDRDQILYTHKGTSGRYVSPIEKSGIYSACFKNDHSPVGDVVIGFSFHADDPNHEVLS

NADATKI

>contig30139 Frame-2F

MCECSMRVLEHEGSDMGQLEFESAFEQSEVVARCIMLSEPLRDAFAELYDLPSAASVTIA

MADTGTKSFEATPAVKCLGLSAVSETGACEIAFAPTSSAFIEFSCAPCNGDGCRTATFHV

ALLQQAFKALAHSNEACLRMNGNGFLSIQHMIESGTGKRAFVDALISPEDTSMS

>contig30184 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66474.1|) 2e-25

MELATVKGKLDTECFIFLVRKDPERYERIAELLRANDEFRAALNSGFDPSDEKMY

>contig30401 Frame-1F

MEKLSIYSRKNDGKLQTFERLHAEGFAYLADNSYIRSGYRLHYSARDCFLSLFELHNETL

NVWTHMVGSFIFLTLMAYLAFSGHALYPTAETTVISRLSTQVWCDDNSFWIVEGHHTPRL

LLACVLPELCPPPADYLPPANYYEVANIIFDHSLQRLPSIERFQALVEKNVGGFSDAIGA

QLEQLRSDLGALSMRLGGQVRGASLEQVQYLKTQLGERVKSLSLFLQDVASQVGADLPMR

FALEELDGVTESVRKGLHILASADGPHNVPHWPIFAFMSSAVICLTCSATFHLMFVVSRP

TYLFLSRVDYAGITILIAGSFYPLIYYSFYCHPWLRSIYLGCISVLASITFVVALLPIFG

TPKFLVARTCIFLALGFFGVVPVSHLVWHFGLFDPHVTVMIGPLLLMGLLYTSGAIIYAT

KFPERFFPGRFDLWFSSHQLWHICVVAAALVHFANALQHYEWRWNTQCQT

>contig31815 Frame-0F

MVILEFAMKQSREPSLKRVACRLAALDDVLLHQILSYAS

>contig32560 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61370.1|) 1e-160

MRMILMCPLRRAGKFLIQGEKVLAEVKVAQRDESRRVLLLNSPVQIKNGTSLDMELWTSQ

THLAPGESGSFSRRGKLMVLTSRSKMPVPICAMFGDEKDSIVVKVDGCKPTIVADLNKLA

AGSTILTLEPEDCDRVGYCLYVTITAHMRKVYREEHQGMIMRGNAREDGELQTYATKYRI

SLLSCLILENTLPIRVQYKIVTNGIPPRVVQTGTLSPGEEVLIHDFQLHAQLMLRLPEMD

SIWSRALNLGDCIYRESMDKSIKTMLGAVGGAKDVIVEFLPSPQKS

>contig32951 Frame-2F

MASTASDSKSRMTYRFLGNSGLLVSKLSLGSWMEVNDKYTEEAWYNMMKFAFEQGVNFFD

NSETYGGGLAERNMGAAIKKGIAEGVWSREDLVLTTKLFYGAKPFYSKVGPNEEGLSRKH

LVEGAKASLKRMGLEYVDVLFCHRSDPHTPIEETVRAMNFIINKGWAFYWGTSMWSAADI

SEACEIADRLGLIRPIVEQPVYSILDRNKVEFEFVDLYKKYKLGLTTWSPLGQGALTGKY

SSGTPEDARMNNEMYKNFVPDFADRVVNADKLKPLVEKLGISMAELALAWCVSNEHVSTV

MIGARTVAQLEQNLKVLDILDKITPEVKAEIDALVPLCRRCRRQTFLRRTATSICNSLES

SWHDHVSALFLFYLI

>contig35060 Frame-0F|Blast-glucan 1,3-beta-glucosidase, putative [Phytophthora infestans T30-4](gb|EEY57657.1|) 1e-142

MARRSAVTVALLASSASALDGKLYGINYDLRRGPDWDAEKCKSTETIAADLKILSTITSN

VRTYSLSDCDVTGVLKSAKDLSLTVWLGVWVSEDSKVYDAEVKVFKELIAGGYIDSNIVG

INVGSEAVYRGDISASEAIKYLASFKKIMQDNDISLPVSITDIADTFIQYPEMLKAGDIV

TVNQFPFWEKINADEGADHFDKRIQPLLKLAGDMEVVITETGWPTGGSAVNGSLASEEMC

AIYLKDFCVLAEKYGWKYYYFAGFDTPYKAEQIDDVNTVESHFGIFDELGTMKPAYKSLT

LTKVKSAKSLSSNLTSSLDSSSEAYGPGTVGTSNMQSSGKKADAPSVSSNTNTGNGTSQL

VAASTPVILGAVLALVWSLYVTCSLLN

>contig35819 Frame-1F

MLKYLASATWLAKNVILLAADDGALDGSDGYAPGTGAYLQAYHLDPVVSGIQGVLPMRAG

VIRAAINLETLSNSRPADTMGIFTAGMNGQLPNLDLVNTAVRALRRHQIPTTLNRQQDNT

SGFNKLNFFKNLNDLYTPPRWKESLRNYLTNLDGMLQFMVTVATGPSGPHANFISYNIDS

ITLSLTTRKTPEDRPLAVRNVMRSLEMVIRALSNLEEKLHQSFFLYVLPNTTTFVSVGEY

IYAVLLVLSPAIVHLLSLATQTTGMRIALALSVVFVIEALCVLLLFGICQFLATPTASLH

SLSFSEVSAAQWFQLATVVSVAQVFIALVITPSLRSVVGFSGCVEVFDWKRKLKKYEAEQ

LKKLLPKSSSDDTKEIGAKTILNSSNGIPPLDSGWRAIKFITMIMLVYFHGILGLLNYPM

ALFCAIPMVHFARVVPFDTATTAQNIWNGLWLLFSSPLMILFLQSWRRQGVGVGLSYIVN

SFAQRLNLLALMYICCIYVVVHTLSLTIFTFSSAVPSGKKTKCD

>contig36155 Frame-0F|Blast-D-lactate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY69329.1|) 0.0

MLGVFSKSARHFAVRSSFSLSQQGRLISIRRNPSEKTLLALKSLLGDRLSTASSVLKQHG

TDESYHAVTSPDAVAFVQSTEEVAAVVKICAAAGTPVIPFGAGSSLEGHISASQGGVSIN

LMGMNNILSIEPENMSCKVQAGVTREQLNVELRATGLMFTVDPGANASIGGMISTNASGT

TTVRYGNMKTNVMALSAVMADGQIIKTGSKARKSSAGYDLTRLLIGSEGTLGVVTEAELR

LFGIPEAEKTMICQFNSIKNAVDTCAMVMQMGIPVARMELMDENAVEAINKYSKLKTPVR

PSLLVEQHGSPSEVEAQSFVVVEIANDFGARDIELATSIEERKRLWSGRHTAWYATMSQR

PGSRGLSTDVAVPFSNLTDVIVETQADLKKSDLFGSIVGHVGDGNFHVMLPFDPENIELM

QKVRDFSDRLVKRAIECGGTCTGEHGIGNGKMSYLRLEHSNSVDVMHTIKKALDPKNIMN

PGKIFYGAER

>contig36586 Frame-2R

MVTLASWLSKWALVRLKKENKAADALLDAETAHERATKGLLVRFSSQTVSCSNAGNLKRQ

ISVMHRRERSRFQCHSRV

>contig37004 Frame-2F

MFERTQNVQHQQSGPLGNLLVFMHPAIGFKQIGASGAIFPRLVSDRVTRLK

>contig40785 Frame-2F

MTAIDIAPSPTSMTVDNDGKKMLEMGGMQNMAWAADTSKFGFKMLVKMGWTAGKGVGKDL

QGQATHVKIARRSENLGIGCSLKQVEVQGWSETAGGFADVLRSLNETYGNKSSSDVDSTD

VVSGSSSTKRKRAKKEKKDKKEKKSKKSKKSEPKVSRRLHYRKNLINKDARNYNAAEMAA

VLGVASSAYK

>contig40819 Frame-0R|Blast-pentulose/hexulose kinase [Brachybacterium faecium DSM 4810]gb|ACU86862.1| pentulose/hexulose kinase [Brachybacterium faecium DSM 4810](ref|YP\_003156452.1|) 2e-06

MNSFVPLLAASLAAGAWLYNYHIQQRKKIFLGFAKLKYYQGLPIVIIFDVGSSSIRASCF

ALVSKAQWVFIDESLQQQHLSSIDDNGEADIVKIEALVEKLMDQMMDFLRATGLSQKVMG

VGFSTFAMNVIGLDAKGNAVTPVYTYAGKRKATAKWSKVLRERLAECGEL

>contig43094 Frame-2F

MLDSTRVSCVEAVDGECEPKVFINMNLDEQSREQLQNVSFYVEVESANMSLLIETECQTQ

RDEWVTFLRNLLPKDNAKTCRDNQEKDVMDEAGDDAVKESELQPVSVSDSSISTRSFMHQ

GKSENLLEDDDPFGMLSLLGSALSPIDGHESSIKMLKYAAPGMFAMDHFGISVERSQTDS

GEISDSGIDVTNTELNNAKDPALAFIPRPRSIQKNQRLLRERSASNISDSLSSSMVKDLL

SSETSRRYSHSALVGSTRDLLNACSRCSKKFGRLIHTPKICASCSHRFCRDHCNQWTPLI

TPDSIKQPNLELSGIPGKAETIVAPDRKRVCTDCHVRQQLLAYLQESGVYYAS

>contig43155 Frame-0F|Blast-tRNA isopentenyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65646.1|) 3e-71

MTALRKVLVVVGSTGAGKTKLSVDLAKAVGGEIVNSDAMQMYRGLDIATAKITEDEKQGV

PHHLFDVIDPTSRCDVLEFKRLALQAIEDILAKGKVPIVVGGTMYYTQSILWKSQLLDDV

LIVNTATNHDEEQTPEALYSRLQKVDSVMASRLHVNNVRKVRQSLRVYDQTG

>contig43586 Frame-1R

MPRPPDEQISPNVPGLKSRPLQLRNEGLIN

>contig43605 Frame-0F

MLETQLPHSPLAPSPLASGAHVERKFHLRKANRDIAALDFLQNIPMRSETAAAAIKQLAP

SRLKADSLNMDSASSVVPTINTGSSKSEPLAGRRLPGMATTVVRMPGLFRYRLITKFPAA

SAVVRRWEVATAQQGIFGARVFFSRGCGYPLATSTIINYNGNETSARRRRAPSMSTTLAL

ESTNYDWRGTSYFRLLHSTWSACDPDRDQEDVHPERFPFSASFLDDPEFRQGRHRHVVRG

DKSLGPIVSSILLYVKPHELKHELNKKFQEKHGWWLQDASLSLSKLRHLKREALMCSQRL

DLQIATVALACVLFEKLVLQHYVTKVNRKLYMAVCFLLAVKFNEPFTSDEHKRVVRKLLK

DFDRTFALPSRDVLTAEFTVYAQLSFNLHVPIAEVHPHFARLLKNMESNPRKYLDDDVFA

SYSALLATEEQSVNFNVTLSGPLNEFDETTDGEVHLSDEEDNQSGEDDHQRGKKQIN

>contig43850 Frame-0F|Blast-pol polyprotein [Anopheles gambiae](gb|AAL56548.1|AF387862\_2) 1e-14

MLNGMAVSWGARKQGGVSLSTMEAEFVAASEVARELLGLREMLREVGVEPELPMQLRVDN

QAAVAQIAGDALR

>contig44172 Frame-2F

MPLPPTHLESLTLHSENECASEDEQEGNDSEGVGDTGLETHGHKGYEIFGIRLANPNVLF

QLSEIDDLEVREWMAQFSIQSSPSLLGGWFPTQMFLPLREIIRLRIAALVGRSNAELETR

RKRLDVIKKQALSDYAEELAGRTLSTKAKKDRTGSKKKVNVDGEIDSASVAPEEDDFALE

RALVLKSAKEDTLLKEVEIENDDEEDEEDDEDLDEVEDLDSSAGVSGNTEALKRNEDA

>contig44198 Frame-2F

MKSSRLIHHNEGANADALSSSQFSRTSAGSSSVTSKSSLKGGKKKKKKTFRPGFGRQLSD

ESAAALQRGDIKEDEVILQQQQENSRISDHSDTSRNTRLATNPTDLAHLLPPVKSGSVLQ

GLTVHHGSKKASGGSVLAGLTVHKSASPALSVPKNEPSADLKPSNLLSGLSIQKTPSTIR

SEKSLESVTVIPEVECNDEPVQLLVSTPASPITPV

>contig44316 Frame-1F

MTVLVTCKRRASCIAWFVSLSIRGPFMVSVPKWSKRVDSSSTKLALVGTDPTADTHGQWC

SPLLPNAVPNRMKAAIPIDALNAGFGR

>contig44446 Frame-0F

MNLAEYWQKLVKLYMPEYGPLSQRESNDIHKSNSAPVPFSRSKFIVFYKVLVQVLSVWKL

RCSFSEF

>contig44815 Frame-0F|Blast-peroxisomal acyl-coenzyme A oxidase, putative [Phytophthora infestans T30-4](gb|EEY56904.1|) 1e-179

MVQVRAYLIKTIAELMGAACTICTRFSAARIQGRTPDNKGEYQVLDYQNQQYKLLPLIAI

SYAALFAGKSLVEMHDSALDVIKKGGSSFGAKLAELHAVASGLKAWLADRVSDGIESCRR

LCGGHGFTQSSNLAHIFAEIVGANTYEGTTDVLVQQHAQYLIKTLMSLPVKNKFTKFLNQ

VQHSGDKMLRCKAQKPEDFGNFELLLDAFQTRTARIVMALASRLKATKNNGKACMVLMTH

ASSAHAELILLEAFILGAQNLPSGAEKDAVTQLCYLFGAWLITKSLGDFRQYDYLSSEQA

VFAHEQVLRLLPIIRKNSVLLTDAWDFSDFELNSTIGRYDGDIYRALVKRAADEPLNKTQ

VPNGYVQFLKPLIQS

>contig45139 Frame-2F|Blast-transportin-like protein [Phytophthora infestans T30-4](gb|EEY59033.1|) 0.0

MLFKPLVEGMLMRILDPHKKVQEAACSAFCTLEEEAGEELGPYLTPILQNLMFAFGKYQA

KNLLILYDAIGTLADSVGDKLNHPELIQILMPPLIAKWNALDDRSREILPLFECLAPVAQ

ALGNGFQEFAMNVYVRCQRIIENELLADAMSEQSPNEFDEGDSELIGCALDLISGLIEGL

QNNSEALLNGSNLLNVLMSCVRHDVMNVRQSAMGVVGDLAKHAPNILRSSLGDLLPVLIE

NIDPELPTVCNNASWSVGEIAIRIGAEIEPYIESCLDRLIGMINRPKLPRNLVENCAITI

GRLGYVCPNVVAPHLQEFAKRWCRALAHVRAPEEKEHCFFGLCYMVKANPNGIVADFMFM

CGAIASLEGQPIQHAELKDMLYQILHGFKTSLGENWAAYFASFPEPLRQFLTTRFNL

>contig45184 Frame-2R

MMRRIAPASRRLFSTAMADTDVV

>contig47230 Frame-2F

MDLSPDGSGTCVRATCYTLRPDCGQALSEI

>contig47560 Frame-0F

MLPFASWNSMFVEMVKVSKGNLQDRAVAAEAAKARISTSLSDSLKLIFSSTKDVVAATST

GATASALGNLSIDGPAASPIITQQARRQAKHSARVFTSSVVDLTLDDESDSSYSASIQAP

TQLHIKTESRGNADNTWLASATAA

>contig49720 Frame-2F|Blast-DNA replication licensing factor MCM8 [Phytophthora infestans T30-4](gb|EEY69900.1|) 9e-84

MASSLVEAATCVWNQYYPEDHFIGIHQPGETRPAHYYRPISDTDGRFQAATTFLDCFRDD

DQWAPLLHCDLTQANVTVVLLHYMELIRTGTADFERALIENIQDVLLCMGIALCMRRHEL

RVEAEEVFTKKRTLPADRTKITVRLHGVTPLLPIATLKADVINRFVSVVGTVVRVSAIKP

LVTRCDFVCAKCNEATSCAFPDGKFVVPQKCVNAPCRGRKLLPNRSSVDTVDYQTIKLQE

TDTSDIG

>contig50814 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60076.1|) 7e-52

MRRLAISTHICPTKVRCRTSANATCMEPQLHSIRVKVSRHASTNHHKTSYHSSSQRGAPN

EVDVASKTTTHRNHANVLLDNETRSFSREFEKPRMDASFLVNNYTAPALAAAFQDREYTL

WQCADLLSEGKLDELKAVLKPYHDFAQHDRDSQRQTSLANALSKRHLERIRKRLSRLPRQ

LTKAHSARAAVVIPLCTFEGKPSVLFTLRSR

>contig50960 Frame-1F

MRNQRQERILKTAKFVAAPSQIKTCARNLTSSVAAKSNIAAPSSATEAVVQNQPSVQLDV

NTSA

>contig52687-0 Frame-2F0

MCGRTRCTLAREEIAKAAGVAPEDFVNSEKYKPVENMGPGRYGPILLQKHREHSDGVKTN

TQLQAM

>contig52687-1 Frame-1R1

MFSTGLYFSLFTKSSGATPAAFAISSRANVHLVRPHMIIICRNAL

>contig52773 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61200.1|) 8e-11

MLKSVKVLDLGWNKITKVMTDINTRSLEVLSLCHNQLYHV

>contig53183 Frame-0F|Blast-RING Finger Ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY65163.1|) 1e-17

MFLRSLYGSRMPQPLHPRVDPQASSYWEEDTASSREISRTMEEADAQNSENHNNGKKIDS

VL

>contig53262 Frame-1F|Blast-glycine dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63500.1|) 2e-96

MAGMKVVVVKSDENGHVDRKDLAAKAAEHSENLSAFMITYPSTFGVFEPGIKDMIELIHS

HGAQVYMDGANMNAQVALCHPGGIGADVCHLNLHKTFCIPHGGGGPGVGSIGVAAHLAPY

LP

>contig53288 Frame-1R

MGANASVTMTRNNTSSQQAKFNAIAALVRSDTSGETPNRRNRRIQDRIVMCQGVLA

>contig53833 Frame-2R

MAVECNRAAWRSLHLIPFGALSELAKWDVVALLLFNLNSIPHEAKTASGWMRFVGKPTSQ

DVDTRALVRQHLYDLIDSDTESSLCLLNAVASIAASCTTQTLDDRHDLVVVAVHELFMAG

FTVESCQQALGANGERAAEPLSILCLAHPWVLSLLITLLYKFHKCAATWI

>contig53958 Frame-0R|Blast-aspartokinase, putative [Phytophthora infestans T30-4](gb|EEY60689.1|) 3e-45

MESSVELHDRWQQLWLDSVLSHGEDGSSFSTSPIDPLLPTSLHPLLQELKNLGRVLQGIK

LTEEASAGIQARVLA

>contig54106 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66327.1|) 1e-80

MDRTSDFVGVTVLFETGQARPHTHRPLSREAHLAQHISDQLRQQELCLRELQGFVVKKSI

IVDDPSAQIAKLTDVLKKELGAVERSIHMFQQVVNAQRGRHEQHHQAHFSVVCQSLKSRC

AKSVKVFHQALQQHTAAIRERSSRRSKFSHGGGNSMVHINAPLFTRTNATDLSGDKVLST

DNGLPYKT

>contig54483 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70497.1|) 2e-17

MKLFPTPTVDDNETRYCFFLPCSTCFQNDAERLEVATQQCSAFLSFAAQQTHAFIWHKHH

FHLDVIS

>contig54717 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70497.1|) 4e-19

MKLFPTPTVDDNETRYCFFLPCSTCFQNDAERLEVATQQCSAFLSFAAQQTHEFLWHKHH

FHLDVISTK

>contig54762 Frame-0F

MASNDIWKEDWRLRSKWFVRRTLAMKMKPIPLNATPPPTRFSDEERSRFIADCIYIRMSL

DSMVVSPRDALLTIFG

>contig54788 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55407.1|) 3e-15

MEQEEGSNPRRYVRASDRRLAEVATQAAARIDIETLQYRRSESTGVTTERSHDGTTVTVT

C

>contig56904-1 Frame-1R1

MTSSCSDRMCLMLLYLRLQDKWKNLTKNTKRKLHKTRNF

>contig57943 Frame-0R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY70002.1|) 3e-31

MHVLSIVAFKWSWVVVVGLAGISGIEYVLAFFFLTFECSAFTELLNEVQLQLHLQEHRMA

RD

>contig58047 Frame-2R

MESVLVGTSHKPWPETSRQPVPPRHDCNLIHVLPKVIATGLRESIKTCPIFKAFYMSLVR

SSGRTWYLNTFRLRGLPISSTLFHNLLCYEFSL

>contig03459 Frame-1R

MVDSDHFPTSLDCFESDNLSGLHANWLDDENLCSLPLADVFTNAKTSRAQDNTAGSLITT

GVTNQPQELNEELIECDAPLLDTVLNFSIDLELSPILEPFDDATVTTSPRQLECRYQKSP

KVVKKIDSPTRNALLATASLQASSEEVRTSNEEHTLSLVVSKRPRTRSSSWLQQEKSTFF

SMFKVKWPKGEHGSSLGFLLRQRFDAISTKVRTKSVMEVQQFYADVIHYISELLKILIND

IDLMNADQVRIAVWCYGKIVSDKRHLDEFQSLDAISFEEKTKLATLLLQSIVRSRRQMLK

AKIDQKLSLIHNRTPISAWVSRSNFSPFSLGKAPEESTKQIYHPAVRIKHPTFLKMSAFS

SPISGTKCCLQQKISSTRKRAISNDCSSVASLEKKTRYLTGAMTFASPVPPLKKKSRLST

TSDVSSFTLQQFQKKVYIKMRMTPLDKQTKESVVLCGCRPKVELKLSSAKKISEIAAHMR

NKWTQVHFLMPRGSVLCFYHKNGTKELSKEDSNMTCFDIWKQCGKKTNGEKVVEVSYKWN

LPSKSIDDANTCGHIMMPLRAPPSLFDQKVTAPAEQTLNSSDDNEILQLPPDLGLNEFIS

QETQEEAETLEALISDSGDEDLNKDVSLVTGRLRRRIKPVLVSKEEFNI

>contig10312 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55290.1|) 1e-14

MNFTGTAMHSTAMCWAAAEGNLAAIRRLREDYDADVNAADYDKRTPLHIAVSDEQLEMVA

YLLQCGANVDA

>contig10583 Frame-0F

MLQMRRLVRAMFDEQRPLLPQRKARVNAIQRAQSWDVNDTDDEPTYVPKAFEGEYNVSFQ

RKPLGVGLVPSSQLYGSWEVSSIQEAEPTDAPFEDKNQDDGTNVAKGDVLIAVNFSCRKA

HLPRAKLAAYLRHCSCPIVMTLRNPQVCGSMDSHAMSTAMYPSSVDYDLQYYSTKVVARA

SSSQWQRSLVHDLVLNAQLANNDKVFKLVQKLMSKSEMDMKSQALVDRRGDAVGKKEREK

SSYGHDSVKPILSELGEFEVTFDKMPLHFVLAPSTRLYGVVEIYDPKDYAPTIQVGDVVM

AINEDRSPLQLSSDEVIDMIAELQAPVTLRFRRPVAYRKYLATYYRNQLKELSSASIASA

MYPLTAEYKQKASKQFAKKAMRPKLLVSQSFMEPETTFSLSKTLTTAGTANEAQSNDFRA

FARKIGDFDRFKLWKGNNSSHGGRPLAGHQSAFLTEKHMQFVRKHLPSYLMCNQMELFYS

TRIHGWNFLSFFDRLENKGPTLLFVQDENDHIFGAFCPASWKQSKTFFGNGRAFVFSLNA

QMRAHMWSGLDSSFMYTQQDAIFVGGGKKGIALCLQLDDRRGFTHACTTFESPPLVESQS

FRCETVEVWGFYGLKV

>contig11081 Frame-1F|Blast-sphingolipid delta(4)-desaturase DES1-like protein [Phytophthora infestans T30-4](gb|EEY60665.1|) 1e-170

MCKVEKSVMPAMAPVQPQVTKPQFIQAHEPQHDFHWTPTDEPHATRRKLIMAKYPEVKKL

FGHCWKTKYICVAVVALQTYLALQAQYMSWPVYLFVLYFVSGTANHGMTMGMHEITHNLA

FKKPLHNKLFGFVANLPVGLPASISFKRYHLEHHRYQGVEGVDVDLPTDFEGKMIANKFT

KFLYILFHAFFYVGRPLIVNPKKPGKWEYINAAVCLSYDCLIYVYGGLSGFLYLLLGTML

GCGIHPVAGHFIAEHYEFTLGYETYSYYGILNRLTFNVGLHNEHHDFPFVAGSRLHEVRA

LAPEFYENLPSHKSWVKVLVDFIMDESMNPFSRVKRQTIEDNDQGKIKSE

>contig14110 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69701.1|) 5e-43

MEGWLRKKGQHVKLWRERYFMIRSTLDGTHFLCYVRKKGDKEPRGWYVLGPGTTVDQVRE

SPSKIETKKLFTFRLGHVNHVVPDESDDNGHLIDITP

>contig14208 Frame-2F

MSQGKKDRIERKRSKKTERLYPRKSHKSHDSKRPKRANKISADDYFLRQTEFRVWLVQT

>contig15535 Frame-1F

MDPKTHLTIHTDDHAEPQPSRDSETQYIKIETPIQEYSCSATFHPDTPRGRRSPYCRSQT

AETSDTEAQHSIHSTSKHGSLEHNLPLRLRKNTDADQSSKGDTTEHTTRMSSIEFRGVSK

LPKRYLTGQFQSNSYFARKLLRLSHFIVLGDLIALGFFYFYKFEDEIGSRESTLYIGSPL

TVLFSSTAPNCSKSLALAALVYHLFPAVLILGLPASGWRLFEPFRREERIDEGGRLQKVK

RTICLQICELVSVGMFVYEALVCGFFIYYVASGKLFQACDFNALAFLFCSGAVVMFYLLF

VLMRAFARFR

>contig15588 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69095.1|) 5e-11 NOT\_ORF

MRME\*MQLNSKTKIMSNSSEECKFNEKTDDEDLPRGLLKVGTLVDVESRTWPGINKQGGA

GRITRVYREKSCEGESEEFFYDVRYVLGGFERKVERVYVHSSKLLKKHSNRERVSREYYH

NDYINRPHLRKQREAQERR

>contig16822 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67747.1|) 1e-06

MWRNLAYGSQQVAEAVPAVAPTKVGMETVISQ

>contig17739 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57614.1|) 2e-29

MWLSNTLPWKVELEALHVLGFTFLTSFLQDRIEKSDFL

>contig18297 Frame-1F

MPLTWAPLYIIAPQFFGIAYTRVNVAKTFCSAALSSFIWLRISRKRKRLRRRSVNGPSSP

LRNLGCRINRIWFWDNIML

>contig20625 Frame-2F

MDHRNNLYGMPADRVGMPNGMPQQQPGMQHHYGMQDMMFDPLPMTNGMYHQPPSIHQQHG

GMGSLMQQPGMVAPEDDPRFVDDLLGAFGNDPTGLGGHQQHLGQMPGHIYDEHHMMPTHS

QTPDLQPVRTQAMPMTTQPPLMQQNNLLGSMHINPMASSSGVRIGIGLQQQQNLGQQAVS

SDAGSLGATISAPLSAPRQAAVAPSSIVLTSTTSKPSNSLRTLATSSNNGGSSDEEGNMD

EDDTQKKKERRRQQVRYASRRRRKKQKDEESFLRDRIAELKEQIRIIGGDLTEQCSQMAG

MSEQALTEAYEKQMVTVQTLRKDNNKLKEQLLQHENFARMIQYGLNALPSDCRDVDRKKI

TGVPMWISDQMNPLKGPTLVVDLNMCHEAVRHAYNELKSFGPTVNSKTNVCYAMGWKTEL

WAASTCLNFRAVRSISDKNIREVANASWDIITSPEKCKRIYPDVKQFRILQKVTDDIVVV

HRIASVASDLSDREFISVAFRLRDGDDYYIGLKSIIVQTEAAENCIRGEECQGWMFIGGT

NETSQWKAHFLGYYDVKGEKDDKVLNQLANEAMFGMLRWESEAMHPLSV

>contig20838 Frame-0R|Blast-phosphoinositol transporter [Phytophthora infestans T30-4](gb|EEY68259.1|) 5e-61

MAINGQSLLLNAPTAYILKNWMDAITQAIKQLKRNSLPPAASSERSPVALPCAVQEASLK

IYNRSITS

>contig21213 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68778.1|) 2e-57

MGLLMLLLAFPFELLGTKFLWWTWHDTDPLLAVRLIGVPCHALFYTYFFAIAFLGVHHIL

RSTLILGEYYEEVHWKSEWSYILLMPLLTTLFAMGFLILCYHVTVHLIGVEAQV

>contig21266 Frame-1F

MFACGMYPRDTAFLQNVLVEVEYQVTRLRKYTSIAIWGGNNENENIMDQFAEVPSFPPGP

HFNRDVAVADFTKLFVDLIYPAIVAVDFSRPFIDTSPSNGLYSADPYVKRWGPSNGVAFG

DVHFYDYKNDCQDHRIYPSARFISEFGFQSWPMATSFHGVTSKEDWNSFESFWTFLKFRE

RHENGTTQMLTQMKRRFNLPFPFSHEIWLEDGFGAIGDGFNQSTIIKRIDSFLYLTQIQQ

SLCYRTAMQTWRRGKNIELGMTMGILYWQLNDIWQGSSWSSIEYSGRWKSLHYVAKREFA

PFIITILEHAFYNFIEVYGVSDLNEDLHVDIVYEIRRTISGTFVKSYNRQAIAIAALESR

LIEKLDVDAFLDYKTTSCDRKSCFMYVHCAATSSATGLKAAFCEDRHHFFAPYKDLNLGL

GNVAISSVVRVEANNSFSFSVKLMATNFVALFVEVDAPNILGYWSSNSFLMVGNATKQLR

FTLAASDDSGKIKADVFWRLVTVNWLQKSYETSIDDVAML

>contig23668 Frame-1F|Blast-RCC1 and BTB domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY57867.1|) 2e-27

MLNNSTRSDVTFVVEGRPLFAHSCVLVARCEPLEKMLDGRMKECFQSEIVISEYT

>contig23714 Frame-0R

MLSAIKTGVQFMLLTFSKSLVIASHLFRVVSASMRAVLSPFFSFFTFFKQEESHLSSAVF

ARKSCQLVGSMIVLNVFFLIAFFKWSTSLLYYVYSEGTSGDANDSTQKSHHFFLYRQ

>contig25451 Frame-1F|Blast-aspartyl aminopeptidase, putative [Phytophthora infestans T30-4](gb|EEY63649.1|) 0.0

MTKLTLCPRTPQTVGAFLNFINKSPSPFHAVYESIQSLTAAGFKRLCEEDSWENVVRPNG

KYYVTRNQSALVAFAVGGKYQCGNGFHVIGAHTDSPCLKVKPISNIESQGWLQVGVETYG

GGLFHTWFDRDLGLAGRVIVRTSDSSFQSRLLLVNRPIMRIPTLAIHLDRQLSQSFSFNK

ETHLRPIIATAARAELEMTTNGKDQPKSKHASVLLQLIAKELNVEIDQICDFELCLFDTQ

GANVGGVLEEFIFSPRLDNLCCSWLATQSLIKSLDNLEDEENVRVAALFDNEEVGSESRM

GAGSNFLQSVAERVSQGKLCSVAAKKSFIVSADMAHGVHPNYSDKHEKNHRPVLHSGPVI

KYNANERYATSGISSFLMKELARRHNVDIQEFVVRQDTGCGSTIGPILSTRTGIRTVDVG

IAQLSMHSIREMCGTEDLVKTLDWFMAFYSDFTSLDKCLKTD

>contig26924 Frame-0F

MKCVSCTASVGLVSILLGTFVQPSTSVETPAVSCLSGELKNLARLFNKDRFHEMFPEALE

LYSFDGLISAANKFSAFANSGNNSTNTLELAAFLAQIAHETDSLKAAEEYARDDFSVWQY

CDNTTVPCAPGRRYHGRGAIQISWNFNYNAAGKALGLDLLNNPDIVITNSTVAWMTALWY

WMTPQKNGCVIHDVVTGVDGFALSTNIINGEFECGPEAINKENDLNRVVLFNGMCQELGV

EALGKISCNA

>contig26991 Frame-0F

MSNKGVQKNRHKRKSLAEDYGGSIGEDLLEYMESEETPGGVQQSADSVGASSNLSRRIQN

RLQKLNDVARSTGGDGETSGYYDFSTLKLKPDHEARPVWVCPNGRIFLEAFSPIYKQAYD

FLVAISEPVSRPEFLHEYKLTPYSLYAAVSVAIETESILKVLERLSKNRLPEGIVAFIKD

CTLSYGKAKLVLHHNEFYVESLYPEVLRKLLEHEHIRAARVKEAAETVAAAAPVASVLHG

GAHAEDADEFIQKEVSAEDQANLQYQKLLNEDYNVADENHSGKLSNDQQKTVHTVSFKIR

KSMVEQVKRACLDLDYPLMEEYDFRNDKTIPDLEMDLKPTTRIREYQEKSLSKMFGNGRA

RSGIIVLPCGAGKTLTGVTAASTIKKSCLCLCTSAVSVEQWTAQFKMWTNIPEKKIARFT

SVAKDFIDPESGVIVTTYTMVAFGGRRARASEEVMQLIQGREWGCILLDEVHVVPAKMFR

KVIGSIACHCKLGLTATLVREDDLIGDLNFLIGPKLYEANWMDLTQSGFLANVSCVEVWC

PMSGEFYREYLRESKSARKRALLYVANPNKFTAAEFLIQYHEERGDKILLFSDDVFALRL

YATKLNKGYIYGGTGERERMRLLQSFRSSPLVNVICISKVGDTSIDLPEANVIIQVSSHF

GSRRQEAQRLGRILRPKANATGGFNAFFYTLISTDTHEMFYSNKRQQYLVDQGYTFKVVT

DLFEPGSFQGVFTRKEDQRALLNEVLSADVESAAKDENAAIRDDEDLSRLELSGHGRKKK

KLASLGALSGADGTAYMEYSAGHGAKQRHNLFRDRYR

>contig27509 Frame-1F|Blast-SNARE associated Golgi protein, putative [Phytophthora infestans T30-4](gb|EEY63582.1|) 1e-113

MYPMVQAQILVACCATTGASLCFMLSYFLGRGVFSNLLAGMIRRFKEKIAQNQSNLFYYL

LFLRITPLLPNWFVNIACPLVGVPFKYFFLATLLGLLPANFIHISTGATLNSAVEASSGS

NVVNFGVLFLLQFVALLPTLFKSKIAKYEKEAFEATKAE

>contig28764 Frame-2R

MLDPDGPLGIHSYYPDDDVTQNTGLGIDETTIRREAFYLSCGLFNCKRTKSFEHSRAELV

YTSCKRIQQLRVFVLNDYVRETLLFVLQQRDVMVLLETVVPLSQFVRATLHHANLNAETP

NATQVKLLAENGVVNFDFQLSEIHPCLEWIVECMIKLIPEEKAIRSTICCVLLVELCGIV

CEAITFHDRRPMVELVSLVELALTYLQTVYLALSKRTTAKMDTLFVANIESPSSMLRAHR

FCPSAFRSIKIDDQLDHLVIQQTDTYNISLARATTDLLAAIVCVAQHCKTSSYERLKNAF

IVS

>contig29684 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57031.1|) 9e-16

MMHSNNELIIATRDGRVLFYRLNPNHTDRD

>contig29918 Frame-2F|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY56654.1|) 1e-150

MYGLSAFKGLLMSRRKPSLDLRHHRLKIISPHSIRIRNLEDRLARSMTSANFSFCGVPLC

VKNRHAAARNFQGLSASGCSHILSPLALSTKKELKPEKAGVKLLVGAGVCLAYELALGHY

LEFIKIMKQTKPQYSYVHLTKEIMHAKGIVGIWDGFFPWGAIQGLAKGSVFAWGHSVART

ALAPLVKDGKISSGMSEVVAGGIGGGFQGFVLSPTLLLKTRVMTDPIFREHMKPLETMTR

SMHIGVRVIQNEGVAALMKGSGMFSLKRVADWSSRFFFSVQAENILYKRNNPDRILTTSQ

QINSSLLGGVLSAALTLPMDVLVAQIQQASKAGVKVSVLELLRQQYQAGGLNQMFSFGTT

GFVARFVHASFTTMIMKTATSVVYEMVEGRK

>contig30941 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64992.1|) 4e-66

MTGKMVDSQHVRSTLERVRCNAHPLYLNGVSCVGTGVFPDAAMSLNHSCIPNVAPSFNPR

TRTLAFHAISEIPRGYTVESAYIDLLQSKKRRQALLHSGFGFDCICQRCYNEVEIGAETS

EDDQERNVMEELLQFINFNRSDIRQQFDSWRQKHTAIFEHDVEAQFALFTVEMQLACAQG

QWVDVIKVADKLLEIWKQCGLPDFYHTTETLHLQICKAAKQAAMLEKSMSSAEKVLTIRR

ICGYLHSELSIKGLHCA

>contig31317 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59513.1|) 6e-28

MAECVEGVHRFTPKERVQLLERSGVSEGMILRFVRETNIINSSRKQTLLEVIDANKEA

>contig32561 Frame-0F

MTVKPTTNGKFMVTPQLEKGKVCLSRGDDQLLHFQWVDRQTGASPEDFIIFPDDAHFAKV

ETGRSDDRVYILQYKNSSRRFFFWMQNKDATRDQELVKKVNDCMNNAQAVASSDGGRVPG

NNVQLDHNAIMQMLGAMGAGEGRTATGGSGQAVQMSELQNILQNMGLPAGAQSAVSSPAT

SAVSSSQASHNGGGSSAAATTASTQHEHDVASMEVDEMDEDELLRLAIEESMRDGGSTNA

SRDNAAAGDSNNSNRPADHGGNDSSGNGGGDMDTPS

>contig34642 Frame-1F

MKGEALEDEIRGKDGDDDKKDDSNEKENKPETQLDLPQDMNANDGGDDNGDDQDDEKLEE

VNEDFEDQYEDHHDINPAEQEEGQKQDELEEEHGDELPEDMQLDNDDMDPEGINSDGEMD

KLDDFENDTVEDEETAGAEEDDDAVDEIEQQDNSVQLGGGGLEDEQEANEEKEEEDAEMA

ENLENIQEEQAARSIAGTQSKDGQDEFIADEQEADDQEMEDVNSTEQNEEQANDDNSDHR

AQKQSNNDNQDTKQQWKPQSEVDSNLDQERPHEKRRE

>contig35818 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70087.1|) 4e-11

MKSKMSARVHKYCNSFSGTLYPQSLLDRTKHGYNLRDIVPCLRQFGELECLEAFLVVSAM

RNKQQVVDSFTATQLVEASSNSIAAFAASKGSEKEKPRMLAQLNAFRDELAALLRIK

>contig36095 Frame-1F

MCYKYSLYSTLLTCQCGVPPNSVAVVCPQPPRVVWTSSWSLTQSVMGYTSVGEAFMWYNS

R

>contig36587 Frame-2F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72305.1|) 1e-12 NOT\_ORF

MSE\*ILKRQVINRFVRHALQSAVDKQKENADKHGRKYE

>contig36851 Frame-0F

MSLKVCLVGSGNWGSAIARIIGENTQKLGAFERDINMWVFEEIINGRKLTEIINSEHESV

KYLPGYKLPENIIAVPDLVEAVNGADILIFCVPHQFLGRMLVSIKEHGLKEGAIAVSLIK

GIDFDKNGVVLVSDLIRKGLGIDCSVLMGANVANEVAAGDFCESTLGCFDLRHGALLREL

FNAPKFRVDVALDPHGVEMCGALKNVVALGAGFCDGLHYGGNTKAAIIRIGLSEMKKFCF

KFFNGVKEDTFFESCGIADLITTCFGGRNRKCAEAFVTQKATWEELEKTMLNGQMLQGTL

TCKEVYTILKEHNAIDQFPLFSAIYRIAFEGADPASVTQLE

>contig37005 Frame-0R

MPIKTRKERCRYFLARVGHTREVLAHSQFRRDFH

>contig39072 Frame-1F|Blast-bifunctional aspartokinase/homoserine dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY60186.1|) 0.0

MELRTLERKSFILRPWPQRLLRLFPFTFGTHSYQKHPGTKIYDRKKVELKRNMSNGSPTA

RNIVSGFSTVDDLALFNIEGTSMVGVHGTSSRLFGALDRVKVNVVLIAQASSEHSICFAV

PIHCAEVAKDVINETFFKEIHVGHIDKTEYIAPISIIAAVGDQMNQTPGVCARFFSALGR

AKINVLAISQGSSERNISAVVHYKDSATALRAVHSSFFLSDQTLSIGVVGLDFEDLSSTS

IGVALLKQYHQQRAYLKQRFNVDIRVRAIGTHMTSQMLLDEDGDITEEALTARKHEFVPF

ERHRFLDHVCADHLPTLAHCRCIE

>contig39186 Frame-2R

MPRIAILLLGACVRSFLYAVPTLHSTLSARPELVTPVSSFYRLQEGAFLYRSTGSPYTGD

VYHQPPLLFALLYLVLQVASPNLQYILSCAVFIAVDLLLALGFARLCERNLKLEEGRRSM

IGGREIWLTHVPVSPLFQPEHLPSTVTFIALMNPYSLASSVAMSTVGFTHLAVLYSLVFA

SEGAVAASMMCVAIATYLSVYPFFLMVPIVLMLHSVKAETILSIGCKCLLICGIWLGVLL

YLSWSLLGNWAFLEETYVWVAMYSDLTPNVGIFWYFFMEVFDRFIPYFLFLLHLHPVIYI

APIYLRLAHRPQAYACALIGIFSLFQAYPSFGDFGFFLSMLALHPKTIMTIENRFIYVLG

LGAATCMLPIMWFLWLFSASGNANFFYNQTLVYQIFNSQLITAFVGATMKRDKDVDTFRA

SQLKKTSDTQ

>contig40061 Frame-1R

MKTLHTIQSGQGACALTAEEEDEMPLLFMDALPLDFRINSHLAAIATFMADSDDDKEKAH

RPNPLLESMKTKRRQTPYSKTVSSNIKRKARNETTSSDTKELQLFLSMFHIK

>contig40115 Frame-0R

MQALQGNCVGKNRPSFIEKEQRAQFDGWEALHGMSTREAQYKNRPHHLNNCRFSATFVHG

IG

>contig40731 Frame-1F

MIESVSVTAQLQGVSPSTAYVAMLPYAYTTNDVAQLFAPFGKLARVIVLRDKQTRRSRGV

AFVQFARAEDCAEAVTRMDKLLLEGLTLSVSLSRDNGRSREFARKRKFTTVQRCFECGES

NHVSYECPRNVLGPRERPVTAGCKSSRKKKKKKFDFHERTHFFNDEGIVNLLAPPEEGDV

SITLLAYSSKTRNPAGVHSSWMKPKLTTATALTHRRPQRKRASYFSDEDASDGE

>contig40818 Frame-0F

MPFPTTSQKLKVCKYVDTTTCLASDSSVGKKHRNCQQLQNVPANLARPETLPSSSLNLCT

LLFCVASYFTPVATLTTL

>contig43028 Frame-2R

MRQDNIGHQLVNITGYLDSDFALIKRTESQSLVAGSLLMECR

>contig43587 Frame-1F

MAASKITLRINTLFSMLVASRVVVASCRCTLRTQAAEFVVVRSLF

>contig43851 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68604.1|) 4e-61

MSNVAVPGQHLATVDGKLQAGIGTYVQEGSIFASTYGKWLIADDFVTVTRANKTVASTQV

LHVGDVVVCRVTKITSRQVMVDILCVSATVLKDAFPGTIRQEDVRNNDIDKLLMEEVFSP

GMLVKAEVLSFGDTRSYFLSTAKPGLGVVRQNLEKN

>contig44173 Frame-2F|Blast-anoctamin-like protein [Phytophthora infestans T30-4](gb|EEY57355.1|) 0.0

MVGIVVLALFGLFVLKHWINDKDNLEKNHISIQYQPSLTLSVTILNAVQILVLNTVYRNV

ARKLNDFENHRTDAEYENHLVIKVFLFQFCNSFASFFYIAFVKRLAEGTCLHEDDCMQEL

RDQLLTLFIIRIVVGNVTEVAVPYLKYRYQLYSERKAVITEVKVGHNYIEEQAKLVPYET

NEAFEDYNEMVIQYGFINLFVVAFPLTPLLALANNMLEVHVDAVKLCFVHRRPFPHPAKD

IGVWFYILRFMTYIALGTNSALILWTSDLFEDQSGMTKALGFVVACQVCLVLALLVERAV

PDTPHEIELLQKRFEHIVNIVFKGMFGGDDSDFHEVAESLDLRIYSNQEWDGMKQRNA

>contig44317 Frame-1R

MVSVPERSKGVDSSSTVFALVGSNPTADTDTHGHWSGARCHGQIRSKRSGKP

>contig45400 Frame-1F

MNEKQRFEVLVFAAVVLASHVDGLGGVAFPTFLGRLLYELGMKSQDVKIDFPVGFETRGN

WVVPFLSPPNVKWPAWLLNDELKLDNFVQIANSETIDFRIDSGLISGECNDEEQPLSLET

IRKILSRVPAESKVHLVLTRGLQKEYFTREETHAAFVREHNL

>contig47231 Frame-0F

MKSRARHLDLLSVTPMDEIEKTVGLASATKGTRKSKRGKLRSKSHLEINKLSKSHPQVHI

GSWVLQQLPILLNGLIRYTSVYIYLLQMSLASG

>contig47284 Frame-1R

MRLIVYKEKHELWCALNDRFHDFRVMVRRLVVRYDARHVLPHNRLDVLRHITFDHLVSLS

HAISGSRSEAAACHKSLFGMLITIRRFG

>contig47415 Frame-2F|Blast-conserved unknown protein [Ectocarpus siliculosus](emb|CBJ49206.1|) 1e-74

MMQWDMIQEGDRLLLGVSGGKDSLSLLHVLLSFQKRAPVRFEVACATVDPQTPSFDPSPL

KDYMRSLKVNYHYLTEDIIERAASEMNGDSLCSYCARMKRGVLYTCCRQFGYNKLVLAQH

LDDLAESFFMSAMHNGQLRTMKAKYWNDQHDVQVLRPLVYVREIELKKFAYDSRLPVINE

NCPACFEEPKERSVGQ

>contig47950 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55310.1|) 1e-43

MSLSKRDREWATSASDGDSAVSAADHDSKRPRLSSSSSPPANSTTYTSQFPASTTEQSSQ

AHSMVALDAIRVQLQNTSDPHLQARLLLQYSSYAASPSVESTAAIDFLFSFLLQNQTQSA

TTQHEGTMTQNTESSGAIVVSAILRGLRELLGVKAEVVEPMIQVDAMGEQLMECMSISDD

FKLRRNMLSIVVDCL

>contig49655 Frame-1R

MPEKQPSKRLTAILLPYQREALAWMVKQEASDYKGGILADEMGMGKTVQAISLLLENKQK

SKLIGNKSATSQKMQTVGGTLVVCPLVAVMQWKSEIERFVEPGHLSIYIHHGVKRFDLIK

KIASHDVV

>contig49721 Frame-2F

MSYGFLLKEFGSTFCTSAAVTI

>contig50648 Frame-2F

MYTPCKALASSDYLRAYVRRLRLGTVAVLRDLTFRLLPLKSGITSMRVKTVSPDKLSCFE

IQCGPLWPVAVATFSSSIIFIIAAKPGVFVKK

>contig50961 Frame-0R

MSSIERETTNKHRVRDAISWHAYTSGVKAGAVTAVIAAAAVFAANKYWPAFRNRLNVSGK

TALIVSPFLGAFTIVAENQLMHGARNPDMYMASLEGSYVKPAHEKSQLKLWQKSANMLYD

HPYRTLIAVGVPLVGGIYSYQHLNKGISASQQIMHTRIYGQAAVVVLLLSSMAFHDYMGK

RGRFTVEEQED

>contig52772 Frame-2R

MSCGRSTLSKIIAMDWKLLRGSHEGGEAPRNSNMKRRRRPLFPAFEADLLN

>contig53182 Frame-1R

MKVLHLLLCTALAISRVSGATIRATASSPAAASPTTLTETSTAPLTATSTETVTT

>contig53216 Frame-2F

MNYIFFNLLKHFLYTQRFAIDFYCANINCSAAASRTQLYRWHFRYVLLNTLELYATSLQP

YSSTLVIILRITFR

>contig53263 Frame-1R|Blast-guanine nucleotide-binding protein-like 3 [Phytophthora infestans T30-4](gb|EEY60643.1|) 6e-49

MGRKQQAAPPRNRCAKRQSIAAQALRGAKSQIGQQNRTVPKNRIGKEQNSQKLQQQREQL

RRHHIGRNRGLVSTLSLTELAGRATQSAQVFNQNQMHQTPHQTQDELVINDASRRAYMKE

LRKVIDKADVILEVLDAR

>contig53832 Frame-2R

MDETSPELIAERYNEVYRRERAHVLFEGRKRRLTGAAWSLMKCVNTGQPFYY

>contig53959 Frame-0F|Blast-calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type, putative [Phytophthora infestans T30-4](gb|EEY62297.1|) 4e-21

MVLRDRGRQVEIPSEELVVGDIVLLATGDLVPADMRLIQSSELQVNEMILTGESNDVLKK

VDIETKPTDKLT

>contig54482 Frame-2R

MLVGDSRCCGKTGQSCQKGCLQSCHSSTERDLIFVVNLKVTDLPLHANHWNVQYSVPFIL

SHLADLSFKHDSD

>contig58033 Frame-0F

MQRFGRIAATTSRVLEPTFLCPTWV

>contig58257 Frame-0R

MFMCFKVSLLAFVANVYRIAWSNGFSALEFAVKSEHTKLREQCLSKGANLNAPTLNGKIS

LHLAATLSNSETIL

>contig58969-1 Frame-2R1

MHAQVHHSLFCLQRPSPDTSFFSLFELHVYNSELLPCTQQHMLQRSPQCVPQQKPRRVLG

SL

>contig58983 Frame-1F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60832.1|) 3e-06 NOT\_ORF

MPK\*MHIGTQYNPATYML\*VIEAGIGSCVKD\*FVEYKKSTLSQSTRERSCFASPDGNVSH

ESLALVCRSAVLNCRRPPP

>contig04035 Frame-1F

MSSLNNGNTNYLDLRGSKDRSWQAHFFFKFPEKSAKSSILAACRIQKVMKFLVVHFKLIL

>contig06576 Frame-0F

MSCVVDFASTKNSKTTALCARNYVEFSGTQQSIKSFIVQRDKLDIKSCTKEAFGSSNLLQ

KKAKRGQQSISSFLTQTGTKRKSHMAGEVIRSKIGSASHRTFNAVHCVDPVASKKSVEEW

GLVLSGRPPPTPICFCGQPSIIRSVIKTGENRGRKFYVCTKPAGEKGNPNARCDFFKWAK

SKSHKKMKET

>contig14306 Frame-2F

MQVTVQIVHNSNGWGGLYLCISTA

>contig16825 Frame-0R

MGQFMDFFRLNSMFYSHTGFYYATWMTIVTTFVYMYCKVYIALSGVQTQIVYSINSTEII

MENSEAYGFDARVFEDMDSVYNTQYYIQAGLFLSLPLICVYFAEMGLRRGLIQFLEMVFT

LGPAFFIFQLGTTMHFFDNNLLHGEAQYKATGRGFKITRETFVLLYKAYAPSHYRKAMEL

IGLCLVYLTFGEFAICDISVAGDENSFAFDYCDTSQSFGVQTFAIWVIAVVWLVAPYIFN

TDGLDWEKTKADVTTWAKWMYATEDYQDKDEVMIGGWIGWWKGELSLYHNTRPIARVTVI

LRECRHFVLMWYVVALEWEILTVGIVFASAVMTILALGLLGAMGGAFRSVRSSLRAIMYF

TVLVFAVIAFFIVTMAVFDLNLRRTLSLFFGYMAALYGLNEASRMYSFATSSIATVEMFQ

QLAFFFDFVFSIAMILPLLVMSAIPFLNIVQTRMMYNKGFSEVVSASSQYAFSLAAFMGM

LGGIGCGWLFHLFTMLESTAGFLSYVTTYDLLDGNVGDGMVTYAFYYACIVGSLVAGGLN

FFIGRRLTIVVGGLLTVLGMLGVSLVQTNGEGLLVPGICLLGSSVGVLLPTLAVYIYEIS

TRDMRGKALLLLGCGFLLGILFASWFSSSSDEVGWVWQVFIATIILSFMTPAVYIFPESP

YWVYMRKGLESCERCLAILRRKESVTEELRMIRDEEASSDDKVGGALVLKFAVGLMLMLV

SGLFVGCVNMYLSNTFRSIEDATYTFVNCIGMQLLGAFFSFFFMDRIDHKRILCCTLVPM

ATLVFVLGWNDMSTFVTGNEEFVMLQIVGLLLYFFAGLGITSVPWVSCVGLFKTKERAVY

VTGYFMLFFVMPVCATYIRSNAAMSGRPYMYLFALTGCSIAAMGLLATMSTRKNGMVCTK

GEMEEERARLRRLRASRRSARTPGTGRSRNFSRSRVKSHSNYQMLESPAGSAP

>contig17084 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66149.1|) 9e-40

MDIGIEGMRVGSKRTINIPSHLGYGCEGMPPTIPGNADLVFEIEIVNA

>contig18931 Frame-0F

MMTLLFSALVQFRIKIQVFT

>contig20882 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68023.1|) 0.0

MNLIANDSAIKMVLRLLFPPDNEVHESIGTEQSLTFPHQFYIPCRLHCLSTLQVLSKLEN

FGLAVLDFELCDILIELVHICPGVGLDALGIIRNICANGAAAKCAFEILQSGVYLEFIGW

MLLVEETFVDDKFESTDHKFESTEQLRLPSAMILYEMVKEKAPLKAESRRALCRFFPPAI

IRTIASCPESIVEYLMADHVTPELVWNADFRNFQRDEILKFLQIYFSSISVADTEDKNYT

SVVETFRIDYTDIYSAPVEGNIYLSLYMKEPTFNLHDPLYFMTCLWSKFEELYKELIYMT

SARHERIDRADDELIQRDINLIDLVGSSLVCLLQYETSLIESVVELHIPTKCCAILNDTL

RSQACEPCVVNAVRLLRVCVMSPMCIKSMQPICSTALSCLMSLVNPTRGGPLHFESAFVL

DIMRRIVKDYPEHGDHDTSSGIVYLATRLNLVGFLLNILENPDSLGRVKANFIVRAEAIE

ILIMVEKDRIQGSSAHQILKKHKKWQKIYRHEATDDVRSMLNEDPFLKLLYPEADRVMRA

LV

>contig21214 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68778.1|) 2e-16

MLISAILQVLIVELIYCNSDRWHAQALVMIVPQHMPLYTILLQAQLYYM

>contig21698 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63515.1|) 2e-69

MLSYMAAALGILSPSESSPPSHTSPTNHKNGFKRMSLRLRSRGWLDRENELFILIPRNAT

ATCNIIFFPGDVQDFHTNMATGPFADYSDYAYESVAELLSKKFGNTCNVWIVRPHRFKHG

AYSSFDNFLTTNEYGAATKYDATGSSTKHLASLMQNTQILLRRQGVNVSTVLPIRLLGFS

KGGIVLNQLVTELVRYSFNKKRSNSGKVRHGSVFASTRQFFAAIQSIHWLDPGNGSLKGT

MPLEEAALAVLARYKHLQLFVHVTPYQYNSRDRAWIKTEVENFIKKMKLRGADSKLIVYN

EGGKGSLASHFHILNDFEVDRPSKLNGDRLLRPRSPERINFAFEPKTLIIR

>contig22048 Frame-2R|Blast-STIP-like protein [Phytophthora infestans T30-4](gb|EEY69226.1|) 1e-164 NOT\_ORF

MLAKMGFKGRLGKKEDGVSAVVEVKQRPAQMGMGFGDFVEASNLRQNRKLQRELNGESAN

DQNAASQDEYFVEDDTLWRKRKTPAISKKHKRAADLAQAVETMITHQKANVVVDMRGPSV

RVLTNVTAASDVNTWNGKVLKPKLGD\*LIYNVRMVVNLAEGKICDLSQKIDIHRERLAGL

KKEAKMMKTQLDMNDVHLQHMQEMVKQIKALDQLREEAT\*SQSVGSLMSLLRCVRRSFPL

EFDAHKLQQLVPSICMPILQDVLKKCDLLDEASSGKVVIQLKLIHEFLNELPSSRGAKDA

TKTGNVLPIIREKTMAEGSELYNFILEETLWPAMMQCINVNWHAKSDPASCIKMFLQFRP

HLSTEFEDAFLSQLVLLRLKKECQRWNPQSDAIPIHEWLLPWLPFLDAAMASLYPDIRLV

LA

>contig22242 Frame-2F

MASCQFNVLLTTYEYIMKDKHVLRKYDWQYIIVDEGHRMKNAQSKFAMTLGSMYTSRNRL

LLTGTPLQNSLPELWALLNFLLPTIFESVDTFEQWFSKPFAQFSGNGESNELSDEERMLV

INRLHQVLRPFLLRRVKASVLDQLPDKVEKVLKCELSGWQKIMYRRIQEGGALLMETTDD

SGKKKGKAKYTSKGLSNVLMQLRKVCNHPYLFQTNGYQIDFDIVRSSGKFELLDRMLPKL

KAAGHRILMFSQMTQLMHVLEDYFSYRGFRYLRLDGSTNADEREQRMFMFNAPDSPFFIF

LLSTRAGGLGLNLATADTVIIFDSDWNPAMDAQAQDRAHRIGQKNEVRVFRLVTNSPVEE

KILARATDKMNMNNLVVEAGKFNNKSKEAERRAMLESLIKMEQEEAAHAAQGDDELLNVL

HDDEINEMMALTDEELVLYHSLDAERKGREAKEWEEYCKQLKIPHIPRTRLMSEKDAPAW

LREANDVMENDIASGKHDKDAWNVEMEAVSGKPRKRKEMSYRDQFTDAEFVKMCEDGIDE

KAMKAVTTNLKEINQGKRKRHDKEELVDPNSVADEDDSNDDDAGKRERKMLCYYYKKVYD

AVVKLKDPTGRLRSDLYMEKPSAVDYPDYYTIVLQPMDLLTIKTRLDKYFYGSHDQFETD

FTLMVGNAQLYNHPESLVVLDALEIDRCVKTKMKPLHIKTMEQIAAAYEKAKKDHKRRSK

NRKDKKRRHH

>contig22718 Frame-1R

MCITIILTIMVVMCWMQLPHDRSPCMEQ

>contig23177 Frame-1F

MADELERKLAQRLAHEKDFPSTGLKKLFFLDETEASVLFRNGVQDEDVANLIKERLNFWV

NVLEMNHRYTLSKDKNFIMKAIRSAYPDLNSLLEALKRLPAGNVL

>contig23524 Frame-2R

MLEYERKYPALHDELSSAYRSFEKTRNRHEKLQIQHENLVRDHKSLVFRNSLKGWSDPSS

EETSEDK

>contig23713 Frame-2R

MMFDTGETRFTQDEVTTTEFESPIRTQRSYLLMERRDMEPSDRHLAEMFLHTLVSSLKAL

CAVRLECLSVTYRFMWHDGSWLQSDVEYPSYATSTEVDNTTFLPKNTSNSRQTNRQKSQS

SSSKRRPRAVDDSALSSRNRGDLEATTPKREGRLTTRSFYYPNKSPTRLRSTLSSGDFSK

LEFASSGLGTNLYDDPILEGQPAPSSPMYNDHERNVSDLYSTASALPHKSFSLELDKSGL

DRCAASTLDTVNKSLLAALIAQHQETEQVFCESHKRLLVLLEKFVRLEYQDHDWALRERA

LTIERELQQEYHEIQAEVHDIQWLQH

>contig26888 Frame-1F|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY57315.1|) 0.0

MAAMTQLRKSRECIRIVLRSGARSTKSPTMLCLDNCACIEGHTTPTFHITEPADEFQPLI

GDIYPVPGEIVRLRVDRAAYIIFYKCDDSGEEQNLKNEMLVTSSSSEDDVDANEWSEDGS

GRIAPPRSYASLGAAGHKVQTDNCFTRDYNHPTRSLGRGLFRASTSVGSAFLKGAAGLVN

KTYQGGANGGVFGFAKGLGMGMLGLGTHTVKGAFRGVGQVTHLVGEMVLGTAPHFSIDGI

LVLTNYRIIWQALSTVDAMEIPLASILSAESFTTAPHVANIEGKHLLRASLAFQNEATCS

EFLGCIWELYSSGGSPSHFLFANLHYQALQQKEATNDMDNIGLRTPSDLFYDAEEDYRRL

KLLDEDCWMRLYDNSTYTMFPSYPDTFVIPSVLDDEDLRELSIYRSASRIPAVVWRHPHT

GALVCRCAQPCTGLSGFVVNADQKLVAALQNATSASGDARFHFFDARSQMAAAANSAQGK

GTEDPRNYPNSELHFCDIANIHAVRSSYASLAAVCQPGQERESSGWLFQLRSTFWFLHLS

SILLTSQKICRYLNQGHSVMIHCSDGWDRTPQLTGMVQLLLDPHYRTIRGLLNLIEKEWC

SFGHLFRYRYGHGEGPGQQELEEQSPVFVQWLDALWQIWRQQPWAFEFNEAFLSALYESI

FSGLHGTFLYNSERQRKQEEAKAPTRSLWFALLEQTETYVNVEYDSAKNFNSIGLVLPFS

SEENDLVMWATHLVYADPVCRKYE

>contig28947 Frame-2F|Blast-hypothetical protein PITG\_01294 [Phytophthora infestans T30-4](gb|EEY61051.1|) 7e-10

MMCSRFLSAATKNALTPTSLYSLFSASPNISVAVVHGAPSQIDWLAAETTPTVMELLNRN

ARRPKKANHGKRPCSHFRRRQKRLGAKKA

>contig29012 Frame-2R

MTSGRFANVFLSLYLGYSTMTIYSRHVDEIDVRFDYA

>contig30872 Frame-0R

MDSPSRERKDRISGGRDSLKLGLGSSEVNLWSTRQFKRFNCSSIESQSYIIVNTTFTYSA

LAKKFCSSSFLISVMIPAVPGVSESLLHLLFLVGAGFEPVTFESTCRYLTTAPGLVLFYL

>contig31310 Frame-1F

MGGMGRFTNHLSDANCRIQDLNEESGPEFAIVASRDIEPGKKTAVDGPDKRFYCYRGSNK

CRDKGLCDDPLISDVVTSRLRYDNKGKPAAGIGV

>contig31549 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62475.1|) 1e-130

MSPAELLKERGNDAFKSAAFEKAIELYGEAIEACNDKPGSALALSCYNNRAACNQQLSNF

SAVIRDCSHVLEYEEKNQKALLRRGLAYEGLERYRLALQDIRALLAINPSIDIANKAQHR

LSNYVRQLKQNN

>contig32566 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67719.1|) 3e-45

MDHATPTANPYLIMGYSVEFPQGKRPFPAQFAVMNKVLTALKTEQHALLESPTGSGKTLA

LLCSTLTFQKQYFKDQMAAQMLRQQDVKWKEQEAKKQALKAQVKALETRMQLLEAQQQLE

SARKLRQIDETPP

>contig32957 Frame-2F

MWDYLRRCGASGFFLPLSGGADSSSVACIVGVMCHLAVEESNKGDEQVIKDVQRIMGTSG

QEYQPLTPADLAGHVLHTTYMGTKNSSSATKKRAEALASEIGCYHLSMGMDLMVDAVVKT

FSLLTGKMPLYLSKGGTIQEDLALQNIQARLRMVMAYLLAQLLPWVRSKTGFLLVLSSGN

VDEALRGYMTKYDCSSGDLNPIGAVSKGDLRKLLCWAAVKYNYPTLQTIEAAPPTAELRP

TDETLGEDADHCQLDEEDMGMTYDELGFFGRLRKIDRCGPYWMFRKLINLWVHVTPAEVA

TKVKRFFFHYSVNRHKMTTLTPSYHAESYSPDDNRFDLRPFLYNSRWTRQFASIDTLAAK

MEENE

>contig35668 Frame-1F|Blast-serine/threonine protein phosphatase [Phytophthora infestans]gb|EEY61167.1| serine/threonine-protein phosphatase PP2A [Phytophthora infestans T30-4](gb|AAN31475.1|) 0.0

MDSRGEMKALDAQIDRLRRAENLTETEIYELCQKAKEILAGESNVQPVRCPVTVCGDIHG

QFYDLLELFRIGGACPDTNYLFMGDYVDRGYYSLESVALLVALKVRHRERITILRGNHES

RQITQVYGFYDECLRKYGNANVWKYFTDLFDHLPMTALIENRVFCMHGGLSPSIDTLDHA

RALDRVQEVPHEGPMCDLVWSDPDDRCGWGISPRGAGYTFGQDITEQFKRSNGLTFIARA

HQLVMEGYQWTHNRGVVTIFSAPNYCYRCGNQAALMEIDEVMADRSGDKVYETCKFIQFD

PAPRDSNFNEKKRTPDYFL

>contig36580 Frame-1F

MCFYCLKAGHQMKQCWYLKADIESETTHDVHKKFCCAVTVDRTPFMVRCLEGYIEGVNRE

RANRRPSSSTTSTSRNHGDYSVSKSVGRDYRPKTDGYVISLPRESTFGLRDQPTSSATST

ATDYRKRSRSVFQPAEGRVLSRDPRLNRSNSVFGSTGVLEEFSPRKRVRSPSFERQLQIH

YS

>contig39181 Frame-2R

MVESSTHTEYLCASLLPLGTGRKVARSSCSIASASMLSGGNSANLIDKVADELASHFKLK

TLGNVGFILGA

>contig40112 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59620.1|) 5e-41

MPLLNQRELQRRRQQLNYSDPRPIESPVHAASTFSRSRANTHKRASIGNHGSSMKGRPSL

VARRGQLNSSRSPCFTDNMTSPRSVWEDNLLNGRSDSTASPRHKVTLNSRLVSLSHTALP

SDRQYIHYPAPQTKSQFNSSHKRRSPFSYPHEEVTDCASNATKRPRLAYRELPKWRQELS

SQDRAKTRERIMLSLHMHSQGNFEKLVLLLSSMEEELLHIKSTSNKVYEYQATELGNPLS

TPRLSVK

>contig40668 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67169.1|) 3e-07

MTLMIWTLINLTSVLLSNIASMLIAYKFYRDWDFRVSSVR

>contig40736 Frame-2F

MRGVHRNSAMLCKISLLTTILLLNTLTTAVTSTDDQSKKSVDVEVTEVEPNGNDKPVPEF

VATNEWQDLLPGQGVPRGLHMRLNLETGKREAKLVDRSDTDAEEFTRLLVTGSDSQETTV

TVLTDYAGDAATDFENGETLSVTDDRLGNYALKEDAEHDEAPRAEPKWNHEKIYEVLQAL

PEPPEVDGMNIHEAHEKLSPAEFRRQVVYLWKKRQAELKEALESLQDDAKYLGKLLKQFK

EAEENGDMNGQISVLEVLEWEVQDLDKTHVFNFIGGFSIMADYLNSTSLPVRASAAWVIG

SAAKNYKDGQDWAIDAGVIPKLLDSIALDIPNKNDVAKDVHEVKKKSIYALSSIVRSNAR

GQRLFLLQNGPEQLAGLFDNAHSAKLHLKVLLFMYDLMIEEPNLELAPEAESTASSLVHL

KKIFQAPKWCERLLTTFVE

>contig40783 Frame-1F

MPFPLRLQLSSGLDTLKWLASRSSASAFARVTRCNCRFATTGPPRHIFANSSVGIGSLPL

APEETEAERELLKSLPEFREAAKILLGQGGDAARLLPNYQRAEKALPQLRRSVEICRSTM

GFHSVYLLAALRHLVATLFIKGDVNEAIKVMHERGDIMQWPSAEHERMLRLLLRFNLPHQ

AESWCQKDVFMKQFPKDETVPLKWTLYELIGLELREGAEQLVKAVEDPLFVQAVETLREK

KDVVLKHEKMSTLKASEVQLGREIPYLLAQYASLSVLSTQALGVDHTTPPTDVQLVSLNQ

AEVLYKEALAWVEKIAAEEKKNALLASGPHAPFGAWVETNLGELLLRKNKPEEAMEWLGK

ALRTLQTDQTGFGGSALAMTRVLGHIAKGSHVLGQAVTSEGLFVTVVEAFEREVQLSATD

RVEFARVLRAYGDLLAKWDKRDADAAKRYEQAARVEDDLAALCKANHSADALHPIFYLPL

>contig43092 Frame-1R|Blast-folylpolyglutamate synthase, putative [Phytophthora infestans T30-4](gb|EEY58400.1|) 1e-30

MLSITKGLETALARSRASKDKEVVVVCGSVFLMAEARQALGYKEPIDSVALNDGKSVDLS

TFQNQLSVAQHKATIAAVL

>contig43467 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63060.1|) 4e-11

MLPMLSSFQSVKTIHEWCTSIASKYQRVDYLINYAESDIVEAFTKAEESTRSVSTFLEIL

CEAMASTCFPDRVPDDESWSIASNGTIVNIASLSEETLLEPLVKRMATKLQSRHVQLNCV

L

>contig44174 Frame-1R

MRPSSTCTKQVQSSIFSMEVVLSQLELASPRRAPSGHKARVSKKCRQLRESALLSKRSNQ

HHSRPRGKCLTKVPCTTTNALHSLRDQVASMTNELESLRAKWAKHIPNKRILVAAHRSAY

EKYATSVAEHVHSDLQQQLRQQQLVFATLQTAILNAPMRSNSQDMFEALHFATHLGHGDD

EREAMLCAHHAQSVATVPSIAYKFFNLANNQVLAHQSAHADETPVSPLA

>contig44440 Frame-2F|Blast-sporangia induced conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70121.1|) 4e-77

MSSVFFDCGIISFRIAVMCCCARSVCDGSRVKPASKRQYYVSYVDRTQEEIGILTEALSL

QYIGHRLSNKMPTHGFRLIATPKQRALNEYGDRVIQFLSFVMQITETGFNRLVKIKEPVA

NNVRMRDFLGLSLNIGEQTIIATSSCDARIEGQGGGIRPSLPSAWLDVDLNVSADLSNCG

KWNERPVINEGTFT

>contig45182 Frame-2F

MEDLNIHSGIKDVHYLESYITASGCTNFLDGLVRLLYVSSTTSASQ

>contig45216 Frame-1R|Blast-protein phosphatase 2C, putative [Phytophthora infestans T30-4](gb|EEY57902.1|) 3e-74

MRILATQILARWARGQCRKVPVVAVRQALILSGLGLSMLAFSQDELTKECSAHMEGQCDA

RYTPSEVEGAFSVPLEREEFVSIKKSRATRLSSASYKANFPIEDKYAVETTESGDVFVAV

LDGHGGWQVSEYARKTLIGNVQNELAYLYKSGTHEPVQDDEDTESNDRVAAAIQRAFGRT

DRDLMSEVASAFK

>contig45407 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67447.1|) 4e-53

MANLEKDLEALDRVLFRLASADDERMLEVLQPLLPQLLLLFPRSQVTPLELQLRDKILQV

VTHVKTRLTALTHPTMPLDALCQVLQHKDLSVFSYNLALLFIEVGFEAATKDEQTKILAT

VIKQISSFSAAYQDSVLRLLVRSLPVSPLAVFPNLKLEDYYEGEHKETSMTNRTTFTSEA

IERQESKRNV

>contig45946 Frame-1F|Blast-aminomethyltransferase [Phytophthora infestans T30-4](gb|EEY62888.1|) 1e-26

MRPSSIRSLSSAATSLKKTPLYDWHVSLGGKMVPFAGYSMPVQYQAGVLQSHLHTREQGK

ASLFDVS

>contig46976 Frame-1F

MPMELVQSYKRQTGRFQVRKQILNPIYKFALW

>contig47283 Frame-2F|Blast-40S ribosomal protein S3-3 [Phytophthora infestans T30-4](gb|EEY56169.1|) 1e-125

MAANISKKRKFVADGVFYAELNELLQRELYGDGYSGVEVRVTPMRTEIIIRATRTQEVLG

EKGQRIRALTSVVQKRFNFPDGAVELYAERVANRGLCSQAQAESLKYRLLGGLAVRRACY

SVVRFIMEAGAKGVQVVVSGKLRAQRAKAMKFNEGYMVKTGNASQEYVDTAVRHVLMRQG

VLGVKVSIMLPHDPTGKVGPKRALDDVVTILEPKEEVYRPYVEPSNPIVPVAPVATSPAP

VDPMYQSTA

>contig47838 Frame-2F

MARPKAAAEDAASSEPRSRSRSRAQSPMPPSPEPMEHASHECLEYLLENQIISHLCEAGR

RDQPSGIMSLAMQFVGALLSRVSYPILPTREVHVSVVTLIQAAARKEVEDPTVRKYLISL

LNILWKKLRGDPVQTEFFFLHADRLMIRRTDFANKANSGTNQFGIAGDDPFLHYHNHHTQ

SEVPELILFTGLLPHMYAVGKIGEKCREALVIAAAVHDKALCRFVLQLTPFCHYAVNGVI

SAFDSLPKTLASTAKIPAINVSLSDSDMEIELSILAVRLRFCCTLAMVARYELEEV

>contig47957 Frame-1F

MIPLDHLCSWCRSSKWQFKCYSCDPRRVKTLCSNCSNLWHFRGFARTHLITTSNGETRSF

LAWSQLNGNDIGNKNEVLETANKNNALNHRSDQGHHDIPPIDLDRTMSTATLEEKESTIA

AVQEDGSRQNDLTQYNGEKQLENLDPRTALEEAPRKPVEDHTIPHVTSTTATVWPVTTSN

TQEEASSISNATSQSLGHTGAHVVANSTNSNVVFASAKESRHPALASATLAAVTPLPPVT

AVTHPN

>contig49058 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64102.1|) 1e-44

MMRRSQLSQSMLGHPPPPKFETLQQTQKYERAMNTFQSVAETMARLSDEDYEAQLGQLQR

LYTPTTEQAEMV

>contig49726 Frame-2F

MDDNYREPLVLFEDLALDRLSSLELLASSYLKYWCVIVESNAENPYPILLQILLRRMSLF

KLLIELVSVSRELQSETSYSVLKKLENLIYERWKSNNLSAARIEIFLQLNAVPDNDFFRA

PLSRIYLSYIKYC

>contig49793 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61750.1|) 1e-104

MVWEEGSPQLLPMAHRRTRNASTGSFPETHADAPELRSDKLRLRLKDREKAAAARAQRPN

HLAFRRIPVLFLLLTASFALGFYAQLLAFFCHVRLGFTAEVLPTSEVSLMEKRTASLIEH

TQRVVFVCKHTNWDFLGFIASPHTILFAHDDVAVPRALEDSLRVVRHTGVDSYMNLHNKT

VTIMSHINAANPRSHLLKQDDEAVIYWPHYYQCLKKCTDIDSCYAGDMHVNLGDVA

>contig50438 Frame-1F

MVQCLGPMCNTLSLISCAPLEQTARKLLKTLQLSRRSPGSTLCVVPAPFELFNMNYHDNI

SITK

>contig52681 Frame-1F

MPSIRSICQGNDISKSLERRSGCLSCLELMVDTACKCNRLPLLISWATSHIPTCSAKRTR

STRKKLSPIKRLI

>contig53185 Frame-1F

MSEGLSPPRKRARRRAEEEIAGTLRSAAHDGAAFASNMPADLHEETEHRQRLAMSSFLSM

ARGRLDAQMPVDAASVEALSAAADALEALSSSSMSLDEPMPMAVAVAAEESTTDDEELQP

FSMAQVEPMVALDGPVALELVYEDVVTFLFNMARGQKTQQLHKGMRTVRKARNAAELLPR

LFTAEDDTGLTLLMIGVRGNDRVLCSMLLDAGADVNFKTEKRTYALLLAAQKGWEEMTKF

LLEHGANEESKNMALIPAAHFGHLPVVLMLLETGGNFNYANKKGTTPLMRAAQEGRDAVV

KFLIKMGA

>contig53509 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64339.1|) 1e-27 NOT\_ORF

MNGTVPELVLFVIPNIVRSIAAMTEAVKLVLTHQALLLVIKAEVEGCMLEEGKVINGREF

SDLARARAYLQEMAERN\*VDVFESVTIAVEKLVEKMR

>contig53835 Frame-2R

MSLNDEKLEPMPPPPAPKAHPMLTLPLPHLYQLHNASIKASTNLDEQLTPLSPPVPHTHP

LIALDDESTHNDKLQRGRDGMAISSHQTIFNRKATIGQQGNSTSLSRDRMKACTGQHQET

LQSGNPLAYEA

>contig54009 Frame-2R

MTTSARSTPKKITPTSTRALLAGSLFFLIATNLRVFAVARSDSGEVDADILTCVCIVSAI

SDGPAPAKQGENTAPSDY

>contig54711 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64254.1|) 2e-11

MTLFATSVAVFAIGTIRRGQIRSS

>contig54764 Frame-1F|Blast-DNA polymerase alpha catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY54777.1|) 5e-35

MQRAKIGGGEGQKITNMFFSTSAGTATSHGAALHGGRQHGTAKHDIDLDSLLDDLTSNPT

ESRSAYAKPLSYSTGISTCEKDTLSLIP

>contig55932 Frame-0F

MKKIKGWENALNGDNSGALAGRRTF

>contig58539 Frame-1R|Blast-60S ribosomal protein L8, putative [Phytophthora infestans T30-4](gb|EEY69751.1|) 9e-16

MIGVVAGGGRTDKPILKAGRAYHKYRVKRNEWPRVRGVA

>contig07026 Frame-2R

MPRIRKSTQLSSERDGSYAPPASARRPSITIKPRQQRERRAPMAFSPMTDRVTRKPRKLK

NVCPLLDSDKHSLLVTPPRPEYKRLERKIKSQAHRLRYPLSFIEAYEAEGWNKSSHDKLK

PGKELEVEHRKLITGQRALIEGLNELKTLYAHEPQVPPMAVFEDVHCSRCGSTEIEQDND

ILLCDSPGCHRAYHQRCQMPIILTCNIPQGEDLWFCEVCLAIFECLKSINSVFGTTYESI

DALFPELNEEELHIANDGRNSATPEEENVATARSNEDDDEEEDEDFVCEDEESDEDEEDP

FQTENGNDDEMVEEVPESAQDLLYLRKEDVIDLN

>contig07242 Frame-1F|Blast-cytochrome oxidase assembly protein, putative [Phytophthora infestans T30-4](gb|EEY64598.1|) 4e-94

MSRAISVRGLMTPGLLKEMGEVRKHFVGLTGLVAGTIFAGSLLAEIDGGQKFPTFPTMNG

RWIPHGLFELKPFWRNFYDNEVLVHFDHRVLALTTLAAYTAVLMKARKPAVWSNLTEDAK

RAMMLAFAAISGQFVLGATMVVNEVPTPLAMIHQGGAALVLGSSLWTVHSLRFARPGGLM

GAAVAAAASKMA

>contig13320 Frame-2F

MWNFIFAVAILAMESAAFFSARPTALETTLNEHLKNNVIPFLSPADNTLSSNNLKTVKTE

LLESLKRFKEECETTKKKAGAYENWAMNHVTQIRDDASIQKLFDTLVLAKSINPKSKYLK

EVIKAVFEPKSHLNPEDAQGWFKFSRDPKNTPEEAAEKLFTSSNLAMLTWFVTYKRIDRP

NLYLATALLLPFGDSLKPMLDFAMKKGYSDLAGKIMNGLEHSIPDVVDFLLFSRELGNPI

FSKKMEIAVAYAEQSGDEGLQSLVVKLRQLYENSLTKYIMWALDVDENDAMALKIQKWAT

VDKPSVPSTTLTNHASPVVVDLTPPNVEDPIPMLTEKTDTVSAQKKISKTIARCFPASKT

RKVTTSTNLPSIEATKIENP

>contig14307 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60832.1|) 2e-09

MYIPPQSSTARRTIVIRHAFAIKKLLVPRR

>contig15533 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63592.1|) 3e-07 NOT\_ORF

MTRLSKSQLTHKEMEIWGVASLTTADFAKRKRSLFLLQWYNYNFDRHK

>contig16824 Frame-1R|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 3e-64

MREHIFTGNASSLAKFKTWQELVFVTLSQRVLADPLYVRMHYGHPDVFDKVLAITRGGVS

KASKGINLSEDVFAGFNCTLRGGVITHVEFMQCGKGRDVALSQISMFE

>contig18291 Frame-2F|Blast-UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase, putative [Phytophthora infestans T30-4](gb|EEY65364.1|) 0.0

MQDEVVPPPPMSTMYLLSLLAIGIASYKAAALIIPIVGRRMPAKLSGKDLCKRGTPAGEI

PIPEALGIVSGLVYVIALIVTVCTVVDNADVRRMMAWGIVSILSMIILGFTDDLSDLRWR

HKLLFPPLASLPLLVHYAGLTAVVLPKPVRFLFEKGTLVYTLLNPIVPLSDSGEIAELGL

FYYVYMGMMAVFCTNAINIYAGVNGLEAGQSLVIGVAVVIQNVLQILLGHDNENYHYTSL

LFMVPYLATTLGLLQHNWYPSRVFVGDTFCYYGGMTFAVCGIFGHFSKTLLLFFLPQVLN

FLYSLPQLFRIVPCPRHRLPKFNAHTGLLEPSTITPASTRSNYTLINLCLVLFGPMKESH

LVLMLLAFQVLCCGLTFYIRYGLSSYFYDFVR

>contig19195 Frame-1F

MYLDNCGGHNSSEILNAALAKTRTKLT

>contig19731 Frame-0F

MNSISTAKDFHAAVAATDEIPLVAYFTAPWCGDCNLVGPKVEKLAEELRGSAVFNLVSAE

ELETLCEEVEVDNFPHFRVYKAGKTLGDHTGSKFDKIEAFIRGLVASDRVGETEDTPEGD

TAVETSSATKTFSSEAKTEGLKKRKERDVTEAQDEQVGKKGKIEEEALKETEQAVSDAEA

SVVAATIEIADNENADVVDLASGMTENAGEVLHESVIEDNAELAQKLAKEAETTRVDVVA

A

>contig19890 Frame-0F

MDLAIVKDKCLNLEFATAGECADSIRLVFSNACLFNPPGHIVHESASRLLKEFETDYTKY

KAKDEAMVKRRETHSCPYCLDNVCGICYEKCINFEPPFVVCLGACRQRIKRHAIYYKSPD

GQYHWCSKCFSSLPEVLSLKSAPASNTDHQTEALEMEYTISKFALLKAKFLDELTEPWVQ

CDQCNGWVHQICALFNACENAIQEEEVLYTCPLCLLEELDANMTKDNLEMSPVDTSVDEF

PLNKQKDLLRSHSPALKRRPYATDFTRSLGFEEEIKEKIFSFQARADSELVEGSITSFVR

SQNLQSCDLSCFMQKWVQQHLNLLGEDIIAQSIVVKVVSSIRSSCHVSSAVREHFKSASQ

AYPQIIDYTSKVIFVFQMINGVEVCIFSMYVQEYDKHCQLHANRNRIYIAYLDSLVYMRP

RHVRTSLFHQILISYLASCKVNGFEYAHIWACPTTRGGDFIYWCHPSFQKNPGKERLLQW

YLSMVRKAKELGVVYACRDLYASEFEHLEVLLDKQLPPHFDGDYWPSEAERLATSPKRGR

KEANLSSAYSANFRKRVSESVKSACESLFVIALHPTCAACKQLIVNVAYWRASRVGAFDL

YYCRKCQSAGAEVMFSYAGQEAVLTEAFPPEFCRKSKMVDAMISCPFLDCRPSMLKNCEE

HHYQFDSYRRAKYSTMMLVYQIFSTQRSAQ

>contig20883 Frame-0F

MTLEFADFRLVNVYCPNHRPNREFSSPYSTIAPGFCTIRFNPRFLIACKALRSIASAAVR

SSHLESAALVLTKRIHS

>contig21260 Frame-2F|Blast-endoplasmic reticulum-Golgi intermediate compartment protein, putative [Phytophthora infestans T30-4](gb|EEY62206.1|) 0.0

MGAIDVLKKWDFYKKIPEDLTVSTLPGVSLSIVGCLIMFVLFILEFNSYLTVDYQYNIVM

DEGLDQNMRINFNITVPDLPCEFASVDVSDMTGTRKHNMTSNIFKIRLDQKGRVVGLADE

TQFKPRFAEDAEYGDLPDSDAAVTILAEDTFEPFLKQHHYVAVDFFAPWCIWCKRMEPVW

TRVAKTLPSLHYGQQVRVASVDCQAHPQLCMKQFIRAYPTILFYKDGDISPVEMYFGDRT

VEAFSKQV

>contig21879 Frame-2F

MVVKDCPRHSDQVKTIEGESDTVSLIPKENGSLFGSFKNTLLAPLKMMVGIKTTETRCSQ

GWIRHLALAPNGNFVSMIDDLGRVAIRQIDVCADVLKWQTIDDVSCKTLSLPIKHLVWLT

SNLLALFLTDGSVVYASFYANSDEAAASQHISSDNDNERVGLPGRLVLIPVRYH

>contig23550 Frame-0R|Blast-ubiquinone biosynthesis monooxygenase, putative [Phytophthora infestans T30-4](gb|EEY62944.1|) 0.0

MQVWDAMGDGFIRFDANKINKDILGHVIEHRVLVRALHDRMNQLAADPQDSAPLKLYCPA

KVKHFQRPTIVSGISDIGLEDGQRLKADVVVAADGGNSIIRSLSALGTWGWDYDQQAVVT

TVKTDGKNETAWQRFFPTGPVALLPMRDGYSSVVWSCTAEMAKELTALSSEAFITRLNEA

YAAPPMSPVPPEFPGLPVLSSLMNGVHQAAATIMSAASLTDPFVAPPKAVAAVGPRVAFP

LKLKHATKYIKPGIALVGDSAHTIHPLAGQGLNLGLGDVNALSNLLVGGVKSGENLSSEY

FLQQYEDERMKANITMQLAMDGFKRMFGPTPDAVSVARNVGMGTLNAVEPLKNQIMKYAM

GL

>contig25336 Frame-0F

MSPRKLETFIKTATGGSRSHKKKLQREVQKLSNWNEIAPFQIESIPRSTVSFPLKQNQNL

NCRV

>contig25457 Frame-0R|Blast-3-hydroxyisobutyryl-CoA hydrolase, putative [Phytophthora infestans T30-4](gb|EEY63647.1|) 2e-07

MEGIYERLEVRDMCMNINFSVAHYE

>contig25549 Frame-0F

MLGSTSDTKRGGVGLSLSSSSPSQREMSSRGSGSELDEAQSAAIEDENAARVLSEIDQLA

SDRVFSSSVSLSDQALQDFVVQLTVVSLSECSGVGPSGTPGGSAPRVFSLQKLVEVADMN

MRTRSRMVWAATWQTLSRHFTTIGCHEDLTVGMYAIDSLRQLSMKFLERVELRDFNFQRL

FLAPFEIIMANATSLETRELVLRCVENLVLARVSNIRSGWKTIWGVLRIAAETYAPGSED

RVVLLGFQVARGVLERHFDCIVDVFVDAVECMLAFAVCGGEEFERRIGERLVLTQLGVDS

IGLIRNVCIDKLASGEVIEPLRVQEITALVSATSAPATAAGAVMATKQAARVGCKKDKTV

TDDPTADGSESDGLLSPSVRARLRYQKHESVRSLEDISPHKGPAFASSMPSRRRADLINS

FEEEQQEMSSVVYNDSTAHMRMWWPVLTALSTLAADCRLDVRLAALDALFSALENHGHKF

SSGLWGHIFKGVLIPILDKLRHLDIIVGKGALVQLKLPLPRTQASSRMPPYTAIKTTATL

CLERLVECFGLFYDIVGFLPEVLFLLRKCMVAGDADMQFSIATARAFEAMLVAYGHKFPR

DVWGLIADELCNVLKCAEPTWVFFALPLDGQRGTSLRSSEAHSNSSSTPSPSRGALTNPS

LSRPPLYLSLYSNVVASLGFTFTATFSPKVLSVEEVEAQRVPSRTHLEVFLALQRIVGNV

LANRREQYLLLSIGQANSLLSCLRESFLFARKVNDAVLLRQYLKRAGWRYGIMLSSSSEL

PT

>contig25866 Frame-2R|Blast-FKBP-type peptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-4](gb|EEY70553.1|) 3e-86

MLLTSTRGFRAVRHKVRPMKENHLCVLHTWPQMPSSNPFSLRTPCTHTVFFSEQATCPVV

SLGDRVHLHMDGKLSSGTLLPSTRDTAPLKFIVGSNQVLPGVEKAVQGMKKGEFKTIALG

PAEAFGAEKQLLTVPLQELHLPEKERQRLAIGQTLELAGGERARIVLLSDETIEIDLAHP

YAGHSLQATLELVDHELYSELHESERLVLPHVVHEGDTVTFPRRGDTVVVHYSGKLAKDN

HEFDSSRNRGEPSRFQIGVGQVICGWDEGVMRMSKG

>contig26997 Frame-0F

MEMAKIPQTPRKRKRIARQSGNLYEYKALCLASLCQKLAQCELLSVGEAELVKAVVNLES

IDVLQRVINSNLLPLRPRMLLFATAMQEQGLKCLEPVVQCWIQTVSEKMLEEVLDATTMS

GSSEPLAKRTKTKSSETIQKNQWKLRCCDFCQGKASIATLRSRLKEWKYLVESSQQTARI

LESNGYEYCSNKAMIALSAFWDPLSVAGLTTTGKAVMKRKRSDLILKNVEAVVPSMLVVD

YKQILQNIMAERFGCVGGEADVLVKVWTSVWKREVKNVFKTKQITLNDAIRQCSIADAYA

GAAVFSEFSDKITHLPGFCIVMEVIRFTCASISGVIAAFAHAWTETYSNFGLFVPEIEAL

GRRGISSTKPILRSYLSKVLLSTEVQFLVGPSAQNELLFVLYEIFFEQVYVGKQNSSFFK

YWDALMSQLDS

>contig27604 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59718.1|) 3e-97

MICSSCHPLMGTCEMKNACPRICNDWLNACRNEYYAHAGAGALAPCYGNALICSPLKSIA

KSGADFCRHMGFHVGSDTDTEGIDCFDGSIPDQLGEIEPSGPWQTQLMGYLKKEAEDPSG

LFIAGCFILITIMLLGKRVARRLGDPFGGDQLNLIEVRLLQQERYQRGERMYDDETDSCS

EEEEASANNIDISERLESE

>contig28058 Frame-1F|Blast-C2 domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY63881.1|) 1e-112

MPQLLVTLLRANSLPVADTYVQGNASDPFVTFQLDDEYMRSSCITKALDPVWQPAETFVF

ELPHPSQATERHLLVQVSDNDRWKLDDLLGELSIPLSSFERRPNEAVIGTYELIVPETLK

AAMKTIETKASIQLDICYLQETDGQQTLCVWENEDYVDGHWTPSHNKERRHWSSFDLQTS

SDNFEQVVPDVPEGLEASGWAYSNKRGDDHGWIYASTYTGPWSSMPSALCYARRRLWQNH

CRPAVACE

>contig28515 Frame-2F

MEDVLVQMIIACVNDQEPPRTTKSTTASQFHDHMTSLLHDLQLACREVSSGNAQRLLHAF

RGAGYTVETVPSDSRMLPTCPSCGHALSKQGMSAPER

>contig28762 Frame-2R|Blast-Solute:Sodium Symporter (SSS) Family [Phytophthora infestans T30-4](gb|EEY54966.1|) 1e-145

MGLVVELGLLDLSLCVIYLISVMIVGLYFTRKEQRKHVLLQSKHLYHQACDAKDRNETNN

VLEVYYLGGRKIPWYALAVADVSSYIDISGTMINTALVYALGIKGMYIEIRGGLCLFLAF

QLAYTGKLSRRCPVKTRGEWIKFRFGSRVDAVILRTIIAITSLISGILATTYFAVGGGKF

FTEFVKLPEWGNLPSDFWAAALLMVVAMLYTIASGYTTVVYTDVYQSLFIFTSFTMVAIS

GFLVHLPETFSVFLPVASMQNERQFVEMNTTRIAWVSAVPPWSLNVPEEASYSMYNSFGY

IIASYSFLQIMRSAAGPGGSGLQSVLATKSEREVRSQTFVAMVLLSLRWAFSAGIAILGI

QYSIDHVGVAIDPERVVPIVISKVLPNGYKGFVLASLVAAALTTFDTTINSASSYWTVDI

YQALLHPQASKRQLLWHARISSLVVMLAGLSLSYNQSDLGLYDHCPGRWLHLALFLLLVL

GSF

>contig28946 Frame-2R

MPETSDPSAPAMPSTEERAALQSSGSVSRSLTSPSRARLLATAGMGSGPAAPDEAHAVRL

NVLNSSVQEARDARNSRLIMWAISMVNFPQIVMAVVLLALYWQSETLCYRIQVWVLLHTV

HLTLTLLVEWTLYCLNGARSNSAIRLREKYMALLSQLKYGLDLAGLFWFLVGNMWVISDG

ARCDDGSVVYQLALWMIIIAYAKIFLPCLLLLALLPILCFCLPCVIRLLSRLQDPMRGKG

ATKEMIDQLEAKVYTVNMFPPDDACCCICLNDYEISQSLRVLPCSHHFHKECVDEWLLVN

STCPTCRKSIFDVSSSGGATVSEEEMLQQV

>contig29013 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68775.1|) 5e-71

MELKVQLLFLPEAVRKMPWKIFVEDFGGDLQNVIKSLSQSQGFASLHPSPSRMRSAPTKF

DIVASTPSSMNYLNEGDYDYESELSKKDFDTWRRRISAFSTPMDRCRVSAVPSTVLRTAR

KGETIYSVRGSPIVPESVDKAKAPTGSLVATFENSLDPTSCCIKLDTERVLDLSRPQDLS

AKSRGEATSKLKALQAKVAQLLLQINHCS

>contig29769 Frame-1F|Blast-ribosomal protein L35 [Phytophthora infestans]gb|EEY65716.1| 60S ribosomal protein L35a-4 [Phytophthora infestans T30-4](gb|AAY43422.1|) 4e-54

MVASKGQPTRLYVKGVFLGYKRGLRNQYSHTALIKIQGLADKKDVDFYLGKKIAYIYKAK

SLKNGTQFRVIWGKVMRAHGSNGVVRAKFAKNLPAEAMSKSVRVMLYPSRV

>contig30183 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58151.1|) 2e-61

MIDLFLDELAYLIRVLVSYTAFLGTICDTLGQQKKTESFQTKVQEWSAVYVLLERFYVFQ

SVHKASVLAEPQEVENGIFVSSLVEDVSFVLNKAFSRASQCVNYHTTLSIVIALVDALES

QYLPAILTLPSQPCLIPT

>contig31100 Frame-2F

MTEAQPTGDYVEAVTPRLLKRMDKATED

>contig31548 Frame-2R

MISTAASSSLSGYLLTEVLLASSGIVSDIKSQRSADVVVLESVLLTDNTNAELQVEASGS

SAVYVSAGTAEVSVRQLQLSAKNTARLQFNVQSVTATEDVTADVEDSATLSLLSSSVMAT

TLEFQAQGTGTVCLSASTVTGTPNDFEGSGQISLPNAEDKHSTTGTGSCEEVTIPTREPA

CVSNDCPGASPSNTPSSSNPSTIASDDTPAAQEGVSTNVEASSSPARSLAALAAAVIAVA

SAVLI

>contig32237 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62219.1|) 1e-12

MPCSLSRIHFHGLVEFPRPSLDFSDIPSALMVPFICRLPPFAIVLFMTLLVHCSVGNATD

MVDMPDDPISGKMVMSHSYNLELNNGQKLRFANQETLDSFLQDPKTGLQGVASVPVSPNH

RKEERKVLCP

>contig32567 Frame-0R|Blast-chorismate synthase [Phytophthora infestans T30-4](gb|EEY61463.1|) 0.0

MSTFGRFFRVTTFGESHCKGVGCIVDGVPPSLALTEADIQPQLTRRRPGQSKLTTPRDEK

DLVSILSGTEKGYTLGTPLALFVPNENVRPMDYKEMDNVPRPGHADYTYQMKYGTRASSG

GGRASARETIGRVASGAVAEKWLKEKYGTTIVCWVSSIGTVEMPRELLNDPKKAIYTRDE

VDTMGSIRILRDPAKWRKVDDSMKQSDIDKVYDDEFVKTSEDVKTPAYIDTAEVVYNRYG

TIVPVPANLNAWLTDDLIPVRCPHPPSACAMSTVVRAVKADNDSTGGVVTCVIRNAPVGL

GEPCFDKMQAVLAHAMMSIPATKGFEIGSGFAGTSKRGSEHNDPFCAGSDGKQPEKLGVT

KNDAGGVLGGITSGADIYFRVAIKPVSTIGRAQSTVGYNGQDTVLEAKGRHDPCVLPRVV

PLVESMAALAIADAAMIQLGRDGSKHEDEWLEQKRKL

>contig32956 Frame-1F

MESKDCSDETEETKLDQQAEVAASIPLLVEDVKKSVALILCVRLVDVTYLEDVFLQAGRN

DLASCQPFLTFSLKTNGEEAKVKLAPQSTTIFPRWLPACNSRTMLSACLLADRSKGMEES

TSHEVGAGAEIVVEIREADKILFGSSVIATAQISLQNYCAAALIAAENELNGSQEVIEFL

APIRVARKSTDWSRAIPNASRIRFVMCCRRTLTTPFAAVESGEEGKCRLDVINELKDILS

AYQLKKELDLLVRSKSQLKLLLERELVDTSTSGTNIPAALRSIPGDTLEEEKKESSLSQY

IAGVNEDSLEARGRGINSVRGSAVSATTEESITDETYENMGDEKRLTAVLIGVSNIQIPI

DIIHRNFKHAHVTTDHIEPKVYCTITYQESTRSALSVVAKASVGSVETNDQDHCGEDGSV

TSLRGAAAIRSSSSHSHLQKIRTYQFPRGQTLGLDLIYRNGRVIVQGVVCDGPCGTLVYE

GKIRIGDSVVAANGKSIVNLHRDASFAVIEKAMRWDEDAGAPILEQAPLAKFTLSFLYQS

TTPERMTHIDTSRPPCAQAT

>contig33977 Frame-0R|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY69472.1|) 1e-104

MGKQKFHAAVWASPSIGVTWTPVLWAQWKFAKALVTAFPTAKVIPAVQHHLRSRNPEFLA

RFQEDPLTSSDMITPRTGCQALEAMIRLQRDTKVSDADSPFCAIPMLFLAGTDDRVSDQQ

AAYKFYTRMGSIDKEFKFFEGLYHMIYEEPEREDVLTYLISWLHKRFPLETRQPIRS

>contig34644 Frame-1F

MRWCAALMDNEKLVLIPNDGFRYVERNNCLFLSNFTVTFNLRYCCTKSRHINTRMRLFER

IALRRLVFKRNGFSVKL

>contig36093 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64981.1|) 6e-14

MTEAGKSFLLCAYSNIDLPAGLLKVKVETLGAYLSESLDQIEM

>contig36581 Frame-0R|Blast-polyribonucleotide nucleotidyltransferase, putative [Phytophthora infestans T30-4](gb|EEY66211.1|) 1e-110

MWGMAEKLGRAKAEAFIESGHVGKLARQEGEREVYATIINGLREHCACTGASVDEVAIQR

AAHDTFQRVLRERILTVASESKNNKITRLDGRSVRTVRSLDMEAGVLPMAHGSSLFARGE

TQTLCSVTLGPLERGIRLRGALHEAREHAELDAPTPYKHAMLHYEFPPFCVNETGRVGGI

NRRMIGHGALAEKAVLPILPSITEFPYTIRMTSEVLG

>contig37003 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55611.1|) 5e-32

MTYYRIGQRLTRTRAVVRALARSSAGKWNSATLEKLVQNSKSRFGSAVTRPLGAAIATFL

DSGVAFNVSSEFLYFDGEDDDGT

>contig39180 Frame-2R|Blast-DNA topoisomerase 2 DNA gyrase B [Phytophthora infestans T30-4](gb|EEY61057.1|) 2e-19

MSISYGLEQADDIFLTNWIGTILGPAG

>contig41644 Frame-0R

MYPFSTTNAKDWRNLLSVYLDAVFFPNLNEFDFLQEGHRLGINESKGELEYKGVVLNEMK

GVLSDSNNLFSTRLQQELMRGTIYEHVSGGDPEMIPLLTYEDLRTFHTNNYHPSNCCFFS

YGDLPLTDHLAYLDQTILNNFEYRSESAATRVDTEGFSLLKTDGKVPQLIVIQGPSGNMS

NEAVDSNNKFCMSKLVDVKSTNSFSTFVLRIVSYLLTNGPASPLYKALIDSKLAHDFSVG

TGFDTSTYYPTFGVGVEGIEGGDASVPAIRNAVQEALKKVVTEGFDKERVAGMLHQLELS

LKHVTGNFGLQLMHGVSSVWAHNGDLIENLQLNSLLERLSTEMASNPKFLEGYVRDYLMR

DDLREVHMLMLPSEDFVRDQERRERETLAMRLSEQSNADLDRIASITDKLERRQQENQPV

ECLPTLTVDDIPRVEEGNFDHIDIFELNSTPTELTCVPSTNEISYLRLLFDLKALPEAYH

RYISIFTSVFGSLGTLRYSYDELPTISANCSGGVSCSAIVAPSLTDAHLERSKQSLLLST

MCLPHKVNETLDLLRELLCETQFLSDDNLGQLRLILQSSATAASNSISSSGASLAGIRSR

VGLTPASLYDELYSGLTQIQQLQDWAQCSEEELRNIARVLQDIARMVFVPENLRLSVVTE

EKLRLQVEQSLTSSLLQPLAKSSSSVDVASLQPIEELKLPLVSPKSYYAYPISVNFVVET

QPSVSFAHENHVPLTVLAQIMSSCFLHQRVREKGGAYGSSVSQLEGSFSMGSHYDPNTLE

TLDAYAESREWAVRGEFSDRDVQEALLSVFASLDAPKTPSMKGRMSFLRGITNEMRQRRR

EQYLSLKRDDLVRVARQFFTDDTPGKCTVIFGKDGDDLSKFSDKGFHVERVASSVQ

>contig43093 Frame-1R

MLLQRLYQVNQFTAVKDGLENMQRLNAAFGDPASQLRVVHVAGTNGKGSVTYKVAKVLER

SGYKTGLYMSPHIASFRERVQINGQFITERDVCNLLSEIFTISAQLRIPATFFEMTTMLA

FMYFAKQGVDYVALETGLGGRLDSTNIVTPALSVITSIGLDHMRVLGNTREAIAREKAGI

IKPHVPVVVGPHTPLTVIMEFATQNNAPLVHVPIQTGFDDDYNAENTAIAREACVQLNAL

HALETGKPCGIEKSIELTNEHIVAALESRPPCRFQVLHVLRPNSNERKVTVVLDVAHNPQ

GIDKLIGLLYKRFPDQKFRFVCGFSADKAIDKVLEKIMNVVRDT

>contig43152 Frame-1F

MSLYAKSSSCSAMSSPIAPHIVVRSLSVTLLCSPESSGSSATIQSGGSRPPQNRYFYKVI

YSMKPRPAVGSSCRTIIAIWP

>contig43466 Frame-1F|Blast-elongation of very long chain fatty acids protein, putative [Phytophthora infestans T30-4](gb|EEY60011.1|) 1e-145

MAAEVLRSYKQWADAQETLFLDWADPSGQYKLSPMRDLPGADFATAFAICVAYVSFVVIG

TLIMKAGVPAMNTSPLQFIYNPLQVVLCSYMCMEAAILAYRNGYSATPCNAFNAENPVMG

NVLYMFYLSKILDFFDTLFIIFGKKWKQLSFLHVYHHLTIFAIYFMNFRVAYDGDIYATV

ILNGFIHTIMYMYYFVSAHTRDIWWKKYLTAMQLIQFVMMNVQGYLMVSRSCKNFPPKVP

VIYLIYIQSLFWLFMNFFIKSYCFKPRKSLATKSKTQ

>contig43949 Frame-1F

MMTVLPLAETTAIASKKRRRSLESVDSSKIFAMPSSLSPRAMPSSPKRATLSFNASKHSN

DGEELLRRSLMSLSLQLKLKMILVEAWASDMNSVVMERNLFAVAKELAILKEMGVYEQHT

CVRFLELARNRMVQLLEQTEHNETLHMEAKQMWTMALIQAQEAVHSSPISPSAVSEFPLL

NGFSANSRDISVLWRAMSIARDRGAQLWHENKPEQALPFLLAADSYMKRFTLKYQRLKVD

HAMLDTLQTLPRVHKRTPTRVSFADEPLVMGIADVEVDRTPICPTKPSKLESLLLRTSRE

FPTPPF

>contig44175 Frame-1R

MSRQSTRLVTQVTILVLGLYCFSAVILWMQWVNIPDNSIATFKFQDQSNRLHTNDKSTES

LLSAWKKHEFQCLEWVETTDEGDEVGTRRECWQRIQAGDAGYCKVRNSTSGQIIHLMHTT

SLSLKDDARFTCEFAFLFSSFRFHAQSYRHDPPLTLDVIQSCGIIMAVYDRVLPSAFASI

RRLRDLGCLLPIELWFRHDELRRENPVLLLLQTQYGPISFRQVFDERIHGFNVKVHALYY

SRFTRVLLLDADNFAVRDPT

>contig44441 Frame-1R|Blast-histone H2B [Phytophthora infestans T30-4](gb|EEY66069.1|) 8e-25

MLPGELAKHAVSEGTKAVTKFTAA

>contig44548 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54960.1|) 7e-07 NOT\_ORF

MMKESSDIAMSRRLCVMLQRHMAAIRYACADK

>contig45183 Frame-2R|Blast-acetyl-CoA acetyltransferase [Phytophthora infestans T30-4](gb|EEY61475.1|) 0.0

MKALAFGAQSLLSGSQQIILAGGFESMSNAPYYIPKARTGYRLGHGSLVDGVIHDGLWDP

YNDQHMGMCGEKCAQDFGFTREEQDAYAIESYRRAVDASDRGFFKTEITPVTIKGRGNQS

KIIDKDEEMYSTKPEKIPTLRTPFKSNGTITAANAPSLNDGAAAMVLMTGAKARELGVPP

LARIRGFADAAQDPMEFTIAPSMAVPLALHHAKLEMSDVDYHEINEAFAVVALANMQLMD

IQHDRINVNGGAVAIGHPIGMSGTRIVGTLINVLKEKDATIGCAAICNGGGGAGAMVIER

LN

>contig45217 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64249.1|) 4e-54

MSDKTKWLPDLAALASLSVALHYFLGLYGLLGALLIIILLECGAKQQQSLNVKGIYSTSG

QEDDASTEEDDEVLTFQETPDEKQRDNFQRSTRVASLNVRDVGSSGEPFKGLEMNSRTPT

AFETELFVGRVLFLVRTQPEDPLYANLFTGKRRMFWIQIQGRFKKAPKGTVYLGGELPAK

IA

>contig45873 Frame-1F

MALWEGLEEEDLHTKTKQSLKPINNNLTGHEFATDDKRSATRPRANGVVETKLSETLRLG

FGWRKAGPTPRSSVGCDVVSTNLSVNDTTNFEVFDARRSRSRSRSSHEVGRRLSRSHSKK

RTLSRHDSLESGRGDFERQRRTQEYFDARNARLTLLSGRQGPRMNQERLSLKPMVATDAP

ALATRARTFDNGMQSDSPLGRQLTEFDLKSPSDVRKDSNPTELVSSRPQQASDGESDQDE

EALRLAMSAMRLYEEERGPNLRVANATRQAALAKMMEVYAREIEQSTSLKSEPYSRGTIS

GTRQLHPVSTTDRLMRRTVSDDRPTPFYDPLLQNVSETIQRPQSSRQCRREDTFTSMHPA

KQTETDIVHRYRDLSDLSSSAFQAFQLNSLHP

>contig46977 Frame-1R

MSAYCRPRQELSYCETSAPVSLPPQFLLQMRRLRKFCTSRLSARRLIVIPIDGV

>contig47369 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53613.1|) 7e-64

MVMTLAVVCAMDYPDSGVIFFDSEHNFSPKRLLQVAIARISCTHRDQKADINELAAALIK

RIRIVKIKSMTEYVSKFKEIEVAMHLLHIKLLITDCVTALFTKVDGLTYAQRQHQMLRMA

RDL

>contig47413 Frame-1F|Blast-Putative gag-pol polyprotein [Oryza sativa Japonica Group]gb|AAM47288.1|AC122146\_7 Putative gag-pol polyprotein [Oryza sativa Japonica Group]gb|AAP52462.1| retrotransposon protein, putative, Ty1-copia subclass [Oryza sativa (japonica cultivar-group)](gb|AAK70633.1|AC091238\_11) 5e-10

MRSEKCNGWVKSMKEEIAALQSNNVWQVVKRPPGSNAVHTNYIRIRQMRNARSSD

>contig47839 Frame-2F

MRTSSPWRSTNGGRKSGRSRADITPVEVDRSITWDSVGGLKSHIEALKEMVMLPLLYPEF

YGKFNVAPPSGVLFYGPPGTGKTLLARALANSCSFNSEREPRATDSAQIGPGKKQRIRRQ

VTFYMR

>contig49727 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69435.1|) 1e-136

MHRNFRRKREILARGKQLLLLSAKFSMLKENDVVNEDADGNKNVQFGLGVKICADRRALN

ANAPVYELKHIFHNKCRCARSHVWEGFVEHPSSEPTRDVVVAFSPAGNPETIRDMWGDFW

SGWAEDELQEFKREMKGFSFSSAINLVTSSVSGDYEPASQLFKFMWSKIGNAWSDGEKTR

IRQSIQNMMAVAMDRGFTEPAGISILEKIMRKPRIQR

>contig49792 Frame-2R|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 2e-27

MHHGHPDVFDKVLAFTRGGVTNASKGINLG

>contig50813 Frame-1R

MDREAARTRMLNLWLMLSTTSAANISVHTNQGTVMHVDNLISNAGQTLLACINLATPVGT

YTHAVLRDHEVAQIEWNLSKTELKTLVYDDLIEMP

>contig52774 Frame-2R

MLRLHQSETEETHSPIEIEIFPSLRVIEMLNMKPRGLQNVHCFAYQLRELHIEHTQMTTL

RQLLAPNSKPWRKLTKLRMKCCELQVLDESVNMLKSVKVLDLG

>contig53210 Frame-1R

MYTVHQSLSVTCKITLETKRFNVLAQKFADLVAGTLERLRLGKCDESRSGLRYSMRLSAL

LD

>contig53401 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65038.1|) 3e-56

MAHYQLELKILDEASMEARARRILASIGIHSIKQDAPLSTFSGGWQVRILFARVLFMEPD

FLLLDEPTNHLDMPSILWLQQYLLTLDKVLETP

>contig53834 Frame-1R

MRIVVASWTHHLMSYKNMADAVRWTRSGAHKRHIDGRNEIRLLQDLAAGDIIHWLARR

>contig54484 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65663.1|) 6e-22

MITMTTDQSPSVELLPIDVNSRERIPGSPLVPGGVSWSEDGRLAVVADSNILVSTFRSRE

LEMFQPDGP

>contig55933 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61577.1|) 2e-42

MLPFALNQSGSIFYVYLLGSADISNAVPICNSLTFVFTAITSRLLGEKPQRSVSTYTGVV

LILLGVAICYDSKG

>contig56253 Frame-1F

MSESRWCDNCHRRFDYCHRQNTSNWLNRFLLS

>contig56327 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70136.1|) 3e-09

MEHVLWYRSDSSKRFVERVLETTRELEKRVETTSRAAGTVFNSNATVSSLLRSFSMNVCL

CNGLEN

>contig56392 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69289.1|) 1e-08

MPTFYYFNDGNFLHSLSFSGADEKILRNNVEQLNDL

>contig58251 Frame-2F

MWFLSRFLLPSIFSRAKLLAPAKLLRVATQAMTITATRLPKRIIRFQL

>contig58538 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69691.1|) 3e-07

MYFCAACKVYVEDTNVTEHDMTTTHMITSSQGVSLQKG

>contig58985 Frame-2R

MSDASDVEELKTEVKGEATKVNSEEANEKTKKDESVDASSSTIDNIAKGSKNGTDGALES

IKNVTDRAKSVADAALESSSVSASASCSGSELINDLTIEQQELSNEKVTLAEAANAAESS

QFIKVGAGVGAFVGMLAVAFAVIIRKVRSRLSGDRFGRDEASVAMKSDLSADEEAFEDDS

VESNGLHRKGMVKEDDDADADGEVEGTFVGP

>contig06628 Frame-1F

MIAGLPSSLIRKKTNSLKEPLNFTKLKKVTTQSRTSSQSLPYPGPRN

>contig07025 Frame-2F|Blast-molybdenum cofactor synthesis protein, putative [Phytophthora infestans T30-4](gb|EEY57844.1|) 1e-111

MAVEACAGCSSLMSELVKLRIKYKKLQSKLHLLEKTPMALSNDQKDVNQGTPVPTSPYSA

FSRVELQRYGRQMLVKEFGVKAQLKLRAARVLLIGVGGLGSPVAMYLAAMGVGTLAIVDN

DHVDRSNLHRQILHDEKGARDCEKKVLSAKRRLLELNPLLQCIVYLTRFTTTNALNLVKE

YDVVIDASDNAGTRYLVNDACAQLQKPLISGSALGFEGQVTVFTYRDDANATGCYRCLYP

KPPLLSRSCAENGVIGVVPGVIGCLQAIETVKVITGVGEPLVGVQCFYDAFDGKFRHFKM

KKKRNPQCLSCSRHSILLKNGSVMAPLDSSHFVQDVVCDDKSACLDLKVQVSAEEFANIR

KAAFAQDIKQNERGSRYVLLDTRSPCQFEMVHFPEAVNIPTNKLMKTDPMEVLATLHGVP

TSEFIKQLSRTAKRTYVICRRGVDSIKVTQWLLDHGIPNVFNITGGYTEYSKEGGVDPTF

PMY

>contig08055 Frame-2F

MRLLLCLLAFIFLSAIYFKHVLKGKSQHPRPNASTVESLRGNVANTSMATQEERAFLEQF

FLKRRIDNVTSAILKQYKKILKLQTMADRGKTLDEWLHRKSGKLFHPMEALQNLRGQLKV

FEWVELLVHFAESKNKNVLSWTSHAKEQLSSICNEPNLLPTIFQDYPKLSLSVLQIVDRI

KGNDALFQKWFLSVSTNTQFSPEALYELLNLSATKTLSILKLFTELQTFEATRKGAEEML

TFMSSNKAISQKLLSEWQKENKHENLVTFWRILPLSQTAGFTSSIFTLWLEAYGKFSRKT

NFLAQDMCFHQLLEEAHFYPVDHGQAVTNPAATSPLFPRNRR

>contig09449 Frame-2F

MTSRDLVGRPLVPFFDSDNNLNDSLQLGNDEREEIDIDARVWDKELGYFVYPSDQKGPKP

VKLANQDIKTDGGSKLLLTPTMMLSSNVPDHLNSMEMESHSLRDGVHSTLNKRGLKPKSQ

SNPRRKNNDKGEEASTTHGVSSKKVKSKNGNPNTGNSSTQSKQKEQLSASGKWAWSAFQS

SPDPAELPMPPFLINAGCTNSNASCLNLVAKAPAVPLPLNPIFSNHASAPIACSLPKGPP

QSLPSRLPVPPDVTTAAPTSIEVSMTQDLRRMLNIG

>contig11295 Frame-2F

MRGLSKRDSGFSGPYNNILDTSKVSYAASSVSLGFSGHSKGSRPEPTDSSSHVSTKVSSR

SFDGILAESAQSPAVLGGSVCGSHKSGSCRVLGSAALGGYGDFSNVNEYVQQDVSSRCSS

KPNVFGEYLRMKEEMQYDEPDRVSLDGPSGVSFSDTISDLDSGKYSFHSVQGISRPPQRL

VDQNGRSSIADSITDSEYAEQSLSRDESDCGSEMSFNDEKYSFSSIDSLNDSQVRESKRE

VEI

>contig11633 Frame-2F|Blast-P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4](gb|EEY66187.1|) 0.0

MADSVASDSDPDAEAKLWNLFEQVFCFLKGMTIYQTRRRLKFTIVSQTVINSLRIFPIIL

GLSFEATLPVLILYVTLVFGWHGTKFLVPKFLLSYKIGMQLTLLVDVIWYYKGYNGKLNS

VSSGTSVLMQGFFSILLTILNIMGFMYGWKLRRIVKAVQNQRECDRAALATMMPSPMRVN

SLHQALSVQSSSEADKDDGPSVRRNIKVARDTPSSKSRRAQSGIIASLLEAFKTSKQRQK

EAAAQEAAPVFCSNLMVTSKYTYYNFIFVFLKMQFSRLANLYTTIVVALCFFDFSPVSPV

ASLTPLLIVFATSALKDVSEDLRRQKGDVQVNSRPAHIVRRNELGDLMHIDGKWQDIEVG

DILLLKNGDQVPADCILLATSRPDGRCYVETANLDGETNLKIRQVASCTKPFVTAEDILE

QHRLEVECDVPNKDLFYFDGVIKIGKATDDAGNNATKDDAKASLTMDNLILRGSESRNAE

WTLGLVIYTGKETKVQMNSVAVPLKRSFVEKTLDTMFVLVLMLLFAISIACTLGNNNWNL

DLAEDMTPWYIKEDANGYIFLSYLILFNNLIPLSMYVTMEGVRFVHARYIENDLEMYDAK

TDTPAQVRNSNINEDLGQIQYIFSDKTGTLTCNEMIFSKCTIAGLRYNDIDVDPAKHVRP

GTRFNDSRLLARLNANHSTKKEIHDFLLLLTICNTVIPEMSSRPTSPTSSSSSYSTHSQP

IKYNASSPDEEALVLAAADLGYVLESRDGPVCNTLIQGKPMSFEILNVLEFNSDRKRMSV

IVRFPDGSIVLYCKGADDIIFDLLSKTQPQGVAHVTRGHLQEYASEGLRTLTTAVRRLTQ

EEYDQWNQLYRQAEYSMNGRAAKIAKVSAIIEVELTLLGATAIEDRLQDGVEESICALRK

AGIKFWVLTGDKKETALSIGMSSHVIDDNMDVIVLGQRDKGSLRARLEELYVDLVEDKWG

SDETSSATSVLWETLKRAILYLWDLIKLALVGRDEEAEARKKRRRLPRRDHGGAEATAAA

GSNNYDEVYPAQLNRNLSESSFGRNLCDHDFEAKKELMTGGTDSMCSADFIDEELEFAMV

IDGKTLALVLDDDIKYLFLAVATQCKSVICCRCSPSQKASVVKLVTEPTLMFSPGNITLA

IGDGANDVPMIQAANVGVGISGKEGRQAVLSSDYSIAEFQYLKRLLLVHGNYSYKRISKL

ILFSFMKNVALSMSNFFLAMQTMYSGLLMYFSIFFTLYNALFTTIPIVIIAMYNQDVSPV

VLMQYPTLYVNGLKNRSFNWLSFFAWCLLGAWHAYVVYAVPFFTNGSVVWYFSSASPSIQ

FDKRDLGLWANGVASYTYLITASTVQVSLMTSNWTRANAISTVGTLCFYYLFTAFFCSVF

GWTETDFYDTEVGYGVLSQLVNEAWFWLGLLFSAIIAVLPNYIAKAGRVLFYPEPSHLMR

EWNRLAKGEDAVVVADSPRLVRRNTGFAFSHFPGETEMALGTFRSSDTHTGMRSDNLGVG

SSMQLPLSSTAVGSSLNAEAIIS

>contig16827 Frame-0F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 0.0

MMLRFVVVWNEIVNSFREGDLLDDKEAAILQYDIRSTGEVFEPVFLSAGKLAEAMGLAMK

LAKEGKSESQLRVALVENDCLSANRSFFTASMYVMNALFGTDDADVVDGFRTIEEISANG

GFLKSFNVRELAALRLAAVELLEEILDLPDPDVPSPHVPNSQVHAMGVIRNFVAKMEVFL

SSVQSFCVDPALQRKFSNSKFCSSANGYMFAARGLVNMFSSDTAMGAATRACLLLSLDRS

EAMPRTMEAQRRLGFFMKSLVMDIPQLRSIKEMRSFSVVTPFYAETVLFSLKALNDPLVN

HPIFQQVEEDGKNLTILKYLTKIHQEEWDNFLERVDVSSAEEAQKNFPEEIRLWASYRGQ

TLARTVQGMMMYEDAIKILHWLEIGSSPDKTAEQKQMQLQDMVRLKFSYICACQVYGKHR

MEGKTQAADIDYLLREYPNLRVAYVDMVEHENGDVSFDTVLIKSEADEIVEVYRYALPGD

PILGEGKPENQNNAISFTRGEFVQTIDMNQQHYFEECLKMPQLLCT

>contig17222 Frame-1R

MQCHAVWCYFFISLGEHKSIGMPKNNNIASFPLKNMQLKVATSQFLPVQAARIAETTPFT

NKSCLG

>contig18946 Frame-0F|Blast-syntaxin 5 [Phytophthora sojae](gb|AAM12664.1|AF404748\_1) 4e-20

MNRTADFTLRCQHYAATNGRASLQKSEHTPLYENAQFNAAASDISKEVYQASKRLQQLTQ

L

>contig20170 Frame-0F

MTPLIAPGIDASPLMTWGEVEGTPTLLGSVAAPERIWSTPIFEVQDTPRREKLANRLESE

ARHRNSNSRAPGNKTPLKRPFKAEETHLSRNIRARVSSARSNFRTPIGSDLQLRASYSTP

LRLPRPPSKTRKTR

>contig24509 Frame-0R

MKLMWLVSLSLVALVSRLSEGQTCGPRLRKDWNALTEAEKTTYRGAIAAAMDSGEYAKFI

EMHTEMMSEREAHRQCMFIYWHRYILTAFENMLRGQGGDFACVTVPYFNWITGSARFTAG

SCSSFGDCLSIATELGGWTSGVTRTLSINGVSNTGRCVNLPPLDHFCQLTSSAPSACARC

VPRSNWGTVRLPASTSYAAIRNQVLSGRNIGEMSSSVEQGCHNNIHANMGSTMGTFAAPA

DPLFWSHHAMVDNLHVIFHRCRVGTARMTFAQKAANPVAWQSCARRNSNVNFEPTDVVMI

RTGLRGNNPIPASTDPVVGRYFAGLPNQYAGLMDTRDLGVHSYGYEISGQLASLFTQCDA

SPTSRRMEETNASTPHANCGAGPDYAALNNFPETDFNGQEDDHQDVVVIDNLGNPVSPDT

PKDDYISDDSAKKVVSWYDQTLDAMGGDSPENMVDLERQACMFEHICLGGTQDFSPEFKE

LWKVKEPRCKTIVDAISNGSQTIQYEAWREDMELAFGCPEPTNDMSSNSGSDGSSQSSKC

GFLHANNTIQLDEPEVNILG

>contig25982 Frame-2R|Blast-hypothetical protein PITG\_17492 [Phytophthora infestans T30-4](gb|EEY67002.1|) 7e-47

MLHAESAACIQEFMHYKLTKQLSRLHRMLLKFESRGIVSRWQRYVARDPTLFNILNDWCR

RDLERIERMEGLLLSNPFLLRLDNKSRYVLEKIIQSIKKSPGKCSAAVENQKLGRREAVD

AN

>contig26921 Frame-0R

MPSSKSKLELIRVSGTLLRDGGLAIGIDTSHMLFDGEAIFTFMTVWGQHYSGVKKEERLV

VSHERQLMNGTNKPSKMEHPEFCVDSDDEVSSKSNIATQTLPAQRYHNFHFSPNMMKKIK

EWTNNKNCGNETTNVSYASTLDAVTALFTLLITRARAHSQDVKITTFVNARLRLEPSLPQ

NYVGNVTFNALSTYANSELQPQVNSEAQVSPETLSKLAHRVRESILRCNNEFMRDA

>contig28516 Frame-0F

MAFEFRLLPFLAIVLTCFISSKGNFHTAVRLVTIHPHNTSAFTEGLVFDDGALIESTGLN

GKSFI

>contig28761 Frame-1F|Blast-hypothetical protein PITG\_15946 [Phytophthora infestans T30-4](gb|EEY63576.1|) 1e-160

MSPLFCMRDLMLKMIELPSSRLKAGPKFEIAVCKSLEHVFGTGMEACLYAATLGIIAVEE

LKIALEIFQIALPRAPDEPKQCFALLSSSHKICDDEFDEALAELDMDNMLEGRDARPVLA

WTIHVCRSKVIELISTNLRVVVQQLVLKYPLTDASTFEELYAIDLLGLVIGTGKVQFLWN

NYMSSTAKSRNLAPRVLSAVLKHSPGLNRLRSVFFKESEADRELCIAWLLGTLDITTFHR

NPVAFKLKDAPFTVNGRMTQEVKAHKLTRIHHSDYWVMLTDGLIFHVLQSDSIEFETMDL

NLLNVLRKVALTCKFRSLFGATRAGLHDAATLYDLHLDVFQSFCRSAGDLWNSYTATSSS

RWHEMNLFRAKMVNPTTGIFVSFLDGYKYNFRQSCREIDRWNYNWHKLAKSFLRQAGGIA

VKGRSIHDIDDSIKSFDERLTGLTTMFQFMYECIDTFLFYCGEMAIGETNLFFSLIELLF

RQMNSAEYPQAIKRLEMQRRQNHRDGAQNINSELRNGFCSASMRFVDSVQLFFACQKYPS

LLHWFA

>contig29634 Frame-1R|Blast-calcium/calmodulin dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY63540.1|) 1e-177

MRCFSCLFDCFGRSESPASPRNDVSTVTAAINVEDRPIAALTPTGSQNSGKVTDLYTLGK

VIGSGSYSVVRESVHKKSKRKFAIKCIKRSELSAEDDEAIQFEVAILKQMQHPNIMTLEE

FFVEQDYYYLVTEFVSGGELFDRIVEKTFYTEKEARDLIKILIGAIQYCHDQNVVHRDLK

PENLLLLSAKNDASIKLADFGFAKTVTKDNSGLVTTCGTPGYVAPEILEGASYGKPVDIW

SIGVITYILLCGYPPFHDESQPLLFKKIRLGQYYYDSPYWDDVSTDAKDFISNMLKVDPK

DRASAKELLEHKWITGTDVATVPLTSALTELRRFHARKKFKAAVHSVQATISMNKTFSGL

GDSVRSTKDAASL

>contig29681 Frame-2F

MDTPEKRKLLWKKLHDTFPEFKEPA

>contig30089 Frame-1F|Blast-myotubularin-like protein [Phytophthora infestans T30-4](gb|EEY53288.1|) 1e-173

MSPPLHIIDARKPIATKGNRLKGKGVENSQHYDNATIEFMGIANIHKMRESLDALKSLVS

PSTVEDGDKHYHNRLENTRWLKHVMRVLSGARRVAEVLHEDGASVLVHCSDGWDRTPQLV

ALAQLILDPFYRSIRGFASLVEKEWCSFGHKFADRIGVGKDITDQPNERSPVMLQFLDCV

WQMTRQFPTCFEFNEKFLLHISDSLISGVYGTFLYNSERERVLDKVWERTESVWTPVLEK

PGPYKNPLYRPTNRVLYPRANLKRVVLWDGMFFRWDPESHPDYMEFMDPVEKLDD

>contig30548 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65843.1|) 2e-93

MMDEEDEFGMSKMTRDADPMEHEAKSAVKDHPDFQFLDVDEIHVAMMSEDKAAVPLWMMH

IPVEKDLRRWTIVEIQIRPDRSWEVIKELIATICIGKGLVMTEEHINSMLFRKKVTRESI

THGVSNSSTYLNVYVRIGVSPSKLRVVDICTLVLDENNLLGAIVLTKRYALWETEDPNQS

HKYALDQLLGALQSTLLSQRLSLSDLYMSTFENSMDTVENAELDEGYVADVKRAFSSEMK

VHMREVCIPLESYAYDQEYACAQMIGLLEPFFQKYGIKLTVEASSKSDVVKDDTNVLVED

ADALTISEDNLMSRKEYAPSLDEHKHTLEENLPLNDQTQLSNTCKIYGEVISELVQNLWK

ACKEDCKVRLNAKIEEKHRQVSTRVEAVQSLRTRAIRAIMESDGAQESSLHQVSGDG

>contig30870 Frame-2R

MNSSYVISRALFIDVIFKTKENFILRS

>contig32281 Frame-2R|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY68476.1|) 5e-57

MRVVCVSDTHGLHNDVLTIPKGDVFVHAGDFTDTGERSEVLAFNEFLGRLPHRYKLVIAG

NHESSFDRAFYPKFWHQYGHPQQYDPNEVRALLTNALYLEDQAVLIEGFLFYGTPV

>contig32955 Frame-2R|Blast-patatin like protein [Phytophthora infestans T30-4](gb|EEY60477.1|) 0.0

MLKIPPLAIKKVLDKYPGAFYRLAQAALSQVEKITAKSLIDHFGLASKIIQVAPLVDVSL

LKQQDTAMHTEEIVDCVADAIGLTEVHLRSTLAACLKVVTRLTNQSIRETEESTDALGVY

IVLDGSVSVQVATASHTYVELYKASKGCEIGIATCFVGSHYVATRHICLEKTILLWIPDA

LFSSFLQLNSVAVKCTRHLLEQYSDLVCVADTSFDWLHLHSGKSLFNRGDRCDSVFTVIS

GL

>contig33398 Frame-0R

MLKRMNSAYDPPRVSVLAASALDLEYAEVQSRLQAEVRDSSLVSIGVESWAVSQKCILVS

CLINRPKPAVFSIESTGVMPPTPAVLVKTIHNTITQVGTGRVSVIVTDTTDGMKQASLML

QDQYSGITILPSCAYVMNQMMTEILGMRTIARTLDICKKLAGFFATDHLARGSFLRVSEH

MHFVDEIAPMGDPDDSSPIGLLECLFKVERGRHILDILLAENGTMNKLIAQAKEEIITLA

FWKDVSLFTELLGPFLEILKMFEADSPLLSTFYHQFTLLWAHLNKFEELASKLQPIVTGY

WETIQHPAIYAAYLLDPRFPLSNLTGEATSEALAYIKRTSNVEAYGTIVDELTRFTARTG

LFADDAILESAQKCSPLHWWKGFIGSSCPNLQRVAMLTLSFPISSGLPKRKREIFKRILL

MNAQYMSEAQSSKAAVVCLNSTLVSSVEDNSVSSETHV

>contig33974 Frame-1F|Blast-serine protease family S10, putative [Phytophthora infestans T30-4](gb|EEY61195.1|) 0.0

MLKLLLSLALLARTAAASPFSGTNYSLTMNTVDEDFCDSTKQLSGYFKISGSKSKNYFYW

FFESRGGPSTDPLIIWLTGGPGCSSILALLMENGPCSVNDDLTLKRNPSSWTERANVMWI

DQPVGVGFSYGDRSEYDTSEKEVGDDMFHFLQEFFVAKPEYQKLPFYVFGESYAGHYVPA

IAHRIFRGNQQMEGSVKINLAGFGIGNGLTDPEVQYKYYPDMAYNNTYGVKAVSYPVYMA

MKAAVSPCRNMIRSCQTTKVACLAAQTFCNAALVAPYSASGLNVYDVRSKCEHFPMCYDF

SHVEAFLNLESTLKKLHISPKSAKWKSCNMEVHAGFTFDWMKNFQQLVPPMLEAGIRGLV

YAGDADFIVNWMGCKAWTLELPWSQHLEFLAAEDKAWTVEGKKAGRIRQVGPLAFQQVFE

AGHMVPMNQPKNALAMLKAFTLREDQIKDIVGDAKQHDFDVEAKIKEDSVMSVM

>contig34647 Frame-0F

MGFYSLRWHGLLKKLGHFLTTSGVADPLYWCRSPKRLG

>contig35064 Frame-2F|Blast-ORM1-like protein [Phytophthora infestans T30-4](gb|EEY54591.1|) 8e-22

MTTHLDTNKNVNWMDSKGFWTFYIMLLASLYMTMPIAFPSHGDALTAVNFIHGV

>contig35468 Frame-2F

MWQFLEQAAKNASVNASGYVNTVQEKAQSFASAVQDEASTLLHSAIGSAPPGPVDELLYE

ELADYKVFASFFSVDEHAHEIKHTVDEQVAIRELYETLVPLTLNHDEFWCRYFFRQAPIH

DLESKCTWTSSEENCKEEAKHVLHEDDSEELGRLRAERDTARRAASQWRQKAR

>contig35734 Frame-2F

METRLTNLPKSGQAPEPWSGPLWLSINDSINYAWNDGQPSPSAKYALAFNMDVKEIMDKV

SAKSGVDAYETSKICTSSSQCDNAFCAIRTNAVSGRCLQPWFGLSHGLVPASLLEKKPVC

SVKHNNVVFEPIDIMGLITFIYAEANLPRLFIGKRYRGDDGSEDAHGRFSVSSYRDVNPG

IFHITASNLLGKLNRSFIIDIHADELVWNQPVHTFKVTKQKLMTLKEAAQEFYKQDSYTW

NADATEIAHVNSQITTVDAVEIVDGKLSVSLP

>contig36090 Frame-2F

MFNQPRNSSEISHMQNVPEVNPIKPEKQNPEGQIGCQDWPFALLFVLNVGVIIALMALWG

IKAVTDSKNNSSELLSGDDTKVVVVIAVGMAFVSMALALLLVKLIVAYARVMILFVLWFN

VGISFALAAYGFIIGNLFIAIIGALIALLNLCYARAVQHRIPFAVANLRVAEGAIAKHGS

TYIVSAAFTIVQIVWVVIWSMALVGVANKIAENDSTDYSTSTRSSYKQPRGSYVAFFFLL

LSFYWGLQVFKNVAHTTVAGTVATFWYQAESKGATAASLKRATTTSFGSICFGSLIVAFL

QALRALAENGRQDGSALACFAECILGCLQSLMEYFNRWAYVYVGIYGYKFTQAGNAVFQL

FKQRGFDAIINDDLIGNVLGFAALGVGLICAGVGALIAELTHTVTFHNSTAFLAILGFVV

GIGVAVTPLAVIDSSVATIFVCFAEDPAALQSSHPELYAFLVQEWHNLYPEIMVQAGYWH

V

>contig36465 Frame-0F|Blast-phosphoenolpyruvate carboxykinase [Phytophthora infestans T30-4](gb|EEY57342.1|) 0.0

MFIRSDFASVANDFQADFTVINACKIVDEDWKAHGLHSEVFVIFNIEKHVAIIGGTFYGG

EMKKGIFSMMNYHLPLNGVMAMHASANIGKNGDTAIFFGLSGTGKTTLSADPKRELIGDD

EHGWDDEGVFNFEGGCYAKTINLCKKSEPDIYNAIQPNAMLENVWIDANNEPDYFNSSKT

ENGRVSYPIYHIPHYRPDSRGKHSQVVIFLTCDAYGVFPPVSKLSAGQAQYHFLSGYTAK

VAGTERGVTEPQATFSTCFGAAFMTLHPTKYANLLKKKLQEHNTLVYLINTGWTGGVYGV

GERMKLPFTRKCVDAVLDGSLNNATFIKDSLFGFEIPTMLDGVPTEILNPKDAWTDKDAY

DETALKLAKAFKENFKQFILPDNDISVFGPNV

>contig36601 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59006.1|) 5e-37

MPAEEAKLKTTPLDPRFPNTNQAQHCWTRYNEFVLCLKTKVGDEEACKRYYQNAASVCPS

AWIERWNDQREEGTFQGVQYAGED

>contig36854 Frame-0R

MLVSIRFAATIAVAILGQATVVKCWDSTQLKVMSFNLRTSLANDPCPSGCWALRKFRAEQ

LVERYEPDFIGTQEGAPDQIDFFIQQLGFTSTGECAGNCDGNERNSIFYKTERWDLLESS

TFALSDTPNVIPSNSWNLQYLRAAVIARFRDKATHQVVCMLNTHFDISRGHDQSSSLVAK

LLSEHCDVADTIILTGDLNTGPESPAIKYLSNQDSLNGSCTPVPMYDTLAAAGVGGPTWV

GSSFGNITVDYKFDYIFLRPDDHTCLLNSLILVDLFDGFSSSDHAVVQSEFSLGKGCTSD

FQKAEPLVSVSCHAYDTTARFL

>contig38698 Frame-0F

MSRKNSRTKIKAQYELEVEKERLRKEKLIKKRERKATKESKSVVKKVSNKVLRRMRIRQM

EKESRGEMVVDKEDKEKNKHTDAKME

>contig38878 Frame-2R|Blast-inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase, putative [Phytophthora infestans T30-4](gb|EEY66049.1|) 0.0

MGETFSLMYERWNKIYRDFYSTKTDTFNLSKIPDVHDCIKYDLLHNSNVGWKCGLELFKL

AEALARCYVSQEYGMDISEKQSIGNRVSQALCAKIRADIVTVMSASAGLEQTPFSSRSLY

GNGNIVDESAVDLADQDIEHNGYRLDPSFAKELQIKSPGTQIRTRLYFTSESHLHTLLNV

LRFQCPSWRSRHEGGEDGEYVISLEQEQYSNEILKRMGINVSDHMTLRKYIFRESKLISD

SSGRALDRVAEINYLAHVVIRVFETPSLPEDSEERFRVEISFSPGVKDGLADSPDGADGV

EDMIYLTRNMTGVMFEDMLAACVSSVQSTSV

>contig39077 Frame-0R|Blast-vacuolar protein sorting-associated protein 28 [Phytophthora infestans T30-4](gb|EEY68147.1|) 3e-77

MDVLKLNIRAVDEIQPLLSEMMSSLTMVRGLPADFSKRDKIEDWLRTMNAMGASDELDEV

QARQLSFDLERAYSSFMAFLNK

>contig39183 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62952.1|) 6e-61

MVTTKRLNLENSRDGDESLSVSSSDGEHEQHLTTETAGQKEVSSSDEESDEEFQIPPGFE

IIRGSGAVTREAVFHNDQELWFFKLPKNLDASVLANVKIKVDEDNVAATPGKVVAKVTAE

EGNKKYVLLNEDRMLTDQLVNALPLALDRARFVLGKPFSRCFSLVDDYVNSVSSPEATNK

VAVEASPVVEKLKIKRLIGKHEKPHKSKKAKHK

>contig41849 Frame-0F

MSAMAKSFYAESRLCANRRIKDELGVTLMYPTYREGFLAQVLEEDKLAKKELKEPICIDY

ALHSSINRRIILINSGCLHAKPYLDLCRIGFRLSRVLGQLVVPCSYQYSDEVDPQVLYGL

QAKTFEMVLTEFLATRGNHAREVIILPLFFSTCATLTDFLPTTINKVWAASTPPALLSIR

ISGCLVEGASDTRVSQILLEGINQVVNFGT

>contig42000 Frame-0R

MKNLLTKLNFGFEQRDQQMFRFGEMLINAAHDCIASGFSCENKSILDEFINISKRFKGQT

FGSQQLASPLLFSIQSCTRVYSDIYETTSAATHTNLCDVLRADARNESQASASVFSLILP

SSKIPSDPLAKFIKLYRV

>contig42109 Frame-0F

MNHDSDDAITAVPTRYAEQISVAYYEREALEFTEQEVKRLNAAVRLQPKLGARSDFFQDV

KNVAKGLPLFLGKHTRFIYDEQDDIVAAVDVTQEALNKGTFCANRRGVRRGIL

>contig42659 Frame-1F

MLTRLTRKPPQLMPSMLEVFGTDKPNPSHYEKNVEKIGEAVKNEAEKKHVPPPMATTVWA

KTRDLGIIERNILATNTLSNVPPAPENSSAINLKEIAFPGAPERPCVTADQACLIEGYVF

PAHKRKLAKKVERLVNKSQGAEDNEGNLVLSDSDESDLANSDTSSSGSFDISDYDENQVV

TLSDLPLFSHLWGLFSSWITHETKLVVAGLSLPAKGKESFNASFLAEKFSKSEADAALRR

AGQIRTERWNSLSLMLNRPLPHVARQLNLASDRFANRRIDAITETFRLREAIDTRNAHQW

TCIATILLLVAYDIKPERSNQVKAVTTLDTSELQQLLQLFYDLRNDSDVEVDMDLTPLPS

NEPDGKDLLKNEKVDDVLPASCRKCRRPKARCICQSRAENGVEGNTSATLEKMFQEALSL

REEYDELLQSDIF

>contig43090 Frame-2F|Blast-phosphatidylinositol kinase (PIK-G3) [Phytophthora infestans T30-4](gb|EEY55051.1|) 4e-18

MWIQFLERAVQHFKPTSELQMSVSTEEGGRRIVPGDLRGPPLSVQPP

>contig43151-1 Frame-0R1

MSSPIAPHIVVRSLSVCRGYNDNLYCLT

>contig43601 Frame-1R

MDEDEGVFLCAAKRGKRHDDLEKGLEFACGGKVDCTDLDTRFSTIEERCDYVYNEYWHAH

REDGASCDFGGTAQLVSISSFKTDRSAIVRCSLF

>contig43854 Frame-0R

MESRPGYEKLWFPGIPNNTIVARCQFQAETGNGSFVQHLLTRHFDETERKVMVWRKFTEG

DGAYAGMHIDETGWNVIRRSPDGKGTVIESISRSIPMPFSSVVNLEGVLKEFADTIIDIG

KEECQKCVRKLDILLRNDARARYPHAI

>contig44176 Frame-0R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY69105.1|) 1e-72

MRGDQRADMSLMTFGGKTNMVLELGKRLLQPEEEWQDKCAAFVELQGLLSDFSMLQKKLY

NAPETVGAEGAANLFTPENVQALTQPFRVTVTDLRSTVVKEACITLSLLAQALGPLRCKI

FLRNVFPTLLDARGGSNKVNTAAVHSCIETIVQATPSRFVLAPILQVLDASKNRDVRESC

IHYTNLALRGWNSAVLEKFRMP

>contig44442 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56120.1|) 2e-40

MLRGDEYSEKADIYSFGVVLAELDTCLPPYAYRQGQKNKGKIDIDYAPLIAAGRASPPFR

FDCPQALRELANQCLDYDPSKRPSAMQIVYNL

>contig44811 Frame-0F

MEGEYDMLTNHVYAELQRTSSHNQHLAAFPATLVHQRRPIGVTNSIFPRIPFFY

>contig45214 Frame-2F

MQNEVGGEGNGADSDLPSSLPSYIPITNQGNNSVGLSFSFNLLARPGAAPDADAAQRQWK

GLGQNQFSYVATGARPGSRRADKAPQATGAQPSPSESMRGMSFYEKSGSTGGQFITADGM

AAPPASLATDMPVALKLGQQLNTPASQISAAQFAASTGGLAMDTALLARVSGTDPSLMGS

EEIKQIMRTPDLLSIYQKLQEEDDRRQRRLERNRASARVRREKKKGMVETYETEVSKLES

SLKMLRSHEFGTGNAQKLVTALEYSSGEHFHHAQMSKEAKMELMARILGNHSRNTDAIRR

SNDENQALITVAIESSEFSRSLRAHLGLTSEQCQRLASLVVPASEETRKLDAIQKCFSAL

RAHDWLYVPGIEAILHQSRNTMTPHQFQKLLSWSLENRASIEQLQIVSTPSAAEVEKNLN

FVFSED

>contig45944 Frame-0F

MDLDSARDMLSTFASPNLSTSETSDEDKYASIKITPALSDELIASSQNSLDKVLELAMTN

ASTDSAWTEEIPTTENVLVHSRDGKPSRIYKCEADISLSPDELFDELYTNLETSNVWNVT

AAESNVICKLDETTDLVHLISAPALGGVISSRDFVNTRTWRRQDGGGYVIANSYAGKSIL

KPQKGITRGENGPTGWVILPHPTSPFKSRLIWILNMDIKGYFPSSVIRKGSIGEVSCFVR

NLRRYIAQNNAASGEYAPEHA

>contig46398 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64519.1|) 1e-114

MLLNTFMFWMMVTEAIICVVLSLPFGQRVSHAVVSFLSKHLGGKDSTANMVATVILALIS

IHFLSDVSTLYRHHSSEEVLSDGMRIRLLTAQRDMYITGFCLFLFLLLRLVYIALVTNLR

LEKSLEAMTKQAEGAAAGYKSLLAENETFKIQTDKLHQLLGDEEGVDKKKKVDALARLVQ

ENADLEAKVKASSEKLQKTESQMAAVTKQAEGQSSAFMKLMDEKSESDKQLEAAKAHEEE

IKRQREKIVKLTEERDALRIQIQDYDFMFAEAKKKAE

>contig47281 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67859.1|) 1e-163

MHTACGTLFPSVAISCRHGSDFVRFQWQVAKLAAAIQHERESAVHDDNLKRTRHREGIVM

VIYPKLLVSAYASIRTLRAINCTLPIELWYCAFEMDMGNGTSLLDGIPKKLQQDYGPVTL

RAIIDAQVIGFNSKVYAITNSEFEHVLFLDSDNVAVRDPSYLFNLPEFEQTGAIFWPDFW

HPGHTIFNIHDDSLLWELLDMPFIDMFEQESGQLLIDKTKCSAPLRMLNLLAFHDPNLFS

RYKLTHGDKDLFRLAWLKTNSPFHMIAYPPGIAGTVRATKFCGMSMVQYDTTGQALFLHR

NARKITGGIEAENTPDEKIWTHLQRFRYRASSLEVRDLKATVKSHLKSSIKYMVDASLKP

SDVLIISYQQLCKKYSIQIYGASPEFHKAQWCYGQPTVTAPMYKTSLLKETVFFGLEDIL

LNFANDAVTLLSKSAVEYIADSIVY

>contig47739 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61776.1|) 2e-90

MYGALTLKTSSSSSRNNLAPPPPTPSPFRYHVREGDTLTSIAQETQTTESALLSLNPLLG

RKVQQVKLYPGQLLVVEEAHAVSLPPPPEYIDNGWGQMHLVRAGETMNGIAALYNTSEDI

LRQDNRRYFPTGERSLLCPGQLLHVRLINTGAMQKDDPASSCGGR

>contig49791 Frame-2R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY57772.1|) 3e-44

MSYPHSRNKQKLSPVAVGERLMETIPILESFGNAKTHRNHNSSRFGKYMRLQFATESHEL

SGASIDTYLLEKSRLVFQPQGERNFHIFYELLHSD

>contig50555 Frame-1R

MNHVYREVDWAVCCIRPMPMLCATRASQQADHSHIEKVAKSCVDAVGVKNISGIRHQPQS

HGELAIGACLKKHLSFKIKKTYIKSRSCSFHHWPAASIEGDQPVTPLQYIGW

>contig50810 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57563.1|) 3e-46

MANAPQFYFIKQALRAYFCSEVSVQDAEDPAHFRAQMLLNDHSPDDDLVASTSNVINVLV

GVSAASYVAQLAVIVYAWHLTGTNPLRFVPIETFETSIDTVTAEFTSQQRIFDVSFTAIS

SFVAAADGGDDRDTLMATTMLVNDIGGARGLLTLLGFRQTVGSRTVAPLTFHQCLAAFA

>contig50964 Frame-0F

MNSLEHVYGRFQEWKAKFPQVYKSTYCELAQTKLFAPYVQAEVLYWDPLTAADAMTTFDD

FLWHRILRQHVRRIGGFDAVDGPMLYQIRNILLEKVYAAVSRYFDPFSNLHSRSLSLILE

EITRHGYLSSVEDMVQSLVNVALEAFSSEASVIIIVAIDESTAESSNDINVFSRYLLKRF

NALLDNLLTLFVALPSGPIAAAGFQCLLQVLDQVLAYARFSQDRQSMQQMNTAMQVVRKL

SGSSYLLQLLKVPNQERELKHMLTLFKP

>contig51079 Frame-1F|Blast-ribonuclease H2 subunit A, putative [Phytophthora infestans T30-4](gb|EEY61842.1|) 1e-36

MSDRQNLQQTLLLASNCPAGCLNNVSVMVGIDEAGRGPVMGPMVYGAAYWPVATNDAMCA

MGFDDSKALSADSRAHLFEKMRSTEDLGCVDEPQMQFQFV

>contig51978 Frame-1R

MQISPPEDAFYGSSQSDQAILEQKCNEIIQQGDVYSNENMLQEAMACYTKAINLVESAEE

HQSVVLMKLGRAKSRCWRKLTRFQSQNTILMTR

>contig52683 Frame-1F|Blast-6-phosphogluconate dehydrogenase [Phytophthora infestans]gb|EEY56494.1| 6-phosphogluconate dehydrogenase [Phytophthora infestans T30-4](gb|AAL76320.1|AF394510\_1) 0.0

MADLSDIGLFGLAVMGQNFALNMASHGFKVSVCNRSPDKVDATVQRAKDEGNLPLVGYKD

MKDFVASLARPRKIIILVVAGKPVDMTIAALSEFMESGDILVDGGNEWFPNSVRRASELV

PKGIHFVGMGVSGGEEGARNGPSLMPGGPKEAFDALEPIITKCAAQVDDGACTTYLGPIG

SGNYVKMVHNGIEYGDMQLIAEAYDILKIAGGLTNEELANVFDDWNKSELESFLIEITAQ

IFAKKDDLTDEGYVLDKILDKTGMKGTGRWTVQEAAERSIAAPTITASLDARYLSARKDE

RVFASKILFGPSEIPAVDKQQLIDDVRQALYASKICSYAQGLNLIREAGVQMGWNVNLGE

CARIWKGGCIIRAKFLDRIKSAYTKDASLISLLVDPDFAAELQARQYSWRRVVSLAVASG

IPAPSFASSLNYYDTFRRERLPANLTQAQRDFFGGHTYERTDREGLFHCAWSAAHHSIGD

VSERIRGNL

>contig52777 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56726.1|) 1e-101

MTRRAATDKYRKLCAARGVRVGRALVDDERVCQYEGKAELDPESGRMYWPVLFLYEQHGT

SDFVQCFGEHDTFIEHLANMFPEDGPYAEWDVKNEFVASKLAVYAAADMVLPYLTPKEWH

VRLSGDKEEDDEEAKRIQLEEKLKSKMQNWIEVSPFCTLQNLLTHKQYVVPGIPVLNIFA

RDSEALNAFLKHIKRRVILLDAQQQVING

>contig53213 Frame-2F

MSPKSMLHLLLRDFVSLLSILALLGCSETTAVVASAGANQANRGLRLPHIRNSAYISADV

EERTRPPPSLVNSLLTDAIHSSQHFIDPIINAVNRQKNEPSVKVQKALAKHIETILTTDS

GKKFVAKCKEISANANLAWPPTSAVSQTLDPFVTVAQLVSVVDERIPNLIKRFAAMDNNV

ERLAASAQMFIDELFDHDQVVNAAVMTDLETQRTGYWIFNVNSNAAG

>contig53837 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54546.1|) 1e-52

MLQRTRNCELTREGFTRLATALRLLLDACLA

>contig54102 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63754.1|) 7e-86

MSGRRSAVTWLDWNEWQNVHTSLFCRDVFEQQRAISRVAAWRSRAQLPVAINATAQLVEL

QLHASMAQHHHHAVGVSSRSHMELSLLYSNAIVRCVNGLVDGSQKGAYALAVSTLAQRIG

IPLWVVDLRHESTHNQLPSLPVLRFAARHLLAWLRVNYWTAQESLLSGQVHLVAHWLFQQ

LPHLTKILNEKMDPA

>contig54487 Frame-0F

MATPAEILHPFTFVKLRKGRHSGEVYHQLRCFEPRCCISYKLYRKHSYDHATNLN

>contig54713 Frame-1F

MATFHGMGSSDNRCIETQAVCLHEVPQKTAIPRSSPKRKQRPASGTVPPDLTTLSASFPI

EKNE

>contig56391 Frame-2R|Blast-protein phosphatase 2C, putative [Phytophthora infestans T30-4](gb|EEY61469.1|) 9e-11

MSRFLAEPVTIKTSESISAPGMSIGKSCMQGWRDSME

>contig58036 Frame-0F

MLCNCSKAYNVKEEASFFKASMLYTQKYLNALQCS

>contig58252 Frame-1R

MRLGSLVAVIVIACVATRSSFAGAKSSALENNDYGKRKRLRSHILPSFGKTDA

>contig59071 Frame-1F|Blast-cytochrome c peroxidase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY57904.1|) 3e-72

MGTKEKTTQHVRDVFYRMGFNDREIVALCGAHAIGRCYPSRSGYSGPWTKAEWTFSNEYF

RELLETNWTIKKWKGPVQYEDPTGTLMMLPSDMVLIEDPLFRKHVEEYANDEALFFHGFS

NAFVKLTENGVKFPVTSGWRQFFGA

>contig04036 Frame-2R

MKFISILFLSSLLSQANAIPTSNEVLAGINAYRTSIGFPRACRNDIVANGAQGAVEAQFI

KFYGGNFDIAQQIDINLSGLDVVTSTINYYSDPESAGAVVKEWLLTNNATILETEVLFGF

GTVTPDNQAYKLLEREKKNGGTASLSSFRSLFSVLLVSSRNAQCP

>contig08054 Frame-0R

MNQEDSVAALQKWNWSSLSQSNGKVVTRPIQGQRDATPSHAKSKEPLLQRDSTTSQLQPS

NSKTISTKCIESSKTTSEAVEEFSKLRIINRLISAKALREEMEGRKFIQLHELDRVPKET

FTNKLDWVTIGVMTRKTLSKAAANGSTYMVWGLSNLEGVELSLFLFGDAYATHWREPLGS

LVAILNATLLPATEKNTFAFKASLAPEIVQLGQAMDFGICKGKTSGETRCRVAINTAKTQ

YCLHHIALNFIKAGKDRPQLNNSAGNIRKTLFADLTKPKNVSAGGFVSTSILQSRASEWK

ASSFKKRKRTSAGASVLDGSIALPAFIERENEGDTALLSNKKELQVVSLMDQLRQPQLFN

TATQHQTINTTTNGNRGFSSRAQKILSAVRSRDGKSFKSVKPKKINMMQFMNP

>contig09448 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65774.1|) 1e-121

MVVTVTFPKPADYSLAASYYCLNASSEADQRDNISKFSSLYKPKLAASVYHNTGNALQIP

RLPLRELNWTNRARFLAMMERHSFVVLTNIGENLERTHNQVLHEFNRFFTSDNEDWKNGC

TSKHVYLNEYGKPFWYAGYEHTNVRDCFRVACGDMSRVIWPSLDFENRWLALQRCMQRIC

DRALSLTVGFDIEPSHTRSDSDFSVCYGLHYPNSEGSGQSEKENIFEHVDPSLYVVEPVS

SVEGLDVYDQHAKQWLQVEKVCVPGKEIVLFCGHALNRATKGRILG

>contig11085 Frame-1R

MECLLLKVTSASIMKRAAKCWQVSKLKIPFVLDLSILIMHLEDYATSVHEPPEIFFEATI

VANFPLLAAISSRSLRSFARSFPAAANT

>contig13407 Frame-1R|Blast-sideroflexin-1-like protein [Phytophthora infestans T30-4](gb|EEY53502.1|) 1e-157

MAFQVPGNMIITGCMMTFYRSIPAVIFWQFMNQTFNSIVNYTNRNASTGVSQDQLLQAYA

AASTASVATALGLNKWVSKRPKLSNSIIGRLVPFAAVAAANCVNIPLMRQVELLNGIEVE

TDDGEKIGKSKRAAVEAVAQVVPSRILMAMPGMFIPPVIMTKLEQRPLFRNNKVVNALTM

IGLTGVCLSFSTPLCCALFPQRSSTAVSSLETELQETIRQRTFHKDPVTHVFYNKGL

>contig14644 Frame-0F

MWQVSTRRLVVAKSFRVRTCALASSLATSGEARADKSDERIAPWNQQTSDDKIKYLSVQV

DRSSLKRTGGALTGSTPVELPKGKSKENVLVHVLRSMIEVKGPLTVAEYMTRALCHPDYG

YYMKKDVFGSEGDFTTAPEISQMFGELVAIWCIATWQQMGMPSHVKIVELGPGRGSLMCD

FLRASKSFPTFYAAIELHLVDISPAMQRIQQETLKCEPILDKKAPEHTMQLPDNGPTARW

HTDFANVPHGPSLIIAQELFDALPVHQFEYTKRGWCERLVDIDFEDGGDHFRFVLSPGPT

PATRVFIGREKLFDPSAASLHVAETQISGIDDLKQISKMAMHETGRLDVADVTSTPVRSA

LAQIGDNIEISPGSIALVQDMAKRISYSGGAALIVDYGNDHPSELSLRGIKKHEFVSVLR

EPGDVDLSADVDFATLKRFSTTDSKVKSVGPVGQGTFLKNMGIEHRLAMLLQNTESEKTQ

QELFSSYERLVNAEQMGTIFKAMALVHKDIGQLVGFEEPSSEAVEHGN

>contig18932-0 Frame-0F0

MRNFIYSLARTQNQFEKCSL

>contig19197 Frame-2F

MRKLNMQRLFRWRRNDNDSPHRWWCNFTHWHSKNAKRSYPIQGLPDTVSGVAYRTGQK

>contig19892 Frame-2R|Blast-ras family GTPase, putative [Phytophthora infestans T30-4](gb|EEY58454.1|) 1e-176

MGGAIPLSAEHGEGLTLLLDEIIPLYETFEQKKNDKETAQKQERGDPQDPRTIKLAIVGR

PNVGKSTLLNKIVRNDRVLTGPEPGVTRDSVEVPWTFQGRLIQLVDTAGIRRYSKRDHDD

QIENLSVRDSFGAIDSAQVVLVVVDMSEPKLFHMDLTIAMRVIEEGRALVLAANKSDLVS

TSVDFWMMQMQKELHDSLAQVRGVPIVPISALTGTGIKKLVPEVLKAYDRWDLRISTGRL

NRWLKAMSRHHPPPTIKGKTLNVKYATQVKARPPTFAVFVSKPSDVPESYQRFLLTQLRE

EFDMVGVPARLLLRGKKDNPFEKRKRFQQRTSSVLYGKQRQMQKGRSHVAPKEDVNGGKS

ELTRKQKTGHFTPRRLKGRK

>contig20171 Frame-1F|Blast-bax inhibitor-like protein [Phytophthora infestans T30-4](gb|EEY53003.1|) 1e-107

MSTFGARTSPQWTMATMMKNSGITEDVQQHLIRVYATLAACVLSAMVSSAVTLMFGPERF

AFVGSSFAATLGSIWLYMEPTQNFKRRFAILMAIAASMGLTVSTLVAVVIQVDSSILVSA

LLLTTLVFLCFTASALIATRRSYLYLGGILSSGLSVVFLTSVIGIFKYSTFLFNLNLYGG

LFLFCGYVVYDTQLIIEKASMGDKDVLAHTLHLFMDLVSIFVRILAALLKGKKGGAPPRN

YNRRT

>contig20539 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61262.1|) 8e-85

MRESLEQRSRLLAAQLQIFERNGRTLTELIAKMLKAREEQETILLAFAKSFEDIAAQEEC

APLAHCLGSLGDCGQKLANESHEVMMLRPEKEILQVIAQIQEWAIVPMKRLLEDGEKAVK

IEFKLQKEYDELKRGSSAREKEKKLRILSDQKRRVENGNALVNLHMEHFDRFRIENMKKI

VNELARSQAFYHAKGLELFAASCQSIATLQPTL

>contig20881 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55857.1|) 1e-43

MCSEQARAELNWSPKLAVLIGSYLSSPLYSLDTGILPNMVSLHLFGANDYVIAASKSQQV

MNIFKDQETRKNSVFTLVHTQGHVIPKCAESLRLFKSFLSL

>contig21217 Frame-1F

MIGNKISRPEEDGNIVRGWINDLVLKPQINIAGGRHRRTFDNESIDVLHSTPIVAVTTGG

RFVGVLDVDRTEFALTWFRQTPPDVAIRPIQGVTRCPYFPSVDDVGSILSLQCQSLRFPQ

LKRVVEMPKPFVLDPAVKNTVDVLLEAKTGSFSATLASNEHDSFQITILIRCR

>contig21914 Frame-2R

MKFFPIFAVASLFTLASAQLDNDAVLDVINRNRFQKGFSFACNNEHVARATQDYAEAVVK

HLAVTGSVPPNGLTPFLLNKTENVISSSPASFYGNYNAESLVKEWAELRGEFISSTEILF

GLGHVDTKSQVYKDALARSDIRGASELRFPHLYVIGLADIKDVKC

>contig22155 Frame-2F|Blast-cell division protein kinase, putative [Phytophthora infestans T30-4](gb|EEY68005.1|) 1e-97

MDKDLKRHMEHTLGKLEPAQIKSFLYQLLNGLAFSHSRGVMHRDLKPQNLLVNAAGELKI

ADFGLARAFSLPIKKYTHEVVTLWYRAPEILLGQEIYSPPVDLWSVGVIFAEMVMKKPLF

AGDSEIDQLYRIF

>contig22634 Frame-1F

MPGKYVIYLNNSQTWVLYTSTRLALRVEYSVVFSVNASGSSLVADSEYFGTIRVALLPED

ANTDIYDEYATCVVLGGTVSMESRTSYTFHWVVEENSCDTSGLLHFALHHQIESMGGPVI

DTTSYGAIILHSATRGQMVAQVTTTPTWSFVEPEADFEVDFYPPDRPSPWLVKKIDLRNT

LEEDILGNWSTWDVDSWYFNGKSFQKYASLCLMASDVSVVGRDTSLLSFCLDKLESLIEP

LLNNTLTPFLMYDTLYRGLISTSIFRANNIYEEFGNSIYNDHHYHYGYFVVASAILKHLD

PNWYRMPELEELIWTMLRDVANPSKKDPYYPCFRHFSWYLGHSYSHGVTSIDNGKDEEST

SEDINFFYGMTLWGRVTGRKAVEDLGSLMLRLDAHAIRTYFLLKRDNTIHPPEIVRNHVT

GIFFDNLVLYNTWFLDEIYAIHGIQMIPVSPINRLARTSTFVAQEWNDILAKQPIIVIEN

SNISWLSLLLVNGATVDPMESLRRLPNATMDDGLSLSWALYNAATRCRDGVKVNMAAEIM

LTIDKTSVISIHTE

>contig25334 Frame-1F|Blast-mannose-1-phosphate guanyltransferase beta, putative [Phytophthora infestans T30-4](gb|EEY62296.1|) 1e-141

MKALILVGGFGTRLRPLTLSCPKPLVEFCNKSIVMHQIEALVAVGVTEVILAVNYQPQVM

LAALESMEKKYHIKISCSHETEPLGTAGPLALARDLLDDGDPFFVFNSDVICEYRLQELL

EYHQQHGAEGTILVTRVDEPSKYGVVLSKNDGQIERFVEKPRDYVGNKINAGIYIFHPNV

LDRIQLRPTSIENEIFPQMAAEHNLYSMVLPGYWMDIGQPKDFLAGMCLHLEYLERTNPE

MLSTGPTFLGNVLVDSSATIGDKCLLGPNVVIGPKCVIED

>contig25455 Frame-2F

MQRVIAMQVRRLQRPMRISNATSFSTKTPEFLDIIYGQDTGVRTVQFNRPEKLNALTLPM

ALHLTHRLHKIEANKTVNAVVFSGNGGKAFCAGGDIRALADNGKDPALRHVALDFFRHEY

RLNYLLATTEMPIISFLNGVTMGGGVGLSMHGKFVVATEKTVFAMPETAIGFFPDVGASY

LLPRLGRRLVEGENYVADVPKSQALKGQGLGTFLALTGERLKSHEVIGFGLATHYLPTSE

YDTLVHHLTGLEFEKNVSQEERDEMIHEALAELETDEAFQEIDQEYLETVEKVFGAHNEN

DTMEGIYERL

>contig25741 Frame-2F

MARLWSSVGVLLWKHWRELQHESRLNRNRVGKRWLFPALVTTIIIPLGLILVLIQKMCEY

NAMLVKPNGGLASLPGFERALSSGSNDTSSVSNDAEYTEHAPFLLTALPLLLAKSNQSLA

FLHRDDALLFLQYLNSQYPGSAELGIPSYVNMTKIIPFSPTASNEAADAIIQEYPTTSGE

HIYATFDLRRADNDPKKASPPLEFSTFFYRKGIMDPSKQDSNDQLFEYYSKEWSFHRPLV

FPDILPFQMA

>contig26920 Frame-1F

MSYRSLHSSKKGPSNIQPSVIDLTTEEEEAEVPSQMEAHLESDDYFEVLKLPRSASGPDV

KRAYRKLAVQWHPDKNRSNARAEEIFKKISGAYEVLSDPEKRKAYAMYGKAGLRGHASAG

EGEDFWPQGHEGFSTQHARDIFNAFFGGNDPFQAFFGSQRQQSGLFEANTFGSMGFGGRM

GGMGFGNMGMPGMNSFFSDGFHSMNGPGTMYSSGTSSSSSTFRDRSGHTITQKTTTITKA

DGRTETVTEEYRNGELVYSSSGNRQLADAGRMQLEGTGQSTNGYMYQRQRF

>contig27592 Frame-1R|Blast-histone-lysine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY69457.1|) 1e-143

MKFNKHTRESNCMLGENCGNRALHQKVYPRFQKFHTVEKGWALRVLEFVKAGQLVIEYVG

EVINEEEKERRLLHHTKNSPEDKNMYIMELGKGEYIDARFKGSVSRFINHSCDPNCHLLK

WRVKGVNRIGITALKDIEPGSELSYDYQFHTKEAIEWKCHCGSKSCRGTMAPDKIRITCV

SPRKKVTKKELIKQRKRALIQEKIQHDRETKSTARRLSLTNYVSMGDRTTTEKMVVRTGP

AVRELQWAKKHKLFNMRDAKHGYNFKLRKELRDARTIRHDRINQELYSVSGSSTTVLSRS

GSPEDC

>contig30404 Frame-2F

MAADGHRVRIAVNEEFRAEIIDRGLEFFPLAGAMRNLHDFIKFLHDTKKANVLQKHLAGR

LVVGPFRDLIFSLWPAANGADPHGRGQGIPGEHFRADALLWHPLLFGHVHIAERLGIPLQ

CFGLLPLSPTFAIPHVLSAFLMDDTSHLGWEFKKTNYLSYGVVDALLWRGMHEILTDFRE

HIGLKRRCNQPSRLVEWQIPHIYLWNPALMHRPIDWGHELSVVGYVTLQDEREIDKMRKY

KWSRSLNEFTLATRLPIIFVGVSANWLASIEIDQLVCQIDKAAEQANVKIIFQACDEEAQ

RSLYHTENIYQVESDIPYSLILRKVVATINWGDPAIVEEGLAAGKPVGICASVSTQYYTA

YMCVAAGVGIPPIDVKTITMESLVLSFRQIVEPKLRKKAVEMAKTFNSDKALETAVANFY

MNLPLRAMRCDIDENKIARIYDPRLELKLSFEAYIAIQPLRFHTDTNDVIYRPLYYDGHT

PAKYSLRSLENDQKVIDKKPYIGLNIIQKALTSLASHSSIESDLEAPRATLTRLSSRVPM

VMEKPVYWSTLEDEEKERTCILKEYEKAIEQHVNSKS

>contig30549 Frame-2F|Blast-peptidase, putative [Phytophthora infestans T30-4](gb|EEY58883.1|) 1e-172

MKLFHPSYCFAAVAFVLTSWPQNQVDACTAIGVTKGASVDGSTLIAHTDDAGDGAADLRL

VRVPAQDHALGSKRAIYNFNGGYPRVVARDRGIQYQPVIDLESGKSQEYSKPMGFIPQVE

HTYAYFDQDYGMMNEEQLSIGESTCGAKTVGWPLDVPEGNNLFGIAELTKIALERCATAR

CAIDMMGSLSEEFGFFSEDSGDMASPDFGDSAEALLIGDKLGEVWVFHVMTGKDHSGAVW

VAQRVPDGHVTVVANAFTIREIDLSQPDWYMASSNVISLAEEMNWWNRTSGQAFDFTAAY

GFADKDAVGPLYTGRRVWRVFDVLAPSLHLDARLGSFSQFATYPFSVKPDHVIETFEIMD

LLRDHYEDTR

>contig31102 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63041.1|) 5e-48

MSVCSIYTQKSSTTVGCYTRGFYELPTGSYNRVILALHNIANQWLSLSRHMECAHMKKLA

WRLRQNSQDMDLVRLACVRPKHKPGDASCQVCAKSLSFLPRRKKTCKSCYHAVCSRCCVK

KLVCVVAPDQSSILE

>contig32280 Frame-1R|Blast-D-2-hydroxyglutarate dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63759.1|) 0.0

MLPRLLRTARSQCSAISSIHHTAATRAFSISARKNALASWNDHDKAYFQQLLNPESVLTD

ADDTEAFTIDWLKKYKAQSNHQMVLKPKTLEQVSSILNYCNDRNIPVVPQGGNTGLVGGS

VPVFDEIVLSMSSMNKVISFDDVSGILVCEAGCVLENLDNYVAKHGYMMPLDLGAKGTCQ

IGGNIATNAGGLRLLRYGSLHGTVLGIEAVLADGTVIDCLSTMRKDNTGYDLKQLFIGSE

GTLGVVTKVSILTPPRSSSRNVAFLACNDFLSCQKAFVEAKKKLGEILSAVEFMDRQSID

MILTQQDWITDPLASPSPFYVLIETSGSNSDHDMEKLEAYLEDVMGSGIVTDGTVAQDEA

QVKKLFMLREDISMSLSSRGYVYKYDISLPIDKYYTIVEDVRKKLAPFGAEVVGFGHLGD

CNLHLNISTLEYDEKVFNALEPYVFEWTSKYRGSISSEHGIGMHKPSFLHLSKSDESIQL

MRQMKEMMDPNGILNPFKILPSSEQTSTW

>contig33975 Frame-2R

MEVPIKEAAERISSITPRPSTTTRSAPSIPRHTACEDDDDSLDAELTKQLTDKLLLRQLE

CEMQKRRPDHFVIGVACRTLGGVPSSLRSQVWKELLGVARTEQPSLDQSILQVEEDLDNQ

RVIAADAIRTRSNERLFQKPETIELVVKLLTYYCKSRSIRYKQGMNEVLAPFLLLTEKRR

PESKGSTPLPEGVIFQCFHALIDRFLPHVFIDKEFRSLQCSLHLYRLLMLYHDPELCHYL

DQHDMTPELYVTPWFMTLFARSLPPEFVFYLWDFFLVEEGPYLLHFVAYALVVAHRDTIL

RADIAMLPQVLSSLTFTSRDDLIQVCGQALVIAESTPNSFNRDLCSVCYGGLKDAIEPFY

NQLHTCSSLRIYPEELIQNLMNRLAFQTKQKQSFELISDATIKHELIRLRSLGSNHSPRL

SQCCHEHEEEEMTPALQFILLDCRPLEEYVKSHLSLSHHIDPTIMERPDALDELMKGFAL

MKGCHFCFVGPSGNLPSSYSRFFLQNAANKTKVPRKESRSNVFKKIHGTIDVTECAASSS

LPLKGFGRQSRRMLSSGKRNVSANKSGHNGVYQVHAEHVSVTRLVFMFLQKGFKYVSRLD

RGFRCLEDSIRSMDQFTQEQLLVASPLPPSIPEPVVVPSSGYMSATTGG

>contig34589 Frame-2F

MPLFSGSNTLRFSLRNHHRHTDADVDSSNSHGSHLNRKPRQEMRPEMHLPDQTTVKSHSL

TTEALQAPSSTLSSSVRSSASTLRSTSNTLIENLSGGENDTDIPEDSESRHSIITPSSSR

VPSMRNSRNSGQTTLRNSHFSLAEYRQLQCSMSYKNRVNSDTYRRSSTTSSHNDPRISER

MSDMLTSFRANEASVSLPDSHSLLHARISELSTNVSCALPHSVEPLAPVDQSSPVLASES

TELTATTRITEV

>contig35065 Frame-1R|Blast-ORM1-like protein [Phytophthora infestans T30-4](gb|EEY54591.1|) 1e-52

MHWVKGSPDDNTIGDYRELTFYEQIDQGRPWTNTKKFLMMIPTFLFLAASVATDYDTQHL

LINFPIWATLILAKLPELDRVRIFGINSTVGIDDHKKN

>contig35238 Frame-2F

MSSPLSSPRSTVMSASPAPVTLENTKELPRARQIVSINEEGTNFTLDEEALRLIFHQVPE

DMKVAIFSVVGAFRTGKSFVLDLFLRYLRHASHGRMLKPDGAQDENTEVWKAWVMEGVTG

SGEEKLEGNSNVEQTDGEKGFSWRAGRKRNTTGIWMWEVPFIRKSHTGEDIAVFLIDTQG

MFDSETSQMLTASIFGLSTLLSSYQIYNVDKRVQEDNLQHLALFTEYGRMALFGDTKSSM

ALSDKQQALQKAASLSDRQGGDVETSDKETSETENDDLDTVKLPKHARPFQRLDFLVRDW

QDFSRNQSLAAKREDMEQYMIELLSCRKQKDLADTREQISSCFEKVACFLLPHPGHAVTE

REYDGSVEAIDSRFLELLTTYLDDLFDPMNLCPKTIHGVTVTSRELYTYIKAYAGLFREA

SIFPEAKTLLEATAEANNINQRDKALIRYKRDM

>contig38178 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63450.1|) 1e-111

MKMYFTCLFRESLNGCLNVIVRGIFNMGKNPGKIAKTLVSASIKSLMMGFLNAPGIGLAK

KLTFLARRNYDALQRPKQSACSSCFKTKKWMLFGLNTYLFQCGVCGTTVCSQCIAHTKQI

LFLGLDAPRSKRPCCATCLRDARRSSRVLIGDQGFQVIADYYLQQRFRSFGQVQSSASAT

VQFPLYPMYSNDTMTREYESSRCRYREKSGLSADMPTNSTAHESLDTDPFSRELDEV

>contig38879 Frame-0F|Blast-acetyl-coenzyme A synthetase [Phytophthora infestans T30-4](gb|EEY58107.1|) 1e-117

MPMKPGSCSKPFFGINFVVTDEHGNEIVGNAVEGHLCIRKPWPGMARTVYGDHSRYLKVY

MSTHQGLYFTGDGCRRDKDGYYFITGRIDDVLCTSGHRIGTAEIESALVAHNLVAEAAVI

GLPHRIKGEGICCFVSLVESVEPSKDVEKELVQQVRAHIGAFAAPDLIVLVPDLPKTRSG

KIMRRVLRKIANGEEHSLGDVSTLADSSVVPMLIENAKAALVGKSF

>contig39076 Frame-0R

MTSIEADTITLRSINDCSSYIILLFAFKPLSTRGALTTEACYHEFCTSVGTVHKSSMFKK

KIRYCDNATS

>contig40469 Frame-0F|Blast-Equilibrative Nucleoside Transporter (ENT) Family [Phytophthora infestans T30-4](gb|EEY61700.1|) 9e-25 NOT\_ORF

MTSKLEYLQRYMSGGCVGACSSNLPISYLYRPCAYSN\*NSIAIQNLDAANRESKKKIKRV

KKNKIETLGTRLVNDDDAWEHSAPSRDEIEKKWELDAAEDEQPLMVTADDTEVADSQDLP

VYVGSDKYLKSMIGNEFSQNSADNDDLSPPRKKVIRLKKEAKLTSEDDFLPQKCSDKTSK

RLEQDKNKSLSPRRRPKNEKKCESVEQDKLAARSRDYRKGADASQRVRETSVSSTKKYCS

VSDGLGSDRKNLRNVLSRSPAHIDRHYRVDSLGRDIIAHSKKSKVRSDSTQKKGSASKHR

RARSRSRSYSRKYRQDLDQKASHSYETNDRRQNRSRSFQSRRRRNGRSPSLRRRRSPRSS

PRKLPQQ

>contig40735 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69437.1|) 7e-13

MRHQVSSCQQIYVKSEVKNVVKALAKRFGSDEALDAAAKEELSLFFEDFLNRV

>contig42001 Frame-2F

MVNMFLPCPLEFRLSRMSILHKDVRKLLYESLWRATTDAHSSLSVLSRSVHLFTLQLYVV

EDFRYFQTIAPASEAKFFDRQLASQIADRFIEWIPQNQPNVLSSVKPRCSILKLLLKLNP

WSSHGGSASMTKLDGDQKHEIGRGIDWLLHRLSRISPECQSVVEQHQVTEQESRDEAARK

LALAQRRKEAQARALRQMQLRQVAFANQMKTVVNESEVGSEEECDIEGEREKHTHLKSET

AMDNNDIEMSTCDGMNDNEFAVECAMCHSGNPENSFMCYVGFAQCSPVLSRLNGGAHDLC

LSTPMDEMHVGEDIPVHVRLCGHSVHHKCWESYHTSQFQRAITGGHHRHALNAVDVTKKE

FLCPLCKSISNVLIPTSTESLRKFLPGMSPQISDTGHVERATATLSQLEMFNWLERTVGK

DSRTLNSNGLSGSSEDASALLLEQKPAPTLSGITDLSGTQQLKQWLEGGLASLCMAIHKV

ACGAMQKSQPERYITSGCNALFHTLLCSFLDTQNSDQLREHLFLEAMCFLPLMLKYVNTR

IPGNASVAPKDLNTRLAHLLFYGGSDILSDGTVVLENEHPSTQTQTRKQSQWAKSEEDAV

FIARLVVLARLVQTLLWYAVTRKEDFSNAMADDLAISKENVTFFMACFCGNRVKSVDAEV

NPEHAVSHQLMLLLNALLQKCDGAFLVQPIIDNRQLLNVVACEVVPLAKAATFMIQTLMK

RATSHHRASTMTASKPIFITQEEVLAVGFVDLNALQLSDQDVDGNKEQAALTKLVFRWVH

RFKTAYEEMYDPHDVLQQWLTTANVDRDLKLSLSSVLIRDLHTTHSTISVFSSGANRTRY

LRTLPRAYVKFYSALAKRRCQACHQFPARPAVCLLCGMLLCAANTCPSIHLDKGGYPDEA

NPGACTIHAKKCGRGSGMFLLVLEGAVLLVYWKLAAYVGSLYVDEYGEEFGERNRELSKG

RPLYLNEERRDRLLRLWLRHEIPNEVVKIQNTSERVIRNSHY

>contig43583 Frame-1F

MDVHRVVTNRQFCNKMWNAVRYALPLLATCDRDRKDGFKSLDVACFRDTMSLADRWILSR

LAAVVIEVNQAIADNQLGVSVAVLQRFFIQELCDVYLEFSKPVLYNNRLANTMDWEVHWN

IKKKQCAQVTLYQCLDYSMRLLHPFIPFVTEELWQRIHGGIESSILCAPYPEKSEMTCWI

DVDAEERMAFLIEVIHGIRSLCHTVKILSSKQTKVSK

>contig43600 Frame-2F|Blast-cryptochrome, putative [Phytophthora infestans T30-4](gb|EEY64672.1|) 5e-90

MRQINQEGWTHHAGRHAAACFLTRGMLYISWSRGASYFQEKMIDMDWPINIGNWLWVSAS

CFFTNYRRVASPSTFPQRWDPQGQFIRKYIPALRNMPDKFVYEPWKAPLKVQRDAGCLIG

KDYPFPIVDSKLAMTRCL

>contig44810 Frame-1F|Blast-nuclear pore complex protein Nup155 [Phytophthora infestans T30-4](gb|EEY53449.1|) 2e-80

MTKALMRDRNENNQILIKQLREQCPIFFSVSDLWHYQGYRSLSNAKLSGSPVARQKLLNE

SLEQFLSSCHMWDTEDSLDVLQGICEDYTFLNYYEGLVKLSLACAKHFHDAAASDLSGVK

EAWKRRCFGCILL

>contig45215 Frame-1F|Blast-protein phosphatase 2C, putative [Phytophthora infestans T30-4](gb|EEY57902.1|) 1e-92

MVKFEQDKLVKEHPGEANVFTCRHPDSCYVKGALQPTRALGDFALKHPEFNGPPYKDGDR

SAGRHFSAPYTPPYITAMPEVKSHTLEEGDKFIIIGSDGLWDYLSNEEAIEVVSEAISRG

NHDLAGRALVERVLQKAAKRYGMTYQDLLSLPPGSNRRRRHDDTTVVVLFFE

>contig45404 Frame-1F|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY61198.1|) 1e-163

MTVWVRAFAIFYDKQDERHTILSSKLAECLKLARDGDQSLKWKFYLLDLLCARLALPDMA

QLFVPTYVDFIEYDEKIERDQISDSKSDVSLRPIDDGVLQNAAVKTGNIKAKWSPAIIRA

SLDSGSLSARCLYDYILGHGPLGLLEACTESIQSGQSDNEFDIDILANAYDEMWDMDRMQ

KVEALECNNRLPGLIDLLRESILLAGWHNFNFNDNYELVHAPLLPLLEKEDFSRPPALNC

RTVLLRSLQDLMIQRLGGSHSEEPSALEFDLSRCAETMTLSDGNRTAKQYTAKQWGMVMA

TTGCPPNTGIHEWGVRLDRCEKDHIFLGVCTRDASVATYVGGDRQGWG

>contig45549 Frame-2F|Blast-serine carboxypeptidase-like family S10, putative [Phytophthora infestans T30-4](gb|EEY54227.1|) 0.0

MQIDDGTPLLLWLNGGPGASSMTGLLTEMGPYRLTKERKLIPHVHSWTNIGHMLFIDQPF

GTGYSSVRDEKGYVNSQEEAAKQLYSGLQVFFRRHPEYKFNPLYVCGESYAGKYALSISH

YIHLKNSGFLNQDGLIINLTGVAIGNGDMWPVLQTRSVPDFAIALGLIDSEQYEDANVQI

SVCEELHRQGRDVDAFHVCHAVTQKIYEAAGTPFIYDIRQSVNTLIDLNMLLSSYFNDDA

VRRALNVPLGTPWKSVDGSAYGTSPAAPPIVRHLQQDEMLDVPIDVFRDLLDNYKVLFYA

GNMDGSVCNNLGVGRIIDRLAWTDTTKYRVAKRQPWMVDGGVAGLVKSAGNMSYVVVLNS

GHLVPADQPEASLDMMRRFINNEPFFTLFRST

>contig45945 Frame-0F

MATGRANAYDSLASPHEAVDMKFSSMQSASSLPVGCDTTLYDHDLVMVFPRREGGEAKKP

DDFTQCSFVQLMMGKDTVRSQRAGNLVVDPFQRVLRTSRCFLDERGCDAVLDSSL

>contig46399 Frame-1R

MQAARHVLALTVARRPRAIFMHSLLLQFHTKRCSSSSSRKPLQNPFEIDLSVLEARQTNL

DHLHDADMQDDICELHQEMSKLFGEEIVENMGDS

>contig46478 Frame-1R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY61424.1|) 1e-43

MLGLFGWTDASQVTLEAHVVLVCTLVGTLGYVAVLKYFTPIVVAVVCLVEPVLIAFMGVA

VDGKEIS

>contig47738 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66702.1|) 1e-28

MSLRRCLYTSALMLVMPSLARSLATEEIYSVSHCAGTPNIIKMVETDNCVPQACTQNDLG

GYNLFVAATCNVKDRFQYSNERLHGFDYVMMEEYKGDGC

>contig48348 Frame-2R

MQLWLQLLQGADALLVCIAAGLLCALYLLGFLVLRNCCRRRHSSEIALVPNAALIVSDME

EPLLENFNYDEELLRTKPVSLPFEYQPSAPPIITIFT

>contig49219 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59278.1|) 2e-78

MSTTSTKWPVVLIHGVLGYGKNRPLWNLWSPYWPEEALAKLNQNHLMVEVGALSSDHDRA

CEAFYQLYGGRVDYGEDHSLEARHARFGATYEQPMYPNWSASNPVHLVGHSLGGTTALEL

YQLLCSDFFNIGSDYRWVVTLVSIAGPLTGSTVTHLFGLHDLHMVPYSLGHVVGSALGMW

FKLHTDWPVLRRVL

>contig49651 Frame-1R

MGIHDAVDSDGPLVVDVHAVTGKMTYTGASEVIANEIGDLGDGGQILITRRIADWLFMYA

DLVAIPCAVDRVGEYTIPMINATLEVFQAIPIELAKRKKKFTTTLKKRVIVQTSGTLDEN

PSSGLTSVAAERRRTLNAWRNRRRQLEQGALRRHATSQSLLGDCEMEINPRKSS

>contig49725 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68521.1|) 9e-42

MVARILLLLAMDKCAFDGKSYKSFNLKAQFVPVYSFLAVLQVCELEPISSKKTAGSKKMK

NLSIFKSWIYRWKDWRMGFTHFVQLQVEPNQDTLWYLLGRRAAGIFPRNQNGADLIIPMF

CSKSDNASC

>contig50965 Frame-0F

MKRCWQWQLQCLSIAVFLQLCVGMFSTDLTLGACEFASESYYIMSTNDSHSPTSVGYLEC

AKATKTDADICKICSCREKKVGVVNGVIVAWAVCVELG

>contig51979 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60202.1|) 2e-42

MAQKLVFVDQVPSYVYQNVTFQATVMLTDSTNVKVTGLQKPLQVLLRYNDSYDVVEDQDA

FLRLNAAATIDADSGMALLSMCVRTLTATCDGRNFCLEVRSIDGEIEPIFSSSVHLVKEK

LHVVTQP

>contig52776 Frame-1R

MIAVEEDLMSLRVPSGNSQLLKFSQDCPLELQELARQCWHESPSERPDAIDVQEELVRVL

EGRLTTSGQPPPNWTPPSYVSAASTLNSLSSFEPSSYMSSSRSVTIADLEGD

>contig53212 Frame-0F|Blast-Hect domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY61850.1|) 1e-29 NOT\_ORF

MDLHALSCIPNLVRLEHKVHYLAMLAEEHLGSIHVSISRTSENNQLDIILQQLHSTLQND

L\*AEMEISLAHGPGVGVGVTRDFLRVFNAAFILQGQLKPHR

>contig53267 Frame-0R|Blast-phosphatidylinositol kinase (PIK-L3) [Phytophthora infestans T30-4](gb|EEY66032.1|) 5e-74

MLDHFAGAFTVLDAADFRDLFITNIHLLYECILQDHAILTIPQHFLANSNVSCWFAEILL

KFLIAQMKDLSVEAEGDLPDTDRVDKVMTIENLRFESMRPVSQVDCASIVLRLFKIVFGS

V

>contig53836 Frame-2F

MTRMPSQILDIHRACRALRSSDGCCQS

>contig54486 Frame-0R|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY57526.1|) 2e-41

MNRESSRSHAVFTVKLVLEERTSAGVKRTRRSCLHLVDLAGSEKQRQTRVQGKRLKEAAQ

INKSLSALGNVIMALVDVCNG

>contig54712 Frame-0R

MILCYIGKGCCVYDSIQYAVDGDVVACVADSKWRIRCFSVCTCY

>contig57748 Frame-1F

MAQKTATDPDKIPGIKKLLRQLNQEVSKSTTLTQKGGLQVPGHIAKELQELQPQFQTLQR

EIEQIDAKLAVYSRQKKRLALVEREIVELPKETKTYRSIGKMFLQTTCKENVAAIKNEDS

FVNDQVSSLGARKNYLTRQKQSVQNNITELLAQCA

>contig57946-1 Frame-0R1

MEIKSNWERSSKIYKLRTENWQPFDYSFFS

>contig58987 Frame-1F

MVFQCVKIGFITTRVVAILCVHLHSHRVELHENT

>contig02617 Frame-2F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY64165.1|) 0.0

MASATNALVAKNSSKAIWDLAIFSFLMLTSKLFKELQSLIYLNVKQTAYIELATLTYEHV

QSLSYDWHVQKKLGDVLRSMDRGVESANSVVSYVFLYLLPTLAESVVVIVIFTMHFELAG

LSFVAFTSLVLYAYLTITITLWRKKYREASIRHDNEYHDKATDALLNYETIKYFGNERHE

VEEYSKVIEKYMRYSMSAQASLSVLNATQSTIIQATVLAALALAVPHVVSDASGRRIDIG

AFVAISVYLTNLFTPLFFLGGIYNMVINSVVDMKKLSELLSVESDVVDSPDAVQLRIFKN

DLENGIDVAFRHVSFHYPSQLASTGVKDLTFTISRGTTTAFVGETGAGKTTISRLLFRFY

DCIAGKILVNNQNIATVTQESLRDAIGIVPQDTVLFNDTILRNIKYGNLNATFDEVVAAA

KAACIYKFIMKLPDQWNTKVGERGLKLSGGEKQRVAIARTLLKNPPFVILDEATSALDTV

TEQEIQDALNRLKANRTMLVIAHRLLTICNAHQIIVMQNGTIAESGTHDELLIRPNSIYA

RMWDAQRKHEDEGSAHDEV

>contig07553 Frame-0F

MLGIAEAFKSNDDGHAAARQQSAQRLHEAYVSQVKRRVWGVRVIRVIHRRRFLMESQNGL

EIYFVDGSSCFFGLEHIGEADLVYATLKERKPPCLAKWGKRLLTADRMLSKSKWTDMWIR

REISNFEYLMALNVSAGRSYNDLAQYPVFPWVLKDYESSELRLDDEDTYRDLRRPIGAQT

PEAIQRARATFENSDPNAPIPAFHYPHAYSHMQSVLYFLLRLAPITSAVLGSDEQQLHPK

AVHEPTFDSIAEAFHMSTHDARHMFELPPEFFYLPELFQSARNKTLARHFFTPGQDYSTT

AGLARNVVLPPWASSPYEFVRLHRLALESDYVSRHLHHWIDLIFGYKQSGTPSIDAMNAY

HIACYPERLDLSTSSDGVRAKLVQRGTIPMQLFRNAHPARMTQDESLEARYPASHSMALL

SSRRQVRRYDLSSKHTAPVTSVRFSNAVNHAVALTALTGSTPGLGSGTGMGAHSTSSTDH

GIVVYTTDSDGVVLAKRYLNAVPDTVRSCPFSMVDVDQWWKLPAGCLVSEGVVFYEQMIS

CGYWDGSWRIHWAADGELLQRIAFHKKPILCMARSEDDFTGDLAVAFGSQDCTVSVWALS

KLSASRSRRLFLKKELPVGGLPWVLLVGHTRPVVAVALNVDLDVVVSASKENIVLLHSLR

GSMALHALALTPGPFETSVIAHLVLSAQGDTLVHSITTHQPCQSRRYSRANSLFSDDKAQ

LTVGGLVGTTTGSMVAGALSSSGYVTPSESSDDRFGHQDGMDQQSELYVVSINGHVVSHD

KLVTRDESTGEHEKNTRPQVLLERGVLFTRSGEYLITACTTGVDAAVEVRNAGMPGSIVR

RIECRRVNATLTSLSMGHDERCIVCGYSDGAVVAYALHFGIADGCKSLVGLDKQARERER

AAFAQATKRDLLRQKRREDFIPTFFRGHSIPMEQNTLWVSRQGKSKVPDALYLTTMQKQF

ALLKQTCNSGDDTYERLLRRLWDALYTRSSCLSSNEKAMTRMVFERVGDTWSRLGFQRPD

PTTDFRAGGMLSLDCLVYFASHYTIQAVRMVSSQVPGSHAHTYPWGPAGINLTCMVARLF

WKFDGELVREQFMNWPLFETEEAFRLVFSEVFVLFDYLWNEMNANYGNFTMVIQATSDRI

RSVLNETPGDLNGVLLALRAQSVSVVPTRRKSVEEVASQPLARNCTRHEGLTASDGTRFQ

PSTPPSKSSRSTWSFTTRLGLGNTHASSCGMDPVETKTLVATTTETSTKSSLKSSTGPTT

ALLVPTGPDIFAGNDFCELGNPSEDPFACLL

>contig09911 Frame-0F

MKVAQFLTLASAFTTVAHAYAASDTPNALIRSFGTKEPHVYDKRRMLTRSESSSNIRLRR

LSLAELDLAEKNVLQDQEAIKTAKHLENEALKKLKKDVMSNNDKDLDKDIAAKLAAEEVE

EEAEEVEKMDEEIEENEVEKELESLFDSVDEDSEDKKDETKKEKDDATPKKKTTPKSSTS

KKEQGSKEIQDSDDDSEEEEVARRRHRLLLALVDLKVTEDAIRKDKKLEKEAKKVENEAL

EKLKADIMASNEKDIDEDMVVKMVAEEVEEEAEEAEKADEDNAETQVEHDLETLLEVEDD

DDSVDEETESSTSKVKQVAEEKTDESDDEDEEEGGRIRFRRRLTQEELKLAEQNIRDDKK

LKKEAKILAAEAKKLLQIDATGSNDEAIDDDIAIKLVAKEMEVKAKEAEELDKGIAEYQM

ENELEELYDAENDDVSDDSETKGSKDSLKQTKITSDVAVSKKKVPTHTDEVQEKDDDDDE

DEDEDEEEDEDDEARRHLRRLSVVDEADVEKEIGEAEAAMKVAEGEDAKASVELVEALKD

SDESEIEDAIKAELAAKEEKAEAEIEEEIGEDLELLDLEKELEVGDAEDGEAEEEEEEDT

SDKAAKKPAKSSKKSKAAGESDKKGKEQSSSDKKTSKTSKQSQTGDSSDQGTKSEDEAEV

PSKKISKKAKTEEVPDEEDDTVPAKKLKKSSKTVQVEEDDDSDDDGN

>contig10940 Frame-2R

MHEQLPLGAVLTAEGDVVIPASRRPNGSTRKPIRIRQGYLPPDEVQKYKTVANRRHEQEL

KRAAEVRSAVVDELSMEKLSLGTKTDVSAARGLLRSSDKCSRKMQGRQHLIKDTRAGMVT

SSEASREQRQQLQLQLTKVKKKLTKMADMGPDSLTARQEVQISKLQQQKVEIIAKLNGAT

FLRTSASADGLRSRLDISL

>contig11200 Frame-1F

MLATARTAPAELHFSSFLTQLKTEPSAEPSTRLDDPSASSPVPSADTFTTNYAPVRPLSS

ASSFHAPSGYYHSTTEVLPPRELPNSIPLWSTAVPSLSTETYGNHNPVLHPLLHHNTSLL

RPNEDELVLDAQMLREVLQEMPSSHVSHRTPLMPGLQLLFASPLPSSDLHSANPPSFYPP

PPSMASSSEMLLPMSQSAASANGHDLPSPSQNFAPPLATNVPLARKKRAPTTRVCKVEGC

TKGIRSRGLCKAHGGGRRCTTPGCTTSDQGGGHCVLHGGGRRCRIDGCKKSAQWRGVCKM

HGGARRCRYGQCSKNGQVKQGYCRMHHNLLTAQRQQQEQLQLQHSLQPLPPLPSMSGKRT

MDGN

>contig11824 Frame-2R|Blast-syntaxin 7-like protein [Phytophthora infestans T30-4](gb|EEY57916.1|) 1e-122

MGDRYQSNQSPRDSSGSMTNERFGKLVTETSKGISNFNQLTRSIAQKMSLFGTPQDSRSN

HVHIKELTEKGNKLVAKINRRLQELNRGAKGAAGRTRRTQINKLSADYKNQVRVFEETCE

RLLESERQSVDFIRRSSQSFRGGDSRQSRKGVEFTNYSEDQIYAQANVIIYDEDDMQRRE

DDIIQINHQLREVNAAFTEIDGLIQDQGETVVEIVENTETAKENVSSALEEVRQAEQRKK

CCAFSKIELFFFVILLLVIFMAVMGILFAAK

>contig12472 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68367.1|) 1e-120

MMDMRQITTPTFAMGVKDLRDPHGQVDSQRSAYGQQQRVEMDMRYKSYDASSNGAQYLQI

HADQRSYEPISLQAGSATRYHIPMDNGALPSVSGGMYKSSTGMDRQAYASRAAPEQSKNL

YSQHWTAKPEIPQHHSDGRVDYFDANKEQHHHQQSQQSTHHLPYPAQSSQYHHHLSPADS

AAAAAAYGQQHASRGYYSHQFPQSSAPGEPSTSQQPPSMIYYSANGYQPHQMHSIQQQQQ

QMQIL

>contig13408 Frame-2F

MVEESLFSSEAAYCSKERSCLPVITSVASLIGYFYVVGTYWRVLAVRQHPAGIMFGMSLY

GAIYQFLFLLDRTVSSVKCTDIGILVDFFHTGQETYMLIFAIDLLLALKNPFSASKGQMT

KYHICGGLWSFLCAMISHFDSTQYALFSFCWFNSGADSLQRTSIRIEKNSNTTLTAGVFF

AVYMVVVYCTSLLAIVRTWNTFVKGLPDTFRTRQRIQRHLKYYVGCYFGYWTVVLVCYAV

LRLLPYSSFEIKGGLKCCVWHLLSCLLLAKGMVHALIWTRTSNILALFEQFRQTGTIILP

VPNNGNWDDNINWALRLEILTSTSKGICQSVDRAEDQARASTDSSSRSLSDASLEEGKRG

PGLTDDYCDRKESYTQIEELLLETHDNHSRNEGVVFKDFAPHVFRCLREVAKVSSASYRN

SLQQTTKEQVSEGKSGAFFYFTQDRKYVVKTLANEELKFFLSILPTYYTYMKRHPDTFMT

RFFGCHGLTMYGKTVFFVVMQSVFATSLPIHERFDLKGSWVGRLEGRKPLGTVATCKFCN

AEYTIRTYEQRCHGRGERHLNHQYDQVG

>contig14180 Frame-2F|Blast-proteasome subunit beta, putative [Phytophthora infestans T30-4](gb|EEY70244.1|) 1e-123

MNSRQRTQSPIVTGTSVIALKYKGGVMMAADTLGSYGSLARFTDQRRLTAVHNATLVGAG

GDFSDFQFIKDKLDELEVYDFNKDDGCGTTAPEIYHYLQRLFYHRRNKFDPLWNTIVVGG

LNQETNEPFLGQVTMIGLAFEGDYIATGFGHHLGMPLLRKQWQPDMEETDARKLLEDCMR

VCFYRDCRTINRVQFAKVTAEGVTIPEPVKMDTKWDYAQFVQTKSEVGSSW

>contig14203 Frame-0R

MMKESRDLLKQLKLMFSTIIRFCKAQENLYTSAMHEKHVVRKRLLVMRRQEFNNSALLAK

DKNNVQVDQDTFAANSKIMSQVEEISDDFCNQFIKLLDIIKQDST

>contig16829 Frame-1F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 4e-53

MQLDYQNSLVSFHNLGILVALWLPVVCIFNYSTQIFFTILQALLGGFQGILMKTGEIRGA

KEMTKAFRVAPQLFDQKVVTLLARSSDAPTSSMESVRMST

>contig19802 Frame-2R

MRMPFITSCRNTFAIHGVVPNVVVLPIQGSLNNSLLSSSPVAFSFSRAKINSGA

>contig20536 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64332.1|) 1e-139

MLEQDEEIFYGFWGSCTNSYRDTEHHKGYQILLKWRDAIQVKANSRGTDGKNSSFRATFD

RLKKCQALPAGARAASVTSNHFFVYTSNVDSHFKRDFDSKEVYELHGSIENWQCAGDVET

GTREPCKKIWKLPLGFRFDLDLTTMKARGAEATTCPECGGKGRPNVLMFHDRQWIANTSE

EERYIAWESVMELMLQEDPTLNLVVLEIGCGTRVPSVRRETEMVVADVIEGCGRPQATLI

RVNIEASRCDHPLILANNSFISIRSKGLKALQGIDYELDNLRVKAKAK

>contig21218 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64188.1|) 0.0

MLLGSQKGHLVQMDTLRMKLTCELQANDLVRDVTFLHNDSLFAVAQKKHVYIYDSTGAEA

HCIRTIPQPRKMEFLPYHFLLSCVSGNGLLTYHDVTIGKQVSTHRTKQGLCDTMALNPWN

AVVNLGHASGIVTLWTPNMSDAVVKMQCHQGPIRSMGIDNSGNYLITAGADRKVKVFDLR

KYQELNNYYLSAAANTLRVSQRGLVAVGFGPNVHVLKGTYSSSSPIRPYMTHQIPGSMIA

SVAFRPFEDVLGVGHATGFNSIVIPGSGEPNFDTYEANPFENHKQRDESEVRSLLEKIRP

EMITLDPNAIGRVDMDPVDEQEKKIHQMRLANGDDMLKKTKKKMRGKNRPSRRLRKKQQN

VVDAKSNSFASS

>contig21373 Frame-2R

MTRTPQAQLYPRLYYMNISWNDDSGQL

>contig21694 Frame-1R

MIQHLQSLLQVKTEEARFKTQSCTERSPVRAGSRSIATTSGRSKASARESSHTGYNILDS

SITSSHHGDNDKENAGLCTHEQASSEPTAANSQAKSPRSMLMPISSNQADFGCLLQESAS

LSRIKRFNRVTTNPFKKLSQAQAQQSDVMNQAVRWARTQGGRIDISTSQTQLPARRKKLA

DRPKNSFLAPTQASLRRVRCLPRRFDHVRRPFVV

>contig21720 Frame-1R

MASRFWAGSSSSEEESDVSDVSDVETTQQQAARAATRWAVQSDSDSDEEVRVVKSAKDKA

LESMARHCTGLRNHMKINDWTQIQTEFDELTKQHERAKKSTTTLPVFYLRTMVALEDFMA

EKVKSKSEQKKMSKENSKALIRMKGKLKKQLESIRLQIDDFRANPMDSSDESASESSSSD

ASSDESDASSSAVSSKDESESSGSEDESTDDEKSGSDDDSDDSDRSWPSKSSSSSSSSED

DDNMPKGRARWLKQTPILTKTTKVKGPKLVKQRETRRDSEEAIPKVLIEEELKLTPSQFD

RRVKEVVAMRGKKGIDLSEQITLMRKLALYARRLGPARQIVATMYLVGTSVFDTSSKIDR

VMSARHWKQVQTNVCTILNLLEKNPEFSLAPLSSEDQADMVRAGREKVTAAQIAAAAAEE

AEQDLHFVDTLPPAGTKGTIKVSGDLVTFVERLSEEYIKALQQTDPHTSEYVARLYDESL

LYDVAERVQTLYARKDPQRAATMALV

>contig22044 Frame-1R

MAHGDEKSMLTKEEKAAKKLSKLARKLEKEKAKAAASESSDKKEKKHKKDKKEKKTGTSK

KRSREADLENDETDPAEETGESELEASRPKKVKNENATHVGGEENPPLDSFRICDVTKKN

LQTRGIYTLFPIQAMTFDKIMDGNDIIGRARTGMGKTLAFALPVIELLLQDKRPRPHGRA

PRVVCMAPTRELAKQVASEFELTGPSLSTVCIYGGASYQSQNHAFRSGVDILVGTTGRVI

DHIDRGNLRLHDCEFLILDEADTMLEMGFREDIQKVFAAMEKMQNECTRKRQTLLFSATI

PKWVKDVADNYMKKAEYVNLVKDSDSQASTDVQHIAIPCHWQGRPTLLASLLGVYASNES

RTIIFAETKKDCNELAVHPEIKTDCQVLHGDIAQEQRETTMKAFREGRLRLLIATDVAAR

GLDMNVDLVINSEPPRKMSGVADVDTYVHRSGRTGRAGKKGICITLYTNRQRDQLNQIEQ

KIGNKLIMRGPPDQEDLIKASAAKALKDINNVDPAMIEMFREKAIEILKTMTPESCLAAA

LACITGHTKPPRRTSLMSGVPDYVTVQFVSSNCIRAKGYVWNALNRDFPENIANDVKQLT

LTEDLMGACFDLPIAGLELLEKQIVDSGFNCPYSIPKQLPNLQKAAYQMRQQSYRGGRGR

GGSFARGGRGRR

>contig22714 Frame-1F

MTSKRLGPHNNKKLMDICLDIKEEDKRPEIQFKSNLILKKRSSPFEGLLSDSMNVCSLKC

MEDQLTLPGLPTMPPNIRLADATSCVTSLEANSKTVDVEELGVAEASQTTQMRQEKSIVV

DYEDSDGDQLEIRESIARCASSACGPVLTDESSDGSLLALQRSPSCSLGVTTVAALSGRS

VTFEQDEAFVNLAFDTSSDTLAEEKMRCSKEHKLCACEVKLHRSLDSCWLVSGGQVYDVT

GLVTVHPGGILSILRKAGGLDCTRDMKFHTKNARKMMEKCFIGKLQQCGDEVDISGRVNC

NIM

>contig22923 Frame-1F

MALHRLNKPITQNEMFGVLRRAKQFKPSTVTFSLYYTYSTERVVDEKIPRPRMLSLRWPS

SAKHLCKSTHSPFTFSHNYT

>contig23528 Frame-2R

MNDLSEALWTFLFGASCVAGLILARRRKLHRFHLQILNAKSADCGRLFGLDIGGTLTKLV

YFQSVDGAAVAQQTQLENLSDLVAHSERQKVKGSLPLIDDFIMRLDTTEEAQREDRLKMV

VPELGGTIHFVNFPTIKMDDITEFVRRRFFHRYIKKIACTGGGAFKFSQLFQSRLGIELV

KTDEMDALIQGLNYVLQYARGECYRFVNVIPDTHGLGRATKEIVPTPEKCNLYPFLLVNI

GSGVSIIKITGKLQYERVSGSSLGGGTFLGLCRALSKLRTFDEAMDASVQGDSNEVDMTV

GDIYGSAGYEHFQLKPETVASSFGKAGSRQLSHPLRDADLARSLLFMITQNLGQLAFLNA

RRANVKQIYFSGNFLRHNEVACRQLAYAINFWSKNEMQAQFFHHEGYFGALGTFLQRFNS

NETEFAESENNAG

>contig23663 Frame-2R

MSTATIAARQVITERLKDNESAVCILAPLDHPQCVQNFYDAWQP

>contig24257 Frame-0R

MRFIRAFFFLPSAADIGVVPRFKRELYTIQHTMTALLFLRDAYFSVGNTSVANYEYLQTS

SGQIHPVNLEVQRVLPKGDLETQEYLVFQDDGSVGPFDPAMPAWQKKHLFRSVRVVKFSF

PMRDRQFGKLYEECFEWRVKVRFEAYKSAHFRVQLEDCEVSRCVNLQPSSFWTMARQPFM

WMHLLIAVIIVLYTILSFKALRRSFHVIRRASKVMKKNAKTSRQKHVKPYEDDRDSDYSK

RYAKQHESLTLWSEITLLLKLKFIQVIVFVSLLLLLASTTWSLLFLEAHMPVRLWHRILH

ATALLLLWSSLVGYLEHDRHIFSIVLTLKWATPRVLQFLLGVSPIFIGYALFGTIYFGNK

IKQFGSLSASMVTLFSLMNGDIIMDTFDAMELHHYYVSGKMYLYSFLSLFMYVVLNIFIA

IVEEAFFATQSTRRRLSHLLSDPNTSGAEVAKETDLPA

>contig24507 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54209.1|) 1e-128

MYFGTMRELFQSGVRSDITLEVGPDREMLRAHRLILTTRCEIFEAMFRPGAMKESWDGVV

RIEDHSPEMVSKMLEFIYTNRVLDLAKLNSNQLIDLLTLSEQYLLLPLKHLCEVAAQDVL

SVGNIGRFLCAAEKFNAAYLKEYCIAYFMNHTSEIIDDENFRDEIESCPSMALTIVRATT

RIPGSLSEPVQKRRRLNMPFDEPEYLSPST

>contig25056 Frame-2F

MPDLLSGDFKTENSNDELQIPSLTFKKSADYVRAFLPLLVAECSNEVKEGLRRSGYSNGG

HLLRYVSEKPREGMRCLNFSIVERDEGLLASSMCKERPNNSYNEKLLRNGDIIFLQAAGE

SQNRSGHIRARTFLGVVLISETEKGRRQTFGTEKSSKIEVEESVSVLFLNDGELDSATTS

VHAFSSELLTSSAIASSEWKVKSLCNLVTSAREYIGLRSVDMLPEHLRSVILTPDAYQST

QSELITITSALDNLRRESSNKSCAQIVKILKRLSGMNVMLTDLRSTSIGKAVNKLRKHDN

ADVKALSTKLKDKWTELIDQKDVLECPPRFVPSDLWEAIKHQYNNSQLQSIHSVLNNYSI

GVSLLQGPPGTGKTKTIMGLLSGLLSLRLPTSAIMPISKLDAQSDDAKGGLTNREAVPTR

QLKGEPKEMLTSSTAAPIFSVSALGSILCRSSNSTSTGPNRRSVQTLKNKESSRSRLEAK

LSSRTNHSNSNLVVKRRIITRAASERLAGRTNNILLCAPSNGAVNELVLRIMTDGLLDSV

GKLTKVCAPSVHPEALKEDFISIVRLGNAGEDAPEIVNSVCLPHIIRREMAIHPKAMGLR

ALQDTQRFLRSSIREFHNKANENDGKQKNRKELAKTHQRLTECTGNIRRLRDEMTAIRAK

TTETILSKANIIACTLSKAGSGDFSNLKHGFDALIIDEAAQAVELSTLVPIRERVARVVL

VGDPKQLPATVKSVVAAKARYDRSLFERIAESGVAPSMLRVQYRMHPFLREFPSKRFYGG

LLTDGPSVMEQIRKTCSGVYARTSFQPFLLYDVENSREEDMNGSKYNREEAAFCINLCQN

MFETCIDVRNNNWSVGFVSPYKEQVRVLRQEITRSKISASVSIEVNTVDGFQGREKDVIV

FSCVRSSKRGGIGFLRDIRRLNVAITRARYCMYVVGNVDTLVRDETWAALVKSARDRRLV

INTKGEPFSMVAKRLESDKYRDLAEHYQLMHSKAVEKCALIVKPKVAVSKAETIAQEAQS

VGATQPSGVKATQSNDCVPQEGDERVSNSNASSKPLCDGNDSKQGIQKPESHKRVAALGA

L

>contig25214 Frame-0F

MEHPRRVQIFQANRLRPIRELTSPLFASVHSIYAVHPFHDFIVGGNSSGRVALWRGVSTT

NEMNNKTTS

>contig25544 Frame-0F|Blast-carbohydrate esterase, putative [Phytophthora infestans T30-4](gb|EEY57726.1|) 1e-71

MQILADPQYLAAVGLEQPVHTFVKGCVGISGAYNIVRLANTSFYGKFITNPPFGERVEQW

RDASIGPTLLKIGESSPLTRMPLLLLTAQEDYHFQEDAQEIERWLTAVGNTSIKRHVIPH

CNHFSIVQHLAKNDFDSNLTML

>contig26242 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65216.1|) 5e-09 NOT\_ORF

MSHYVVVDARLSLSTENFCCLPGTPQLHRPKMVLNSCQKQMLQARSGSTSILSLQASDAS

PVNRCAHT\*GPKPT\*NFHQNTRPRHTSSAMTTRQADPLCEKSWHSSQ\*MKINRQEFWRRF

SK

>contig27502 Frame-1R|Blast-DNA polymerase I, putative [Phytophthora infestans T30-4](gb|EEY65558.1|) 4e-60

MEIAREFGYTRTLLGRYRRLPDAMLMDDTMAAKKARGHAERAAINTPIQGAAADVVMQAM

LRVHQNTRLKELGWEMVSQIHDEIIVEGPEESVDEAIKLVVHLMENPFEKPLSVALEVEA

NVNESP

>contig27609 Frame-0F

MKIIYCSRTHSQISQFVREIRKTKFANHIRVVSLGSRKNLCTNPKVSKLESDVRMTDKCL

DMMQSSKTKDGKKVCKCPFYEKELLGQYKNHALAHVQDIEDLHTLGEHMSVCSYYGTRES

IPLAQIVTVPYSMLLSKDTRETLGIDVENNIVIFDEAHNIIDAINNTYKVEITSKQLVLA

RRALWSYFSKYEKRLKGKNSFYIKQLLSILELMTKFLRQANKAAFKAASSREDDKELGVA

QMMTINDFLFSARVDNFNMFKILEYLKESDLAKKLMGFANSLQTSCQAAETLLDNDTDEG

YQSRHASPLRIVEAFLKALTNTGGDGRIFVQPHN

>contig28055 Frame-0R

MTSNLVDNASYFDDDTHVIPPHAQELLSSLSSFSLQSLADSAVLELTGHHTSEPQPQVDN

EAFAAMCAIVTCFARDVRPQTSIEQ

>contig29913 Frame-2F|Blast-long-chain-fatty-acid-CoA ligase, putative [Phytophthora infestans T30-4](gb|EEY57424.1|) 1e-156

MRGNLAVRAEHCLALRFGAMNALRKTVLRGRNVFLGYRNAASTSLSTELLGDDSKELYTM

IDDSDGWLRMRQRAFLTPTGFLRLNDPRDFLVLSTGDWIPIQPFECAMMKLMPELVRAVL

IGDGRTFLSALFFLKTSVGGSRMIAGNSKHVNGRRLDDEALKVGHSIKSAAMTVGEAIRC

QQWAVHFDVVLEKLPDVCCISGHRVRKWILMAADFSVETGELDPDTGDVCRRGVAHKYHA

LLESLYN

>contig30546 Frame-2F|Blast-cell 5A endo-1,4-betaglucanase [Phytophthora infestans]gb|ABG91064.1| cell 5A endo-1,4-betaglucanase [Phytophthora infestans](gb|ABG91063.1|) 0.0

MSMSGRPSGVGRGSFSAGRSSEVERIIAAADVDTTFAGKKARYRGRRSTWPGALALFLLA

IVSIAGLTYYGIKVKDGVNETVASSEASEESRFSDGTQIIDGSPTDPASELATTNPKMYA

DRKCEQPNYISKNGRIYAQLSDGTSTQIDIKGVNWKGMEDPKGVPKGLWDNMVDGDSLYR

YAYFFHYNKFNVVRFPLSIDAVMRNTDIDSNLVNSNSNRALATASRYNTLLSLLVQGLGQ

FNIGVVLDFHVLSALEDDRSGLWYGTSIQLKDIKTAITNLAEAMCDSTHFNIIGIDLKDG

LNKDATWGDGSDTDWSVAATELGNHMLTECPKWLAFVQGVQGESHKDLYGERSLKNTFLP

GSDLSGVSTNPITLETDNKVVYAPKFFSSSYSPRLFFFGDGETSGNLLKNYVELADADLL

ANIKLHMNYSFGAAFDTGMAVVLSSFGGLVGDLDATDMQTSSRIIENVIGQMAGSTAPYL

AGGFWWTLNPDTAWPYPAPDNSNSTEQGLVGDTWRVANMDVLKALAAMNKTMDSVKFIPC

ST

>contig31178 Frame-1F

MPLDSIREAHASFSFGISEPQSGNISSVFIKINTKRSTDGTAAFVHAIRLASYNGPIAET

VADRSASVTTVVVNGILFQVFTNKVDDVTTFTYIPSQDAMQFVGNLMDFPNSLPYSTTFP

LDLVSIEAGF

>contig31192 Frame-1F

MKRHGSAEGSRLLVAIVLAA

>contig31530 Frame-1F|Blast-translation initiation factor eIF-2B subunit beta, putative [Phytophthora infestans T30-4](gb|EEY56937.1|) 1e-110 NOT\_ORF

MATPTKELTEWLDEWPVVRELVDELVLSLKRRQLHGSYETAKMTTSVLSKVLATVEWSTA

GEILDKIRQLGHMLTKAHAHELAIGNVVRRVLYIIREEHLNALKLPSYGNGLRTIAAPTS

NVSSNRNNNLSRSLDTILTPGTDTDLSIPITDLKLSVMEGIAELVDEIDNLHVNIADQAM

EYIHTEYSGLPLLRQIS\*WLMCCGISHYSEVILTFGRSLSVEAFLKTAAKKRSFKVIVVE

SAPSLNGQHMAHALAESGIHVTVIPDSAVFALMARVNKVVVPAAAVVANGGLIAQSGLQN

IALAAKKCSVPVVCVAGLIKLSPLYAHDLDVLRELLAPSSIYNYEDTVDN

>contig32166 Frame-1F

MDAPTQVAYLRNVLRITEYVGGLRERVLGLVIDQLVAIDVEIKLDESEEDVFTMDDFLDD

NMLAPDDASQQVDKMADKLDQMMLVMFKYIEECAASSSSTFSAGGSVATIDSTDGGVDIR

QAALVFKYLLKVFEHSILNTHRSKYPQFLLFYVCRIDPQFQDIFISQLLAASLDPQTPAT

MRQSCGAYLASFLARAKYISVAYLQKALYHLLKWLHDQMDIYDETLQEQQRVCDPYAASE

IYTELRKESQNVEITGAHGFQENIFVSSLQTVCYMLCFRGLEIAISDNGTGYEFLRSLGW

ERLLITSDGYCPLAYCQQTVATEFLNLAEAFDLVSDECLERVDQAIGSASVSTSKSSKSM

ERSKKPTSGSSTATTLLDQRQPLETFFPFDPYLLRRSFQYIGPLYLYWKHADPTSPENYK

RLESVKDTIRLMRRGAHIECYGSEEEEGTNDDDTSVGGSASIPINFTSASYDAESHMGSL

DRDYTSPGSSYDMKDHVDDRVACKRSLPSRCMFNPSPALSASSPPSRLPPLGATNAFILG

GFDGDEDDGF

>contig32364 Frame-1F

MDNLIQRYGHITCVNLIDKAGKSSTVRDQAQLGSAFGKYAKKYNTLSKSGDGLSSVGSSA

ALSMPMSPARNVLSPQQKSTPNALPPPLAGNGSNGVGTSSTGGSLAGSPTSASMAINSDK

VPGSVGSATLQALMSLPARIHPPPSIPVPLAPTSISQLFAEPVAYVWFDFHHECRKMAWH

NLSKLLTEVEEQFTQYGWFECDGEGRLLSRQRGVFRVNCMDNLDRTNVVMSLFARRTMLM

ALQLYPFDVVKDDNGNSVLDSPYESFEVVFKNAWADNADYVSRMYAGTGALKTDFTRTGR

RTLAGALQDGVNSITRYYLNNFSDGIRQDAFDLLVGNFAPDKRDESPFTFQQQHSLMHLM

LEVALATCAIVTVSLSTRPELPVATRVRDGVIAAVVLFFVTGYVIMKKGTFRSIGRRYVC

KPAFSSSGYIRRKTS

>contig32834 Frame-0F

MCRPIESRDSISVMGLSAAALFPGYQVSSKASANQAAQISRDAPAWSTSGGRDNMNMVNM

ATPPALPVYPFLSSDMPNMPWNAATSTTNLLRMGLPSDQYSIAIATCEGTPEVSVLESNF

EAQELEELLEYSVPVDSDSNSIDKDKPDLSGEGFGGMELSILYSFLMDRPDENSKKHGEI

DDGILNLDMLTGSPVEGLVESLESDCKGTDFLMMTCRHQEPHMMIPTVSPTTVVAKSRRL

CKSEGCPKRSRSNGLCISHGGGRRCAIKGCDKSSQGGNLCIRHGGGKRCSYKGCGKAAQT

NFLCKAHGGGPRCQFSGCSCSSQGGGFCRSHGGGKRCMFDGCDKGTQRGEFCALHGGSRL

CEVPNCMRNDRGGGLCATHGGGKRCIVEWCYKPCRRKGLCSAHLRQVEEAVSR

>contig33301 Frame-0R

MIIAIATFSLILGLLTLVANLVPQVSNIAFAARSATSSFRTQTLIIAVHH

>contig34586 Frame-1R

MTSCHRVIKCWTMSTPCVTPSSWISFHRTFQLARRNNA

>contig34847 Frame-2F

MHLERRHLPAFSSRIRASSVCWNARHVLYAQTMFIGPNLSAIIKVLSRQCQQRREPIFGR

CSASTPVLVVTGFSDLKVRFIFHPQAR

>contig36944 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY62844.1|) 1e-104

MVCMNSAFRKILRLSTTARRTMDTGEIVTFVSVDSDRVLSAYKLGMWCTISPLMLLVVGV

LISTQMDVLVAVAALVTIAIVMQTSLLLSRKIGAYRRQISRLSANRLKVTNEMLQGIRVV

KYYSWEGFASDLIGEIRDREIALLRKYNRVRLANTVLMFLAPTLLNLVCFSTTIVLGNTL

DIPSTFTIVALTNACRT

>contig38696 Frame-1F

MKELKIKKPRVGDNGLVKRKTSTSKRMRPKRNSDGDSNQARKKKKGLEVDLSIYRPPASL

TEVAPARVISTRLTARVQLKEVAAHECDKTMSSQKPKTE

>contig38876 Frame-0F

MKQKHSLQLENIELQLRSMEETYELHQRAVLLASQSKTLDVLALSGPVYLAPMVLMPDTL

KALTCVTFVIGNSLEVIEEKMKRLRGERIPGTKAILVESEDEANNIKQSIVDYGVALLER

KRNENPVR

>contig39079 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57560.1|) 2e-59

MLFRSRAFNFGLASGIHRTLNSTRMPSALIPIADGSEEIEAITLANVLTRGGVEVTLATV

GNKPNNVVTMSRGVMVKGDMAIEACAGKSYDLVLIPGGMPGAKHIRDSKEVVALLQKQKN

DGNLYGAICAAPAVVLHSLGLLAPGVATSYPSFEPQMEGVEYKHDDVIVNGKCVTSRGPG

TAMAMGVKLVELLCGHEKAQSVAQDLLYTPSP

>contig39871 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62990.1|) 3e-34

MVVETAIVISGIGKEINDEMLKKMYCAYGPIARVKHNGSNSAQVVFTSKKDALKATRATN

GAIVHGKTLKVTFQRKFKQSTEPCRGFVAGICRKGDMCKYYHVTDDATYARSSTPAV

>contig40237 Frame-0F|Blast-cystathionine beta-lyase [Phytophthora infestans T30-4](gb|EEY60664.1|) 0.0

MLERSYVTQLVSGSGQAEPEKIFVPRYEAEATPKRARAHLDGNEALEIDEVNRNMLKNGA

SDEFSMSTRIVSFEACKDDPHGSATMPIYQTSTFAQPSGTTFGAYDYTRSGNPTRAALER

QMAELENGHRAFAFTSGMAALSAVSRLAHVGDEIVLSDDSYGGTYRLLSKVATKNGINVK

YVDLSGEHGPKNLLAALTDKTKLVMMESPTNPMQRICDIKRLAEAAHTVNALLSVDNTMM

SPILQNPLDLGADIVVHSATKFICGHSDTMSGIVIAKDPDICRDVYFYQNAEGTGLAPFD

CWLLLRGVKTMSLRVLTAQKNAAEVASFLKDHPLIKTVHYTALLPKKSPESMIHDSQARG

CGSVVCFRTGSLAFSQHLLTVTKLFKITVSFGSVNSLISLPGAMSHASIPEEVRKAREFP

EDLVRLSIGIEDAKDLIKDLSQALQSYVAP

>contig40466 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59046.1|) 5e-29

MVFLMTLVDQLEDKLQQDRVHIIKSEIKADTSDLLQPCQDQAVHGHDDVTA

>contig43023 Frame-0F

MLTSVIKILTTPGPDGILTLMPFNEPEPACLKIVEENLWLTAVKQTISLLMQIVVSDHRK

FLTSQANNSVQETIADDFNAPASAIRLLKMYQLVLLSKAVALTNLSASSNELEQQVISRR

RLQLQDAIVQLSFLCLHAYRDLVDNIVTSQAEESFFFTEAEAAQLLDVPPYKFPLLSEVL

PWFLTCLCLLQR

>contig43485 Frame-1R

MTESGRRRVEQKGRFTITEIIPGSPSSAQLSSLTFLDDEMSIADFSTVDVALPTGDSCSE

MAPLSLQQAPVEPSETVIDTIVASNARTTEKSLDGQPHETVSAPSISALTSAAEAEGAAV

SSVSEVFSPLKAELPSQKYTSPKKMAQRIRRIKRR

>contig43944-0 Frame-1F0

MGRHIARGLWKNVVLQVRKFASSGKLMIDIRAGFLHSATFSAVKFLLGNELSQLINVFTD

CSLVVSV

>contig44178 Frame-1F|Blast-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65844.1|) 1e-69

MLSTLWWITLALAVLVTQCYKIIVRFLQLLLHTYFRKIVINGLNNFPREGPVILCPNHPN

MLVDAILVMTEAASYGRSTYVWAKGSLFKNPFAAFILKKLGAVPVYRPRRKDASLADEDS

QKTPQELDAANRVMFEQTWRVLSEGNVMVLFPEGTSYTAPK

>contig45087 Frame-0F

MADFHMTEPEETEIELIFADETTQEFDIGEAPQDDDDDIMEDKDDEIRDDADMVYHKHSG

PVYSIKVNPLDPRMVITGGGDDAGVIWNLENGNILYKLLGHQDSIVSVDFNHDGKYAATG

GYDGVVKVWDVATGNQLTNLVGPTQEIEWICWHKKGDVVLAGSGDGTVWMWLATTGECMH

VFAGHEDGVTCGTFTGSGKMIVTGSTDCTVRVWNPKTGECNHVFRGHGFHAEPVTFVVCH

SSQPLSLSGSQDGTACLTQVQTKRILATLSHVTAAPGVPVTISDTTASTGNSVECGGFCN

TMNWAATGCLGGYVRIWDLGTYQCRHTCRHPAGVIKLLWHPTLPTVYACTVEGLIYVWDA

RTGKLLKSLAGHSDMVLDMTFIPDVNDNSVVKLLTASDDESVRLYQV

>contig46477 Frame-0F

MLQSANDLKNELADVDLSNSGPSSDALMGLYLNMDNSVSTALEVNNDRPPLELELSVTQA

TLYA

>contig47364 Frame-0F

MTALPAINPACTLLSTQLSNLEESESTQFISPDIDIEHESKSNSLMQEMDSSSVDIVSDT

NSETGDDSLYWDEVKEE

>contig47834 Frame-2F

MRTNATMDRGSNDTESRDFHKLETNLKELLGRAFILMKQAGRDTNTVNFLDLAEATAQLS

HETADAQKTIMQNTYRNLKARYGDLTVAYFIAAAKSRHDIASELERCQLDDWASQGLKLQ

QVFSLLNINSANGNALLNPLLLTCLAYAKKIESVTSTDLIFFYNSLRRRFTDLAFANMVS

SLDITDHSILNELALNMRHMLMDELRNDDPVDLFHRLFKEVDMGNIIRNSAILIW

>contig50113 Frame-2F|Blast-inositol-3,4-bisphosphate 4-phosphatase, putative [Phytophthora infestans T30-4](gb|EEY65488.1|) 3e-74

MGFKDGGLRRLLQQLASQSPPDPRLRERIEMREDIVRSQVLAIAGASFLNAVGLAATRGG

QHRQRLKFA

>contig52612 Frame-2R|Blast-adenosylmethionine-8-amino-7-oxononanoate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY69924.1|) 3e-41

MRSQVDVYRSLRLPVVLVGDGKLGGISTTMSALETLLIRGYDVAAICLIEQDGLENKAA

>contig52779 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67190.1|) 8e-45

MHAALAGHLHLVQRLSRRNPKKFQRCCQEAMDSAAEFGHLDVVQWLHHNRQEGCTTDAMD

MAACNGHLEIVQWLHENRKEGCTRNAIDFAAQRGHLKVVQWLHYNRLEGATHYAIDNAAS

YGHLDVIKWLHNHRHEGCSQSAVLNAISAGHEHVARWLVLNRKRDCVGKMSFVEYVAGRG

HCNIDKLTGKHPYLQELIDADYGNT

>contig53505 Frame-0R

MAKNQIHTLLFFSTAGSNQQAKEQQRMVLITACTSSGPPDSSLESVYAM

>contig53570 Frame-2R

MQLHKAPIDANMSTRRTLRFIIWINFIYLANNYNGLGSKTICEEILRHADDIATTDVLLE

AFSYAQQLLSKPI

>contig53952 Frame-0F|Blast-phosphatidylinositide phosphatase SAC1-like protein [Phytophthora infestans T30-4](gb|EEY54523.1|) 2e-68

MPIADKKKHYELVVQDDNLVLLHPIHPLRLHIPRIVSCDASLDLSVEHDKDFQHVHGRRM

AFDAIYGIFWLLRGPYLAVVTQSKLVCKGVKGTEIRVVQQLELLLIPTQDLPILSPQQEE

DERTYINMIVGNIAAQKLHFSKDYDLTHTLQRIAAFDGKSGT

>contig54768 Frame-0F|Blast-chromodomain protein, putative [Phytophthora infestans T30-4](gb|EEY56485.1|) 1e-23

MSLDESSVLIDRALVTMCQNLPESLGLYNTAKDQLSLAAIRTVPLLEQVGPDSRKLALIR

DWMR

>contig57141 Frame-0F

MVGLSASELQNETLFPGDTIEYYSM

>contig57747 Frame-0F

MQLGPVFAAVLAKSRLQVCGCAQAVFDDFRSRGDQLLG

>contig57949 Frame-1F

MIITIFLLLVVQVSSRALGIRRLGVHICCWLCLKSYYV

>contig58038 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60028.1|) 1e-16

MTTFITAARELQALLCDVGEDFVVRYLDLSAKISVQMLCHNDIGFEADISSISSAEQRNL

IALSAILRRLLDAATRDRMTFLLPHISNDKGELSSSCRIE

>contig58540 Frame-2R

MAVNENSPLLHGRSDQQRTRPPLRRALYVIVPLALVAIATIFLLVGSNKSSILSKRAPAT

N

>contig58988 Frame-0R|Blast-V-type proton ATPase 16 kDa proteolipid subunit, putative [Phytophthora infestans T30-4]gb|EEY61710.1| V-type proton ATPase 16 kDa proteolipid subunit, putative [Phytophthora infestans T30-4](gb|EEY61709.1|) 9e-56

MAGVLGIYGLIVAVIIQGSIEPPNGNFPKYGSYSGFAHLAAGLCCGLSGLAAGMAIGVVG

DAGVRAVGQQEKLFVNMILILIFAEALGLYGLIVALILSQKKSDCPSE

>contig59334 Frame-1R

MDLRRDESASIWTQLHASSPSSSHASPTPAARSGLAMTVLSPTRSVLLFGGADGKTFFED

IFL

>contig02616 Frame-2R

MGHTSVGETLSRYIYFIGKIPFCSI

>contig04153 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67585.1|) 0.0

MQNMRAQIDEKGFGATVEVELRLGRITSCLQEARCRPSQEGMDAAVVLEDEQMKAVGAKF

VPGVSDLDFKSFMRGVEGMLRGDAYSKHKEEQVVHNMGQSKRVVQDVDPQTNMRGTPMVQ

VKERLGSIDIFMPRCQYDVRVSISCEYPLSEFEGDVNAMPAAENVRHKDRVSAVGRELRV

DITKVLEESTNQRSFEVEVELSEPVVNGWLSQTDENDQSWKSAVEMSSLLWKMVKYFMPN

SGQAFKRNWDFPGATEVQNAYQGRLGVRGKFSGTMPVGFARWHIPLVQSREYFVSEKTDG

VRFFLVVAGGKTVLIDRSNSPFAASGLDLLKLVLPEGTVLDGELVFHQKDKRYVYIAFDI

IATGPFAEDSHVDKPFIERLRILNDFLSEEGPYASGIRNLEINRHAILIILRKKWVPHRH

IMEIFHQIQRVQKRDHSFARIYSDDKRVHYTDGMVFCPNTKYVTNTNQEYLKWKWSDLIT

VDFLVTLNSSSDGIQLSCGGPRNTHIELDNIVQLDPKDAQMVHKLVLRTPTHQAVLEFAF

NADKGLWNFKCARPDKDCANYIRTVLGSLVNMAEGISEEELQYRLTNPNGQEWISHMKTM

RRTLLDQHK

>contig09446 Frame-1F|Blast-hypothetical protein PITG\_07336 [Phytophthora infestans T30-4](gb|EEY53646.1|) 1e-15

MNCHEAEEQKAFQVQHGEKYIQLKNYTDQLEAELRETKSKMQTLTTSNDELREVKFF

>contig13359 Frame-2R|Blast-116 kDa U5 small nuclear ribonucleoprotein component, putative [Phytophthora infestans T30-4](gb|EEY61932.1|) 0.0

MEESLYDEFGNYIGPELHSSEDESSSASESDPTSDHESEEAIKDAGRPMDALVLHNDEDN

AIVLHEDKQYYPDADEVYGDAEVLVMEEDAQAIEQPLIEPVKIKTFSVLEQKIPRTTYST

HFLTSLMDHPQLIRHVAILGDLHHGKTLFTDLLVQQTHVDKWDPALEKRYTDTRKDEQDR

KVSIKSTPVSLVLPTSKGKHFLLNILDCPGHVNFSDESTAALQLADGAVLVVDAIEGVMM

NTERLVKAALRANVAIVVVLNKVDRLIIELKLPPADAYFKLLHTIEEINAIITANTLSSD

ETRRVSPELGNVCFASGQHGWSFTLESFASVYADTYPSIPPSTLATRLWGDKYYNPQTRT

FTTKPPYAGALRSFVQFVLEPLYKLYTKVLNGDPKELSASLRAMKLRLRKEELNLNPRPL

LKLVLGKFFGNVTTGFMDMIVRYVPSPLVTAATKLEQLYTGNQSKDLRLVQGIQSCDPKA

PLMLNIVKLYSSPDGTTFRAFGRIYSGQVCALKEVKVLGESYSTDDDEDMCTRTIESVAI

AEGQYNIQVNRIPAGNWVLLEGIDASITKSATITDADEMLLQTEQVGIFRPLHLAFHTSA

VVKLAVEPLNPAELPKMLEGLRQISKSYPLVQTKVEESGEHIILCTGELAADCILHDLRR

MYAAIEIKVADPVVAFCETVIEQSSVQCFAETPNRKNKFTMISEPLDVGLDKDIESNRVS

LSHNVQDVVAFFETKYQWDVLAARSVWAFGPEHNGPNVLLDDTLASEVDKTMLLSVQESL

IQGFQWSCREGPLCDEPIRNTKFKLVDAMMASESIYRGGGQVIPTARRVAYSAFLTATPR

MLEPMYALEIQCPADTVSSLYQVLSRRRGHITHDAPKAGSPLYTVRGFVPVIESFGLETD

LRVFTQGQAFVTQVFDHWALVPGDPLDTSVVLRPLEPAPVNDLAREFMVKTRRRKGLSED

VNVSKYFEEPMRRELARHDLEMQYLL

>contig18949 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66936.1|) 4e-12

MPRSYYNSVMKFWLFSSASLAACVALLVYTYMTRQQFYPSIIYLVTSKISLLVLGNAGLV

LTALFGRLVKTLFLGPLRDAEV

>contig19199 Frame-2F

MDGRDIERRAAVLGFGSNMCGKRLLQNVNN

>contig23662-0 Frame-0R0

MQKSACHAVGTNPIVATPPSQSRQKKRPSLGLPQTL

>contig23662-1 Frame-1R1

MRSERILLLQPHHLNHVRKKDHHSDYLKHL

>contig24506-0 Frame-1F0

MRAPIYVRSSLKIRGYLDCDGCSKGCLPISVENLIS

>contig25215 Frame-1F

MPSPPSMKKANAGPGYYDLIKEAVLALKERSGSSRHAIDKFVAAKKGSSYSKSRLNIALK

RGVEAGKLVPVKGSFKLAADEKKVAKKPIIKSPVKKVSSSKKPLSVPAKKLVSKKSVAKK

MTSKKSLKNAKKPTAKKIAKKSKKVSSKKPKTIKKKMVKKSAAKKPAKVAKK

>contig25884-0 Frame-0R0

MGTKHEPNLSCPRKPWRSLLTSSINSLK

>contig26243 Frame-0F

MIAAILRHGRSVLKYCKSYGVEVQSIQ

>contig26661 Frame-2F

MTSCSVHRKAYVRSCTARNPKLTTHQRQKHPYPRIAICRRYREVVWFLVIIYKKYYDCFL

GSSYPFELPPLFAILYPYSAVKR

>contig27503 Frame-1R

MYEQYLLNCLLQLMQTTAARNLGLLNFKCIVIKWPCQPLVLKRGS

>contig27608 Frame-1R|Blast-ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY65798.1|) 3e-93

MEALDELGRILVNLSRIVPGGVVVFFPSYRFEESAVHRWQATKVYDQIQAKKSIYNEPKK

SDQLADVLMRYTAACSRDFHNGSGAILLSVVGGKMSEGINFSDELARCVVMVGMPYPNAR

DVELAEKMAFLDKRNPKAGRMYYDSLCMKAVNQSIG

>contig28021 Frame-2F

MGRRWQLRNKENFINYVKLELQLLSKEWMIILPCVIMQYVHAIFHNLAYYIQGRYLSTEQ

RFTLHDLGFELMPELTGFQSDISEYLVFAAIFGPAIILVLTIPLFRQEPGRPRYLVIVLK

RTLMQISICLVFRIISFLVTALPGSADHCELKFNDACLAANPNDPVLCVIPNLDFDPPDS

TEIFTRLNALKGCGDLMFSSHTIYTVSLILTVWKYWPNKYGISIMVCVQIAIAFLIVASR

KHYTLDVFTALYAVPLFWLALEAYYKDINNKDMKLTVKTIYDFYQVDVTSDANDGMVPLH

TSDLLPPQAVPLNSVHVALTEEDSQSGNTSFQRKNSV

>contig28054 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55319.1|) 4e-37 NOT\_ORF

MEVVPSLQRVLENTSENNLEL\*SRQGHT\*ILVCSVGFDFAHVVDVNWRLDYVLRTSSAGS

VYETMYFVQLQLQSPCASESRLKSMTFSCSVEELRVLVYRIQEATNEVEKLAAGTAAT\*K

LKTNARSMVCFFTRLAFTKIYFGLLQNGNLKIKKKSVDVPA

>contig28195-0 Frame-0F0

MSKCQLSDGEASVASIANLAKKRKKTHNEDAVQSNALFSIQHNESVGEGAVELNVKPKKQ

RKRFKNVPKQQRVG

>contig28195-1 Frame-0R1

MDATEASPSESWHLDMIQKQTFEKS

>contig29912 Frame-0F

MVQDPTTRLTIRAKVQREQNMAVNETKRWDARTQKCQLCMKSPGFKKLWMLSLGEYTYLA

LPSRRQLHPRHCVIVPIDHTCSFAQADEQVCDEIRRFQAALATMCEHVYNMSIVFLEQTS

APDRKRHTLMECIPIDSNLAMDMPLYFKQELLQANSDWSTHQAIIDTNQGGIKRHVPPTF

PYFHIEWHSRNGRGGYAHVIEDDSVFPRNFGVNVVAGLLDVMPTRRQQGHLQYENRRVLD

FLKDWKAFDWTQSLEGGELTL

>contig30132 Frame-0F|Blast-2,3-bisphosphoglycerate-dependent phosphoglycerate mutase, putative [Phytophthora infestans T30-4](gb|EEY64196.1|) 5e-66

MFDKEHVKKIRNDYYTRFPGENGESCEDIYNRTIPFFNSFILPHLAAGRNVLVSSHGFVI

RTIIKYLDGMDAIDFNEQMKLEKSAPDKCSLLAPTGVPLIYKYEKGKFTKLAQTCRDRAE

SLSRSSAP

>contig31193 Frame-1R

MALMLSTSRSPARVTTFLLVQASSLVQYLQNSTRCNLILPIKHF

>contig31531 Frame-2F

MVTGDNITTARSIASKCGITQPGDGSLIMDGQTFRSRVLDSNGNIIQSEFDRIWPLLRVL

ARSSPKDKYTLVSGLMQSNVAPHGPQVVAVTGDGTNDAPALKKANVGFAMGISGTAVAKD

ASDIILMDDNFNSIVNAIKWGRNVYDSIAKFLQFQLTVNVVAISLAFIGAVILEQSPLSA

VQMLWVNLIMDSFASLALATEEPTPALLERKPYPKTEPLISKKMAKHIIGQSIYQLVVLL

AIVFAGEKWFEIPSGRRPDLPEETKDDPTIHMTIVFNTFVWAQLFNELNCRKIHDEINIF

SGITKNRVFLYVCVLQVALQYAMVQHTGDWFKCKPLSASQWFACIALGFVSMPLGLLLRS

ISMTKIASWMGICREVDTDEARRTSSNNGQELWVRSFARIRAQIRVIKAFRKGLQSKALI

KEC

>contig33300 Frame-0R

MFEVQIVRQRRASVGLQALQRRFTMSLTDQCLTIKAGPSSPVSSSVLNIATSRIKSVRIR

GRLLRLVVVSGYTLTYE

>contig34510 Frame-2F

MNRRALARKAAGVRVAAPSSAAAGFDNVSQKLELQLQKGDYYGALQMYKTLFIRLLKGDA

VGTDQQEKAVSLALKAALKLIDHEQNTASIEMANLMISVFTDFHHPVDDAHKELIRQIDV

AFQTKPQFSTDLAVFLKNAVKWSSNEGARKRGDPELQSMLARAYCVAGDFTLAMKHFLHS

ESPQELADALFHWSLQGYPSESDLYLARAVLQLVSLENLRDANRVCEVYVAKCEQSGRPT

DLPLFNFTRFLLLTLERDALPLFRTLQEHYAPALARDSSFNSYLNVIGQKFYGLQPPRSG

LSSLLEMFSNGTQ

>contig34648 Frame-0F|Blast-STIP-like protein [Phytophthora infestans T30-4](gb|EEY69226.1|) 9e-79

MCYQDALALARDVSVEMPSISSSSRDKKTPPRSASCHSVSLKDVIENLAISYDLKFVPKG

VHNGQQVYAFGKHQIILEQGVVFARESKG

>contig34846 Frame-2R

MPKELISPYIECASNRRPFLPTL

>contig35236 Frame-2F|Blast-atlastin-like protein [Phytophthora infestans T30-4](gb|EEY69647.1|) 7e-40

MHHKACLQEAMNVFDDGARMGRRSEIVRYRQEVADLIERERHRYLEMNAERDPYKNLEFY

LIPGCLALALLVFRV

>contig36022 Frame-1R

MVITPGELHVFVTAKSSCFYYRIKATQTQFLRILRITFLREG

>contig37450 Frame-1F

MARERNCYLSGRGGNKRSTQPIRQVPASVYPSL

>contig37656 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69408.1|) 1e-176

MTLVGIKCGELILLDAEGHPASPSLVQNGDKRTQILCGGLGLKLKPLGIFLLQRAGIQRG

DAFILVLDNDRTSVACLLAAMSLHCICALVGKSRSHLVDYIKLESGICKVLTVDDTNESV

SVQTDAIQVEPGEEAASILWFKEKNICKVGGVCLLTSGTEGGKPKIVLCAWNRMLLQGLS

TNQQLFPTRPARIICGASITHAYAINTIFALYTSPYDAQSELCFASSAVGLYTLLMQRSE

MFTALYATPGIYTALAAMPPTQLYADVPYCAGTRLCVPLFQKIRDNYGLLLMQNYGSTET

GGIAAWSLYGKAFSDEVKEMERNNKLLYAGSTWPGVEMQILNYGELVVKTPWQSVGYIKE

GQLFQKYQICCTSDCGQVTQDKDGVNCIWLERRVRDSVEFYWHDQRKACKPETIEEVMIS

HPNVTDALILTQNVNDRKQGIIRARVVLNTDIAAAASTIKRWCVRNNLPAMRESLHIELV

NYLPCSSAGKPAYT

>contig38697 Frame-1F

MVNTYFINIFKIPPSSKPKAFSCGSNLDETSDSFLLTEPWEQQRRFQLYRLIRMIKSLRH

L

>contig39078 Frame-0F|Blast-nucleolar protein, putative [Phytophthora infestans T30-4](gb|EEY66010.1|) 2e-82

MEITVEEGDLLYFPRGVIHQACTDENEFSTHVTISVYQHTSWANFLEVALPRIIRQAFDS

NVEFRKGLPVGYLNYMGTQFVADTVKATEFTATCKKLVGKLAAYVIEKDLQEAADEAAMD

VLANRLPPLGENQSKEDDEFSRSLLDSNFNVHFKNRSHVRLTMGEDA

>contig41510 Frame-2R|Blast-CASP-like protein [Phytophthora infestans T30-4](gb|EEY57173.1|) 2e-14 NOT\_ORF

MHNAGLNYWKAFDRDSKRVLLDSQGSTMKSEKEASVRSRKKLAETAKQLRPLTINAEKLR

VWGRCLKPTKRRLTT\*RAVLSFPRAPSFSFAKDCMLPLTLHQP

>contig41846 Frame-0F

MNRVHSLFFEKLGRSRKFAEDLRFMMCRGFRVIVFSQYAAIRLNFDGLFSSLFTILSPGV

YSSQ

>contig43945 Frame-1R

MMPPLPQFNASYISKPPFDHATKWHGAAQTNRVSLEILNLFLRNN

>contig44179 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57034.1|) 4e-82

MGRRSTSPRRSRSRSPRRARPRSRSSSRGGRRSIPLKRSRSHSRVNYSRTRARSRSPDRQ

RDRSRGRNRRGRSRSVGRVRSEPISLLVRNLAPDISQDELRQAFSRHAGDILDVYIPKEY

SSNRPRGFAFIEFADARVGRDVKLEMDRTQLGGREIAVLFAKQHRKSPQEMRRILHQPNE

GSPKRSFQRRSKSRSRSSERRSASPNERSLASPRRASFSSKQEISNADSHSDATRGKESA

MDTE

>contig44544 Frame-0F

MKSAVISPALSIWWKLGALSGASGVLL

>contig45086 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54214.1|) 4e-06

MVASSAQLYAQCYDELDLASNFALYSWMTTARWRFAIENQGLPAIWFNPDSENQPRSLEY

FTFHNGRTFFSRSVRLPSIILPLKL

>contig45305 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66086.1|) 3e-39

MDATSVYPNAVPVLAATGLGVTLSGNDPDHVPLMPDFINDSRRRFAPDSSAVDVSGVIQL

HVRNALGYSFLRPHQRNKLQMNLVGNSNVKKAEWNTQASFYRNNYRHFVPHDLMMDYLKN

ECPPQDDCFNLSKWQGNAIAGVNCGQDGHVVFYPTGHVLQQACAWYSKGESAKNLSCSST

KIETGAPIRQFSVMGCRDAYHSTSAAK

>contig45547 Frame-0R

MCIDITTSGFVSYRKPTDILAAFFIEFVFGSAVIAAIRSQ

>contig46397 Frame-2R

MLMELSEYEAKRQRRIEANQRVLQALHVIKIPRHTSTHANKKKELHPVRRSLRQLQQTER

AAELEETEIKTVMALRELPSRRKRSKVESLELVERKELFNLPISPLSTQNQGKTVHLSSS

QISIELENFHSQWLGTQLLPMGKNTVMQSMCPPGYVAKFSKMSGVLPWKNAIALFVNLES

DSPYDNVFRHEVVNGITSVYFQWFGQHRWHDESPLVRRLRNTERGSESLRFHETYNNKSD

INKEPVLLFLRQTQGPYIYCGRLGYLGHLHASKPLEFRWQLLDADSLHWENLLRQLTYSE

>contig47835 Frame-1F

MGGIQSAINYAQHVLAKPVRDSNHDKLERRRVALMLVNLILQQQLLYTTSNEPFPHTEVE

PLHHKPDEKREAWLVEFFKTNRDFVTAEVVDLCLSRHQLEKAILVATLRNEVPETLDKII

NKGLASVISEDLVMYLVESGHASALASPHSRLILRSFPIQIQVKILLAYPPAILQHRDWL

VRNLAAISQDLCCELARKIDPTQPETTDLSQSATAAYSMSAKRRFTTDIATSEFMQVAPE

EQVELFLTLLLHLNHQVHCSGENGRLKVAENGKDYSQARLESLLKDLAAQYRPPIMVSRC

VDYENWTAAACIYEAHGELVEALDCRLHSHNSCPSPCVASSASSDTQQPNDSSSSSMPDK

SKFQEQMREELLGLLNSLVVQNHSSEVVSEQICAAILARILVKWFDFNLERTVLEDYLLE

ATVF

>contig48346-0 Frame-0F0

MSNLQCVVANVKRVWTEPSLMISFSHA

>contig49217 Frame-2F

MVTQRVVPICPNGVSSYHAGKVALDEMLAHFDEPPHAVEQTEAQDDDDGTATLGLAVNTQ

N

>contig49280 Frame-2R|Blast-hypothetical protein PITG\_10137 [Phytophthora infestans T30-4](gb|EEY56590.1|) 2e-35

MSILRVGLQQYPDCLAMKFNLVLLLLRTGDEMTASALWMKARGWNFHAETNAVTGVASPV

DSAAACQIAAVSASAYVPFISEHVQGNLDGECGVSAQQLVFLDALIIKSWRKRWNSQLAD

NTIQFIEYLESRGSTDLLSKVKKSL

>contig50112 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65789.1|) 8e-46

MSSSHPRFRVTDESETSQRLRERAQQLEWKRILDEQVQEKARIKEKEEAERRRSEEGTAK

EEARYLREQQLQAQRRVGLNSPARDNAALSNTTG

>contig50435 Frame-1F|Blast-ATP-dependent helicase, putative [Phytophthora infestans T30-4](gb|EEY57215.1|) 8e-20

MLQSMRLYGFQHAVYLPAVKKLII

>contig51700 Frame-1F|Blast-NPL4-like protein [Phytophthora infestans T30-4](gb|EEY59551.1|) 0.0

MIVRVRSKNGTWRVEDLTPASTIADIKRWIYEHHSIAPAQQHVSLDQSGLRQTTDTDTLS

ELRLGHGDMLFLGYEGHTVAMGGALGTKINADGTLTRVAYHERADKQAFRPGLKSLRDMK

MHWTLGEFVRMDAQFDFKICAQKDPHVATVHLDSASCNDFQAYLRQFAFQQSRCGWLYGS

VDDKTKEVVVEFIYEPPQEGNPHGFEVLNDPYADKVDAIAEALGSEKVGWVFSHPPREDG

DFHFSAREIMLAAQLQADAGGKNSMFVTLKVTLDKQGQASFEAFQVSDQCVEMFAAGALM

ENESNSNACAVSETFTALVEAKPAVEVDNNFFLCVVPVVPHESTLRCEFPKLNREGAYRN

RVALKSQLQLHRDVPFVKRISDFQLLVFLSDFLDVQTDIPPICQAVRDPSIPLDTGYQIL

IDSIAGNQ

>contig51977 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67672.1|) 1e-40

MEENLMYGVNHKKLDMTQTTYSMPVNEMQQWEISIKDYRKESIWNCNLIDNHTRVTRQLT

AAHYCHTMSHPFHMHSTHFQVSDMDDTTDPDGILFDVGEWRDTLPLFRGGVQIRFTPR

>contig52613 Frame-1F

MSHALSASYCKSAPDDQSCIFSSTSHFSFPSVAFDCRRICSGSESCEDKVFGLHAMRCWN

ACSMTINDQEKTSHSLSMICTYFLCTRRRHAVHRTWIVAHLYKKSVAAGVHQVKSLVSIR

PNLSTYCITLDPALFQRHSCDMSESREPFGVFERLD

>contig52778 Frame-2F

MGDQKGSSTRSDRNLTTPAAMSGIDWSIFKNGEEDAFGWLLRNNVTSFLMSDDAADVKTN

DILLCNDVKIDCTIGKSAVDGRSHFSEISKASAVIAANEAHSNARLPVMQLEENLRYLPP

QSVANLVSLLQTRHQLHDRSCSAEVSSKHHDDENTAEMGKKLTITSKAEKMDRSVSVVQN

AGQKASIRTRSISAKRSAEQLFIADSSRPFKQKKSGADGSITEVDCEKKQLRRV

>contig53283 Frame-0F|Blast-DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY57466.1|) 6e-29

MTFAELMRLVEAAALRKLPDLSMDSARKLLTRFQTRNEQSIRHIIDDWPLHWPVVNVPST

PAKAMPQPQHVGQPKLDVLTSRVSPRPSLAESPNRVAMAAAAMTHLLASSSLTTNSCIAE

TRRPSLMRSKTSNVMLPDAATKEMVSVDPRVRSEGDSDAVMVV

>contig53504 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61841.1|) 6e-44

MMLRGLITEHFKLFGDEFPRIAGLVGELYFPKKHTFRHKISKVVEHRCDSFLEYLLG

>contig55230 Frame-2F

MQRLGVAIATIPALLHNYVASGISDLPAPVRSRDMIDYLQCQVCQTPELTGSVQDS

>contig56455 Frame-0R|Blast-40S ribosomal protein S13 [Phytophthora infestans T30-4](gb|EEY55889.1|) 3e-37

MGRMHSHGKGMSKSARPYKRSPPSWLKVSAEDVEDHICKFAKKGLTPSQIGVILRDSHGI

AQVKSVTGSKVLRLLKK

>contig56680 Frame-2F|Blast-PREDICTED: hypothetical protein [Mus musculus](ref|XP\_001478231.1|) 5e-06 NOT\_ORF

MVRCGTGTIS\*LSVFFSRFAALTALRASSSSVSTRVK\*LSASRSRRRRSQRFMSASSGQF

PSLTSNRRYSLASSHDKSFTESSSTAVST\*NVVNIYWTSTFVAKLSTTELTATPRS\*RIS

\*TSSKLFGIFITFPTPSSFHTTIK\*STTALPTV\*NSG\*ASASTAHRARSDTGCSRCSTFT

I\*RGQFFISVCWAYSTNHTAL\*RKKGFSTISSAL\*SVAYKSRNGSGLGSLILRRDCKISD

L\*TESVFGSGRPFKSSSTNKCNTNSSSSTSKTDFHEEGSMYRAYSIQIKNTGSVRK\*FSN

FASCRPSSENILAASKVCFHFSNNGSLKSIPPSEAAWSISANSALL

>contig58963 Frame-1F

MSHKSRTLRLLCLHGMYQDASTFAGKIMPLRCDNMNVEFVCIDGPFTVVPPIVKRTKGER

TRVVSSKTGIKNEFRAWWRQQGPHQNDRCGSMYERNVLISFLREKLAEAG

>contig58989 Frame-2F|Blast-calcium-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY57833.1|) 6e-67

MPWVLRAKDAATKRRWLVALSDCIDILVWLRHYQVGAVVGVGGNGVVQELEDKRDGTVFA

VKVLDVAKFRHREQAVAEIEILRSITNNITHPNLVKIHKVYEELQKVYIVQEMCTGGELY

DRIVQRGKLSEQDAANILRQLMSALEAL

>contig59612 Frame-1F|Blast-heat shock 70 kDa protein [Phytophthora infestans T30-4](gb|EEY57393.1|) 2e-08 NOT\_ORF

MEKLTSTENKMTIMNAPELFFQADISRKVSEVK\*FDLDLEDNAKETVAEAEEFEPEDEAI

KIYIDTKKSLKN

>contig06325 Frame-1F|Blast-acyl-CoA desaturase [Phytophthora infestans T30-4](gb|EEY56644.1|) 1e-167

MMSFAQFKKEANWFMVYYLSVVHLGALEGLRRLFFCKWETYPLFLIIYYFTGLGITMGAH

RLWAHRSYKANGPLRFVLMLCNCLANQGTIFHWCRDHRVHHKYSDTVADPHDSNRGFFFS

HMGWLMVKKDSRVLEAGTKLNYDDLWADWTVVLQEKMNPWGQLFMCFVLPTILGVTVINE

DWKNALFILGFLRYVAVLHATWLVNSAAHFYGYQIYDNMPPRENWFVSLGAMGEGWHNWH

HKFPYDYATSEYGVTAQYNPTKLTIDVLALFGLVTHRKRATDIWLKTQESKQKGAAFVDP

NGDDPTLAFSKLKAKAN

>contig06875 Frame-2F|Blast-arginine N-methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY70137.1|) 0.0

MVASNLRDISPDKKKEWESSSDFANYFCTYAYIYHQKQMLTDDLRMKSYHDAIFKNQNHF

KDKVILDVGTGSGILSIWAAQSGARKVYAVEATNIAHQARKVISANGQDHIITVIQSKME

DVELPEKVDVIVSEWMGYFLLRESMFDSVIVARDRWLKADGSMFPSHASIFIAPMCNEDN

SIKRFNEFTSAMDGWRNFVDNTKASWGVDMSVLGNDFRKEQEQYSLHTSSWKELKIEDLV

GDEVEIASWDLKSCKLNDIKEVKASFSMPISIMSRFGGIAGWFDVEFKGCKENPAETEVT

LTTSPFVQPTHWGQQVFPLYPPMQVCVGDMVVGNIAVMRRAENQRLMNVKFDFRIHRLED

DSATMSGPPNTAVFQIE

>contig07029-0 Frame-1F0

MKLLTYKQRLITTGDQLAEFNDLNQLDSFSCTSPDDSVMD

>contig08341 Frame-2F|Blast-prolyl endopeptidase, putative [Phytophthora infestans T30-4](gb|EEY62978.1|) 0.0

MKKAMKNSGLLAEKLVYPNVRRSDIVETLHGVQVEDPYRWLEDPDLPDTRDFVEKQNDVT

QRVFAQMPFVDDVKARMTELFNYAKYSAPRKHGGKYVFSKNDGLQNQSVLYIQDELRGEP

RVLLDPNSLAEDGTAALSSHAFSEAKNGDDKLFLAYGISRGGSDWQTIKVMAAHDNNNTL

DDTVEWVKFSGISWTHDDQGFFYSRYPPPEKMKDDQHDDQEGPKRGTETDANMNHQVWYH

KLHTPQSEDKLVYAYPTEPTFNVSAEVSDDGMKLLLYVQDGCKNANMIHIADLSGFNTFL

SGTQETTISVIKLVDTMDDAYSYILNDGDFYYFKTNANAPRERVVRTKISEDTTAFVWDE

VIPEQQDAIVIESVHPVAPNLLVVQLVRNVHNEMHVYNLDGVFQYEISLPSVGTVNVASK

RTESEFFYHFISFLYPGSIFRLDLSTKCADSGAAPPAELFRETKVKGFDPSQFEAQQVFY

PSKDGTKIPMFLVKRKNALKNGELPVYLYGYGGFNISLTPAFSVSRLVFVQHFNGMLALP

NLRGGGEYGEQWHQDGMLHKKQNVFDDFHGAAEYLIQEGYTNPSKIAIHGGSNGGLLVAA

VGNQRPDLYRCIVGAVSVVDMLRFHKFTIGHAWRTEYGDPEVADDFHCIRRYSPVHNVPR

ADSPMMQKLSERGGFPSVLLTTGDHDDRVVPLHSYKLIAELQHQLGTSESQTNPLLIRID

TKSGHGAGKPTTKIIEETSKVFAYIAWNLCAPFVA

>contig11088 Frame-1R

MFRNSKPNKNKRRRIAEGESENDTCENIPLVPIPNERFAINTFSTGGAKTAKNVVQTRMI

ESEREIVPMQYAGDATYETQIDTEKDRDARAVLERSIKANQDGSADANSGQIYRGQAAYK

SYITKKDSQVGMNKYTGTQGPIRAQTWARAISRFDYQPDICKDYKETGFCGYGDSCKFLH

DRGDYKSGWQIEKEYAEKEAKRQKRLQEGR

>contig13712 Frame-0R

MPPPTSFRPSTNATDAPTTAPPTAMPTLSSTAASGTSSLTSDLSDSSTASPTNTNSPDVN

NSNNSDPATKRGTASSKGLATWQIALIICCGLLVFIVAVVSVLSCYCKARSRLFENEDDQ

PDVSYYQQPQHNIRENTFESSVATAPTLVRPPLLPHGRRSGSLGIFTNECKPGDTNASNS

GTADRLNVGLVPVFSLENSTRLTGSFPNERILSGSSLNDCRPSHSNKSFIRQLSLENGRA

LAVEL

>contig13767 Frame-2F

MNMKLFPKQAVSFPSISAMSIATEYAMEFLSESQKRGIAGICACLLPAVTDGSTSLAWSK

MYLKLVIEHFVGLSSAQTEAYLPILTSRRQALVQKDHEPSVATVAELDLSPFLALLVPGP

ESDTLHGLKRWTQKLQHRTKRNTFDTIEGFRLEIVKQLLWFSVKSVGYDARTRT

>contig15093 Frame-2F

MGDYGQYDVPKADEMINFKVGQPAPAMLPLDKIREAAALKFAETDPMFLQYGVIKGYPKF

RATLAEFLTKGYQHEVDPEKLFVTNGVTGGLALICSLFLQAGDLVFMEEPSYFLALSIMK

DFKINVRQIRMDEDGLDIDELERLLQRGIVPKMLYTIPTCHNPTGRTLSTVKRQRLVELS

VQYKFLIVADEVYQLLSFPHVTPPPPMFTFDTHDTVLALGSFSKILAPALRLGWIQGSHT

LLRKIEGCGQLDSSGGISPVISGIVHAAIASGLQQEHLDTTIKTLWGRADALMKELKVCL

PAGVTFEVPDGGYFVLVRLPDGMNANDLLPIAQKHKVMFLPGASFSRNMKNYLRLSFSWY

DLPDMQLGARRLADAIREYQNVLATDSSNKGENCTNEGQGVRIAVHGYTGRLGSLIVSEL

NHCTDTSVQYAGPIVARGETVQVPDLNKVDVIIDVTLPAGTKNLIQYLLQEKEIGKISQL

PALIIGTTGALPSEELEAYSKHAPVVLRSNFSVGVPLVSELIKNVAFKLPSEGWNVEVTE

IHHTKKLDAPSGTAKTLVKSLASTGAPCLGENGQAPTHSLRLGDEVGQHTVLFAGPGERI

EIVHQATRREVFAIGAVRIATRAPSLPRGLHSD

>contig19800 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60395.1|) 2e-27

MELKRNVAFILEYRNPRKLVSEPGYFFTHLVSSIAFIEELNGSSLTISLDEFNKELQKSQ

AASGGVLTNMPRACNEEEEEKGTYKKDPWNGRKSHDVKVEQWPLPTVLEIRAKRLALQHS

>contig20534 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53975.1|) 1e-114

MSQVIAPWDLQNIVEQIQDFLCCLPSHLRPTLLSKPWLSESYDCVASHRKGMYANPFMCK

SQSDKFRLVVKDDDFLNILDDAELSDSDAETTASISSAFHHIEPLTRADSIHSENSEIDS

LSGRSTFACMSAGASSDLNANLQESITPSITSTTLSAVGPIRNFSHQPHLLKNANFSERD

VLLYPSSGCRVNRRHRKLPSRERWDIKRSMYYVVDLSASEGLRLFGYNMSSAFVEALTTH

LARVITWTKLRNNLLRSLLLEKVGISVAAPIGSAVLQPRSFFVALNTTNQAGKGVGKSYV

VPCADSTVSFINFQSPVLSILPSNEWFPKSLDASHLRSTDGTALGAYLQEAQTQSALEVV

EALYARPRRKSSTYSSDLVPPPRTPDLSREISGSSFGNH

>contig21982 Frame-2R

MFRHAAARAAPIPFQRGFAASALKVDNPYTGETFCEVAYDSKAIAHAKLDAAGKAQLDWK

NVPLSERQALCTKWTTVLKRNADSIAHEISGMMGKPVKQAQNEISGTIDRAMALIELSDE

ALRADYFPEADGLFRQITCEPVGVVYIIAPWNYPLMTAVNSIIPAVLAGNAVLLKHSPRT

PLCGEHFQKTFEQAGFPNHVLQSSFVEHDTASEIIQRSETAFVSFTGSVRGKRDMLLKTN

FILW

>contig22158 Frame-1F

MSAGIANTTSSKWADDVGTGKSSEAGRENVTEWEPDLVPEHSNTDANTVESCISSTETRK

TGVSAEYMNSFDGKNIVDKNGDETENGTRCKVLPLNDNIRVAGEEPPVDNVLDASDDTKT

KQRLAEAVAAATLKTLGNESAVESANSSAIPKEEFLGTKSLDSKEGARVEEATDKDETL

>contig22716 Frame-2R

MASSVYLNPKEATVLVKCKNVFRLTKSFGKTSSTPIRTSRNDLFRAAIDEDDLIHNSWGS

SELLSLFARRSSGIARIRSACISPKSLDLFAKSRPYKNLKLNNCFLRIVEQNLYLEK

>contig23661 Frame-1F

MRPAGFVTFRSLKAAQSCTQILQSAEPTQMHVQPAAPVDDVVWENIGLSKNTKDTWLLIS

LALSAAIILLWTVPTGLVVSFAKVSTLEREWSWLATTIDKHPWVAAVLEQLSPLLLAIMT

ALAPLIFGVLSKREGHAFASQIDASLLNKLVIYQIYVTFLLPIIGGTVIDAVIGSSTTNL

NASAILTLISDSVAVQSSFFITYLMVKTGLNLTLELLRVTPILKAAIYQVFAPKLTPRER

ASPWLGLTSLAHPGTFTASDQVSEYFLILMLVLVFCAIAPILNYFAFVYLVLSDLVYRWA

VFCVYEPSTQTAGTFFPSLYRFIVGALIFSQVIMASVLATKQVALPATFAIILPFLTLAF

HLFVASRYPKIALNLPLDQAVMIDSRRFRQMDDLNACLRTCTCSQPCWSASR

>contig24053 Frame-2F

MCYSTILGRFKDGQDSELETSLGVVDFSPSAVGLLQCKNDVIVAPNGTLFCPKSYRHGVL

PLILDEILSTRIMVKKAMKSAKNSKQKRLEKVLYARQLALKLISNVTYGYTAAGFSGLMP

CAQLADAIVQTGRCTLEATVRLIEERSEWNAKVVYGDTDSVFVLLTGRSKTDAFQIGQEI

ANAVTASNPRPVTLKLEKVYMGCFLVSKKRYVGNKFENPTQKVGTIESKGIETVRRDSCG

VVKHALKTSLSTLFESCDLSKVKEKLERFWIQIIENRVPLKEFIFAKEVRLGTYSNGSAP

PAALVSIKAMGKDSRAEPRYAERVPYVVVNGSPGARLMDLVVSPDEYFSKRKRYSINYHY

YINKQIIPSLERLFLLTGANIRSWYATLPRTSVKARQYAFDNPSPTSTIGCGFRSIDSFY

LSKHCRLCGSIGINALCQNCSANPQRSLLAIHTAFARHEKAVMALKVACTACADRDAFGN

CNNYTCPVWNHIKLFEVDKTTLT

>contig24505 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54209.1|) 3e-25

MYSCLMQKTQRFSSLFRHYSKHHGLPRESLDFFFT

>contig25216 Frame-0F

MSGWVSSWLQGKSNEESKTQGYQSGGNALSDSSVVPSADEIRRKRLQKLQEQQEGTLSAN

QSTIDGKYDVIMTNPEALPPQTSAKPSVEDLIPAPTPAVAPIEPQKLKKAGLIPEIYIND

MLQRVLRVTLSPTLKNTELLHLPHFEAKQLSAQNSSEVLYSRIIMNPVDLPGGTQHPLAA

VTYLEKVYYRCRDEIQKLQSSFLRLSADKKKEALECLSSIREMCINYSATALTDPEIFPF

EAGTINFDAFEKVVRLQSNAQTPEFVDGIVAILEESSGTLQIFSPIFQKLLAELFLINPP

SLLSNFYNNMHILTALCRNKALATAFTQMPGFLLTPGPPKTGLRLQDATALGILVRFSCN

KDPAILQMFSNITKRTKNDVENSILAIRAKLNSVQTTVSDIVTLLLKAGGSAREQVMTWL

EEAMQVNAERAKENPDINITSSNGMFVNLTMVLLRLCGPFLAPDSGKTKLIKTEYLTMQN

HLFPYDETTLVSCGTDSGLAQHDTRQIGKTSDFNFITRCYFVTARAMHLGPVGMIGQYMR

LLRQLSYFQSRMSAPDADPRLKAHFDQMATTKMIMDAELLHPDFIHEMIRFSLLTSAVVS

SICAGSSYLDRRLLVLPLPAPDNKTSALLQHVPEHLVDDLCTILKFVARLQPNALNTFEL

KALLTMILIFLSSPSYVHSPHLRAKMSEVLFHIFLPSEESEERETAGTAFGMELLRTDPL

AQQHLAPCLLALYGDAEHTGFYEKLEHRYNIACLLKYLWKLEGHKSSFLRISEDRGSFVK

FAHGLMNHINSLVTDALIALYEIKALQEEMQNIAQWVALEESVREQKQSLLSDKERTVTS

SLQLANETIHMMSYLTSEIQEPFVKMPELEDRLVSMLNSVIVKLTGPRGVELKVKNPEQY

KFRPKVMLQEIVQTLLHFAHYPSFLLAVATNGYYDGPVFRKCAHIVARTQLLEPSDVQKF

NTFVVEVEKAAEGAANLDEVLGEIPEEFLDPLIFTLMKDPVLLPSGYSMDRSCITQHLLN

DQSDPFTRVPLTIEQLQPNSDLKMKIEQWIQEQQQKHAAM

>contig25887 Frame-2F|Blast-2,4-dienoyl-CoA reductase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY60614.1|) 1e-139

MQLQISMLRPHGPSTLRTALVRTRSTATPRTAPMLKTMLPLGTFEGKVALVTGGSTGLGK

GIATKLSDLGATVAIMSRKKGVVEAAASEIEALTGNKVISLTGDVRDAEQVKKALDELDE

HAGVPTIVINNAAGNFISPFERLNAKGFGTIVDIVLKGTANVTLDAGKRMIHHGHGGVFL

NITTTYAETGSGYVVPSAAAKAGVSAMIKSLAVEWGKYGIRFVGIAPGPIKTKGAFDRLD

PSGSFEKVMIENNPLKRFGEVDELANLATYMTSDYASWLNGEIIRFDGGETVANAREFNM

FGSVSQEKWDELEAIIRDSNTKSKK

>contig28022 Frame-1F

MSCSKEFITCQVLLDHLVFAVNKASVLELVKRGNIKNQMIYNPLFPKSTMTPSAQRFPEG

>contig28196 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64042.1|) 1e-168

MCSTLKELRLRDLAVDPVALNKLITKNAESLRVVDLLGCHTIRGEDIRTLAQCSQLRDLS

LWGCHNVDNASIEHVIQHCSQLERLNLRYAHKVDDKVVASIALHLKQLKDLNLRYCYKVS

DKGVARLCESLPRLRSLNLSQCARLTDAAIMRVATSMTCLKELRLWGCIKLTSNSVLSIS

EGLPELTLLDLRGRDKFEAVIGGPTALKFLIETYRSKLARWEQAQGEQMGVFKRPSMIAA

AA

>contig28949 Frame-0F

MQIILANHWLSRRFCFKKCLSSNKIQHSLAMTIFSWAHPVASPSHQRTASSFD

>contig29911 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY58105.1|) 2e-94

MVGFENLEASLNSFDQLCFNYWIEKVHHFYVQNTLAINFTDLEDESQHVGKRLTLHAHVN

ITSEQEQCLQLFEEKPHGIFDLLTGMTKVRAPKDDDFVTKLFSGNVGMGSLTRPNMGTDA

MNDYLAPSKDWQLLFIVQHHCGKAT

>contig30131 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57131.1|) 3e-11

MKRLSVMMEQGGSIHMLYLVLFVVVVFVLLYFAIRSH

>contig30409 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65370.1|) 0.0

MKFIDLCDLGTLLPGDDFVSKRSDGLRRDEGSSSNGAIGLCDFDEVQSEKLWWIFNRWRN

AKSKYMEGKIETSEFYTCNIRYLRTLLDAFDPQQIAVLYFGGNESSSAKSVLPAGGTSIS

PAKNAGNPNGMLDFDVSRMNTHALIQDHRLVLSIGYEYIRDDHTSFGSHPKLQFKVFGVC

DGDTRAWRQEIPRPEWYLSEYDMLEAEDAAVGAGVLRTLRIFGAKLLVKLLGFLLLENSV

VVVGNSYPQIQEVTTSLLKLLEPFRWQHTFLPFVPVSSWRFLYDAAYQHAQAELAARPKS

RRSFTRLSHDWRAWSSGIGGSGGESSFSSSHGSTNSLTCGSLISGEKVEEEPPFLLGATA

DTWHNCLAFSRKCGNDPRVLSTCLVVVDLADVDALTTDKSLRNAVPLPRKWRRQFLERMQ

KIAKQRHKTRVKTSRRHMAQQLVG

>contig30544 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55996.1|) 3e-15

MFVASTSSHCFLNDVHEYSHLWHVTQQHHYFQKTVKMILEMSALQLLFLPPVLLVVSGLA

LYNFQCVFRFLTRNLKSYMTLPAVQFLKPCK

>contig30948 Frame-0R

MKLLTKLQSDTQRSGEASRQSHKRSLESLNDTLHAETLRQQKSSKTTLRPKKQKMGVNEV

KIVDEEDESKKDSESSEAEFIPELRNSPPHKKVRGRDSTMKKQQVAHEKKETKTATESAG

TSQPTSRDHLAVVVAKIRADKVASQKSDTNIHPEVKFKSGALSKIKADASLKAEHGTFED

HESGASSKLEAIIPGASSTSAIVVDESDEEEVDEEDEYEDEDEAGKVSNSSTDDDQDLFD

LNEEDVYVVEAILCVKEGRSLMTAGRRQKEADLYLVKWDGYNELTWEPDENIPRRLIEMF

RERERAKRACQYQIKVAHERREVI

>contig31961 Frame-2F

MFMRHCESVEVNELIQVKNECVTLLHTRGAKLKLNPSLLSICSDYDTVHPCLLLIATSTT

SH

>contig32238 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53446.1|) 2e-34

MSTYLLLVLRGLEILVEDEIRSKLQVERLEICSVQENVRPPYLQVMQGQAAVGRIILQTK

SSVAEVQKLRSVQAALAFLAKNDDIITNSDIGVMQI

>contig32959 Frame-2F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY70130.1|) 1e-112

MDNGRSLYVGELLLNGKRLSKDYRRVAACVQQYDLLYPTLTVKECIIYSAQLRLPATLSD

AVKHAMVDRVIAELDLTHVANSRIGSDGGSSGWRGVSGGEKRRVSIGMELVTSPQILILD

EPTSGLDSFSAHSVVQLIKELANHGRIVVLSIHQPSARSFLQLDKIMLLGKGKMLYSGAP

AESINFFQDLGFKCHK

>contig33394 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65897.1|) 1e-103

MTVKPSQTTLHYDAYQNLLVVLYGRKKVTLYSPPDMQKMYPFPIYSKSANHSQVNIIQPD

LEKHSQFLEASAHRFEIMAGDALIIPEGWWHQVDSDEYTIAVNYWWNGMREKLVADKQMV

PYYARVLLEELVKQCYETRLLALQRASENDYKCDNESCAVAAFLAANNQAERERLLMSLD

STTFAKVQEFLASSHEKEWRKLLSNASVDFAAVLTNSWERDELDDHFLNALFSALESEEE

TIKEELANKQAQFRRTCAMQMYQLLFG

>contig33978 Frame-0F|Blast-methyltransferase domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY54688.1|) 1e-142

MSIKSTINKKLEELVEKAGVIKNVLDDPKSVVCDDIWTEERERLAREHLRQDTSAIPEFW

QRKYEQEAALSWNKFYKRNSTNFYKDRHYLHQVFKELGEVPKDGEKRTLLEIGSGVGNAA

LPLLEINPALNIVAIDFAALAIDLLMAQPLYDASRVVATVCDITKDALPDAAFANGGVNF

ALLLFSLSALHPDKMKAAVKKVVAAIKPGGRLFFRDYGRYDQAQLRFRAGSKLQENFYVR

QDNTRAYYFSTEEIDELFTEAGLVSIENEYIRRQYANRQQNVVRFRVWVHAIFEKPLKAV

GATHIYE

>contig34513 Frame-0F

MSKRGPFFSSNTAPRNPYYRHSQSQRPRASTTEWLYRFLGALVVVMLFLGTYESFRGVEP

LLVAPTYIDPQAKDAIISTEKRNHLKLRSATAGQDSQPSQKLSSSPLRLKIMTFNLRFAG

TSDGHNGWQYRKDHVADLIDRYHPVLMGTQEGLKAQLLELEGLLKMPYERFGVEREKNGE

FEQIFYDPTVLERLDDGNFWLSEKPDTSGIKGWDANCVRMVTWGKFRIHATQQELFFFNT

QLDHVGRTARAEGSRLLSQRIQLIAGNAPVFLVGDFNTYRYASTYKYFTSQEDGPHFYEA

WPAAEKQIGNVSYTYHGWAGVKNDGEKTAVRAANHIDWIFFRPQMTVLQTEVITENRNGR

YPSDHYPIQAEILFPSAVDLPPPTG

>contig34584 Frame-0F

MTHKFHGCFWSVVAVAGTVTAAVVFYKYASRRNRESEESELHTATEMQIATECQECEECI

TDDESEEKEDLDNSQK

>contig34845 Frame-2R

MGRAAARKGRMKKARKRTAPVAAVQLYRIGLRASNTSSSDNTVLVQNNSRDI

>contig35068 Frame-2R|Blast-ubiquitin family protein, putative [Phytophthora infestans T30-4](gb|EEY58892.1|) 6e-68

MADELIIKVVSGASESLHVNVDLATTSVLALKQHIETKNAQQYPLSAQRLIFQGQILQDD

KLLTDYRVTAGCALHLTLTPGTTAGPATACASSAPPAELRTFLQQMRAAEPPEQYATAVR

TLQKICANVVDHPNEEKYRKLRVDNSVLKAKLLDRTAGQDCVKLLGFQEAVQANHVVL

>contig35464 Frame-0R|Blast-60S ribosomal protein L21-1 [Phytophthora infestans T30-4](gb|EEY58295.1|) 3e-82

MPHSFGNRARTRDMFARPFRQSGMIRMSTYLRTFKVGDYVDIKANGAVHKGMPHKYYHGR

TGRVFNVTKRAVGVRVNKVVGNRVIHKHINVRIEHVHQSKCRLGFLTRVKENELKKKEAR

ATGVRAQIKRVPAQPKAAYTLKTKGSKPITMAAQPFVDLM

>contig36021 Frame-0R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY69332.1|) 1e-136

MTTPLGLETKAQRCIFVTYIGLWVSYGMLSELAKRQGVHFNSACAVVLQSLLKLLLATYM

YMTTETITTSSLAARIRFMLAQVRTHARLILFYIIPSGLYVVYDVLSYINLRAFDASTYF

LLMQFRLVVTGVLHQLMFSKRLNRNQWLSLGVITIGCTIKTLSTQDTDGSARFGVNYNGP

RPVAYLLLLTQILSGTFAGVYNEVLLKKQVAITVNLQNVFMYFNSIIGTMIMLGMGMTGQ

TAQDALTISNFSELFSPYVLPMVLIMSFTGIVTSLFLKQLDSIRKAIASAMELVFLPLLC

AVLFGQLITLYTMAAIVFVGFGVYLYALPVKVLSTAELPKYRKVTHQEMVQDENDSLDTP

IDVAESPSAVNRLRC

>contig36858 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY61121.1|) 6e-79

MQVLAAPAVALRFIVQVLPIIELAPRGIEGTTYGLVITFRHLAIALGSVVYNAIGSYFAV

HEEDVRFDSNATRMQVFVTYVIVWIMQLASLGFLKFLPRQKLEVQQLRYYGGYSTSAGWL

VIGVLLSVLTLVTTTNMLSLFKSTSCLRVAGGTGCAT

>contig37105 Frame-1R|Blast-chromodomain-helicase-DNA-binding protein, putative [Phytophthora infestans T30-4](gb|EEY65872.1|) 1e-46

MTDYYFLNKTDSIPERMLGIVIKMTKEVGGD

>contig37453 Frame-1R

MVSPPLASVNPSLPAMLSLLSFVRSYVAEVRQSPG

>contig38175 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60177.1|) 2e-54

MHGLKPLPFQAGVDIERDASAINPDIWSPYYPHVVMLPSGLMQVHPGPLQSLKVWPRGGV

VTIGFRCGVTAHKQSNIICDDSDGHGCYLQRGRIPAVDCHFCLHTQWLFLVMTTWRTSTL

>contig39110 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61853.1|) 6e-45

MELLIRRSTSACALPQGHIIIATYRSKRSQAKREVLRVSSGFNAVEKKITWKEIKRHKDQ

HKAERDKTLPNAKRPQHPTVEELDQKWAKIRMRTKAVPSAVLPARARKEIENKRRMWRLG

LITDDEEEKNGGAGAFEPRSKGITGHQSKFERKTSSTSNDGRSSKAEKEA

>contig40068 Frame-1F

MERQLNLRTEGENLQLFHHHFRHRRGLRFPMPLMELTTENILVESFEEGLRLHDVLTQLE

PSRRQNMARVVLDAYLRMVFLDNFAHGDLHPGNLLFRNPTESFPTAGVVAIDAGIVTKLD

PKELRNLVELFHAVATGHGYKAGELMIARSYDGQKELNARQCTDLESFCKGMEAIVNEAL

GWQLRLKNVHVGALLRQVLELCCTHHVKLEGKYASIVVSIAVLEAVGRKLDPDINILAVA

LPIITQALLQ

>contig40666 Frame-2F

MAGMVELNAWRNLVSYGAHLQPIRLQVLQNAEHRIVPSAALPILSQANQDSSIIKNEEPE

AESSIDLSTVEESNEASPLLQNEISNVESTNETSNDTIIPPYVCEALNGGEQMALNVGGP

VWAMDWLPSKPFNNAAALAAEISKRNQKRPQGSSASSKMAFEGKENNLADSINGTVGADS

KLEWRYLALATHPPCHVEDGKVVKATPPDHYYDAPESARNLIQLWAIPVQWPKKVDTTLC

KSAMVKPRLVYAIDHESGVGWDMQWCPLANKFPKTKGRENILGILAVCFGDGTMKVFEIP

VIPEKRLQIEPVNEEFELVERNIPIAIAKLPQIIQLCVHWSPHYWNLILTGGSDGSVALW

NIKMAVNKCASEGNTPTELDFIEPQRRFHDADTVGKQEAFDWGSGWVAVRAVAWSPFDEH

LFATTGNVIPSFQI

>contig40811 Frame-1F|Blast-40S ribosomal protein S17, putative [Phytophthora infestans T30-4](gb|EEY60339.1|) 7e-61

MGVRTKTVKGSAVKIIEKYYSRLTLDFDTNKRVCDEVAIIPSKRMRNKIAGYITHLMKRI

QHGQVRGISLKLQEEERERRMDFVPEVSAIDTENIEIDNDTKDLLAHLDLKLAGVHVPQ

>contig43487 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54884.1|) 1e-121

MLSSTDSMQSTQPSRSSSPQYPGPDYRYSAQNMRNIAVPPRSSTGRAKTEQVVLEFLYKV

AELIIQSRVNFHAEPDLRRGSRRARFNLDIEEVPIVRDAMAAWKEDVTLPLAIDIYWDAG

SHTILLERWSVTFVADGEHAFAYLSSTQDVIQQLKEVCKRISVLLRALFSFMRQLPAHRL

FTQSYPSMLSYTLHGAVASDAVHAFETQRVATSSYSFMPITTPFGNLKVTAVYRRDCDPF

TELRELAAPLRILQDDFIIQDYVPSSPEFASASAPVSRSTTVETPTREHEHRTGSFVPVS

GPPPTSNYEKDALSSRRSSPRSIPVT

>contig43946 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58623.1|) 5e-32

MLDRYFLSDEDFVAVLNQFPNTFAFGQVFRCTLDVKKSFSRALTLVHELTNSLRAFQEFE

QLP

>contig44547 Frame-2R

MARHCPPAPHQTRTRLCGPLHALSCFSHGHVRSFCSSCKGGQDWQLLRFFICDGFRTATQ

YTHVRCKGQRH

>contig44961 Frame-0F

MRLLNTDRNDANILVRKRRSQSMGHAEFELIPIDHGYCLPQFLEIGWCDWCWFNWPQLQH

PLSAGDRAYILSLSPQDDVARLAERIPLRRACRRNIIIASMTVQKGVRANLILFEIARIM

CREDLDTLSTLEQLCIKAFSQLQVIKQRKQNGTHLYRIHIPQSIASAAEESEPIVVEEET

ESVLVATRPSQREAFHNLRLIIDSPSCQHSSRFGRSPIASGAHSPPGFWANNAPFSTDDE

DDEFQKCCVASSDTENGLNADKSNRSRFLLNWDKSASNALIDAAQQVGSKSTGSLATLAS

AACNGSTIFSEYSSSRSPAFSIIDVEDDKDEFEMLNDALDGDVQDENLFLSILGRLLDER

IDILSGN

>contig45085 Frame-1F

MTLRIDTEMELLRRKCFAERNALWGNVTPDQFEFKPTPSDAWTPHPANDKLLLRKMKMHG

AFDGSGREFYPPETTHEKDLDVVEYVRDRPWPPQEFALKPVAKTSRGRIGKRKAAPMAAI

LEPLPLLAKTCRECKTQSTPLWRTQTRTVKTKKQVVKNVAMNNVAMNLANSFMAQNMATL

KPLMTEMRVVNENVVVDVCLECYLKLERADLFDKKRLELKRRKRSKKSVSASAALSEKKR

SRHPIHGLKKQKKQEISEANEAAAVDQGHENGAASGAVVLNLTQEEIEAAKGSSRDRKKD

RNHRQKDKKKKKKHRRKRDHLDESESDNLSLNALPASLEEVVPAYQYTMPQTSAVEMNAD

RHVEVLAPDEPEAGDSAFEEELLAPARFSSRKRRSVQYTESPVVADAPASALKNRKASSS

SRTARSKRTSTSVAPAPATTSVPPVSSVKKRSRSKKELARERELRALGQYCPVCNEVYED

DDPNTFVCCDSCELWVHGTCDSSLTAESIAAMANTEDKYICPLCAGR

>contig45409 Frame-0R

MSNDDVVRFLIEKRHDAFDDVAINLLVEGYVRGSLDNMAVVLVALT

>contig45544 Frame-0R

MKIGISYSSWINLPNAIFPGGRTAAVGERARYILRQAHDLNLAMGIAH

>contig45948 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61881.1|) 0.0

MNRGPDQYLASFEYWCSRWNLMCAPLMFSQHSMQVLTTSRDKYSKNAAEQSIRDALMITP

DPCLFLLQSVVSLRYLDLTFRTLGKLAKQLLTVVSDKLSMEFRHAEYCVSQFSHLSVHIV

KELDDVVYLHRSHREELLAFCHDAFDNDSIDKTMGFLMRRPELYNKETAAYLGPKFAEMF

VSGGVSNVLKFYKSEFESSLEMRRQFIREVINLEIATTEEEGNDVDSCTFKHASKAVKEF

KLQHEAEFLPYIMKARTAMPKPVYADASAAPADEIAYLKCPLAQNHIVVVDNDETLLLAM

DVLMRDCVKRLGLDVEWRPDSRATVPSKCSILQIACDDYVFIIDFLAMRLGDMEELLEHL

FSSQNIVKIGFAIDGDIKRLRWSFPEFKCFDTFANVLDFSFETLVATTHFVNGTVVPAHC

NDISASNLLQHRCRRRLGLSACIKQALNYPLSKLLQVSDWERRPLTPQQVSYAALDAYCL

LMLQDSVAVK

>contig46394 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55771.1|) 1e-108

MRSRLVRHLLRPPIASQTPRRYASQFSPSLFVPSNSSSNLAQTTSTRCYSQSHNTNNNST

ISEPESTTYLGVVYNAAKVKKYSAEIEIESHVISGGDYWTGLEAAKAYDELVTLYCDLDE

PRNFPESSIIATKDDHGNEIEWQAPDAGSRHADLIPCVPKTYLTIQEVQEALERENAIDV

YTINLAGKSSLADYMVFATGRSQAHMRRMADLLIQSIRTRAIMDDFDYIVEGRDCDDWMI

ADCNTIVIHLMSAKTRRILALEDHWENMVEDKHRIYGNMSEDEYMDKFGTSEFMEDLDEN

ELESDCNSTDDAKIDWK

>contig46978 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61828.1|) 3e-23

MISDCPPVAAYAAGIAMEVEGPPKHPRQTERLLHSLRVRGDLSPLLFIGLSDGTLRSYVV

DGRVGVLRWQ

>contig47238 Frame-1R

MLSSKKMLAICAAAAIAMASMTEATSYAAPDSNDTPGSDPYGNPTEPSTSPT

>contig47735 Frame-2R|Blast-DNA replication licensing factor MCM6, putative [Phytophthora infestans T30-4](gb|EEY63344.1|) 6e-68

MATTSSSNGASVGTKRARGGAPALNPSAAPVELLIDATAEAVSARFFQFLCSYGQQDETD

EGIRPAKINYSHQAEVMRHTETSSLFVDFSHVLEFDPDLAQALQAQYYRWEPYLRRSVFE

FIRHEDAAYTINEDANKTQREFFVNFYNFQHVSQYEN

>contig47959 Frame-2R|Blast-glycerol kinase 1 [Phytophthora infestans T30-4](gb|EEY66864.1|) 0.0

MCVREALAMSSIDPSQLQAIGITNQRETALIWDRATGKPLYNAIVWHDTRTLDIVHRLKK

GEGEHFPGTGADRFRAVTGLPIATYFSAVKIMWLFENVPGLRAKAEAGNVMFGNIDTWLI

WKLSGGIDGGVHVTDVTNASRTNLMRLDTLQWDDDIIKCLDIPKSILPIIRSSSEVYAIG

HNDSVIPGIPISGALGDQQAALFGQTCFLPGEAKNTYGTGCFFMMNTGTKPTPSTKGLLT

TIGYKIGDEPAVYALEGSISYAGSLVQWLRDNLKLINSAPDVEKYAMQVKDNGGVYLVPA

FSGLFAPHWRDDARGVMVGLTSYVTRDHICRAALEATAFQTQEVVAAVEGDSGVHLTKLK

VDGGMVVNQTLMQFQSDILNVPVVRLANAESTALGAAYAAGLAVGFWKTMEELRENWQVS

ATWNPDMKAEKRSYLVHRWSKAVERTLNWVEE

>contig48345-0 Frame-0F0

MEVVCFDCKCIQYSKLFFSAKATFVYRMSCTIGPKGLFAQPTVKANA

>contig48345-1 Frame-1F1

MDTQSREWKSSVSTVNVSNTQSSFSVQKQLLCIGCHVPLAPKAFSRNQQLKQTP

>contig49214 Frame-2F

MVFTSFSTISTVFKMKKQTCVLAMTSMLATASEYIGVFLLKLSKLFMSGATDEREKTPLF

VDVACQTDDLTAAVHYYYDVQKHDDSRSSFTKEFDISNDQMDCSTSDDSDWSEASQGDNS

LIRVKHYLCMCGSCPHYKEISTD

>contig49728 Frame-1R

MLAALLERSHNSRLIFFPDSCTPISSALTPSCTGSHGVWMCVPCLQCIAAINKNEGPRNR

IFDEAISC

>contig50111 Frame-0F

MTRLATTFQRPAHAFGLAQHRSYNFPNLMCTGNNEAPKRAPDSVASSRRLGKGADFCNGH

RAIIERAIDRHCNLSRWLMQSFIMETRCCHAHARRCKRVVLYTAQIVLVVIDGLTRFIVC

INEAVEYNCRGRKIMLVIDETSEGTEIAG

>contig50436 Frame-2F

MVFSSSIVGIVALASAYFAASTAAQDMPIPWDGTGKGLDVATLNKKFMIHILTMRNGAEN

GNVTKYVAIEENGRAPAYNGDSSVIEIGVDAEAIFQQQKTFRRS

>contig50559 Frame-0F

MTSTDGSEDDSRLGSRESYTHSSVKWNDRSTQSYEQNQAPFEEQANSRCIGSRLYTRQGQ

SDEEERDSVVSFSGENSFFPSAGRPSSLYGGSQSSFASHRMNQSSVASTDHDGSSIASFG

VSSAGATFGGSEHISESGAYSDGSISETPSMVNSSNASTAFGTDFPSASEGQFSAPGTTI

GGSDNASDEEFSDDNASETTSINENMSANLRSASEYGASSMQYNSETIASRDAQEPFAES

APNTNLVTKFEESKSAALSSVYGSLDNSNDEKPCASSSGLFSTSQQAVSGPVAASSIPSG

VTHQLGSITQEEIFPSAASLFGATTGADIPNPFSAFSASANITKPSDAPELPTLNVENLV

TAGSSTSFFESPHATSVKHSHSSGH

>contig50641 Frame-0F

MKHAGLRLPTSACNQVSIEMNYRDHAKITAVGPAIHYFLI

>contig51075 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66319.1|) 4e-34

MSWNEFQHLRLPFWLKSYAKLFHFVEKVAQVEYAANRDPFAVAVFYVLLGKNNLLASLFK

MANETRIAELLSNNFNDSR

>contig53507 Frame-2F

MLKKKEKLEQMRELGRGGLTKGLQFLRTAANNASVDNIEASSTPSLPSVEGEDTKSNRLS

YEELLALTMKLTRQNKLMKIQFQTIKRKEEAISKSETDVQALRSFLELELGLDVAACIRT

DNGRGGSIDMDALTEKYRMIAPMQQEEETKPQAIVESVDLLNLSPVAAQRMKDNDVPSKD

DQGIVFDEIEIHEAMQQVERMREVLKQNAQEMQALERKRAERDA

>contig53950 Frame-1R

MNTVPVAVAVELKSLNVFQSESDE

>contig54007 Frame-2F|Blast-cyst germination specific acidic repeat protein precursor [Phytophthora infestans](gb|AAC72309.1|) 1e-10

MSLRKSSTAAALAGILAASLVSANVDVSVNRDATYTLSESCGLPCSGNGLHP

>contig54780 Frame-2F

MTLPLHRARQCNFTRVWAADATTAESVLDLQQQQPATWSATNASGVSITNGALELQNTTL

R

>contig55563 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66086.1|) 1e-64

MPRQPLISWIQPQNYSGEQDFLFGAVDDVNLSRNGQDSRGYIVSTLKRHKVTTLFPYERN

RKRKGTKVMSLMPLRSNGDDAEYSELPQTNIEQFVASEATLDLRMDDGGEYTHLTGLCAL

CDETLESASIYQLNSLGDLFSHRVSVSRSQIKSYHSAIQPELPSGIAATDNLMDESASRF

LPIPVDAILPEHDTESLQRFITLPVKALRRQFPRLSDNKEAPNTEDDRSYNVTHALDAIA

FVNLQIKDSRTSQAKQNKIRLNGASNKLKRGVATKS

>contig56614 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57888.1|) 3e-22

MISLQIENIQAVLFHDRTSDAACAALKIYLKRILERFIEMFQHELEQLQPQLQATATPTA

K

>contig56683 Frame-2R|Blast-endomembrane protein 70-like protein, putative [Phytophthora infestans T30-4](gb|EEY69817.1|) 4e-31

MLYFGYMAIISGALALLTGAVGVGASLWFTRKIYASIKVD

>contig57745 Frame-2F

MRLHVTFTCATCATKQCSRDAENLNRCGYKPLSPSSHCRQSELITNIPAQCSRLHFLYGF

KKIRNVL

>contig03451 Frame-1F|Blast-elongation factor 1-gamma, putative [Phytophthora infestans T30-4](gb|EEY57157.1|) 1e-112

MKLYTFPGNYSVFKVLIAAEYNGINIELPEFDMAKDIKSKAFMAKTPLGKVPLLETEEGC

IFESGAIARYVARLRPDTGLYGKTFFESGQVDAWIDFSAFEMEVPLEVWVHPIIGVGKFN

AAALAKAKADVKKALQIIENHLLLRTYLVGEQVTLADIVVASALVYPFKFILDKEFRKPF

SAVTRWFSTVVNQPEFQAVVGDVPLIDVALTAEGDNSNTKAVKKDASKKEKKENATPKED

TPKPKKG

>contig05772 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54775.1|) 2e-07

MEAHAPLHLPEIKVTSAEHTRQLEKRFTYLWTSAHALLPTNSTLAHHM

>contig06579 Frame-2R

MKQEVKFVTWNINGLRAVLQRLNQNLHDFLTSLDADIICLQETKMTRSELDEEFVRPRGF

DAFYSFCRHRGGYSGVVTFVKSNLPTIAAEEGLTGLWQTEDSVGHVGSMHYELPSTLVKD

LEGGGRCVITDHQSFLVLNTYCPALASAERLEYKLYFHKLLQDRVDTLRAAKKPVIVVGD

INIAHQRIDHCDPQANDADCSFEDHPCRKWMNSFVEVPVKERNKLLLKLQRVDNICKNTS

RKLVDLFRHFHPDQTKAFT

>contig08058 Frame-0F

MCYGFLDSTFSKEQQANLDVLATCTNDCSFRWTTFLPLCEGPASMLLTNEGHVYSTIDEN

HFKCTA

>contig10231 Frame-2R

MCDVGLLVFFLFLVRLKSKVPCLFKGPTVVTHMTIRSERNRSCLATSAQRGKKENVARKA

RKCILKERTV

>contig10943 Frame-1R

MTKPVDLRINYNLGSMNDKYTMPPSSRDLVLVLNLYCDFILKRRAIH

>contig11298 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70076.1|) 3e-28

MQCAVSATSTRALCWLRLWSNKKETLTVMKGRRRALLRAHAFVSLARLVMASDTSKFCSS

IVSCLKDGSATCDTKTGTCPPCIYTLDSTHTCWEKDNSTNTCPFTGVRYDC

>contig14183 Frame-2F|Blast-vacuolar protein-sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY66104.1|) 4e-73

MRTQPLASSFLKLSFKDGGRDDFFNPLAASLKRKAWRDSQPSHLSDRRLVKRQFNAADAG

IAGIMRR

>contig14648 Frame-2F

MAPSQVTLEAWLASTRRLLSIEQEEEVHTMRQELAQLNDTENPNVLTHLTLSHLSTGLFG

RTLLQFSFPSIYLRHAKVHHITVGDLVQIRLQATILGTGIVSRLEERTISVAVNSDHDDV

DEAKLVAAKANITLDRLVNNATYNKLTNALDQLTKSEFGAAQAVIDVVFSENQPTWETPV

REITPFTIGLNKSQVEAVQFALASQDLALIHGPPGTGKTTTVIEFLLQAVCTCHYKVLVC

APSNIAVDNVLAKFANKCVEFGKIVPIVRVGHPARVVSSIVKYCFDARIQEADGTKIVRD

IRRETKHLQRKLHTLRDSSERKQLRRELKSNRKDIREREQRIAREIVQQSRVVFATNVGA

ATTVLRDVTFDVVVIDEAAQALEIACWVPILKAKRCVLAGDHLQLPPTIKSKVAATSGLD

VTLFDRMTHLERMQPVIKLLDTQYRMHEDISAWSSRAMYKGELKDFECVAKRKLHELPHV

SIPLRRSCVECDIIVN

>contig15092 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56873.1|) 3e-45

MTSALGVSVLSLVMSEVKQSKEKQFTDRHGDMLASLPQEDLKLVEAASELVERGLVVRIT

ATPSRREFYRVESRNKYKRNGSYHDVNRSVDSGSNSFDATTIRGSGASYYNCFSHYCTCA

AFHDTVVKSHPTAMCKHILARLLADATGQFQSMQVEDLHFAQMLSGSMSVCE

>contig18150 Frame-1R

MRLRDRFVAFLVAIVALCPHVEPLRIPKGSKQPLKHEGMITQTDPSFNEITLQRDEPT

>contig19801 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60395.1|) 6e-27

MELKRNVAFILEYRNPRKLVSEPGYFFTHLVSSIAFIEELNGSSLTISLDEFHTELQKSQ

AASGHVLTNMPRACNEEEEKNKTYKKDAWNGRKSQDVKEEQWPLPTVLEIRAKRLALRHS

>contig21370 Frame-0F

MEDRSRCKGGVQSQQSYVQQQVAASQQQFPAYQHQMQAQAQLHPYQYQQYQNQQQQQSKV

PVMHQNRNIGYRNTTTATSSGAQKPSKTGAKMGIKSGMTVEDLKRLTQKRMQQSGLSNPA

TPKNVALDSFSSTRSATPKINMTVVKTTSTPANVATPPVVPKTGMSVQELKQLTALRVAS

QNAPVHASEITGFVSKAMLNNATKSHYRDNSRTSEISGNTPKRSYHARSNSGSQYGSAYY

SSFGNNLSQSHGPLSSESKNDLSSIRGHR

>contig21983 Frame-2R|Blast-branched-chain-amino-acid aminotransferase [Phytophthora infestans T30-4](gb|EEY63223.1|) 0.0

MVLVQSLKSLGRMTSRHSAAFSTGANISFANIQIDRTKNPRAKLPKEELKFGKTFTDHML

EVDWEQGKGWGDPIIRPYGPISMDPASAVLHYALECFEGMKAYVDAKGHIRLFRPDMNMK

RLNRSMKRLLLPEFDGDELIKCLQELLRLDKDWVPQGEGYSLYIRPTGISTQASIGVGVS

EKAKLFIILSPVGPYYPEGFNPVKLLASDRYIRAWPGGTGGFKVGANYAPGILPQYDAQD

RGYSQNLWLFGPNHDITEVGTMNLFIYWINEQGEKELITPPLSRGDILPGITRDSILHLT

REWRDFHVTEGNITMKQVQKASQDGRILEIFGSGTAAVVSPVSTINYMDEDLIIPLNGSD

GKAGKLAERIWKDLSDIQYGRRDHPWSIVLDAA

>contig22159 Frame-1R|Blast-eukaryotic initiation factor 4E, putative [Phytophthora infestans T30-4](gb|EEY66244.1|) 9e-71

MRKVLNLPQFVALEYKRHDMSLNDNSSFRNTTLWRSDKNDGNSREGSSNGDRASSGSRYP

RGDKTAGHQRSAWNRDGKRSFFKSDGNDNGQQRSSKSSEHKGEGGD

>contig22638 Frame-2F

MRTTQTTDVPEAPAISPPKTPTVQQESSLKIPVVQSTSTVNTPNTAVLHAVNVSNSGRSK

TSMSNSKLCAKLRVEISQVELGIAIDANEDEVNLKVVAIAPLPSGGSRIAFHSGETIIIR

ELDEKDTLVSTSATVKVPMHDFADMYADESGFVLLGTRDAEGGGTLNCGNPSNLCGVAPN

PSVPCYDMYLVRYDGTKETWATKLTTSSAALPPYSTGKTGSDVYMIWWYAHHGRIASDGT

NWAAYFGCAISTSESGCINIHQGDRMKVVNPSGAIVTQPDSFDWGCSHSGYERLTYDSRK

KGYASICKT

>contig23178 Frame-1F|Blast-importin alpha-2 subunit [Phytophthora infestans T30-4](gb|EEY66875.1|) 2e-16

MSSPAAKMPERKSLFKKGIDADESRRSRMETTVQIRKTIKEDRMNQRRR

>contig23660 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62480.1|) 1e-102

MAELKPLSPVLKADISEKVNSIQVKPESVNKRGLKLDTNLVQSLDGGYLKQFEEAKVNGI

PTATLPAHFALLSTTCIYEPGYTTSPRGKRRISQTQGVPFGLQHDEAHKEDSEDAENGKV

GDDVESHALINNDLNLPVFTNAELSAMIDLPSNLPTTTTSAAPSPVHGIDDPMPYSYPDS

SSMSTDVANLMYDQEIPVVISMFSSIFDESQNFHQQLLDHSESTNGNAAAPAPPVVVTGQ

IMPPGAPVLPRDIANAASISHVAAVSKADPSTSPEPFDYFSPSGYANAANQFLGSYGQQV

QPFFLNREVTPNAAVFPSCQQVPESINSQLVASMTMANTTDLDTMNCNYRGAKDGRGGRL

QQSKVAQPSKSHLPALRAASASATTTSSSKLMRLAFTPDIADFKLVQIFHQFCDPVAMVL

TLPRFQQLLLFHQIKEESAGPTNSATETKQGGSDTANSIVVTSEAETIFKALDINSVGAL

DLERFMHSYQICNRCTEVKRRANQALCASQGQMLNSTALERHLMEDVVPVVVRVVPTSFE

GHKVKSCDHYQWTWCEGFEKTGNDKCRGTNRHDKCPKYLANCTLWKHKLPPKSRKPKLQQ

ENVDSPTKKLKHFS

>contig25459 Frame-2F|Blast-Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4](gb|EEY58372.1|) 2e-90

MGDRGLGMDFMLAGMATSGACVVSNPMEVIKTRMQLQGELAHNVTSGSVPVVRYRNFAHA

FYTICRTEGLRGIQRGLLPGISYQIFMNGPRLGLFVPLQKVFGATDPTSVWFPVRNVCAA

ATSGMIGACIGSPFYLVKARIQAASTAGKINAQYAYDGMIDGFRQILNTDGVAGLYRGAT

AAVPRVAIGSGTQLATYTQAKTVVLAAGFEDGIQVHLGASTLTGLVVTTAMNPMDVVSTR

MYSQKVVNGKGKLYSGLLDCISKTMKSEGIRGFYKGWSAHYMRLGPHTIFTFLFWEKAKT

LAAEFGY

>contig25547 Frame-2F

MSLLCSNTKPGVRGYTERGV

>contig26663 Frame-0F

MWKCAAALDYDAFRSDVVPYIGVLDIFGFEDFEPKNRNSFEQLLINYANETLQSVFNACI

FEAEQTLYKQEQIDFPTNHSLSFPLSIRNQTNSINKLDLLDHMSPSGDLVVYADNRECLN

LIASRHGGLFATIDNVSRLPMPSDRKLNERLHTLFKRHPCFPTPHPKDLRDTFQICHYAG

TVTYTIDSFVDKNNNIISDQFEELLKHSSSRVLHDSSCHSSNRARSDSIVSPKSAGLSPL

PGGSASSKRLKGGSTSNLFSMQMKGLTSELEGTNCNFIRCMKPNTQMKVGLFDRPYVVEQ

LRCSGTVQACEVLRVGLPTRILYAEVVDVYRNLLPNDIFCRFNANDKLFTQAILYVYDFS

TSAYRMGTSRLFFRTGKIALLDKLLTPAPVTIKNLGQELVRFLRK

>contig26887 Frame-1R

MRGSLPSQTSTIWQVMAYLQAKVCQYFDCTVFPIISTYKHTSTSAWRVPMRRYNEMDWCV

QG

>contig28470 Frame-0F

MMRRRESNLTLDDEAETTVEIERLDQPWMALEVFEQLWLHATQQVCSSCTFSKYTQQAGD

RMIRTQKHQNQNSINSSTAANNPFQQQLMEALGDDLVIFPTSPKSPLVILAYASIIDEFG

LKTLLLAQMEQLRDSEQICITIKNTDPAPRSKMIAFLCLLQQRLQPIQVPKRPDPRSGNT

SLLFQEESDLDRIINLESTPITLSPCIRTPPLSPLSSAMKAPVRSPDSDLEIEPLARGRS

HTIRYRTARDITFEGYLSKKSDVLMRWKATYCVVEDDTLAFYETREDFISNSKIIGRIQL

QAIEDEDIGKPNGFRVIAEGGHANHLSSRTAFEKEQWKRVILIAIDQVPEVARPFVAFAS

QPLEPHSFYRLLGSLLRQEVEDFALLFRSMHPDIVVTSNFPPIVPFWGQYRRYDGVLLFI

STLLDTVTVDHFSLKEVIELVRGDADFVDEAGNSSEALMSPLPINSSIVSSTPTTMSPLP

SASTPSAQWSKRIVVTGKETYNLLHTDARRVTQLFVHELWLDHKDRLVRWHLNGDAVALS

VAFDDAPRGENIRLVLPGEASAISHSIPPGTFYVQMLRAEQLHVEETTAGPDTSKKPSPS

NPSNPPGVKGYPVYARCILEEGTHMEQTLRGLDIKEGQDSTRDELATAFHKSPRKENIRP

SKGTRFFRGLRRAAGISSERTVTTFGDASGCVTHLCKCMPVVTSNDHHKGGILNPNWCSN

LRLEFPGCTRGFTYFLKVEVFQSRFLLSDELLGVCKINVTPHLSLVHGSADAKANGALPR

WHNLCDQYNDCKESWAPPTVFRGRIQVGIIFAPNIPSATSFPQYQVLRRMASDGSLIESR

RGSANETLLHSLSSYNLHEGLWSEQKALVKAFSFSSDKGVESQPLQNLNNEKNGYSQLTH

DSHSFYGKSTRFDVPKKYQLIKVVGAGTYGEVVAASDIESGTTVAIKKVTNAFQDLLDTK

RILRELCLLRQLSHPNLIRLYDVLRPERLSYLEDIYLVTDLMETDLHRVIHSTQTLTDEH

VAHFMRQILRALAYLHSANVLHRDLKPSNILVTSTCEAKICDLGLARYVDHSKAKRSNDS

AKDTFVELTEYVVTRWYRAPEILLSGCKYDTPSDLWSAGCILGELLGRKPLFPGTSTINQ

LNKIFNVLGTPEIGYIAQIHKEAAQRWVHRQRRRVKIPFEELYPNANQQALDLLAKLLVY

DPKERLTAVEALKHPYLREAFRSMGDYTEEDVAYGYDEAEQKEDVFVGTIHCLNDSVADS

KETMQKAVFEQVCHFHPEAREFEDWLKQHDQKYSVDPESGKLEPISSQG

>contig29334 Frame-0R

MGVNFDPNGAFEETSSRRSSLKEGDDLNAKKYLKHREMVDGELESELKTTPFEKYGLHIG

QKTKSSSLLAAINPFSRKSRSAGDNTSLYKMVGYFKGLIRVIEREDEKPLFDFNTLLQTL

PYEVRIYVLDGVGFAPMDIGLNGRPGKSDPYLRLKLGDKKISDRKNYFENTTDPDFYKMF

MFNAKLPGASILTIEAMDHDLIGGDDLIGKTTIDLEDRLFDSRWQAMGKMYETSSRLRLK

PLETRTLNIFTSRAPMGTLKLWVDILSPALAHDYPAIDISLPPPVDMELRVVVWKARNVP

SFDAMEDMNDLFFRCWMEGSEYQETDIHWRAKKGKGSFNWRMKFPITLGHKQLNTKIPYF

HIQGWDKDVLSANDAIGEHTLDLGPYFRQAIQLKTNVQVYEDDDETRKKKKKASSDDDAA

VKKIREATGLWDDDDPSDSKWLKLEALDHKTNTRNFMGEVCVSLELVPAENAKKNPVGHG

RSSPNNSPYLPPPAGRLSFSLNPFKVLNDLLGPSICHRLTCCLCCVLFMVFVYFLAPFIN

VAIIALRG

>contig30219 Frame-0R

MQIPGLDDAKWFAGTQKSLSIIGLDTNAQKTLFKILAGVLLLGEVLFETKGESGSRISSG

SALTNVAKMFGLPSSKIEDALCNRTVITRNDSVTVPLAPVEAAENRDALAKTIYSKMFDW

MVVKINAAISTDESRIKGQIGVLDIFGFEDFVHNGFEQFCINYANEKLQQKFTTDVFKTV

EDEYIREGLQWDHITYQDNQGIVEVIEGKMGIIALMNDHLRQPRDTEEALVNKIRTNHQS

KKNGDVNESIAFPKVKRTQFIINHYAGSVTYETVGFMEKHRDMLQKDLLDLIQLSTMSLL

PELFEESEVTPEVGNGRTKKGPKSLGSQFKTSLAELMDNIKTTNSHYVRCIKPNSNKSPT

EFNKRMIVEQLRSAGVIEAIRITRSGYPSRLSPQELATRYAIMFAPSMHSKDVRRTCSVF

MASIGRKSPLEYQMGKTLIYFKSGVMEELEAMKSDFMYYEARTIQRFALGFLARRRLRHK

IRAAVVLQSYARMSLDFKEYHFQRRAIVKIQRGWKTYKAIPFEPEYNEYPEDEYNDGGEW

VDDDDRDMGDDFDEDLNSFRGNRGRSVADRMETFKVAHSDRRGSVKRLNDLSARAKSYMK

PRSGSGSTASSSGISLEDENSMLKIENRNLKYDLELMREQCIELQAIILEIHKSRKR

>contig30545 Frame-0F

MRSSKLLPTFAFIKLQRLSTARTVSSETTGSDAFTFSGAAAKAQPSN

>contig32165 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54356.1|) 2e-12

MSMASRLRHFVNSPTGPKTTHFWGPVANWGFVLA

>contig32239 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53446.1|) 1e-128

MLQLAQHTFGDVVLDSMCGIGTLPICAADFTSNGVYALGGELHQSPSKKAGRNARTRPRF

VNIVRWDSTHLPLRSHCIDRVLIDMPFGLRCGTQRQNNKMYPKVLKELHRILRPNGRAVL

LVMSKKLFKGVMKDLQFQIEAEHMVSIGGLGGAIYVIQPIDMLL

>contig32837 Frame-0R

MREKIIKAEPSQNLKTGIMTFSSSASCDASTGLVQISGHDVSSDQLQPPSSVSSAAAATS

TISSTNSVAQRQDKYAVGGRGRGRGRGKRSLEVKNANLKSPRKPKRPRTFSFDDMAVGDM

SRASEPPDRNPLAPCGACKEWLVKVAEANPSFRVVTFENSRCRNVYIHQLM

>contig32958 Frame-2F

MIRSRIKRESSPNFASLATRPLDSEIREHNMTAQIDIGSPLAKTESPPFMKEITSINTPR

EQNELALEEAVMNLKTLGTFATSSSLLPISKPKVETYKFDDSITIPPRSMVIEIRVIFAR

TMQNIFRHRSLLVLHTALSVSLAVFGGLIFNHVTNDLAGFQNRMGAFYFILTFFGFASMS

SMDLFIGERPIFLREAGAMYYGAFSYFLAKATLDTCLLRILPASLFASIFYWIMGLQATT

DRFLLFLLTIVLFNVAAGAICLLVGVVSSRVGPANLGATVVLLVMLLFGGFLLNSQSIPT

AVGWLKHLSIFSYAFEILMTNELKGLILKFDAPGYPAIPIYGEVYLKTLGMDFANRYYDV

AALSLIAVSLQVLAFLFLSLQVPLHRSMIEIEGDNLIRREEM

>contig33302 Frame-0F

MMTASHTLARRLSQGLYGKAEFLENCCPKAETISLMRLFHYFPYEHFASLTNNQSLSNNF

KEFIGSSPHTDWGFLKLILQDPGGGLQIYHNQKWMDVPYVAGALVANAGDYLSLVTNGNC

LSPVHRVLLNKRERYSLVFFYYPDFDAVVPNFENDLNIATKGKAFNTLLDGTVRNVNGCF

GEYHMDKWANVQREV

>contig34844 Frame-2R|Blast-hybrid signal transduction histidine kinase, putative [Phytophthora infestans T30-4](gb|EEY61857.1|) 3e-91

MTPRNSNEMACSHLVDAAEAPIFGVNTQGHIVFFNKKAAKVSEYWPAEVMGEDLVSFLID

EDHRDQVAAVFGKALAGIETANFEFPLITKNGRKVDILLNATPRYNYAGVIIGVVGIGQG

ITERIVQEQEYSRLIDTANAPIVGVDKQFCVTIWNKKAATITG

>contig35234 Frame-0R

MLPLTDALPNYLRTRSANLRVISGVSDGGLRAIQKLLQAVLCHHMTYPEGNDCLLAPLGN

QTLPKYVIQSLFLPAIDRQFSTAVIDFPSRAVRIELMSTIR

>contig35465 Frame-2F|Blast-GMP synthase [glutamine-hydrolyzing], putative [Phytophthora infestans T30-4](gb|EEY55088.1|) 0.0

MQATFRGQNRTLLGNSMGDAFPVTNRKQVAILDFGSQYSHLIARRVRELHVFCELYSCLV

SSDELRQHQLTGIILSGGPQSVYDESAPHIQPDVWNLIEEMELPVLGICYGLQELAYTNK

GVVAPSQHREYGKAFVTRKSEIDCGGLFQGLPEMFQVWMSHGDKLHKNPDGFVDIATTNN

SEHAAIVNVARKFYGIQFHPEVTHSPLGKDILRNFVVNICKSPTDWDMRSIADAFIEEVR

ETVGPEGHVIGAVSGGVDSSVAAVLLQRALGHRFHAVLIDNGLLRKDEASEVVDRLHSKL

GINLKCIDASHRFLEALKGVTEPESKRKAIGNLFIDLFQEEAERIGHPVDFLLQGTLYPD

VIESISYKGPSATIKTHHNVGGLPEKMHLKLIEPLRELFKDEVRELGMALGIDEPSVWRH

PFPGPGLAIRVLGEITPEALDILRHADSIFIEELRNSGHYKTTGQAFCVLLPIKSVGVMG

DGRTYEKVIAIRAVSTSDYMTADWYHMPYEVLSRMSNRIINEVRGVNRVVYDISSKPPAT

IEWE

>contig35810 Frame-0R

MTRVSNEMREGIESIQTIYELGKRSFLNKPSNEEDGPRHTPKTTIISWERVF

>contig36486 Frame-1R

MRRSRNDSKSTPPESMNGGDHVVESLDLPIVEWEGYVTKRGHLVRNWKMRFFTLEGNLVS

YYENKVDARNRSHLKGRVNVASVKVDKVAKNGHGFDFSFETTEGKVFH

>contig36947 Frame-1R

MRNHMGLSCFTLAFLASLHSVTASTLTTAAQDAYQVDLPIGSRSASRTLMPEPPLPKLTS

WAIRILKTTPASFEWTVSKKIEPSAFYLMRVPTDTTKWHVSDHVARFKHLLAQLANAFGE

IEASELLARALSAKLGEHKLAMLVENAENELDPTVLAIEKGIYAAW

>contig38174 Frame-2R

MTSCAVSSSGFSCSLGPKDQINVSFFCRFYTFPKLPIKLHIRNINCASAHMNA

>contig39872 Frame-1F

METESSHEKSRLNAIELKVKDVQGKLQTRLPAKYKNLVAMVCGAKWRSRTFKPKNAASVI

KKIRLELGAFDYSVKEQAELLTRYLIELDGVLSYGNSEIRRARKALVILVQQLLPLADEF

MARGAKLKHFGQRVLGGIECLPTTALKPIDSNADFGDMRFEPLARESEHIESMLEDKEDA

NKDIKMEQLLSMNKGENRNVEENQINGGADKDDMAVEDDANDGDADEVIAAREKGVAAAR

SDDARIINAALEDDDITVEDDNEAVGDDDEAVEDDREAVSDNDEAVSDNDEAIS

>contig40739 Frame-0F|Blast-Rab5 family GTPase, putative [Phytophthora infestans T30-4](gb|EEY54592.1|) 1e-100

MSQSKTCHFKLVLLGDTAVGKSCLVVRFVRDEFFEFQEPTIGAAFLTQTVGLEDGMTVKF

EIWDTAGQERYRSLAPMYYRGAAAAIVVYDVTNKDSFTGAKSWVKELQRRGDPNVVIALA

GNKADLEARRKVEYEEAHQYAEDNDILHMETSAKTAVNVKDLFVAIAKRLPKNPIQPERE

AFPITPPQASKSKSG

>contig40810 Frame-2R

MALAVLFTLVIAGCTLATVLSAEALLSKAALCEVDVDKSRPVINMLQVSEEPANQYPRVL

CFAVTYSSQHHTRVQAVAETWGQRCDKLLFFSNMSDTIIVGANTSRERHFDIVHFDIIAD

HKHLWLRTRAALKYLYDHFRHEFDWFYKCDDDTYVIVENLRSYLKRPEILQRVNRAPMQI

GHRFSMPTQVLDYYIKNSTLRAEWHIHWDRMIYNSGGSGYVMNRLYLDTFVKSLPETTCL

SDTASSTMPEDAAVAFCMIWNDVYPWDTRDHHGRDRWHALNPRLISRTWRNRNDWYERYH

IGLGGLRSSNECAAPDSVAFHYVKPVLMYHLERSLYFCRSKYNDIAAFNEHNGLAIGDKV

MVV

>contig41512 Frame-0R

MASSNKSCFATTHAQPRRSWGGIRSVV

>contig41585 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60002.1|) 3e-47

MEFLSRLESEDHQARVVDPIKTQFGELHHSTDHVFKTVIAPKNDKQNFDASNASCSERVY

ATPKGCFVNPEFPLDAIDVKRFITYCDPETE

>contig41844 Frame-2F

MSRHQSAFLRQEAMATSSNQATEEVLQRGNNFANPRGYPRAKAHILFDEDTGDQVVKHNE

SEWDARNYTWVSRKLPASELAKYGPASSDNTQRDLSDSIHHTASSNDISERDEDVTYSTI

GRKRKEYGNYEERWKRSYEIVASVQDKAPEDSRYSDSKLTKALALYPNIPVASPRFAIKD

IIAFKTLTLCLETCQPVLSEWKCGQIQAMDAPCG

>contig42452 Frame-0F|Blast-dihydrodipicolinate synthase, putative [Phytophthora infestans T30-4](gb|EEY69164.1|) 1e-142

MTLKLRGAFTALVTPFTDDGTAVDYAKLRELVEWQIQEGINGLVPMGTTGECPTVSHEEH

DRVISEVVSAARGRVPVIAGTGSNNTAEALRLTRAAKKHGADACLVVCPYYNKPTQKGLY

AHFKAVADVGLPVVVYNIPGRTNVNLTPETIAELYKLPNIIAIKESTGSLDQAMEIAALC

DITILSGDDNLTLPLMAMGSTGVISVLSNASPKKVLAITDSMLKGDYVTARKASLENFFL

VKSLFCEANPQPIKKLLHLMGKCSPSVRAPLVECESSTENVISRLAKEHKLI

>contig42654 Frame-0F

MYALPAFPLQNSQNDAIIAQWCAQMTAFLAMHGQNLLAWHPKWLQFVTEREEDKGARMHM

TAVDFILQPFPMAKVVIPRGAQEKVVMHVHSDNEMQQYIVWRFELEDYDVDFSVSYAPEP

YAQPLEI

>contig43859 Frame-1F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72305.1|) 1e-08 NOT\_ORF

MRLHPTSLMYRRISHRTSSLLCAD

>contig44191 Frame-0R

MCVRLRVYDNLCMVANSIITTYSQLQSIYGNLCMVAHSIITTYSQLQSILE

>contig44533 Frame-0R

MAADREHLALLKPTGEVFVNGLSSSYDDQYPESERLRSLVTHEDFSQTLAVINDALMDHW

PCLPCKGFGYGCCICTLGLSLYCATTQVAEAENRLKMQLQHINEQIKYKEKGVQWRLERS

WWKRSSFIEISVCAQGSKTSEVGASDEMMSDRVL

>contig45130 Frame-0F|Blast-aquaporin, putative [Phytophthora infestans T30-4](gb|EEY55401.1|) 2e-60

MVRIDDKVESDYLGVQEQDVRMSSEPMKYYQIKSLLFRQCLAEFLGTLVMIMFGDGVVAQ

VVLSQSTKGGYLSINLSWGLGVLFGIHVSGGVSGAHLNPAVTTTLAVYGRMEWRKVPYYI

FSQIAGAFIAALLVWIVYFPMLKVIDPE

>contig45219-0 Frame-1R0

MTLVRKDPYVSIYDIGMQRSLCIDCLHCRQTPLTTKSASIVNL

>contig45219-1 Frame-2R1

MYRSTTLVCKDPYVSIACIADRHPSPQKVLRSLTFSRPKVRSCVGALLRSVVSKEFLDL

>contig45493 Frame-2R|Blast-manganese superoxide dismutase [Phytophthora nicotianae](gb|AAY57577.1|) 1e-117

MPFELPKIPYDYNALEPFVDTATMNIHHTKHHQAYVNNINNYIASDKGSALQGKSILEVV

QAATEAPVRNNGGGHYNHSLFWTWMTSPGSTNTAPHGALKSRIDEDFGSLDQMKQEFNAA

ASSRFGSGWAWLGVKADGKLAITSTINQDNPLMPNVDQPLIPILGLDVWEHAYYLKYQNR

RPEYISAFWNVANWDKVVEYYDNFASKGKPVNI

>contig45545 Frame-1F

MVERQPTMSLQAWIATRNECLTVADKLIDPVSIVAAYGDNDRSIVAKSDFQAGTELVALK

QGVFLNGTNWLKHFVGEEKESLNAKVDSMQLSSTIKTSLALLAEVARGNSSDYCGYIQQL

PTTLMLPFCWESKLCELLQHTTAFSLLDDKVVLDLYENHAKPLMTTFSAIWPTEVSTLST

FQWAYSMVVSRAFNVENATEPTLLPVIDMANHSVHNPAAHIVMIDASTFQLIALREVKKS

EPVTISYGELSNAQLLCRYGFVLPTVLPSDSIHITSLELTNAFQAFLHNSDIDNEDSSQI

RLGKATLKSNPAKRVKVDHLEKDGHSLFFTLNDKEEQDFGLGDALLNFVMTNNYPAEHLD

DVLAMILQEKDKKYCACLLKASEIASCETKAIRQLTLHERLICRRVLLGLKSLEEGSDVS

EDDDES

>contig46302 Frame-2F

MKGRFFQDEPNENQTAIDELLQKCVIPRSLMSPEDALFAAKFMERLHTFATPQMSTLQYI

HKVNMKVSAIVLCATEREASNFGIFMKETLGMVLRWYQNGATYDDEAIHGKIGLSLDLND

GKKRLAHRQFKAAYSRWHLNLELVYTTALSSGEYMRIRNSLVVLTKLIDVFPTGRGTADV

ILGIVETLTNEDREDVKIMAKRYFALLTKRKTSLIDDKLLRTRGMLASSLNPIAFNNEPK

DATSQLDQDKKVADSDRKADTKLDITSELTLSRGESQELESGEIIPGKSTGNSSSSINSL

AETKQREIQSSVSNPNIRSGRGSSADSAHDRRSRPERKDTIDSRKNIAEEYHDSEEGRER

WGHRGTSPALGGRSGSINSR

>contig46395 Frame-0R

MPLSTQKSYGRQRVMKKELSTASAFTAELSHRLSAIYQSPAQERIHYLEGRLVELMEELK

SLKTKNKHLNFEVDKRDNLISKCRNDLIR

>contig46474 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62334.1|) 1e-111

MGSCLSLEDISVSQLEAQAGGPNLWYEPADPKFQNRRAIPRLRDALIKRNLALPLCILIC

QMRSRIEYHEDKRLPHLKLLGRVFDTCQLTFSQLLQFLSGVVHPLVYRKMLPSVAALVHD

YNVEPELAMSLCRPAMRSDDPILQTAPRGIHAIGASTTASDEAACNGTTTTDASSGEICW

YMYNTNFLDDIRKALRPESSSTSKFEDPFTGLTPEVYATFWGLKLYDIHIPFQQYESEFC

VCA

>contig46979 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69607.1|) 2e-12 NOT\_ORF

MLLNRIRLEHITNNLCYNPAKYGVEEISRLRSFCEAPVMRYSETRLRKGIEDE\*TIIQGM

AEGHIVSISCPQFVKKIFNAKDQLRF\*ATK\*VQEEGELSFSLAVKEQFRLAGNIHRH

>contig47239 Frame-1F

MSYGNVTMPSESPSEWQIGALLLRVIEIEDKVSLRHSSCLRDNGVVVIDRHKIVIVVSTL

NGIGKLVRRRN

>contig47837 Frame-1F

MTLDLFKLQKEASSLRNDLAMATEALEVHATKAKDYEGRYIQSENDVVKLKKQVGEMRDR

HHENFEMLRKEKETEFERVDAERQALVKDKKELCREKDQLELCCTTLKRELESVRTYEEE

LDALLSNKTLELESLSVDLSDTKKALSDRMALATRLQTENMNLAGKLAEQVALIESALRD

AANSRKAQETMKTQVQTATTEIQQMKTKEDHLQQDLDQIRRELQQQSDAFQREREKADMA

LQVAVVRENQKFQREKERLETESKHKSKLALQAVLEKEK

>contig47958 Frame-0R

MSKLWQSCPSRTCKFIAVAPRFLPKPQKPFMLVCCHSSPLATALLLPQSSAEATWPRHDE

IQKQF

>contig49057 Frame-1F

MDRATPDWCGSLSFESIRPPAVHETSMVADERTAADAPTGPLVDEIGKVEPDSVVGEKRA

FRDDEDVNAFVHAVPQTSVDDAGDSQDSQATQDDDIHNVVATLKASVGVDMAFDAAASIV

PPPEALKMESSTPVQDAVMAAAVASVDPHATANVKFDSKRMARVSFNSWFDFDSYFEIYM

QETYQPFRMRSSCSVEAYRRNQQKVMLNNKSSRGRRAEFPDEAIHHHRIYMCTHAMKARC

RGANTRPGQKYRGIGCMAKINVKITPADNPSKYMVIVTD

>contig49215 Frame-0F

MEWLYFSSDKLISDPGNESISNPFASKRVTRSEATLSTASATQSMAAPPHPEAETYHAYW

RQPRTKFCSRLPIFNRGNGILLTSIDTGG

>contig49282 Frame-1F

MSGDIKEIGAAEKRICHKLPIFSGFCAIEQTKQDCDINWMAYEADSEYSPVFLSLEELME

RHLEPLMCMGIASTFLDSNFIYVKEGDEAHADFLSYLGVRQISKVDFFSKYLVPR

>contig49729 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64814.1|) 1e-106

MKICNFGASTTRAAELSRDRVAGNLHYTAPEAVSGAWYDPVRADVWSLGAVFFVLLTGSP

LLRLPFPECRGFELVKTVGCRGVLKLWNMDNLFSAATMDLLAKMLVVDPAKRLKSMKEVL

EHPAMLATAHTEHSLIAV

>contig50110 Frame-1F

MRLVGEEAFWALERLFRFINTTLSRMSVAGSIAKQRASFISNDAELFVIESMDLQGLNLL

YDVALCTENASVSCQAINYLIYLHLHVGSNLRRYEVWKDFVNNCFRRL

>contig50558 Frame-1R

MFDKGSDSQFDATIHNVMEGNQGRSEVSMSDGKSSLTNRGQQSGAVMGSSESASSMILLQ

LDANNEPIHPRLILRQQQEHVKVHMEQYVREYVAYLSAQQMSRQARNNAEASPLKAFAVQ

TDENGSLVGRSLSPLTTSPVATERDVEASHTVSYAQGKCYASERTL

>contig50969 Frame-0R|Blast-abnormal spindle-like microcephaly-associated protein [Phytophthora infestans T30-4](gb|EEY64421.1|) 2e-93

MVLEAQRRDVQVKELKHKVGTRAACCIQKKYRSYQCIKQNVAATQIQTLVRGWHLKTWYR

TCRYSACVIQQNVRVWRRQRQLCALQSFYSMLLNYRRLQREEEERLEQIRQDRLDRLQKK

LAHRAARRIQAVYSLYVFQKRTVAATFIQAVARGYLNRLQYAVIWNSVVVLQRAFRSWLV

RSRFCRALYRHRAAVENSEVCTWVGFSPFSV

>contig51975 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54321.1|) 1e-62

MSLLVEVGAYEAAFVLNVLHQEMHIHDRPLGFHQSILLYMMELVSTHYLLLCRHLPALID

TIMACLEPTKPDRRRRCLPLSTRCLHGLVRRFPMVDFHQETQRLALGTMDAVIVIYDLRT

ATKWRVLDGHGSAV

>contig52611 Frame-1R

MGVLWNFVLTSLLLTNAVCILHEKRFLRSHGWHKVDSSQGMTIKNQIVGFLIAVQYLR

>contig53281 Frame-1R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY66249.1|) 2e-36

MLSEEDNQCVIISGESGAGKTEASKQIQNYIAGVSGSGAGVDKVKRTFLESNPLLEAFG

>contig53506 Frame-0F|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY57349.1|) 7e-21

MTSLDNVAKEKELIEASLVEMKQALLKSEAAAAKVQQNLDAIQTQG

>contig54006 Frame-1F

MLRLGRSAAFEATSSGGIVTSALHSNLHVQLEHRGLKGLQCIYQTQSSCHSKPGVKRG

>contig54073 Frame-2R|Blast-HECT E3 ubiquitin ligase, putative [Phytophthora infestans T30-4](gb|EEY69908.1|) 2e-23

MVLCRLIESATPLGEAMFRGLPEPTPQIYDLSDMAPT

>contig55232 Frame-1R|Blast-RNA polymerase II-associated protein 1, putative [Phytophthora infestans T30-4](gb|EEY54443.1|) 5e-25

MALFAALETFCRLERVQGAQHSFHQLGLFIDAATEEAGKCIHSLLKSSSEFDVAIVQLLT

TILRFLATACCHTTKYHLETAGIVQVRKLIQSDIVILKLLPQLNTTVKSRELLVAIVQFH

L

>contig56457-1 Frame-2F1

MGGEKVGRHVVHCRLFNRKTLMG

>contig56457-2 Frame-2R2

MPPDLLATHLLQLAQQLLVLLRDVDILNDYDS

>contig56682 Frame-2R|Blast-endomembrane protein 70-like protein, putative [Phytophthora infestans T30-4](gb|EEY69817.1|) 4e-31

MLYFGYMAIISGALALLTGAVGVGASLWFTRKIYASIKVD

>contig56804 Frame-0F

MATFLPSDDVQILAVNMHNSFSRLSRHWAQSSVSWHAFIHAPCHYCRLLCFRRNECQGLD

FGR

>contig57142 Frame-1F|Blast-phospholipase A2, putative [Phytophthora infestans T30-4](gb|EEY63036.1|) 5e-09

MLLPSVLWLSCALISYSEGAPIDFPDLTKFKQECEPFRCRPKRTPAPVK

>contig57744 Frame-2R

MFLSTLYELLSLFDALGHFRDRPSAINEFSRGWMCVFV

>contig58543-0 Frame-2F0

MSLACIAFKNDEFSCSRRCDGQGDVQFVLSGAISTFAAWVKHAILFVLIPLAAAISFSSF

FLRCQMLKRQTNLSRQSANICSFWRLS

>contig58543-1 Frame-0R1

MAPERTNCTSPCPSHRREQLNSSFLKAIQASDIKN

>contig59140-1 Frame-1F1

MDASLEAAVQLFTATKESTGGTGVANELTTKKKLVVLSMPLGPDSCQQRM

>contig00758 Frame-2R|Blast-5-methlytetrahydropteroyltriglutamate-homocysteine methyltransferease [Phytophthora infestans T30-4](gb|EEY58407.1|) 0.0

MTVDSATLGFPRMGPNRELKFALEKFWRQKITEDELYTIAHTVEEANWRKQLDAGVNRIG

VGLFSLYDHVLDWTYYLGLAPERFASVPVGLSQYFAMARGVDGIPALDMTKWFDSNYHYE

VPELNAKSTPKANFGNYLETIKRALKTLGPNKTVPILLGPLTYLALSKYDGATLDELLVK

ILPLYTTLLNDLASLGVEQVQVHEPSLVGAQAEELAKHLVTVYGANATKGAIQHPNVAIN

LATYFEEINHKVYQWFLTSPVSALSLDFTRGDNISVLQKYGFPANKRLGAGLIDGRSVWK

FNPDTILSQVTAIKIVLANASNSHLTIQTSSSLQHVPYTTECETGLNTGETDGLLGVLSF

AYEKLNELEVVKTIAKIGAAAAKAEIDGVQQAWDVYYEKNPAKPVVQNRLASVTELDFQR

PCPFAERRPYQHKGLPVLPTTTIGSFPQTPQIRALRRNLKAHEISLEHYRAKIDEQIAYN

IGIQEALGLDILVHGEPERTDMVEYFAEKLNGFAFTQNGWVQSYGSRCVRPPIIFADLER

PTNMTVREFVVAQSFTSKPVKGMLTGPVTILNWSFPRQDISRKDQAFQLGLCLRDEVVDL

EAAKCCIIQVDEPALREGMPLKPSKKDDYLTWAVDAFRLATGVAKKETSIHTHMCYCEFA

DCMHAIDAIDADVNSIENARSDDETIRSFQAIGYTRDLGPGTYDIHSPVVPPKDGIVQKL

QSFLNLLPATQVVVNPDCGLKTRKWPETIAALRNMVDATLEVRASL

>contig09915 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54819.1|) 3e-66

MPSKRNRVPCNWVDVAKMGTIVGTSRFVPLRVPLDAKYTPQLYDNSGEIWTPADFLELQK

AQHLNIKMIIDLTNTFKYYDGVEEFKESGVQYVKLKIEGFNAPPDIRDVANFMKTVDEFL

ANEPNGTIAVHCTHGLNRTGYLLVTYMVKRLGYTVTEALEA

>contig10931 Frame-1R

MTLRDTCEKPVEKVVKPRRLKEISTPVCKSEVLLQTTEALSLPFPRGSTAANVAAAMNAI

MTNPTKLASFSSVTKPTTQTGGGTVAMSNFNKAFSALSSSVSMTSTASSVSISTVASTKV

IQAKPGGESSFASTTLKEVAETKEKSENQRVPIFSLSKD

>contig12476 Frame-1F

MNKFLVRGLGFFNDAYDLFIMNIINVVLTEQYGKDVYTSTMKSWLSAAALIGAVVGQLLF

GYLGDVFGRRVNMIATCGLLIIGGILCTVAYGGSASGTLWFLFAARLILGIGIGGEYPLA

ASSTAEDASSVSDRNQRVALTFSLQGLGSLTAAILGNLLIQALAGGDKGENAASRLETVW

RLLFGIGVIPAIVVCYWRITAEETEAYKATEELRNVATTTDSVAKRARLSFILRHYGVSL

LGTAGTWFLFDIVFYAQNLFSASILTVVGVKDASIQVITTQNAFVAFMALPGYYVAVYYI

NRLGRKIIMLQGFAVMTVLFLVLAIFWNSIKEKAVLFIILFGLALFFSNFGPNTTTFVMP

TEMFPTPIRSTCHGISAAAGKAGAAIGTFGFSIWVENESFGYAGAFYTFAAITLIAIPLT

WFCMFDNDQGFDDMDDEFYRKLNGADDVTRESFNSVANREKNGMYKATETPF

>contig14207 Frame-1F

MDDLSTKDAMELFTDEFSRDWNRGKLARQFYEGLPDAVVEQTKRTRHQWGFVATLGDKER

FELATTKDSVNVATKQKQMFINDVKDAASSKTGGTSTGNKRQINEEENSTCEFDRKRLRA

ERRRKHQHLDVIMDELVPKATGREAQIEKRRQFGNKLHGAARDREDARDGLDLSEDFLMG

GRDDLKRRLAQRDLARSHKQEQRQQKLADYQAKESARMDKFLEDMGLAGPNGKGGKQMAI

ASRRTP

>contig15095 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62459.1|) 7e-52

MARGVRIGTKADVLKTLRSLLRVTRARGSQESIRDCKFAQKLLSQYRARQFENDREKMRA

YRAEASDYLMLLQGVEEQRCLWALDAGVEKGLTGQEIVNASARRVGLEVPEMYAEKHAED

ERKQATAAQYLAGKRTASS

>contig19899 Frame-2F|Blast-CCR4-NOT transcription complex subunit, putative [Phytophthora infestans T30-4](gb|EEY67624.1|) 8e-95

MVSFASPLFWQINYLVTNLSKKNFKTSVAELNQLVELYGEDARIFLLNCLVQGVDFRDTR

GQKDALKIQLLTHEVAQASSRPNFTTFICEAIEGSSPYSSPISECHVTENFLNIFSKTLK

LSLPQQVTVGLAFAQGNNFERSAQAIQFLRAKIPEISLCDTKFPPDVLHSLVFVLRMKKE

FHDDVTEAELLLASVSSPHLTEMGSLEMAPLTIGNLQHVDCEPVTE

>contig20697 Frame-2R

MRRRLLFRCALYLHYLTPLTLIKRYEYNG

>contig20837 Frame-0R

MEYTIKYAANHICACDACAASATQKMLIVLDARGIGIRDMGGEAFEYIRRCTAMMQRHYP

QRSLRIFIVNVPAWFGMAWKGVKPLLNEATRAKTFILSESETTAALLKCVDAENLPVEYG

GSCMCVGGCDINSSHQRLQRVLVDRIIESKSMESDEQIHTKTHVHSHERLPSSEVAPRKG

SILPTLRPSFKKDFSGTVFDKLRFGSIFRTVK

>contig21269 Frame-1F

MSEDEEEEVSEAKWVQCDSCKKWRTVPKDFNLDAMPKHWYCHMNTWDTRFASCAVAEEVV

KTKLSPPANKNKRRNKLKVKSKSTASSAGDDIGYSSNESGRFKRSGGSIRGSMTDVTSVD

EKEKSGRPKHKDKGTKKRKMTKQLKEKYREVKWVQCESTQCGKWRVVPSSINFDRLPAVW

YCHLNTWAPELAKCSAPNPTEVDTIWFNKTTKEGRVSKKARAASISGNVTPASSVATTAS

GGGTAIVAIAGVSGINRVGMMTGQSTFSNNSCAMHSVKGRGGRTHNNTNGTGVKKTVLEW

AQCEKCNKWRKLPQHIKSSTLPDKWYCSMNHWDLSRAKCSIPEEADQEPLPVAPHSGSRW

HKVGHKGQRPRRGKLSYSDLLYGSTGQLRKAYTLESSTLSFEYEGTTYYRDDQYKNSSMY

VSPAAMSAAATMAGWSDQIMQETQCNSDVKVDALAPPTPPQASIDQVAAVLLESMDLRRR

RSVIELFDAVNAAYQRSEATINGLASLAMVTAALGQLEHRGLVERVGECLNEKMEKETEQ

QRRIESLFNGAFSVPIHYRKVPTRPLKASKCWKFGAKVLALSSAANSS

>contig21377 Frame-1F

MNGRVTTVTYFVFFCFWEFLPTVLLLCLVSSKAGGVGAPKHGSASQKLPDYGIFHIINTN

EGKLLTASSLGTSASSSYGTRPVGDPERGRPRWTHGGDLFQDPLRYDSDDGPVPSLPHHY

LNNYHGEVSNNSTHYYE

>contig22552 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64066.1|) 4e-74

MYNTDEYNTLIKSLRLELEKAQIRTKVNALVDRQKQQKQRLTQQIARAEEQRKREAAQNI

RREQATYRFKALEARKETQTDRMEREKERYEKQSSTTHILFFDVVRDQSVRNTEEDTRIK

EKVEFTKSKDSFQQDTTQWNSDMAQWSKHRA

>contig23667 Frame-2F

MENFETLIYQLNQWLSISEALRPVANSKELVVALADRLTKLQYSSKDLTPANPSSARTRQ

MRAMGCLAESTISLYQRHLIKWLAKDTHVMVHSESIKK

>contig24055 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57655.1|) 2e-54

MNVSNFGNQSSSNGNLLPLKRVKLLSCRSDVHGPGHAIWMKLNTPLTKQRSDTKDGLAVV

ISVRDYWKHLSVNERQQILLVDDPELVKQLYKLNIGLLCVGLMQRHLKAVNRLSTSKSKT

VVPQRSSSISGLLPTVACILDQVVTLPSTQAATQNSPIEKTYDLLEAMEFLNVDTGILTI

KFEVVKDTCRLFEILGDVLTGFLTSHHVLRRSSFYQLFVTESEMINTWPNFQRLIAMLLE

QLILRSYVNYLEKQAAHQMEQL

>contig24503 Frame-0R

MLLHQWGTLLLVVLATHTNATVEGNELQQQQEKISTTQWPSLLFVIKTERSFINGHTDFS

IVANPIVSADESTVAYDIFATFTVGTNLYNYTRVGSAAYLETMMVDSSTSLIQCLQSELD

DLPPIDAIIAAVNQATPVSNQLKVCTSKDVYQVTVGTLTFALCASSNSGFEMFAHDLKIA

VSYLDEPVNIIPPNYLEECITEVKPSQVSSIGRSLLTGEQVVTDESRSLFSFAFAEDACS

CKSKPRPCVFIHGFGVKEEFPVLRSSLRYWGNFIADRAPCCTVMKFAQLNTVNYTWTNAT

QQQKVCDRALAVSHTSSGRLIKDTIIVSHSMGSLILAGAIANGTCKLDASTTWVSTGAPM

FGTMASDFAQKVCTEDTNLLAEELAVIKHQCPVKKALKSLVYQNGLYITPSLREAYAAAQ

GAYRKNVDAAMCSEGYSGILSSHQVQFWLLAKLIPHKSHKNDGTVEFQSCVKGLNISRFH

NTYKSRFYRTKLNHFDMQFRTGDSIWNEAKMPLKWFECLL

>contig25052 Frame-1F|Blast-propionyl-CoA carboxylase beta chain, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63650.1|) 0.0

MRIPRNYLRLVHQTRIPTRWMSAVPDGAASSILTPAARKLAFQHDLEQARKRALEGRGTT

RVEKQHEKGKLTARERIDLLLDKGTFREYDMLKSHRCSDFGMQTQQFPGDGVVTGRGLIN

GRLTFVFSQDFTVFGGSLSETYAEKIVKVMKKAMELGAPVIGLNDSGGARIQEGVASLAG

YADIFQLNVLASGVIPQLTMVMGPCAGGAVYSPAMTDYIFMCRDSSYMFVTGPDVVKTVT

NEEVTQEELGGATTHTKTSGVAHCAFDNDVEAIREMRRFFDFLPLNNTEKPPTRTSDDNR

FRLVPTLENIVPPDPNVPYNMKEIIHQIVDSFDFFEIMPDYARNMIVGFGRMEGRVIGLL

ANQPMELAGCLDINSSVKGARFVRFCDAFNIPIVTLVDVPGFLPGTDQEYGGIIRHGAKL

LYAYAEATVPKITVITRKAYGGAYDVMSSKHLRGDINYAWPSAEIAVMGAKGAVEIIFRG

QNVEENTADYERKFANPMV

>contig25881 Frame-2R|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY54027.1|) 1e-131

MVFGNHDEAGGFPKTKIIEMLSKKTHSYTSSGPKTVDGIGNYMLNVTAPIAGVWGVKNTT

VFRMYFLDSGAKAHTEMYPFVFAEYDWIKQSQIDYYRQLSEAGRAERHSSVEFVLPAVMF

FHIPLAEFAYSSDGCKGERHERLNDQGMNLRFLSTLSQMNEIKAAFVGHDHLNEYCCLVD

GVQLCYGGGTGFGRAYGSPDFSQRARVIEWTVDNNERHNIRSWKRHYDDVSRVFSEEV

>contig26246 Frame-0R

MEMESHEEKLHNMIIDSKRAAAKDDMKRHTARIKEEQRERARLERAGIGGSGFGTPSSFG

SSLSNAFKSPRSGSNSFMNSPRSPAATSPTSLNSRPEPGLSKSAGMKLGVSSQSQGVGLG

RGGKSFMDAMAAEDGLKEIPPMSVAVETVQKPEVIAAVSHDPIGAVVEEKMTVMLTRDGA

LQQLEVKGSLFVSVNDPSAGCCRLKLRTNGADGITFQTHPKVDKRLYDSESVLALRDPSK

PFPTTRVAFLRWSLKTQDESMLPLNITCWPEEEGDGQINVSVEYSLDRDMVLENVNVVLP

LGGQDAPSVAHVDGLYQHNAAEGSLLWHQDQIKSTNNTGTLEFTIRGNKVDAFFPISVSF

FSRNVYSDVIVEAVQKVDDGSSITFGFEKLLSANSYQIV

>contig26664 Frame-2R|Blast-tRNA pseudouridine synthase D (TruD), putative [Phytophthora infestans T30-4](gb|EEY58382.1|) 1e-129

MQVRKTSVALQPSAAPSIASPKNNLRRSIDRDENSMRLIFLLAMLPIVPKRLHLGDLRGN

RFSLAIRDLPHDEFLSTKQIQDAIRSWRDHGFINYFGLQRFGTKSIATHVIGRAILQRNY

QGVVDLLLSPQEGDASLIRKARQAFQENHNIEAALQALPPYLVAERALLHGLQTHGATAY

ALAIQSIPRHLRMMYTHAYQSYVWNKVASERLKHLSREVPVAGDLVIPHEIITIDVVEET

IVETNDEESGRMTKKSRGNTALTRGEESVILVTPENVSQYTIYDVVLPLPGYSVTYPTNA

MKELYEEILKADGIDFYTLERVTNSEYHLPGSYRHVLRKPQDVAYKVKRFNDSTLPLLET

DVDHLLNRPVKVSIPDGK

>contig26880 Frame-2F

MHSLGTSILGHPSPKLSCAGRVEIFSSGNNGSLEVFIIFEEGNRSAFWTMADTLQGAIVR

SGRQWRRKHRHQHNDIVV

>contig27599 Frame-1R|Blast-expressed hypothetical protein [Trichoplax adhaerens]gb|EDV22439.1| expressed hypothetical protein [Trichoplax adhaerens](ref|XP\_002114983.1|) 2e-08

MKAITSHHNQLITSTHNRVAWWTLVEMFVLVIVSLAQISFLRRTLEVRRIL

>contig30083 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68222.1|) 2e-66

MYLEVLHSISMLPQTIETLERTDETILTQRAAALQEKHVFVFERGCCVFWGLSREEESWH

LMMLAPFFLRETGQVDPQVMDFSYGDRSSIAKDTIVLCSMTVAEKIAISFAMSQSATLGA

FETRVGDRIRSTRHIPSSLASVGSIQYSQDDTSKLIGQLFIELADVNIHSNVLDEPEYFF

NSQDNDDFKYLYEKMLKYQDVANRVAILNKRLSILRDLVGVLNQQLTHHQGSKLEWIIIW

MLVFQVIIAIGWEIFLKDIMGCFR

>contig30542 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64537.1|) 6e-14

MNVSRIFAKQLTTGHTQLCPWRENPSPEAFAM

>contig31109 Frame-1R|Blast-homeodomain transcription factor, putative [Phytophthora infestans T30-4](gb|EEY61507.1|) 9e-19

MNPLLYNITRVVVLSAFSSTASDFFGFKLKLWKLKA

>contig31448 Frame-2R

MTGIEVAQPRYAVRLDHQFPISTVTVLADP

>contig32162 Frame-2R

MRLTALVSHAVESLIPLNVSVTASSRSCCSICLPLGTLNATSPMVISEGNFVIKVAMFFR

DAIPVFIPAPVAVERLRFLREEMVFHVLLLVLPYKQRFCPHCCSFTSRHVHNRLVRRQLE

RVVVFTLTR

>contig32360 Frame-1F

MGKKTNWTTAEDQTLCRVWMNASDLKLQGGDQKASNFWNAVRELFHQEIITTVERPLNGL

KVRWTRINKDSQKFACILNEIQTIEKKVDERNGSAAVALFTEQQWIDEAKDAFYRHYNVK

FSFEGCWKQLRYSSKWLQLFANSTNHPISVMDAPSTSTMVKNESGRAPSTSSSEDEISTT

NEGAYRTATDFAPPAAVSTSMPNTNNESMFATATAAINQTFTNSNVFAIPLSHKRPANVS

FESLATISNQQLQELIVTWVEQLKRQNDLMVDQNAIALLRIDGEMLSDAEAQQCFETLRA

RYFKKVRRSYKNN

>contig34843 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57592.1|) 1e-08

MANAAMVVYCFDTLQSHFNGSAEPTPYFDVHQE

>contig35233 Frame-0F|Blast-atlastin-like protein [Phytophthora infestans T30-4](gb|EEY69647.1|) 4e-32

MLLIMMSTGQVMFKRVKTVLSIVKSAIDASKEDSKEKND

>contig35660 Frame-2F

MRFGLFAVGTGANENGASMSFLNLAFPRLSDQFFI

>contig35817 Frame-0R

MRERKFLIIVGALVVCAPAHSAAEKHRIGLRQETTSSKTKLPSASIEDRAMSDWIKIFRG

AANVDPTDVAVPKSSVISKVQQALQNAADGAKLAEDLDTYSIFTLLLSGLPTSWFKSLYG

KAFTFNPEKATTVLQRVFAEVGKLPSRSEDVDIQSALLFTTTQVSISLAKTLVGKYASFI

PHLATLMDRSFGNPTAPAIEKLAKDVGKFALMDAGSWVLSKFINPLTEKKLWISYGSTTA

GTSRGGHFSIDMQQGRVKISMNALDETLIPNAGINTNRARAPRLRLNQPTSVARPDPTIN

RLGSATVNFDHVEP

>contig37103 Frame-1F

MLRIHDNKLLRSISTLPVLIVVLIMTLEYYIFMTEHWVPEYRRSVDFYVLSMILEASVFH

FAVGCTVVAYYKVVLTDPGYVTPTLVQCVKDAMQAAIEEGGNSSSLVLKTCQKCKLLKPF

RAHHCSFCNRCVLKMDHHCPWVANCVGQDNYKFFFHFVVYAFIALFMCVWVLFKPFQTAL

FSKRGADSFSSLVVVGFVLGSALGFSLLGIIAVHSYLLVQGGTTIECHEYGRAFPFNQGW

RNNISDVFGEMTKDWLLPTTPVRKQRFLLQPAALHQIIACSCIDDLYDQEDDSFL

>contig37455 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58679.1|) 2e-48

MELTQKLTSNIINIHCKYRFTFDSNELVTWFSAEWDLVNALQEVLADLSDVSTVLLGANI

SSSTGQIKVDDIHATESKLVIDPRHNVEFLLS

>contig37653 Frame-0F|Blast-nucleoside diphosphate kinase B [Phytophthora infestans T30-4](gb|EEY55644.1|) 2e-76

MARERTYIMIKPDGVQRHLVGEIIKRFENKGYKLVALKLARPSVEHLEAHYADLSGRPFF

PSLIAYMSSGPVTCMVWEGNNVVLEGRKMLGATKPTDSALGTIRGDFCVDVGRNVCHGSD

SVESAEREIYLWFPEGIIEWGANDEAWVYEN

>contig38692 Frame-2F

MANEVEAVLAKEKKMELCGIVTPTTSVLSHYTRERIQKKHPRCIFFHGCVSCALTLLLQD

VCTILPWLDTVRKTIADFVAVFHGKYTLQTEIKTNQNLQTAAEFPEISSICASLEDVLKC

EKVLYTIVARRDFVEASTPVEHENRKRVQDFVLNENFVRDLVNSLDILRPLQQQLQHFQE

NQPPLSEVVSNLVELLTIFSSLEWMSKKEKALITSCVSERFNAIYGDSHGVASTLDPRYL

GKALDDKKMHEVENFLVRFCEHEDHSVDILSQLQRYKTMVLELKETNQAYWQQLQSGAIK

PTEFWEEHRNHFPHLHELAVAVFSLPSSSVSRSPSFGAQMQVILSRFGNKLPSS

>contig39116 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67851.1|) 2e-14

MSKPSKLIKIRKRLEESSKSRSRIRSSANRLQSATCASPRESEKITTSSVFKPKKKLLES

DLVLCENEISAELQAIKKESSDFQNKG

>contig40462 Frame-2F

MVNFVPISCSPVCMKFIQAQRYELFIISRLWHGRFHVVSLTNRMMITTKTNEIVGNDTFP

RLETQMMTRES

>contig40660 Frame-1R

MGKAVGGGISRVGHVGRSILHVGKSQGNKQQGEVYQTDDSTAAELLSAGYSFSSESQSTK

KYVCGYLHKISDSKWGKKRSWHRRWFVLDRQRGVLSYYRHNPAKHMPTSSSQGNIVHMAD

SPIPLIKADSSTAPTPVASSGTTGEFNISSGRSRGNLKVEERDTQSAVQSTAATEDLMSR

EDQVQAQEQQQTLLYLNEAHPWYRGALDLNMRNVSLLFEKTLARNAPTRFFFQVSTLALH

DIDLKRGTQYKLCADTETNYNLWTSAIAEVVNRKDSRNGTTISNDSPMLFHQQVHRQQLN

HKQTEELVICESDHGGIADSGQDSLSPSKKLKQKSYDISKTSSHPKRKVPPHIVTQFPVI

LDGGQPDASSWHLCFHIDGIKQCLIVGFMLNIVAIRCLATEHVLWKLLVCIAVSGLFALN

TYNPTPRQRLRPGSRGESLVD

>contig41843 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY55879.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53029.1|) 3e-39 NOT\_ORF

MSQLAMSDIKIKQEKSNGFQANKDEEATDHEVAVGNPHCTHVVYMLINI\*VSAAFEAASE

GKSMERLNALLVHACSCDHSQCPDQRFNDLCSHMKRFLRAACWASHNERWLMYPVATAVV

ELFAYHALHCQAQQCDVPMCRQLRN\*VFL

>contig42455 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66019.1|) 1e-107

MYPIYCISFILNTIWYQEIADDAYVQLHGKPSPTPVSDMIRDELYRAILVAFFLLQTVLS

YLIPVIGPATSFIHLSWLYALYCFEYKWSLAGWSLERRLAHLEQNWAYFAGFGSPFTLAT

FFVPNFVSKGIFALLFPVFMLLAIACDPISEGNEAFKKLPIFHFSRWWTLQLLRRIGKST

GLKTKKQRAVNKQKRIERS

>contig42653 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64767.1|) 2e-34

MPMPHPRTPATPGSQTSTAYVSLKTRLHTPMAEPEMVVWLRDLSLAITTSHKPNEDICFE

LVVRRKHPNSSHLSVEATMWTQSRPISDFSMLRQNLLRDLQQGHSCSAECKWLYAVVKQH

FPKTQTMLAPCALKTERWRVALLRVLT

>contig44318 Frame-2F|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY60597.1|) 1e-77

MVKLNARAIQTYFLIEDGNRAHPDRYRDNKVMGILFDNKVNYATWFSGEKYAIHGIQMLP

ATAVTEFVRSHDFVEQEWNQVLSREPIVQNDELSNPWLSLLYMNYATLNKSFALEKLRTV

KMDDGLSRSWAMYIAATRP

>contig44534 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66659.1|) 2e-62

MVTNDSVSLSALRGLMDLLAATQRYRELAAMLLSLVFYDRELIRSLRVTDDVLDIAKFYR

HRLPVWILDLVHEYVTLTKLQLQTETQDANTAPVSCVLAAKFDKRARGVSNLQANWRMRY

VQLTEKEILYFKHEKD

>contig44967 Frame-2F|Blast-adenylate kinase, putative [Phytophthora infestans T30-4](gb|EEY58525.1|) 1e-125

MSLAAVPTTSLLSELRKRIECAGKKERRTIFIGPPGCGKGTQSPRVKDEYCLCHLATGDI

LRAAVAAGTDMGKKAKAAMESGALVTDEIVVGIIKDAIKSPECSRGFILDGFPRTVVQAK

KLDEMLAEENAQVDTVVNFDIPDSVLMERISGRRVHPASGRSYHVKFAPPKVEGKDDITG

EPLIQRKDDNEATLSSRLQAFHKQTQPVIDFYRKQGKLTKVNAHTDMNKVTEQIRKSLGS

D

>contig45083 Frame-2R|Blast-eukaryotic translation initiation factor 3 subunit A, putative [Phytophthora infestans T30-4](gb|EEY61754.1|) 0.0

MSHFFHKPENALKRARELLAIPNVDAGVLKRTKHSALEILHDALIAKKNRTWQPTHEELM

ILYLDICLELQMGRVAKDGLHQYRNLCIQQNSTSLETIIKHFVTQAERKLAAAKKESNEL

NLLAAAKVDLDAAQTPEDVMLSTTTFEGSNDRTDREVVVPWLRFMWETYRTVLDILKSNS

KLESLYMVTAMQAFDFCTEYQRKIEFRRVCEIMRNHLSSLQKHTATPTSQSTRQMRSWDG

FTLESVERLLEVRYRQLQVATDLELFSEAFRTIDDINNIMNLVEQTPRVDLLVTYYEKLA

QIFQVSKNHLFHAYALYKWYSLRVAGLQGLVGTQVLKGLPVLVSEEEHKEMATRVVLAAL

SIPLLDFEFAPSVFGDAVSSSGASIADNSLSSATRDKNTRMAALLGFTTTPTRGNLLEDI

VAAGILPKASTATSELFHRVELQEVDPLQIVKQLDPFLKIIRSDPLAKAYVNEVERLVVR

RVLFQLTRVYASVTISHMRSIFLGLDVSYEEIEALIARSRSLSTVAHTSAPNLSSLYRRS

ATQHGSNNAETFSADAVASAQTRTKIRIDQVEQCIRFTDAVDLEANAAQLSLLGERLAHA

IRKVPAGALTSSAARDQQSKELFATCRSRLKMQRSEMLAR

>contig45300 Frame-2R

MCNAEKTCAASASSPHCKLVNASAIVNANIHNGKNQ

>contig46305 Frame-0F

MEKGGVTVAKVGEQLHGKELDDDKSRILRELQTSRLEVHELQQVVEELRDEQRL

>contig46392 Frame-1F|Blast-phosphoglucomutase, putative [Phytophthora infestans T30-4](gb|EEY69540.1|) 1e-107

MSTCMEEQWLAKAQQWIEWDVNAGTKSQLEELVMAKNIDRIRDLFSSRVAFGTAGLRAVM

GVGPTAMNDLVVLQTAQGICKYLLQQFGDQAKSMGVAIGYDHRQQGTLSSKRFAELTASV

CLHDGFKVYFYEGFVATPLVPFCIEQKRCAVGVMVTASHNPKVDNGYKVYWSNGSQIIPP

HDEGIAKMILANLAPWRVYNESLDTLKHTFKQLFHNPTDEVTNKYFEQARARLCRYPETN

AA

>contig47360 Frame-2F

MFHGKTLGIYSLGLYDVPDNPKWVILGILFLTISLVVINLLSYAMLEYYRHESTLVLPLT

SLSETILARQSYAMLS

>contig48343 Frame-0R|Blast-conserved oligomeric Golgi complex subunit, putative [Phytophthora infestans T30-4](gb|EEY65325.1|) 1e-136

MGLLMKTIKKRMTRPLNALSFSLVDSCTIQCDLNFLLKRIWKFYVKGIQVLRSEVIEGLI

TPRIALVGYTEPVMLRMIQDAQERLILCMQKYIRDEIEGFVPSPSDLDYPTKLKAAENVN

APLYATWYPSLEHTLMCLSKGYHYVKVEIFEELAQDAIQICAASLVMASADITANHGELH

GSLFLVKHLLTLREQITPFEIQFAQRSKSLDFTSSADALNELLVDASTLFRFSGLNGIVN

LVSRGMPQIQETTADVKKALEQELRKSCTHFIEIVLQQLAQPLLDLLKQIAHEQQMQHAT

ALDFRQCAFTAPTEVYDVLASLSHQLGDVQLRIRETVHLYLRNASTEMILLKPVQQNLLD

AVRNVSALMKRTYTCEELQSCQEITAIVLQQLDAF

>contig49050 Frame-1F

METSPLLKKACDALKKPSAWHDFIDLSYMAAQVSMATLARAAILSIDSLFLGNLGIRELA

AASLAQIWTSPALYCVWASASALNT

>contig49212 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58623.1|) 4e-68

MDVLLKKVWTLEKKRLTMSKRCGDHVAMEQQMEFQTAKLETLHLARLKSHLDQLRQLRTV

EASIHTSDRAISYFQVEQYLTRVLQDPNLVAHVKKMRSCCGGSNGREDLDLVPEGVNFYG

GITHGSPLAAIVDHLKYCLDVLIFFEKKVTLEEEGVFSRVPQSFYRG

>contig49285 Frame-1R|Blast-ARP2/3 complex 20 kDa subunit [Phytophthora infestans T30-4](gb|EEY61997.1|) 1e-86

MSKKLLLNPVLICRNEQEKCLIEPSINSTRVSMCIKKADEIETILSHKFNRFLMQRAEQF

IIMRRVPVRGYDMSFLVVHQHLENMYKHKLIDFIITFMEDIDKEISEMKISLNARGRIVA

TEFMKQFT

>contig50647 Frame-1R|Blast-exportin-T, putative [Phytophthora infestans T30-4](gb|EEY56559.1|) 2e-47

MADMTEFERAVLIAFQCAAASTGNQQMQTLKLQAENFCAAIKSQADGWQAELQLFKQSEH

EQVKFYALQALQETLVNGIIDDVALAIRVEFFTWLQSHVAYVENTAPYLKTKLAVVMTLL

MKRDYPDRWPTAFAELLALLPQGA

>contig51705 Frame-1R

MPANCFKAYVTRRRPILAQGGSTHLQTSLRIFYNGCLRLHFMVCTTDLHPLERSCMDG

>contig51792 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60185.1|) 1e-107

MSAIVEAVFGSYDIKIAKQWRDEDLLHREQQKQWREDSIQRDTEWRRADLERERRLVKLE

SEKRLVGARLQQVQSVSQLSAILAFFSIMFLQEMKSLHRDTSQPLIIVYGTVGALEFLCM

LLCTLTCTLLLLALTRFVTHTLDGEIYRLSDHDMDTISPFTNWWRIKCEKEWLLAYQLFR

SGASFFLVAMGLACWIVLSRSTIAAITVSVLCLCGLLYYNLRIASRWRYLVNPSGL

>contig51972 Frame-1R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY59915.1|) 2e-18 NOT\_ORF

MENMHEELLLHVLHNVSNVTSLYVYGRHFLLEKTRFIRLEVNERNCYILKSAFS\*A\*STM

GDGETGR

>contig52616 Frame-2F|Blast-mitotic checkpoint protein, putative [Phytophthora infestans T30-4](gb|EEY56318.1|) 8e-37

MATQDTELQAPPSDGVSCLRFGARAQLLVASWDATLRVYEGTRQRSCIELVAPVLSCSYG

QSDSEAFAGGLDCVLKHVDLTTRKITKLSTHAAAVRSVGFSSELGLAVSGGWDGAMRIFD

VRNGGNAQVDEIKLPGKVFGMDVHGHLLAAVTSERQVVVFDLRNLAQPVVQKESPLKFQI

RCIRL

>contig52689 Frame-2R

MPTQMLSRALQYPRASVLRSASSLMKYHVGLRTTQLGADALAKQEQHLRTQGVVALNLNT

PVFQVFGSNTDTGKTIISAGICRSAATIAAKHGGRVEYIKPLQTGMDGSFQGDASFVKAH

AILATEKLAELNCSTLFSWKTPVSPHLAA

>contig53219 Frame-0R

MFRLFYGSVNGNLRLLSLAETGKTRA

>contig54074 Frame-0F

MCPKNACFKFGHAAMYPSSKIALLRVTGMRQLVKGWTVEPYIGQCLKYDNAWSQTTCPSA

ITSIARDDDIARNLQLDETINNCNHARFKLLIHV

>contig55987 Frame-1R

MAAILTAASIMALGCFAVWLGGGWKVAKWRVFETFAVTSAMRRNIGILRYDGRVKDCKLR

LRPFSSQIPVYLAEKSVLAGPLAIFWPYPQT

>contig56685 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60157.1|) 3e-19

MGSGLESKHLDRMATLGRQVGSFINTPLKFIPGTNYHYAE

>contig56803 Frame-1R

MQLRYIFTIVMATLAAPHSSAFVATGVNPSLRRLAT

>contig57145 Frame-1R

MPSLYHVLHSGPYLPPSTKWFASPKSGLKKDETQKNELPNSKSRGPGL

>contig58544 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54961.1|) 7e-21

MAERVEGVHRFTSEERIRLLEGAGVSEGIILRISRETSIINCSRRQTLLEDIAAKKEARK

LIRQQEQL

>contig59147-2 Frame-1R2

MAMMMATRTAAATAAMETRIATLTS

>contig59330 Frame-1F

MKLNIDVYDSAGKLIYCTRTVIEMAKCVEKIKKK

>contig06173 Frame-0F

MCAHSQIHACEESLNISLQVTFHYHRVPDVYGLLQLLNIIKIFDISL

>contig10237 Frame-0F

MVTNSASLADSIDELEDEHEDAAVFNADVASATNSHERELAASVASLDDLLDLPFKDPCF

KSAAQRDFQDKETDQKGLETTNERSIHGRENERTSLNDSVKLDQVYEEEMDQKEIAWDNA

LVKESFQEIRDVHDILKNQLTCHVLVKKKMIDEIQEILQSLQMELHFERHSTIAIGSAAI

SLPRVDTNRSLVGDCCYRCGFSGELAELEIERGVRELYCEECWELFFYSDEQESSLVLET

NQNTMIETKPLSTDEDALDEALKYSFHDSMVTREDILNPWRNLQNRDAMSPSSSRDSNAS

SITGCASEVWL

>contig13328 Frame-2R

MADDTHAATNIISAHIDSSFSPPFPPSSPEEPTLKQAPLQRRPLFRSMREALESTGQMKE

EQGGYVVKRHSGHPQQTSFRSSEAVRSKSKHTKQRSGSKANNISRISEVTEADAAGYTVI

RRRSSCDESNLSALNTASNFQASVIHKTRSSNPSRAGKTQPQRSRRGSMSAPQGNIRAAA

VTPTPSFSLQTDSQTCPAASRLVIQPIPSLTPAASGWVAKACIPAD

>contig14206 Frame-1R

MNAERQSARLKRRAERLGLPPREHCINNGIRHSSVGSSDVNSAHAHGSSDPICSSDNCRR

QPTPTSSTTAACRTLSDRSPRDINTLVGKLLNKIYGAPSSMTTRRTVVRLIDSMATAQQT

DALTVLEKIKRKISADATKFYSDSQATVMKLNEVYSRFVRLKNLDNKTEALLLLYGLMDT

TPPPMVSRKKSNHLENAAAMSIDSNMKEPMLDASGSATSGSHDRSESMPAPLLNLENHSV

PPAASITMAATDVELLEESFKFAVGIAQVNKPSRGKSSSPRTHARMLDSESKGIPNVALE

CLTFDVPEEVLMRDVLYALQAIESRYLYFDNAADRFQIIKSAGVPTPMRELIYMQCELGW

VFRKISEYIKQHRRELAYGLVGQSFCHVLNTELANYYRLIAVLAAQIDDDVETRQPHERR

TSNLTLRTLSVWLRDPLDKMRLIARLIDSVEGLRGGALASGVHSHVLHGDPGVSQFVQRV

LKQIAAPLVRMIKRWVFEGELDDRHGEFFVVADPSVSDDQFWDKRYTLNLKMLPTFISIE

LAKKILVIGKSINFIRQCCGNADWVMDAAKEAAVIGVEFDNENAYVAELKRLEAVIENVS

NSTNKYLIRSLTEKFQLLDHCLALKRYLLLGQGDFIQYLMDLLGPELSKRGSQVYRHTLT

NVLETALNASNAKFESADILGRLDVELLQGSPAETGWDIFCLHYNLQAPVNSVIPATSIF

QYQQIFSFLWRMKRIEHSLSASWSKDMNLGHEVQGCVPGIRPVLHKSQLMRSEMIHFITN

LLNYMMFEV

>contig15094 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68592.1|) 4e-90

MLVWQDVFTEDEVMSDSNKVIPCKDMEGNEISGMFQVESKMVAKGADNVDIGCGDAFGGD

DAQVDDSVETVNNIIDDSIGFGYIETGFETRAELKTYLKSYFRKIMKHLKSTGVDEGTLN

RFKTDAPEIVKYLVSMFKELQFYMFKSCDSEAGLAYAYYPDGALAPTFCYIKWGLKEVKF

>contig17229 Frame-0R

MPTDRPLTRLEQIQVKLWEEQEARFRDESAALPASTHETDAPVRRRRSSSSEGSAKRRGV

KLPSYFRSVEIQGHGAPTGESPSAKPPPFPKVLGTHSGQTISVADDEDHLEDGLAMTFGS

LLRFEDLRPTEDSVRLSFESMPLNESGAFSIDQTIASNVAIRTLYERILVLTNKQHELEV

LPEADGAEKEEVARELKVLYDQLRVEKDS

>contig18156 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59914.1|) 3e-50 NOT\_ORF

MHGDLRGFCAYLSVPLSYS\*TNARIKFVDKAPVTYAFSIAVGAASSTSLLFNRGHLLALD

RDAVLSRSQYWRLFSSQLTFQNGLAVSLGLYFVFQFRVLERQLGSRKFGSILFFTLLISG

VMQHVALRSVPSLTNTIPGGPYPVIGAFAVYYI

>contig19177 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57156.1|) 6e-15

MQSSPGGVRVPSCSSEKGVIVDCQNFAEKLRNTLSEMASA

>contig20762 Frame-0R

MGSESRRRSVTSSVGNDANCESEGLEDSLLLDAEMLLEKAQKMGLPSQMSVKRISLFDIP

DLQILEISDELNDPIGTESTHLRDGEETLRQWLRRRRHSTDDADDSDGEDHEQGNNVDGS

GVAEEREEASG

>contig23558 Frame-2R

MHSIFQKNGRGGTSPCDVRKFNFVLCQWRHGHCAVGKLDGAMEIIDELPAYFQSCNVRVE

PTSNDGVCVAVRTSAMFPQLASFPSISSLHCCSVITVHVDMVRNLVVNPQNFASTCEAKI

>contig23666 Frame-0R|Blast-3-deoxy-D-manno-octulosonic-acid transferase [Bartonella henselae str. Houston-1]emb|CAF27078.1| 3-deoxy-d-manno-octulosonic-acid transferase [Bartonella henselae str. Houston-1](ref|YP\_033118.1|) 5e-10

MMTEVHFELSKRLPKDQHLLTLIIPRHPHRTSVIIKQLYQKFPEISIGLRSRDGLPTNGA

DVFIVDT

>contig24252 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66514.1|) 1e-27

MFELIELKPELPSASILKKYFSQNKLQEENFLLHQLIGRLQALVKRKQVDATPAIEHNLA

KSIFDGFSNLSSASTIQALLEVLINPDMSSLNANFLLEA

>contig24502 Frame-2R|Blast-ubiquinone/menaquinone biosynthesis methyltransferase ubiE [Phytophthora infestans T30-4](gb|EEY54009.1|) 2e-09

MHSVVTLPLRHNARLVRSLSSASSFLSTPNADLRKHWSSKTHFGFQEVPVEEKERMVASV

FHNVAEQ

>contig25541 Frame-0F

MEKRLLRRNTIPMVGSGKFLLFEQQNKDVVKELEYNAEIFLRTPAGETAFYRAVGRKPLS

VLPPHPNAGEASSYDNSTEGRIRKAHESGGVVRHDDALSSLAALYGTDLSIMKHRRNLTV

KIPDCRNTIQKLDLHIPDQYGVSPESSTLLVFAEESPINTRGWMVTLSLGSPSYKGSGIV

EVKWTPTGNFKSVLALTCDFFRHNCCTPRAMSIATKSSEGADLRTMLPLKFKALPDRTIN

LKFKWCFTSNSGFASSTPLASCVGRSILENLSKSTELCAGQIDFLYHSSSSPQDNLDQTM

PILLSSVGVAMAKGTHRSLYFEMETFDLGEHQLGEDVRSHLVFYNRSHQALQYVLLAGSR

DQGSVSTSSFSPPYLVGGEMTFDNATGTIEAGCSVRATFVYRGSAPGQHTEQIFLRNLNG

DRLDTSVAVISVRISRPVYVRVPELDPQSTGQLEILDLGPCYVTPEMQDTAVDSPFASCR

FSKVHKLTLQSQVEDPLIICASSNLRTQCYVYEDARLHHEATRVYMKGKQSIDLYVAIRP

RVSLDAIKSGSTRDLFGGIRVQLFGLQLNSDEQEEEKSDMVAEFTVKFVGIAGASIARVT

PSIIDLGVEYNSGQLQMCQTHEASFELINLSKALPFRYRIFLTSATENYSDDDDSLHISL

KHEKGEILPGETGLVEFRVMAYTNGLFRSRIMVENVHYPGKLSFVDVVLFVDSGILKCDV

AAAAAEQMILHGQRFDMARESLQSVDIGCVNVIRLEDELTDGCAPFGGDHESASRKYRIY

GEHSSGHFVEMESCRSVQLMSPPDA

>contig26665 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53147.1|) 5e-08

MVDAEPSQILDHVFLGNRTHARDRKILQRLRITHILN

>contig27507 Frame-1F

MKEVTSITSSPDAQMYMHIQSNWSDSDQSCWLDVYKRDVRIVASSVHEDAQNKRLVAEAQ

CTPSSHYDLPLSAASAARPESHLPQIVGRESFWVDVEVNCQTNTSSKKLRTVFQAPNETV

NMPMSTDIGPVGIPAIQLYTLDLSKNERYVIVGGADGFCMLWDYQNRTQMLPLKGHVADV

TCTRFFPSSQVVLTGSLDFTLRIWSISGHCAAVLKGHQGGVQDVVVIGRGRNVLSCGTDG

LIQLWNCGTQNVVARWANDDQSPVHCLSIMEDNTQLLVEDKTQINTSENEVETDGKVFFA

GLDNGETLGVDVRARGAILNLEGLAGSIVSCATTSAPVSQPMLFTGSEDGLLTIWDLRHP

>contig27598 Frame-2R

MAFIKACVSLTVSRFTLSSYTKSSSSCTCSAASIKLNHAIRHRLSISFRQYST

>contig28050 Frame-0F|Blast-Equilibrative Nucleoside Transporter (ENT) Family [Phytophthora infestans T30-4](gb|EEY61700.1|) 0.0

MTRSASMMFAIFFFIGVGSSLPWNVFITAQAYFQRRLEGTTYEDAFLNWFSMAFNVSTLM

TMLIRTVVIAERMAGAVRTVLVSLVAIMIIMFMHCTWTRMPEFHGYPFFYMTMLSIFLVA

CASTLMQEGLLRIVATFPPQYTQAVVSGQSFAGLAVSLSNFIILWGKSHDDVGLLSVVHA

NSDLCAFLYFVLVFITLVLCLLVFAILTQMTLFRQYYAIDQLAIRKVKYLDECSSEADTI

DGMDLSPRKHLLEEEEEEEGDISKKVDVLKVAFKIRWYAAAMFFIFIVTLGVFPGITSAI

QSIDPEKCIFSLKLFTPFTLILFNASDFVARLSASWWPKLGQGKLFLISIARLIFFPLLM

LCNLQNESHEVISAVVFRSDIEAMFFIAACAFSNGLLCTLAFMEYPSLLRQNAEKETGGS

IIYFVLSIGLTAGSLMSFVLRAM

>contig28476 Frame-2F|Blast-Resistance-Nodulation-Cell Division (RND) Superfamily [Phytophthora infestans T30-4](gb|EEY58756.1|) 2e-43

MITFYHLGALSSRYPVLTVVSAAICSAFLCLGLLTMKIQTDPQGLWVPPNSVAATEQKRF

NELFGPFYRIEQLLFFVESDPNPNLDHTLVPSATCDANHDLIQRRFLIQMAKVQTQITNT

LIYSHDEANVSLSLET

>contig29916 Frame-2R

MAMAVVCEESFVRRISSMLADYKEAVTDSIAHPSRLYVLVFTGPNGTLFLHSLYFLN

>contig30082 Frame-1F|Blast-DNA excision repair ERCC-8-like protein [Phytophthora infestans T30-4](gb|EEY59812.1|) 2e-66

MVSAFCYLLDRSVGLPSRAYSDNLHARESTTLLKHSPSTSNYIFRQGMRVWSFALDPVEQ

RFLFVGTSKSQLLVFDLETLDEADFLGHLAYSTTNALDPICTADAKTRNAPTLQFGISMV

DWYPADGGICISSSLDEHVKIWDAETFSCVSSLHLRSAVFGA

>contig30495 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68281.1|) 2e-84

MLVRIVRFLLLALTDLAMIPALNIMKRNRRHFELFVGVLHLGVSFIFNAAEALDTELFLK

ENEWHFISDVLSVSYFLMLCVHVMDYKNENHNIVLRYVAFAGAWITKTKDDWSSVIFQAL

LVICYLLGVFYRRTFTPGADISPLIKQNVTYAMGCLAALLVVLIVIVFFDEDDSPDALGL

AMGMLHITAGALFYYAWLSVPCMDSKKDDIIPKYSSYV

>contig30543 Frame-0F

MHKNAKLLKGMEDLKVAEAVATKILWEASKSDDTMSAMDTKTFAVRLSASVLSPDDTCVS

PDVLVTAAFLFGSGWQFHGKDEKDVGILSCGSCNRQWQAFRVPGSNEVDAETNEYKAKRF

KTEIAPAVDLLSQHRYFCPWITERKSTIGDVNAGSKLNMFVKLPGWKQYA

>contig32163 Frame-2F

MLLKLRKGFRAPTRCPVSLSCTFASHAGIIGSLSNVLDGALNLKSAAFVESDAHMSKLTL

ELRERVAKARQGGSEAARKRHEIRLKMLVRDRIDSLLDPGSPFLELSPLAAYDMYGGDVP

SAGIVTGIGRISGVECMVLGNDATVKGGTYFPLTVKKHLRAQEIAQENRLPCVYLVDSGG

AFLPLQDEIFPDRDHFGRVFYNQATMSALGIPQIAVVMGSCTAGGAYVPAMSDESVIVKG

NGTVFLGGPPLVKAATGEIVTPEELGGADVHCRTSGVIDHYANNDAHALDITRRIVSNIN

YRPEPSVTQTKVEEPRFSPDELSGIIPVDSRKPFDVRKVIARIVDGSRFDEFKKEYGVTM

VTGFAHLYGNPVGIVANNGILFSESSVKAAHFIELCSQRGIPLLFLQNITGFMVGKKAEH

GGIAKDGAKMVMAVANTKVPKITCIIGGSYGAGNYGMCGRAFSPRFLYMWPNARISVMGG

EQAAGVLAQVQRDNYELRQEAWSAEQEATFKQPILDKYALESSAYYSTARLWDDGIIDPK

DTRKVLGLSLSVALNSKPQETKFGVFRM

>contig32732 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58767.1|) 0.0

MSSTDASPASDNGALVNELNALVESTNFDDKICLEDFTLIRVIGKGSFGKVTLVRKKNNS

KVFAMKILTKSHLLKRKQVEHTKTERRVLSVASHPFIVGLHYAFQTQAKLYFVLDYCPGG

ELFFHLSRMGKFDEEMARFYAAELVVALEHLHSLGVVYRDLKPENILLDEMGHIKLADFG

LAKDEVTEIDSGAMSLCGTPEYLAPEVLARKGHGTAVDWWGLGMVLYEMLTGLPPWYTRN

RQELFARIREAPLEIPNYLSRDAASLIQSLLHREPDKRLGSRGAGDVKAHRFFCTVDWDG

LLWAEPPFKPSDPQSKEEGDTSNFDKEFTELPVSGTPLSKSSGGSALPKSMFTGFTYEAP

TLSYGSNTSQSKVDVSSTPYI

>contig34583 Frame-1R|Blast-regulator of microtubule dynamics protein, putative [Phytophthora infestans T30-4](gb|EEY65123.1|) 6e-07

MLMVLVTIVSSALPLSYQFEDTYFMEIPLFQPLLWIAAGIFQLQLLGYFIKFLFTSISDT

RLHLLKRNETLPANLTLFGSKAVSLRVPPCPRKCKGN

>contig34842 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64435.1|) 4e-74

MSKASGYTQGQDWEAAGWGSRAPPRGAAKQVALNSARRAGNVVTEAKHNAGTNKGAHSAA

NVNMRKLEEDTDNFKHDAVDRSLSQALMKARMEKKMNQKQLGTLINEKPQVIAEYESGRA

IPNGQIIAKLNRALGVQLPRGPKKKKAPAT

>contig35661 Frame-2F

MDDRWGEDGSIRGLQAVYGGCGKENSYSKGKGPQYTRVIPKFLQKYHQLPAIEAKFETLP

KPADEEDVGLDEVQQAAIDKYIANNTKKSIGNVCDRIGDEQQEHYPKKKKNQQAVVRLGQ

NLACHGTKNKNKRKRIDTPCLSNSRLLSFSVDDE

>contig38172 Frame-1F|Blast-protein transporter Sec24 [Phytophthora infestans T30-4](gb|EEY59671.1|) 2e-32

MAPHDDTSNRVDAILTSIRAERLPCQKIVVMREGDPTEGRFFWKLVEDRASFPGGSYSYS

EFLGQISRMSLSGGR

>contig38604 Frame-2F|Blast-glycosyl hydrolase, putative [Phytophthora infestans T30-4](gb|EEY61621.1|) 2e-48

MASPDSVSIRHGHFVDAQGRVRILRGVNLGGSSKFPFGYQHTDRHSSSSFFDGARSVSFV

NRPFPLNEARGHFARLQRWGLTLLRLIVTWEAIEHGGPGVYDDAYLQYVKALVTIAAD

>contig39117 Frame-0R

MSDLIARPMGVRSIPKVVLLIAEIMRHSLVNKFIFRRSQGVRLMALLMRSLPPHYLTNDL

FIAIERLRSAVMS

>contig39188 Frame-0F|Blast-AP-3 complex subunit delta, putative [Phytophthora infestans T30-4](gb|EEY62953.1|) 4e-33

MEFESMMGALSASSNGKRRKAAKKAKSRDILEDDLMPDGARSSDEDNRGTRKKFGLIDE

>contig40816 Frame-2R

MGLLDFRRCQWDAKLLELIGMEMTKMPLLADSSVPFMGLNAIYTRHWPELRNVPLFLGVS

DGAAANIGSKCVDSSRIAVTIGTSAAIRVVLSLDVMKTSKVPNGLWCYRFGKDHVLLGGA

LSDGGSMYKFFCERLRLSDEG

>contig42652 Frame-1F

MSVSAWANNVRTETIHHCFRHCSIQSEPADVLPVLED

>contig43026 Frame-2R

MELLGESMSMLRMSPDSIHGVPLAKAVSVGLEMLDCIEAFHRHGYVHRDIKASNFALSAV

SERNPTKPQRYYIIDFGLSRQHLGEERQVLPARQVAEFRGTSMYASLSSHRRQELGPKDD

LWSWFYLVMDFLRGELPWAADAQLKNRQTVLRLKEHYTEASPNLLVENLPGATQLLEMME

YLQSLKYQDIPDYKHIRKQLQAVKQRTLVFENSDSGDDEASVDKKEAQMVADIDAVNWNS

FESMREKALCWVEKAEAYTNNDGALNRLLTIAKRHETFFFCEGLSFQEQIRVQNAVYLIE

KTSRGRGSVFAPPPIQSFVKRRQSEQKLRSDALRKRRERDLQVRQSLDVSKEERTPKTAS

TIGSSGTAAGGDKTKEDGNKGGSCPPVKSESSMDVSDAEAIDTSVSQRHDLMPASQPYFQ

QSHVKLVSQGPPLHHRSRGSHVSGSIPPASSPRIPSSRIMTYGPERPSLPPPKPPGRYLA

NSKVISPSRNHVPFEIQHANSAPRNGNLEQHASRQQYDTAA

>contig43589 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60031.1|) 1e-10

MVPLFPFVMIHVQLISNLSCYVVLRYRVLASSH

>contig43941 Frame-1F

MSPEYIVHTNTYSIRHFARMSSTALP

>contig44197 Frame-1F

MRIVVPSSTSRIDDYEHHLPARNVSHFDNDINPQRNRCGGSESTGFNQRFKSSKRQNLPD

HFIPKSILWSPRQQLNAARDFNSPARSSKSLVGISSLEYQKDLVRSHTKEPEPLTVEQIN

TADRLRISAMRLNSEERQGD

>contig44966 Frame-0F

MLVQSFDESRQAGSSCTAASALTIFKTLLRHSFVSRNKEPRCDTTHELGVQIVQQTFEPL

VMILHAMDDEKVLTAGSECLKWMVLVAVESLAAYTTASGQNGIDTLLLVSAQLLSPTASD

ASAICVGGLITQILLKLGPRLPPSTVQSILSAVCARLATTDSPALVQSLCMVFARLVHSY

GSDFLNVLEQLPSNDWECSSMLPFVFRTWMEKQPDFYGLYCIKVTITALLKAVEWHDRRL

EAILVPRRTMDTLSGSCTGIQTRSKSRGTRASDHTPTVHFLTAFVVCLAKTLAQLADEED

EWVSSDDESSDSESCDEAVGTVTSSVFAPAENYQLLSDCLETEEGVEMQDGGEPEEEFEA

YFDPINDVDLKIVIRQALQGMSENSI

>contig45301 Frame-2F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY55551.1|) 1e-157

MKLVPRKALRTTVDKMIESVGLTEIRHALIKTLSGGQKRKLSVALALLGGSSLVFLDEPT

SGMDPYSRRFTWNLLQQSRENRVIVLTTHFMDEADILGDRIAILADGHLQCAGSSLFLKK

RFGAGYNLTLIKTTDHSCDALIVEAFLRQYVPGVKCLSHSGSELVFQLPTTSSEVFPTML

EQLDDRMPSLGIQQYGISVTTLEEVFLRLSRDHDNKVEQNLTAPASLKPLTARGAVNMPF

TAYTRIEPSRWTQYVALLTKRFQIAKRDFKTCAYAIGIPLIFLIILALLPEVEIADFIPD

YASNLPTAADQRQCAESDNITALIDQGFNGSAC

>contig46472 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55840.1|) 1e-106

MALDSKRISIAVSSAAAAGQHDAAKLLLKFGLRHCVPVDAGSFAHVVESAPDDTKRLKIA

ELYVHAKECGLVSRIEGLDSSIVNYLLHYAILDGNYKHMMELLHEMQLCRNLMSNRTLRE

LFKSIAQFRANIRGKGKQIDANQRLNECPTIKELFERFPNVIPCTVHSFSQGILQSLHGG

DLSVALGLMHAAHRHQDVKLRPEIYSQLLYPLLAGGQRGGDELSDASVFERLRVERCFDK

QYPKQRAHLNSLIVNICQSNNDFLTLLVCLDRWQAQGHQPMSRRVTMRVF

>contig48342 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64471.1|) 1e-18

MCKWKEYGSFATRLHGEASDVDLAVFGATKEFGLTNQQGVKPLADHMHDLEAYVDVSAFT

RASISLLIDVVIVTLHEKSDSKSCELRRSAQDSVSAIPSKINSANPG

>contig49284 Frame-0F

MRHHARSAQLKPSVMLFHVVLLLSSHWIAGLRLVAFNDSFVPGDNSPGKLRQSSHLVASR

LDEDSDDSIQQVSGVVEDRMDLDSKKNAILAKETAVAESSWTAP

>contig50431 Frame-0F

MHSIKLPCCPEVDGVVRGSMYQSGYVFVEAERDGYMDVMHSLQINFKSTSRLPHFLLNSA

LKRRILSVVTISREIQTSRMGRQTLLRKKDLMPKRARALCANCSRKFSLFVRKTRCRVCG

EVVCQPCAPPIVISTSQGPTKTRVCTNCCHHKAPVEDYEPDYEDSRRLQNHTRYSDILQD

QHDHPDMYHEDEEDSMDEDGDEDGLEEQSDYSVFAQSRFTDASRDSMAASQLNASKYQYD

PQYDSSSHFDTSSVMDESQYYLDGSSD

>contig50646 Frame-1F

MLRDNLMTQTLFLELPVLESHLPSILQVTGIITNDIDDESMALRKRVLKLGLELVRILVA

GLYEGVTKVSFDALALRDRSRKQQELTKIQSLVARQEALMGAIGELVCCESDRLTDVRLE

AIDFLRLVSQANGGVQMIVLNMYAVPSGRPVIAELMKLDVGKDRDYIPVAAAASSLLDAL

FEENEGACMAIVQHIQTPPPLSLSAEFDGTKNVLHTQIHNRSAGRVLLDALMVNLDFIHQ

FKDSADIEMLESNLVVAWKASHRLTKLLEKSSFCQELALRVPD

>contig51072 Frame-1R

MMLASIEVLECEQRGSRFTEWFPGALILAQDLPEILHIDNSNVSRFFVSLSLFVACKTSG

LLGSCFCADKRFQEVSSLLFRNGIEECGTKERMIYPYKESECWS

>contig51704 Frame-0F

MDWTAFKRSAQRFRHSLISQLDSSNFHLSVYSVTLLMRSFMRAIGLGGLFHRSTVRASTV

NAAAAFDLSHGSRLSSIYERPQFLFFCGSDTLARSSVEHTLPKHSVLASQFCEAAAQTQS

TIDHRMPVFFKSRFSPSQFADC

>contig53218 Frame-2F

MTLRILLLWHEALGSDEEQATDEEIQARVLYFQNDGNNDTSPISSLHLVQGLLKFMRMLR

RKDRCKMKTKWTPEWASVALTQNFLFVLEVEPQIFMAI

>contig53409 Frame-2R

MLQEKDEERRKWEIEHKERVEHLQFEHQEVIQSLSLELQQENEKRQQKSMNLQRKCVLLE

LVLSREREEKSQAQVEHNGKLETKVCELTKWKESHASQACEAKHREVQVAQMQAEREPKV

KE

>contig53957 Frame-0F

MLGGRDYRAYSSSSDHTFSESDMAHPMLPSPSGSPQPLSGSDVSSFSVFGSKSEHSDNGV

PDCGMDVM

>contig56684 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60157.1|) 4e-17

MGSGLKSNHLDRMATLGRQVGSFINTPLKFIPGTNYHDAK

>contig57144 Frame-2F|Blast-peptidyl-prolyl cis-trans isomerase ppi1 [Phytophthora infestans T30-4](gb|EEY70464.1|) 8e-25

MASSAPSKPSTHVVFETTVGNFTMELYTVHAPRTCWNISELARRGYYNNTIFHRIIKDFM

I

>contig57742 Frame-0R

MPCSRISAITAFQQLLPFSARYATESRTLPTLLPGMSSHQ

>contig58967 Frame-0F|Blast-calcium-binding atopy-related autoantigen-like protein [Phytophthora infestans T30-4](gb|EEY56604.1|) 2e-31

MFLVSHVNQHHIEKWVERVDNLKHLSGHVTEQEFLDFNVFLEHLDELKVAMDLVTQGHGV

N

>contig01324 Frame-2F|Blast-SUMO-activating enzyme (SAE), putative [Phytophthora infestans T30-4](gb|EEY66754.1|) 1e-105

MMEEEATFSAAEAAVYDRQMRLWGVEAQKRLQRSHVLVSGLTALGSELVKNLVLAGIGVT

LHDSKITTLAAASSQFFLQEQDVGKNRAEACLSRVQELNPLVQVVCETKPLDKLPDDYFK

QFSVICIIGADQVTELRLDALCRSVGTAFYAARSFGFEGLVFADLGDHIFRRNVAGTDAK

PGDSITISFPSLKQSENVQWNSLQSARKRAPQLPQVFVKNQLLRGYKTQLGIKEVADNDA

TKFIDYARKQFQLNGLSENYLSADELQ

>contig06620 Frame-0F

MKIGVLAGLVAACITVTQSATTLAQHHEERNIEVVRSDTLRRRLQNAKETNKTSKAAANS

ESRSMNPVQELSSSDSVNGPVEFTESFGSPVGKEFSDASSVIPGQIVSSISIWANTRITG

VNIQISAPQEQSFEHGEREGIPITLALTLGEYIVSMEAHWGIYNGVTLIYYVCFTTNLQA

TIQGGTKTKNRRTVLMPENYQLAGLFGHSDGDITQLGAIMTTAPMLAYLPNVPTTPMNTG

STQNNLPPASLSSQPGNSPSQLGNPPMT

>contig07322 Frame-1R

MDVLSIQNGQFVDQHGRVALLRGVNLGGSSKLPFGYGHTDDQDMRDFFDGAATVSFIGRP

FPLAEADMHLSRLQRWGFTLLRLIVTWEAIEHAGPNLIDYDYLDYIYAVVKKAAEYNMHV

YIDPHQDVWSRWTGGDGAPMWTLECIGFEPRHFEPTKAAYCLETCGCIPSEAPKMMWPTN

YAKLACATMFTLFWGGHKFAPKCCVNGVPVQEYLQSHYLASMMALAEKLKKLPNVVGFGT

MNEPSQGFIGVKDLKKNVGSFHSGYAPTPFQGMALGEGIPQDVEVWDVGLYSLLRNKPSK

VETIDPKRFRAWQEHCVCVWRNAGVWEIDANGSPHLVQPDYFANVNFSQDFYVPFATRFA

EHLHEIIPAAMVFIEVPPLGFSDTCFPHIQAIPHAVNAMHWYDAVTLVTTTWCSYFTVDH

WTRKLAFGNKALRRVHQRQLAHIASLGRTYMAHAPTLIGETGIPFNLNHARAYISGDYSA

QIEAMDNTIATLESQVVSYVLWNYTADNSHAFGDLWNREDCSLSSRDSEALAIRLQSRDG

SARGLKAFARPSARKIAGQPLLSTFTMATKEYVLEYVAHNIKTAALTEIYVPYVHYPSGY

RITSSDGHCTVEKHESYDIVLYTHDTKVRTHRVC

>contig09441 Frame-1F

MDASDLRGWHEVEQTLMALDLPPVPPTSDPHRLLGYVLQILPRYMEIEMLVTHLRLYASS

LEQDMEQVKSYSRLLTREAISEREKKQFLERYAAQVVQERNDLLHSQGFQKKKATGHYVW

HSCCRKSKTQPSDPAPSIIALRGEKLHEVRKQLETLHEELHNQEQLRNELGFLLKKMQRE

HDSKV

>contig09980 Frame-0F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65895.1|) 0.0

MSVLFAMLAIIALLQSTATAAPVDSVIIVRGNKLYNAKTGERFFMKGLTYEYAVSDEYYD

KYSKAVIEENLAGLEFNTLRLYNIHPGSSYKKFMDDMAKLGVYVMVSASPDNDEYYGKYR

YSTITKKLSCTGKVSTSGGAKTVDQTETCYPALLLEYGKKIIQNFAQYDNTLGVVVANEI

MQEDLTSASCVKAYVADLKKWMAVNGKKLRILPLAYAAADSSNDKVSNADDYHVIKVQGL

LCGDKMINGMMAESIDIYLINEYRWCPDSTFAEAFQRYINMAQGIPIVVAFGEYGCKLSK

STPRDWTMVPYLYEEPSKTKEFSAVWSGGLAYSYGEAKLSKDSLFPMFTGGSIDFLSTPS

SKPTTVTRI

>contig14072 Frame-2R

MKSQSQIERIRLVSPPRLSQRHEKGHTLKGTKGSKKNTLQHNQPSSSVSRHRTTMLGQCP

PGCGSRLSFMGKTSIKRPMVATASRGNGGVIRPWI

>contig14205 Frame-1R

MMLAQRGCLKGLVSKHVRRCSDNVSKIFKAHTTLSVSKSLPVVSLTTELRERVKIAPLAV

TYNPTVVEQGWQQYWQQALRPSTHPDSSKRSDKVFRMILPPPNVTGALHIGHALTITIQD

VIARWHCMRGFDVQWLPGLDHAGIATQSVVEKKLRKERGLSRYDLGREAFVDQVWQWKHQ

FGDRILNQMDHLGALVTKNQAYFTLDTKRSEAVRRAFVHLYEKGLVSRKQRMVHWCPKLQ

TAISDIEVDVEQLEKPTTKILPGKCAAVEFGVRHRFKYQVADSQEFVQVDTTRPETIFGD

VALAVHPDDKRYQALHGKYVLHPFSRKRIPIITDNLLVNMELGTGVVKITPAHDSNDFEC

SQRHQLPIVQVIDKSGKLCGQIEKRFQGLDRFEARQLVVEALKDMQLYVDKFDHPMALSL

CSRSGDVIEPLLMPQWYVDCSHMAKRAADNVRNGVMTIQPTSLAHTWFSFLDNIQEWCVS

RQLWWGHRIPAYRLKAGAIQRSNAQDKWFVATSIAQARQKAEVEFNCQLQNDDLEQDVDV

LDTWFSSGLLPLSVFGWPHAHDDNCREDQSPLDVMETGSDILFFWVARMAMLCEEFTGRV

PFKKILLHPMVRDKTGRKMSKSLGNVID

>contig14869-1 Frame-2F1

MWFSAWRQKLQLLIIVFFIFVAFAASNAAWIP

>contig15097 Frame-1R

MLFQLHDVVIGRFARTNHRNRRRSGGASKDKPMRTYIARKRPSIRRRAYIKLGHRLQSAF

E

>contig16027 Frame-0R

MYYQCESEIPLRIGSPNSLPQAAVALTENSLTPRQTRLRARLTDFYIKYNPSAVDRIDKI

LKRYHGREAQLWSDLAQKYSTEVDETIKLGLGDFVFYSVLVARAAKYDFSAMIGCFISVL

MGLGGTLILLGVHKKALPALPISILLAVTMYFWLRSVFVSFASSALKFGVPL

>contig17064 Frame-0R

MKSAVPSELDSNRQKHSNDLRIDTNQSLHGAIQTQACENHGSGKLQMLPPQVSLPLQPKQ

TSCLETLERPSTNLPSPSLMRSSSSQLSKGSNFVFVSSDLAREDVNRVLEAIHQMGGKFG

LDFDLKRDSETGLFSTSVTHLITKAVPSIRNVCPFNSMRCKRTAKYMRALAEGTFIVDFS

WISASLAAGRWLTEDPFEMAGDIYSDAIGKPHEGHLRRIQTGRRNSIFSLLCFVLLVSEN

EFEFQFTSVRTLVNNFGGTIVPAENFSQQKANPRSRRTPIGVVSKTTLPSVAKAKWLQFQ

IP

>contig18155 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59914.1|) 4e-09

MLVTVTKMKRILTFVFFVEFIPKLHPRMLRVWGVYFTDKSSTYILMLVLFARD

>contig18649 Frame-1R

MTSSTEGVAAEGGHLVAMNASQIDANMDTEARVLMHD

>contig20761 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63906.1|) 3e-51

MYLERRSVLFMGIQSISMQDGSEYLNEEELRESWTLLIDDRRVRLTCESSLIPPFASLYT

ADIQLEMVCQTSNEFYLHLAAGCYVRLRAESNIMRDIIVLTIRAFTNLAVVAVDLNPSDS

VSPRSRQSCAKAHH

>contig20835 Frame-0F

MQSPGNNQGTIGVGRCLLDGQLLGSTPCAVTMADRSSPTQDMLVTNHPLLDYKTTGDPSG

PLSIKSGLSVSLANDSEMVQLVVQVFRSVSPQNVLPTTGVDMANSKYLIPTTLAPGRETT

GKFATETRMDFSNLTRGSDVHTFMENDPFVSSLSSGTLSEALNGNLRHVVVDEILRVPRS

TFALPIAYLDFLEEQALERSRFLQKQLHAMEDFPRETERLITEVDFLRKKQEEYLKQRQF

LIRQEKRLLTEQSDGKFFMAAERAGTVFAASDSPGALNASTAISGAAGANDADAVAPFKR

STYKNLNLWQFLPTNMQDQFLCTCKPPRSDTALSRLSSRPFVWHTMTMGCPAAHTKGFAN

GGYPATGPIETVSLIGLGDDDPVVAKNQEGESSSPTSPVISSKLGTLHHTSSCADDSLAA

FKLRLELQDRLSVIGSQILSAAAACILASLDLAVNGSAF

>contig21375 Frame-1F|Blast-DEAD/DEAH box RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY58225.1|) 0.0

MAQQQFATNEENWKASLKRPEKDTRVQTEDVTNVKGNEFEDYFLKRELLMGIFEKGFERP

SPIQEEAVPIILAGRNVMARAKNGTGKTAAFIIPCLEKTDTSKKHIQVLILIPTRELALQ

TSAIVKEIGKHMGIECMVSTGGTSLKDDIMRLYQTVHILVGTPGRVMDLANKGVADLSQC

STVIMDEADKLLSPEFQPLLEQLINHTAKQRQICLFSATFPVTVKAFKDKFVDNPYEINL

MDELTLKGVSQFYAFVEERQKVHCLNTLFSKLDINQSIIFCNSVNRVELLAKKVTELGYS

CFYIHAKMNQAHRNRVFHEFRNGATRHLVCSDLFTRGIDIQTVNVVINFDFPKNSETYLH

RIGRSGRYGHLGLAINMITYDDRFNLYRIEQELGTEIRPIPPVIDRNLYCK

>contig21726 Frame-2R

MWNTERSNTEGQRWWLDIYHKLIYELAWLIGKPGIAFEHLHADETWKEKEPDTDKKFLKW

LLRVAKFRAKGGQFDDNDFIRLLKYTTSAYQQAKLFVWLQHAQDFPSMNEFAKKQLWRMK

GDPNTRFTVYQVLVDNGETPASIFRNDYNNEIGATFVNWLFYVKMFRDTRDYSEEELFRL

LTKHHSNEAVIKVFTSLAMSTSHKVPYYLVNKMLAYLISKPETTQLVFDTWLASRIHPAA

ARKILLPGDQFDPYSVLFGCWLNYVRQFREISNTFSDDDFSLLLSKTKSDTDLVKALSSF

RNDPRLQNLVETGLVYMKIFMDFKRSLKDRVG

>contig22550 Frame-0R

MLSRHITASLRRAFSSTYFKASLQAVWTQSNGHQSFIPTWKLYAVGATAVGVTMCPSLCE

SKVEEVETSGPPGVRRPDLPVFSLDEVQKHTGAHKNGTWVVYRHGVYDITKFIASHPGGT

KILLAAGRSIEPFWQLYAAHNHADVHKILETLRVGNLRQEDVELLETVRKERYGKGPYSK

DPPRHPALNVNSSMPFNAEPPVELLMQSFITPNDLFFVRNHLPVPEVDIETFTLKIAGLG

IDQERNVEFTIDDLKSKFQHHTITTTIQCAGNRRAEMSSVKQVNGLSWDTTALSTATWTG

VLLSDVLASIGITDESSLSEKSFEMGQADQNSVMQHVQFEGLDADLEG

>contig22712 Frame-1R

MGMTEYMIKDYVAKNPKRSLESIKALLAKLAKGKNIDSDVLSDDMKLQEVKHAMDNNAHV

GTSRDAELYHKNNF

>contig23665 Frame-0R

MKRRFLLNYEWLNCLSLVLSNPRTPCSLLFHLARLKAH

>contig24501 Frame-0R|Blast-ubiquinone/menaquinone biosynthesis methyltransferase ubiE [Phytophthora infestans T30-4](gb|EEY54009.1|) 1e-113

MNDFMSGGMHRLWKDAFVDTLHPVGPIKCLDVAGGTGDIAFRIAKKLSKSLRGINGSEVT

VCDINSSMLQVGLERAAKVLPNLDQSLFRWVEGNAEHLDFEDNQFDVYTIVFGIRNVTHV

DRAIQEAYRVLKPGGRFMCMEFSQVPNPIIRQIYDTYSFNVIPLLGEKVANDRSSYQYLV

ESIRQFLPQEEFKAMIQDAGFKHVTYTNYTFGVTAIHSGFKF

>contig28475 Frame-2F

MLQAQWVPQRIDGASMWKPRARHAHSSVVVGGDQVFVFGGKDATSTTFFNDLFYYDAPLN

QWVQPRGTVTGQVPQPRAFAGLTASTDGRTLFLFGGTDGKHEFGSLFRYDVQHCRWDSLA

GATVGDRPSCRINHSLTYVAPHHLVLFGGRQRALRQNELYIYNITTRSWRLMLDSSAPKI

GRTAHATVLFHSEPAGPRAVQELIIFGGYAGKHEWLNDLYVLSLSQAAL

>contig29915 Frame-2F

MADGVVCEESFVRRISSMLADYKEAVTDSIAHPSRLYILVFTGPNGTLFLHSL

>contig30135 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64195.1|) 8e-48

MSASSPAAKVKTINVSVSFRAEVKSFNVYCMKVEVGVATFLLAAVVAAAGILVDKVCQRG

CKACGCGDGKCCNSVRPSERRYQLPRAHVEHWDTRDGRCDPSWSNLAPKCSPSRQGDKSR

ALIGTLILLRHGQSVWNRNPNRPKDLWRYAGSIDIPLRFCG

>contig30188 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66474.1|) 1e-35

MEPNGSLAKKKAPPKPRKRKISDVGAASKDGMSSAKRFSTDSAAEMVSYESAAEAHTGQT

AQLKPFVRGELVESIKQMLFGFGDVSEPHDETAELMEDIVVEYIHA

>contig30496 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65647.1|) 1e-60

MAKAKAALATQYRRLGAKKNKSKVRHIVEIVRPWKYLQFEELIKEDRDIVVERLQKEVAD

VPATCSYAVRGVNQVVRAISRREVQVVVFASNPESLAFGHLPLLCRLHRVPICVLHLSSK

TFGRVFKLKSMVAVGMKAYVSRPVKAEHEAQSTTAIKEPQILTEAEQQKLASITDFLIAK

ASKRT

>contig30878 Frame-1R

MLVILVIAVALALIILRTYYKHKCAGTNAQNNDTTATLMSKGEVDTGKGSFISNDDLLRN

FRLPQSDVSTVKSWGSGRLWLCEYRGKKVMVKRVESEVTDSYVTKALIVEARTLSTISHP

NITNLLGVTWLAGTDFAVVTEFMAKGDLKTVLTSAEVDLDISAKLSMCFDVASALAYLHE

TERILSVKQLSSRKVLINEALDCKLSLFECVPSTDNSRGPITYGLDKIVWLPPEIITRSS

PMDARKHNIYAFGVLASEILTRTAPYKSLIDKLGNTMSDIELVSRVRRQDPLRPHENRQE

FSSVPAIVRQLIEQCLSYAPMSRPTARDLVKVLSFAKNEVTTISL

>contig31543 Frame-0F

MRREISILKTLDHPNIIKLYDVCEGTRHLHLVTELCTGGELFDRIIARGHYSEADAAVLV

RKISDAVKHCHDRDICHRDLKPENFLFATKSEDAELKVIDFGLSRMDDGLSAGVMTTRVG

TPYYIAPEVLGRHYDKSCDLWSIGVIMYILLCGYPPFYGDTDPEIFASVRAGRYDFDSPE

WTNVSHEAKHLISHLLRVDASKRLTAEEVLLHPWLSGSAPRSSMTLNPNIFASLKRFTGN

NKLKKAALGVIADLATEGEIAELKKQFMAIDTDGNGVITVSELAEALRDTGLGMIEEEVL

ELVKGIDIDGDGLVDYPEFLAATMKRNLANQKEHLMNAFNYFDTTNTGHINKADLVQFMG

SEEQAQEIIDDVDANGDGVISFEEFVAMMDRKGYGDDSGMDSTDDSSFLSAAHYNSGQTN

FTKGTEL

>contig31965 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59800.1|) 2e-68

MSTDQLIRTQNSRVLQAFRAIGVVTDAVPIVWYGMGKESFATASLGKSFVVYNCDKLSPV

LVSPQLPKRIAALAVQSKQQLTFTACGRQVIVWKRVARIKTLIGHKGGIKQLLTVGNVLF

VLDDEREITVWDLNTMERVHTLSFPTTFTPTVMLH

>contig32362 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY61544.1|) 2e-98

MFIEPVVFSILSSIFPTIRIWPDVTFSTLIELYSEMIGLFGLQHEFWYYHELLDYVTSRT

NRKVVLTGHSMGGGIARLVGSIVGATSVTFSPPGFVQSYSKLVHHIGGKSMKVDRASLHH

RNFAVVPEYDPVTMIDAQAGMTQKISCDTPL

>contig32418 Frame-0F

MNRHALAEASSLHDGPVPVYLMGEIANSTKASDRDAEKTADYILRRLNKSNLNVKLKALQ

IIAFCIREGSPTFSDAIREEEQEILAYIQFSGPPDPVYGDEKYRRIRVAAQEALVCLNDG

FLSSQKVESPQLEQETPQCASRPWQAQEGESAQSYNHSNGVYNQGQSERQLSSVGGSWGQ

PLGSSRPTPYQDNPSVGYNNAAACYNGPAGGGYNAPSPGLNGRSRNFQAPNEVGNGHMGK

SLHGSNESYGQNIENSGCYEYNQAGTSSVNTPNIPQQQPSGFNSWAASAGTGLTTKTAGA

GVWSSSGYQKKDSASDNEPRYNPSTLRDNRPTVLVGHTLSFPKPAGGFGRSNASAPSGLG

GFESGTYNPNAVRSAVAENSFNGGNNARSNFGGGYQSGGPPSFMDNASRPAHRIGSLGLP

VNGQPLNNVPTTALGKKAEVLKKMGTAALEKWDRRNMDKSMASSLADNDELRAGPQVIDH

GFFQLNGQQGTGGGDTSRDYERTMIDSLCASAGLSRAPSADDLKRFLDLAQTLDAQTIGD

ILLDKLEDDTWQVRLKGLHVVLGLLDSPGAKLYQEFFEANLEVIKELRKDVKPSVVSKTL

QLLRALGHADKAIRAPPSGARCSNSTQTQRGSPITKTHHEVDLLGLSSLSLESAPGPTNK

RVINTLDLLGSANHSQLPPPPAHRQEVSLLDGFDAVKSSRSSDQTSYCPSLQQHYQQPLQ

DKHKTFGHFGKELYAVTNSPRGASMVVAAQPHGTCDDRRLGGGQSAFNFM

>contig33471 Frame-2F

MESSPSDSFVESQQCSADPSAFVGYHIPVNSSKAARLPPQETQSSFKLVLDLNAPLTDDS

APIGTNPFDGLFASDTQDDENAAVQTLVQEKNKSKPLTKTKYQQHRPRSPPPTMLKTVEI

AWRARRQKIANNNIVVNTIIQDSDLSEDLAPIVYNDGGLKVCEEDEEKQAPKKSIEEYSD

QETEYDKEIECTQDLGDEEMTGSYERASVENEAK

>contig36098 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69792.1|) 1e-110

MEETFTNAKWSAYAKTYSSVFESLTARWAVDAVQIAHHEILHLLQQYEATSCTTPFHFVD

VGCGPGNLSFEFARRYLTLPTDIRITASDISDGMLKQLMEKLMADPALNSFAPKFCTLQS

DGMFLSEVADSSVDAIGSNFGLSIFPNRMQGYATAFRVLKEEGLLVMTTWSDKSSQIVWF

DTITDAFNAAGPSEDKLQFPSTTVGSDRERVMNELHEAGFRDVRVYSTTHTIVFDDPKAM

IQAMMTNPFAAKFLKRLSKDRIEQMLIELMESDAQKNFYQDERMARIDGADGFVDKKP

>contig36609 Frame-2F|Blast-kinesin-like protein [Phytophthora infestans T30-4](gb|EEY58749.1|) 1e-127

MARSSPASNEMGNVRVYCRARPQNAKELAMASSQHCVLTENERIEVKSSDGSVQKFTFDR

VFGEDNDQKSVFENVALPVVQDIMAGYNATIFAYGQTSSGKTYTMEGANIDHSELQGIIP

RTATEIFNNVMNADENMEFIVKVSYIEIYMERIRDLLDPYKSKVNLQVREDAQRGIFVEG

MTEMCVTSAMELLAAMRAGAANRAVAATGMNEGSSRSHSVFMVTLFQRNLENQATKAGKL

YLVDLAGSEMVRKTGATGRQLEEA

>contig37457 Frame-0F

MDASPLDLPSRSIILDHVWDPLEDSEVAFFDDLEEDMRTECSKHGTVEHVHIVANGSVIV

RFAELKAAIACLKVLNGRWFAGRQLEARFDQATAENSSDAETKVEAFLASLGE

>contig38690 Frame-2R

MASTRSLRAWYNDEGKWFDRNTSRDVLCHFQERELFLGLIRIFLSHVISFDTVEGHFNTA

KCDVKGRVCEGIGPESSRCYRRI

>contig39114 Frame-2R|Blast-3-hydroxyisobutyrate dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY67769.1|) 1e-129

MVLPAKPRVGWIGTGVMGASMVGHILRHGYDVTVYNRTPSKCDKLKEKGATVAYSPAEVA

KVSDIVFGIVGYPNDVRKVFLDPESGVLSSIKSGGVIVDMTTSEPSLAKEIYDAAKLEGV

SSLDAPVSGGDIGAREGSLSIMVGGDAHTVEVIMPLFKIMGRNIRHMGGAGAGQNTKMVN

QILIASNMVGVVEGLIYAQKSGLDIEEAIRAVSAGAASSWSISNLGPRIAKRNFNPGFSV

DHFVKDMGIALKEAER

>contig39877 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59112.1|) 1e-53

MVVPGSNVDVDIGSLPVWRPYYQFRRRQDGIYLVARLHGTDSRNVRVQWNEQSSVLRITG

FCLPTHKDIVMSRLSGAPTFGRFEIIEQFPPNVFNVQEATQQMFEDGTLQIYLPYYALRY

PLRYRPASLLQAQDCFVW

>contig40662 Frame-0F|Blast-NADPH-dependent diflavin oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY61274.1|) 0.0

MVPPSQAIPRLLVLYGSETGTAQDVAEFVHQRACNRQLVDTQALAMDDFPVVQLLPECNT

VVFVVSTTGDGEAPQNMRNSWHSLLRKSLGPQWLKGVRVAIFGLGDSSYAKYNAVARRLQ

ARLLQLGASELIDRGLGDDQHVNGYFGALNSWLEKLWTEILKLHPLCEGTTIDDTPKPIE

HRYSVIMHDAGAPEVHEAKQMTPKSDSSRFYAPPRTAVGTDQGLILASVEINRRITAESW

EQDVRHLVLNICSGSSIVKASKPFYRAGDVAVVYPDNVLGVDDMLTRLKLNGDAVITINA

ANGSKQFDFPSPVSLRDIFTKYLAVLQSPRRSFFEQISLFASNAEEKDKLEELASAEGVD

LFYDYCVREKKTYAEVLADFPSVNIPLIILLQLIPRQQPRSYSISSSGLLHPETVHLTVA

IVNFLTPYKRRRNGICSSFFLSIDPCKEKKCIPMWIKKGLFAPPDLERDMLLIGPGTGLA

SMRAMVQERHFLRKQADKVKVNSKVLYLYFGCRHKSKDFLYNDELSEFVASGDITELHTA

FSRDQNHKIYVQTLLAENKETIFEFIMKGKGCVYIAGSAKRMPTDVYEVIRDILRLVGQL

SLSAAEIVMKTLIRNKRYVVESWS

>contig41517 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65537.1|) 1e-113

MSRCRSNSSSSSLSQAESGSGDVCANTPFDYELTFLKGNPWPDAPLTSTEEERIQVIQRL

NLSQDFANTIIRGLLELACATINCHVAAVSVVTKSTSLFVTTIGLVGDQVPRDVGVDAHA

IMSREPLVVLDIRKDIRFAKNPLALSMQVNFFLGIPIFIKETGVVVGALCFVDKDARKRM

RGSDLRALQLIAARMMEKMDAQNNEMTEKIPEGVRLL

>contig43098 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58177.1|) 7e-91

MWSSLLLFVIPFGVCVAQSPHASRSPHASSVSVIDKSSSEMVTSLYNICPVVNKFLDEYD

HRSAEEIKADAADDVMMSYMINHPNNTLWDFFKIEVKQKSKMARMLPFHTRVADAVKDVV

DFSLDSVIYLAHSIADAVTWVANSIREPSVGAKEVKDFFTEFSENIKLVWRLMKEDPKDT

SENLAGGLLLHIMHHPAEFTAETVLLVATGFAVIGGLIFSVETIFGALSSSVTSVLMSVL

VFLHIIDDPLLIVTPLITSIVNSASALNSNGSVADNTSLTIDRIQPLKTCQIPREFRPIF

SSRDICLSTPIQVRYLIFGTSKRTFEMSYEERTAAYNRFHDFACCFLGNEEYEVTTPMLD

KETLKSNLVSTPVKIQNCSQLLSQYDASTVWRSDVPDRSEPQDYRSVVGKVKVNQDRSDY

>contig43159 Frame-2R

MACTQRNFAIVDQITLNIVTKVAAEDFCSENIAHVVHILRAAMLFVSKFNDRPFGFQSEF

QLHSNSSLWQSFMSFVPVGYCVGESGHDQVSDVNGKRGHSLSARSLVSVSGSLLVHVPAK

GN

>contig43483 Frame-2F

MGHNDLVGHQHVGCADLLREVEDRVEPKLHVFGHVHEGYGCSYSSDGTITYINASLCTHD

YEPVNQPIVFELIGPPKRGWSIPTLSLTAPSTGMAMPRSFSTNDVSSISKVWIRDNKNVG

RLPTGDVPQDYDLMMHEWLRSCSQKPAFSQNEFVAIKSSEILQKEKLHDFRVDGTASGLL

FESTLKLRPVRNVEKRALRYLFSQGFREPKSESDTVLELDSQNETKKNDLLTSMKMSKGI

GILKGSNQNYKISRRMTVAVLDHINEYEEEMDHCDREHVQLVRKDAAILFEGPSLLTQNA

QYRRLKKTLQRRSAVPMLDALTEEPKIKKEEVVDAVLEQNKVANDDTVAYAAASTVIECA

LCKYKVSGHVHFGLPPPSSLEILKDVKHDGEQTENLIETYSRAENLPLNRLSSWF

>contig44543 Frame-0R|Blast-hypothetical protein PPL\_10453 [Polysphondylium pallidum PN500](gb|EFA75881.1|) 6e-22

MLKNWETASRYQMIHSVVLLVTPMCRRPGLAGGLIATGTLLFSGSLYAMTLTDQRKLGII

TPIGGVAMVAGWLALLL

>contig45081 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55988.1|) 7e-85

MNPPVCFVRPTADMMVKPGHPHVTSDGYVKIPYTCDWRPDFTLLELVAHMCSIFGNIPPV

FRRPGTARVPNRASISSSSVGSGIGGYFQPGSYAQTHPPQPSPYA

>contig45188 Frame-0F

MRMRLVMDDRNCPMCKQPLERVVVSTIPRPYDSFELWGDAAGPNSALDELSDMIYVDCKA

HYVELRKLREFECRMKHCREVKHSLENLKDHLAHDHGVGFCELCLTHQSFFIQEQEVFTK

GALKGHNTGRSRGGPAGQKHANTGRDFHPICQFCRRRFYGDKELYEHLERDHFKCHLCKV

ENEYFRNYASLETHFRRKHYLCEDRNCLEMRFIVFPNDVEYQAHMGSIHGVHNRLQLNFQ

VSRGGGNPIGGPTNTSFADEVPDHWNFGASSHPPSPAVELQDAFPALPMPAGPSPTPILR

PAIARPVAMHVQSLLPARQLMAPPRAQIMRNQRLAHALGVVRPGLANGEAASFEDEMKTP

NYSEALISWGKANASYLAVVERRLERIVREPTCHSVSLRVMSGEERALMHQLASFYGIVS

ESFGEDPHRRISFFKRVDAHVPSITLSAHISKLNELARAAQASSRLKFLPLRSNTPTQQT

APVLARPLGAVNRGWEHISPRHVPSIADAWSDDDEEKSENDTVNLQTCKEE

>contig45302 Frame-2R

MLRASRLYSLMRSSCYASRMMSSSKLSLHQLLQRESIKGVRVLVRGDLNVPLKRNATPAT

ITDDTRIRALLPTLKMLQSAGARTILCSHLGRPGGEAKDELRLTPVAARLSELLKCPIKK

LDDCIGPQVDASIDKLQDGEIVLLENVRFYEQEIENDRNFAKQLAHDAKIYVNDAFGTAH

RAHASTEGVTNYIKTNVAGSLLEKELKYLSGAMDAPVRPLGAIIGGAKVSTKISVLKSLL

QKCDKILIGGGMIFTFYKAQGLGIGKSIIEEDKVELAKEILEEARERGIHIVLPTDVVVA

EKFDADASSKVVAANAIPSEWVGLDIGPKSLITFAEALKECKSVLWNGPMGVFEFPKFAA

GTFGVARALAECTESGIITIVGGGDSVAAVEQAGLGTRMSHISTGGGASLELLEGKVLPG

VAALNNAE

>contig46307 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65919.1|) 9e-49

MNIVFVCTSNTCRSPVSEEFAVEYFRRKLNMSREQQEEKGIVIRSAALTDAFEPEGSPAS

KYAKDVMKKYQLDLSTHRSQLLTEQMCKDADYVVCVASGMVHKVTEKFPVTKERQGVLCA

FTRDVPDPWHMSYDTYMENIAQIEETTREFLDQHVTW

>contig46390 Frame-0R

MKQVISSIRRQWTTQILAAVQGLCRCSRRLIHRRPSTRWYCLDCDTSLILAGFKPVCPFL

TKHITKSYLPELFCNY

>contig46471 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70311.1|) 2e-70

MDQEWYDGSDSKCLSISAWSFTISDYQLARFLAVYYPDSVDAQIVVLSRWMKNDPSSSYP

LEKILELSSAGVVSSFVLTKVLVDALDTCGSDLYVMMNPNIAMTLWRNLAELVTALDEDE

FLRDQLESEATGVSNQVTLLELGAQHLWWKRVYLARPNTVQEIVAITNQNSDLMKVYIYR

AAVAQRLFSDTPPIAEALFSAMQSSEVAFSHEHVRLYKSFFTVASL

>contig47731 Frame-0F|Blast-Resistance-Nodulation-Cell Division (RND) Superfamily [Phytophthora infestans T30-4](gb|EEY64845.1|) 1e-172

MEHFEIYEKYGLDMKHFSNCLYSPTTSDVALCTELKSALEGEDSLPSTMSDCPCLSTFGS

PMNLYNTYLGGFPDGAESNYTLFLDSLAFVSSILNYNYADDDKNEPAIKWEREYIKAMKK

EAKSNAVFDIFFFADISVQDEVDAESSNGMGPVAISYCLMIIYIALGINRLKYGRDFFIS

SKILAGFCGVMSIVCGVASTIGLFMWFGVKLQLIIMEVVPFLSLAIGVDNIFLLIHAMTE

KEDQLRREQPSIFVGLGQNPKEIEAITTTIVSESLAYIGPSIFMASVAESVAFAFGSISA

MPVVLWFAAMASCAVAVNFCLQITLFLSILTLDKRRELSGKYDIIFRRSSSVAEPA

>contig48547 Frame-2F

MMAFGNNNTDDSMSERLLGEDEATNSDPPIDGYELISERETLVFENDFFREQQRLSKRGG

FFQTYLMEKMLPG

>contig49210 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62254.1|) 6e-64

MRLNFRSFSDMMVVLLVFVSGIVLHKALAQLDTHESSARVNVWERSFSAFRDTPASIVES

MSFEVLQYNLFGRPYEVSKDGQRERLLRVPESLHRISETIDIVTFAEADIQTQRDEMLTE

FQQFGFHFWTTILHDPDPFTSLLNGGVMVVSKWPIIREAQHVYRDACHYSDCLAAKGVKY

ARVLKTVNDTSKVFNVFAT

>contig49658 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63104.1|) 1e-141

MVASESPSPEEEVAYLRQLERDYYALLGVPRDASSTEIRNRFLSLSREFHPDRRRQDNSA

IVAAANAQYAVLDRAYKVLFDPVKRNIYDQYGEKGVQALEQKSLPPRHTVGTHLKSADEV

QRYVQKILYCMNQQALEAQFSSDSRMSMNLDASAFVQAPMQGFQSLFQRGARCIKRTEMS

ILQRVELPLTPSTSLTLGGYMYDKNATGASGSFTAALSYRSIHPSTPSFTLTSQLGDAPK

LHCQISQPVSPYTVFLLVPEIDEHGLNLAVGLNRMLSVHMHGAMMWSLRNGLFGSMNQSS

GPTTTMATIGVNTGGPTVTLQCRRLLHVAMTIKVAIQASLQTGISVVASASREISNRTRI

AFSLALARAGVTLRVGFTRGSVRFVMPVFLSPFSAQSA

>contig49799 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54952.1|) 7e-10

MEFWLTTWRSVVVMFKLAVQGFECGPWAVRNSPMMLFASTCAIMLIAANNG

>contig50432 Frame-0R

MYRRLSWGSSTILDITCQKKV

>contig51071 Frame-1R|Blast-anthranilate synthase component 2, putative [Phytophthora infestans T30-4](gb|EEY56306.1|) 1e-101

MTTRVLLIDNYDSFTYNIYQYMAQLGAHVEVKRNDQITLDEIRDMKPDRIMISPGPGYPK

DAGISCDVIRHFAGIVPIAGVCLGHQCMFEVFGGKVDHAGEIVHGKASVMVHDGKGLFKG

MASEFKAIRYHSLVGMPETLPDALEVTATVKGTNIIMGVRHKQFKVEGWQFHPESILTED

GLRLIQNFLEL

>contig51707 Frame-2F|Blast-multidrug resistance-associated protein 1, putative [Phytophthora infestans T30-4](gb|EEY56177.1|) 1e-14

MQLNPCGAAIEDEQLWAALRAVR

>contig52614 Frame-1R

MNQGASELPALAAVKVASAPDARSAADVNALDWSESAENSHSRDDEFVSLPQGPSLSYER

KIRLHKYAENRARSCLGLLSETSGALWKIHDCKNDIGVYKPSSDWSESVSAKAVVFANAA

FPNVLKTVYDLKTSDKFKLFMRKV

>contig53503 Frame-2F

MEASQMPIHSPVNEIASVLQFTSRCCILPETLQSRPRGVSQYVLCSIDDNRFAICRISAT

SLSRTRQVFVDESITLQRDSKYFKDVQTSLVAHNTIESDKNIALENSDLLWISRNAVRSA

VAVTLELLPC

>contig53576 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53356.1|) 5e-16

MFGVSSNDWRPLVANFQRQVKDKSTSLVTEDIDHVIRVCLQHDRVREASDAICQGEKHGL

VATFESHFQVCYSW

>contig53954 Frame-1R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY54200.1|) 2e-53

MCAKKSGWDRDRSRLERQKKDLECQLKDAKHTLTGFSQAIEQLEIKMQRKGAEMQTRCLE

LENELSEKLDE

>contig54784 Frame-1F

MKLELHAVVAGQIPSRIFRSLPELRTWPFARTSVQARKSATTLWHLRIPSVQSLKTLRSS

AYAVVHGRTSSASYTPTPFRGFSRHASGNSVEINILKLQEHLWYTP

>contig55985 Frame-0R|Blast-thyroid receptor-interacting protein 13 [Phytophthora infestans T30-4](gb|EEY65004.1|) 5e-67

MTAMVFSDLKVNPLVIAWNRVVLLHGPPGTGKTSLCKALAQKLSIRLAYRYPNAVLLEIN

AHSLFS

>contig56452 Frame-2F|Blast-cellulosomal scaffoldin anchoring protein [Trypanosoma cruzi strain CL Brener]gb|EAN82436.1| cellulosomal scaffoldin anchoring protein, putative [Trypanosoma cruzi](ref|XP\_804287.1|) 5e-11

MASIPSRSTTTNTFVSRSPATNAPVLTNPPPVSTNPPVSTNPPVSTNPPVSTISPVSTTS

PVSTSPVSTTSPVSMD

>contig56908 Frame-0F

MVLSSVARVSSRSLQGIRSQTFRLLSTS

>contig57147-1 Frame-2R1

MNFNIAIWPTYSLITNLCLFFRKLMTQAPCAHQVVKYSV

>contig58546 Frame-2R

MDYATVKFCISGWIDAICLIDKYNASLLESVALPLAKDDSVLSIRGEA

>contig59079 Frame-0F|Blast-callose synthase, putative [Phytophthora infestans T30-4](gb|EEY63082.1|) 6e-28

MVLLTQAFAPQLINGTFASKFVREGESCYVGQDMTPPFLYKLKYMAFW

>contig05776 Frame-2R

MRNGSSNGNPENYVTIDPEGRSPAYNGDNSVINIGVDAKARFQNQTNLRRSELVQKVVAN

TKGTTFFRTSVMKKTPFLNKFAWQIIFPEVKTFEIRVDATKSPPMLIYLNNGTWDAKYET

EFVFGTWYNIGIAVKAATTGTGSVLDFYMSEGNEDLELKVTHEVVSEFPKDYEFHFGPLV

YFETETPPTMADNQDILSYNGVMILDEVETSGSEKGVQTSGSGKGEQTSGSGKGSTYGPM

VGGESDPVIKPAKCARK

>contig06269 Frame-1F

MTVSPVWADLGERRNPTLAELQAFTGYATCDDPGTNVTCFPVSGTDGLSLKPGGVTLTGL

ASSLSSDYFNAYVGVTRTYFPITSLNKTLDFKGVTLHRFSTLRDTFKFTSTRDIGTGVPV

DGLHQLSFIADFLAYLSGPFFINSHPSLLEAVDMSTRDGTKMTHDSMYNPEGELV

>contig08344 Frame-2R

MPLRSSLFDLGSSRVLTFGDSRRNVQHPIGDDAEVDTNLRPELVKCPEFLLTGLELEKRT

TLHILHKKGRRFESPWRPLFVGIYARTLFYFTDLGGWPRGVVPLVDAEVKAVDRIFRHGD

AVSGGDDCGPCWKVTSSSGRVLLFRASSHDARMEWVDKLRQATGLYKRNSMDGKAALALV

QRLSRSSSSVSSTSSVSASSTVMLQSPRHRRRKLTFEHDLEQSELLVDALHVIGKQREEM

GELRRRLEELETMRDQLQHMEDEKRSVDIQNKTFRTKKSRSDGEKLFFEECWANAKKIDL

DTMLDEVAIELCNGYRGSTISDTLSEDDTPSSEGEDDGAINVNVKACNQRKEKIAIASSQ

SFVNESNEMVSYDEDGKLIDVELGIIALEKSERDSTIKKSSLLKQKSKSVEKFSSSYQMT

VLLPKSYELGNVSLTKTEIAAEFDFSLLINRDPESVLARENVENDFYAFNLKKSHSCDGS

FDSAAGVGNGFLQQQTMELAEIARNLQSSFHTESKILMAPSKVSLNDPEGQPSFSDVTDF

DENQISSNGSSESIFSITQDDLCYSEEDGESERLSEFEA

>contig09246 Frame-2R

MASCSASSRETSSTQGTTASTAQVSAGILSVDIIGARNLPPAVLGSLLKWTSSYANPYVV

LSLDQERFVSTVKLHDLNPSWKETARLNVPLPTEADVFQSEELTRTLDKTYPLGKNKGGY

TTRKHTGDALAAANAVLGYRQYCPCTPELNVQVFHRSDTPRDASSSLRDPLIGAVVVPLL

SCLMSNVSSARGWYHLVNEDDENVGQLQLALTFDVSATSQFVEPRKGDLMRLTGFGGRHY

YAKILPISARLEVLEVFQDQVLVETRSPEDWPLRFELHRNLLHIVHRPSLIHDASTQLQT

HVMRLSELRVITSAHHLWHLVPETRRQQVENSMAFVAFFGAQAYAIVIQSIQEGWHAGVS

SGVQTLKTSTKDAYGQLKHEFKRVYWCAPPHQVLETEGYDDNVIDCGPRMHRGRIVSAFT

ADCVAVDDDLDESDLECYQDEDAVPEQLICPITGCPMLDPVVAADGHSYERDAIQKWLTN

SAISPMTGMHMSTKQVFSNFTLRQLSEEVQATRRQQVTRRRSRKPSAEDYEGKETSDLSG

>contig15096 Frame-2F

MSTTVIKRSCHSQMATPVGSTKPRTQTDLELMDVNLNKHKVENVVDSKCDMTANGNLKAD

ELLLATVDATTKCNASETSRILVDQAKRRLKIQMQFVENARKRIENETHPDMTQKMQLLL

EERDRLLRVAKQRGDYFEHGTSVIFNYECDEANAEYELQCGRLRQDMLDEINHEMEILHD

QQKGGHTHARATTRKTRSTRNKPELDLSFVHDTAQKIKKRAGGYVFQPLENRLGQLEIDQ

DVRELTTSYEATKKRRMEFDT

>contig18723 Frame-1F|Blast-triosephosphate isomerase + glyceraldehyde-3-phosphate dehydrogenase [Phytophthora infestans](emb|CAA45835.1|) 0.0

MAFHQVFKTQARQMSSSSRKFFVGGNWKCNGSLRQAQELVGMLNTATIPSNVEVVVAPSQ

VHAATVKASLRPDVRVSGQDVWKHGNGAFTGETSAEMLTDLGAEYTLVGHSERRERGETN

ETVAQKAAYALDKGLGVIACIGETKELREANQTVAFITEQLDAYAAEIKDWTNVVIAYEP

IWAIGTGLTASPEQAQEVHASIRAWLKEKISREAADKTRIIYGGSVGASNAPELSQKNDI

DGFLVGGASLKPDFIQIINAQNPTTKLGGAVNVAINGFGRIGRLVLRAAATNPLINIVAI

NDPFISTTYMEYMLEYDTVHGKFNGSLSHDEQHIYINNKPIRVFNELNPANIKWSEEQVQ

YVVESTGAFTTLEAASAHLKNGVEKVVISAPSNDAPMFVMGVNHELYEKKMHVVSNASCT

TNCLAPLAKVVNDKFGIKEGLMTTVHAVTATQKTVDSPSKKDWRGGRGACFNIIPSSTGA

AKAVGKVIPSLNGKLTGMSFRVPTADVSVVDLTARLVNPASYDEIKKAIKNASENEMKGI

LGYTEKAVVSSDFIGDSRSSIFDADAGIALTDDFVKLVSWYDNEWGYSSRVLDLIEYMVK

ND

>contig20531 Frame-1R

MHVIQEMGEAVFVPSGWYHQVQNLDDTISINHNWFNGYNVRELWRFFKAELAAVNQELED

LKEIGLVGYAFDAKCQEVMLANTGINYLEFRELLYAKAGKLLKEIFFVESNSLLPMGNDQ

LRHLKYNVFFKS

>contig20629 Frame-1R

MDVSLRNVLSQCWFAEALAQVLERAFTQCHVEKYMLISLGDAVIAEQGTVLSKLVSGFLR

RDEATDFIKGGCYTHVNDIDTLQQWLTKQAATGFDSAPGTFFVVYAPCEANTEKVTSKLQ

ECFEDIMLLVLLHPARFLGLRTSNDATESSSMYYLDHLGDTKLKLNTDWHQALSYIRHPF

RLLRHQAGYHFVAEFIRLILEPKPMEMTPKNTFGPARLTMFATIKQVPFQLLLLILRWSY

FHPAVVSACAERLNRQMHLIPQERIRLEIAALQRSEEQIWRDLYPSIEPQRKLFAADSNR

IQGALSNLPTIPFDINVSKLVRLSECRLWDTQKQFYKDHGIRAWSSGQIPYGISSTSFLA

AAYARLAVDFLLSNADSIQTSSKSTSSPNCFVWEAASGSCKFLHSFMVHFTEIIEAHDVF

KRRLLVPLVVATDLSEDVLTSRRQMACFRPYMERKQLDFAFFDTADFVNEGPVGSHKQNT

LYLMNLQRQWLVGRDGPVVVVGNYFLDSLRTDVYAVSLQQNLTHKADKSAVGYNVDHRDG

DDYCLYTAFLDKHTSSIADMNVRLFPTPDFKRQTIYKNGRLNAMLAEILDEFYSRDTKGA

NSKPISTSGLVLFPVEALELFLSLIDSNSSDTIYPIAFLTGDAPFSFRDAISSTCIITSN

ETPEGQANKEYLGLELPQLSPHPDCFCLPVDFEIFDICFKYLDRSTARVLTNSMYCSAPG

NDTFGVFFATFKSQTLDECASVQNVKSKMQHLSFSHEFARFTPTDNDLLWGMLKFDDSAH

YFAEDTLVALLAQSYWDYDLFVVLQWELLRRLKQHNHLDSKRLRRNLIESGTKSWRTFYQ

LEQGCKTIDTMRNLQLDRWFYG

>contig20694 Frame-1R

MIGSNCHPGRGGVLCLSCPGGSYSPGRFSKCLPCDPGTNSDHIGAEKCDACPRGHFNLEF

GMTECQACPLGSFSAKEGSIKCALCPPGSFVGVKGSEACSLCPSGSITVSSGNINCTLCG

IGETTSKAGATECHSCRNKPEHSEFNLRGNCSYACSKGRNGLDCKTPFERLMKPIGGPIG

FAILLLTITGLILGSWGYISVRSSRSELHRYAHYKAQRLRDELSLATLTRTLTPRLIGQD

LKNHVARLYFAGDNHLKNAWRLNPYFLPSNLREIIEEETFAEFASTCNKLVEWNPSNWEG

WLYFLLFVTVPPISTLFVRKRQLHRVKSLSKYIVQYGGRFFRDMNFRVHGTQLKLGFSSD

FSLGYLDVMISQSRSSLSLNLITFQAV

>contig20760 Frame-0F|Blast-aldehyde dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY59138.1|) 0.0

MYGPVTEIPAFPDVLKQDTHADVVALRASFATGATKDMKMRKSLLRSLKRLLVENEAAIV

EAVWKDLHKHPVELFATETALIQAEIQEFTDYIDDWSKPKPKLTNVANLPGLSYIRPEPL

GVVCIIGTWNYPIHLLLMPLVAALGAGNCVILRLPGEDTTRYVNNLLLQLLDRYMDKSYV

RVVYGGVDETKKMLQEHYDLIFATGGTFLGKIVAQAAAQYLTPTVLELGGKSPCIIDHTA

DLKLAAKRIAWGAFVNGGQTCVRCDYLMVDEKVGDQFVKLLEKEINIQYGGANVKESDSF

GRIINKRMYDRLAGILDKDREHVTYGGDTDAMQLFIAPTLLNFRSDFDSFASSASMSDEI

FGPLLPIYYFSSGDLSEPITFVSKREKPLALYCFSSNGKNKERVVNETSAGSMVLNDLLM

QLSNSNVPFGGVGGSGMGSYHGHFGFKAFSHYKTVIYKNSLLDLPQRYAPYTQSKKLILS

IVLYPLSRLHMRLLKTLFFGLVLAAITSIIGHYA

>contig20980 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61369.1|) 8e-81

MRGTRLMYDRWLQSSPLLTKGVTSAILFGLGDQIAQRIDKFDENERDGCEAYNCYGLQRT

AKMMVWGGFVFAPVGHVWYNFLEKAVRGTGMTAVAKKVAADQVVFSPPLSLAFFTYSGVS

ETLSLRNAVDTAATKLAPTLAVNWTVWPLVHVCTFGFVPLQYRILFINVVNIGWSAFLSR

MATQEDGRVSTAQKFEDYLIQQMEETEETTIVS

>contig21693 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63793.1|) 2e-85

MGGSFEYTGAPFYAGISSLKTGADLCHVFCVEEAAIPIKCYSPELIVHPLLCSDAALARI

EKSKRAEVLMDAVERIGRVLSRLDSLVIGPGLGRDASVQQIVRRVIAKTKETGLPIILDG

DALFLVYMEPDIVKGYTNAILTPNAMEYARLCVATCLLPNIDVAQAAKVPPAQLSEALGF

SVIVQKGCLDTFSDGAI

>contig22249-1 Frame-2R1

MDSCRIPTQSLQWRRMAGSFRCLLFGFSFI

>contig23664 Frame-2R|Blast-hypothetical protein PITG\_21328 [Phytophthora infestans T30-4](gb|EEY60469.1|) 2e-23

MSAQSFRLWQLPGLRKFSKSIVGLFTLVICQDEHVIFVLHHNPFIVFHISSAY

>contig23718 Frame-2F

MLDSFETEGEICIVTEYAQGELYQVLEDGSNLPEEEIRKIAIQLIQALHVIHSNRIIHRD

MKPQNILIGSRQQIKLCDFGFARAIAHDSSLLRSVKGTPLYMAPELVLEKPYHYTVDLWS

LGVILYELAVGKPPFYTDRIVSLIQMIVSDDVEYPSTMSAPFQSFLKGLLSKDPAQRLQW

PKILHHAFIQETPKEIESRLRREKENRTLPRFFRDNDNSPEVDDEKIMISSVERLGLCDD

WKMCDPKIGQQHVKPEVSNKSGNYGDDQ

>contig24500 Frame-0R|Blast-calcineurin-like phosphoesterase [Phytophthora infestans T30-4](gb|EEY65311.1|) 1e-163

MIVAVYGDMGTEANSIATNKYVNALTGKVEFIYHIGDISYADNDFLTAKTAFGFFYEELF

NKFMNSLTNVMRHLAYMVVVGNHEAECHSPTCLLSDSKQRQLGNYSAYNARFRMPSPESN

GALNMWYSFDYGSVHFTTISSETDFPNHPSNAYLSKQTYGNFGNQLAWLEADLKAANGNR

ALVPWIVVGMHRPIYTIRSCDANGVPTNEYESLKVQKAFESLFIKYQVDLVYQGHVHAYE

RLFPTADSKPIMDGVSMDGTTYTNPKAPVYVVAGIAGNSEGLYQFKDPLSPPWLAFMTNK

HYGITT

>contig25051 Frame-0R

MLSRWLPAAPRTLRNSQLSAFSLRAVQHPYNALRQYSSPSNAGGGVPGDFVCHLRDVGVT

IPGGKRLFEHVSLGFLRGAKIGLLGPNGSGKSTLLKVIAGVRQDFDGERWIKDGLKVGYL

PQEPHLDPHKNVYENIMDGMKESEMLLSQFDQVSMAMGEPEADFDALLEEQSQLQDRIEQ

LNCWDLSHEVAKAMAALRVPAAEANVEVLSGGERRRVALCRLLLEKPDLLLLDEPTNHLD

AESVHWLEDYLQKYRGTVLSITHDRYFLDNVAGWVLELDRGETYAYEGNYTQWLTQRRNR

FNMQLKSDSIRAKQIASEIAWSRDHQGSKKATKARVRKLQEMESSGSQASLRVEEGQIVV

PSGSRLGNKVIQVHNLRKQLDNGRVLFKKLSFEIPRHAIVGIVGGNGMGKSTLLNIIAGI

EAPDEGSVELGKSVSLGFVSQSREELSGRRTVYEEISGDNEFVEIGGDRINTRAYIASFN

LRGPMQEKQVSRLSGGERNRVHLAKMLLGGHNVVMLDEPTNDLDVDTLRSLENALTTFDG

VSLVISHDRWFLDRICSHIIAFEGNGKVGFYDANYTEYERQRKQQFASD

>contig25543 Frame-0R|Blast-carbohydrate esterase, putative [Phytophthora infestans T30-4](gb|EEY57726.1|) 8e-38

MIAHRWKELAYVAKFSHALQALDISIPRKASLGEKLPTCVFVHGGSWQRGDKCGGLNQGL

DEAFVRAGFIGVSVNYRLSPEVQHPEHAKDVAAAVKWLYCNVTK

>contig25882 Frame-0R

MKCYHQNSYAILCCVEIFEVCGRLNNWFCKQNFIAGSF

>contig26612 Frame-0F

MAPKSKAKKVVTSLPDFDHEPLKTKPVPKKLIDSTRFVFGVDLDDPRDAEDDENTLAPVA

KYVILAMICLMSFAVRLFAVVRYESVIHEFDPYFNFRTTKYLASEGFLEFLDWFDDRAWY

PLGRIIGGTIYPGLMYTAALVYWVLNLLNISINVRNTCVFLAPLFAANTAIASFLLTKEV

TKRSSAGLLAAAFTGIVPSYISRSVGGSYDNEGVAIFALLFVFYLWIKAVHTGSMFWSAA

CALAYFYMVAAWGGYVFIINMIPIYVLVMIVAGRYSPRLYIAYSTFYTLGSLMAMQVPFV

GFNVIKQAECAGSHGVFVLLQVYGFVHWLRTYISAASFRRLVLGGAAIVVSGFALALVVL

QLMGKVQWTGRSLTLLDPTYASKYIPIIASVSEHQPTTWTSYFFDLHILVPFAPVGLYFL

FQNLTDGGIFVILYGTVSWYFAGVMVRLMLTLAPIACILGAVGISSTLCKFMGVLARPST

FVVSLDGVQSVHKLVALSVIGGLLMMMLSYSFHATYVSSMAYSSPSIVIEAGRTQTGERV

NFDDYREAYFWLRQNTDANAKIMAWWDYGYQMSAMANRTVIVDNNTWNNTHIATVGRALA

STEEDAYPILQSLDVDYVLVIFGGVTGYGSDDINKFLWPVRIGSGVYPNDMPAERDYYSV

SGSFDIGPGGSKILHNCLAYKLCYYRFGEVMTDYQHPPGFDRARNAEVGVKNIQLTHMEE

AFTSEHWIVRIFKVKKQPNVEPTTAVKTARLSAAAATEKDISKERTRFLGCTRAEDLLGN

DRVYAGGTSGANYNLALFLAKEKNKRYFAIARVANEGHAFAFNKLPVNIADLDGNDEGCT

RPCKDSKSHVCGCADGGCTEMNVDPGEGQEHNRRWAIYERETV

>contig26667 Frame-0F

MVIAYLMKLHSMTFEHALAFVVERRPMANPNENFRQQLQEYGRHLQRKVPKSKETRSARG

PAGPQLPSSTTFEKKVLNIGPHLPPGFTKEADSDNCGDGSDGIDGGDGQPNNAVDKTVSE

SQLSSQIKRIRTNEGERPSKKKK

>contig28027 Frame-2F

MCELQLENAESDQQRENGHETSMTAALSLVSENFGAAAHYIPGAIAMMSIPAYLLILTRA

KRWNGEIIKKRGSIHRRRHCGGSGSTKRKRRKARK

>contig28474 Frame-1F|Blast-peptidyl-prolyl cis-trans isomerase B precursor [Phytophthora infestans T30-4](gb|EEY60785.1|) 1e-142

MNSVRENTRNGGDSVRRRHDTEFASRLLDIFVVWPTCHFSVAIMSWLGRPSQRLLRSQRY

SRPVLFCKTAPFSSSASNAGRLSSLTSLQKISLGLSAMFGGGYVIGYAFGPFSSLEDLFG

VKAVSGAPAYTGELIVTDKVFFDIGINDDYVGKIVIGLYGEVQPRTVENFRALCSGEKGA

SRAGPPLWYKGSHFHRIIPGFMIQGGDFTQHNGRGSESIYGRRFDDEDLSVPHSGPGTLS

MANAGANSNGSQFFICTGDTPWLDGKHVVFGRVLEGMDVVDIISSCGRRSGKPNAAVKIL

NCGVLDANTTTQRNAEEPIAPKCLTRDEMNERLASLRAVESNFKVQKNDIDATLYGQVMT

EIKHEKKRIKKKLAELEAND

>contig29763 Frame-2F

MLTRSRSKASKQPVFIDDNWNDAYIQAKDEQIDALLATSQRGWNDLEEENSEAFDSDSDE

DAWHSDSDESEDNDEDWLERPHRLPKYTFSQRWVAGGGLLQNVCWTLAGVAVAPVLLYAS

LPRYEKPLWPLQSPHFVGFLSKVSLNVLSLTVAAAALYGALCGVEPLAMTNVLQWRHIEL

EPLTQCRENLLRGVRDFFQNAVDFVSGWPTAPLRQSDDGIRTVVDSLNAPMVYELALLAA

GVLVMLTCFYRAWAKILVLLIIATYVAFNVNMEIKMQQRAAIEIYSLDPDFAFVNESIFV

AIDGHNLEVGGSVAWMPYWDGLHQQEAHVCPKRFPQQLKEGGVFVTFSQVDEYVPCYLSA

KETASAVLIDGEIQPSNSFQCYENVRLRVKDHRSVPGWSLHLPQQKEEET

>contig30303 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65074.1|) 2e-16 NOT\_ORF

MEASGAFLVHHFTSLYLKAGHRVCFVSSVNQCP

>contig30541 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64537.1|) 2e-17

MDALLSSWYDATAPIDARVRENPLVFAFTGDISGLSDFKRFKNSESKSFKSVSRPWDHAD

FMARVSSFSIASWFAKPDLINPLECARYGFSNVGLDKLQCNW

>contig30879 Frame-0R

MTDWLTMPSLERGLNQITTKHSNNQVESDGVNVFTKAQWQALKLYFSILDLDGSGLLMEE

SFVVLLAEQDSDAYATEDELSLLLEVMDCNADKLITEQDFLFFARSAMMRWKKDSSGANT

DMRRPK

>contig31195 Frame-0R

MLSRENLPPQVAQRVARELRKLVMQPLDGIRYLPQREEQLSEIYAEIRGPEHTPYEGGYF

KVKLTLTVSFPEQPPRGVFLTRIFHPNVSQPAGDICVNTLKKDWKVTLGLAHVLQVIRCL

LIVPFPESSLNDEAGKLFLDSYGDYARRAKLWTKIHASSRFTADVDSEKMSGKTITTQSA

TSRHSNSGNQHKRPADNGPSLEGMEESTKKSTYVSDVENSLKKKKNNKKKSITRL

>contig31964 Frame-1R

MATGSYFENQEIEPLADPTLTENSPVEQLALTTNSTLTTFPASDAPTDAVLSPATIAGII

VAGIVAVAAVAVFASYRKNQQKRTRRDSIEII

>contig34840 Frame-0R

MFQPTCFDKELPSFRCLYSVYTRCFCRVLSI

>contig36024 Frame-0R

MGPSKIIFWCWCLQVFLADADSPDCITCKKILPDTKIKGRMNEPADDYVNLPT

>contig36099 Frame-0F|Blast-lysophospholipid acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY61084.1|) 0.0

MDSVVTLLGRLQPYAELATPFKFSYLHGQVDQLSASIGLGTDQLCYVLCLFAAYPLAVVY

KLLPNGSLKHIFDILLGVCMAQFVLSSGWVHSFIASSVTYILVKFGPPHYAPGIVFLFNM

LYISSSHIYRLYVDYMGWTLDFTGPQMLLVLKLTSFAYNYYDGVVDQTFQNKGSHLSADK

KRVYASRQKLAIYEIPTPLEFFGYVYSFTTFLAGPAFEIREYLDVTSGRKFQFNGKMKQP

SSVLAAFSKLVVGSFLMAAFAMYAPMYPLSNLHDPQIAALPLFAQMRELYITLIFCKVKY

YSAWKVAEGSTVLCGFGFEGFHEDGTSRGWNGVSNMDILGFEFSQSIRAASRAWNKGTQN

WLERYVYTRTGNSLVATYFISAFWHGFYPGYYFFFMS

>contig36943 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59830.1|) 5e-08

MGLSELPFDEPVIIWSVTKKLSLQNPLGSKKARCLSGNRDIYNQLRHILRLFELASNVRF

ELIEWRLCRRCWKAMLQRSFWDSQGVSKRLLL

>contig37009 Frame-0F|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY58784.1|) 1e-126

MMMRRPPGDRMCSAVTFFPFYAAHRMLSCLGYSQSVRLKSGRTVIISSEIAQGGFSFVYK

ARDPENGESFALKKILCQTDEQVHSTKAEIQAHYNFKHPNIMPLIDYAVISTQTDILTYY

LLFPYMENGTLRDMIDTAINQDVRISEAQILDIFLKICRAVAELHIKVPPLAHRDIKPEN

IMLSDEGEPLLTDFGSVTVADVTISGRCDALLLQEQAACHSSMAYRAPELYDALGHSHIN

SATDVWSLGCLLYALAFGYSPFECSFYDSGVVRVVECSYLAVIGSIKFPKNCPYSPKFCN

MIRWILTLDASARPTVFDIIERLHSLND

>contig37456 Frame-2R

MLFYIGRKLSGFAMSNAVVVSKKDEYMSLVHDPLIYAIVDFTRTSLFCT

>contig38170 Frame-1R|Blast-protein transporter Sec24 [Phytophthora infestans T30-4](gb|EEY59671.1|) 0.0

MNPFVQWVDNGRRWRCNLCGVSNDVASSYFCHLTSNQMRQDYYERPELSSGSVEVIAPSE

YMMRPPQPPCYVFVIDVSATAVASGSVQIAVNTIKAQLDNLLGAPRTRVGFLTYDNSIHF

YNLKSNLKAPQMMVVPDLDELFIPIPDELLVNLSDSREIVEMLLETLPTIHQNASSAETA

LGPAIRVAFKLMSSIGGKMLVFQNSLPSTGIGALRNRENPSLYGSDKEHTLLQAADTFYR

TNAIDFCRQQVSVDLFLFSSTYTDIASMGSLSKYSAGQVYYYPSFNAERDGEKFSKELAH

CLVRETAWEAVMRVRCTKGMRLANFYGNFFLRGPDLLALPTCNADSTFAVELTHSDALLT

STTISVQAGLLYTNSSGERRIRVHTVCIPVTKLFAEIFRQVDQDALCNIMAKNALEIAIK

TGLNSGRSRLQAQCMDIVSAYRSSGAYGAKQASGYQLHLTESLQLLPLYIMSLLKNSTLR

GGTDLNVDERAFLQYELNNMPVELSQAYIYPRMFALHNMPPEAGLPALEDLAAENAHSAT

AKSVVLPPVVNLSIERLQCDGVFLLDDALTLYLWVGRSVSPELLNSLFGIPSLEGVDC

>contig38871 Frame-0R

MKLAACEAARQDIATNANGVSATWEKERQTLKAQLELETKKCTQLKDFNARLMSGLKSLK

KENNELKDHAASALKPAASLGKVPLPSPPLSPQQHPAPTFAAPPTKSAAALTSLSSSPQL

EVRSGPAAVQSSIVESKAKPVVPSVGVEATSAASAPPAPPNITSPSKDLTTVSTQADKTT

AEVVSTAESSSTPPPNVPAQATTFTSVAPPLPVLSAPAPPLPVLATLALPVVASRSPAPV

AEPALSIPALLKPAPTVPTLPKATPTVPAPLIPAPIVLPGAGETGEAGTNIALPAPPAVA

PQKAASKSSSDESAAMTAEEQLRQFALRSIKKQVGDATRFTLTNAPASIAEAKLATATAT

ENKSVLETKEQLTLDIDSSIGAFGSGGPSGLVFGKPGVSLPIPSPASPAVSQSPHEPLSG

ENVPPESLRRSQRLARFGSDATNSAAASSIIGGGSTTKRPLGGAVEGTLSVQKVAKTSEY

QTTKTTTAITTITNPSLPDSESKQEEDTSPGKLKTTELHSTPPST

>contig40119 Frame-0F

MPGVAGCVLHRNSTLNQLSN

>contig41840 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70257.1|) 1e-46

MFLSHEIGHGFGLPDFYGPETKPSGEFPNSIMMAYSSTTITPSDGWLLRRILDHVRSRYE

F

>contig42456 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66019.1|) 1e-33

MSKAASAGFREFCGGVQHAVSLHQILLFYIQSRLVCVSSLKCFVLNGLIFLGSIYFFDKA

VIPVIHMFGELLYRSFSYG

>contig42650 Frame-0F

MYLSNQGLQLNALSLEKTIARVGKHGGFVTSRKKLLHEIVQSDLQFRFEQMLLVDKGLFE

LACQAFHSFMRSYATHSSDTRNIFHVRSLHFGHVAKSFALRDPPASSKLRDTGLNSKKGS

LQKRKERFAKQQAVVAQKQKKVRDEKRRYAHNVSEFAN

>contig43024 Frame-1F

MKGLILLGLVVAAASADEIDPLEAKFASPSLSANTSMLANSSLPTFSSQSEFASTSVSFA

GSNAFGSGSASSNVDTTILDEEDTSDSAASNSTDNVMVGDSESGSNGSVEIIIESDKSTD

SEFSSSESATGVPPFNSYTDSSSGPSYNSSSSSEAVSIQLATLQASTFIFVAISVLM

>contig45080 Frame-2F

MAFRKYVLDHHLNYSDFLSDGETKYKMVTLAQANCYHGDTLGVMNVAEKSVFNEKQHPWY

RPEGVFLKVPTIALRDGKYVISIDSTIAGIAKSQELPSLNAAFDKSRDESPLAEAYRTHV

ARMIDETEATKNLHVGAALIEPVLMGSGGMFLVDPLYQRMLVQECRTRRIPVIYDEIFSG

WWRLGVESARDLLGVDPDIACYAKLLTGGVVPMAVTLASEEIFNTFYADSKGEALLHGHS

FTAYPIGCAAAVTALDMYQIFSNSSSHTVDITRVYWNLDVLTNLSTRPYIERTFAIGTVA

CVELVSESAGYASTEAAELIQMLRKNGVYARSLGNVLYMMCSPLTTREDCDKYLSTLIRQ

IEILQTK

>contig45189 Frame-0F|Blast-putative dolichyl-phosphate beta-glucosyltransferase [Phytophthora infestans T30-4](gb|EEY53237.1|) 4e-19

MLREIILIRLCYSVGIWKNTDGGFRLANRPAGL

>contig45303 Frame-2F

MTERKEWTPPCHAACSTCAFSTLFPVFTYLLLPAGVIALVKLGEAYLLLFLGQLLLAIGA

VEWSWLAFRICQRLLLAAKLHEDSLTTFSADRAAAIQEDPTHLTLQTHTQHASDEEARRL

RALEDQSLRREVPGDSYINLLNETIRPKSFAIAPLTDKICSGRWYLAAFFLATVGAAVSV

ALGYAMEYRVFDSSNPTSGWKMMVGASAEAAFVSIFCGSLAPTGADAVVLVVYQACVLAA

SMNAYLKLQLNVIASIAQVDPLFTILAGAIIIILFRVVTSKVVMHSLLLVLCDVLGLVCI

VAPLIAFADLIDQAMSQSFKNQLALFLLVVLAADVGDCLAKYLQLHRPQALNCCHRIEFK

TEASSYEVEALAISLTCGAIMIAADWLGMGGADLTIIEVVVLFCSIALGQWCRLWMAHIR

QMAKVSTSAFYFPEGSRTCGVLDRMTVFLVAIIVYYP

>contig45541 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69886.1|) 2e-29

MYEKEFPLPLCQIERIIQNMKHALYEAYWNHANLAPSTESVAFGLFVVEVATRFMRVLYN

RCSRQPFCNVTSWII

>contig45879 Frame-2F

MMRKESLGVPHSSHAHLHSYVGACRESARLSRFHSTISYNDTSRFSTSNDSSKQKLK

>contig47833 Frame-2R

MDVIQAKDPQFALIINLAKKAFREIQRHGYAQGYSLAGFDEREHMQGPSGGLTKLELRTR

KDSRSGALPKTGTGTRRLEKEGDETPLYYEVHLVLDAQERLSVIAAWELSEKDPPRGQNR

QQIMRLSIQPTAAMLERDLSYNTENSSVATWLLAGGLAMIAAGVLIMYNTRRPMPERKPR

RRSSDIWELVDKNDMPITTRKPQEVLESDQLGKKND

>contig48546 Frame-2F|Blast-Phosphatidylinositol-3-phosphate5- kinase (Fab-like; PIPK-A1) [Phytophthora infestans T30-4](gb|EEY53276.1|) 0.0

MRSDILNPRILLIASALDYQRMKEAISSLESVACQELEYMHIVTEKILTLNPDIVMFEGH

VHRVAEELLFKASVSVVKNVRLLDLQRIARCTGASVLTSYDHIDKMSDVGIIGTCKRFYV

MLSDQEPKSARKIALKANVDGTYVVEDGGCYSHQQTKRIQRQNIVFEGGITSKGCTLCLR

GGNSDIFAEVTNVLIAIIRAAYNMRLQRSLLAAYGYIAPSQNCERSVAEEWFAKSSTSLY

ISLKSNSLSMRAALKEAQAMCKWCKANTHFNNISSLRVVHGAEDAEEGSLTSGTVVQSRY

TNWCTCGAKSSKSLRDRILFSTCWSILEGKTASKAEMMCIDFYSSNDMSVGNFFDSFCFS

SSKVEFKRAFLSSKLSISHDTGRLIVRVKDLSEFKDTSDQLPPAEFLRGFTYKSVLQLIR

SDEVLMWSRNLSGE

>contig50433 Frame-0R|Blast-phosphatidate cytidylyltransferase, putative [Phytophthora infestans T30-4](gb|EEY55709.1|) 6e-15

MLQPSTAVQTSPLTSSYCSLRHAPPPPTHTSRWPAFFRYNVVQRTLSAAVLAPSLTVFLW

LSPV

>contig50819 Frame-0R|Blast-CRN-like CRN4 [Phytophthora infestans]gb|EEY61565.1| Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|AAY43398.1|) 5e-27

MNEPCEFDVNIRNKRLTDKFIENNRNRKVLDEAQVTELHESMSLTQEPCKFNVDTTFGDV

DGSALAFIGVERPFNRCLNLQARVARVLALKNGWVEESYDFPDFWDDVDLDNKMDIFLRS

LPEADI

>contig52615 Frame-0F|Blast-integrator complex subunit, putative [Phytophthora infestans T30-4](gb|EEY65797.1|) 1e-118

MITRSSFAVTVSETQSAMERELVKVISDCIGSDGKVVIPIYRVGYFHDLLTILLERLQQI

ENATGKAAKCPIYLSDAAMEYPSRFLPLLSRTCTPTIKNLLREKNPHALNLQAFDWKLLH

QPGPFVLFTGPANISQGDSLRALKAIASEPKNLIVLSEYCTPGTINYSLYADPARKRVSK

RLGVSVECGVHYQPCGDEVDAKSIVQLVSCVAPSQVILDFTAAENLKFVK

>contig53577 Frame-2R|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY53674.1|) 2e-19

MTSAMNHREIWLASLAQVHGTTLTLSHGVSAENILVVA

>contig54077 Frame-1R

MDVVTNSTRFAWTLSCETMKIVLAVHHAAVIFSVGKMLNFLMLCSRL

>contig55236 Frame-2R

MDSSKLADPFTLVQQDMVNVNDSIKRILGSDHPVLAAVARYFFEHDGGKKVRPT

>contig56398 Frame-0F|Blast-UDP-N-acetylhexosamine pyrophosphorylase, putative [Phytophthora infestans T30-4](gb|EEY65532.1|) 2e-15

MKVLAVARNDEFAPIKNAPGAASDS

>contig56453 Frame-0R

MDSTTTEPASLIATLLKKHARTSQSQQDRRPTTLSRKLSNNVFPALSFHFNLSNRILGR

>contig56909 Frame-0F

MVLSSVARVSSRSLQGIRSQTFRLLSTS

>contig57146-0 Frame-0R0

MPSLYHVLHSGPYLPPSTKWFA

>contig57740 Frame-0R

MLYHLLAQQAFRLDQTYFGYPLPPRHSKCILLSLRIRNPPLSLNRD

>contig58532 Frame-1R|Blast-3-phosphoinositide-dependent protein kinase, putative [Phytophthora infestans T30-4](gb|EEY58380.1|) 1e-91

MACMVFQLLVGRPLFRAENEYLTFQQILNHPAEEFAYPSGFPPVAQDLIDRILLQDPSKR

LGAGTDEDGMGYKALKAHVFFEGIDWDMVGSAQPLYMPEIGQLPPTDYDGAKEDWLFAGV

ATELQVSSGLV

>contig58547 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58210.1|) 3e-11

MMTGDHYQQCEPELAAYCCKCENDNPVAIRHSCRKCLGGYGHSLYVTRITARQYGFTGKL

SEVYESERHNSCIQNKWCEWG

>contig59333 Frame-1F|Blast-Amino Acid/Auxin Permease (AAAP) Family [Phytophthora infestans T30-4](gb|EEY68993.1|) 1e-65

MQFGSETRDNILLNFSPAYVAQYPSVRAPLLLGQLCMALALILTTPIAMWPFRSCVLSVY

LRVKNGVQTPSHKATYSEYVWVTVVGLSLIVTCSIFVPSVKIPLSIVGSVSGSLLIFIMP

ALFYLLQSPGPICT

>contig59614 Frame-1F

MDTTVSHVDVSRKSAKRWQIVDALSGVLSADASVAQLGERQTEDLKVPGSIPGRG

>contig03885 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64112.1|) 1e-37

MATLSEDEQELIHRDREVHPECFYSTALSKSCRSINGDSKCEIIKKIYRQCPNSRKELIS

NRTEIMEDEHGGESTADDFDDRERMGPIKGGEQFPGAFFQQ

>contig08035 Frame-1F

MPGVLPGVTPGVNPGVIPGVEPGFVPGEKAAGPNAASGLSDKTFEVPSLMLRKHHQHKKD

DEESEREETIVAKIVVTGNSTDLLNMFEVAPLHSRRNDGLTLHLKNENAYGKGYVQTQIF

LFEKNLLRRVTTAFAGDVVLNDDVVMVRDTEADVSFACVGDGNLYFESKVNATLGSLEVE

VTGSGVVQMKIPFMNLDGNLNVEVAGSGVVALITDSFAADSVKTTLSGSGNIVMDTNKLL

LQKLEASVYGSGTSSFATTGSVDKETLKLSGSGQLLAGSIVARRSDVEVWGDGELFVQVT

DKLTVSTSVWGRVGYVNTTPSNIKIKGWWFWREASSIVYSAAVNKVVIYEPAVVPTKRPV

YFSIETSKSALSNDPDYVIVKTEQKQADLMTMSLSSVQHIDESQGLFYAIIGASVMVANV

VAARSWAARRSRRQYTRLR

>contig08408 Frame-2F

MLTFQFVAVKVIRVYDQQKRHQMVRELKSLFVNFVPLATASIPSLAVLDTTATQAACNEL

VLFYDAYTNPDMGSV

>contig11389 Frame-2R

MPLKWLHRRRSADDATKLQSSHNEPQPLMEWTTRGHNRHPNNPTHLNDANAAFTKEKASR

LHKPRRRFTIHGLSYHQKHHENAGWSRSVPPEEVVDTLSSPYPSIIYIDCPP

>contig12447 Frame-1R

MPWSISSIMEPVSTKAEDQLVWFALYLVVYLAFYFFTSPFVGNRELLNSWTPYVYFSMVL

YAWLISAAALHTPVHALGLLDSTIKQPISLLFPFFSASFVFLIVLEVPMALFLSRITKRL

GFSWTVAHVSLARSFMNVLRNSAAISVACVALIMHCDATYDCAASPEEPTTYNSHACAQI

FSFLQSDDVETVVPASYGGAVLIWCMGMLLAITNLVLERYSGIRMIASFGWFSNQPEDDE

MNERSENGHEVVPPEQNLPMVPWYSMLLFDTVFDLLISLKIFLGRFDMRTMQRALHPNDE

EYCFDHLADKNDVWLDFMADCGDGFNSSYQIARLLAQPQLEVECNVFDTDQQRTGVVDET

GKPKTKTMVRVFPRGDALVIGGDLAYPHPDDKTYETRLFRCFEYAMKPPELYHPSAISTQ

KKLPSGCSSLRQYEGPSVFAIPGNHDWFDGLNTFTRYICQRDWLGGWLLPQKTSYFSIKL

PHGWWLFGVDLALENDVDTEQFGFFERVVTTQMGPHDAVIVVTHEPRWLLNVYEDTSNVD

IKLSYLIEKILKGRVAVRLAGDIHNYMRHSLVEATQQLKRPASMRFKMPQSNVSKTNLSR

RHSFSYRVEKHFPHMTQPEKFGANDPNHQTEVSSRRERPAAHLIISGGGGAFLHPTHIPS

TKLTSNGGSYEQKLCYPPAEVSRRYAVLNVLGFRRLNWRFDAIGGVGYFVLVFSMFPRCS

VGSIYAAATHWEAAARFGQELVHVLYDMVTTSYVSLGCSIVMLLGTIGFADATTLSKRCV

MGILVSCCHYVAAFTILLVYECLFEVASVRGGLGREGEHTLYLFFSSTLPDFSAIRKYDF

FGLASLYGDFMRLCMTIFD

>contig13387 Frame-0F

MIQRRSDRKYQTVHAIRRRERSQRRSVLKKQVSMAVAQQLFYEHQQQKTLGIPLPQHHPL

HVLIANANDKTTATPNEVVSSAAPVQRTSCPLKLKFCPQSSHGNHVTPFHRSANVLPTGL

LFKREPRPTTTGSCPPKAVLKKIVPSTSTDQKNMESLMNDSFGYMPIATCSGNKETWSDD

DIEFLQTVLLA

>contig14100 Frame-2R

MEQSVGHGNEERRAFERSLNVRDSEHEGRTAANHEHKSYSLFINKTDKRVHETKLTATAT

PFAGKRKREESGEAVTTDFIAYAREHIHSQEAGEEGFSIDPSERAVEHRASKVVRREILI

ASPAANDDEDWEGNAPLEVKMEEVEAVVTYSEHFDLQPIDIILHVFSFLVTATNLQNMTQ

VSKKWRELISRRSLYRSLSSVTSEGSVNWINFKNLGIKNKGTEGTCIKCCQRSTGKILAM

KKARVFPKGEGVPYYMLRELAVLKGIKHDHIASLELISLAKDELHVFFPYVDRTLHEIIN

PTGDPNGGRVLPEAVIRKLLHQLLDAIAYCHRRGVLHRNLKPKHLLIKTSDTEVLSDAML

QVSDFALVRATGIPRRTYTMEVVTLWYRPPEILMGLRGYSSAVDIWSVGCIFAEMAQGKP

LFTGISEIDQLFQIFSKLSTPTSETWPGFSSLPNYHFEFPHWKRRPLNRLFPGISDLGID

LLTKLLIYNPDQRITAEDALRHPYFSSKAPTFLPLTPKIPMDQMCYTMSRARNGPTPEHV

ELFHAYLRQTEMDSWKEIKYLSRQKTLRPAHRSMLVDWLIEVVDVFEMCLRTAFLAVNYT

DRYLDIVMVKKTQFQLLGATCLHVASKCEDVSYIGVEDLAMCADNVYTSVEVLEMEEKLL

NTLNFTLSVPTALDFLNIYERMIPPIQKKTSMLAHYLLELALQEYQFLKYLPSVVAACCL

SMAMFTMDGFPMTKELVDACQYNWSDLKECMGELRTLYSNSPSNNLAVIKKRYSKAERCQ

VANVLPPTSFNMAF

>contig15086 Frame-0F

MDGEMDAVVAAGTRKDLQKSLKKTLKRHYRRERKDRNRKETKQQDMNTTVSTMPSYALLT

QWRNNCRDWCCHLFAYATPTHEALNLIQQYAPIVEIGAGTGYWSSLLQRTGVDIVAFDKT

PPHSNKTLFNDYHGQVPPFCTVQEGGPEVLSHDSMATKKSLLLCYPPPNDPMALQSLQLF

QGDVVLHIGEWQGDTGDSCFENELERCFRLVQEVLLPNWGNSAYSLTVWRRQTQALMPIA

WRGMSCFHCGKTRSEVATQGTSLRRCKVCKTNVYCSSSCAQMDVIGHEAEHAMRLVFLQE

PSLEIATSSRRFENEAYYSKLKMFELNDQVVTVKRNGNAMIQGHSKELFQSDVMKLDSPV

DEEISATGTSQMMQHAA

>contig15598 Frame-0R

MVLLKSLRKTASQGLRQSFALYSTERVFPNFSIYGSSSAFQVTPNAPQYTNNGNYLKTKR

VG

>contig15976 Frame-1F|Blast-elongation factor 3, putative [Phytophthora infestans T30-4](gb|EEY66162.1|) 0.0

MAPYAPTDGISKLAIDQSKHFTDALTEALKSPAGQQKVAAEKVSELIIGDANLSFGVVSH

ELRKALTGDDADAKIVASHVMDDLMQKNAERVEAYLVPLLSLFLDLLADKKPAVRPVAEE

AALTIISSANKNSTIRILPILFNGLDRTKKWQTKKGSLELIAELSKIAPYQVGRCLPDII

PQVTDCMWDTRKEVKVAARETMTKVCNVVGNMDIEPFIPALVSCLANPTEVSECTHKLAS

TTFVKTVEAPALAIMEPLLKRALAEGKTAVKRQAAVIIDNMCKLMDDPAEAQLFIPKLLP

GLKKVIETQADPECREVATRAHETLFVAGGSMEVSEDELKVDYANIHNVVVESIAANPAA

VKAQIDTFTVDYVTGICFFLVVARNFNKAVFEKEITAYFKAFIKPEEIKPLAHEIRERCF

KENKSIFIEDVDCDEGIPDLCNCEFSLAYGGMILLNNARLRLKRGHRYGLCGPNGCGKST

LMRAISNGQLEGFPSRDELKTVFVEHNLQASEAELSVVDFILVDEDLKNTPRKEVRDTLA

GVGFTAEMQAQGVGTLSGGWKMKLELARAMLQKADILLLDEPTNHLDVKNVAWLEQYLTS

LTNVTSIMVSHDSGFLDTVCTNIIHYETRKLKIYKGNLSKFVEQKPEAKAYYELESDNVK

FVFPEPGFLADIKNKGKPIIRLTNCSYQYPGTTKPSINNISVTCALSSRIAVLGPNGAGK

STLIKMLTGEVEPTGGQVWKHPSMRFAYVAQHAFHHIESHLDETANQYIQWRFQSGEDKE

LLAKETRKLSNEEKEHYKKPVNWEGEKRVLEEIICRRKFKKSFEYELKWEKCPVDENAWV

PREKCEKWGWDKLLQIADDREAARANLQARPPTAIAVQKHLDCFGLGAEFGTHSRMRGLS

GGQKVKVVLAAAMWLNPHILVLDEPTNYLDRDSLGALASAIKEFNGGVVMITHHNEFSSA

LTQETWNVENGRLLIEGQQVEDKT

>contig16036 Frame-1F

MQHSAAFGSYVESVGTIASVLFALINRCGYYDVKPRDSTIIRQAKIVYVSLLESVQKERG

EWQGFISSIDSRAPIVAEELETLSPRNLLLSKLKNNSTPSQLSVLNEILDVSLRNLMGPI

VPFELYTRQRKLLLSESLAVPPSLSALLAIRGIVEN

>contig17707 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69723.1|) 2e-36

MLAIRRATAAVRSCAFAVPAQVMSASNFKDKEKAVEAVYFNKQDEKALRKLLQKMKGQTD

VVDKKGLEDHVDHDTKGLKAIPGLNLNDEQIQALLKWKHQH

>contig18997 Frame-2R

MDFHDSEFAFQELPLRYTELDFDDLDASPRPSVDSIGNEDALDIDDGMEFHDSNVGLDYQ

LDDVVFQEADVELEIDTHSSRRVDEERTIRLKAYAIFDSGNEFIYDLVVKQAAELCHCSF

ASLSFLDARREYIKASAGIVSQVTEVLRPHSILARLMERLQAPRMESVVIFDATLDPELS

THVLVMEAPRLRFFMAVPCRARDGSVLGALIVADSTPRRTVTPFERTAVGQLADQVDALL

EDRRLRHVEHVHEMTKSTDLLRDQLVDLLSQSYSTGLQMQQNERQMELSTTSCTLREDA

>contig20143 Frame-1R

MDEGAFVESLFAPEMRSPIATSSFSRALPSCGRVKAPSNGTFVPPPPNVLLSSGMLLSHY

QVPYLPPPEDAPLFVRLHDDDMFGQMLNDQDFQDFHGFKKDPEASATKSVNSLLLEPLEL

PRNNDMCGLKDTLSTNSAPMRSSPNGYTLDSNLMPGFPPGGHHYFASNYAPYRTQSPGTP

TWLRDGSDALATQPFQKNPLPKHRILMDMAMLPHQPSPGAVDMFHPMATTLTLQSPTGLW

LAKPKNTSHTFVRGRQDGPFVDALKPAGESLASVIP

>contig21272 Frame-1F|Blast-phosphatidic acid phosphatase [Phytophthora infestans T30-4](gb|EEY59651.1|) 1e-79

MATYDRKEGQLSDVIEESDDTPFYVSDASAVHSYTAAIVQFIRNYRLLEFGSTLILYFFG

VVFANIDVHERPIRGIQVRLSESTSVWSLDPTIDEVKLSEQVPLWLLQALGIGIPIATNL

IVNYVLPLFGHVRVIPHDTRDFLLSLFQSVALSIFLTQFIKNVTGRFRPSFYDMCGWDFD

VMWDGVTNLCTDDDGEKEGRKSFPSGHASFAWASMLVLT

>contig21368 Frame-1F

MPRQKDTKRIDPTLARQPGDVGTDAEPHNVFKASGSPIISPRSIRHCLEESSFDISGKAR

KKLNGGVTLPHASVFNENARSAAAAVALQAKEAQEALEAEQVTNATLQELSGVQLVVHQM

LTTHTRTLTHLRIEQADFPNTRLSLKQVETMLSPVVSLCNALRAEHFGIHVPTVEIARTM

NDVHYWKLWESDSIDIGIFFMPPNSAIPLHNHPGMSVVTRVLYGTATVTSYDILSDTEAK

RLEAGSEIVYEDDTFSFDAVNPTKGSVSWARVSREGRFKQGTTTWLDPRRFNLHHIQASS

DIGCALLDIMVPPYDNANRDCHHFQILEQKVVHKERLFKMLESLKPDSHMELTSNDTIDA

SPASS

>contig22655 Frame-0R

MQPFVSLMSLFAAIMQAITVPENIKCKLQFQRGGGH

>contig22769 Frame-0F|Blast-beta-glucan synthesis-associated protein, putative [Phytophthora infestans T30-4](gb|EEY62157.1|) 4e-29

MRYAANNFCQRNNSEVQSYATVRAALAAGIEDNMCSLR

>contig22844 Frame-1R

MFARDTLVLLFAIVYRVNYCLKKLHLLTVVSNAATGNATSYQYCRSQFPRRSYSVECLFH

KAEYTLRIQFGSLYPIVYRI

>contig23160 Frame-2R

MQRQPKMKMQKHPEMNSMTAEAMELERDMSLSDVTKSPACAHDVAAFCQREANIVALLRQ

APNEVKPRKVVEAVRIMRLCMISHHELLTTDCVKTLSAGLSEVPRTIGSNPAINVKAFDN

DKDVGDDSSMEINIYYSRHHDGAGHALRSSDALAANNIQTGASSSTLSTVLVHPLMWVFV

VPFFVIGVYVTVARMAKFMRRRREERRIESKLYMPVN

>contig24929 Frame-0F

MCKSTSKLLGNGEERAKVDVATDATCYTEPTEKSSEGNTDSLPKKRHKLKLLLLGDSGVG

KTSLMRVFSGDEFSESMLATAGVDFKLRHINVGDEAITLQIWDTAGQERFHRITSTYYKG

ANGIVLVYDVSDRRSFDNVGYWMNNIRQYSTPVQMPAMLLVGNKIDLPNRVVTLEEGQAA

ASQYGCRFIETSAKTSENTNGALETIARDAYLMSIN

>contig25320 Frame-0F

MALLEIFSSFEGSVSGASQNKKRKTLPPVTHQKATSIKAAPWDIDKFIAFMQAVYGSSKV

SHPGSDAKYCVTFSKFADTDTGRKLLQSDGFVSLIIHECKIATKSKLITQFLQSRGYSAK

SLTSGGSREDDGDQKISSDGVFKGDAETKASGSNILRQPVVLHGFSADQNILKCLENLRQ

EYCARSCTDAAGSDTSAFLPDVHMPPWKLTYKLYCDFQVEWETSDATNASDSDMAPLEPL

EILAFKPPTRLLLHGLITLNDMHASGLAEANRWLTWITASQASSGARDKVVVSNSVARAL

RLLLYLFQSRVDSASLNEALWTSPRLYNKLDTQMQDVLSMCSGIYPSWCDSLVTHCKFLF

PRDLREKLFRSTSFGCTRSLHWFRTQMNIDDSSSDSIGGVGIFNQEITITPIPKERVKVY

RANILESAEVVMKLHAKRKAILDVVFVGEKGYGSGVTAAFYSTTAHALHTLSENQTKHYW

IFGEDDEARAADAKTFCSDGFNEIAEEAAVIRHSNGLFPYPHRKPDSKLVNRFRLVGRLA

GKALMDERLLPLPLSPQFMKLVVGESFGLNELEDIFLSHGRIVYSMYKASKQLTAGKENV

QIEDLVVEDWLDAVGLTFIDPLSQEPLVAGGDEIAVSSSNLALFVRAVLELWLDLGIRAQ

VLAFREGINEVLPVKKLRLLFVSELLSLLCGEQDIQWNAQSLLKDTKLAHGYTKDSQPVQ

YFFEVLEEMSVAERRAFLLYATGCPNLPPGGFKALKPPFEVVRRVVDNLDVDRALPFART

CTNTLHLPAYSSKNVLAKQMMFAIANSRGVIDRD

>contig25773 Frame-1F|Blast-Cation Diffusion Facilitator (CDF) Family [Phytophthora infestans T30-4](gb|EEY55872.1|) 1e-117

MSYFRGVRFFSHAKSQAMAESSLLTSPSSPNGYGTRSITPGSIKADDRFRRSQVSHAFLL

KKEENAEAQHLASTSGTTLRVQVAINVSLAANVALSIVKIYAAFTSGSLAVLSSLVDSIL

DLTSQALFWYSDKRMHTPSVEYPAGRRRLEPIAVIISATLMGMAAIEVIQQSAGALLKGL

RGHQRELNISFSTMAVLLCAIVMKLLLWYVCAKIASHSSSADALAQDHRNDVFSNSVAVT

AAFVSHSFMRLWYLDSVGAMLISVYIAISWLATGKEQVERLVGLQAEQGFIDQIRMLGDI

HHPMMRTDIVRAYHFGNNYLVEMEVILPEDMCVKDAHDISLSLQNKVEELDNVERAFVHV

DYLERNYDEHKDPTLRRDSV

>contig26501 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55342.1|) 3e-76

MPSRNASGNLRYRQFERLMEKDVIDLDQLRKLSWGGIPTKYRPTAWRLLLGYMPSKKDRC

DAMLKRKRQEYVELLQQYYYIPDTDRGSREQTTLRQILVDIPRTNADVRLFQNERIHQSM

ERVLYIWAIRHPASGYVQGINDLMTPFLVVFLSAF

>contig26695 Frame-2F|Blast-M96 mating-specific protein family [Phytophthora infestans T30-4](gb|EEY67456.1|) 1e-133

METVMQRRTRQQLAGFNGIVSNVVGNVQGSTWDLLLDKDTYDALLAGAETAYYEVDEVLA

ANGLNILETACANARLREGSEGMYVDIFTNKMLPFDFKTAAEAVWTHFRGSEKHRGNLYE

NILKDVESSSDTVAEMFAIEFMANDLAADFRVKQVVRRYIEDDRQVVVWVSTASALENSK

SPFASFGFQEKGYVISKRVRGCGNVSMFQTCCLVSPQMSEAGSFDLSTVSTFTEFVLSFM

FATITSSL

>contig26934 Frame-1F

MTVLTLIETWQQDFGHKYPSLVAGYSVLVERGYIFPHEREKKQNESEHKEATDTHHKRLN

QAKKQQRDREMKRIVPEMEHVLIEMHQVFEILVPTLDSLYLENSDEVKSVEAHETEEEEE

IEWESVNSENEEAPVDNYTHDCDSEVGVEAMDMNEIVQAYGLGSSSYRLTIEISKNICEE

SSENDALFKSLADGALCIRKRFLPILKDWEQHSTLEKHSSQSQRDVLKRIKHLQDQMTRA

LLQWEDLSQGSRHFQQEKAAVSAIVSMPLDSYKLPIKRKQYQ

>contig27537 Frame-1F

MGAETRAGRLSVENFVYDCKVYGEGWEDRKARIQSESPMGKLPGWNLFSVIVKTNDDLRQ

EVFTMQLIQKLQSIFEFEAPLLWLRTYRIVATGANIGLLETITDACSLDHLKKTFPGGNL

AQYFRSVYGNMSSSEFRAAQRRFVESMAAYSLVSYVLLLKDRHNGNILLSSEGRVIHIDF

GFILGIAPGGMFSLEDAPFKLTKEMVDVMGGLTSPSYKHFRRCLYDGLVVLQKYHSEIVA

LVQTTGQHSPFPCFQGAKLARIIAKLRTRLCVGLSRRRIQLRVEHLLRKSYNAWGTRQYD

SFQQRSNNVHP

>contig28572 Frame-0R

MRLAPLTGLHPWSDTTGEVVKVWQWRAISSARPHHLHYNQCRLSSIVISTNKKGAPLH

>contig28891 Frame-0F

MHLPPAHLSSIDTFVALRSSAMINTPQQLYSQFDGFKPPLGDTAVDFMMKVSPTYLNKTY

VEDFPSSGFYSMNLAILPPETTYADVRSFNDADDEYTVHASQVDFCSERFFDDVFLQISP

DYGCLV

>contig29993 Frame-1F

MNHIVLDLCAIVNYSPIEHLYVKNGKRCKALLETHGSQVKAMLVLQLHLMGKRLPSSDFV

TDLRMVLDHVPQLVQAAIRICAHLQLTSLVRAGIGLAQAIAQASWPEEDTNGLKQLPHVA

MAVETELRLEWHVSSIMALQALVGEKTTKKKLMDWFRIRHGWTHFQIQELVRRVESIPRL

EVKVMVHQSDVKVVLTTLNDQGTQMVAVTSRFQKPQPYGYYVLLTIDEGDKEELVQLAHV

AWQPTMLITLSRIESGV

>contig31804 Frame-1R

MACWLRSAATPTTLQKNWSKVSQWVVMMVGGMVVGWVWKKKKCVALSTMEAEIVATSQTV

TEIMGIVELLLKIGVPIQPGSILHVDNQAAIAQIQIEDTSGREKHIDVRYKFIKDEREVL

KSQYCESKNMRAHILTKTLLAPRLNELSRLVMLVR

>contig32849 Frame-0F

MRRRPSGKTPHVSRREPARHAVVMVLGDVGRSPRMQYHALSLARLSSNLRVTLLGYTGES

CVPDVARQNNINVLTFSPLLQRLPRKFFVLVAPMKVFLQLLQLFWLLLVTVGSLDLVLLQ

NPPTIPTFVVVWLCCRLKGAKFVIDWHNLGYTLLAISIGKGHPLVKVAKWVERVFGRKAD

ANFCVTHVMQMWLHETWQIKATVLHDKPPPFFKPTTLELQHELLTRVGDQLQHCNDLVAW

EKQANIEDTLLTRKRKKNCHFTGMKGKDVVQSRDNRPAMVISSTSWTADEDFGILLSALE

HLNARTSSLDVTEFPNLLVVVTGKGPQKAMYLEKIQTLAFQRIRIATM

>contig32935 Frame-1F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY64739.1|) 0.0

MWDIHRHQINQQQVWLAAGSLSGLYLSYKILVGLYKELVITRALDSQGLHRPKSTLPVLG

NTLDVMFFHKDRLQDWITEQSQISDGKPWVLSIIGRPQTLIITSPEACEDVFKAQFDNFG

RGDELVDLQHDIFGEGVAGVDGEKWLKQRRIASHMFSTKMLRDVMDEVIIEKSIKLRDIL

AQCAKDDRVVPMNSLLGKFSSDVFTKIGFGVDLHGLDGDVNSEMDHPFIKAVDGYAEVFG

ARLQSPMWFWKLKRFLNIGDERMLKRCIKVATDLLNEVMLKSMASKSAVDWETKTDLLTL

FVDTTGNTNVSDQRDAMMNFFLAGKETTSFSLAWIIVNLNRYPRVLAKLRTQIRENLPEL

MTGKLQVPTIDDLNKIPYIEAVLKESLRLCMTGVHRTPRRSTTLREGTFVPFGTHVVMSV

YAAARMSSVWGDDAAEYNPDRWIDAESGKMKQMNSFQFITFGGGPHQCVGMRFAMLEMQT

VIAVLFSRFNIKTVEDPFKITYDYSVTLPVKGSLECTIHEASAPAF

>contig32940 Frame-2F

MHNLFVATAILNKKLRSIQVHIAQRQACAFFQSLVIKKVLRVNKDAMLCRDRMFELEERQ

SLRDSSSLDRRATVTRSTKKNLNKYDFESQEYIAT

>contig35123 Frame-0R|Blast-NADH ubiquinone oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY56224.1|) 2e-60

MGMVFRASPRQTDVMIVAGTLTNKMAPALRRVYDQMPEPRYVVSMGSCANGGGYYHYSYA

VVRGVDRIVPVDIYVPGCPPTAEALLFGLMQLQKKVKGSKSLLLKLRK

>contig35794 Frame-2F|Blast-ethanolamine kinase, putative [Phytophthora infestans T30-4](gb|EEY55443.1|) 1e-128

MQWLMSVLPSALNCNGRDLIYNLNTDETTKQALAFASDVVFSHNDLLSGNILHNKEWNRV

QIIDYEYGGYNFRGFDLANHFCENCGFELDLALYPSVEKQMAFFKGYMSTAAPELLAQLE

ANNELNAFLRALNGVVSRYALASHLLWGYWALVQTVHSKIDFDFLQYAAKRFDAFDKQRE

LFCESTI

>contig35893 Frame-2F

MRMSGFIAMVLFASIANCSSFSNVKNVAQVSGQDQYKHHLKGHHDTWAASKTDVVVEERI

FSDFSNLMRRINEHVASRLESIRNSHYWDIFKTGIVEGIGHGIGFMLVSLCLHY

>contig36038 Frame-0R

MKLQLKAHVRMCDCKLIRHERHDSQLPQAHITSTQPVEMHMQLLKCLNNDKSCTESLYKI

PADKHFD

>contig36144 Frame-0R

MAPKHGVHHDIIPWESDRISSDSPSSQDVLINWLTTPANATRWCHEKRKRLLHEILQLLQ

TNGMTHRTVQDVSGKISSIENSFTTATAFLLQTGELEAFNQGVAAQEIVETVRTLCPQYR

ELQRLFGVKKGKKKLPKDGLSASNGAASDSMETRTESSLDTKDGSRAKDIETPSLEETTF

AVETGVEASNSEQKKPTSADSVASCDAEKHHLASMKQRIHNDNGHGDNNGGARYSNERMT

SHILDAEKETNGNEKDVRRLDVAEEKERDDGDEKMKVLRRFGVKTGVRSPFKTKWQHQIE

FSKSSDDKEISDEDGRNDGDSDEDDIVHNEEWIPLAQRHKLHSTNVVKVDNPRHKDVDNA

DDKEDDSDQLDANDKNVRNSEENEETEDEELETIALKRGSKSAADFNEESSTSEHDKDDL

EEEVPPTQLTTRSDLNEEPIKDQSKQEKDVIERSKNEIDCRTSQKHSMASNELYRAKATK

RLRTERVHNDRLKDLERVAFIKRAKQEQDQRNTLFELERATLECELEAKQVQLTMERALA

RKRLRSAGIEPAEVDRVLPL

>contig36939 Frame-1F

MGSTRVQSIGAGYGTVELLPMSPILPLSTMLPRDSSDYLFKFLVLVQVFMYLEAGAVPSL

LQQFTLTFRLSPQEQGLLGAIVYISISLASPWCSTLFRRFDPRQLLGVSLVANNLAVLGL

ACTPTSAWYSKSLLISLRGFVGLTQAFSCVYSPLWVHDYAPKAKRGTWMSYLQGAVPVGI

TLGYLAGSVTIWLASHGPEATGTFIQSGMDAIGSKSATETNASVDFMSGIDDDAMRLCHG

IYCWRWPFLTQFVLILPLSILIFFVPREHIRLRSTSRRSIVIVDEEEDEVSSAPPSTSPT

NDDDRLLTSPSENSSELNEPSFQSTDVHEEEESKSRWSNLWLLLQHRVYVFVVMGLSGLF

FVVAGVQFWTTLYLETNTEDSTYEIHLSYLLVSGTGPIMGVFFGGWLIDQCGGYSGPYQQ

MQALRVCMIFGGAGCLAALPVSYVHNTFFIALFLWLMLFCGGSILPACSGIVISAAPPQL

RPLASSVAYTSYNLFGYAASNYIPGFIMNFIIDPNAEADEGGSGLDSSRSCNPACTYRIG

FRIVLFWTVWAFFCLTCGAIESGKIYAATRTTPSDRDGKHTAIDTTTLHQSSKKNVV

>contig37033 Frame-0F|Blast-50S ribosomal protein L1 [Phytophthora infestans T30-4](gb|EEY59617.1|) 1e-118

MTMGVLSAFCAVNNRVLCSTSSSLRSLSTLKTYASKPIRSPTAFGLVPRSFNVIKSPVDI

QTAVNKCKAQKVRNFDETIDIAVQLGVDPRKPNQSVRGVVSLPNGTGKEVRIAVFARGPK

AEEAIAAGATIVGAEDLIEQVLSGNLEFDRCIATPDVMPLVGRVARILGPRGLMPNPKLG

TVTQEVGDAIAAARSGQVDFRAEKKGIIHAGVGKMSFTEDALLENVRAFMVALSDAKPEG

AKGKYIKAVHLSSSMGPSYNLDTKYLDPSSTYFMRFE

>contig37446 Frame-2R

MTTLPSLYMETVSLSDDAPGTVAAASDTTVLDVVSIKSQIVQPEVLKPSKETAEICVPVL

DSATIGDGTLSNSGTSNGQSTGTQHRNSHQNPQLPPLR

>contig39127 Frame-1F

MAAELPLPLSSDFFPPIVLSIDEIMHYRRLSNERVAQLVSIIDDADCFYRWNDIKVRNDR

RVQKAQFLDIQPSSKSPIIQHPSTLYKSSFHIVDVQVEEILQAIAKVRTKEARRVSKYLY

GDEMADTQTLLTFPTSMNHVKPSYSYRALKWCLLQAKKHEKRLDFCYVEYAGTRKAHPIA

SNTLVGFCIQESIAMNRKVPTLEQYNILRGQFRRTGIVITQSRQSNILQVTAIAQVDGTM

ESAAIRETMEILMVDYVASIYRIKGLLEHERMKKLQFLDKWHWVSAKQRKTCSVCLRGFY

IFHRKYHCTSCGEVVCSTCAPLRELDEGPLNERTRALRVCSICIAQASSVCGVSHLSRFT

ESDDERNLDTLTCTTNIGTEIYGKSRRDSKHRGIARQAIEDTCCRSSEQGTPVHLPPLRS

RQRCSRRRDCEYSSESDSIDQLKRRTFEFVQREQRANVVKHSTRSTFVFSKATRSDALKE

LVEQVCQIQDPMNVVISEAEEDEDCHSILRKSHPEVKRNDESYEQFIKIRETFDLSSVEF

NSMLDTSDHNASVSPSSTLSGHFESDVAFHVTEKTDTGRSSISQSDVMPRSLQLSISSQS

LGHQDASEYLSPLLPATENALDTKQAMKQGRQQTCQPELAASLHASCMAIEASRGDQRSI

DPVA

>contig39866 Frame-2R|Blast-protein phosphatase, putative [Phytophthora infestans T30-4](gb|EEY63804.1|) 1e-180

MQTVLRARGRALVAARPPHQSRSSPPSLISSQLGMQPTNARRWARLPSFFSTSTDHNLEL

LASGSIQRDDKSRFWIGLTLATVGMAAAVNQSNADAKESVEGEKGDAIQIAERIHDRKVD

GHAEVQESEKTKGTLQKRKTSVRDGKVLVSTAAVRGDREYMEDTSYVSSCKRFAAVYDGH

GGSAVSQYLRNQLYAMLAPGLAELEQEMHAEKNESTNGTTKSTRRQKITTILRETIQKLD

QDVIAKDEWKFQGSTAVGVLMFEDVLYSLNVGDSRAVLCRAGHAVELTRDHKANDPHERR

RIESLGGLVRWFGYVDAQGEPIEPYGAYRVNGNLAVARAIGDRDSRPFVIGDAEVRQYDI

EYDKDEFIVIASDGLWDVFSSTEVIELVQDVMSGELGGREAWSSGGHSDTRVPIFEWSQQ

YTSDRSMIKAARRRRKLQIAKYLVQEALFRGTSDNVSVIVVWLR

>contig40123 Frame-0F

MLSAERKETVTGTAAAICGCIKYKLTTSHQMPLVSSRTSNLVFATKTHNLLLLSRSHLET

RNEGDEKSPSLLHYCSASFESLECSLKPFAESKTDHRF

>contig40808 Frame-0R

MAATHPEDLVLEYDMLQLVDGDESDTSHLYDVTASPVDSSDVEELFPNCSDGASSTEATT

CKISCASLACASAGASCRTTLALSSPEVETNTPNDFAAFLLDGEQFLRDMEKVVKIGLET

QKYFTALEQSDGAIDLNAFSDLEIPASPCPSAPSSVGDSPHRNDRGDFGCEYQDSRNGHD

PSCFTLPHSDSIFSIMSETSSLGHTTDGSVTTSPVPSIVNELGSTHENIATHEFKATHEE

DMATREMMASYVNMATLENMATDEADEVEMDEIMADELNLLEKEVKYLDAQKDYLQTRVT

SSRRRRLSIKQRRPNEQSNRSVKSQEEKQLLLELVTQQQVYQDNFKAMLVFAPVNDVRLA

LMTPMESYIHLNANLHDRRQTILSLREEKLAMTYKFIEHKATGLDWTQPHQYSDVFEKFG

KQYCVNFAISKYEGVSVFQVGRALYEQIAGNDEAMNRAMGSTTIRESIDTIKCNFMHQRI

VSSMQWEDDKTEKMPDMESNAIFYCQFGDNSAILATDYIDRDELHPYDTSNRIRKDISSG

VVLSSHVDDNGMKYVVMKRYLLAKYHMYPHKVTQQQQDRYFADIPKCQDTMKSLMIDRLQ

RNGDGMCGRED

>contig40893 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61370.1|) 4e-87

MIRSHEFLPFAWVKPNGPWRVACRTGSKVGRVKMVSRNYGIYDFANLDRERNLDALRYRM

FGSKSKTITGDIVVDRASRVLVFRDHDTNKPPRYILEVKIVAVRLKTALILKPDSTAELI

AETDNHGAKTTESKELKTAHVYRFDSDLEFACDSRPKKLTLNFYESHEDPTGRLQDMSSI

GIPDESSCTSNPREDDDFVKPAFNSIELE

>contig43038 Frame-0R

MDEVELMRQQRDERAQEAKANELQIHEL

>contig43614 Frame-1F

MDVARMRESVMLTTTFLKHNLYVSYA

>contig43799 Frame-2R

MRTVYVCAHFTDFIYVLLTLSS

>contig44112 Frame-1F

MVEEVTVTFHVNESNQGVLATLVLTNYRIWFVPYRRVRGLLHEDVHTLPVSKIQKASIQQ

QKRSNNHVVTVLILDNMDAGHYHVTLSPIARLRDSVRDFSRDAELKRVKTLHHIVREIEW

LQIENCFCSPDDWNHVIASEGDLLLENDLLQDGPKHSSFMMPPLMVRALSHNYSKYPKHP

FRKENTERLSVSAGPLERPKIKPHPSEFAAFRSPTREKLSNHFQLAMRRRIRYNPDVEFT

RQGALSHPRWRQCDLNVHYQLCPTYPSFLMVPSCLNDEIIQAAACFRSKSRFPALTWIHP

RTGAPLCRSSQPNTGVLRSTNSE

>contig44978 Frame-1R

MHSRHSFVASALACALLSSHDSLVAADYTVKAAASPNENTWQGYGTSLCWWANVFGERAD

VADALFTLKPSVTLEGATGEIPGLGFNIARYNVGGSSKGVVNVSGTDVAMKMSSKMPDFK

FMESFMVGLETNDLSSPIWNWEADSKQRAMMKLAVDRGVDQIEAFSNSPPWWMNKNLATA

GGDDGTVDNLKTENHEAFALYLASVVKKARNDWGIEMNYVELFNEPSETWWQFPGGQEGC

HFSFEAQQAILPLLRKQLDAMDLQDVAIAAADENSPTRALENLKSLSANPNAVDTVEKWN

THGYEGLKAYRGPDRHGLNEPISQLGMDLWNSELGEEDGTGLTMAETIGLDINEMGVSGI

VYWQALDSGGWGLIQSNPGDNWIGEANPKYYVMAQYSRHIRPGMKIL

>contig45128 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68023.1|) 2e-63

MLSLDHESVHLVWSKQTREELRVALYAEIKRFTRFQISSGSKKARWNFEDFIVPYPSLID

EVVVGECYISILAHLDSKLFFFGTIPEEDHFIVLTPEQLSVRNPAAVLAALHVRVLRENI

YAEHRNDLKTSILCIKSMGVVAAAYARSMKISMIFEEVDHLWT

>contig45410 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53567.1|) 3e-30

MTISGPLYRRTPRLFNRSKPGEWSLVWCELEVERGELLVSLDSDGRSRNASIPVKNCELA

HVRSDGRDCIE

>contig45843 Frame-2R

MEVSSELGDASSYASNFVSIEVQWLQFLPSSA

>contig46316 Frame-1F

MSSNEAKDGLRVPERQPMYSGPNSSSSFGRRLKSRQPHAIGHVPRRPHVPPPPPPQILQP

PYDPNETDYVMAESERQMPGSEMPYFRTDSAPNAQGFPNGMLETGIKYSIMNTLTEDNKL

SRPMHVNSVDESSEDSFDNGSYVTDKIQAATNEGIGWFHAKIKVENTIHWANNYKIQCCM

FLIFICGAAMTVTFADNDAKTSVGLVAGSLITIFCCSAVVYTFLTRPTWRKHPNPIIFFR

SICDICLVVVLLITELYKCCKGDCSQSLTGASCTATAALTQFFLWTSESWFFVMAIDMLS

SLQSPFTDYKSNVRRYHGFVWITG

>contig47294 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57010.1|) 8e-38

MQQLASVLDNLHSPSSHVQTPLTHVEEQIDLQSEAALAIHRRVENVLAMYQQMILVLSEK

CVEYDALLNQI

>contig47319 Frame-2R

MSLVEIAAIGVDGPTPSPLSLFVLCSRIATASSSSTKLHVQLLDPPILYETEVTSEQKPR

ALDCSGDNYVETVGLALRPQSDVPSRFELRWSKKLRTLTLMERAAFSMKFCTISFEISES

NDNWRLLLHQVTTEQQHLRQLLDAKQTRMIKLENILKQKEQLLETALTAKQSVEDDLVKG

FCAVLNAKKDEIRRLQTEAPRLEVASSRLKQPILKKARKAMGAKLKRKEKAVSRIESDEE

MATDVDEEDTKRAKQEAINAYNHVATDSKPTSVQISSADDLLSSMDEIIKNEHEA

>contig47849 Frame-1F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY53370.1|) 5e-32

MEQFILSYRSLPTLFQWIYLFIALPFAVLSNQWNPFQTRWRSWVCFLIIVFNLSFQLWLA

NATRYATNAYVTVVREYTTC

>contig47935 Frame-2R

MEKYGGDVALTPLHDACAGGRHHDVLFLLEHGADPDTLGEQVIGCFRRTPLHWAAMRGHA

RIIRLLVRYGVNVNARDVFGRTPLAWACVLNRTRAVEALLASNADVNLRDAQGDPLLCIC

AAGACASIKRGSKTVAGKQNKFGDECVDEVDWEETADEGGDLGATLSGQKALARELDPCI

FQLLLTHGVDLHATRASNGDSALHVALRRRHQTAAILFVRAGLSLTAVNFLGQRA

>contig48556 Frame-0F|Blast-eukaryotic translation initiation factor 6 [Phytophthora infestans T30-4](gb|EEY66247.1|) 1e-130

MATRCQFENSNEIGVFSKLTNSYCLVCVGGSENFYSTFESELAEHIPVVHASIAGCRFVG

RVAVGNKRGLLLPSTTTDQEMQHIRNALPDTVVVQRVEERLSALGNCIATNDHVALVHTD

LDRETEEIVADTLGVEVFRQTVAGNALVGSYSALSNQGCLVHPRTSVEDQEELSSLLQVP

VVAGTVNRGSDVIGAGLVVNDWTAFCGLDTTSTEISVVESIFKLQNAHPSSIASTMRSAL

IDSMT

>contig49784 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62407.1|) 2e-09

MGTYVEDYLESMYMLPSEIKRNFDLMRELDK

>contig49946 Frame-0R

MRLFDTAFSDHDERNAKTENESDAKTVSSTYGALDTAITLASPCVSLSMLEDELTQGYEQ

GAFADGMYELLHLPIFCLIVFGLTTVYFVVTGVQYWSTIFMIKSLHASKYLVNGLFVIVS

GTGPILGVFYGG

>contig50449 Frame-1F|Blast-nucleoporin-like protein [Phytophthora infestans T30-4](gb|EEY55485.1|) 1e-75

MNATKIFRRFSSQHSDFVHDMSFDFYGKRLATCSSDRKIKIWEEHGQDWHLEHEWNAHQA

SVWKVEWAHPEFGQILASCSFDRTVSIWEDEGLYLNASASSSDSVAVTGGAPIASVGLKE

GWRNQAQLVDARDSVHDVKFAPRHLGLRL

>contig50540 Frame-0F

MTACSVPNGLAFLNLSIVRSTSVVVMGMHDQQDFLPRIQRSHLQASKLLTQSRDSKLRRF

HHHVTDKLPEDVLKLKQKILESHPIKLTRFSLTHFRRVTTPPVDIPDALNNEFAVKSLVS

GKTVPLTLSMWKHGKSMMKHLDMIDERVSYQ

>contig50823 Frame-2R

MGSVPLLVGLPARCRPALMLSSSFSGADSRRRTIFSTPSTSMSSSAFEGDNTHVSERKGL

FEIDDDTGESLETFHERVKLRQRTKQSEMKALKAQLEAAQERAEEFEIRLNEVNQDKDAW

TIRVKDCQRVIEKRNK

>contig51716 Frame-0R

MDMSDDSGNTHHISRESYSFLSDIERSVVER

>contig52627 Frame-2F

MQSLENEELHQRMRPRRSLKRPLSKVSRNGLPPPLIYRPRPPLMYEYEAFEDDDDILMSE

DEEMAYEYGARYRPRIVHRNRFDSVSSEHWSSFAEQTYPQNCKRHRGTQDSSFYKHDDHN

FDRQNRERADISSSHLTDPSDDDIVSSEPYPLQANCSNQVEVSTENGSTVSSSCDYNFGH

VVEDGETPETLSNNCTQTD

>contig52692 Frame-2F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY64041.1|) 3e-26

MDLSKLQNHACVFKTYQSSNAMNETAP

>contig53471-0 Frame-1F0

MKTLVISSTIALMLLALPTSVNAHGQLILPVPRLITQQYRAKCGALDGAGDQELQYAPV

>contig53967 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54486.1|) 1e-78

MNCVKGEIHNVLSMMRVNARWASVHRFTKEIPASTQSPMMRAFKQLHYELQSVIDLSDVD

TVTYLLPFVMVIESERTSGLITGAAISAVNKFLLYGLITSESLRADVAINRIAVCVSRCR

FEETHRADDEAVLMKLLELVEYCVRCDAGHLISGD

>contig54171 Frame-0F|Blast-elicitin-like protein [Phytophthora infestans T30-4](gb|EEY59954.1|) 2e-22

MAELYAEVAEEERRLHRGPSQRQYWDRKTFTSFAEQQRAMEQSSTLYIGNLSFFTSEA

>contig55226 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60649.1|) 2e-55

MAAEAEAALNALRKLESNKVCINCGSYNRFGHQNICEKVRTFVCSNCKSAHQSFSMRVKS

VSMSNWSMEEVNELRDENGGGNAAAERIWLGRWDESSMRKPTKEDSLDYYKQFINSVYNE

K

>contig57156 Frame-2F

MRLFQISATILAGAKGLNANAAPRCFPSDFMFGSATAAYQVEGAWNEGGRTPSIWDDFCR

SNHSNVACANVADDFYHRYRQDVNLMVKTGLESSRFSISWSRVMNWEPATKRMRPNPEGL

AFYHALVDELHAHKIAPILTLYHWDLPLELHTELSPQGWLNPCIVDHFVDFATLMYHELG

KKVNIWTTFNEPLTFTIAGYASGTGAPGFKDSDTLAYIVAHNVLRSHAAAVKVFRELKTV

SPPVLHPNARIGIVLNSDAAYPLDKHNPLDVAAAERKMQFELGWFLSPLVTGDYPAIMRE

RVGDRLPKFTQEETAYLSNRMTCTCLITIRRN

>contig59240 Frame-2R

MLNKLQKEGLFGNESKLKLLKSLARKSDERLLTTFKASYVDGLVKDSAFDKAFSVENALE

LAEEAAVSRIAN

>contig01316 Frame-1F

MEGMLNYFVPEDGDSSEHLNVVPLPRVESLCLQHIKESFPLLGDFHFRFKTAFEGTYVWL

DIVNDADPIPDFNGLVIAKISRLQRESPTSSIYCHNAHKTNIEATDLIETAEPPSSPIKR

EEPQLPQKVFNNDLVGLMADPVPSSTPSVATPVIPQQNNITSSQAAPDPFDVFGGSNTAP

MKPTPISANISATNGPRGLSPTTMGPHVRAFGALGGFHPMASGNPSPMAPRIPSGMNISQ

MHMGIIQPPVGMQQTQKPNSFQGLQWQGMGQQQQQQRNPNQRW

>contig03466 Frame-0R

MLSKLTLTSNKLTTFSNLEVPDSITYLDVSWNAITSFDGMALPDSMTQLFLGGNPITSVS

GVAFPSSLTLLYIHNLELSSLEGATFPDSIQYLSLVQSGLSSIDGVQFPGQLQYIDISFN

SITALPTGLPSTVVQVTATNNQFTQLSQYTFPSSIATLNFSGNPIETIRGVSFPMALSKL

DFGSNEIQSFEISRSDYSTFKDLQEFNVVIAQSSCSTSGAELVAVLGHNICVISDELFDS

TYGSASSRAESTLSSPISDSGGSSTVLIVILCLAAVLVAALAAFAYRTYRVRETKDVTRR

MDCNNFFANNTLMDTASPMGGQHYRTKSQDMNSLNSSFSGKVTMMGGTSMESALVKYRVP

ASEVQIDRTIAKGGYGVVYLATYQNRPIVVKKILPEKAADDRNLRAFIDEIKLISSLSHA

KVVRFIGVSWSMLSDMAVLMEYMPNGDLDMLLKQQQERQKTYPKEFDWYQNSSVLPAKAS

IALDVLEAIVYLHSFPSPIIHRDLKSKNVLLSSSYEAKLSDFGISREWQVDATMTAGIGT

MAWIAPEVLRGERYTEMADIYSFGVILSELATCVKPFDGVTNALIVLKVTSEEKPDLGAN

CPEDIRELAERCLSFHASDRPSASVAHYELRTLLKLHSAFEL

>contig07358 Frame-0F|Blast-calcium-binding protein, putative [Phytophthora infestans T30-4](gb|EEY59271.1|) 1e-172

MSLFSRRKTPEQLVKLLRDALADPSATAKPLKDGTPVEEITKRLSEMKVLLYGDGEQDAK

AEKCVQLAELLIASGLIPRLITGLYKLPFEARKQFAQVYNNLMRRDLAGFVSYVERKPEI

ISALVSGYENSEVALNCGTMLRELIRHEILAGKILYSPNVWKFFDVYVHLPNFEVGSDAF

ATFKDLFTRHKTLAATFLTSNFDVVFAKYNCLLMSENYVTRRQSLKLLGEILLDRSNFDI

MMKYIGEKENLKMMMNLLRDTSANIQFEAFHVFKVFVANPKKPETISLILVNNREKLIAY

LKNFQNSKEDPQFIEEKALLIRTLEGLKVGEAACEAASSSSKSASQ

>contig08041 Frame-2F

MKLSVCLAFMAVARETAFAWTFDASEVNHHEGIDGEHQPLQRTWTITSTAQLEQLYLAVP

GRVFVELDPSLLPMTKNPEEKAPSKELPNVPVKVNSATERPGVLPGVTPGVRPGFIPGVV

PGFVPGENPAEHNEGPRWKKNESSLVDKTVEVPSKATSTKIPVTSSPDTIATEVPGVLPG

VTPGVRPGVIPGVEPGFVPGENPAGQKAGSGLADKSSETPRL

>contig10206 Frame-1F

MQAKLGNRWSIIAQQLKGRTEDAVKIRWKSLMRGRRASTKDDKTSTESPGAASDVVESPS

SDPEYIKLKAAEASSTRQINYKNATTSPRVFVKREQDIVSGTSPSSSSEGAIAGKMVNSV

FVKPTQPLAQPRMTAAMGNTMQSVNDLVAASIHNFQMSQRFYPSSAGTALYSGNTNQLMP

IGNHQFAMSGNYNVNIQPQQLVLQHPSQLIQQQLMPQSYPLPHGYPMHQQSMGLMPHYVV

PTSFSTSTQMPVSTALQRSLSMPLTPTHTPQALAMTNAPYHPAHTTSIHQGFSGAPLHPR

TASLSALTGTFSQSLSGTSTGGVSAFSGNVSTSNIGNSPSAANAGAKGLNTPREEWGSSQ

TPRSQMIMTEGHASAYELFHQQRLRLMLQERDKQGMTLSSAPSPGQALLTKELEANKERQ

ARQAIMHKGWKSAVESMVSFNSVNDLSALEDQQRFDGLLEKVSLSALDPSDEEMLEQAVD

IISG

>contig11858 Frame-1F

MVKACWGSVILMCTLALHPYNEIAQAREESVLRAVNASTKGEVLQSHFEERAPSYTDLAR

MAAGFAEKIHNYISS

>contig12240 Frame-0R|Blast-protein phosphatase 2C, putative [Phytophthora infestans T30-4](gb|EEY56002.1|) 6e-67

MAASLDLASLHAMAQTLQSSFLSQVIVLLLFVLVLRYVAASWRNSFTPYEVQTCPPINPH

VHYRYGVSQMQGRRPYMEDRFTAIADLNGDPTQSFYGIFDGHGGDGAAEYCVQAMCQNII

RDPLISKEPIEALKNGFLRTDH

>contig13463 Frame-1F|Blast-Ufm1-specific protease, putative [Phytophthora infestans T30-4](gb|EEY69016.1|) 1e-147

MCTKVFQAQMLANQVKLLLLTDSMGTITTSNKVQMIKAGAVRTDRSRHLASWLFLQHYTS

LSYLSHEHIQHVLVEMGDKPASFQGSKDWIGSVEVGYVLDELFGVRFRTLTVSSGAHLPD

VARELLYHFETHGTPVMMGGGQLAFTILGVDLNEVTGTCAFLTLDPHYTGDEDLEIIQHQ

SVALEGYKAIPCSWRKTTTFAKNAFYNLCLPQRPCEGV

>contig14875 Frame-0F|Blast-U6 snRNA-associated Sm-like protein LSm4, putative [Phytophthora infestans T30-4](gb|EEY55692.1|) 1e-37

MLVELKNGDTYNGHLVNCDTWMNVNLREVICTSKDGDRFWKMPECYIRGNTIKYIRVPN

>contig15502 Frame-2R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY57906.1|) 9e-32

MDVKRLLWESKLAVALCLLIMARCVDRVLYTRITYDYTEFLWYFTNVILPIAFLVSSAPV

VAYKIYFT

>contig17056 Frame-1R|Blast-peptidase family U48, putative [Phytophthora infestans T30-4](gb|EEY66429.1|) 6e-07

MYTSLFGAYATFIFLRTGWIFFHARYCFPFLRLEKSCIESSSNIPNLCDVGHFASIFLVH

IFCN

>contig17250 Frame-1F

MEDAVMAFYCQHNLLCANESTTNNIVTAKQRSALFQDVDVNARVSSSREKSIGSVFELLD

ETQKAQLFDAAKQAKERVLESKAMETMPDRLELCTNKDDKAFRATISASIAQRFTSSRVV

KMDDFNEGMKTNESMYSPAQRSTSRWFPKALLCKRFQLKGMCSSDSPAIDNEKKLDLFDK

ELVPHFVKYAADRAACRDSMEKKVHVKGIENESRSSLEQVEKASNALLQSIFEPSDEYLS

EEESGENSSEEETVELIKVAVHDQLKEKQRDAVRSEVLNEDNKLFGVVASRDERMEEVQR

KVKGVEESSQERHRRVKKERKSHKKHKKRRDGKETRKKKRV

>contig18444 Frame-0F

MIIRAVSESESETDDDRLSADNTALSHRRSVFDSSGSAKHVTSDRDSGAARCLWFAVCGV

LVLLVLVDLAAVFDPSPDTFALLPLLIRTLRLGEAIIVPLTASMLNQFAGTALVSVWMYT

RELSFGASNSTWLRSARYGLWIVGALLFLGHVVSCLYILFALVESNGNRTKFWLGRKHFK

LSTGSYGQA

>contig18655 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56769.1|) 3e-46

MIGVAIPVIVLFVDCFVQIYRERQVFGLLAPRNEPEHLVVAGYPAKSATCMERVFLIGSI

LGLCIGTGILAARINSNHFLTETGAIVELWMVTFAIAVAVGLFLYSTLMCIVIFSIRSRL

KWLHEPRAIVETNQCSSSSWSDDNNIVGP

>contig19146 Frame-1F

MERSECILCHRKRNEFSCASCTSSMLQQRRTMLAALQADVAVLRKKTESALNMKNPLFRA

ELRLNDCIEQVRRVAEMVMKTREKLCTERIAVLERTSMLEKRSLVMVEVQHKLQNDCQQA

KSLHAPVLECLDYQIQWANENAAKVRGDRLRKLFALFALIPEKVISEEADEKVADPFSRL

PDVRRQRKLKKDVPVFYRTIAGLPLPKSGKFENVPPEVVAAAFGKVIHLLNCLVKYLKIT

YPHPMIFNGSFSTIGNTTEGAGCHTLYPDGSIGFGRGVSMLHENVEFLCASQGVPLENIH

STDLLGNLLQIYKSSRLGTICNNQETL

>contig21273 Frame-1R

MFLQLCVLAGCDYCPSVRGVGIMTAYKLVRDFKTPMEVFKALQQLKGPAVPDDYESHFYA

AILTYRHQLVFDPRDAKLKMLHPLDISNDILPLVDQGLHFLGDVELRDSVVAAIASGHVH

PVTHESYRWKDAAASTLFTEEQATSHSKTSMTRSSTSSESNDILSSHLHRRHYRNSKALD

ELAFEETMYSAPPAVVRVQYEKPRPSSRSSWTHLDSVLGSSDHIVNFRSPKVSENFQPLA

ALHDPPAVRRTSGIKTYNLKEFERRPNRDHVKRVRNPTNRRRDGKGSGFEGEVLCRVDQG

QVPSLIRSSKYRRDAARDNDVNSLLNEQNARLAQQKRQRITPSPSSPLSSRGSSASSGNP

LIRPTLSDCGQQPCFSENSGVLNSQMPRRYDSYKSGNSIVPKPTSHYAFATFAEEKWDRI

LQDEIEDRHSHQRREEDPVLESSSSDIM

>contig22038 Frame-0F|Blast-ADP-ribosylation factor family [Phytophthora infestans T30-4](gb|EEY59698.1|) 6e-19

MGMAFSRVFERLFGKKEMRILMVGLDAAGKTTILYKLKLGEVVTTIPTIG

>contig22272 Frame-0F|Blast-exonuclease 1, putative [Phytophthora infestans T30-4](gb|EEY59632.1|) 8e-76

MDRISALLHNGIAPYVVFDGGPLPMKNKIETERRRTRQKYRELGIQHYKNKRYSEARKCF

ARAVDVSPYMAHQVIQQLKARKVAYVVAPYEADAQLAYLVKNGIADGVISEDSDCLPFGC

QTVLFKMDRDNVAQEIKMANFKKNKGLSFHMFTDQM

>contig22939 Frame-2R

MRVFLSLRKLRKLVDKSYFEDGLEQLVIYRHPRTGVLASAASGNGTCTAPLDGMVSLKCM

FREQRFLLMPTKLIMVMNPEAFVLIEKIPDQNDDSSSYHGEGQGIVKVFASIHRTYCTVD

LRDDRVLKVTVRSITPVRGCRTGRKNCHVAQKLGMLKEWSVTLMFPTAEDCAQAQTHINV

SGTEVRAFKLQQIETSLTVHLQVSQSSNGMWYGPFFASTEANSEEDEALNTNKLYSEVDE

DEDKVEDKDENEGEDEDQDEVEVEDENGGEDEDEKKKIEDEDGEEEK

>contig23679 Frame-1R

MVLSSRVRIPRLSQRSRIRAPMPSHAALPGERCDVTSASSNDAAVTLRQYREKSCFTLYR

DKLRLLSFH

>contig24047 Frame-1F

MYFRMHHAGYTVAAQKCATAKRCCSNRCCSNRCCHSRQLSLCTSRCAIRSNAEQSEKDDS

DSTDRLQVALTRSREYFLSWSKVDFVRIQARDF

>contig24432 Frame-1F|Blast-cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|EEY59924.1|) 0.0

MIFPVVMLAVFAFLPTSAQSDTRNHPIVYSVSEEGSCHGSSTEDVCLKNHCAWCECAAVP

SSCYTIAEAEKLPSAIFKCKKVELYSSWDLTTVPSTSAELSRLFESWKFHHAKSYDSAMQ

NELRRGIFEINARSVAMHNTKADKKFTMELNEFADLTWDEFQSWYLGAPQQCSATESNGV

EYGDVPAQKDWRADEAVSPVKNQGKCGSCWTFSTTGCLESHVKLKHGKFTILSEQNLLDC

AQNFDNHGCNGGLPSHAFEFIKYNQGLDTEETYPYEAKEGKCKFNTHHVGVKVNQVMNIT

TRDEEELKAAVGSAGPVSIAFQVVSDFRFYKSGVYESTECHSGEKDVNHAVLAVGYGVED

GKNHWIVKNSWGTKWGMDGFFQIKRGVNMCGVADCASYPIVA

>contig25321 Frame-0F

MSCSFMELPPNRRAAVISILILLIGLVFGLSLHANAHIPQPWNRVSSIIGWIYFFCWSVS

FYPQVFLNRARQSVVGLSLDYTMLNMLGFMCYSIFNVAFYYSESVQQQYMRRHDGHRNAV

ELNDVFFSLHAALLVAVSLYQCYLYPRGDQTLKPITILWSFGTCVAALLFGLVILFTGNA

TTSIVFNTLNLLYMLSYVKLLTSLVKCLPQIVLNYQRKSTVGWTIWNVLLDMAGGVLSIG

QQVLDAKATNDWSAMTGNPVKFSLGFVSIFVDVVFLLQHYVFYADRTKFLGGESDPFLPK

EVATGATI

>contig26694 Frame-1F|Blast-M96 mating-specific protein family [Phytophthora infestans T30-4](gb|EEY64933.1|) 2e-12

MLLHDDEREALEAALSLVDDFPHVTPVCGDPQLASEALRGLSLPSCSLGVPTSTDTGGDG

EDGIVDEELESLLLEVGLSSSLLLYQKMKSGTSAEDFTAHETPSSTSGACKANNDLKSEH

QEQDHGTALQSSHEKYSTNGKTKKRVRLNPNRARDNRKNELAYLRNKVKQMEEQVMSLRQ

SFSEYKPFGMATTATRSILNSADTPPLWRDMASTQQLRR

>contig28573 Frame-0R

MEARKRAMASIATRQAAFQAMVDSEETEEDQKKDDVGLVEATQSNLGKRKIEALGKTNTK

HQKKANERCYYCILCHDNSAQGQIGMAAYVHQSTVLAPEFRPEANEALGSEGRKVRDHVK

KVIEKMELCSGGGCLTSSDSDTATSPTLRAFATSFPEWYMDGSLEDQLTRNNTARNSPPS

PATRNPNADRMRFGISMLEGEPIQTDEEMDVLEGVLDLREDQQLFPMDMRGAVSLDLRDN

RVEPRRLGGRELVGARNGAIRGHGGSMYDSDDDGNDDSSTRFRLERMPPGFGRTHESAKL

YLTPCGLHVRTCQHAVHINCLERYITSLHDKAMRGEEFDGVQAIDPDSAMTQFLCPLCKT

LSNFLIPTSEPRVSILKDDEREQKRFVSRAEQDVVSAWDKILQDQLSIPGWYRSVLGRDG

GFEDDEIETEHDMWRDYFEDTLWEPHGSLEKGAPFLWAACAYTLASFLTVAEDEYRKVSG

TDAMFDPLIDQCPLSLEKELESLTCVTKFCRWTCSLLEHCSDAKVIWETAKRCCPINTET

KREFRKFTKVLGSIDACLRGTILGLLVADTFTAFVVSSVIADELDTVWQFIPVFTAADLL

QHLHAEFFEPTELERTSLYQDKHSLVADSESEKSNPTAAKVANALASAHRLTRSGRKISS

ATLTNPSVQQLKKQIETSDGMESEVYAALQLLERMAEAYSTEKLKPLTTVLNVQSRLQHI

LASNASFVRRMKLFWRCLVNSNIRVFASKSIHIPTILDIARSSDTTFNQLWHWCMDRILS

KNFLGSSTGGEKCEHTEGCSEAYVASMFILRKVPNQPRLIDLPTQYDELYSQMAGHKCTR

CEKAPCDPGLCLICGEYLCCGDSCCTRAFMPHGPPVGECTRHAAECGGGVGIILLLEQCR

IAIVGGNMAAYFPSPYVDSHGEEDVGLQRGRPLRLDMTRYRNLESLWLNHRIFTEVSRQR

NQRDPQYTINLSYL

>contig29718 Frame-2R|Blast-Mitochondrial Tricarboxylate Carrier (MTC) Family [Phytophthora infestans T30-4](gb|EEY57963.1|) 1e-19

MPSAVALFPQIGTISADNVEEEFRSRTDCHGQPIRHFIYNKGI

>contig29909 Frame-1F

MRAEKANWRDDEMNRIIMEMRERFQSEMSTTSFWTALAKKNGLEMDSQEMLTLQKSMEHS

FLVSNPQSEDKMAAPLSADAAVAASVAAINGSSDSTLSRTRSVSKESTWNNACAAFEALR

VVVWKHSFLPRLQFCADDTTNIWNRITDLDADESFAHISTGDKLLSINGRAIDDSVQTDD

DLNDVFAAYASPIIMKFEASDVAPGKCKVHDYAVTWSNGPLGVTLKDDCATQKIPIVNRL

TKKSGSVAVKQNIAIGDVLVAINNIDTIQLGCSLSMSILKKVQLPAKLRFRGVGGPAASV

SKSNGKPSVQVAPRSNRNVSRPPSLMKQDSGMVMVEERASSIMNLSLSMSRPHKYTVNWG

EGPLGLTIIPGLNEGDLPVIKKVTGTGNSAGIDKAQVGDFLESMNGIVTSAMHFEDIVSY

LKTAPKPVLLCFRAAIDEDEMRGRPSSYRSNNNTALSARSDASYTHRDSASRHTGSPDHV

HASPMSHHAAEIVRQVPREVSSHVYKVVWGSGPLGLTVDAKPQAGAFIKRIGTHGAAAHL

PQDCVGDDVTHINDMDVSRVAFQDIVAHLKNVQRPVTLFFRRQALNSSHHDRQNSYSSNS

DGSSSAVYDAPVSKPSKRIAAPGMDDTGAQYYNLVWQDGSPLGLSLRGADETSEYPFITR

VTGTGSAAHLPQSALNDCLISVDGRSVHAREKSFEEVMTLLKVMQKPLTLTFQVRKGSSV

PAPPHSAPVPVQYQQRAPSPPPPPMHVPQSQPRKAVKAQESYTWRQNRTGPPSVPTPPLP

PTSSSLPGASNGMIGDGSTTNLSRSVDRGLGGGVNSGNENKFSSIQAPFLMQNKLSTGRR

QKMLKGLKK

>contig30411 Frame-1R

MACINGDKTSRVCAIERHSYDSLCISRRQQSSRVKALSSYIQFGRTYTFITRKLLVMLDV

DHFCCLSVHLRHLRHYFFVSLLSMCNVLFQSLASS

>contig30464 Frame-2F

MPVKGIGKEFRFILLFESNNII

>contig30842 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59431.1|) 1e-128

MTVLLPFFIANGNWFLLALSVPVAAVVALIHPRLRLHCGSLARRSTKRLYLLWGLLLLGA

ILGVLGVALEIYYFRGCPNSVVFHSEIEDLARFVYELCARANLQYWVAFGNLLFIMRGQR

RIPVGDTDSDIGVLKSAFLQQFGSVSNFSLVAKQDALVTLQRPVYVVYHTERELVQIYLD

EVLRGSHADIWLYWEELDQKTQTKWLIHKDRTIRGKRLLYDQVLPVRKESAVFLNVSVTM

PRNASFLAQAEYGASFMTPLTMRMECIENMWNGYTFYKTAFWIKASYATIFTVMVAVVTL

LTATWIQPLRRSLQFENLETDEAELIKVDSNIAHTTCRKAVV

>contig31979 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65857.1|) 3e-11

MYEADVIPKTMFAIVLEYLNDIQGAARKVSNLIDAMLINNFTTPRC

>contig32295 Frame-2R

MLPGEMGGQAVAEIIFGRINPSGRLPITYPKTPGTIAIPYNHPVNTRCRDGPCKMEWDFG

HGLSFSMFKYGAVSLSESTVFSTDFSSLDVSVFVTNAGPMAGKETVMLFLIQPYRIISVP

EAKQLKKFSKIYLQPGETEKVTFSLTSEDWGVFDPQIGRGFRRIVESGEYVIAIKPETEC

NVYDEDSMANNPLCAKFTILDK

>contig32941 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68279.1|) 2e-47

MITYAGSLAAEVAELRSLLLQTKTSGNHRDLNQLLQQKEKALAAVKPQQDEPMEIVPQLV

KVTATRPAPIDSVTFTEISRFSWEDDGYGKELVMVYIMSGVEGVGNLPKENVTCHFGKSS

FDLKIIGLDNKNY

>contig34507 Frame-0F

MMFATNGIRQQTWRFYNANRTSKNRKNEKFIWKITILSHYRPVSAVRFLLVKPHKQQSPS

FINMGQAPQINTLHSSNMSRKHDGILLPSLSIHSCTPKQNGITCTTENPFSFGSLQDLLT

STTSRFNDSNLLPTRNELPSIEDAQVTLDRAVIALNARYYQDALKLYLEGGYAMANAVEI

QSSPTVRDLVARKAFETLEWCISLSDLIEGQEKDQNPRPGVHKVGMPVASWNEDWVGSRL

SKEESRCIWYTPVRCPDPSDFSNLGYRLRCVETGRNPQLLICITMYNEGPQQLQATLTKL

ANNLAYLMDQNIKDKRKSFAGEDAWQNVLVCIVADGREQ

>contig35795 Frame-2F|Blast-alkylated DNA repair protein alkB-like protein [Phytophthora infestans T30-4](gb|EEY68761.1|) 1e-08

MKAYKACEKRWKSSMINDLLLDGALVDVRNLSTEQQKNVCRVGSWKWSQNLEERPVLG

>contig36145 Frame-2F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY61800.1|) 0.0

MPAPTTELLKRLCTGKFVPDNSSLKSEPGDFLHLFVSHRAQLKEFLQYIVEVETVSNTSI

GNTLLEMVLSDDDDGESGSRSVEEKEEAVLRILDNPRVKYDEDHALIHLQMHSMKKGKRY

LYNKLHMYHMLVQFHIEENDDQSILEEVRKHGEKDPNLWSLALKYFAERGPLPKGAVGGE

EWKELKQLLVLIDTNPAIPPLQVVQVLSQSRELPVSVIKQYVVSQLASDEKKIEEDEDKI

KAFKSDTKQMKEEISQLSSRAVVFQATKCDLCNHDLDLPAVHFMCQHSFHLNCISETDRE

CITCSMDHRHIVGLKTQLDQKAGNHEQFYNQLETAADGFHTIAEYFGKGIFKSSEVVLDE

GSFETRFSAEF

>contig36404 Frame-2F

MMRVPLRDRGSLEQFLCCALLSAKSIVIAKTDNSDVDDEEFRRKARHQTKMALVNYFHKE

ASRVIWSANRPHTHDRLLLGGSMHEDEASSVNGIELESRLQLVCDSPQCSTPIQRESRCA

FKRCRTCCYRMQRLVARSLRHANMKARQSALNALQAELAATISLGKERILSDPVIPWCEA

HCNKRRRGETF

>contig36471 Frame-1R

MSSMVLASLVMLGAVVLTLEIQRQLLFARILSALVMLLGWVLLLSSEQQLQAICCAVVYH

GLAEGLRQWQRSFPCVFERRKDRKVVLWLLFWARVYTWGTTLGGIAVLTVVSRSHESTRV

SYWHESIILALYHEIVEVLVMLYFADEEVPYIWHRRIGHWLGALLVGFLKSSGRLEAALR

GPLLAEMSSVALISVLLVVMWFSIKIPWDRIAEASTSSLFQDESYTENEPEIVDENREQL

>contig36615 Frame-2R

MLVTDDDKLNDFFTKFLHQLSSWLLKGEAKKLVLVITGIETQEVLERWAFEVHAEDGVGE

SAPALKPQKEIMAEIQAIIRQITASVSFLPLLDEQCTFDLLVYTDKNSEVPALWEESDPR

FIKDSAEVRLRSFSTKVHMVNAMVAYKNPEADI

>contig36938 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56801.1|) 1e-143

MSCVAEAMYKRSGFRRLCMTSSPMVNASEDEHRRIVTKLCAQGLLVDIIDGGDSKGEMHS

GYLILLVRAPEPVVLSLVKQFRIQMWMDHGAVVDMEQDVAQRRNDPLTPAERIEIVDYII

EQRARLSKSDVWIHDLFPMHNQSVTNTLIHRWVASWRLHELNDKKVLRSLRYNFGEKVAY

YFAFLKYYNTWLIPLAAIGILLELLRGVITMTTYMRLLPFWGLGVSVVWGFGFLKSWERE

NACMQYEWTGKLHVKQIEYCNKQFYGQFRVNSLTGDVEVVYPAWRRLPKYFCVILFMLAQ

LLIMLVLVASWVTIYEILKATYKESHIFSIQWFLILLEGCIFGFFVDVVQWNMVVTKMGA

LFTHWENYRTEEQYERALISKLFLLDFLNYYTWFFSLAFVFVIPGLGNYLTNCLNHMFSG

DAMNCCFGPYVDQDGSCITCPVGDKDATCIQCVGLFTFDRRHVDLGAMFVTPIVITQLLN

ILLRLVAPILVRKRREYAQERADVQAQQRVRDAGAMKILGSL

>contig39126 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59840.1|) 5e-65

MERNRWLRALKTPARRKSRSWSIGSSEEVTVAMSSFDSDGHCRFDRLSIPIYKSGWIKKK

SSLLGLWKCYFFVYQGLMLSYYNSDKSYEVPQKRGYVESVKTRRHSSLLDVPNAGNTVAS

AVLELVITLGLPLNQVLHLRFRSVIEARDWRRVLQPDGTHYSLARK

>contig39867 Frame-0R

MDTLCDPRFQTNPFVTGPLAVRFLAGAPLFTVENECVGAVCVLDTAPRDSLQESQIATMQ

NLAHLAMVMVQERREAQHQVARALAASSHLVATRQVLPKTTSSDLVPLSSYSETSMVVQG

RERPKEDPVLKEQMIQLLHKASQVRDQVNQQTHKQQAGLKSSGE

>contig41507 Frame-0R

MSELGQQARNTYASGAPANYVPGLGRGAVGFTTRSDIGPARAPMTQDGTQDAPFLPPAGR

GRGVEIPGSGFGPSAGRGSGTAGMGGFGREKDENEDFGDYSETNYDEFSGYSSRGLFQDT

PYDADDKEADDIYDQVDERMDTRRKRRRELKQLEELKKARKEMPKISDQFADLKSSLQHM

SDADWERIPDIGDYSLKYKTNTPLQKRHEMFAPVPDSILGANAGQSLNGTITPAGNGSET

PSGITSSVTGLAGARGAQLSHKLDKMSDSISGQTVVDPKGYLTDLNSLKLTSDAEIGDIK

KARLLLRSVTMTNPKHGPGWIAAARLEEVAG

>contig43039 Frame-2R|Blast-plectin-like protein [Phytophthora infestans T30-4](gb|EEY55919.1|) 1e-39

MSELGSTGGSKLRFERQAAERVARELMDMKIETAHLRERLRLRVGGDITAAELEAEAFAL

QTALGEAQKMLKVREAELQSAEVKYQKAMRGLMQMDEAWKVSIEQTKEAQDAKQKAERCL

TEERLRC

>contig43615 Frame-1F

MKKQAAKAVVLRWTKPFLRLIPATAIAKSATKARMDSN

>contig43798 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63999.1|) 2e-51

MFPSNDGYHSSTHAATRDSSDNLLGHTAIGDFHLHSVCSDGKLKPSEVVAKAATNGVTYM

SLTDHDTMSGVNEAIIAAQKLGVFVIPGVEISAEVKGGEN

>contig44113 Frame-1F|Blast-mitochondrial inner membrane protease ATP23 [Phytophthora infestans T30-4](gb|EEY67990.1|) 1e-09 NOT\_ORF

MELTRKTFRSATLNASEEEKRRQKCEFMRENALTKCKRTALKTAFTFEKLIMRKLL\*RAG

SRVKFLVDVMEKTGCSL

>contig45129 Frame-0R

MRNTTTKHLIIILSFARTVLHRTSLTSATAIYPSECNKIGRSFIDELILVELPILRIKCG

RAGIVYSLHVHRHGEALNGRALQL

>contig45411 Frame-2F

MRLCGILMKEEEKAMARCDDKISNQLFGNGAILFMLLFESYALPNLSTFPSQLIDLVHLL

HERLGQHGLCGMTFISEPGSDIVSRSNSCFLKSCVLILDKFMHHNASVWIEKKPREPEQK

GL

>contig45842 Frame-2R

MEVSSELGDASSYASNFVSIEVQWLQFLPSSAGISLQCYCIDHGLKHKQILAQCKYELAF

RDVSLFTHPHNRPFQ

>contig47941 Frame-0F

MASDGSMSVMLPMVSMMLLLVFAGGLWFLLTRNQLRGTSHSFLARVLLQDQDTITRLDIE

RGEAQAERWRCLVCEFSNAMDRPTCVLCGTKNSKREEPSRLKHSIAGREERVSSTSSITM

LTRPSLAASVVSTNSRPSLRPLRLSTLNPRQKYARRRKEWVRCVGE

>contig50448 Frame-2R|Blast-nucleoporin-like protein [Phytophthora infestans T30-4](gb|EEY55485.1|) 3e-60

MYEAIDVMNLSHWPLQEEFLADKAGATCVSWNNSRFDVPMIVVGGNGDVAKVWGFNNSYR

RWQVVVELVGHADAIHDVCWAPNMGRSSHLLATASKDRTVRIWRLTIQ

>contig50541 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56579.1|) 5e-96

MDGIYSDSTEDLRASKTLLKHKLVNGSIMNVSERRSLDAPYRFAGIKWFAAKAAWGLTKH

RDVLAYERMGTTTDATGKELAYHVLHSIDHPDWPIDAIKGIKREHQVTCFLYRKRHDNHV

ECFIWSTVYNLDSVVQRVAAYVLAGSLLSVTECVKSARAKKFSILMKHAP

>contig50765 Frame-0R|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY59571.1|) 1e-29

MMLLVLAPLFALLLTLWGVIGLILTLPPKPVAAASLAVTWTLYFCLPHIPLRLLDWPLVV

TLGLAVLTQLSRSDSLVVHGMITV

>contig50822 Frame-2F|Blast-oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY57986.1|) 1e-37

MLRKTSADVVVVGAGVAGCSAYYHLARVNAHNSNYKPLLVDALPPFSLTSANGSFSYRNW

FPRDDEAPIRELVVHSIDKMDDICKNTNNALG

>contig52626 Frame-0R

MSEKKKNAKDIDDDVKSLNSISSSLSDDSSVLSSPSQRPQQRPRFDSKASWADSTRFDMG

RADSRASEVSARDLRLTGLGTRASVSQHRQRSDSRASRLSRTSSRSSMNSMVRGGRQSFV

SNFGVTKGKKRL

>contig52693 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68416.1|) 3e-12 NOT\_ORF

MCLSRDSPNKRKVVSLNFMVEEAYMLWDCALQT\*ELTL\*MLRRFLQGELYDARGKHVQLE

AVFPTCLQLDLCMHETIFSLGGARLELG\*DARALESI

>contig53470 Frame-2F

MDEAADSYGFGSFSELFDRSPAQIAKHLDLGALSPFFMSERLLSRFRRHRHRDERSALHH

HVAAKF

>contig53584 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60028.1|) 1e-24

MHWNVIKDGGGNRRILLRLQTSDGRTRKIHVPFKQYHELRHSVALILKDMNQV

>contig53966 Frame-2F

MWHDLLYHVAKNAAFGVPHEVVLAAIKTLQTLLQVSSAGDLELLAQSQPVRAGVGMRVVG

GALLSSSMPVSAHVTNRRPTSLYRDPALWNEAFSTLLHLCDERQLAALQDKEHVRLWCED

DEQEIASAVVAVLVALYLQAKDFEFKERTEAVEKMLHVFRVLVFRHVLEPLSTIKSTMMT

ST

>contig54703 Frame-0R|Blast-ATPase [Phytophthora infestans T30-4](gb|EEY56694.1|) 1e-30

MHLTLTMMLMNLQARANLPLLFLACTTSSCDTQDLPDDLLALFNENPTVSLTS

>contig55227 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62433.1|) 8e-28

MDALYDVKDVPVIIERFDTVFVSQRMDCTLGLDELISELAQSMALKSSLAGFTFAAQLIR

RSNSSIQYKNRWIQSDARLIETALSVIYSIDVSDLIGGIPSSVDTDNHM

>contig57157 Frame-1F|Blast-RecName: Full=GMP reductase; AltName: Full=Guanosine 5'-monophosphate oxidoreductase; Short=Guanosine monophosphate reductasegb|AAN31473.1| GMP reductase [Phytophthora infestans](sp|P59075.1|GMPR\_PHYIN) 1e-08

MPRLEYEVRLDFKDVLIRPKRSKLQSRLQVDVEREFCFR

>contig59159 Frame-1R

MLKLFKPLHWHLLLFKIKRDP

>contig59348 Frame-0F

MSNASTCDTYYKTHTAAREVEKVDIHDP

>contig00028 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61962.1|) 2e-13

MEILPLDYGAGVKVSFTDGSSCVKGKTMTTTFHFECDLGSGTTSKPATVSVNDDDKCDWN

IVWKTAYACPICDDDYFNELRSTCNGGEQLGLVCSQARVLWWCRDGEHKYHFHVLRERCG

AEYKGFVLGVCCHCCHWVYCLASVDGHSHYSSQVPQCLQ

>contig03887 Frame-2F

MPEHPPFPQPDPPHYSFQPSQEKDGRD

>contig05764 Frame-1F

MHRLGRETLFRQVCVSRSARWTSIANASTLSSPHTLYTIYQQRVHDGIMTYDPIQLHAVH

QFDALYDAIVQYNGGTNVTTKPKKTSWWPQRIQQHFNTIPRLNQTPKGLYLYGGVGCGKT

YLMDMFYDHVPVQSKRRVHFHAFMLEVHHQMHVLRQQGLHDDAIPRIADHLLQTSWLLCF

DEFQVTDVADALILRRLFTALLARGVVMVATSNRPPHDLYKNGLQREVFQTFLDLLTERC

TVVSLEASKTDYRVVQSVVHTEKVYEWPSTPYTQAAFEHAFQARCDGEEIIETFVTTHGR

SVRIPEAATNARVCRFSFQDLCEKPLGAADYLAIAEKFSTVFVRTIPRLSAENLNPVRRL

ITFVDCMYDRGV

>contig06251 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70345.1|) 1e-22

MHSDIIVLLTETIVRCEKLQQENADQLQNLMQLSIFSASVSDRTSVSSSCVFFENTGKLD

NHEALDTDAVDSGAFNSPVTTSRFENGVKGLESFGRPVSLQLLVSQGGYVEA

>contig08859 Frame-0R|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY57356.1|) 2e-54 NOT\_ORF

MDKV\*SSRYILILTLISLFQLQILNEVPFLHKLDSPRVLKFFDWYESSNHIWLVLEYCMG

GDLLNLITQDKQLPESTIQSFGIELVAGLQYLHINSILYCDMKPANILIDEFGSL

>contig13385 Frame-0F|Blast-C2 domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY58865.1|) 1e-176

MGNSSSTSSTPDKTVLDVELELVSAKDIAAGDYFDMKAALKGKVASSDAYALIEVGGQKM

AWTRPILDTREPVWNEKFFFRNVKPDTICNLYLLDEDFDGDDALGQTQFTATNTEGSVTT

FELPIARNGNAAGVILVNVKSHFTEPYGDGQLQQYGPVHYSAHLSIASGIFTQSMTDDDK

LQSSAYHVQLHNIQLILPNDHEWNKNYPTIEKIFSPDHPESPVLRKAVAAEHELVYCHAA

TTQYGQLYEPSDFFKLVNYGQRLEKRVLFTYAITPTGWYFSETGAAFLKDMLSKHMLHSG

AAFSVKYAGEFHIEHNLFGKYKLVIDNNSGTYAPPMADLPKLKAIFEVNFPGISIEAKDR

DDEEVKKARQEILNAWT

>contig13460 Frame-1R|Blast-endoplasmic reticulum-Golgi intermediate compartment protein, putative [Phytophthora infestans T30-4](gb|EEY68747.1|) 8e-94

METPLVDVSKIVTKNLATYKYFVSIVPSRYIYLNGKSVVTFQYSVTEFETSSQGSNGQIS

FPGVIFSYDFSPIAVDYVETKPSLLHFLTSTCAIVGGVFAVARMIDGAIYSVSKKID

>contig15501 Frame-0F|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY57906.1|) 1e-179

MRQFPHYKYMLMALFDTLYNLLGAFPTPHIGGNMANVLNQLNLPFNMVLSYLFLQTRFKR

GHILGSILVLYGGMVNLIPVLTGQDTANAPDPSAGWITLYIVSLLPAAASNVYKEIGLKD

VDLDIWYANIWISFYQLLIGLATIWTVRIQAFSDPPVPWSDFPSYIWKAHECFMGNPVEL

NGNTLLCNSGVLTVFLVFIVFNTMYNQLMLYIFKEGSSVLFVVSSAVGLPLTDLLYMVPL

LTGTSASQTFTIYDGFSLVVLVMGLLVYHSEKEERKRGTESIEKSPMYASPSLQKTHLMR

KRRGKVVYRQSPRIRRTGSNNDISQRLIGRNTPKSTYGSSTNVPRDNTDDFV

>contig17055 Frame-2F

MNCLSPPLVSVPPGEWFCPDCEKERGKEGEKEFIRRTKAESADKEDLIAIALNGSDGTLP

SAKTSSSKKSKKYKYKQNSRLSPDRSTGLSKKPRAHRSSSREVSPPPKKEGTLQKKLDGR

KKNSSQLPITSSRAQIISDPDGSLGDDELRSEEKCFICGFGGELIVCEFTGCTKVYHQLC

LGAYPFPKDEDAIWFCPRHTCALTGEKESFEDGERSLGRPKHAFARKINVKKWLWKCNQC

PIAISDEALPQLPQGQIVSKRARIFVCQHCYIHAPPKVQLSKRLEKIWSTLATNRQGMPF

CGPLLCGVEPIDKDLKESQVQVHLYKVLARIRRLEYEESAVFSRDIDEIVAVALDVIADR

SAPLIGAAKTLTIIRNEQFAIHGAKLIFLDSKIRRGETEKSDGLDDESSLVARRWPLRWR

QECSPFEDKYYAQLEAKSLDEWTAFVTAAPLSANGDEYDNQNIAGAYISGELSETEDVQR

HSESAEGRYPSYASANDLSGSSAAKGTRPGLSLSEGTDVMIALEELSRPGLGNRKRKFGG

VQANRLDNMDAREFFLSPSTSEMQHMFDQQSTALRSALEAHSTLQRSWLISQQNMLGLGE

SDGFSVGEGRLAAELRLANKNLRQRLRNKDKLVDQLTSDHMALRAEVINLHRELSKIKTH

ARELEDRFAVAQVANGDRVGDLENNDAISNGDAANAPNRSLNELHFF

>contig20611 Frame-2R

MLTLPLYLGTVLGCVVSMLWVVSLKQLTAKSFFRRILLLLASVLGTMLGASLVLFIMQRW

NAWKEKEESLNGAISETEVKDLDVFTRTPLACTATLNRYFIIEKKRPDLKKRFCEIHKRI

QEKDGKEAKVAVFVSGPATLQLEVLTQAQNYQLPNFQVFRKSFLL

>contig22657 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63744.1|) 7e-56

MIRTSNLRMEYCLHGSDQQNFAESHFNLGLGAWISCLGQLMAYVQARDSSIKLPYKVAKH

SIGGHSVIFLKKKQKEWTKALKYALTDLKWLLTWVSTRAYNSSTSPSTVIATSRKAALAS

TANSS

>contig23540 Frame-1R

MYSIIFRPCVSQWSRKTCGVLRDTRSLQGLCAS

>contig24431 Frame-0F|Blast-hypothetical protein PITG\_02637 [Phytophthora infestans T30-4](gb|EEY64109.1|) 2e-23

MILQRFIDPTNPGFDPLRVGSDDVFAASAAIGDVD

>contig25069 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53180.1|) 9e-37

MPPKADSLFRWIEDRECEILKNTSSSWGRVLDAGTGRHSLSWLLKGDASSFIEEVVAVTG

EEPLANELSIDFSPSNTPHATPFKVMTGNWQNEKFLALEKPFDV

>contig25357 Frame-2F

MSFNFGTSATPTSGFQFGATTNAPSSSAAPSTSGFSFNASSSAPTASSSFSLNATPT

>contig25807 Frame-2F

MKLLSKLSLRLVTTGRKSIDTSRSAGGVRFRLQGRNHRTRVQPCQRALQ

>contig25872 Frame-2R

MFRNLIHNRYRPLFFLSRRLISCKRKQRERL

>contig25898 Frame-0R

MRSDDAKIRLAQEMVTQIQDSFREDLKRLNWLDEPTREAALDKLGSVTKHIGHSTLEETF

PFQLRSDASFVENLQVVSNYELDRDIARIGNSINRDEWVTTGAVVNAFYVPRANRIVLPD

GILQSPFFAQDRHFVRNFGSIGSIIGHELTHGFDSSGRHYAGDGNLRDWWSNVTSNEFLK

RSEGLVTQYNSYEVLSQTGSGKRLGYTNGKITLRENIADNGGVKIAFAAYQKYTTDQETQ

DDSSSMSQAERNLSVNVADKLFCISFAQSFCSKRSDASII

>contig26275 Frame-0F|Blast-vesicle-fusing ATPase, putative [Phytophthora infestans T30-4](gb|EEY55016.1|) 0.0

MAFEAAVVGLPGNSYAFTNCVYVHLDDFRSLVKKTPQGVVTKDELRAHGLNVWINRKFVV

AAKPHKEILPGTVAVGTMQRMCVGLPLNQTCEVSVYTCASTPKNVLSTVTFEIQQVLTRA

QGNDLRVVDCTLLKDLFETEYIHQVFAVGQLMAVRCDGLPLRLQCINIDTVDGDTSSSDS

CSPRVGAYLQGAIINFTKGKDALIRLANQSSGMTRTVFKPDFDFTKLGIGGLDKEFNDIF

RRAFASRLFPTDVIQKLGIQHVRGMLLFGPPGCGKTLIARKISQALTAKEPKVVNGPEIL

DKFVGESERKIRELFSDARKDQEELGDESDVHIIIFDEIDAICKQRGSSRDSTGVGDSVV

NQLLTQIDGVDSLNNVLVIGMTNRKDMLDEALVRPGRLEVQIEINLPDEKGRAQILKIHT

DRARDKGALHSKVVADLDNCLDPTKFVSDDPDYKNLVQRTKNFSGAEIEGLVRAATAHAL

SRGTDGRTMHAIANYNPEISMEDFALALEEVKPKFGAPSDQLALYYKNGLIPYGSSFTDV

REALARVIDQVRSNDKTSLMSVLLHGERGSGKTALATYCAVASEFPLVRMVKASELISRT

ESGKCSYVYNVFEEAYRSPLSIIILDDIERLMDYVGLGPRFSNLVLQGLMVLVRNPVPVA

GRKLVVIGITSNIAAMHAVELSDVFDMCLEVPQLTEKHELDVVLKHTGLPVADDQKEEVL

KLLSDRPISVKKLLLVTEMAKEELNRTGESDITAQQLIECAYKF

>contig26608 Frame-2F

MARAQQVESVKEALQNALEVNDPKIVEQKLGQSIKIGFCSPLFSALFDHYSMLQNSANEE

DAAEISGDMDGLHAAVEFLTRRVNANAEIREDAVELLVSEMEEFSNPPEDGDAVQYDEAE

REKILLTVGTLRRTLEARIAAAARLETTLALPMEASSVGALEVSINAAREAGVHERLLIK

AEDKLTSARKRSVHSGERRRLSGRGPLLRNDSDTSSQLSTQNEEGRPRCDTTEWPGMATQ

DESVDPTSDKKDSVEKDALAFNHFENLRGFNSQSERALAKKLCWESRAISQSLSVLDDTS

DEGASTYAPSGQMALSINRSILGYMRDRIVFYREMLAQYILQIGLIKPSLVDEIYLQLMK

QLTKNPKRDSSIRGWSLFAMCVTSFPPSLALQKYVILFLKAQVADSNSFWRLVRNFAAYA

LKKLENVLEHGATGFIPSIDEIRGYEARPPFLATIQLLDGTPLADAFPVTPELTVTQLVE

ICSHFLGLEDHVVNFLGLTTISERAVLGKTSPSGQATTPTTSPFMSARHEGDDPTADSHG

GASAKEMALSMALRTSTSTSTSLSSYFHKFIAAPSFLNADVFLGDIFEKELIRGRDVRFV

LKIRLHPVYMLQYIDDMYDRLVYIQVQDEIVKGNLPVLEEKALIRLTAIAVAVDCEDAPP

LSMEEMMEMNLLEYLPQEWQVAHDEEEWAELVLDMLTDNLLDEHDALFPVSELQRTYIEE

VTRHRLYGACFFPSKLVNRGSGVNACFGLELPHYFVIAVNGYGLHILGRDGSMLAFCEYA

EIVYCGGSYPQYKFCFQKASDLTAPVDEVIVTTKYADELDAL

>contig27580 Frame-2F

MSVRSESGHSRNSSNVSSNPPPLPTPGSAPMPPTSTAARFSIFDSVTPEVTQSNPLDQLL

QQQHQVPPAAPPAPHPISSSNQFLQQFLASSSSSIPTTSNHMHSFPPMSAPTSLLPQFQQ

NLGAFPPPRSASVPPAFPQFHPVPSFSSVNGGPFPAAPRTTPTFSVDGSRGNGLGESASS

SITGSPRRAGSAIGYGTADVPTTPPGVTLGGETVNYYSNGDNTTRASRSLEVMPITLYNS

ERTSQLGNLISVNEHFISYPIRNGLIRVISQSSVDRLLLRKHEHHAVTELAFFSSKSDLF

LSSGTDHCIAIWSIQIDPMSRELIKLVPTQAQRVKWHPSDCNKIAIANGSIVFITELSHV

GADGTGAENLYEISVVCGQTSGQINDMAFSPGSGECLVTAGSDGLVQVYRVQERLPGQPA

EFIQRFDPFQGEAVNSLHFYDGNFFNQPGLLIGGGSNTRFSLWNAALTENTAPVCYQTVK

VHDDFREGSALLHETILDPSTQFLFVANRSKPVIYAFHLAQSSDSCTPRQFDNVTEFAIA

YPVLSMGLLNRINPGQPARDGSDSISASDGLNFTMQLYCLQTQAIQRYLVGANECYLPVA

RGSIENEIETGENIGQTVGAMTTEGEGSYQTAAESPRAAPAVMPAPETEIDVQAPDEVDA

EEDVENSDQHAPLRSAYNGLPRALTSPGARSNRSSRGIGTRSLHLATNDDAVSVSASSAT

NDDGNLPSLRFYSRSSPSSSVRAFQDESSVQYDLSVDDTASESQQQTLLAFLRRMETAQI

QRDEELRDQMRAVIGSLGNHLTAQVSMQVEKSIQKQLQSVLVPAMGRIVLHTMENNFMKP

VQNGFQHVISEKLIPLMEQKLSDSLATALPDQLANGVDEMILRVVEDVRQPVRDSFRECF

QDILIPSFQAATQKMFEQINDTFVQGTRSAFESSGQSTSNVKVANQLDQLTRVVESLSQK

VEQLNVAFNSRIANGAIVPAAKTAEESQLEAQQNTVLDFLFYLSRNDWEEAFKFALGAQN

VNLVMFACRQCDPRVVLGCHPPKLSQTLILCLVQQLGADLVDDLETKLNWLRESLLVMDV

RDQTIAGFVTSVLQELQAALMSVPVQSRESQYTLLHHVLNSMLNSA

>contig31110 Frame-2F|Blast-homeodomain transcription factor, putative [Phytophthora infestans T30-4](gb|EEY61507.1|) 0.0

MAIPVKRAMSISELRNTILVKVKATPPRLFYRKVAELAAIVLSVVPLALRCTIQCQEMDC

LPTTQEPLEVLVWICQFLKELSTNRLLQHCQMLLSGASVISISCMLSTYYLASIVFTALA

DAEVTYHRRFLYAKCFTALTSSRRSRLAKLPHFRLKNVVNIKAWISLRGGRTWLKRQGRQ

RAADEIVSTSFLIILVLLVVMGMQAVSDGSPSLSPESIVHIEVAMWCMLSTVFMLRFMML

GSNINRKYQNTSLLLTEQMNVYLRLLAKPHKKDKLLVSNNVLKLACKLL

>contig31433 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59508.1|) 5e-22 NOT\_ORF

MSLRELLMWSLTTAVTECSEAQLVTLVLIVVVVAVALLSYFVVAPEYEKHLNKQYSASVH

AASSPLFHDQKERNQLLARMKLRKHKSLDT\*DSESGSSGEDTLSGCPIQRRQRPFRA

>contig31558 Frame-1F

MTAQLQPLVIELAVEGMMCMKNCGLAVQSALHSVEGVADAVVNFDQRSARVECVPGASVT

ANELVDAVESVGFGAAIKPSATLKTDGGSLTLELLVEGLMCQKNCGTTVQNALRGVDGVA

TAVVNFEQRKATVTLLGPCSTTLEELVDIVECVGFTASAYDATRAAAIKLQAQKAQQMET

ENVVLDVPDATGHPRAVFHVEGMSCAACVKAIEDFVGHMEGVLLCRVGLISQKADILFDR

DLIKNEQITLQKCIQDAGYNATFSHVVEPGDDDSLEIKFRVTGMTSAACGKKIETAVGNL

PGVTKVVVHLSLNKAHVHFKQLSKTGPRDVQECINALGFSAEVASETIDQNAMSKSEVTK

WRKLLTTAMIFSLPAMLIHMVFMYIPAIEMILMTRVINAVTLKLLLLFLLATPVQFGVGQ

RFYVATWKALQHGAMGMDFLVVAGTSMSYMYSLVSLIGSAVHENYNGHHFFESSAMLITF

VTLGKYMESMAKGKTADALF

>contig32296 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65875.1|) 2e-33

MLISAGVKPPTHPLWDNIEA

>contig32421 Frame-2F

MIYNALPKACQTFCMSATLSPELEKLKRSVLHNPAVVKLEEGATDGKLQQFYLPVKSGDK

DLLLYALLRLGVVSGKVIFFVNSTDAAYRLKLFFEQFVIKSAVLNAKLPHNSRQHIIEEF

NRGLFDYLIATDDSVDRDENNYEDEDDEEEENKSTEDAVFDDGAEYDAASDLLDEEENKN

DSKEYNITEVNGAVDVGEDEDEASENEQEEDKVKKKTIKTVGAKRGQADDASYGVSRGVD

FRGVQFVINVDFPKSVRTYTHRIGRTARGGASGTALSLVSKDDAMEERALKRVQSKQVAV

RSETNEVMAQPAELAFDLKEIDCFRYRVEDVRRAVTRVAVCEAQLADVKKEMLNSERLAA

HFEANPRDLNVLEHDKVVGSARVQPHLATIPDYLVPIELQPPAPVRTKKKFNKLNKRQRL

ADVKRRTDNDPLHTFVAPDADDKKTTVEDR

>contig32937 Frame-1R

MLIIWKRLIARFHATYLNFLFNIAVATNRLCIST

>contig35796 Frame-1F|Blast-alkylated DNA repair protein alkB-like protein [Phytophthora infestans T30-4](gb|EEY68761.1|) 4e-08

MEAYKACEKRWKSSMIDDLLLDAALVDVRNLSTEQQKNACCVGSWKWSQNLEERPVLA

>contig36407 Frame-0F

MPKERRVAFSGAEVIEYDALLAPVIKFCGAHGLRNTETLALECEARGLHVSKAHLTLQYI

KELQLSLRSRGFEPISDDLKELQTQRRVIELLSTWASLDELHRPLITDILDPKAVRRAQL

ATKQLTGCVDDGYVFGRRFITVSTFVDMMSSEEILKMARERATKLPELDKKQRSDIKVRQ

RELVGLFGKARGRPLRSLTLRQTIEEAEARGMVLPEGRLMKGKKNKRAWVDVLRPVMLAE

LKASKIRQQQEIMLRTKLIQELELGKRTGDKKNV

>contig36498 Frame-0F

MDVKIALDAEIMKYRRILDREEHRVAVATPNTLGHKRKKEATRNVASKRTKRTSTETNVL

VSPVQIAAIDLKKDRITLKNTSNDAIPLGNWVVRGQMDQTFRFPETYVMRPHSTLTVHSS

KRNKNAKNERQKGEDSFLANKFSLNVKGDFVVLMTSDDVPVSIKSEGLPEDEVRAIEADL

RADFMDDDAPPSGSCALM

>contig37444 Frame-2R

MEVAHRRAKVIANEVKEMRHLDKDVKGATTTKFSAVEAVGIISGAFVTSFQRAKHLMGAE

KKEYNLLSGSSPITGMSKLDDPDTDGDGLQLSPDALRNDTKRFRTPPLKPALKRISVYSA

AALESNKKFTQMHQPMTKMGIQWHEDVLDDDEEFIEDKSDSSPESLSLIMDEENSSARPP

ILNFKSKCDEPKTPRSKKKRKKLVRSMMRRLTPPEKEELYRQRPDLMIVPNWAQKYREEL

AGEDSTHWNTWLLAMISVLVVLLLVFLLLIVRQRAAASAQRAD

>contig39190 Frame-0R

MGNTCCSWYSKSEPDIEDHVDASLENKLLEKQEDDVEVTTAEEEAWRQRREQLRDEQDMS

MKSNDGDDPEDDVRSRRSHDWDLSNHRADQSAALEDDNDNEAFGIEEEIIRDSVNEYQHG

ADEAIIFGRLTQLTAEDSYATNIESIQGDDDLRVFRDSEQDSTTALSVSLLQSSSPSSFR

GSTPCSSYPDELREQDQQKYGNDITSGTTKQRV

>contig39864 Frame-2F|Blast-pre-mRNA-splicing factor ATP-dependent RNA helicase, putative [Phytophthora infestans T30-4](gb|EEY62021.1|) 1e-169

MKSLGINDLLHFDFMDPPPEKALIRSLEQLYALGALNGLGELTKLGRRMAEFPLDPMMSK

ALLASEKFGCVEEVMTICAMLSVNNSIFYRPKDKAVHADNARLNFARGGGGDHITLMNVY

NQWVETNYSTQWTYENFVIMRSLKTARDVREQLEGLCDRVELERTSNRSDHEPLRKAICA

GYFYNTAKLDSSGHYKTVKKAQSVHIHPSSCLIKLEEVPRWVVYHELAFTTKEYMRNVIP

IKSEWLTELAPHYYKTKDVEDARSKKMPKAVGRAG

>contig40121 Frame-1F

MIGYSCCQQQYLTDLTHVKAHLVTVIMR

>contig42444 Frame-1F

MNAIVQALAALPEFVTAVLDEGNLLRAIQMHLNRNSKGKTMEQVKTVFNKWRTSGDAKQL

PLQYTLSQMLQRVANGSETPINPEPLKNVMGKKNSIFATHFQQDAHEFLLNLVSEYEQEL

VQMVHDVTAKIQEEATTSSTAQNSSLVHFFRNDLKTKSAAQEKSDRSVDAKLDLICRLTP

AKSFRAEFNRTLTCRKCGYSRKQPETFYDFSLDLPCKSFSEPQCIAEQEPQAQPSPEKQC

FCDLTAVSAREGYYCCPKASCSYQQKIENGVEPAKSPAKPTIAVMKSTVSPLMSTGDCAS

RPQHIELGSLIRKQFDIEVLQVNCEQCKEGREAQSAYEIQSLPSVLVFHLKRFEVNPHTG

DLYKRCDPIVPPAKIDLANFINLASSTGGETRYAL

>contig44363 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60536.1|) 1e-103

MRFLDAPADVAGGEAVTHWVVELIWSRLDPITPRFEANEAVMTALFELYGWCLQTLRHGM

APQLGGIATLIVRVFEQRRFVAPLECASVAVDVFAKDASAEIVESFRGLMGALSQSAFQF

FILHSLAESPDVLRSFFELAYRFLLFCPAAVLCTAEFPVLLDLSLACLGNQDRPSTNAIL

MFLTFLLNESAFKLASFTPTINASVLD

>contig44433 Frame-2R

MTLASFTRNIGANNGKSNSIRHSNHSDEAGSFKTYTPAGRRYIVMTVLVMCMSTSCGR

>contig44558 Frame-1F

MLVAAAATDEQMKLTSTCLEDGVIDSKVLEAIVLPTIANPFRHVGIKWRLRDSRDYVCLD

MTGMDRRNRDGEVLGYSISHSVAFAQVPSFTNFGIERANMSMCCLFRQKTRETVECYARG

FFDIPSDSKDLLTSLSIHATATQWLNVVSKYADCAEMKKLVWRMRKNSGLPVNGPMAIEP

TTTQTSSQSDKSTKECSVCTRSFKLSMLRRTCKICQREMCSSCSVKKLVCVLAPDRRTVF

DKKRTFCTECRYTVTQCDALMIAKDEIRALQRTKCSAKMHTEEDDDAVRTMPVFNYLVQR

DPNFT

>contig45412 Frame-0R

MFGVSETAKQHEQNPVGMGNYKSMTSENVHEMFGGLNEYERFTTAQYYRQRSHIAPAAIG

RRATNLAERKQFRANYSKLPTQKATMMWLAFPVALMVLWGVNVSIIRNDSKKR

>contig45467 Frame-1F

MDISTLPLGTQEVLSDLISDRGLSAWQVVLGVRIPADSDESVDIIYGNALAESLQEERIN

RKRKRNCEHKDSVIEKPTWSCFIVYPAVSSLTSPTINIKRIVQLQQRADANDPTVAPSTR

QTFLCLTDGANISYYVLKNPDLG

>contig45841 Frame-0F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY70221.1|) 1e-140

MASQQRYYKATETSLDMLTRLSKRHSGVTHWLRSNRQSCVWMEKWLVAHRGVDGYLQQRK

TVLVKPNSTSSWVNVSVLSSGLIKAIDRSITKLLPRIRDILDPEAVVEHFYDSDDNPKRL

VGKRVRVKWAKDKWYEGTVQEFNEETYEHFVAYDDGDKRSYHMSEKQFYVVK

>contig46314 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65927.1|) 1e-113

MTSADSSRREFCMVASSSYEMTHWVCAIQNAINSGNRSTFDGATDFQQLWTDAGIQGFLI

RYGVRKCSSRNRLQTRVLELNFAEQTLTNSRRGETLTTFHFTDIRNVSMGSVRSRGEDYG

LSIDFCGRHRSWPIFLDTVEARDDLFAILQRIVHNNVSGDDLERRSCRLTLKTGHLEMKN

AGPHATLRGRLFVCLYENCIMFYPADGDTNTRPWYVSTLKGLRLSV

>contig47421 Frame-2F

MHFFCMGMPISCSNSILPTFPPSSAMLRQFLASIVDR

>contig47942 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58623.1|) 1e-127

MLTIRWQGGIWSSRRQSTSGECSRNTKDASSASTGALTTYPLVYWQRLGVLKSLLDLFAL

FCRVAPEHHQWSIISLCFEPLLSTLYQPATSAEGSASSAPWSEHDSVSTGTSICSSFVAI

CSEYVKPSIYRSIGSSPSQHGELTPTTKLSQIWSFYLTALVPHAPMHICKHIYQYLTRLA

WEHWCLTLEVVQQMCALVQTEKQQLSRVAIESTDEIVPPLASRLSPYPFVSWLVRDILCR

TTWKATNTWLDAQSETVCSSFLLAFAKLCIELVLDMPHFQLQSGPAVSANALPP

>contig48554 Frame-2R

MNELRRALKVLSVQRNAPYYMQHSSPQRVEARCPSWRQRKRRVGDIKDSDIVASECDFVV

SANRHANGRVYVTRAIFIHSATCSVLNARIAANTETATTEAEKSRASTVTASALLETALP

YMGQLATSRGGRDAVKPKDVSDIMKEKFGVQPSYMTAWRALSAFRKQRKQEDSSSYMKIA

GYLRAFAATNAGSVVSFEHQDSASAQVLATKPGAKIFARAFLCPTPLHDALKNCRGSMLL

SVFMVTSAFGGVVLTATAQDAMGDNVPIAIGLAPAETQTEWQFFLQQLQKAFSDFDHSIA

SLVHNRGDSLTSAIQSV

>contig49229 Frame-0F

MKTSDVRVQETQRTLEMMQVEFDQWKLDNACVQVELQERFESEERVLECQGEGSNAANSR

AVDATGVDESRECGVDITFNDGFCVVGSCERRFIKSTRGFESK

>contig49661 Frame-2F

MTSRNIVFGSSNSLLTYSGRSMAHKFIIIMRKPIMRAYSHKPMT

>contig50191 Frame-0F

MAIGRRNEQLQLSVTTLKRNFHVREEETQQLLLGLGALNAVAKELAALQKDYWECSSKNA

VLIQESLEELSNCSAQVDTLKRCRDVTITQLQDFRLDCLQKMNNLASRLDGLADSSSLEA

ESFVTDVEAMNPKQQAVKELKDELIQVRKRVIRSELATSVPSCSNLESTTPPESIERMNL

ALEMLDKLHAEMFQLKQSLVQDNLSFRQHFETLLMQQMACVQDVQDNEAERIHEEMDHMR

SGMCEILKDIHRLKERTKYLVPSMARVGFRKSSKVPLPHEPRWFGGRSGERIDEHRSIAI

SHSGGFSMATRLCSNNLPHTEHDFSDDIHCPGVLSIVSDACYARPRHPRSSKSSNSSPGR

SDEDNWLMTTENAPAADQRPAQPCQSPHYSSCSSSLSGRLSAYRDETATPTAEQFEQRLL

EQHRLFWISEGAG

>contig50542 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY65284.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54655.1|) 9e-64

MLVLVEIFFVTLVFKLVVMGSYQDKIFKQVMAAHGFKELVEDEKHHASCTRACCSCFRVS

LWLRLVLLVVTLPINLLPIVGSVIYAWLNGTIVAWEYHLLFFELKNFTFAQQKAYVTDHK

VQYSAFGMLAVLLEMIP

>contig51714 Frame-0F

MRAREDCFFQNCARPICLLFYDHCRQIH

>contig51949 Frame-0F

MKVVVIFLLVVFTLQDSKRFQGAIACSTSSECAWGHSCVAGESHNAVQACVPHTVCGGPS

MGNCPRKNERLA

>contig52690-0 Frame-2F0

MDSTATPRRSETDDDGENRLNGRSTFEPVFSDLAEINKKKIHSETKLASEAAVNNAPSPT

RSGVIIQHVEEPTVLSLKSG

>contig52690-1 Frame-2R1

MTPLRVGDGALFTAASDANFVSLWIFFLLISARSEKTGSKVLRPLSRFSPSSSVSERLGV

AVLSMSSSDGKFRNSSSPLSISAPCSLSSSSTSSSTPPNTNRLISAELWSSIIPKGEETP

ST

>contig53200 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4]gb|EEY65284.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54655.1|) 3e-17

MTSYVVQGMAYFAMRPRLWLMTMFPLLLTIIVAVASVIILFSVAFAPQAEWFEEAGLSNW

TSW

>contig53473 Frame-0F

MQNANIAPKQRLSVRAITTQTTSKQRLSMRHERAVASVRRSCIRFMFLYCDVTVGDVRVF

VLPCRGYFFHRRLNLRLSMSLT

>contig53518 Frame-1R|Blast-nardilysin, putative [Phytophthora infestans T30-4](gb|EEY61296.1|) 1e-90

MLFMGSTKYPDENEFEAFLSAHGGYSNGATDTEVTSYTFEVGPASLETALDMFAQFFISP

LLKAQVLDRELSAIESEFSQALQNDRIRSQQVLCDVSPMTHPYHRFSWGNKKSLQTEPET

SGVDVRQHIVDFYGKFYSANIMKLVVCGENTLDEL

>contig54018 Frame-1R

MHYLQISWPLCLQRFDKLLLALSRLAREVPIALAGLYFLLALMICILQLCKFGH

>contig54087 Frame-1F

MQRRLKLFSVLCASNFANRREELGSVQKSGVQFPSLPWCASYSLSSCPLNQASIAPITEA

SPDNL

>contig54173 Frame-0F

MHGGGVHTRCLQDVELCSRLYTIKRLGRYSTSHPRE

>contig55224 Frame-2F

MLEDRKSFYNDLQIERTNYRADHSIDAIRKKYARTLEMRTESTMSMSTRDVTLATSTLR

>contig55901 Frame-0R|Blast-tafazzin-like protein [Phytophthora infestans T30-4](gb|EEY53093.1|) 1e-67

MIRAIFDKVEQGAWVHIFPEGKIVQDEPLGGRPSPRREEIGRLKWGVGKLIARATTRPIV

VPVYHYNMEKLMPQDDQNRVISVLPKKNLNLGVIVGEPLSFDDLFERYAHNCVARDSPWE

TQEQEKALYSAITRRIENALLALEKKTHSWPQ

>contig56261 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65363.1|) 1e-17

MKSSVFNEEIKERPLNTQRFDSRKTAYTMCREVLRIIMSQKKVVNFCSEKQKIILSNTGL

Q

>contig56694 Frame-2F

MKEGRLRMKKALVPYSRASNASAL

>contig00029 Frame-0F

MWTALGLCAGGFLASRAYATEPQLRYGFGDCVDEKRTLYYYIKGDGTCSANSTGQVLAKP

PVHGLRCDVHCARGFYLGANFSGPTPVSSCERCPQGKYSLGGGKLFSQRTNAWTSPLPVE

LETDCMTQDMFTGEWKHNCNPWSASKDGSLISSGENSGVLENFGGTKLYSTLRIGATFVR

DGYVTFKYRVDAELPYDGLLFQVDDTAGAESVSQSDGWKEKVVPVTMGAHVLAWHYRKDY

TGDVGEDKAFLKVIEVVGTAYSDLHCHTCGGDMTNSGGSLCAFCDVDEYAAAKSNSELEF

TCYTCPDNTHAPKGSIGISSCVEQRPCSLDDVNATYTPCTNGLRNVTYSWRQPQTCELQQ

TSSIQLPKAEQGVECASCARGYQLGKGDECEPCGTNQVRSVTGQCTICRAGTVVVKTLEF

GVGTPDGWEEWPSIVDATAATKAGWKLTKSGVLLAQHTSPDDESGRWKRPSRTVLLFHVL

FEHSGSLTITYNLSGVPTFEDIGSRAWVELEIRDVGANSIKIKREMNITGSSYDVASSSS

TSDVTDEFTATHLLHGSENGEYSQVIPINVTTAVLKEIALVVRATSAEAKRAMEVRVMFL

GLVGTRDGAGVTCENCPMGYAPFESEGTGCHVCPAGTFADTEDPSGIVACVKCPLNTYSK

EGASTCTPCGANTYSEVGAITCAAPQALTVKASPTASLSSSSEVVSSALGGLQVTYNLSL

LEALVWGNASLFLDDTVYGNATSLLSTTRVHASIPFEADGQSFWFSGLFRPLGTGWKEKV

PGQIVDEQVDTNKDVAHVVIASITNPREAGHFFQQNSGLYGNVLCSAPP

>contig08490 Frame-1F

MTEDDVETYCVRLPSSKRTHEASKPEQILNETHQVMPPLAEEPSVSVNRVHHDNMASTVS

VATPPVVSQGTSRQRPKVLSLNANAPAFVRITNATSSPSTKQAPLRVQIPETIVNENEEE

EEEEEEEETIKEDDDCESDESVEGTPEEINELIGKPVERIVTKEGCGIDVVQGAVASYFP

ATKMFRVMYYDGECSDLPYHEVFNSIPADLRPLGSGHLKKRKSDERSRNGDTDDASPQLC

KTRKLSTNFSASLKRGGSPTSPTIQENDMALIDTVEHNIVRKVLFIIVSTVNNAMMKSQL

VVLSSTDLKDEEALKAFVRKDGLTSLAELISKWDNRVETEQGLLLVLKILAVLPGITKEA

IMDSRIGKRVRAIEKRGDYQDLSIPGLASWVINKMKADVTEAQDTSERETNKASQEATKH

SQGSNGLRRSTSSHRSDGKRDDRTATTSKGAPNTSANKFSTSSPVTTGVAGLKRSNSANH

LLNLMNSHNGRNASTTRSDRDIFGNRVIVEKKRRLGTAQNWRARRSTVVLDQVTRRVTEK

AQDVGGLKPLEVVQEDWKPSKITFAGTDSVCSFDKEVEVSKLLVFRPSGSPKTPTFGRGK

PLTGQLKSILRVRLSPRPASRLSTSKETSAPPKIHVTTRSESDSIVVLSPRSRATLEATN

ESPTFNTSRLSYVVSPTEKKKHSFSPPPCIPVSEQPPLGFIENDENTIIFHEDNRVKHLN

ARDEELHHTATTTLSPVVSEDESADVLETSCSDTNECVSKVGTTNPTTCSSKSTERNVER

TSADSTSHDLIRLSVYS

>contig09255 Frame-2R

MPECLCFLLHTMLPKVTSGAQEEPGLFLTNTISPMYSELRRDSDKKTSKGARAPHREIRN

YDDFNEFFWTKKCLKYDYTNIGEAFANYDKKGRPKIVKKTFNETRSWTRAIISFRRIFFM

NCALFLATLGFSINMVLLCPDSAIMYGEDIQPASGSRVLEILGKKYAAPPGALVENQDDT

LSDTIETGTGAGNQCLYAKLATCLGVPFFTSASTTFGTLPQDFRELLRLVPFTKCVEKTV

GRCKCYHDLIDGCFSGTGNADEISGEGSVASVVYDQRECAPAWLAQVKSVLNQEGDGLLN

CDMCQIDITSLAQNPTRLMDLMQGLINTGRSDQGAMALLGGLAMIGLVCVCELQNRFFSG

IGMGFVGRSMPVPMKTYCRYTCFWLVLYVVKLIFDYQFVIKTLVETTLLVYSAESSDYLQ

YSHFMLQITFHNLLYVLFLWIPAWMVFLYDAQIFYSVLSVIYGSFAGFNLRIGELRSFRI

LRLTFKSIPGVFNRKLVPNIAEEQAKKKKKTKKNKMDKDEMVMPVRRFERISMSQGSKPL

TVKTQKYSSLLDHRDDEDVYSEMKTPNGTDEVMSMQSSRSSNIGSITGVSGAEFERTIPF

AMAWNRCLTSLREADVISDRELNVLSYLIDSKDTVGRKLYPPAFLTAGKLDESIDIVLEC

SALYEKLKSDKKKKEKVLQKIETTMRERLTKDDLRVESILGSYKFSSQVLRILLGDEHKE

LDDCYNFIEEMASHQQILKGLKLDTLYHCRAAAAELMKSILEVPKKSTETSIKFQRSLYK

VIDSVESVINCLKTVLTKQENLVQMLNDTPLKPNSFFFPGDSQHYASVQLQKIVNDEAAL

DIVSRAYQLLTVDNFDAEPRSEEGRRRLRFFANSLFMDMPEAKPIRKIRSLTVSTPYYNE

IVMYSIKDLTAQNDDCVKLLYYLQTIYPFEWENLLERIVAKDMTEALKKNPEEVQLWASY

RGQTLARTVRGMMYNAEAIRFLHWLEIGENEPMHQLSCSCNKCCKLNEMVDLKFNYVCTC

QIYGKQKDEQKQQAQDIDFLLRKHLNLRVAYVDGPKKVKDAPPKFFSVLVRAQDEKIVEI

YRVELPGDPIIGEGKPENQNHAIIFSRGELLQCIDMNQDGYLEEALKMPNLLSTMDRGTE

KRPLTIIGFREHVFTGGVSNLASFMSIQELSFVSLGQRMLALFHVRQHYGHPDIFDKLFA

MSCGGTAKASKGINLSEDIFAGFNSTLRGGRVSHEEFIQVGKGRDVGMQQLTLFEAKLSS

GAGEAVISRDAMRMASRLDFFRLHSWFYGNLGWYFTQSLTVVGVYFFIYGKVYMALSGHG

>contig10204 Frame-1R

MRLDVVSRATRAAQRFSAQFPGQKLRVIHASATLRAGLAFEATQAHQKGRYAPLLPMAAA

IALMGVASMNGDSASCEGPAKPVSRDTVSQAMLKEVVAKLNRIESAVANPHRHSDGLNVG

VDVVLGAQWGDEGKGKLVDSLSQSYDVIVRVAGGSNAGHTIVHEGKKYKFHLVPSGILNP

NAICLIGNGVVVHLPSFLDELEELKRMGIDYQGRILISDRAHMVLDLHQEVDGINELRRG

RNKIGTTKKGIGPAYSSKMLRNGVRVGDLRYFEDFTEKMRDLVQFYKDNYPELEADVEAE

IKVYRDMKDKILTMTVDSVSYLNNAYVAGKKILVEGANATMLDIDFGTYPYVTSSNPSIG

SVCTGGGISPNRLNGIIGIVKAYCTRVGEGPFPTELHDNVGEHLGTVGAEFGTTTGRPRR

CGWLDIPQMRYSNMVNGFTELNLTKLDVLTGLQKVKIGVAYWHKGKKLDGMPSNLQLLQD

SVVEYEELEGWAEDISKCKTFDELPAAAQKYVLRVEELLGTHIKWIGVGPDRFDVITRPH

PLEKAYIS

>contig11957 Frame-0R

MTEPMRDEYQGGDHRGGGPPLNPPYGPRDDFRRRSDSRDNFDMRYRTPRGPSRSRSPHRG

RDTFDSGARVDGTRRDTRVPEPLVSYKVWMMRQTDELAPEVYQQRYEEYKKKHIQRMLRA

FFELHKREEWLQERYSPALRHRVEKVQMSHQMNEAKLFYERVRTGVASICLDEVTPVENN

ALTSSGDFVNDLEDSARVLYVRRVPCACPVGTLSEAIKKAGGPFLHLYLSDPMKKKAYDF

DRSAYIIYESTVAASEAMPKIHNTFVEDGNSFPPFRLQVSPHRARAPLKTPSYLSVPERL

TVDYHQSLRLAMALDARLYLGANEKRMQFGIEALLASEEVLVKYPTDKHKLDVIVAYLRR

VHHYIYYAGVQCLDMGDIMHAHPALFCRPPPSARDLEEEKARQEAQVDTGIETKGCTKEE

MNHEIDEKDVVAVSASTDTAKAIGGWAGALDEKVQTYIQELALENIEVKRSKARALVDEI

EAREEAALESTYSNYGEKASDDGKHRCRLCTKLFKAMDFVKKHIRNKHPELVVDKIAEVG

ESYMWEQYREDEQRPMPPLETSNSMPGGAVLGGRAGGSNGGRLNGGYRGRPDRDFNNGGR

GSYRDDGYRGRGPSMRDERMQRSSFDRRSPPRYGGGNYRRSPSSRGPALPRFPDNELPID

PRQVSTSYRDLDNLQDTEVELSFDALDSLPPPKKKTKV

>contig13331 Frame-0F|Blast-solute carrier family, facilitated glucose transporter, putative [Phytophthora infestans T30-4](gb|EEY57438.1|) 0.0

MRRRSFRSERDYPQLRPRSSWANLTRFVHKQGEHKPLLDDEDETAEPSYTYPLLLSCLVA

VINAFQYGYNTAVTGAMNPAVIFPNHSNMMWALCVSSFAIGGPIGSIVGGQLSTLLGRRR

TMFANSCLFVLAGAVMACAINMYMLIAGRFLVGIASGTATVMVPLYLGELAPPNLRGALG

TTYQLAMVLGILWTIIMAFGFAGPSLSAMQPGWRLIFGFTGILGFVQLILAPCLVESPRW

LLTNGKAKEAKQTLQRLRQTDDVFEELDSISAANFSETGDAPGVGQVLRDQSIRLPLIVA

VVLQIAQQLSGINAVMFYASSFFKSAGLANPLMGIALVYIVNVMATIVALMLMDSAGRRP

LLLWSVMGMLVSSGVLTMGLLDLVPYASFCSVGGVMSFVWFFEIGLGPIPWLIAAEMFPA

KSRTTATSIATMVNWLGLFLIGIFFPTMQEVLKDYIFVPFAALLVLALGFSYKFVPETKG

KTVDEILNELNAK

>contig14176 Frame-0F|Blast-mitochondrial carnitine/acylcarnitine carrier protein, putative [Phytophthora infestans T30-4](gb|EEY55598.1|) 1e-101

MSEEVATNKPTSGVVSFVTGGFGGMCLVATGHPLDLIKVNMQTQPKALPGQQPMYLNAVD

CARKMVAKDGFRGLYRGMSAPLIGVSPIFATCFWGYDMGKLIAIKATGQSPTAPLSMGQI

MFAGGFSAIPATVVMAPGERIKCLLQIQAQAIERGEPKLYDGMIDCAKKLYRTGGLSSIF

RGWEATLLRDVP

>contig14280 Frame-1R

MQEAVVQSEQAARSGDVELSLRCVEKVELLKQKRREALRQITAGSFNVVDTVNQKLRVCD

VCGAFLSIFDSERRLADHFGGKLHVGYVQIRRKLKELAEKKSNIQQVERRPIQGLRSRPR

IREEQHRIKRPERESREPRKKRSRSRARQPNKRSRDHGSKFRRSISTSWSRSRSPERRQR

RNYRHRR

>contig14653 Frame-2F

MEFARRLSHTSEMLQTSTMKDARRPEKLHVNTNIARSPKVSHEPNQDATPTSSPQLGPQS

TPSSTHHADAQRRRRSHSECLLLAKTSGTTDLPGSCAEYISNVKQILARNDDQLMDLKRR

RSMNLSHPSLFK

>contig14792 Frame-2F

MLQHFFCALCVVALIACLHFVAAAAAANQPLLKMQQNRSLASSVKGVKGLVDVFGSTLPK

STVVRSDLLKIEGDVKNSVKNAVESWSTISSNFLKITLDEEN

>contig16035 Frame-0R

MKLSISSARNIRMPLAFMKRQTGAGGGHDRREIGASRMSGQLPSILSSISLTAAVYLLVT

ELNGQPRHRSREQIVSSVS

>contig17054 Frame-0F|Blast-peptidase family U48, putative [Phytophthora infestans T30-4](gb|EEY66429.1|) 3e-15

MRFSVTATTAVVACSVVAAAYVGVLYTLPHAIRRLPRDHPTHHTGTLLAYLYLLCNLSIC

AGSLL

>contig18657 Frame-1F

MYVLSVSILQKTILRKLPCQLDVG

>contig21903 Frame-1R

MPRKDRVKYRFLQSRNKQNFKRVITAHKEMPVLSGASAYAFYQSPFCRLFLRSLIIIIET

KGDVPIYF

>contig21976 Frame-0R

MHVVGHRLAGQVAVITGAAGGIGRKSAILFAKQGAKAVVCADINVNAAAETVQLVHEELK

KLGKNDTVAVAVQVDVSSAKDVENMVKMTEKDFGALNVLFNNAGIMHSADDDAINTQEDV

WDLTMNINVKGVFLGCKYGIPAMLRAGGGSIINTASFVGILGAATPQLAYTSSKGAVIAM

SRELATIHARENIRVNALCPGPLNTELLQKFLDSEEKKQRRLVHVPMGRFGEAAEMAKAA

LFLASDDSSYITGTSFMVDGGISSAYVTSEGRVDPFGGPSEV

>contig22568 Frame-0R

MPLEPPPSLTIEPWTSPVQNEQYFIANACRITMVKSISQ

>contig23541 Frame-1R|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY55978.1|) 1e-171

MGKGNATWVKQRRDRFEEEIRLFYRDEIRHKQELMLTRLEKVSPFSKFPILGNRFLLLRL

RGKGGNGEVWDVVDYVNNKQLCALKLSTSIRHAQREHHMHSKLNHPNIVRVGENPFLIRY

QQHQYTAFTVTSVQSDLQQLIEVYEHLDDDSAYRVLAQLLNALKYLHEDMGIAHYDLKPS

NVLIDHDGSVKLTDFDLTRDVRTATFNSTAGTLRYLPPECFRPSRSDCEATAEKADMWMV

GILYCMMVTGKHPILPDKSTQAEVKTIMSRYAGEFRYARPVSDLSRWILEGCLHPHPRCR

PTAAQLMVALQNELPQY

>contig25323 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60761.1|) 1e-96

MLLEIVQLSVILWRTCHQTYWHSHPRRIFFHIVLLLSCGLRLLFWLGLCKSPVLTVGVAC

LWWSNTLVLLCTAAVIFQWSSALTAGRETAQERHRSKRITLLHVLVCLHSIHFIWTTVLC

IRVIVIGLPTSSSDIEDDSKHAHVLLLTHRMMNIVTLAYDVVVASYVAIQLKERVLTAAV

SDDMKKKSVVQMSLLMTLLIASLTLQMLMDVPYVILNRGELRQLLSLEAFCILKYVLPSL

CLNVAFLYIMRRVEQRDSTR

>contig25356 Frame-1F

MTANRSSAISWNVDFSLPGIVDDTYWSESYVSLNFPSVKMEYLQTAKVDFEYDSFQNKEL

TAIAHITMLLRLDSFDRGSLVIIKLCQSGPDPSWLGIYQREVQVDGVWYSLFEGYVNTML

FQTFVPKLCTTAYKGNTKAFLNQLGLDRSHRLAAIRAGFMMRSGVDAVLNVNNHYMTYTA

AVDPSPRMFR

>contig25770 Frame-0R|Blast-asparagine synthetase [Phytophthora infestans T30-4](gb|EEY60662.1|) 0.0

MCGIVAIVRSMKPDAELRQAALAAGKKIQHRGPDWNGVRVFGERGIAIEHERLAIIDPES

GAQPLVSSDPERRVTCGVNGEIYNYKELAAGLKTPYQFLTKSDCEIIIPLYLEHGPDFVH

LLRGMFSFVLYDYRNDFFLAARDHMGITPLYYGYGADGSVWFASEMKALEDDCVRFEVFP

PGHVFTSDTETCKPWYRPNWFEPGHMGKTPLDLLVLREAFEASVKRRMMSDVPWGVLLSG

GLDSSLVASIAVREKQKLVAQGSEWINKIHSFTIGLENSPDLKAAQEVAEFLGTIHHSYT

YTIQEGLDAISEVIKHLETYDVTTIRASTPMFLMSRKIKAMGIKMVLSGEGADEVFGGYL

YFHKAPNAEAFHHETVAKLQALHQYDCLRANKSTSAWGLEARVPFLDADFLDLAMNIDTR

EKMIDAKANKFEKFIIRKAFDDKEHPYLPEKILWRQKEQFSDGVGYGWIDSLKKLADKTV

TERQMKHAQRLFPYNTPQSKEAYWYRSIFQHHFHREVAAQTVPGGPSIACSTPAAIEWDD

AFKNAADPSGRAIAGVHVDAYAG

>contig25806 Frame-2R|Blast-tRNA-specific adenosine deaminase, putative [Phytophthora infestans T30-4](gb|EEY65141.1|) 4e-27

MLADCSLYVTCEPCIMCAGALAHVFIKHVYFGCHNDRFGGCSSVLSLHERSALPDSKLHR

GYMCVSGILKDEAIALLKKFYVSENPRVENSKKKRKLANLN

>contig26274 Frame-0F

MEELQNTPINASGRIGNMNDHAPCCSTVKYAILNTLNFSWTDDLLQTKFCDRALRFSNGN

ATIITNTVIVTYSFSGLAIAMAVATGKCSFGSGSTWVALGTPMIGTLAADR

>contig26502 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55342.1|) 2e-91

MVQRMEELVRRCDAELFAHIVERESVQFVQFAFRWMNCLLMRELPLDGIVRIWDTYLCED

SGFESFHVYVCAAILMTFGETLKTLEFQDLVLFLQSLPTKDWKENEIEPLLSRAFILQSY

FADAPSHLTCQAAQ

>contig26696 Frame-2F

MDEYSQHVAHLPRSEKPGLPLNQSFSSAYMLVYVRDGENDIHAIHDDLPMQSKDYNKSYA

ITETPDLVKTYRWQLNPVPIPQELVTRFHEEETIVARRKRAQQTEYLYMNVRIVSDTSVA

NLKRITRTLDFAGFNNCSTIRIRIKRAASIWQLYTRVYHITGVPLSRQRLWKVITRENRT

TRPDQALGPDVYNCCVESLIEDDASLKAPVKLYLQILDALSETPLHAIQVSKGLSRRKTK

TAPARLYRYFLDEFVPLEDEGTKEATIGPEEGGTGVLGDDWERSGINSAPALASDDILLF

IKFYDVTKELDHRLEYVGNVVVDSRITGAELEEYLHDALSIPLAKMLILYEEIQPTTVSE

IQPDATLGALEIQNGDIICYQYATNLGTTIVLNAVDEVPDASELIYTGPDGEPVKTILSS

NSDEKNIQDTFVASDSEPFHRIKHTERYPDVPLYFQYLLDRIEVTFYRYGLGEEKSFTLS

LLLSNVYDEVIDAVAAHLGLKPSQRLFLRLYQHSPINHLPMKSPLRHSRYAGDTQTTLEE

LLTEYMDRTNIMYIEVLEHPITEIEAKKELDVYLSSYDECFASTEPTTSLSLHRHVELLV

RPTDTVNELLQLLREGFGLPLDTPLRACEVVQHGTMITHVVEKGTELSRYWGRGHVSDPN

TAELLVELIPSYEVADKTSTNDSIQDARWFYKGVVHFNFQHDSEKWIHPHGVPCMVRFQE

KDTVGDLKERIRQRMGISASNFAQWSLALVKNLKASRLLNIYNDMDEDAVDEFPMSRLME

LCGEDFEALGSIGLEHADPTPPLRHLSNRRLETGIHIR

>contig26937 Frame-0F

MADPKQRRKLAYALQADLLFNPDFSLTPEVIEIMQVFFADLEPDARGTISCSTLADEIAR

LDPNAETTRRLQKDLADMDERIDFSAFCKYVMRWKVQSPEAVQTVYNSWASQIVALDFDM

THNLFFDLKSEAKPRNWKSLFGTDQQLQQRRKLHKGFDNVNHEVEDASNAKCGLHAEDTL

NPEARQNKVDNMKNIFSDATAAAANKISILTVSKSFVAGSMAGIIAKSTLAPLDRVKIIF

QVNDQRKFTFRNAAKMARDIYVNDGFRALFRGNLLNIFRVIPYAGLQHSGFDYFRHSFHA

YNFRKAERNHCTEMPKLSSVQLVTAGSLAGGLSLVVAYPLDIIRARYMVQMGKQRHTSIY

DAVAAMYKVEGMRSFSRGLLPSILGTLPYTGIGFSLNERFKNWTLEYKYRHLEDKGPKPQ

AIHLNPVTKFVCSYFAACIAQT

>contig28953 Frame-2F

MHSPALSGAIVRRKNSTSRKSNDTHRAQFGTESPQNNLSQHRRRHRSWVDNDSLSYKRES

TTLLIAKTSPIDQSSARKFQKSISSHHLPHLSSAVMYGVINSILTIPCMYGYAAIIFSHP

DFVSFMPALSKLVMFSSVVHQVMFTLLSSLPFAIGQVQDAGLIFLSAIATSICNSLGEET

SLKAKVTTTVVSIGLATASLGVVLVLLGKFKLAGLVSYLPMPVVGGYLAYIGLFCLFAGL

SLCTGLVINDFTSMLQIWDMHYILLCFPGILGGVILLLVSQRCENSFALPAAILLMPLLF

YLLLVLIGVSFDEARDFGWVSPASDPAGLTQMFDLFDLSQMHWDQIPKQLTTWLGMTFVV

AFSSCLDVAAIEMDMGSQLDINHELKSVGWSNVVSGLFGGYTGSYIFSQTVFTYRSKTNS

RVVGMCVIISELAIVLVPLSVVSLVPRFFFAATLIFIAIDLMLEWLVHVYQKILPREYVV

LWLSFIAINMVSLELGMVLGIGFAIINFLLGYAQVRVVSRRSRSSAAVRKLAARTLVGQK

RDAIVYLELYGYLFFGSSVQILEDVQKSVLIRKSFKIMEKEFFKESDTEPQCMDDSGIPL

TPLSKRDIPVVCLDGSPAPHSKGLPTEYVVMDFKRVSGMDATAARSAFMILQQHCKRHKI

TVIFADVLPEIRMLLLKNEIADKRSFFDNAESALEFCENQFLLHTAHVQKITDHHESMSV

LLHRFMGEPDNSSLFQGIDHFFRKYEVPQGYDFYRVASYPDRFYFLACGRVALFINNDGS

EAPGKPLSVLENVIPGAMFGRGRLFWPPISPNGCQGC

>contig29558-0 Frame-0F0

MKIVAIGTWLMEVFAHVLLRKECIELMNDFIVLI

>contig29558-1 Frame-0R1

MCKHFHEPRTDRNDLHGNTKIAIEPG

>contig29697 Frame-0F|Blast-dentin sialophosphoprotein precursor [Tursiops truncatus](gb|ACN91299.1|) 4e-09

MEEKSKKMTDDGVNYGMYSATSRSDESDIQGVSLDNFVAKGKSADDLLALDDCNSASNGD

SSEEDDGDDQSISSDSDDNVFVNHFSTSSTTHKSKSSSKTYTFYKTSHVIGVANENPSKA

STGRKFDKKDLFGKKNALKDDTVTPELDSFATSGVDDHLRVGMDNAPSHENDFLQLEDAP

ATKAASKSIKPLW

>contig29990 Frame-2F

MLTRGEKESRMAVPQGTPTEIKCEGYLTKRGHLFTNWKTRYFTLRGNVLEYFSSEEKSKK

YGAVTVEKVATWSGEAHGFMFYTSKQIPYYVYASSEAERSKWLRALKDFMVETEEVSCEG

YLTKRGHLVPSQRMAYYVLNGRSLRHYADQLAYRDNQSAMADVEIRSVALWDGEANGLMF

MTVTGNVFYVIADTVGEQQKWLSTVLKSTGSVPEPVSCAGYLTKQGHKRKSWKKRYFILR

GNTISYYSDYDMANNAKGKPLAEVLVEDVQKWEGEPFGFMFMTNEQVPYYVYADNDRERS

KWMNALNKLNVVAEEPTVEKKRCSNCNAVLTGSRFCGACGYNLRGTTIGDRTSRGHGGMD

DDIDGRDDIDDESTPFDELEALSEGA

>contig30466 Frame-2R

MSGAMSGGGTRARSGGMSSTLASGLSENEIRDLQEKASSLRNELGHIRDEKESLEKELVH

LKRTIEQYEKELPKIDLNVSATKTRLIDLKKNKITLEKQTKLSPGAKKNVEKLMATKVAK

EAEYSSTKLKVDMMAAKLAKIKEQILDVGGEKLRKEQDVANKITKQIAEKTKQMTKIRVD

YRNSQKNTEKNVLALKKIGEDIEAAKSKMEETREQITAMEEKALAVLQRCETVQDQVTTK

EKALRKDEAKYRKLKKEYDVMASAEVDLTNSLEDCEKMLEENGKKESYWKSKLTSLHAAF

ITEQEHNAGILEDERYLPARKRHKKNKNTDGNDDMDKKHKEEMEEKNDEEEEDANLIDTL

EKLPVLNTTALSRFSKEEMKYEISVLEQQRDELKANVNMGALAEYKQKENEYKARVLELE

ESTRLRDAKRHEYDELRRKRLDEFMTGFRIITLKLKEMYQMITLGGDAELELVDSLDPFS

EGVVFSVRPSKKSWKNISNLSGGEKTLASLALVFALHHYKPTPLYVMDEIDAALDFKNVS

IVGNYIKQRTRNAQFIIISLRNNMFELADRLVGIYKTNDATKSVTINPKIYEQGTTKGTT

TPVTKKPGTSSMNTPMSVSLPSLKKARRSSQQSIPSPHAQQNTTNMSTPLQDRTNQSHE

>contig30840 Frame-1F

MFFFRCDSILLSSSVGAFCKQVTTHDVGNYNFLSTHGKRIEENTVAPYGGQSMNIIDGCD

>contig31111 Frame-1F|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY67944.1|) 2e-09

MLLVPRDEPARVWYYVSDTVVKRVLVEHVLQCEAYMLFYRRRRNDKVIVRATSPRIETEC

SSTETAL

>contig31807 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68151.1|) 1e-97

MLRRSLLSTLHQKRTIASTIRNMNNGSMAMESSLEASKEQDCWNCHHATDCCSFFCTACK

AIQPIDTGCHCDYFEIFKVPKSFNLEPRSIEQTYWNLQKRLHPDLYGSKSELEKKLSAVN

SAVINDAYKILKEPNTRINYLLTLHGVDALGETASTSVDSELLMQTMEIRERIAEAADVD

ALEKIRKEISKHIDAIINKLGKVYDRNQDLESTERYAVELQYMVKCAEETETREEELDGY

>contig32297 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65875.1|) 2e-48

MRGLNLGGVVEFCRVLTCQPQLLLPQLSVKDMTEVPFQKLRDRGFRGVIFDKDNTLTIPH

EIAIPSHFASSLDECRRVFGDSGVVVFSNSAGSVDDKDGNQATKIEEELHVAVLRHKHKK

>contig32943 Frame-1F

MKVKPSFPLHFFLARCKTAGEMIGRKLWCIRLRASSPGGFHLPKRRRLLASSFDKIGFGS

VGRPIVERGIMEQMYVTIQNRAEGATVPELRDVLGVPTFKLPYKLAQGLIANYNISVEQV

ILG

>contig35120 Frame-0F|Blast-NADH ubiquinone oxidoreductase, putative [Phytophthora infestans T30-4](gb|EEY56224.1|) 1e-37

MLSLARRSGAVARNSAFRCASSVPVTSSTPAPAERGNIQELLSGNATARNGVEYVVSRVD

DLVNWGRKSSLWPMTFGLACCAVEMMHS

>contig35458 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66595.1|) 2e-49

MSGPLGRIVAQVIVMGAGIVSKAFVQAYQQAVHNARSGNAGVMAAKTVARKKEMSTQQAR

EILNFSSSDPAPSLNDIQKQFSRYFEANDPAKGGSFYLQSKIFRAKEALERSILDESPRQ

NDKAKD

>contig35797 Frame-0F|Blast-alkylated DNA repair protein alkB-like protein [Phytophthora infestans T30-4](gb|EEY68761.1|) 2e-19

MGGVSRRCYHGVARVFPTRCSLDFYKFDAISRSKAHYDELEYVKRYLNSQRININIRQVY

PGEISTSKKDSQTHSPQIAIN

>contig36147 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68178.1|) 1e-46

MAHIETKDPFGFVGTHVVRRKPRRSGEEHGWLTRYNEALDCYTLFVPGGGEPRILSRGEV

MKYLSAPNIELHDNDQDEFPPPVKDTTTSRYLGVKVLRQSHQVLSLNRSGEVDDIW

>contig36406 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68534.1|) 1e-84

MDAGDTHGTSSSSTAESSTVKNEGRNWNKLRVVLEASPTTMLLGNPDMNAAWRLFLYGNG

SPTHHLGLLTGSPTEVDVLSMLKVGDSGDNAPSEVEAIMPPRCRRQVFLRNARGERLGYA

VSWINEDAVGDVFRDTKIPIGENILQHKTELYRDMKNVFCGHSLELEKAFKAQGPFWGRS

YVFWNGGRPMTYIYEVFSPALEKYMGKVMLK

>contig36473 Frame-1F

MLSMVKSSQSVGTSKGNSSSSNTSASIEPGSPVAIAIASLAQGGNINLQELDKCRLYKPL

THQPLIQSQDDESSLHNDWHSNSGANQAAAVLTSVSRISLPTVAVKGPKKRSTKSKCSPG

LRSGKWTLEEEAFTNMIIYYFKRGLLDVEDGTSLRWYLAKRLNCEAMRVTKKLKGNSSIG

KQIFRSIENTPANRQAIRHAREDLCVVEARFLESLSGSGGGLPTRNTPSKPMPSSLTVSV

CGRKILPSMKNSESHIELAPMPQPKSEDARLLLHFFCEAHDTGSEDEPEEEYKVEDGSIS

IDLSHKFGKKRPLSSVVNEIKPSLKKGNTLLEVQEVGYQQENRLAVKIQDTNY

>contig37030 Frame-1F

MLLLHNNQVSKIQENLAEAVANLEFLMLTGNRIAQFSEVDHLTSFAKLDTLSLSGNPVTK

RKYYREYVIFKLPQLRVLDFHRIRPRDREAANAFFTSIVGQRAMQVAHDERVAESAQAVK

SVAVKIKEVVPAVGVVLPPPPSQASVLLVKEVLVEAELPKKTVVAEPMKKAEVLTKTAEA

EQIEKAKPLKMAADTSSAKKVKAMKMVSEAEPMEVTIESKAEPADVEMEHSDEEAVAPYS

PPKPIGQMTVVILREE

>contig42030 Frame-1F

MIPNVNVIDWQHRSLSSSQHSSPVMASASGLGSVTRLDERYVKPLDDLALDNQTESSGHS

IEISAVLKEPRPFAMSFLRPHQERLHRSMFESFNRMSDTPVKENINSLVPASVQFLMSRS

LEEEKDLSAKSDKEKAYLYKKVVNGVK

>contig44432 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63945.1|) 6e-06

MPRPETQLPRDLNSYDRSKLFKDGCGTFDDKRPKERWSQGRYTMYE

>contig45578 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57202.1|) 1e-77

MLWVGVKIAVLAAVVACYVSPQLLLQPLVGKHLGKAEVDASARVLRSFMTLMSYSLATMR

SSWFWVLAAVAALQLTFWGLQLAQESIVGLSVENEKKFLLIGTVACFGTIVSIILFGDYG

DAKARFRKRLMAFYSKHNPEKLHEVDDLIKKYELNEELLFERLHRKYNALAAGATNHSVM

KTIDESEFLYEEAEEERVEPDEETTACKENTTTFLRKDSGRNKRDSVAQEIQKKTRPDAI

FLEIEDYGELDGTPPVSPRTAATLAYTCRQSSTLIKDAIAVAQQAQQERIEFRIANIDSK

RGDGYAGH

>contig45840 Frame-1F|Blast-O-sialoglycoprotein endopeptidase, putative [Phytophthora infestans T30-4](gb|EEY53253.1|) 1e-132

MARQICLNNPDIAFLQINHLEAHILASRLPHAETSRPEFPFVVLLVSGGHCCLVLAKGLG

DYELLGNTLDDSIGEAFDKVARMLNASALEGGQSVHWGKLIEDMAARGNDRAFNFTEPMK

HRKDCDFSYSGIKTAMLREVKKLSELNLSTKEDLCASFQRTAVDQLITRTRRACKWSKER

MGDIVTSLLCAVVWRRMSTFAAAWRQQQGKKGS

>contig46315 Frame-0F|Blast-phosphatidylinositol-4-phosphate-5-kinase (Pi-PIPK-D2) [Phytophthora infestans T30-4](gb|EEY57162.1|) 1e-141

MRLRVLHSVTIYVIAIIIYWGLSFCIYVPFLVQGDNRSSWVAQMMNFMITCKGYFDFVVW

FQMNDFHESSKKGKGKKAGVDVDVDLSPQVNLALRCEVLYYTTTGIIQAVRDTQHLPPGA

NQQELYLQPQGTEDNRGSLGVDEYMIRTRPKAALGKGTLFIDYCP

>contig47158 Frame-0F

MKAKRLENPTTMLHSRRLQSTRRGYSASETVTWASPNATHVRSRPRGTQATSVATSKQEA

DWALAQQEVRPEMQADYAKDRVAEAEDHGFLPISKLHFGAFGDVRTMTLETVNFLIRVLE

DVWLCISAKMRGCKLEKSSYCFTYVAEKAGAVG

>contig47943 Frame-0F

MKKASLLRGTVKLCMGCRRNTCRRCREWCTVFRLEYRTQKPCKERFCMPCISDVTRVTVS

SFYISSLNEFTSTSIDLQSSIESSVKYDHSSHSSSPREISDCDLDQWFPATQEPPLHHLE

GLATFVERASVASAKDMQWNRNELQYFSNLLRESGHFQPNESTSSSTAATRHDSPTRTTQ

SQSFDPTNSMPLPRPVKIDGTHRAYMSEDFTLLHLQALSVDELD

>contig49295 Frame-0F

METNHGLCRCVAESTANVTSIKQIRWISASLMSKRAGLPGAIVCSQAKDSNYLTLIYPPP

DGRSTDDTLMDIYKAKKLTWPVATIESINYAQVTAFEVAQEQVDFSPRNDSFLPCFTLG

>contig49787 Frame-2F

MMPLLDSGSFMSVDNVEVLASVNIGTNESSFRTVYLSRRIMLAMHTLLQEADDFNSMNQL

DAITANSSIFLLQSITQRLKSFKDRNAEFIFRFQVRQATNERLISSWRPWQHSHASYWKA

ETVVASQTPR

>contig50190 Frame-1R|Blast-acyl-CoA dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY65023.1|) 7e-79

MRAIGVAERCLELMIQRAKTRTAFQQLLAENALVCSQIAKSRCDLNSARLLTLHAAHHMD

LHGNKVAQQAIAMSKIVVPQMALDICDRAIQIHGAAGVSQDFILSYLYATVRTLRIADGP

DEVHMRTIAKLELSRSKL

>contig50536 Frame-1R

MACATTSLRRSPSTSSLNGSCKCSPLMLMLPKSFDGLLVIQDPLQPDNNVGKSWYRISQV

SEILSTFLTL

>contig51715 Frame-0F

MKLLIVLRSASSSLNLSLGSSVSHQVETLTIPITRSPNVGIKKLRLVGHFPDPLAFLNPN

QKIAKSNKSDR

>contig52691 Frame-0F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72292.1|) 8e-06 NOT\_ORF

MEISYAMKKGVLSIRHTQCFDRMIKRSSNTNVNLFET

>contig53201 Frame-1F

MPLSASLPSENNLRLLGQTGLFSCK

>contig53586 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70608.1|) 6e-38

MDENGCYAILASDFVDEDLRYPYRPNERIRRDMMSVAMVASYRDTTANATAQGEDEMVVI

ITRWALSIVRRPGMVISNRVWDELRYSHVCWADLMFNCVRQTLGLPVV

>contig53964 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62334.1|) 8e-25

MDVLSFVLVSELSRPQKSMKSDGTNVSLWLTSLANFSGSFYRKYPNVELAGLLQYLIQRL

QNWASVDLIV

>contig54019 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60002.1|) 1e-62

MANAFLEKIRETAGGVDSLDSESLWSCPICTFVNESTAVVCGACNEPDPKLQDQDACRQL

QRQGWRCGKCTFINQPDDESCAICELTMDGQRGVPRGMWMCAGEQGGCTFFNLMTNFYCE

VCNRARPDLASTRF

>contig54172 Frame-2F

MCNFALSGKGLDGSDEENQWLEVFQDALQLQEHAFGDQFSQHRILDVILKHLLVSRSVKS

NDVQNLVKYWIALDIEAVDHVTTKL

>contig55298 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69570.1|) 2e-22

MLANVAAAATDAPSSSEFLMDGTTTYCWEVDTSIYSNTVDKSLVNMISAQGNGCPLKLSI

AIPTD

>contig56387 Frame-1R|Blast-COP9 signalosome complex subunit 1, putative [Phytophthora infestans T30-4](gb|EEY57774.1|) 7e-10

MATLEGFDMEVYAAKYSGRNRIERLLFLAKTSPALEAEATRA

>contig56628 Frame-2R

MASVLLKRVVPAASRSFSSYTKLWDLFSTTKVPAAKPVAPQYMMNMRDNLEFALERMRLA

RRPFVLQLLDQTARLVKKSNHGKRPCSHNRRRLKRFGRRSNK

>contig56930 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61532.1|) 4e-28

MSRPREIEYGVYGRVLFCGQLEKRRDGAVRGGWASRLFVLTPESLHYYRKATEFELLGEE

RGH

>contig58529 Frame-1F

MPSTLTEAETADFATSKVLDQAPQKASEAPTLCQEKNSDRRRRFTLNKLTRKHHAITEAE

NEDAADVSYPVSTDSFSDLSLKESGLVHTVGPQDFDLLCVIGQGAFGKVIQVRHQPTGEI

LAMKIVSNKYIVQHNSVSCLQAERDIMTKISHPFLISLKYAFQTKSNVYLVMPFVAGGEL

FHHLHRQGLLLESSAKFYAAEIVLALEHLHSKGIIHRDLKPENVLLGADGHICLTDFGLA

KEMAAVK