```
gi|85111610                                        1 ----------------------------------------------------------------MIQPL-VKASRPRLWVCSD-CL---------LRR
YKL134C                                            1 ----------------------------------------------------------------MLRTI-ILKAGSN------------------AS
Cre02.g073400|Cre02.g073400.t1.3                   1 -------------------------------------------------------------------------------------------------
Vocar20013694m.g|Vocar20013694m                    1 -------------------------------------------------------------------------------------------------
gi|32565901                                        1 -------------------------------------------------------------------------------------------------
CMS132C|CMS132CT                                   1 -------------------------------------------------------------------------------------------------
gi|268637658                                       1 -------------------------------------------------------------------------------------------------
Esi0033_0093                                       1 -----------------------------------------------------------MLAVRRSSGAGGGTNTCRR-WF----------AR
tr|M1C3Y6|M1C3Y6_SOLTU                             1 -------------------------------------------------------------------------------------------------
GSVIVG01018572001|GSVIVT01018572001               1 -------------------------------------------------------------------------M---------TV
GRMZM2G450659|GRMZM2G450659_T01                    1 -------------------------------------------------------------------------------------------------
LOC_Os06g47210|LOC_Os06g47210.1                    1 -------------------------------------------------------------------------------------------------
Cucsa.251510|Cucsa.251510.1                        1 -------------------------------------------------------------------------------------------------
Glyma04g13088|Glyma04g13088.1                      1 -------------------------------------------------------------------------------------------------
Medtr3g009160|Medtr3g009160.1                      1 -------------------------------------------------------------------------------------------------
Bra029169|Bra029169                               1 -------------------------------------------------------------------------------------------------
Carubv10025983m.g|Carubv10025983m                 1 -------------------------------------------------------------------------------------------------
AT5G51540                                          1 -------------------------------------------------------------------------------------------------
Eucgr.K00152|Eucgr.K00152.1                        1 -------------------------------------------------------------------------------------------------
30147.t000467|30147.m014196                       1 -------------------------------------------------------------------------------------------------
Potri.015G129300|Potri.015G129300.1               1 -------------------------------------------------------------------------------------------------
416778|416778                                     1 -------------------------------------------------------------------------------------------------
Phpat.016G041000|Phpat.016G041000.1               1 -------------------------------------------------------------------------------------------------
gi|71999758                                        1 -------------------------------------------------------------------------------------------------
gi|85107353                                        1 -------------------------------------------------------------------------------------------------
YCL057W                                            1 -------------------------------------------------------------------------------------------------
gi|66801567                                        1 ---MTIEASDAGG----------------NGASAVV---SAA---ASDGVPDSR----------------DAVNARKS-RWSAVLDWARS---P------
CMS446C|CMS446CT                                   1 -------------------------------------------------------------------------------------------------
gi|4507491                                         1 -------------------------------------------------------------------------------------------------
gi|14149738|ref|NP_065777                         1 -------------------------------------------------------------------------------------------------
LOC_Os01g67590|LOC_Os01g67590.1                   1 -------------------------------------------------------------------------------------------------
Bra004244|Bra004244                               1 -------------------------------------------------------------------------------------------------
Bra004078|Bra004078                               1 -------------------------------------------------------------------------------------------------
Carubv10019853m.g|Carubv10019853m                 1 ----------------------------------------MKIKE----------IVFSRLGLTFFL------
AT1G67690                                          1 -------------------------------------------------------------------------------------------------
Eucgr.B03454|Eucgr.B03454.1                       1 -------------------------------------------------------------------------------------------------
Medtr3g086000|Medtr3g086000.1                     1 -------------------------------------------------------------------------------------------------
Glyma11g37410|Glyma11g37410.2                     1 -------------------------------------------------------------------------------------------------
Glyma18g01380|Glyma18g01380.1                     1 -------------------------------------------------------------------------------------------------
Cucsa.394790|Cucsa.394790.1                       1 -------------------------------------------------------------------------------------------------
GSVIVG01010319001|GSVIVT01010319001               1 -------------------------------------------------------------------------------------------------
29929.t000212|29929.m004709                       1 -------------------------------------------------------------------------------------------------
Potri.010G054500|Potri.010G054500.1               1 -------------------------------------------------------------------------------------------------
164651|164651                                     1 -------------------------------------------------------------------------------------------------
Phpat.018G066900|Phpat.018G066900.1               1 MHTFTECVREKGGHPGRGIRAREQQPRRRKEEAKIGPLGATGLQPNFATAVQNSHLGTPYTTITQKKREIQNPGSVMELVSVVAPPGRRMLQHTLRAKGGPFFA------
Phpat.019G060600|Phpat.019G060600.1               1 -------------------------------------------------------------------------------------------------
Esi0023_0135                                       1 -------------------------------------------------------------------------------------------------
85692|85692                                       1 -------------------------------------------------------------------------------------------------
97633|97633                                       1 -------------------------------------------------------------------------------------------------
119899|119899                                     1 -------------------------------------------------------------------------------------------------
97030|97030                                       1 -------------------------------------------------------------------------------------------------
Cre13.g572900|Cre13.g572900.t2.1                  1 -------------------------------------------------------------------------------------------------
Vocar20008539m.g|Vocar20008539m                   1 -------------------------------------------------------------------------------------------------
439159                                            1 -------------------------------------------------------------------------------------------------
Eucgr.L02517|Eucgr.L02517.1                       1 -------------------------------------------------MLTVVACTTRIAL------SR
GSVIVG01031425001|GSVIVT01031425001               1 -------------------------------------------------------------------------------------------------
GRMZM2G133919|GRMZM2G133919_T01                   1 --------------------------------MAHARP--------HP------RQPIRFL---AAAAMLLLSSAIFT------
LOC_Os02g58340|LOC_Os02g58340.1                   1 ----------------------------------------------------MVFLIVSASSF------
PGSC0003DMG400030613|PGSC0003DMT40007866          1 -----------------MKY----------------RRIGSPPSRI--------LYGSTTTPSL---IL---TLLLILMATRF---S--L-SR
Carubv10000350m.g|Carubv10000350m                 1 -------------------------------------------------------------------------------------------------
Bra006067|Bra006067                               1 -------------------------------------------------------------------------------------------------
Bra028579|Bra028579                               1 -------------------------------------------------------------------------------------------------
Carubv10025914m.g|Carubv10025914m                 1 -----------------MKR----------------IRI--------------------MATL---VI---A--NMLMATPTSRASLNLLRR
AT5G65620                                          1 ----------------------------------------------------MLMATPTSRASLNLLRR
Bra024401|Bra024401                               1 -------------------------------------------------------------------------------------------------
Medtr5g030940|Medtr5g030940.1                     1 --------------------------------------MRHEALIGLL---LISNMLMATRLTLTF--SLSR
Glyma01g02480|Glyma01g02480.1                     1 --------------------------------------MRRSSLVGAL---LIANMLMATRLTLTL--PFSS
Glyma09g33490|Glyma09g33490.1                     1 --------------------------------------MRRSSLVSAL---LIANILMATRLTLTL--PFSR
Cucsa.273340|Cucsa.273340.1                       1 --------------------------------------MEKKSVVLRAL---LIANMLMASRIILAA------
GSVIVG01003850001|GSVIVT01003850001               1 -------------------------------------------------------------------------------------------------
Eucgr.I00597|Eucgr.I00597.1                       1 -------------------------------------------------------------------------------------------------
Eucgr.I00594|Eucgr.I00594.1                       1 -------------------------------------------------------------------------------------------------
28333.t000012|28333.m000566                       1 ----------------------------------------------------MASRMSFSR------
Potri.007G004600|Potri.007G004600.1               1 -------------------------------------------------------------------------------------------------
Potri.014G004600|Potri.014G004600.1               1 --------------------------------------MAETRKVHPVGAVL---LIINLLMASRISLSR------
Potri.014G010100|Potri.014G010100.1               1 -----------------MPTRHKRENENKNN----------KTISTLHTTQ--------HMAETRKLHPAGAVL---LIINLLMASRISLSR------
28658.t000001|28658.m000032                       1 -------------------------------------------------------------------------------------------------
30484.t000001|30484.m000014                       1 -------------------------------------------------------------------------------------------------
```

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gi|85111610                                          24 TLSPLLRQQRRRFTGFTAHAPK----------------TLTGTIPVTHKNGDTKHDDSL----------------------------------------LRSIFD
YKL134C                                              15 IPSPSRQNKLLRFFA-------------------------TAGAVSRTSPGS------------------------------------------------IKKIFD
Cre02.g073400|Cre02.g073400.t1.3                      1 ------------------------------------------------------------------------------------------------------------
Vocar20013694m.g|Vocar20013694m                       1 ------------------------------------------------------------------------------------------------------------
gi|32565901                                           1 ----------------------------------------MLRSVI----------------------------------------------LRHSRTISR
CMS132C|CMS132CT                                      1 ------------------------------------------------------------------------------------------------------------
gi|268637658                                          1 ----------------------------------------------------------------------------MKKEIG--NVLFKSINN
Esi0033_0093                                          24 SPAPRTLSRL-TWHGRKCDTPAVAAVSATARPAAAASGRFLAGGDDFRSNGFRRRNAHSVATTS-------RQPQRQQRIS--------SWLSPSSS--SLLATA-AR
tr|M1C3Y6|M1C3Y6_SOLTU                                 1 ------------------------------------------------MHALI-------RKCAA-AHVR---------ANT----------
GSVIVG01018572001|GSVIVT01018572001                   4 TPFRRFITVL-VRLNLQFKTTTTTN---------LVILRLIRSRRSSQVTGGVTSGHPKMLTLV-------RRAASSLCLR--------FLH----------
GRMZM2G450659|GRMZM2G450659_T01                        1 --------------------------------------------MNQL-------------------------------S-ASAMLSR
LOC_Os06g47210|LOC_Os06g47210.1                        1 ----------------------------------------------------------------------------------------------------------
Cucsa.251510|Cucsa.251510.1                            1 --------------------------------MSAAMWSVV----IRRSSWE-IL------RQI----------------
Glyma04g13088|Glyma04g13088.1                          1 ------------------------------MLWSLA-------VARNKTVQLF------RH---------------
Medtr3g009160|Medtr3g009160.1                          1 ------------------------------MWKLT-------SRF-----------------RPHINS
Bra029169|Bra029169                                    1 ------------------------------MWKLT-------RRL-----------------QPHINS
Carubv10025983m.g|Carubv10025983m                      1 ------------------------------MWKLT-------RRL-----------------QPHINS
AT5G51540                                              1 ------------------------------MSTLL-------R-------------------R
Eucgr.K00152|Eucgr.K00152.1                            1 ------------------------------MSALI-------RRYAAVLCHK--------RMLKPNYP--T-LVLTCHV
30147.t000467|30147.m014196                            1 --------------------------MMR----------WGAARRNSSRLWSQS-------RRYIAGHGSK---------QRQDPCSS--SVAELECVV
Potri.015G129300|Potri.015G129300.1                    1 ------------------------------------------------------------MFRRIPLGRFL-------TRK------IHNQTNGLIVPTTNVQKQQKRQILFKMGNE
Phpat.016G041000|Phpat.016G041000.1                    1 ------------------------------------------------------------------------------------------------------------
gi|71999758                                            1 ------------------------------------------------------------------------------------------------------------
gi|85107353                                            1 ------------------------------------------------------------------------------------------------------------
YCL057W                                                1 ------------------------------------------------------------------------------------------------------------
gi|66801567                                           50 -----WLALRTEYLQMNGSTPWF----VP-A------------LSGSAI-----VVALL--GTVVVVRAYRRRQDVQKGRVGINASAGTDPAAAQRT--RRAAYR
CMS446C|CMS446CT                                       1 ------------------------------------------------------------------------------------------------------------
gi|4507491                                             1 ------------------------------------------------------------------------------------------------------------
gi|14149738|ref|NP_065777                              1 ------------------------------------MIAR----------------------
LOC_Os01g67590|LOC_Os01g67590.1                        1 -----------------------------------------------------------------------------------------MS---
Bra004244|Bra004244                                    1 ----------------------------------------------------MS----ED----DEGNEKK----T--QGS---
Bra004078|Bra004078                                    18 -----WVHQRARGFSLPVALFLF--------------L--SLFSLSRENSRGEM----TE----NEGNDKK----M--EGS---
Carubv10019853m.g|Carubv10019853m                      1 ----------------------------------------M---TE----NEGNDKK----I--EGS---
AT1G67690                                              1 ------------------------------------------------M---TE----NEGNDKK----I--EGS---
Eucgr.B03454|Eucgr.B03454.1                            1 -----------------------------------------------M----TE----SQGSREK---A----T---
Medtr3g086000|Medtr3g086000.1                          1 ----------------------------------------M---TE----NEGKREK---M----E---
Glyma11g37410|Glyma11g37410.2                          1 ----------------------------------------M---TE----SEGKCKK---M----G---
Glyma18g01380|Glyma18g01380.1                          1 ----------------------------------------M---TE----IQGNTQK---M----Y---
Cucsa.394790|Cucsa.394790.1                            1 ----------------------------------------M---TE----IQGNTQK---M----Y---
GSVIVG01010319001|GSVIVT01010319001                    1 ----------------------------------------M--VRE---
29929.t000212|29929.m004709                            1 --------------------------------MEM----TE----NQS--------D--KTS---
Potri.010G054500|Potri.010G054500.1                    1 --------------------------------AE----SEADTAK----L--RIK---
164651|164651                                          1 ----------------------------------------------------------------------------------------------------------
Phpat.018G066900|Phpat.018G066900.1                  105 -----IVAAHHLH-LLPSSSSSSSSSSSP-A-----------------PSSSKTRSCCPAAAAS--RLACCPREWSQSDLLLRGRS----SSGLRVG----T--RGV---
Phpat.019G060600|Phpat.019G060600.1                    1 ----------------------------------------------------------------------------------------------------------
Esi0023_0135                                           1 ------------------------------------------------------------------------MDPPDEFRA-----KQV
85692|85692                                            1 ------------------------------------------------------------------------------------------------------------
97633|97633                                            1 ------------------------------------------------------------------------------------------------------------
119899|119899                                          1 ------------------------------------------------------------------------------------------------------------
97030|97030                                            1 ------------------------------------------------------------------------------------------------------------
Cre13.g572900|Cre13.g572900.t2.1                       1 --------MMHVARLL-----------RKSALRPAANL--ATRRFNVVSAQRFAS-----------SEARVPASGRRA--FGGLSS
Vocar20008539m.g|Vocar20008539m                        1 ----------VCGQL------------RRESVQDCSLWQKQTSCRMERCWRRRYSS---------SSCAVPA-------------
439159                                                 1 ------------------------------------------------------------------------------------------------------------
Eucgr.L02517|Eucgr.L02517.1                           16 SVH-RHRPHL--------HRYAR----RH-H-----------SLSSKLSFFCPLWSSS---FSLCLRNPRSS----------PT---------SRSL
GSVIVG01031425001|GSVIVT01031425001                    1 ------------------------------------------------------------------------------------------------------------
GRMZM2G133919|GRMZM2G133919_T01                       30 ----TARLPLAVSARLPNPTNTT----R----------LIFAGLPASSPV--RAFCPRA--------
LOC_Os02g58340|LOC_Os02g58340.1                       12 -LIRLPLVARARLPNPTSSS----YT-S----------RSRSRALLLLPASSPL--RAFCPAS-------
PGSC0003DMG400030613|PGSC0003DMT40007866              41 S-------A-HFCLR--PTSSFS----PS-S----------TKNLLQCRSCSLWSSS---FSLCLHTFRKS----------TS---------PGNR
Carubv10000350m.g|Carubv10000350m                      1 ------------------------------------------------------------------------------------------------------------
Bra006067|Bra006067                                    1 ------------------------------------------------------------------------------------------------------------
Bra028579|Bra028579                                    1 ------------------------------------------------------------------------------------------------------------
Carubv10025914m.g|Carubv10025914m                     32 APHPKPNANKYYYSS--SFSSSS----HS-R----------PSTLRKSYSCPLWSSS---FSFCLPPPRST-----------TS---------TSL-
AT5G65620                                             18 SPKPKY-----F-----SSSSC----HF-R----------PSTFRKSYPCPLWSSS---FSFCLPPPRST-----------TS---------TSL-
Bra024401|Bra024401                                    1 ------------------------------------------------------------------------------------------------------------
Medtr5g030940|Medtr5g030940.1                         30 SSRSRI-HPLL------KRTSCS----FF-N----------PKHSHKSLPCPLWSSS---FSFCIDSLHKS-----------TS---------PSFT
Glyma01g02480|Glyma01g02480.1                         30 ----SI-PPLL------NRTYRS----LS-H----------LKQFPKSHPCPLWSSS---FSFCLHTLRKS-----------TS---------PLRA
Glyma09g33490|Glyma09g33490.1                         30 ----SI-SPLL------SR---S----LS-Q----------LKQFPKSHPCPLWSSS---FSFCLHTLRKS-----------TS---------PIRA
Cucsa.273340|Cucsa.273340.1                           27 ----SI-HPLLVRRT--HSLSIS----IS-S----------PHRLPKSFPCPLWSSS---FSFCLHNRRKS-----------VT---------SSSI
GSVIVG01003850001|GSVIVT01003850001                    1 ------------------------------------------------------------------------------------------------------------
Eucgr.I00597|Eucgr.I00597.1                            1 ------------------------------------------------------------------------------------------------------------
Eucgr.I00594|Eucgr.I00594.1                            1 ------------------------------------------------------------------------------------------------------------
28333.t000012|28333.m000566                           10 ----SI-PPI-----L--KRSPFS----RI-T----------PKHFPKSHPCPLWSAS---FSFCLQSLHKS-----------ST---------PIIS
Potri.007G004600|Potri.007G004600.1                    1 ------------------------------------------------------------------------------------------------------------
Potri.014G004600|Potri.014G004600.1                   30 ----SI-LLLQ-RTN--NHFPYS----HF-T----------PKRFPKSYPCPLWSSS---FSLCLQTLHKS-----------ST---------TTAT
Potri.014G010100|Potri.014G010100.1                   55 ----SI-LLLQ-RTN--NHFPYS----HF-T----------PKRFPKSYPCPLWSSS---FSLCLQTLHKS-----------ST---------TTAT
28658.t000001|28658.m000032                            1 ---------------------------------------------------------------------------------------------MNR
30484.t000001|30484.m000014                            1 ------------------------------------------------------------------------------------------------------------
```

```
gi|85111610                                        73 SPET-----WKQHSC--------DK-----------H-----------GRNVCLFRNAYLTSPHCFLDFAHVSLGKARALVDKVLNA-----------QSLDEYRAIVRH
YKL134C                                            48 DNSY-----WRNINC--------QD-----------NNNSKISQYLFKKNKTCLFKNPYLTSPDGLNKFSQVSLQQAQELLDKMRND-----------FSMSGKLTYIMN
Cre02.g073400|Cre02.g073400.t1.3                    1 ------------------------------------------------------------------------------MLLAEVLD----------TTPEDGVEVVAL
Vocar20013694m.g|Vocar20013694m                     1 ------------------------------------------------------------------------------MLLAEVLD----------TTPEDGVEVVAL
gi|32565901                                        16 NSWV-----ARAH--------------------RSE-VDKET-CLFGNKNLKT-ESFNE-PAAVKKSTDALIQELLTP------------SQNPRTSLQI
CMS132C|CMS132CT                                     1 ------------------------------------------MLCSRCLFGLRGLHVPQDWQTIKHQTLKACNDLVYKILS----------NREGSVLQD
gi|268637658                                       16 KNNS-----IRLI-----------------------TSTNNSSNENVCLLGIKE-KTPKCWEDLFHKKNEKINEIRDHIIPIK------INQESTIEQLKETLYY
Esi0033_0093                                       113 QGTG-----RRSHATGLQG-----VA----------GVGSASEDPAGGALTLCVAGVLGLHRPEDFAPLAAAAVVSDRLRKPISTG--------EVSTPLGILRG
tr|M1C3Y6|M1C3Y6_SOLTU                              18 -----NFIHI-------------------STSTAPSIKET-CLYGFHHLKTPKCFQRFVDDAHERSCELVNYIAG----------MPSSHEIIRA
GSVIVG01018572001|GSVIVT01018572001                71 ------NQCNL-----------------ERIGSHRLHTSCLYGFDLLKTPKCFQRFVDEAHERSCELVTYISG----------MPSSAEIVRA
GRMZM2G450659|GRMZM2G450659_T01                     1 ------------------------------------------------------------------------------M-------------------------M-----
LOC_Os06g47210|LOC_Os06g47210.1                    13 AASL-----RRAAAA-----------------AFSTAAARPETGCLYGFDVRRTAKCFSRRFVDDAHERSDELVAYIGQ----------LEPSAEIVRA
Cucsa.251510|Cucsa.251510.1                          1 -----------------------------------------------------------------------------M-----------------------------
Glyma04g13088|Glyma04g13088.1                      22 ---------KRNILL-----------------GVAIRTFSTPTCLYGFPHLKTPKCFQPFVDAMQRSGLISYICS----------KRPAAEVMRA
Medtr3g009160|Medtr3g009160.1                       19 ---------KNLPL------------LLRHRSF-STTCLYGIPHLKSPKCLQPFVDEALQRSCELVNYISS----------KFSASELMRA
Bra029169|Bra029169                                15 NSWL-----IRHL----------------SS---GEATCLYGFDHLKTAKCFQRFVDAHERSCELVNYISG----------MPSSHDTIKA
Carubv10025983m.g|Carubv10025983m                  15 TRWL-----IRHF----------------RSGGSGDATCLYGFDHLKTAKCFQRFVDAHERSCELVSYISG----------MPSSHEIIKA
AT5G51540                                          15 TRWL-----VRNF----------------RNGGAGDATCLYGFDHLKTAKCFQRFVDAHERSCELVSYISG----------MPSSHEIIKA
Eucgr.K00152|Eucgr.K00152.1                          1 -----------------------------------------------------------------------------M------------------MPSMGVIRA
30147.t000467|30147.m014196                         8 AAWK-----LRSLHS----------------DLSETRNLSTTCLYGFDHLKTPKCFRQFVDEALQRSCELVNNISV----------TLHSSAEIIRA
Potri.015G129300|Potri.015G129300.1                32 STWV-----APQL----------------NGAAATTCLYGFDHLKTPKCFQPFVDEALQRSCELVNYISS----------MPSSAEVLRA
416778|416778                                      46 SPDD-----GRDA----------------HELLRKNPVGLYGVEALKTAKCFRAFAETALAKSEDLIARVKE----------LEPSMETIKC
Phpat.016G041000|Phpat.016G041000.1                 1 -----------------------------------------------------------------------------M------------------MPSMGVIRA
gi|71999758                                        45 TPAR-VVGYYVVHPVIPEET---------V-----ENNCFMYNIAKNEDWPKLATAEPRELYECTVRMLM----------DYGATVMEHMEHLATLPAEHRKFENVVEP
gi|85107353                                         1 -----------------------------------------MTGMVDNPQPPGLRNHTPESVTHAFEAWADKHRAALDAIVAD----------VNLSDPQTVTFENVMRP
YCL057W                                             1 MRLL-LCKNW---FASPVIS---PLLYTRSL----YSM----ANTTSLFIAPQAPPNWSFTPSDLSGKTNEILNNSNNFYDSMSKV-----------ESPSVSNFVEP
gi|66801567                                       124 TRAP-DAERLSEGGQDSE--------VERSISQHARTERSE-KRHSVGHTCHKHIAFRVDMSVADLKAETQRILAEERALADHISSLYELVRGGAPLLKPPLDFDHTFQL
CMS446C|CMS446CT                                     1 ---------------------------------------MKPPAHCAGD----MADAASPCSVVNDLRWDLSLQQCHEERTRELIEQTKRVVDQWGTQ------------EFEDVSYESTLKA
gi|4507491                                          1 -----------------------------------------------------------------MKPPAHCAGD----MADAASPCSVVNDLRWDLSLQQCHEERTRELIEQTKRVVDQWGTQ
gi|14149738|ref|NP_065777                           5 -CLL-AVRSLRRVGCSRILL---RMTLGREVMSPLQAM-------SSYTVAERNVLRWDLSPEQLKTRTTRELLVQTKQVYDAVGML--------GIELVVTYENCLQA
LOC_Os01g67590|LOC_Os01g67590.1                     3 -LRR-RERRVIAAACAAALV---AVGLNLAF----SAVAAHR--RRERKELPC-FTAQVNLSPEQLKRRTAPERVVSKKPEITYDAVAAVL--------PLDKVSFENVIAP
Bra004244|Bra004244                                15 -NL--TKLKLVTLTCAAGLL---GLAVSFAI----PAFKSQKHKS-KKKGLPCCDTVCVNLSAKELLDHADEIHSISTRVHDAVAALV--------PLNKVSYENVVLP
Bra004078|Bra004078                                16 -NPK-KLKLVFTCAAGLL---GLAVSFAI----PAFNSHKQKS-KKKCLPCCDSVCINLSAKELLDHADEIHKISTRVHDDAVALV--------ALDKLSYENVVLP
Carubv10019853m.g|Carubv10019853m                  64 -NPK-KKLNLVFTCTAGLL---GLAVSFAI----PAFNSHKQKS-KKKGLPCCDTVCVNLSAKELLDHADEIHHKSTRVHDAVAALV--------SLDKLSYENVVLP
AT1G67690                                           15 -NPK-KKLNVVFTCAAGLL---GLAVSFAI----PTFKSHKQKS-KKKGLPCCDTVCVNLSAKELLDHADEIHKISTRVHDAVAALV--------PLDKVSYTNVVLP
Eucgr.B03454|Eucgr.B03454.1                         12 -KPR-RENQLLAHTCAAAVL---AVAVNLAV----SAVRAHR--RREKSKPAERIVQRSKEVHDAVASV--------PLDKVSYTNVVLP
Medtr3g086000|Medtr3g086000.1                      13 -KLK-KGRGMIAHTCTAAVL---AIAVNLVI----AAVKHQKEKNAKKKDLAG--SKVRVNLSFSEIVKEANQILAKSKEVEHNLVASV--------PLDKVTHANVISP
Glyma11g37410|Glyma11g37410.2                       3 -KEK-RRGIILAFTCAAAIL---AIAANLAI----TAIKYQKAKNAKKKDLAG--SKVRVNLSASEILKEAEQIITNSNKVHDAVAASV--------PLDKVTHANVISP
Glyma18g01380|Glyma18g01380.1                      13 -KEK-RGRSFIAFTCAAAVL---GIAANLAI----TAIKYQKAKNAKKKDLAG--SKVRVNLSASEILKEAEQIITNSNKAHNSVASV--------PLDKVTYANVISP
Cucsa.394790|Cucsa.394790.1                        13 -KRK-TQSKLLVFTCGAALL---AVAVNLAI----VAICKR----KKKELPC-FELRPNLSASEILKEAEVHDAVASV--------PPNKVTYSNVISP
GSVIVG01010319001|GSVIVT01010319001                 5 -KKD-RRYNLLALTCSAALL---ALAINLAI----SAVNAHT--KKRKRRPLAG-SNVRVNLSATEILQLANSITSKSKAVHDAVAGSV--------PLDKATYANVVLP
29929.t000212|29929.m004709                        15 -QKK-RGRNMITLTCAAAIL---ALTASFAI----SALNSRR-KKSKKRDLEC-STVRVNLSPNEILKEANRILTAKSKEVHDAVASV--------PLDKVTYANVVAP
Potri.010G054500|Potri.010G054500.1                13 -KHK-RERNLLAHTCAAALA---ALALSLAI----SALNSRR--KKSNKKDLSG-SNARINLSASEILKEANRILTAKSKEVHDAVASV--------PLDKVTYANVVSP
164651|164651                                       1 ------------------------------------------------------------------------------M-----------------------------
Phpat.018G066900|Phpat.018G066900.1               176 -IVK-WK-DVAVMGAAAAST---VVHAGMVR----SMVR---RSHAVVSVSDGINVRLGLSASEHLSHADFIHSTSTSVHDAVAAV--------PLDQVSYDNVIAB
Phpat.019G060600|Phpat.019G060600.1                 1 --MV-RK-EAVVASVAAAGL---AVTARVVM----GMLR---RSHS--NISDGIQVRLKLSAVDHLRHTDNILATSTSVHDAVAAV--------PLDQVTYENVMRP
Esi0023_0135                                        13 AEGLPADTPLPPHFLRDLEANKAKEAEAEREKER--QAVRSSNHYMQQDGLHKHETIAPEAAKEAFDVLHEDLETGFAKFHEDLV----------DFTSGEHW-----
85692|85692                                         1 --------------------------------------------------------------------------EEHLVALLAC----------NEHSWESLAIH
97633|97633                                         1 -------------------------------------------------------------------------------M--------------------P
119899|119899                                       1 ----------------------------------------------------MPLLVSVGCLHEHNRVHEHVPVCVKQVVKHELKEKDLLQLSCFPASSF----GENGGDLVEALVHP
97030|97030                                         1 ----------------------------------------------------MPLLVSVGCLHEHNRVHEHVPVCVKQVVKHELKEKDLLQLSCFAASSF----GENGGDLVEALVHP
Cre13.g572900|Cre13.g572900.t2.1                    53 TPAVWSA---KRFNSSSRAMT-AEAAHVEAAV-AP--AVSVADNPLLAHVSFFPKPDQVKPEHVVPGCVKHLMAQCHHEIIDKLSA--------VEPSWSGLVHP
Vocar20008539m.g|Vocar20008539m                    41 --VAFGA--KRLHGSRTIMTNTEAAAVEAVVSSA--SIPEPPNPLLAHVSFPKPDQVKPEHVVPGCVKHQLLSEEHAEIDLESE--------VTPSWSGLVHP
439159                                              1 --------------------------------------------------MAAL--AIDKELNPLLAHVGGSLPLYDKVDAHVVPGCRQLLEDEAELVKLQN--------LKRDWESLVHP
Eucgr.L02517|Eucgr.L02517.1                         66 STTCSSAS---ASASTPPI-------APRAPPMA--DAGVESNPLLHFDFFPPPDAVEPKHVVPGCIKHLPAFRSLLAKNLESDLVELETT--------VEPSWPKLVEP
GSVIVG01031425001|GSVIVT01031425001                 1 ------------------------------------------MAAERNPLLEDFVFPPPDDVVEPKHIRPAFRSLLAKNLESDLYELETT--------VEPTWPKLVEP
GRMZM2G133919|GRMZM2G133919_T01                    69 --------------RPSPS-TCAA------FSST--MAASDNPLLADFDFFPPPDDVEPSHVRPGCHELLTRLEGELKEKG--------IEPTWAKLVEP
LOC_Os02g58340|LOC_Os02g58340.1                    57 -------------RRPSPA-TCSAA----YASS--SMATDDNPLLADFDFFPFDRVEPIHVRPAVRTLLARLEGELTDLEKG--------VQPTWCKLVEP
PGSC0003DMG400030613|PGSC0003DMT40007866           90 PRKSITVRSFSPSS-----A-S----ISDHPSKM--SMASDDNPLLKDFDFFPPPDDVVEAHHVRPGIRALLKKIDEELSALEKT--------VEPSWPKLVEP
Carubv10000350m.g|Carubv10000350m                   1 -----------------------------MAS--EDSLSSNPLLQNFDFFPFPDSVDAHHVRPGIRALLQQLEAELLQLEKT--------VEPSWPKLVEP
Bra006067|Bra006067                                 1 -----------------------------MAS--EDSLSSNPLLQNFFFPPPDDVVDAHHVRPGIRALLHQLEALLQLEKT--------VEPSWPKLVEP
Bra028579|Bra028579                                 1 -----------------------------MAS--EDSLSSNPLLQNFDFFPPPDSVDAHHVRPGIRALLQLELELQLEKT--------VEPSWPKLVEP
Carubv10025914m.g|Carubv10025914m                  88 -----SFHPFSS-SSPPSMS-SAAAA----AVDS--AQTLSSNPLLQFDFFPPPDSVDAHHVRPGIRSLLQHLEAELELEKS--------VEPTWPKLVEP
AT5G65620                                          65 ------SSSSFRPESSPPSMS-SAAAA-AVESVVS-DETLSSNPLLQFDFFPPPDSVDASHVRPGIRALLQHLEAELELEKS--------VEPTWPKLVEP
Bra024401|Bra024401                                 1 --------------------MS-SATAAAASSSVSD--ESLLSNPLLQDFDFFPPPDSVDAHHVRPGIRALLQELEGELEQENS--------VEPSWPKLVEP
Medtr5g030940|Medtr5g030940.1                      82 CSAS------------SM--A--------AS-----ALDVEANPLLKEFVFPPPDDVVEAHHVRPGIRALLEKLERDLEELERS--------VEPSWPKLVEP
Glyma01g02480|Glyma01g02480.1                      78 SSSL----------STPSM--A--------AS-----SLDECNPLLQNFFFPPPDDVVEPKHVVPGIRALLEHELELEKS--------VEPSWPKLVEP
Glyma09g33490|Glyma09g33490.1                      75 SSSF----------SPSMA--A--------SSPL--NDAVECNPLLQNFDFFPPPDFVEPKHVVPGIRALLGKLEAELELEKS--------VEPSWPKLVEP
Cucsa.273340|Cucsa.273340.1                        79 H--YFSSRSS--HSA-PSMA-A--------FGGI--DQTPQSNPLLLDFDFFPPPDAVKADHVIPGRTMLNQLENDLIELESK--------VEPTWPKLVDP
GSVIVG01003850001|GSVIVT01003850001                 1 -------------------------M--------ATVP--QSTPEVNPLLLDFDFFPPPDAVKADHVRPGIHALLKKLYSDLSEERT--------VEPSWPKLVEP
Eucgr.I00597|Eucgr.I00597.1                         1 --------------------------MA--NNGVESNPLLRDFDFFPPPDDVVEAHHVRPGIHALLKKLYSDLSEERT--------VEPSWPKLVEP
Eucgr.I00594|Eucgr.I00594.1                         1 --------------------------MA--DAGIESNPLLRDFDFFPPPDDVVEAHHVRPGVLALLKKLENDLEELERT--------VEPSWPKLVEP
28333.t000012|28333.m000566                        58 AAPSLSFSPC--YSSLSSMA-A---------ATTT--DISLQSNPLLKDFDFFPPPDDVVEAHHVRPGIRALLKNLESDLEELEST--------VEPSWPKLVEP
Potri.007G004600|Potri.007G004600.1                 1 ------------------------TVVDESNPLLQDFEFFPPPDDVVEAHHVRPGIRALLKNLESDLEELERT--------VEPSWPKLVEP
Potri.014G004600|Potri.014G004600.1                81 TPPS--ISNC--YSSISMD-------------PVVDEANPLLQDFEFPPPDDVVEAHHVRPGIRALLKNLESDLEELERT--------VEPSWPKLVEP
Potri.014G010100|Potri.014G010100.1               106 TPPF--ISNC--YSSISMD-------------PVADEANPLLQDFEFPPPDDVVEAHHVRPGIRALLKNLESDLEELERT--------VEPSWPKLVEP
28658.t000001|28658.m000032                         4 TNVIIAASVAAVHSI---------AHAEPASMLP--MSNPFAKFSALFFGVPAFDKIKNEDYLAPAFEEGNRQNAHEIEATANN--------KAAPTFDNTIVA
30484.t000001|30484.m000014                         1 ------------------------------------------------------------------------------M-----------------------------
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gi|85111610                                          137 LDRLSEILGRVLDMADFVRVTHPDQQIQRTASMAWDMMYEYMN-----------------QL-------NTMTGLVDQLVQAMDNEQ--------------------
YKL134C                                              123 LDRLSDTLGRVIDLCEFIRSTHPDDAFVRNAQDCHEQMFEFMN-----------------VL-------NTDVSLCNILKSVLNNGE------------------
Cre02.g073400|Cre02.g073400.t1.3                       1 M-------------------------------------------------------------MYQRLSEALAAYEAGLRALSNRTAPEL--------
Vocar20013694m.g|Vocar20013694m                       21 IDEMSDQLGRTYDANECCRNVHSDERWRQMAGKACVQLGEYIS-----------------RV-------NHHEGMYQRLSTALAAYESSLAALEKRETPRL-----
gi|32565901                                           78 VDDLSNETGKSADLAECVRQLHSEPEFRNAAEDVSRNFCELVE-----------------SL-------NTNTALYQKLKSSEITES--------------
CMS132C|CMS132CT                                      49 FDELSDTLGQVLDASELARNVSAEPEHVEASESVFRELSQYMQ-----------------EL-------NCDENLCGALLRKQDA-------------
gi|268637658                                          87 IDGLSRELGDLMDPAQFVMNVIPYGPHKIESHKAFLKMSDTVN-----------------RL-------NANSDLYQLLLVLRDHK--------------
Esi0033_0093                                          191 VDAISNTVGVIDAADFVRNAHADEGFRVEAADEAFSVLAEYIQ-----------------DL-------NADDSLYEALCGVVEEG----------------
tr|M1C3Y6|M1C3Y6_SOLTU                                 78 MDEISDTVGSVIDSAELCRHTHPNREEFVDEASKASLRVNEELH-----------------YL-------NTNHSIYKAVNKAEKDS-------------
GSVIVG01018572001|GSVIVT01018572001                   131 MDEISDAVGSVVDSAELCRHTHPDREEFVEEANKASMRINEYLH-----------------YL-------NTNHSLYHAVLKVEKDR------------
GRMZM2G450659|GRMZM2G450659_T01                         1 M-------------------------------------------------------------------------------------
LOC_Os06g47210|LOC_Os06g47210.1                        78 MDEISNTVGSVVDSAELCRNTHPDKEFMDEADKASMRIYEHLQ-----------------YL-------NTNTTLYNAILKAESEG-------------
Cucsa.251510|Cucsa.251510.1                            1 M-------------------------------------------------------------------------------------
Glyma04g13088|Glyma04g13088.1                         83 MDEISDTVGSVVDSAELCRNTHPDREEFVEEATKKASMKINEYLH-----------------YL-------NTNHPLYDAVVKAEQEC-----------
Medtr3g009160|Medtr3g009160.1                          78 MDEISDTVGCVVDSAELCRQTHPNREEFVEEADKAKINEYLHVSWLRSATTYFQLYLGCTYL-------NTSHPLYDDALRKAEKDG------------
Bra029169|Bra029169                                    73 MDEISDTVGCVVDSAELCRQTHPDREEFVEEAAHKAAIDMNDYLH-----------------QL-------NTNHTLYAAVRKAEQDS----------
Carubv10025983m.g|Carubv10025983m                      76 MDEISDTVGCVVDSAELCRQTHPDREEFVEEANKAAIEMNDYLH-----------------HL-------NTNHTLYAAVRKAEQDS-----------
AT5G51540                                              76 MDEISDTVGCVVDSAELCRQTHPDREEFVEEANKAAIEMNDYLH-----------------HL-------NTNHTLYAAVRKAEQDS-----------
Eucgr.K00152|Eucgr.K00152.1                            1 M-------------------------------------------------------------------------------------
30147.t000467|30147.m014196                           73 MDEISNTVGCVVDSAELCRNTHPDREEFVEEANKASMRINEYLH-----------------YL-------NTNHPLYDAVVKRAEQDG---------
Potri.015G129300|Potri.015G129300.1                    91 MDEISNTVGCVMVDAAELCRNTHPDKEFYDEANAASLKLYKNYLH-----------------YL-------NTNHTLYDAVVHVES-SD---------
416778|416778                                         107 MDDISNTVGCMVVDAAELCRNTHPDKEEYDEANAASLKLYKNYLH-----------------YL-------NTHKSLYDAVVHVES-SD---------
Phpat.016G041000|Phpat.016G041000.1                    11 MDDISTVGSVVDAAELCRNTHPDEYVEESNHASMKVYEYLQ-----------------YL-------NSHPVLYKAIVGVESSPD---------
gi|71999758                                           129 LLTEEYEVNFAFQTLV-LKMLTLMEDCNRKLFDAD--LHHIKI-----------------MCARDQMEKLTNKLFQDAIKQLYE---------
gi|85107353                                            61 QLEFENQKF--SHNLRFYQHVSENSDLRETTRKMAKWYDNIWT-----------------DM-------NMRGLVFRAREVLYHKSGLAASR---KQNS----
YCL057W                                                83 FMLFENELGPIINQLTFLQHVSSDKEIRDASVNSSMKLDELNI-----------------DF-------SLRHDIFLQHARVWQDVQ------------
gi|66801567                                            51 TDKLDVKFRNIESSLTFLANASTDEKVRDVANEVEATLSKYSI-----------------AT-------SMREDLYQAYVDCCKQNN--------------
CMS446C|CMS446CT                                      224 WADMEAKHAARRSSVTFPSFVSPHSDIRAASVEAQRELAKLDV-----------------EL-------SSRAPVYRVLRPHADEYEIQLRDALRRQRSSLHAPVASRE
gi|4507491                                             68 LADVEVTYTVQRNILDFFPQHVSPSKDIRTASTEADKKLSEADV-----------------EM-------SMREDVLYQRIVWLQETCD---------
gi|14149738|ref|NP_065777                              92 LADVEVKTYIVERTMLDFPQHVSSKDVRRASAEADKRLDSHFQ-----------------QC-------RREDLVFRIVHLQETCD-----------
LOC_Os01g67590|LOC_Os01g67590.1                        91 LAELDAQQFPLVQACVLPRMVSPEDEVRRASAEAEKRLDSHPQ-----------------SC-------RKREDVYRVIRIYAA--K----------
Bra004244|Bra004244                                   104 LAELEARQLPLIQCCVIPKMLSPHDNVRKASAEAEVKIDAHFQ-----------------SC-------RKREDVYRVIRIYAA--K----------
Bra004078|Bra004078                                   105 LAELEARQLPLIQCCVVPKMISPLDNVRKASAEAEMKIDAHIL-----------------SC-------RKREDVYRVIRIYAA--K----------
Carubv10019853m.g|Carubv10019853m                     154 LAELEARQLSLIQCCVFPKMLSPHDNVRKASTEAEQKIDAHIL-----------------SC-------RKREDVYRIINIYAA--K----------
AT1G67690                                              105 LAELEARQLSLIQCCVFPKMLSPHDNVRKASTEAEQKIDAHIL-----------------SC-------RKREDVYRIINIYAA--K----------
Eucgr.B03454|Eucgr.B03454.1                           101 LAELEAEEFPLVQSCIYFKMVSVGDDVRQASAQAERRIDAHLN-----------------IC-------SKREDILVVKAFAV--R----------
Medtr3g086000|Medtr3g086000.1                         103 LAELQAQQFFPLIQSCLLFKLVSTREDREVRKASAEAERRIDAHLN-----------------IC-------SKREDILVVKAFAV--R----------
Glyma11g37410|Glyma11g37410.2                          93 LAELQAQQFPL-------------DVRKASAEAVRRLDAHFD-----------------TC-------SKREDVYLVIKAFA------------
Glyma18g01380|Glyma18g01380.1                         103 LADLEARQLSLIQCSCVFQKMVSTREDVRKASAEAERRIDAHLD-----------------AC-------SKREDVYLVIKAFAV--R----------
Cucsa.394790|Cucsa.394790.1                            99 LADLEARQLSLIQCCVFPKLISTSDDVRKASAEAEKRIDAHAQ-----------------MC-------SKREDVYCVVKAFA------------
GSVIVG01010319001|GSVIVT01010319001                    94 LAELEAQQFPT-------------EEVRKASAEAEQRIDSHVL-----------------MC-------SMREDVYCVVKAFVA--R----------
29929.t000212|29929.m004709                           104 LADLEAQQFPLIQSCVIPKFWVSTLEDVRKASAEAERRIDAHVS-----------------TC-------SEREDVYRVVKAFSV--K----------
Potri.010G054500|Potri.010G054500.1                   102 LADLEAHQFPLVQSCVFPKLVSTLEDVRKASAEAERRIDAHVS-----------------MC-------SKREDVYRVVKAFAS--K----------
164651|164651                                           1 M-------------AVQSCVIPKFVNPARDVRDASVEAEQRIDSHVL-----------------KC-------RLREDVYRVVKAYAE--K----------
Phpat.018G066900|Phpat.018G066900.1                   262 LANLQAEEFALVQSCVFPALVSTSKEVRDASSEAEKRLDAYNV-----------------KC-------SMREDVYRVVKAFSE--K----------
Phpat.019G060600|Phpat.019G060600.1                    84 LANLEAEEFALVQSCVFPALVSTSKEVRDASSEAEKRLDAYNV-----------------KM-------GQSKLVYDALKFLQVPAC----------
Esi0023_0135                                          104 -----------------------------LNVVTIFQ-----------------KM-------GQSKLVYDALKFLQVPAC----------
85692|85692                                            22 LEWIMETLIVSCSVVNHFQHMKDSKNLRGKAIQBIEARRKDEDL-----------------KF-------AQSKPLFDSKALQSPN----------
97633|97633                                             2 FERILDHLIVVWGIVSHLKDVKDSDALRPAVDEAQELRTNELL-----------------RL-------GQSKALYCAFEKI--------------
119899|119899                                          62 FERILDRLIVVWGIVSHLKDVKDSDALRAAVDEAQELRTNELL-----------------RL-------GQSKALYCAFEKI--------------
97030|97030                                            62 FERILDRLIVVWGIVSHLKDVKDSDALRAAVDEAQELRTNELL-----------------RL-------GQSKALYCAFEKI--------------
Cre13.g572900|Cre13.g572900.t2.1                      141 LERTSDRHQRVVWGIVSHLKGVKDSPELRAAVEEVQPENVKLSI-----------------RL-------SQSKPLYCAFKALPEGFA---------
Vocar20008539m.g|Vocar20008539m                       129 LEKISDHEQRVWGIVSHLKDVKDSPELRAAVEEVQPQPEKVKLST-----------------RL-------SQSKPLYAFKALREGGQ---------
439159                                                 63 LERITDRLIVTVWGIVEHLKAVKDSSELRAAVEEVQPEKVAPLL-----------------RL-------GQSKPLYAFKELQDGFG---------
Eucgr.L02517|Eucgr.L02517.1                           148 LEKIIDRLIVVWGIVNHLNSVKDSPELRSLIEEVQPLEAKVEFQL-----------------RL-------GQSKPIYNAFKAIQESPD--------
GSVIVG01031425001|GSVIVT01031425001                    58 LEKIIDRLIVVWGIVNHLNSVKDSPELRSLIEEVQPLEAKVEFQL-----------------RL-------GQSKPIYNAFRAINRNSSD-------
GRMZM2G133919|GRMZM2G133919_T01                       140 LERIVDRLEVHWGMVDHLKSVKDSADLRAAVEEVQPFVKVSFQL-----------------RL-------GQSKPIYSAFNAIRNSSD--------
LOC_Os02g58340|LOC_Os02g58340.1                       130 LERIVPSLEVVWGTVDHLKAVKDSSDLRAAVEEVQPDKVKFQL-----------------RL-------GQSKPIYNAFNAIRNSSD--------
PGSC0003DMG400030613|PGSC0003DMT40007866              172 LEKIIDRLIVVWGAVMNHLKDNPELRSLIEEVQPEKVKFQL-----------------RL-------GQSKPIYNAFKAIRESSD---------
Carubv10000350m.g|Carubv10000350m                      62 LEKIIDRLIVVWGAVMNHLKAVKDAPELRAAIEEVQPEKVKFQL-----------------RL-------GQSKPIYNAFKAVRESPD--------
Bra006067|Bra006067                                    62 LEKIIDRLIVVWGAVMNHLKAVKDAPELRAAIEEVQPEKVKFQL-----------------RL-------GQSKPIYNAFKSIRESPD--------
Bra028579|Bra028579                                    62 LEKIIDRLIVVWGIINHLKAVKDAPELRAAIEEVQPEKVKFQL-----------------RL-------GQSKPIYSAFKSIRESSD--------
Carubv10025914m.g|Carubv10025914m                     169 LEKIVDRLIVVWGMVNHLKAVKDAPELRAAIEDVQPEKVKFQL-----------------RL-------GQSKPIYNAFKAIRESPD--------
AT5G65620                                             150 LEKIVDRLIVVWGMVNHLKAVKDAPELRAAIEDVQPEKVKFQL-----------------RL-------GQSKPIYNAFKAIRESPD--------
Bra024401|Bra024401                                    74 LEKIVDRLIVVWGIVNHLKAVKDAPELRAAIEEVQPEKVKFQL-----------------RL-------GQSKPIYNAFKAIRESPD--------
Medtr5g030940|Medtr5g030940.1                         149 LEKIVDRLIVVWGMVNHLKAVKDNSELRSAIEDVQAEKVKFQL-----------------RL-------GQSKPIYNAFKAIQDSPD--------
Glyma01g02480|Glyma01g02480.1                         147 LEKIVDRLIVVWGMVNHLKAVKDSSELRSAIEDVQAEKVKFQL-----------------RL-------GQSKPIYNAFKAIQESPD--------
Glyma09g33490|Glyma09g33490.1                         147 LEKIVDRLIVVWGIVNHLKSVKDSADLRSAIEDVQAEKVKFQL-----------------RL-------GQSKPIYNAFKAIQESPD--------
Cucsa.273340|Cucsa.273340.1                           157 LEKLVDRLIVVWGIVNHLKSVKDSADLRSAIEDVQPDKVKFEL-----------------RL-------GQSKPIYNAFKAIQESPE--------
GSVIVG01003850001|GSVIVT01003850001                    64 LEKLVDRLIVVWGIVNHLKSVKDSADLRSAIEDVQPDKVKFEL-----------------RL-------GQSKPIYNAFKAIQESPE--------
Eucgr.I00597|Eucgr.I00597.1                            61 LEKIVDHLIVVWGMINHIRKAVKDVLLRAATGKVLVSEMVKFQL-----------------RL-------GQSKPIYNAFKAIQESPD--------
Eucgr.I00594|Eucgr.I00594.1                            61 LEKIVDHLIVVWGMINHIRKAVKDTAELRAAIEEVQPEKVKFQL-----------------RL-------GQSKPIYNAFKAIQESPD--------
28333.t000012|28333.m000566                           139 LEKIVDHLIVVWGMINHLKSVKDTAELRAAIEEVQPEKVKFQL-----------------RL-------GQSKPIYNAFKAIQESFQ--------
Potri.007G004600|Potri.007G004600.1                    61 LEKITDQLAIVWGMINHLKAVKDSPELRAAIEEVQPEKVKFQL-----------------RL-------GQSKPIYNAFKAIQESFQ--------
Potri.014G004600|Potri.014G004600.1                   154 LEKIAPQLTVVWGMINHLKAVKDSPELRAAIEEVQPEKVKFQL-----------------RL-------GQSKLIYNAFKAIQDSFQ--------
Potri.014G010100|Potri.014G010100.1                   179 LEKIAPQLTVVWGMINHLKAVKDSPELRAAIEEVQPEKVKFQL-----------------RL-------GQSKPIYNAFKAIQESFQ--------
28658.t000001|28658.m000032                            88 MEKSGQLLSRVVSSVFGNLSGANTNDTFKALERELSPKLAAHSD-----------------AI-------RLNSKLYAKIKALYDKRD--------
30484.t000001|30484.m000014                             1 -----------------------------MARHYS-----------------KI-------GTNAALFARLDALWESFD----------
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gi|85111610                               200 -----------------------------------------------------VSTTWSEERMVAEVLKLDE-AKSAVHLPKD-AEDKLVHLSSAHSQTGT-------------------NEIQ
YKL134C                                   186 -----------------------------------------------------VSSKLSAEELKVGKILLDDE-LKSGLYMNPD-VREKFIQLSQEISLVGQ-------------------ELIN
Cre02.g073400|Cre02.g073400.t1.3           28 -----------------------------------------------------RPWQMGGWCRESVLVAQRLKQDM-EQAGIHLPAA-QRARVAELAAANGHFAA-------------------AENA
Vocar20013694m.g|Vocar20013694m            98 -----------------------------------------------------GPQQLAGWCSESVLVAQRLKQDM-ELGGIHLPSLEQRNRHAELAAANGHFGT-------------------AENA
gi|32565901                               141 -----------------------------------------------------S--RLDLVDKRTLTLLLDDH-EQSGVHLKDN-QKEQFVQLSSEIFDAGA-------------------RFQQ
CMS132C|CMS132CT                           110 --------------------------------------------------------VTCEQALVRSLQRDELALRGGASLSFS-KRKHVAAVQNEILEWSM-------------------R---
gi|268637658                              149 -----------------------------------------------------HYHQLFPNDHQLFLNEMLKKES-EVNGLNLPK-EKYLEIMKLKDEIFAQGS-------------------MSIE
Esi0033_0093                              254 -----------------------------------------------------AMDGFTGLQRHVGLHMALS-ERGGLHLSGE-ERAEVVALQNEATRMER-------------------LPEH
tr|M1C3Y6|M1C3Y6_SOLTU                     140 -----------------------------------------------------N--SLTHEAHRAARFLRMDL-EKGGIHLCSE-KLDRANELAIDHIQLSR-------------------LYNE
GSVIVG01018572001|GSVIVT01018572001        193 -----------------------------------------------------N--LLSKEAKRAAHYLRVDL-EKGGIHLAAD-KLDRVNQLHVERAHLCREMVLYMEINSTDMLIRLWAIMFSE
GRMZM2G450659|GRMZM2G450659_T01              1 -----------------------------------------------------------------------------------------------------------------------
LOC_Os06g47210|LOC_Os06g47210.1            140 -----------------------------------------------------V--MTTEAARRAATTLRVDE-EKGGIHLDPE-KLLEHVRHLNLEHAQHGR-------------------KFSE
Cucsa.251510|Cucsa.251510.1                  1 -----------------------------------------------------------------------------------------------------------------------
Glyma04g13088|Glyma04g13088.1              145 -----------------------------------------------------H--MGSEEAQRGVRNLRADH-ERGGIHLCPE-KLDRVNKLNIELSQLFCR-------------------EYNE
Medtr3g009160|Medtr3g009160.1              158 -----------------------------------------------------H--MGSAEAQRGIKSLRVEM-ERGGIHLCPE-TLDRVNKLDIGLSHLCR-------------------EYNQ
Bra029169|Bra029169                        135 -----------------------------------------------------N--LLTKEASRTAHHLRMDL-ERGGIHLSPE-KLDKVNNLTTNLFQLCS-------------------EFSG
Carubv10025983m.g|Carubv10025983m          138 -----------------------------------------------------N--LLTKEASRTAHHLRMDE-ERGGIHLDPE-KLDKVNSLTTNLFQLCR-------------------EFSE
AT5G51540                                  138 -----------------------------------------------------N--LLTKEASRTAHHLRMDE-ERGGIHLDPE-KLDKVNNLTTNLFQLCR-------------------EFSE
Eucgr.K00152|Eucgr.K00152.1                  1 -----------------------------------------------------------------------------------------------------------------------
30147.t000467|30147.m014196               135 -----------------------------------------------------H--LLTKEAQKAAHHLRIDL-EKGGIHLSSE-KLDRVNQLNMDLFQLSR-------------------EFSE
Potri.015G129300|Potri.015G129300.1        153 -----------------------------------------------------H--LLTKEAHEAAANQLRIDE-EKGGIHLPPE-KLARVNQLHLSILQLSR-------------------EFTE
416778|416778                             169 -----------------------------------------------------A--LLTTEEAKRAAKTLRIDE-ERGGIHLPPE-KMSRVNENNLELTRLGR-------------------EGTE
Phpat.016G041000|Phpat.016G041000.1         74 -----------------------------------------------------I--LLTTEEARRAATLRMDE-ERGGIHLPSD-KLRRVNDLNLEITRLGR-------------------EEGE
gi|71999758                               193 -----------------------------------------------------AKDGLSEEWQSRLLEWYLLEI-KASGLDKHDDKTLKVLGSWSKFVDEYRS-------------------KYIT
gi|85107353                               131 ---------------ARYITEDIAKNAGF-------------------------EDASAIALEEWWKEA-IRLGLYPSKPQRDRENQIQKRVEAIKS-------------------EEKN
YCL057W                                    146 -----------------------------------------------------SKADSVERETFKYVEKSYKDY-IHSGLELDE-GNRLKIKEIKKKLSVNSI-------------------NFSK
gi|66801567                               114 -----------------------------------------------------DFKESDLSKELQRYVEKTLEGH-EKNGLQLPK-EKRKLKEIMTKLSDNSI-------------------KFSK
CMS446C|CMS446CT                           309 SRREQLRHKRESILEQAAHDQDYDDFGRQTPLGAQAAAALGFTLEHVEYMRFTVRDL-ERHGAHLDD-QLRERLVDLRTRLADLCI-------------------EYQR
gi|4507491                                 131 -----------------------------------------------------KDSLRPETARYLERLRLKLG-KRNGLHLPR-ETQENIKIRKKKLSLLCI-------------------DPNK
gi|14149738|ref|NP_065777                  155 -----------------------------------------------------LGKIKRPETARYLEKSLRMG-KRNGLHLPR-QVQNEIKSMKKRMSLLCI-------------------DPNK
LOC_Os01g67590|LOC_Os01g67590.1            152 -----------------------------------------------------GERIGLEATRFVQCMVREG-EKNGAKLTQ-SKKTEMRKMKSHMDELSL-------------------KYIQ
Bra004244|Bra004244                        165 -----------------------------------------------------GESISPEAKFYLQCLVRDE-EDNGLNLTA-TKREEVDNLRRAIDELSL-------------------RYVQ
Bra004078|Bra004078                        166 -----------------------------------------------------GESIAPEAKCYLQCLVRDE-EDNGLNLTT-TKREEVGRLKDEIDELSS-------------------RYVQ
Carubv10019853m.g|Carubv10019853m          215 -----------------------------------------------------GESIAPEAKCYLQCLVRDE-EDNGLNLTA-VKREEVERLTNEIDELSL-------------------RYIQ
AT1G67690                                  166 -----------------------------------------------------GESISPEAKCYLQCLVRDE-EDNGLNLTA-IKREEVERLKYEIDELSL-------------------RYIQ
Eucgr.B03454|Eucgr.B03454.1                162 -----------------------------------------------------GDWMSPEATCYLQFLVRDE-ERNGLNLAT-AKREEVQRLKSQIDELSC-------------------QYVQ
Medtr3g086000|Medtr3g086000.1              164 -----------------------------------------------------GDWMNAETKSFVQILVRDE-ERNGLNLTA-SKREELLRIKAQIDELSI-------------------IYIQ
Glyma11g37410|Glyma11g37410.2              138 --------------------------------------------------------------VRDE-ERNGLNLTA-SKREELQRLRDQIDELSF-------------------KYIQ
Glyma18g01380|Glyma18g01380.1              164 -----------------------------------------------------GEWMNAEAKRFVQILVRDE-ERNGLNLTA-SKREELQRLRAQIDELSF-------------------KYIQ
Cucsa.394790|Cucsa.394790.1                160 -----------------------------------------------------GEQTSAEQKCFIQCLVRDE-ERNGLNLTT-SKRKELLDRVQIELSL-------------------RYIQ
GSVIVG01010319001|GSVIVT01010319001        142 -----------------------------------------------------GEWISPEANRYVQCLVRDE-ERNGLNLTS-TKRREVQRLRAHIDELSV-------------------LYIK
29929.t000212|29929.m004709                165 -----------------------------------------------------GEWMNPEAKHYVQCLVRDE-ERSGLNLTV-TKREEAQRLTNEIDELSL-------------------RYIQ
Potri.010G054500|Potri.010G054500.1        163 -----------------------------------------------------GEWMNPEAKHYIKCLVRDE-EQNGLNLTV-TKKEEVQRLRAQIEELSL-------------------RYVR
164651|164651                               53 -----------------------------------------------------KEDLPPETQRFVNHLVRDY-ERLGLNLTP-EMKSEVLVKDKTIGELCI-------------------TLQK
Phpat.018G066900|Phpat.018G066900.1        323 -----------------------------------------------------KVTLEPSAQRFVDRVVRDY-ERLGLNLSP-EIRKEVERLKTTLGELCI-------------------EEQK
Phpat.019G060600|Phpat.019G060600.1        145 -----------------------------------------------------KEPLSPCAQRFVDRVHRDY-ERLGLNLSP-DIRRKVEFLKTTLGELCI-------------------EEQQ
Esi0023_0135                               132 -----------------------------------------------------RRLMTEAQIRVVDASVKQM-ELGGVGLSG-EAKEEFNKIQLELADLST-------------------KFSN
85692|85692                                 85 -----------------------------------------------------FQNSSDAQKRTVESYMKKV-IISGVHLEDD-GQKKLFNQYEKELVELTR-------------------KFSD
97633|97633                                 60 ---------------------------------------------------------------------------------------------------------------------- ----
119899|119899                             125 -----------------------------------------------------FDTLNEAQQRVVTGRLKLA-ILNGVALPDH-ERKVHENEIQELEKLN-------------------KFSE
97030|97030                                120 -----------------------------------------------------------------------------------------------------------------------
Cre13.g572900|Cre13.g572900.t2.1           204 -----------------------------------------------------VSGLTAGQRRIVDNELRDE-VHGGVALEG-EAKERFNAIQQELTQHAT-------------------KFSN
Vocar20008539m.g|Vocar20008539m            192 -----------------------------------------------------VSQLTPAQQRIADNELRDE-VHGGVALEG-EAKERFNAIQQELTQHAT-------------------KFSN
439159                                    126 -----------------------------------------------------FKNLTEAQKRIVEARLKDA-TLNGVALEG-EEKKRFNEIQEIELFGT-------------------KFSE
Eucgr.L02517|Eucgr.L02517.1                211 -----------------------------------------------------WNLLSDAQKRIVEAQIKEA-VLSGVALED-GKRREFNKIQELEKLSK-------------------KFDE
GSVIVG01031425001|GSVIVT01031425001        121 -----------------------------------------------------WEALNDARKRIVEAQIKEA-VLNGVSLED-NKREYFNEIQQELKLSQ-------------------KFSE
GRMZM2G133919|GRMZM2G133919_T01            203 -----------------------------------------------------WDSLSDEARKRIVEAQIKEA-VLSGVALED-EQRRKFNQIQEELEKLTQ-------------------KFSE
LOC_Os02g58340|LOC_Os02g58340.1            193 -----------------------------------------------------WETLSDEARKRIVEAQIKEA-VLSGVALED-EQRSKFNQIQQELEKLTQ-------------------KFSE
PGSC0003DMG400030613|PGSC0003DMT40007866   235 -----------------------------------------------------WDSLNDARKRIVEAQIKEA-VLSGVALED-DKREQFNKIQELEKLSH-------------------KFSE
Carubv10000350m.g|Carubv10000350m          125 -----------------------------------------------------WKTLSEARQRLVEAQIKEA-VLSGIALED-DKREEFNKIQELEKLSH-------------------KFSE
Bra006067|Bra006067                        125 -----------------------------------------------------WNTLIEA-----PQIKEA-VLSGIALED-DKREEFNKIQELEKLSH-------------------KFSE
Bra028579|Bra028579                        125 -----------------------------------------------------WNTLSEARQRLVEAQIKEA-VLSGIALDD-DKREEFNKIQELEKLSH-------------------KFSE
Carubv10025914m.g|Carubv10025914m          232 -----------------------------------------------------WSSLSEARQRLVEAQIKEA-VLIGIALDD-DKREEFNKIQELEKLSH-------------------KFSE
AT5G65620                                  213 -----------------------------------------------------WSSLSEARQRLVEAQIKEA-VLIGIALDD-DKREEFNKIQELEKLSH-------------------KFSE
Bra024401|Bra024401                        137 -----------------------------------------------------WSSLSEARQ-----PQIKEA-VLTGIALDD-DKREEFNKIQELEKLSH-------------------KFSE
Medtr5g030940|Medtr5g030940.1              212 -----------------------------------------------------WKTLSDARKRIVESQIKEA-VLNGVSLED-DKREQFNKIQELERLSE-------------------KFGE
Glyma01g02480|Glyma01g02480.1              210 -----------------------------------------------------WQTLSDARKRIVESQIKEA-VLNGVSLED-DKRESFNKIQEKLSQ-------------------KFGE
Glyma09g33490|Glyma09g33490.1              210 -----------------------------------------------------WQTLSDARKRIVSQIKEA-VLNGVSLED-DKRESFNKIQEKLSQ-------------------KFGE
Cucsa.273340|Cucsa.273340.1                220 -----------------------------------------------------WNTLNDARKRIVESQIKEA-LHGVTLEG-DKREQFNKIQEELERLSH-------------------KFDE
GSVIVG01003850001|GSVIVT01003850001        127 -----------------------------------------------------WQTLSDAQKRIVDSQLKQA-VLNGVSLED-DKKBHFNKIQQEELKLSQ-------------------KEEE
Eucgr.I00597|Eucgr.I00597.1                124 -----------------------------------------------------WKMLSDAQKRIVEAQIKEA-DHKGIALED-GKRREFNKIQELEKLSK-------------------QFDE
Eucgr.I00594|Eucgr.I00594.1                124 -----------------------------------------------------WNLLSDAQKRIVEAQIKEA-VLSGVALED-GKRREFNKIQQ------------------------------
28333.t000012|28333.m000566                202 -----------------------------------------------------WQSLSDAQKRIVEAQIKEA-VLNGVALED-DKREQFNKIQEELERLSQ-------------------KEGE
Potri.007G004600|Potri.007G004600.1        124 -----------------------------------------------------WTSLSDAQKRIVESQIKEA-VLNGVALDD-DKREQFNKIQEELERLSQ-------------------KEGE
Potri.014G004600|Potri.014G004600.1        217 -----------------------------------------------------WPSLSDARKRIVESQIKEG-VLNGVALDD-DKREQFNKIQEELERLSQ-------------------KEGE
Potri.014G010100|Potri.014G010100.1        242 -----------------------------------------------------WPSLSDARKRIVESQIKEG-VLNGVALDD-DKREQFNKIQEELERLSQ-------------------KEGE
28658.t000001|28658.m000032               151 -----------------------------------------------------RLRLDASKYLLERYETDL-VRACAQLSD-ADKAKLKAMNAELAKFQT-------------------TEAQ
30484.t000001|30484.m000014                 27 -----------ALGPTLEETRVLERHWLGF-VKACAKLPK-PEQERLSAVNEKLAGLGA-------------------QFGQ
```

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gi|85111610                                  251 HMEP----------KIFYTTVEKSRMMGMDPVEV----------------------------------------KRMASMGKVY-VQTLSHQASIALRTVRDDHAEHQLFMA
YKL134C                                      237 HTDY----PGSNSVKIFCKDLDNSKVSTFLLKQL--------------------------------------NKD-VKGQNYKVPTFGYAAYALLKSCENEMVRKKLWTA
Cre02.g073400|Cre02.g073400.t1.3              82 ALTD----SRKV-------------G--------------------------------------------RAPTGMGRFVPLEPFSVAGVMAGEPNESVRRAVVAA
Vocar20013694m.g|Vocar20013694m             153 ALTD----PSRV-------------G----------------------------------------------RVRLGLGRSVSLEPSQVAALLVSEPHEAVRRQVYMA
gi|32565901                                  190 NCDRIV-SVCKF---------DQAKYGLFSQIYTPV---------------------------------------SNSLDHSKRRMVYNT
CMS132C|CMS132CT                             155 -VTA--------V-F--------------R--------------------------------------------DAEKSPGKRF---------------------------
gi|268637658                                 200 QSLNSYKHPPNVTLNIEYSSLV---GHLELKYFQ----------------------------------------QLPPKKPDGNVPFIPTDYLVAGILKYIPDNIFYVHHL
Esi0033_0093                                 305 NILA---KRAAFQV-N-----RKDLHLGTFEFILSRIP----------------------------------------QPEGQPADRFTLLTQSLMSDVIKNARSGALFRVAMFL
tr|M1C3Y6|M1C3Y6_SOLTU                       189 NIIT---DPGHVDI-FPASRIPKELHLLVSPIYRNLP-----------------------------------GSSKGSW---GLRDKTKEKGFRLATESSTLQGFLQCAPDAGVRKVAVVQ
GSVIVG01018572001|GSVIVT01018572001          262 NIIT---DPGSVDI-FPASRIPKRLHHLFKPIYGHNS-----------------------------------STLRGSS---GSRDNIKEKGFRIATEPGTLSSILQWASDAGVRKVRMAFIQ
GRMZM2G450659|GRMZM2G450659_T01                1 ---------------------------------------------------------------------------------------------------RKKQVAIV
LOC_Os06g47210|LOC_Os06g47210.1              189 NVMN---KPGFVDI-YPASRIPRNMQRHFKSIHRIKP-----------------------------------WGDEEQR---NQMDLTKQKGLRHVTESGTLSTALRWVSDEBIRKQVALV
Cucsa.251510|Cucsa.251510.1                     4 NINI---DPGYVDI-FPPLRMPNNLHHLAKPIYRSSE------------------------------------SF---GSRSSKKENGFRLMTESDSLSSILQFLSDDEVRKMAVVK
Glyma04g13088|Glyma04g13088.1                194 NIVM---DPGYVDI-YPSSRIPKNLHYLVKPIYCSKS-----------------------------------LITKDLS---GSGDWLKEKGFRLITTNPQTLTSVLQFSDDEVRKMVYIR
Medtr3g009160|Medtr3g009160.1                207 NIVT---DPGSVDI-YPASRIPKNLHLFPIYKSEP-----------------------------------LITKDIS---ESKDTVKEKGFRLITTEPRTLDSVLQLSSDDEIRKMVYIQ
Bra029169|Bra029169                          184 NIAD---DPGHVDI-FPVSRVPRHLHHLLTPVYGGSP-----------------------------------RGYKGSA---HASKHRGFRHFTQRTLSSILQWTSDEEVRKMVYVE
Carubv10025983m.g|Carubv10025983m            187 NIAD---DPGHVDI-FPGSRIPRELHLLNPTYRSTE------------------------------------RGPRGST---RAMFKSKQKGFRHNTQRTLSSILQWTSDEEVRKMVYIQ
AT5G51540                                    187 NIAD---DPGHVDI-FPGSRIPRHLHHLLNPTYRSTS------------------------------------GGSRGST---RSAHKSKQKGFRHNTPRTVSSILQWTSDEEVRKMVYIQ
Eucgr.K00152|Eucgr.K00152.1                     1 --MAV--DMGSVDV-FPATCIPKELHRICKPIYRSTS-----------------------------------GMSMGST---KSTSNMQEKGSRHITFPAELSSVLQWVADEEVRKMAYIE
30147.t000467|30147.m014196                  184 NISI---DPGHVDI-YPASRIPKETHHLLTPIHRFTS-----------------------------------GASGGSR---GPWNNTKEKGFQLITPPRTLVSVLQWNSDDEVRKIAYIK
Potri.015G129300|Potri.015G129300.1          202 NITI---DPGYVDI-FPASRIPKNLHIHLLKPVHRFTS-----------------------------------GSSSGSL---GSWNNMKEKGLRLITTEHRTLVSVMEWVSDEEVRKMVAVQ
416778|416778                                218 NMQL---SQGHVDV-FPASKVPESLHHLMQPIRSHSK-----------------------------------SWK-------SKSEDTGLRLWSTDAGVVSSVLKWVPDAEIRKEVVIC
Phpat.016G041000|Phpat.016G041000.1          123 NMMR---DQGQLDI-FPASVIPKSTQHMMKPIWMEKD-----------------------------------GRVGWSRRSKFVAHDDSNMGLRVVTEPAVLSSVLKYVADSEVRRRVYMV
gi|71999758                                  245 GVMSTNDQQTFVVH-----HQKVIKDAHPHVHQKLHVD------------------------------------------EQNWLSGPWRGRMTPHTIYLFMQYCGDRQLRATAWEK
gi|85107353                                  193 HHASDKG---CNWF--------TPARLDGMDNDIIDQL---------------------------------------AKGT---GENEGRLKVKNSPARKRMWTA
YCL057W                                      198 NLGEQKE---YITF-------TKEQLDGVLFDSIHTQF---------------------------------------ETIKSDKDSNETLYKVTFKYHDIFAVLKLASSAQTRKQA-FL
gi|66801567                                  167 NIADDKT---KLSF-------SMEQLNGFLSKYEDVIFLKYEDVIFLTKKYCTVAFTRKAVEFA
CMS446C|CMS446CT                             397 NLNEENT---RLWF-------SAEBLAGCMSPDFHEGL---------------------------------------RSRPNPAKPRSELEFEVELKYFPHYFPIMKHCSVEKTRRILEKL
gi|4507491                                   181 NLNEDPT---FLPF-------TLQBLGGLPEDFINSL---------------------------------------MEDEKLKVTLKYFPHYFPLLKKCHVFETRRKMEEA
gi|14149738|ref|NP_065777                    205 NLNEDDT---FLVF-------SKABLAGLPDDFIDSL---------------------------------------TDDDKYKITLKYFPHYFPTVEKKCCIFETRRRMEMA
LOC_Os01g67590|LOC_Os01g67590.1              202 SLNDSHN---FLLL-------NEEDLAGLPLEFFKEL---------------------------------------TNGKLKVTLTSYHVTFPILEHCEVGSTRRLIAVA
Bra004244|Bra004244                          215 NLNEDSS---CFFF-------TEABLAGLPLEFIQSL---------------------------------------DK-------TQNKEFKLITLESNHVAALLELCQIAKTRRTVAMA
Bra004078|Bra004078                          216 NLNEDSS---CFFF-------TEABLAGLPVEFIQSL---------------------------------------DK-------TQSKEFKLITLESSHVAAILELCQIAKTRRTVAMA
Carubv10019853m.g|Carubv10019853m            265 NLNEDSS---CFFF-------TEDELAGLPLEFFQSL---------------------------------------EQ-------THNKEFKLITLESRHVAAILELCQIAKTRRTVAMA
AT1G67690                                    216 NLNEDSS---CFFF-------TEDELAGLPLEFFQNL---------------------------------------RK-------TQNKEFKLITLESRHVAAILELCQIAKTRRTVAMA
Eucgr.B03454|Eucgr.B03454.1                  212 NLNDDCS---YFLF-------SESELHGLPLEFFKNL---------------------------------------DK-------AQNDKYKVSLRSQNVAAWLELCHVGATRRTVATE
Medtr3g086000|Medtr3g086000.1                214 NLNDASA---FLFF-------NESELAGLPEFFKGL----------------------------------------DK-------SENCQLKHSLRSHVTAVLEFCRVGTTRRMVSRA
Glyma11g37410|Glyma11g37410.2                173 NLNDDSR---FTLF-------TKABLAGLPLEFFKGL----------------------------------------DK-------SLNCKFKHSLRSHVTAVLEFCRVGTTRQVVSGA
Glyma18g01380|Glyma18g01380.1                214 NLNDDSK---FFLF-------TEABLAGLPEFFKGL----------------------------------------DK-------SENGKFKHSLRSHLVAAVLEFCRVGTTRRMVSGA
Cucsa.394790|Cucsa.394790.1                  210 NLNDDGT---MFLF-------SEABLDGLPEFFESL----------------------------------------DK-------TENGKFKVWMRSHVTAVLELCRVGTTRRMVAVA
GSVIVG01010319001|GSVIVT01010319001          192 NMSDEST---FLLF-------SETELAGLPEFIQSL----------------------------------------DK-------AENGKFKVYLRSRHVILVLELCRIGMTRRTVAVA
29929.t000212|29929.m004709                  215 NLNDDSS---FILF-------SEABLAGLPPEYFKNL----------------------------------------DK-------AENGKFKLITLRSHNVLALLEFCQVGTTRRMVAAA
Potri.010G054500|Potri.010G054500.1          213 NLNDDSS---CFLF-------SEABLVGLPPEYFKSL----------------------------------------DK-------AGNDKYKITTLRSHNVLALLEFCQVGTTRRMVAAA
164651|164651                               103 NLAQLNE---VFLF-------NEDELAGLPEYFKNL----------------------------------------RK-------GKHEKLKLPLDARYHFLAVYNGVGSTRKALAVA
Phpat.018G066900|Phpat.018G066900.1          373 NMNEENR---RFYF-------TDSELAGLPADFIKEL----------------------------------------NR-------DSEDKLEVELKYFHYFPIMEKCHIGSTRRAMATA
Phpat.019G060600|Phpat.019G060600.1          195 NMNEENR---RFSF-------SESELAGLPADFIKEL----------------------------------------TR-------DSDGKLEVNLKYFHYFPIMERCQVGSTRRAVAIA
Esi0023_0135                                 182 NVLDAVKAHSLTLW--------DKADVDGLPASALGVAAQSAKLMGDMKAWTETELKLLSVKAELEHSKAACEGCATPLEGPWRLILMPSYLFCMQHLKNREVREKVYRA
85692|85692                                  135 NILDSIRKVGKIVT--------SVEEVEGLPATSLALAAAKAAA-------------------------------SECGVEVASPELGPWLPFKIPKSSYFRVMFHLKNRKARPELYLA
97633|97633                                   60 -----RKLFGKIVT--------BISVLEGLPETALSLAACAAV-------------------------------SNGYAGNAKSGPWLITLLSSMYSAVMKFARNRPLREEVYRA
119899|119899                               175 NVLDSHKLFGKIVT--------BISVLEGLPATALALAACAAV-------------------------------BNGYAGNAKSGPWLITLLSSMYSAVMKFARNRPLREEVYRA
97030|97030                                 120 NVLDAHKSFGKIVT--------BISVLEGLPATALALAACAAA-------------------------------BNGYAGNAKSGPWLITLLSSMYSGVMKFARNRPLREEVYRA
Cre13.g572900|Cre13.g572900.t2.1             254 NVLDAKAYKKLIT--------QPEEVAGLPATSLGLAACAAV--------------------------------REGHACAAESGPWLITLLFPSSFPVMTHAKNRELREEVYRA
Vocar20008539m.g|Vocar20008539m             242 NVLDATKSKKLIT--------WPADVAGLPATSLGLAAQCAV--------------------------------REGHECATPHSGPWLITLLFPSSYLPVMTHAKNRPLRVEEVYRA
439159                                      176 HVLDSTKKVQKIVV--------DKADIEGLPPTALGLAAQOAC--------------------------------SKGHECANAENGPWMTLLPSYMPVMKFAKNRALREEVYRE
Eucgr.L02517|Eucgr.L02517.1                  261 NILDSTKQEKLIT--------DKKDIEGLPATALALAAEMAL--------------------------------SKGHENDTAENGPWVLTLDAPSYRSSVMQHAENRPLRLEEVYRA
GSVIVG01031425001|GSVIVT01031425001          171 NILDSTKQEKLIT--------DKKBIEGLPATALAMAAEMAL--------------------------------SKGHENDTAENGPWVLTLDAPSYRSVMQHAENRPLRLEEVYRA
GRMZM2G133919|GRMZM2G133919_T01              253 NVLDATKKEEKLIT--------DKKBIEGLPATALGLAACAAV--------------------------------SKGHENATAENGPWVITLDAPSYIPVMQHAKNRPLRELEEVYRA
LOC_Os02g58340|LOC_Os02g58340.1              243 NVLDATKKEEKLIT--------DKNEIEGLPATALGLAAQOAA--------------------------------SKGHENATAENGPWVITLDAPSYLPVMQHAKNRPLRELEEVYRA
PGSC0003DMG400030613|PGSC0003DMT40007866     285 NVLDSTKKEEKLIT--------DKKDIEGLPATALGLAAQOAV--------------------------------SKGHENATADPGPWVITLDAPSYLFVMQHAKNRPLRLEEVYRA
Carubv10000350m.g|Carubv10000350m            175 NVLDATKKEEKLIS--------DKNEIEGLPFSALGLAQQOAV--------------------------------SKGHENATABPGPWVITLDAPSYLFVMQHAKNRPLRLEEVYRA
Bra006067|Bra006067                          169 NVLDATKKEEKLIT--------DKKEIEGLPSALGLFAQQOAV--------------------------------SKGHENATABPGPWIITLDAPSYLFVMQHAKNRPLRLEEVYRA
Bra028579|Bra028579                          175 NVLDATKKEEKLIT--------DKKEIEGLPSALGLFAQQOAV--------------------------------SKGNENATADTGPWLITLDAPSYLFPVMQHAKNRPLRLEEVYRA
Carubv10025914m.g|Carubv10025914m            282 NVLDATKKEEKLIT--------DKKEIEGLPSALGLFAQQOAV--------------------------------SKGHEHATAENGPWVITLDAPSYIPVMQHAKNRPLRLELEVYRA
AT5G65620                                   263 NVLDATKKEEKLIT--------DKKEIEGLPSALGLAAQOAV--------------------------------SKGHENATAENGPWIITLDAPSYLPVMQHAKNRPLRLELEVYRA
Bra024401|Bra024401                          183 NVLDATKKEEKLIT--------DKKEMDGLPSALGLAAQOAV--------------------------------SKGHENATAENGPWIITLDAPSYIPVMQHAKNRPLRLELYRA
Medtr5g030940|Medtr5g030940.1                262 NVLDATKKEEKLIT--------DKTEIEGLPATALGLAAQOAV--------------------------------SKGHENATAENGPWIITLDAPSYIAVMQHAENRPLRLEEVYRA
Glyma01g02480|Glyma01g02480.1                260 NVLDATKKEEKLIT--------DKKEIEGLPATALGLAAQOAV--------------------------------SKGHENATAENGPWIITLDAPSIAVMQHAENRPLRLEEVYRA
Glyma09g33490|Glyma09g33490.1                260 NVLDATKKEEKLIT--------DKKEIEGLPATALGMAAQOAV--------------------------------SKGHENATAENGPWIITLDAPSIFAVMQHAENRPLRLEEVYRA
Cucsa.273340|Cucsa.273340.1                  270 NVLDATKKEEKLIV--------DKHEVDGLPATALGMAAQOAV--------------------------------SKGHENATAENGPWIITLDAPSYLPVMQHAKNRPLRKEVYRA
GSVIVG01003850001|GSVIVT01003850001          177 NVLDATKNPGKLIT--------DKKDIEGLPATALGLAAQOAV--------------------------------SKGHEKDATAENGPWIITLDGPSFLSVMQHAKNRSLRKEVYYA
Eucgr.I00597|Eucgr.I00597.1                  174 NVLDATKKEEKLIT--------DKKDIEGLPATALGLAAQOAV--------------------------------LPKGHENATABPGPWIITLDAPSYTMSVMQHAKNRPLREEVYRA
Eucgr.I00594|Eucgr.I00594.1                  163 ----------------------------------------------------------------------------GHENATABPGPWVITLDAPSFMSVMQHAKNRPLRLEEVYRA
28333.t000012|28333.m000566                  252 NVLDATKKEEKLIT--------DKKBIEGLPATALALAAQOAV--------------------------------SKGHEDATAENGPWMITLDAPSYIMSVMQHAKNRPLRLEEVYRA
Potri.007G004600|Potri.007G004600.1          174 NVLDATKKEEKHIT--------DKKEIEGLPATSLGLAAQOAV--------------------------------SKGHADATAENGPWIITLDAPSMSVMQHAKNRPLRLEEVYRA
Potri.014G004600|Potri.014G004600.1          267 NVLDATKKEEKHIT--------DKKDIEGLPATSLGLAAQOAV--------------------------------SKGHTDASAENGPWIITLDAPSFMSVMQHAKNRPLRLEEIYRA
Potri.014G010100|Potri.014G010100.1          292 NVLDATKKEEKLIT--------DKKDIEGLPATSLGLAAQOAV--------------------------------SKGHTDASAENGPWIITLDAPSFMSVMQHAKNRPLRLEEIYRA
28658.t000001|28658.m000032                  201 NVLEEANASALVVD--------TRELLAGMSDKALDAAAAAAK--------------------------------AKGMDGKFLEPVVNTIGQASLAVLTNRAVREKLMAL
30484.t000001|30484.m000014                   77 NVLADEKSWALLLS------EEADLAGLEDYLREAMAAAAR--------------------------------ERGFEGKYAVTKSRSIIEPFLTSSERRDLREQAFHA
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Identifier	Pos	Sequence
gi|85111610	312	SR--TASR---------RTVHTLEELMLLEGESAKLSGFESVGHLVLHDRMVASTPESVRQELQALSENTRPQAQQEVADLTAAK----------RAHKGGDATLEPWDK
YKL134C	304	LH--SCSD---------KQVKRLSHLIKLRAILANLMHKTSYALYQLEGK-MAKNFRDVQDFLLTVMNNTIEKTANELKFIAELKANDLKKPLT-TNTDEILKLVRPWDR
Cre02.g073400|Cre02.g073400.t1.3	127	AG--RSPA---------CNRELLERMVAVRAEMAQLQGYPSYAALRTGNSLAGTEAAVVGFLTGAADVRPLMEQELQAMAQLKAFDSRNIA-TSEPSAPVSLAAWDV
Vocar20013694m.g|Vocar20013694m	198	AG--SSPP---------CNERLLEEMIAVEREMAQMQGYPSYAALRMAAGSIARTEAAVVTFLEQVAAEVRPMAERELQTLMHLKAFDMRNSR----HPSASTGISAWDV
gi|32565901	231	FY--RHDD---------IQESYLQHLISSRHQLSQLTGFESFAHR-AQRNSLLENYDTVRSFLWGVVEKCRGAFEKELAVLIDVSAQCSQQDN--NNGNNLISTIAEFDL
CMS132C|CMS132CT	171	GS--ANVN---------IAWNSLTALLNKRSELAQVLSYVPSVAHF-VALDKLLRHHHGVVSELNSVSSMLNEVRRKRQHDSLSLQRSRCS--------------------
gi|268637658	270	QSISNCYD---------SVLNHLVQLLSKRYQLAKTLGCENVSFY-ELKNKLLKTPT------QDLSKEYKEKSDEELNKLIEIKKRMEPNN------PNNDKIFSFDL
Esi0033_0093	371	GN--SVAA---------ENVQVLERLMAVRHKLALRVGFDSHAHR-MASEKNENPEEIARTLEALSAGIRELKAFQEASMLRQAKMEVE----------SSELYAQDL
tr|M1C3Y6|M1C3Y6_SOLTU	268	GN--SVPH---------ANLAVLEKLIATRHEIAQLMGFHKSYAEF-ALHSTMAASPEVVMSELFEMSKVVRFKADQEFAIQNFKRENSC----------DPNGELDPWDE
GSVIVG01018572001|GSVIVT01018572001	341	GN--SVPH---------ANLAVLEKLIAARHEIAQLMGFHKSYAEF-AVRPNMAASPEVVMSELFEMSKMIRFKPKADQEFKAIRDEKKARTC---------QICEDELDPWDE
GRMZM2G450659|GRMZM2G450659_T01	10	GN--SEPR---------ENLGVLEKLIARRHEIAKIMGCKSYAEF-AIRPNMAASADVVMSELENMSNTVKHKAEEEFKTIHNFKRRTCN--------EKSADELDPWDE
LOC_Os06g47210|LOC_Os06g47210.1	268	GN--SEPR---------ENITVLGKLINAADELAKIMGCKSVGDF-AIRPNMAASVDVVMSELFKDLSGVVRHKAGEEFKRIQDFKRNVCN--------EKSAKELDPWDE
Cucsa.251510|Cucsa.251510.1	78	GN--SEPR---------ANLGVLEKLIATRHSLAQLLGYVRSYAEF-AVTPNMAASPAVVMSELQELSKKMVQAKSIEEPKLVMKFKREKCI--------NKFEDELDPWDE
Glyma04g13088|Glyma04g13088.1	273	GN--SVPH---------ANVDVLKRLISARHELAQIMGCVRSYAEF-MVKPNMAAVSPKVVTSELFLESKMVQAKSIEERKLVMKFKREKCC----------RSDGDLRPWDE
Medtr3g009160|Medtr3g009160.1	286	AN--SVPH---------ANVDVLEKLIATRHSLAQLLGYVRSYAEF-AVKSNMAASPKVVMSELFEMSKVVQAKSTEEFNLITKFKREKCC--------QNNGDLDPWDE
Bra029169|Bra029169	260	GN--SVPH---------ANHGVLEKLIASRHELAQMMCGNSYADF-MVEPNLAASPKVVTSELQELSRTVKPKADQEFIAIRDEKREKCC--------DKSAELEPWDE
Carubv10025983m.g|Carubv10025983m	266	GN--SVPH---------SNHGVLEKLIAARHEISQMMCGNSYADF-MVEPNLAASPKVVTSELQELSKTVKPKADQEFIAIRDEKREKCC--------NKSAELEPWDE
AT5G51540	266	GN--SVPH---------ANHGVLEKLIAARHELSQMMCGNSYADI-MVEPNLAASPKVVTSELQELSKTVKPKADQEFIAIRDEKREKCC--------NPSAELEPWDE
Eucgr.K00152|Eucgr.K00152.1	79	GN--SVPV---------ANLGVLEKLIAQITGYASYAEF-ALKQNMAASPDVVMSELLESMKVVREKADKEFNAIQNFKRQKSC----------QCVDLEPWDE
30147.t000467|30147.m014196	263	GN--SVPH---------ANIKVLEKLIAARHELAQIMGYKSYAEF-MVKPNLAASPKVVTSELNEMSQLVRFKADKEFLAIRNFKKQKCC--------KKCIDLEPWDE
Potri.015G129300|Potri.015G129300.1	281	GN--SVPH---------ANLEVLEKLIAARHELAQLLGYNSYAEF-VVKPNLAASPEVVISELFNEMSKVVRFKPKADQEFLAIKKFKREKCC--------QRCIDLEPWDE
416778|416778	290	SH--STAK---------NNLLVLDKLIESRHELAQLIGENSYAEF-ATAPTMACGSEVVQSFLHDLLSQTQSKANEELFKMFESGA-----------RSSSLIEPWDE
Phpat.016G041000|Phpat.016G041000.1	205	GN--CVPK---------ARLRVLLEKLIGARHELAQLLGYNSYAEF-ATAPTMAASNAVVSELQELSIRIRGKADEEMKTLAELSKQVDTS--------CSSTSINAWDE
gi|71999758	315	WTSKWGF------DHDFYNNSINIEELRHNNEGLAKTLGYSSVAEH-RLANKMAASPETVRGFINAQRRIRPVVIDRMESWSAWAGRCELI----------TGEEQAYDM
gi|85107353	259	MENKC-P---------ENVELFKEAMLLRDEAARLLGYPDHATL-RIESRMAKTPRAVNNLFNDLRTRLAPLATKEINQFLQTKKSDCET------RNLPFDGSFYHWDW
YCL057W	266	ADQNKVP---------ENEALLLDTLKLRDELASLLGYDTVANY-NLYDKMAEDSTTVMNFLNDLKDKLIPLGRKETQVLQDMKAEDVKK-----LNQGADPNYYIWDH
gi|66801567	232	NGSKCIK---------ENTPILEETCKLRFEAAQLLGFKDWASY-KSNYKMVKSNDNIQSFLEERMRKLLTPHAVTEYDRLKQLKKRIYLEKGG--NPETYDDHYYSWDN
CMS446C|CMS446CT	466	FHSRCVP---------ENVFLLEETVRLRDEAAKLLGYSHAAF-VLEMRMANSPENVEAPLHRLSKRLDRAAHAEPSEPRILKRKDNLERYGVLLGLEPDNEIRMWDL
gi|4507491	244	FNCRCKE---------ENCALLKELVTLRAQKSRLLGLTHTHADY-VLEMNMAKTSQTVATFLDELLAQKLKFPLGEQERAVILELKRAEKCER-----RGLPFDGRIRAWDM
gi|14149738|ref|NP_065777	268	FNERCKE---------ENLPILQQLLFLRTKVAKLLGVSTHADF-VLEMNMAKSTPESRVTAPLDDLSQKLKPLGEEQERFILNLKRAECKD------RGFEYDGKINAWDL
LOC_Os01g67590|LOC_Os01g67590.1	264	YGGKGGK---------ENLALLEKLVQLRHRLARLLGYNHADY-AIEPMPERTSSRKVEFLEDLSEQLNGLARNEESVLKDLKMKEEEGD----AQE------SVEDL
Bra004244|Bra004244	278	YGKRCGD---------ANIPVLQKLVQSRHRIARLLGYAHFADY-ALDHRMSKTSTRVVIRFLEDLSSNLTPLASREDSFLKDLKRKEEGD----LPE------SVEDL
Bra004078|Bra004078	279	YGKRCGD---------ANIPVLQKLVQSRHRIARLLGYAHFADY-ALDHRMSKTSTTVVIRFLEDLSSSLTPLAIREFSILKDLKRKEEGE----IPE------GVEDL
Carubv10019853m.g|Carubv10019853m	328	YGKRCGD---------ANIPVLQKLVQSRHRIARLLGYAHFADY-ALDRRMSKTSMRVVIRFLEDLSSSLTPLAIREFSILPDLKRKEEEGE----IPE------GVEDL
AT1G67690	279	YGKRCGD---------TNIPVLQRLVQSRHRLACVVCGYAHFADY-ALDRRMSKTSMRVVIRFLEDLSSSLTPLAIREFSILTDLKRKEEGE----IPE------GVEDL
Eucgr.B03454|Eucgr.B03454.1	275	YGNRCGE---------INLSILENLVQLRHKLAKLLGYSNYADY-ALDCRMARKFLIKVFEFLEDLSASLTNMADRELSVLKDLKKREEEGD----VPL------IVEDL
Medtr3g086000|Medtr3g086000.1	277	YGNRCGE---------ANLSILESLVQQRHKYARLLGYSCYAEY-AVDVRMAKTPIKVVEFINDLSVRVTEMATKEDIVLKDLKKKEEGE----FPE------GIEDL
Glyma11g37410|Glyma11g37410.2	236	YGNRCGE---------INVSILERLVQQRHKYARLLGYSCYAEY-VIDVRMAKTPKVVEFIKDLSTSLTGLALKEINILKDLKKKEEGE----FPE------GIEDL
Glyma18g01380|Glyma18g01380.1	277	YGNQCGE---------INVFILERLVQQRHKYARLLGYSNYADY-AIDVRMAKTPKKVVEFIKDLSTSLTPLAMKEINILKDLKKKEEGE----FPE------GIEDL
Cucsa.394790|Cucsa.394790.1	273	YGKRCGE---------VNLSILERLVELRHKLARLLGYSNYADY-AVHYRMARSSAKVVEFLENLSDSITLAAKEIASLKNLKKQEEEGE----SPE------GVEDL
GSVIVG01010319001|GSVIVT01010319001	255	YGKRGGE---------ANPSVLKSLIQLRHRLARLLGYSNYADY-AVAPRMASSSKVEFLEDLSSASVNELAAREIDMLKDLKRKEEGE----FPE------GNEDL
29929.t000212|29929.m004709	278	YGKRCGE---------VNLSILERLVELRHKYARLLGYSNYADY-AVDLRMAKTSKVVEFLEDLSASLTEMATREITVLRDLKKKEEGE----FPE------GIEDL
Potri.010G054500|Potri.010G054500.1	276	YGKRCIA---------V---------ELRHKVARLFGFSNYADY-AVDLRMAKTSTKVVEFLEDLSASLTPLARETALALDLKKKEEGE----LPE------GMEDL
164651|164651	166	YDKRCIA---------ENLFIFHNVVKLRHKIAKIIGYFGYSNYAEY-VTSSRMAKSFTNVKNFLLSLSAKMSSVAAAELNKLKALKKAEYGE----EE------GMEDL
Phpat.018G066900|Phpat.018G066900.1	436	YDQRCMD---------QNVTILEKVIEMRSAMAQLLGCHKNHAEY-AIATRMAKSFFVTVKSELEDTSNKISPLAKKETAKLEAMKRQEEGD----EPE------GLYDM
Phpat.019G060600|Phpat.019G060600.1	258	YDQRCMD---------ENLPILEKVVAMRNAMAQLLGVRNHAEY-AIAIRMAKSPLKVKTFLENLSSKMSPLAKKETAKLQAMKRREEGD----EPE------GFHDL
Esi0023_0135	286	FTHLRASSVSVGEDGKSLDNEHIARVLELKKTMASLLGYGSYAEV-SLASKMAPSVPAVDDLTAMFREKSYPAAERELLEFRAYAKEKGND----------EETLWDV
85692|85692	212	YRNKASTC------EFMNTPVLTRILELRNLKAKLLGYNIVISMLLKMAT-LDKANELELHESRSGAWDGALEEDALKALAASGYG----------NYELMPWDL
97633|97633	132	DILVASGE------SFDNFPVITRILELRQQKAELLGYENH----SMLQKMAT-LDSCHALLEKLHSGSRDAAIRDMREFEEEVRSENSE----------EDENLFHWDL
119899|119899	252	DVLVASGE------SFDNFPVITRILELRQQKAELLGYENH----SMLQKMAT-LDSCHALLEKLHSGSRDAAIRDMREFEEEVRSENSE----------EDENLFHWDI
97030|97030	192	DILVASGE------SFDNFPVITRILELRQQKAELLGCENHAQV-SLLQKMAT-LDSCHALLEKLHSGSRDAAIRDMREFEEEVRSENSE----------EDENLFHWDI
Cre13.g572900|Cre13.g572900.t2.1	331	YILTRASSC------DADNGPLIERILTLRGEKARLLGFSSFADL-SMASKMAT-LSRAHALLEKLRAASYGCAALADRDEVQAYAASGQFQ----------GDEFWWDI
Vocar20008539m.g|Vocar20008539m	319	YLTRASSC------DSDNGPHIERILELRAEKARLLGYDNFADL-SMASKMAS-LDKAELSLEKLRSASHAAEAIRDDKDEVQEGATSGQFE----------QDPEWWDV
439159	253	FIHLVASEC------DLDNTPVINKLIELRMEKEKLLGYKNYAEV-SMAMKMAT-TETANELLEKLRLSSWDGALKDFEFLKSLSKSKNAF----------EADDLSHWDL
Eucgr.L02517|Eucgr.L02517.1	338	YVLRASSC------DHNNTPIIARILKLRLEKAKLLGYNNYAEV-SMAMKMAT-VEKAAELLEKL--------------------------------EANDIKQWDI
GSVIVG01031425001|GSVIVT01031425001	248	YVIRASSC------DHNNTPIIARILKLRLEKAKLLGYNNYAEV-SMEMKMAT-INKAAELLEDLRSASWNNAAIQDMEDIENLAKAQDAI----------EANDIKQWDI
GRMZM2G133919|GRMZM2G133919_T01	330	YLTRASSS------DLDNTPIIQILKLRLEKAKLLGYKNYAEV-SMAQKMAT-VERVEELLEKLRAASWDHAVKDMEDLKVQAKDSGSP----------EANDITHWDL
LOC_Os02g58340|LOC_Os02g58340.1	320	YLTRASSG------DLDNTPIISQILKLRLEKAKLLGYKNYAEV-SMAQKMAT-VDRVEELLEKLRAASWDPAVKDMEDLKAQAKESASP----------EANDIAHWDL
PGSC0003DMG400030613|PGSC0003DMT40007866	362	YLTRASSG------DLDNTPIINQILKLRLEKAKLLGCENHAQV-SMLKKMAT-VEKAAELLEKLRSASWDPAVKDLKDECKSQGQSP----------EADDINHWDL
Carubv10000350m.g|Carubv10000350m	252	YLSRASSG------DLDNTAIIDQILKLRLEKAKLLGYRNYAEV-SMATKMAT-VEKAAELLEKLRSASWPAVQDIEDLKSGAKNGGAA----------EADSIIHWDI
Bra006067|Bra006067	246	YLSRASSG------ELDNTAIIDQILKLRLEKAKLLGYSNYAEV-SMATKMAT-VETADELLEKLRSASWDPAVQDIEDLKSGAKNGGAA----------EADSFIHWDI
Bra028579|Bra028579	252	YLSRASSG------DLDNTAIIDQILKLRLEKAKLLGYSNYAEV-SMATKMAT-VEKAAELLEKLRSASWAPAVQDIEDLKSGAKNQGAA----------EADSLIHWDV
Carubv10025914m.g|Carubv10025914m	359	YLTRASSG------DLDNTAIIDQILKLRLEKAKLLGYNNYAEV-SMATKMAT-VEKAAELLEKLRSASWDAAVQDIEDLKSGAKNQGAA----------ESDSLTHWDT
AT5G65620	340	YLSRASSG------DLDNTAIIDQILKLRLEKAKLLGYNNYAEV-SMMKMAT-VEKASELLEKLRSASWDPAVQDMEDLKSGALSQGAL----------EADSITHWDI
Bra024401|Bra024401	260	YLTRASSG------DLDNTAIIDQILKLRLEKAKLLGYNNYAEV-SMTMKMAT-VEKAAELLEKLRSASWDAAVQDIEDLKSGALSQGAL----------ESDSMTHWDT
Medtr5g030940|Medtr5g030940.1	339	YLTRASSG------DLDNTKLIEQILKLRLEKAKLLNYNNYAEV-SMATKMAT-VDKAAELLEKRKASWDAAVQDIEDLKKGSKDQGAL----------EADDLITHWDV
Glyma01g02480|Glyma01g02480.1	337	YVSRASSG------DLDNTGIIDQILKLRLEKAKLLNYNNYAEV-SMATKMAT-VDKAAELLEKLRRSSWDAAVQDIEDLKESKSQGAL----------EAGDLITHWDI
Glyma09g33490|Glyma09g33490.1	337	YVTRASSG------DLDNTGIIDQILKLRLEKAKLLNYNNYAEV-SMATKMAT-VDKAAELLEKLRSASWDAAVQDVEDLQDEAKKGGAP----------EAGDLITHWDI
Cucsa.273340|Cucsa.273340.1	347	YITRASSG------EMDNTPIIEQILKLRLEKAKLLGYNNYAEV-SMETKMAT-VEKAAELLEKLRSASWNAAVQDVEDLQDEAKKGGAP----------EANDINHWDM
GSVIVG01003850001|GSVIVT01003850001	254	YVTRASSG------DLDNTEIIGQILKLRLEKAKLLGYNNYAEV-SMATKMAT-LDKAAELLQKLRSASWDAAVQDMEDLKRASKSQGAV----------EANDINHWDM
Eucgr.I00597|Eucgr.I00597.1	251	HVTRASSG------DTNNTPIIDQILKLRMEKAKLLGYNNYCEV-SMATKMAT-LDKAAELLEKLRSASWDAAVQDMEDLKRASKSQCAK----------EYDDLRHWDI
Eucgr.I00594|Eucgr.I00594.1	203	HVTRASSG------DLDNTFIIDQILKLRLEKAKLLGYNNYCEV-SMATKMAT-VEKAAELLEKLRSASWDAAVQDMEDLKIGSKSQGAK----------EANDITHWDI
28333.t000012|28333.m000566	329	YVTRASSG------DLDNTPIIEQILKLRLEKAKLLGYNNYAEV-SMATKMAT-VEKAAELLEKLRSASWDAAVQDMEDLKISGKNQCAM----------EANDITHWDT
Potri.007G004600|Potri.007G004600.1	251	HVTRASSG------DLNNTAIIDEILKLRLEKAKLLNYNNYAEV-SMATKMAT-VEKAAELLEKLRIASWDAAVQDMEDLKISGKNQCAM----------EANDITHWDT
Potri.014G004600|Potri.014G004600.1	344	HVTRASSG------DLNNTAIIDEILKLRLEKAKLLGYNNYTEV-SMATKMAT-VEKAAELLEKLRSASWDAAVQDMEDLKISGKNQCAM----------EANDITHWDT
Potri.014G010100|Potri.014G010100.1	369	HVTRASSG------DLNNTAIIDEILKLRLEKAKLLGYNNYTEV-SMATKMAT-VEKAAELLEKLRAASWDAAVQDMEDLKISGKNQCAM----------EANDITHWDT
28658.t000001|28658.m000032	272	SLARCGHC------GKYDNTQVVLSLAKLRAEKAMLLGYPSLAAY-ALEDQTAHDPDAVNKMMSEFARPAVANAKKEGAEIQQVIDKEKC----------GFQLAAQDW
30484.t000001|30484.m000014	148	WVARGANG------GKTDNREHIRETLALRAEKAKLLGYANFAEL-KLDNTVAKTEDAVNDLEMTVWAKAATRAAEEERIAALIABEGR----------NHEVMPKDW

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gi|85111610                                          401 DFWAESIRQAI-KS-RQKRED----LSSYESLGTVLQ-GLSRIFTRLYGIREVFREP-----------MPGETWHP----DVRRLDVVSDV----EGHVAVLVCDLFY--
YKL134C                                              401 DYYTGKYFQLN-PSNSPNAKE----ISYYETLGNVLQ-GLSDLFQIYGIRLEPAIT-----------DEGETWSP----DVRRLNVISEE----EGIIGIIVCDLFE--
Cre02.g073400|Cre02.g073400.t1.3                     224 EYYASRARQAL---VTSPPGA----LLRYTALFSVLA-CVRTLLRAVFRIELVLGPA----------AAGEGWAA----GVLRAEAHHPD--LGPLGTVVLDLGE--
Vocar20013694m.g|Vocar20013694m                      293 EYYAARARQRI---ITSSSSA----VLRYTAVFSVLA-CVQHLLRRVERMELRVSPA----------APGEGWAP----GVLRCDAEHAD--LGPLGTVVLDLADRC
gi|32565901                                          327 GFLMHLYRESAYDIAQ-VSQQ----SSLFETFNSIWN-CFSTLTRRLYGVRLIEEPL----------TSGEMWNS----SGVMKLQAVLEQ----NNELGVIYVDVSI--
CMS132C|CMS132CT                                      249 ----------------SLARR----LQRYLGVDSVLE-VLSGLLCELFGIRIYRLRQ----------NQVRGVIWHP----SVEHAMLVD-A-RNGNFVGEVFFDLFA--
gi|268637658                                         357 PFYKNQMSKEFYKSHSLEKEE----LSQYETLENVLN-GLNIIVNKLFNSQLKIVPM----------NNGESWDK----SVIKFNLLRND--ENKTILGIMYLDPWE--
Esi0033_0093                                         458 SYYMGYVKSRE--CNLLDSVV----LSEYETLGGCLE-GLRMVCRGLSLSLSLEQVPI----------EPGENWAGRSGGGVKLVLRHEQ----EGVLGTIYLDLHR--
tr|M1C3Y6_SOLTU                                      357 AVFTWLMKSAK--MKLESSV-----KS---------------------------------------------------------------------------------
GSVIVG01018572001|GSVIVT01018572001                 430 AMLTGMMKSSA--MNLDSSV-----VASYFPLHQCIE-GLKVEVESLFCATERSIPL----------APGESWHP----DVLKMSLHHPD--EGDLGYMLILCE--
GRMZM2G450659|GRMZM2G450659_T01                       99 DMFTGMMKSSV--MDLLASV-----IAKYFPLSQCLK-GLNVEVESLFGATEHQIPM----------RDGGSWHP----DVIKLRLHHPD--EGDLGFMLDLKS--
LOC_Os06g47210|LOC_Os06g47210.1                     357 DMFIGMMKSAV--HNLLVSV-----VAAYFPLSQCLK-GLNVEVESLFGATEHQIPM----------GDGGSWHP----DVMKLSLHHPD--EGNLGFMYLDLYS--
Cucsa.251510|Cucsa.251510.1                          167 AYYTSMMKSTA--HNLLDSVV----IASYFPLSQCIE-GLKVLVKSLFGASEYNIPL----------APGGSWHP----DVLKLSLQHPE--ELSLII--------
Glyma04g13088|Glyma04g13088.1                        362 LYYMTMMKSSS--MKLDASV-----VGSYFSLSNCIE-GLKVLVNSLFGATERIIPL----------APGESWDP----HVLKLSLDHPE--EGDIGYMLILYS--
Medtr3g009160|Medtr3g009160.1                        375 LYYTTMMKSSV--MKLDSLV-----AASYFSLSNCIE-GLKVLVNSLFGVICHRIPL----------APGESWDP----QVLKLCLHHPE--EGDLGYMLILKS--
Bra029169|Bra029169                                  349 LYYTSMMKSSV--NDVPTSV-----VASYFPLSQCIE-GLKVLVESLFGATEHTVPL----------APGESWDP----B------------GDLGYMLILYS--
Carubv10025983m.g|Carubv10025983m                   355 TYYTSMMKSSV--NDVPTSV-----VASYFPLQCIE-GLKVLVESLFGATEHTIPL----------APGESWDP----DVLKLSLHHPN--EGDLGYMLILYS--
AT5G51540                                            355 TYYTSMMKSSI--NDVPTAV-----VASYFPLQCIE-GLKVLVESLFGATEHTIPL----------APGESWHP----NVVKLSLHHPD--EGDLGYMLILYS--
Eucgr.K00152|Eucgr.K00152.1                          167 TYYTAMMKSSH--KDLDSSV-----VASYFPLRCIE-GLKVLVESLFGATEHSVPL----------APGGSWHS----DVLKMALHHPE--EGDLGYMYLLYA--
30147.t000467|30147.m014196                         352 ALHTGMMKSSA--QNLLSSI-----VASYFPLAQCIE-GLKVLVNSLFGATEHNVPM----------APGESWHP----DVLKMAFHHPE--EGDLGYMYLLYS--
Potri.015G129300|Potri.015G129300.1                 370 AYYTGMMKSSA--HNLLSSI-----VASYFPLSQCIE-GLKVIVKSLFDASEHQVPV----------APGESWHP----DVLKMSLHHPE--EGDLGYMYLLYS--
416778|416778                                        373 AYYTGMYKARA--QNLLSKV-----ISSYFPLERCLN-GLKVTVKSLFDASEHQVPV----------APGEVWHS----DVQKWELRHST--EGCLGHMFDLYS--
Phpat.016G041000|Phpat.016G041000.1                 295 SYYAGLLKART--MDLNAGV-----VASYFPVGQCIE-ALRIICQLLFGATEEQVPL----------APGEAWHP----AVQKMCLRHPS---EGELGHLYLDLLYA--
gi|71999758                                          409 PLVCRKEABHH--YDVNPLD----LMNHFPFWPTFQ-NIMGVIGHIPNLEFKDITDK----------GLEKAHA----DVRIYSVGDK----FSGQHYGRLYIDPYD--
gi|85107353                                         352 AFYASQISKQE--FDLLNKK----VAEYFPIDSAIT-GMLRFFGVLFGVVRLTAEDLERISPTGVADDVMYHR----DTIMFSVWND-ESEGNDFLGVILVIDAHP--
YCL057W                                             360 RYYDNKYLLEN--FNVFLEK----ISEYFPLEATIT-GMLETYETLFNLKFIETKDS----------QNKSVWED----DVKQIAVWNMDDPKSPNFVGWIYFDLHP--
gi|66801567                                         329 AFYNNVMLVQD--MQVENNL----VKEYFPFEVVIK-GIENCYELLNVKFTEVP-----------AYQFWHE----SVKMYSCVDT--ADSNKLLGHFYIDLFP--
CMS446C|CMS446CT                                     565 RYYMTKYEQQ---LQIFHTK----IAEYFPLERVLS-NMLDIYCELLGLAFVHLT----------QCQRWHE----DVRLFEVRDA--QNAALLGYFYLDLHP--
gi|4507491                                           338 RYYMNQVETR---MCVFQNL----LKEYFPVQVVTH-GLLGIYCELLGLAFHHEE----------GASAWHE----DVRLYTARDA--ASGEVVGKFYLDLYP--
gi|14149738|ref|NP_065777                           362 YYYMTQTFELK--MSLFQBF----LKEYFPIEVVTE-GLLNTYCELLGLSFEQMT----------DAHVWNK---SVTLYIVKDK--ATGEVLGQFYLDLYP--
LOC_Os01g67590|LOC_Os01g67590.1                     352 LYYMKRAELK---VDLFTGE----LKQYFPVDLVLS-CILKMFCDLFALFEEMK----------DAHTWHD---TVRLFSVWDA--SGSDLGYFFLDIFS--
Bra004244|Bra004244                                 366 LYYIKFVELQ---FDLLFGD----IRQYFPVSLVLP-CILKICDLFGKFKIEEVT----------EILVWYY---DVRAFAVFDS--GSGKLLGYAMLDMFS--
Bra004078|Bra004078                                 367 LYYIKFVELQ---FDLLFGD----IRQYFPVSLVLS-CIFKICDLFGIKIKEEVT----------ETDVWYY---DVQAFAVFDS--GSCKLLGYFLMLDMFT--
Carubv10019853m.g|Carubv10019853m                   416 LYYIKFVELQ---FDLLFGD----IRQYFPVNLVLS-CIFKICDLFGIKFEEVT----------EVDVWYH---DIRAFAVFDS--GSCKLLGYFYLDMFT--
AT1G67690                                            367 LYYIKFVELQ---FDLLFGD----IRQYFPVSLVLS-CIFKICDLFGIKFEEVT----------EVDVWYH---PIRAFAVSDT--DAKKTIGYFYLDIYH--
Eucgr.B03454|Eucgr.B03454.1                         363 LYYVKFTFQEQH--FDLLFGA----IKQYFPVKLVLS-CILKIFQDLFDLRFEEIA----------DPEVWHC----DVRLFSVIDL--SSGDLLGHFYLDVMVR--
Medtr3g086000|Medtr3g086000.1                       365 LYYVKFVEEQS---YDLLFGE----IKQYFPIGLVLS-CIFKIFCDLFGLRFEEIA----------GAEVWHC---DVRVFAVFDL--SSSELLGCYCYLDLFS--
Glyma11g37410|Glyma11g37410.2                       324 LYYVKFVEEQD---YDLLFGE----IKQYLPISVVLS-CIFKIIQDLFGLRFEEIA----------RADVWHG----DVI------------------------
Glyma18g01380|Glyma18g01380.1                       365 LYYVKFVEEQG---YDLLFGE----IKQYFPISVVLS-CIFKIIQDLFGLRFEEIA----------GADVWHC---DVCVFSVLDL--GSSELLGVCVFFDLFS--
Cucsa.394790|Cucsa.394790.1                         361 LYYVKRAEFQE---FNLLFVT----VKQYFPVSLVLS-CIFKINCDLFGLRFEEVI----------DAEVWHY---DVKLVSVFDL--NSGELLGYFYLDIFS--
GSVIVG01010319001|GSVIVT01010319001                 343 LYYMKRVEEQY---LDLLFGV----LKQYFPINLVLP-CIFKIFCDLFGLRFEEIA----------DVEVWHS---DVRAFSVFDL---SSELLGYFYLDIHP--
29929.t000212|29929.m004709                         366 LYYVKFVEEAQ---FDVVFGA----LKQYFPVDLVLS-CIFKIFCDLFGLRFQEIK----------DAEVWHS---DVSVISVFDL---SSAELLGYFYLDLFS--
Potri.010G054500|Potri.010G054500.1                 355 LYYVKFVEEAQ---FDLLFGA----LKQYFPVDVVLS-CILKITCDLFGLRFQEVA----------DAEVWHG---DVSVFSVFDL---SSEELLGYFYLDIYM--
164651|164651                                       254 LYYVKFVELE---FQAITEK----LNEYFPVEVVTN-GLTQIYCELFGISFWLIFE----------ERGAWHP---DVRLFAVSDT--DAKKTIGYFYLDIYP--
Phpat.018G066900|Phpat.018G066900.1                 524 RYYIRKSEEAD---FNVYET----VRQYFPLNIVTA-GLLQIYCDLFGLFRKEVS----------DPDVWHP---EVQKFSVTDE--NTGENMGYFYLDLHP--
Phpat.019G060600|Phpat.019G060600.1                 346 RYYIRKAEPLE---FKVFYET----VKQYFPLNVVTA-GLLQIYCDLFGLFREEVV----------KPTVWHP---EVQQVAVSDT--ETGEMNGYFYLDLHP--
Esi0023_0135                                         384 AFWSBRRKEL---MAFSFED----LRPYFSLEEVLE-GMYDDARLFGVSITPAD----------GEA--EVWNP----DVRRFN1KDT--ASGEHVASFYLDAWS--
85692|85692                                         303 PLWWMERLREAR--LDMSEEE----FRPFEAFFEVLE-GLRPYFSMEIDAAD----------NLVATSIWED----DVREFRVKDM--DTKETEAYFFLDPFS--
97633|97633                                         221 PLWWTERFREAK--LDMNDE-----LRPYSMENVLD-GLFSLAKRLEGVHIEELE----------ENT--EVWDK----EVKLVKVAEC--ASGENLGYFYLDPFS--
119899|119899                                       344 PLWWTERFREAK--LDMNDASFPSKAWPYSMENVLD-GLFSLAKRLFGVHIEELE----------ENT--EVWDK----EVKLVKVAEC--ASGENLGYFYLDPFS--
97030|97030                                         284 PLWWTERFREAK--LDMNDEE----LRPYSMENVLD-GLFSLAKRLFGVHIEELE----------ENT--EVWDK----EVKLYKVAEC--ASGENLGYFYLDPFS--
Cre13.g572900|Cre13.g572900.t2.1                    421 TFWAERLRESK--YDVNEEE----LRPYLALFSVLQ-GLRGLANRLFGVEVVPAD----------GEA--PVWHK----DVREFKVLK---ACAAAYFYLDPYS--
Vocar20008539m.g|Vocar20008539m                     409 TYWAERLRESK--YNISDEE----LRPYALPKVMD-GLFNLANRLDIVRVVPAD----------GMA--PVWHP----DVDLFKVLK---ACQPKAYFYLDPYS--
439159                                              345 TYWSERLREDR--YDVNEEE----LRPYSLPKVVD-GLFNLAKYLFGVQIEPAD----------GMA--PVWNK----DVSEFQVKDL--ACEPLAFFYLFPYS--
Eucgr.L02517|Eucgr.L02517.1                         340 NFWGERLRLK---YDINEEE----LRPFISLPKVIN-GLFNLAKMLELDVEPAD----------GLA--PVWNN----DVKEYCVKDS---LGIPIAYFYLDPMA--
GSVIVG01031425001|GSVIVT01031425001                 422 SFWSERLRESK--YDINEEE----LRPYAALPKVMD-GLFLLANHLEGVTVEPAD----------GLA--PVWWS----DVKEYCVKDS--SSSEVAYFYFDPYS--
GRMZM2G133919|GRMZM2G133919_T01                     412 SFWSERLRESK--YDINEEE----LRPYALPKVMD-GLFNLANRLFGVTVEPAD----------GLA--PVWNS----DVKEYCVKDS--SNSEVAYFYFDPYS--
LOC_Os02g58340|LOC_Os02g58340.1                     454 TFWSERLRESK--YELNEEE----LRPYSLPKVMD-GLFNLSAMLFGIEIEPAD----------GVA--PVWNN----DVRFYCVKDS--SCNPIAYFYFDPYS--
PGSC0003DMG400030613|PGSC0003DMT40007866            344 TFWSERLRESK--YDINEEE----LRPYSLPKVMA-GLFGLAKTLFGIDVAPAD----------GVA--PVWNS----DVRFYCVKDS--SCNPIAYFYFDPYS--
Carubv10000350m.g|Carubv10000350m                   338 TFWSERLRESK--YDINEEE----LRPYSLPKVMA-GLFNLAKTLFGIDVVPAD----------GVA--PVWNS----DVRFYC1KDS--SCNPIAYFYFDPYS--
Bra006067|Bra006067                                 344 TFWSERLRESK--YDINEEE----LRPYSLPKVMD-GLFSLAKTLFGIDIEPAD----------GLA--PVWNN----DVRFYCVKDS--SCGPIAYFYFDPYS--
Bra028579|Bra028579                                 352 TFWSERLRESK--YDINEEE----LRPYSLPKVMD-GLFNLAKTLFGVEIEPAD----------GLA--PVWNN----DVKEFCVKDS---SCSPIAYFYFPYS--
Carubv10025914m.g|Carubv10025914m                   451 SFWSERLRESK--YDINEEE----LRPFSSLPNVMD-GLFNLAKSLFGIEIEPAD----------GLA--PVWNN----DVRFCVKDS--SSSEVAYFYFDPYS--
AT5G65620                                            431 TFWSERLRESK--YDINEEE----LRPFSSLPKVMD-GLFNLAKTLFGIEIEPAD----------GLA--PVWNN----DVRFCVKDS---SCGPIAYFYFDPYS--
Bra024401|Bra024401                                 429 SFWSERLRESK--YDINEEE----LHPYSLPNVMD-GLFDLAKSLFGIEIEPAD----------GLA--PWWDK----DVRFYSVHNS--SCGSIAYFYFDPYT--
Medtr5g030940|Medtr5g030940.1                       429 TFWSERLRESK--YDINEEE----LRPYSLPKVME-GLFSLAKMLFGIDHIQPAD----------GLA--PVWDK----DVRFYSVHNS--SCGSIAYFYFDPYT--
Glyma01g02480|Glyma01g02480.1                       439 NFWSERLRESK--YDINEEE----LRPYSLPKVVE-GLFNLAKMLFGIDVGPAD----------GLA--PVWNN----DVREFYRVKES--SCNFVAYFYFPYS--
Glyma09g33490|Glyma09g33490.1                       346 GFWSERLRESK--YDISEEE----LHPYSLPNVVE-GLFNLVGTLFGIEIEPAD----------GLA--PVWNS----DVRFYCVKDS--SCNPIAYFYFDPYS--
Cucsa.273340|Cucsa.273340.1                         343 KFWSERLRESK--YDINEEE----LRPFSSLPKVTE-GLLVGLFGIEIEPAD----------GLA--PVWNS----DVRFYCVKDS--ASPIAYFYFDPYS--
GSVIVG01003850001|GSVIVT01003850001                 295 KFWSERLRESK--YDINEEE----LHPFSSLPNVIF-GLLVGTLFGIEIEPAD----------GLA--PVWNN----DVKFYCVKDS---TCNPIAYFYFDPYS--
Eucgr.I00597|Eucgr.I00597.1                         421 GFWAERLRESK--YDINEEE----LRPFSLPKVMD-GLFNLAKTLFGIDIESAD----------GLA--PVWNN----DVKFYCVKDE--LCNPIAYFYFDPYS--
Eucgr.I00594|Eucgr.I00594.1                         343 GFWAERLRESK--YDINEEE----LRPFSLPKVMD-GLFNLAKTLFGIDIEPAD----------GLA--PVWNN----DVKFYCVKDS--LGSPIAYFYFDPYS--
28333.t000012|28333.m000566                         436 GFWAERLRESK--YDINEEE----LRPFSSLPKVMD-GLFNLAKTLFGIDIEPAD----------GLA--PVWNN----DVKFYCVKDS--LCNPIAYFYFDPYS--
Potri.007G004600|Potri.007G004600.1                 461 GFWAERLRESK--YDINEEE----LRPFSSLPKVMD-GLFNLAKYLFGVQIEPAD----------DLT--PVYDM----DVRVWDVPDA----NCKQSALBLGPYFA--
Potri.014G004600|Potri.014G004600.1                 364 AFLSDKVREAR--FNFLQNQ----LRPYELNSVLTN-CVFYAANKYVGLILKEKER----------CV---PAYHP----DVRVFEIRDR----SDKLVALFLGLYFA--
Potri.014G010100|Potri.014G010100.1                 240 RHYAEKIRTRK---FDFSETE----LRPYLQLEKIIA-ACFDVAGRLFGIKAVEQK
28658.t000001|28658.m000032
30484.t000001|30484.m000014
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gi|85111610                                          483 -----------------------------RELKSPNPLHFTLRCSEELSPHEIA-----------ETAHTQAENP------------
YKL134C                                              484 -----------------------------RNGKTSNPAHFTVCCSRQIYPSETD-----------FSTI-------------------
Cre02.g073400|Cre02.g073400.t1.3                     305 -----------------------------RSGKYPSAVTFPITCGRQLPGGDVE-----------AALAS------------------
Vocar20013694m.g|Vocar20013694m                      376 GGSGRSGQTHTTAKYTTRHRIDVVLTYIPDRPGKYPSAVTFPITCGRQLSPPSSS------------------------------------
gi|32565901                                          411 -----------------------------RPGKAVGDCHYTVRCSKQ------------------------------------------
CMS132C|CMS132CT                                      320 -----------------------------RDGKMPGALHYALRGSERR------------------------------------------
gi|268637658                                         443 -----------------------------RQDKATGCVNHFIGLGYKKFKILKN-----------NLKNN-------------------
Esi0033_0093                                         543 -----------------------------REGKFGHALHFTVRCGC-------------------------------------------
tr|M1C3Y6|M1C3Y6_SOLTU                                   -------------------------------------------------------------------------------------------
GSVIVG01018572001|GSVIVT01018572001                  511 -----------------------------RKDKYPGCLHFAIKGGRR------------------------------------------
GRMZM2G450659|GRMZM2G450659_T01                      180 -----------------------------RKGKHPGCAHFAIQGCRR------------------------------------------
LOC_Os06g47210|LOC_Os06g47210.1                      438 -----------------------------RKGKYPGCAHFAIRGGRR------------------------------------------
Cucsa.251510|Cucsa.251510.1                          241 -----------------------------------------------------------------------------------------
Glyma04g13088|Glyma04g13088.1                        443 -----------------------------RKGKYPGCAHFAIKGARR------------------------------------------
Medtr3g009160|Medtr3g009160.1                        456 -----------------------------RKGKYPGCAHFAIKGCRR------------------------------------------
Bra029169|Bra029169                                  419 -----------------------------RKTKYPGCASFAIRGGRK------------------------------------------
Carubv10025983m.g|Carubv10025983m                    436 -----------------------------RKTKYPGCASFAIRGGRK------------------------------------------
AT5G51540                                            436 -----------------------------RKGKYPGCASFAIRGGRK------------------------------------------
Eucgr.K00152|Eucgr.K00152.1                          248 -----------------------------RKGKYPGCAHFAIKGGRW------------------------------------------
30147.t000467|30147.m014196                          433 -----------------------------RKGKYPGCANFAIKGGCR------------------------------------------
Potri.015G129300|Potri.015G129300.1                  451 -----------------------------RKGKYPGCAHFAVKGGCR------------------------------------------
416778|416778                                        454 -----------------------------RKEKYPNCAHFTLKGGRR------------------------------------------
Phpat.016G041000|Phpat.016G041000.1                  376 -----------------------------RPGKFPGCAHFTLKGCRN------------------------------------------
gi|71999758                                          491 -----------------------------RQNKRGGWNVLLARPESKE------------------------------------------
gi|85107353                                          447 -----------------------------REGKYHVLNFPLELGHQR------------------------------------------
YCL057W                                              446 -----------------------------RDGKYGHANFGLSSSFMI------------------------------------------
gi|66801567                                          410 -----------------------------REGKYGHAAVWPLIPGYER------------------------------------------
CMS446C|CMS446CT                                     645 -----------------------------REGKYGHAAVWPLQPSCVR-PS-----------KVQETTAPRGKVG-------------
gi|4507491                                           418 -----------------------------REGKYGHAACFGLQPGCLR------------------------------------------
gi|14149738|ref|NP_065777                            442 -----------------------------RGKYNHAACFGLQPGCLL------------------------------------------
LOC_Os01g67590|LOC_Os01g67590.1                      432 -----------------------------REGKYAHTCVVALQNRCLC------------------------------------------
Bra004244|Bra004244                                  446 -----------------------------REGKFSQSCVVALQNNALF------------------------------------------
Bra004078|Bra004078                                  447 -----------------------------REGKFSHSCVVSLQNNALF------------------------------------------
Carubv10019853m.g|Carubv10019853m                    496 -----------------------------REGKCNHSCVVALQNNALF------------------------------------------
AT1G67690                                            447 -----------------------------REGKCNHSCVVALQNNALF------------------------------------------
Eucgr.B03454|Eucgr.B03454.1                          443 -----------------------------REGKYGHSCVVFLQNRSLS------------------------------------------
Medtr3g086000|Medtr3g086000.1                        445 -----------------------------REGKYGHSCVVFLQNSALT------------------------------------------
Glyma11g37410|Glyma11g37410.2                        381 -----------------------------RGKYGHTCVLALQNSALT------------------------------------------
Glyma18g01380|Glyma18g01380.1                        445 -----------------------------REGKYGHTCVLALQNSALT------------------------------------------
Cucsa.394790|Cucsa.394790.1                          441 -----------------------------REEKYIHTCVVALQSSALL------------------------------------------
GSVIVG01010319001|GSVIVT01010319001                  423 -----------------------------REGKYGHICVVALQNGSLS------------------------------------------
29929.t000212|29929.m004709                          446 -----------------------------REGKYGHTCVVALQNGALS------------------------------------------
Potri.010G054500|Potri.010G054500.1                  435 -----------------------------REGKYGHTCVVALQNGALS------------------------------------------
164651|164651                                        335 -----------------------------RDGKYSHACVCPLQPSST-------------------------------------------
Phpat.018G066900|Phpat.018G066900.1                  604 -----------------------------RDGKYTHACVCSLQPGCLM------------------------------------------
Phpat.019G060600|Phpat.019G060600.1                  426 -----------------------------RDGKYTHACVCSLQPGCVQ------------------------------------------
Esi0023_0135                                          465 -----------------------------RPENKRGGAWMGVCIGARKALG------------------------------------------
85692|85692                                          386 -----------------------------RPLEKRGGAFVSSFVAK----------------------------------------------
97633|97633                                          301 -----------------------------RPHQKRSGCWMGVVFNRSHAAV------------------------------------------
119899|119899                                        429 -----------------------------RPHQKRSGCWMGVVFNRSHAAV------------------------------------------
97030|97030                                          365 -----------------------------RPHQKRSGCWMGVVFNRSHAAV------------------------------------------
Cre13.g572900|Cre13.g572900.t2.1                     500 -----------------------------RPAEKRGGAWMAEVVGRSSLLA------------------------------------------
Vocar20008539m.g|Vocar20008539m                      488 -----------------------------RPAEKRGGAWMAEVVGRSRLLA------------------------------------------
439159                                               425 -----------------------------RPSEKRGGAWMDIVVGRSRVLA------------------------------------------
Eucgr.L02517|Eucgr.L02517.1                              -------------------------------------------------------------------------------------------
GSVIVG01031425001|GSVIVT01031425001                  420 -----------------------------RPSEKRGGAWMDVVFGRGSTFS------------------------------------------
GRMZM2G133919|GRMZM2G133919_T01                      502 -----------------------------RPSEKRGGAWMNVVFSRSRVLA------------------------------------------
LOC_Os02g58340|LOC_Os02g58340.1                      492 -----------------------------RPSEKRGGAWMNVVFSRSRVLA------------------------------------------
PGSC0003DMG400030613|PGSC0003DMT40007866             534 -----------------------------RPSEKRGGAWMDEVVSRSRVLA------------------------------------------
Carubv10000350m.g|Carubv10000350m                    424 -----------------------------RPSEKRDGAWMDEVFSRSRVMA------------------------------------------
Bra006067|Bra006067                                  418 -----------------------------RPSEKRDGAWMDEVFSRSRVMA------------------------------------------
Bra028579|Bra028579                                  424 -----------------------------RPSEKRGGAWMDEVFSRSRVMA------------------------------------------
Carubv10025914m.g|Carubv10025914m                    531 -----------------------------RPSEKRGGAWMDEVVSRSRVMA------------------------------------------
AT5G65620                                            512 -----------------------------RPSEKRGGAWMDEVFSRSRVMA------------------------------------------
Bra024401|Bra024401                                  432 -----------------------------RPSEKRGGAWMGEVFSRSQVMA------------------------------------------
Medtr5g030940|Medtr5g030940.1                        511 -----------------------------RPSEKRQGAWMDEVVARSRVLS------------------------------------------
Glyma01g02480|Glyma01g02480.1                        509 -----------------------------RPAEKRQGAWMDEVFARSRVLS------------------------------------------
Glyma09g33490|Glyma09g33490.1                        509 -----------------------------RPAEKRQGAWMDEVFARSRVLS------------------------------------------
Cucsa.273340|Cucsa.273340.1                          519 -----------------------------RPSEKRGGAWMDEVFSRSCVLA------------------------------------------
GSVIVG01003850001|GSVIVT01003850001                  426 -----------------------------RPSEKRGGAWMDEVVARSRALSRDGTKARLPIAHMVCNQTPPVGNKPSLMTFREVETVFHEFGHALQHMLTKQDEGLVSG
Eucgr.I00597|Eucgr.I00597.1                          423 -----------------------------RPSEKRGGAWMDEVVARSRVLS------------------------------------------
Eucgr.I00594|Eucgr.I00594.1                          375 -----------------------------RPSEKRGGAWMDEVVGRSRVLS------------------------------------------
28333.t000012|28333.m000566                          501 -----------------------------RPSEKRGGAWMDEVVSRSRHLS------------------------------------------
Potri.007G004600|Potri.007G004600.1                  423 -----------------------------RPSEKRGGAWMDEVVSRSRVLS------------------------------------------
Potri.014G004600|Potri.014G004600.1                  516 -----------------------------RPSEKRGGAWMGEVVSRSRVLS------------------------------------------
Potri.014G010100|Potri.014G010100.1                  541 -----------------------------RPSEKRGGAWMDEVVSRSRVLS------------------------------------------
28658.t000001|28658.m000032                          444 -----------------------------RSNKRGGAWMNATVSQSSL----------------------------------------------
30484.t000001|30484.m000014                          319 -----------------------------RSSKRSGAWMSSFQSQHKLPL------------------------------------------
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gi|85111610                                          518 ------------------------------------------------HVLIPSF----------------------------------------------------
YKL134C                                              513 ----------------------------------------------------------------------------------------------------------
Cre02.g073400|Cre02.g073400.t1.3                     335 ----------------------------------------------------------------------------------------------------------
Vocar20013694m.g|Vocar20013694m                      431 ----------------------------------------------------------------------------------------------------------
gi|32565901                                          429 ----------------------------------------------------------------------------------------------------------
CMS132C|CMS132CT                                     338 ----------------------------------------------------------------------------------------------------------
gi|268637658                                         473 ----------------------------------------------------------------------------------------------------------
Esi0033_0093                                         560 ----------------------------------------------------------------------------------------------------------
tr|M1C3Y6|M1C3Y6_SOLTU                                   ----------------------------------------------------------------------------------------------------------
GSVIVG01018572001|GSVIVT01018572001                  529 ----------------------------------------------------------------------------------------------------------
GRMZM2G450659|GRMZM2G450659_T01                      198 ----------------------------------------------------------------------------------------------------------
LOC_Os06g47210|LOC_Os06g47210.1                      456 ----------------------------------------------------------------------------------------------------------
Cucsa.251510|Cucsa.251510.1                          241 ----------------------------------------------------------------------------------------------------------
Glyma04g13088|Glyma04g13088.1                        461 ----------------------------------------------------------------------------------------------------------
Medtr3g009160|Medtr3g009160.1                        474 ----------------------------------------------------------------------------------------------------------
Bra029169|Bra029169                                  437 ----------------------------------------------------------------------------------------------------------
Carubv10025983m.g|Carubv10025983m                    454 ----------------------------------------------------------------------------------------------------------
AT5G51540                                            454 ----------------------------------------------------------------------------------------------------------
Eucgr.K00152|Eucgr.K00152.1                          266 ----------------------------------------------------------------------------------------------------------
30147.t000467|30147.m014196                          451 ----------------------------------------------------------------------------------------------------------
Potri.015G129300|Potri.015G129300.1                  469 ----------------------------------------------------------------------------------------------------------
416778|416778                                        472 ----------------------------------------------------------------------------------------------------------
Phpat.016G041000|Phpat.016G041000.1                  394 ----------------------------------------------------------------------------------------------------------
gi|71999758                                          510 ----------------------------------------------------------------------------------------------------------
gi|85107353                                          466 ----------------------------------------------------------------------------------------------------------
YCL057W                                              465 ----------------------------------------------------------------------------------------------------------
gi|66801567                                          429 ----------------------------------------------------------------------------------------------------------
CMS446C|CMS446CT                                     679 --------------------------------------------------TPSTGTSHVH-------------------------RASET
gi|4507491                                           437 ----------------------------------------------------------------------------------------------------------
gi|14149738|ref|NP_065777                            461 ----------------------------------------------------------------------------------------------------------
LOC_Os01g67590|LOC_Os01g67590.1                      451 ----------------------------------------------------------------------------------------------------------
Bra004244|Bra004244                                  465 ----------------------------------------------------------------------------------------------------------
Bra004078|Bra004078                                  466 ----------------------------------------------------------------------------------------------------------
Carubv10019853m.g|Carubv10019853m                    515 ----------------------------------------------------------------------------------------------------------
AT1G67690                                            466 ----------------------------------------------------------------------------------------------------------
Eucgr.B03454|Eucgr.B03454.1                          462 ----------------------------------------------------------------------------------------------------------
Medtr3g086000|Medtr3g086000.1                        464 ----------------------------------------------------------------------------------------------------------
Glyma11g37410|Glyma11g37410.2                        399 ----------------------------------------------------------------------------------------------------------
Glyma18g01380|Glyma18g01380.1                        464 ----------------------------------------------------------------------------------------------------------
Cucsa.394790|Cucsa.394790.1                          460 ----------------------------------------------------------------------------------------------------------
GSVIVG01010319001|GSVIVT01010319001                  442 ----------------------------------------------------------------------------------------------------------
29929.t000212|29929.m004709                          465 ----------------------------------------------------------------------------------------------------------
Potri.010G054500|Potri.010G054500.1                  454 ----------------------------------------------------------------------------------------------------------
164651|164651                                        353 ----------------------------------------------------------------------------------------------------------
Phpat.018G066900|Phpat.018G066900.1                  623 ----------------------------------------------------------------------------------------------------------
Phpat.019G060600|Phpat.019G060600.1                  445 ----------------------------------------------------------------------------------------------------------
Esi0023_0135                                         487 ----------------------------------------------------------------------------------------------------------
85692|85692                                          403 ----------------------------------------------------------------------------------------------------------
97633|97633                                          323 ----------------------------------------------------------------------------------------------------------
119899|119899                                        451 ----------------------------------------------------------------------------------------------------------
97030|97030                                          387 ----------------------------------------------------------------------------------------------------------
Cre13.g572900|Cre13.g572900.t2.1                     522 ----------------------------------------------------------------------------------------------------------
Vocar20008539m.g|Vocar20008539m                      510 ----------------------------------------------------------------------------------------------------------
439159                                               447 ----------------------------------------------------------------------------------------------------------
Eucgr.L02517|Eucgr.L02517.1                              ----------------------------------------------------------------------------------------------------------
GSVIVG01031425001|GSVIVT01031425001                  442 ----------------------------------------------------------------------------------------------------------
GRMZM2G133919|GRMZM2G133919_T01                      524 ----------------------------------------------------------------------------------------------------------
LOC_Os02g58340|LOC_Os02g58340.1                      514 ----------------------------------------------------------------------------------------------------------
PGSC0003DMG400030613|PGSC0003DMT40007866             556 ----------------------------------------------------------------------------------------------------------
Carubv10000350m.g|Carubv10000350m                    446 ----------------------------------------------------------------------------------------------------------
Bra006067|Bra006067                                  440 ----------------------------------------------------------------------------------------------------------
Bra028579|Bra028579                                  446 ----------------------------------------------------------------------------------------------------------
Carubv10025914m.g|Carubv10025914m                    553 ----------------------------------------------------------------------------------------------------------
AT5G65620                                            534 ----------------------------------------------------------------------------------------------------------
Bra024401|Bra024401                                  454 ----------------------------------------------------------------------------------------------------------
Medtr5g030940|Medtr5g030940.1                        533 ----------------------------------------------------------------------------------------------------------
Glyma01g02480|Glyma01g02480.1                        531 ----------------------------------------------------------------------------------------------------------
Glyma09g33490|Glyma09g33490.1                        531 ----------------------------------------------------------------------------------------------------------
Cucsa.273340|Cucsa.273340.1                          541 ----------------------------------------------------------------------------------------------------------
GSVIVG01003850001|GSVIVT01003850001                  506 IRGIEWDAVELPSQFMENWCYHRYFSNQKKLIYFFVLKSNRRNYAPISHCQRSWVVLFSLAKMLFGIDIEPADGLAPVWNNDVRFYCVKDTAGSPIAYFYFDPYSRPSEK
Eucgr.I00597|Eucgr.I00597.1                          445 ----------------------------------------------------------------------------------------------------------
Eucgr.I00594|Eucgr.I00594.1                          397 ----------------------------------------------------------------------------------------------------------
28333.t000012|28333.m000566                          523 ----------------------------------------------------------------------------------------------------------
Potri.007G004600|Potri.007G004600.1                  445 ----------------------------------------------------------------------------------------------------------
Potri.014G004600|Potri.014G004600.1                  538 ----------------------------------------------------------------------------------------------------------
Potri.014G010100|Potri.014G010100.1                  563 ----------------------------------------------------------------------------------------------------------
28658.t000001|28658.m000032                          463 ----------------------------------------------------------------------------------------------------------
30484.t000001|30484.m000014                          340 ----------------------------------------------------------------------------------------------------------
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gi|85111610                                              525 -ESAEFAANDGMAYSRSQDCAIKQLETIALVCDEPQQSHN------------RPA---LLLSHF-----------QLETLFHEMGHA-----------------IHS
YKL134C                                                  513 ------------QVGENPDCTYFQLPVISLVCNFSLILIA------------SKKSLCFLQLS-----------EVETLFHEMGHA-----------------MHS
Cre02.g073400|Cre02.g073400.t1.3                         335 --------NARRRGGTGGGCQRQLPVMALLASATGRCPS------------TGVPALTYE-----------ELRVLLHELGHC-----------------VHN
Vocar20013694m.g|Vocar20013694m                          431 ------------SSSSSRGDCNRQLPVMALLASASGTCPA------------SGQPAMSYR-----------ELRVLLHELGHC-----------------CHN
gi|32565901                                              429 ------------LSDCTWQMPILVFSLGLVDGHSS------------QWRNSRVSLH-----------SAETMFHELGHA-----------------MHS
CMS132C|CMS132CT                                         338 ------------LRDGSSQLPSAALVCDEPPII------------RKAGMQHY-----------QLETLLHELGHV-----------------LHT
gi|268637658                                             473 --------LKNEDDDDEYNDEYNLPKCSITCSFTQNNFN------------EPLKSKLQHS-----------DVETLFHEFGHA-----------------LHT
tr|M1C3Y6|M1C3Y6_SOLTU                                   560 ------------PLPTVVLVCNFGLLEPPPDGGNAKQSKERSGKDDGRLMSHS-----------EVETLFHEFGHA-----------------LHS
GSVIVG01018572001|GSVIVT01018572001                      529 ------------LSETEYQLPEIKIENQISF------------------------W-----------ILL*-----------------------------
GRMZM2G450659|GRMZM2G450659_T01                          198 ------------LSDSNYQLPIIALVCNESGACR------------LTARLNHG-----------DVETLFHEFGHA-----------------LHS
LOC_Os06g47210|LOC_Os06g47210.1                          456 ------------LQDSNYQLPIVALVCNFSSSSK------------TMARLNHW-----------DVETLFHEFGHA-----------------LHS
Cucsa.251510|Cucsa.251510.1                              241 ------------------------------------------------------------------------------------------------------
Glyma04g13088|Glyma04g13088.1                            461 ------------ISQTEYQLPIVALVCNFSGSRNP------------SAVRLNHW-----------EVETLFHEFGHA-----------------LHS
Medtr3g009160|Medtr3g009160.1                            474 ------------ISQTEYQLPIVALVCNFSGSRNP------------SAVRLNHW-----------EVETLFHEFGHA-----------------LHS
Bra029169|Bra029169                                      437 ------------ISDTEYQLPVLALVCNFSRASDS------------SVVRLNHS-----------EVEVLFHEFGHA-----------------LHS
Carubv10025983m.g|Carubv10025983m                        454 ------------ISETEYQLPVIALVCNFSRACDS------------LVVRLNHS-----------EVEVLFHEFGHA-----------------LHS
AT5G51540                                                454 ------------ISETEYQLPVIALVCNFSRACDS------------SIVRLNHS-----------EVEVLFHEFGHA-----------------LHS
Eucgr.K00152|Eucgr.K00152.1                              266 ------------ISSTEYQLPIVALVCNFSGSHNS------------SLARLNHW-----------EHETLFHEFGHA-----------------LHS
30147.t000467|30147.m014196                              451 ------------FSETDYQLPVVALVCNFSGSRSS------------SNVRLNHW-----------EVETLFHEFGHA-----------------LHS
Potri.015G129300|Potri.015G129300.1                      469 ------------ISETEYQLPVVALLCNFSGSPCS------------STVRLNHG-----------DVETLFHEFGHA-----------------LHS
416778|416778                                            472 ------------TSETEYQLPVVALVCNFSKPLSS------------MSALFHHW-----------EVENLFHEFGHA-----------------LHS
Phpat.016G041000|Phpat.016G041000.1                      394 ------------ISESDYQLPVVALCNFATPDCN------------TLPLLNHW-----------EVETLFHEFGHA-----------------LHS
gi|71999758                                              510 ------------RGLDKIVYFIGSAIAPTSN------------GPSLLHHQ-----------QLQQLFHFGRS-----------------VQL
gi|85107353                                              466 ------------TDGTRFYESTAIVCNFSPAPTKD------------KPSLLKHN-----------HIVDLFHELGHG-----------------IHS
YCL057W                                                  465 ------------DDTTRSYEVTALVCNFSKSTKD------------KPSLLKHN-----------EIVTLFHELGHG-----------------IHD
gi|66801567                                              429 ------------ADGEKQYPVAAMLCNFTKPTPT------------TPSLLTHD-----------EVVTLFHEFGHV-----------------MHN
CMS446C|CMS446CT                                         694 ------ATNALQLNAMHSADCERQVPVAAMVANLSKSSGG------------RPSLLRHE-----------EVVTLFHEFGHV-----------------MHH
gi|4507491                                               437 ------------QDGSRQIAIAALVANLAKFTAD------------APSLLQHD-----------EVETLFHEFGHA-----------------MHQ
gi|14149738|ref|NP_065777                                461 ------------PDGSRMMAVAALVVNFSSQPVAG------------RPSLLRHD-----------EVRTLFHEFGHV-----------------VHH
LOC_Os01g67590|LOC_Os01g67590.1                          451 ------------SNGTRKVPVANLISQCPKEFDG------------NSALLRHP-----------EVETLFHEFGHV-----------------VHH
Bra004244|Bra004244                                      465 ------------SNGACKIPVALLIAQLAKDG-G------------EAVLPGGS-----------EVVNLFHEFGHV-----------------VQH
Bra004078|Bra004078                                      466 ------------SNGACQIPVALLIAQLSKDGSG------------EALFPGGS-----------EVVNLFHEFGHL-----------------VQH
Carubv10019853m.g|Carubv10019853m                        515 ------------SNGACQIPVALLIAFEAKDDSG------------EAVLPGGS-----------LVVNLFHEFGHV-----------------VQH
AT1G67690                                                466 ------------SNGACQIPVALLIAQEAKDGSG------------EAVLPGGS-----------LVVNLFHEFGHV-----------------VQH
Eucgr.B03454|Eucgr.B03454.1                              462 ------------FNNVAQIPVVLLITQFPKDISG------------HPGLLRVS-----------EVVNSFHEFGHV-----------------VQH
Medtr3g086000|Medtr3g086000.1                            464 ------------ISCARQIPVALLISQCQKDSEF------------SPGLLRTS-----------EVVSLFHEFGHV-----------------VQQ
Glyma11g37410|Glyma11g37410.2                            399 ------------SSGARQIPVALLISQCQKDADG------------SSGLLRFS-----------EVVSLFHEFGHV-----------------VQQ
Glyma18g01380|Glyma18g01380.1                            464 ------------SNGAQQIPVALLISQCQKDADG------------SSGLLRFS-----------EVVSLFHEFGHV-----------------VQQ
Cucsa.394790|Cucsa.394790.1                              460 ------------SNGTRCIPVALLLSQLQNDVDG------------HAGLVRGT-----------EVVNLFHEFGHV-----------------VQH
GSVIVG01010319001|GSVIVT01010319001                      442 ------------SNGARQIPVALLISQCQKEVDD------------HTGLLRFS-----------EVVNLFHEFGHV-----------------VQH
29929.t000212|29929.m004709                              465 ------------SNGARQIPVALLISELQKGIAG------------HPSLLRFS-----------EVVSLFHEFGHV-----------------VQH
Potri.010G054500|Potri.010G054500.1                      454 ------------YSGCERQIPVALLISQLQKGNCG------------HSGLLRFP-----------EVVSLFHEFGHV-----------------VQH
164651|164651                                            353 ------------NSGCQLPVAAMLANFRRGH------------AALLSYP-----------EVETSFHEFGHVASTCAIPFALPFLNMFILQMHH
Phpat.018G066900|Phpat.018G066900.1                      623 ------------IDGCTRQLPVGAMLANFTKFTTE------------KPSLLGHN-----------EVETLFHEFGHL-----------------MHH
Phpat.019G060600|Phpat.019G060600.1                      445 ------------KDGTRQLPVAAMLANFTKPSAE------------KPSLLGHA-----------EVETLFHEFGHA-----------------MHH
Esi0023_0135                                             487 ------------RSPVAYLTCNGSPPVGD------------TPSLLMFR-----------EVETLFHEFGHG-----------------LQH
85692|85692                                              403 ------RSRALAPECCDIRLPACIIVCNQTPPLGD------------NPSLMTHD-----------ELKTLFHEFGHA-----------------LQH
97633|97633                                              323 ------------QKGCVVRLPVAHLVCNQAPPLPD------------QPSLMTHADKFDGALMIETLQVTMLFHEFGHA-----------------LQH
119899|119899                                            451 ------------QKGCVVRLPVAHLVCNQAPPLPD------------QPSLMTYE-----------VVTMLFHEFGHA-----------------LQH
97030|97030                                              387 ------------QKGCGVRLPVAHLVCNQAPPLPD------------QPSLMTYE-----------VVTMLFHEFGHA-----------------LQH
Cre13.g572900|Cre13.g572900.t2.1                         522 ------------PPGCAVRLPVAHMVCNQMBPVGD------------KPSLMTFR-----------EVETLFHEFGHA-----------------LQH
Vocar20008539m.g|Vocar20008539m                          510 ------------PPGSAVRLPVAHMVCNQMBPVGD------------KPSLMTFR-----------EVETLFHEFGHA-----------------LQH
439159                                                   447 ------------PRGCSSVRLPVAHMVCNQTPPVCN------------SPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Eucgr.L02517|Eucgr.L02517.1                              ---- ------------------------------------------------------------------------------------------------------
GSVIVG01031425001|GSVIVT01031425001                      442 ------------CDGCASPRLPIAHHVCNQTPPMGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
GRMZM2G133919|GRMZM2G133919_T01                          524 ------------RNGCLAARLPVAHLVCNQTPPVGE------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
LOC_Os02g58340|LOC_Os02g58340.1                          514 ------------RNGCSPVRLPVAHLVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
PGSC0003DMG400030613|PGSC0003DMT40007866                 556 ------------RDGCSNARLPVAHMVCNQMPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Carubv10000350m.g|Carubv10000350m                        446 ------------QKGCSSVRLPVAQMVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Bra006067|Bra006067                                      440 ------------QKGCSSVRLPVAQMVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Bra028579|Bra028579                                      446 ------------QKGCSSVRLPVAHMVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Carubv10025914m.g|Carubv10025914m                        553 ------------QKGCSSVRLPVAHMVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
AT5G65620                                                534 ------------QKGCSSVRLPVAHMVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Bra024401|Bra024401                                      454 ------------QKGCSSVRLPVAHMVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Medtr5g030940|Medtr5g030940.1                            533 ------------PDGCNSSRLPVAHMVCNQTPPVGS------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Glyma01g02480|Glyma01g02480.1                            531 ------------RDGCSARLPVAHMVCNQTPPVGE------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Glyma09g33490|Glyma09g33490.1                            531 ------------RDGCTSARLP------------------------------------------------------------------------------LQH
Cucsa.273340|Cucsa.273340.1                              541 ------------QDGCAFARLPVAHMVCNQTPPVGE------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
GSVIVG01003850001|GSVIVT01003850001                      616 RGGAWMDEVVARSRALSRDCTKARLPVAHHVCNQTPPVCN------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Eucgr.I00597|Eucgr.I00597.1                              445 ------------RDGCAHARLPVAHMVCNQTPPVGT------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Eucgr.I00594|Eucgr.I00594.1                              397 ------------PDGCASTRLPIAHMVCNQTPPVGT------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
28333.t000012|28333.m000566                              523 ------------RNGCTAPRLPVAHMVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Potri.007G004600|Potri.007G004600.1                      445 ------------RNGTAPRLPVAHMVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Potri.014G004600|Potri.014G004600.1                      538 ------------PNGCTAPRLPVAHMVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
Potri.014G010100|Potri.014G010100.1                      563 ------------PNGTAPRLPVAHMVCNQTPPVGD------------KPSLMTFR-----------EVETVFHEFGHA-----------------LQH
28658.t000001|28658.m000032                              463 ------------MGTHPVVLNHLNIPKPNPG------------BPTLLTYD-----------EVRNLFHEFGHA-----------------LHG
30484.t000001|30484.m000014                              340 ------------KNCHVGELPIIYNVCNFAKPAEG------------RPALLSLD-----------DARTLFHEFGHA-----------------LHG
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gi|85111610                                        587 ILARTSFQNVS----GT-RCATDLAELPSTLMEYF-AALPSVL-ALFARHY-----------------------ETDNPLEYEWVDNKI--REARRE----------
YKL134C                                            567 MLGRTHMQNIS----GT-RCATDFVELPSILMEHF-AKEIRIL-TKLGKHY-----------------------GTGETIQADMLQRFM--KSTNEL----------
Cre02.g073400|Cre02.g073400.t1.3                   391 LLSRTKYQHLW----GT-RCAQDLVEVPSHLFEYW-ATDPLVM-GLMARDRSNDSS--------------AAAGAGGGGEPLPAULKELI--AGRAAT----------
Vocar20013694m.g|Vocar20013694m                    483 LLSRNKYQHLW----GT-RCAQDLVEVPSHLFEYF-ASEPRVM-GLLARDRSGCAA--------------GAGGDAEEGEPLPEELFRQLA--AGRSVA----------
gi|32565901                                        477 ILGRTKYQHVA----GT-RCPQDFSELPSNLMEYF-FSDLGVM-TDHIRRT----------------------DRPEEQLSIESAATLL--ASRHSL----------
CMS132C|CMS132CT                                    382 IMSRTRFQHLS----GT-RGPMDFVELPSTLMENF-WNQDLL-QQFAIN-------------------------GERQFLAELE--EARQEA----------
gi|268637658                                       530 LMSRCNFQHLC----GT-RGPTDFIELPSTLMENF-SWNQDLL-QQFAIN-----------------------SMCKEPISNEMVTNLK--KIRNLE----------
Esi0033_0093                                       617 LLSRTELQHVS----AS-VP---------D----AV-HRVERGL-RQQRRHY-----------------------RTQEAPLPAULDGLH--RSKLLE----------
tr|M1C3Y6|M1C3Y6_SOLTU                                 --------------------------------------------------------------------------------------------------------
GSVIVG01018572001|GSVIVT01018572001
GRMZM2G450659|GRMZM2G450659_T01                    243 LLSRTEYQHFS----GT-RVALDVAELPSNLFEYY-AWEYRVL-KTFPLDE-----------------------TTCDAIPEKEVKALN--MSHNME----------
LOC_Os06g47210|LOC_Os06g47210.1                    501 LLSRTEYQHFS----GT-RVALDVAEMPSNLFEFY-AWEYRVL-RKFPVDE-----------------------TTGDEIPEKEVKALN--ASRNME----------
Cucsa.251510|Cucsa.251510.1                        241 --------------------GSRYY-ASDYRVL-KTFAKHY-----------------------STGBILPEKEVKSMQ--GAKMME----------
Glyma04g13088|Glyma04g13088.1                      507 LLSRTDYQHFS----GT-RTVLDLAELPSNLFEYY-AWEYRVL-KKFARHL-----------------------STGEELPQKEVESMQ--GARDME----------
Medtr3g009160|Medtr3g009160.1                      520 LLSRTEYQHFS----GT-RVALDLAELPSNLFEYY-AWEYRIL-KTFARHY-----------------------STGDAIPEKEVESML--GAKNME----------
Bra029169|Bra029169                                483 LLSRTEYQHFS----GT-RVALDLAELPSNLFEYY-AWEYRIL-RRFARHL-----------------------STGETIPEKEVKSLQ--GARNME----------
Carubv10025983m.g|Carubv10025983m                  500 LLSRTDYQHFS----GT-RVALDLAELPSNLFEYY-AWEYRIL-RRFGRHY-----------------------STGETIPEKEVNSLQ--GARNME----------
AT5G51540                                          500 LLSRTDYQHFS----GT-RVALDLAELPSNLFEYY-AWEYRIL-RRFGRHY-----------------------STGETIPEKEVNSLQ--GARNME----------
Eucgr.K00152|Eucgr.K00152.1                        312 LLSRTDYQHFS----GT-RVALDLAELPSNLFEYY-TCEYRVL-KTFAKHY-----------------------STGETIPEKEVESMQ--GAKKME----------
30147.t000467|30147.m014196                        497 LFSRTDYQHFS----GT-RVVLDLAEMPSNLFEYY-AWEYRVL-RTFAKHY-----------------------STGEIIPEKEVKAMQ--GARDME----------
Potri.015G129300|Potri.015G129300.1                515 LLSRTEYQHFS----GT-RTVIDEAELPSNVFECF-AWEYQVL-KTFAQN------------------------SSGETIPEKEVVSMN--QAKKML----------
416778|416778                                      518 LLSRTEYQHFS----GT-RTVIDEAELPSNVFECF-AWEYQVL-KTFAQN------------------------SSGETIPEKEVVSMN--QAKKML----------
Phpat.016G041000|Phpat.016G041000.1                440 LLSRTELQHVS----GT-RTVLDESELPSGLFEHY-AWEYRIL-RQFGRHY-----------------------LTGETIPEKMVASMN--EAKRML----------
gi|71999758                                        552 LLSQSPYRDIS-IPWSFFYASDWDAADMFPTFLQMF-VTKPNLI-ATLSSFHQIT-------------------KQSLIEEHANSVALTISRA----------
gi|85107353                                        511 LVGQNKESRPN----GPGSVPWDFVEAPSQMLEFW-TWRAEYI-KRLSKHYLT-------------------GEQMSDDMAERIA--ASRHEL----------
YCL057W                                            510 LVGQNKESRPN----GPGSVPWDFVEAPSQMLEFW-TWNKNEL-INLSSHYKT---------------------GEKIPESPINSLI--KTKHVN----------
gi|66801567                                        474 MSTKVHYSMFS----GT-SVERDFVECPSQLFEFW-CWNKDVLVNKLSGHYKDH------------------SKKLETDFVERMI--AAKNLN----------
CMS446C|CMS446CT                                    751 LCSKPRFARFS----GT-RVERDFVEAPSQMLENW-CWDRQAL-ERLSGHYERLAPRTPRDDGQSESAGAGAGTGGALVPEPLSTLIERLQ--QTRRCL----------
gi|4507491                                         482 LCSQAEFAMFS----GT-HVERDFVEAPSQMLENW-VWEQEPL-LRMSRHYRT---------------------CSAVFRELLEKLI--ESRQAN----------
gi|14149738|ref|NP_065777                          506 ICAQTHFARFS----GT-NVETDFVEVPSQMLENW-VWEVDSL-RRLSKHYKD---------------------CSPILADLLLEKLV--ASRLVN----------
LOC_Os01g67590|LOC_Os01g67590.1                    496 ISNRATFSRFS----GL-QLEGDFAELPSLLENW-CYENISL-LMMSGFHQDI--------------------TKSITSEACQSLK--RERDIF----------
Bra004244|Bra004244                                509 ICNRASFARFS----GL-RVDPDFREIPSKLLENQ-Q-----------DI-----------------------TKPLVDEVCKTLK--RWRYSE----------
Bra004078|Bra004078                                511 ICNRASFARFS----GL-RVDPDFREIPSQLLENW-QCYESFII-LKLMSGYRQDI------------------TKPLVDEVCKTLK--RWRYSE----------
Carubv10019853m.g|Carubv10019853m                  560 ICNRASFARFS----GL-RVDPDFREIPSQLLENW-CYESFTL-LKLISGYRQDI------------------TKPLVDEVCKTLK--RWRYSE----------
AT1G67690                                          511 ICNRASFARFS----GL-RVDPDFVEIPSQLLENW-CYESFTL-LKLISGYRQDI------------------TKPLVDEVCKTLK--RWRYSE----------
Eucgr.B03454|Eucgr.B03454.1                        507 ICNRASFARFS----GL-RVDPDFVEIPAQLLQNC-CYESFSL-LKLISGFHQDL------------------TKPVNDEMCLSLK--RWRYSE----------
Medtr3g086000|Medtr3g086000.1                      509 ICNRASFARFS----GF-RVDPDFVEIPACLLENW-CYESFSL-LKLISGFHQDI------------------TKPILKDDICKSIK--RWRNSS----------
Glyma11g37410|Glyma11g37410.2                      444 ICNRASFTRIS----GL-CVDADFVEIPAQLLENW-CYESYSL-LKLISGFHQDI------------------TKPLTDDICKSIK--RWRISE----------
Glyma18g01380|Glyma18g01380.1                      509 ICNRASFTRIS----GL-CVDPDFVEIPAQLLENW-CYESYSL-LKLISGFHQDI------------------TKPLKDDICKSIK--RWRTSE----------
Cucsa.394790|Cucsa.394790.1                        505 VCNRAPFTRIS----GL-RLDPDFVEIPAQLLENW-CYESVSL-LKLISGFHQDI------------------TKPLKDEVCKSLK--KWRHSE----------
GSVIVG01010319001|GSVIVT01010319001                487 ICNRASFARFS----GL-RVDPDFVEIPARVFENW-CYESFSL-LKLMSGFHQDI------------------TKPIEDRMCESLK--RWRSSE----------
29929.t000212|29929.m004709                        510 ICNQASFARFS----GL-RVDPDFVEIPALLLENW-CYESFSL-LKLISGFHQDI------------------TKPIKDEICRSLK--RWRYIF----------
Potri.010G054500|Potri.010G054500.1                499 ICNRASFARFS----GL-RVDPDFVEIPALVLENW-CYESFSL-LKLISGFHQDI------------------TKPINDEICKSLK--RWRNSE----------
164651|164651                                      412 ICSRPSFARFS----GL-RVSPDFEEIPAQVFENW-CSEKSSL-KMMSGHYDT--------------------REPVLDSFCEILV--RKKKTH----------
Phpat.018G066900|Phpat.018G066900.1                668 ICSRSVFARFS----GL-RVEEDFVEAPSQMLENW-CLESASL-KMMSGHYEDT-------------------NQPLEQEIIEALM--QKKRAE----------
Phpat.019G060600|Phpat.019G060600.1                490 ICSRASFAKFS----GL-RVEEDFVEAPSKMLEYW-CSEKSSL-KIMSGHYKDS------------------KQPLPQDICEALM--KKKRAH----------
Esi0023_0135                                       527 MLTTMVDGDCA----GINGVEWDAVELPSGFMENW-CYHKPHV-DQFAKHLETG--------------------ETLKELFDKLC--MQRYTM----------
85692|85692                                        455 MLTQEVIFVS----GMQNVEWDAVELPSGFMENW-CYEKDHL-SSFAKHYKTG--------------------ELLPESLFQKIK--SSRTLRA----------
97633|97633                                        381 LLSKQDEGIVA----GSEGIEWDAVELPSGFMENW-CYDRNTL-MSFAVHYRTG------------------QELPEALYTKLK--SSRTFF----------
119899|119899                                      498 LLSKQDEGIVA----GSEGIEWDAVELPSGFMENW-CYDRNTL-MSFAVHYRTG------------------QGLPEALYTKLK--SSRTFF----------
97030|97030                                        434 LLSKQDEGIVA----GSEGIEWDAVELPSGFMENW-CYDRNTL-MSFAVHYRTG------------------QELPEALYIKLK--SSRTFF----------
Cre13.g572900|Cre13.g572900.t2.1                   568 MLTEVFDGHAS----GIRNIEWDAVELPSGFMENW-AYDRALL-YSFAKHYETG------------------EELPEELFSRLK--AAKNYR----------
Vocar20008539m.g|Vocar20008539m                    556 MLTEVFDGFAS----GIRNIEWDAVELPSGFMENW-CYDRALL-YSFAKHYETAALPRVD---------LLIPGVRVARELPLPEELSRLK--AAKNYR----------
439159                                             493 MLTKQDEGIVA----GIHGVEWDAVELPSGFMENW-CYDRKTL-MSFAVHYKTG------------------EPLSEDVYEKLK--AARTER----------
Eucgr.L02517|Eucgr.L02517.1
GSVIVG01031425001|GSVIVT01031425001                488 MLTKQDESIVS----GSHGIEWDAVEIASGFMENW-CYQRKEF-RGLGRHVVKV-------------------ASDSSCELGIDLL--QKINLLLVQYLFSELD
GRMZM2G133919|GRMZM2G133919_T01                    570 MLTKQDEGFVS----GIRGVEWDAVELPSGFMENW-CYHKNTL-ISIAKHYETG------------------ETLPEELYAKLV--AAKNGR----------
LOC_Os02g58340|LOC_Os02g58340.1                    560 MLTKQDEGFVS----GIRGVEWDAVELPSGFMENW-CYHKNTL-ISIAKHYETG------------------ELLPEELYAKLV--AAKNER----------
PGSC0003DMG400030613|PGSC0003DMT40007866           602 MLTKQDEGIVA----GQIEGDAELPSGFMENW-CYHRDTL-MGIAKHLETG------------------ETLPEDLYKKLL--AAKTER----------
Carubv10000350m.g|Carubv10000350m                  492 MLTKEDEGIVA----GIRNIEWDAVELPSGFMENW-CYHRDTL-MSIAKHYQTG------------------ETLPENVYKKLL--AARTER----------
Bra006067|Bra006067                                486 MLTKEDEGIVS----GIRNIEWDAVELPSGFMENW-CYHRDTL-MSIAKHYQTG------------------ETLPEDVYKKLL--AARTER----------
Bra028579|Bra028579                                492 MLTKQDEGIVA----GIRNIEWDAVELPSGFMENW-CYHRDTL-MSIAKHYQTG------------------ETLPEDVYKKLL--AARTER----------
Carubv10025914m.g|Carubv10025914m                  599 MLTKQDEGIVA----GIRNIEWDAVELPSGFMENW-CYHRDTL-MSIAKHYETG------------------ETLPEEVYKKLL--AARTER----------
AT5G65620                                          580 MLTKQDEGIVA----GIRNIEWDAVELPSGFMENW-CYHRDTL-MSIAKHYQTG------------------ETLPEEIYKKLL--AARTER----------
Bra024401|Bra024401                                500 MLTKQDEGIVA----GIRNIEWDAVELPSGFMENW-CYHRDTL-MSIAKHYQTG------------------ETLPEEIYKKLL--AARTER----------
Medtr5g030940|Medtr5g030940.1                      579 MLTREDEGIVA----GIRGIEWDAVELPSGFMENW-CYHKKTL-MGIAKHIETG------------------ESLPEEVYQKLV--AARTER----------
Glyma01g02480|Glyma01g02480.1                      577 MLTKQDEGIVA----GIRGIEWDAVELPSGFMENW-CYHRETL-MGIAKHIETG------------------ESLPEEVYLKLV--AARTER----------
Glyma09g33490|Glyma09g33490.1                      540 --------------------------------------------------------------------------------------------------------
Cucsa.273340|Cucsa.273340.1                        587 MLTKQDEGIVS----GIREIEWDAVELPSGFMENW-CYHRDTL-MGIAKHYETG------------------ESLPEEVYLKLV--AARTER----------
GSVIVG01003850001|GSVIVT01003850001                679 MLTKQDEGIVS----GIRGIEWDAVELPSGFMENW-CYHRDTL-MGIAKHYETG------------------ETLPEDVYLKLV--AARTER----------
Eucgr.I00597|Eucgr.I00597.1                        491 MLTKQDEGIVA----GLRGIEKDARELASGFMENW-CYHRETL-MGIAKHYETG------------------ESLPEAVYRKLL--AARTER----------
Eucgr.I00594|Eucgr.I00594.1                        443 MLTKQDEGIVA----GLRGIEWDAVELPSGFMENW-CYHRETL-MGIAKHYETG------------------ESLPEDVYVKLL--AARTER----------
28333.t000012|28333.m000566                        569 MLTKQDEGIVA----GIRGIEWDAVELPSGFMENW-CYHRETL-MGIAKHYETG------------------ETLPEDVYVKLL--AARTER----------
Potri.007G004600|Potri.007G004600.1                491 MLTKQDEGIVA----GIRGIEWDAVELPSGFMENW-CYHRETL-MGIAKHYETG------------------ESLPEEVYLKLL--AARTER----------
Potri.014G004600|Potri.014G004600.1                584 MLTKQDEGIVA----GIRGIEWDAVELPSGFMENW-CYHRETL-MGIAKHYETG------------------ESLPEEVYLKLL--AARTER----------
Potri.014G010100|Potri.014G010100.1                609 MLTKQDEGIVA----GIRGIEWDAVELPSGFMENW-CYHRETL-MGIAKHYETG------------------ESLPEEVYLKLL--AARTER----------
28658.t000001|28658.m000032                        505 MFSNVKYPREA----GT-RVPRDFVELPSQVNEMW-SVWPEVL-ANYAKHYQTG--------------------APMPQELLDKVI--ASKKEN----------
30484.t000001|30484.m000014                        386 MLSNVTYPSVS----GT-GVSRDFVELPSQLYEHW-LTVPAIL-MEYAVHYETG--------------------APIEQALLDKVL--AARTEN----------
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gi|85111610                                              652 EALDTENQHILAMLDQELHSSKAVQG--HI----------------------------------------------------PSTEIFHSLQRQFSTAPEDPQGHAWQGFHGHLV
YKL134C                                                  632 QNGETYSQAKAMLDQSLHDEKIISDIDNF-------------------------------------------------------DVVENYGALERRLKVL--VDDQSNWCGREGELH
Cre02.g073400|Cre02.g073400.t1.3                         467 AALELQQQLVLSLADQWLFGENPHAPTAAA----------------------------------------------GAGSASSWNSSDVWRKAVEMASSV-PYVPGTHSPELRVGELT
Vocar20013694m.g|Vocar20013694m                          559 AALELQQQLVLSLADQWLFGEGHGHAGVGAGGGGGAGGA--------------------GGGLEGAGGGSYTGAAGSHIWRKAVHVASSV-PYVPGTKPELRVGELT
gi|32565901                                              543 TAHETVQQAAYGLYPLEVHGPIAAPQIASGRM---------------------------------------------------TT---TELFHDIMNKTMPHI-QRSPDSALQHRPHTV
CMS132C|CMS132CT                                         441 VVAEIALQTPHAALPLALHSHDHPGWGNEARS-----------------------------------------------------KIKRIIAEVVREYGRL-EQVLYRDGIPYMPHII
gi|268637658                                             594 QGIETQEQLSLAFLPLKLHTVETDKNTSTNIG-------------------------------------------------------DTNMSPAQILSTLHQQQIGI-HGTVSNFHLTSFNHLF
Esi0033_0093                                             670 AGLGIQTQLHLYATLDQQLFGRQPEGGVWS---------------------------------------------------SASHUADALQERIAGL-PRCECAFWHSRFGHFT
tr|M1C3Y6|M1C3Y6_SOLTU                                       ------------------------------------------------------------------------------------------------------------------------
GSVIVG01018572001|GSVIVT01018572001                         ------------------------------------------------------------------------------------------------------------------------
GRMZM2G450659|GRMZM2G450659_T01                          308 PATELQRQHFYSIMPLTHFGEGSSKPMDT---------------------------------------------------MSTV-ADLRRKETWSG-KYAEGTHWHTRETHLV
LOC_Os06g47210|LOC_Os06g47210.1                          566 PATELQRQHFYSIMPLTHFGEQGSKPMDT----------------------------------------------------HSTV-ADLRRKETSW-KCVEGTHWHTRETHLI
Cucsa.251510|Cucsa.251510.1                              281 AATELQRQLLYALLDQTLFGEKLTSERDT-----------------------------------------------------VSVV-ADLKRQYTSW-KHVDGTHWQSQFGHLL
Glyma04g13088|Glyma04g13088.1                            572 AATDLQRQHFYALVDQTLFGEQPFPHGDI-----------------------------------------------------SSVV-AKLKREFTSC-EHVEGTHWEARFSHLL
Medtr3g009160|Medtr3g009160.1                            585 AATDLQRQHFYALADQTLHGEQPHPLGDV-----------------------------------------------------SSVL-AELKREHTNL-EHIEGTHWEARFSHLL
Bra029169|Bra029169                                      548 AATEMQRQVFYALIDQMLFGEQPATSRDV-----------------------------------------------------SKLV-AELKREHTSW-NHVEGTHWHIRFSHLL
Carubv10025983m.g|Carubv10025983m                        565 AATEMQRQVFYALIDQMLFGEQPETARDV-----------------------------------------------------SHLV-AELKQQHTSW-SHVEGTHWHIRFSHLL
AT5G51540                                                565 AATEMQRQVFYALIDQMLFGEQPETARDV-----------------------------------------------------SHLV-AELKRQHTSW-NHVEGTHWYIRFSHLL
Eucgr.K00152|Eucgr.K00152.1                              377 AATELQRQVFYALVDQTLFGDQLAGQRDT-----------------------------------------------------SSVV-ADLKRQFTSW-RHVEGTHWQTRFSHLV
30147.t000467|30147.m014196                              562 SATELQRQVFYALVDQTLFGEQPASSRDT-----------------------------------------------------SSIV-ADLLKRQHTSW-KHVEGTHWQIRFSHLV
Potri.015G129300|Potri.015G129300.1                      580 AATELQRQVFYALADQTLFGEQPASPNDM-----------------------------------------------------SSIL-AEFKMQHTSW-KHVEGTNWQIRFSHLV
416778|416778                                            582 GVTELLRQVLYAMVDQKLFFGQPLPAGGT-----------------------------------------------------TGVL-VEMQELSKNW-KHIEGTHWQSKFGHMI
Phpat.016G041000|Phpat.016G041000.1                      505 SATEIGRQVLYALLDMTHFGLQPLPAKDT-----------------------------------------------------TAVI-ADLKLKYWGV-RHVEGTHWHTRENHLV
gi|71999758                                              623 SLWETYRTLFWSDFDLSIYEMEDRKQK----------------------------------------------------FWLDMYKQM-YEEYFFFKRAKNDYQPGSFPLFI
gi|85107353                                              576 QAFRNLWQLSSHIFDMEVHSPKSRAALEN----------------------------------------------------MFFTKRYNELRNE----LTGMKGPEAI---
YCL057W                                                  576 GALFTLLRQLHHGLFPMKVHLCKDLQN--------------------------------------------------------LSHLCLTWNQLRQDISLISNGGTLSKGYDSTGHIM
gi|66801567                                              541 VALFYLRQLQLALFPNALHSGNPANF-----------------------------------------------------TNTADLYHRI-ATDVALNENQKGTNPGGSFGHLL
CMS446C|CMS446CT                                         842 IALQTRRQLVLALFDQALHHAPTREKLEREYGADRRNSRNRSRSRASGHRNSQQQQQQQQQQQQLSSSSEMLVDGILTAELLALL-QRRIGLVPMTFGTHMGASFGHLM
gi|4507491                                               547 TGHFNLRQLVLAKVDQALHIQTD----------------------------------------------------------ALPAEEYAHLCQ-EILGVAATFGTNMPATFGHLA
gi|14149738|ref|NP_065777                                571 TGHFNLRQLVLSKVDQSLHANTS----------------------------------------------------------LPAASEYAKYCS-EILGVAATFGTNMPATFGHLA
LOC_Os01g67590|LOC_Os01g67590.1                          562 ATGKLIKQEHLLCLFDDQIHTGEN---------------------------------------------------------VNHDELIKDFHPKVMLGTHPLECTNSPASGCPRHA
Bra004244|Bra004244                                      561 SATKSIQEHLYCLFDQKIHISDD----------------------------------------------------------VDFHQLIRSLHPKVMVGLPVVEGTNNPASGCPRAV
Bra004078|Bra004078                                      578 SATKSIQEHLYCLFDQRIYSDDD----------------------------------------------------------VEFGQLIRSLHPKVMVGLPVVEGTNNPASGCPRAV
Carubv10019853m.g|Carubv10019853m                        626 SATKSIQEHLYCLFDQIIYSDDD----------------------------------------------------------APLLQLIRSLHPKVMIGLPVVEGTNNPASGCPRAV
AT1G67690                                                577 SATKSIQEHLYCLFDQIIYSDDD----------------------------------------------------------APLLQLIRSLHPKVMIGLPVVEGTNNPASGCPRAV
Eucgr.B03454|Eucgr.B03454.1                              573 SATKLKQEHLYSLFDQIIHSADD----------------------------------------------------------IDHAELFKHLHPKVMLGLPVLEGTNPATCGPRCA
Medtr3g086000|Medtr3g086000.1                            575 SATKLKQEHLLCIFDQIIHSADN----------------------------------------------------------IDIRELFKHLHSKVMLGLPVLEGTNNPASGCPFSV
Glyma11g37410|Glyma11g37410.2                            510 SATKLKQDHLLCLFDQIIHSADN----------------------------------------------------------IDIQELFKHLHPMEMLGLPILEGTNPASYCPSTV
Glyma18g01380|Glyma18g01380.1                            575 SATKLKQDHLLCCLFDQIIHSADN---------------------------------------------------------IDIQELFKHLHPMEMLGLPILEGTNPASYFPSTV
Cucsa.394790|Cucsa.394790.1                              571 SATKLKQEHLLYCLFDQIIHCAEN---------------------------------------------------------VDIIELFKHLHSKVMLGLPVLEGTNNPASGCPCSA
GSVIVG01010319001|GSVIVT01010319001                      553 SATKLKQEHLLYCLFDQIIHSTED---------------------------------------------------------VDMVKLFRDLHTPKVMLGLPMLEGTNPASGCPRSA
29929.t000212|29929.m004709                              576 SATKLKQDHLLYCLFDQIIHSADN---------------------------------------------------------VDIVELFKHLHPKVMLGLPVLEGCANPASGCPRSA
Potri.010G054500|Potri.010G054500.1                      565 SVTKLKQEHLLYCLFDQIIHSTDN---------------------------------------------------------VDIVELFKHLHPKVMLGLPMLEGTNPASGCPRSA
164651|164651                                            478 AGHLTKHQILLALFDLIVHSSDQ----------------------------------------------------------FETVSVLEQLHTQVMEGIPMLEGTDLSTSFTHLM
Phpat.018G066900|Phpat.018G066900.1                      734 SGHLTKRQLLFGGLFDQSIHMREK---------------------------------------------------------AHTAAVLKELTPKVMEGLPMLEGTNNSASFGHMA
Phpat.019G060600|Phpat.019G060600.1                      556 AGHLTKRQLLFGGLFDQTIHMRDK---------------------------------------------------------VHTAAILKDLTPKVMGIPMLEGTNNSASFGHMA
Esi0023_0135                                             593 AGSAMLRQLYFGQX----------------------------------------------------------------------------------------------------------
85692|85692                                              522 --IDMFNQVLLAAVLLKHSNFFFNGLTT------------------------------------------------------KIHHVYSEL-SLKTQIPHCMHGEQYLCSFSHIS
97633|97633                                              447 SASNVLFYLVSRSLHLLKLHAHLEAVNSK----------------------------------------------------EIYNLCNKV-AGEIL-IPPLPEDKSICKFLLH
119899|119899                                            564 SASNVHLYLVSRSLHIDLKLHAHLEAVNSK---------------------------------------------------EIYNLCNKV-AGEILILPPLPEDKSICKFLLH
97030|97030                                              500 SASNVLYLVSRSLHLLKLHAHLEAVNSK-----------------------------------------------------EIYNLCNKV-AGEILILPPLPEDKSICKFLLH
Cre13.g572900|Cre13.g572900.t2.1                         634 SGTMMRQLHHSCVDLLEHSRFVFGQGK------------------------------------------------------TVFDVDNEV-ASRLLVPGPLHEDRHLHCFSHIF
Vocar20008539m.g|Vocar20008539m                          639 SGTMMRQLHHSCVDLLEHARFKFGQGK------------------------------------------------------SVYDVDQEV-AARHLVMKLHEDRHLHCFSHIF
439159                                                   559 AASLMRQLHFAMTLLELHGRFKVGGSE------------------------------------------------------TVYDVNHRV-AEKTQVLFPLPEDRFLCSFLHIF
Eucgr.L02517|Eucgr.L02517.1                              564 FLSEIFTLLRYHSVDLLELHTKYHLDGSE-----------------------------------------------------TIYLFLDDRV-GRRVNVIHLLPEDKFLCSFSHIF
GSVIVG01031425001|GSVIVT01031425001                      636 AGTLSLSLRQLRFASVDMEHLHTTYDENGSV----------------------------------------------------SIYDVDDRV-AEKTQVLAPLHEDRFLCSFHIF
GRMZM2G133919|GRMZM2G133919_T01                          626 AGTLSLRQLRFATVDLLELHATYDENGSL------------------------------------------------------SIYDVDDRV-AETTQVLAPLHEDRFLCSFSHIF
LOC_Os02g58340|LOC_Os02g58340.1                          668 SIYLVDDVRV-SKKTQVLFPLPDDKFLASFSHIF
PGSC0003DMG400030613|PGSC0003DMT40007866                 558 AGSLSLRQLKFATVDLLELHTKYMPGGSE-----------------------------------------------------TIYDVDQRV-SIKTQ----------------
Carubv10000350m.g|Carubv10000350m                        552 AGSLSLRQLKFATVDLLELHTKYVPGGSE-----------------------------------------------------SIYDVDQRV-SMKTQVIPPLHEDRFLCSFSHIF
Bra006067|Bra006067                                      558 AGSLSLRQLKFATVDLLELHTKYVPGGSE-----------------------------------------------------SIYDVDQRV-SLKTQVIPPLPEDRFLCSFSHIF
Bra028579|Bra028579                                      665 AGSFSLRQLKFASVDLLELHTHYVPGGPE-----------------------------------------------------SIYDVDQRV-SVKTQVIPPLPEDRFLCSFSHIF
Carubv10025914m.g|Carubv10025914m                        646 AGSFSLRQLKFASLDLLELHTNYVPGGPE-----------------------------------------------------SIYDVDQRV-SVKTQVIPPLHEDRFLCSFSHIF
AT5G65620                                                566 AGSFSLRQLKFASLDLLELHTNYVPGGPE-----------------------------------------------------SIYDVDQRV-SVKTQVIPPLPEDRFLCFSHIF
Bra024401|Bra024401                                      645 AGTQSLRQHKFATVDLLELHTKYVPGGQE-----------------------------------------------------SIYDVDHRV-SEKTQVIPPLPEDRFLCSFSHIF
Medtr5g030940|Medtr5g030940.1                            643 AGSFSLRQLKFASVDLLELHTKYVPGGPE-----------------------------------------------------SIYDVDDRV-SEKTQVIPPLPEDRFLCSFSHIF
Glyma01g02480|Glyma01g02480.1                            540 ----------------VHTKYVPGGPE-------------------------------------------------------SIYDVDDRV-SEKTQVIPPLPEDRFLCSFSHIF
Glyma09g33490|Glyma09g33490.1                            653 AGSLSLRQLRFASVDLELHTKYVPGEPE------------------------------------------------------LCSFLSPSD-CKGTQVIPPLADDKFLCSFSHIF
Cucsa.273340|Cucsa.273340.1                              745 AGSLSLRQLRFATVDLLELHSKYVPGGSE-----------------------------------------------------TIYDVDQRV-CKGTQVIPPLHEDRFLCSFSHIF
GSVIVG01003850001|GSVIVT01003850001                      557 AGSLSLRQLKFATVDLQLHLHNYVPGGSE-----------------------------------------------------SVHDVDQRV-WEKTQVIPPLPEDRFLCSFTHIF
Eucgr.I00597|Eucgr.I00597.1                              509 AGSLSLRQLKFASVDLQLHTKYVPGGSE------------------------------------------------------SVYDVDQRV-SERTQVLFPLPEDRFLCSFSHIF
Eucgr.I00594|Eucgr.I00594.1                              635 AGSLSLRQLRFASLDLLELHTKYIPGGSE-----------------------------------------------------SIYDVDQRV-SKETQVIPPLPEDRFLCSFSHIF
28333.t000012|28333.m000566                              557 AGSFSLRQLRFASLDLLELHTKYIPGASE-----------------------------------------------------SIYLVDQRV-SKETQVIPPLPEDRFLCSFSHIF
Potri.007G004600|Potri.007G004600.1                      650 AGSFSLRQLKFASLDLLELHTKYIPGAIE-----------------------------------------------------SIYDVDQRV-SERTQVIPPLHEDRFLCGFSHIF
Potri.014G004600|Potri.014G004600.1                      675 AGSFSLRQLKFASLDLLELHTKYIPGALE-----------------------------------------------------SIYDVDQRV-SKFTQVIPPLHEDRFLCSFSHIF
Potri.014G010100|Potri.014G010100.1                      570 EGFRTTEYLAASILDQKHQLGVSQMPSD------------------------------------------------------VLSPEAQSL-KQAGVDYAPVPPRYRTTYFSHVF
28658.t000001|28658.m000032                              451 AGFNTVEFTSSALVPMAFHTRGYVEDPMA-----------------------------------------------------V---QAQVL-AEIGMPKSIV-MRHATPHFQEHVF
30484.t000001|30484.m000014
```

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gi|85111610                                         713 ---GYGSTYYSYLFDRVIAQRVWNVVENSGQGGAALQ----RENGEELKENLLKWGGSKDEWKCLAGALKD-ERLEGGGEKAMKLVGSWGGQRGTKSDQLV---------
YKL134C                                             693 ---GYGATYYSYLFDRTIASKIWYALGEDD----PYS----RKNGDKLKKHLLKWGGLKDPWKCIADVVEC-LMLEKGGSDAMEFIAQSHKS*-----------
Cre02.g073400|Cre02.g073400.t1.3                    537 ---IWGGSXYGLVVYARCLAAQLWRASGLAE---APLD----PGACELLRERLLAPGGALEPLELLTGHAEAAEAGEGAGS--PVG-SSATHQARGRQVRLALQRQRGQQQ
Vocar20013694m.g|Vocar20013694m                     646 ---IWGGAYYGLVYARCLAAQLWKLTGLEE---APLD----SGPAAAGAS----PGA-------------------------VA---AAARLRRLEPWQVAKLRQR----
gi|32565901                                         608 ---QLGAKYYSLVVARASACLIWQQRLL-N---DPFS----RKWGDC-WAEVQSHGGGHHLAVLLEKILGGFRPT----------ENDLTQALSKESQHLANLDAVTV--
CMS132C|CMS132CT                                    505 ---GYGGCYYSYLLARILAALVWNRLERDS---KLSM----AAACELLRNGFFRFGASKEPRELLATVLNGBE------------PSFRGLAEAIGMADSQYATLPVLASAN
gi|268637658                                        662 --YMGASYYSYLLAKDYSKRLWINHEDSG---KQLN----LEKGQFYQQNFLKPGASIDPSLILNKEINKNK-------------------------------------
Esi0033_0093                                        730 ---GYGASYYAYLYAKMFTSAIWERHFA-K---DPLN----SDACELLWKELLIHGGAKDPHBMLRVLLGE-EQGSGGDAGLRAGVTSLTKDTGAVAT*-----------
tr|M1C3Y6|M1C3Y6_SOLTU                                   --------------------------------------------------------------------------------------------------------
GSVIVG01018572001|GSVIVT01018572001                 367 ---TYGAGYTYLYVARCFATTIWQEVCQ-E---DPFS----RSAGSAIHDKFLRFGGSKDPSSLLKDLAG-DAVIRNSGSGIIPNASSLCKEIGLL*----------
GRMZM2G450659|GRMZM2G450659_T01                     625 ---NYGAGYYSYLYARCFATTIWQEVCQ-G---DPFS----RSTGSAIRDKFLKHGGCAKDPSALLKDFVG-DSIIINSGGGIIPDISSLCKEVGL*-----------
```

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gi|85111610                                          ---------------------------------------------------------------------------------------------------
YKL134C                                              ---------------------------------------------------------------------------------------------------
Cre02.g073400|Cre02.g073400.t1.3             634     QQQQG---GGGGAHEAMPGGGLLQ-----YLEGGYA---P---R----SDYYLET-LKTGIAA*-------------------------------------
Vocar20013694m.g|Vocar20013694m              710     --------GVEKALAPAAEGGFLQ-----ALEGGFA---P---R----PEQYLEM-LRKGSGSPEGLRST*------------------------------
gi|32565901                                          ---------------------------------------------------------------------------------------------------
CMS132C|CMS132CT                             595      --------RSELCAEPSA----------------------------------------------------------------------------------
gi|268637658                                         ---------------------------------------------------------------------------------------------------
Esi0033_0093                                         ---------------------------------------------------------------------------------------------------
tr|M1C3Y6|M1C3Y6_SOLTU                               ---------------------------------------------------------------------------------------------------
GSVIVG01018572001|GSVIVT01018572001                  ---------------------------------------------------------------------------------------------------
GRMZM2G450659|GRMZM2G450659_T01                      ---------------------------------------------------------------------------------------------------
LOC_Os06g47210|LOC_Os06g47210.1                      ---------------------------------------------------------------------------------------------------
Cucsa.251510|Cucsa.251510.1                          ---------------------------------------------------------------------------------------------------
Glyma04g13088|Glyma04g13088.1                        ---------------------------------------------------------------------------------------------------
Medtr3g009160|Medtr3g009160.1                        ---------------------------------------------------------------------------------------------------
Bra029169|Bra029169                                  ---------------------------------------------------------------------------------------------------
Carubv10025983m.g|Carubv10025983m                    ---------------------------------------------------------------------------------------------------
AT5G51540                                            ---------------------------------------------------------------------------------------------------
Eucgr.K00152|Eucgr.K00152.1                          ---------------------------------------------------------------------------------------------------
30147.t000467|30147.m014196                  719     ---------------------------------------------------------------------------------------------------
Potri.015G129300|Potri.015G129300.1                  ---------------------------------------------------------------------------------------------------
416778|416778                                        ---------------------------------------------------------------------------------------------------
Phpat.016G041000|Phpat.016G041000.1                  ---------------------------------------------------------------------------------------------------
gi|71999758                                  760     IQDEMEMSENQRR--------------------------------------------------------------------------------------
gi|85107353                                  712     GRDP-----------VIEGASSEEDPAIEHHP-F-----------------------------------------------------------------
YCL057W                                              ---------------------------------------------------------------------------------------------------
gi|66801567                                          ---------------------------------------------------------------------------------------------------
CMS446C|CMS446CT                                     ---------------------------------------------------------------------------------------------------
gi|4507491                                           ---------------------------------------------------------------------------------------------------
gi|14149738|ref|NP_065777                            ---------------------------------------------------------------------------------------------------
LOC_Os01g67590|LOC_Os01g67590.1                      ---------------------------------------------------------------------------------------------------
Bra004244|Bra004244                          710     AQMEVSMSLNALTRLPLKNTGRLE-EFGLARHSLFTSRTPCLERAQRRKALVVEAKGKKGMAARQYQRTPPPMPKIEDDGNPR------FVIFIRM--ANVYLWYPLSII
Bra004078|Bra004078                                  ---------------------------------------------------------------------------------------------------
Carubv10019853m.g|Carubv10019853m                    ---------------------------------------------------------------------------------------------------
AT1G67690                                            ---------------------------------------------------------------------------------------------------
Eucgr.B03454|Eucgr.B03454.1                          ---------------------------------------------------------------------------------------------------
Medtr3g086000|Medtr3g086000.1                        ---------------------------------------------------------------------------------------------------
Glyma11g37410|Glyma11g37410.2                        ---------------------------------------------------------------------------------------------------
Glyma18g01380|Glyma18g01380.1                        ---------------------------------------------------------------------------------------------------
Cucsa.394790|Cucsa.394790.1                          ---------------------------------------------------------------------------------------------------
GSVIVG01010319001|GSVIVT01010319001                  ---------------------------------------------------------------------------------------------------
29929.t000212|29929.m004709                          ---------------------------------------------------------------------------------------------------
Potri.010G054500|Potri.010G054500.1                  ---------------------------------------------------------------------------------------------------
164651|164651                                        ---------------------------------------------------------------------------------------------------
Phpat.018G066900|Phpat.018G066900.1                  ---------------------------------------------------------------------------------------------------
Phpat.019G060600|Phpat.019G060600.1                  ---------------------------------------------------------------------------------------------------
Esi0023_0135                                         ---------------------------------------------------------------------------------------------------
85692|85692                                          ---------------------------------------------------------------------------------------------------
97633|97633                                          ---------------------------------------------------------------------------------------------------
119899|119899                                        ---------------------------------------------------------------------------------------------------
97030|97030                                          ---------------------------------------------------------------------------------------------------
Cre13.g572900|Cre13.g572900.t2.1                     ---------------------------------------------------------------------------------------------------
Vocar20008539m.g|Vocar20008539m                      ---------------------------------------------------------------------------------------------------
439159                                               ---------------------------------------------------------------------------------------------------
Eucgr.L02517|Eucgr.L02517.1                          ---------------------------------------------------------------------------------------------------
GSVIVG01031425001|GSVIVT01031425001                  ---------------------------------------------------------------------------------------------------
GRMZM2G133919|GRMZM2G133919_T01                      ---------------------------------------------------------------------------------------------------
LOC_Os02g58340|LOC_Os02g58340.1                      ---------------------------------------------------------------------------------------------------
PGSC0003DMG400030613|PGSC0003DMT40007866             ---------------------------------------------------------------------------------------------------
Carubv10000350m.g|Carubv10000350m                    ---------------------------------------------------------------------------------------------------
Bra006067|Bra006067                                  ---------------------------------------------------------------------------------------------------
Bra028579|Bra028579                                  ---------------------------------------------------------------------------------------------------
Carubv10025914m.g|Carubv10025914m                    ---------------------------------------------------------------------------------------------------
AT5G65620                                            ---------------------------------------------------------------------------------------------------
Bra024401|Bra024401                                  ---------------------------------------------------------------------------------------------------
Medtr5g030940|Medtr5g030940.1                799     INTR---ILTYVLRSPF-------------LHSIF-SDFPCTENPETAFTYFWITDS-CPLTMKEVI-HRPPFEVLSQSSNLMKMLHYNFHLILKMELKEKEEKIPSMAR
Glyma01g02480|Glyma01g02480.1                        ---------------------------------------------------------------------------------------------------
Glyma09g33490|Glyma09g33490.1                        ---------------------------------------------------------------------------------------------------
Cucsa.273340|Cucsa.273340.1                          ---------------------------------------------------------------------------------------------------
GSVIVG01003850001|GSVIVT01003850001                  ---------------------------------------------------------------------------------------------------
Eucgr.I00597|Eucgr.I00597.1                          ---------------------------------------------------------------------------------------------------
Eucgr.I00594|Eucgr.I00594.1                          ---------------------------------------------------------------------------------------------------
28333.t000012|28333.m000566                          ---------------------------------------------------------------------------------------------------
Potri.007G004600|Potri.007G004600.1                  ---------------------------------------------------------------------------------------------------
Potri.014G004600|Potri.014G004600.1                  ---------------------------------------------------------------------------------------------------
Potri.014G010100|Potri.014G010100.1                  ---------------------------------------------------------------------------------------------------
28658.t000001|28658.m000032                          ---------------------------------------------------------------------------------------------------
30484.t000001|30484.m000014                          ---------------------------------------------------------------------------------------------------
```

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gi|85111610                                               --------------------------------------------------------------------------------------
YKL134C                                                   --------------------------------------------------------------------------------------
Cre02.g073400|Cre02.g073400.t1.3                          --------------------------------------------------------------------------------------
Vocar20013694m.g|Vocar20013694m                           --------------------------------------------------------------------------------------
gi|32565901                                               --------------------------------------------------------------------------------------
CMS132C|CMS132CT                                          --------------------------------------------------------------------------------------
gi|268637658                                              --------------------------------------------------------------------------------------
Esi0033_0093                                              --------------------------------------------------------------------------------------
tr|M1C3Y6|M1C3Y6_SOLTU                                    --------------------------------------------------------------------------------------
GSVIVG01018572001|GSVIVT01018572001                       --------------------------------------------------------------------------------------
GRMZM2G450659|GRMZM2G450659_T01                           --------------------------------------------------------------------------------------
LOC_Os06g47210|LOC_Os06g47210.1                           --------------------------------------------------------------------------------------
Cucsa.251510|Cucsa.251510.1                               --------------------------------------------------------------------------------------
Glyma04g13088|Glyma04g13088.1                             --------------------------------------------------------------------------------------
Medtr3g009160|Medtr3g009160.1                             --------------------------------------------------------------------------------------
Bra029169|Bra029169                                       --------------------------------------------------------------------------------------
Carubv10025983m.g|Carubv10025983m                         --------------------------------------------------------------------------------------
AT5G51540                                                 --------------------------------------------------------------------------------------
Eucgr.K00152|Eucgr.K00152.1                               --------------------------------------------------------------------------------------
30147.t000467|30147.m014196                               --------------------------------------------------------------------------------------
Potri.015G129300|Potri.015G129300.1                       --------------------------------------------------------------------------------------
416778|416778                                             --------------------------------------------------------------------------------------
Phpat.016G041000|Phpat.016G041000.1                       --------------------------------------------------------------------------------------
gi|71999758                                               --------------------------------------------------------------------------------------
gi|85107353                                               --------------------------------------------------------------------------------------
YCL057W                                                   --------------------------------------------------------------------------------------
gi|66801567                                               --------------------------------------------------------------------------------------
CMS446C|CMS446CT                                          --------------------------------------------------------------------------------------
gi|4507491                                                --------------------------------------------------------------------------------------
gi|14149738|ref|NP_065777                                 --------------------------------------------------------------------------------------
LOC_Os01g67590|LOC_Os01g67590.1                           --------------------------------------------------------------------------------------
Bra004244|Bra004244                              811 AGGTTAKIMVAAKDNLLGKYIYKDTIARNIAAVIYRDEKEIQKTAIKQHRVLRTATEFRYG---------YKLVVML--SKLLSSVIGSSENGNMRAALSTSDVIELPTQ
Bra004078|Bra004078                                       --------------------------------------------------------------------------------------
Carubv10019853m.g|Carubv10019853m                         --------------------------------------------------------------------------------------
AT1G67690                                                 --------------------------------------------------------------------------------------
Eucgr.B03454|Eucgr.B03454.1                               --------------------------------------------------------------------------------------
Medtr3g086000|Medtr3g086000.1                             --------------------------------------------------------------------------------------
Glyma11g37410|Glyma11g37410.2                             --------------------------------------------------------------------------------------
Glyma18g01380|Glyma18g01380.1                             --------------------------------------------------------------------------------------
Cucsa.394790|Cucsa.394790.1                               --------------------------------------------------------------------------------------
GSVIVG01010319001|GSVIVT01010319001                       --------------------------------------------------------------------------------------
29929.t000212|29929.m004709                               --------------------------------------------------------------------------------------
Potri.010G054500|Potri.010G054500.1                       --------------------------------------------------------------------------------------
164651|164651                                             --------------------------------------------------------------------------------------
Phpat.018G066900|Phpat.018G066900.1                       --------------------------------------------------------------------------------------
Phpat.019G060600|Phpat.019G060600.1                       --------------------------------------------------------------------------------------
Esi0023_0135                                              --------------------------------------------------------------------------------------
85692|85692                                               --------------------------------------------------------------------------------------
97633|97633                                               --------------------------------------------------------------------------------------
119899|119899                                             --------------------------------------------------------------------------------------
97030|97030                                               --------------------------------------------------------------------------------------
Cre13.g572900|Cre13.g572900.t2.1                          --------------------------------------------------------------------------------------
Vocar20008539m.g|Vocar20008539m                           --------------------------------------------------------------------------------------
439159                                                    --------------------------------------------------------------------------------------
Eucgr.L02517|Eucgr.L02517.1                               --------------------------------------------------------------------------------------
GSVIVG01031425001|GSVIVT01031425001                       --------------------------------------------------------------------------------------
GRMZM2G133919|GRMZM2G133919_T01                           --------------------------------------------------------------------------------------
LOC_Os02g58340|LOC_Os02g58340.1                           --------------------------------------------------------------------------------------
PGSC0003DMG400030613|PGSC0003DMT40007866                  --------------------------------------------------------------------------------------
Carubv10000350m.g|Carubv10000350m                         --------------------------------------------------------------------------------------
Bra006067|Bra006067                                       --------------------------------------------------------------------------------------
Bra028579|Bra028579                                       --------------------------------------------------------------------------------------
Carubv10025914m.g|Carubv10025914m                         --------------------------------------------------------------------------------------
AT5G65620                                                 --------------------------------------------------------------------------------------
Bra024401|Bra024401                                       --------------------------------------------------------------------------------------
Medtr5g030940|Medtr5g030940.1                    890 AGGITNAVNVGI-------AVQAD----------WENREFISHISLNVRRLFDFLVQFEATTKSKLASLNEKLDVLERRLELLEVQVGNASAN----------------
Glyma01g02480|Glyma01g02480.1                             --------------------------------------------------------------------------------------
Glyma09g33490|Glyma09g33490.1                             --------------------------------------------------------------------------------------
Cucsa.273340|Cucsa.273340.1                               --------------------------------------------------------------------------------------
GSVIVG01003850001|GSVIVT01003850001                       --------------------------------------------------------------------------------------
Eucgr.I00597|Eucgr.I00597.1                               --------------------------------------------------------------------------------------
Eucgr.I00594|Eucgr.I00594.1                               --------------------------------------------------------------------------------------
28333.t000012|28333.m000566                               --------------------------------------------------------------------------------------
Potri.007G004600|Potri.007G004600.1                       --------------------------------------------------------------------------------------
Potri.014G004600|Potri.014G004600.1                       --------------------------------------------------------------------------------------
Potri.014G010100|Potri.014G010100.1                       --------------------------------------------------------------------------------------
28658.t000001|28658.m000032                               --------------------------------------------------------------------------------------
30484.t000001|30484.m000014                               --------------------------------------------------------------------------------------
```

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gi|85111610                                         --------------------------------------------------
YKL134C                                             --------------------------------------------------
Cre02.g073400|Cre02.g073400.t1.3                    --------------------------------------------------
Vocar20013694m.g|Vocar20013694m                     --------------------------------------------------
gi|32565901                                         --------------------------------------------------
CMS132C|CMS132CT                                     --------------------------------------------------
gi|268637658                                        --------------------------------------------------
Esi0033_0093                                        --------------------------------------------------
tr|M1C3Y6|M1C3Y6_SOLTU                              --------------------------------------------------
GSVIVG01018572001|GSVIVT01018572001                 --------------------------------------------------
GRMZM2G450659|GRMZM2G450659_T01                     --------------------------------------------------
LOC_Os06g47210|LOC_Os06g47210.1                     --------------------------------------------------
Cucsa.251510|Cucsa.251510.1                         --------------------------------------------------
Glyma04g13088|Glyma04g13088.1                       --------------------------------------------------
Medtr3g009160|Medtr3g009160.1                       --------------------------------------------------
Bra029169|Bra029169                                 --------------------------------------------------
Carubv10025983m.g|Carubv10025983m                   --------------------------------------------------
AT5G51540                                           --------------------------------------------------
Eucgr.K00152|Eucgr.K00152.1                         --------------------------------------------------
30147.t000467|30147.m014196                         --------------------------------------------------
Potri.015G129300|Potri.015G129300.1                 --------------------------------------------------
416778|416778                                       --------------------------------------------------
Phpat.016G041000|Phpat.016G041000.1                 --------------------------------------------------
gi|71999758                                         --------------------------------------------------
gi|85107353                                         --------------------------------------------------
YCL057W                                             --------------------------------------------------
gi|66801567                                         --------------------------------------------------
CMS446C|CMS446CT                                     --------------------------------------------------
gi|4507491                                          --------------------------------------------------
gi|14149738|ref|NP_065777                           --------------------------------------------------
LOC_Os01g67590|LOC_Os01g67590.1                     --------------------------------------------------
Bra004244|Bra004244                             910 DQLKTVFDKVKDFFGDAKESFGKISSLNPGTDEETEGSPDDKAKVQG*
Bra004078|Bra004078                                 --------------------------------------------------
Carubv10019853m.g|Carubv10019853m                   --------------------------------------------------
AT1G67690                                           --------------------------------------------------
Eucgr.B03454|Eucgr.B03454.1                         --------------------------------------------------
Medtr3g086000|Medtr3g086000.1                       --------------------------------------------------
Glyma11g37410|Glyma11g37410.2                       --------------------------------------------------
Glyma18g01380|Glyma18g01380.1                       --------------------------------------------------
Cucsa.394790|Cucsa.394790.1                         --------------------------------------------------
GSVIVG01010319001|GSVIVT01010319001                 --------------------------------------------------
29929.t000212|29929.m004709                         --------------------------------------------------
Potri.010G054500|Potri.010G054500.1                 --------------------------------------------------
164651|164651                                       --------------------------------------------------
Phpat.018G066900|Phpat.018G066900.1                 --------------------------------------------------
Phpat.019G060600|Phpat.019G060600.1                 --------------------------------------------------
Esi0023_0135                                        --------------------------------------------------
85692|85692                                         --------------------------------------------------
97633|97633                                         --------------------------------------------------
119899|119899                                       --------------------------------------------------
97030|97030                                         --------------------------------------------------
Cre13.g572900|Cre13.g572900.t2.1                    --------------------------------------------------
Vocar20008539m.g|Vocar20008539m                     --------------------------------------------------
439159                                              --------------------------------------------------
Eucgr.L02517|Eucgr.L02517.1                         --------------------------------------------------
GSVIVG01031425001|GSVIVT01031425001                 --------------------------------------------------
GRMZM2G133919|GRMZM2G133919_T01                     --------------------------------------------------
LOC_Os02g58340|LOC_Os02g58340.1                     --------------------------------------------------
PGSC0003DMG400030613|PGSC0003DMT40007866            --------------------------------------------------
Carubv10000350m.g|Carubv10000350m                   --------------------------------------------------
Bra006067|Bra006067                                 --------------------------------------------------
Bra028579|Bra028579                                 --------------------------------------------------
Carubv10025914m.g|Carubv10025914m                   --------------------------------------------------
AT5G65620                                           --------------------------------------------------
Bra024401|Bra024401                                 --------------------------------------------------
Medtr5g030940|Medtr5g030940.1                   966 ---PSLFAT*----------------------------------------
Glyma01g02480|Glyma01g02480.1                       --------------------------------------------------
Glyma09g33490|Glyma09g33490.1                       --------------------------------------------------
Cucsa.273340|Cucsa.273340.1                         --------------------------------------------------
GSVIVG01003850001|GSVIVT01003850001                 --------------------------------------------------
Eucgr.I00597|Eucgr.I00597.1                         --------------------------------------------------
Eucgr.I00594|Eucgr.I00594.1                         --------------------------------------------------
28333.t000012|28333.m000566                         --------------------------------------------------
Potri.007G004600|Potri.007G004600.1                 --------------------------------------------------
Potri.014G004600|Potri.014G004600.1                 --------------------------------------------------
Potri.014G010100|Potri.014G010100.1                 --------------------------------------------------
28658.t000001|28658.m000032                         --------------------------------------------------
30484.t000001|30484.m000014                         --------------------------------------------------
```