```
27490.t000003|27490.m000041                  1 ------------------------------------------------------------ 0-----------------------------------------------
Phpat.1Z035600|Phpat.1Z035600.1              1 ------------------------------------------------------------ 0-----------------------------------------------
gi|392884626                                 1 ------------------------------------------------------------ 0-----------------------------------------------
gi|530420285                                 1 -------------------------------------------------------MPWLL 5SAPKLVPA---VANVRGLSGCM--------------LC---SQRRYSL
gi|11559925                                  1 -------------------------------------------------------MPWLL 5SAPKLVPA---VANVRGLSGCM--------------LC---SQRRYSL
gi|530420287                                 1 -------------------------------------------------------MPWLL 5SAPKLVPA---VANVRGLSGCM--------------LC---SQRRYSL
YER078C                                      1 ------------------------------------------------------------ 0MLHRINPVRFSMQSCQRYFSKLVSP----------L----EQ--HKS
gi|85089070                                  1 ------------------------------------------------------------ 0-----------------------------------------------
CMA107C|CMA107CT                             1 MSSSVRYGALRTLQGVAARGAHTAAFRQQCGDRGSLLRALGKRAEAPVAQGCKQTRNDAE 60SWPRGL----ARGPGRAFFSNHTGYQDAYRQQRASEVAAAEEKEMLL
Cre01.g046150|Cre01.g046150.t1.3             1 -------------------------------MLTRVVAGLM-------RAGH--TAPSVP 20ALRGLM----CGRTGS-------AP-------RAPHIC---SRE---
Vocar20008388m.g|Vocar20008388m              1 -------------------------------MLARVVAGAA-------AG-H--RDITLT 19TTF-SL----SGRNAFSLSLTHIAA-------VFNRFC---TTH---
gi|66812452                                  1 -------------------------MNNICKL-NKFIISKS---------SS--SLSS-- 21-TSSKIKTNCLIKNAKMFSSSL----------NLNRFY-------ST
89300|89300                                  1 ------------------------------------------------------------ 0-----------------------------------------------
Phpat.012G034000|Phpat.012G034000.1          1 ------------------------MRMKSCKEVERLLSGKF---------GH--MLARMA 25AWRSLVPVSWRL-CCREVSSTQ----------KIG--HE-NGQYFAT
GRMZM2G135045|GRMZM2G135045_T01              1 ------------------------------------------------------------ 0---------MAM-AARLLRATE---------VASRFLS-ASHGFVQR
LOC_Os12g37640|LOC_Os12g37640.1              1 ------------------------------------------------------------ 0-----MATAVRL-LRRSLRGGE---------AAPRFLS-ASQNLVRL
PGSC0003DMG400002792|PGSC0003DMT40000722     1 ------------------------------------------------------------ 0---------MQA-LRRNPLHR----------ISSRFL---NQV-VKT
Bra030767|Bra030767                          1 ------------------------------------------------------------ 0---------MQV-LARNLAQ-----------RVS--R---SQV-ISR
AT1G09300                                    1 ------------------------------------------------------------ 0---------MQF-LARNLVR-----------RVS--R---TQV-VSR
Carubv10009008m.g|Carubv10009008m            1 ------------------------------------------------------------ 0---------MQV-LARNLVR-----------RVS--R---PQV-IIR
Cucsa.090530|Cucsa.090530.1                  1 ------------------------------------------------------------ 0---------MRT-LVQKLLP-----------RTT--F---KQV-VAF
Eucgr.B01688|Eucgr.B01688.1                  1 ------------------------------------------------------------ 0-----------------------------------------------
Eucgr.L00254|Eucgr.L00254.1                  1 ------------------------------------------------------------ 0-------MALHM-LARKFLQR-----------AP--P---RQA-ISS
GSVIVG01031262001|GSVIVT01031262001          1 ------------------------------------------------------------ 0---------MQI-LRRKLLQ-----------RSS--F---IQG-VGR
Glyma10g28690|Glyma10g28690.1                1 ------------------------------------------------------------ 0---------MQG-AVRKL-TR----------IIS--H---RQV-VGF
Glyma20g22820|Glyma20g22820.1                1 ------------------------------------------------------------ 0---------MQG-AVRKL-TR----------IIS--H---RQV-VGF
Glyma20g22820|Glyma20g22820.2                1 ------------------------------------------------------------ 0---------MQG-AVRKL-TR----------IIS--H---RQV-VGF
30128.t000390|30128.m008929                  1 ------------------------------------------------------------ 0----------MI-PLRNLFQR----------RVP--F---KQG-TAC
Potri.013G007100|Potri.013G007100.1          1 ------------------------------------------------------------ 0---------MQI-LVRKLLQR----------ATP--F---KQG-IVR
Cre02.g083065|Cre02.g083065.t1.2             1 --------------------------MHKVG-----VSGAS-------------WNRPAS 16AWRGHAHA------------------------ARAAQVP-------T
Vocar20010463m.g|Vocar20010463m              1 ------------------------------------------------------------ 0-----------------------------------------------
gi|164428892                                 1 ------------------------------------------------------------ 0-----------------------------------------------
gi|66825133                                  1 ------------------------------------------------------------ 0-----------------------------------------------
Cre07.g342920|Cre07.g342920.t1.2             1 ------------------------------------------------------------ 0-----------------------------------------------
Vocar20011350m.g|Vocar20011350m              1 ------------------------------------------------------------ 0-----------------------------------------------
NP_490843.1|                                 1 ------------------------------------------------------------ 0-----------------------------------------------
Esi0137_0095                                 1 ------------------------------------------------------------ 0-----------------------------------------------
gi|260593665                                 1 ------------------------------------------------------------ 0-----------------------------------------------
gi|149589008                                 1 ------------------------------------------------------------ 0-----------------------------------------------
gi|260593663                                 1 ------------------------------------------------------------ 0-----------------------------------------------
gi|164425919                                 1 ------------------------------------------------------------ 0-----------------------------------------------
Glyma01g37350|Glyma01g37350.1                1 ------------------------------------------------------------ 0-----------------------------------------------
Eucgr.C03941|Eucgr.C03941.1                  1 -------------------------MN--------------------------------- 2----------------------------------PLFP-------SI
Phpat.022G059200|Phpat.022G059200.1          1 ------------------------------------------------------------ 0-----------------------------------------------
80851|80851                                  1 ------------------------------------------------------------ 0-----------------------------------------------
Glyma08g03391|Glyma08g03391.1                1 ------------------------------------------------------------ 0-----------------------------------------------
GRMZM2G021110|GRMZM2G021110_T01              1 ------------------------------------------------------------ 0-----------------------------------------------
LOC_Os02g13140|LOC_Os02g13140.1              1 ------------------------------------------------------------ 0-----------------------------------------------
Glyma05g36260|Glyma05g36260.1                1 ------------------------------------------------------------ 0-----------------------------------------------
Medtr8g101720|Medtr8g101720.1                1 ------------------------------------------------------------ 0-----------------------------------------------
Cucsa.397160|Cucsa.397160.1                  1 ------------------------------------------------------------ 0-----------------------------------------------
Bra011117|Bra011117                          1 ------------------------------------------------------------ 0-----------------------------------------------
AT4G29490                                    1 ------------------------------------------------------------ 0-----------------------------------------------
Carubv10007150m.g|Carubv10007150m            1 ------------------------------------------------------------ 0-----------------------------------------------
Eucgr.C03666|Eucgr.C03666.1                  1 ------------------------------------------------------------ 0-----------------------------------------------
GSVIVG01015237001|GSVIVT01015237001          1 ------------------------------------------------------------ 0-----------------------------------------------
29912.t000128|29912.m005402                  1 ------------------------------------------------------------ 0-----------------------------------------------
Potri.006G149500|Potri.006G149500.1          1 ------------------------------------------------------------ 0-----------------------------------------------

27490.t000003|27490.m000041                  1 ----------MT 2IGGKTI---EQ----------ALASLSDMTAGAV------PIGKDEH-LQRIARAQAY-- 40---------MQAQGIAAIYINAG----------
Phpat.1Z035600|Phpat.1Z035600.1              1 ------------ 0-----------------------------------------MEKLKKLRQQ-- 10---------FEAAGIDGILVTNG----------
gi|392884626                                 1 ------------ 0-----------------------MLRSGRSLPMWPSRIPNEEY-AMRRTNLMNL-- 30---LKKEVKT--GEKQVVVVMKGA--RKSYIAP
gi|530420285                                34 QPVPERRIPNRY 45LGQPSPFTHPH-----------------LLRPGEVT----PGLSQVEY-ALRRHKLMSL-- 82---IQKEAQGQ-SGTDQTVVVLSN--PTYYMS
gi|11559925                                 34 QPVPERRIPNRY 45LGQPSPFTHPH-----------------LLRPGEVT----PGLSQVEY-ALRRHKLMSL-- 82---IQKEAQGQ-SGTDQTVVVLSN--PTYYMS
gi|530420287                                34 QPVPERRIPNRY 45LGQPSPFTHPH-----------------LLRPGEVT----PGLSQVEY-ALRRHKLMSL-- 82---IQKEAQGQ-SGTDQTVVVLSN--PTYYMS
YER078C                                     32 NTFTNRVRIPIE 43AGQPLHETRPF-----------------LIKSGELT----PGISALEY-YERRIRLAET-- 80---LPPK---------SCVILAGN--DIQFAS
gi|85089070                                  1 ---MIISAADLE 9FGQPVYETHPH----------------ILQPGELT----PGITAQEY-HERRSKLAFA-- 46---LPEN---------GIAILASS--ELKYRSG
CMA107C|CMA107CT                           104 LRK--LRLKLTRP 114VSQATGHTHPH-----------------LLDIDQVT----PGIPLAEY-RARRQALAAL-- 151---MPPH---------SLLILPAA--PEQ
Cre01.g046150|Cre01.g046150.t1.3            44 FSTAPSPEERPPF 56AGQPISSTHPE---------------LLAPGQLT----PGVTAAEY-AARRRQLSEL-- 93---LPPG---------SIAVLPSA--ATTYM
Vocar20008388m.g|Vocar20008388m             49 INR------PCSP 55AGQPTAATHPE---------------LLAPRELT----PGIEASEY-RARRHRLSQL-- 92---LPPG---------GSAVLPAA--ATTYM
gi|66812452                                 51 NNTNNNKLKKPLS 63IGQATFETHPY---------------LLDKNEIT----KGIKMKEF-KDRREKLMKN-- 100---FPIG---------SVVVIFTP--PEPM
89300|89300                                  1 ------------ 0-GQPTPETHPE---------------LLEAGEIM----PGISAAEF-HQRRKSLMSI-- 36---LPRN---------SLVAIGSA--PIKTMSD
Phpat.012G034000|Phpat.012G034000.1         59 RRWYSQPWTAPYD 71AGQPTSESHPQ---------------MLSGDELF----PGISLRDF-KERRTALRSR-- 108---LPTE---------SMVILSAA--SVKQ
GRMZM2G135045|GRMZM2G135045_T01             28 AAYT--AGGIVD 37VGQPTPQSHPE---------------LLADGEIT----PGITNEEY-ISRRKKLLEV-- 74---LPEK---------SLAIIASA--DQQMMT
LOC_Os12g37640|LOC_Os12g37640.1             32 VA-N--NTRSVD 40VGQPTPRSHPE---------------LLAEGEIT----PGITSDEY-IFRRKKLLEV-- 77---LPEK---------SLAIIASA--EQQMMT
PGSC0003DMG400002792|PGSC0003DMT40000722    24 SAYS-T-KKIYD 33AGQPTPATHPQ---------------LMKEGEIT----PGITSEEY-MQRRKKLLDF-- 70---LPEN---------SLAIVAAA--PTKMMT
Bra030767|Bra030767                         21 YAYS-T-QRVRD 30IGQPTPASHPH---------------FMSEGEVT----PGIRVEEY-IGRRKKLAEL-- 67---LPQN---------SLAIVSSA--PVKMMT
AT1G09300                                   21 NAYS-T-QTVRD 30IGQPTPASHPH---------------LMAEGEVT----PGIRIEEY-IGRRKKLVEL-- 67---LPEN---------SLAIISSA--PVKMMT
Carubv10009008m.g|Carubv10009008m           21 NAYS-T-QRVRD 30IGQPTPASHPH---------------LMAEGEVT----PGIRIDEY-IARRKKLVEL-- 67---LPEN---------SLAIISSA--PVKMMT
Cucsa.090530|Cucsa.090530.1                 21 RGYC-T-DKILD 30IGQPTAASHPE---------------LMKEGEIT----PGITADEY-ITRRKRLLEL-- 67---LPEN---------SLAVIAAA--PVKMMT
Eucgr.B01688|Eucgr.B01688.1                  1 ---------MID 3VGQPTPATHPE--------------LLNEGEIT----PGITAEEY-VSRRNQLLDL-- 40---LPEK---------GLAIIAAA--PIKMMTD
Eucgr.L00254|Eucgr.L00254.1                 23 HSFS-S-KRMID 32VGQPTPATHPE---------------LLNEGEIT----PGITAEEY-VSRRNQLLDL-- 69---LPEK---------GLAIIAAA--PIKMMT
GSVIVG01031262001|GSVIVT01031262001         21 CGYC-S-KNIVD 30AGQPTPASHPQ---------------LLNEGEIT----PGITSEEY-VSRRKRLLEL-- 67---LPEN---------SLAIVASA--PVKMMT
Glyma10g28690|Glyma10g28690.1               21 RSYC-TDKVVVD 31IGQPTSASHPQ---------------LLKDGELT----PGISTEEY-ILRRKKLLDL-- 68---LPEK---------SLAIIAAA--PVKMMT
Glyma20g22820|Glyma20g22820.1               21 RSYC-TDKVVVD 31IGQPTSASHPQ---------------LLKDGDLT----PGISTEEY-ILRRKKLLDL-- 68---LPEK---------SLAIIAAA--PVKMMT
Glyma20g22820|Glyma20g22820.2               21 RSYC-TDKVVVD 31IGQPTSASHPQ---------------LLKDGDLT----PGISTEEY-ILRRKKLLDL-- 68---LPEK---------SLAIIAAA--PVKMMT
30128.t000390|30128.m008929                 21 YAYS-T-NKVFD 30IGQPTPATHPQ---------------LLKEGEIT----PGISNEEY-ISRRKKLLEI-- 67---LPEK---------SLAIIAAA--PVKMMT
Potri.013G007100|Potri.013G007100.1         22 RTYS-T-NKVHD 31IGQPTPATHPQ---------------LLKEGEIT----PGITTEEY-ISRRKRLLEL-- 68---LPEK---------SLAIIAAA--PMKMMT
Cre02.g083065|Cre02.g083065.t1.2            33 SRV-G-VTAAAGA 43GGASSSA-AATATAAPPAAASSPAAPDWSERFRV------RSVPEQF-RETRQKVC---- 91---------KEFLAGGLLYLESGEAPARNG
Vocar20010463m.g|Vocar20010463m              1 ------------ 0------------------------------------------------------------- 0---------------------------------
gi|164428892                                 1 ------------ 0-MANSGQEHEIHYN-------------LVEDDEF------DIVNIV--VEGTDGI-HSAG 37AAPSASVVEELDAPKSGLIYLRGFDEPLYPYSD
gi|66825133                                  1 -----MSVHPRN 7QGKDD-CCEKTHLD-----SQYSPGYYWLGNNTL------KVPLVLH-KENRQRLVSQ-- 52---ILSKHK-DQVKENSFILLESGKSTMQYDTD
Cre07.g342920|Cre07.g342920.t1.2             1 ------------ 0-MATA-QTHAVGLD-----IPIEADTYHMGPGTL------RISRKAFHGKLRSRLLER-- 45---LQAVL---PEDQRGLIFLEGGKEQHQYTSD
Vocar20011350m.g|Vocar20011350m              1 ------------ 0------------------------------------------------------------- 0---------------------------------
NP_490843.1|                                 1 ------------ 0------------------------MTFQLSEKTF------KVPVDLF-TENRHRLVDA-- 27---LKS-----KVPANSVVLLQGGVEKNRYNTD
Esi0137_0095                                 1 ------------ 0------------------------------------------------------------- 0---------------------------------
gi|260593665                                 1 ------------ 0-------------M-----AAATGPSFWLGNETL------KVPLALF-ALNRQRLCER-- 33---LRKNP---AVQAGSIVVLQGGEETQRYCTD
gi|149589008                                 1 ------------ 0-------------M-----AAATGPSFWLGNETL------KVPLALF-ALNRQRLCER-- 33---LRKNP---AVQAGSIVVLQGGEETQRYCTD
gi|260593663                                 1 ------------ 0-------------M-----AAATGPSFWLGNETL------KVPLALF-ALNRQRLCER-- 33---LRKNP---AVQAGSIVVLQGGEETQRYCTD
gi|164425919                                 1 ------------ 0-------------------------MTTTAA--------RMDFE-TTLKGKYPAKRH 23AQRVADYIRNKMPGASGVLYLEGRATKLLEDND
Glyma01g37350|Glyma01g37350.1                1 ------------ 0------------------------------------------------------------- 0---------------------------------
Eucgr.C03941|Eucgr.C03941.1                  9 NIFR-PSIFPGT 19LGRAAIATKPLPPM-----APSPSPSSSLSPPPV--------PMELH-VRNRDKLLKS-- 63---LRQSLRDAGRPLHGFVFLQGGGEQARHDT
Phpat.022G059200|Phpat.022G059200.1          1 ------------ 0----------------------M------EVSMELH-AVNRKKLLSR-- 18---MSDQVKSMGQPVNGVILLQGGDECTRYCTD
80851|80851                                  1 ------------ 0------------------MARHRPPSF------SMLREMH-VHNRKKLQNA-- 26---MAEKLKSIGQRLAGVVLLQGGEERYRDCTD
Glyma08g03391|Glyma08g03391.1                1 ------------ 0---------------------------------MRDE-QRCRWSFMSK-- 14-TGRSSSLPFVNTCPSLLVLLQDGEEQTRYDTD
GRMZM2G021110|GRMZM2G021110_T01              1 ------------ 0-------------------MAASPTSSLAPPVV--------PMELH-AGNRDRLVAA-- 29---LRGHISASARPLHGLVLLQGGEEKTRYCTD
LOC_Os02g13140|LOC_Os02g13140.1              1 ------------ 0-------------MAAA-AAAAPPSSSSLAPPEV--------PMELH-AGNRDRLVAA-- 35---LRAHLSASGRPLRGLVLLQGGEEQTRYCTD
Glyma05g36260|Glyma05g36260.1                1 ------------ 0---------------------------MRDEHPKL--------WMELH-VKNREKLLTS-- 23---LRQHLSDSSRSLHGFVLLQGGEEQTRYDTD
Medtr8g101720|Medtr8g101720.1                1 ------------ 0------------------------------------------------------------- 0---------------------------------
Cucsa.397160|Cucsa.397160.1                  1 ------------ 0-----------------------MALPSLLTPPPV--------PVELY-VTNRQKLLNS-- 27---FRQHLSDSSRPLQGIVLLQGGDERTRYDTD
Bra011117|Bra011117                          1 ------------ 0----------------------------MSALTPPPV--------PMELH-AVNRRKLCDS-- 24---LRRHLSSSDRPLDGFVLLQGGEEKNRYCTD
AT4G29490                                    1 ------------ 0----------------------------MSSLSPPPI--------PMELH-AGNRKKLLES-- 24---IRRQLSSSNRSLDGFVLLQGGEEKNRYCTD
Carubv10007150m.g|Carubv10007150m            1 ------------ 0----TTKSVPVPLAGKN-KKLIPIVMSSLTPPPI--------PMELH-AGNRKKLVDS-- 44---IRRHLSSSNRSLDGFVLLQGGEEKNRYCTD
Eucgr.C03666|Eucgr.C03666.1                  1 ------------ 0-------------MAPP-SAAAPPAPSSLSPPLV--------PMELH-VRNRDKLLKS-- 35---LRQSLRDAGRPLHGFVILQGGEEQARHDTD
GSVIVG01015237001|GSVIVT01015237001          1 ------------ 0-------------MESH-REANSMASSSLTPPEV--------PMELH-AINRGKLVKS-- 35---LLQHLTESTHPLHGFVLLQGGEEQTRHDTD
29912.t000128|29912.m005402                  1 ------------ 0----------------------MASTSSLTPPKV--------PMELH-VTNREKLLKS-- 27---LRQHLTETSRPLHGFVLLQGGEEQTRHCTD
Potri.006G149500|Potri.006G149500.1          1 ------------ 0----------------------MASSSRLPPPKV--------PMELH-AKNREKLLKS-- 27---LRQHLTETSRPLHGFVFLQGGEEKTRYCTD
```

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27490.t000003|27490.m000041                       55 --------------------------- 54-----ANLTYFTGTKWHASERMVGAILPAQGAV------------------EYIAPAFE 90ESTLKDFMLVDGAVNCW
Phpat.1Z035600|Phpat.1Z035600.1                   25 --------------------------- 24-----QNRRYLTNFTGT-----YGVVLISQDQAK-------------LLTDFRYTAQA-- 59QAQAADFEI-----VFL
gi|392884626                                      57 DVPHAF--------------------- 62--RQKSHFRYLNGITTP---DCYYIMQSGI--------------SESSKETNILFA---- 99DRRSAYDELWEGALPTE
gi|530420285                                     109 NDIPYTF-------------------- 115--HQDNNFLYLCGFQEP---DSILVLQSLP-------------GKQLPSHKAILFV---- 153PRRDPSRELWDGPR
gi|11559925                                      109 NDIPYTF-------------------- 115--HQDNNFLYLCGFQEP---DSILVLQSLP-------------GKQLPSHKAILFV---- 153PRRDPSRELWDGPR
gi|530420287                                     109 NDIPYTF-------------------- 115--HQDNNFLYLCGFQEP---DSILVLQSLP-------------GKQLPSHKAILFV---- 153PRRDPSRELWDGPR
YER078C                                           99 GAVFYPF-------------------- 105--QQENDLFYLSGWNEP---NSVMILEKPT-------------DSLSDTIFHMLV---- 142PPKDAFAEKWEGFR
gi|85089070                                       66 AVFFPF--------------------- 71--RQDSNFLYLTGFSEP---DSLAIIQKTG--------------PKPGDYVFHLFC---- 108RPKDPRAEQWSGPWSG
CMA107C|CMA107CT                                 167 FYSMDVPHRY----------------- 176--RQHTDFLYFTGCLEP---QAALVVYKPRSAAVDASAIEPGPQPDALQAEFLLFV---- 227RARDASRELWD
Cre01.g046150|Cre01.g046150.t1.3                 111 AGVIPWPY------------------- 118--RQDPDFYYLTGLLQH---GL-AVITAARTHGAEIS------GGGGGGGKFVLFI---- 162DAPNAQRAKWDGA
Vocar20008388m.g|Vocar20008388m                  110 SGVIPWPY------------------- 117--RQDPDFFYLTGLMQH---GL-AVLTAPAPGKASIQ------T------HVSLLG---- 155YPSPNQRERWDGA
gi|66812452                                      117 MSYDIPWSF------------------ 125--RQNTNFNYLTGFNEP---EAVLVLVKTS-----------------ELDHQSYLFV---- 160RERNEEKEKWDG
89300|89300                                       56 IIPYPY--------------------- 61--RPDSDYLYYTGCQQP---GGIAVIKANG--------------------DLCMFV---- 92SDPDPERSVWDGTLADK
Phpat.012G034000|Phpat.012G034000.1              125 MTDVVPYPF------------------ 133--RQDADYLYYTGSQQP---EGIAVLYDDA---------------------DLCMFM---- 164PNWDPERETWNG
GRMZM2G135045|GRMZM2G135045_T01                   93 DVVPYPF-------------------- 99--RQNGDYLYITGCTQP---GGVAVLSEET--------------------GFCMFM---- 130PDTNKEDLVWQGETA
LOC_Os12g37640|LOC_Os12g37640.1                   96 DVVPYSF-------------------- 102--RQNGDYLYITGCAQP---GGVAVLSEET---------------------GLCMFM---- 133PDTSKEDVVWQGQT
PGSC0003DMG400002792|PGSC0003DMT40000722          89 DVVPYNF-------------------- 95--RQDADYLYITGCQQP---GGVAVLGHDC--------------------GLCMFM---- 126PEPSLQDVLWQGEVA
Bra030767|Bra030767                               86 DVVPYTF-------------------- 92--RQEADYLYLTGCQQP---GGVAVLSSEH--------------------GLCMFM---- 123PEPTPNDIAWQGEVA
AT1G09300                                         86 DVVPYTF-------------------- 92--RQDADYLYLTGCQQP---GGVAVLSDER--------------------GLCMFM---- 123PESTPKDIAWEGEVA
Carubv10009008m.g|Carubv10009008m                 86 DVVPYTF-------------------- 92--RQEADYLYLTGCQQP---GGVAVLSSDR--------------------GLCMFM---- 123PESTPNDVAWQGEVA
Cucsa.090530|Cucsa.090530.1                       86 DVVPYTF-------------------- 92--RQDADYLYVTGCLQP---GGLAVLSHDF--------------------GLCMFM---- 123PETKPYDVLWNGKIA
Eucgr.B01688|Eucgr.B01688.1                       60 VVPYTF--------------------- 65--RQDADYSYITGCQQP---GGIAVLGHEC--------------------GLCMFM---- 96PEATPQDVLWQGYVAGV
Eucgr.L00254|Eucgr.L00254.1                       88 DVVPYTF-------------------- 94--RQDADYSYITGCQQP---GGIAVLGHEC--------------------GLCMFM---- 125PEATPQDVLWQGYVA
GSVIVG01031262001|GSVIVT01031262001               86 DVVPYTF-------------------- 92--RQDADYSYLTGCQQP---GGIAVLGHEC--------------------GLCMFM---- 123PESHPHDVIWQGQIA
Glyma10g28690|Glyma10g28690.1                     87 DVVPYTF-------------------- 93--RQDADYLYITGCQQP---GGVAILGHDC--------------------GLCMFM---- 124PEAKPNDVIWQGQIA
Glyma20g22820|Glyma20g22820.1                     87 DVVPYTF-------------------- 93--RQDADYLYITGCQQP---GGVAVLGHDC--------------------GLCMFM---- 124PEAKPNDVIWQGQIA
Glyma20g22820|Glyma20g22820.2                     87 DVVPYTF-------------------- 93--RQDADYLYITGCQQP---GGVAVLGHDC--------------------GLCMFM---- 124PEAKPNDVIWQGQIA
30128.t000390|30128.m008929                       86 SVVPYTY-------------------- 92--RQDADYLYITGCQQP---GGVAVLGHDC--------------------GLCMFM---- 123PEATKHDIIWQGQVA
Potri.013G007100|Potri.013G007100.1               87 DVVPYTF-------------------- 93--RQDADYLYITGCQQP---GGVAVLGHEC--------------------GLCMFM---- 124PEATRHDVIWQGEVA
Cre02.g083065|Cre02.g083065.t1.2                 113 SDV-FHRH------------------- 119--RSHSHFVYVTGCMAP---GYGALIDAET---------------------GHFTLLA---- 151PRLPEEAAYWVGA
Vocar20010463m.g|Vocar20010463m                    1 -MHRH---------------------- 4--RSNSYFVYVTGVELP---GFAALLEPES----------------GHFTLLA---- 36PRLPEEAAYWVGAVPTLEQ
gi|164428892                                      71 Q-GPPF--------------------- 75--RQQRHFFYLSGADFP---GCAVTYDIPR-----------------QELILWI---- 107RRNDPRLSLWYGTTPS
gi|66825133                                       82 H-EPLF--------------------- 86--KQERYFFWTFGSDIP---DCFGIVGLDE----------------QATSILCI---- 119PKLPAEYATWMGEIRS
Cre07.g342920|Cre07.g342920.t1.2                  73 G-EPLF--------------------- 77--RQEAYMHYLFGVQEN---DWFGALCVKT-----------------GKSYLFA---- 109PRLPDSYAVWMGKLKS
Vocar20011350m.g|Vocar20011350m                    1 --------------------------- 0-------MHYLFGVQEA---DWFGALCVKT-------------------GRSLLFM---- 27PRLPESYAVWMGRLKGPDE
NP_490843.1|                                      53 AADLPF--------------------- 58--RQESYFFWTFGVNES---EFYGAIDVRS-------------------GGKTTLFA---- 91PRLDPSYAIWDGKINNE
Esi0137_0095                                       1 --------------------------- 0------------------------------------------------------------------- 0---------------
gi|260593665                                      61 T-GVLF--------------------- 65--RQ---------------------------------------------------------- 67---------------
gi|149589008                                      61 T-GVLF--------------------- 65--RQESFFHWAFGVTEP---GCYGVIDVDT-------------------GKSTLFV---- 97PRLPASHATWMGKIHSK
gi|260593663                                      61 T-GVLF--------------------- 65--RQESFFHWAFGVTEP---GCYGVIDVDT-------------------GKSTLFV---- 97PRLPASHATWMGKIHSK
gi|164425919                                      57 E-AEPF--------------------- 61--RQRRYFYYLTGCPLA---DCHYMYDLDA-------------------DKSTLFI---- 93PPIDPDSVIWSGLPVSV
Glyma01g37350|Glyma01g37350.1                      1 --------------------------- 0------------------------------------------------------------------- 0---------------
Eucgr.C03941|Eucgr.C03941.1                       93 DH-TELF-------------------- 98--RCVVVSAIWFG*------------------------------------------------ 109---------------
Phpat.022G059200|Phpat.022G059200.1               49 H-TPLF--------------------- 53--RQESYFAYLFGVKEP---GFFGTLDLSN-------------------GKSALYC---- 85PRLDPEYAVWLGEIQPP
80851|80851                                       57 H-LELF--------------------- 61--RQESFFAYLFGVREP---GFYAAIDIAT-------------------GQSILFV---- 93PRLDPDYAVWLGEIHPP
Glyma08g03391|Glyma08g03391.1                     47 H-LKLFMYPNPEPRHFNLSIPNSICFA 72LRGQESFFAYFFGVIEP---GFYAAIDVAT-------------------GNSILFA---- 106PRLPSEYAVWLGVIKP
GRMZM2G021110|GRMZM2G021110_T01                   60 H-LELF--------------------- 64--RQESYFAYLFGVQEP---GFYGAIDIAS-------------------GQSILFA---- 96PRLPADYAVWMGEIKPL
LOC_Os02g13140|LOC_Os02g13140.1                   66 H-LELF--------------------- 70--RQESYFAYLFGVREP---GFYGAIDIVS-------------------GQSILFS---- 102PRLPADYAVWMGEIKP
Glyma05g36260|Glyma05g36260.1                     54 H-LELF--------------------- 58--RQESYFAYLFGVIEP---GFYAAIDVAT-------------------GNSILFA---- 90PRLPSEYAVWLGEIKPL
Medtr8g101720|Medtr8g101720.1                      1 --------------------------- 0------------------------------------------------------------------- 0---------------
Cucsa.397160|Cucsa.397160.1                       58 H-LELF--------------------- 62--RQESYFAYLFGVIEP---GFYGAIDIAS-------------------GKSILFA---- 94PKLPPDYAVWSGEIKPL
Bra011117|Bra011117                               55 H-AELF--------------------- 59--RQESYFAYLFGVREP---DFYGAIDVGS-------------------GKSIIFI---- 91PRLPEDYAVWLGEIKPL
AT4G29490                                         55 H-TELF--------------------- 59--RQESYFAYLFGVREP---DFYGAIDIGS-------------------GKSILFI---- 91PRLPDDYAVWLGEIKPL
Carubv10007150m.g|Carubv10007150m                 75 H-AELF--------------------- 79--RQESYFAYLFGVREP---DFYGAIDIGS-------------------GKSILFI---- 111PRLPDDYAVWLGEIKP
Eucgr.C03666|Eucgr.C03666.1                       66 H-TELF--------------------- 70--RQESYFAYLFGVIEP---GFFGAIDITS-------------------GNSLFFV---- 102PRLPSEYAVWLGEIKP
GSVIVG01015237001|GSVIVT01015237001               66 H-AELF--------------------- 70--RQESYFAYLFGVREP---GFYGAIDIAT-------------------GKSILFA---- 102PRLPAEYAVWLGEIKP
29912.t000128|29912.m005402                       58 H-LELF--------------------- 62--RQESYFAYLFGVKEP---GFYGAIDVAT-------------------GKSILFA---- 94PRLLADYAVWLGEIKPL
Potri.006G149500|Potri.006G149500.1               58 H-IELF--------------------- 62--RQESYFAYLFGVKEP---GFYGAIDIAT-------------------GKSILFA---- 94PRLPADYAVWLGEIKPS

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Phpat.1Z035600|Phpat.1Z035600.1                   72 AAKESVYS-EVARIAEEMGITK-------------------LG 94FEEDNLTY---------------SLHRKYA------------EVVKGELVA-TAGVIE 124
gi|392884626                                     117 SEWEKTAKFTECVPTSRIL-QTLEKVCD--K---GTAVF--FD 151STS-------------------DDLLYKF---------------VQAKANSVREINHFIE 17
gi|530420285                                     168 SGTDGAIALTGVDEAYTLEEFQ-HLLPKMKA--E---TNMVW--YD 205WMRPSH-----------------AQLHSDYMQP-------LTEAKAKSKNKVRGVQQLIQ
gi|11559925                                      168 SGTDGAIALTGVDEAYTLEEFQ-HLLPKMKA--E---TNMVW--YD 205WMRPSH-----------------AQLHSDYMQP-------LTEAKAKSKNKVRGVQQLIQ
gi|530420287                                     168 SGTDGAIALTGVDEAYTLEEFQ-HLLPKMKA--E---TNMVW--YD 205WMRPSH-----------------AQLHSDYMQP-------LTEAKAKSKNKVRGVQQLIQ
YER078C                                          157 SGVYGVQEIFNADESASLNDLS-KYLPKMIN--R---NDFIY--FD 194MLSTSNPSSS-----------NFKHIKSLLDGSGNSN---RSLNSIANKTIKPISKRIA
gi|85089070                                      125 LQAAEDVFNADFTGDIAKVE-TLLPPILR--G---AGKVY--TD 160ITPSTPVTGQ------------------------LV---TTLLSHLHLPPAPLAGLVH 1
CMA107C|CMA107CT                                 239 GPMIGIEDAPAMFGIPNVYPVERLG-ALVAEIMHGG------------ 273-----EPTPPSLFFDAN-VNSEFTKRVGTALAPDKSMESAAGAAWQSFASRLCSPVP
Cre01.g046150|Cre01.g046150.t1.3                 176 TLSREVAAAEFGADEVAYMHEMP-RRLAALASAAA---SSSST--SS 216SSSSSSSTTPLLLFDSDRVGGHHYSTLMALLKP----------ALETPGRIAPLRPLL
Vocar20008388m.g|Vocar20008388m                  169 SIGREAALRIFGADEVYWMHEMP-RKLQELVKS------------- 200-------SEPILYDTDRVGAYHHSALTVALRP----------ALEQPGRVAPLRPLL
gi|66812452                                      173 ARCGGENVKKYFGIDFGYNLTNRDIPILGKLLKSTT---DGKLY--CN 215TTP----------------WNQLSNKLEPFLE-------------N---IKFYTVESL
89300|89300                                      110 EAALSVFHANETYTIAEIP-KYFGEMVK--Y---ASGVY--CN 144ENI-----------------LSPTFRKVSKIQE-----------AFEQNKLRSLSPHSS 17
Phpat.012G034000|Phpat.012G034000.1              177 KLAGPDEASRVFGADVTHSLRRLR-KVLPDIIR--R---AKTVF--CD 216LGS--------------LTPVVAELEAFQS----------ALQQGRVRSLNRY
GRMZM2G135045|GRMZM2G135045_T01                  146 GVEAAVDFFKADKAFPLSQMQ-KILPELIE--Q---SKGVY--HN 182VNT-----------------T-SSYKNLDAFRR-------------ASLNNKVKDLTNYTD
LOC_Os12g37640|LOC_Os12g37640.1                  148 AGVEAAENFFKADKAFPLSEMQ-KILPEMIE--R---SKVVY--HN 185VKT-----------------LSPSYKNLDSFRR-------------ASLNNKVKDLAYYTD
PGSC0003DMG400002792|PGSC0003DMT40000722         142 GVDAALDIFKADLAYPISRLP-EMLSRMIE--S---SSIVF--HN 178VKT----------------TTSSYMELEAYRK------------AVNNCKVKDFSVYTH
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Vocar20010463m.g|Vocar20010463m                   56 LQEQYGADRVVYLDELK-GLLAAA-------GASTLHTLPG 88C-AEKLTGKIPP--------------------------------GCHVLTDLLPATLD 113RC
gi|164428892                                     124 IDESKSKSDVSDVRYIDGLT-AYLHAVLTPENGGGGGPLYVLSP 166DQLPKLS-PSPP----------QYS---FFKGMH--------GSASRGLKIDTTSLLPAIE 2
gi|66825133                                      136 KEYYKSIFLVDQVLYVDEMM-DYL---KSKNA----STIYTILG 171TNTDSGSTFVEP----------Q------YPG-----------LRETFNVNNTLLFPEIA 2
Cre07.g342920|Cre07.g342920.t1.2                 126 LEEWRAKYGVDAVHWVDEMA-DVI---RGLQP----PCLHVLHG 161KNTDSGLDVLPP----------A------AP-----------PP-GIPLEQQHLFPALT 1
Vocar20011350m.g|Vocar20011350m                   47 FKAKYGVDAVHYVDEMS-EVL---RGLAP----PCLHVLHG 79VNTDSGLQVPHP----------A------AP-----------NT-GIPLDMDTLFDIIT 110EH
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Esi0137_0095                                       1 ----------------------------------------- 0------------------------------------------------------------------ 0------
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Carubv10007150m.g|Carubv10007150m                128 LSHFKETYMVDMVFYVDEII-QVFNEQFKGSG--N-PLLYLLHG 167LNTDSSNFSKPA----------S------FEG-----------IE-KFETDLTTLHPILA 1
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Potri.006G149500|Potri.006G149500.1              112 SCFQQQYMVSMVYYTDEIV-GVLHELSNVLE--K-PLLFLLHG 150LNTDSNNFSKPA----------E------FEG-----------IE-KFEKDLTTLHPILT 18
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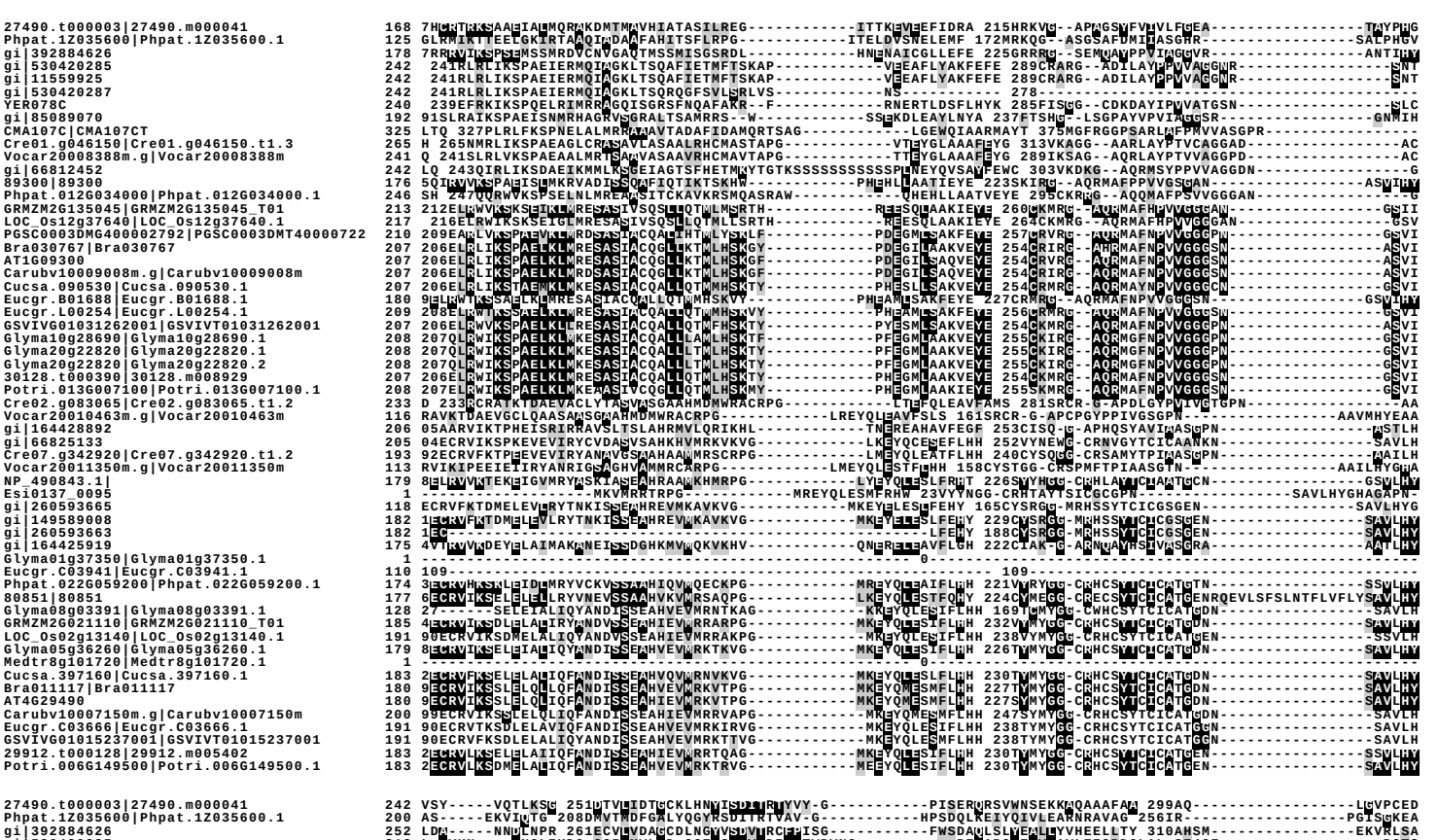
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Phpat.1Z035600|Phpat.1Z035600.1              267 DAFARDFIAEKGYGER---------------- 282---------FG-HGMGHGVGLDIHEEPFMSTRC---------------TAILQPGMNRE- 316---SILPEI-
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gi|530420285                                 381 LENIYSMMLTLIGQKLKDLGIMK------NIKENNA 410---FKAFIFQRMLKMPQRSFGVLVYELRMM------------------------- 437------
gi|11559925                                  381 LENIYSMMLTLIGQKLKDLGIMK------NIKENNA 410---FKAARKYCPHHV-GHYLGMDVHDTPDMPRSL----------------PLQPGMVITI 450EPGLYI
gi|530420287                                 279 ---------------------------------- 278------------------------------------------------------------- 278------
YER078C                                      379 LHDIHEKSITLMKQELKNLGIDK------VS----- 403---GWNVEKLYP-HYIGHNLGLDVHDVPKVSRYE----------------PLKVGQVITI 443EPGLYI
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CMA107C|CMA107CT                             484 AASLEHLHRVCVRMIAENLYELGFFG------RRHRVDE 516IIERGLYGRYFP-HALGHYLGMDTHDTHQLSKAI-----------------PFRAGMVITV 559EPG
Cre01.g046150|Cre01.g046150.t1.3             415 SIRDLHHLCIDVLSQGIRDLGLRP------GASLAE- 444-IRGSMYRDYFW-HSLGHYLGLDTHDTHLVGHDR-----------------PLAPGAVITV 486EPGLY
Vocar20008388m.g|Vocar20008388m              380 SIRELHALSIDILSEGLLDLKLLP------RASLAE- 409-IRNHLYRDFYW-HSLGHYLGLDTHDTPLIGHDR-----------------QLEPGTLITV 451EPGLY
gi|66812452                                  393 ETLNSIHLKSVELIQAHLKRLGIIN------ESNP--- 421----NDYRLYYP-HSIGHYLGMDTHDTLDFDYGV-----------------TLEPGMIITI 460EPGI
89300|89300                                  318 IHSHSMQLLSKALIGLGIKG------QGHS--- 341--P-PDVGKFNP-TAIGHYLGMDVHDSGGVSRGE-----------------SLRPGMVLAI 381EPGLYFPKD
Phpat.012G034000|Phpat.012G034000.1          385 VTLSQIHSRSVALLWEGLLKLGLVT------GPFD--- 413--LFK-FYSFNR-TQIGHYLGMDVHDCSTVSLDR-----------------PLQPGVVITI 453EPGL
GRMZM2G135045|GRMZM2G135045_T01              353 NEIHNHSVKLLIKGFQELRILE------KGKS--- 378--I--QYNYLNP-TAIGHSLGMDIHDSMTLPKDK-----------------PLEPGVVITI 417EPGVYIP
LOC_Os12g37640|LOC_Os12g37640.1              356 INEIHNHSVKMLIKGFQELGILE------KGKS--- 382--I--QYNYLNP-TAIGHSLGMDIHDSVKLSKDK-----------------PLEPGVIITI 421EPGVYI
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Eucgr.B01688|Eucgr.B01688.1                  322 IHKYSVDMLCKGFKEIGLLK------DDRS--- 345--ILHSYHQLNP-TSIGHYLGMDVHDCSTINYDR-----------------PLKPGVVITI 386EPGVYIPYN
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GSVIVG01031262001|GSVIVT01031262001          347 RQIHHYSAEKLLHGLKELGILK------DSRN--- 372--IYHSYHQLNP-TNIGHYLGMDVHDCHSLGDDQ-----------------PLKPGVVITI 413EPGIYIP
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gi|164428892                                 324 -L---------AAMYREAM--------------- 332---------------------MDRDDVEQNVVGPP---------PPYKGRQRLRENMVVTI 363EPGIYFHR
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Medtr8g101720|Medtr8g101720.1                  1 ------------------- 0MVTSNLGPIFMP-HGLGHLLGIDTHDPGGYPKGLE-RRKEPGLKALRTARVLQEGMVITV 58EPGCYFIDALLL-PAMNNPEISKFF
Cucsa.397160|Cucsa.397160.1                  330 MHKLAEKILLESLIEGSVLV--------GDVMD 354MMAARLGAVFMP-HGLGHFLGIDTHDPGGFLQGLG-RPEEPGLSSLRTVRDLKEGMVITV 412EPGCYFIDA
Bra011117|Bra011117                          327 MHKLAERIILESLKKGSILT--------GDVEE 351MMLERLGAVFMP-HGLGHFMGIDTHDTGGYPLGVE-RPKEPGLKSLRTARDLLEGMVITV 409EPGCYFIKA
AT4G29490                                    327 MHKLAEKIILESLKKGSILT--------GDVDD 351MMVQRLGAVFMP-HGLGHFMGIDTHDTGGYPKGVE-RPKKPGLKSLRTARDLLEGMVITV 409EPGCYFIKA
Carubv10007150m.g|Carubv10007150m            346 DMHKLAERIILESLKKGSILT--------GDVDD 371MMVQRLGAIFMP-HGLGHFMGIDTHDTGGYPKGVE-RPKEPGLKSLRTARDLLEGMVITV 429EPGCYFIK
Eucgr.C03666|Eucgr.C03666.1                  337 DMHKLAERTILQSLREGNILF--------GDLDH 362MMVERLGAAFMP-HGLGHLLGIDTHDPGGYLQGLE-RPKEPGLSSLRTVRELLEGMVITV 420EPGCYFID
GSVIVG01015237001|GSVIVT01015237001          337 DMHKLAEKLILDSLKKGCIVV--------GDVDD 362MMVKRLGAVFMP-HGLGHFLGIDTHDTGGYLEGLE-RPKEPGLKSLRTVRDLQEGMVITV 420EPGCYFID
29912.t000128|29912.m005402                  330 MHKLAERTIIESLKRGLILV--------GDVDD 354MMTERLGAVFMP-HGLGHFLGIDTHDPGGYLKGPK-RSKEPGLRSLRTARELQEGMVITV 412EPGCYFIDA
Potri.006G149500|Potri.006G149500.1          330 MHKLAEQVILESLKNGCIIV--------GNVDD 354MMIERLGAVFMP-HGLGHFLGIDTHDPGGYLKGLE-KLKGPGLKALRTIRELQEGMVITV 412EPGCYFIDA

27490.t000003|27490.m000041                  375 ----------------------------FGVRHEDHFYMTENG--PK--- 391-----------------------WFT---EPAHSIDD-PFGLQR----------
Phpat.1Z035600|Phpat.1Z035600.1              323 ---------------------------GGVRVEDDLVVTEVG--NE--- 339----------------------VLT---HSPRDLIV-L*-------------
gi|392884626                                 398 -------------WPV-----KEF--RGI-GYRIEDDVATSEAG-GIE--- 423-----------------------LLT--AAVPRDPIE-IQRLMGTAE-------
gi|530420285                                 438 ----------------------------------------------- 437-------------------------------------------------------
gi|11559925                                  457 PED----------------DKDAPEKF--RGL-GVRIEDDVVVTQDS--PL--- 486------------------------ILS--ADCPKEMND-IEQICSQAS----
gi|530420287                                 279 ----------------------------------------------- 278-------------------------------------------------------
YER078C                                      450 PNE-----------------ESFPSYF--RNV-GIRIEDDIAIGEDT--YT--- 478-----------------------NLT--VEAVKEIDD-LENVMQNGLSTKF
gi|85089070                                  406 D----------------DDRFPEHF--RGL-AVRIEDSVVVDVES--PL--- 433----------------------ILT--TEAVKEVVD-IEALRE---------
CMA107C|CMA107CT                             563 VYVPVA---------------DGDAPAAF--RGL-GMRIEDDVVIRPGGAAPE--- 597----------------------ILS--AGIPLQARD-IEAVMREIAT
Cre01.g046150|Cre01.g046150.t1.3             492 IPDD------------PRY-----GPL--AGL-GVRLEDDVLVTAAG--AQ--- 520-----------------------VLS--DQAPVAIEE-VEELAGSAVEAA
Vocar20008388m.g|Vocar20008388m              457 IPDL------------PQF-----GVF--RGI-GVRIEDDVLVTSSG--CR--- 485-----------------------VLS--DQVGHCNCT-AS--YGIVRD*--
gi|66812452                                  465 YISKY---------------DSNVPEKY--RGL-SIRVEDDVVIPNLNNSPL--- 498-----------------------VLT--HLAPKEISE-IESIMSNK---
89300|89300                                  391 ----------------ADVPDRY--RGI-GIRIEDEVLITDSG--YE--- 416-----------------------VII--CFLACGSKL-----------
Phpat.012G034000|Phpat.012G034000.1          458 YIPAK----------------QTIPEKF--RGI-GIRIEDEVLITATG--YE--- 488-----------------------ILT--AEAPKEIEE-IEQFLAQSPND
GRMZM2G135045|GRMZM2G135045_T01              425 AA-------------PVLNERAPSRY--RGM-GIRIEDEVLITDDG--HE--- 456-----------------------VLT--ASVPKEVSH-LTTLMNMGRGGSAA
LOC_Os12g37640|LOC_Os12g37640.1              428 PPV-------------PILKENAPDRY--RGI-GIRIEDEVLITESG--HE--- 460-----------------------VLT--ASVPKEISH-ITTLMNMGSNS--
PGSC0003DMG400002792|PGSC0003DMT40000722     301 ----------------------------------------------- 300-------------------------------------------------------
Bra030767|Bra030767                          417 SS-----------------FNCPERF--QGI-GIRIEDEVLITETG--YE--- 444-----------------------VLT--GSMPKEIKH-IETLLNNHCHENAA
AT1G09300                                    417 SS-----------------FDCPERF--QGI-GIRIEDDVLITETG--YE--- 444-----------------------VLT--GSMPKEIKH-IETLLNNHCHDNSA
Carubv10009008m.g|Carubv10009008m            417 SS-----------------FDCPERF--QGI-GIRIEDEVLITETG--YE--- 444-----------------------VLT--GSMPKEIKH-IETLLNNHCHGNAA
Cucsa.090530|Cucsa.090530.1                  419 SI-----------------FQGPQRF--AGI-GIRIEDEVLITESG--YE--- 446-----------------------VLT--GSIPKEINQ-IESLLNNFCFGSTM
Eucgr.B01688|Eucgr.B01688.1                  396 -----------------LNCPEWY--QGI-GIRIEDDVLITDTG--YE--- 421-----------------------VLT--GSMPKEVKH-ITALLNDCNMAEQAES
Eucgr.L00254|Eucgr.L00254.1                  423 YT-----------------LNCPEWY--QGI-GIRIEDDVLITDTG--YE--- 450-----------------------VLT--GSMPKEVKH-ITALLNDCNMAEQA
GSVIVG01031262001|GSVIVT01031262001          421 SF-----------------FDGPERF--RGI-GIRIEDEVLITETG--YE--- 448-----------------------VLT--GSMPKEVKH-IETLLNNFCHGVNT
Glyma10g28690|Glyma10g28690.1                420 SS-----------------FNVPERY--RGI-GIRIEDEVLITETG--YE--- 447-----------------------VLT--ASIPKEVKH-IESLLNNFGQLKSL
Glyma20g22820|Glyma20g22820.1                420 SS-----------------FNVPERY--RGI-GIRIEDEVLITETG--YE--- 447-----------------------VLT--ASIPKEVKH-IESLLNNFCHGMGA
Glyma20g22820|Glyma20g22820.2                420 SS-----------------FNVPES*------------------------- 427-------------------------------------------------------
30128.t000390|30128.m008929                  419 ST-----------------FDVPERY--QGI-GIRIEDEVLITETG--YE--- 446-----------------------VLT--DSMPKEVRH-IESLLNNYSHKGGM
Potri.013G007100|Potri.013G007100.1          420 SI-----------------FDGPDRY--RGI-GIRIEDEVLITETG--YE--- 447-----------------------VLT--GSMPKEVKH-IESLLNNYSCGNGM
Cre02.g083065|Cre02.g083065.t1.2             462 LIPPLLA-KARADPKVAPFINFDLAESLAAGGLGGVRIEDNVLLLDGS--KGARA 513GAGTGAGAGVSGGVSGAGVQGRLFNLTVAAGCAKEMRE-VEDVMAEEWRPA
Vocar20010463m.g|Vocar20010463m              360 -RARNDPGVAPFLDFDAAEALVRCGLGGVRIEDNVVVLAEA--PPPAA 404----------LAAAPPLGLQGRLYNLTVAAGVAKEMAE-VEEVMRQEWRPEAAML*--
gi|164428892                                 372 PYIQSFFLSNPDHAKYINTKVLDKY--WDIGGVRIEDCILVTKDG--YE--- 416-----------------------NLT---TAPKGKEA-LKIINAGIPGFGGDG
gi|66825133                                  439 HLLT-QALSNPETAKFFNLTELDKY--RNIGGVRIEDDILVTETG--CD--- 482-----------------------NLS--KNLPRTIDE-IEAFMLK--------
Cre07.g342920|Cre07.g342920.t1.2             433 VLLL-PALEDPVQSKYLVRDVVMSY--LQLGGVRLEDNVVVTEGG--AE--- 476-----------------------SLT---RVPRSVEE-VERVMAGGDWPQ*--
Vocar20011350m.g|Vocar20011350m              356 -PALEDPDKAKYLVRDAVMSY--MSVGGVRLEDNVVVTETG--IE--- 395--------------------RLT---HVPRSPEE-VEAVMAGAPWP*-------
NP_490843.1|                                 419 LLN-EALADPKKSEFLVKSEIDKY--RGSGGVRIEDDVIIRASG--NE--- 461-----------------------NLS---DLPRTVEE-IENFMASGGEWTEKVI
Esi0137_0095                                 224 PEVAPFLVTSELARF--RGFGGVRLEDDVVVTADG--VR--- 258---------------------NLT---NCARTVED-VEAVMAGRITNRNQLFKKCYT 290
gi|260593665                                 358 LD-EALADPARASFLNREVLQRF--RGFGGVRIEEDVVVTDSG--IE--- 399-----------------------LLT---CVPRTVEE-IEACMAGCDKAFTPFSG
gi|149589008                                 421 LLD-EALADPARASFLNREVLQRF--RGFGGVRIEEDVVVTDSG--IE--- 463-----------------------LLT---CVPRTVEE-IEACMAGCDKAFTPFS
gi|260593663                                 380 LLD-EALADPARASFLNREVLQRF--RGFGGVRIEEDVVVTDSG--IE--- 422-----------------------LLT---CVPRTVEE-IEACMAGCDKAFTPFS
gi|164425919                                 407 IIE-PFLKDPKHSKYINADVLEKY--WDVGGVRIEDNLVITKDG--TY--- 449-----------------------NLT---TAPKDPEE-MEKIIQQS--------
Glyma01g37350|Glyma01g37350.1                145 VL----TAQHF--LCLHSSTINSFIHV---------- 165---------------------------------------------------------- 165----
Eucgr.C03941|Eucgr.C03941.1                  110 ----------------------------------------------- 109-------------------------------------------------------
Phpat.022G059200|Phpat.022G059200.1          413 LLV-PALEDPAQRNFFVEPALEVF--RHTGGVRLEDDILVTANG--QD--- 455-----------------------NWV---VKEVNNLGLLEQTVCYSMFKVL*--
80851|80851                                  433 VLD-PALEDPVLSRFLNREAIDKF--RGFGGVRLEDDVIVTSDG--CE--- 475-----------------------NLT---NCPREISD-VEDVMAGGPWPRT*--
Glyma08g03391|Glyma08g03391.1                207 ----------------------------------------------- 206-------------------------------------------------------
GRMZM2G021110|GRMZM2G021110_T01              424 LLT-KTRDDPISSKFFNWQEVEKY--KSFGGVRIESDVYVTAQG--CR--- 466-----------------------NLT---NCPRETWE-IEAVMAGAPWPLPASS
LOC_Os02g13140|LOC_Os02g13140.1              429 ALLI-PARDDPVSSKFFNWEEIEKY--KSFGGVRIESDVYVTAHG--CK--- 472-----------------------NLT---NCPRETWE-IEAVMAGAPWPVRAT
Glyma05g36260|Glyma05g36260.1                418 LLL-PAMNSPETSKFLNQEAINRF--KGFGGVRIESDVLVTATG--CY--- 460-----------------------NMT---KCPREMRE-IEAVMAGAPWPAQKI*
Medtr8g101720|Medtr8g101720.1                 83 NQEVISRF--TGFGGVRIESDVLVTAAG--CY--- 110-----------------------NMT---KCPREIHE-IEAVMAGGPWPVKKT*----- 136-------
Cucsa.397160|Cucsa.397160.1                  422 LLD-PALKNSKTSKFFNVEAVNKF--RGSGGVRIESDLLVTANG--CR--- 464-----------------------NMT---NCPRETWE-IEAVMAGSPWPIVSKS
Bra011117|Bra011117                          419 LLV-PAMENAKTSKFFNRETIERF--KNIGGVRIESDLVVTANG--CK--- 461-----------------------NMT---NVPRETWE-IEAVMAGGSWPPVATG
AT4G29490                                    419 LLF-PAMANATTSKFFNRETIERF--RNFGGVRIESDLVVTANG--CK--- 461-----------------------NMT---NVPRETWE-IEAVMAGGPWPPTK--
Carubv10007150m.g|Carubv10007150m            438 ALLI-PAMEKTTTSKFFNRETIERF--RNFGGVRIESDLVVTANG--CK--- 481-----------------------NMT---NVPRETWE-IEAVMAGGPWPLVTT
Eucgr.C03666|Eucgr.C03666.1                  429 ALLD-PAMESANTSKFFNHDVIGRF--RTFGGVRIESDVLVTATG--CK--- 472-----------------------NMT---NVPRQTCE-IEAVMAGAPWPPSK*
GSVIVG01015237001|GSVIVT01015237001          429 ALLA-PAMENSETSKFFNHEIIGRF--KSFGGVRIESDVHVTSNG--CK--- 472-----------------------NMT---NVPRETWE-IEAVMAGSPWPLDKS
29912.t000128|29912.m005402                  422 VLA-PAKEASSTSKFFNSEAIGRF--KGFGGVRIESDVHVTSNG--CN--- 464-----------------------NMT---KCPREIWE-IEAVMAGAPWPLNKVS
Potri.006G149500|Potri.006G149500.1          422 LLA-PAMESSNTAKFFDREAISRF--KGFGGVRIESDVHVTAGG--CQ--- 464-----------------------NMT---KCPRQISE-IEAVMAGSPWPLN*--
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27490.t000003|27490.m000041                409 ----- 408------------------------------------------------------------ 408
Phpat.1Z035600|Phpat.1Z035600.1            352 ---- 351------------------------------------------------------------ 351
gi|392884626                               445 ----- 444----------------------------------------------------------- 444
gi|530420285                               438 -------- 437------------------------------------------------------------ 437
gi|11559925                                508 -------- 507------------------------------------------------------------ 507
gi|530420287                               279 -------- 278------------------------------------------------------------ 278
YER078C                                    504 EEDQVAPL 511*------------------------------------------------------------ 511
gi|85089070                                452 ------ 451--------------------------------------------------------- 451
CMA107C|CMA107CT                           620 TSAHY------ 624------------------------------------------------------------- 624
Cre01.g046150|Cre01.g046150.t1.3           545 AAAEAAARA 553GGAQPRALPLPPRGPPAALWQMMYGRAAAAAAAEAVGLPGTGAAAGASAREQGAAAVS* 611
Vocar20008388m.g|Vocar20008388m            506 ---------- 505------------------------------------------------------------ 505
gi|66812452                                519 ---------- 518------------------------------------------------------------ 518
89300|89300                                429 ----- 428----------TLSRCPPRFFQRPFRKR*------------------------------ 445
Phpat.012G034000|Phpat.012G034000.1        512 NDLTEKPSLF 521----C*------------------------------------------------------ 522
GRMZM2G135045|GRMZM2G135045_T01            483 DAHGHEL 489----RAACS*------------------------------------------------- 494
LOC_Os12g37640|LOC_Os12g37640.1            484 -MMDAHEL 490----RAACS*------------------------------------------------ 495
PGSC0003DMG400002792|PGSC0003DMT40000722   301 ------- 300------------------------------------------------------------ 300
Bra030767|Bra030767                        471 QSFAGFS 477----S*----------------------------------------------------- 478
AT1G09300                                  471 RTSPVSL 477----CKVKGLHTNRNPRRLF--------------------------------------- 493
Carubv10009008m.g|Carubv10009008m          471 QSFANFS 477----S--QG*------------------------------------------------ 480
Cucsa.090530|Cucsa.090530.1                473 HGPKFMK 479----ASTC*------------------------------------------------ 483
Eucgr.B01688|Eucgr.B01688.1                450 WNSAR 454----DVSI*--------------------------------------------------- 458
Eucgr.L00254|Eucgr.L00254.1                477 ESWNSAR 483----DVSI*------------------------------------------------- 487
GSVIVG01031262001|GSVIVT01031262001        475 ENQNNMR 481----AASIS*------------------------------------------------ 486
Glyma10g28690|Glyma10g28690.1              474 *------- 473------------------------------------------------------------ 473
Glyma20g22820|Glyma20g22820.1              474 MDSQNN* 479----------------------------------------------------------- 479
Glyma20g22820|Glyma20g22820.2              428 ------- 427------------------------------------------------------------ 427
30128.t000390|30128.m008929               473 EKEDCMQ 479----VASSWQSH---------------------------------------------- 487
Potri.013G007100|Potri.013G007100.1        474 EAQNNLE 480----AASS*------------------------------------------------- 484
Cre02.g083065|Cre02.g083065.t1.2           564 EAMSRVVG* 571-------------------------------------------------------- 571
Vocar20010463m.g|Vocar20010463m            449 -- 448--------------------------------------------------------- 448
gi|164428892                               443 QA---- 444GGGSS------------------------------------------------------ 449
gi|66825133                                502 ------ 501----------------------------------------------------------- 501
Cre07.g342920|Cre07.g342920.t1.2           500 ------ 499----------------------------------------------------------- 499
Vocar20011350m.g|Vocar20011350m            418 -- 417--------------------------------------------------------- 417
NP_490843.1|                               489 ESRVS 493DFLSK------------------------------------------------------- 498
Esi0137_0095                               291 DA*------------------------------------------------------- 292
gi|260593665                               428 PK-- 429------------------------------------------------------------ 429
gi|149589008                               491 GPK-- 493----------------------------------------------------------- 493
gi|260593663                               450 GPK-- 452----------------------------------------------------------- 452
gi|164425919                               469 ----- 468----------------------------------------------------------- 468
Glyma01g37350|Glyma01g37350.1              166 ------------------------------------------------------ 165
Eucgr.C03941|Eucgr.C03941.1                110 ------- 109--------------------------------------------------------- 109
Phpat.022G059200|Phpat.022G059200.1        481 ----- 480----------------------------------------------------------- 480
80851|80851                                500 ----- 499----------------------------------------------------------- 499
Glyma08g03391|Glyma08g03391.1              207 ------ 206---------------------------------------------------------- 206
GRMZM2G021110|GRMZM2G021110_T01            494 SMVVA 498AENSND-ISKAS*----------------------------------------------- 509
LOC_Os02g13140|LOC_Os02g13140.1            499 NNSLSK 504AS*-------------------------------------------------------- 506
Glyma05g36260|Glyma05g36260.1              487 ----- 486----------------------------------------------------------- 486
Medtr8g101720|Medtr8g101720.1              137 ------------------------------------------------------ 136
Cucsa.397160|Cucsa.397160.1                492 ISI*- 494----------------------------------------------------------- 494
Bra011117|Bra011117                        489 NNTTK 493*----------------------------------------------------------- 493
AT4G29490                                  487 ----- 486----------------------------------------------------------- 486
Carubv10007150m.g|Carubv10007150m          508 ENNSTK 513*---------------------------------------------------------- 513
Eucgr.C03666|Eucgr.C03666.1                498 ------ 497----------------------------------------------------------- 497
GSVIVG01015237001|GSVIVT01015237001        499 SIHSEN 504GREGK*----------------------------------------------------- 509
29912.t000128|29912.m005402               492 ASS-- 494----------------------------------------------------------- 494
Potri.006G149500|Potri.006G149500.1        489 ----- 488----------------------------------------------------------- 488
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