```
gi|17532463                          1 ----------------------------------------WALASSNATS--MESLFG 16NPFRPKKERVVVEEKPFEYTPSAYVQMIDQMIGLKTRPWNPERTPIK
gi|56606061                          1 ----------------------------------------MAAAPNA---------- 8-------GGSAPETAGSAEAPLQYSLLLQYLVGDKRQPRLLEP---G-
gi|66810255                          1 ----------------------------------------MANISD---------- 6----------------EELKKILSDN-----AHKF----MFA----E
CMS209C|CMS209CT                     1 ----------------------------------------WSAGTSPVS--------- 9---------------RKSEEADVVTRL-----PL-----NLQFP-----
YDL217C                              1 ----------------MV-YTGFGL--------------EQISPAQ--------- 15----------------------KKPYN-----E-----LTPEEQ---
gi|164426913                         1 ----------------MVRCPRWGEPFT------ARRRRTRAWDAEGRPRG--------- 29----------------------ALPYP-----ESSFVAVVQEEEKEE
Esi0063_0018                         1 ----------------------------------------WPADDRRHG----ECC- 13-----NQQGPE----GLRSLHPQLGSR-----LPFFLPWVPRPAAGA
Cre01.g021050                        1 ----------------------------------------WGSTDEERVASSATAST- 17-----SSADPS-PPAPPPPVEKNKKKF-----DPI------------
Vocar20010161                        1 ----------------------------------------WSSADEERVASSASAST- 17-----SESGVQNPSAAATSPTKKKEW-----HPI------------
30209.t000032|30209.m001533          1 ----------------------------------------WGVNEI---------- 6---------NDSASSSKKEAGPEPTVL-----QLF------------
GRMZM2G357152                        1 ------------------------------------------------------- 0-------------------------------------------------
GRMZM2G007080                        1 ----------------------------------------WASPDP-SA-----AD-- 10-------------AGTGGESTSQAAAV-----EPI------------
LOC_Os03g18500                       1 ----------------------------------------MASPEP-AA--------- 8--------------GADGASASQTAVV-----EPL------------
Potri.001G281200                     1 ----------------------------------------MASNENPGS-----ESN- 12-----NNGGAA-SSSSTSKDGETHTQI-----QPF------------
Potri.009G076400                     1 ----------------------------------------MASNDNPGS-----ESN- 12-----INGGDAAASSSTSKVGETPTQI-----QPF------------
Carubv10010466                       1 ----------------------------------------MADSSA--A-----EP- 9---------T-GPTPSTVGSDENATQI-----QPL------------
AT3G10110                            1 ----------------------------------------MADSSA--A-----EP- 9---------TTGASSPPVASDENSTQI-----QPI------------
AT1g18320                            1 ----------------------------------------MADSSA--A-----EP- 9---------TTGASSPPVASDENSTQI-----QPI------------
Bra016560                            1 ----------------------------------------MPNDSS--A-----EP- 9---------AA----GSSGSNENVTKI-----EPI------------
Bra031026                            1 ----------------------------------------MADAN--A-----EP- 8---------AA----GSSSSNESVTQI-----EPI------------
Cucsa.151920                         1 PSSLLPSPTPSRPSPFSIFLSRSDSPFFFLSHFFISLLHSTSMASTSG--D------G-- 50---------SS--LDPPTSSDAQLPPI-----QPV------------
Eucgr.K02762                         1 ----------------------------------------MASNSA--S-----ET- 9---------AG--WDSSGLKEAEKPHL-----QPL------------
PGSC0003DMG402019636                 1 ----------------------------------------MSDPA--T-----E-- 7---------SN--DAQSSSEEVKKPQI-----EPI------------
GSVIVG01024670001                    1 ----------------------------------------WSSNSG--S-----E-- 8---------FT--WDSSSSTEAEKPQI-----EPI------------
Medtr4g077950                        1 ----------------------------------------MADESQ--K-----A-- 8---------VS--WDSVNSKEVEKPQI-----QPL------------
Medtr4g078050|Medtr4g078050.1        1 ----------------------------------------MADESQ--K-----A-- 8---------VS--WDSVNSKEVEKPQI-----QPL------------
Glyma09g35780                        1 ----------------------------------------MADDSA--K-----G-- 8---------IE--NASLNSTRLENPQI-----EPI------------
Glyma12g01980                        1 ----------------------------------------MADDSA--K-----G-- 8---------IE--NASLNSTQLENPQI-----EPI------------
230551|230551                        1 ----------------------------------------WVDQSA---------- 6----------EPPAQDSDGSSAPPPPV-----EPL------------
Phpat.012G063000                     1 ----------------------------------------MA---------------- 2--------------GNADAGPSSSGE-----SPL------------

gi|17532463                         64 ---PIQ-MLTLPE 72MSRGERWIQWGMENCTVKASISGVLGVGVGFAFGLFTASVDPQLSMV------------ 119--------------GGDPTKQLTLKQTWKE
gi|56606061                         46 --SLG-GIPSPA 54KSEGQKMIEKAMESCAFKAALACVGGFVLGGAFGVFTAGIDTNVGFD------------ 101--------------PKDPYRTPTAKEVLKDM
gi|66810255                         25 NGVRDFLPNIKN 36IAPYNEMQYNLMDNCLVHGVRGMVAGGAHGFLFGALFTPNSGF---------------- 79----------TPEPTTPTPLYRQVMDGFKEQG
CMS209C|CMS209CT                    30 -----------E 30RNPSEKFNEMVLESCAFKAVAAAIAGGGLGVALGLTTGGFSAEL---------------- 74----------DRAVEAQSPWHEQLRAYGKALA
YDL217C                             28 --GE--------- 29--RGAEMIMNFMTSCPGKSVVSGVTGFALGGVLGLFMASMAYDTPLHTPTPANTAATA 87GNIGVGGISRTVQVSDLPFRQQMKLQFTDM
gi|164426913                        50 EEEEEE-VVVVVV 61VVVMVAMMQKAMESCFAKTVMSGGAGFALGGVFGMFMASMAYDTPYHSPTTPGTGPGANP 121AAAGIPGY--KPVDLSSMPLREQLKHGFKD
Esi0063_0018                        47 ----AD-----AM 50PTPP-----VLTESCGFKLIMGTVGGAGMGTVFGLFLGAMGDMQ---------------- 89-----PLQMINGREVPQAPFREQARLMYKQT
Cre01.g021050                       42 -----------EM 43PTPEVLMAQEFMNNCFVKSAMSGAMGGVAGLAFGLFMSSFENAH---------------- 87-----GGMDSIPDGTAQRSTRAVLKEMFTNM
Vocar20010161                       43 -----------TM 44PTQQELAAQEFMNNCLVKSAISGAMGGIAGFAFGLFSASMENAH---------------- 88-----GGLDTVPELGPEKTTRVILREMFQNM
30209.t000032|30209.m001533         28 ---------RM 29PSMEEIRAQEVWDNCAVRSVASGVLGGGLGLFMGLLLGSLDNPL---------------- 73-------------MQDQMTGREQFIYIAKQMG
GRMZM2G357152                        1 ----------- 0---------------MDVPDLKYARGGLGVLMGLFTGALENPI---------------- 28-------------MAEEMTARQQIVYTLKQMGS
GRMZM2G007080                       28 -----------RM 29PTVEEIKGQDIWWNCAVRSVVSGVMGGGLGVLMGLFFGALENPI---------------- 73-------------MAEQMTARQQTVYTAKQM
LOC_Os03g18500                      25 ----------RL 26PVPEEIKGQDIWWNCAVRSVVSGVMGGGLGVLMGLFFGALENPI---------------- 70-------------TAEEMTARQQIVWQAKQMG
Potri.001G281200                    37 ----------RM 38PTIEEVRAQDVWNNCAVRSVASGVMGGGLGLFMGLFLGALDNPI---------------- 82-------------MQDEMTGRQQFIYTAKQM
Potri.009G076400                    38 ----------RM 39PTIEEVRAQEVWNNCAVRSVASGVMGGGLGLFMGLFLGALDNPI---------------- 83-------------MQDEMTGRQQFIYTAKQM
Carubv10010466                      30 ---------RM 31PTIEEIRAQEVWNNCAVRAVTSGVMGGGLGLMMGLFLGALDNPI---------------- 75-------------TNDTMTARQQFVFTAKQMG
AT3G10110                           31 ---------RM 32PTIEEIRAQEVWNNCAVRAVTSGVMGGGLGLMMGLFLGALDNPI---------------- 76-------------THDTMTARQQFVFTAKQMG
AT1g18320                           31 ---------RM 32PTIEEIRAQEVWNNCAVRAVTSGVMGGGLGLMMGLFLGALDNPI---------------- 76-------------THDTMTARQQFVFTAKQMG
Bra016560                           27 ---------RM 28PTIEEMRAQEVWNNCAVKSVASGVMGGGLGLMMGLFMGALDNPI---------------- 72-------------WHDTMTGRQQFVVTAKQMG
Bra031026                           26 ---------RM 27PTIEEMRAQEVWNNCAVKSVASGVMGGGLGLMMGLFLGALDNPI---------------- 71-------------TNDTMTGRQQFVFTAKQMG
Cucsa.151920                        70 ----------RM 71PTVEEIRGQDIWDNCAVRSVVSGVMGGGLGLMFVGLFGASTDTSM---------- 115-------------VQDEMTARQQFVNTAKQ
Eucgr.K02762                        29 ---------RL 30PTHEEIRGQDIWNNCAVRSVFSGIMGGGLGLMGMLLGALDNPI---------------- 74-------------MQDQSCKQHIYVAIKQMG
PGSC0003DMG402019636                27 ---------RM 28PTVEEIRGQDIWNNCAVRSVVSGVMGGGLGLFMGMFLGALDNPI---------------- 72-------------MQEEMTRKQLYVQAKQMG
GSVIVG01024670001                   28 ---------RM 29PTVEEIRGQDIWNNCAVRSVASGVMGGGLGLIMGLFLGALDNPI---------------- 73-------------MQEEMTARQQFIYTAKQMG
Medtr4g077950                       28 ---------SL 29PTVEEIRGQDIWNNCAVRSVVSGVMGGGLGIAMGLFLGALDNPW---------------- 73-------------MQEQMTGKQQFIFQAKQMG
Medtr4g078050|Medtr4g078050.1       28 ---------SL 29PTVEEIRGQDIWNNCAVRSVVSGVMGGGLGIAMGLFLGALDNPM---------------- 73-------------MQEQMTGKQQFIFQAKQMG
Glyma09g35780                       28 ---------RL 29PSVEEIRGQDIWNNCAVRSVVSGVMGGGLGIFMGLFLGALDNPL---------------- 73-------------MQEEMTGRQQLIYQAKQMG
Glyma12g01980                       28 ---------RL 29PSVEEIRGQDIWNNCAVRSVVSGVMGGGLGIFMGLFLGALDNPL---------------- 73-------------MQEEMTGRQQFIYQAKQMG
230551|230551                       27 ---------RL 28PTFEEMKAQDVFNNCAVKSHVSGVMGGGWGIFMGLLFGALDNPL---------------- 72-------------NPDQMTVRQHFTHAAKQMG
Phpat.012G063000                    18 ---------RL 19PSPDEIRAQDIFNNCAVRTAVSGVMGGGWGIFMGMLFGALEQPL---------------- 63-------------HTDMMTARQHFVHAAKTMS

gi|17532463                        136 MSSRMKSYGKNFGSIGLMFSGTECALETIR 165AKSDWRNGTYSGGIVGGLLGL--------RAGIMPAVWGA-AGFAVFSTIIDHYMRG--- 213---------- 2
gi|56606061                        119 GQRGMSYAKNFAIVGAMFSCTECLIESYR 147GTSDWKNSVISGCITGGAIGF--------RAGLKAGAIGC-GGFAAFSAAIDYYLR----- 194---------- 19
gi|66810255                        102 RSGLRSAKSLSIITLVYTGTECAIEKAR 129GRTDKLNPIYAGCTIGAVFAG--------RAGFMAAVGGC-VGFAVFGMIMDHFMVFFF- 179---------- 179
CMS209C|CMS209CT                    97 AQIRTYSKNFALWGAIYTIAECSVEKYR 124ARHDLWNSLIAGCAIGAVLASQPRASMSARTRGQQMSVGC-LGVAAFSCAHDYWLEHRHA 183---------- 183
YDL217C                            119 GKKSYSSAKNFGYIGMIYAGVECVIESLR 147AKNDIYNGVTAGFFTGAGLGY--------KAGPQMALMGG-AGFAAFSAAIDLYMKSEDG 198RPPQNDFKE* 20
gi|164426913                       150 MGQRSYSTAKNFAKVGALFSGIECGIEGTR 179AKNDLGNGVAAGCLTGAIAK--------NGGPQAAAVGC-AGFAAFSAAIDAWMRMPSE 230ED-------- 2
Esi0063_0018                       116 ADRSLSMGRNFASFSAIFMGSECVIEKMR 144GKTDMMNSVYAGCATGAAAFGM--------KQGPQMACFGC-VGMMTFSALMDKLMGH*-- 192---------- 19
Cre01.g021050                      114 RTKSVSYAKGFAVMGALFSFNECVVEKWR 142AKHDAANPVIAGCVTGAMMAH--------SGGPQMCFGG-ASFGAFSYVIEKYLNSDH* 192---------- 19
Vocar20010161                      115 RTKSVSYAKGFALMGALYSFNECVIEKWR 143AKHDKANPALAGCVTGAMMAH--------SMGPTMCWGG-ASFMAFSTAIEYWMES*-- 191---------- 19
30209.t000032|30209.m001533         93 RSTSSCKTFAVMGLVFSAAECIVEKAR 120AKHDTTNTVVAGCVTGGSMSA--------KVYTKIMAHLNDILFEKLKLEVLSYNLCLQQ 172L--------- 173
GRMZM2G357152                       49 RSISNAKTFAVMGLIFSAAECTIKKVR 75AKHDTTNTAVAGCVTGGALAV--------KVGPKATCFGC-VGVCCVLSGN*--------- 117---------- 117
GRMZM2G007080                       92 GSRSTSNAKTFAVMGLIFSAAECTIEKVR 120AKHDTTNTAVAGCVTGGALAV--------KGGPKATCFGC-VGFAAFSVAIEKFFDRHT* 170---------- 17
LOC_Os03g18500                      90 RRSINNAKTFAVMGLIFSAAECVIEKAR 117AKHDTTNSAVAGCVTGGALAA--------KGGPKATCVGC-VGFAAFSVMIEKFLDRHS* 167---------- 167
Potri.001G281200                   101 GRRSWSSCKTFAIMGLVFSAAECVTEKAR 129AKHDTTNTVVAGCVTGGTMSA--------KGDLLLCCCSM---LFSY*---------- 165---------- 16
Potri.009G076400                   102 GRRSWNSCKAFAIMGLVFSAAECVAEKAR 130AKHDTTNTVVAGCVTGGAMSA--------KGGPKAACFGC-AGFAAFSVLIEKFLDRHT* 180---------- 18
Carubv10010466                      95 QRSWNSCKTFAVMGLVFSAAECIVEKAR 122AKHDTTNTAIAGCVTGGSMSA--------RGGPKAACIGC-AGFATFSVLIEKFFDRHT* 172---------- 172
AT3G10110                           96 QRSWNSCKTFAVMGLVFSAAECIVEKAR 123AKHDTVNTAIAGCVTGGSMSA--------RGGPKAACIGC-AGFATFSVLIEKFFDRHT- 173---------- 173
AT1g18320                           96 QRSWNSCKTFAVMGLVFSAAECIVEKAR 123AKHDTVNTAIAGCVTGGSMSA--------RGGPKAACIGC-AGFATFSVLIEKFFDRHT- 173---------- 173
Bra016560                           92 QRSWSSCKTFAVMGLVVSAAECIVEKAR 119AKHDIINTAVAGCVTGGTMSA--------RGGPKAACMGC-VGFATFSVLIEKFFDRHT* 169---------- 169
Bra031026                           91 SRSWSSCKTFAVMGLVFSAAECIIEKAR 118AKHDTTNTAFAGCVTGGSMSA--------RGGPKAACIGC-AGFATFSVLIEKFFDRHT* 168---------- 168
Cucsa.151920                       133 MGRRSWGSAKSFAVMGLIFSAAECVVEKAR 162AKHDMTNTIVAGCVTGGSISA--------KGGPKAALAGC-AGFAAFSALIEKFLERHT* 212---------- 2
Eucgr.K02762                        94 QRSWNSAKTFAVMGFVFSAAECVVEKAR 121AKHDTTNTVVAGCVTGGTMSA--------RGGPKAACAGC-AGFAAFSVLIEKFLDSH*- 170---------- 170
PGSC0003DMG402019636                92 RRSWSSCKTFAVMGFVFSAAECTVEKVR 119AKHDITNTAVAGCVTGGALSA--------RGGPKAACMGC-AGFATFSVLIEKFLDRYH* 169---------- 169
GSVIVG01024670001                   93 SRSWGSAKTFAVMGLIFSAAECVVEKAR 120AKHDTTNTVVAGCVTGGAISA--------KGGPKAACVGC-AGFATFSVLIEKFLDRHD* 170---------- 170
Medtr4g077950                       93 RRSWSSAKAFAVMGFVFSAAECVVEKAR 120AKHDITNTFVAGCTTGGAISA--------KGGPQAACMGC-AGFAAFSVVIEKFLERHQ* 170---------- 170
Medtr4g078050|Medtr4g078050.1       93 RRSWSSAKAFAVMGFVFSAAECVVEKAR 120AKHDITNTFVAGCTTGGAISA--------KGGPQAACMGC-AGFAAFSVVIEKFLERHQ* 170---------- 170
Glyma09g35780                       93 RRSWSSAKAFAVMGFVFSAAECVVEKAR 120AKHDITNTVVAGCATGGAISA--------KGGPKAACAGC-AGFAAFSVVIEKFLERHQ* 170---------- 170
Glyma12g01980                       93 RRSWSSAKAFAVMGFIFSAAECVVEKAR 120AKHDITNTVVAGCATGGAISA--------KGGPKAACAGC-AGFAAFSVVIEKFLERHQ* 170---------- 170
230551|230551                       92 SKSLHMAKAFAVMGAIYSGTECIIEKAR 119AKHDMTNTMVAGCVTGGSLSA--------KAGPKAACVGC-AGFAAFSVVEKLFDRAA* 169---------- 169
Phpat.012G063000                    83 SKSVQMAKTFTVMGAIFAGTECVFEKAR 110AKHDATNTVEAGCATGGSMSA--------RAGPQAACIGC-AGFAAFSVAIEKVFDRHN* 160---------- 160

gi|17532463                        214 13
gi|56606061                        195 4
gi|66810255                        180
CMS209C|CMS209CT                   184
YDL217C                            208 7
gi|164426913                       233 32
Esi0063_0018                       193 2
Cre01.g021050                      193 2
Vocar20010161                      192 1
30209.t000032|30209.m001533        174
GRMZM2G357152
GRMZM2G007080                      171 0
LOC_Os03g18500                     168
Potri.001G281200                   166 5
Potri.009G076400                   181 0
Carubv10010466                     173
AT3G10110                          174
AT1g18320                          174
Bra016560                          170
Bra031026                          169
Cucsa.151920                       213 12
Eucgr.K02762                       171
PGSC0003DMG402019636               170
GSVIVG01024670001                  171
Medtr4g077950                      171
Medtr4g078050|Medtr4g078050.1      171
Glyma09g35780                      171
Glyma12g01980                      171
230551|230551                      170
Phpat.012G063000                   161
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