```
LOC_Os03g09870|LOC_Os03g09870.1              1 -------------------------MAAKRGSESDG----------DELGGGGAAEGT-- 23-SPND---------------------GGASPPPLAAAPAVCFIRSAG
GRMZM2G072415|GRMZM2G072415_T01              1 -------------------------MAARRGREWDG----------DEQGAAL------- 18-----------------------------PTPAPLGAPVVCLLSSAG
LOC_Os10g22039|LOC_Os10g22039.1              1 ---------------------MAARRGRGRGREWED----------DDLGVGG------- 22-----------------------------GQPPHLAAPVVCLARSAG
68615|68615                                  1 ------------------------------------------------------------ 0---------------------------------------CVIKGVGD
Phpat.023G040200|Phpat.023G040200.1          1 --------------MAMVPSGRGDEG--VGGGEWTD----------SGDGFNDSSSSA-- 32-SPEA---------------------GN-WSAGGPNHPTFCFFKGVA
Phpat.024G046400|Phpat.024G046400.1          1 --------------MAMVPSGGGDDVSGGEGGSWTN----------SDDGLIDSSSSA-- 34-SQEP---------------------GS-WSVGGPNHPTFCFFKGAA
LOC_Os12g33020|LOC_Os12g33020.1              1 MAS-----------------GGGDARRRKEEGEEDGFS-------SDGGD--TTDAESSD 34ERAGAGAGRRAVPGANPILSRLAVSRNPSPLAAATAAPGVCLLRFAW
GRMZM2G112640|GRMZM2G112640_T01              1 MVG-----------------GGGDPRPEDE----PFS--------DGDAT--ESDTDES- 28-PPQGISARRPGATTNPILTRLAVSRNPSPLAAATAAPGVCLLRFAW
GRMZM2G092286|GRMZM2G092286_T01              1 MAR-----------------GGGDRSREDD----PFS--------DGGTT--GTDSDES- 28-SPRGVGARGPGSTSNPILTRLAVSRNPSPLAAATAAPGVCLLRFAW
GRMZM2G120530|GRMZM2G120530_T01              1 MAR-----------------GGGDRSREDD----PFS--------DGGTT--ETDSDES- 28-SPRGVGARGPGSTSNPILTRLAVSRNSSPLAAATAAPGVCLLRFAW
27613.t000023|27613.m000630                  1 ------------------------------------MATADSPNTNNNNNT--ADSDLED 22INANP---NPNSPSNA-----------LLPSSSTSPAVCLLRSAG
Glyma0121s00230|Glyma0121s00230.2            1 ------------------------------------------------------------ 0-----------------------------------------------
Glyma08g43515|Glyma08g43515.1                1 ------------------------------------MASD-------AT--VNSVSEVN- 14NAPNP----R----------------KSEGPSSTPSPTTSLLLSAAT
Glyma18g09772|Glyma18g09772.1                1 ------------------------------------MASD-------VT--VNSVSDVN- 14NAPNP----T----------------KSVGPSSTPSLTASLLLPATT
Glyma18g10010                                1 ------------------------------------MASD-------AT--VNSVSDVN- 14NAPNP----T----------------KSVGPSYTPSPTASLLLPAAT
Bra002900|Bra002900                          1 ------------------------------------MAAENPSNGVDVDTSHDSDSND-- 22---------NR---KAS-----DLTNHDSSMALTVPSTAVCLGRFAG
Bra028975|Bra028975                          1 ------------------------------------MAAE---DSPDVDTSLDSDSNH-- 19---------NANANADV-----KLNNHDSSNAVAIPSPAVCLVRFAG
Bra026412|Bra026412                          1 ------------------------------------MSADDSSNATDIDAKLGSDSNL-- 22---------NSGGDDAA-------DNDSSKAL-TIPAPAVCLVRFAG
AT4G26670                                    1 ------------------------------------MAANDSSNAIDIDGNLDSDSNL-- 22---------NTDGDEAT-------DNDSSKALVTIPAPAVCLFRFAG
Carubv10005731m.g|Carubv10005731m            1 ------------------------------------MAADDSSNAIDIKGNLDSDSNL-- 22---------NTDGDEAS-------DNDSAKALATIPAPAVCLFRFAG
AT5G55510                                    1 ------------------------------------MAAENSSNAINVDTSLDSDSKP-- 22---------NRDANDMT-------DHDSSSKALVIPAPAVCLVRFAG
Carubv10027112m.g|Carubv10027112m            1 -------------------------------KLQRGSSAMAAEDSSNVDTSINSDSKP-- 27---------KYEANDVT-------NHDS-SKTLVIPPPAICLVRFAG
Cucsa.042410|Cucsa.042410.1                  1 ------------------------------------MADS--------------SKDVSP 10DADNL----LTNSSDSP-----N-SSDAIVPSPPFTGPALCLFRFAG
Medtr5g094300|Medtr5g094300.1                1 ------------------------------------MATA---DSDGVTPPH--DEDSSD 19SSVPN----SP------------------NSAIVPAAPSVCLVRFAI
Glyma02g46620|Glyma02g46620.1                1 MLRRDNITHSHPKESRREEKQRGRRHRRRGSTSSSSMATP---DSDATTQPQ--DSDTA- 54--PNS----SP------------------PNALVPAAPAVCLLRFAT
Glyma14g02050|Glyma14g02050.1                1 ----------------------------MSSSSSSSMATP---NSDATTQTQ--DSDTV- 26--PYS----NS------------------PNALVPAAPAVCLLRFAT
PGSC0003DMG401022191|PGSC0003DMT40005712     1 ------------------------------------MA------TPATSPNSESDSDVET 18S-PVA----NPSPGQNP-----Q-FTSDALTTAIPSSPVVCLLRFAG
Eucgr.F03519|Eucgr.F03519.1                  1 ------------------------------------MASP---MSPNA------DPDAES 15DAANP----SSTA-DSP-----N----ALAPSGSTSPPVVCLLRFAG
GSVIVG01037765001|GSVIVT01037765001          1 ------------------------------------------------------------ 0-----------------------------------------------
Potri.001G360300|Potri.001G360300.1          1 ------------------------------------MATA---NSPNTSNN--SDSDVED 19--PNP----NPSSNNNN-----A----SIIPSAESSTPSVCLIRFAG
Potri.011G088500|Potri.011G088500.1          1 ------------------------------------MATA---NSPDASNNNNTDSDVED 21TSPNP----NLSINKNN-----G----FLISSAESSSPSVCLLRFAG

LOC_Os03g09870|LOC_Os03g09870.1             49 DFAGGAFIGSIVG 61YG-----------------QGLFTKKGFKGSFSTAGSSAKTFAVLSGVQSLVVCLLRRLR 104GKDD---------IVNAG-IAGCCTGLALS
GRMZM2G072415|GRMZM2G072415_T01             37 DLAAGAFVGSLVG 49YG-----------------KGLITNQGTKACLSIAGSSAKTFAALAGVQSFIMCLLRRLR 92GKDD---------MINAG-MAGCCTGIALSF
LOC_Os10g22039|LOC_Os10g22039.1             41 DLAAGAFVGSLVG 53YG-----------------QGLLTNKGMKGSLSSAGSSAKTFAALSGVQSFILCLLRRLR 96GKDD---------MINAG-VAGCCTGLALSF
68615|68615                                  9 AMSGAVMGSVFG 20FG-----------------TGLFQKKGFKGALHSGASSAKTFAILSGIHGFVTTLLIQIR 63GKKD---------AINAG-IAGCATGIALSAP
Phpat.023G040200|Phpat.023G040200.1         57 DGLAGGLMGSVFG 69FG-----------------SGLFKKQGFKGSLREGGSSAKTFAILSGVHSIVSCYLKKVR 112GKED---------AWNAG-IAGCATGLALS
Phpat.024G046400|Phpat.024G046400.1         59 DGLAGGLMGSVFG 71FG-----------------SGLFKKQGFKGALREGGSSAKTFAILSGVHSIVSCYLKKVR 114GKED---------AWNAG-IAGCATGLALS
LOC_Os12g33020|LOC_Os12g33020.1             82 ESAAGSLVGAVVG 94YG-----------------KGLVTTKGFKGSFADAASSAKIFAVLAGVQSLVACTLRQLR 137GKDD---------VLNAG-IAGCCTGLALS
GRMZM2G112640|GRMZM2G112640_T01             75 ESAAGSLVGAVVG 87YG-----------------KGLVMRKGFKGSFPDAASSAKIFAVLAGVQSLVACSLRKLR 130GKDD---------GINAG-VAGCCTGLALS
GRMZM2G092286|GRMZM2G092286_T01             75 ESAAGSLVGAAVG 87YGADLGR---WGWTPCGLGKGLVTMKGIKGSFADAASSAKIFAVLAGVQSLVACSLRKLR 144GKDD---------GINAG-VAGCCTGLALS
GRMZM2G120530|GRMZM2G120530_T01             75 ESAAGSLVGAVVG 87YG-----------------KGLVMMKGIKGSFADAASSAKIFAVLAGVQSLVACSLRKLR 130GKDD---------GINAG-VAGCCTGLALS
27613.t000023|27613.m000630                 54 DAAGGAFMGSIFG 66FG-----------------SGLIKKRGFKGSFVEAGSHAKVSN----MDKLESYVYGQN- 104---K---------LSEVGFSCGICFWVGLF
Glyma0121s00230|Glyma0121s00230.2            1 -----MLSMGLF 7SG-----------------AGLIKKKGFKGSFIEAGSNAKTFAILSGVDSLVVCILGRLR 50GKDD---------AINAG-VAGCCAGLATSFPG
Glyma08g43515|Glyma08g43515.1               42 STACGALTGSLFG 54YG-----------------AGLIKKKGFKGSFMEAGSQAKTFAVLSGVDSLVVCIFGRLR 97GKHD---------AINAG-LAGCCAGLATSF
Glyma18g09772|Glyma18g09772.1               42 STACGALTGSLFG 54YG-----------------AGLIKKKDFKGSFIQAGSNAKTFAILSGVDSLVVCILGRLR 97GKDD---------AINAG-VAGCCAGLATSF
Glyma18g10010                               42 STACGALTGSLFG 54YG-----------------AGLIKKKGFKGSFIEAGSNAKTFAILSGVDSVVVCILGRLR 97GKDD---------AINAG-VAGCCAGLATSF
Bra002900|Bra002900                         53 DAAGGAVMGSIFG 65YG-----------------SGLFKKKGFKGSFADAGQSAKNFAILSGVHSLVVCLLKKLR 108GKDD---------AINVG-IAGCCTGLALS
Bra028975|Bra028975                         53 DAAGGAVMGSVFG 65YGDTSYSLLHTVWS----CSGLFKKKGFKGSFADAGQSAKTFAVLSGVHTLVVCLLKKLR 121GKDDGETHPASPSSINVG-VAGCCTGLALS
Bra026412|Bra026412                         53 DAAGGAVMGSIFG 65YG-----------------SGLFKKKGFKGSFADAGQSAKTFAVLSGVHSLVVCLLKQLR 108GKDD---------AINVG-VAGCCTGLALS
AT4G26670                                   54 DAAGGAVMGSIFG 66YG-----------------SGLFKKKGFKGSFADAGQSAKTFAVLSGVHSLVVCLLKQIR 109GKDD---------AINVG-VAGCCTGLALS
Carubv10005731m.g|Carubv10005731m           54 DAAGGAVMGSIFG 66YG-----------------SGLFKKKGFKGSFADAGQSAKTFAVLSGVHSLVVCLLKQVR 109GKDD---------AINVG-VAGCCTGLALS
AT5G55510                                   54 DAASGAFMGSVFG 66YG-----------------SGLFKKKGFKGSFVDAGQSAKTFAVLSGVHSLVVCLLKQIR 109GKDD---------AINVG-VAGCCTGLALS
Carubv10027112m.g|Carubv10027112m           58 DAASGAFMGSVFG 70YG-----------------SGLFKKKGFKGSFVDAGQSAKTFAILSGVHSLVVCLLKQIR 113GKDD---------AINVG-VAGCCTGLALS
Cucsa.042410|Cucsa.042410.1                 48 DSVAGAFMGSIFG 60YG-----------------SGLIKKNGFKGSFAEAGSCAKTFAVLSGVHSLVACMLKTLR 103GKDD---------VINHG-VAGCCTGLALS
Medtr5g094300|Medtr5g094300.1               45 DSAGGALMGSVFG 57YG-----------------TGLFKKKGFKGSFADAGSSAKTFAVFSGVQSLVVCILKRLR 100GKDD---------VINAG-VAGCCTGLALS
Glyma02g46620|Glyma02g46620.1               78 DSAGGALMGSVFG 90YG-----------------AGLFKKKGFKGSFVEAGSYAKTFAVLSGVHSLVVCILKRLR 133GKDD---------VINAG-VAGCCTGLALS
Glyma14g02050|Glyma14g02050.1               50 DSAAGALMGSVFG 62YG-----------------AGLFKKKGFKGSFVEAGSYAKTFAVLSGVHSLVVCILKRLR 105GKDD---------VINAG-VAGCCTGLALS
PGSC0003DMG401022191|PGSC0003DMT40005712    55 DSAAGAFMGSIFG 67YG-----------------SGLIKKKGFKGSFGEAGASAKTFAVLSGVHSLVVCFLKRLR 110GKDD---------VINAG-VAGCCTGLALS
Eucgr.F03519|Eucgr.F03519.1                 49 DSAAGAFMGSIFG 61YG-----------------AGLVKKKGFKGSFAEAGSSAKAFAVLSGVHSLVVCFLKRLR 104GKDD---------VFNAG-IAGCCTGLALS
GSVIVG01037765001|GSVIVT01037765001          1 ------MGSIFG 6YG-----------------LGLVKKKGFKGSFAEAGSSAKTFAILSGVHSLVVCFLKRLR 49GKDD---------VVNAG-VAGCCTGLALSFPG
Potri.001G360300|Potri.001G360300.1         52 DSAAGAFMGSIFG 64YG-----------------SGLIKKKGFKGSFGEAGSCAKTFAVLSGVHSLVVCFLKRLR 107GKDD---------VINAG-VAGCCTGLALS
Potri.011G088500|Potri.011G088500.1         56 DSAAGAFMGSIFG 68YG-----------------SGLIKRKGFKGSFGEAGSCAKTFAVLSGVHSLVVCFLKRLR 111GKDD---------VINAG-VAGCCTGLALS

LOC_Os03g09870|LOC_Os03g09870.1            125 FPGTPQALLQSCATFAAFSCIMEGLNKQQA 154AMAQTLGGSALTV------------SHQNGGVLPPFTLPPLLDASDALSSCCQPLV--LK 200PKH*--------
GRMZM2G072415|GRMZM2G072415_T01            114 PGAPQAMFHSCVTFAAFSCIMDGLSKQQA 142AMALTLDVKSPTV------------KYEEGRVIPPFTLPPLLDALDPLGSFCQTLI---K 187PKH*---------
LOC_Os10g22039|LOC_Os10g22039.1            118 PGAPQAMFHSCVTFAAFSCIMDGLNKQQA 146AMAATLASKPSTI------------KHQEGDVLPPFTLPPLLNASDALASCCQAFL---K 191PKD*---------
68615|68615                                 86 GNPAALLQGCATFGVFSYFVERMNTTQP 113AIAATLTGKKKSR--------------------------------------------126-------------
Phpat.023G040200|Phpat.023G040200.1        133 TPGTPQALAQSCLSFGAFSFLLEYMNHTRP 162AIAATSSE-SQSSHLPQINVNNHLHLHFNLPALPPFTLPPLAFPGAL-SFLNQELANRTR 220PL*---------
Phpat.024G046400|Phpat.024G046400.1        135 APGSPQALAQSCLSFGAFSFVLEYMNHTRP 164AIAATVTSVLQPSSSRQFNIINHHHWHLNMPALPPFTLPPLSFPSQL-SFLNLESANRTR 223PL*---------
LOC_Os12g33020|LOC_Os12g33020.1            158 FPGAPQTMIQSCLTFGTFSYIIEMLNKQEP 187ALARPSITGTKDL-------KAGH------RVLPPFTLPLPQEAMEGFSSFQNFLS-KFQ 233GK*---------
GRMZM2G112640|GRMZM2G112640_T01            151 FPGAPQTLIQSCLTFGTFSYIIETLNKQQP 180ALALPLATEIKDQ-------KAGQ------SVLPPFTLPLPQDAMDGFSKFQNFLSSKFQ 227GK*---------
GRMZM2G092286|GRMZM2G092286_T01            165 FPGAPQTLIQSCLTFGTFSYIIEKLNKQQP 194ALALPPATGVMDP-------KAGQ------SVLPPFTLP-PLDAMDEFCKFQNFLSSKFR 240GN*---------
GRMZM2G120530|GRMZM2G120530_T01            151 FPGAPQTLIQSCLTFGTFSYIIEKLNKQQP 180ALALLPATGVMDP-------KAGQ------SVLPSFTLP-PLDTMDEFSKFQNFLSSKFR 226GN*---------
27613.t000023|27613.m000630                123 GGGAPQALLQSCLTLGAFSFIMERLNKQQP 152ALAHSFSLRNKHE-------YSASRPLPNAPHHLTLSVPLPNELKAAFSFFCNSLKKTSS 205-NFPTAL-----
Glyma0121s00230|Glyma0121s00230.2           74 TPQSLLQSCIAYGALSFIIEGLTKQRS 100ALAYPMSKKTSVR-------NQD-------QSYIYMFFIRGFYFK--YGIFS-------- 136--LPHLHVNQKAAVY
Glyma08g43515|Glyma08g43515.1              119 PGTPQALILNCLTYGAFSFMIEGVTKKRS 147ALAYPMSKKTSA*------------------------------------------------ 159-----------
Glyma18g09772|Glyma18g09772.1              119 PGTPQSLLQSCIAYGALSFIIEGLTKQRS 147ALAYPMSKKTSVR-------NQV-------LLKIVSVEIQTYDLSPLLSPFT-------- 185--LKSFFPNH*--
Glyma18g10010                              119 PGTPQSLLQCCIAYGALSFIIEGLTKQRS 147ALACPMSKKTSVR-------NQG-------IIPTSH*----------------------- 169-----------
Bra002900|Bra002900                        129 YPGAPQAMLQSCVTFGAFSFILEGLNKRQT 158ALAHSVSSRHDQT-------RSL---K--DDLPLSLALPIHEEIKGAFSSFCKSLTKPKK 206LAFPSSR*----
Bra028975|Bra028975                        151 FPGAPQAMLQSCLTFGAFSFILEGLNKRQT 180ALAHSVSLRHDQS-------RSL---K--DELPLSLALPIHEEIKGAFSSFCDSLTKPKK 228LAFPRPH*----
Bra026412|Bra026412                        129 FPGAPQALLQSCLTFGAFSFILEGLNKRQT 158ALAHSVSLRHQTG-------NFGDHQQ--RPLQLSLALPIHEEIKGAFSSFCKSLTKPKK 209I*---------
AT4G26670                                  130 FPGAPQALLQSCLTFGAFSFILEGLNKRQT 159ALAHSVSLRHQTG-------LFQDH-H--RALPLSLALPIPEEIKGAFSSFCKSLAKPRK 209F----------
Carubv10005731m.g|Carubv10005731m          130 FPGAPQALLQSCLTFGAFSFILEGLNKRQT 159AMAHSVSLRHQTG-------HVQDH-H--RPLPLSLALPIHEEIKGAFSSFCKSLAKPRK 209F*---------
AT5G55510                                  130 FPGAPQAMLQSCLTFGAFSFILEGLNKRQT 159ALAHSVSFRQQTR-------SPQ---H--DLPLLSLALPIHDEIKGAFSSFCNSLTKPKK 207LKFPHAR-----
Carubv10027112m.g|Carubv10027112m          134 FPGAPQAMLQSCLTFGAFSFILEGLNKRQT 163ALAHSVSLRHQTR-------SLH---H--DLPL-SLALPIPNEIKGAFSSFCKSLKKPKM 210LEFPHAR*----
Cucsa.042410|Cucsa.042410.1                124 FPGAPQALLQSCLTFGAFSFILESLNKRQP 153ALAHPIFSRTRSE-------M--ERNR--PPLVLPLQFALPVELKGAFSSFCKSLEKSRR 202CSW*--------
Medtr5g094300|Medtr5g094300.1              121 FPGAPQDLLRSCLTFGAFSFIMEGLNKQQP 150ALALPMSWKTGVQ----------HNAR--PPLVLPLQLPLPNELKEAFSFFSESLKKRNK 198GAYPTS*-----
Glyma02g46620|Glyma02g46620.1              154 FPGAPQALLQSCLTFGAFSFIMEGLNKQQP 183ALAVPMSWKKTVQ----------HNAC--PPLVLPLQLSLPDELKDAFSFFSESLKKRSK 231GPYPTS*-----
Glyma14g02050|Glyma14g02050.1              126 FPGAPQALLQSCLTFGAFSFIMEGLNKQQP 155ALAVPISWKKPVQ----------HNAS--PPLVLPLQLPLPDKLKDAFSFFSYSLKKRSK 203GPYPTSR*----
PGSC0003DMG401022191|PGSC0003DMT40005712   131 FPGAPQALLQSCLTFGAFSFIIEGLNKQQP 160ALALTSHMNVNS------------RQQ--FGVLAPLSLPLPNELKESFSFFCQSLKNRRH 206GSG*--------
Eucgr.F03519|Eucgr.F03519.1                125 FPGAPQALLQSCLTFGAFSFIIEGLNKQQP 154ALAYPYAQKKRIQ-------N---DLP--TLPAIPLPLPLPDELKGAFSSFCESLRKPNK 202GKRSVAH*----
GSVIVG01037765001|GSVIVT01037765001         73 TPQALLQSCVTFGVFSFIIEGLNKQQP 99ALAHPFSMRNERG-------G--KKAL------PPLAFPLPDELKESFSHFCRSLQKPNK 144GNFPAAH*--------
Potri.001G360300|Potri.001G360300.1        128 FPGAPQALLQSCLTFGAFSFIIEGLNKKQA 157ALAHSISSRNKCD-------Y--HSKP--CPLALPLSVPLPDELKGAFSFFCKSLRKPKS 206ANFPAAAP*---
Potri.011G088500|Potri.011G088500.1        132 FPGAPQALLQSCLTFGAFSFIIEGLNKQQP 161ALAHSFSSRNKRD-------Y--HNVT--CPVALHLAVPLPDELKRAFSFFCKSLRKPKS 210GNFPAVS*----

LOC_Os03g09870|LOC_Os03g09870.1            204 --------- 203
GRMZM2G072415|GRMZM2G072415_T01            191 -------- 190
LOC_Os10g22039|LOC_Os10g22039.1            195 -------- 194
68615|68615                                127 ------- 126
Phpat.023G040200|Phpat.023G040200.1        223 --------- 222
Phpat.024G046400|Phpat.024G046400.1        226 --------- 225
LOC_Os12g33020|LOC_Os12g33020.1            236 --------- 235
GRMZM2G112640|GRMZM2G112640_T01            230 --------- 229
GRMZM2G092286|GRMZM2G092286_T01            243 --------- 242
GRMZM2G120530|GRMZM2G120530_T01            229 --------- 228
27613.t000023|27613.m000630                212 --------- 211
Glyma0121s00230|Glyma0121s00230.2          150 GAKMI* 154
Glyma08g43515|Glyma08g43515.1              160 -------- 159
Glyma18g09772|Glyma18g09772.1              194 -------- 193
Glyma18g10010                              170 -------- 169
Bra002900|Bra002900                        214 --------- 213
Bra028975|Bra028975                        236 --------- 235
Bra026412|Bra026412                        211 --------- 210
AT4G26670                                  211 --------- 210
Carubv10005731m.g|Carubv10005731m          211 --------- 210
AT5G55510                                  215 --------- 214
Carubv10027112m.g|Carubv10027112m          218 --------- 217
Cucsa.042410|Cucsa.042410.1                206 --------- 205
Medtr5g094300|Medtr5g094300.1              205 --------- 204
Glyma02g46620|Glyma02g46620.1              238 --------- 237
Glyma14g02050|Glyma14g02050.1              211 --------- 210
PGSC0003DMG401022191|PGSC0003DMT40005712   210 --------- 209
Eucgr.F03519|Eucgr.F03519.1                210 --------- 209
GSVIVG01037765001|GSVIVT01037765001        152 ----- 151
Potri.001G360300|Potri.001G360300.1        215 --------- 214
Potri.011G088500|Potri.011G088500.1        218 --------- 217
```