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Potri.T1457000|Potri.T145700.1
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Medtr7g036950|Medtr7g036950.1
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Glyma07g36311|Glyma07g36311.1

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Vocar20003543m.g|Vocar20003543m 336 --- 335-----PEAELEL-----WVS-ATIKST--ARR 355-G-KNSLNMGEVPLARNALDT-----
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CMT063C|CMT063C 452 --- 453-----PEAM 455GEPRTSENGDAVDTEDEPSTKSK---KRP-SKK 465-----RR
Cre17.g729800|Cre17.g729800.t1.2 347 EL 348GSKRRKRRDDGEVEEDVVEVIVSSGNGAASPAVNGNGSGSRK-GEKFPAL--KAR 397EA-AAKATA--SAGA-----G-----GSEEGKD
Vocar20010438m.g|Vocar20010438m 351 EL 352GAKRRRNEAGEVEEDVVEVIVSSGNGAASPAVNGNGSGSRK-GEKFPAL--KAR 409EA-AAKATA-----G
LOC_0e03g62750|LOC_0e03g62750.1 367 --- 366-----PEPAIKSDPLP-KVGKPPASQEPPEPGPQR-GERFRKL--KEE 405BS--RRKVFLEKAEQT---EQAGTQAG-I-VDGK-QN
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Potri_010G051900|Potri_010G051900.1 470 --- 469-----QLQIQKPVSELS---VQTKRQEKFTPEGLRP-GERFRKL--KQD 510EA--RRRQREEBERK---AEAAGRQSMENNE--H
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Bra032799|Bra032799 373 --- 372-----SQPLVQKSVSELS-PRDK--GSEKVTSEGPKP-GERFRKL--KEE 412EA--RRRQREEBERK---AEAALS--NQNTD-SAQE
AT1624490 76 Q-LVQKSVSELSKI--PRDK--GSEKVTSEGPKP-GERFRKL--KEE 113EA--RRRQREEBERK---AEAALS--NQNTD-SAQE
Bra040623|Bra040623 367 --- 366-----SELVQKSVSELSKI--PREK--GGKVTSEGPKP-GERFRKL--KEE 409EA--RRRQREEBERK---AEAALS--NQNTD-SAQE
AT1624490 374 --- 373-----SELVQKSVSELSKI--PREK--GGKVTSEGPKP-GERFRKL--KEE 409EA--RRRQREEBERK---AEAALS--NQNTD-SAQE
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Glymal1g37590|Glymal1g37590.1 379 --- 378-----SMKLNST--TAEEARLS-EKTSSEGPQP-GERFRKL--KEE 413BA--RRRQREEBERK---RKALEAARETKVD
Glymal1g01540|Glymal1g01540.1 373 --- 372-----SISKLNST--KAEARQS-EKTSSEGPQP-GERFRKL--KEE 407EA--RRRQREEBERK---RKALEAARETKVD
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Eucgr.B03237|Eucgr.B03237.1 384 --- 383-----SESEVNS--T-NKVEEKILTVEGPR-GERFRKL--KEE 417BE--RRRQREEBERK---RKALEAARETKVD
Pphat.003G132900|Pphat.003G132900.1 400 --- 399-----LPPPSA--T-ATADAPTSTSTKDR-GTRFKQL--KEE 432EA--RRRQREEBERK---RKALEAARETKVD
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Bra035669|Bra035669 367 --- 366-----AQP-GERFRKL--KEE 382BK--RRRQREEBERK---RKALEAARETKVD
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Bra004536|Bra004536 291 --- 290-----AQP-GERFRKL--KEE 290-----RKALEAARETKVD
Bra040305|Bra040305 304 --- 303-----AQP-GERFRKL--KEE 303-----RKALEAARETKVD
432 --- 431-----AQP-GERFRKL--KEE 303-----RKALEAARETKVD
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gi|268637951 374 --- 373-----F 374KNKPNRANSE--Q--EKKD-----KLLKELQDRYDLLLKKKQ 408EIKLFGKNNK
Esi0025_0161 492 --- 491-----F 492-----ASK-E 496DLERWGGGGEGASGEASRAAAE
gi|66811452 363 --- 362-----I 363SLFNDGKPKK--E--I-----KYAPEL----- 382
gi|28395049 320 319DIFAAFNTKFI--S--R-----K----- 333----- 422
gi|71960488 327 --- 326-----326AISQVLSYK--N--K-----AIPFSMADR---Q-R 351DASSFKKAGT--RKALEAARETKVD
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YER154W 346 --- 345-----M 346GIPQSLKHNQ--K--A-----RDQA--HGRQOLMD-- 371-----NEKKL--QSEFK
gi|223718097 420 --- 419-----I 419GLESFPPKQGW--N--A-----EMTRRERERQMRNQ-L 449ELA--ARGPL--RQFTT
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Bra040348|Bra040348 231 FEQPKDQSVV--V--HEDPPLS----- 248----- 419
Bra000424|Bra000424 365 --- 364-----H 365FQPKDQSVL--G--HDDPPMS----- 384
AT2646470 376 --- 375-----H 376FABPKDQSVV--G--QEKPPM----- 396
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Potri_003G139800|Potri_003G139800.1 168 --- 167-----H 167----- 167
Eucgr.B00058|Eucgr.B00058.1 372 --- 371-----H 372QAPSSREKDE--N----- 385
Eucgr.B00060|Eucgr.B00060.1 224 SQAPSSREKDE-----G----- 236----- 455--GT
Bra010053|Bra010053 433 QPS-----F 436DLFAALKMKKA--M--M-----TQDTON----- 387
AT5662050 368 --- 367-----H 368DLFSLKMKKA--M--M-----TQDTON----- 387
Carubv10026454m.g|Carubv10026454m 350 --- 349-----H 349----- 387
PGSC003DM400005839|PGSC003DM40001495 368 --- 367-----H 368DLFSLKMKKA--M--M-----TQDHSQ----- 389
GSVIVG01019529001|GSVIVT01019529001 372 --- 371-----H 372SLSLKMKKA--L--M----- 385
Eucgr.B00060|Eucgr.B00060.1 381 --- 380-----H 381SLSLKMKKA--L--M----- 397
29651.t000009|29651.m000289 377 --- 376-----H 376SLSLKMKKA--L--M----- 393
30190.t000068|30190.m010832 375 --- 374-----H 375SLSLKMKKA--L--M----- 391
Potri_006G073000|Potri_006G073000.1 361 --- 360-----H 361DLFSLKMKKA--G--RKE----- 376
Potri_018G140100|Potri_018G140100.1 362 --- 361-----H 362DLFSLKMKKA--A--RKE----- 377
Potri.T145700|Potri.T145700.1 362 --- 361-----H 362DLFSLKMKKA--A--RKE----- 377
Cucsa.107400|Cucsa.107400.1 378 --- 377-----H 378FSLKMKKA--A--RKE----- 397
Medtr7g036950|Medtr7g036950.1 373 --- 372-----H 373SLSLKMKKA--A--RKE----- 392
Glyma07g31320|Glyma07g31320.1 374 --- 373-----H 374SLSLKMKKA--S--A----- 386
Glyma13g25140|Glyma13g25140.1 430 SP-----F 432SLFALKQATS--A--A----- 444
Glyma07g36311|Glyma07g36311.1 375 --- 374-----H 375SLFALKQATS--A--A----- 387

Esi0227_0023 343 342----- 342----- 342-----
Cre06.g251900|Cre06.g251900.t1.2 340 VDDSTAAGTATMA- 374VT-A-----GATA-----AAMDPSKVNRRCKRRR---LTSL 401---V---QDGSTASAAVAG---
Vocar20003543m.g|Vocar20003543m 376 ---DLPETTAALT-DVIK- 389SS-Q-----TDSS-----PLVDLSNVNRFCKRRR---LSSL 416---V---QDANGAQIF
Esi0099_0095 450 449----- 449----- 449-----
CMT063C|CMT063C 420 NSA*----- 422----- 488-----
Cre17.g729800|Cre17.g729800.t1.2 418 ---A----- 417----- 417-----
Vocar20010438m.g|Vocar20010438m 435 SD-----A-GGD 440NI-DEQ-----ESH-----ENEPIIANGNGGLSHSTNEMIP-NGSM 474KEDII---QESTDSHSSVD
GRMZM2G136854|GRMZM2G136854.T01 152 VSSGD 156Q-DQQ-----GSH-----BNGPVVASINGGVNHRNEKTO-NLSS 190E---KEAADHS
GRMZM2G426200|GRMZM2G426200.T01 243 ---ASSGD 247KN-DEQ-----EPH-----EIGPIVANSNGVNHRSNETE-NFSS 281E---KEAADHSSVSKP
PGSC0003DMG40001740|PGSC0003DMT40002790 412 QED-KSDTADVA-VGNHRAK 463LS-A-----VG-ET-----ADGSVAV-NGKPSH-----BG 484---R-VE-Q-QSD
Potri.008G182000|Potri.008G182000.1 438 DSSSFTRNGNSP-VGAAVIDD 458AS-T-----AAIH-----SSALKVVV-NGDLSGQDQKQDETSVIV 492EKSEVSAPTEDY-QAKRE-
Potri.010G051900|Potri.010G051900.1 536 ENDELENESSFERNGRGS-VGAVVIDD 563MS-A-----VAFHD-----SSALKVVV-NGDLSGQDQKQDETSVIV 597ETSEVSAPTEDY-
29929.t000274|29929.m004771 444 SER-E-NGVSM-SGADVDD 460KF-----AH-DS-----SAAGVII-NGEINSSS-----SG 484---R-VE-Q-QSD
Bra032799|Bra032799 442 HEG-KSDTG----- 449-----AE-ET-----GDGSAAV-NGKPSIQKDETTNDKLGTV 479---HDAEQ-Q-HSH---E
Bra040623|Bra040623 151 ---150-----AE-ET-----GDGSAAV-NGKPSIQKDETTNDKLGTV 180---HDAEQ-Q-HSH---E
AT1624490 435 QDE-KSDTADVA-VGNHRAK 463LS-A-----VG-ET-----ADGSVAV-NGKPSH-----BG 484---R-VE-Q-QSD
Bra012507|Bra012507 442 QED-KSDTADVA-VGNHRAK 463LS-A-----VG-ET-----ADGSVAV-NGKPSH-----BG 484---R-VE-Q-QSD
Carubv10009320m.g|Carubv10009320m 406 ---Q-----TVEGGNQ-VVND-LVK 450NS-Q-----SVADDD-----PSISGVV-NGN-GKDLGNQNSSTS 484D---TANDEGSAHL
Medtr3g086250|Medtr3g086250.1 442 KTLLEETVEVENQ-TGGDLVVE 461KS-R-----SLASDD-----PSISGVV-NGNPLSKDLGNQNSSTS 497E---TENNEGSAHF
Glyma1g01540|Glyma1g01540.1 433 ETFEKTVEBENQ-TGGDLVVE 452KS-R-----FVASDD-----PSISGVV-NGNPLSKDLGNQNSSTS 488E---TENNDGSAHF
Cucsa.394650|Cucsa.394650.1 442 ANS-TKREYR-TGGDLVVD 443GN-DSFQSLTTHNS-----SMIEVVV-NDSESNESKDKQMYTR 483E---SESESV
Eucgr.B03237|Eucgr.B03237.1 450 SSMFGV-NNETR-P-PLVNK 466ST-BEPOYANTHYL-----SNGGVVV-NGNLSFPELQDE-NAS 503---DKGAAV
Pphat.003G132900|Pphat.003G132900.1 459 RDNLRAQLAQEAQ-KSAASAGE 480TS-DEAQVSDGK-----EDSDNSK-----EQA-L- 504---AANG
Pphat.010G066400|Pphat.010G066400.1 460 RDNLRAQLAQEAQ-KSDASEE 481TS-DEEQO-NEEK-----EDSDTSK-----EQA-L- 504---ATNG
LOC.Os01g05800|LOC.Os01g05800.1 414 ---DMD 253EE-S-----DDEE-----TEEGGPV-----EEA-SST- 273---GSDKPPF- YG
GRMZM2G110063|GRMZM2G110063.T01 250 ---DMD 413E-S-----D-ET-----TEEGGPV-----EEA-S-T- 431---SSDKL
GRMZM5G839422|GRMZM5G839422.T01 410 ---DMD 313-----D-ET-----TEEGGPV-----EEA-S-T- 431---SSDKL
12954|12954 314 ---ESEE 408GS-D-----DEEE-----EVR-----EGA-LAS- 424---S-TSKP
Bra035669|Bra035669 405 ---ESEE 420GS-D-----DEEE-----EAR-----EGA-LAS- 436---STGPK
Carubv10023172m.g|Carubv10023172m 417 ---DSD 407GS-D-----DEETK-----DKGDDV-----EEA-YVS- 427---SGSKQ
GSVIVG01024995001|GSVIVT01024995001 404 ---DSD 409GH-D-----DEETK-----DKGDDV-----EEA-YAS- 429---SADKV
Cucsa.213790|Cucsa.213790.1 406 ---DSD 404GS-D-----DEETK-----DKGDDV-----EEA-YAS- 424---SSKVV
PGSC0003DMG40000401|PGSC0003DMT40000106 401 ---ASDD 406GS-D-----TESD-----NKQEDA-----EEA-YAS- 426---KVGEEV
Glyma1g14960|Glyma1g14960.1 403 ---ASDD 406GS-D-----TESD-----NKQEDA-----EEA-YAS- 426---KVGEEV
Glyma1g06920|Glyma1g06920.1 403 ---ADEE 416GS-D-----EDSP-----DKGDEVL-----EGA-YAS- 436---TGSQT
Eucgr.B02380|Eucgr.B02380.1 413 ---DSD 405ES-D-----DEETK-----AKGEV-----EEA-YAS- 425---SSKQV
29876.t000003|29876.m000246 402 ---DSD 407DS-D-----DEETK-----AKGEV-----EEA-YAS- 427---SASKV
Potri.009G029100|Potri.009G029100.1 399 ---DSD 401DS-D-----DEETK-----DKGDEVL-----EEA-YAS- 421---SASKV
Bra004536|Bra004536 291 ---DSD 303-----DEEE-----EVR-----EGA-LAS- 424---S-TSKP
Bra040305|Bra040305 304 ---KVEAL-----FALGKIYS- 490-EKQLWSKASLYHGLV-----LRKTKERELVIAASLGAGVALFNLGKRSEALEI- 538-MSVFTMDVPDPLSQ
Pphat.008G051300|Pphat.008G051300.1 478 YLQAM-----VILGQALL- 404-QKDFAEAAKYLEQAASKLL-DACPTVEVEVDLLIVASQWAGVSNTRQKTSSEGITH- 460-LERVANBEPNDPKSKAHYL
Carubv10016975m.g|Carubv10016975m 392 ---VYRAL-----VLMGRVLL- 434-LKIVNDANAYPERAIKLSLGHASADADEVLLIISQWAGACERQKRAH- 491-FERVANQEPEDPCKKYF
Eucgr.B01387|Eucgr.B01387.1 422 YVYRAL-----VLMGRVLL- 434-LKIVNDANAYPERAIKLSLGHASADADEVLLIISQWAGACERQKRAH- 491-FERVANQEPEDPCKKYF
Glyma1g47545|Glyma1g47545.1 401 YIGAL-----VVMGQTL- 413-QKMYEABARHLEAIKSLFLAGNTEVVDLLIISQWAGVACVROGNAEGVAH- 470-FERVANBEPEDPCKKYF
GSVIVG01019145001|GSVIVT01019145001 426 VYRAL-----VVMGQTL- 413-QKMYEABARHLEAIKSLFLAGNTEVVDLLIISQWAGVACVROGNAEGVAH- 470-FERVANBEPEDPCKKYF
gi|85104274 432 ---AAAADTS 429APASAPL-----KPSLDT 427APAVNVL-----MSNPSVGA- 445---MSRPP-GS- 260
Cre16.g690200|Cre16.g690200.t1.2 423 ---KPSLDT 427APAVNVL-----MSNPSVGA- 445---MSRPP-GS- 260
Vocar20001462m.g|Vocar20001462m 412 260----- 418----- 418----- 418-----
Esi0170_0057 419 ---PS-SSKSKPIFMK 394KK-----AAERAR-----EAV-AKASKVRHEELKQHGERS---GED- 549---396
gi|268637951 383 ---PS-SSKSKPIFMK 394KK-----AAERAR-----EAV-AKASKVRHEELKQHGERS---GED- 549---396
Esi0025_0161 519 ---PS-SSKSKPIFMK 394KK-----AAERAR-----EAV-AKASKVRHEELKQHGERS---GED- 549---396
gi|66811452 383 ---PS-SSKSKPIFMK 394KK-----AAERAR-----EAV-AKASKVRHEELKQHGERS---GED- 549---396
gi|28395049 334 ---PS-SSKSKPIFMK 394KK-----AAERAR-----EAV-AKASKVRHEELKQHGERS---GED- 549---396
gi|71960488 363 ---PS-SSKSKPIFMK 394KK-----AAERAR-----EAV-AKASKVRHEELKQHGERS---GED- 549---396
Esi0028_0040 357 AP-----PSMAGPVGK 368AKTFSFASAA-----AGTPKVVLRVSRPKPAGDR---GKTA- 402---366
YER154W 382 EK-----HNPLQ-----PGKDNF- 474-PNIPSSSKPKS-K-----RSSDN-APVDATRMKIPESPP-QR- 422---487
gi|223718097 463 ---HNPLQ-----PGKDNF- 474-PNIPSSSKPKS-K-----RSSDN-APVDATRMKIPESPP-QR- 422---487
CMT118C|CMT118C 399 ---SGLD----- 395-----QPD-ASALGYKVKNEPKK- 413---403
GRMZM2G064804|GRMZM2G064804.T02 392 ---SLE----- 385-----QPD-ASALGYKVKNEPKK- 413---403
LOC.Os10g37690|LOC.Os10g37690.1 382 ---PGVDSPIADK 228ECCQSSPASPVSFVNFSPVMDKESQSS-SSVLCDDRILDLIA-----DRS-SSVLSQRFSDFENRA- 268---428
GRMZM2G055880|GRMZM2G055880.T01 219 ---SSK 251DPSMSSSSSSVPGRR- 1-SK-SSVLRIRITLEROL- 286---419
LOC.Os03g02480|LOC.Os03g02480.1 411 ---SSE 387DPSMSSSSSSVPERRI- 1-SK-SSVLRIRITLEROL- 422---424
Pphat.011G106700|Pphat.011G106700.1 420 ---SSE 387DPSMSSSSSSVPERRI- 1-SK-SSVLRIRITLEROL- 422---424
Bra040348|Bra040348 249 ---SSE 387DPSMSSSSSSVPERRI- 1-SK-SSVLRIRITLEROL- 422---424
Bra000424|Bra000424 385 ---SSE 387DPSMSSSSSSVPERRI- 1-SK-SSVLRIRITLEROL- 422---424
AT2046470 395 ---SSE 387DPSMSSSSSSVPERRI- 1-SK-SSVLRIRITLEROL- 422---424
Carubv10023251m.g|Carubv10023251m 397 ---T-295-PPPGVSNPGDS-----KKARLVH*----- 315---449
73518|73518 295 ---T-295-PPPGVSNPGDS-----KKARLVH*----- 315---449
Potri.001G091800|Potri.001G091800.1 416 ---ASPLVPEPSSKPGVPR- 1-SP-ASVLSQRLRSLEKQV- 167---388
Potri.003G139800|Potri.003G139800.1 168 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
Eucgr.E00058|Eucgr.E00058.1 388 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
Eucgr.E00060|Eucgr.E00060.1 239 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
Bra010053|Bra010053 456 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
AT5G62050 388 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
Carubv10026454m.g|Carubv10026454m 350 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
PGSC0003DMG400005839|PGSC0003DMT40001495 388 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
GSVIVG01019529001|GSVIVT01019529001 386 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
Eucgr.E00060|Eucgr.E00060.1 398 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
29651.t000009|29651.m000289 394 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
30190.t000068|30190.m010832 392 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
Potri.006G073000|Potri.006G073000.1 377 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
Potri.018G140100|Potri.018G140100.1 378 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
Potri.T145700|Potri.T145700.1 378 ---K 239*----- 455---QTQPLVPMNRI- 1-S- 1-LSPVSKRLKALESQV- 418---484
Cucsa.107400|Cucsa.107400.1 400 ---LTAQ 403---PSQSPQSQSDRK-----NGS-SSVLRIRITLEROL- 435---438
Medtr7g036950|Medtr7g036950.1 395 ---ASA 398NQQLPVESSKQPTKISSSSSS-SSVISQRLRSLEKQV- 423---481
Glyma07g31320|Glyma07g31320.1 387 ---TT 388NQSSSIPESAKSHSNKISS-----SSVISQRLRSLEKQV- 423---481
Glyma13g25140|Glyma13g25140.2 445 ---TR 446NGSSSTPEASAKSHSNKISS-----SSVISQRLRSLEKQV- 423---481
Glyma07g36311|Glyma07g36311.1 388 ---T 388NGPNSMPVEPSKHPKKTSS-----SSVLRIRITLEROL- 422---

Esi0227_0023 343 ----- 342----- 342
Cre06.g251900|Cre06.g251900.t1.2 415 -ASA*----- 417----- 417
Vocar20003543m.g|Vocar20003543m 428 PA---ATTSV*----- 434----- 434
Esi0099_0095 450 ----- 449----- 449
CMT063C|CMT063C 489 ----- 488----- 488
Cre17.g729800|Cre17.g729800.t1.2 423 ----- 422----- 422
Vocar20010438m.g|Vocar20010438m 418 ----- 417----- 417
LOC_Os03g62750|LOC_Os03g62750.1 492 P-----TSHDAKRS--RDEENEQDAV*- 510
GRMZM2G136854|GRMZM2G136854.T01 200 ----- 199----- PDVHKL--TDRENGNDV*- 215
GRMZM2G426200|GRMZM2G426200.T01 296 ----- 295----- MLPPAHL--TDQNGNDV*- 313
PGSC0003DMG400010740|PGSC0003DMT40002790 412 ----- 411----- 411
Potri_008G182000|Potri_008G182000.1 510 *----- 509----- 509
Potri_010G051900|Potri_010G051900.1 610 -ARDEQ-P-----DNKRKE-----AVEVNGSV 629ATTDD--KITEDAHQAKRA*----- 646
29929.t000274|29929.m004771 492 -----ENKQ-----KVQI----- 499
Bra032799|Bra032799 489 -----ET*----- 490----- 490
Bra040623|Bra040623 191 T*----- 191----- 191
AT1024490 495 -----R----- 499----- 499
Bra012507|Bra012507 497 -----EE*----- 498----- 498
Carubv10009320m.g|Carubv10009320m 406 ----- 405----- 405
Medtr3g086250|Medtr3g086250.1 496 N-----AV--N-KKNLEKE-----SREVLSTR 514VTNK-QAHGEDSDRVSKD*----- 532
Glymal1g37590|Glymal1g37590.1 509 N-----NVEIN-EKILDKK-----PREVLTTT 529TTNK-QPPAETKD*----- 543
Glymal1g01540|Glymal1g01540.1 500 N-----NVEIN-EKILDKK-----PREVLTTT 520TATNK-QPPAETKD*----- 534
Cucsa_394650|Cucsa_394650.1 488 ET-----TV-RVAKD-AKNGEE-----QRE*----- 506----- 506
GSVIVG01000594001|GSVIVT01000594001 492 N-----YVDVYDE-QHNGKL-----EKVIEV 514-CTDN-KPGEETLQPRREQPTREEV*- 539
Eucgr_B03237|Eucgr_B03237.1 510 TN-----NDA----- 514----- 514----- BRSDN-----* 519
Pphat_003G132900|Pphat_003G132900.1 509 AVGD-----SSGK----- 516----- 516----- QASRKRKRSP* 528
Pphat_010G066400|Pphat_010G066400.1 509 AVGN-----SSAK----- 516----- 516----- IK-GRSKRSP* 527
LOC_Os01g05800|LOC_Os01g05800.1 443 PN-----YS GK----- 448----- 448----- KGRKRKRSP* 460
GRMZM2G110063|GRMZM2G110063.T01 285 K-----Y----- 285----- 443----- KGRKRKRSP* 455
GRMZM5G839422|GRMZM5G839422.T01 438 PN-----YS GK----- 443----- 443----- KGRKRKRSP* 455
12954|12954 314 ----- 313----- 313
Bra035669|Bra035669 430 LP-----DVGG----- 435----- 435----- RRSKRKRSP* 447
Carubv10023172m.g|Carubv10023172m 443 LP-----DVGG----- 448----- 448----- RRSKRKRSP* 460
GSVIVG01024995001|GSVIVT01024995001 433 VPQ-----YAGP----- 439----- 439----- RRSKRKRSP* 451
Cucsa_213790|Cucsa_213790.1 436 PA-----YNRG----- 441----- 441----- RRSKRKRSP* 453
PGSC0003DMG40000401|PGSC0003DMT40000106 433 PN-----YS GP----- 436----- 436----- RRSKRKRSP* 448
Glymal1g14960|Glymal1g14960.1 433 QN-----YSRE----- 438----- 438----- RRSKRKRSP* 450
Glymal2g06920|Glymal2g06920.1 433 QN-----YSRE----- 438----- 438----- RRSKRKRSP* 450
Eucgr_B02380|Eucgr_B02380.1 443 PE-----LNRP----- 448----- 448----- RRSKRKRSP* 460
29876.t000003|29876.m000246 432 PD-----TSRP----- 437----- 437----- RRSKRKRSP* 449
Potri_001G237800|Potri_001G237800.1 434 PD-----TSRP----- 439----- 439----- RRSKRKRSP* 451
Potri_009G029100|Potri_009G029100.1 428 ED-----YSRP----- 433----- 433----- RRSKRKRSP* 445
Bra004536|Bra004536 291 ----- 290----- 290
Bra040305|Bra040305 304 ----- 303----- 303
Pphat_008G051300|Pphat_008G051300.1 555 HRYFKACITLGSVLSQEGRKNKALKLLKAAKYEPVMEKVFIP 597QLEKEL-GIRS*----- 607
Carubv10016975m.g|Carubv10016975m 481 DALVLYSAIPNRRRRAAKYLRRVAVDPSFSELL-K 518QCEDDTLTSSSSDSTHKT*----- 539
Eucgr_B01387|Eucgr_B01387.1 498 YDGLVLLAVCLSTGKKAEEKLRLAVADSSHRYLL-E 536LEKDDDLINLVLNRRADY*----- 557
Glymal1g47545|Glymal1g47545.1 512 DGLLLAATLTDAGQAAKYLRRVAVYKPKYKFL-E 549QCEDD-DPTSDLRERRD*----- 568
30128.t000480|30128.m000919 491 DTLIFLALNREGRAAAYLRVAVAFNPAFKELL-E 528QCEDE-EFGSDLVNRRDY----- 548
GSVIVG01019145001|GSVIVT01019145001 515 DGLLLAATLVRREGRAAAYLRVAVAFNPAFKELL-E 552CERED-GFVNDLVSSRRDY*----- 572
gi|85104274 457 -----KGRKNH----- 462----- 462
Cre16.g690200|Cre16.g690200.t1.2 446 -----KARR----- 449----- 449
Vocar20001462m.g|Vocar20001462m 443 -----KARR----- 448----- 448
Esi0170_0057 261 ----- 260----- 260
gi|268637951 419 ----- 418----- 418
Esi0025_0161 550 -----GPK*----- 552----- 552
gi|66811452 397 ----- 396----- 396
gi|28395049 334 ----- 333----- 333
gi|71960488 367 ----- 366----- 366
Esi0028_0040 403 ----- 411----- 411
YER154W 397 -----FNNKK*----- 402----- 402
gi|223718097 488 -----YFWDHDLG----- 495----- 495
CMT118C|CMT118C 423 -----KARR----- 426----- 426
GRMZM2G064804|GRMZM2G064804.T02 414 -----KARR----- 423----- 423
LOC_Os10g37690|LOC_Os10g37690.1 404 -----KARR----- 413----- 413
GRMZM2G055880|GRMZM2G055880.T01 269 -----KATGESRE*----- 276----- 276
LOC_Os03g02480|LOC_Os03g02480.1 429 -----KARR----- 436----- 436
Pphat_011G106700|Pphat_011G106700.1 420 -----KARR----- 419----- 419
Bra040348|Bra040348 287 -----KDQKKK*----- 293----- 293
Bra000424|Bra000424 423 -----KDQKKK*----- 429----- 429
AT2046470 425 -----KDQKKK*----- 431----- 431
Carubv10023251m.g|Carubv10023251m 427 -----KDQKKK*----- 433----- 433
73518|73518 316 ----- 315----- 315
Potri_001G091800|Potri_001G091800.1 450 -----KARR----- 459----- 459
Potri_003G139800|Potri_003G139800.1 168 -----KARR----- 167----- 167
Eucgr_E00058|Eucgr_E00058.1 389 -----KARR----- 388----- 388
Eucgr_E00060|Eucgr_E00060.1 240 ----- 239----- 239
Bra010053|Bra010053 485 -----KGRKNSSKK--R*----- 495----- 495
AT5G62050 419 -----KGRKNSSKK--K----- 429----- 429
Carubv10026454m.g|Carubv10026454m 419 -----KGRKNSSKK--R*----- 429----- 429
PGSC0003DMG400005839|PGSC0003DMT40001495 350 -----KGRKNSSKK--R*----- 349----- 349
GSVIVG01019529001|GSVIVT01019529001 422 -----KGRKNSSKK--R*----- 443----- 443
Eucgr_E00060|Eucgr_E00060.1 430 -----KGRKNSSKK--R*----- 438----- 438
29651.t000009|29651.m000289 415 -----KGRKNSSKK--R*----- 423----- 423
30190.t000068|30190.m010832 413 -----KGRKNSSKK--R*----- 421----- 421
Potri_006G073000|Potri_006G073000.1 418 -----KGRKNSSKK--R*----- 427----- 427
Potri_018G140100|Potri_018G140100.1 412 -----KGRKNSSKK--R*----- 420----- 420
Potri_T145700|Potri_T145700.1 412 -----KGRKNSSKK--R*----- 420----- 420
Cucsa_107400|Cucsa_107400.1 436 -----KGRKNSSKK--R*----- 446----- 446
Medtr7g036950|Medtr7g036950.1 439 -----KGRKNSSKK--R*----- 446----- 446
Glyma07g31320|Glyma07g31320.1 424 -----KGRKNSSKK--R*----- 431----- 431
Glyma13g25140|Glyma13g25140.2 482 -----KGRKNSSKK--R*----- 489----- 489
Glyma07g36311|Glyma07g36311.1 423 -----KGRKNSSKK--R*----- 430----- 430

