

403021|403021 1 MGSLGHEHPNAAIRRVASAIKEAQAANKHGQLEKPKINPSRQCFAKGIYGLRLIVLH 60APAGDFYSFIGCFSEHHVFEKALPAHLGIKDYARILGEEELATFAE
422696|422696 1 ----- 0 -----
Medtr2g036910 1 ----- 0 -----
Glyma09g06470 1 ----- 0 -----
Glyma15g17695 1 ----- 0 -----
Medtr4g127630 1 ----- 0 -----
Glyma13g00660 1 ----- 0 -----
Glyma17g06820 1 ----- 0 -----
GRMZM2G005209 1 ----- 0 -----
LOC_Os06g07160|LOC_Os06g07160.1 1 ----- 0 -----
Bra038838 1 ----- 0 -----
Bra038562 1 ----- 0 -----
Carubv10013910 1 ----- 0 -----
AT2G19080 1 ----- 0 -----
29462.t000013|29462.m000385 1 ----- 0 -----
Potri.018G147700 1 ----- 0 -----
Potri.006G077100 1 ----- 0 -----
Potri.T161600 1 ----- 0 -----
Cucsa.081250 1 ----- 0 -----
Eucgr.C00132 1 ----- 0 -----
Eucgr.C00132|Eucgr.C00132.1 1 ----- 0 -----
GSVIVG01010902001 1 ----- 0 -----
PGSC0003DMG400008514 1 ----- 0 -----
405344|405344 1 ----- 0 -----
Phpat.004G037800 1 ----- 0 -----
Phpat.012G046000 1 ----- 0 -----
Esi0338_0018 1 ----- 0 -----
YMR060C 1 ----- 0 -----
gi|85114751 1 ----- 0 -----
tr|A8IDQ8|A8IDQ8_CHLRE 1 ----- 0 -----
tr|D8TKNO|D8TKNO 1 ----- 0 -----
gi|392895600 1 ----- 0 -----
gi|56789715 1 ----- 0 -----
gi|17507265 1 ----- 0 -----
gi|1326108 1 ----- 0 -----
gi|119616246 1 ----- 0 -----

403021|403021 108 TYHSLPPPPKME 120SMHDALEVLVEETIRQ---DARDWENDVAKLYPVLLVDFLPGNDGTFGNCSGLTDDTE 176EPDGVPM---DELCAELIDPTKLPFTVTVT
422696|422696 1 ----- 0 -----
Medtr2g036910 1 ----- 0 -----
Glyma09g06470 1 ----- 0 -----
Glyma15g17695 1 ----- 0 -----
Medtr4g127630 1 ----- 0 -----
Glyma13g00660 1 ----- 0 -----
Glyma17g06820 1 ----- 0 -----
GRMZM2G005209 1 ----- 0 -----
LOC_Os06g07160|LOC_Os06g07160.1 1 ----- 0 -----
Bra038838 1 ----- 0 -----
Bra038562 1 ----- 0 -----
Carubv10013910 1 ----- 0 -----
AT2G19080 1 ----- 0 -----
29462.t000013|29462.m000385 1 ----- 0 -----
Potri.018G147700 1 ----- 0 -----
Potri.006G077100 1 ----- 0 -----
Potri.T161600 1 ----- 0 -----
Cucsa.081250 1 ----- 0 -----
Eucgr.C00132 1 ----- 0 -----
Eucgr.C00132|Eucgr.C00132.1 1 ----- 0 -----
GSVIVG01010902001 1 ----- 0 -----
PGSC0003DMG400008514 1 ----- 0 -----
405344|405344 1 ----- 0 -----
Phpat.004G037800 1 ----- 0 -----
Phpat.012G046000 1 ----- 0 -----
Esi0338_0018 1 ----- 0 -----
YMR060C 1 ----- 0 -----
gi|85114751 1 ----- 0 -----
tr|A8IDQ8|A8IDQ8_CHLRE 1 ----- 0 -----
tr|D8TKNO|D8TKNO 1 ----- 0 -----
gi|392895600 1 ----- 0 -----
gi|56789715 1 ----- 0 -----
gi|17507265 1 ----- 0 -----
gi|1326108 1 ----- 0 -----
gi|119616246 1 ----- 0 -----

403021|403021 203 WDVSSRSKDEKPMRLSEYKRGKHLVLTVRPP 233FHLPTACPRS-----L-----STYLYLCLAKKPFVLEHSNA----- 265-----
422696|422696 41 SRSDKKEFVRLSEYKRGKHLVLTVRPP 67SFHLPTSCPRC-----L-----STYLYLCLAKKPFVLEHSNA----- 99-----DNLNF
Medtr2g036910 1 ----- 18CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 50 ----- FPDSDQIF
Glyma09g06470 1 ----- MATFPESTQNNLVVRRK 19CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 51 ----- FPDSDQIF
Glyma15g17695 1 ----- MATFPESTQNNLVVRRK 19CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 51 ----- FPDSDQIF
Medtr4g127630 1 ----- MAEVLNVVRRK 12CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 44 ----- FPDSDQIF
Glyma13g00660 1 ----- MAEVLNVVRRK 12CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 44 ----- FPDSDQIF
Glyma17g06820 1 ----- MAEVLNVVRRK 12CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 44 ----- FPDSDQIF
GRMZM2G005209 18 --SAMASAAAVWMAARKVLVRRK 41CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 73 ----- FPDSDQIF
LOC_Os06g07160|LOC_Os06g07160.1 2 --ASAAAAAAWMAARKVLVRRK 25AFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 57 ----- FPDSDQIF
Bra038838 1 ----- MEGDQTSGGFLLVRRK 18CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 50 ----- FPDSDQIF
Bra038562 1 ----- MEGDQTSGGFLLVRRK 18CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 49 ----- FPDSDQIF
Carubv10013910 69 --THTNAIMEGDQTSGGFLLVRRK 91SDFLPTGCPQC ----- L ----- SAYIFLKLKSOVPEFLDYHFN ----- 123 ----- FPDSDQIF
AT2G19080 1 ----- MEGDQTSGGFLLVRRK 17SDFLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 49 ----- FPDSDQIF
29462.t000013|29462.m000385 1 ----- MEGDQTSGGFLLVRRK 17SDFLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 49 ----- FPDSDQIF
Potri.018G147700 1 ----- MEGDQTSGGFLLVRRK 17SDFLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 49 ----- FPDSDQIF
Potri.006G077100 1 ----- MEGDQTSGGFLLVRRK 17SDFLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 49 ----- FPDSDQIF
Potri.T161600 1 ----- MEGDQTSGGFLLVRRK 17SDFLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 49 ----- FPDSDQIF
Cucsa.081250 1 ----- MEGDQTSGGFLLVRRK 16SDFLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 48 ----- FPDSDQIF
Eucgr.C00132 1 ----- MEGDQTSGGFLLVRRK 18CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 50 ----- FPDSDQIF
Eucgr.C00132|Eucgr.C00132.1 1 ----- MEGDQTSGGFLLVRRK 18CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 50 ----- FPDSDQIF
GSVIVG01010902001 1 ----- MD-ELDNQKLLVRRK 10CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 48 ----- FPDSDQIF
PGSC0003DMG400008514 1 ----- MEB-ARERKLLVRRK 17CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 49 ----- FPDSDQIF
405344|405344 1 ----- MEGDQTSGGFLLVRRK 17CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 49 ----- FPDSDQIF
Phpat.004G037800 1 ----- MEGDQTSGGFLLVRRK 17CFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 49 ----- FPDSDQIF
Phpat.012G046000 6 --SSSSAWAESSGSADLVVTRFE 29AFGLPTGCPQC ----- M ----- SAYIFLKLKSOVPEFLDYHFN ----- 61 ----- FPDSDQIF
Esi0338_0018 5 --EHGDAMPVRSWNP-LRAAFKSWGR 27IEGPLELQPGPVITHGSALDMVVVQFRPAWELCAHLEFVRLVRRV ----- EN- 76 ----- SSMYMSAAAGLYP
YMR060C 1 ----- MVKGSVHLWQK 11DGKASLISVDS ----- I ----- ALVWFELNCTSEAKSMVAGLQVFSN ----- 50 ----- NTDL--SSGKLP
gi|85114751 1 ----- MTLEPFWWGP 10AGGLPISDAFC ----- M ----- ATVTMFAQTLAADYL-----LVQS 42 ----- SPSA--VPSHLP
tr|A8IDQ8|A8IDQ8_CHLRE 1 ----- MSGNVCIKRWPE 13GGLSLSHAC ----- M ----- QAELMPLMGAQAVE-----ACPT 45 ----- SSS--SPGGLP
tr|D8TKNO|D8TKNO 1 ----- 0 ----- 0 ----- 0 ----- 0 ----- 0 -----
gi|392895600 14 --A--LSMNAADWED-VSLFPTFLN 34DQAMMYDFADP ----- M ----- AQOTFIRMTSIFLNVR-----QRPN 66 ----- VDFI--SPGVVPE
gi|56789715 7 --AFVSGTAAAPFWENATLYQQLHG 30EQILSDNAAS ----- M ----- AQOAFQMCNLEPIKVV-----CRAN 62 ----- AEFM--SPGKVP
gi|17507265 1 ----- M ----- EPHIFPS 8DFGLPTIDVDS ----- L ----- QFLACSKMCSFVRVI-----QSTR 40 ----- PWR--SPGSLFP
gi|1326108 1 ----- MAAPM-----EFCWSG 12GGLSVDLDS ----- M ----- ALTMARFTGALKLVH-----KISN 44 ----- PWQ--SPGTLPE
gi|119616246 1 ----- MAAPL-----EFCWSG 12GGLSVDLDS ----- M ----- VMAAFVFGALKLVN-----VIDN 44 ----- TWR--GSRGVP

403021|403021
422696|422696
Medtr2g036910
Glyma09g06470
Glyma15g17695
Medtr4g127630
Glyma13g00660
Glyma17g06820
GRMZ2G005209
LOC_Os06g07160|LOC_Os06g07160.1
Bra038838
Bra038562
Carubv10013910
AT2G19080
29462.t000013|29462.m000385
Potri.0188147700
Potri.006607100
Potri.T161600
Cucsa.081250
Eucgr.C00132
Eucgr.C00132|Eucgr.C00132.1
GSVIVG01010902001
PGSC0003DMG400008514
405344|405344
Phpat.004G037800
Phpat.012G046000
Esi0338_0018
YMR060C
gi|85114751
tr|A8IDQ8|A8IDQ8_CHLRE
tr|D8TKNO|D8TKNO
gi|392895600
gi|56789715
gi|17507265
gi|1326108
gi|119616246

484 D-DGKQLKQKA---GGGGDMS---RE---ODGKNFHE 512FVKLKSNSVDEEDVCDANVESFKAISRLIGEMSGDTL---DPLLDRCPLKGDYKIYLE 570KTY
270 ----- 269 -----
261 GGF-S-TSSSKFKRKRKPKRKHOOHKKDDKRYK- 287-RRAKYFV-----VAQLVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 330
262 NGR-S-TSSSKFKRKRKPKRROPFKBEETLR- 288-RRAKYFV-----VAQLVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 329
262 NGR-S-TSSSKFKRKRKPKRROPFKBEETLR- 288-RRAKYFV-----VAQLVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 328
256 -Q-S-TORRFBKPKRKRH-RTBEETKFK- 275-RKGYFV-----VAQLVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 314
256 --K-S-HSSSKPKSKPKRRE-KTBEETKFK- 279-RRAKYFV-----VAQLVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 320
256 --K-S-HSSSKPKSKPKRRE-KTBEETKFK- 279-RRAKYFV-----VAQLVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 321
285 PRRRPSA-DHSYKPKPKRKRRE-RTBEETKFK- 313-RRAKYFV-----VAQLVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 352
271 NKRASG-GRVYKPKPKRKRRE-RTBEETKFK- 298-RRAKYFV-----VAQLVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 337
175 ----- RKGRKPKSKPKRRE-KTBEETKFK- 196-KRKFYF-----AAQFLAVVYVLSVMSGGGSS--DELEYEDDD* 231
158 ----- GKGRKPKSKPKRRE-KTBEETKFK- 279-RRAKYFV-----AAQFLAVVYVLSVMSGGGSS--DELEYEDDD* 314
329 SFS-----RRGSKPKSKPKRRE-KTBEETKFK- 353-KRKRFFL-----AAQFLAVVYVLSVMSGGGSS--DELEYEDDD* --- 389
258 ----- RKGRKPKSKPKRRE-KTBEETKFK- 279-RRAKYFV-----AAQFLAVVYVLSVMSGGGSS--DELEYEDDD* 315
227 ----- 226 ----- 226 -----
195 ----- 194 ----- 194 -----
257 TRR-S-NSSSKPKRKRKPKRRE-KTBEETKFK- 283-RRAKYFV-----VTQVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 323
257 TRR-S-NSSSKPKRKRKPKRRE-KTBEETKFK- 278-RRAKYFV-----VTQVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 284
262 RRGF-Y-NWSSKPKRKRKPKRRE-KTBEETKFK- 288-RRAKYFV-----GAQLVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 330
260 RGGP-S-HWSSKPKRKRKPKRRE-KTBEETKFK- 286-RRAKYFV-----AAQFLAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 327
260 RGGP-S-HWSSKPKRKRKPKRRE-KTBEETKFK- 286-RRAKYFV-----AAQFLAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 327
259 RRGF-S-NWSSKPKRKRKPKRRE-KTBEETKFK- 285-RRAKYFV-----VTQVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 326
259 RRGF-S-NWSSKPKRKRKPKRRE-KTBEETKFK- 285-RRAKYFV-----VTQVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 326
264 HASSGRDMDKGNPKRKRRE-KTBEETKFK- 292-RKGYFV-----NRQVAVVLFVLSLMSGGADSG-ESVLDLDDGGLDFGMDG* 330
265 KLGSK-----EREER-AMKA-RSSSDLLR- 297-RRAKYFV-----IAQFLAVVYVLSVMSGGGSS--DELEYEDDD* 322
277 NQDFK-----ERDNP-ER-KRBEKDFK- 288-RRAKYFV-----IAQFLAVVYVLSVMSGGGSS--DELEYEDDD* 336
282 KKSQ-----SED-----RL-RDAM----- 299-----LRADYVNSHN----- 309
282 -----E-----L-LNSMSNKIDD 293FVHHPSPNNRQDPQ-FREQGN-----VMSLYNHWACKYI* 327
326 -----ACD-----SALSIVGR 336FVAVIDD-----IPMLGREMS-----RWVAQRQRVAEENSA-----ETQLVVR 376RSVGSERSLL
148 -----G-----QKRAPDPEVH-----P-----SAAELFRRH-----TWL----- 174-----GAGT
211 -----QKTPAPTV-----P-158----- 210-----SSAERQFRHS-----YYWL----- 210-----GAGT
264 AK-----ADWEAAATTT----- 265--EEASESL--PEEPPMRDA-----TLNLT----- 286
256 PA-----PTEBEETKFK-RRQVLSVLAG 276LA----- 280
264 PA-----QETVDANLQK-LHQLVNKESN 286LTERMDNRRQSPQLPPRKL-----TL----- 309

403021|403021
422696|422696
Medtr2g036910
Glyma09g06470
Glyma15g17695
Medtr4g127630
Glyma13g00660
Glyma17g06820
GRMZ2G005209
LOC_Os06g07160|LOC_Os06g07160.1
Bra038838
Bra038562
Carubv10013910
AT2G19080
29462.t000013|29462.m000385
Potri.0188147700
Potri.006607100
Potri.T161600
Cucsa.081250
Eucgr.C00132
Eucgr.C00132|Eucgr.C00132.1
GSVIVG01010902001
PGSC0003DMG400008514
405344|405344
Phpat.004G037800
Phpat.012G046000
Esi0338_0018
YMR060C
gi|85114751
tr|A8IDQ8|A8IDQ8_CHLRE
tr|D8TKNO|D8TKNO
gi|392895600
gi|56789715
gi|17507265
gi|1326108
gi|119616246

574 E-PSVSIIAESRAPSFEEIDTLNNEVLLWVGTSACNLKMGQPAIYNAPVPGYMGF- 628-----
270 ----- 269 -----
330 ----- 330 -----
329 ----- 328 -----
315 ----- 314 -----
321 ----- 320 -----
322 ----- 321 -----
328 ----- 327 -----
322 ----- 321 -----
232 ----- 231 -----
315 ----- 314 -----
390 ----- 389 -----
316 ----- 315 -----
227 ----- 226 -----
195 ----- 194 -----
324 ----- 323 -----
285 ----- 284 -----
331 ----- 330 -----
327 ----- 327 -----
328 ----- 327 -----
328 ----- 327 -----
327 ----- 326 -----
327 ----- 326 -----
331 ----- 330 -----
327 ----- 326 -----
337 ----- 336 -----
310 ----- 309 -----
328 ----- 327 -----
388 LAGAGLTLAIN-VAG-LGIYV-YRYSRLLG-APLQVWRPLVGLG- 429-SFGAA-----GAMFAGLA-----
251 --GAGAAVVAAYLLSG-Q-----GGGGVGV-PAQ-----QA-----AGV 279PQQRERQQPQVAAKETAIAIVSHVIDTQQRDTIGVEQAPGPMVAVGATKQVPR
179 AIASVLSLGR-----YIQFAT-VME-----QGAVVQGVGV 209AAKQKEDVAPAGADVTRQLPHLQASLQKHSRPPGE--QPQPPSRAAGLETP 26
264 ----- 263 -----
281 ----- 280 -----
310 ----- 309 -----
310 ----- 309 -----

403021|403021
422696|422696
Medtr2g036910
Glyma09g06470
Glyma15g17695
Medtr4g127630
Glyma13g00660
Glyma17g06820
GRMZ2G005209
LOC_Os06g07160|LOC_Os06g07160.1
Bra038838
Bra038562
Carubv10013910
AT2G19080
29462.t000013|29462.m000385
Potri.0188147700
Potri.006607100
Potri.T161600
Cucsa.081250
Eucgr.C00132
Eucgr.C00132|Eucgr.C00132.1
GSVIVG01010902001
PGSC0003DMG400008514
405344|405344
Phpat.004G037800
Phpat.012G046000
Esi0338_0018
YMR060C
gi|85114751
tr|A8IDQ8|A8IDQ8_CHLRE
tr|D8TKNO|D8TKNO
gi|392895600
gi|56789715
gi|17507265
gi|1326108
gi|119616246

629 ----- 628 ---KGLYCTGASCKAVSYAFSGV-----DGPVILALGDDMLVFPK-AGEVKL 671-----QFIVQVEK*
270 ----- 269 -----
331 --- 330 ----- 330 -----
330 --- 329 ----- 329 -----
329 --- 328 ----- 328 -----
315 --- 314 ----- 314 -----
321 --- 320 ----- 320 -----
322 --- 321 ----- 321 -----
328 --- 327 ----- 327 -----
322 --- 321 ----- 321 -----
338 --- 337 ----- 337 -----
232 --- 231 ----- 231 -----
315 --- 314 ----- 314 -----
390 --- 389 ----- 389 -----
316 --- 315 ----- 315 -----
227 --- 226 ----- 226 -----
195 --- 194 ----- 194 -----
324 --- 323 ----- 323 -----
285 --- 284 ----- 284 -----
331 --- 330 ----- 330 -----
327 --- 327 ----- 327 -----
328 --- 327 ----- 327 -----
327 --- 326 ----- 326 -----
327 --- 326 ----- 326 -----
331 --- 330 ----- 330 -----
323 --- 322 ----- 322 -----
337 --- 336 ----- 336 -----
356 --- 355 ---QGTAAAGSTTAAA-AAAEAAA-----AGKATAANESLPVK-----388-Y--TVISIAAFMV-----LSNLSLRG
328 --- 327 ----- 327 -----
443 --- 442 ----- 442 -----
337 VPD 339SAGGPPGGGRPA-GE-ALSVS---ST-----GLEGGKAAA 370RAGGKAAEGAAVPAEAAIRIGGAAAKQGVV-
268 7AGASGGTSAGRQKAKAAAVAAAKGAASTGRAAKGAAGATVERAGAAAKAGSKAGGEAAV 327RGAQAGASGAAKMVEQASGMKMASQGVGRAAAVAREAPGVVVS
211 --- 210 ----- 210 -----
264 --- 263 ----- 263 -----
313 --- 312 ----- 312 -----
281 --- 280 ----- 280 -----
327 --- 326 ----- 326 -----

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403021|403021      680 ----- 679 -----
422696|422696      270 ----- 269 ----- 269 -----
Medtr2g036910     331 ----- 330 -----
Glyma09g06470     330 ----- 329 ----- 329 -----
Glyma15g17695     329 ----- 328 ----- 328 -----
Medtr4g127630     315 ----- 314 ----- 314 -----
Glyma13g00660     321 ----- 320 ----- 320 -----
Glyma17g06820     322 ----- 321 ----- 321 -----
GRMZM2G005209     353 ----- 352 ----- 352 -----
LOC_Os06g07160|LOC_Os06g07160.1 338 ----- 337 ----- 337 -----
Bra038838         232 ----- 231 ----- 231 -----
Bra038562         315 ----- 314 ----- 314 -----
Carubv10013910    390 ----- 389 ----- 389 -----
AT2G19080         316 ----- 315 ----- 315 -----
29462.t000013|29462.m000385      227 ----- 226 ----- 226 -----
Potri.018G147700  195 ----- 194 ----- 194 -----
Potri.006G07100  324 ----- 323 ----- 323 -----
Potri.T161600     285 ----- 284 ----- 284 -----
Cucsa.081250      331 ----- 330 ----- 330 -----
Eucgr.C00132      328 ----- 327 ----- 327 -----
Eucgr.C00132|Eucgr.C00132.1      328 ----- 327 ----- 327 -----
GSVIVG01010902001 327 ----- 326 ----- 326 -----
PGSC0003DMG400008514 327 ----- 326 ----- 326 -----
405344|405344      331 ----- 330 ----- 330 -----
Phpat.004G037800  323 ----- 322 ----- 322 -----
Phpat.012G046000  337 ----- 336 ----- 336 -----
Esi0338_0018      408 ----- 407 ----- 407 -----
YMR060C           328 ----- 327 ----- 327 -----
gi|85114751       443 ----- 442 ----- 442 -----
tr|A81DQ8|A81DQ8_CHLRE 401 ----- --VGVEGAKSAVEGAQAVTGA 419AVRGTQGA-- --KAASGAAKSGIEALPYRLL 447SGWLHVLMVLSAVGAAAARG
tr|D8TKNO|D8TKNO   373 ----- ATKGAASARRAVGT 387AAVYARSAVQTGRGAASMGAWAAGADAVQRGAMRVAQGIQTLFHLWYFAVVLPLYRLA 447AGSLHMGWLAGNSAASAARGVWFFLD
gi|392895600      211 ----- 210 ----- 210 -----
gi|56789715       264 ----- 263 ----- 263 -----
gi|17507265       313 ----- 312 ----- 312 -----
gi|1326108        281 ----- 280 ----- 280 -----
gi|119616246      327 ----- 326 ----- 326 -----

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403021|403021      680 ----- 679 -----
422696|422696      270 ----- 269 ----- 269 -----
Medtr2g036910     331 ----- 330 ----- 330 -----
Glyma09g06470     330 ----- 329 ----- 329 -----
Glyma15g17695     329 ----- 328 ----- 328 -----
Medtr4g127630     315 ----- 314 ----- 314 -----
Glyma13g00660     321 ----- 320 ----- 320 -----
Glyma17g06820     322 ----- 321 ----- 321 -----
GRMZM2G005209     353 ----- 352 ----- 352 -----
LOC_Os06g07160|LOC_Os06g07160.1 338 ----- 337 ----- 337 -----
Bra038838         232 ----- 231 ----- 231 -----
Bra038562         315 ----- 314 ----- 314 -----
Carubv10013910    390 ----- 389 ----- 389 -----
AT2G19080         316 ----- 315 ----- 315 -----
29462.t000013|29462.m000385      227 ----- 226 ----- 226 -----
Potri.018G147700  195 ----- 194 ----- 194 -----
Potri.006G07100  324 ----- 323 ----- 323 -----
Potri.T161600     285 ----- 284 ----- 284 -----
Cucsa.081250      331 ----- 330 ----- 330 -----
Eucgr.C00132      328 ----- 327 ----- 327 -----
Eucgr.C00132|Eucgr.C00132.1      328 ----- 327 ----- 327 -----
GSVIVG01010902001 327 ----- 326 ----- 326 -----
PGSC0003DMG400008514 327 ----- 326 ----- 326 -----
405344|405344      331 ----- 330 ----- 330 -----
Phpat.004G037800  323 ----- 322 ----- 322 -----
Phpat.012G046000  337 ----- 336 ----- 336 -----
Esi0338_0018      408 ----- 407 ----- 407 -----
YMR060C           328 ----- 327 ----- 327 -----
gi|85114751       443 ----- 442 ----- 442 -----
tr|A81DQ8|A81DQ8_CHLRE 469 ----- AVWSLDTAAWAGDGAYSRLLSGVSLNRGMDAAISATPP 507LVKQQLARAAVVAAPQGRDLDSLNSKSPSQVGSIFSGLASAAAAAGKQQLMA-- 562-----
tr|D8TKNO|D8TKNO   475 ----- SATWAGELAYRWLLDGMVRNMGMDAAISATPP 507LVKQQLARAAVVAAPQGRDLDSLNSKSPSQVGSIFSGLASAAAAAGKQQLMA-- 562-----
gi|392895600      211 ----- 210 ----- 210 -----
gi|56789715       264 ----- 263 ----- 263 -----
gi|17507265       313 ----- 312 ----- 312 -----
gi|1326108        281 ----- 280 ----- 280 -----
gi|119616246      327 ----- 326 ----- 326 -----

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403021|403021      680 ----- 679 -----
422696|422696      270 ----- 269 ----- 269 -----
Medtr2g036910     331 ----- 330 ----- 330 -----
Glyma09g06470     330 ----- 329 ----- 329 -----
Glyma15g17695     329 ----- 328 ----- 328 -----
Medtr4g127630     315 ----- 314 ----- 314 -----
Glyma13g00660     321 ----- 320 ----- 320 -----
Glyma17g06820     322 ----- 321 ----- 321 -----
GRMZM2G005209     353 ----- 352 ----- 352 -----
LOC_Os06g07160|LOC_Os06g07160.1 338 ----- 337 ----- 337 -----
Bra038838         232 ----- 231 ----- 231 -----
Bra038562         315 ----- 314 ----- 314 -----
Carubv10013910    390 ----- 389 ----- 389 -----
AT2G19080         316 ----- 315 ----- 315 -----
29462.t000013|29462.m000385      227 ----- 226 ----- 226 -----
Potri.018G147700  195 ----- 194 ----- 194 -----
Potri.006G07100  324 ----- 323 ----- 323 -----
Potri.T161600     285 ----- 284 ----- 284 -----
Cucsa.081250      331 ----- 330 ----- 330 -----
Eucgr.C00132      328 ----- 327 ----- 327 -----
Eucgr.C00132|Eucgr.C00132.1      328 ----- 327 ----- 327 -----
GSVIVG01010902001 327 ----- 326 ----- 326 -----
PGSC0003DMG400008514 327 ----- 326 ----- 326 -----
405344|405344      331 ----- 330 ----- 330 -----
Phpat.004G037800  323 ----- 322 ----- 322 -----
Phpat.012G046000  337 ----- 336 ----- 336 -----
Esi0338_0018      408 ----- 407 ----- 407 -----
YMR060C           328 ----- 327 ----- 327 -----
gi|85114751       443 ----- 442 ----- 442 -----
tr|A81DQ8|A81DQ8_CHLRE 563 ----- --AVGGA-- 567----- --PPSEDLVEQARLLVWHVWVWVGRQLQLTAAA--
tr|D8TKNO|D8TKNO   575 ----- LVEQVNAALHAAFDPRDVSLEMEKGEPPQEQGGQPQGGAPSGAAKGGAA 625ALRSVDVLHDKLLDQARLLVWHVWVWVGRQLQLTAAAEEVAAVTRGMWSWLLRCVAHL
gi|392895600      211 ----- 210 ----- 210 -----
gi|56789715       264 ----- 263 ----- 263 -----
gi|17507265       313 ----- 312 ----- 312 -----
gi|1326108        281 ----- 280 ----- 280 -----
gi|119616246      327 ----- 326 ----- 326 -----

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403021|403021 680 ----- 679 -----
422696|422696 270 ----- 269 ----- 679 -----
Medtr2g036910 331 ----- 330 -----
Glyma09g06470 330 ----- 329 ----- 330
Glyma15g17695 329 ----- 328 ----- 329
Medtr4g127630 315 ----- 314 ----- 314
Glyma13g00660 321 ----- 320 ----- 320
Glyma17g06820 322 ----- 321 ----- 321
GRMZM2G005209 353 ----- 352 ----- 352
LOC_Os06g07160|LOC_Os06g07160.1 338 ----- 337 ----- 337
Bra038838 232 ----- 231 ----- 231
Bra038562 315 ----- 314 ----- 314
Carubv10013910 390 ----- -- 389 ----- -- 389 -----
AT2G19080 316 ----- 315 ----- 315
29462.t000013|29462.m000385 227 ----- 226 ----- 226
Potri.018G147700 195 ----- 194 ----- 194
Potri.006G071100 324 ----- 323 ----- 323
Potri.T161600 285 ----- 284 ----- 284
Cucsa.081250 331 ----- 330 ----- 330
Eucgr.C00132 328 ----- 327 ----- 327
Eucgr.C00132|Eucgr.C00132.1 328 ----- 327 ----- 327
GSVIVG01010902001 327 ----- 326 ----- 326
PGSC0003DMG400008514 327 ----- 326 ----- 326
405344|405344 331 ----- 330 ----- 330
Phpat.004G037800 323 ----- 322 ----- 322
Phpat.012G046000 337 ----- 336 ----- 336
Esi0338_0018 408 ----- 407 ----- 407
YMR060C 328 ----- 327 ----- 327
gi|85114751 443 ----- 442 ----- 442
tr|A81DQ8|A81DQ8_CHLRE 597 ----- 596 ----- 596
tr|D8TKNO|D8TKNO 681 GAALG 685LLAAMAAAGGAVVAAGAWALASGVRQLRMAATLEVRARRMWSPLRALRAIDMVSALAGP 745LLRTPPLPSPRGRALGGEKVAEAEQPGVRKDEEEK
gi|392895600 211 ----- 210 ----- 210
gi|56789715 264 ----- 263 ----- 263
gi|17507265 313 ----- 312 ----- 312
gi|1326108 281 ----- 280 ----- 280
gi|119616246 327 ----- 326 ----- 326

403021|403021 680 ----- 679 -----
422696|422696 270 ----- 269 ----- 679 -----
Medtr2g036910 331 ----- 330 ----- 330
Glyma09g06470 330 ----- 329 ----- 329
Glyma15g17695 329 ----- 328 ----- 328
Medtr4g127630 315 ----- 314 ----- 314
Glyma13g00660 321 ----- 320 ----- 320
Glyma17g06820 322 ----- 321 ----- 321
GRMZM2G005209 353 ----- 352 ----- 352
LOC_Os06g07160|LOC_Os06g07160.1 338 ----- 337 ----- 337
Bra038838 232 ----- 231 ----- 231
Bra038562 315 ----- 314 ----- 314
Carubv10013910 390 ----- -- 389 ----- -- 389 -----
AT2G19080 316 ----- 315 ----- 315
29462.t000013|29462.m000385 227 ----- 226 ----- 226
Potri.018G147700 195 ----- 194 ----- 194
Potri.006G071100 324 ----- 323 ----- 323
Potri.T161600 285 ----- 284 ----- 284
Cucsa.081250 331 ----- 330 ----- 330
Eucgr.C00132 328 ----- 327 ----- 327
Eucgr.C00132|Eucgr.C00132.1 328 ----- 327 ----- 327
GSVIVG01010902001 327 ----- 326 ----- 326
PGSC0003DMG400008514 327 ----- 326 ----- 326
405344|405344 331 ----- 330 ----- 330
Phpat.004G037800 323 ----- 322 ----- 322
Phpat.012G046000 337 ----- 336 ----- 336
Esi0338_0018 408 ----- 407 ----- 407
YMR060C 328 ----- 327 ----- 327
gi|85114751 443 ----- 442 ----- 442
tr|A81DQ8|A81DQ8_CHLRE 637 ----- 636 ----- 636
tr|D8TKNO|D8TKNO 783 EKPAHPEAAAKAEDTKPEGKG 805EGRAKGMVATAAAAAAPLFEAIRGGQAYARDSLAATRFVQSLVPKDPEREAEAAARAVE 865AFAELSAVLRSDDRAFTTT
gi|392895600 211 ----- 210 ----- 210
gi|56789715 264 ----- 263 ----- 263
gi|17507265 313 ----- 312 ----- 312
gi|1326108 281 ----- 280 ----- 280
gi|119616246 327 ----- 326 ----- 326

403021|403021 680 ----- 679 -----
422696|422696 270 ----- 269 ----- 679 -----
Medtr2g036910 331 ----- 330 ----- 330
Glyma09g06470 330 ----- 329 ----- 329
Glyma15g17695 329 ----- 328 ----- 328
Medtr4g127630 315 ----- 314 ----- 314
Glyma13g00660 321 ----- 320 ----- 320
Glyma17g06820 322 ----- 321 ----- 321
GRMZM2G005209 353 ----- 352 ----- 352
LOC_Os06g07160|LOC_Os06g07160.1 338 ----- 337 ----- 337
Bra038838 232 ----- 231 ----- 231
Bra038562 315 ----- 314 ----- 314
Carubv10013910 390 ----- -- 389 ----- -- 389 -----
AT2G19080 316 ----- 315 ----- 315
29462.t000013|29462.m000385 227 ----- 226 ----- 226
Potri.018G147700 195 ----- 194 ----- 194
Potri.006G071100 324 ----- 323 ----- 323
Potri.T161600 285 ----- 284 ----- 284
Cucsa.081250 331 ----- 330 ----- 330
Eucgr.C00132 328 ----- 327 ----- 327
Eucgr.C00132|Eucgr.C00132.1 328 ----- 327 ----- 327
GSVIVG01010902001 327 ----- 326 ----- 326
PGSC0003DMG400008514 327 ----- 326 ----- 326
405344|405344 331 ----- 330 ----- 330
Phpat.004G037800 323 ----- 322 ----- 322
Phpat.012G046000 337 ----- 336 ----- 336
Esi0338_0018 408 ----- 407 ----- 407
YMR060C 328 ----- 327 ----- 327
gi|85114751 443 ----- 442 ----- 442
tr|A81DQ8|A81DQ8_CHLRE 703 AAYRSTRRLAAASLAALGDMAGNTAADLARRYRVPLPKLAWLHSRAT 749QLAKDQAVASFAAVAGAGPAHLVASVQGTPIAPVGGSGQIGGTPAAGPL
tr|D8TKNO|D8TKNO 885 WRLAQASMAALTDLAGNLITDVARRYHIPKFEWFKGKAA 925QLAQNRAIASFAKIAGTGPASVVAGMVGAPMPLAAGGKGYESGDDKNGRQGEQAAGGGE 985G
gi|392895600 211 ----- 210 ----- 210
gi|56789715 264 ----- 263 ----- 263
gi|17507265 313 ----- 312 ----- 312
gi|1326108 281 ----- 280 ----- 280
gi|119616246 327 ----- 326 ----- 326

403021 403021	680	----- 679-----	679
422696 422696	270	--- 269-----	269
Medtr2g036910	331	- 330-----	330
Glyma09g06470	330	- 329-----	329
Glyma15g17695	329	- 328-----	328
Medtr4g127630	315	- 314-----	314
Glyma13g00660	321	- 320-----	320
Glyma17g006820	322	- 321-----	321
GRMZM2G005209	353	-- 352-----	352
LOC_Os06g07160 LOC_Os06g07160.1	338	- 337-----	337
Bra038838	232	231-----	231
Bra038562	315	- 314-----	314
Carubv10013910	390	--- 389-----	389
AT2G19080	316	- 315-----	315
29462.t000013 29462.m000385	227	- 226-----	226
Potri.0188147700	195	-- 194-----	194
Potri.0066077100	324	- 323-----	323
Potri.T161600	285	- 284-----	284
Cucsa.081250	331	- 330-----	330
Eucgr.C00132	328	- 327-----	327
Eucgr.C00132 Eucgr.C00132.1	328	- 327-----	327
GSVIG01010902001	327	- 326-----	326
PGSC0003DMG400008514	327	- 326-----	326
405344 405344	331	- 330-----	330
Phpat.004G037800	323	- 322-----	322
Phpat.012G046000	337	- 336-----	336
Esi0338_0018	408	-- 407-----	407
YMR060C	328	- 327-----	327
gi 85114751	443	- 442-----	442
tr ASIDQ8 ASIDQ8_CHLRE	801	- 800-----	800
tr D8TKN0 D8TKN0	987	KATTGGREQEVEG 999	
gi 392895600	211	-- 210-----	210
gi 56789715	264	-- 263-----	263
gi 17507265	313	312-----	312
gi 1326108	281	- 280-----	280
gi 119616246	327	- 326-----	326