

gi|85116624 1 ----- 0 -----
YNL310C 1 ----- 0 -----
CMT595C 1 ----- 0 -----
gi|66800951|Dd 1 ----- 0 -----
Esi0238_0026 1 ----- 0 -----
Cre07.g334850|Cre07.g334850.t1.2 1 ----- 0 -----
tr|Q9TXQ4|Q9TXQ4_CAEEL 1 ----- 0 -----
gi|124249392 1 ----- 0 -----
AT3G54826 1 ----- 0 -----
Carubv10018399m.g|Carubv10018399m 1 ----- 0 -----
Bra003197|Bra003197 1 ----- 0 -----
Bra007101|Bra007101 1 ----- 0 -----
GSVIVG01016242001|GSVIVT01016242001 1 ----- 0 -----
PGSC0003DMG400027152|PGSC0003DMT40006983 1 ----- 0 -----
Cucsa.308490|Cucsa.308490.1 1 ----- 0 -----
Phpat.010G079800|Phpat.010G079800.1 1 ----- 0 -----
Eucgr.G02856|Eucgr.G02856.1 1 ----- 0 -----
Glyma10g35330|Glyma10g35330.1 1 ----- 0 -----
Glyma20g32180|Glyma20g32180.1 1 ----- 0 -----
Medtr1g094720|Medtr1g094720.1 1 ----- 0 -----
GRMZM2G064608|GRMZM2G064608_T01 1 ----- 0 -----
LOC_Os02g57430|LOC_Os02g57430.1 1 ----- 0 -----
9162|9162 1 ----- 0 -----
29595.t000008|29595.m000284 1 ----- 0 -----
Potri.008G037300|Potri.008G037300.1 1 ----- 0 -----
tr|D8TZD5|D8TZD5_VOLCA 1 ----- 0 -----
Phpat.005G013800|Phpat.005G013800.1 1 ----- 0 -----
AT5G27280 1 ----- 0 -----
58719|58719 1 ----- 0 -----
Phpat.021G072000|Phpat.021G072000.1 1 ----- 0 -----
PGSC0003DMG400025127|PGSC0003DMT40006469 1 MEILIELKDALIKQYDKGTSSGGNIKDDDELISATISCDDESNKDRTEQEQQDIENSIDQV 60ILDSPRSELGNFTNINTEDNKSKSSSERAINNQKSLKIHIPLTNP
AT1G68730 1 ----- 0 -----
Cucsa.284080|Cucsa.284090.2 1 ----- 0 -----
Potri.010G132400|Potri.010G132400.1 1 ----- 0 -----
Glyma01g23015|Glyma01g23015.1 1 ----- 0 -----
Glyma02g14430|Glyma02g14430.1 1 ----- 0 -----

gi|85116624 1 ----- 0 -----
YNL310C 1 ----- 0 -----
CMT595C 1 ----- 0 -----
gi|66800951|Dd 1 ----- 0 -----
Esi0238_0026 1 ----- 0 -----
Cre07.g334850|Cre07.g334850.t1.2 1 ----- 0 -----
tr|Q9TXQ4|Q9TXQ4_CAEEL 1 ----- 0 -----
gi|124249392 1 ----- 0 -----
AT3G54826 1 ----- 0 -----
Carubv10018399m.g|Carubv10018399m 1 ----- 0 -----
Bra003197|Bra003197 1 ----- 0 -----
Bra007101|Bra007101 1 ----- 0 -----
GSVIVG01016242001|GSVIVT01016242001 1 ----- 0 -----
PGSC0003DMG400027152|PGSC0003DMT40006983 1 ----- 0 -----
Cucsa.308490|Cucsa.308490.1 1 ----- 0 -----
Phpat.010G079800|Phpat.010G079800.1 1 ----- 0 -----
Eucgr.G02856|Eucgr.G02856.1 1 ----- 0 -----
Glyma10g35330|Glyma10g35330.1 1 ----- 0 -----
Glyma20g32180|Glyma20g32180.1 1 ----- 0 -----
Medtr1g094720|Medtr1g094720.1 1 ----- 0 -----
GRMZM2G064608|GRMZM2G064608_T01 1 ----- 0 -----
LOC_Os02g57430|LOC_Os02g57430.1 1 ----- 0 -----
9162|9162 1 ----- 0 -----
29595.t000008|29595.m000284 1 ----- 0 -----
Potri.008G037300|Potri.008G037300.1 1 ----- 0 -----
tr|D8TZD5|D8TZD5_VOLCA 1 ----- 0 -----
Phpat.005G013800|Phpat.005G013800.1 1 ----- 0 -----
AT5G27280 1 ----- 0 -----
58719|58719 1 ----- 0 -----
Phpat.021G072000|Phpat.021G072000.1 1 ----- 0 -----
PGSC0003DMG400025127|PGSC0003DMT40006469 108 TRTFSAITYLLRD 120DMINQSSKKCGPNRQKQLHINRKLKHAEMKIRGAFIELYKGLEYLKIYRNLNMLAFVKI 180LKKFQVTKNQVLPYLRVVSSEYFNSD
AT1G68730 1 ----- 0 -----
Cucsa.284080|Cucsa.284090.2 1 ----- 0 -----
Potri.010G132400|Potri.010G132400.1 1 ----- 0 -----
Glyma01g23015|Glyma01g23015.1 1 ----- 0 -----
Glyma02g14430|Glyma02g14430.1 1 ----- 0 -----

gi|85116624 1 ----- 0 -----
YNL310C 1 ----- 0 -----
CMT595C 1 ----- 0 -----
gi|66800951|Dd 1 ----- 0 -----
Esi0238_0026 1 ----- 0 -----
Cre07.g334850|Cre07.g334850.t1.2 1 ----- 0 -----
tr|Q9TXQ4|Q9TXQ4_CAEEL 1 ----- 0 -----
gi|124249392 1 ----- 0 -----
AT3G54826 1 ----- 0 -----
Carubv10018399m.g|Carubv10018399m 1 ----- 0 -----
Bra003197|Bra003197 1 ----- 0 -----
Bra007101|Bra007101 1 ----- 0 -----
GSVIVG01016242001|GSVIVT01016242001 1 ----- 0 -----
PGSC0003DMG400027152|PGSC0003DMT40006983 1 ----- 0 -----
Cucsa.308490|Cucsa.308490.1 1 ----- 0 -----
Phpat.010G079800|Phpat.010G079800.1 1 ----- 0 -----
Eucgr.G02856|Eucgr.G02856.1 1 ----- 0 -----
Glyma10g35330|Glyma10g35330.1 1 ----- 0 -----
Glyma20g32180|Glyma20g32180.1 1 ----- 0 -----
Medtr1g094720|Medtr1g094720.1 1 ----- 0 -----
GRMZM2G064608|GRMZM2G064608_T01 1 ----- 0 -----
LOC_Os02g57430|LOC_Os02g57430.1 1 ----- 0 -----
9162|9162 1 ----- 0 -----
29595.t000008|29595.m000284 1 ----- 0 -----
Potri.008G037300|Potri.008G037300.1 1 ----- 0 -----
tr|D8TZD5|D8TZD5_VOLCA 1 ----- 0 -----
Phpat.005G013800|Phpat.005G013800.1 1 ----- 0 -----
AT5G27280 1 ----- 0 -----
58719|58719 1 ----- 0 -----
Phpat.021G072000|Phpat.021G072000.1 1 ----- 0 -----
PGSC0003DMG400025127|PGSC0003DMT40006469 210 KALKLADEVEREIPKHFEDDKKAMKYLKP 240TQKRESHAVTFPIAQTKELKYRVDVFLICTTGMFVAVIGVLPFLHLLTVAKGYSYNOIQAIIPA 300LLLLVIFILLLV
AT1G68730 1 ----- 0 -----
Cucsa.284080|Cucsa.284090.2 1 ----- 0 -----
Potri.010G132400|Potri.010G132400.1 1 ----- 0 -----
Glyma01g23015|Glyma01g23015.1 1 ----- 0 -----
Glyma02g14430|Glyma02g14430.1 1 ----- 0 -----

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gi|85116624 1 ----- 0----- 0-----
YNL310C 1 ----- 0----- 0-----
CMT595C 1 ----- 0----- 0-----
gi|66800951|Dd 1 ----- 0----- 0-----
Esi0238_0026 1 ----- 0----- 0-----
Cre07.g334850|Cre07.g334850.t1.2 1 ----- 0----- 0-----
tr|Q9TXQ4|Q9TXQ4_CAEBL 1 ----- 0----- 0-----
gi|124249392 1 ----- 0----- 0-----
AT3G54826 1 ----- 0----- MI 2KKASF-
Carubv10018399m.g|Carubv10018399m 1 ----- 0----- 0-----
Bra003197|Bra003197 1 ----- 0----- 0-----
Bra007101|Bra007101 1 ----- 0----- 0-----
GSVIVG01016242001|GSVIVT01016242001 1 ----- 0----- 0-----
PGSC0003DMG400027152|PGSC0003DMT40006983 1 ----- 0----- 0-----
Cucsa.308490|Cucsa.308490.1 1 ----- 0----- 0-----
Phpat.010G079800|Phpat.010G079800.1 1 ----- 0----- 0-----
Eucgr.G02856|Eucgr.G02856.1 1 ----- 0----- 0-----
Glyma10g35330|Glyma10g35330.1 1 ----- 0----- 0-----
Glyma20g32180|Glyma20g32180.1 1 ----- 0----- 0-----
Medtr1g094720|Medtr1g094720.1 1 ----- 0----- 0-----
GRMZM2G064608|GRMZM2G064608.T01 1 ----- 0----- 0-----
LOC_Os02g57430|LOC_Os02g57430.1 1 ----- 0----- 0-----
9162|9162 1 ----- 0----- 0-----
29595.t000008|29595.m000284 1 ----- 0----- 0-----
Potri.008G037300|Potri.008G037300.1 1 ----- 0----- 0-----
tr|D8TZD5|D8TZD5_VOLCA 1 ----- 0----- 0-----
Phpat.005G013800|Phpat.005G013800.1 1 ----- 0----- 0-----
AT5G27280 1 ----- 0----- 0-----
58719|58719 1 ----- 0----- 0-----
Phpat.021G072000|Phpat.021G072000.1 1 ----- 0----- 0-----
PGSC0003DMG400025127|PGSC0003DMT40006469 312 CFPNIIYKSSRYRFRVIRNIMFSPLYKVVMLDFPMADLQCSQVPMMLRN 360LEYVACYIYTGSKYTDYGYCMRTKYRDLAYAVSFLPHYWRAMQCARWDFEGHKS
AT1G68730 1 ----- 0----- 0-----
Cucsa.284080|Cucsa.284090.2 1 ----- 0----- 0-----
Potri.010G132400|Potri.010G132400.1 1 ----- 0----- 0-----
Glyma01g23015|Glyma01g23015.1 1 ----- 0----- 0-----
Glyma02g14430|Glyma02g14430.1 1 ----- 0----- 0-----

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gi|85116624 1 ----- 8S----- TMSCI--TRLGSAAQSL--KT-----
YNL310C 1 ----- 06ATPLRHLLTK-----PR-----GVV-----AGNTFA-----
CMT595C 1 ----- 0-MKRFVGVVS-KQILLIKNIKN--MNNCKLI--SFSMIK-----
gi|66800951|Dd 1 ----- 7P-GGQ-----A-----SACTIQR-----
Esi0238_0026 1 ----- 0-MHRTAARG--S-NQQ--HRFF-----LQ-----
Cre07.g334850|Cre07.g334850.t1.2 1 ----- 2-ARRFLDAF-RHR--LQSPSL--ESTCPIH-----SFANM-----
tr|Q9TXQ4|Q9TXQ4_CAEBL 1 ----- 5S-MRRALS-VLVLNQQ--PRVP-----LFO-----
gi|124249392 1 ----- 5S-MRRALS-VLVLNQQ--PRLP-----LFO-----
AT3G54826 8 IVLRFQNFTEMRVSEFLLSLRLSMAA--RL-----7RIGRFSLCP-----KHQQT-----PI-----IKEPESWQ-----
Carubv10018399m.g|Carubv10018399m 1 ----- 4QIQRIILBLLS-----TKTYI-----SQGLFMS-----
Bra003197|Bra003197 1 ----- 2-ARRFLDAF-RHR--LQSPSL--ESTCPIH-----SFANM-----
Bra007101|Bra007101 1 ----- 5S-MRRALS-VLVLNQQ--PRVP-----LFO-----
GSVIVG01016242001|GSVIVT01016242001 1 ----- 5S-MRRALS-VLVLNQQ--PRLP-----LFO-----
PGSC0003DMG400027152|PGSC0003DMT40006983 1 ----- 7RIGRFSLCP-----KHQQT-----PI-----IKEPESWQ-----
Cucsa.308490|Cucsa.308490.1 1 ----- 4QIQRIILBLLS-----TKTYI-----SQGLFMS-----
Phpat.010G079800|Phpat.010G079800.1 1 ----- 2-ARRFLDAF-RHR--LQSPSL--ESTCPIH-----SFANM-----
Eucgr.G02856|Eucgr.G02856.1 1 ----- 7RIGRFSLCP-----KHQQT-----PI-----IKEPESWQ-----
Glyma10g35330|Glyma10g35330.1 1 ----- 8MLQRIILSL-F-AAD-RAQN--L-LP-----AEASOR-----
Glyma20g32180|Glyma20g32180.1 1 ----- 5F-QRRFLSI-FSRQT--HHPIT-----QE-SWY-----
Medtr1g094720|Medtr1g094720.1 1 ----- 5F-QRRFLSI-FSRQT--HHPIT-----QESSWY-----
GRMZM2G064608|GRMZM2G064608.T01 1 ----- 7DQ-RRFISGTSQSFHD--RH-----PIFQ-----
LOC_Os02g57430|LOC_Os02g57430.1 1 ----- 7LRRRSLA-ATAGS--FAMVE--LR-----GP-----
9162|9162 1 ----- 6PLVRRSGAG-VLNGS--PAGAS--TR-----GP-----
29595.t000008|29595.m000284 1 ----- 0-----MHGGP-----LTLKSSLLSR-----
Potri.008G037300|Potri.008G037300.1 1 ----- 7LQRRNVLSV-L-THN--NQLGSS--FN-----KEPAGQ-----
tr|D8TZD5|D8TZD5_VOLCA 1 ----- 7LQRRNVLSV-L-THN--NQLGSS--LN-----KEHEWK-----
Phpat.005G013800|Phpat.005G013800.1 34 HEHCWSKLVKNGSREMKLDRDLGLRSEKLLSPVGAASCRFDDAEPEPAYS 29D-----S-----ETPAGAS-----
AT5G27280 1 ----- 0-----MHGGP-----LTLKSSLLSR-----
58719|58719 1 ----- 0-----MHGGP-----LTLKSSLLSR-----
Phpat.021G072000|Phpat.021G072000.1 1 ----- 25SKLQRPVLGV-----ESPWTSTKG-----LTLKSSLLSR-----
PGSC0003DMG400025127|PGSC0003DMT40006469 418 HLV 420NLGKYVSA--MLAAGKVKVAYEKEKNMGWLLCLVIV--SSVATVYQVYDVPKVD 470G--LQCHS--KNPWLRLNMLRRKFLIYFYSMG
AT1G68730 1 ----- M--ANTAAGWSVPLA-PIYS 17P-----VNTKP--IN-----FHFS-----
Cucsa.284080|Cucsa.284090.2 1 ----- M--ASMAAATTVFSSPTLL 18Q-----HS--FNPGT--R-----RHS-----
Potri.010G132400|Potri.010G132400.1 1 ----- M--AATAFLSGSFL 14P-----TLTCMK--PMPKPK--Y-----PLL-----
Glyma01g23015|Glyma01g23015.1 1 ----- M--AATAFLSGSFL 14P-----TLTCMK--PMPKPK--Y-----PLL-----
Glyma02g14430|Glyma02g14430.1 1 ----- M--LAPMAA-SALYSPIFL 17P--P-----LMH-----

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gi|85116624 28 ----- 27----- -TTTTSFPLNYFVHSSSCCQRFVMSPPQQTQQRGD--- 63----- -INYTPRQKHTIPRPSQP---S
YNL310C 1 ----- 0----- -MIPRTRTLL--QSKIPETRYFARCAWAP--RVRY-----N-- 30----- -V-----CRTLP--AAL--
CMT595C 37 ----- -S 37----- -TW----- -HRSBLAHLPRARACQKHCSSAGLVY-----A-- 66----- -RAEEPKE--ASRFTGTAGAL--
gi|66800951|Dd 37 ----- -36----- -QQPI--QKFLSSVFNFNFK-NLNQ--RF----- 59----- -Y-----CKKQQQPNNS--STA
Esi0238_0026 1 ----- 0----- -1SSASERLRA--AQSSTASFPTE-----AV----- 42----- -SSTCTGSSCRRGF-CSGGGS--A
Cre07.g334850|Cre07.g334850.t1.2 20 ----- -SC 21SSASERLRA--AQSSTASFPTE-----AV----- 42----- -SSTCTGSSCRRGF-CSGGGS--A
tr|Q9TXQ4|Q9TXQ4_CAEBL 1 ----- 0----- -APRLLSRV--QPR--AF-CLRH-----LW-----G-- 28----- -RGARPEV--HGRRAWAGWR--RS
gi|124249392 9 ----- -V 57ST--EQL-----SLSNSIFSRSHV--YGR--HF-----Q-- 80----- -RQLSVIREANEASV--TNVCNS
Carubv10018399m.g|Carubv10018399m 27 ----- -V 27ST--EQL-----SLSNSIFSRSHV--YGR--HF-----Q-- 80----- -RQLSVIREANEASV--TNVCNS
Bra003197|Bra003197 28 ----- 27----- -GKL--AQSNSIFSRSHV--YGR--LF-----W 50----- -RQLSVIREANEASV--TNVCNS
Bra007101|Bra007101 28 ----- 27----- -GRL--AQSNSIFSRSHV--YGR--LF-----W 50----- -RQLSVIREANEASV--TNVCNS
GSVIVG01016242001|GSVIVT01016242001 31 ----- 30----- -FLPSA--S--AA--RDQF--MAM--CF-----G 48----- -RHFSE--TAATNGCCSSN
PGSC0003DMG400027152|PGSC0003DMT40006983 28 ----- -SV 29----- -FARAFAGFNNL--CSR--EN-----G 48----- -RHFSE--TAATNGCCSSN
Cucsa.308490|Cucsa.308490.1 36 ----- 35----- -HFGKHF--RHR--EN-----G 47----- -H--EATPALAGSKDNEDNKI--R
Phpat.010G079800|Phpat.010G079800.1 34 ----- -VV 35TIPRIYAPA--AFPEPSVPTTI--RAL--HL-----S 62----- -H--IRYLCAKPKDNLPS--S--S
Eucgr.G02856|Eucgr.G02856.1 35 ----- 34----- -ILPSA--S--ALFRRNLI--HBR--GL-----K 54----- -HQAENEDLNKQE--W--S
Glyma10g35330|Glyma10g35330.1 29 ----- 28----- -SPTSAI--NSYGF--HOR--GV-----M 46----- -HTNPKKPVCDVENEADTH--K
Glyma20g32180|Glyma20g32180.1 30 ----- 29----- -ASSGH--S--AA--RDQF--MAM--CF-----G 47----- -HTNPKKPVCDVENEADTH--K
Medtr1g094720|Medtr1g094720.1 31 ----- 30----- -SFPAP--A-----TA--GLR--SH-----L 44----- -KAGASDTHTEP--QD-----Q
GRMZM2G064608|GRMZM2G064608.T01 30 ----- 29----- -LFPAP--V-----AA--GIR--SH-----W 43----- -HMEASNNSDRNQD--I
LOC_Os02g57430|LOC_Os02g57430.1 1 ----- 0----- 0----- 0----- 0-----
9162|9162 1 ----- 35----- -FLPST--T--SIFARNDP--YGR--RF-----Q 55----- -HOSNPASQPEDSQNHSSC--P--N
29595.t000008|29595.m000284 36 ----- 35----- -LPSA--S--SIFARNDP--YGR--CF-----Q 55----- -HAKPANCNENHENG--F--K
Potri.008G037300|Potri.008G037300.1 27 ----- -DQYYNV 32RGAAFVPPRVE--ERESAQKCCAMRAKES-LHQQ--AV--AQPMALTLISDG 80PLVDVPEVAEDAEVQAALPQETS--SGTIVH--
tr|D8TZD5|D8TZD5_VOLCA 98 ----- 97----- -EVSPPDLKKEISPEAGAV--VSSL--STSL--QT--LSKDRAMG-- 135----- -ILLNAAG--STAGWT--
Phpat.005G013800|Phpat.005G013800.1 39 ----- 38----- -RLSNK--KEDKDYDQHS--SSSS-LFNN--RT--LSQEMAMG-- 74----- -LVLQAA--SGKWT--DSG
AT5G27280 1 ----- 0----- -LSQEMAMG-- 9----- -LVLQAA--SGKWT--DSG
58719|58719 57 ----- -KNV 59TSFVFLVHSPFT-----KAYK-KGST-KFGI--HW-----Q 87----- -RRVCR--RWRCHLEE
Phpat.021G072000|Phpat.021G072000.1 500 LNLVLRRLAWLQTVL--HYNF 51GTVDYR--VEGFLAALLEVNSHWNYI--RSST-ITYQK--RR--ASEH-- 557----- -LAKPANCNENHENG--F--K
AT1G68730 30 ----- 29----- -ASFYK--PFRFVKQ--NPIELH--RKT--RVV--EV--VTFPKQ-- 65----- -RNRSF--SFGSLAD
Cucsa.284080|Cucsa.284090.2 33 ----- 32----- -ITSEK--PIV--SS-KA--NPNQV--IRSR-NFCT--AF--VSRK-- 66----- -RYKVL--TVSSHVDG
Potri.010G132400|Potri.010G132400.1 35 ----- 34----- -PNSYK--PIS--FS-T--NPLR--LSHT--EA--ILPKR-- 62----- -SRKFL--VSGSVDG
Glyma01g23015|Glyma01g23015.1 1 ----- 0----- 0----- 0----- 0-----
Glyma02g14430|Glyma02g14430.1 23 ----- 22----- -PKPMH--PIC--CF-NP--LPPSILS--RSK-FSGA--AV--APQKL-- 55----- -PRRFL--RWRGLHGH

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gi|85116624 239 ----- 238 ----- 238 -----
YNL310C 175 ----- 174 ----- 174 -----
CMT595C 213 ----- 212 ----- 212 -----
gi|66800951|Dd 211 ----- 210 ----- 210 -----
Esi0238_0026 161 ----- 160 ----- 160 -----
Cre07.g334850|Cre07.g334850.t1.2 271 ----- 270 ----- 270 -----
tr|Q9TXQ4|Q9TXQ4_CAEBL 120 ----- 119 ----- 119 -----
gi|124249392 179 ----- 178 ----- 178 -----
AT3G54826 224 ----- 223 ----- 223 -----
Carubv10018399m.g|Carubv10018399m 194 ----- 193 ----- 193 -----
Bra003197|Bra003197 189 ----- 188 ----- 188 -----
Bra007101|Bra007101 197 ----- 196 ----- 196 -----
GSVIVG01016242001|GSVIVT01016242001 355 DFMDGMGLGML 365VEGLGELKLGELLDTPPPGIDEATAISKASIVMQFLESQYSIFTRIVFDTPAPTHTLRL 425LSLPDFLDASIGKILKQKLASATSIAKSV
PGSC0003DMG400027152|PGSC0003DMT40006983 204 ----- 203 ----- 203 -----
Cucsa.308490|Cucsa.308490.1 187 ----- 186 ----- 186 -----
Phpat.010G079800|Phpat.010G079800.1 201 ----- 200 ----- 200 -----
Eucgr.G02856|Eucgr.G02856.1 189 ----- 188 ----- 188 -----
Glyma10g35330|Glyma10g35330.1 189 ----- 188 ----- 188 -----
Glyma20g32180|Glyma20g32180.1 190 ----- 189 ----- 189 -----
Medtr1g094720|Medtr1g094720.1 200 ----- 199 ----- 199 -----
GRMZM2G064608|GRMZM2G064608.T01 188 ----- 187 ----- 187 -----
LOC_Os02g57430|LOC_Os02g57430.1 189 ----- 188 ----- 188 -----
9162|9162 76 ----- 75 ----- 75 -----
29595.t000008|29595.m000284 200 ----- 199 ----- 199 -----
Potri.008G037300|Potri.008G037300.1 200 ----- 199 ----- 199 -----
tr|D8TZD5|D8TZD5_VOLCA 250 ----- 249 ----- 249 -----
Phpat.005G013800|Phpat.005G013800.1 254 ----- 253 ----- 253 -----
AT5G27280 213 ----- 212 ----- 212 -----
58719|58719 106 ----- 105 ----- 105 -----
Phpat.021G072000|Phpat.021G072000.1 194 ----- 193 ----- 193 -----
PGSC0003DMG400025127|PGSC0003DMT40006469 668 ----- 667 ----- 667 -----
AT1G68730 171 ----- 170 ----- 170 -----
Cucsa.284080|Cucsa.284090.2 174 ----- 173 ----- 173 -----
Potri.010G132400|Potri.010G132400.1 170 ----- 169 ----- 169 -----
Glyma01g23015|Glyma01g23015.1 101 ----- 100 ----- 100 -----
Glyma02g14430|Glyma02g14430.1 162 ----- 161 ----- 161 -----

gi|85116624 239 ----- 238 ----- 238 -----
YNL310C 175 ----- 174 ----- 174 -----
CMT595C 213 ----- 212 ----- 212 -----
gi|66800951|Dd 211 ----- 210 ----- 210 -----
Esi0238_0026 161 ----- 160 ----- 160 -----
Cre07.g334850|Cre07.g334850.t1.2 271 ----- 270 ----- 270 -----
tr|Q9TXQ4|Q9TXQ4_CAEBL 120 ----- 119 ----- 119 -----
gi|124249392 179 ----- 178 ----- 178 -----
AT3G54826 224 ----- 223 ----- 223 -----
Carubv10018399m.g|Carubv10018399m 194 ----- 193 ----- 193 -----
Bra003197|Bra003197 189 ----- 188 ----- 188 -----
Bra007101|Bra007101 197 ----- 196 ----- 196 -----
GSVIVG01016242001|GSVIVT01016242001 457 FGQETTRQDAADKLERLRERMVXVRELF 485DSTDFVIVTPTVMMAISSRLHASLKRENVPVKLIVNQLPFPSTSDCKFCAMRRK 545QMRALDMIKDDPE
PGSC0003DMG400027152|PGSC0003DMT40006983 204 ----- 203 ----- 203 -----
Cucsa.308490|Cucsa.308490.1 187 ----- 186 ----- 186 -----
Phpat.010G079800|Phpat.010G079800.1 201 ----- 200 ----- 200 -----
Eucgr.G02856|Eucgr.G02856.1 190 ----- 189 ----- 189 -----
Glyma10g35330|Glyma10g35330.1 189 ----- 188 ----- 188 -----
Glyma20g32180|Glyma20g32180.1 190 ----- 189 ----- 189 -----
Medtr1g094720|Medtr1g094720.1 200 ----- 199 ----- 199 -----
GRMZM2G064608|GRMZM2G064608.T01 188 ----- 187 ----- 187 -----
LOC_Os02g57430|LOC_Os02g57430.1 189 ----- 188 ----- 188 -----
9162|9162 76 ----- 75 ----- 75 -----
29595.t000008|29595.m000284 200 ----- 199 ----- 199 -----
Potri.008G037300|Potri.008G037300.1 200 ----- 199 ----- 199 -----
tr|D8TZD5|D8TZD5_VOLCA 250 ----- 249 ----- 249 -----
Phpat.005G013800|Phpat.005G013800.1 254 ----- 253 ----- 253 -----
AT5G27280 213 ----- 212 ----- 212 -----
58719|58719 106 ----- 105 ----- 105 -----
Phpat.021G072000|Phpat.021G072000.1 194 ----- 193 ----- 193 -----
PGSC0003DMG400025127|PGSC0003DMT40006469 668 ----- 667 ----- 667 -----
AT1G68730 171 ----- 170 ----- 170 -----
Cucsa.284080|Cucsa.284090.2 174 ----- 173 ----- 173 -----
Potri.010G132400|Potri.010G132400.1 170 ----- 169 ----- 169 -----
Glyma01g23015|Glyma01g23015.1 101 ----- 100 ----- 100 -----
Glyma02g14430|Glyma02g14430.1 162 ----- 161 ----- 161 -----

gi|85116624 239 ----- 238 ----- 238 -----
YNL310C 175 ----- 174 ----- 174 -----
CMT595C 213 ----- 212 ----- 212 -----
gi|66800951|Dd 211 ----- 210 ----- 210 -----
Esi0238_0026 161 ----- 160 ----- 160 -----
Cre07.g334850|Cre07.g334850.t1.2 271 ----- 270 ----- 270 -----
tr|Q9TXQ4|Q9TXQ4_CAEBL 120 ----- 119 ----- 119 -----
gi|124249392 179 ----- 178 ----- 178 -----
AT3G54826 224 ----- 223 ----- 223 -----
Carubv10018399m.g|Carubv10018399m 194 ----- 193 ----- 193 -----
Bra003197|Bra003197 189 ----- 188 ----- 188 -----
Bra007101|Bra007101 197 ----- 196 ----- 196 -----
GSVIVG01016242001|GSVIVT01016242001 559 LSNLTLIQAPLVDVIRGVVPALQFMGDIVWK* 589
PGSC0003DMG400027152|PGSC0003DMT40006983 204 ----- 203 ----- 203 -----
Cucsa.308490|Cucsa.308490.1 187 ----- 186 ----- 186 -----
Phpat.010G079800|Phpat.010G079800.1 201 ----- 200 ----- 200 -----
Eucgr.G02856|Eucgr.G02856.1 190 ----- 189 ----- 189 -----
Glyma10g35330|Glyma10g35330.1 189 ----- 188 ----- 188 -----
Glyma20g32180|Glyma20g32180.1 190 ----- 189 ----- 189 -----
Medtr1g094720|Medtr1g094720.1 200 ----- 199 ----- 199 -----
GRMZM2G064608|GRMZM2G064608.T01 188 ----- 187 ----- 187 -----
LOC_Os02g57430|LOC_Os02g57430.1 189 ----- 188 ----- 188 -----
9162|9162 76 ----- 75 ----- 75 -----
29595.t000008|29595.m000284 200 ----- 199 ----- 199 -----
Potri.008G037300|Potri.008G037300.1 200 ----- 199 ----- 199 -----
tr|D8TZD5|D8TZD5_VOLCA 250 ----- 249 ----- 249 -----
Phpat.005G013800|Phpat.005G013800.1 254 ----- 253 ----- 253 -----
AT5G27280 213 ----- 212 ----- 212 -----
58719|58719 106 ----- 105 ----- 105 -----
Phpat.021G072000|Phpat.021G072000.1 194 ----- 193 ----- 193 -----
PGSC0003DMG400025127|PGSC0003DMT40006469 668 ----- 667 ----- 667 -----
AT1G68730 171 ----- 170 ----- 170 -----
Cucsa.284080|Cucsa.284090.2 174 ----- 173 ----- 173 -----
Potri.010G132400|Potri.010G132400.1 170 ----- 169 ----- 169 -----
Glyma01g23015|Glyma01g23015.1 101 ----- 100 ----- 100 -----
Glyma02g14430|Glyma02g14430.1 162 ----- 161 ----- 161 -----

