

```

gi | 66806813 | 1 | ----- | 0 | -----
gi | 17506651 | 1 | ----- | 0 | -----
YNR017W | 1 | ----- | 0 | -----
gi | 85084169 | ref | XP_957257.1 | 1 | ----- | 0 | -----
gi | 298712788 | 1 | ----- | 0 | -----
gi | 5454122 | 1 | ----- | 0 | -----
CMO311C | CMO311CT | 1 | MQSRPDLFGFFPYTRALDRDSSVVVVVACKKTYGPPCRAISRHGCEPELAFRHMGCVCVS | 60GYRETRRNLLSVLVQASRRGMCCFEHSHAQLSVGAQRRCRGRWRCAA
LOC_Os04g47900 | LOC_Os04g47900.1 | 1 | ----- | 0 | -----
Cre10.g434250 | Cre10.g434250.t1.2 | 1 | ----- | 0 | -----
LOC_Os02g45100 | LOC_Os02g45100.1 | 1 | ----- | 0 | -----
73724 | 73724 | 1 | ----- | 0 | -----
85570 | 85570 | 1 | ----- | 0 | -----
GSVIVG01016813001 | GSVIVT01016813001 | 1 | ----- | 0 | -----
Carubv10016391m.g | Carubv10016391m | 1 | ----- | 0 | -----
AT3G04800 | 1 | ----- | 0 | -----
Phpat.011G020000 | Phpat.011G020000.1 | 1 | ----- | 0 | -----
Phpat.011G020100 | Phpat.011G020100.1 | 1 | ----- | 0 | -----
Medtr1g081230 | Medtr1g081230.1 | 1 | ----- | 0 | -----
Glyma10g30280 | Glyma10g30280.1 | 1 | ----- | 0 | -----
Glyma20g36660 | Glyma20g36660.1 | 1 | ----- | 0 | -----
Cucsa.291760 | Cucsa.291760.1 | 1 | ----- | 0 | -----
Eucgr.B01693 | Eucgr.B01693.1 | 1 | ----- | 0 | -----
Eucgr.B02109 | Eucgr.B02109.1 | 1 | ----- | 0 | -----
GSVIVG01035979001 | GSVIVT01035979001 | 1 | ----- | 0 | -----
30128.t000070 | 30128.m008609 | 1 | ----- | 0 | -----
Potri.005G051800 | Potri.005G051800.1 | 1 | ----- | 0 | -----
Potri.013G039200 | Potri.013G039200.1 | 1 | ----- | 0 | -----
LOC_Os03g02390 | LOC_Os03g02390.1 | 1 | ----- | 0 | -----
GRMZM2G064600 | GRMZM2G064600.T01 | 1 | ----- | 0 | -----
GRMZM2G077760 | GRMZM2G077760.T01 | 1 | ----- | 0 | -----
GRMZM2G368041 | GRMZM2G368041.T01 | 1 | ----- | 0 | -----
LOC_Os10g37530 | LOC_Os10g37530.1 | 1 | ----- | 0 | -----
29706.t000055 | 29706.m001325 | 1 | ----- | 0 | -----
Potri.001G198100 | Potri.001G198100.1 | 1 | ----- | 0 | -----
Potri.003G044100 | Potri.003G044100.1 | 1 | ----- | 0 | -----
Bra016597 | Bra016597 | 1 | ----- | 0 | -----
Bra025966 | Bra025966 | 1 | ----- | 0 | -----
Carubv10012124m.g | Carubv10012124m | 1 | ----- | 0 | -----
AT1G17530 | 1 | ----- | 0 | -----
Carubv10020993m.g | Carubv10020993m | 1 | ----- | 0 | -----
AT1G72750 | 1 | ----- | 0 | -----
Bra008046 | Bra008046 | 1 | ----- | 0 | -----
Bra016036 | Bra016036 | 1 | ----- | 0 | -----
PGSC0003DMG400002488 | PGSC0003DMT40000636 | 1 | ----- | 0 | -----
PGSC0003DMG400043220 | PGSC0003DMT40009364 | 1 | ----- | 0 | -----
Eucgr.F03162 | Eucgr.F03162.1 | 1 | ----- | 0 | -----
Cucsa.360430 | Cucsa.360430.1 | 1 | ----- | 0 | -----
Medtr8g018780 | Medtr8g018780.1 | 1 | ----- | 0 | -----
Medtr2g099550 | Medtr2g099550.1 | 1 | ----- | 0 | -----
Glyma13g42300 | Glyma13g42300.1 | 1 | ----- | 0 | -----
Glyma15g03070 | Glyma15g03070.1 | 1 | ----- | 0 | -----

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gi | 66806813 | 1 | ----- | 0 | -----
gi | 17506651 | 1 | ----- | 0 | -----
YNR017W | 1 | ----- | 0 | -----
gi | 85084169 | ref | XP_957257.1 | 1 | ----- | 0 | -----
gi | 298712788 | 1 | ----- | 0 | -----
gi | 5454122 | 1 | ----- | 0 | -----
CMO311C | CMO311CT | 108 | QRSVHPCCSTLR | 120RRGASIVLVSTAAEVRVMSIWSRLTDKRRSNKPPDA | --SGEKSDIL-GAGTSLDSRAD | 176PAPDHL--WA | -----
LOC_Os04g47900 | LOC_Os04g47900.1 | 1 | ----- | 0 | -----
Cre10.g434250 | Cre10.g434250.t1.2 | 1 | ----- | 0 | -----
LOC_Os02g45100 | LOC_Os02g45100.1 | 1 | ----- | 0 | -----
73724 | 73724 | 1 | ----- | 0 | -----
85570 | 85570 | 1 | ----- | 0 | -----
GSVIVG01016813001 | GSVIVT01016813001 | 1 | ----- | 0 | -----
Carubv10016391m.g | Carubv10016391m | 1 | ----- | 0 | -----
AT3G04800 | 1 | ----- | 0 | -----
Phpat.011G020000 | Phpat.011G020000.1 | 1 | ----- | 0 | -----
Phpat.011G020100 | Phpat.011G020100.1 | 1 | ----- | 0 | -----
Medtr1g081230 | Medtr1g081230.1 | 1 | ----- | 0 | -----
Glyma10g30280 | Glyma10g30280.1 | 1 | ----- | 0 | -----
Glyma20g36660 | Glyma20g36660.1 | 1 | ----- | 0 | -----
Cucsa.291760 | Cucsa.291760.1 | 1 | ----- | 0 | -----
Eucgr.B01693 | Eucgr.B01693.1 | 1 | ----- | 0 | -----
Eucgr.B02109 | Eucgr.B02109.1 | 1 | ----- | 0 | -----
GSVIVG01035979001 | GSVIVT01035979001 | 1 | ----- | 0 | -----
30128.t000070 | 30128.m008609 | 1 | ----- | 0 | -----
Potri.005G051800 | Potri.005G051800.1 | 1 | ----- | 0 | -----
Potri.013G039200 | Potri.013G039200.1 | 1 | ----- | 0 | -----
LOC_Os03g02390 | LOC_Os03g02390.1 | 1 | ----- | 0 | -----
GRMZM2G064600 | GRMZM2G064600.T01 | 1 | ----- | 0 | -----
GRMZM2G077760 | GRMZM2G077760.T01 | 1 | ----- | 0 | -----
GRMZM2G368041 | GRMZM2G368041.T01 | 1 | ----- | 0 | -----
LOC_Os10g37530 | LOC_Os10g37530.1 | 1 | ----- | 0 | -----
29706.t000055 | 29706.m001325 | 1 | ----- | 0 | -----
Potri.001G198100 | Potri.001G198100.1 | 1 | ----- | 0 | -----
Potri.003G044100 | Potri.003G044100.1 | 1 | ----- | 0 | -----
Bra016597 | Bra016597 | 1 | ----- | 0 | -----
Bra025966 | Bra025966 | 1 | ----- | 0 | -----
Carubv10012124m.g | Carubv10012124m | 1 | ----- | 0 | -----
AT1G17530 | 1 | ----- | 0 | -----
Carubv10020993m.g | Carubv10020993m | 1 | ----- | 0 | -----
AT1G72750 | 1 | ----- | 0 | -----
Bra008046 | Bra008046 | 1 | ----- | 0 | -----
Bra016036 | Bra016036 | 1 | ----- | 0 | -----
PGSC0003DMG400002488 | PGSC0003DMT40000636 | 1 | ----- | 0 | -----
PGSC0003DMG400043220 | PGSC0003DMT40009364 | 1 | ----- | 0 | -----
Eucgr.F03162 | Eucgr.F03162.1 | 1 | ----- | 0 | -----
Cucsa.360430 | Cucsa.360430.1 | 1 | ----- | 0 | -----
Medtr8g018780 | Medtr8g018780.1 | 1 | ----- | 0 | -----
Medtr2g099550 | Medtr2g099550.1 | 1 | ----- | 0 | -----
Glyma13g42300 | Glyma13g42300.1 | 1 | ----- | 0 | -----
Glyma15g03070 | Glyma15g03070.1 | 1 | ----- | 0 | -----

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gi | 66806813 1 ----- 0 ----- MFA 3PCPDKIWDA ----- GGAFA
gi | 17506651 63 ----- QL ----- 64KSAGVGVSRQMTFVYQM ----- D ----- PSMFA ----- SQQPQYIMPEGGVAGKGF EF 108ALGHGWAGVAGVGV
YNR017W 50 ----- 49 - GMEVDTRQLHPLAGL ----- DKG - VEYLDL EEQLSSLEGSQG 86LIPSRGWTDDLCYGTGA
gi | 85084169 |ref | XP_957257.1 6 ----- TRESGVV ----- 12DDYSDASAKMCPG ----- KSEELQVVLKRWGIG ----- NKETLBYISL EDPPLDAG - AS 96VLPSRGTDDLCYGTGA
gi | 5454122 7 ----- 28ADLAGVETGMSLPSYLVNVE ----- H ----- FRMIVG ----- DTEFILDTC ----- N 57 - IKGQVFRMIVGAL
CMO311C | CMO311C 185 ----- QVDDVSWP ----- D 1941EENENGSRVPSFNLDH - QARTV - APALGIYATRRGSKSGVYLFABE ----- YH 242VYHKSWGGL
LOC_0e04g47900 | LOC_0e04g47900.1 1 ----- MAA ----- ADQA 8YDQRPSPRSTKPKPEE - GLT - ISRFEDLDP ----- LSPFLFEE ----- AL 50 - RSRNCCEDTTFYGTGY
Cre10.g434250 | Cre10.g434250.t1.2 45 ----- LRDV - QPNATLGA 57AGLSAPGKLYNPFYGLSTQA - I - GTFKHLRFLP ----- EOPFLFEE ----- AS 101 - VRRRMTQHLQYCGY
LOC_0e02g45100 | LOC_0e02g45100.1 1 ----- MSRA ----- VDA 7QOEPTGRFVSPDRPE - GLA - FPTSYRANVDP ----- LSPFLFEE ----- KF 51 - RRRRWTGNNHTFYGTGY
73724 | 73724 3 ----- SCS - SRSAGERK 17GABEITL ----- D - FYGTSGGASGAL ----- K ----- SLPFLFEE ----- AL 62 - FRRRWTGNNHTFYGTGY
85570 | 85570 3 ----- TSSSSSFAFERK 18FKADGQVLPSPYSEHFG ----- TMDQWMLK ----- TFLFEE ----- AT 59 - FRRSLEGTTFYGTGY
GSVIVG01016813001 | GSVIVT01016813001 41 ----- EEDQTLTLEFTH ----- MDO ----- RT 59SQDNDNKRKLYNYPYODL - QIE - H ----- ONIKKLE ----- TSPFLFEE ----- SV 99 - AORF -
Carubv10012124m.g | Carubv10012124m 5 ----- MNP ----- S - T 9GDQQQRYKRYNYPYODL - NLY - Y ----- ROLVDP ----- TSPFLFEE ----- AT 49 - KRLSWGNNHTFYGTGY
AT3G04800 1 ----- MNH ----- S - T 9GHOQQRYKRYNYPYODL - NLY - Y ----- ROLVDP ----- TSPFLFEE ----- AT 49 - KRLSWGNNHTFYGTGY
Phpat.011G020000 | Phpat.011G020000.1 5 ----- MNDDRQPSG - GAVF 14GEGGQGGQRYNYPYODL - VYGAADL - KSLSEV - RHL - S ----- SLPFLFEE ----- NV 59 - VORRNSWGLHTFYGTGY
Phpat.011G020100 | Phpat.011G020100.1 1 ----- MNDDRQPSG - GAVF 14GEGGQGGQRYNYPYODL - VYGAADL - KSLSEV - RHL - S ----- SLPFLFEE ----- NV 59 - VORRNSWGLHTFYGTGY
Medtr1g081230 | Medtr1g081230.1 1 ----- M - ADG - S - T 6NPEBHQKRYNYPYODL - NLY - H ----- DRYVLP ----- TSPFLFEE ----- AL 47 - RKRSSWGLHTFYGTGY
Glyma10g30280 | Glyma10g30280.1 1 ----- M - ADS - S - S 6NSKHHTRVHYPY - QDLN - V - H ----- OKVNL - TSPFLFEE ----- AL 46 - RTHRSWGLHTFYGTGY
Glyma20g3660 | Glyma20g3660.1 1 ----- M - ADS - S - S 6NSKHHTRVHYPY - QDLN - V - H ----- OKVNL - TSPFLFEE ----- AL 46 - RTHRSWGLHTFYGTGY
Cucsa.291760 | Cucsa.291760.1 1 ----- M - ADS - S - S 6NSKHHTRVHYPY - QDLN - V - H ----- OKVNL - TSPFLFEE ----- AL 46 - RTHRSWGLHTFYGTGY
Eucgr.B01693 | Eucgr.B01693.1 1 ----- MSF ----- GFS - G 9DPEGRKTRVNY - QDL - H - V - H ----- KNLVDP ----- TSPFLFEE ----- TL 49 - KPHRSWGLHTFYGTGY
Eucgr.B02109 | Eucgr.B02109.1 1 ----- MSF ----- GFS - G 9DPEGRKTRVNY - QDL - H - V - H ----- KNLVDP ----- TSPFLFEE ----- TL 49 - KPHRSWGLHTFYGTGY
GSVIVG01035979001 | GSVIVT01035979001 1 ----- M - ADG - S - T 43TDSRKRKRYNYPYODL - QVE - H ----- KNLVDP ----- TSPFLFEE ----- AL 50 - KPHRSWGLHTFYGTGY
30128.t000070 | 30128.m008609 1 ----- M - M - 2DSDNKKYTLHFYQDLN - V - A ----- OSYKLP ----- TSPFLFEE ----- AL 43 - CORRSWGLHTFYGTGY
Potri.005G051800 | Potri.005G051800.1 1 ----- M - M - 1NDPNDHKYKRYNYPYODL - NLY - V - A ----- ONLYKLP ----- TSPFLFEE ----- SL 42 - HORRSWGLHTFYGTGY
Potri.013G039200 | Potri.013G039200.1 1 ----- M - M - 1NDPNDHKYKRYNYPYODL - NLY - V - A ----- ONLYKLP ----- TSPFLFEE ----- SL 42 - HORRSWGLHTFYGTGY
LOC_0e03g02390 | LOC_0e03g02390.1 5 ----- RLFSGCGTRDRRT - 18 - - - - DASGRRLVNY - QDL - H - Y - ROLVDP ----- TSPFLFEE ----- SL 55 - AORRSWGLHTFYGTGY
GRMZM2G064600 | GRMZM2G064600.T01 5 ----- RLYPF - SDDRRD - A - A 20PFS - S - E - R - NY - QDL - H - S ----- ROLVDP ----- TSPFLFEE ----- AL 58 - AORRSWGLHTFYGTGY
GRMZM2G07760 | GRMZM2G07760.T01 5 ----- RYSPG - GTDRRD - A - A 20PFS - S - E - R - NY - QDL - H - S ----- ROLVDP ----- TSPFLFEE ----- AL 58 - AORRSWGLHTFYGTGY
GRMZM2G368041 | GRMZM2G368041.T01 5 ----- RLFPSSGDDR - 14 - - - - SDAERL - NY - QDL - N - M - Y - SYRTL - D - L - S ----- TSPFLFEE ----- AL 53 - AORRSWGLHTFYGTGY
LOC_0e01g37530 | LOC_0e01g37530.1 5 ----- RLFPSSGSSGD - 16 - - - - ASGPGRRVNY - QDL - S - T - Y - SYRTL - D - L - S ----- TSPFLFEE ----- SA 56 - AORRSWGLHTFYGTGY
29706.t000055 | 29706.m001325 4 ----- SI - SDH - D - T 10NRTENRNY - NY - QDL - N - L - P - H ----- ODLVDP ----- TSPFLFEE ----- SL 50 - AORRSWGLHTFYGTGY
Potri.001G198100 | Potri.001G198100.1 4 ----- ED - NN - S - D 9NPQPKGTRVNY - QDL - H - L - P - S ----- OTVLP ----- TSPFLFEE ----- SL 49 - HORRSWGLHTFYGTGY
Potri.003G044100 | Potri.003G044100.1 4 ----- ED - NN - S - D 9NPQPKGTRVNY - QDL - H - L - P - S ----- OTVLP ----- TSPFLFEE ----- SL 49 - HORRSWGLHTFYGTGY
Bra016597 | Bra016597 4 ----- T - D - D 5HTSSESRLHFYQHL - N - V - H ----- NAQVLP ----- TSPFLFEE ----- SL 47 - KRSSWGLHTFYGTGY
Bra025966 | Bra025966 3 ----- T - N 4HSSDDESTRVHFYQSY - ELP - H ----- KAOVLP ----- TSPFLFEE ----- SL 46 - KRSSWGLHTFYGTGY
Carubv10012124m.g | Carubv10012124m 1 ----- M - M - 1NDPNDHKYKRYNYPYODL - NLY - V - A ----- ONLYKLP ----- TSPFLFEE ----- SL 42 - HORRSWGLHTFYGTGY
AT1G17530 4 ----- NR - SSD - H - G 10 - ESDNTRVNY - QDL - H - V - H ----- KSOVLP ----- TSPFLFEE ----- SL 49 - KORRSWGLHTFYGTGY
Carubv10020993m.g | Carubv10020993m 4 ----- NR - SSD - H - G 10 - ESDNTRVNY - QDL - H - V - H ----- KSOVLP ----- TSPFLFEE ----- SL 49 - KORRSWGLHTFYGTGY
AT1G72750 4 ----- NR - SSD - H - G 10 - ESDNTRVNY - QDL - H - V - H ----- KSOVLP ----- TSPFLFEE ----- SL 49 - KORRSWGLHTFYGTGY
Bra008046 | Bra008046 5 ----- NR - SSD - H - E 11S - DENRNY - NY - QDL - N - V - H ----- KSOVLP ----- TSPFLFEE ----- SL 50 - KORRSWGLHTFYGTGY
Bra016036 | Bra016036 5 ----- NR - SSD - H - D 11SDENRNY - NY - QDL - N - V - H ----- KSOVLP ----- TSPFLFEE ----- SL 53 - KORRSWGLHTFYGTGY
PGSC0003DMG400002488 | PGSC0003DMT40000636 4 ----- QHQSPNH - T - G 13DNDGKRYNYPYODL - QVE - H ----- KTLVLP ----- TSPFLFEE ----- SV 53 - AORRSWGLHTFYGTGY
PGSC0003DMG4000043220 | PGSC0003DMT40009364 4 ----- H - G - D 7NNDGKRYNYPYODL - QVE - H ----- KTLVLP ----- TSPFLFEE ----- SV 47 - AORRSWGLHTFYGTGY
Eucgr.F03162 | Eucgr.F03162.1 4 ----- RSSNQDS - S - 12 - P - N - R - Q - D - L - Q - A - P - H ----- QSLKLP ----- TSPFLFEE ----- SL 51 - KORRSWGLHTFYGTGY
Cucsa.360430 | Cucsa.360430.1 4 ----- RSNRDTD - A - E 13PDS - S - Q - R - NY - QDL - H - S ----- ROLVDP ----- TSPFLFEE ----- AL 52 - RRRSWGLHTFYGTGY
Medtr1g018780 | Medtr1g018780.1 4 ----- M - M - N - S - 6DPQKRYNYPYODL - NLY - H ----- QSLKLP ----- TSPFLFEE ----- AK 44 - RKRSSWGLHTFYGTGY
Medtr2g099550 | Medtr2g099550.1 4 ----- HSPDHS - S - 12 - - - - SPNPPR - NY - QDL - E - V - H ----- RNLVLP ----- TSPFLFEE ----- NO 50 - RKRSSWGLHTFYGTGY
Glyma13g42300 | Glyma13g42300.1 4 ----- OTPDQSS - S - 12 - - - - PKTPPR - NY - QDL - E - V - H ----- RNLVLP ----- TSPFLFEE ----- AR 50 - RKRSSWGLHTFYGTGY
Glyma15g03070 | Glyma15g03070.1 4 ----- OTPDQSS - S - 12 - - - - PKTPPR - NY - QDL - E - V - H ----- RNLVLP ----- TSPFLFEE ----- AR 50 - RKRSSWGLHTFYGTGY

gi | 66806813 19 IGVYVLMGVVNIIGKPKRSP - 38 ----- NKRVLYTFALLRKK ----- SPKFGCFNFWGS 65LFFG
gi | 17506651 125 CA ----- - - - - RGLGELMN - PE ----- 137 ----- TRKVMGKPMTRMVMNAHKH ----- GSGFQPSVAVF
YNR017W 104 MYLLGLGKIGSGFSMGQGLQNP - 125 ----- PMSGKGLQNTVNLNHRK ----- GFLGNNA - MAL 15
gi | 85084169 |ref | XP_957257.1 114 TYLTNLTIGGAVGGLGQLQSA - 135 ----- GQPPKLRNLSVLAWVLR ----- GPYLSAGVAV 16
gi | 298712788 73 YITGIGGGAAGVRECFKAP - 93 ----- NRRSRVLSIMNAGK - GSYENTF - LAT 124Y
gi | 5454122 84 CHGALGAGV - 103 ----- QNMAWSPKPNVQLNMTQ - GALWANT - GAL 136
CMO311C | CMO311C 254 TFWGYSYIGGKIGSGFREGIQKGNEMVAELVSVPTGAGGPKAAT 302BLVSHVSKALRLNALNAVGR - GGRGNAGV
LOC_0e04g47900 | LOC_0e04g47900.1 69 LVLRBRGALGKLRRA - EEN - 87 ----- ERCSKLRVNRVLSGGHA ----- ARKSGNNGVIGL 37
Cre10.g434250 | Cre10.g434250.t1.2 117 GYLAGGAVGAGLYKVFYKPE - 140 ----- VVDTLKLKLRVNLNCTGSF ----- ARPNSCGLLGL 10
LOC_0e02g45100 | LOC_0e02g45100.1 70 LAGATSGALVGLRRA - AEN - 88 ----- ERCSKLRVNRVLSGGV ----- GRVGNRIGVIGL 121E
73724 | 73724 80 YLGAVALGAGGCFDFGI - RSR - 99 ----- BVDDTLKLRVNRVLSGGH ----- GRVGNRIGVIGL 132L
85570 | 85570 77 YLGAVALGAGGCFDFGI - RQI - 98 ----- BVDDTLKLRVNRVLSGGH ----- GRVGNRIGVIGL 129N
GSVIVG01016813001 | GSVIVT01016813001 104 YLGAVALGAGGCFDFGI - RQI - 98 ----- BVDDTLKLRVNRVLSGGH ----- GRVGNRIGVIGL 129N
Carubv10012124m.g | Carubv10012124m 68 LTESLIGANKTJEDGI - RSN - 86 ----- ERCSKLRVNRVLSGGLA ----- ARKSGNNGVIGL 119MF
AT3G04800 68 CTCVILGAFKCTEAM - RAA - 86 ----- ERCSKLRVNRVLSGGLV ----- ARKSGNNGVIGL 119MF
Phpat.011G020000 | Phpat.011G020000.1 77 YLGAVALGAGGCFDFGI - RSQ - 96 ----- BSGDMLKLRVNRVLSGGHR ----- GRVGNRIGVIGL 129F
Phpat.011G020100 | Phpat.011G020100.1 77 YLGAVALGAGGCFDFGI - RSQ - 96 ----- BSGDMLKLRVNRVLSGGHR ----- GRVGNRIGVIGL 129F
Medtr1g081230 | Medtr1g081230.1 66 LTAGALGAGGCFDFGI - RSN - 84 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 116FF
Glyma10g30280 | Glyma10g30280.1 65 LTAGALGAGGCFDFGI - RAA - 83 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 116FF
Glyma20g3660 | Glyma20g3660.1 65 LTAGALGAGGCFDFGI - RAA - 83 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 116FF
Cucsa.291760 | Cucsa.291760.1 43 LTAGALGAGGCFDFGI - RAA - 81 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 116FF
Eucgr.B01693 | Eucgr.B01693.1 68 LTAGALGAGGCFDFGI - RAA - 86 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 119FF
Eucgr.B02109 | Eucgr.B02109.1 69 LTAGALGAGGCFDFGI - RAA - 87 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 120FF
GSVIVG01035979001 | GSVIVT01035979001 63 LTAGALGAGGCFDFGI - RAA - 81 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 113MF
30128.t000070 | 30128.m008609 62 LTAGALGAGGCFDFGI - RAA - 80 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 112MF
Potri.005G051800 | Potri.005G051800.1 61 LTAGALGAGGCFDFGI - RAA - 79 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 112MF
Potri.013G039200 | Potri.013G039200.1 61 LTAGALGAGGCFDFGI - RAA - 79 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 112MF
LOC_0e03g02390 | LOC_0e03g02390.1 73 YLGAVALGAGGCFDFGI - RNA - 92 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 125L
GRMZM2G064600 | GRMZM2G064600.T01 76 YLGAVALGAGGCFDFGI - RGA - 95 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 128M
GRMZM2G07760 | GRMZM2G07760.T01 78 YLGAVALGAGGCFDFGI - RGA - 97 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 130M
GRMZM2G368041 | GRMZM2G368041.T01 71 YLGAVALGAGGCFDFGI - RGA - 90 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 123M
LOC_0e01g37530 | LOC_0e01g37530.1 74 YLGAVALGAGGCFDFGI - AGA - 93 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 126M
29706.t000055 | 29706.m001325 68 YLGAVALGAGGCFDFGI - KSF - 87 ----- BPTDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 120I
Potri.001G198100 | Potri.001G198100.1 68 LTAGALGAGGCFDFGI - RSP - 86 ----- BPTDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 119MF
Potri.003G044100 | Potri.003G044100.1 66 LTAGALGAGGCFDFGI - RSP - 84 ----- BPTDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 117MF
Bra016597 | Bra016597 66 LTAGALGAGGCFDFGI - RSP - 84 ----- BPTDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 117MF
Bra025966 | Bra025966 65 LTAGALGAGGCFDFGI - RSP - 84 ----- BPTDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 116FF
Carubv10012124m.g | Carubv10012124m 30 LTAGALGAGGCFDFGI - RSP - 88 ----- BPTDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 811FA
AT1G17530 68 LTAGALGAGGCFDFGI - RSP - 86 ----- BPTDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 119MF
Carubv10020993m.g | Carubv10020993m 68 YLGAVALGAGGCFDFGI - KSF - 87 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 120V
AT1G72750 68 YLGAVALGAGGCFDFGI - KSF - 87 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 120V
Bra008046 | Bra008046 68 YLGAVALGAGGCFDFGI - KSF - 87 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 120M
Bra016036 | Bra016036 71 YLGAVALGAGGCFDFGI - KSF - 90 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 116FF
PGSC0003DMG400002488 | PGSC0003DMT40000636 71 YLGAVALGAGGCFDFGI - KSF - 90 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 123L
PGSC0003DMG4000043220 | PGSC0003DMT40009364 66 LTAGALGAGGCFDFGI - KAS - 84 ----- BPTDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 117MF
Eucgr.F03162 | Eucgr.F03162.1 69 YLGAVALGAGGCFDFGI - RNI - 88 ----- BPTDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 121M
Cucsa.360430 | Cucsa.360430.1 70 YLGAVALGAGGCFDFGI - RSP - 89 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 122L
Medtr1g018780 | Medtr1g018780.1 63 LTAGALGAGGCFDFGI - RSP - 87 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 114FF
Medtr2g099550 | Medtr2g099550.1 68 YLGAVALGAGGCFDFGI - RSP - 87 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 120L
Glyma13g42300 | Glyma13g42300.1 68 YLGAVALGAGGCFDFGI - RSP - 87 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 120L
Glyma15g03070 | Glyma15g03070.1 68 YLGAVALGAGGCFDFGI - RSP - 87 ----- BSGDMLKLRVNRVLSGGH ----- GRVGNRIGVIGL 120L

