

Esi0237_0006 1 ----- 0 -----
gi|17553472 1 ----- 0 -----
YJL104W 1 ----- 0 -----
gi|27363461 1 ----- 0 -----
gi|85097602 1 ----- 0 -----
CMP334C|CMP334CT 1 ----- 0 -----
tr|A8J4S6|A8J4S6_CHLRE 1 ----- 0 -----
tr|D8TX81|D8TX81_VOLCA 1 ----- 0 -----
CMK200C|CMK200CT 1 ----- 0 -----
Medtr4g116100|Medtr4g116100.1 1 ----- 0 -----
Medtr1g098440|Medtr1g098440.1 1 ----- 0 -----
402411|402411 1 ----- 0 -----
Phpat.012G064600|Phpat.012G064600.1 1 ----- 0 -----
Phpat.018G069100|Phpat.018G069100.1 1 ----- 0 -----
Phpat.021G010400|Phpat.021G010400.1 1 ----- 0 -----
76729|76729 1 ----- 0 -----
PGSC0003DMG400029559|PGSC0003DMT40007600 1 ----- 0 -----
GRMZM2G164475|GRMZM2G164475_T01 1 ----- 0 -----
GRMZM2G048434|GRMZM2G048434_T07 1 ----- 0 -----
LOC_Os10g33910|LOC_Os10g33910.1 1 ----- 0 -----
Bra019621|Bra019621 1 MELPPRVLYPRRFHASPSKYTAAAPDLRDKLATLVDRNEKVKKAYHQLQSQIASGLAEA 60GEVFESLAIPLMKLVGLKTSEMESEGRHSTFIFNTERHHMDDTSSQNG
29964.t000004|29964.m000153 1 ----- 0 -----
AT5G61880 1 ----- 0 -----
PGSC0003DMG400029557|PGSC0003DMT40007599 1 ----- 0 -----
Bra003369|Bra003369 1 ----- 0 -----
Bra007441|Bra007441 1 ----- 0 -----
Bra014546|Bra014546 1 ----- 0 -----
AT3G59280 1 ----- 0 -----
Carubv10018261m.g|Carubv10018261m 1 ----- 0 -----
PGSC0003DMG400014859|PGSC0003DMT40003849 1 ----- 0 -----
PGSC0003DMG400025578|PGSC0003DMT40006572 1 ----- 0 -----
Potri.012G108600|Potri.012G108600.1 1 ----- 0 -----
Potri.015G106600|Potri.015G106600.1 1 ----- 0 -----
GSVIVG01008650001|GSVIVT01008650001 1 ----- 0 -----
Glyma02g08820|Glyma02g08820.2 1 ----- 0 -----
Potri.014G151200|Potri.014G151200.1 1 ----- 0 -----
Cucsa.197950|Cucsa.197950.1 1 ----- 0 -----
Cucsa.181450|Cucsa.181450.1 1 ----- 0 -----
Eucgr.A00221|Eucgr.A00221.1 1 ----- 0 -----
Eucgr.L00545|Eucgr.L00545.1 1 ----- 0 -----
Eucgr.H00433|Eucgr.H00433.1 1 ----- 0 -----
GSVIVG01013542001|GSVIVT01013542001 1 ----- 0 -----
Glyma06g20480|Glyma06g20480.2 1 ----- 0 -----
Glyma16g27940|Glyma16g27940.1 1 ----- 0 -----

Esi0237_0006 1 ----- 0 -----
gi|17553472 1 ----- 0 -----
YJL104W 1 ----- 0 -----
gi|27363461 1 ----- 0 -----
gi|85097602 1 ----- 0 -----
CMP334C|CMP334CT 1 ----- 0 -----
tr|A8J4S6|A8J4S6_CHLRE 1 ----- 0 -----
tr|D8TX81|D8TX81_VOLCA 1 ----- 0 -----
CMK200C|CMK200CT 1 ----- 0 -----
Medtr4g116100|Medtr4g116100.1 1 ----- 0 -----
Medtr1g098440|Medtr1g098440.1 1 ----- 0 -----
402411|402411 1 ----- 0 -----
Phpat.012G064600|Phpat.012G064600.1 1 ----- 0 -----
Phpat.018G069100|Phpat.018G069100.1 1 ----- 0 -----
Phpat.021G010400|Phpat.021G010400.1 1 ----- 0 -----
76729|76729 1 ----- 0 -----
PGSC0003DMG400029559|PGSC0003DMT40007600 1 ----- 0 -----
GRMZM2G164475|GRMZM2G164475_T01 1 ----- 0 -----
GRMZM2G048434|GRMZM2G048434_T07 1 ----- 0 -----
LOC_Os10g33910|LOC_Os10g33910.1 1 ----- 0 -----
Bra019621|Bra019621 108 ARSDDLNNQIRRS 120KEENYAAKVDSARKEIVHNHKGQLRQLVHMLRQIETQVNSHRGDIVQMLDDGRNSPQEFI 180QKSLYLSSVHSRNDTFFATVKLLRILF
29964.t000004|29964.m000153 1 ----- 0 -----
AT5G61880 1 ----- 0 -----
PGSC0003DMG400029557|PGSC0003DMT40007599 1 ----- 0 -----
Bra003369|Bra003369 1 ----- 0 -----
Bra007441|Bra007441 1 ----- 0 -----
Bra014546|Bra014546 1 ----- 0 -----
AT3G59280 1 ----- 0 -----
Carubv10018261m.g|Carubv10018261m 1 ----- 0 -----
PGSC0003DMG400014859|PGSC0003DMT40003849 1 ----- 0 -----
PGSC0003DMG400025578|PGSC0003DMT40006572 1 ----- 0 -----
Potri.012G108600|Potri.012G108600.1 1 ----- 0 -----
Potri.015G106600|Potri.015G106600.1 1 ----- 0 -----
GSVIVG01008650001|GSVIVT01008650001 1 ----- 0 -----
Glyma02g08820|Glyma02g08820.2 1 ----- 0 -----
Potri.014G151200|Potri.014G151200.1 1 ----- 0 -----
Cucsa.197950|Cucsa.197950.1 1 ----- 0 -----
Cucsa.181450|Cucsa.181450.1 1 ----- 0 -----
Eucgr.A00221|Eucgr.A00221.1 1 ----- 0 -----
Eucgr.L00545|Eucgr.L00545.1 1 ----- 0 -----
Eucgr.H00433|Eucgr.H00433.1 1 ----- 0 -----
GSVIVG01013542001|GSVIVT01013542001 1 ----- 0 -----
Glyma06g20480|Glyma06g20480.2 1 ----- 0 -----
Glyma16g27940|Glyma16g27940.1 1 ----- 0 -----

Esi0237_0006 1 ----- 0 -----
gi|17553472 1 ----- 0 -----
YJL104W 1 ----- 0 -----
gi|27363461 1 ----- 0 -----
gi|85097602 1 ----- 0 -----
CMP334C|CMP334CT 1 ----- 0 -----
tr|A8J4S6|A8J4S6_CHLRE 1 ----- 0 -----
tr|D8TX81|D8TX81_VOLCA 1 ----- 0 -----
CMK200C|CMK200CT 1 ----- 0 -----
Medtr4g116100|Medtr4g116100.1 1 ----- 0 -----
Medtr1g098440|Medtr1g098440.1 1 ----- 0 -----
402411|402411 1 ----- 0 -----
Phpat.012G064600|Phpat.012G064600.1 1 ----- 0 -----
Phpat.018G069100|Phpat.018G069100.1 1 ----- 0 -----
Phpat.021G010400|Phpat.021G010400.1 1 ----- 0 -----
76729|76729 1 ----- 0 -----
PGSC0003DMG400029559|PGSC0003DMT40007600 1 ----- 0 -----
GRMZM2G164475|GRMZM2G164475_T01 1 ----- 0 -----
GRMZM2G048434|GRMZM2G048434_T07 1 ----- 0 -----
LOC_Os10g33910|LOC_Os10g33910.1 1 ----- 0 -----
Bra019621|Bra019621 210 MNINELLGSVDTGVTDLMQALSKNMCNFMK 240YVGNLAAEVKGGPCVQLMKVNMERANADTRRELEDARERIRLAERKMEALSRLKKA 300DQVQLMTSSAR
29964.t000004|29964.m000153 1 ----- 0 -----
AT5G61880 1 ----- 0 -----
PGSC0003DMG400029557|PGSC0003DMT40007599 1 ----- 0 -----
Bra003369|Bra003369 1 ----- 0 -----
Bra007441|Bra007441 1 ----- 0 -----
Bra014546|Bra014546 1 ----- 0 -----
AT3G59280 1 ----- 0 -----
Carubv10018261m.g|Carubv10018261m 1 ----- 0 -----
PGSC0003DMG400014859|PGSC0003DMT40003849 1 ----- 0 -----
PGSC0003DMG400025578|PGSC0003DMT40006572 1 ----- 0 -----
Potri.012G108600|Potri.012G108600.1 1 ----- 0 -----
Potri.015G106600|Potri.015G106600.1 1 ----- 0 -----
GSVIVG01008650001|GSVIVT01008650001 1 ----- 0 -----
Glyma02g08820|Glyma02g08820.2 1 ----- 0 -----
Potri.014G151200|Potri.014G151200.1 1 ----- 0 -----
Cucsa.197950|Cucsa.197950.1 1 ----- 0 -----
Cucsa.181450|Cucsa.181450.1 1 ----- 0 -----
Eucgr.A00221|Eucgr.A00221.1 1 ----- 0 -----
Eucgr.L00545|Eucgr.L00545.1 1 ----- 0 -----
Eucgr.H00433|Eucgr.H00433.1 1 ----- 0 -----
GSVIVG01013542001|GSVIVT01013542001 20 KHISC 24WNAMIVSLAVHGYCEEALRLFSTMEMSVDGARP 57NRV
Glyma06g20480|Glyma06g20480.2 1 ----- 0 -----
Glyma16g27940|Glyma16g27940.1 1 ----- 0 -----

Esi0237_0006	156	-----	155	-----	155	
gi 17553472	137	-----	136	-----	136	
YJL104W	150	-----	149	-----	149	
gi 27363461	126	-----	125	-----	125	
gi 85097602	141	-----	140	-----	140	
CMP334c CMP334CT	115	-----	114	-----	114	
tr A8J4S6 A8J4S6_CHLRE	67	-----	66	-----	66	
tr D8TX81 D8TX81_VOLCA	139	-----	138	-----	138	
CMK200C CMK200CT	135	-----	134	-----	134	
Medtr4g116100 Medtr4g116100.1	140	YIVSISKTVQINEABHVWESKYIK	1648	QQTQNYQEMVCAPPPLVLTALRIMSNITRDI*	195	
Medtr1g098440 Medtr1g098440.1	85	-----	84	-----	84	
402411 402411	112	-----	111	-----	111	
Phpat.012G064600 Phpat.012G064600.1	116	-----	115	-----	115	
Phpat.018G069100 Phpat.018G069100.1	122	-----	121	-----	121	
Phpat.021G010400 Phpat.021G010400.1	118	-----	117	-----	117	
76729 76729	135	-----	134	-----	134	
PGSC0003DMG400029559 PGSC0003DMT40007600	149	-----	148	-----	148	
GRMZM2G164475 GRMZM2G164475_T01	114	-----	113	-----	113	
GRMZM2G048434 GRMZM2G048434_T07	117	-----	116	-----	116	
LOC_Os10g33910 LOC_Os10g33910.1	117	-----	116	-----	116	
Bra019621 Bra019621	518	-----	517	-----	517	
29964.t000004 29964.m000153	162	PFVDLTEPAQLVGI	-Q	176	VSKTASAQRHVTSS	190
AT5061880	114	-----	113	-----	113	
PGSC0003DMG400029557 PGSC0003DMT40007599	139	-----	138	-----	138	
Bra003369 Bra003369	149	-----	148	-----	148	
Bra007441 Bra007441	115	-----	114	-----	114	
Bra014546 Bra014546	115	-----	114	-----	114	
AT3G59280	117	-----	116	-----	116	
Carubv10018261m.g Carubv10018261m	117	-----	116	-----	116	
PGSC0003DMG400014859 PGSC0003DMT40003849	104	-----	103	-----	103	
PGSC0003DMG400025578 PGSC0003DMT40006572	115	-----	114	-----	114	
Potri.012G108600 Potri.012G108600.1	115	-----	114	-----	114	
Potri.015G106600 Potri.015G106600.1	130	-----	129	-----	129	
GSVIVG01008650001 GSVIVT01008650001	117	-----	116	-----	116	
Glyma02g08820 Glyma02g08820.2	107	-----	106	-----	106	
Potri.014G151200 Potri.014G151200.1	140	-----	139	-----	139	
Cucsa.197950 Cucsa.197950.1	120	-----	119	-----	119	
Cucsa.181450 Cucsa.181450.1	117	-----	116	-----	116	
Eucgr.A00221 Eucgr.A00221.1	117	-----	116	-----	116	
Eucgr.L00545 Eucgr.L00545.1	117	-----	116	-----	116	
Eucgr.H00433 Eucgr.H00433.1	117	-----	116	-----	116	
GSVIVG01013542001 GSVIVT01013542001	254	-----	253	-----	253	
Glyma06g20480 Glyma06g20480.2	117	-----	116	-----	116	
Glyma16g27940 Glyma16g27940.1	117	-----	116	-----	116	