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Es10011.0084	1	0
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GRMZM2G324991 GRMZM2G324991.T03	1	0
g1 17553678 ref NP_498202.1	1	0
g1 71999683 ref NP_501576.2	1	0
g1 46593007 ref NP_003356.2	1	0
g1 94538354 ref NP_004270.2	1	0
CMM104C CMM104CT	1	0
g1 111226358 ref XP_001134518.1	1	0
Es10098.0070	1	0
g1 85119638 ref XP_965680.1	1	0
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Vocar20014031m.g Vocar20014031m	1	0
Carubv10000696m.g Carubv10000696m	1	0
AT3602090	1	0
Carubv10013366m.g Carubv10013366m	1	0
Bra021477 Bra021477	1	0
Bra039151 Bra039151	1	0
146300 146300	1	0
LOC_0s03g11410 LOC_0s03g11410.1	1	0
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Potri.0176092400 Potri.0176092400.1	1	0
Glyma15g0360 Glyma15g0360.1	1	0
Glyma08g46020 Glyma08g46020.1	1	0
Glyma18g31550 Glyma18g31550.3	1	0
Eucgr.H00078 Eucgr.H00078.1	1	0
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g1 66003202 ref XP_635444.1	1	0
Vocar20001314m.g Vocar20001314m	1	0
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CMK260C CMK260CT	1	0
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g1 24308013 ref NP_055975	1	0
g1 453222763 ref NP_490888.2	1	0
g1 50592988 ref NP_003357.2	1	0
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Cre12.g509750 Cre12.g509750.t1.2	1	0
Vocar20001024m.g Vocar20001024m	1	0
Cre17.g722800 Cre17.g722800.t1.2	1	0
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448827 448827	1	0
Phpat.0116047500 Phpat.0116047500.1	1	0
183257 183257	1	0
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Phpat.0130074200 Phpat.0130074200.1	1	0
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GRMZM2G174137 GRMZM2G174137.T01	1	0
GRMZM2G166646 GRMZM2G166646.T01	1	0
LOC_0s01g09560 LOC_0s01g09560.1	1	0
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AT1651980	1	0
Carubv10008921m.g Carubv10008921m	1	0
Bra014305 Bra014305	1	0
Bra018939 Bra018939	1	0
Bra030405 Bra030405	1	0
Bra022162 Bra022162	1	0
AT3616480	1	0
Carubv10015621m.g Carubv10015621m	1	0
29912.t000079 29912.m005353	1	0
Potri.0086193200 Potri.0086193200.1	1	0
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LOC_0s05g44916 LOC_0s05g44916.1	1	0
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LOC_0s01g53700 LOC_0s01g53700.1	1	0
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Cucsa.116810 Cucsa.116810.1	1	0
Cucsa.021700 Cucsa.021700.1	1	0
Glyma13g43000 Glyma13g43000.1	1	0
Glyma15g02390 Glyma15g02390.1	1	0
Medtr8g014660 Medtr8g014660.1	1	0
Glyma07g01720 Glyma07g01720.1	1	0
Glyma08g21380 Glyma08g21380.1	1	0
30146.t000067 30146.m003490	1	0
Medtr8g102230 Medtr8g102230.1	1	0
Glyma05g36040 Glyma05g36040.1	1	0
Glyma08g03580 Glyma08g03580.1	1	0
Glyma14g13370 Glyma14g13370.1	1	0
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Eucgr.C03704 Eucgr.C03704.1	1	0
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GSVIVG01016955001 GSVIVT01016955001	1	0

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34269.t000001 34269.m000014	1	-----	0	-----	0
GRMZM2G007715 GRMZM2G007715.T01	1	-----	0	-----	0
GRMZM2G118074 GRMZM2G118074.T01	1	-----	0	-----	0
GRMZM2G324991 GRMZM2G324991.T03	1	-----	0	-----	0
g1 17553678 ref NP_498202.1	1	-----	0	-----	0
g1 71999683 ref NP_501576.2	1	-----	0	-----	0
g1 46593007 ref NP_003356.2	1	-----	0	-----	0
g1 94538354 ref NP_004270.2	1	-----	0	-----	0
CMM104C CMM104CT	1	-----	0	-----	0
g1 111226358 ref XP_001134518.1	1	-----	0	-----	0
Es10000.0070	1	-----	0	-----	0
g1 85119638 ref XP_965680.1	1	-----	0	-----	0
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Cre12.g523850 Cre12.g523850.t1.2	1	-----	0	-----	0
Vocar20014031m.g Vocar20014031m	1	-----	0	-----	0
Carubv10000696m.g Carubv10000696m	1	-----	0	-----	0
AT3G02090	1	-----	0	-----	0
Carubv10013366m.g Carubv10013366m	1	-----	0	-----	0
Bra021477 Bra021477	1	-----	0	-----	0
Bra039151 Bra039151	1	-----	0	-----	0
146300 146300	1	-----	0	-----	0
LOC_0s03g11410 LOC_0s03g11410.1	1	-----	0	-----	0
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Cucs.081570 Cucs.081570.1	1	-----	0	-----	0
29630.t000033 29630.m000008	1	-----	0	-----	0
PGSC0003DMG400001355 PGSC0003DMT40000343	1	-----	0	-----	0
Potri.004G118900 Potri.004G118900.1	1	-----	0	-----	0
Potri.017G092400 Potri.017G092400.1	1	-----	0	-----	0
Glyma16g10360 Glyma16g10360.1	1	-----	0	-----	0
Glyma08g46020 Glyma08g46020.1	1	-----	0	-----	0
Glyma18g31550 Glyma18g31550.3	1	-----	0	-----	0
Eucgr.H00078 Eucgr.H00078.1	1	-----	0	-----	0
GSVIVG01011510001 GSVIVT01011510001	1	-----	0	-----	0
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g1 66803202 ref XP_635444.1	1	-----	0	-----	0
Vocar20001314m.g Vocar20001314m	1	-----	0	-----	0
Es10268.0010	1	-----	0	-----	0
CMK260C CMK260CT	1	-----	0	-----	0
g1 85109350 ref XP_962874.1	1	-----	0	-----	0
g1 24308013 ref NP_055975	1	-----	0	-----	0
g1 453222763 ref NP_490888.2	1	-----	0	-----	0
g1 50592980 ref NP_003357.2	1	-----	0	-----	0
Es10111.0016	1	-----	0	-----	0
Cre12.g509750 Cre12.g509750.t1.2	1	-----	0	-----	0
Vocar20001024m.g Vocar20001024m	1	-----	0	-----	0
Cre17.g722800 Cre17.g722800.t1.2	1	-----	0	-----	0
GSVIVG01021441001 GSVIVT01021441001	1	-----	0	-----	0
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Phpat.003G045700 Phpat.003G045700.1	1	-----	0	-----	0
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LOC_0s01g73550 LOC_0s01g73550.1	1	-----	0	-----	0
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GRMZM2G166646 GRMZM2G166646.T01	1	-----	0	-----	0
LOC_0s01g09560 LOC_0s01g09560.1	1	-----	0	-----	0
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GRMZM2G068336 GRMZM2G068336.T01	1	-----	0	-----	0
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Carubv10008921m.g Carubv10008921m	1	-----	0	-----	0
Bra014305 Bra014305	1	-----	0	-----	0
Bra018939 Bra018939	1	-----	0	-----	0
Bra030405 Bra030405	1	-----	0	-----	0
Bra022162 Bra022162	1	-----	0	-----	0
AT3G16480	1	-----	0	-----	0
Carubv10015621m.g Carubv10015621m	1	-----	0	-----	0
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LOC_0s05g44916 LOC_0s05g44916.1	1	-----	0	-----	0
GRMZM2G005036 GRMZM2G005036.T01	1	-----	0	-----	0
LOC_0s01g53700 LOC_0s01g53700.1	1	-----	0	-----	0
Potri.001G191100 Potri.001G191100.1	1	-----	0	-----	0
PGSC0003DMG400000289 PGSC0003DMT40000078	1	-----	0	-----	0
Cucs.116810 Cucs.116810.1	1	-----	0	-----	0
Cucs.021700 Cucs.021700.1	1	-----	0	-----	0
Glyma13g43000 Glyma13g43000.1	1	-----	0	-----	0
Glyma15g02390 Glyma15g02390.1	1	-----	0	-----	0
Medtr8g014660 Medtr8g014660.1	1	-----	0	-----	0
Glyma07g01720 Glyma07g01720.1	1	-----	0	-----	0
Glyma08g21380 Glyma08g21380.1	1	-----	0	-----	0
30146.t000067 30146.m003490	1	-----	0	-----	0
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Glyma05g36040 Glyma05g36040.1	1	-----	0	-----	0
Glyma08g03580 Glyma08g03580.1	1	-----	0	-----	0
Glyma14g13370 Glyma14g13370.1	1	-----	0	-----	0
Eucgr.F03085 Eucgr.F03085.1	1	-----	0	-----	0
Eucgr.C03704 Eucgr.C03704.1	1	-----	0	-----	0
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GSVIVG01016955001 GSVIVT01016955001	1	-----	0	-----	0

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GRMZM2G118074 GRMZM2G118074.T01	1	0	0
GRMZM2G324991 GRMZM2G324991.T03	1	0	0
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g1 71999683 ref NP_501576.2	1	0	0
g1 46593007 ref NP_003356.2	1	0	0
g1 94538354 ref NP_004270.2	1	0	0
CMM104C CMM104CT	1	0	0
g1 111226358 ref XP_001134518.1	1	0	0
Es10000.0070	1	0	0
g1 85119638 ref XP_965680.1	1	0	0
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LOC_0s01g51390 LOC_0s01g51390.1	1	0	0
Cre12.g523850 Cre12.g523850.t1.2	1	0	0
Vocar20014031m.g Vocar20014031m	1	0	0
Carubv10000696m.g Carubv10000696m	1	0	0
AT3G02090	1	0	0
Carubv10013366m.g Carubv10013366m	1	0	0
Bra021477 Bra021477	1	0	0
Bra039151 Bra039151	1	0	0
146300 146300	1	0	0
LOC_0s03g11410 LOC_0s03g11410.1	1	0	0
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PGSC0003DMG400028380 PGSC0003DMT40007295	1	0	0
GSVIVG01012193001 GSVIVT01012193001	1	0	0
Cucs.081570 Cucs.081570.1	1	0	0
29630.t000033 29630.m000008	1	0	0
PGSC0003DMG400001355 PGSC0003DMT40000343	1	0	0
Potri.004G118900 Potri.004G118900.1	1	0	0
Potri.017G092400 Potri.017G092400.1	1	0	0
Glyma16g10360 Glyma16g10360.1	1	0	0
Glyma08g46020 Glyma08g46020.1	1	0	0
Glyma18g31550 Glyma18g31550.3	1	0	0
Eucgr.H00078 Eucgr.H00078.1	1	0	0
GSVIVG01011510001 GSVIVT01011510001	1	0	0
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g1 66803202 ref XP_635444.1	1	0	0
Vocar20001314m.g Vocar20001314m	1	0	0
Es10268.0010	1	0	0
CMK260C CMK260CT	1	0	0
g1 85109350 ref XP_962874.1	1	0	0
g1 24308013 ref NP_055975	1	0	0
g1 453222763 ref NP_490888.2	1	0	0
g1 50592980 ref NP_003357.2	1	0	0
Es10111.0016	1	0	0
Cre12.g509750 Cre12.g509750.t1.2	1	0	0
Vocar20001024m.g Vocar20001024m	1	0	0
Cre17.g722800 Cre17.g722800.t1.2	1	0	0
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448827 448827	1	0	0
Phpat.011G047500 Phpat.011G047500.1	1	0	0
183257 183257	1	0	0
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Phpat.003G045700 Phpat.003G045700.1	1	0	0
Phpat.013G074200 Phpat.013G074200.1	1	0	0
LOC_0s01g73550 LOC_0s01g73550.1	1	0	0
GRMZM2G167767 GRMZM2G167767.T01	1	0	0
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GRMZM2G166646 GRMZM2G166646.T01	1	0	0
LOC_0s01g09560 LOC_0s01g09560.1	1	0	0
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GRMZM2G068336 GRMZM2G068336.T01	1	0	0
AT1G51980	1	0	0
Carubv10008921m.g Carubv10008921m	1	0	0
Bra014305 Bra014305	1	0	0
Bra018939 Bra018939	1	0	0
Bra030405 Bra030405	1	0	0
Bra022162 Bra022162	1	0	0
AT3G16480	1	0	0
Carubv10015621m.g Carubv10015621m	1	0	0
29912.t000079 29912.m005353	1	0	0
Potri.008G193200 Potri.008G193200.1	1	0	0
Potri.010G036700 Potri.010G036700.1	1	0	0
LOC_0s05g44916 LOC_0s05g44916.1	1	0	0
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LOC_0s01g53700 LOC_0s01g53700.1	1	0	0
Potri.001G191100 Potri.001G191100.1	1	0	0
PGSC0003DMG400000289 PGSC0003DMT40000078	1	0	0
Cucs.116810 Cucs.116810.1	1	0	0
Cucs.021700 Cucs.021700.1	1	0	0
Glyma13g43000 Glyma13g43000.1	1	0	0
Glyma15g02390 Glyma15g02390.1	1	0	0
Medtr8g014660 Medtr8g014660.1	1	0	0
Glyma07g01720 Glyma07g01720.1	1	0	0
Glyma08g21380 Glyma08g21380.1	1	0	0
30146.t000067 30146.m003490	1	0	0
Medtr8g102230 Medtr8g102230.1	1	0	0
Glyma05g36040 Glyma05g36040.1	1	0	0
Glyma08g03580 Glyma08g03580.1	1	0	0
Glyma14g13370 Glyma14g13370.1	1	0	0
Eucgr.F03085 Eucgr.F03085.1	1	0	0
Eucgr.C03704 Eucgr.C03704.1	1	0	0
GSVIVG01015273001 GSVIVT01015273001	1	0	0
GSVIVG01016955001 GSVIVT01016955001	1	0	0

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440930	440930	1			M	1SRVFSC	---CQAHPRVV	---TEGILLAEFL	---QAW	28GERER		
GRMZM2G083984	GRMZM2G083984 T01	1			0					0		
28753.1000003	28753.10000078	1			0					0		
CMQ089C	CMQ089CT	70	ETRVPAVRQVHRLPAPLLRFRKVPVHFLAASLTLRTRYTRACP	C	112ARVLACHRNCLPTCQRNLPMYTCAYVACLHEAFVRARTMRLGGDFPV					QVHFC 16		
Es10011.0084		1			0					0		
34269.1000003	34269.m000014	1			0					0		
GRMZM2G007715	GRMZM2G007715 T01	11		AGIIGK	---LYIA	20	IAKHR	---SNLKMVG	---VTA	---KDILEGGNTVI	---F6GAG 52QQQ	
GRMZM2G118074	GRMZM2G118074 T01	1			0					0		
GRMZM2G324991	GRMZM2G324991 T03	1			0					0		
g1 17553678	ref NP_498202.1	1			0					0		
g1 71999683	ref NP_501576.2	1			0					0		
g1 46593007	ref NP_003356.2	1			0					0		
g1 94538354	ref NP_004270.2	1			0					0		
CMM104C	CMM104CT	1			0					0		
g1 111226358	ref XP_001134518.1	1			0					0		
Es10098.0070		1			0					0		
g1 195119638	ref XP_965680.1	1			0					0		
GRMZM2G027505	GRMZM2G027505 T01	1			0					0		
LOC_0s01g51390	LOC_0s01g51390.1	1			0					0		
Cre12.g523850	Cre12.g523850.t1.2	1			0					0		
Vocar20014031m.g	Vocar20014031m	1			0					0		
Carubv10006696m.g	Carubv10006696m	1			0					0		
AT3002000		1			0					0		
Carubv10013366m.g	Carubv10013366m	1			0					0		
Bra021477	Bra021477	1			0					0		
Bra039151	Bra039151	1			0					0		
146300	146300	1			0					0		
LOC_0s03g11410	LOC_0s03g11410.1	1			0					0		
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GRMZM2G100511	GRMZM2G100511 T01	1			0					0		
Phpat.0166072700	Phpat.0166072700.1	1			0					0		
PGSC0003DMG400028380	PGSC0003DMT40007295	1			0					0		
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g1|79998683|ref|NP_501576.2|
g1|4683007|ref|NP_003526.1|
g1|14538354|ref|NP_004270.2|
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Bra021477|Bra021477
Bra039151|Bra039151
146300|146300
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Potri.0176092400|Potri.0176092400.1
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Glyma08g46020|Glyma08g46020.1
Glyma18g31550|Glyma18g31550.3
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g1|453222763|ref|NP_498888.2|
g1|50592888|ref|NP_003357.2|
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g1|668083202|ref|XP.635444.1|
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g1|24308013|ref NP_055975 253 -252- LAAAGGVNDH -ELVKLASDAFAGVPPD 267EDAA -TSV
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g1|5952988|ref NP_003357.2| 228 -219- LIG-LGVNDH -VLQVAGFPLNMRG 243L -G
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g1|66803202|ref|XP.635444.1|
Vocar20001314m.g|Vocar20001314m
ES10268.0010
CMK260C|CMK260C
g1|85109350|ref|XP.962874.1|
g1|24308013|ref NP.455975
g1|453222763|ref NP.490888.2|
g1|5952989|ref NP.003357.2|
ES10111.0016
Cre12.g509750|Cre12.g509750.t1.2
Vocar20001024m.g|Vocar20001024m
Cre17.g722800|Cre17.g722800.t1.2
GSVIVG01021441001|GSVIVT01021441001
448827|448827
Phpat.0116047500|Phpat.0116047500.1
183257|183257
Phpat.0046049300|Phpat.0046049300.1
Phpat.0036045700|Phpat.0036045700.1
Phpat.0136074200|Phpat.0136074200.1
LOC_0501g73550|LOC_0501g73550.1
GRMZM2G167767|GRMZM2G167767.T01
GRMZM2G174137|GRMZM2G174137.T01
GRMZM2G166646|GRMZM2G166646.T01
LOC_0501g09560|LOC_0501g09560.1
GRMZM2G103725|GRMZM2G103725.T01
GRMZM2G068336|GRMZM2G068336.T01
AT1051980
Carubv10008921m.g|Carubv10008921m
Bra014305|Bra014305
Bra018939|Bra018939
Bra030405|Bra030405
Bra022162|Bra022162
AT3616480
Carubv10015621m.g|Carubv10015621m
29912.t000079|29912.m005353
Potri.0086193200|Potri.0086193200.1
Potri.0106036700|Potri.0106036700.1
LOC_0505g44916|LOC_0505g44916.1
GRMZM2G095036|GRMZM2G095036.T01
LOC_0501g53700|LOC_0501g53700.1
Potri.0016191100|Potri.0016191100.1
PGSC0003DMG400000289|PGSC0003DMT40000078
Cucsa.116810|Cucsa.116810.1
Cucsa.021700|Cucsa.021700.1
Glyma13g43000|Glyma13g43000.1
Glyma15g02390|Glyma15g02390.1
Medtr8g014660|Medtr8g014660.1
Glyma07g01720|Glyma07g01720.1
Glyma08g21380|Glyma08g21380.1
38146.t000067|38146.m003490
Medtr8g102230|Medtr8g102230.1
Glyma05g36040|Glyma05g36040.1
Glyma08g03580|Glyma08g03580.1
Glyma14g13370|Glyma14g13370.1
Eucgr.F03985|Eucgr.F03985.1
Eucgr.C03704|Eucgr.C03704.1
GSVIVG01015273001|GSVIVT01015273001
GSVIVG01016955001|GSVIVT01016955001
139 VYN-DSGLFGIHASSEHK-FV-----DGLVESQNLVKST 171KNATISLV---LVNLKPQVVVNKDIDRQILTY-----G-----SLQKNL-----
582-VEN-ITAFTSVYN-DSGLFGIHASSEHK-FV-----DGLVDIVG-DEKST 623KNATISLV---LVNLKPQVVVNKDIDRQILTY-----G-----SLQKNL-----
AVANLIVLVSNVQGVSVCHPRGTPVIVYEAHGAHFRFQDSLPTAIEQG--A 311DLA-VQSTHVMCSLTQSSMLHM-----SGDQVDVK-----
10TALIEDITAYDNRGQSTSTFEVAASP-SD-----GV 340SQE---ATI-----
681ATRV-YAHSESR-DPGLQIYCFI-TP-----HD 352LDDTS6IM-----
338LAAY-ATPEYKYG-DAGLLGVSCI-SD-----NH 368LDD---LV-----
LCYS-IYAFHWGFS-DTGIFGIHAAT-GG-----EN 309LPE---LV-----
Q-KAAZND 485TAS-VMSFNMMYK-DTGLFGVYAVA-KA-----NC 513LDD---LA-----
323IAES-VMSFNMMYK-DTSLFGVYAVA-KA-----DC 351LDD---LA-----
359IAES-VMSFNMMYK-DTGLFGVYAVA-KA-----DC 387LDD---LA-----
3246VNVN-LOHNNYK-DTGLFGVYAVA-DA-----HD 352LDDTS6IM-----
156TIEV-FUSPIMCYK-ETGLVGYAVA-NP-----ES 343IDN---LI-----
336LCUS-TQTSFCYCA-ETGLLGAHFVC-DR-----MK 364IDD---MM-----
345LCNS-FQSNTSYT-DTGLWGLYMC-ES-----ST 373VAD---ML-----
387NAVS-AQNTTSVY-DTGLFGVYAVA-HP-----PD 415LDD---VV-----
25LAES-YSTFTCYQ-DTGLFGNYVC-QP-----ER 353VDD---LV-----
373CHS-ITNTQYK-UTGFGVYAVA-QP-----EH 401EE---LT-----
331LATS-FMSNTSYV-DTGLFGVYAVTKL-----DR 369VDD---LV-----
353LAES-LMAFNTNYR-DTGIFGIYITM-PP-----DT 381LQD---LS-----
348LAES-MIAFNTNYR-DTGLFGICTIA-QP-----DS 376LYD---LS-----
G 351LADA-FMAFNTNYH-DTGLFGVYGVY-DR-----DR 379SEU---FM-----
352LADA-FMAFNTNYH-DTGLFGVYGVY-DR-----DR 380CEU---FM-----
NE 383IAES-IMAFNTNYK-DTGLFGVYAVA-KA-----DC 413LDD---LA-----
NE 387IAES-IMAFNTNYK-DTGLFGVYAVA-KA-----DC 415LDD---LS-----
NE 417IAES-IMAFNTNYK-DTGLFGVYAVA-KA-----DC 445LDD---LS-----
NE 383IAES-IMAFNTNYK-DTGLFGVYAVA-KA-----DC 411LDD---LS-----
NE 385IAES-IMAFNTNYK-DTGLFGVYAVA-KA-----DC 413LDD---LS-----
348IAES-IMAFNTNYV-DSGLFGVYAVA-KP-----DV 376LDD---LA-----
NE 383IAES-IMAFNTNYK-DTGLFGVYAVA-KP-----DC 412LDD---LA-----
ND 386IAES-VMSFNMMYK-DTGLFGVYAVA-KA-----DC 414LDD---LA-----
ND 386IAES-VMSFNMMYK-DTGLFGVYAVA-KA-----DC 414LDD---LA-----
G 352LAEN-VQAFNTNYN-DAGLFGVYATA-KP-----DT 380LDD---LC-----
NE 389LAES-VMAFNTNYK-DTGLFGVYAEA-KP-----DC 417LDD---LA-----
EC-MMAFNTNYK-DTGLFGVYAVA-KP-----DC 270LDD---LA-----
NE 384IAES-IMAFNTNYK-DTGLFGVYAVA-KP-----DC 412LDD---LA-----
NE 367IAEN-MMAFNTNYK-DTGLFGVYAVA-KP-----DC 395VDD---LA-----
NE 385LAES-MMSFNNTYK-DTGLFGVYAVA-KP-----DC 413LDD---LS-----
DE 382IAES-MMAFNTNYK-DTGLFGVYAVA-KP-----DS 410LDD---LA-----
DE 383IAES-MMAFNTNYK-DTGLFGVYAVA-KP-----DS 411LDD---LA-----
NE 379VAES-MMAFNTNYK-DTGLFGVYAVA-NK-----DC 407LDD---LS-----
NE 384VAES-IMAFNTNYK-DTGLFGVYAVA-KP-----DC 412LDD---LS-----
NE 383VAES-IMAFNTNYK-DTGLFGVYAVA-KP-----DS 411LDD---LS-----
NE 393IAES-MMAFNTNYK-DTGLFGVYAVA-KP-----DC 421LDD---LA-----
MMAFNTNYK-DTGLFGVYATA-KP-----DC 230LDD---LA-----
VYSSH 505RVKN-CHAFVFN-KVSLFGISLTT-QSGFL-----534-QD---GI-----
07IV-N-SEAFNLTYG-DSGLFGVYAEV-EGATV-----6K 337TVS-----
09FVHS-CAPNHSYV-DSGLFGIYTLQ-RARPRAE-----PPRPPQGE0GR 353EGP---LSLFFRCSEGAASLQVTLRRRFSFPLDGHHPFAS
LNRFY 431IAE-IAFSPMHD-ETGLLGIAGA-AD-K-----LR 409AGQ---LW-----
RHP 401WVQS-CTGFNHCYT-DSGLFGIHASA--E-S-----GR 429LPE---LA-----
411WVS-CVAFNHSYT-DSGLFGIAASC--Y-P-----GR 439TLP---ML-----
HH 372WMYN-ATSYHHSVE-DTGLLGHMISA--W-P-----RQ 400VRE---MV-----
H 366WYS-AIAHNSYS-DSGVFTVASS--P-P-----EN 394IMU---AL-----
310QFVHS-CAPNHSYV-DSGLFGIYTLQ-RARPRAE-----TA 346AGQ---VI-----
317AAPS-ACSPSYV-DAGLVGVYTC-PD-----GQ 345AGA---LS-----
E 347VFTS-VNPFAYK-ETGLVGVYASG-AP-----GK 375AGK---VV-----
A 368WVHS-CAPNFTFN-ETGLVGVYASCDPP-HV-----AK 374AGU---LV-----
QS-FSAFNWIFN-NTRIFGIYASTGSD-FV-----271-AK---AI-----
KYE 373KVQS-CTAFNINYN-UTGIFGIHATSSGE-FV-----402-PH---LV-----
D 364KVQS-CTAFNINYN-UTGIFGIHATSSD-FV-----393-PN---LI-----
RE 371WVHS-CTAFNINYN-UTGIFGIHATSSG-VI-----400-PY---LV-----
WE 371WVQS-CTAFNINYN-UTGIFGIHATSSG-LV-----400-PK---LV-----
WE 371WVQS-CTAFNINYN-UTGIFGIHATSSG-FV-----400-PK---LV-----
358VFTS-CTAFNINYN-UTGIFGIHATSSD-FV-----379-AK---AV-----
355FVES-LSAFSNVYD-DTGLFGIYLTSSD-HI-----38-MW---QR-----
351350LVDS-FSAFNNDV-DSGLFGIYLTSSD-FV-----379-AK---AV-----
D 362QIKS-ISAFAKDVHS-NTGIFGIHTSDAS-FV-----391-PK---AI-----
D 362QIRS-IAAFKDVHS-NTGIFGIHTSDAA-FV-----391-PK---AI-----
802-----MLNLRID--UNQS 813CQ-----WL-WP-ELAPGINHCTAVQ-R-----834-----
227-----DSTPE-IS-----
362VQ 363EVQS-CTAFNINYN-UTGIFGIYATSSG-PA-----392-AK---AI-----
362VQ 363EVQS-CTAFNINYN-UTGIFGIYATSSG-PA-----392-AK---AI-----
361VQ 362VQS-CTAFNINYN-UTGIFGIYATSSG-PA-----391-AK---AI-----
365VQ 366VQS-CTAFNINYN-UTGIFGIYATSSG-PA-----395-AK---AI-----
363VQ 364VQS-CTAFNINYN-UTGIFGIYATSSG-PA-----393-AK---AI-----
354VQ 355VQS-CTAFNINYN-UTGIFGIYATSSG-PA-----384-AK---AI-----
358VQ 359VQS-CTAFNINYN-UTGIFGIYATSSG-PA-----388-SU---GI-----
360HP 361EVQS-CTAFNINYN-UTGIFGIYATSSG-PA-----390-ST---GI-----
363VQ 364VQS-CTAFNINYN-UTGIFGIYATSSG-PA-----393-SU---AI-----
366VH 367KQVS-CTAFNINYN-UTGIFGIYATSSG-PA-----396-SS---AI-----
362VH 363KQVS-CTAFNINYN-UTGIFGIYATSSG-PA-----392-SS---AI-----
355FQ 356QIES-CTAFNINYN-UTGIFGIYATSSG-PA-----381-SS---AV-----
355VH 356QIES-CTAFNINYN-UTGIFGIYATSSG-PA-----385-SH---AV-----
361VQ 362LVS-CTAFNINYN-UTGIFGIYATSSG-PA-----391-HK---AV-----
360VQ 361VQS-CTAFNINYN-UTGIFGIYATSSG-PA-----390-PV---AV-----
361VQ 362VQS-CTAFNINYN-UTGIFGIYATSSG-PA-----391-PK---AV-----
347VQ 348QVHS-CTAFNINYN-UTGIFGIYATSSG-PA-----377-AK---AV-----
347VQ 348QVHS-CTAFNINYN-UTGIFGIYATSSG-PA-----377-AK---AV-----
363VQ 364QVQS-CTAFNINYN-UTGIFGIYATSSG-PA-----393-PK---AV-----
361VQ 362QVQS-CTAFNINYN-UTGIFGIYATSSG-PA-----391-PK---AV-----
361VQ 362QVQS-CTAFNINYN-UTGIFGIYATSSG-PA-----391-PK---TV-----
349VQ 350QVHS-CTAFNINYN-UTGIFGIYATSSG-PA-----379-PV---AV-----
366VQ 367QVHS-CTAFNINYN-UTGIFGIYATSSG-PA-----396-SK---AI-----
368VQ 369QVHS-CTAFNINYN-UTGIFGIYATSSG-PA-----398-SK---AI-----
366VQ 367QVHS-CTAFNINYN-UTGIFGIYATSSG-PA-----396-SK---AI-----
138-----
361VQ 362QVQS-CTAFNINYN-UTGIFGIYATSSG-PA-----391-AK---AV-----
362VQ 363QVQS-CTAFNINYN-UTGIFGIYATSSG-PA-----392-AK---AV-----
362VQ 363QVQS-CTAFNINYN-UTGIFGIYATSSG-PA-----392-SU---AI-----
362VQ 363QVQS-CTAFNINYN-UTGIFGIYATSSG-PA-----392-AK---AV-----

420946|420946 208 --- 207 --- STQFMSIFDDLCKVAEKMACYGGDGLLAKWLASG-AMSS- --- SGS 248G- NYIAPGENRCPVPIFY- --- VECTLSA
440930|440930 653 G --- SLQKNL --- 659 --- STQFMSIFDDPCCKVAEKMACYGDVVKRVALLDKGT- TL- --- 695 --- RLRIIVRASRFF
GRMZM2G083984 GRMZM2G083984_T01 342 --- 341 --- VSQCLQLLQ- SSSPSYLL- --- 359 --- SSLSAARADU-SONRN- IFDEPAIAIS
28753.1000003|28753.10000078 347 --- 346 --- KAIWAQIUELN- --- NGV 361T-AAELHRVKAAYVADYVKRDSVFY
CMQ089C|CMQ089C 361 --- 614 --- RILWEEIEQIKK- --- SAA 374T-EEFVAMAKNRNLNLYQNEHTNT
ES10011 0084 372 --- 371 --- WYTHHLLH- --- IV- --- HKV 385T-DAEYDAAKTLTKNHYVQNSGC
34269.1000001|34269.1000014 315 --- 314 --- PVIDELHKK- SA- --- SSI 328E-QKEIERAQAQIRALLMGQSPAPAR
GRMZM2G007715 GRMZM2G007715_T01 519 --- 518 --- FAIMHEMSK- LS- --- YRV 532T-EEDVIRARNQLKSS
GRMZM2G118074 GRMZM2G118074_T01 357 --- 356 --- FAIMHEMSK- LS- --- YRV 370T-EEDVIRARNQLKSSILHLDGS
GRMZM2G324991 GRMZM2G324991_T03 393 --- 392 --- FAIMHEMSK- LS- --- YRV 466T-EEDVIRARNQLKSSILHLDGS
g1|17553678|ref NP_498202.1| 361 --- 360 --- KSVAMHEMSK- LA- --- SAA 374T-EEFVAMAKNRNLNLYQNEHTNT
g1|7199683|ref NP_501576.2| 349 --- 348 --- DSVLQGVH- --- NNT 362D-EAADVRAKRSLLHNTLLMDGSP
g1|46593007|ref NP_003356.2| 370 --- 369 --- FVLQGVQWMR- LC- --- TSA 383T-ESEVARGKNILRNALYSHLDGT
g1|94538354|ref NP_004270.2| 379 --- 378 --- HVVQKEWMR- LC- --- TSV 392T-ESEVARGKNILRNALYSHLDGS
CMM104C|CMM104C 421 --- 420 --- YEIQMQLTG- MA- --- YKL 434D-ESEVERAKQLTSLHLDGS
g1|111226358|ref|XP_001134518.1| 359 --- 358 --- AEMLEKQOR- LA- --- TSC 372N-KNEVERNKQKLLATLMQYDGTSK
ES10009 0070 407 --- 406 --- QVLEHVR- MC- --- QV 420G-EEFVAMAKNRNLNLYQNEHTNT
g1|95119638|ref|XP_965680.1| 366 --- 365 --- HPSLREWTR- LC- --- SNV 379S-EAEVERAKQLTSLHLDGS
GRMZM5G827505 GRMZM5G827505_T01 387 --- 386 --- RLIMEFR- LA- --- SOV 400S-ETVVARANQLKSSILHLDGS
LOC_0501951390|LOC_0501951390.1 382 --- 381 --- QLIMEFR- LA- --- FEV 395S-ETVVARANQLKSSILHLDGS
Cre12.9523850|Cre12.9523850.t1.2 385 --- 384 --- YAIMSNLFR- MC- --- FEV 398R-DAVVARAKNLKSNLFFQDS
Vocar20014031m.g|Vocar20014031m 386 --- 385 --- YSIMSHLT- MC- --- FDV 399R-EADVVRANKQLKSNLFFQDS
Carubv10000696m.g|Carubv10000696m 419 --- 418 --- HAINVAVTK- LA- --- YRV 432S-EADVVRANKQLKSSILHLDGS
AT3602090 421 --- 420 --- YAIMNVTK- LA- --- YRV 434S-EADVVRANKQLKSSILHLDGS
Carubv10013366m.g|Carubv10013366m 451 --- 450 --- YAIMNVTK- LA- --- YRV 464S-EADVVRANKQLKSSILHLDGS
Bra021477|Bra021477 417 --- 416 --- YAIMNVTK- LA- --- FRV 430S-EADVVRANKQLKSSILHLDGS
Bra039151|Bra039151 419 --- 418 --- YAIMNVTK- LA- --- FRV 432S-EADVVRANKQLKSSILHLDGS
146300|146300 382 --- 381 --- WVITRENT- MV- --- YHV 395R-EADVVRANKQLKSSILHLDGS
LOC_05039114|LOC_05039114.1 423 --- 422 --- FAIMHEMSK- LS- --- YRV 436T-EADVVRANKQLKSSILHLDGS
GRMZM2G091563 GRMZM2G091563_T01 420 --- 419 --- FAIMHEMSK- LS- --- YRV 433T-EADVVRANKQLKSSILHLDGS
GRMZM2G100511 GRMZM2G100511_T01 420 --- 419 --- FAIMHEMSK- LS- --- YRV 433T-EADVVRANKQLKSSILHLDGS
Phpat.0166072700|Phpat.0166072700.1 426 --- 385 --- YVIMHEIGR- LI- --- YRV 399D-EADVVRANKQLKSSILHLDGS
PGSC0003DM6400028380|PGSC0003DMT40007295 383 --- 422 --- YVIMHEIGR- LI- --- YRV 436S-EADVVRANKQLKSSILHLDGS
GSVIVG01012193001|GSVIVT01012193001 276 --- 275 --- YAIMLETSK- LP- --- YRV 289S-EADVVRANKQLKSSILHLDGS
g1|981570|Cucs.081570.1| 418 --- 417 --- YAIMVETTK- LA- --- YRV 431S-EADVVRANKQLKSSILHLDGS
29630.1000033|29630.10000808 401 --- 400 --- WAIMVETTK- LA- --- YRV 414S-EADVVRANKQLKSSILHLDGS
PGSC0003DM6400001355|PGSC0003DMT40000343 419 --- 418 --- YCINRETSK- LC- --- YRV 432S-EADVVRANKQLKSSILHLDGS
Potri.0046118900|Potri.0046118900.1 416 --- 415 --- WAIMVETTK- LC- --- YRV 429S-EADVVRANKQLKSSILHLDGS
Potri.0176092400|Potri.0176092400.1 417 --- 416 --- WAIMVETTK- LC- --- YRV 430S-EADVVRANKQLKSSILHLDGS
Glyma16g10360|Glyma16g10360.1 413 --- 412 --- WAIMVETTK- LA- --- YRV 426S-EADVVRANKQLKSSILHLDGS
Glyma08g046020|Glyma08g046020.1 418 --- 417 --- YCINRETSK- LA- --- YRV 431S-EADVVRANKQLKSSILHLDGS
Glyma18g13550|Glyma18g13550.3 417 --- 416 --- YAIMVETTK- LA- --- YRV 430S-EADVVRANKQLKSSILHLDGS
Eucgr.H00078|Eucgr.H00078.1 427 --- 426 --- YAIMVETTK- LA- --- HRV 440S-EADVVRANKQLKSSILHLDGS
GSVIVG01011510001|GSVIVT01011510001 236 --- 235 --- YAIMYEISK- LC- --- YRV 249S-EADVVRANKQLKSSILHLDGS
g1|111226878|ref|XP_001134603.1| 539 --- 538 --- ELVQOELL- L- --- RSSM 552T-QUELERAKNATISSAVLNLES
g1|66803202|ref|XP_635444.1| 341 --- 340 --- LTITSEIV- --- ASKT 352A-QUELERAKNATISSAVLNLES
Vocar20001314m.g|Vocar20001314m 315 --- 410TPPHAPRSPLYMASRVACGRQAPPGDAQHVVLGTGGGGVSNPAHSRTPHTGT 470N-RVSL-ELERAKNATISSAVLNLES
ES10268 0010 466 --- 465 --- HVFCEHFT- LA- --- T- --- VPV 480T-DEEFSRRMKNKVNIT
CMK260C|CMK260C 435 --- 434 --- EIIECIK- MG- --- Q- --- V 447T-RAELVRANKQTQKSVFMNL
g1|85109350|ref|XP_962874.1| 445 --- 444 --- QVMCRELRA- LT- --- TDHGYSAL 463E-ELERAKNATISSAVLNLES
g1|24308013|ref NP_055975 406 --- 405 --- EIITKFIIL- MG- --- G- --- TV 419D-TELERAKNATISSAVLNLES
g1|453222763|ref NP_490888.2| 400 --- 399 --- ILVHQITQ- LQ- --- Q- --- GV 413E-PTELARAKTQLRSHLMNLEV
g1|59592898|ref NP_003357.2| 352 --- 351 --- KAYVQVTK- LA- --- QGN 36LSNTHVQAANKKLVYKVNESKAT
ES10111 0016 351 --- 350 --- QALASCFSG- LA- --- TAS 364MA-EWAS-ALASAVSRALNKLE
Cre12.9509750|Cre12.9509750.t1.2 381 --- 380 --- DAITKVKQS- LA- --- KGV 394TDVQ-LATAKNMELRASVAT
Vocar20001024m.g|Vocar20001024m 380 --- 379 --- DAITKVKHS- VA- --- KGV 393SDGQ-LAQAKAMALGERATTAT
Cre17.9722800|Cre17.9722800.t1.2 402 --- 401 --- HVMCHELESVEN- --- G 414TNRIELERAKNATISSAVLNLES
GSVIVG01021441001|GSVIVT01021441001 276 --- 275 --- DIAVAGELLSVS- --- PGQ 299DVQVQLTRAKSTKSAVLNLES
448827|448827 405 --- 404 --- LTITSEIV- --- ASKT 352A-QUELERAKNATISSAVLNLES
Phpat.0116047500|Phpat.0116047500.1 407 --- 406 --- LTITSEIV- --- ASKT 352A-QUELERAKNATISSAVLNLES
183257|183257 398 --- 397 --- DLATDELTVAT- --- GGE 412VTELERAKNATISSAVLNLES
Phpat.0046049300|Phpat.0046049300.1 405 --- 404 --- LTITSEIV- --- ASKT 352A-QUELERAKNATISSAVLNLES
Phpat.0036045700|Phpat.0036045700.1 405 --- 404 --- DLACEQITLAVT- --- PGK 419VSEAEQIRAKNSTISSAVLNLES
Phpat.0136074200|Phpat.0136074200.1 405 --- 404 --- DLACEQITLAVT- --- PGK 419VSEAEQIRAKNSTISSAVLNLES
LOC_0501973550|LOC_0501973550.1 384 --- 383 --- DITTELIAT- --- PGK 419VSEAEQIRAKNSTISSAVLNLES
GRMZM2G167767 GRMZM2G167767_T01 389 --- 388 --- LIISO- --- PGQ 398VTELERAKNATISSAVLNLES
GRMZM2G174137 GRMZM2G174137_T01 384 --- 383 --- DIAVSELIAT- --- PGK 398E-VELVRAKNSTISSAVLNLES
GRMZM2G166646 GRMZM2G166646_T01 396 --- 395 --- DLATRELTSLAT- --- PGQ 410VDQSLDRAKASTKSAVLNLES
LOC_0501095560|LOC_0501095560.1 396 --- 395 --- DLATRELTSLAT- --- PGK 410VDQSLDRAKASTKSAVLNLES
GRMZM2G103725 GRMZM2G103725_T01 835 --- 834 --- SVLERAVVHTA- --- PGQ 252VKKTTC-AV- AVAILVQR-
GRMZM2G068336 GRMZM2G068336_T01 239 --- 238 --- SVLERAVVHTA- --- PGQ 252VKKTTC-AV- AVAILVQR-
AT1651980 397 --- 396 --- ELAAKELKDVA- --- GKK 410VQVQLDRAKSTKSAVLNLES
Carubv10008921m.g|Carubv10008921m 397 --- 396 --- ELAAKELKDVA- --- GKK 410VQVQLDRAKSTKSAVLNLES
Bra014305|Bra014305 396 --- 395 --- ELAAKELKDVA- --- GKK 409VQVQLDRAKSTKSAVLNLES
Bra018939|Bra018939 400 --- 399 --- ELAAKELKDVA- --- GKK 413VQVQLDRAKSTKSAVLNLES
Bra030405|Bra030405 398 --- 397 --- ELAAKELKDVA- --- GKK 411VQVQLDRAKSTKSAVLNLES
Bra022162|Bra022162 389 --- 388 --- ELVASENNAVA- --- GKK 402VQVQLDRAKSTKSAVLNLES
AT3616480 393 --- 392 --- ELVASENNAVA- --- GKK 406VQVQLDRAKSTKSAVLNLES
Carubv10015621m.g|Carubv10015621m 395 --- 394 --- ALVDEKNAVA- --- EGR 408VQVQLDRAKSTKSAVLNLES
29912.1000079|29912.10000353 398 --- 397 --- ELVASENNAVA- --- GKK 412VQVQLDRAKSTKSAVLNLES
Potri.0086193200|Potri.0086193200.1 401 --- 400 --- ELVASENNAVA- --- GKK 415VQVQLDRAKSTKSAVLNLES
Potri.0106036700|Potri.0106036700.1 397 --- 396 --- ELVASENNAVA- --- GKK 411VQVQLDRAKSTKSAVLNLES
LOC_0505944916|LOC_0505944916.1 386 --- 385 --- DLAKRELTSLAT- --- PGK 408VQVQLDRAKSTKSAVLNLES
GRMZM2G05036 GRMZM2G05036_T01 390 --- 389 --- DLAKRELTSLAT- --- PGK 408VQVQLDRAKSTKSAVLNLES
LOC_0501953700|LOC_0501953700.1 390 --- 389 --- DLAKRELTSLAT- --- PGK 408VQVQLDRAKSTKSAVLNLES
Potri.0016191100|Potri.0016191100.1 396 --- 395 --- DLAKRELTSLAT- --- PGK 408VQVQLDRAKSTKSAVLNLES
PGSC0003DM6400000289|PGSC0003DMT40000078 396 --- 394 --- DVAVKELIAT- --- PSE 409VQVQLDRAKSTKSAVLNLES
Cucs.116810|Cucs.116810.1 396 --- 395 --- DLAKRELTSLAT- --- PGK 410VQVQLDRAKSTKSAVLNLES
Cucs.021700|Cucs.021700.1 396 --- 395 --- DLAKRELTSLAT- --- PGK 410VQVQLDRAKSTKSAVLNLES
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Glyma08g03580|Glyma08g03580.1
Glyma14g13370|Glyma14g13370.1
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Eucgr.C03704|Eucgr.C03704.1
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708 E-----TWLSLSAWPLPAGDWKKSLDGDGF6AVD 735AAARFSLRKE-----DLEAKISDPSYKNS---RLTPEAWARQNYIRVVPKADQGLE 784
385 E-----KDLRLARIPGTSVLDLP 402CFASDFF-----AI---DLRLITLSASNLQLSGYEADDILYE 436GHOIVSELVGT
387 QAOIQIQELETTHHPYPSLLOSNAAARQAVTSEQVQ 420AVAKKYL-----LP---DQTLVLS---LWPQ-----440PMTA
389 QKAGFMAKELLYTONLQQLSEFAQIQKVDASVVR 433EATSRRVY-----YD---RDIAAIVG---VG-----451
409 GDAAGTIAAGDVQFGRRRVPAEMVARIIDAITTKEIK 444ASADEIT-----ND---QDHALAM---VG-----462
355 AGQ|RMMLYGRPSINQMMERLEGITVERLI 387DLAGRFL-----FD---TVPTLSA---IG-----405
548 IQLHLDGSTATVEDIGRQLLTGRRIPTELFARIVVVDASTVK 591RVANRFI-----FD---QDVAVIA---MG-----6
394 TAVVDDIGRQLLTGRRISLTFARIDAVDASTVK 429RVANRFI-----FD---QDVAVIA---MG-----447
431 AVVDDIGRQLLTGRRIPTELFARIDVVDASTVK 465RVANRFI-----FD---QDVAVIA---MG-----483
393 QKAGFMAKELLYTONLQQLSEFAQIQKVDASVVR 433EATSRRVY-----YD---RDIAAIVG---VG-----451
388 VCEIDIGRQLLTGRRIPTELFARIDVVDASTVK 421DVCRNVE-----LE---QVSAAV---VG-----439
407 TPVCEIDIGRQLLTGRRIPTELFARIDVVDASTVK 442EICSXYI-----YD---QDVAVIA---VG-----460
416 TPCEIDIGRQLLTGRRIPTELFARIDVVDASTVK 451EVCXYI-----YD---RDIAAIVG---VG-----469
456 DSNVAEDIGRQLLTGRRIPTELFARIDVVDASTVK 480-----RD---VSPAIVA---IG-----449
398 VCEIDIGRQLLTGRRISLTFARIDVVDASTVK 431RVASTLL-----RD---VSPAIVA---IG-----449
442 GFATTEIDIGRQLLTGRRIPTELFARIDVVDASTVK 479RVANRFI-----ND---EDHMAA---LG-----509
404 VVAEDIGRQLLTGRRIPTELFARIDVVDASTVK 438DFANKKI-----WD---QDIAIA---VG-----456
424 TAVTENNGRQLLTGRRIPTELFARIDVVDASTVK 459ETAKYEI-----ID---KWOSSRN---VG-----477
419 TAVSENNGRQLLTGRRIPTELFARIDVVDASTVK 454ETAKDFI-----ID---KDTALIA---VG-----472
421 THHWESIGRELLVYGRIPKAMFARIDAVDASTVK 457AVADRFI-----YD---QDMAVAS---AG-----475
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496 GADIGRQLLTGRRIPTELFARIDVVDASTVK 490RVANRFI-----SS---KPSLAA---YG-----546
499 HLESRLVLFEDIGRQLLTGRRIPTELFARIDVVDASTVK 481RVANRFI-----RS---RPTVVL---YG-----523
468 ESNTVVCEDIGRQLLTGRRIPTELFARIDVVDASTVK 506RVATRLM-----GG---MANNAG---QG-----539
487 MVELEDIGRQLLTGRRIPTELFARIDVVDASTVK 522RVAKRVF-----RG---KPAVAA---LG-----495
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272 271-----PTMASGWN---VDKVPPEYFICKR 487
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g1|71999683|ref NP_501576.2| 440----- 439-----
g1|46593007|ref NP_003356.2| 461----- 460-----
g1|94538354|ref NP_004270.2| 470----- 469-----
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g1|85119638|ref|XP_965680.1| 457----- 456-----
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Bra039151|Bra039151 510----- 509-----
146300|146300 473----- 472-----
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g1|66803202|ref|XP_635444.1| 429----- 428-----
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CMK260C|CMK260CT 524----- 523-----
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g1|453222763|ref NP_490888.2| 490----- 489-----
g1|59592980|ref NP_003357.2| 443----- 442-----
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Phpat.003G045700|Phpat.003G045700.1 511----- 513-----
Phpat.013G074200|Phpat.013G074200.1 511----- 513-----
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Bra018939|Bra018939 505----- 506-----
Bra030405|Bra030405 503----- 504-----
Bra022162|Bra022162 494----- 495-----
AT3G16480 498----- 499-----
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Glyma15g02390|Glyma15g02390.1 488----- 491-----
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Glyma08g03580|Glyma08g03580.1 507----- 509-----
Glyma14g13370|Glyma14g13370.1 138----- 137-----
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Eucgr.C03704|Eucgr.C03704.1 503----- 506-----
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GSVIVG01016955001|GSVIVT01016955001 503----- 506-----

420946|420946 440930|440930 34269.t000001|34269.m000014 GRMZM2G083984 GRMZM2G083984 T01 28753.t000003|28753.m000078 CMQ089C|CMQ089CT ES10011 0084 34269.t000001|34269.m000014 GRMZM2G007715 GRMZM2G007715 T01 GRMZM2G118074 GRMZM2G118074 T01 GRMZM2G324991|GRMZM2G324991 T03 g1|17553678|ref|NP 498202.1| g1|71999683|ref|NP 501576.2| g1|46593007|ref|NP 003356.2| g1|94538354|ref|NP 004270.2| CMM104C|CMM104CT g1|111226358|ref|XP_001134518.1| ES10098 0070 g1|85119638|ref|XP 965680.1| GRMZM5G827505|GRMZM5G827505 T01 LOC_0s01g51390|LOC_0s01g51390.1 Cre12.g523850|Cre12.g523850.t1.2 Vocar20014031m.g|Vocar20014031m Carubv10000696m.g|Carubv10000696m AT3G02090 Carubv10013366m.g|Carubv10013366m Bra021477|Bra021477 Bra039151|Bra039151 146300|146300 LOC_0s03g11410|LOC_0s03g11410.1 GRMZM2G091563|GRMZM2G091563 T01 GRMZM2G100511|GRMZM2G100511 T01 Phpat.0166072700|Phpat.0166072700.1 PGSC0003DMG400028380|PGSC0003DMT40007295 GSVIVG01012193001|GSVIVT01012193001 Cucs.a.081570|Cucs.a.081570.1 29630.t000033|29630.m0000808 PGSC0003DMG400001355|PGSC0003DMT40000343 Potri.004G118900|Potri.004G118900.1 Potri.017G092400|Potri.017G092400.1 Glyma16g10360 Glyma16g10360.1 Glyma08g046020 Glyma08g046020.1 Glyma18g31550 Glyma18g31550.3 Eucgr.H00078|Eucgr.H00078.1 GSVIVG01011510001|GSVIVT01011510001 g1|111226878|ref|XP_001134603.1| g1|66803202|ref|XP 635444.1| Vocar20001314m.g|Vocar20001314m ES10268 0010 CMK260C|CMK260CT g1|85109350|ref|XP 962874.1| g1|24308013|ref|NP 055975 g1|453222763|ref|NP 490888.2| g1|59592980|ref|NP 003357.2| ES10111 0016 Cre12.g509750|Cre12.g509750.t1.2 Vocar20001024m.g|Vocar20001024m Cre17.g722800|Cre17.g722800.t1.2 GSVIVG01021441001|GSVIVT01021441001 448827|448827 Phpat.011G047500|Phpat.011G047500.1 183257|183257 Phpat.004G049300|Phpat.004G049300.1 Phpat.003G045700|Phpat.003G045700.1 Phpat.013G074200|Phpat.013G074200.1 LOC_0s01g73550|LOC_0s01g73550.1 GRMZM2G167767|GRMZM2G167767 T01 GRMZM2G174137|GRMZM2G174137 T01 GRMZM2G166646|GRMZM2G166646 T01 LOC_0s01g09560|LOC_0s01g09560.1 GRMZM2G103725|GRMZM2G103725 T01 GRMZM2G068336|GRMZM2G068336 T01 AT1G51980 Carubv10008921m.g|Carubv10008921m Bra014305|Bra014305 Bra018939|Bra018939 Bra030405|Bra030405 Bra022162|Bra022162 AT3G16480 Carubv10015621m.g|Carubv10015621m 29912.t000079|29912.m005353 Potri.008G193200|Potri.008G193200.1 Potri.010G036700|Potri.010G036700.1 LOC_0s05g44916|LOC_0s05g44916.1 GRMZM2G005036|GRMZM2G005036 T01 LOC_0s01g53700|LOC_0s01g53700.1 Potri.001G191100|Potri.001G191100.1 PGSC0003DMG400000289|PGSC0003DMT40000078 Cucs.a.116810|Cucs.a.116810.1 Cucs.a.021700|Cucs.a.021700.1 Glyma13g43000|Glyma13g43000.1 Glyma15g02390 Glyma15g02390.1 Medtr8g014660 Medtr8g014660.1 Glyma07g01720 Glyma07g01720.1 Glyma08g21380 Glyma08g21380.1 30146.t000067|30146.m003490 Medtr8g102230 Medtr8g102230.1 Glyma05g36040 Glyma05g36040.1 Glyma08g03580 Glyma08g03580.1 Glyma14g13370 Glyma14g13370.1 Eucgr.F03085|Eucgr.F03085.1 Eucgr.C03704|Eucgr.C03704.1 GSVIVG01015273001|GSVIVT01015273001 GSVIVG01016955001|GSVIVT01016955001

403 KL-----TERVALEE---K-----L- 415-KEE-----TLKRK 832 LQKDSREIVSLKE 844EITKL-----TERVAKLEEETSK-----L 863-KER----- 472 --- 471----- 471----- 455----- 455----- 452 EGGLETQFTLRTAEEVTVTLVG 815SLLAGGTHG6DREPPGSLMVAENVSDMFDQGSRHRDKFAISELLENVGARVSFGVTRNRLR 875FRGRCLRKDLPVVASLLNEQL 795 --- 462----- 462----- 466 --- 405----- 405----- 609----- 609----- 448 --- 447----- 447----- 484 --- 483----- 483----- 451 --- 451----- 451----- 440 --- 439----- 439----- 461 --- 460----- 460----- 470 --- 469----- 469----- 481 --- 480----- 480----- 450 --- 449----- 449----- 498 --- 497----- 497----- 457 --- 456----- 456----- 478 --- 477----- 477----- 473 --- 472----- 472----- 476 --- 475----- 475----- 477 --- 476----- 476----- 510 --- 509----- 509----- 508 --- 507----- 507----- 542 --- 541----- 541----- 508 --- 507----- 507----- 510 --- 509----- 509----- 473 --- 472----- 472----- 475 --- 474----- 474----- 511 --- 510----- 510----- 511 --- 510----- 510----- 477 --- 476----- 476----- 514 --- 513----- 513----- 366 --- 366----- 366----- 367 --- 366----- 366----- 475 --- 474----- 474----- 456 --- 455----- 455----- 510 --- 509----- 509----- 507 --- 506----- 506----- 508 --- 507----- 507----- 504 --- 503----- 503----- 509 --- 508----- 508----- 508 --- 507----- 507----- 518 --- 517----- 517----- 327 326----- 326----- 326----- 326----- 628----- 628----- 629 --- 628----- 628----- 428 --- 428----- 428----- 546 --- 546----- 546----- 529 --- 528----- 528----- 523 --- 523----- 523----- 540 --- 539----- 539----- 496 --- 495----- 495----- 490 --- 489----- 489----- 443 --- 442----- 442----- 437 --- 436----- 436----- 470 --- 469----- 469----- 469 --- 468----- 468----- 508 --- 507----- 507----- 464 VL 465LQ-----NGELVIEDKMEKAL-----EI 483ISETCWEDIE-----EAKQRRLHDMAGLETGLLP 488827|448827 515 --- 514----- 514----- 507 --- 506----- 506----- 514 --- 513----- 513----- 514 --- 513----- 513----- 514 --- 513----- 513----- 490 --- 489----- 489----- 394 --- 393----- 393----- 490 --- 489----- 489----- 506 --- 505----- 505----- 506 --- 505----- 505----- 835 --- 834----- 834----- 272 --- 271----- 271----- 834----- 834----- 504 --- 503----- 503----- 504 --- 503----- 503----- 503 --- 502----- 502----- 507 --- 506----- 506----- 505 --- 504----- 504----- 496 --- 495----- 495----- 500 --- 499----- 499----- 502 --- 501----- 501----- 508 --- 507----- 507----- 511 --- 510----- 510----- 507 --- 506----- 506----- 496 --- 495----- 495----- 500 --- 499----- 499----- 500 --- 499----- 499----- 508 --- 507----- 507----- 505 --- 504----- 504----- 506 --- 505----- 505----- 435 --- 434----- 434----- 492 --- 491----- 491----- 492 --- 491----- 491----- 508 --- 507----- 507----- 506 --- 505----- 505----- 506 --- 505----- 505----- 493 --- 492----- 492----- 511 --- 510----- 510----- 512 --- 511----- 511----- 510 --- 509----- 509----- 138 --- 137----- 137----- 506 --- 505----- 505----- 507 --- 506----- 506----- 507 --- 506----- 506----- 507 --- 506----- 506-----

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GRMZM2G324991 GRMZM2G324991.T03	484	-----483-----483-----	483
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Carubv10000696m.g Carubv10000696m	495	-----494-----494-----	494
AT3G02090	508	-----507-----507-----	507
Carubv10013366m.g Carubv10013366m	542	-----541-----541-----	541
Bra021477 Bra021477	508	-----507-----507-----	507
Bra039151 Bra039151	510	-----509-----509-----	509
146300 146300	473	-----472-----472-----	472
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Cucs.a.081570 Cucs.a.081570.1	475	-----474-----474-----	474
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Potri.017G092400 Potri.017G092400.1	508	-----507-----507-----	507
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Glyma08g046020 Glyma08g046020.1	509	-----508-----508-----	508
Glyma18g31550 Glyma18g31550.3	508	-----507-----507-----	507
Eucgr.H00078 Eucgr.H00078.1	518	-----517-----517-----	517
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g1 24308013 ref NP_055975	496	-----495-----495-----	495
g1 453222763 ref NP_490888.2	490	-----489-----489-----	489
g1 59592983 ref NP_003357.2	443	-----442-----442-----	442
Es10111.0016	437	-----436-----436-----	436
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Vocar20001024m.g Vocar20001024m	469	-----468-----468-----	468
Cre17.g722800 Cre17.g722800.t1.2	508	-----507-----507-----	507
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448827 448827	513	-----512-----512-----	512
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183257 183257	507	-----506-----506-----	506
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GRMZM2G174137 GRMZM2G174137.T01	490	-----489-----489-----	489
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LOC_0s01g09560 LOC_0s01g09560.1	506	-----505-----505-----	505
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Bra018939 Bra018939	507	-----506-----506-----	506
Bra030405 Bra030405	505	-----504-----504-----	504
Bra022162 Bra022162	496	-----495-----495-----	495
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LOC_0s05g44916 LOC_0s05g44916.1	496	-----495-----495-----	495
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Cucs.a.116810 Cucs.a.116810.1	506	-----505-----505-----	505
Cucs.a.021700 Cucs.a.021700.1	435	-----434-----434-----	434
Glyma13g43000 Glyma13g43000.1	492	-----491-----491-----	491
Glyma15g02390 Glyma15g02390.1	492	-----491-----491-----	491
Medtr8g014660 Medtr8g014660.1	508	-----507-----507-----	507
Glyma07g01720 Glyma07g01720.1	506	-----505-----505-----	505
Glyma08g21380 Glyma08g21380.1	506	-----505-----505-----	505
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Glyma08g03580 Glyma08g03580.1	510	-----509-----509-----	509
Glyma14g13370 Glyma14g13370.1	138	-----137-----137-----	137
Eucgr.F03085 Eucgr.F03085.1	506	-----505-----505-----	505
Eucgr.C03704 Eucgr.C03704.1	507	-----506-----506-----	506
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g1 94538354 ref NP_004270.2	470	-----469-----469-----469-----	470
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LOC_0s01g51390 LOC_0s01g51390.1	473	-----472-----472-----472-----	473
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Carubv10000696m.g Carubv10000696m	510	-----509-----509-----509-----	510
AT3G02090	508	-----507-----507-----507-----	508
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Cucsa.081570 Cucsa.081570.1	459	-----458-----458-----458-----	459
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Glyma16g10360 Glyma16g10360.1	504	-----503-----503-----503-----	504
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Glyma18g31550 Glyma18g31550.3	507	-----506-----506-----506-----	507
Eucgr.H00078 Eucgr.H00078.1	518	-----517-----517-----517-----	518
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ES10268.0010	529	-----528-----528-----528-----	529
CMK260C CMK260CT	524	-----523-----523-----523-----	524
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g1 24308013 ref NP_055975	496	-----495-----495-----495-----	496
g1 453222763 ref NP_490888.2	490	-----489-----489-----489-----	490
g1 50592980 ref NP_003357.2	443	-----442-----442-----442-----	443
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183257 183257	514	-----513-----513-----513-----	514
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Phpat.003G045700 Phpat.003G045700.1	514	-----513-----513-----513-----	514
Phpat.013G074200 Phpat.013G074200.1	498	-----497-----497-----497-----	498
LOC_0s01g73550 LOC_0s01g73550.1	431	-----430-----430-----430-----	431
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Bra018939 Bra018939	505	-----504-----504-----504-----	505
Bra030405 Bra030405	496	-----495-----495-----495-----	496
Bra022162 Bra022162	500	-----499-----499-----499-----	500
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GRMZM2G324991 GRMZM2G324991.T03	484	3-----		483-----
g1 1753678 ref NP_498202.1	452	1-----		451-----
g1 71999683 ref NP_501576.2	440			439-----
g1 46593007 ref NP_003356.2	461	60-----		460-----
g1 94538354 ref NP_004270.2	470	69-----		469-----
CMM104C CMM104CT	481	480-----		480-----
g1 111226358 ref XP_001134518.1	450			449-----
ES10098 0070	498	497-----		497-----
g1 85119638 ref XP_965680.1	457	6-----		456-----
GRMZM5G827505 GRMZM5G827505.T01	478	77-----		477-----
LOC_0s01g51390 LOC_0s01g51390.1	473	72-----		472-----
Cre12.g523850 Cre12.g523850.t1.2	476	475-----		475-----
Vocar20014031m.g Vocar20014031m	477	476-----		476-----
Carubv10000696m.g Carubv10000696m	508	507-----		507-----
AT3G02090	508	507-----		507-----
Carubv10013366m.g Carubv10013366m	542	541-----		541-----
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Bra039151 Bra039151	510	509-----		509-----
146300 146300	473	72-----		472-----
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Cucsa.081570 Cucsa.081570.1	475	474-----		474-----
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g1 24308013 ref NP_055975	496	495-----		495-----
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g1 59592980 ref NP_003357.2	443			442-----
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183257 183257	507	506-----		506-----
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Phpat.003G045700 Phpat.003G045700.1	514	513-----		513-----
Phpat.013G074200 Phpat.013G074200.1	514	513-----		513-----
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GRMZM2G166646 GRMZM2G166646.T01	506	505-----		505-----
LOC_0s01g09560 LOC_0s01g09560.1	506	505-----		505-----
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Bra018939 Bra018939	507	506-----		506-----
Bra030405 Bra030405	505	504-----		504-----
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Glyma08g21380 Glyma08g21380.1	506	505-----		505-----
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AT3G02090
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Bra039151|Bra039151
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GSVIVG01012193001|GSVIVT01012193001
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Glyma18g31550|Glyma18g31550.3
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g1|59592988|ref|NP_003357.2|
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Glyma08g21380|Glyma08g21380.1
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Glyma14g13370|Glyma14g13370.1
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GSVIVG01015273001|GSVIVT01015273001
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1272 ----- 1271

835 ----- 834

