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Glyma.02G152800	Glyma.02G152800.2MRPRVAYS.....	FP	10
Glyma.10G021500	Glyma.10G021500.2MRPRVNYS.....	FP	10
Lj5g0004781	Lj5g0004781.1MQRVAFS.....	LP	9
Glyma.03G209400	Glyma.03G209400.1MQRMAYT.....F.....	SFP	11
Glyma.19G206800	Glyma.19G206800.1MQRMAYT.....F.....	SFP	11
Lj1g0015670	Lj1g0015670.1MKRMVCS.....	FP	9
AT3G62980	AT3G62980.1MQKRIALS.....	FP	10
AT4G03190	AT4G03190.1MGLR.....	FP	6
AT1G12820	AT1G12820.1MNY.....	FP	5
AT3G26810	AT3G26810.1MNY.....	FP	5
Glyma.16G050500	Glyma.16G050500.1MMNY.....	FP	6
Glyma.19G100200	Glyma.19G100200.1MMNY.....	FP	6
Lj1g0006513	Lj1g0006513.1MMNY.....	FP	6
Glyma.16G146400	Glyma.16G146400.1MNC.....	FP	5
Glyma.02G065300	Glyma.02G065300.1MNF.....	FP	5
Glyma.08G059500	Glyma.08G059500.6MECR.....RKKENQNP.....S.....	TFP	18
Glyma.07G189800	Glyma.07G189800.5MECR.....RKKENQKSN.....S.....	TFP	17
Lj4g0012889.1	Lj4g0012889.1MECRI.....RKKESPEPNILN.....QAS.....	PFP	23
AT4G24390	AT4G24390.1MTEE.....DSSAKMSEDVEKYLNLNPPC.SSSSSSSSAAT.....FTNKSRNFKSSPPPCP	51	
AT5G49980	AT5G49980.1MTQD.....RSEMSEDDDDQQSPPLDLPS.TAIADPCSSSS.....SPNKSRCISNSQT	FP	51
Glyma.04G093500	Glyma.04G093500.1MNQI.....	DDG...RTLSPLP	14
Glyma.06G095400	Glyma.06G095400.1MKQI.....	DDGDDEQRSLSPLP	18
Glyma.02G211800	Glyma.02G211800.1MRDKS.....ESH PSTNSEDDHRSSPLLDLAC.AEITESSNSKTR.....TCGPFPGSG..PSEPQAP	FP	57
Glyma.14G179500	Glyma.14G179500.1MREK.....ENHPSTNSEDDHRSS.LLDLAR.AEITESSNSKTR.....TCGSGLGSGSGTSEPQAP	FP	57
Lj1g0027142	Lj1g0027142.1MRDN.....HPPPTSDDDHRSSSLPDLARGGQITDSSSSKTRPGPGS.....SSSSLPQPGS.SSELQAQ	FP	62
Glyma.02G254300	Glyma.02G254300.1MTAR.....	RLS	7
Glyma.14G062100	Glyma.14G062100.1MEDRDAKRMAT.....	RLS	14
Glyma.11G227300	Glyma.11G227300.1MTEDRNVKRT.....	RVV	13
Glyma.18G030200	Glyma.18G030200.1MTEERNVRKT.....	RVV	13
Lj3g0010583	Lj3g0010583.1MEENRSVRCK.....	HVV	13
Lj6g0020395	Lj6g0020395.1MAAAAAATEDRSARRN.....	RLV	18
AT2G39940	AT2G39940.1MEDPDIKRCKLSCV.....	ATV	17
consensus	*	**	

Glyma.02G152800	Glyma.02G152800.2	EEVLEHVFS...	FI	EC	D	K	R	G	S	I	S	L	V	C	K	S	W	Y	E	I	E	R	W	C	R	R	R	V	F	V	G	N	C	Y	A	V	S	P	A	T	V	V	N	R	F	P	K	V	R	S	I	A	I	K	G	K	P	H	F	A	D	F	N	L	V	P	E	G	W	G	A	Y	V	G	P	96									
Glyma.10G021500	Glyma.10G021500.2	EEVLEHVFS...	FI	EC	D	K	R	G	S	I	S	L	V	C	K	S	W	Y	E	I	E	R	W	C	R	R	R	V	F	V	G	N	C	Y	A	V	S	P	A	T	V	V	N	R	F	P	K	V	R	S	I	A	I	K	G	K	P	H	F	A	D	F	N	L	V	P	E	G	W	G	A	Y	V	G	P	96									
Lj5g0004781	Lj5g0004781.1	EEVLEHVFS...	FI	D	N	D	K	R	S	S	I	S	L	V	C	R	S	W	Y	E	I	E	R	C	C	R	R	N	V	F	V	G	N	C	Y	A	V	S	P	E	M	V	V	K	R	F	P	R	V	R	S	V	T	L	K	G	K	P	H	F	A	D	F	N	L	V	P	D	G	W	G	G	Y	V	S	P	95								
Glyma.03G029400	Glyma.03G029400.1	EEVLEHVFS...	FI	W	S	E	R	D	R	N	A	I	S	L	V	C	K	S	W	Y	E	I	E	R	W	C	R	R	K	V	F	V	G	N	C	Y	A	V	S	P	L	M	V	I	K	R	F	P	E	L	R	S	I	A	I	K	G	K	P	H	F	A	D	F	N	L	V	P	E	G	W	G	G	Y	V	C	P	97							
Glyma.19G206800	Glyma.19G206800.1	EEVLEHVFS...	FI	W	N	E	R	D	R	N	A	I	S	L	V	C	K	S	W	Y	E	I	E	R	W	C	R	R	K	V	F	V	G	N	C	Y	A	V	S	P	L	M	V	I	K	R	F	P	E	V	R	S	I	A	I	K	G	K	P	H	F	A	D	F	N	L	V	P	D	G	W	G	G	Y	V	C	P	97							
Lj1g0015670	Lj1g0015670.1	EEVLEHVFS...	FI	Q	V	D	T	D	R	N	A	I	S	L	V	C	K	S	W	Y	E	I	E	R	W	C	R	R	K	V	F	V	G	N	C	Y	A	V	S	P	M	I	V	I	K	R	F	P	E	V	R	S	I	A	I	K	G	K	P	H	F	A	D	F	N	L	V	P	E	G	W	G	G	Y	V	C	T	W	95						
AT3G62980	AT3G62980.1	EEVLEHVFS...	FI	Q	L	D	K	D	R	N	S	V	S	L	V	C	K	S	W	Y	E	I	E	R	W	C	R	R	K	V	F	I	G	N	C	Y	A	V	S	P	A	T	V	I	R	R	F	P	K	V	R	S	V	E	L	K	G	K	P	H	F	A	D	F	N	L	V	P	D	G	W	G	G	Y	V	Y	P	W	96						
AT4G03190	AT4G03190.1	PKVLEHILS...	FI	D	S	N	E	D	R	N	S	V	S	L	V	C	K	S	W	Y	E	I	E	R	K	T	R	K	R	V	F	I	G	N	C	Y	A	V	S	P	A	A	V	T	R	R	F	P	E	M	R	S	L	T	L	K	G	K	P	H	F	A	D	Y	N	L	V	P	D	G	W	G	G	Y	A	P	W	92							
AT1G12820	AT1G12820.1	DEVI	E	H	V	F	D	...	F	V	A	S	H	K	D	R	N	S	I	S	L	V	C	K	S	W	H	K	I	E	R	F	S	R	K	E	V	F	I	G	N	C	Y	A	I	N	P	E	R	L	I	R	F	P	C	L	K	S	L	T	L	K	G	K	P	H	F	A	D	F	N	L	V	P	H	E	W	G	G	F	V	H	P	W	91
AT3G26810	AT3G26810.1	DEVI	E	H	V	F	D	...	F	V	T	S	H	K	D	R	N	A	I	S</																																																																	

Glyma.02G152800	Glyma.02G152800.2	IKAMAAAYP.WLQETRLKRMVIADECLELIAKSFKN.FQVLVLTSCEGFTTDGLAAIAANCRNLRELELRESEV...DDICGHWLSHFPD	181
Glyma.10G021500	Glyma.10G021500.2	IKAMAAAYP.WLQETRLKRMVISDECLELIAKSFKN.FQVLVLTSCEGFTTDGLAAIAANCRNLRELELRESEV...DDICGHWLSHFPD	181
Lj5g0004781	Lj5g0004781.1	IKAMAAACP.SLEETRLKRMVITDDCLDLIAKSFKN.FRVVLVTSCEGFTTHGLAAIAANCRNLRELDLRESEV...EDICGHWLSHFPD	180
Glyma.03G209400	Glyma.03G209400.1	IAAMARAAP.CLEETRLKRMVITDESLELIAKSFKN.FKVLVLTSCEGFTADGLTAIASNCRNLRELDLQESEV...EDLSGHWLSHFPD	182
Glyma.19G206800	Glyma.19G206800.1	IAAMARAAP.CLEETRLKRMVITDESLELIAKSFKN.FKVLVLTSCEGFTTDGLAAIAANCRNLRELDLQESEVE...EDLSGHWLSHFPD	183
Lj1g0015670	Lj1g0015670.1	IAAMSRAAP.WLEETRLKRMVISDESLELIAKSFKN.FKVLVLTSCEGFTTDGLAAIAANCRNLRELDLQESEV...EDLSGHWLSHFPD	180
AT3G62980	AT3G62980.1	TEAMSSSYT.WLEETRLKRMVITDDCLELIAKSFKN.FKVLVLSSCEGFSTDGLAAIAATCRNLKELDLRESDV...DDVSGHWLSHFPD	181
AT4G03190	AT4G03190.1	TEAMAAKSS.SLEETRLKRMVITDECLEKIAASFKD.FKVLVLTSCEGFSTDGIAAIAATCRNLRVLELRECEIV...EDLGGDWLSYFPE	177
AT1G12820	AT1G12820.1	IEALARSRV.GLEELRLKRMVITDESLELLSRSFAN.FKSLVLVSCEGFTTDGLASIAANCRHLRELDLQENEI...DDHRGQWLNCFPD	176
AT3G26810	AT3G26810.1	IEALARSRV.GLEELRLKRMVITDESLELLSRSFVN.FKSLVLVSCEGFTTDGLASIAANCRHLRDLDLQENEI...DDHRGQWLSCFPD	176
Glyma.16G050500	Glyma.16G050500.1	IEALAKNKV.GLEELRLKRMVVSDESLELLSRSFTH.FKSLVLVSCEGFSTDGLAALAANCRFLRELDLQENEV...EDHKGQWLSCFPD	177
Glyma.19G100200	Glyma.19G100200.1	VEALAKSRV.GLEELRLKRMVVSDESLELLSRSFTH.FKSLVLVSCEGFSTDGLAAIAANCRFLRELDLQENEV...EDHKGQWLSCFPD	177
Lj1g0006513	Lj1g0006513.1	IEALAKNKV.GLEELRLKRMVVSDESLELLSRSFVN.FKSLVLVSCEGFTTDGLAAVAANCRFLRELDLQENEV...EDQKGQWLSCFPD	177
Glyma.16G146400	Glyma.16G146400.1	IEALARSRV.DLEELRLKRMVVSDESLELLSRSFVN.FKSLVLVRCEGFTTEGLAAIAANCRFLKDLDLHENVV...TDLKGQWLSCFPD	176
Glyma.02G065300	Glyma.02G065300.1	TEAMVKSRV.DLEELRLKRMVITDKSLELLSRSFVN.FKSLVLVSCEGFTTDGLAAIAANCRFLKELDLQENEV...DDHRGQWLSCFPD	176
Glyma.08G059500	Glyma.08G059500.6	LVVFAKQYP.WLEELRLKRMVITDESLEFLALQFPN.FKALSLLSCDGFSTDGLASIAATNCKNLTELDIQENGI...EDKSGNWLGCFPD	189
Glyma.07G189800	Glyma.07G189800.5	LVVFAEKYP.WLEELRLKRMVITDESLEFLALKFPN.FKALSLLSCDGFSTDGLASIAATNCKNLTELDIQENGI...EDKSGNWLSCFPD	188
Lj4g0012889.1	Lj4g0012889.1	LVVFADKYP.LLEELRLKRMVITDESLEFLALSFPY.FKALSLLSCDGFSTDGLAAIATSCKNLTELDIQENGI...DDKSGNWLSCFPE	194
AT4G24390	AT4G24390.1	VAATAKAYP.WLEKVLKRMFVITDDLALLAESFPG.FKELTLVCCGFGTSGIAIVANKCRQLKVLDLMESEV...TDDELDWISCFPE	226
AT5G49980	AT5G49980.1	VSTMAQAYP.CLEKVDLKRMFVITDDLALLADSFPG.FKELTLVCCGFGTSGISIVANKCRKLKVLDLIESEV...TDDEVDWISCFPE	226
Glyma.04G093500	Glyma.04G093500.1	VTALSQSYHSSLNKLHLKRMSTLTDHDLTLISHSLPS.FQDLTLTCCEGFGTTALAALASNCRLLRVLELVECVVEV.GDEELDWISCFPE	192
Glyma.06G095400	Glyma.06G095400.1	ATALSQSYPSLNLHLKRMSTLTDHDLTLISHSFPS.FQDLVLTCCEGFGTTALAALASNCRLLRVLELVECVVEV.GDEEMDWISCFPE	196
Glyma.02G211800	Glyma.02G211800.1	ASALAQAAP.WLEKLHLKRMVITDADLALITADSFAG.FRELVLVCCGFGTTPGLAAVASKCRLLRVLELVESVVEVEDDEEVDWISCFPE	235
Glyma.14G179500	Glyma.14G179500.1	ASALSQAAP.WLEKLHLKRMVITDADLALITADFAA.FRELVLVCCGFGTTPGLAAVVSCKCRLLRVLELVESVVEVEDDEEVDWISCFPE	233
Lj1g0027142	Lj1g0027142.1	ATALAQAAP.WLEKLHLKRMVITDEDLAVVADSFSG.FRELVLVCCGFGTTPGLAAVASKCRLLRVLEVVSLEVPVSEDEVDWVSCFPE	240
Glyma.02G254300	Glyma.02G254300.1	VRVISQYFD.CLKSLHFRMIVRDSDLQVLARSRGHVLQALRLENCSTGFDGLYYIGRYCRNLRVLFLEESSL...VEKDGDLHELAL	179
Glyma.14G062100	Glyma.14G062100.1	VREISQYFD.CLKSLHFRMIVRDSDLQVLARSRGHILQALKDKCSGFDGLYYIGRYCRNLRVLFLEESSL...VENDGDWLHELAL	186
Glyma.11G227300	Glyma.11G227300.1	VKEISQYFD.CLKSLHFRMIVKDSDLRLNLRDRGHVLSLKLDKCSGFTTDGLFHHGRFCXSLRVLFLEESSI...VEKDGEWLHELAL	185
Glyma.18G030200	Glyma.18G030200.1	VKEISQYFD.CLKSLHFRMIVKDSDLRLNLRDRGHVLSLKLDKCSGFTTDGLFHHGRFCXSLRVLFLEESSI...LEKDGEWLHELAL	185
Lj3g0010583	Lj3g0010583.1KNLRALLEESSI...DEKDGEWLHELAV	53
Lj6g0020395	Lj6g0020395.1	VLEINQYFD.CLKSLHFRMIVKDNDLLLAQSRGPVLSLKLDKCCGFDGLLHVSRCRNLRVLLLEESSI...DEKDGEWLHELAL	190
AT2G39940	AT2G39940.1	VTEISNNLR.QLKSVHFRMIVSDLDLRLAKARADDLETCLKDKCSGFTTDGLLSIVTHCRKIKTLLMEESSF...SEKDGKWLHELAQ	189
consensus		* * * * *	

Glyma.02G152800	Glyma.02G152800.2	S..YTSLVSLNISCLG.NEVNLSALERLVSRCPNLQTLRLNRRAVPLDRLATLLRGAPQLVELGTGAYTT.EM.....RPEVFNLAEAA	260
Glyma.10G021500	Glyma.10G021500.2	S..YTSLVSLNISCLG.NEVNLSALERLVSRCPNLQTLRLNRRAVPLDRLANLLRGAPQLVELGTGYTIT.EM.....RPEVFNLAEAA	260
Lj5g0004781	Lj5g0004781.1	S..YNSLESLSNISCLS.NEVNLPALERLVSRCPNLQTLRLNRRAVPLDRLTNLLRGAPQLVELGTGAYTA.EM.....RPEVLANTLEAA	259
Glyma.03G209400	Glyma.03G209400.1	S..YTSLVSLNISCLN.HEVSLAALERLGGRCNLRTRLRLNRRAVPLDRLPNLLRCQPQLVELGTGVYST.EM.....RPEVFSNLLEAA	261
Glyma.19G206800	Glyma.19G206800.1	S..YTSLVSLNISCLN.NEVSLSALERLLGRCPNLRTLRLNRRAVPLDRPLNLLLCQPQLVELGTGVYST.EM.....RPEVFSNLLEAA	262
Lj1g0015670	Lj1g0015670.1	S..YTSLVSLNISCLS.NEVSLSALERLLGRCPNMKTTLRLNRRAVPLDRLPNLLRQCQPQLVELGTGVYSYA.EM.....RPDVFSNLAAA	259
AT3G62980	AT3G62980.1	T..YTSLVSLNISCLA.SEVSFSALERLVTRCPNLKSKLNRAVPLEKLATLLQRAPQLEEELGTGGYTAEV.....RPDVYSGLSVA	260
AT4G03190	AT4G03190.1	S..STSLVSLDFSCLD.SEVKISDLERLVSRSPNLKSKLNPAVTLDGLVSLLRCAAPQLTELGTGSFAAQ.L.....KPEAFSKLSEA	256
AT1G12820	AT1G12820.1	S..CTTLMSLNFACLK.GETNVAAALERLVARSPNLKSKLNRAVPLDALARLMSCAPQLVDLGVGSYEN.EP.....DPESFAKLMTA	255
AT3G26810	AT3G26810.1	T..CTTLVTILNFACLE.GETNLVALERLVARSPNLKSKLNRAVPLDALARLMACAPQIVDLGVGSYEN.DP.....DSERYKLMAV	255
Glyma.16G050500	Glyma.16G050500.1	N..CTSLVSLNFACLK.GEVSLGALERLVARSPYLKSKLNRSVPFDALQRIMMRAPQLSDLGIGSFVH.DP.....ESEAYIKLKNT	256
Glyma.19G100200	Glyma.19G100200.1	N..CTSLVSLNFACLK.GEVSLGALERFVARSPNLKSKLNRSVPVDALQRIMMRAPQLSDLGIGSLVH.DP.....ESEAYIKLKNT	256
Lj1g0006513	Lj1g0006513.1	S..CTSLVSLNFACLK.GDVNLGALERLVARSPNLKSLRLNRSVPIEALQRILMQAPQLADLGIGSFVH.NP.....FSDAFSKLKNT	256
Glyma.16G146400	Glyma.16G146400.1	C..CTSLVSLNFACLK.GGINAGDLERLVARSPNLKSLRLNHTVPLSAQRILMQAPQLADLGIGSFVH.DP.....RSEVYNNMKNA	255
Glyma.02G065300	Glyma.02G065300.1	C..CTSLVSLNFACLK.GQINLGALERLVARSPNLKSLRLNHTVPLNALQRILRRAPQIVDLGIGSFIP.DP.....NSNVFIKLMNT	255
Glyma.08G059500	Glyma.08G059500.6	S..FTSLEVLFNFANLH.NDVNFDALKLVCRCKSLKTLKVNKSVTLEQLQRLLVHVHPQLGELGTGSFSQ.EL.....TAQQCSDLESA	268
Glyma.07G189800	Glyma.07G189800.5	S..FTSLEVLFNFANLH.NDVNFDALKLVSRCKSLKTLKVNKSVTLEQLQRLLIVHVHPQLGELGTGSFSQ.EL.....TSQCCSDLESA	267
Lj4g0012889.1	Lj4g0012889.1	S..FTSLEVLFNFANLP.NDVNSDALEKLVSRCKSLKTLKVNRSVTLEQLQRLLVRAAPQLCELGSGFSFEDL.....TAQQYSEIESA	274
AT4G24390	AT4G24390.1	G..ETHLESLSFDCVE.SPINFKALEELVVRSFPFLKKLRLNRFVSLVELHRLMLVRAPQLTSLGTGSFSPDNV.....PQGEQQPDYAAA	307
AT5G49980	AT5G49980.1	D..VTCLESIAFDCEV.APINFKALEGLVARSPFLKKLRLNRFVSLVELHRLLLGAPQLTSLGTGSFSSHDEE.....PQSEQEPDYAAA	307
Glyma.04G093500	Glyma.04G093500.1	IDAQTYLESILVFDCEV.CPINIEALERLVARSPSLRKLRNLRYVMSQLHRLMHRAPQLTHLGTGSFSASEL.....DQELDFASA	272
Glyma.06G095400	Glyma.06G095400.1	SDAQTHLESILVFDCEV.CPVNFDALERLVARSPPLLKRRLNRYVMSQLHRLMHRAPQLTHLGTGSFSASEL.....DQELDFASA	276
Glyma.02G211800	Glyma.02G211800.1	T..QTNMESLVFDCEV.VPINFEALEGLVARSPRLKKLRLNQFVSMQAQLYRLLRAPQLTHLGTGSFSATEAGVVG.....DQEPPDYAAA	317
Glyma.14G179500	Glyma.14G179500.1	S..QTNLESILVFDCEV.VPINFEALEGLVARSPRLKKLRLNRYVSMALYRLLRAPQLTHLGTGSFSATEAGAVGDQEPDYQEPDYAAA	320
Lj1g0027142	Lj1g0027142.1	T..QTHLESILVFDCEV.YPVNFEALEGLVARSPGLKKLRLNRFVSMPLLYRLMLRAPQLTHLGTGSFSDEEA.....LEQEPDYASA	319
Glyma.02G254300	Glyma.02G254300.1	N..NTVLETILNFYVTDIANVRIQDLELIARNCPNLNSVKIITDCEVLD.LVNFFQYASALEEFFCGGSYNE.E.....SEKYSAMSLP	256
Glyma.14G062100	Glyma.14G062100.1	N..NTVLETILNFYLTDIANVRIQDLELIARNCPNLNSVKIITDCEVLD.LVNFFRYASALEEFFCGGSYNE.E.....SEKYSAISLP	263
Glyma.11G227300	Glyma.11G227300.1	N..NTVLETILNFYLTDIADVKIQDLELLAKNCPNLNSVKILTDCSEILD.LVNFFKHASALEEFFCGPTYNE.E.....PEKYSAISLP	262
Glyma.18G030200	Glyma.18G030200.1	N..NTVLETILNFYLTDIADVKIIEDELLAKNCPNLNSVKILTDCSEILD.LVNFFKHASALEEFFCGPTYNE.E.....PERYSAISLP	262
Lj3g0010583	Lj3g0010583.1	N..NTILESFNFYSTDVAAVKIEDLELLAKNRPNLNSVKITEYE.....NKYC.IYNE.E.....PERVYVISLP	114
Lj6g0020395	Lj6g0020395.1	S..NTVLESILNFYLTDIADVKIEDLELLAKNCPNLNSVKITEYEISN.LVNFFRQASSLEEFFCGIYNE.E.....PEIYSAISLP	267
AT2G39940	AT2G39940.1	H..NTSLEVLNIFYMETFAKISPDKLETIARNCRSLVSVKGWDFEILELVGFFKAAANLEEFFCGSLNE.DIG.....MPKEYMNLVFP	269
consensus		* * * * *	269

Glyma.02G152800	Glyma.02G152800.2	FSGCKQLKGLSGFWDVLP	SYLPAVYPICSNLTSLNLSYAT.	IQSPDLIKLVGQCESLQRLWVLDY	IEDAGLEVIAASCKDLRELRFVPSD	349
Glyma.10G021500	Glyma.10G021500.2	FSGCKQLKGLSGFWDVLP	SYLPAVYPICSNLTSLNLSYAT.	IQSPDLIKLVGQCESLQRLWVLDY	IEDAGLEVIAASCKDLRELRFVPSD	349
Lj5g0004781	Lj5g0004781.1	FSGCKQLKGLSGFWDVLP	SYLPAVYPVCSGLTSLNLSYAT.	IQSPDHIKLVSQCGSLQRLWVLDY	IEDAGLDVLAASCKDLRELRFVPSD	348
Glyma.03G209400	Glyma.03G209400.1	FSGCKQLKSLSGFWDVLP	SYLPAVYPICSRSLTSLNLSYAI.	IQSSDLIKLISQCPNLLRLWVLDY	IEDAGLYALAAASCKDLRELRFVPS	350
Glyma.19G206800	Glyma.19G206800.1	FSGCKQLKSLSGFWDVLP	SYLPAVYPICSRSLTSLNLSYAI.	IQSSDLIKLISQCPNLLRLWVLDY	IEDAGLYALAAASCKDLRELRFVPSD	351
Lj1g0015670	Lj1g0015670.1	FSGCKQLKSLSGFWDVLP	SYLPAVYPVCSGLTSLNLSYAT.	VQSSDLVKLISQCPSLQRLWVLDY	IEDAGLDVLAASCKDLRELRFVPSD	348
AT3G62980	AT3G62980.1	LSGCKELRCLSGFWDVLP	SYLPAVYVCSRLTTLNLSYAT.	VQSYDLVKLCQCPKLQRLWVLDY	IEDAGLEVLAASCKDLRELRFVPS	349
AT4G03190	AT4G03190.1	FSNCKQLQSLSGLWDVLP	SYLPAVYVCPGLTSLNLSYAT.	VRMPDLVELRRCSKLQKLWVMDL	IEDKGLAVASYCKELRELRFVPS	345
AT1G12820	AT1G12820.1	IKKYTSLRSLSGFLEVA	PLCLPAFYPIQNLTSLNLSYAAE	IQGNHLIKLILQCLRLWVLDY	SIGDKGLAVVAATCKELRELRFVPS	345
AT3G26810	AT3G26810.1	IKKCTSLRSLSGFLEVA	APHCLSAFHPICHNLTSLNLSYAAE	THGSHLIKLIQHCKKLQRLWVLDY	SIGDKGLVAVASTCKELRELRFVPS	345
Glyma.16G050500	Glyma.16G050500.1	ILKRKSLTSLSGFLEVA	PHCLAAATYPCPNLTSLNLSYAAE	IQGSDLIKLIHQCKKLQRLWVLDY	SIGDKGLDVAVASTCKDLQELRFVPS	346
Glyma.19G100200	Glyma.19G100200.1	ILKCKSLTSLSGFLEVA	PHCLAAATYPCPNLTSLNLSYAAE	IQGSDLIKLIHQCKKLQRLWVLDY	SIGDKGLGVAVASTCKDLQELRFVPS	346
Lj1g0006513	Lj1g0006513.1	ILKSKSLTSLSGFLEVA	PHCLAAATYPCPNLTSLNLSYAAE	IQGSDLIKLIHQCKKLQRLWVLDY	SIGDKGLGVAVASTCKDLQELRFVPS	346
Glyma.16G146400	Glyma.16G146400.1	ILKCMSLTSLSGFLEVA	PHCLSAATYPCPNLTSLNLSYAAE	IQNTSLIKLISQCGKLQRLWVLDY	SIGDKGLGVAVASTCKDLQELRFVPS	345
Glyma.02G065300	Glyma.02G065300.1	IEECKSLTSLSGFLEVA	PHCLSAATYPCPNLTSLNLSYAAE	IQNTSLIKLISQCGKLQRLWVLDY	SIGDKGLGVAVASTCKDLQELRFVPS	345
Glyma.08G059500	Glyma.08G059500.6	FKNCKNLHTLSGLWVATA	QYLPVLSACTNLTFLNFSYAP.	LDSDGLAKLIVHCPKLQRLWVLDY	VEDKGLAVGSHCPLLEELRFVPA	357
Glyma.07G189800	Glyma.07G189800.5	LKNCKNLHTLSGLWVATA	QYLPVLSACTNLTFLNFSYAP.	LDSDGLAKLIVHCPKLQRLWVLDY	VEDKGLAVGSHCPLLEELRFVPA	356
Lj4g0012889	Lj4g0012889.1	FNNCKNLHTLSGLWVATA	QYLPVLSACTNLTFLNFSYAP.	LDGDDLAKLIVHCPNLRRLWVLDY	VEDKGLAVGSHCPLLEELRFVPA	363
AT4G24390	AT4G24390.1	FRACKSLVCLSGFREI	WPDYLPATYPACANLTSLNFSYAN.	ISPHMLKPIISNCHNIRVFWALDS	IRDEGLQAVAAATCKELRELRFVPA	396
AT5G49980	AT5G49980.1	FRACKSLVCLSGFREI	WPDYLPATYPACANLTSLNFSYAN.	ISPHMLKPIISNCHNIRVFWALDS	IRDEGLQAVAAATCKELRELRFVPA	396
Glyma.04G093500	Glyma.04G093500.1	FAACKSLVCLSGFREI	WPDYLPATYPACANLTSLNFSYAD.	ISADQLISVIRHCHKLQTFWVLDY	TICDEGLQAVAAATCKDLRELRFVPA	361
Glyma.06G095400	Glyma.06G095400.1	FASCKSLVCLSGFREI	WADYLPATYPACANLTSLNFSYAD.	ISADQLKSVIRHCHKLQTFWVLDY	TICDEGLQAVAAATCKDLRELRFVPA	365
Glyma.02G211800	Glyma.02G211800.1	FEACRSVCLSGFREI	WADYLPATYPVCANLTSLNLSYAD.	INTDQLKSVICHCHKLQIFWVLDY	SIRDEGLQAVAAATCKDLRELRFVPA	406
Glyma.14G179500	Glyma.14G179500.1	FEACRSVCLSGFREI	WADYLPATYPVCTNLTSLNLSYAD.	VNTDQLKSVIRHCHKLQIFWVLDY	SIRDEGLQAVAAATCKDLRELRFVPA	409
Lj1g0027142	Lj1g0027142.1	FAACRSVCLSGFREI	WADYLPATYPVCTNLTSLNLSYAD.	VNTDQLKSVIRHCHKLQIFWVLDY	SIRDEGLQAVAAATCKDLRELRFVPA	408
Glyma.02G254300	Glyma.02G254300.1	AKLSRL.....GLTYITKNE	MPVFPYAAALKKLDLLYAM.	LDTEDHCTLIQRCPNLEVLES	RNVIGDRGLEVLARCCRRLLKRLRIERG	340
Glyma.14G062100	Glyma.14G062100.1	AKLSRL.....GLTYITKNE	MPVFPYAAALKKLDLLYAM.	LDTEDHCTLIQRCPNLEVLES	RNVIGDRGLEVLARCCRRLLKRLRIERG	347
Glyma.11G227300	Glyma.11G227300.1	AKLCRL.....GLTYIGKNE	LPIVFMFAAAILKKLDLLYAM.	LDTEDHCTLIQRCPNLEVLES	RNVIGDRGLEVLARCCRRLLKRLRIERG	346
Glyma.18G030200	Glyma.18G030200.1	AKLCRL.....GLTYIGKNE	LPIVFMFAAAILKKLDLLYAM.	LDTEDHCTLIQRCPNLEVLES	RNVIGDRGLEVLARCCRRLLKRLRIERG	346
Lj3g0010583	Lj3g0010583.1	AKLCRL.....GLTYIGKNE	LPIVFMFAAAILKKLDLLYAL.	LDTDDH.....	DRGLEVLGSCCKRLKRLRIECG	178
Lj6g0020395	Lj6g0020395.1	AKLCRL.....GLTYIGKNE	LPMMLFAAAILKKLDLLYAL.	LDTDDHCTLIQRCPNLEVLES	RNVIGDRGLEVLARCCRRLLKRLRIERG	351
AT2G39940	AT2G39940.1	RKLCRL.....GLSYMGPNE	MPILFPFAAAILKKLDLLYAL.	LETEDHCTLIQRCPNLEVLES	RNVIGDRGLEVLARCCRRLLKRLRIERG	353
consensus		* * * * *	* * * * *	* * * * *	* * * * *	

Glyma.02G152800	Glyma.02G152800.2	P	F	G	L	.	.	E	P	N	V	A	L	T	E	Q	G	L	V	S	V	S	E	G	C	T	K	L	Q	S	V	L	Y	F	C	R	Q	M	S	N	A	A	L	D	T	I	A	R	S	R	P	N	M	T	R	F	R	L	C	I	E	P	R	A	P	D	Y	L	T	H	Q	P	L	D	A	G	F	G	A	I	V	E	H	C	K	D	L	Q	R	L	437		
Glyma.10G021500	Glyma.10G021500.2	P	F	G	L	.	.	E	P	N	V	A	L	T	E	Q	G	L	V	S	V	S	E	G	C	T	K	L	Q	S	V	L	Y	F	C	R	Q	M	T	N	S	A	L	D	T	I	A	R	N	R	P	N	M	T	R	F	R	L	C	I	E	P	Q	A	P	D	H	L	T	H	Q	P	L	D	A	G	F	G	A	I	V	E	H	C	K	D	L	Q	R	L	437		
Lj5g0004781	Lj5g0004781.1	P	F	G	L	.	.	E	P	N	V	A	L	T	E	E	G	L	I	S	V	S	E	G	C	P	K	L	Q	S	V	L	Y	F	C	R	Q	M	S	N	A	A	L	N	T	I	A	Q	N	R	P	N	M	T	R	F	R	L	C	I	E	P	R	T	P	D	Y	L	T	H	Q	P	L	D	A	G	F	G	A	I	V	Q	H	C	K	N	L	Q	R	L	436		
Glyma.03G209400	Glyma.03G209400.1	P	F	G	L	.	.	E	P	N	V	S	L	T	E	Q	G	L	V	S	V	S	E	G	C	P	K	L	Q	S	V	L	Y	F	C	R	Q	M	S	N	A	A	L	H	T	I	A	R	N	R	P	N	L	T	R	F	R	L	C	I	E	P	R	T	P	D	Y	L	T	L	E	P	L	D	S	G	F	G	A	I	V	E	Q	C	K	D	L	Q	R	L	438		
Glyma.19G206800	Glyma.19G206800.1	P	F	G	L	.	.	E	P	N	V	A	L	T	E	Q	G	L	V	S	V	S	E	G	C	P	K	L	Q	S	V	L	Y	F	C	R	Q	M	S	N	A	A	L	H	T	I	A	R	N	R	T	N	L	T	R	F	R	L	C	I	E	P	R	T	P	D	Y	L	T	H	E	P	L	D	S	G	F	G	A	I	V	E	Q	C	K	D	L	Q	R	L	439		
Lj1g0015670	Lj1g0015670.1	P	F	G	F	.	.	E	P	N	V	A	L	T	E	R	G	L	V	S	V	S	E	G	C	P	K	L	Q	S	V	L	Y	F	C	R	Q	M	S	N	A	A	L	H	T	I	A	R	N	R	P	N	F	T	C	F	R	L	C	I	E	P	Q	A	P	D	Y	L	T	L	Q	P	L	D	S	G	F	G	A	I	V	E	H	C	K	G	L	Q	R	L	436		
AT3G62980	AT3G62980.1	P	F	V	M	.	.	E	P	N	V	A	L	T	E	Q	G	L	V	S	V	S	M	G	C	P	K	L	E	S	V	L	Y	F	C	R	Q	M	T	N	A	A	L	I	T	I	A	R	N	R	P	N	M	T	R	F	R	L	C	I	E	P	K	A	P	D	Y	L	T	L	E	P	L	D	I	G	F	G	A	I	V	E	H	C	K	D	L	R	L	437			
AT4G03190	AT4G03190.1	P	D	L	D	.	.	A	T	N	I	P	L	T	E	Q	G	L	V	F	V	S	K	G	C	R	K	L	E	S	V	L	Y	F	C	V	Q	F	T	N	A	A	L	F	T	I	A	R	K	R	P	N	L	K	C	F	R	L	C	I	E	P	F	A	P	D	Y	K	T	N	E	P	L	D	K	G	F	K	A	I	A	E	G	C	R	D	L	R	L	433			
AT1G12820	AT1G12820.1	V	H	G	E	.	E	D	N	N	A	S	V	T	E	V	G	L	V	A	I	S	A	G	C	P	K	L	H	S	I	L	Y	F	C	K	Q	M	T	N	A	A	L	I	A	V	A	K	N	C	P	N	F	I	R	F	R	L	C	I	L	E	P	H	K	P	D	H	I	T	F	Q	S	L	D	E	G	F	G	A	I	V	Q	A	C	K	G	L	R	R	L	434	
AT3G26810	AT3G26810.1	L	L	G	.	.	G	G	N	T	A	V	T	E	E	G	L	V	A	I	S	A	G	C	P	K	L	H	S	I	L	Y	F	C	Q	Q	M	T	N	A	A	L	V	T	V	A	K	N	C	P	N	F	I	R	F	R	L	C	I	L	E	P	N	K	P	D	H	V	T	S	Q	P	L	D	E	G	F	G	A	I	V	K	A	C	K	S	L	R	R	L	432		
Glyma.16G050500	Glyma.16G050500.1	P	F	G	.	.	.	N	P	A	A	V	T	E	K	G	L	V	A	I	S	M	G	C	P	K	L	H	S	I	L	Y	F	C	H	Q	M	T	N	A	A	L	I	T	V	A	K	N	C	P	N	F	I	R	F	R	L	C	I	L	D	A	T	K	P	D	P	D	T	M	Q	P	L	D	E	G	F	G	A	I	V	Q	S	C	R	R	L	R	L	432			
Glyma.19G100200	Glyma.19G100200.1	P	F	G	.	.	.	D	P	A	A	V	T	E	K	G	L	V	A	I	S	M	G	C	P	K	L	H	S	I	L	Y	F	C	H	Q	M	T	N	A	A	L	I	T	V	A	K	N	C	P	N	F	I	R	F	R	L	C	I	L	D	A	T	K	P	D	P	D	T	M	Q	P	L	D	E	G	F	G	A	I	V	Q	S	C	R	R	L	R	L	432			
Lj1g0006513	Lj1g0006513.1	P	F	G	.	.	.	N	P	A	A	V	T	E	K	G	L	V	A	I	S	A	G	C	R	K	L	H	S	I	L	Y	F	C	H	Q	M	T	N	A	A	L	I	T	V	A	K	N	C	P	N	F	I	R	F	R	L	C	I	L	D	A	T	K	P	D	P	D	T	M	Q	P	L	D	E	G	F	G	A	I	V	Q	S	C	K	B	L	R	L	432			
Glyma.16G146400	Glyma.16G146400.1	R	V	G	G	.	.	N	G	P	T	R	V	T	E	K	G	L	V	A	I	S	M	G	C	P	E	L	H	S	I	L	Y	F	C	H	Q	M	T	N	A	A	L	I	T	V	A	K	N	C	P	N	F	I	R	F	R	L	C	I	L	D	P	T	K	P	D	P	D	T	M	Q	P	L	N	E	G	F	G	A	I	V	Q	S	C	K	Q	L	R	R	L	433	
Glyma.02G065300	Glyma.02G065300.1	R	V	G	R	.	.	N	D	P	A	G	V	T	E	K	G	L	V	A	I	S	M	G	C	P	K	L	H	S	I	L	Y	F	C	Q	Q	M	T	N	A	A	L	I	T	V	A	K	N	C	P	N	F	I	R	F	R	L	C	I	L	D	P	T	K	P	D	P	D	T	V	Q	P	L	D	E	G	F	G	A	I	V	Q	S	C	K	Q	L	R	R	L	433	
Glyma.08G059500	Glyma.08G059500.6	P	F	D	E	.	.	G	I	V	H	G	V	T	E	S	G	F	I	A	V	S	Q	G	C	P	R	L	H	Y	V	L	Y	F	C	R	Q	M	T	N	A	A	V	A	T	V	V	Q	N	C	P	D	F	T	H	F	R	L	C	I	M	H	P	G	Q	P	D	Y	L	T	Q	E	S	M	D	E	A	F	G	A	V	V	K	T	C	T	K	L	Q	R	L	445	
Glyma.07G189800	Glyma.07G189800.5	P	F	D	E	.	.	G	I	V	H	G	V	T	E	S	G	F	I	A	V	S	Q	G	C	P	R	L	H	Y	V	L	Y	F	C	R	Q	M	T	N	A	A	V	A	T	V	V	Q	N	C	P	D	F	T	H	F	R	L	C	I	M	H	P	G	Q	L	D	Y	L	T	Q	E	S	M	D	E	A	F	G	A	V	V	K	T	C	T	K	L	Q	R	L	444	
Lj4g0012889.1	Lj4g0012889.1	P	F	D	E	.	.	E	A	I	G	H	G	V	T	E	S	G	F	I	A	V	S	R	G	C	P	R	L	H	Y	V	L	Y	F	C	R	Q	M	T	N	A	A	V	A	T	V	V	Q	N	C	P	D	F	T	H	F	R	L	C	I	M	N	P	G	Q	P	D	Y	L	T	H	E	P	M	D	E	A	F	G	A	V	V	K	T	C	S	K	L	Q	R	L	452
AT4G24390	AT4G24390.1	P	R	E	.	.	.	D	S	E	G	P	V	S	G	V	G	L	Q	A	I	S	E	G	C	R	K	L	E	S	I	L	Y	F	C	Q	Q	M	T	N	A	A	V	A	T	V	A	M	S	E	N	C	P	L	T	V	F	R	L	C	I	M	G	R	H	R	P	D	H	V	T	G	K	P	M	D	D	G	F	G	A	I	V	K	N	C	K	L	T	R	L	483	
AT5G49980	AT5G49980.1	P	R	E	.	.	.	D	S	E	G	P	V	S	E	L	G	L	Q	A	I	S	E	G	C	R	K	L	E	S	I	L	Y	F	C	Q	R	M	T	N	A	A	V	I	A	M	S	E	N	C	P	E	L	T	V	F	R	L	C	I	M	G	R	H	R	P	D	H	V	T	G	K	P	M	D	E	G	F	G	A	I	V	K	N	C	K	L	T	R	L	483		
Glyma.04G093500	Glyma.04G093500.1	T	R	E	.	.	.	E	I	E	G	P	V	S	E	V	G	F	E	A	I	S	R	G	C	R	K	L	Q	S	I	L	F	F	C	Q	R	M	T	N	A	A	V	A	M	S	N	N	C	P	D	L	V	V	F	R	L	C	I	I	G	R	Y	R	P	D	P	E	T	L	E	P	M	D	E	G	F	G	A	I	V	M	N	C	K	L	T	R	L	448			
Glyma.06G095400	Glyma.06G095400.1	T	R	E	.	.	.	E	I	E	G	P	V	S	E	V	G	F	E	A	I	S	R	G	C	R	K	L	Q	S	I	L	F	F	C	Q	R	M	T	N	A	A	V	A	M	S	N	N	C	P	D	L	V	V	F	R	L	C	I	I	G	Q	Y	R	P	D	P	V	T	L	E	P	M	D	E	G	F	G	A	I	V	M	N	C	K	L	T	R	L	452			
Glyma.02G211800	Glyma.02G211800.1	A	R	E	.	.	.	E	T	D	G	P	V	S	E	V	G	F	E	A	I	S	Q	G	C	R	K	L	E	S	I	L	F	L	C	Q	R	M	T	N	A	A	V	A	M	S	K	N	C	P	D	L	V	V	F	R	L	C	I	I	G	R	Y	R	P	D	P	V	T	Q	E	P	M	D	E	G	F	G	A	I	V	M	N	C	K	L	T	R	L	493			
Glyma.14G179500	Glyma.14G179500.1	A	R	E	.	.	.	E	T	D	G	P	V	S	E	V	G	F	E	A	I	S	Q	G	C	R	K	L	E	S	I	L	F	F	T	Q	R	M	T	N	A	A	V	A	M	S	K	N	C	P	D	L	V	V	F	R	L	C	I	I	G	R	Y	R	P	D	P	V	T	E	E	P	M	D	E	G	F	G	A	I	V	M	N	C	K	L	T	R	L	496			
Lj1g0027142	Lj1g0027142.1	A	R	E	.	.	.	E	S	E	G	P	V	S	E	V	G	F	E	A	I	S	K	G	C	R	K	L	E	S	I	L	F	F	C	Q	R	M	T	N	A	A	V	A	M	S	K	N	C	P	D	L	L	V	F	R	L	C	I	I	G	R	Y																														

Glyma.02G152800	Glyma.02G152800.2	SL...	SGLLTDRVFEYIGTYGKKLEMLS	VAFAGSDSLGLHHVLS	GCDNL	RKLEIRDCP	.FGDKALLANAAKLE	TMRS	LWMSSCLVSYGAC	523
Glyma.10G021500	Glyma.10G021500.2	SL...	SGLLTDRVFEYIGTYGKKLEMLS	VAFAGSDSLGLHHVLS	GCDNL	RKLEIRDCP	.FGDKALLANAAKLE	TMRS	LWMSSCLVSYGAC	523
Lj5g0004781	Lj5g0004781.1	SL...	SGLLTDRVFEYIGTYAKKLEMLS	VAFAGSDSLGLHHVLS	GCDNL	RKLEIRDCP	.FGDKALLANAAKLE	TMRS	LWMSSCLVSYGAC	522
Glyma.03G209400	Glyma.03G209400.1	SL...	SGLLTDRVFEYIGTYAKKLEMLS	VAFAGSDSLGLHHVLS	GCDNL	RKLEIRDCP	.FGDKALLANAEKLE	TMRS	LWMSSCLVSYGAC	524
Glyma.19G206800	Glyma.19G206800.1	SL...	SGLLTDRVFEYIGTCGKKLEMLS	VAFAGSDSLGLHHVLS	GCDNL	RKLEIRDCP	.FGDKALLANAEKLE	TMRS	LWMSSCLVSYGAC	525
Lj1g0015670	Lj1g0015670.1	SL...	SGLLTDRVFEYIGTYGKKLEMLS	LAFAGSDSLGLHHVLS	GCDNL	RKLEIRDCP	.FGDKALLANAAKLE	TMRS	LWMSSCLVSYGAC	522
AT3G62980	AT3G62980.1	SL...	SGLLTDRVFEYIGTYAKKMEMLS	VAFAGSDSLGLHHVLS	GCDNL	RKLEIRDCP	.FGDKALLANAAKLE	TMRS	LWMSSCLVSYGAC	523
AT4G03190	AT4G03190.1	SV...	SGLLTSDKAFKYIGKHAKKVRMLS	IAFAGSDSLGLHHVLS	GCESL	RKLEIRDCP	.FGDTALLEHAAKLE	TMRS	LWMSSCLVSYGAC	519
AT1G12820	AT1G12820.1	SV...	SGLLTQVFLYIGMYAEQLEMLS	IAFAGSDSLGLHHVLS	GCKML	RKLEIRDCP	.FGNAALLADVGRYET	TMRS	LWMSSCLVSYGAC	520
AT3G26810	AT3G26810.1	SL...	SGLLTQVFLYIGMYANQLEMLS	IAFAGSDSLGLHHVLS	GCKML	RKLEIRDCP	.FGDTALLADVSKYET	TMRS	LWMSSCLVSYGAC	518
Glyma.16G050500	Glyma.16G050500.1	SL...	SGQLTDQVFLYIGMYAEKLEMLS	IAFAGSDSLGLHHVLS	GCKML	RKLEIRDCP	.FGNVALLTDVGKYET	TMRS	LWMSSCLVSYGAC	518
Glyma.19G100200	Glyma.19G100200.1	SL...	SGKLTDQVFLYIGMYAEKLEMLS	IAFAGSDSLGLHHVLS	GCKML	RKLEIRDCP	.FGDMALLTDVGKYET	TMRS	LWMSSCLVSYGAC	518
Lj1g0006513	Lj1g0006513.1	SL...	SGQLTDQVFLYIGMYAEQLEMLS	IAFAGSDSLGLHHVLS	GCKML	RKLEIRDCP	.FGNMALLADVGRYET	TMRS	LWMSSCLVSYGAC	518
Glyma.16G146400	Glyma.16G146400.1	SL...	SGQLTDQVFLYIGMYAEQLEMLS	VAFAGSDSLGLHHVLS	GCKML	RKLEIRDCP	.FGDSALLMDVGKYET	TMRS	LWMSSCLVSYGAC	519
Glyma.02G065300	Glyma.02G065300.1	SL...	SGQLTDQVFLYIGMYAEQLEMLS	IAFAGSDSLGLHHVLS	GCKML	RKLEIRDCP	.FGDSALLMDVGKYET	TMRS	LWMSSCLVSYGAC	519
Glyma.08G059500	Glyma.08G059500.6	AV...	SGYLTDLTFEYIGKYAKNLETLS	VAFAGSDSLGLHHVLS	GCPKL	RKLEIRDCP	.FGNGALLSLGKYES	TMRS	LWMSSCLVSYGAC	531
Glyma.07G189800	Glyma.07G189800.5	AV...	SGYLTDLTFEYIGKYAKNLETLS	VAFAGSDSLGLHHVLS	GCPKL	RKLEIRDCP	.FGNGALLSLGKYES	TMRS	LWMSSCLVSYGAC	530
Lj4g0012889	Lj4g0012889.1	AV...	SGLLTDLTFEYIGKYAKNLETLS	VAFAGSDSLGLHHVLS	GCPKL	RKLEIRDCP	.FGNAALLSLGKYES	TMRS	LWMSSCLVSYGAC	538
AT4G24390	AT4G24390.1	AV...	SGLLTDEAFSYIGEYKGLIRTLS	VAFAGSDSLGLHHVLS	GCPKL	RKLEIRDCP	.FGDVALRSGLHRYN	MRFLWMSSCLVSYGAC	569	
AT5G49980	AT5G49980.1	AV...	SGLLTQAFRYMGEYKGLVRLTS	VAFAGSDSLGLHHVLS	GCPRL	RKLEIRDCP	.FGDVALRSGLHRYN	MRFLWMSSCLVSYGAC	569	
Glyma.04G093500	Glyma.04G093500.1	AV...	SGLLTDRAFNYIGTYGKLIRTLS	VAFAGSDSLGLHHVLS	GCPNL	RKLEIRDCP	.FGDVALRSGLHRYN	MRFLWMSSCLVSYGAC	534	
Glyma.06G095400	Glyma.06G095400.1	AV...	SGLLTDRAFNYIGTYGKLIRTLS	VAFAGSDSLGLHHVLS	GCPNL	RKLEIRDCP	.FGDVALRSGLHRYN	MRFLWMSSCLVSYGAC	538	
Glyma.02G211800	Glyma.02G211800.1	AV...	SGLLTDRAFNYIGTYGKLIRTLS	VAFAGSDSLGLHHVLS	GCPNL	RKLEIRDCP	.FGDVALRSGLHRYN	MRFLWMSSCLVSYGAC	579	
Glyma.14G179500	Glyma.14G179500.1	AM...	SGLLTDRVFEYIGMYGKLVRLTS	VAFAGSDSLGLHHVLS	GCPNL	RKLEIRDCP	.FGDVALRSGLHRYN	MRFLWMSSCLVSYGAC	582	
Lj1g0027142	Lj1g0027142.1	AV...	SGLLTDRAFNYIGTYGKLIRTLS	VAFAGSDSLGLHHVLS	GCPNL	RKLEIRDCP	.FGDVALRSGLHRYN	MRFLWMSSCLVSYGAC	581	
Glyma.02G254300	Glyma.02G254300.1	ALYLRPGGLTDVGLGYIGQYSPN	VRWMLLGYVGETDAGLLEFSK	GCPSLQKLEMRGCSF	FSEYALAI	AATQLNSLRYLWVQGYAS	SPSCR	518		
Glyma.14G062100	Glyma.14G062100.1	ALYLRPGGLTDVGLGYIGQYSPN	VRWMLLGYVGETDAGLLEFSK	GCPSLQKLEMRGCSF	FSEYALAI	AATQLNSLRYLWVQGYAS	SPSCR	525		
Glyma.11G227300	Glyma.11G227300.1	ALYLRPGGLTDVGLGYIGQYSPN	VRWMLLGYVGETDAGLLEFSK	GCPSLQKLEMRGCSF	FSEYALAI	AATQLNSLRYLWVQGYAS	SPSCR	524		
Glyma.18G030200	Glyma.18G030200.1	ALYLRPGGLTDVGLGYIGQYSPN	VRWMLLGYVGETDAGLLEFSK	GCPSLQKLEMRGCSF	FSEYALAI	AATQLNSLRYLWVQGYAS	SPSCR	524		
Lj3g0010583	Lj3g0010583.1	ALYLRPGGLTDVGLGYIGQYSPN	VRWMLLGYVGETDAGLLEFSK	GCPSLQKLEMRGCSF	FSEYALAI	AATQLNSLRYLWVQGYAS	SPSCR	274		
Lj6g0020395	Lj6g0020395.1	ALYLRPGGLTDVGLGYIGQYSPN	VRWMLLGYVGETDAGLLEFSK	GCPSLQKLEMRGCSF	FSEYALAI	AATQLNSLRYLWVQGYAS	SPSCR	523		
AT2G39940	AT2G39940									

Glyma.02G152800 Glyma.02G152800.2	KLLGQKMPRLNVEVIDERG.....PPDSRPES.....SPVEKLYIY	559
Glyma.10G021500 Glyma.10G021500.2	KLLGQKLPRLNVEVIDERG.....PPDSRPES.....SPVEKLYMY	559
Lj5g0004781 Lj5g0004781.1	KLLGQKMPRLNVEVIDERG.....PPDTRPES.....SPVEKLYIY	558
Glyma.03G209400 Glyma.03G209400.1	KLLGQKMPRLNVEVIDERG.....PPDSRPDD.....CPVEKLYIY	560
Glyma.19G206800 Glyma.19G206800.1	KLLGQKMPRLNVEVIDERG.....PPDSRPDD.....CPVEKLYIY	561
Lj1g0015670 Lj1g0015670.1	KLLGLKMPRLNVEVIDERG.....PPDSRPDS.....CPVEKLYIY	558
AT3G62980 AT3G62980.1	KLLGQKMPRLNVEVIDERG.....APDSRPES.....CPVERVFIY	559
AT4G03190 AT4G03190.1	KLLSQKMPRLNVEVIDEH.....PPESRPES.....SPVERIYIY	554
AT1G12820 AT1G12820.1	KRLAQNSPRLNVEITINENENNG..MEQNEEDER.....EKVDKLYLY	560
AT3G26810 AT3G26810.1	KRLAEKAPWLNVEITINENDNNR..MEENGHEGR.....QKVDKLYLY	558
Glyma.16G050500 Glyma.16G050500.1	KLLAKKMPRLNVEIFNENE.....QEDCSLEDG.....QKVEKMYLY	555
Glyma.19G100200 Glyma.19G100200.1	KLLAKKMPRLNVEIFNENE.....QEDCSLEDG.....QKVEKMYLY	555
Lj1g0006513 Lj1g0006513.1	KRLAEKMPRLNVEIFNENE.....QEECSLEDE.....QSVEKMYLY	555
Glyma.16G146400 Glyma.16G146400.1	KALAEKMPRLNVEIFNENK.....KVDRDVDDG.....QKVEKMYLY	556
Glyma.02G065300 Glyma.02G065300.1	KALAKKMPGLNVEIFNGNE.....KVDRDVDDG.....QKVEKTYLY	556
Glyma.08G059500 Glyma.08G059500.6	RLLAKEMPRLNVEVIKEET.....YET.....HQAQKVVVY	562
Glyma.07G189800 Glyma.07G189800.5	RLLAQEMPRNVEVIKEES.....YET.....HQAQKVVVY	561
Lj4g0012889.1 Lj4g0012889.1	RLLAKEMPRLNVEVIKEEG.....CYE.....GPAQRVVVY	569
AT4G24390 AT4G24390.1	RGVSHALPNVVEVFGADG.....D...DDED...TVTG...DYVETLYLY	606
AT5G49980 AT5G49980.1	KDIFARAMPNLVVEVIGSDD.....D...DDNR.....DYVETLYMY	602
Glyma.04G093500 Glyma.04G093500.1	REVARMLPHLVLVINSEE.....D...KADD.....TEILYMY	565
Glyma.06G095400 Glyma.06G095400.1	QEVAAQTLPHLVLVINSEE.....D...KADG.....TEILYMY	569
Glyma.02G211800 Glyma.02G211800.1	QEVARVLPNLVFEVINNNNS.....E...ENAG.....DEVETLYMY	612
Glyma.14G179500 Glyma.14G179500.1	QEVARALPNLVLVINNNNN.....E...ENAGDEEENAG..DEVETLYMY	622
Lj1g0027142 Lj1g0027142.1	QDVARALPHLVLVEVINKED.....E...AAVD.....DTELLYMY	613
Glyma.02G254300 Glyma.02G254300.1	DLLAMARPYWNIELIPSR.....VVVSNQQEDPVV.....VEHIAHILAY	559
Glyma.14G062100 Glyma.14G062100.1	DLLAMARPYWNIELIPSR.....VVVSNQQEPPVV.....VEHPAHILAY	566
Glyma.11G227300 Glyma.11G227300.1	DLLAMARPFWNIELIPSRK....VAMNTNSDETVV.....VEHPAHILAY	565
Glyma.18G030200 Glyma.18G030200.1	DLLVMARPFWNIELIPSRK....VATNTNPDETVV.....VEHPAHILAY	565
Lj3g0010583 Lj3g0010583.1	NLLAMARPFWNIELIPSR.....VVTKNNMDEPVV.....AAHIFAY	312
Lj6g0020395 Lj6g0020395.1	DLLAMARPFWNIELIPSR.....VVVNNNMGPVVS....VHHPAHILAY	565
AT2G39940 AT2G39940.1	DLMQMARPYWNIELIPSR.....VPEVNQQGEIRE.....MEHPAHILAY	571
consensus	*** *!*****!*** * **	

☐ non-conserved
☒ similar
☒ ≥ 50% conserved