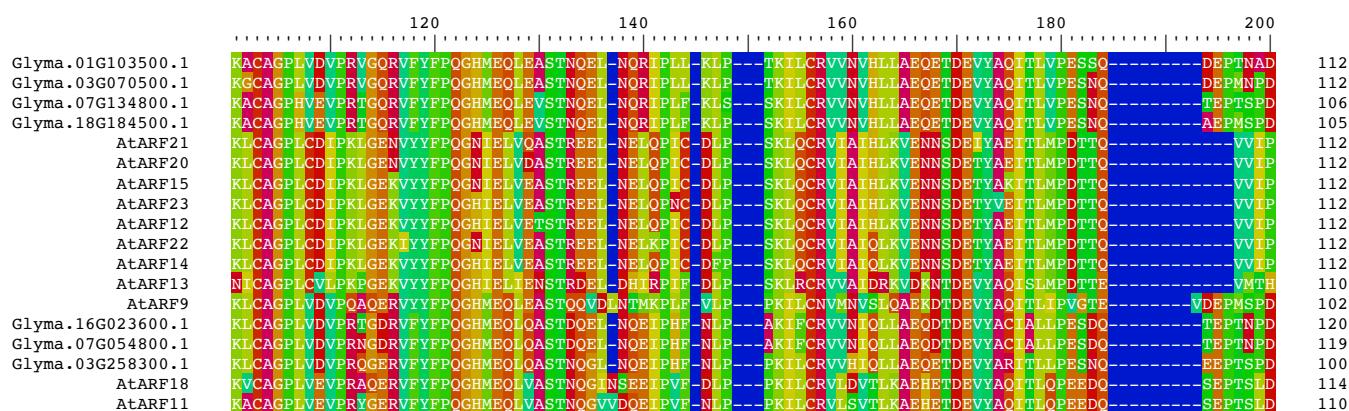


Consensus MLGLQELVPIXXXXXXXXXXXX+-++XX++++++-----+-----+-----+XXXXXXXW 35

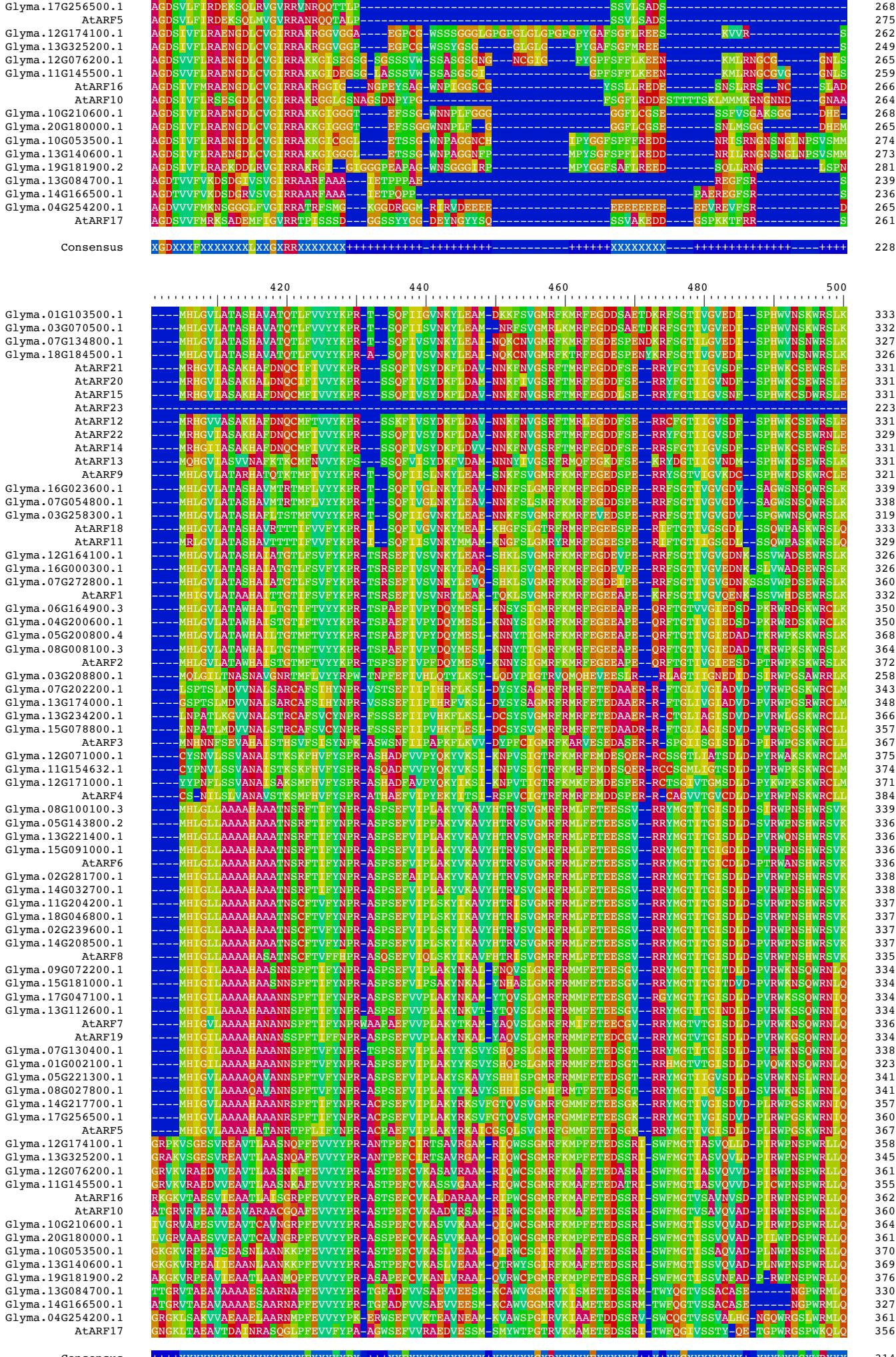


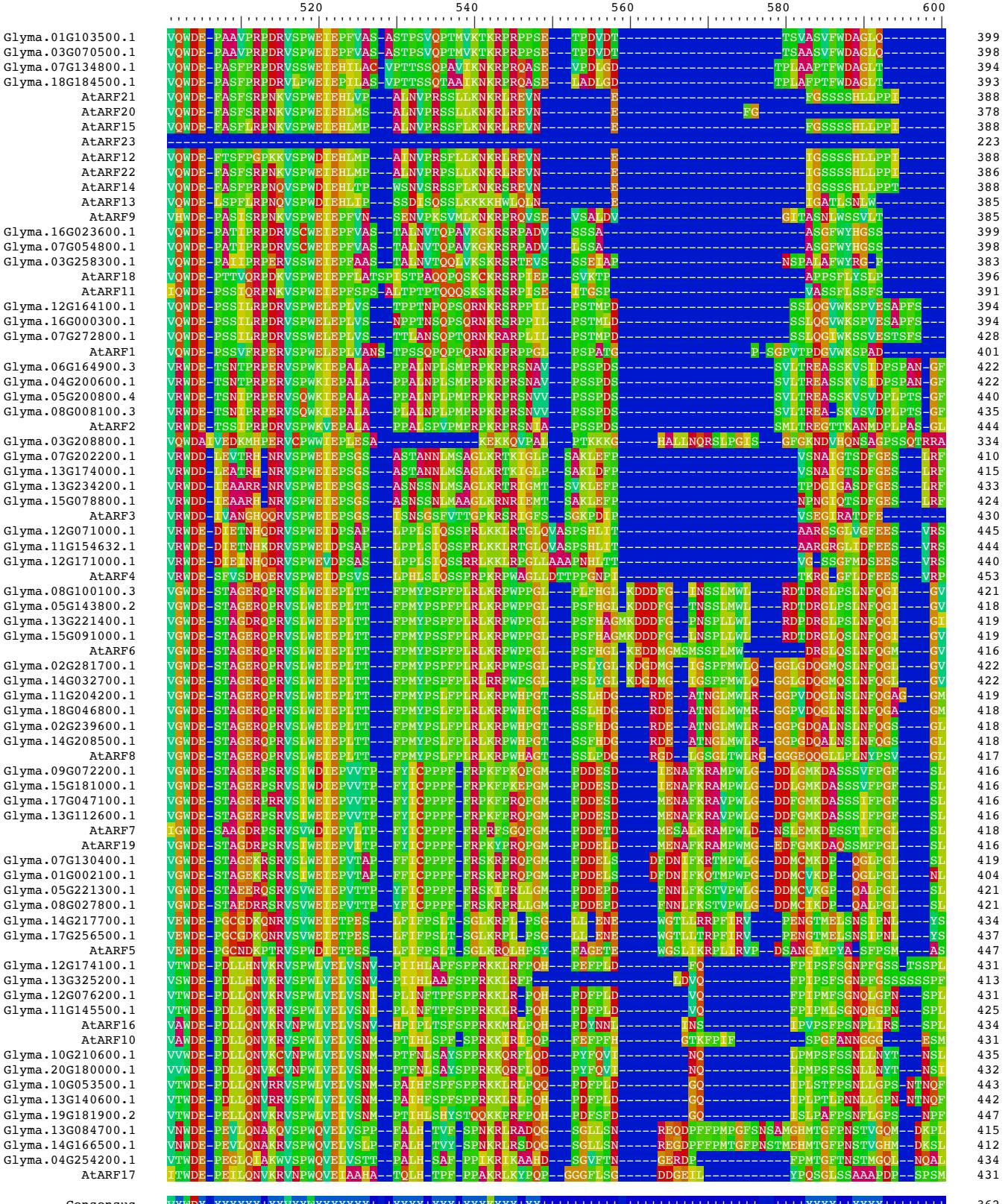
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Glyma.16G000300.1	HACAGPLVTLPREGERVYYFPQGHMEOLEASMNQGL--EQQMPSF-NLP--SKILCKVNVHRLRAEPETDEVYAQITLLPEADQ-----SEVTSPD	104
Glyma.07G272800.1	HACAGPLVTLPREGERVYYFPQGHMEOLEASMNQGL--EQQMPSF-NLP--SKILCKVNVHRLRAEPETDEVYAQITLLPEADQ-----SEVTSPD	137
AtARF1	HACAGPLVTLPREGERVYYFPQGHMEOLEASMNQGL--EQQMPSF-NLP--SKILCKVNVHRLRAEPETDEVYAQITLLPEADQ-----SEVTSPD	110
Glyma.06G164900.3	HACAGPLVTVPREKERVYYFPQGHIEQEVEASTNQVA--DOHMPVY-DLP--PKILCRVINVOLKAEPDTDEVFAQVTLPEPQNQ-----DENAVEKE	128
Glyma.04G200600.1	HACAGPLVTVPREKERVYYFPQGHIEQEVEASTNQVA--DOHMPVY-DLP--PKILCRVINVOLKAEPDTDEVFAQVTLPEPQNQ-----DENAVEKE	128
Glyma.05G200800.4	HACAGPLVTVPREGERVYYFPQGHIEQEVEASTNQVA--DOHMPVY-DLP--PKILCRVINVMIKAEPDTDEVFAQVTLPEPQNQ-----DENAVEKE	146
Glyma.08G008100.3	HACAGPLVTVPREKERVYYFPQGHIEQEVEASTNQVA--DOHMPVY-DLP--PKILCRVINVMIKAEPDTDEVFAQVTLPEPQNQ-----DENAVEKE	142
AtARF2	HACAGPLVTVPQRDDRVFYFPQGHIEQEVEASTNQAA--QOMPLY-DLP--SKLCLCRINVLDKLABADTDEVYAQITLLPEANQ-----DENAIEKE	150
Glyma.03G208800.1	MNVELKAEAYASDEVYAQTVTLPEVVKQDNICF-----EEEVNID	38
Glyma.07G202200.1	HACAGPLISLPKKGSVVVYFPQGHLEQ-----HLH--DFPLPASANIP--SHVFCRVLVDVLHAAEFGSDEVHCQVLLVPETEQVH--QR-LREGEEFD	117
Glyma.13G174000.1	HACAGPMISLPKKGSVVVYFPQGHLEQ-----HLH--DFPLPASANIP--SHVFCRVLVDVLHAAEFGSDEVYCQVLLVPESEQVH--QR-LREGEEFD	122
Glyma.13G234200.1	HACAGPLISLPKKGSVVVYLPQGHFE-----HQV--DFPVTAIY-DIP--PHVFCRVLVDVLHAAEFGSDEVYCQVLLVPESEQVH--QS-LREGEEIVAD	140
Glyma.15G078800.1	HACAGPLISLPKKGSVVVYLPQGHFE-----HVO--DFPVNAF-DIP--PHVFCRVLVDVLHAAEFGSDEVYCOVLLVPESEQVH--HS-LREGEEIVAD	131
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Glyma.11G154632.1	HACAGPLTSLPKKGNNVVVYFPQGHLEQAVASFSPFT--PLEIPTY-DLQ--POQIFCRVNVNVLQLLANKENDEVYTQVTLPPQAELEG--MY-LEGKELEEL	146
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Glyma.08G100100.3	HACAGPLVSIPAVGSRVVVYFPQGHSEQEVASTNREV--DGHIPNPYPSLP--PQLICQLHNLTMHADTETDEVYAQMTLQPLNPCQ-----QEKGAY-LP	116
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AtARF6	HACAGPLVSIPAVGSRVVVYFPQGHSEQEVASTNKEV--DAHIPNPYPSLP--PQLICQLHNMTMHADAETDEVYAQMTLQPLNPOE-----QEKGAY-LP	113
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AtARF7	HACAGPLISLPAPGSVVVYFPQGHSEQEVAASMQQT--DF-IPSYPNLIP--SKLICMLHNVTLNADPETDEVYAQMTLQPLVNKY-----DRDAI-LA	112
AtARF19	HACAGPLVSIPPVGSVVVYFPQGHSEQEVAASMQQT--DF-IPSYPNLIP--SKLICMLHNVTLNADPETDEVYAQMTLQPLVNKY-----DRDAI-LA	111
Glyma.07G130400.1	QACAGPLVNLLPPSGTHVYFPQGHSEQEVAASLNNDP--HSQIPNPYPNLP--SKLLCCLLHNLTLLADPETDEVYAQITLQPVPSF-----DKDAL-LR	114
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AtARF5	HACAGPLVCIPQVGSLSVYFPQGHSEQEVAASRTTA--TSQIPNPYPNLP--SQLLCQVQNVNTLHADKETDEIYAQMTLQPLNSE-----REVPI	136
Glyma.12G174100.1	HACAGGMVQMPPVNSKVFVYFPQGHAEHQAQSNSVDFGA---ARI--PIP--PILLCRCAAVFKLADPETDEVFAFLRNVPRLNSE-----LD-YEDSDGNG	99
Glyma.13G325200.1	HACAGGMVQMPPVNSKVFVYFPQGHAEHQAQSNSVDFGA---ARI--PIP--PILLCRCAAVFKLADPETDEVFAFLRNVPRLNSE-----LD-YEDSDANGE	100
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Glyma.11G145500.1	HACAGGMVQMPPVNSKVFVYFPQGHAEHQAQSNSVDFGA---ARI--PIP--PILLCRCAAVFKMNPANTEDEVFAFLRNVPRLNSE-----LG-PDSDAAGD	95
AtARF16	HACAGGMVRMPMNSKVFVYFPQGHAENAYDCVDFG---NI--PIP--PMVLCRVLAIKYMADAESDEVFAFLRLIPLKDE-----Y--VDHEYGDGE	105
AtARF10	HACAGGSMSVQIPSLINSTVYFPQFAOGTHEAHAPPDE--HAPRVP--PILLCRVLVSVSKFLADEFADTDEVFKAITLQPLPGND-----LD-LENDAVIGL	97
Glyma.10G210600.1	HACAGAMVQMPPLNKTFVYFPQGHAEHAKGVYFGF-----KHNQTRVP--PLIPCRISAMKYMADPDTEDEVYKMRUPLTPIREHEI-----LD-SQDDCFGLN	107
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Glyma.19G181900.2	GACAGGMVQMPPVNAKVFVYFPQGHAEHACGPVDFR-----VYPKP-----PFICQCKVAKIRYMPADPETDEVYVFLRVLPLTRNE-----GD-FEDDAVGGI	119
Glyma.13G084700.1	RACAGAAVQIPKLSRHSRVVYFPQGHMERA-SPSHYLS--PLIRSLP--FVPCHVSSLDFLADPFSDEVFAFLLTPLSQSQQQPFO-----NDTKEARND	103
Glyma.14G166500.1	RACAGAAVQIPKLSRHSRVVYFPQGHMERA-SPSHYLS--PLIRSLP--FVPCHVSSLDFLADPFSDEVFAFLLTPLSQSQQQPFO-----NDTKEARND	100
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AtARF17	RACAGASVQIPVLSRHSRVVYFPQGHMERA-SPSHYLS--PLLSTLPSTSVPVCIIITSIQLLADPVTDEVFAHLLIQPMTOQ-----O-FTPTNYSRF	103
Consensus	XXCAGXXXXXPXXXXXVXYFPQGXXEX+++++XX++-+++++X+++XXX--XXXXCXXXXXXXXXXXXDEXXXXXLXPXXXX+-+--+----+X+XX	104

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Glyma.01G103500.1	PC-----TAEPPRAPVHSFSKVLTAASDTSTHGGFSVLRKHATECLPVLQDMQSPTPTQELVQALDHLGYEWRFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	205			
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AtARF21	TQ-----SENFRPLVNSFTKVLTAASDTSTAYGGFSVPKKAIECLPPLQDMQSPLQPAQEILIAIDLHDNQWRFRHNYRGTQPRHSLTT-----GWNEFTSKKL	205			
AtARF20	TQ-----SENQFRPLVNSFTKVLTAASDTSTAYGGFSVPKKAIECLPPLQDMQSPLQPAQEILIAIDLHDNQWRFRHNYRGTQPRHSLTT-----GWNEFTSKKL	205			
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AtARF23	TB-----NENQFRPLVNSFTKVLTAASDTSAQGEFSVPCKHAIECLPPLQDMQSPLQPAQEILIAIDLHDNQWRFRHNYRGTQPRHSLTT-----GWNAFTTSKKL	202			
AtARF12	TQ-----NENQFRPLVNSFTKVLTAASDTSAHGGFFVPKKAIECLPPLQDMQSPLQPAQEILIAIDLHDNQWRFRHNYRGTQPRHSLTT-----GWNAFTTSKKL	205			
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AtARF14	TQ-----NONQFRPLVNSFTKVLTAASDTSGVHGVFSVPKKAIECLPPLQDMQSPLQPAQEILIAIDLHDNQWRFRHNYRGTQPRHSLTT-----GWNAFTTSKKL	205			
AtARF13	NT-----TMDTRRPVYFFSKILTAASDVSILSGGLIIPPKQYAEICFPPLQDMQSPLQPAQEILIAIDLHDNQWRFRHNYRGTQPRHSLTT-----GWNAFTTSKKL	205			
AtARF9	PS-----PPELQRPKVFHSFSKVLTAASDTSTHGGFSVLRKHATECLPPLQDMQPTQTPQELVQALDHLGFEWFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	195			
Glyma.16G023600.1	PN-----ISEPPQKQFHSFSKVLTAASDTSTHGGFSVLRKHATECLPPLQDMQPTQTPQELVQALDHLGFEWFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	213			
Glyma.07G054800.1	PN-----VSEAPQKQFHSFSKVLTAASDTSTHGGFSVLRKHATECLPPLQDMQPTQTPQELVQALDHLGFEWFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	212			
Glyma.03G258300.1	PS-----PPFTQKQFHSFSKVLTAASDTSTHGGFSVLRKHATECLPPLQDMQPTQTPQELVQALDHLGFEWFKHIFRQGPRRHLLTT-----GWNEFTSKKL	193			
AtARF18	PF-----IVGPTQKQFHSFSKVLTAASDTSTHGGFSVLRKHATECLPPLQDMQPTQTPQELVQALDHLGFEWFKHIFRQGPRRHLLTT-----GWSTFVTSKRLV	207			
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Glyma.16G000300.1	DP-----LPESPRTCTVHSFSKCTLTAASDTSTHGGFSVLRRHADDCLPPLQDMQPTQTPQELVQALDHLGFEWFKHIFRQGPRRHLLTT-----GWSVFSSSKKL	197			
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Glyma.05G143800.2	AE-----LGT-PSKQPTNPFCKTLTAASDTSTHGGFSVPKKAIECLPPLQDMQPTQTPQELVQALDHLGFEWFKHIFRQGPRRHLLTT-----GWSVFSAKRLV	206			

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AtARF6	AE--LCV-PSRQPTNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDFSQOPPAQELMARDLHDNEWKFRRHIFRGQPKRHLTT--GWSVFVSAKRLV	206
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AtARF8	IE--LGI-PSKQPSNYFCCKTLTASDTSTHGGFSVPRAAEKVFPPLDYLOPPAQELIARDLHDVEWKRHIFRGQPKRHLTT--GWSVFVSAKRLV	205
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Glyma.17G047100.1	SD--IGLKQNROPTTEFFCKTLTASDTSTHGGFSVPRAAEKILPPLDYSMQOPPAQELVARDLHDNTWTFRHRYRGQPKRHLTT--GWSVFVSTKRLF	205
Glyma.13G112600.1	SD--MGLKQNROPTTEFFCKTLTASDTSTHGGFSVPRAAEKIFFPPLDYSMQOPPAQELVARDLHDNTWTFRHRYRGQPKRHLTT--GWSVFVSTKRLF	205
AtARF7	SD--MGLKLNROPTTEFFCKTLTASDTSTHGGFSVPRAAEKIFFPPLDYSMQOPPAQELVARDLHDNTWTFRHRYRGQPKRHLTT--GWSVFVSTKRLF	206
AtARF19	SD--MGLKLNROPTTEFFCKTLTASDTSTHGGFSVPRAAEKIFFPPLDYSMQOPPAQELVARDLHDNTWTFRHRYRGQPKRHLTT--GWSVFVSTKRLF	205
Glyma.07G130400.1	SD--LALKSKPQDPDFCKQLTASDTSTHGGFSVPRAAADKIFFPPLDYSMQOPPAQELVARDLHDNTWTFRHRYRGQPKRHLTT--GWSLFVSGKRL	208
Glyma.01G002100.1	SD--LAESTKPPPDDFKQLTASDTSTHGGFSVPRAAEKIFFPPLDYSMQOPPAQELVARDLHDNTWTFRHRYRGQPKRHLTT--GWSLFVSGKRL	193
Glyma.05G221300.1	SD--IFLRSKPQPEFFCKQLTASDTSTHGGFSVPRAAEKIFFPPLDYSVOPPAQELVARDLHDNDVNVRFRHRYRGQPKRHLTT--GWSLFFIGKRL	211
Glyma.08G027800.1	SD--ISLKLSKPQPEFFCKQLTASDTSTHGGFSVPRAAEKIFFPPLDYSLSQSPVQELVARDLHDNDVNVRFRHRYRGQPKRHLTT--GWSLFISGKRL	211
Glyma.14G217700.1	SD--FGHKHSKHPSEFFCKTLTASDTSTHGGFSVPRAAEAKLFPPLDVTIQPPTQELVVVRDLHDNTWTFRHRYRGQPKRHLTT--GWSLFVGSKRL	227
Glyma.17G256500.1	SD--FGLKHSHKHPSEFFCKTLTASDTSTHGGFSVPRAAEAKLFPPLDVTIQPPTQELVVVRDLHDNTWTFRHRYRGQPKRHLTT--GWSLFVGSKRL	230
AtARF5	PD--FGMLRSKHPTEFFCKTLTASDTSTHGGFSVPRAAEKLFPLPPLDYSOAOPPTQELVVVRDLHDNTWTFRHRYRGQPKRHLTT--GWSLFVGSKRL	237
Glyma.12G174100.1	-----AEGSEKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSAEAPPVQTIAVNDVGEVWKRHRYRGTPRHLTT--GWSFVNQKKLV	188
Glyma.13G325200.1	-----AEGSEKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSAEAPPVQTIAVNDVGEVWKRHRYRGTPRHLTT--GWSFVNQKKLV	189
Glyma.12G076200.1	DV--AEPSCCEKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSAEAPPVQTIAVNDVGEVWKRHRYRGTPRHLTT--GWSFVNQKKLV	188
Glyma.11G145500.1	DA--AEPSSCEKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDCTAEPPVQTVAVNDVGETWFRHRYRGTPRHLTT--GWSFVNQKKLV	188
AtARF16	DS--NGFESENSEKTP-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDVAEAPPVQTIIAKDVKHGDVWKRHRYRGTPRHLTT--GWSNFVNQKKLV	199
AtARF10	TPPSSDGNNGKERPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDVAEAPPVQTIIAKDVKHGDVWKRHRYRGTPRHLTT--GWSTFVNQKKLV	194
Glyma.10G210600.1	JN--S-GGVEVNEKEPPTSFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSAEAPPVQTIIAKDMGOCWKFRHRYRGTPRHLTT--GWSTFVNQKKLV	202
Glyma.20G180000.1	SA--GGGGVQDQQEKEPPTSFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSAEAPPVQTIIAKDMLGQCWKFRHRYRGTPRHLTT--GWSNFVNQKKLV	203
Glyma.10G053500.1	-----ITQDKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSVDPVQNLAKDVGETWFRHRYRGTPRHLTT--GWSTFVNQKKLV	197
Glyma.13G140600.1	-----TRDKPA-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSADPPVQNLAKDVGETWFRHRYRGTPRHLTT--GWSTFVNQKKLV	196
Glyma.19G181900.2	N--GSENKDPSK-SFAKLTQSDANNGGGFSVPRYCAETIFFRLDYSADPPVQNLAKDVGETWFRHRYRGTPRHLTT--GWSFVNQKKLV	210
Glyma.13G084700.1	DD--DEDREN-NCGVV-SFAKILTPSDANNGGGFSVPRFCADSCFPPLDFRADPPVQLLSVADIEHGVWFRHRYRGTPRHLTT--GWSKFVNQKKLV	196
Glyma.14G166500.1	EE--NRDR-NCGVV-SFSKVLITA-SANNGGGFSVPRFCADSIFPPLNQADPPVQNLIVTDVHGFWVFRHRYRGTPRHLTT--GWSKFVNQKKLV	191
Glyma.04G254200.1	AA--SASAQTCENNQVV-SFSKVLITA-SANNGGGFSVPRFCADSIFPPLNQADPPVQNLIVTDVHGFWVFRHRYRGTPRHLTT--GWSKFVNQKKLV	202
AtARF17	GR--FDGDVDDNNNKVT-TFAKILTPSDANNGGGFSVPRFCADSVFPLNQFIDPPVQKLYVTDIHGAUWDFRHRYRGTPRHLTT--GWSKFVNQKKLV	198
Consensus	+X+XXXXXX+XFXXKLTxDXXXXXGGFXVXXXXAXXXPxLDXXXXXPQXXXXDXXXXXWXFXHXXRGXPXRXXXX--GWXXFXXXKXLX	192

	320	340	360	380	400	
Glyma.01G103500.1	AGDTFVFLRGDNGELRVGVRRLARQASSMP-----SSVISSQS					243
Glyma.03G070500.1	AGDTFVFLRGDNGELRVGVRRLARQASSMP-----SSVISSQS					243
Glyma.07G134800.1	AGDTFVFLRGDNGELRVGVRRLAPLOSSMP-----SSVISSQS					237
Glyma.18G184500.1	AGDTFVFLRGDNGELRVGVRRLAPVQSSMP-----SSVISSQS					236
AtARF21	KGDVIVFVRGETGELRVGIRRARHQQGNIP-----SSIISIDC					243
AtARF20	KGDVIVFVRGETGELRVGIRRARHQQGNIP-----SSIISIDC					243
AtARF15	KGDVIVFVRGETGELRVGIRRARHQQGNIP-----SSIISIDC					243
AtARF23	VGDVIVFARGETGELRVGIR*					223
AtARF12	AGDVIIVFVRGETGELRVGIRRARHQQGNIP-----SSIISIDC					243
AtARF22	AGDVIIVFVRGETGELRVGIRRAGHQQGNIP-----SSIISIES					241
AtARF14	EGDVIIVFVRGETGELRVGIRRAGHQQGNIP-----SSIISIES					243
AtARF13	VGDIFVLLRGENGEELRFGIRRRAHQQHIP-----SSVISANC					243
AtARF9	AGDIFVFLRGENGELRVGVRRLAQQNSMP-----SSVISSHHS					233
Glyma.16G023600.1	AGDAFVFLRGFHGQIRVGVRRLARQSPMP-----SSVISSQS					251
Glyma.07G054800.1	AGDAFVFLRGEHGQIRVGVRRLARQSPMP-----SSVISSQS					250
Glyma.03G258300.1	AGDAFVFLRGENGELRVGVRVARQSPMP-----SSVISSQS					231
AtARF18	AGDAFVFLRGENGDLRVGVRRLARQSTMP-----TSVISSQS					245
AtARF11	AGDAFVFLRGETGDLRVGVRRLAKQSTMP-----AVSISSQS					241
Glyma.12G164100.1	AGDAFIIFLRGENGEELRVGVRRLMRQSNMP-----SSVISSHS					235
Glyma.16G000300.1	AGDAFIIFLRGENGEELRVGVRRLMRQSNMP-----SSVISSHS					235
Glyma.07G272800.1	AGDAFIIFLRGENGEELRVGVRVMRQOSNVP-----SSVISSHS					268
AtARF1	AGDAFIIFLRGENEELRVGVRHRMRQQTNP-----SSVISSHS					241
Glyma.06G164900.3	AGDAFIIFLRGENEELRVGVRAMRQOQNV-----SSVISSHS					259
Glyma.04G20600.1	AGDAFIIFLRGENEELRVGVRAMRQOQNV-----SSVISSHS					259
Glyma.05G200800.4	AGDAFIIFLRGENEELRVGVRAMRQOQNV-----SSVISSHS					277
Glyma.08G008100.3	AGDAFIIFLRGENEELRVGVRAMRQOQNV-----SSVISSHS					273
AtARF2	AGDAFIIFLRGENEELRVGVRAMRQOQNV-----SSVISSHS					281
Glyma.03G208800.1	AGDSC1IFVRCGESGELRVGIRRANEINSNIQS-----SSLISGHS	S				168
Glyma.07G202200.1	SGDAVFLFLRGEDGELRLGIRRRAOLKSGST-----FSAISGQO					252
Glyma.13G174000.1	SGDAVFLFLRGEDGELRLGIRRRAOLKSGST-----FSAISGQO					257
Glyma.13G234200.1	SGDAVFLFLRGDDGKRLGIRRRAOLKSAGS-----FAPVSGQO					275
Glyma.15G078800.1	SGDAVFLFLRGDDGKRLGIRRRAOLKSGST-----FAVPSGQO					266
AtARF3	SGDAVFLFLRGDDGKRLGIRRRAOLKSGST-----ISAQYNQN					276
Glyma.12G071000.1	SGDAVFLFLRGENGELRLGIRRRAVPRNDLP-----ESVIGSQN					283
Glyma.11G154632.1	SGDAVFLFLRGENGELRLGIRRRAVPRNDLP-----ESVIGSQN					282
Glyma.12G171000.1	SGDAVFLFLRGENGELRLGIRRRAVPRNDLP-----ESIVGQS					279
AtARF4	SGDAVFLFLRDGGELRLGIRRRAVPRNGLP-----DSIEKNS					294
Glyma.08G100100.3	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					247
Glyma.05G143800.2	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					244
Glyma.13G221400.1	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					244
Glyma.15G091000.1	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					244
AtARF6	AGDSVLFIWNDKNQNLGGIRRAQPNVMP-----SSVLISSDS					244
Glyma.02G281700.1	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					246
Glyma.14G032700.1	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					246
Glyma.11G204200.1	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					245
Glyma.18G046800.1	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					245
Glyma.02G239600.1	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					245
Glyma.14G208500.1	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					245
AtARF8	AGDSVLFIWNEKNQNLGGIRRAQPNVMP-----SSVLISSDS					243
Glyma.09G072200.1	AGDSVLFIIRDEKQQLLGGIRRAQPNVMP-----SSVLISSDS					243
Glyma.15G181000.1	AGDSVLFIIRDEKQQLLGGIRRAQPNVMP-----SSVLISSDS					243
Glyma.17G047100.1	AGDSVLFIIRDEKQQLLGGIRRAQPNVMP-----SSVLISSDS					243
Glyma.13G112600.1	AGDSVLFIIRDEKQQLLGGIRRAQPNVMP-----SSVLISSDS					243
AtARF7	AGDSVLFIIRDGKAQLLLGGIRRAQPNVMP-----SSVLISSDS					244
AtARF19	AGDSVLFIIRDEKSQMLGGIRRAQPNVMP-----SSVLISSDS					243
Glyma.07G130400.1	AGDSVLFIIRDEKQQLLGGIRRAQPNVMP-----SSVLISSDS					246
Glyma.01G002100.1	AGDSVLFIIRDEKQQLLGGIRRAQPNVMP-----SSVLISSDS					231
Glyma.05G221300.1	AGDSVLFIIRDEKQQLLGGIRRAQPNVMP-----SSVLISSDS					249
Glyma.08G027800.1	AGDSVLFIIRDEKSQMLGGIRRAQPNVMP-----SSVLISSDS					249
Glyma.14G217700.1	AGDSVLFIIRDEKSQMLGGIRRAQPNVMP-----SSVLISSDS					265

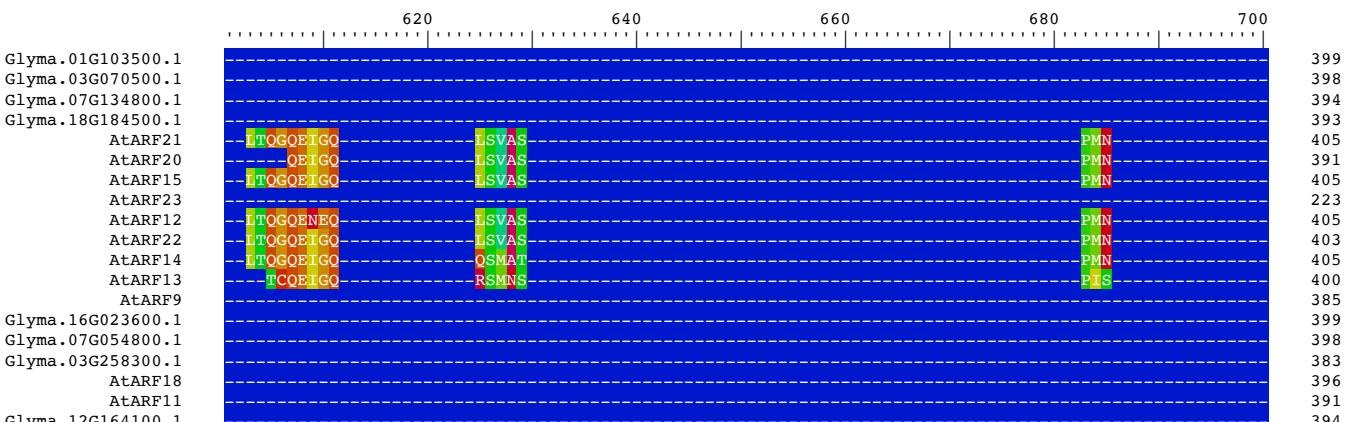




Consensus

VXWDX-XXXXXX+XXVXXWXXXXXXXX+-+XXXX+XXX+XXXX~~XXXX~~+XXXX+XX+++++++-+-----+----+XXXX++XXXX++++++

362



	720	740	760	780	800
Glyma.01G103500.1			QADMAQKNVLAESKW		414
Glyma.03G070500.1			QADMAQKRNVLAEISKR		413
Glyma.07G134800.1			QCDMTQLRVMTESKR		409
Glyma.18G184500.1			QSDMAKLSVMAEIKR		408
AtARF21		I-SLRYRDTEAAMNPS			421
AtARF20		T-SLRYRDTEADAMNPS			407
AtARF15		T-SLIVRETTEDAMNPS			421
AtARF23					223
AtARF12		I-SLRYRDATEDAMNPS			421
AtARF22		I-SLTYRDTTEDVMNPS			419
AtARF14		I-SLRYRDITEDAMTPS			421
AtARF13		VPEFSYPNAILEDSKFLS			417
AtARF9		OPHEFAQSCTI-SQW			399
Glyma.16G023600.1		NELSQLGAATAEVQVS			414
Glyma.07G054800.1		NELSQLGAA-AEVQVS			412
Glyma.03G258300.1		QDPTIALGSS-TEVQVS			397
AtARF18		QSQDSINASLK			407
AtARF11		QSHESNPSPVKI			402
Glyma.12G164100.1		VCDHQHGRDVYPSTNF			410
Glyma.16G000300.1		YRDHQHGRDVYPSTNF			410
Glyma.07G272800.1		YCDPQOGRGLYPSPPK			444
AtARF1		-TPSSVPLFSP			411
Glyma.06G164900.3		FSTLRGNTESNEFDT			446
Glyma.04G200600.1		FSTLRGNFAESNESDT			446
Glyma.05G200800.4		LSTLRGNFAESNESDT			464
Glyma.08G008100.3		LSTLRGNFAESNESDT			459
AtARF2		YSTLRTKHTESVECDAT			468
Glyma.03G208800.1		PLQRAPSTDIIIRPSKVP			367
Glyma.07G202200.1		YDSTNAQSHQVSDLRR			441
Glyma.13G174000.1		YDSFNAQSHQLSDLRR			446
Glyma.13G234200.1		EDGINAQSPRLYELGR			464
Glyma.15G078800.1		PFDCINAQSPFWLYELGR			456
AtARF3		-ESLRFQRV			438
Glyma.12G071000.1		GCDTVTKP-PGFEMMSSP			478
Glyma.11G154632.1		GCDTVTKP-PGFEMMSSC			477
Glyma.12G171000.1		GCDTVTKQ-PEFEIRSP			473
AtARF4		GFDMNRRILDFAMQSH			487
Glyma.08G100100.3		YOSDMYQAAAALQDMWTSNFSKQHPT			463
Glyma.05G143800.2		YOSDMYQAAAALQDMWTSNFSKQHPT			460
Glyma.13G221400.1		MOTDMYQ---AAAQDNRSI-LPSKQHSA			458

Glyma.15G091000.1		MQTDMYQAAAAAVQDMRSLDPSKQLSA-	461
AtARF6		MONDVYOAAMAAALDMRGIDPAKA-AA	458
Glyma.02G281700.1		LOPELYQAITSAAQFQEMRTMDISKS-SQ	463
Glyma.14G032700.1		LOPELYQAITSAAQFQEMRTMDISKS-SQ	463
Glyma.11G204200.1		DQNQQYQAMLAAGLQNLGSGLMLKQ	459
Glyma.18G046800.1		DQNQQYQAMLAAGLQNLGSGLMLKQ	458
Glyma.02G239600.1		DHNQHRYQAMFASGLQNLGSGLMLRQ	458
Glyma.14G208500.1		DHNQHRYQAMFASGLQNLGSGLMLRQ	458
AtARF8		DNNQQYQAMLAAGLQNLGSGLMLRQ	457
Glyma.09G072200.1	Pooooo	DNNQQYQAMLAAGLQNLGSGLMLRQ	457
Glyma.15G181000.1	PPooo	DNNQQYQAMLAAGLQNLGSGLMLRQ	541
Glyma.17G047100.1	QQQQQ	DNNQQYQAMLAAGLQNLGSGLMLRQ	542
Glyma.13G112600.1	QQQQQ	DNNQQYQAMLAAGLQNLGSGLMLRQ	557
AtARF7	Loooooooooooo	DNNQQYQAMLAAGLQNLGSGLMLRQ	557
AtARF19	SLNHOQQQSOSQOQQQOLQOQQQLOSQOHSNNNQSOSQOQQQOLQOQQQOLQOQQQOLQOQQQOL	DNNQQYQAMLAAGLQNLGSGLMLRQ	612
Glyma.07G130400.1	Hooooooooo	MSQQVQ	526
Glyma.01G002100.1		TLGTVLLPQQQLGDITQQFRQND	526
Glyma.05G221300.1		TLGTVLPQQQLGDITQQSRQND	511
Glyma.08G027800.1		ALGAVTQPLQLQGDITQQFR-NRN	527
Glyma.14G217700.1		ALGAVTQPLQLQGDITQQFR-NRN	527
Glyma.17G256500.1		AMQESAAATR-GPLQEMKTTIAAEENOMP	482
AtARF5		AMQESAAATR-GPLQEMKTTIAAEENOMI	485
Glyma.12G174100.1		EMQNIVMGNGGLGDMKMQPLMMNQK	496
Glyma.13G325200.1		AGIQGARH-AQIC	451
Glyma.12G076200.1		AGIQGARH-SQIC	433
Glyma.11G145500.1		AGIQGARH-AQFG	451
AtARF16		VGLQARHNAHQYYG	445
AtARF10		AGIQGARQAQQLFGSPSP	460
Glyma.10G210600.1		GGIQGARH-AQFG	456
Glyma.20G180000.1		AGMQGARH-AHYC	463
Glyma.10G053500.1		AGMQGARH-AHYD	462
Glyma.13G140600.1		AGIQGARH-ANYC	467
Glyma.19G181900.2		AGMQGARH-DLYSP	435
Glyma.13G084700.1		AGMQGARH-DLFSP	432
Glyma.14G166500.1		AGMQGARH-DAFS	454
Glyma.04G254200.1		AGMQGARH-YDFGS	451
AtARF17		Consensus	366

	820	840	860	880	900	
Glyma.01G103500.1	NDNTGTWHHMOT	-DMNSKSNSGNT	MIRNOTEWSWLS		SPh-SS	454
Glyma.03G070500.1	NDNTGTWHHMOT	-DMNSKSNSGNA	MIRNOTEWSWLS		SPh-SS	453
Glyma.07G134800.1	SDSSSHMRHHNS	-KSNNNNGI	SMNOTEAWWSL		Sp-----	441
Glyma.18G184500.1	SDSSSHMRHHNS	KSSNNCI	SMNOTEAWWSL		Sp-----	440
AtARF21		RLLMSY	PVOPMPKLN			437
AtARF20		RLLMSY	PVOPMPKLN			423
AtARF15		RLLMSY	PVOPMPKRN			437
AtARF23		KLLMSY	PVOPMPKLN			223
AtARF12		RLLMSY	PVOPMPKLN			437
AtARF22		RLLMSY	PVOPMPKLN			435
AtARF14		RLLMSY	PVOPMPAKLN			437
AtARF13		GLLLNH	SLLATIPNENY			433
AtARF9	SSPOOCHRHDANE	-DAKKSD-	WLN		NS-----	422
Glyma.16G023600.1	KENQVVPCSLRQ	-KDIINSNPIDAN-	NSSISSRVRMEGVWPS		SPh-LN	459
Glyma.07G054800.1	KENQVVPCSLRQ	-KDIINSNPIDAN-	NSSISSRVRMEGVWPS		SPh-LN	457
Glyma.03G258300.1	NENPVWV-STRQ	KE-INGNPMS	SSKVRVEGNRPS		SPh-----	433
AtARF18						407
AtARF11						402
Glyma.12G164100.1	NSTATGFLGFGG	-NCYA				426
Glyma.16G000300.1	NSTATGFLGFGG	-NCYA				426
Glyma.07G272800.1	NSSATNFIGFSG	-NSVS-			P-----	463
AtARF1	PAKAAATF-GHEG	-NKSFCV				428
Glyma.06G164900.3	AEKSVVWPPTAV	DDEKMDVST	SRYGSESWMS		MGRNEP	484
Glyma.04G200600.1	AEKSVVWPPTAV	DDEKMDVST	SRYGSESWMS		MGRNEP	484
Glyma.05G200800.4	VEKAAVWPPVAD	-DEKIDVST	SRYGSDSWMS		MGRHEL	501
Glyma.08G008100.3	AEKSGVWPPATD	-DEKIDVST	SRYGSDSWMS		MGRHEP	496
AtARF2	PENSVWVQSSAD	-DDKVDVVS	SRYGSESWMS		SARHEP	506
Glyma.03G208800.1	CYPVSNYPRIAATG	NSIGIPQV	IRG		SRFGENR	378
Glyma.07G202200.1	CYPGSNYPRIAATG	NSIGISQV	SSNVSS		NCIGFSE	476
Glyma.13G174000.1	CYPGSNCSTGIPPTG	NNIRMPHP	SSNVSN		NCIGFSE	481
Glyma.13G234200.1	CYPGSNCSTGIPPTG	NNIRVPHP	ASDFSC		NCIGFSE	499
Glyma.15G078800.1	CYPGSNCSTGIPPTG	NNIRVPHP	ASDFSC		NCIGFSE	491
AtARF3	LOGEIEFPGFINT	SDGGAGAR	RGRFKG		TEFGD	471
Glyma.12G071000.1	SHPNLGSAEV	--RKVSSSEI	NSVHPP		SYAGFVE	509
Glyma.11G154632.1	SHPNLGSAEV	-RKITSSSEI	SSVHPP		SYAGFVE	508
Glyma.12G171000.1	SHPNLASTGV	-RKIAAAEF	MRVHPS		SYAGTVE	504
AtARF4	ANPVLVSSRVKD	-RFGFVDA	TGVNP		ACSGVMD	519
Glyma.08G100100.3			SSIQF		QNFPNOTS	479
Glyma.05G143800.2			SAIQF		QNFPNRTS	476
Glyma.13G221400.1			SLLPF		QNFPNRTA	474
Glyma.15G091000.1			SLLQF		QNFPNRTA	477
AtARF6			SLLQF		PGFSMOSP	474
Glyma.02G281700.1			SLLQF		SNVPSAHA	479
Glyma.14G032700.1			SLLQF		SNVPSAHA	479
Glyma.11G204200.1			QLMNF		YHLYLQSG	475
Glyma.18G046800.1			QMMNF		YHLYLQSG	474
Glyma.02G239600.1			QIMNP		FNYLQSG	474
Glyma.14G208500.1			QMMNF		FNYLQSG	474
AtARF8			OFVQI		OYLOQSA	474
Glyma.09G072200.1	QQRQQPQEQQQSCQ	-OTIMNNGAVA	VSYSQLOQQQNLIS			625
Glyma.15G181000.1	QQRQQPQEQQQSCQ	-OTIMNSGTVVA	GSIPPOQQCPSP			626
Glyma.17G047100.1	OHLGQQPKQQQSSQH	-ATTIMNNGVVA	GSIPPOQQCPSP			641
Glyma.13G112600.1	OQLGQQPKQQQSSQH	-ATTIMNNGVVA	GSIPPOQQCPSP			634
AtARF7	NOLYNGOOAAQHOSQOASTHHL	OPLOVLSGSMS	GSIPPOQQCPSP			711
Glyma.07G130400.1	-Q-OQIYNNGTIA	VANQVSCQSPNQPTGFS	GSIPPOQQCPSP			600
Glyma.01G002100.1	POGQVO	-SQLLHPQNMVTNNILQQ	GSIPPOQQCPSP			569
Glyma.05G221300.1	POGQVO	-AQIYVHPQNMVTNNILQQ	GSIPPOQQCPSP			554
Glyma.08G027800.1	PDQAH	-TQLLNPNQVQTNILHQ	GSIPPOQQCPSP			570
Glyma.14G217700.1	PQNEAH	-TOLLNSQRVVQTNILQQ	GSIPPOQQCPSP			570
Glyma.17G256500.1			LNLNH		HSTPDQPN	496
			LNLNH		QSTPDQPN	499

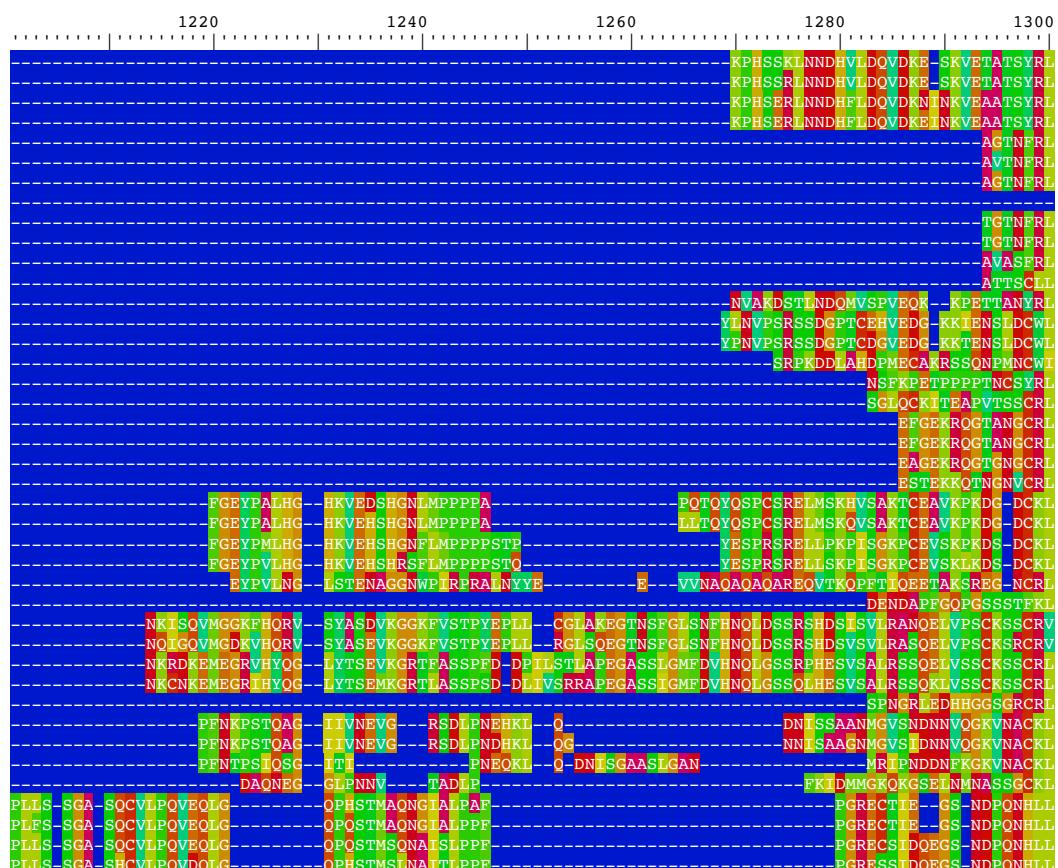
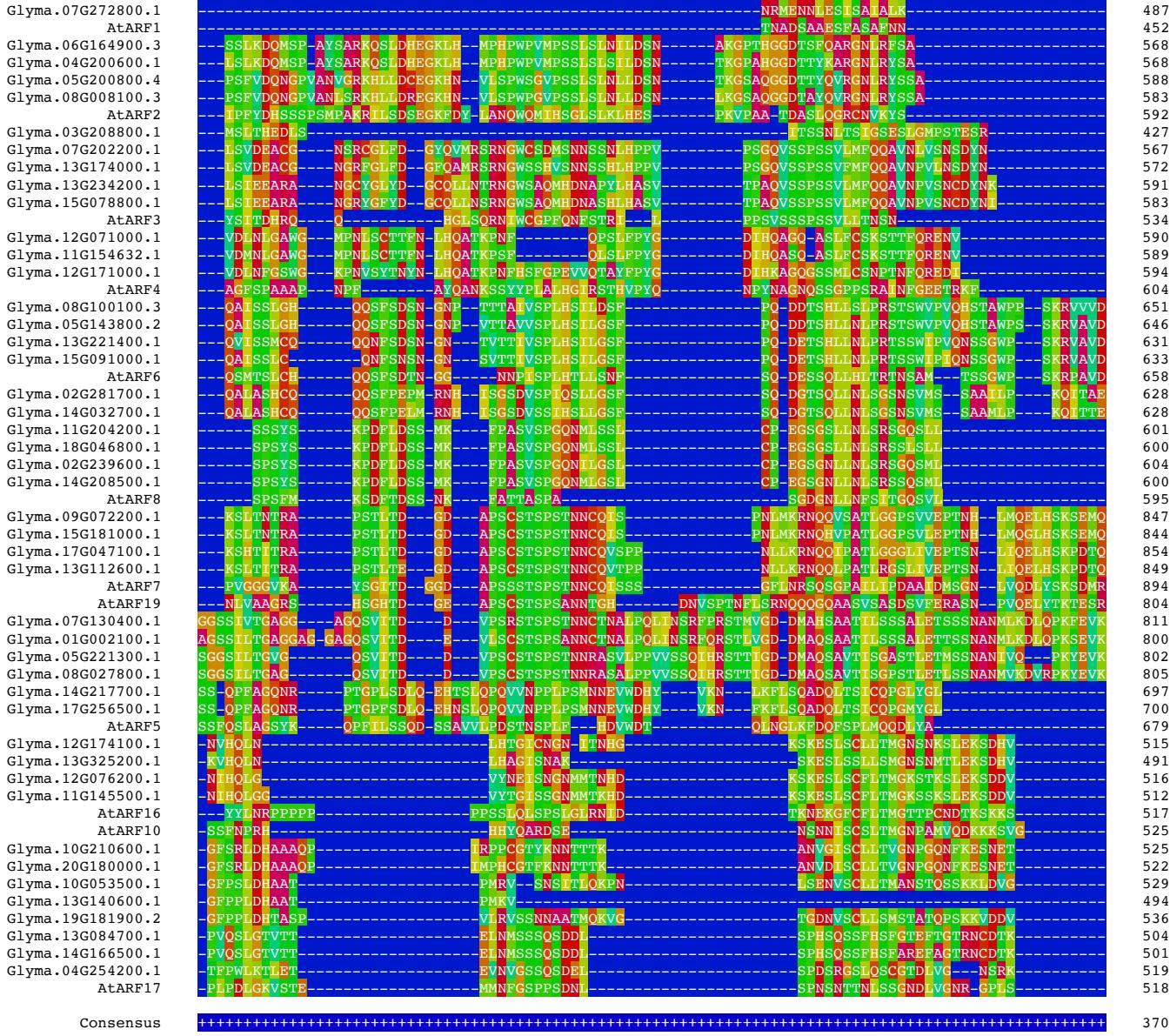
	SEVQ	PQN	KLTVNPS	511
Glyma.12G174100.1	ISL	SDLHN	SDLHN	460
Glyma.13G325200.1	ISL	SDLHN	SDLHN	442
Glyma.12G076200.1	KSL	SDLHLN	SDLHLN	460
Glyma.11G145500.1	KSL	SDLHLNN	SDLHLNN	455
AtARF5				
AtARF16	LSS	SDLH	SDLH	465
AtARF10	SLL	SDLNLSSY	SDLNLSSY	471
Glyma.10G210600.1	LSP	SDFPF	SDFPF	464
Glyma.20G180000.1	LSP	SDFPF	SDFPF	461
Glyma.10G053500.1	LSL	SDLHL	SDLHL	471
Glyma.13G140600.1	LSL	SDLHL	SDLHL	470
Glyma.19G181900.2	ISL	SNLHP	SNLHP	475
Glyma.13G084700.1	LSF	SNFLNDN	SNFLNDN	445
Glyma.14G166500.1	SSF	SNFLNDK	SNFLNDK	442
Glyma.04G254200.1	SRF	CNYPTDM	CNYPTDM	464
AtARF17	FNP	TGFITGGN	TGFITGGN	461

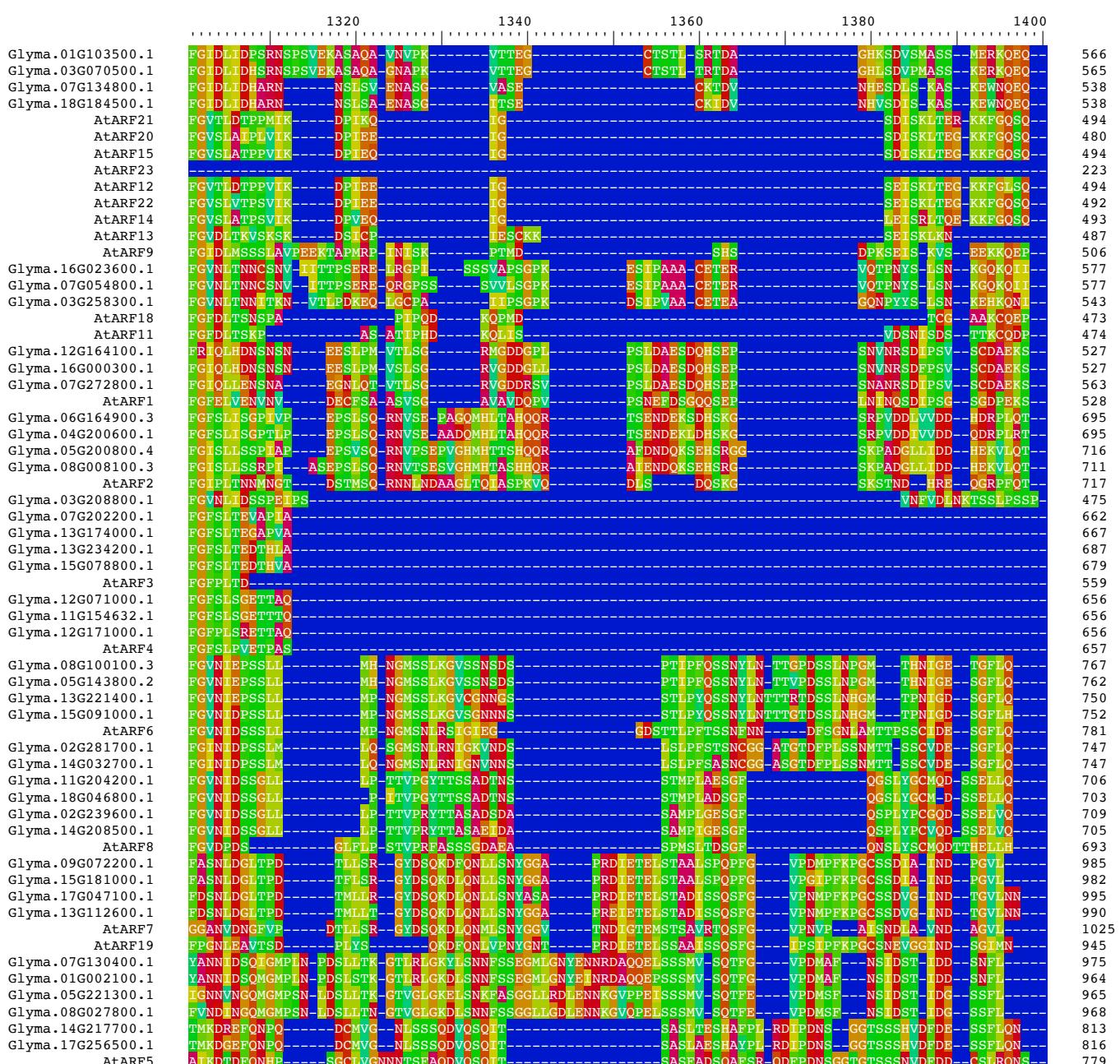
Sequence logo showing the conservation of amino acids across a set of Glyma and AtARF proteins. The x-axis represents positions 920, 940, 960, 980, and 1000. The y-axis lists protein accessions. The legend indicates the following color scheme: C (blue), P (green), S (yellow), T (orange), A (red), D (purple), G (pink), F (light blue), I (light green), V (light orange), H (light pink), K (light purple), and N (light blue).

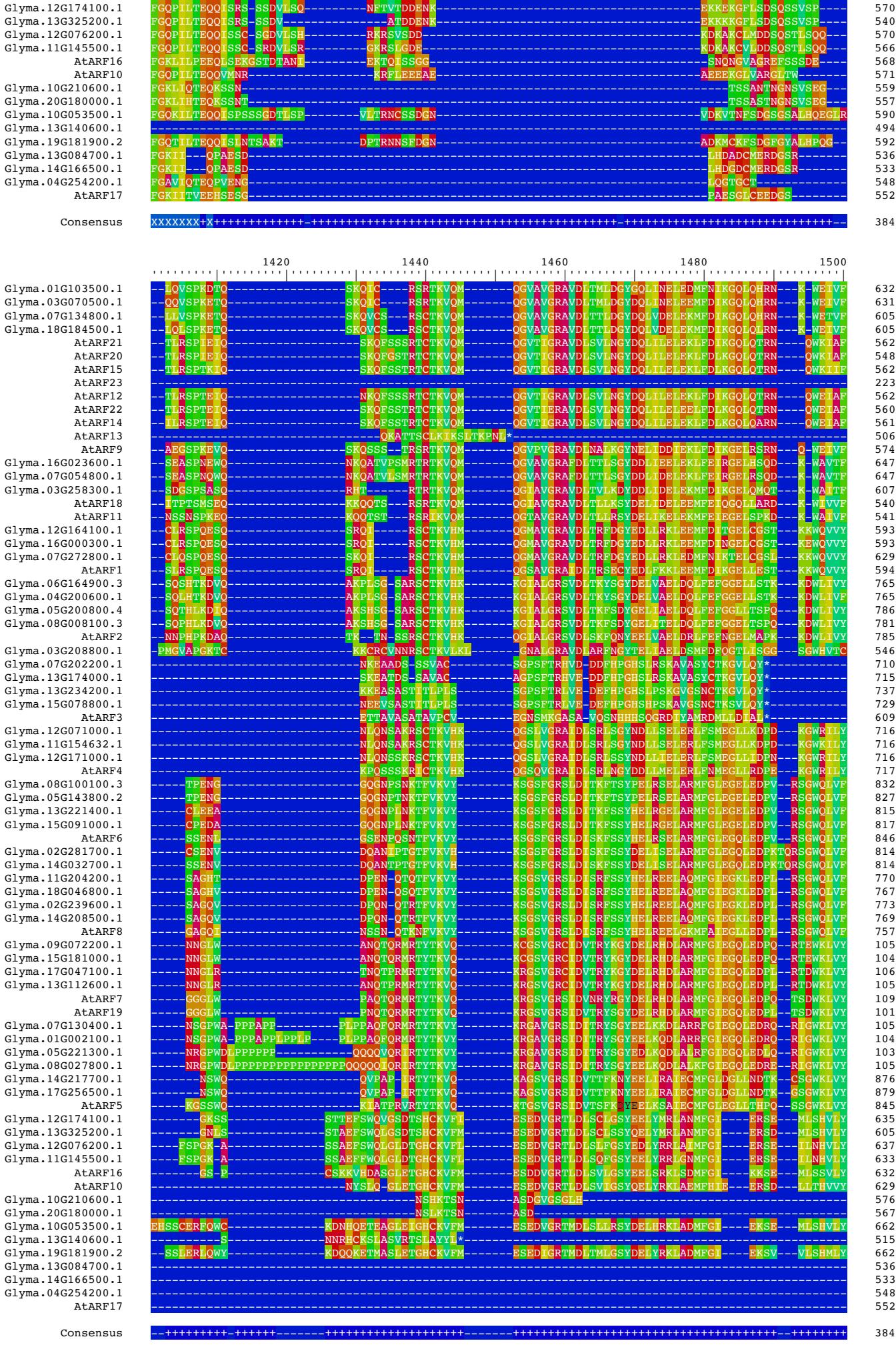
Position	920	940	960	980	1000
Glyma.01G103500.1	CP	SHLFQD			
Glyma.03G070500.1	CP	SHLFQD			
Glyma.07G134800.1		QLYQD			
Glyma.18G184500.1		SQLYHD			
AtARF21	N	NOMVTOIE			
AtARF20	N	NOMVTOIE			
AtARF15	N	NOMVTOIE			
AtARF23					
AtARF12	N	NOMVTEME			
AtARF22	N	NOMVTOIE			
AtARF14	N	N-VVTPPIE			
AtARF13	NS	DOMIQPRK			
AtARF9					
Glyma.16G023600.1	VT	PNLFSID			
Glyma.07G054800.1	AT	PNLFSDE			
Glyma.03G258300.1	SK	PNLFMD			
AtARF18		LFQD			
AtARF11		LFQD			
Glyma.12G164100.1	SN	KSIYWS			
Glyma.16G000300.1	SN	KSIYWS			
Glyma.07G272800.1	SN	KSIYWS			
AtARF1	SI	GSAFWP			
Glyma.06G164900.3	TY	SDLLSGFC			
Glyma.04G200600.1	TY	SDLLSGFC			
Glyma.05G200800.4	TY	PDLISGFC			
Glyma.08G008100.3	TY	PDLISGFC			
AtARF2	TY	TDLISGFC			
Glyma.03G208800.1	NO	HPFLKQDEL			
Glyma.07G202200.1	SFRF	QKVLOGQE			
Glyma.13G174000.1	SFRF	QKVLOGQE			
Glyma.13G234200.1	SFRF	QKVLOGQE			
Glyma.15G078800.1	SFRF	QKVLOGQE			
AtARF3	SYGF	HKVLOGQE			
Glyma.12G071000.1	TNRE	PRVLQGQE			
Glyma.11G154632.1	TNRF	PRVLQGQE			
Glyma.12G171000.1	TNMF	PRVLQGQE			
AtARF4	LDRE	PRVLQGQE			
Glyma.08G100100.3	PLM	OTOLIQQSPF	SQQAFFNSQENPHP	SPSQSQAOTQTHFQOHLQHQHSF	NNQN
Glyma.05G143800.2	ALM	OTOMIQQSPF	PQQAFFNSQENPHSP	SPSQSQAOTQTHFQOHLQHQHSF	NTQN
Glyma.13G221400.1	ALM	OAOMLQQSO	PQQIFGNTQENQHS	POSQAHLQOHLQHQHSF	NSQH
Glyma.15G091000.1	ALM	OAOMLQKSQ	PQQIFCENNQENQHS	OSQFOTQAHLQOHLQHQHSF	NSQ
AtARF6	SLV	OPQMLQQOI	SQQQQQLSQQQQQQQ	OLSQQQQQLSQQQQQLSQ	QQQQ
Glyma.02G281700.1	SEV	ORQLPPOSQ	LONTLLHNPOENQVP	AOSOLLOQCLERYHPY	SDQO
Glyma.14G032700.1	SEV	ORQLPPOSQ	PONTLLHNYPENOVP	AOSOLLOQCLERYHPY	SDPR
Glyma.11G204200.1	NSN	SPLQLQQQQ	PIQQSVSS-NMLQPO	TNVLTENLSQHLLQPKHNN	QFVO
Glyma.18G046800.1	NSN	SPLQLQQQQ	PIQQSVSS-NMLQPO	AVHLTENLSQHLLQPKHNN	QFVO
Glyma.02G239600.1	NPN	PPQLQPO	AIQQSVSNNLQPO	AQVMAENLSQHLLQKSHNN	REDQ
Glyma.14G208500.1	NPN	PPQLQPO	AIQQSVSNNLQPO	AQVLAENLSQHLLQKSHNN	REDQ
AtARF8	SHN	SDMLMQQQQ	QQQASR-HLMHQ	TQIMSENLPQNMROEVSN	OPAG
Glyma.09G072200.1	QQ	ASLLQRQQQQQQQ	TOLOSSPLQLQQSLSORA	QQQKPLISTSSPLQLSQL	715
Glyma.15G181000.1	QQ	ASLLQRQQ	QQOTOLOSSPLQLQQSLSORA	QQQPMOTMCQQNSSEQOPQLLQQQ	712
Glyma.17G047100.1	QQ	ASLLQRQQ	QQOTOLQOSPLQLQQNLPQRALQOPPATQMLQNPSEQQLHILQLLQKLOQQQQ	QOLLSTSTPLQLSQL	721
Glyma.13G112600.1	QQ	ASLLQRQQ	QQOTOLQOSPLQLQQNLPQRALQOPPATQMLQNPSEQQLHILQLLQKLOQQQQ	QOLLSTSTPLQLSQL	716
AtARF7	QQCOPPGINGQNQCTTLLQKA	HQAAQOQIFQOSLLEO	PHIQFQLLQLQRLQQQQFTS	POSQ	773
AtARF19	MHN	SSQLLRNQQ	EGSSLHSLQQLNLSQN	SIAPPVSSSLQPQISA	676
Glyma.07G130400.1	QQ	QTIGQNO	PQNLQISPMEDHV-QQLQMS	DNQIQOLQLLQKQKOTLLAQ	635
Glyma.01G021000.1	QQO	QOTIGQNO	HQNLQISPMEDHV-QQLQMS	DDQIQOLQLLQKQKOTLLAQ	622
Glyma.05G221300.1	OKH	QOTTLGLNE	ROIIVFQSPMPDHFNQOLMS	DNQVRFOLLLQKQQQTLLAQ	638
Glyma.08G027800.1	OKD	QOTTFQGNE	RQNVFQSPMPDHFNQOLMS	DNQVRFOLLLQKQQQTLLAQ	638
Glyma.14G177000.1	ALN	MQSLLKNKDQ	PEKLHPLGKDNHISSGIVI	DKPKSESEVLPDVIVDYPSEMGCIERVAANP-VNQG	565
Glyma.17G256500.1	ALN	MQSLLKNKDQ	PEKFHPLAKDNHLPMSGIVI	DKPKLECEVLPDRVIVDYPSEMGCNNEKVAVNP-VNQG	568
AtARF5	ASN	TSGQEON-I	SOSMSAPAKENSTLSCSS	GRVQHGLEQSMEQAOASQTTSTVCNEEKV	570
Glyma.12G174100.1		NKLQLG			466
Glyma.13G325200.1		NKLQLG			448
Glyma.12G076200.1		NKLQLG			466
Glyma.11G145500.1		NKLQLG			461
AtARF16					465
AtARF10	TGN	NKLHSP			480
Glyma.10G210600.1		NKLPLAD			470
Glyma.20G180000.1		NKLPLAD			467
Glyma.10G053500.1		SKLQSG			477
Glyma.13G140600.1		SKLQSG			476
Glyma.19G181900.2		NKLQSG			481
Glyma.13G084700.1		SYLYMGSG			453
Glyma.14G166500.1		SYLYMGSG			450
Glyma.04G254200.1		SRLCMGN			471
AtARF17		PPQLFTN			468

Sequence alignment of AtARF proteins from various species. The alignment shows conservation across the amino acid sequence. A color scale at the top indicates hydrophobicity: blue (most hydrophobic), green, yellow, orange, red (most hydrophilic). A Consensus sequence is shown at the bottom.

Position	1120	1140	1160	1180	1200
Glyma.01G103500.1	VI	DD	S	K	I
Glyma.03G070500.1	V	D	S	K	V
Glyma.07G134800.1	T	D	S	K	V
Glyma.18G184500.1	T	D	N	K	S
AtARF21					
AtARF20					
AtARF15					
AtARF23					
AtARF12					
AtARF22					
AtARF14					
AtARF13					
AtARF9					
Glyma.16G023600.1	V	I	D	S	K
Glyma.07G054800.1	A	T	D	S	K
Glyma.03G258300.1	P	N	N	S	V
AtARF18					
AtARF11					
Glyma.12G164100.1	S	P	N	T	S
Glyma.16G000300.1	R	M	N	T	S
Glyma.07G272800.1	S	R	M	N	T
AtARF1					
Glyma.06G164900.3	T	S	G	D	P
Glyma.04G200600.1	A	S	G	D	P
Glyma.05G200800.4	T	H	G	D	B
Glyma.08G008100.3	A	H	G	D	H
AtARF2					
Glyma.03G208800.1	T	N	I	D	P
Glyma.07G202200.1	H	K	S	L	G
Glyma.13G174000.1	I	F	S	P	V
Glyma.13G234200.1	I	L	P	S	P
Glyma.15G078800.1	I	L	P	S	P
AtARF3					
Glyma.12G071000.1	T	V	C	L	T
Glyma.11G154632.1	I	C	S	L	T
Glyma.12G171000.1	I	C	P	R	S
AtARF4					
Glyma.08G100100.3	O	H	I	P	Q
Glyma.05G143800.2	O	H	I	P	Q
Glyma.13G221400.1	H	H	I	P	Q
Glyma.15G091000.1	H	H	I	P	Q
AtARF6					
Glyma.02G281700.1	O	L	S	Q	A
Glyma.14G032700.1	O	L	S	Q	A
Glyma.11G204200.1	A	-	O	O	T
Glyma.18G046800.1	A	-	O	O	T
Glyma.02G239600.1	T	Q	O	R	T
Glyma.14G208500.1	T	Q	O	R	T
AtARF8					
Glyma.09G072200.1	Q	Q	Q	Q	Y
Glyma.15G181000.1	L	Q	Q	N	Q
Glyma.17G047100.1	L	Q	Q	N	Q
Glyma.13G112600.1	L	Q	Q	N	Q
AtARF7					
Glyma.07G134000.1	P	H	H	O	S
Glyma.01G020100.1	O	T	S	H	L
Glyma.05G221300.1	Q	R	L	D	K
Glyma.08G027800.1	Q	R	L	D	K
Glyma.14G217700.1	L	A	N	P	T
Glyma.17G256500.1	L	A	N	P	T
AtARF5					
Glyma.12G174100.1	N	O	L	K	P
Glyma.13G252200.1	N	O	L	K	P
Glyma.12G076200.1	N	O	L	K	P
Glyma.11G145500.1	N	O	L	K	P
AtARF16					
AtARF10					
Glyma.10G210600.1	A	M	F	I	L
Glyma.20G180000.1	M	L	L	G	T
Glyma.10G053500.1	M	L	L	G	T
Glyma.13G140600.1	L	F	S	T	A
Glyma.19G181900.2	L	F	S	T	A
Glyma.13G084700.1	S	F	G	N	N
Glyma.14G166500.1	S	F	G	N	N
Glyma.04G254200.1	S	F	G	K	S
AtARF17					
Consensus	+++++	-----	+++++	-----	-----







Glyma.01G103500.1	TDDEGDMMVLVGDDPWP-----	EFCNMVRRIFICSSQDVKKMCGS-----	KLPIS-----	SVEDG-----	TVISSL-----	TTET-----	692
Glyma.03G070500.1	TDDEGDMMVLVGDDPWP-----	EFCNMVRRIFICSSQDVKKMCGS-----	KLPIS-----	SVEDG-----	TVISSL-----	TTET-----	691
Glyma.07G134800.1	TDDEGDMMVLVGDDPWP-----	EFCNMVRRIFICSSQDVKKMCGS-----	KLPIS-----	SMGE-----	IVISLN-----	TTET-----	664
Glyma.18G184500.1	TDDEGDMMVLVGDDPWL-----	EFCNMVRRIFIYSSQDVKKMCGS-----	KLPIS-----	SMEE-----	IVTSID-----	TTET-----	664
AtARF21	TDSGDEMVLVGDDPWP-----	EFCNMVKKLIYSSKEEVKNL-----	SSK-----			SLSS-----	606
AtARF20	TDSGDEMVLVGDDPWP-----	EFCNMVKKLIYSSKEEVKNL-----	SSK-----			SLSS-----	592
AtARF15	TGSDEDEMLVGDDPWP-----	EFCNMVKRIFYIQKR-----			R-----		593
AtARF23							223
AtARF12	TDSDEDKMLVGDDPWP-----	EFCNMVKKIFIQKR-----			R-----		593
AtARF22	TDSDDDMLVGDDPWP-----	EFCNMVKKILIFKRG-----	GOK-----		LEVO-----		598
AtARF14	TNNNEEDKMLGEDPWP-----	EFCNMVKKIFIYSSKEEVKNL-----	SRK-----		SLSS-----		605
AtARF13							506
AtARF9	TDDEGDMMVLVGDDPWP-----	EFCNMVKRIFIWSKEEVKKMTPGN-----	QLRMLLR-----	EVEITL-----	TTTSKID-----	NHSN-----	638
Glyma.16G023600.1	TDDENDMMVLVGDDPWP-----	EFCNMVKRIFIICSRIDLKKMKC-----	CKLPAS-----	SSEVE-----	VILLSPDSQRND-----	ETQOSHMP-----	716
Glyma.07G054800.1	TDDENDMMVLAGDDPWP-----	EFCNMVKRIFIICSRIDLKKMKC-----	CKLPAS-----	SSEVE-----	EILLSPDSQRND-----	ETQOSHMP-----	716
Glyma.03G258300.1	TDDGNDMMVLVGDDPWP-----	EFCFTVKRIFIICSRIDLKKMK-----	KHSSS-----	SSVGE-----	ETLLSD-----		662
AtARF18	TDDEGDMMLAGDDPWN-----	EFCKMAKKIFIYSSDEVKKM-----	KLKIS-----	SSLEN-----	EEYGNESE-----	NRSRG-----	602
AtARF11	TDDEGDRMLVGDDPWN-----	EFCKMAKKIFIYSSDEVKKMRS-----	KSLLG-----	D-RG-----	TIVNLESDO-----	RTVHV-----	601
Glyma.12G164100.1	TDNEDEDDMMVGDDPWL-----	EFCSEVRKIFIYTAEEEVKSLSPK-----	GLPIS-----	EEVKPSKNDSEA VAN PED OSS-----	VPGC-----		665
Glyma.16G000300.1	TDNEDEDDMMVGDDPWL-----	EFCSEVRKIFIYTAEEEVKSLSPK-----	GLPIS-----	EEVKPSKNDSEA VNPDQD OSS-----	LGPCC-----		665
Glyma.07G272800.1	TDNEDEDDMMVGDDPWD-----	EFCGMRVRKIFIYTAEEEVKSLSPK-----	RPLPMN-----	EKVNPSCQDSEAIVNPDQD OSS-----	MGpsc-----		701
AtARF1	TDDEDDMMVGDDPWN-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	KLAVN-----	ARMQ-LKADAENGNT EGRSSS-----	MAGRS-----		665
Glyma.06G164900.3	TDNEGDMMLVGDDPWO-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	OSVMASDGA DADAVK CPHQKF-----	NSENGLDA-----			843
Glyma.04G200600.1	TDNEGDMMLVGDDPWO-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	HSVTASEGADTKDVKCOPHQKF-----	NSENGLDA-----			843
Glyma.05G200800.4	TDNEGDMMLVGDDPWO-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	OSASEG-ATDT QEI KCOLNN-----	SASDT-----			858
Glyma.08G008100.3	TDNEGDMMLVGDDPWO-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	OSASEG-A ADAQEIECOLN-----	SSSDT-----			853
AtARF2	TDEENDMMLVGDDPWO-----	EFCAMVCKIYIYPKEEIQKMSPGT LSSKNEEN-----	AVVGE-----	SDADAKSASANPSL-----	SS-----AGNS-----		859
Glyma.03G208800.1	TDDEGDMMQLGDYWPQ-----	DFLGVVQRMIIICPKEGTDNLKPGS-----				SANP-----	590
Glyma.07G202200.1							710
Glyma.13G174000.1							715
Glyma.13G234200.1							737
Glyma.15G078800.1							729
AtARF3							609
Glyma.12G071000.1	TDSENDIMVVGDDPWH-----	EFCDVVSCHKIHIYTQEEVEKMTIG-----	MISDDTHS-----	CLEEAPVIMEASKSSSVGQPDYSPATAV-----			792
Glyma.11G154632.1	TDSENDIMVVGDDPWH-----	EFCDVVSCHKIHIYTQEEVEKMTIE-----	MISDDTHS-----	CLEEAPVIMEASKSSSVGQPDYSPATAV-----			792
Glyma.12G171000.1	TDSENDIMVVGDDPWHLPFWC-----	EFCDVVSCHKIHIYTQEEVEKMTIG-----	MISDDTHS-----	CLEOAPVMVEASKSSSVGQPDSSPTVVRM-----			799
AtARF4	TDSENDIMMVVGDDPWH-----	DFCNVWVKIHIYTKEEVENA-----	NDDNKS-----	CLEOAAALMMEASKSSSVGQPDSSPTVVRM-----			788
Glyma.08G100100.3	VDQENDVLLLGDPWP-----	EFCNVSVGKIIKIISPQEVQQMG-----	IQR-----	SNGVC-----	EDPRNLSTGTITV-----	GSLNY-----	907
Glyma.05G143800.2	VDOENDVLLLGDPWP-----	EFCNVSVGKIIKIISPQEVQQMG-----	IQR-----	SNGVCDDYAGREDPRNLSTGTITV-----	GSLNY-----		908
Glyma.13G221400.1	VDRENDVLLLGDPWP-----	EFCNVSVCWIKIISPQEVQQMG-----	IQR-----	SNGICDDYVSQDPRNLGTCTV-----	GSDLY-----		896
Glyma.15G091000.1	VDRENDVLLLGDPWP-----	EFCNVSVCWIKIISPQEVQQMG-----	NQR-----	SNGICDDYVSQDPRNLGTCTV-----	GSDLY-----		898
AtARF6	VDRENDVLLLGDDPWE-----	EFCNVSVVCIKILSPQEVQQMG-----	VDKLP-----	SNCNCDFGNRSDFPRNLNGNLASVG-----			933
Glyma.02G281700.1	VDRENDVLLLGDDPWE-----	EFCNVNNVWYIKILSPLEQVQKMS-----	KVLSPSTS-----	GDKLSTPVSQCDNYSVSQELR SRSRNGMASM-----			896
Glyma.14G032700.1	VDRENDVLLLGDDPWE-----	EFCNVNNVWYIKILSPLEQVQKMS-----	KVLSPSTS-----	GDKLSTPVSQCDNYSVSQELR SRSRNGMASM-----			896
Glyma.11G204200.1	VDRENDVLLLGDDPWE-----	EFCNVNNVWYIKILSPEDIQKMG-----	QKMG-----	GKLN-----	GSLEY-----		844
Glyma.18G046800.1	VDRENDVLLLGDDPWE-----	EFCNVNNVWYIKILSPEDIQKMG-----	QKMG-----	GQRLNGTGAESQD IVSGPPSI-----	GSLEY-----		841
Glyma.02G239600.1	VDRENDVLLLGDDPWE-----	EFCNVNNVWYIKILSPEDIHKG-----	HKG-----	GQRLNGTGAESQD IVSGPPSI-----	GSLEY-----		847
Glyma.14G208500.1	VDRENDVLLLGDDPWE-----	EFCNVNNVWYIKILSPEDIHKG-----	HKG-----	GORIN-----	GSLEY-----		843
AtARF8	VDKENDILLLGDDPWE-----	EFCNVNNVWYIKILSPEDVHQMG-----		HCEGSGGLFPQNP-----		THL-----	811
Glyma.09G072200.1	VDHENDILLVGDDPWE-----	EFCVSCVQSIKILOSSSEVQQMS-----	LDGDLGHVPV-----	NQACSGT DNGNAWRQGYEDNS-----	A-----	ASFNR-----	1125
Glyma.15G181000.1	VDHENDILLVGDDPWE-----	EFCVSCVQSIKILOSSSEVQQMS-----	LDGDLGHVPV-----	NQACSGT DNGNAWRQGYEDNS-----	A-----	ASFNR-----	1122
Glyma.17G047100.1	VDHENDILLVGDDPWE-----	EFCVSCVQSIKILOSSSEVQQMS-----	LDGDLGHVPV-----	PNOAYSGT DSGNAWRQGYEDNS-----	A-----	ASFNR-----	1136
Glyma.13G112600.1	VDHENDILLVGDDPWE-----	EFCVSCVQSIKILOSSSEVQQMS-----	LDGDLGHVPV-----	PNOAYSGT DSGNAWRQGYEDNS-----	A-----	ASFNR-----	1131
AtARF7	VDHENDILLVGDDPWE-----	EFCVNCVQSIKILOSSSEVQQMS-----	LDGDLGHVPV-----	PNOACSGT DSGNAWRQGYEDNS-----	A-----	TSFNR-----	1165
AtARF19	TDHENDILLVGDDPWE-----	EFCVNCVQNIKILSSSEVQQMS-----	LDGDLAAIPTT-----	NQACSET DSGNAWKVYEDETSAA-----		ASFNR-----	1086
Glyma.07G130400.1	VDHESDVLLVGDDPWE-----	EFCVNCVRCIKILSPQEVQKMS-----	LDGDFGNGLQ-----	NQACSSSD-----		GGNT-----	1110
Glyma.01G002100.1	VDHESDVLLVGDDPWE-----	EFCVNCVRCIKILSPQEVQKMS-----	LDGDFGNGLQ-----	NQACSSSD-----		GGDT-----	1104
Glyma.05G221300.1	VDHENNDVLLVGDDPWE-----	EFCVNCVRCIKILSPQEVQKMS-----	LDGDFGNGLQ-----	VPAGSSSD-----		GGNA-----	1099
Glyma.08G027800.1	VDHENNDVLLVGDDPWE-----	EFCVNCVRCIKILSPQEVQKMS-----	LDGDFGNGLQ-----	VPAGSSSD-----		GGNA-----	1113
Glyma.14G217700.1	VYQESDVLLVGDDPWE-----	EFCVGCVCIRIILSPSEVQOMS-----	SEEGM-----	LOGM-----		NV-----	930
Glyma.17G256500.1	VYQESDVLLVGDDPWE-----	EFCVGCVCIRIILSPSEVQOMS-----	SEEGM-----	LOGM-----		NV-----	933
AtARF5	VYQESDVLLVGDDPWE-----	EFCVGCVCIRIILSPTEVQOMS-----	SEEGM-----	INDLK-----		TSVS-----	902
Glyma.12G174100.1	RDAAGALKQTGEEPFS-----	EFMKTAKRILTII TDSNNKDSRVRWITGIRNAE-----		HGLD-----		GIFA-----	700
Glyma.13G325200.1	RDAAGALKQTGEEPFS-----	EFMKTAKRILTII TDSNNKDSRVRWITGIRNAE-----		HGLDAA-----		SIFIA-----	670
Glyma.12G076200.1	RDAAGALKQTGEEPFS-----	EFMKTAKRILTII TDSNNKDSRVRWITGIRNAE-----		HGLDAA-----		SIFIA-----	701
Glyma.11G145500.1	RDAAGALKQTGEEPFS-----	EFMKTAKRILTII TDSGSKNIKRAFITGIRNGE-----		HGLD-----		SIFIA-----	697
AtARF16	RDASGAIKYAGNEPFS-----	EFLKXTARRITII TEQGSE-----		HGLD-----		SVVV-----	670
AtARF10	RDANGVIKRIGDEPFS-----	DFMKTAKRILTII TIKMDIGGDNRKWTWITGIRGE-----		NGID-----		ASTK-----	693
Glyma.10G210600.1	--QGSPINNSDGGS-----	PWYKDQHKSDLGTDNVT-----				CAIA-----	612
Glyma.20G180000.1	--QGSPINNSDGGS-----	PWYKDQHKSDLGDNVNT-----				CAIA-----	593
Glyma.10G053500.1	RDSTGAVKRSIDESFS-----	DFTRTAKRILTILMDSGSN-----				NVGV-----	700
Glyma.13G140600.1							515
Glyma.19G181900.2	RDITGAVKHIGDEAFS-----	EFTKXTARRITIILMDNSD-----				GRGI-----	700
Glyma.13G084700.1	--GS-----	NKLKTVEAICYFSK-----					551
Glyma.14G166500.1	--GS-----	NKLKTVEAICYFSK-----					548
Glyma.04G254200.1	--CTGDECQCOR-----					ALNS-----	562
AtARF17		KESSDNETQLSLSHAPPSPFK-----				HSNSNAGS-----	585
Consensus	+++++-----XX-----	XXXXXXXXXXXXJXXX-----	+++++-----	-----	-----	-----	401

Glyma.01G103500.1 * 693
Glyma.03G070500.1 * 692
Glyma.07G134800.1 * 665
Glyma.18G184500.1 * 665
AtARF21 * 607
AtARF20 * 593
AtARF15 * 594
AtARF23 * 223
AtARF12 * 594
AtARF22 * 599
AtARF14 * 606
AtARF13 * 506
AtARF9 * 639
Glyma.16G023600.1 * 717
Glyma.07G054800.1 * 717
Glyma.03G258300.1 * 663
AtARF18 * 603
AtARF11 * 602
Glyma.12G164100.1 * 666
Glyma.16G000300.1 * 666
Glyma.07G272800.1 * 702

AtARF1	*	666
Glyma.06G164900.3	*	844
Glyma.04G200600.1	*	844
Glyma.05G200800.4	*	859
Glyma.08G008100.3	*	854
AtARF2	*	860
Glyma.03G208800.1	*	591
Glyma.07G202200.1	-	710
Glyma.13G174000.1	-	715
Glyma.13G234200.1	-	737
Glyma.15G078800.1	-	729
AtARF3	-	609
Glyma.12G071000.1	*	793
Glyma.11G154632.1	*	793
Glyma.12G171000.1	*	800
AtARF4	*	789
Glyma.08G100100.3	*	908
Glyma.05G143800.2	*	909
Glyma.13G221400.1	*	897
Glyma.15G091000.1	*	899
AtARF6	*	934
Glyma.02G281700.1	*	897
Glyma.14G032700.1	*	897
Glyma.11G204200.1	*	845
Glyma.18G046800.1	*	842
Glyma.02G239600.1	*	848
Glyma.14G208500.1	*	844
AtARF8	*	812
Glyma.09G072200.1	*	1126
Glyma.15G181000.1	*	1123
Glyma.17G047100.1	*	1137
Glyma.13G112600.1	*	1132
AtARF7	*	1166
AtARF19	*	1087
Glyma.07G130400.1	*	1111
Glyma.01G002100.1	*	1105
Glyma.05G221300.1	*	1100
Glyma.08G027800.1	*	1114
Glyma.14G217700.1	*	931
Glyma.17G256500.1	*	934
AtARF5	*	903
Glyma.12G174100.1	*	701
Glyma.13G325200.1	*	671
Glyma.12G076200.1	*	702
Glyma.11G145500.1	*	698
AtARF16	*	671
AtARF10	*	694
Glyma.10G210600.1	*	613
Glyma.20G180000.1	*	594
Glyma.10G053500.1	*	701
Glyma.13G140600.1	-	515
Glyma.19G181900.2	*	701
Glyma.13G084700.1	*	552
Glyma.14G166500.1	*	549
Glyma.04G254200.1	*	563
AtARF17	*	586
Consensus	*	402