

Supplementary Data

PROMOTER ANALYSIS OF MADS-BOX GENES IN EUDICOTS THROUGH PHYLOGENETIC FOOTPRINTING

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Table S1: Motif occurrence in randomized datasets

SUBFAMILY	motif loss	motif length	number of motifs
SEP3	-	9	12.55
SEP3	-	10	1.36
SEP3	-	11	0.00
SEP3	-	12	0.00
SEP3	+	12	4.36
SEP3	+	13	1.36
SEP3	+	14	0.27
SEP3	+	15	0.09
SEP3	-	9	0.00
AP1	-	10	0.00
AP1	-	11	0.00
AP1	-	12	0.00
AP1	+	12	17.64
AP1	+	13	4.82
AP1	+	14	1.64
AP1	+	15	0.36
AGL12	-	9	11.64
AGL12	-	10	1.09
AGL12	-	11	0.27
AGL12	-	12	0.00
AGL12	+	12	3.27
AGL12	+	13	1.09
AGL12	+	14	0.27
AGL12	+	15	0.00
AGL3	-	9	139.18
AGL3	-	10	66.18
AGL3	-	11	26.36

AGL3	-	12	9.45
AGL3	+	12	8.09
AGL3	+	13	2.45
AGL3	+	14	0.55
AGL3	+	15	0.18
ANR1	-	9	8.27
ANR1	-	10	2.18
ANR1	-	11	0.55
ANR1	-	12	0.18
SVP	-	9	209.36
SVP	-	10	126.27
SVP	-	11	61.18
SVP	-	12	22.71
SVP	-	13	8.00
SVP	-	14	2.27
SVP	-	15	1.00
AGL6	-	9	11.36
AGL6	-	10	0.73
AGL6	-	11	0.00
AGL6	-	12	0.00
AGL6	+	12	1.09
AGL6	+	13	0.45
AGL6	+	14	0.09
AGL6	+	15	0.00
AGL18	-	9	211.09
AGL18	-	10	138.82
AGL18	-	11	66.73
AGL18	-	12	26.82
AGL18	-	13	10.64
AGL18	-	14	4.18

AGL18	-	15	1.18
STK	-	9	17.27
STK	-	10	1.82
STK	-	11	0.09
STK	-	12	0.00
STK	+	12	2.27
STK	+	13	0.55
STK	+	14	0.09
STK	+	15	0.00
AGL14	-	9	0.00
AGL14	-	10	0.00
AGL14	-	11	0.00
AGL14	-	12	0.00
AGL14	+	12	1.27
AGL14	+	13	0.36
AGL14	+	14	0.00
AGL14	+	15	0.00
AG	-	9	10.55
AG	-	10	1.36
AG	-	11	0.00
AG	-	12	0.00
AG	+	12	3.82
AG	+	13	1.00
AG	+	14	0.45
AG	+	15	0.18
AGL24	-	9	0.00
AGL24	-	10	0.00
AGL24	-	11	0.00
AGL24	-	12	0.00
AGL24	+	12	1.18

AGL24	+	13	0.27
AGL24	+	14	0.18
AGL24	+	15	0.00
AGL15	-	9	193.64
AGL15	-	10	106.18
AGL15	-	11	43.27
AGL15	-	12	15.91
AGL15	-	13	5.36
AGL15	-	14	1.91
AGL15	-	15	0.73
SEP1-SEP2	-	9	0.00
SEP1-SEP2	-	10	0.00
SEP1-SEP2	-	11	0.00
SEP1-SEP2	-	12	0.00
SEP1-SEP2	+	12	2.18
SEP1-SEP2	+	13	0.45
SEP1-SEP2	+	14	0.18
SEP1-SEP2	+	15	0.00
PI	-	9	0.09
PI	-	10	0.00
PI	-	11	0.00
PI	-	12	0.00
PI	+	12	0.45
PI	+	13	0.09
PI	+	14	0.00
PI	+	15	0.00
FUL	-	13	5.64
FUL	-	14	1.82
FUL	-	15	0.73
AGL42	-	9	0.55

AGL42	-	10	0.00
AGL42	-	11	0.00
AGL42	-	12	0.00
AGL42	+	12	5.27
AGL42	+	13	1.82
AGL42	+	14	0.27
AGL42	+	15	0.09
SOC1	-	9	2.18
SOC1	-	10	0.18
SOC1	-	11	0.00
SOC1	-	12	0.00
SOC1	+	12	1.64
SOC1	+	13	0.27
SOC1	+	14	0.18
SOC1	+	15	0.09

Table S2: Number of motifs of a certain size in one-to-one subfamilies

SUBFAMILY	size 11	size 12	size 13	size 14
AGL3		19	7	
ANR1		11	3	
AGL15		14	5	
AGL18		19	6	
FUL			17	6
SVP			14	7
AP3			10	3

Table S3: Number of motifs of a certain size in two-to-one subfamilies, no losses allowed

SUBFAMILY	size 9	size 10	size 11	size 12
SOC1	17			
STK			15	
AG				16
SEP3	11			
AGL12	10			
AGL6		7		
PI	6			
AGL16		16		
AGL24				12
AGL32	3			

Table S4: Number of motifs of a certain size in two-to-one subfamilies, losses allowed

SUBFAMILY	size 9	size 10	size 11	size 12
SOC1			20	
STK			15	
AG				22
SEP3			24	
AGL12			14	
AGL6			18	
PI		23	5	
AGL16		17		
AGL24			21	
AGL32			8	

Blue numbers indicate that the high number of species-specific motifs is omitted (see below)

Table S5: Number of motifs of a certain size in “many” subfamilies, no losses allowed

SUBFAMILY	size 8	size 9	size 10	size 11
AP1		8		
SEP1-SEP2		13		
AGL14	8			
FLC			8	
AGL42		8		

Table S6: Number of motifs of a certain size in “many” subfamilies, losses allowed

SUBFAMILY	size 8	size 9	size 10	size 11
AP1		8		
SEP1-SEP2		10		
AGL14	14			
FLC				25
AGL42				13

Blue numbers indicate that the high number of species-specific motifs is omitted (see below)

Table S7: Summary of comparison between FootPrinter motifs and motifs from public databases

SUBFAMILY	FootPrinter motif	database motif	sequence	score	length motif
AG	tAAAAAgAAAA	GT1GMSCAM4	GAAAAA	0.24	6
AGL12	CnTCCATCTCT	SO_GAG-motif	AGAGATG	0.33	7
AGL12	ATcTTTntT	NODCON1GM	AAAGAT	0.17	6
AGL12	ATcTTTntT	OSE1ROOTNODULE	AAAGAT	0.17	6
AGL14	TAGGGtTT	TELOBOXATEEF1AA1	AAACCCTAA	0.18	9
AGL14	TAGGGtTT	UP2ATMSD	AAACCCTA	0.18	8
AGL14	TAATCTtT	NODCON1GM	AAAGAT	0.24	6
AGL14	TAATCTtT	OSE1ROOTNODULE	AAAGAT	0.24	6
AGL15	GAAGGAAAAAnAn	PYRIMIDINEBOXHVEP148	TTTTTTCC	0.3	8
AGL16	AACgACgTCT	BO_TGA-element	AACGAC	0.39	6
AGL18	TATCnTATCTnT	AT_GATA-motif	GATAGGA	0.16	7
AGL18	nTTTTAnGGTTT	TELOBOXATEEF1AA1	AAACCCTAA	0.27	9
AGL18	nTTTTAnGGTTT	UP2ATMSD	AAACCCTA	0.3	8
AGL24	gcTAGGGTTTC	UP2ATMSD	AAACCCTA	0	8
AGL24	ctTGGATCTGA	AGMOTIFNTMY149	AGATCCAA	0.18	8
AGL24	gcTAGGGTTTC	TELOBOXATEEF1AA1	AAACCCTAA	0.39	9
AGL24	TTCTCTCTCTCT	CTRM CAMV35S	TCTCTCTCT	0	9
AGL24	TTtTTTCTTTtT	GT1GMSCAM4	GAAAAA	0.24	6
AGL3	TTATCTTTAAAA	NODCON1GM	AAAGAT	0	6
AGL3	TTATCTTTAAAA	OSE1ROOTNODULE	AAAGAT	0	6
AGL32	AGAGnGGTTAA	GT1CORE	GGTTAA	0	6
AGL32	AGAGnGGTTAA	AT_GT1-motif	GGTTAA	0.05	6
AGL32	GnAGTTAATT	MY148LEPR	GTTAGTT	0.34	7
AGL42	nTTTAGGGTTT	TELOBOXATEEF1AA1	AAACCCTAA	0	9
AGL42	nTTTAGGGTTT	UP2ATMSD	AAACCCTA	0	8
AGL6	GTTAGTTTGAA	MY148LEPR	GTTAGTT	0	7
AGL6	AACCAAAntTT	REALPHALGLHC1491	AACCAA	0	6
ANR1	TCTTTTnTCCTT	PYRIMIDINEBOXHVEP148	TTTTTTCC	0.3	8

ANR1	AAAnATTGGCAT	LEAFYATAG	CCAATGT	0.34	7
AP1	AAAAGGAAA	PYRIMIDINEBOXOSRAMY1A	CCTTTT	0.12	6
FUL	nTTTTnTTTTTCT	GT1GMSCAM4	GAAAAA	0	6
FUL	TCTCTCTCnTGnT	CTRM CAMV35S	TCTCTCTCT	0.27	9
FUL	nATAAAATnTTGT	LECPLEACS2	TAAAATAT	0.3	8
PI	TAGAGAGAGA	CTRM CAMV35S	TCTCTCTCT	0	9
PI	TTATCTTTc	NODCON1GM	AAAGAT	0	6
PI	TTATCTTTc	OSE1ROOTNODULE	AAAGAT	0	6
SEP12	TAGGGTTn	UP2ATMSD	AAACCCTA	0.12	8
SEP12	aAACCCTAA	TELOBOXATEEF1AA1	AAACCCTAA	0.16	9
SEP12	TATAGaTAA	AT_GA-motif	ATAGATAA	0.37	8
SEP3	TCGACACGTGn	CACGTGMOTIF	CACGTG	0	6
SEP3	TnTCGACACGT	GADOWNAT	ACGTGTC	0	7
SEP3	TCGACACGTGn	HA_ABRE	CACGTG	0.14	6
SEP3	TCGACACGTGn	SO_G-box	CACGTG	0.14	6
SEP3	TCGACACGTGn	PS_G-Box	CACGTG	0.24	6
SEP3	TTAAGGTTAnG	AT_GT1-motif	GGTTAA	0.3	6
SEP3	CTCCACCnTCC	PC_A-box	CCGTCC	0.31	6
SEP3	TCGACACGTGn	BJ_G-box	CACGTG	0.33	6
SEP3	TCGACACGTGn	BR_G-box	CACGTG	0.33	6
SEP3	TCGACACGTGn	CA_G-box	CACGTG	0.33	6
SEP3	TCGACACGTGn	CR_G-box	CACGTG	0.33	6
SEP3	TCGACACGTGn	NT_G-box	CACGTG	0.33	6
SEP3	nTTTGAAAATA	PS_BoxI	TTTCAA	0.33	7
SEP3	TCGACACGTGn	ZM_ABRE	CACGTG	0.33	6
SEP3	TnTCGACACGT	ACGTABREMOTIFA2OSEM	ACGTGKC	0.34	7
SOC1	CnTTTATCCT	SREATMSD	TTATCC	0	6
SOC1	cTTTTtTTc	GT1GMSCAM4	GAAAAA	0.34	6
SVP	AACTAGGGTTTTnT	UP2ATMSD	AAACCCTA	0	8
DEF	naAAAGATT	NODCON1GM	AAAGAT	0	6
DEF	naAAAGATT	OSE1ROOTNODULE	AAAGAT	0	6
DEF	AAcCAAAtc	REALPHALGLHC1491	AACCAA	0.12	6

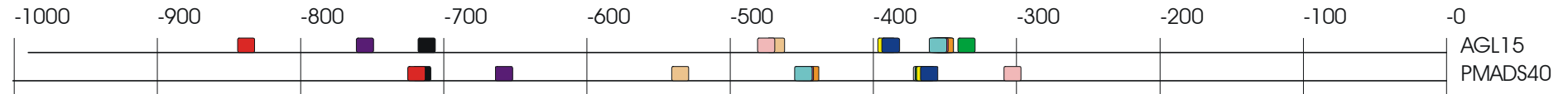
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DEF	nGATTAAt	PC_Box4	ATTAAT	0.35	6
DEF	ATTCTAtTT	BOXIINTPATPB	ATAGAA	0.34	6
DEF	nnATATTCTAT	-10PEHVPSBD	TATTCT	0	6
DEF	TTGACGTTTAC	HEXMOTIFTAH3H4	ACGTCA	0	6
DEF	nCCACCTGCAC	INTRONLOWER	TGCAGG	0	6
DEF	AnGCnAACCAA	MY148AT	WAACCA	0	6
DEF	AAAnGCnAACCA	MY148AT	WAACCA	0	6
DEF	nCCACCTGCAC	RAV1BAT	CACCTG	0	6
DEF	TTGACGTTTAC	TGACGTVMAMY	TGACGT	0	6
DEF	GCnAACCAAAT	MYBATRD22	CTAACCA	0.34	7
DEF	GAACTTACCTTT	INTRONUPPER	MAGGTAAGT	0.27	9
DEF	GaTAACtGAG	MY149AT	TAACCTG	0.24	6
DEF	GACCTTTTAg	PYRIMIDINEBOXOSRAMY1A	CCTTTT	0.24	6
DEF	TtTTTTCcAA	GT1GMSCAM4	GAAAAA	0.24	6
DEF	TtTTTTCcAA	PYRIMIDINEBOXHVEP148	TTTTTTCC	0.36	8
DEF	tTaCTTTAG	NTBBF1ARROLB	ACTTTA	0.24	6
DEF	TTATAAcAAAACc	AACACOREOSGLU148	AACAAAC	0.2	7
DEF	TTATAAcAAAACc	MYBGAHV	TAACAAA	0.2	7
DEF	nGACGGAAAGnAA	PC_A-box	CCGTCC	0.31	6
DEF	TcCATCTCTc	SO_GAG-motif	AGAGATG	0.33	7
DEF	TtTcCATTtT	AT_Gap-box	AAATGrAGA	0.19	9
DEF	TTTTAGGGTTTG	TELOBOXATEEF1AA1	AAACCCTAA	0	9
DEF	TTTTAGGGTTTG	UP2ATMSD	AAACCCTA	0	8
DEF	TAACtNACCTT	PC_Box-W1	TTGACC	0.34	6
DEF	TTTATCa	PS_LAMP-element	CTTTATCA	0.36	8
DEF	CnAATTAACAnA	GARE1OSREP1	TAACAGA	0.34	7
DEF	AACTAAnAnCAA	MY148LEPR	GTTAGTT	0.34	7
DEF	AAntTTTTTAGnT	SEF4MOTIFGM7S	RTTTTTTR	0.34	7
DEF	AgAgAGAG	CTRMCAMV35S	TCTCTCTCT	0.26	9

AGL3	TTTTTATTTnnG	-314MOTIFZMSBE1	ACATAAAATAAAAAAAGGCA	0.37	20
DEF	AAAAtAAAA	-314MOTIFZMSBE1	ACATAAAATAAAAAAAGGCA	0.14	20
SEP3	TAaAAtAAA	-314MOTIFZMSBE1	ACATAAAATAAAAAAAGGCA	0.32	20
DEF	AAAAnAAAA	3AF1BOXPSRBCS3	AAATAGATAAAATAAAAAACATT	0.24	21
PI	TTTtATtTA	3AF1BOXPSRBCS3	AAATAGATAAAATAAAAAACATT	0.32	21
SEP3	ATaGATaAA	3AF1BOXPSRBCS3	AAATAGATAAAATAAAAAACATT	0.32	21
AGL14	CAAACtAt	AACAOSGLU148	CAACAACTATATC	0.25	14
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DEF	TAAaaAaAA	ATRICHPSPETE	AATATACTAGTATTATTTACTAAAAAAAATC	0.37	31
DEF	TTtAGtAAC	BOX3PVCHS15	TATTGGTTACTAAA	0.32	14
AGL14	TTTatTaT	C2GMAUX28	AATAATAATAATAATAAATA	0.29	20
DEF	TtTCCATT	CARG1ATAP3	GTTTACATAAATGGAAAA	0.12	18
DEF	CnTACCtTT	CARG2ATAP3	CTTACCTTTTCATGGATTA	0.38	18
DEF	CaTTTtTA	CARG3ATAP3	CTTTCCATTTTTAGTAAC	0.25	18
AGL14	TAATCTtT	CGF1ATCA149	GATAAAGATTACTTCAGATATAACAAACGTTAC	0.18	33
PI	TTTtATtTA	COREOS	AAKAATWYRTAWATAAAAMTTTTATWTA	0.17	28
DEF	AAaATAAaA	ELEMENT1GMLBC3	GATATATTAATATTTTATTTTATA	0.22	24
SEP3	TAaAAtAAA	ELEMENT1GMLBC3	GATATATTAATATTTTATTTTATA	0.32	24
DEF	AAATtAtT	ELEMENT2GMLBC3	CTTAAATTATTTATTT	0.25	16
DEF	AgAgAGAG	GAGA8HVBKN3	GAGAGAGAGAGAGAGA	0.26	16
DEF	AgAgAGAG	GAGAGMGSA1	GAGAGAGAGAGAGAGAGA	0.26	18
AGL14	ATATGATA	IBOXLSCMCUCUMISIN	AGATATGATAAAA	0	13
AGL16	TTCTTTGnAA	JERECRSTR	CTCTTAGACCGCCTTCTTTGAAAG	0.24	24
PI	GGAGAgaaA	LE_5UTRPy-rich	TTTCTCTCCTCTyTy	0.27	15
DEF	AaCAAAaA	LE_E4-ERE	CACAAGTTTGTTTTGTTTTTACTACCAACAA	0.37	32
STK	TTTTgTTtTTA	LE_E4-ERE	CACAAGTTTGTTTTGTTTTTACTACCAACAA	0.39	32
AP1	TCTTTATAT	LE_E4-TATA-box	ATCCATTTCTATATAAAGAAACATA	0.33	25
DEF	CCaTtT	LE_H-box	ACCATTTTCACTC	0.31	13
SEP12	AAACATAAA	MARARS	WTTTATRRTTW	0.27	11
DEF	TTTCCATTTTT	P_MADSAQ2	AnwnnAAAAATGGAAA	0.32	16
DEF	CCaTtT	PC_FP56	TCCCCATTTTACCCT	0.31	16

AGL14	TTTTCATT	SO_Pc-CMA2a	CAACCAATGAAAA	0.33	13
DEF	AAAAAaAa	ZM_LS7	CAGATTTATTTTA	0.36	14

one-to-one comparisons

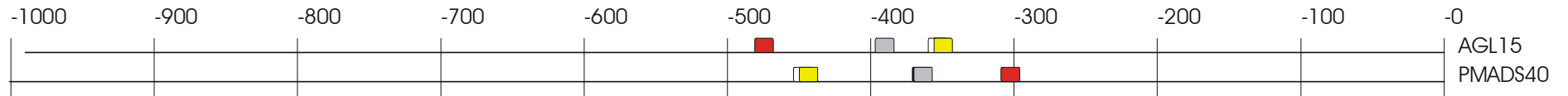
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Motif8 0.001470307 Agggaaggaaaa Atggaaggaaat	Motif9 0.004222421 agagaaaataca aaggaaaataca	Motif10 0.001922271 aactacttaca aactgcttaaa	Motif11 0.001017905 gtttctaattgt gtttctaactgt	Motif12 0.000339302 attgttgctctg agtgctgctctg	Motif13 0.001922271 gggaaggaaaaa tgaaggaaaata	Motif14 0.007163036 aaggaaaaaaga aaggaaatga

Fig. S1

Subfamily: AGL15, size: 13, allowed mutations: 2

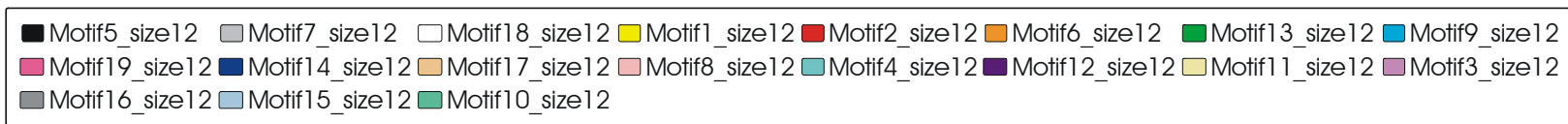
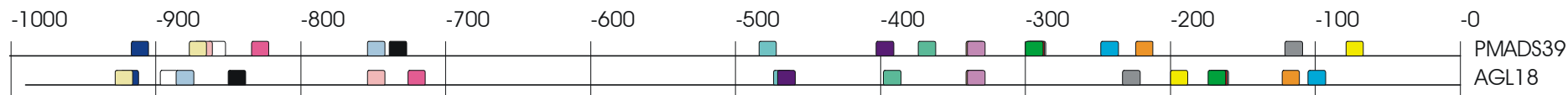


Motif1_size13
 Motif4_size13
 Motif5_size13
 Motif3_size13
 Motif2_size13

Motif1 0.001771909	Motif2 0.000301602	Motif3 0.001809609	Motif4 0.000452402	Motif5 0.000640903
gaaggaaaaaaga	gtttctaattgtt	aaggaaaaaagag	agagaaaatacac	aggaaggaaaaa
gaaggaaaataca	gtttctaactgtt	aaggaaatatgag	aaggaaaatacac	atgaaggaaata

Fig. S1

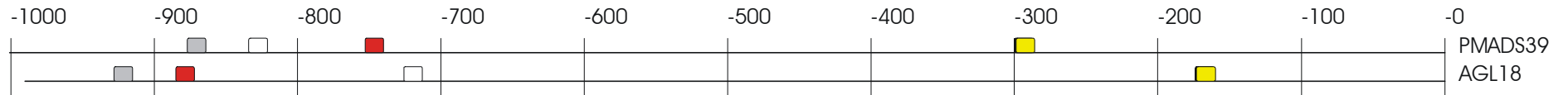
Subfamily: AGL18, size: 12, allowed mutations: 2



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Motif8 0.025334529 tttctttcaat tttttttcatt	Motif9 0.00591893 aaattggataat aaatttgagaat	Motif10 0.002262012 aaatactaact atatcctaact	Motif11 0.00584353 ctacttttctt ctaatttcctt	Motif12 0.010292152 aaataaactgtt aaataaaaagtt	Motif13 0.007200737 aaaattctaaaa agaattctgaaa	Motif14 0.035551281 ttttcttctt tttctctcctt
Motif15 0.007426938 atctaaataaaa ttctaaagaaaa	Motif16 0.002488213 atcaagattgg atcagaattgg	Motif17 0.020282703 ttttagggttt atttaagggtt	Motif18 0.006333632 aattaatcaatt attgatcaatt	Motif19 0.008218642 gatttatttat gattgatttgt		

Fig. S1

Subfamily: AGL18, size: 13, allowed mutations: 2

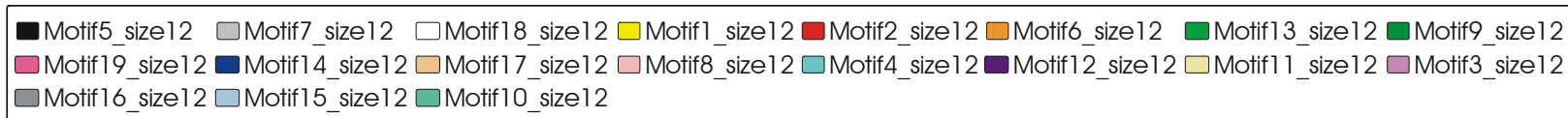
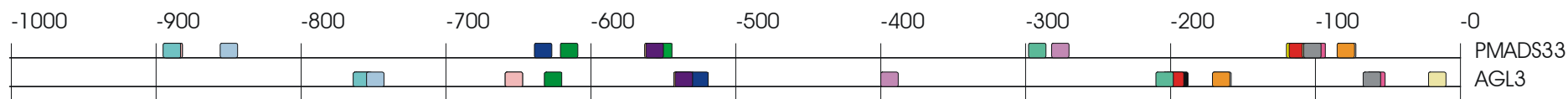


Motif1_size13
 Motif4_size13
 Motif5_size13
 Motif3_size13
 Motif2_size13

Motif1 0.001131006	Motif2 0.000829404	Motif3 0.001017905	Motif4 0.001206406	Motif5 0.004712524
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agaattctgaaag	tctaaagaaaacc	gaattctgaaaga	ctaatttcctc	gattgattttgt

Fig. S1

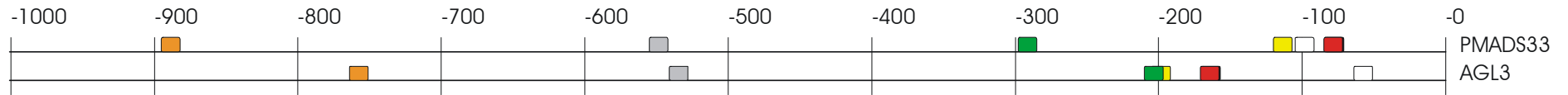
Subfamily: AGL3, size: 12, allowed mutations: 2



Motif1 0.000301602 atcctgccccta atcatgccccta	Motif2 0.000226201 ccttgcctaga tcatgcctaga	Motif3 0.005768129 aaagttgaaaa aaagttgataag	Motif4 0.002224311 gttatcttaaa gttatattaga	Motif5 0.000188501 tgcctagagaa tgcctagatta	Motif6 0.001244106 taaacaagatct gagacaagatct	Motif7 0.002224311 ttatcttaaaa ttatcttaaaa
Motif8 0.008482543 ttatcttaaaa ttatatttagaa	Motif9 0.003807719 agtgaagataa agtgaagagaa	Motif10 0.002412812 aatcaattaatg aaccaattcatg	Motif11 0.026314734 agagaagaagga agagaagagaga	Motif12 0.061112011 atcttctttt atcttatttc	Motif13 0.037511691 cttttatttta atcttatttc	Motif14 0.005014126 ttgaaaaaaca ctgaaaaaaca
Motif15 0.003581518 agaatagtttc agaatcttttc	Motif16 0.003430717 gagaagaaggag gataaaaaggag	Motif17 0.038491896 gattttctttt aattttatttt	Motif18 0.000904805 aaacaagatcta agacaagatcta	Motif19 0.010216752 aagaaggagag aaaaaggaggag		

Fig. S1

Subfamily: AGL3, size: 13, allowed mutations: 2

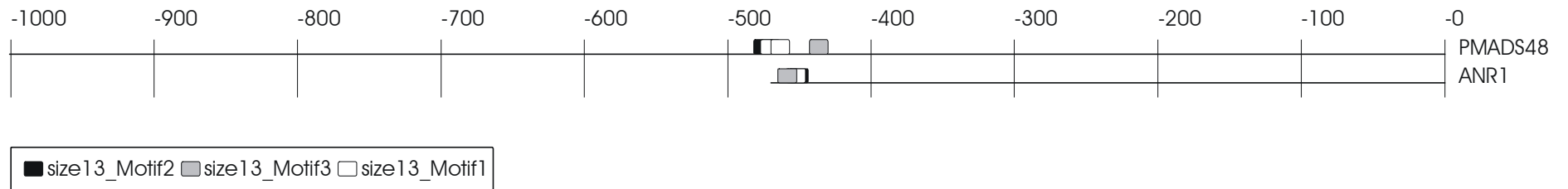


Motif1_size13
 Motif4_size13
 Motif7_size13
 Motif6_size13
 Motif5_size13
 Motif3_size13
 Motif2_size13

Motif1 0.000339302	Motif2 0.000263901	Motif3 0.001093306	Motif4 0.00399622	Motif5 0.000377002	Motif6 3.77E-05	Motif7 0.005504228
aaacaagatctag	aatcaattaatgc	ggtatcittaaaa	ttttattttacg	taaacaagatcta	atcctgcccctag	aagaaggagaaga
agacaagatctat	aaccaattcatgc	ggtatatttagaa	ttttattttctg	gagacaagatcta	atcatgcccctag	aaaaggaggaga

Fig. S1

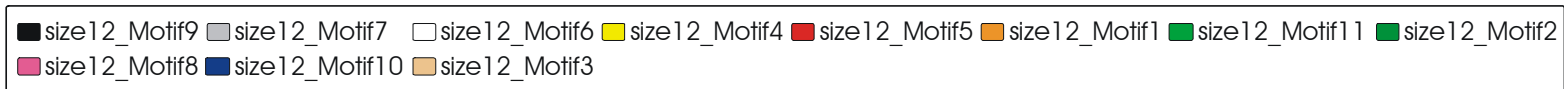
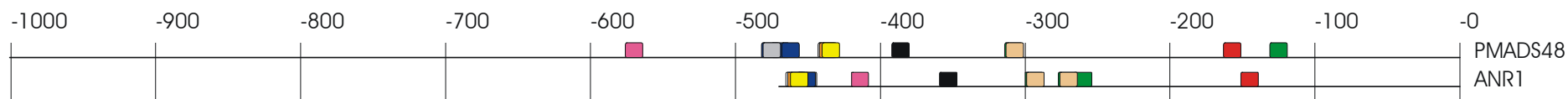
Subfamily: ANR1, size: 13, allowed mutations: 2



Motif1 0.001055605	Motif2 0.008369443	Motif3 0.00980205
ttctcttttcc	ctcttttcct	ttgtcttctt
ttctccttcc	ttctttcctt	tttcttgctt
ttctccttcc		

Fig. S1

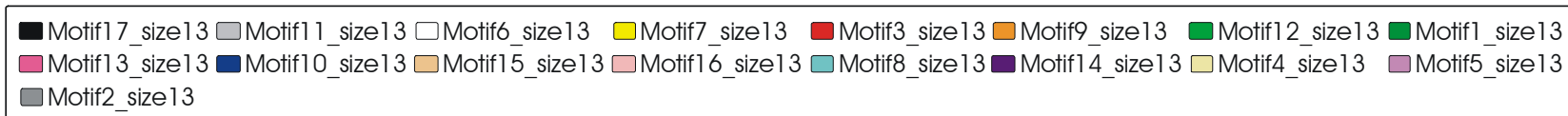
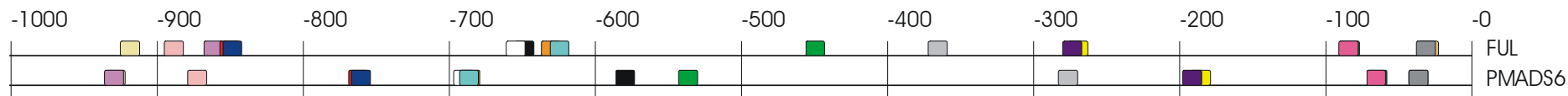
Subfamily: ANR1, size: 12, allowed mutations: 2



Motif1 0.020659705 tgctttctct ttcttgctct	Motif2 0.00188501 accactaatcaa agcactaatcaa	Motif3 0.000377002 agtctaataac agtctaataac agactaataat	Motif4 0.016437284 tccttctctt tcttgctctt	Motif5 0.010254452 tggatgtgtt tcgattgtt	Motif6 0.025409929 ttgtcttctct tttcttgctct
Motif7 0.010933056 tccttttcct tcctttctct	Motif8 0.000678603 aaacattggcat aaagattggcat	Motif9 0.021338309 tgtctttatta ttcttaatta	Motif10 0.002563613 ctcttttcct ttctttctct ctcctttctct ctcctttctct	Motif11 0.001131006 gagtctaattaa gagtctaattaa tagactaattaa	

Fig. S1

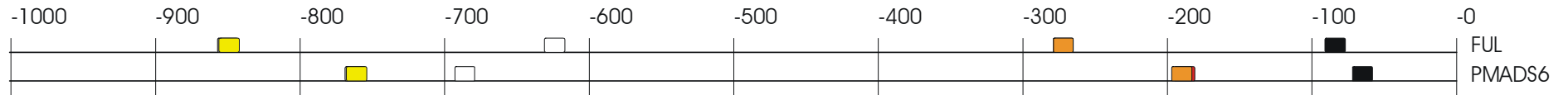
Subfamily: FUL, size: 13, allowed mutations: 2



Motif1 0.005240327 caaaagaaataaa cataagaaagaaa	Motif2 0.002412812 tctctctgtgct tctctctgtgt	Motif3 0.000565503 ttgctctataaaa ttgcaattataaa	Motif4 0.008746444 attttaatgttt attttagtttt	Motif5 0.004147021 tattttaatgttt tattttgtgttt	Motif6 0.003581518 agctagaaaaaaa aaccagaaaaaaa	Motif7 0.029142248 ttttctcttgt tttttcttct
Motif8 0.04316672 agaaaaaaaaaaa agaaaaataaaa	Motif9 0.066013036 gaaaaaaaaaaaa gcaaaaagaaaaa	Motif10 0.000452402 gctctataaaat gcaattataaaat	Motif11 3.77E-05 atcgacaacgcat ctcgacaacacat	Motif12 3.77E-05 tacgggaaggaaa tacggtacggaaa	Motif13 0.003732319 acaaaagaaataa acataagaaagaa	Motif14 0.034571076 ctttcttttct gttttttttct
Motif15 0.001847309 tctctctgtgct tctctctgttct	Motif16 0.003204516 aataaaatttgt gataaaatattgt	Motif17 0.000754004 aaaaacacctgct aaaaaaactgtc				

Fig. S1

Subfamily: FUL, size: 14, allowed mutations: 2

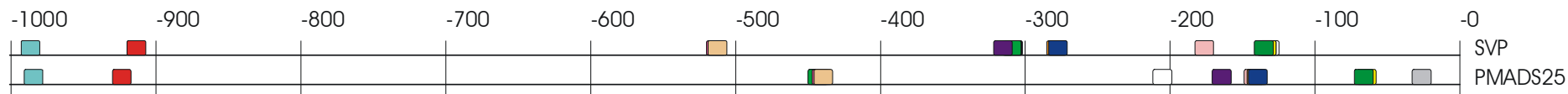


Motif2_size14
 Motif6_size14
 Motif3_size14
 Motif5_size14
 Motif4_size14
 Motif1_size14

Motif1 0.044900928	Motif2 0.00188501	Motif3 0.022695515	Motif4 0.038831198	Motif5 0.000188501	Motif6 0.000188501
ttttttttctct	acaaaagaataaa	agaaaaaaaaaaa	ttcttttctctt	tgctctataaaat	ttgctctataaaa
ttttttttcttt	acataagaagaaa	agaaaaattaaaa	ttttttttcttt	tgcaattataaaat	ttgcaattataaaa

Fig. S1

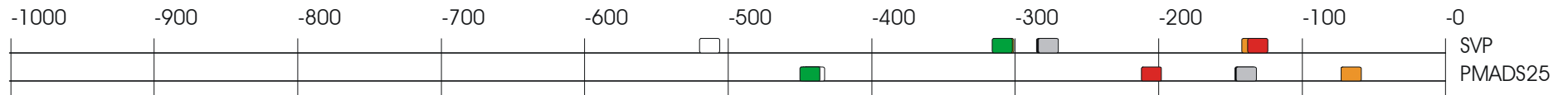
Subfamily: SVP, size: 13, allowed mutations: 2



Motif1 0.000678603	Motif2 0.001168706	Motif3 0.003543818	Motif4 0.000640903	Motif5 0.004712524	Motif6 0.001771909	Motif7 0.002450512
agttttcctgtc	aactagggttgt	acatttcaaaaa	cicictaaattta	aaaatatttaca	ctttctcttcc	atccctttcttt
ggttttactgtc	aactagggtttt	agatttcaaaaa	ctcacaataattta	aaaataatataca	ctctctctttac	atctcttcttt
Motif8 0.000377002	Motif9 0.002752114	Motif10 0.000980205	Motif11 0.000113101	Motif12 0.000452402	Motif13 0.000490102	Motif14 0.000678603
tctaaattagca	agttcttcttt	ccagttcttct	gttttcctgtct	ctctaaatttagc	tttctgtcttc	tttctgtcttct
tctaaattagca	atcttctcttt	ccatcttcttct	gtttttactgtct	ttctaaatttagc	ttctcatgtcttc	tctcatgttcttct

Fig. S1

Subfamily: SVP, size: 14, allowed mutations: 2

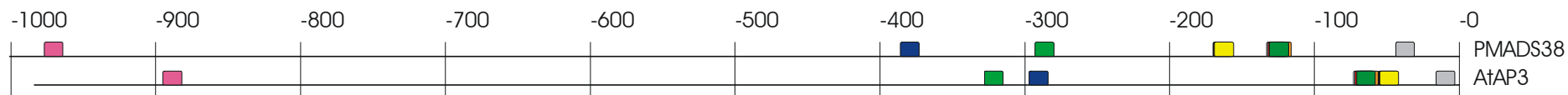


Motif7_size14
 Motif2_size14
 Motif6_size14
 Motif3_size14
 Motif5_size14
 Motif4_size14
 Motif1_size14

Motif1 7.54E-05	Motif2 0.000188501	Motif3 3.77E-05	Motif4 0.000527803	Motif5 0.000829404	Motif6 0.000150801	Motif7 0.000339302
agttttcctgtct	tctaaatttagcaa	gltttcctgtctt	ccagttcttctt	ctttctcttct	ttttcctgtctt	ctctaaatttagca
ggttttactgtct	tctaaatttagcaa	glttttactgtctt	ccatctcttctt	ctctctctttact	ttctcatgtctt	ttctaaatttagca

Fig. S1

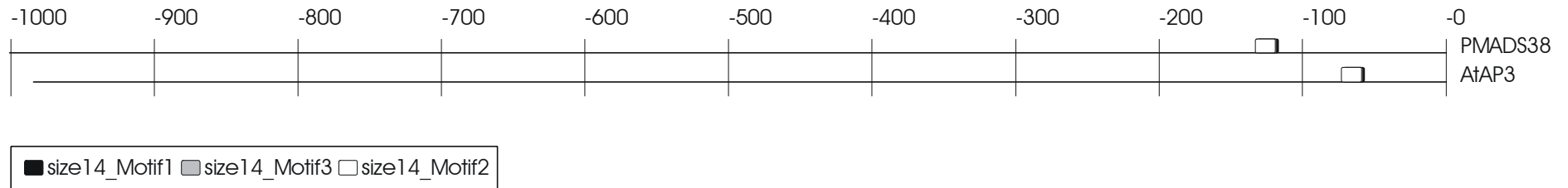
Subfamily: AP3, size: 13, allowed mutations: 2



Motif1 0.000490102 ctgtcctctcca cttctcctctccc	Motif2 0.002375112 acaagagagaag ttaaagagagaag	Motif3 0.000414702 atgattaagca attatttcagca	Motif4 0.000829404 tcttctcattata tcttctcttata	Motif5 0.001621108 ttcttctcattat ttcttctcttat
Motif6 0.000640903 ttctcattatc ttctctttatc	Motif7 0.000603203 aagatcaatccat aagatgaatacat	Motif8 0.002525913 tttcttctcatta attcttctctta	Motif9 3.77E-05 agctttggctccc agcaatggctccc	Motif10 0.001017905 tcttgctctctcc ccttctcctctcc

Fig. S1

Subfamily: AP3, size: 14, allowed mutations: 2

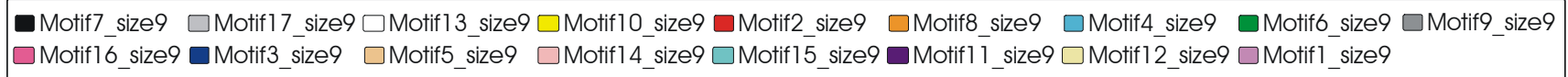
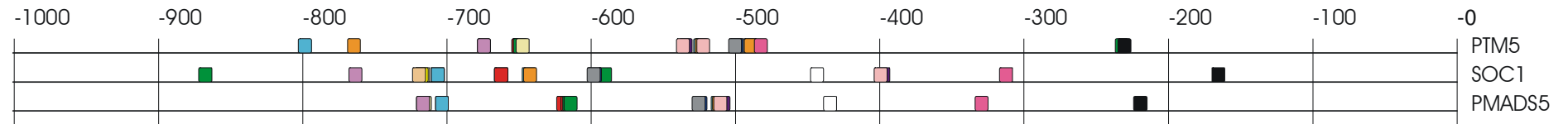


Motif1 0.000226201	Motif2 0.000980205	Motif3 0.000414702
tcttctcattat	tttcttctcattat	ttcttctcattata
tcttctctttat	attcttctctttat	ttcttctctttata

Fig. S1: Motifs detected through FootPrinter in the promoters of one-to-one Arabidopsis and poplar MADS-box genes. Next to every motif, its occurrence per 1kb of random promoter sequence is mentioned.

two-to-one comparisons

Subfamily: SOC1, size: 9, allowed mutations: 2, no losses



Motif1 0.072007366 **Motif2** 0.196757301 **Motif3** 0.034834977 **Motif4** 0.089123253 **Motif5** 0.153816782 **Motif6** 0.090970563

ctttttaa	actctttt	tcctctct	ttgtttct	agtttttt	cttctttc
ctttttat	actttttt	tcattctct	ttaattct	actctttt	cttttttc
ctttttgt	actccttt	tactctct	ttatttct	actttttt	cttttttt
	cctttttt			cctttttt	tttttttc

Motif7 0.179603714 **Motif8** 0.118642504 **Motif9** 0.030989558 **Motif10** 0.066050736 **Motif11** 0.04320442 **Motif12** 0.091045963

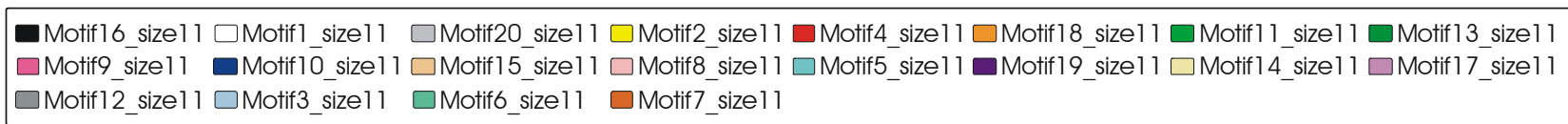
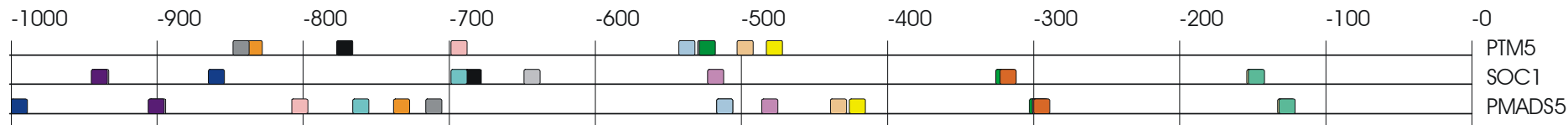
atttttta	aaaaagggt	tcctctct	ttttttgt	aaactata	tttttgtc
ttttttta	aaaaaagt	tcattctc	ctttttat	aaactact	tttttctc
atttttgta	aaaaaact	ttactctc	ctttttgt	aaactatt	tttttgtc
					aaaaacta

Motif13 0.025824631 **Motif14** 0.071366463 **Motif15** 0.053270371 **Motif16** 0.02744574 **Motif17** 0.566746983

catgatct	ataaactta	taaaaagggt	ttcaattaa	ttgtttct
cattctctt	caaaactta	taaaaaagt	ttcaattga	ttttttct
cattctctt	aaaaagtta	taaaaaact	ttcaattga	tttattct

Fig. S2

Subfamily: SOC1, size: 11, allowed mutations: 2, losses



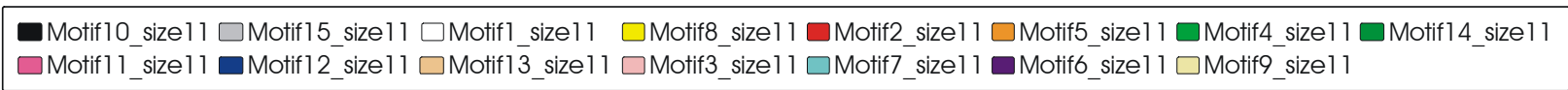
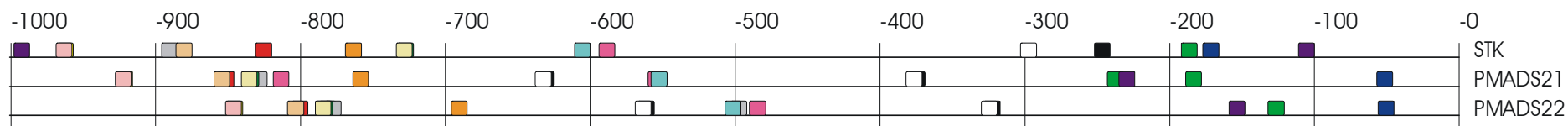
Motif1 0.00203581 ataagtaaagg ataaggaaagg	Motif2 0.005768129 attgaatatct attaaatatct	Motif3 0.004825625 tacaaaactta taaaaagtta taaaaactta	Motif4 0.001055605 ttgcatcctc ttgcatcctg	Motif5 0.00199811 attacacaca attaccacaa	Motif6 0.006182831 tcttgattca tcttgaatca	Motif7 0.000414702 gcatcctcaa gcatcctgaa	Motif8 0.008633344 actaaaaata actaaaaata
--	---	--	---	--	---	---	---

Motif9 0.000377002 tgcacctca tgcacctga	Motif10 0.008557944 tctctatctt cctctatctt	Motif11 0.001244106 gttgcacctt cttgcacctt	Motif12 0.006032031 ttttcacctt ttgtcacctt	Motif13 0.011159257 taaaaaagtta taaaaaactta	Motif14 0.004335522 ctcttgattc ctcttgaatc	Motif15 0.002978315 cattctctaa cattctctca	Motif16 0.015080077 aatagatgaa aataaatgaa
---	--	--	--	--	--	--	--

Motif17 0.000754004 ccctttatcct ccttttatcct	Motif18 0.001244106 tttagcgagtt tttagcaagtt	Motif19 0.005164926 aataagtaaag aataaggaaag	Motif20 0.01172476 ataaaaaggtt ataaaaaggtt
--	--	--	---

Fig. S2

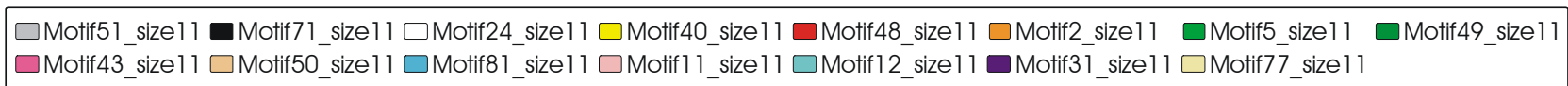
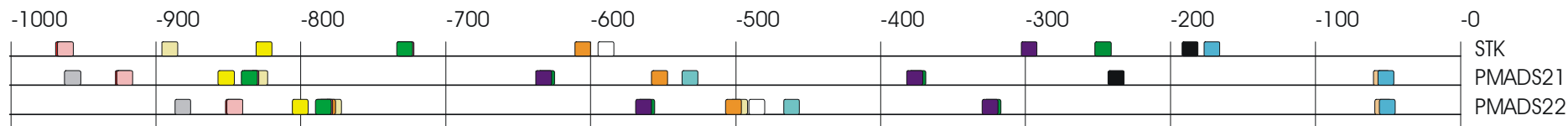
Subfamily: STK, size: 11, allowed mutations: 2



Motif1 0.01760599	Motif2 0.010254452	Motif3 0.000904805	Motif4 0.034194074	Motif5 0.007087636	Motif6 0.122299422	Motif7 0.015080077	Motif8 0.001809609
ttctgaaatc	acttttctgt	catgctagatt	aagctttttt	ttctcccctt	ttttgtctta	tacatatctt	atgctagattc
ttctaaaatc	acttttctgt	catgctagatt	atgctttttt	ttctcccctt	ttttgtttta	ttcatattct	atgctagattc
ttctaaactc	atgttctgt	tctgctagatt	aaactttttt	ttctcctott	ttttttttta	tacatatgtct	ctgctagattc
Motif9 0.007540038	Motif10 0.005089526	Motif11 0.01372287	Motif12 0.022544715	Motif13 0.008143241	Motif14 0.00784164	Motif15 0.022582415	
tttccatatt	cttgaatcaa	tttacaatatt	catatataata	tccacttttct	tctccatattt	tatttcttagt	
ttctcatatt	cttaaatcaa	tttacaatctt	catatataata	tccacttttct	tcttcatattt	tatttcttatt	
cttccatatt	cttgatcaa	tttacaatctc	tatatataaca	ttctcttctt	tctccatattt	tatttcttctt	

Fig. S2

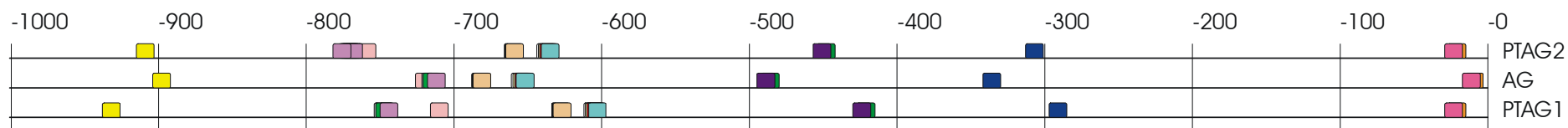
Subfamily: STK, size: 11, allowed mutations: 2, losses (only motifs shared between Arabidopsis and poplar)



Motif2 0.003770019	Motif5 0.00188501	Motif11 0.000452402	Motif12 0.000867104	Motif24 0.002337412	Motif31 0.004410922	Motif40 0.002563613	Motif43 0.00196041
tacatatattct	ttctccatatt	atgctagattc	ctttgagcta	atttacatctt	ttctgaaatc	acttttctgt	tctccatattt
ttcatatttct	ttctcatatt	atgctagattc	ctttgagcta	atttacatctt	ttctaaaatc	acttttctgt	tcttcatattt
tacatatgtct	ctctccatatt	ctgctagattc			ttctaaactc	atgtttctgt	tctccatattt
Motif48 0.000226201	Motif49 0.001281807	Motif50 0.002186611	Motif51 0.010367553	Motif71 0.025447629	Motif77 0.005655029	Motif81 0.005655029	
catgctagatt	ctgaaatcaa	gcgcatatata	tagtaaaataa	aaactttttt	tatttcttagt	catatataata	
catgctagatt	cttaaaatcaa	gagcatatata	taggaaaataa	aaactttttt	tatttcttatt	catatataata	
tctgctagatt	cttgagatcaa				tatttcttctt	tatatataaca	

Fig. S2

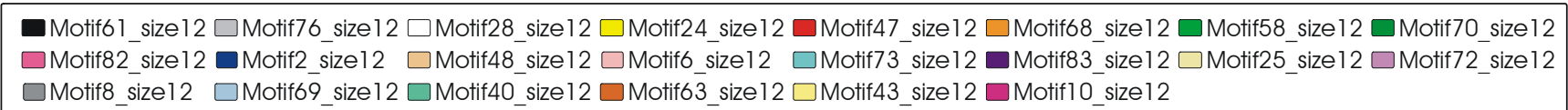
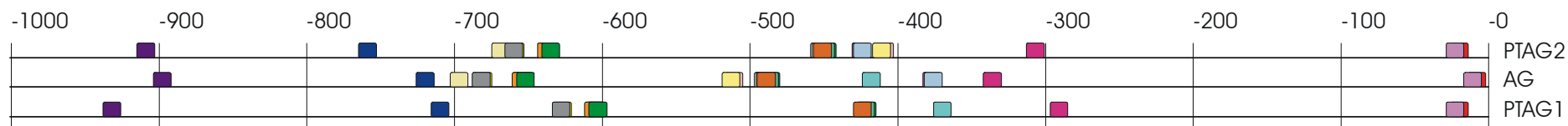
Subfamily: AG, size: 12, allowed mutations: 2



Motif1 0.000452402	Motif2 0.000640903	Motif3 0.00199811	Motif4 0.000339302	Motif5 3.77E-05	Motif6 0.000301602	Motif7 0.012064061	Motif8 3.77E-05
ttgctccattt	tttcaaaaagt	aaattacaagga	gtttggatcag	atgccacctct	gctccattttc	taaaaaaaaaa	ctccagattgaa
ttgctccattt	tttcagaaagt	aaattacaaga	gtttggatcag	ataccacctct	gctccattttc	gaaaagaaaaa	ctccagattgaa
tacctccattt	tttcagaaaat	aaataaaaaga	gcttggagcag	ataccatctct	cctccattttc	taaaagaaaaa	ctctagatttaa
Motif9 0.746162196	Motif10 0.746162196	Motif11 0.000942505	Motif12 0	Motif13 0.000188501	Motif14 0.000414702	Motif15 0.000565503	Motif16 0.000640903
aaaaaaaaaaaa	aagataaaaaa	ctccattttct	tgcccactctt	ttggatcagct	cactgtttggg	tgctccatttt	ctcactgttt
aaaaaaaaaaaa	aaaaaaaaaaaa	ctccattttct	taccacactctt	ttggatcagct	cactgtttgg	tgctccatttt	catcactgttt
aaaaaaaaaaaa	aaaaaaaaaaaa	ctccattttct	taccatctctt	ttggagcagca	cactctttgg	acctccatttt	ctcactcttt
aaaaaaaaaaaa	aaaaaaaaaaaa						
aaaaagaaaaa	aaaaaaaaaaaa						
aaaaagaaaaa	aagaaaaaaaat						

Fig. S2

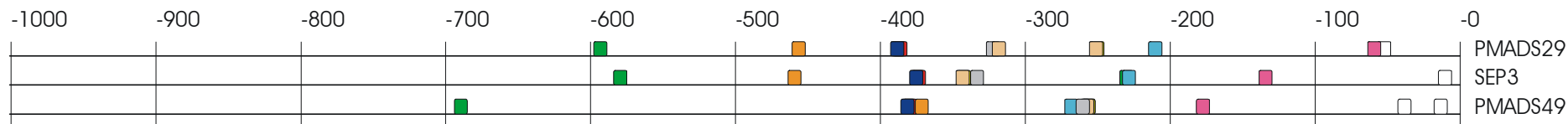
Subfamily: AG, size: 12, allowed mutations: 2, losses (only motifs shared between Arabidopsis and poplar)



Motif2 0.00199811 aaattacaagga aaattacaaaga aaattaaaga	Motif6 0.006522133 tcttctcatca tcttctcataa	Motif8 3.77E-05 atgccacctct ataccacctct ataccatctct	Motif10 3.77E-05 ctccagattgaa ctccagattgaa ctctagatttaa	Motif24 0 tgccacctctt taccacctctt taccatctctt	Motif25 0.001244106 ctttataaatg cctttataaatg	Motif28 0.000640903 tgcttcactgt tgcttcactct	Motif40 0.000716304 tcactgtttgg tcactgttttg tcactcttttg
Motif43 0.005391127 tctcttctcat tatcttctcat	Motif47 0.000150801 ttggatcagcta ttggatcagcta ttggagcagcaa	Motif48 0.000754004 gcttcactgtt gcttcacttct	Motif58 0.000414702 cactgtttggg cactgttttgg cactcttttgg	Motif61 0.000565503 tgcttccattt tgcttccattt accttccattt	Motif63 0.000640903 cttcactgttt catcactgttt cttcacttctt	Motif68 0.000452402 ttgcttccattt ttgcttccattt taccttccattt	Motif69 0.000904805 tctgatcttct tctgatcttct
Motif70 0.000942505 cttccatttct cttccatttct cttccatttct	Motif72 0.000339302 gttttgatcag gttttgatcag gctttgagcag	Motif73 0.004524023 ttcttttctgt ttcttttaigt	Motif76 0.000301602 gcttccatttc gcttccatttc ccttccatttc	Motif82 0.000980205 ttctgatctct ctctgatctct	Motif83 0.000640903 ttttcaaaaagt ttttcagaaaagt ttttcagaaaat		

Fig. S2

Subfamily: SEP3, size: 9, allowed mutations: 2



Motif1 0.030914157 **Motif2** 0.045730333 **Motif3** 0.098020499 **Motif4** 0.057530493 **Motif5** 0.130254163 **Motif6** 0.314872002

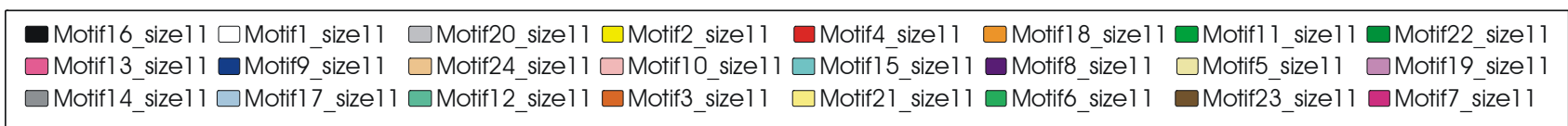
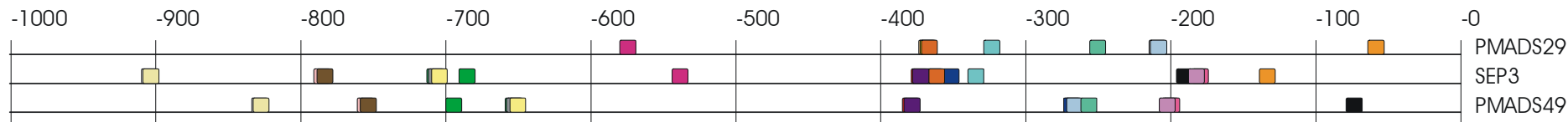
tcaagtaat	atagataaa	tttgaaat	ttcttcaa	taacatttt	aaaacgaaa
taaagtaat	attgataaa	tttgaaact	ttcttaaa	taaaatttt	taaaagaaa
tagagtaat	atagattaa	tttgaaat	ttcttaaaa	taaaaattt	agaagaaa

Motif7 0.040263805 **Motif8** 0.110650063 **Motif9** 0.036983888 **Motif10** 0.221790228 **Motif11** 0.048105445

gttgaaaa	ttaacattt	ggttgaaa	tagaataaa	tttcaatta
gttgaaac	ttaaaaatt	tggttgaaa	taaaacaaa	tttctatta
tttgaaaa	ttaaaattt	ttttgaaa	taaaataaa	tttcaagta
	ttaaaaatt			
	ttaaaaattt			

Fig. S2

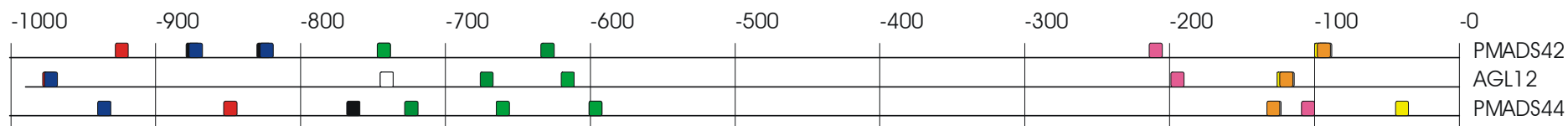
Subfamily: SEP3, size: 11, allowed mutations: 2, losses



Motif1 0.00188501 ttaaggttagg ttaaggttaag	Motif2 0.000904805 tctaagcatgg tctaaacatgg	Motif3 0.000980205 ctaagcatgga ctaaacatgga	Motif4 0.016324183 gtttgaaaata tttgaaaata	Motif5 0.001168706 taaggttaggt taaggttaagt	Motif6 0.002940615 tctccacctc tctccaccgtc	Motif7 0.012591864 aaagcatcaaa aaaacatcaaa	Motif8 0.021866111 tttgaaaatat tttgaaaataa
Motif9 0.002752114 atagggttaatt atagagtaatt	Motif10 0.001017905 tgtcgacacgt tttcgacacgt	Motif11 0.00987745 tctcatttca tctcttttca	Motif12 0.012780365 ttaaattttc ttaaattttc	Motif13 0.002865215 tgagattgta tgagatttca	Motif14 0.001093306 ctccaccttc ctccaccgtcc	Motif15 0.024693626 tttctttcaa tttctttaa	Motif16 0.002148911 gagaagtgtg gagaattgtg
Motif17 0.001771909 aaagtaattct agagtaattct	Motif18 0.013044266 atagataaaaa attgataaaaa	Motif19 0.004222421 tttgagattt tagtgagattt	Motif20 0.001545708 taaagtaattc tagagtaattc	Motif21 0.001357207 ccaccttcat ccaccgtcat	Motif22 0.002752114 gtgagattgt gtgagatttct	Motif23 0.001658808 tcgacacgtgt tcgacacgtgg	Motif24 0.001847309 atctaagcatg atctaaacatg

Fig. S2

Subfamily: AGL12, size: 9, allowed mutations: 2

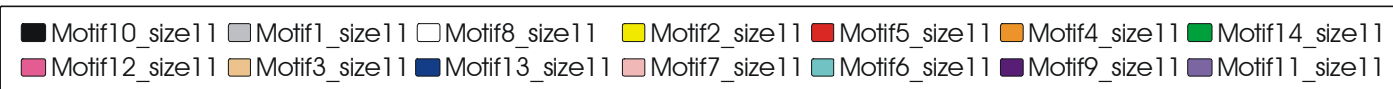
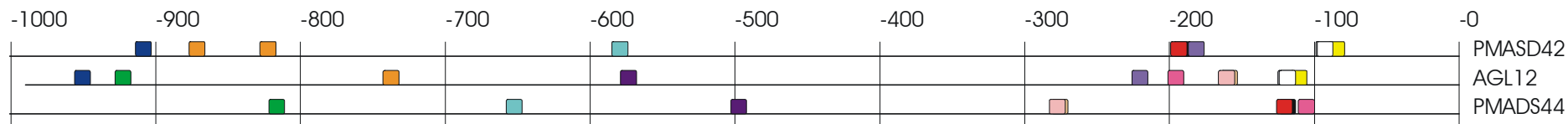


Motif1 0.146729146	Motif2 0.091385265	Motif3 0.079849006	Motif4 0.001281807	Motif5 0.005579628
atcttttt	ataaaaca	ttctgttt	gctagtca	gaagctagt
atctttgt	aaaaaaca	ttctgtct	gctagtcca	taagctagt
atctttct	ataagaca	ttctgttg	gctattcca	taagctgt
atttttgt				

Motif6 0.154495386	Motif7 0.133345578	Motif8 0.033779372	Motif9 0.005617329	Motif10 0.001583408
gtttttgt	gtttttgt	tctgttta	gcatgagat	agctagttc
atctttgt	ggtttgtt	ttttgtta	gcacgacat	agctagtcc
atttttgt	gttttctt	tcattgtta	gcatgacat	agctattcc

Fig. S2

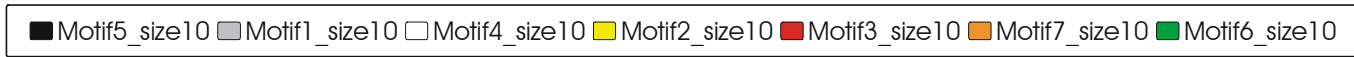
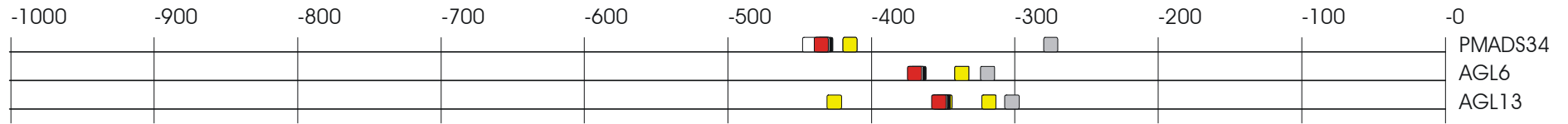
Subfamily: AGL12, size: 11, allowed mutations: 2, losses



Motif1 0.000301602 aagctagtca aagctagtcca	Motif2 0.000942505 caaactagtg caaactagtgt	Motif3 0.017078187 aagaacagag aagaacagat	Motif4 0.025673831 tttgttcat tttgtttaat	Motif5 0.00384542 ccattctttt ccatgctttt	Motif6 0.000188501 cacgcctcatg ctcgcctcatg	Motif7 0.004599423 cgaagaaacag caaagaaacag
Motif8 0.000829404 agctagtcaa agctagtccaa	Motif9 0.002450512 cctccatctct cttccatctct	Motif10 0.006597534 attctttttg atgctttttg	Motif11 0.00784164 gagattatata gagaatata	Motif12 0.000942505 tggcatgagat tggcatgacat	Motif13 0.003506118 ttaaagatgaa gttaagatgaa	Motif14 0.001131006 tgatttacatc tggtttacatc

Fig. S2

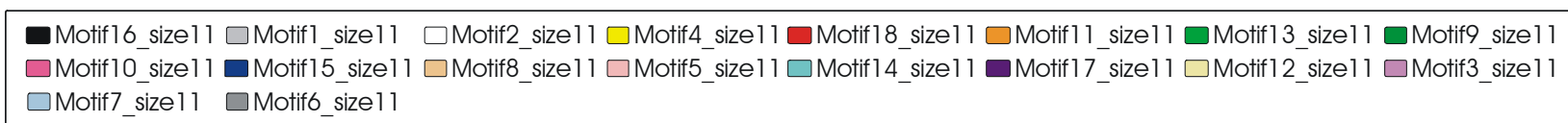
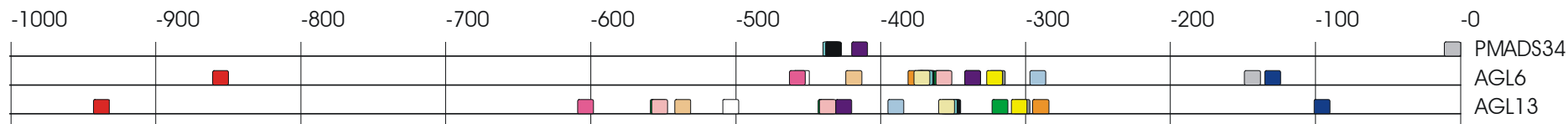
Subfamily: AGL6, size: 10, allowed mutations: 2



Motif1 0.002865215	Motif2 0.016135682	Motif3 0.008369443	Motif4 0.009010346	Motif5 0.023977322	Motif6 0.009010346	Motif7 0.016135682
ctgctaataa	attccattc	cagaatttc	aaaatttca	aatttcaat	agaatttca	attccattc
ctagctataa	attccattt	aggaatttc	ggaatttca	aatttcaat	ggaatttca	attccattt
ctagctataa	attccatac	aagaatttc	agaatttca	aatttcatt	agaatttca	atttcattt
	atttcattt					atttcattt
	attaccattt					attaccattt

Fig. S2

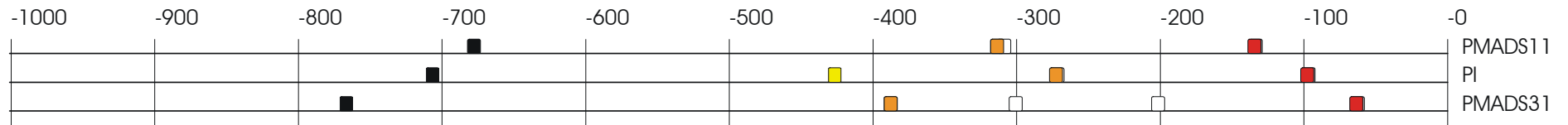
Subfamily: AGL6, size: 11, allowed mutations: 2, losses



Motif2 0.00776624 agttgaaatt agttgaact	Motif3 0.004071621 agaatttcaa ggaatttcaa agaatttcat	Motif4 0.001809609 aatctagctat actctagctat	Motif5 0.000263901 ggtccgactgt ggtccaactgt	Motif6 0.000754004 tctagctataa tctagctataa	Motif7 0.005353427 tcatttggtc tcgttggtc	Motif8 0.009010346 agcaaaaaaga atcaaaaaaga
Motif9 0.000301602 tgggccgactg tggccaactg	Motif10 0.002186611 gtagttgaa gtagttgaa	Motif11 0.00584353 aataaaaggaa aataaacggaa	Motif12 0.011347758 aaaggaattt aaaagaattt	Motif13 0.012101762 attccattt attaccattt	Motif14 0.002186611 cagaatttca aggaatttca aagaatttca	Motif15 0.003506118 aaagtaataca aaagtaattca
Motif16 0.003129116 gaatttcaat gaatttcaat gaatttcatt	Motif17 0.009123446 attccattct attccattt attccatact attaccattt	Motif18 0.018850096 aaccaattt aaccaaaatt				

Fig. S2

Subfamily: PI, size: 9, allowed mutations: 2

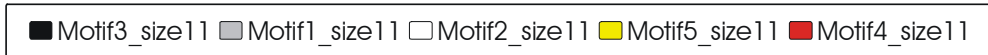
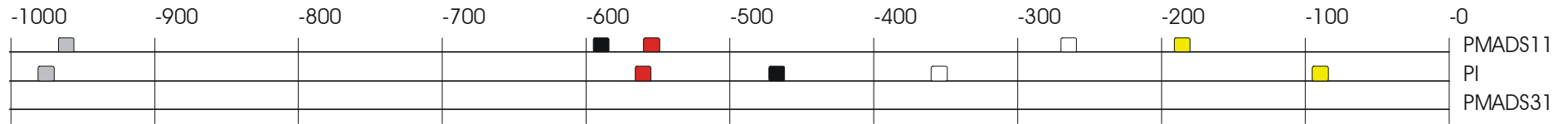


Motif4_size9
 Motif6_size9
 Motif2_size9
 Motif1_size9
 Motif5_size9
 Motif3_size9

Motif1 0.031856662	Motif2 0.033703971	Motif3 0.031856662	Motif4 0.171573573	Motif5 0.00591893	Motif6 0.006936835
aggagggag	ggagaaaa	aggagggag	tttcattta	agctcctct	gctcctcta
aggagagag	ggagaggaa	aggagagag	ttttattta	tgctcctat	gctcctatt
acgagagag	ggagagaca	aggagagaa	ttttatata	tgctcctct	gctcctctt
	ggagagaaa				

Fig. S2

Subfamily: PI, size: 11, allowed mutations: 2, losses

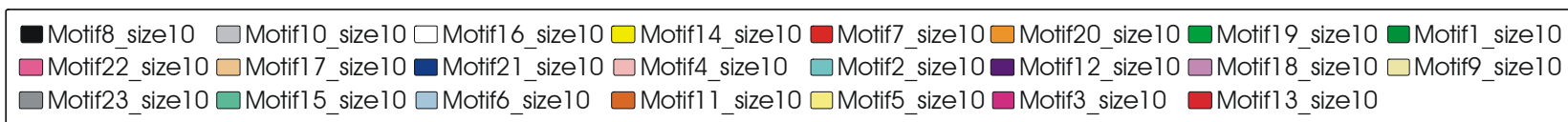
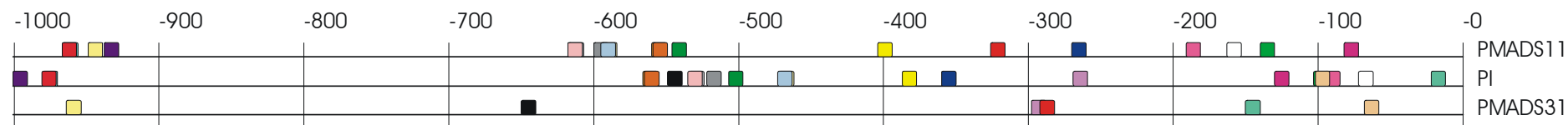


Motif1	0.006446733	Motif2	0.00599433	Motif3	0.000527803	Motif4	0.005579628	Motif5	0.004825625
tatgttcgatt		aagccaaatca		cagaagagacc		taaaggttga		cttctcgttct	
tatgtttgatt		aagcaaatca		cggaagagacc		taaaagttga		cttctgttct	

Note: Sequence V.898 seems to be very divergent compared to the other poplar paralog (Il.730). However, when lowering the motif size to 10, some motifs can still be detected in sequence V.898.

Fig. S2

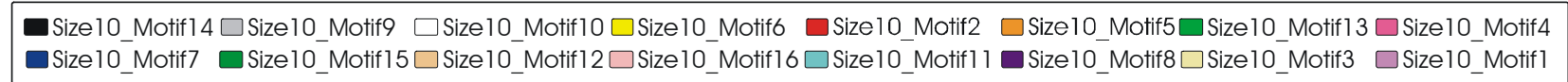
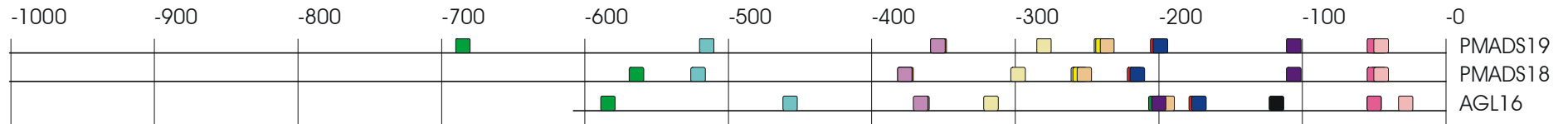
Subfamily: PI, size: 10, allowed mutations: 2, losses



Motif1 0.01172476 tttactaca tttctctaca	Motif2 0.01768139 atgttcgatt atgtttgatt	Motif3 0.008369443 tatctcctca tatctcatca	Motif4 0.021338309 cttatctttc tttatctttc	Motif5 0.016550384 gtacaaaaat gtagaaaaat	Motif6 0.00384542 cagaagagac cggaagagac	Motif7 0.001771909 agcttcgcag agtttcgcag	Motif8 0.014627674 ttcatgtgaa ttcatatgaa
Motif9 0.004787924 agaagagacc ggaagagacc	Motif10 0.009048046 ttatctttcg ttatctttcc	Motif11 0.02556073 aaaggttga aaaagttga	Motif12 0.014062172 tgcaacttc ttcaacttc	Motif13 0.014665375 tatgttcgat tatgtttgat	Motif14 0.011687059 atcgatcaca atcaatcaca	Motif15 0.04324212 agaaaaagat agaaagagat	Motif16 0.006899135 tatatcctct catatcctct
Motif17 0.003204516 tgctcctatt tgctcctct	Motif18 0.031178059 aaaaagagtt aaatagagtt	Motif19 0.004297822 aagctcctct atgctcctct	Motif20 0.017907591 taaaggtttg taaagtttg	Motif21 0.01575868 aagccaaatc aagccaaatc	Motif22 0.011046156 cttctcgttc cttctgttc	Motif23 0.008897245 atatccagaa atatctagaa	

Fig. S2

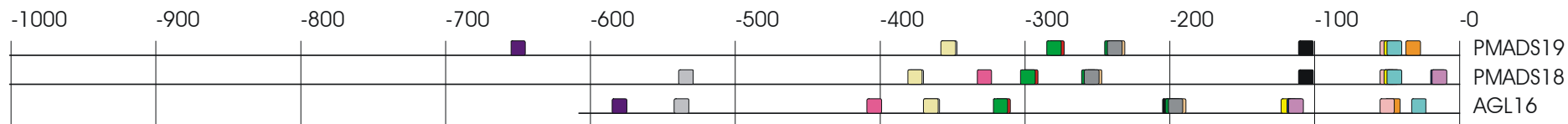
Subfamily: AGL16, size: 10, allowed mutations: 2



Motif1 0.014250672	Motif2 0.022770916	Motif3 0.014627674	Motif4 0.020659705	Motif5 0.009952851	Motif6 0.001508008	Motif7 0.03340237	Motif8 0.028425945
aaaaaaccac	cctctctct	tccttatata	gttggtgatt	aaaaaccact	acgacgtctc	tctctcttc	aaacacacat
aaaaaaccac	cctctctct	tccttatata	gttggtgatt	aaaaaccact	acgacgtctc	tctctctcc	aaacacacat
agaaaccac	tttctctct	tgttatata	gatgatgatt	gaaaccact	accacatctc	tctctctcc	aaaaccacat
Motif9 0.00188501	Motif10 0.016286483	Motif11 0.153741382	Motif12 0.001734209	Motif13 0.093119474	Motif14 0.016286483	Motif15 0.014250672	Motif16 0.018774696
aacgacgtct	gttgattatt	aattataaaa	acgtctctga	atztatatat	gttgattatt	aaaaaaccac	tgattattgt
aacgacgtct	gttgattatt	tattttaaaa	acgtctctga	atztatattt	gttgattatt	aaaaaaccac	tgattattgt
aaccacatct	gatgatgatt	aattttaaaa	acatctctga	atttaaat	gtttattctt	acaaaaccac	tgatgtttgt

Fig. S2

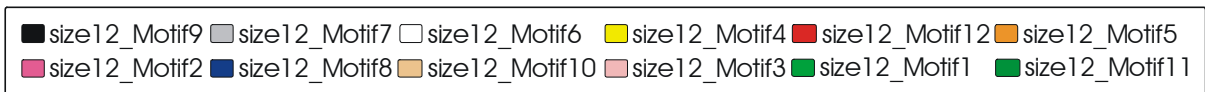
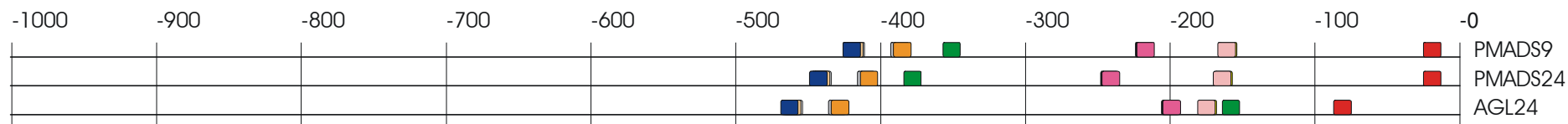
Subfamily: AGL16, size: 10, allowed mutations: 2, losses (only motifs shared between Arabidopsis and poplar)



Motif3 0.02940615 atccttgga atccttgaa	Motif5 0.016286483 gttgattatt gttgattatt gtttattctt	Motif7 0.018774696 tgattattgt tgattattgt tgatgtttgt	Motif8 0.00188501 aacgacgtct aacgacgtct aaccacatct	Motif11 0.050895259 ttcttgga ttcttgaaa	Motif12 0.041470211 aaattgaact aaatttaact
Motif13 0.014627674 tccttatata tccttatata tgtttatata gttgattatt gatgatgatt	Motif17 0.010329853 aaaaccacta aaaaccacta aaaccactt	Motif19 0.023147918 ttaagaatgt taaagaatgt	Motif26 0.014778475 gttggtgatt gttgattatt gttggtgatt	Motif28 0.061300512 atgattttaa atgatttgaa	Motif31 0.002186611 cgacgtctct cgacgtctct ccacatctct
Motif35 0.009952851 aaaaaccact aaaaaccact gaaaccact	Motif39 0.028425945 aaacacacat aaacacacat aaaaccacat	Motif40 0.001734209 acgtctctga acgtctctga acatctctga	Motif41 0.004222421 cttatatagc cttatatagc tttatatagt	Motif42 0.130141062 aataaacaaa aataaactaa	

Fig. S2

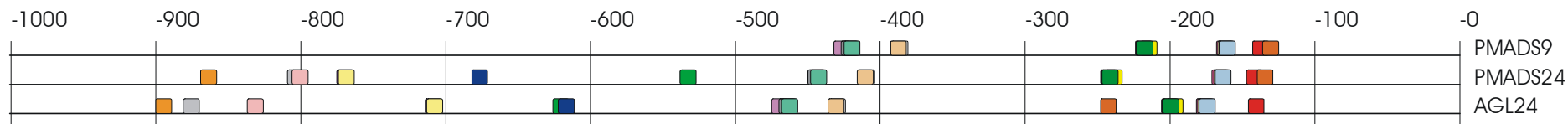
Subfamily: AGL24, size: 12, allowed mutations: 2



Motif1 0.000490102	Motif2 3.77E-05	Motif3 0.000150801	Motif4 0.000150801	Motif5 0.000150801	Motif6 0.000867104
gtttagctataa	cagttctttgc	ttggatctgaac	tggatctgaact	ctcgaacacaca	ttagctataaaa
gtttcgctataa	cagttctttgc	ttggatctgaac	tggatctgaact	cttgaacacaca	ttcgctataaaa
gtttagctaaaa	ccattctttgc	atggatctgac	tggatctgatct	cttgaacacaaa	ttagctaaaaaa
Motif7 0.000414702	Motif8 0.000226201	Motif9 3.77E-05	Motif10 0.000867104	Motif11 0.041130909	Motif12 0.048934849
ttctgaacaca	tgtttagctata	tcagttctttg	ttagctataaa	ttctctctctct	tttttctttt
ttctgaacaca	tgttcgctata	tcagttctttg	ttcgctataaa	ttctctctctct	tttttctttt
atcttgaacaca	tgtttagctaaa	tccattctttg	ttagctaaaaa	ttctctctctct	ttcttctttgt

Fig. S2

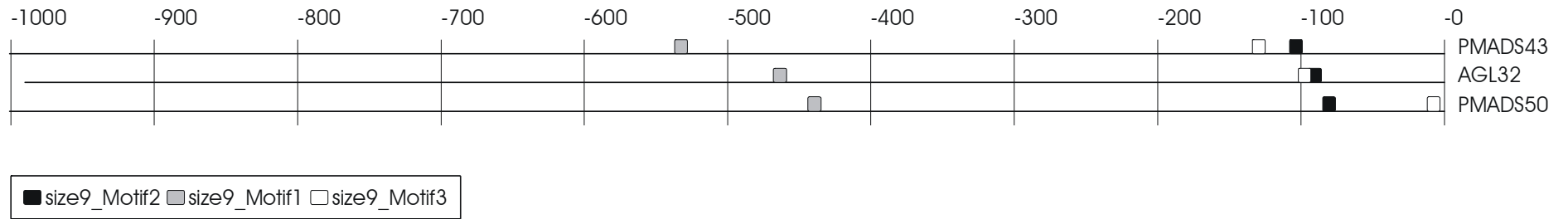
Subfamily: AGL24, size: 11, allowed mutations: 2, losses (only motifs shared between Arabidopsis and poplar)



Motif6 0.000226201	Motif8 0.006786035	Motif11 0.001093306	Motif17 0.002073511	Motif18 0.000678603	Motif20 0.007389238	Motif21 0.003091416	Motif23 0.000829404
ttgtttagcta	aacagaaaaac	tgtttagctat	gctagggttc	ctggatctga	attattatc	ttctttgcat	gtttagctata
ctgttcgcta	aacagtaaac	tgttcgctat	gctagggttc	ctggatctga	attataaac	ttctttgcat	gtttcgctata
ctgttagcta		tgtttagctaa	attagggttc	tatggatctga		ttctttgctt	gttttagctaaa
Motif28 0.001583408	Motif29 0.013006566	Motif30 0.003732319	Motif34 0.000904805	Motif35 0.000565503	Motif40 0.010631454	Motif43 0.002073511	Motif44 0.001017905
tcagttcttt	gtgatttttt	acagaaaaact	tctgaacaca	cagttctttg	ttaatcataa	ttctgctaaa	ttctgaacac
tcagttcttt	gtgattcttt	acagtaaac	tctgaacaca	cagttctttg	ttaatcataa	ttctgctaaa	ttctgaacac
tccattcttt			tctgaacaca	ccattctttg		ttcttcttaa	atctgaacac
Motif46 0.002073511	Motif51 0.001055605	Motif54 0.018623895	Motif56 0.005466528	Motif65 0.000452402			
ttgatctgaa	gatccctgtt	aattaagttt	taagtttgta	tgatctgaac			
ttgatctgaa	gatcactgtt	aattatgttt	taactttgta	tgatctgaac			
atggatctgat				tgatctgatc			

Fig. S2

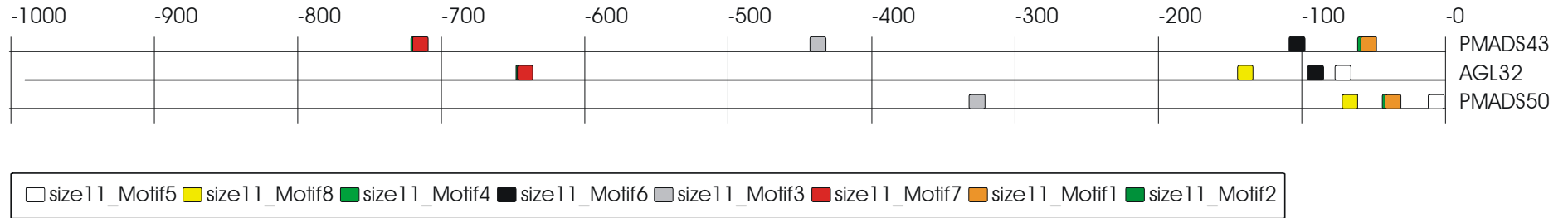
Subfamily: AGL32, size: 9, allowed mutations: 2



Motif1 0.075362683	Motif2 0.016701185	Motif3 0.139113708
aaaaaagag	tgagttaat	ttagtggtt
aagaaagaa	tgagtcaat	tttttagtt
aagaaagag	ttagttaat	tttttggtt

Fig. S2

Subfamily: AGL32, size: 11, allowed mutations: 2, losses

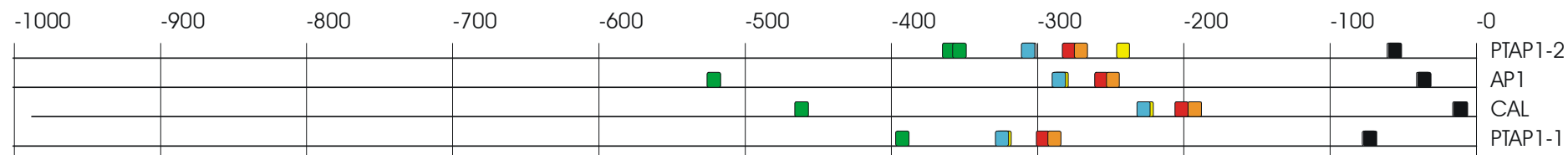


Motif1	Motif2	Motif3	Motif4	Motif5	Motif6	Motif7	Motif8
0.002752114	0.002111211	0.001017905	0.006597534	0.00784164	0.003204516	0.001847309	0.007728539
aaagatggta	agagtggtaa	agaagggctaa	aaaaagatggt	ttttagtga	gtgagttaatt	gagtggtaaa	aatatttagt
aaagaaggta	agagaggttaa	agaatggctaa	aaaaagaaggt	tttaagtga	gtagttaatt	gagaggttaa	aatattgtaat

Fig. S2: Motifs detected through FootPrinter in the promoters of two-to-one Arabidopsis and poplar MADS-box genes. Next to every motif, its occurrence per 1kb of random promoter sequence is mentioned.

“Many” comparisons

Subfamily: AP1, size: 9, allowed mutations: 2

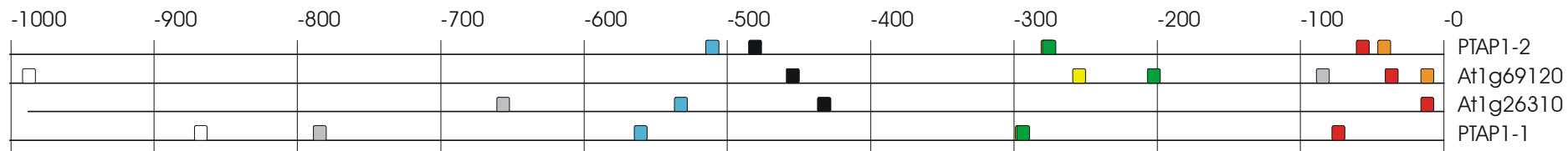


Motif7_size9
 Motif4_size9
 Motif6_size9
 Motif5_size9
 Motif3_size9
 Motif1_size9
 Motif2_size9
 Motif8_size9

Motif1 0.007728539	Motif2 0.124071331	Motif3 0.039811403	Motif4 0.029029148	Motif5 0.018925496	Motif6 0.008934945	Motif7 0.074193977	Motif8 0.011950961
actccggt	aaaaggaaa	aagaaacca	ggttat	cagtgaaa	ccagtgaga	ggtat	gccagtgag
actctggt	aaaaggaaa	aaaaacca	ggtat	caatgagat	ccaatgaga	ggtat	gccaatgag
actgtggt	aaaaggaaa	aagaaacca	ggtct	cagtgagca	ccaatgaga	ggtctta	accaatgag
actctggt	aaaaggaaa	tagaaacca	agttat	caatgagaa	ccaatgaga	ggtat	accaatgag
	aaaatgaaa			caatgagaa			

Fig. S3

Subfamily: AP1, size: 9, allowed mutations: 2, losses (only motifs shared between Arabidopsis and poplar)

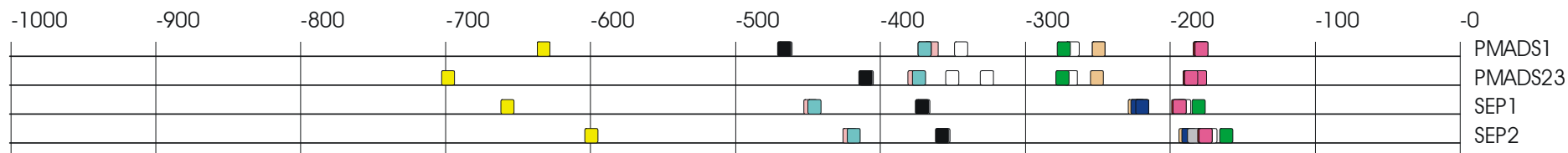


Motif28 0.01771909	Motif76 0.010329853	Motif107 0.029029148	Motif108 0.01172476
gaaaccact	ataactact	ggttatfff	aaaccactc
aaaaccact	ataattact	ggttatfff	aaaccactc
aaaaccact	ataactact	ggttctfff	aaaccactc
		agttatfff	

Motif129 0.055984785	Motif156 0.035249679	Motif185 0.109179755	Motif221 0.002902915
tcfttatat	taaaaaagg	tgtatatat	ccgctgtca
tcfttatat	taaaaaagg	tgtatatat	ccgccgtca
			ccgccgtca

Fig. S3

Subfamily: SEP1-SEP2, size: 9, allowed mutations: 2

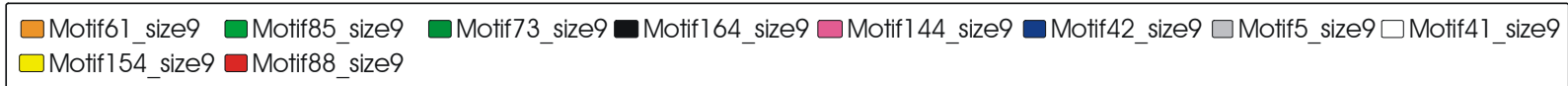
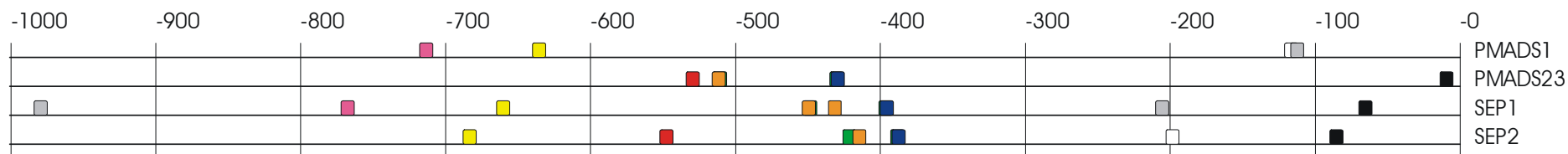


Motif1 0.116305092	Motif2 0.123505828	Motif3 0.035626681	Motif4 0.1573229	Motif5 0.022657815	Motif6 0.040376905	Motif7 0.165805443
ttctcttc	agtaaagaa	ctgttctt	ttcttatct	acatggatt	ttcttgaaa	tttctatc
ttctcttc	agtaaagaa	tgtgttctt	ttcttatct	acatgaatt	ttcttgaaa	tttctatc
tttctctg	agagaagaa	ctgttctt	ttttttct	acatgaatt	ttcttgaaa	tttttttc
tttctctc	agaaaagac	cttctctt	ttctttct	aaatgaatt	ttctcaaaa	tttctttc
	agaaaagaa	ctgtctctt			ttctcaaaa	
					ttcttaaaa	

Motif8 0.18280823	Motif9 0.413759605	Motif10 0.120112811	Motif11 0.039924503	Motif12 0.413759605	Motif13 0.039924503
aaagaagta	cctcttctt	tagggitta	ttgttctg	cctcttctt	ttgttctg
aaagaagaa	ctgttctt	tagggtaa	ttgttctg	cctcttctt	ttgttctg
agagaagaa	cttcttctt	tagggtttc	tttctctg	cttcttctt	ttgttctta
aaagaagaa	ctgttctt	tagggtttc	ttgttctta	ctgttctt	ttcttctg
	cttcttctt		ttcttctg	cttcttctt	ttgtcttg
			ttgtcttg		

Fig. S3

Subfamily: SEP1-SEP2, size: 9, allowed mutations: 2, losses (only motifs shared between Arabidopsis and poplar)



Motif5 0.002525913 **Motif41** 0.009311947 **Motif42** 0.161469921 **Motif61** 0.024015022 **Motif73** 0.038718097

agctagtac	ctctagcta	taaccctaa	aagtagaga	ctaacccta
agctagtac	ctctagcta	aaaccctaa	aagtaaaga	caaacccta
		aaaccctaa	aagcagaga	caaacccta
			aagtagaga	

Motif85 0.033892472 **Motif88** 0.024467424 **Motif144** 0.099113804 **Motif154** 0.016851986 **Motif164** 0.032686066

agtagagaa	cttaattag	aaacataaa	caaacatga	tatagttaa
agtaaagaa	cttaattag	aaacataaa	caaacatga	tatagataa
agtaaagaa			caaatatga	tatagataa

Fig. S3

Subfamily: SEP1-SEP2, size: 11, allowed mutations: 2, subsets

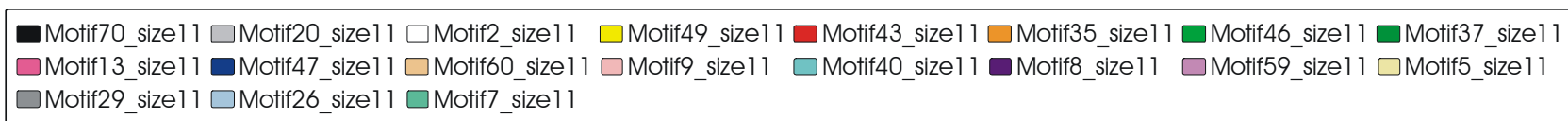
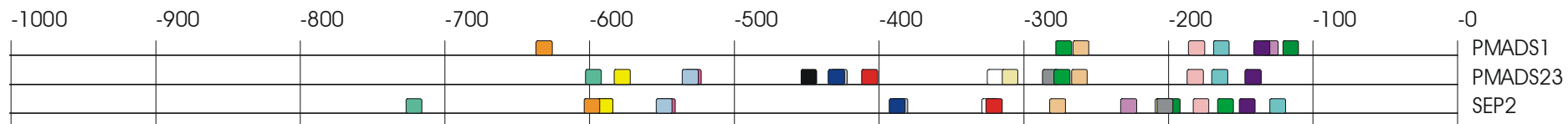
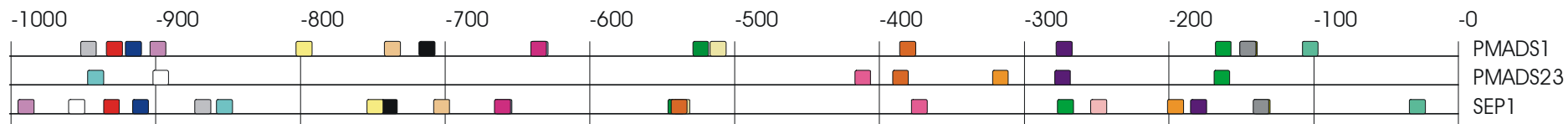


Fig. S3

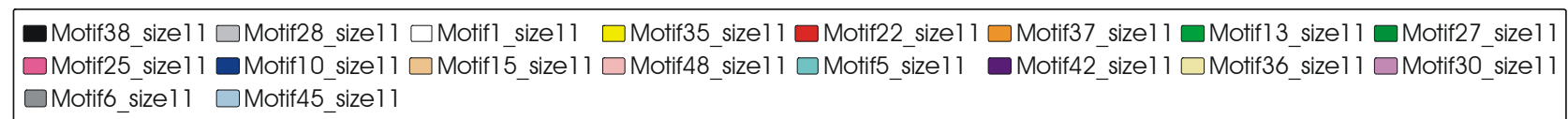
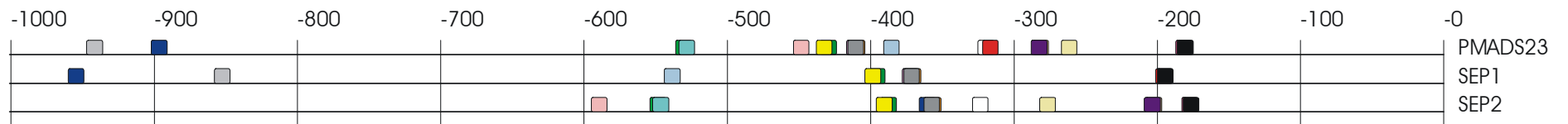
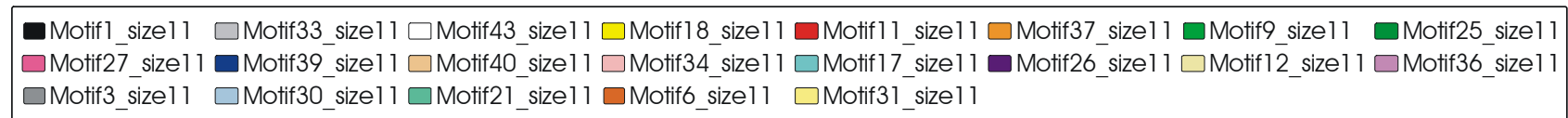
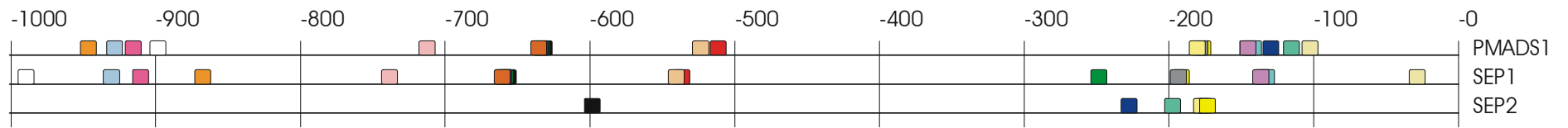
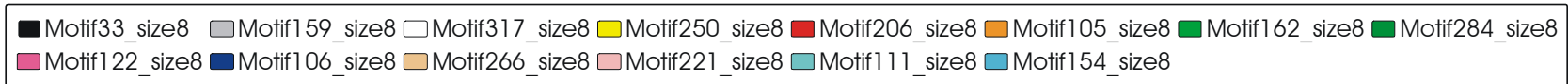
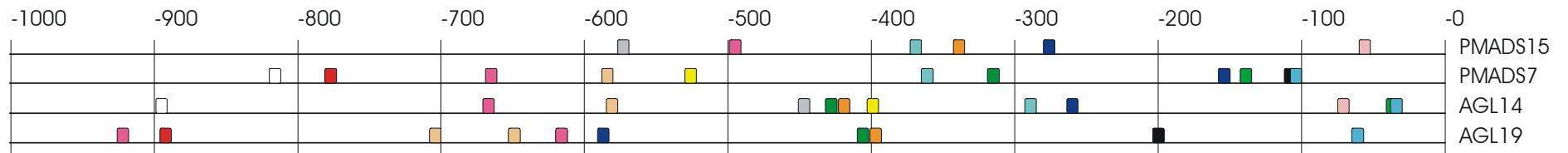


Fig. S3

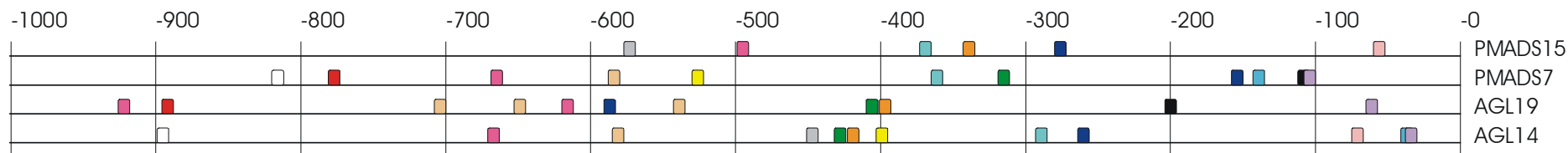
Subfamily: AGL14, size: 8, allowed mutations: 2



Motif1 0.116305092	Motif2 0.098095899	Motif3 0.058849999	Motif4 0.074307078
ttttgat	tttcatgt	catcaatc	caaactag
ttctgat	tttcatgt	cattaatc	caaactat
ttctgat	ttttatgt	catcaatc	caaattat
ttgtgat	ttttatgt	aatcaatc	caaactat
	tctcatgt		
Motif5 0.302280138	Motif6 0.164372836	Motif7 0.129010056	Motif8 0.412402398
tttattgt	tctacttt	tcatcaat	agaagaaa
tttttat	tataattt	tcattaat	agaagaaa
tttattat	tctaattt	tcataaat	agaagaaa
tttaatat	tctaattt	tcataaat	agaaaaaa
tttattat			

Fig. S3

Subfamily: AGL14, size: 8, allowed mutations: 2, losses (only motifs shared between Arabidopsis and poplar)



Motif33 0.184542439 **Motif105** 0.267595961 **Motif106** 0.118680204 **Motif111** 0.139076008 **Motif122** 0.156003394 **Motif154** 0.114570883 **Motif159** 0.195437794

attcaaat	tagggttt	caatatct	taatcttt	tgccaaaa	aaataact	ttgttatt
attcaaat	tagggctt	caatttct	taatctat	tacaaaaa	aaataact	ttgttatt
	tagggttt	caatttct	taatcttt	tacaaaaa	aaataactg	

Motif162 0.189631965 **Motif206** 0.116455892 **Motif221** 0.271742982 **Motif250** 0.088897052 **Motif266** 0.040716207 **Motif284** 0.129010056 **Motif317** 0.045994234

tcaaaata	atatgata	tttccatt	catttcaa	tatagatt	tcacaaat	gtagtatt
tcaaaata	atatgata	tttccatt	catttcaa	tatagact	tcataaat	gtagtatt
				tatagact	tcataaat	

Fig. S3

Subfamily: AGL14, size: 8, allowed mutations: 2, losses, subset

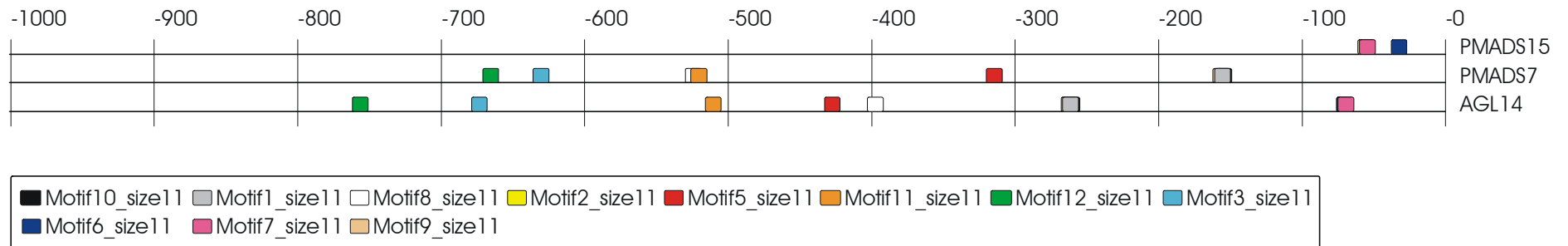
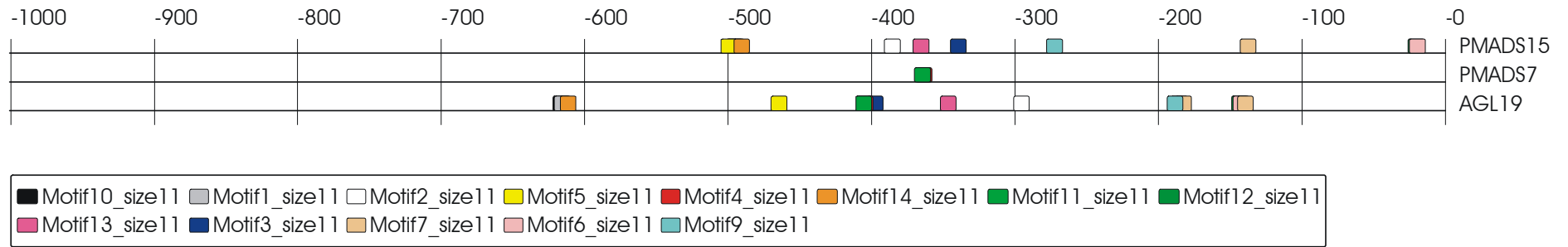


Fig. S3

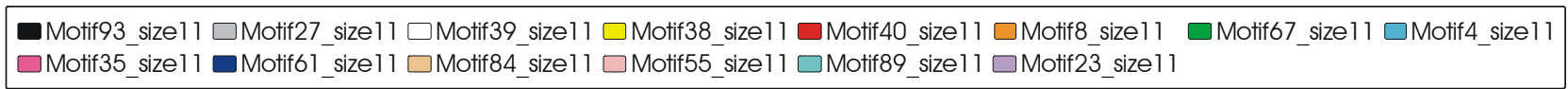
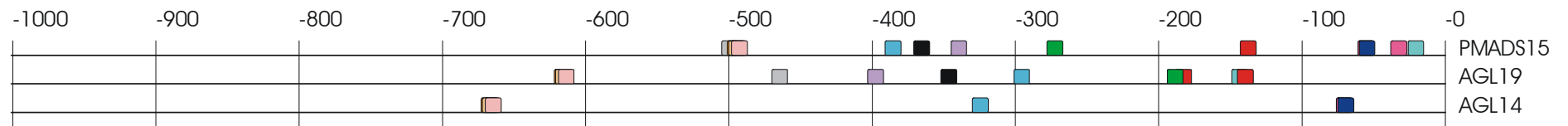
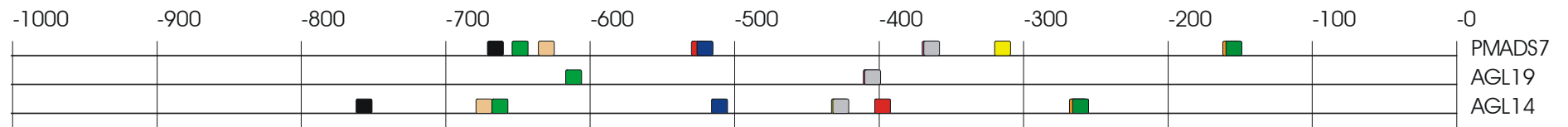
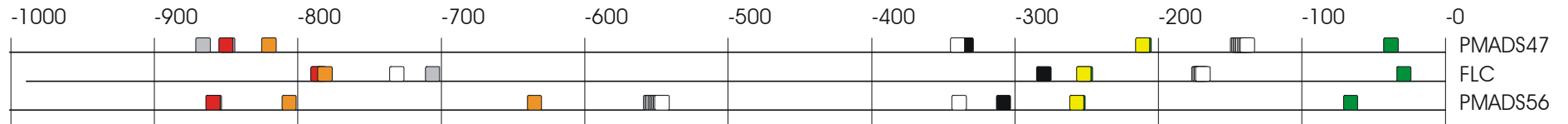


Fig. S3

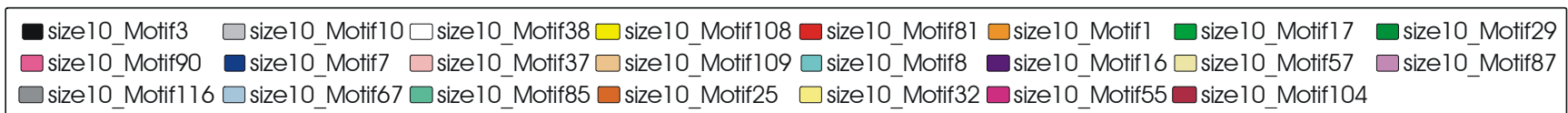
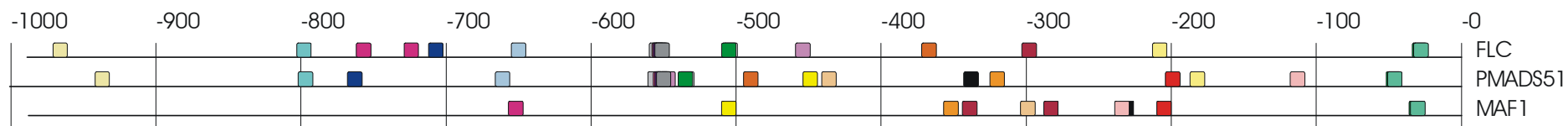
Subfamily: FLC, size: 10, allowed mutations: 2



Motif1 0.065937635	Motif2 0.007389238	Motif3 0.004222421	Motif4 0.015343978	Motif5 0.014778475	Motif6 1.518488325	Motif7 0.072082767	Motif8 0.002865215
taaaaataa	acacgtggca	aaattagggc	aataattaat	tacacgtggc	aaaaaaaaa	aaaaataat	aaaagtagca
taaacaataa	acacgtggca	aaattagggc	aatatctaata	gacacgtggc	aaaaaaaaa	aaaatataat	aaaaggatca
taaaaagaa	acacgtggca	aaattaggtc	aataactaat	aacacgtggc	aaaaaaaaa	aaacaataat	aaaaggagca
					aaaaaaaaa	aaaaaagaat	
					aaaaaaaaa		
					aaaacaaaa		

Fig. S3

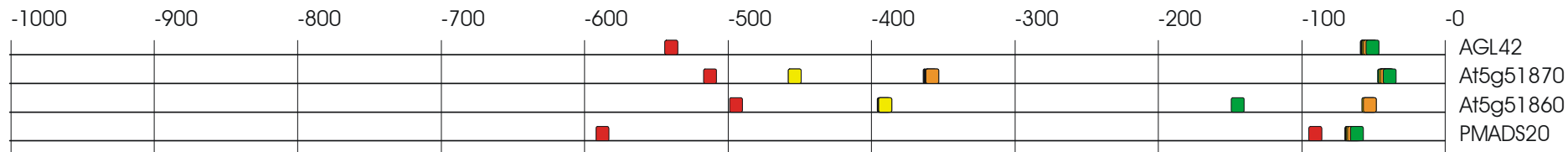
Subfamily: FLC, size: 11, allowed mutations: 2, losses (only motifs shared between Arabidopsis and poplar)



Motif1 0.005617329 cactacttc ctctacttc	Motif3 0.001206406 accgactgga accgactga	Motif7 0.080301409 caaaaaagaa caaaaaataa	Motif8 0.026088533 agaagaaatt agaagtaatt	Motif10 0.021413709 tgaaaaacac tgaaaaaac	Motif16 0.071818865 aaaacacatt aaaacaaatt	Motif17 0.004222421 aaattagggc aaattagggc aaattaggtc	Motif25 0.003581518 aggtctttc aggtctttc
Motif29 0.083355124 ttgttttta attgtttta	Motif32 0.043430621 atatttggt atttttggt	Motif37 0.001621108 ctaaccgact ctaadcgact	Motif38 0.014439173 ttgttttac ttgttttac	Motif57 0.037134689 aattgtatt aaattgtatt	Motif67 0.013157367 tgtatttag tgtcttttag	Motif81 0.002563613 aacgacaagc aactacaagc	
Motif85 0.002375112 aattagggca aattagggca aattaggtca	Motif87 0.050254356 caaatttaa caaatttaa	Motif90 0.093194874 aaaaacacat aaaaacaaat	Motif108 0.003355317 aaacgtattg aaacgtatgg	Motif109 0.038227994 taaaaagaga caaaaagaga	Motif116 0.055268481 aaacacattt aaacaaattt		

Fig. S3

Subfamily: AGL42, size: 9, allowed mutations: 2

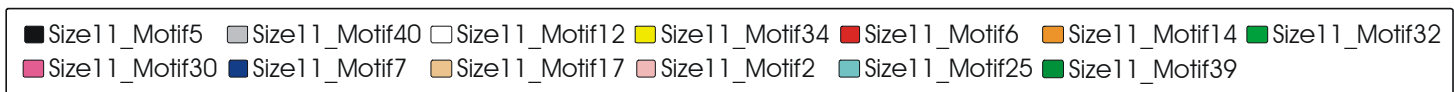
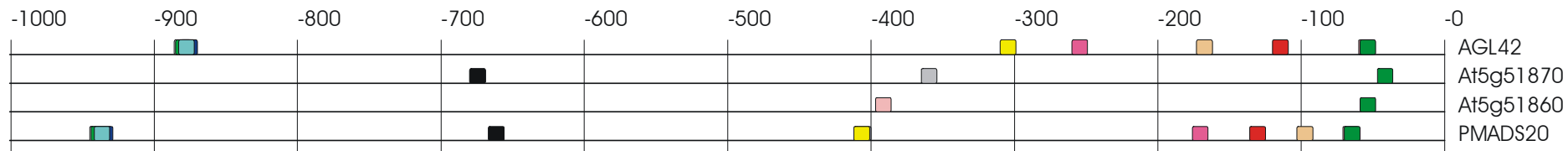


Motif7_size9
 Motif4_size9
 Motif6_size9
 Motif5_size9
 Motif3_size9
 Motif1_size9
 Motif2_size9
 Motif8_size9

Motif1 0.054702978	Motif2 0.015758680	Motif3 0.304806050	Motif4 0.054702978
tagggttc	gggttcat	tctttttt	tagggttc
tagatttc	gggttcaa	tctgtttt	tagggttc
tagggttc	gggttcaa	tctatttt	tagggttc
tagggttc	gggttcca	tctttttt	tagggttc
tagggttc	gggttcaa		
Motif5 0.161469921	Motif6 0.161469921	Motif7 0.050555957	Motif8 0.124787634
ttagggtt	ttagggtt	tctagggt	ttagggtt
ttagggtt	ttagattt	tctagggt	ttagggtt
ttagggtt	ttagggtt	ttagggtt	gtagggtt
ttagggtt	ttagggtt	tctagggt	gtagggtt
	ttagggtt		

Fig. S3

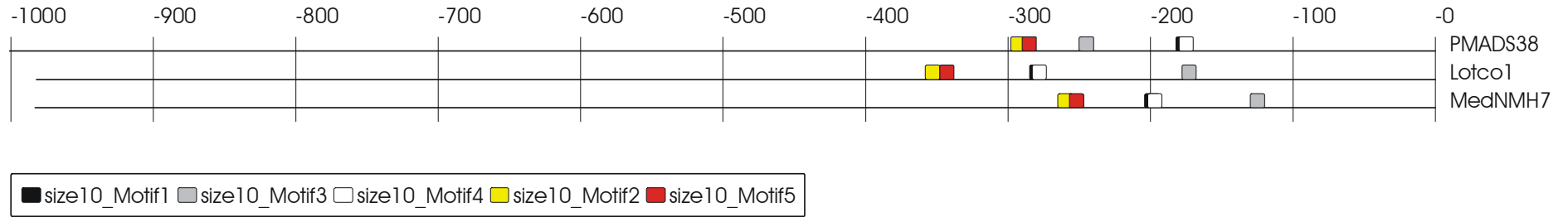
Subfamily: AGL42, size: 11, allowed mutations: 2, losses (only motifs shared between Arabidopsis and poplar)



Motif2 0.023223318	Motif5 0.001734208	Motif6 0.002073510	Motif7 0.003129115	Motif12 0.014665374	Motif14 0.004599423	Motif17 0.000904804
ctttagggtt	cttaatttac	atttggtgaga	tctcaatgata	tgttttctcaa	ttctcaatgat	tactagcttct
gtttagggtt	cttaatttac	attcggtgaga	tctcaattata	tttttctcaa	ttctcaattat	tactagcttat
Motif25 0.007276137	Motif30 0.011724759	Motif32 0.010028251	Motif34 0.005428827	Motif39 0.017304388	Motif40 0.016097981	
tttctcaatga	ttgtaaaattt	tgtttctcaat	atttctagggtt	tttagggttc	ttctagggtt	
tttctcaatta	ttgtagaattt	tttttctcaat	atttctagggtt	tttagggttc	ttctagggtt	
				gttagggttc		
				gttagggttc		

Fig. S3: Motifs detected through FootPrinter in the promoters of “many” Arabidopsis and poplar MADS-box genes. Next to every motif, its occurrence per 1kb of random promoter sequence is mentioned.

a. Three organisms



a1. Arabidopsis-Brassica-Solanaceae

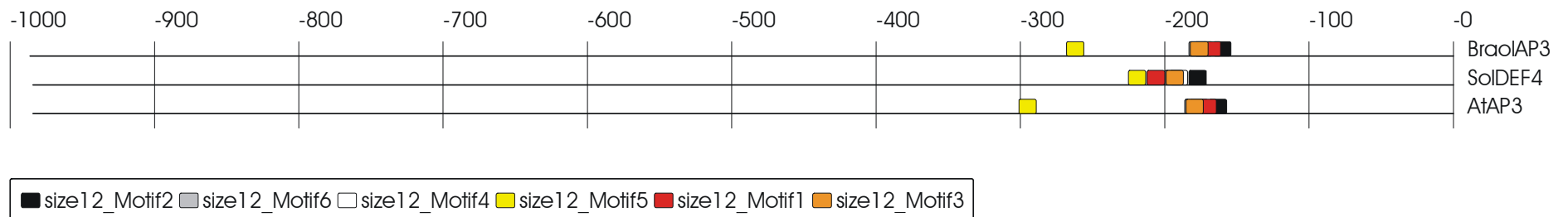
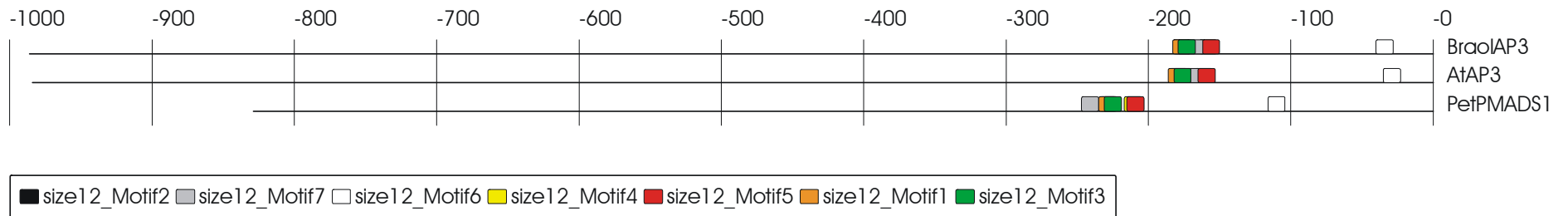


Fig. S4

a2. Arabidopsis-Brassica-Salicaceae/Fabaceae

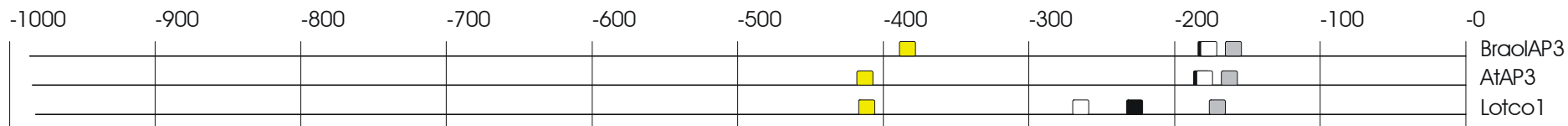
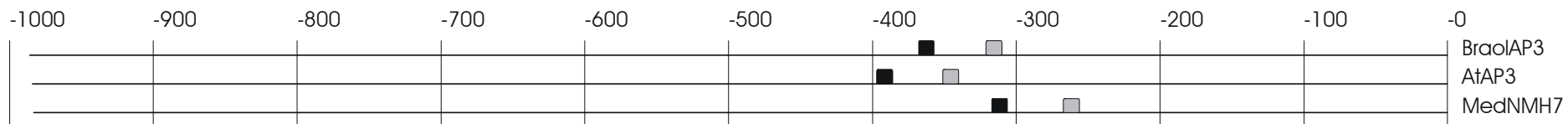
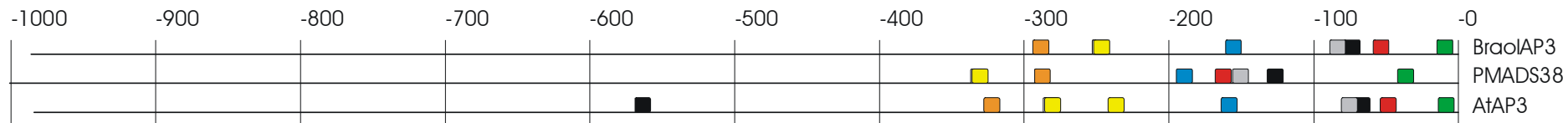


Fig. S4

a3. Arabidopsis-Salicaceae/Fabaceae-Solanaceae

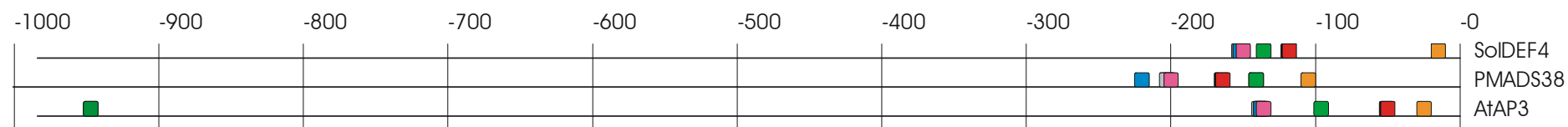
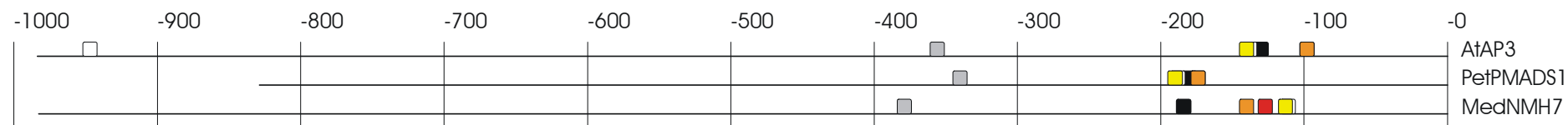
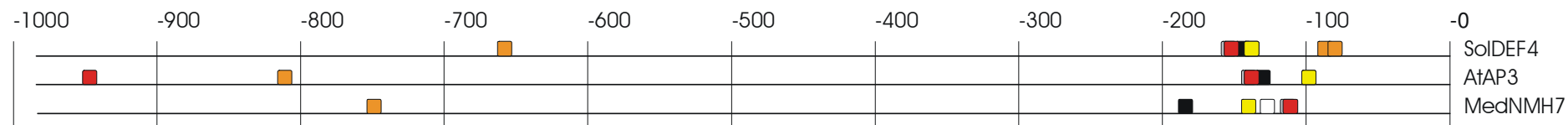
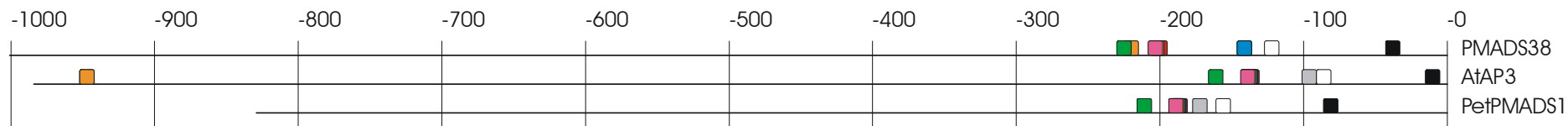


Fig. S4



a4. Arabidopsis-Salicaceae/Fabaceae

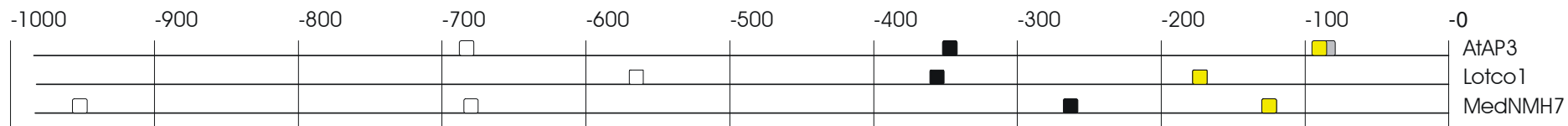
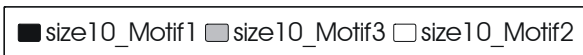
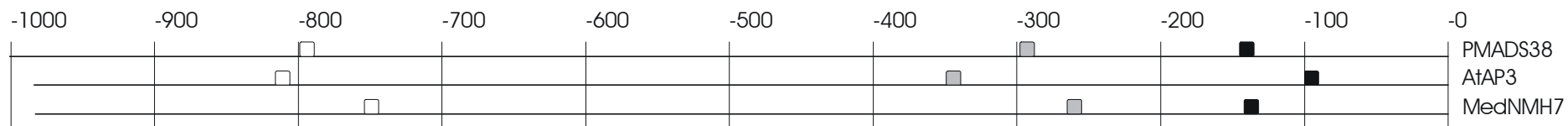


Fig. S4

a5. Arabidopsis-Solanaceae

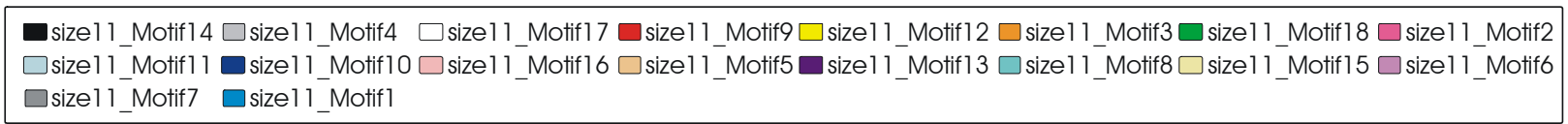
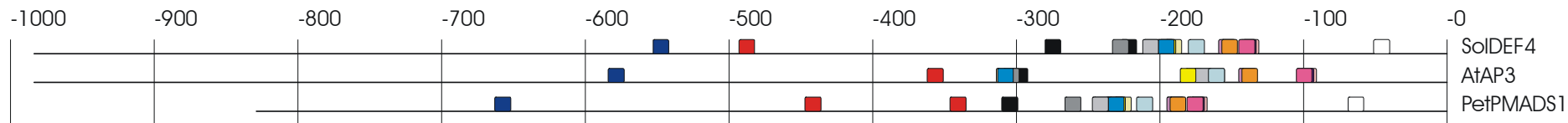
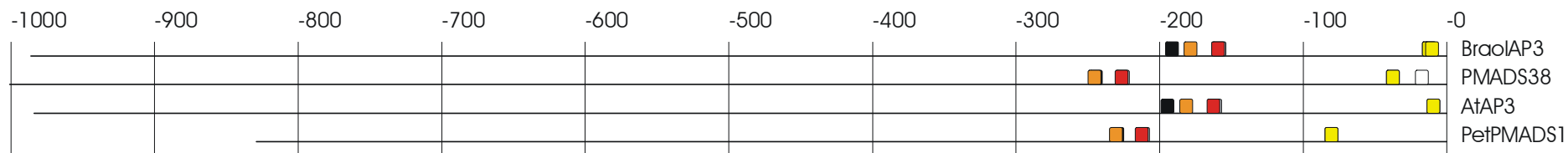


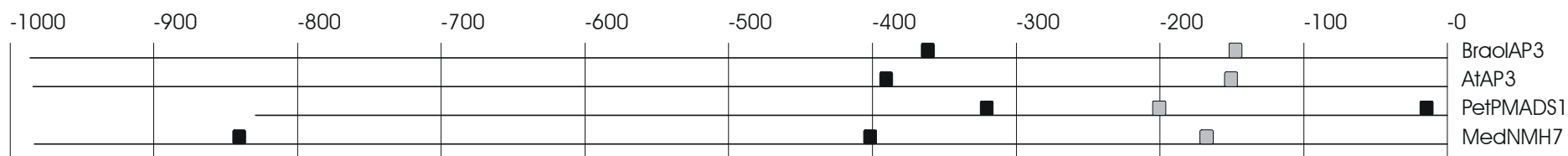
Fig. S4

b. Four or more organisms

b1. no motif losses allowed



■ size9_Motif5 ■ size9_Motif4 □ size9_Motif2 ■ size9_Motif6 ■ size9_Motif1 ■ size9_Motif3



■ size9_Motif2 ■ size9_Motif1

Fig. S4

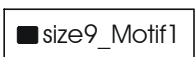
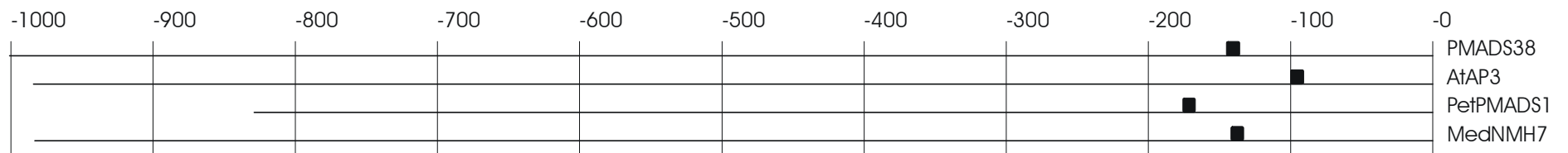
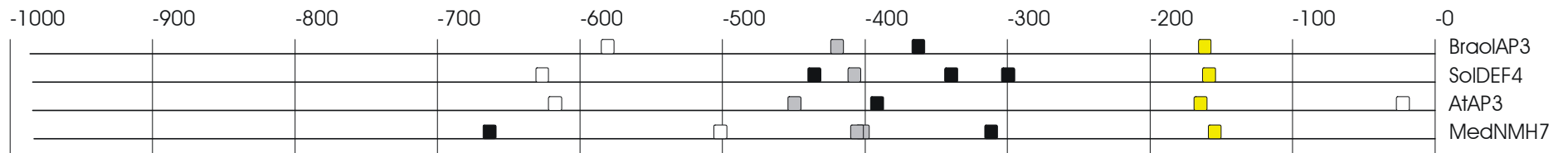
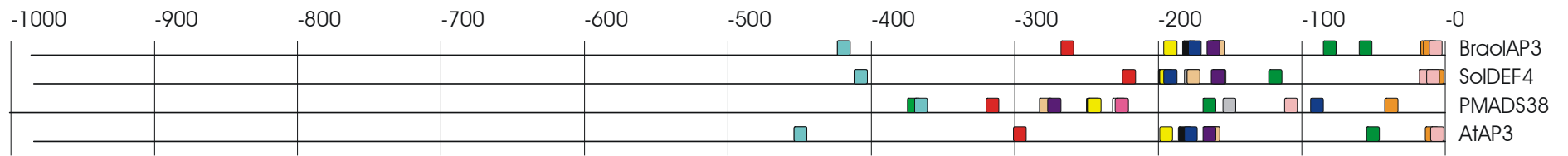
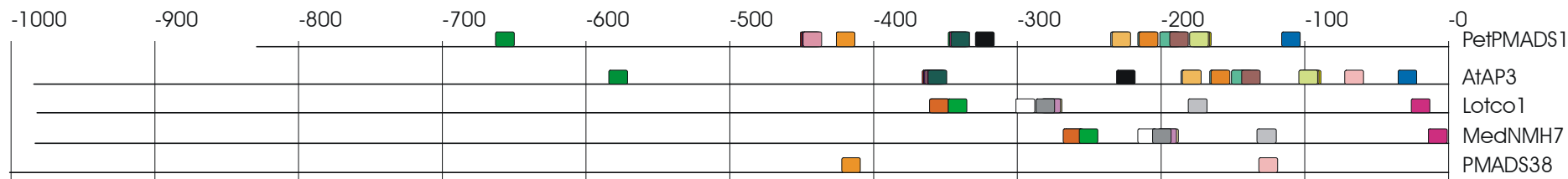


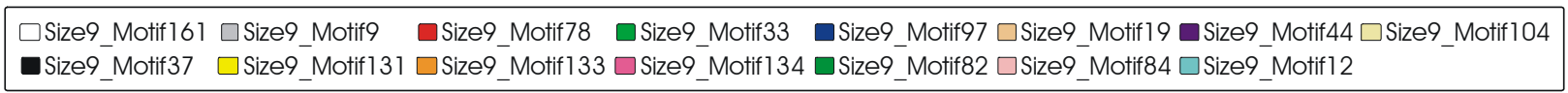
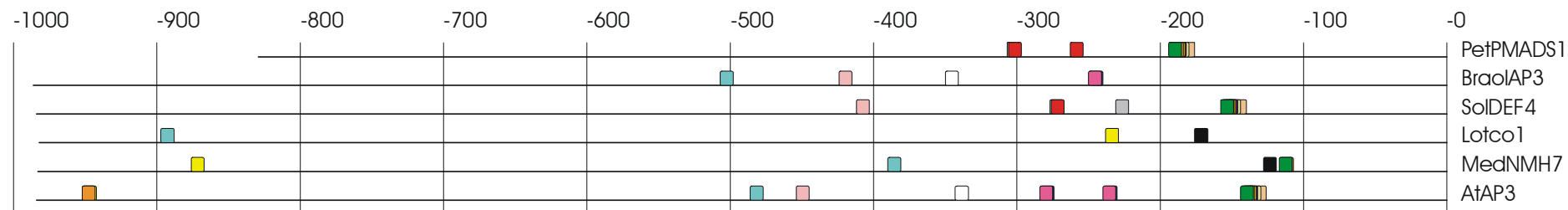
Fig. S4

b2. motif losses allowed



Motif1 0.00599433	Motif2 0.000678603	Motif3 0.000226201	Motif4 0.000452402	Motif5 0.000377002	Motif6 0.000339302	Motif7 0.000188501	Motif8 0.001017905
aacatataatct	caactttatcttt	ttataagaaacc	gttaataaattga	aactccatctctc	caactccatctct	acctttcatggat	taattgtataaaa
aacatatttatat	ctgctttatcttt	ttatacaaaacc	gttaataaattca	aactccatctttc	taactccatcttt	acctttcacggtt	taaattgtataaaa
Motif9 0.000414702	Motif10 7.54E-05	Motif11 7.54E-05	Motif12 0.000150801	Motif13 0.001621108	Motif14 0.00203581	Motif15 0.000263901	Motif16 0
ctttccattttta	ggcaataactttcc	ctccgtaataaaa	gcaataactttcca	ttcttctcattat	tcttcaacaaaaa	aaaagcatggaca	ggacggaagcaa
ctttccattttta	ggcaagcctttcc	caccgataataaa	gcaagcctttcca	ttcttctctttat	tctacaagaaaaa	aagagcatgcaca	tgacggaagtaa
Motif17 0.000263901	Motif18 0.000678603	Motif19 0.000490102	Motif20 0.000603203	Motif21 0	Motif22 0.000904805	Motif23 0.000452402	Motif24 0.000716304
tccgtaataaat	acatttataagaa	gaaatataatagat	actttccattttt	gacggaagcaag	ccgtaataaatt	actccatctctct	ttcatcaactct
accgataataaat	acagttataacaa	gaattagatagat	cctttccattttt	gacggaagtaaa	aagtaataaatt	actccatctttct	ttatcaaaattct
Motif25 0.007389238	Motif26 0.000226201	Motif27 0	Motif28 0.000226201	Motif29 0.000339302	Motif30 0.001017905	Motif31 0.000603203	
aattaaaaaatc	tataagaaccct	aagggtccccact	cctttcatggatt	ccgtaataaatt	tttcatcaactc	cgtaataaattg	
aattaaagaata	tataacaaccct	agggtccccact	cctttcacggttt	ccgataataaatt	ttttcaaaattc	agtaataaattc	

Fig. S4



Motif9 0.008557944	Motif12 0.115400287	Motif19 0.020735105	Motif33 0.056512587	Motif37 0.044523927	Motif44 0.057794394	Motif78 0.005278027	Motif82 0.018209193
acaagtgac	ttttctta	ttagtaac	ttccattt	ttatcttg	tccatttt	caagtgact	ctttcatt
acaagtgac	ttttgtta	ttagtaac	ttccattt	ttatctata	tccatttt	caagtgact	ctttcatt
acaagtgac	ttacttta	ttagtaac	ttccattt	ttatctta	tccatttt	caagtgact	atttcatt ctttcatt
Motif84 0.047389141	Motif97 0.011347758	Motif104 0.024354324	Motif131 0.057417392	Motif133 0.056512587	Motif134 0.009048046	Motif161 0.016097982	
aaccaaac	tgtcttga	catttttag	ttccattt	ttccattt	gtgtcttgt	gctaaccaa	
aaccaaac	tgtcttga	catttttag	ttccattt	ttccattt	gtgtcttgt	ggaaaccaa	
aaccaaac	tgtcttga	catttttag	ttccattg	ttccattg	gtgtcttgt	gcaaaccaa	
			tccatttt	ttccattt			

Fig. S4: Motifs detected through FootPrinter in the promoters of Arabidopsis and poplar AP3 homologs. a. Promoter comparisons between three organisms (belonging to different plant lineages). Sequences of motifs are available upon request. b. Promoter comparisons between more than three organisms.

Protein sequences of Poplar MADS-box genes used in this analysis.

```
>PTAP1-2
MGRGRVQLKRIENKINRQVTF SKRRTGLLKKANEISVLCDAEVALIVF SHKGLFEYSTD
DSYILERYERYSYAERQLVATDLD SQGNWTL EYNRLKAKVELLQRNHRNYLGEDLDSMSL
KELQNLEQQIDTALKHIRARKNHLMSQSI SELQRKEKAIQVQNNMLVKQEEAPEARNEL
GHTLEPIYSFHLGGYGA
>PTAP1-1
MGRGRVQLKRIENKINRQVTF SKRRTGLLKKAEISVLCDAEVALIVF SHKGLFEYSTN
ACMEKILERHERYSYAERQLVATDLD SQGNWTL EYNRLKAKVELLQRNHRNYLGEDLDSV
SLKELQNLEQQIDTALKLIRERKNHLMYQSI SELQIKLYPIG*RQNKSYMNVRRSEPYTQ
VEKAIKEQNN
>PMADS6
MGRGRIQLKRIENKINRQVTF SKRRSGLLKKAEISVLCDAEVALIVF STKGKLF EYATD
SCMERILERYERYSYAERQLLANDDPENHGSWTLEYAKLKARVDVLQRNQRHFMGEDLDS
LNIKELQNLEHQIDSALKHVRSRKNQLMYESI SELQKK
>PMADS14
MGRGRVQLKRIENNISRQVTF SKRRTGLLKKAEISVLCDAVAVIVF STKGKLF EYSTD
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