Appendix Table of Content

Additional references (Appendix Table S1)

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Cerutti H, Osman M, Grandoni P and Jagendorf AT (1992) A homolog of Escherichia coli RecA protein in plastids of higher plants. Proc. Natl. Acad. Sci. USA. 89:8068–8072.

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Pfalz J and Pfannschmidt T (2015) Plastid nucleoids: evolutionary reconstruction of a DNA/protein structure with prokaryotic ancestry. Front. Plant Sci. 6:220. See artwork on the cover of the eBook: The proteins of plastid nucleoids – structure, function and regulation.

Appendix Legends

Appendix Figure S1| (Related to Figure 1) Genetic analysis of the *pap8-1* mutant. A The two phenotypic classes [WT] and [albino] from a *pap8-1*/+ segregating progeny and their ratio in **B** calculated from N=604 plants. **C** Box plot (Min, 1st quartile, median, 3rd quartile, Max) of cotyledon width 5 days after germination (DAG) in wild type and albino plants grown *in vitro* under 30 µmol.m^{-2}.s^{-1} of white light.

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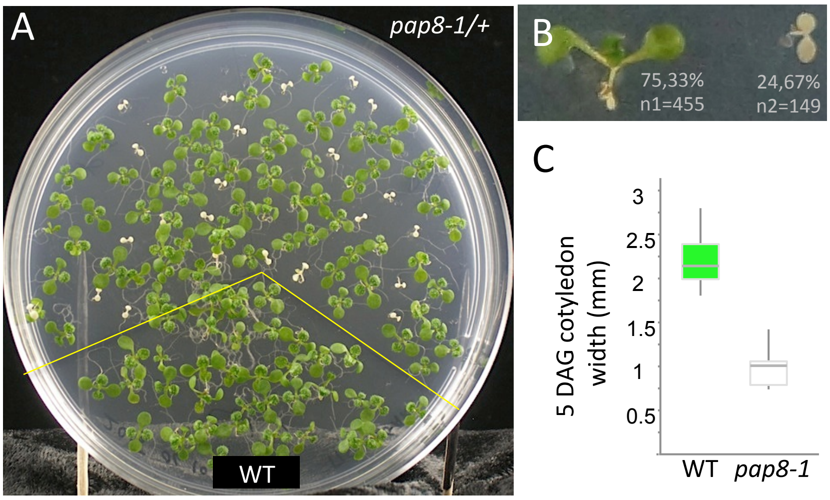
Appendix Table S2| Output from PlantPan3: Search for transcription factors binding sites. Annotations as on the corresponding website; position is given relative to the transcriptional initiation site.

Appendix Figure S1



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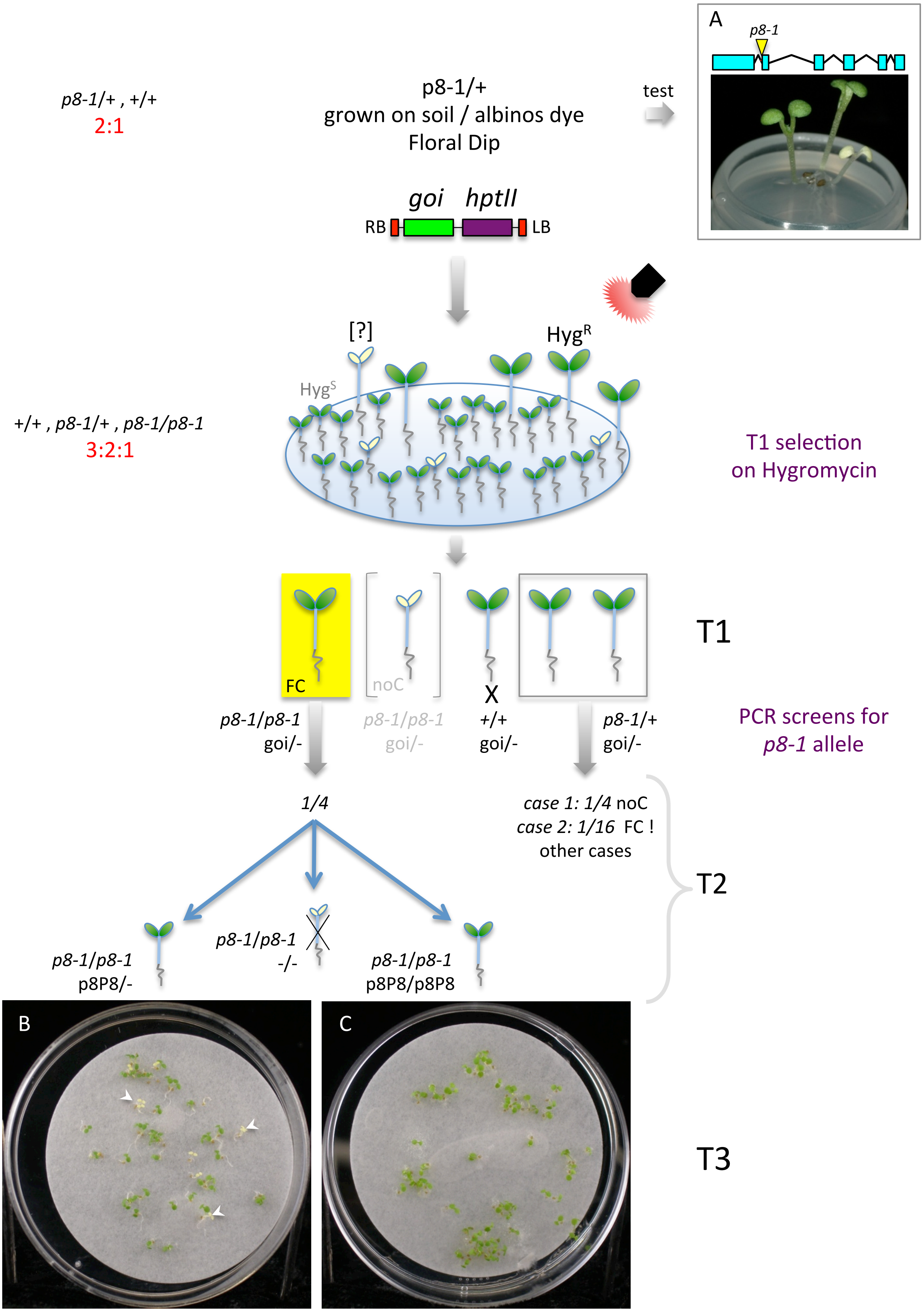

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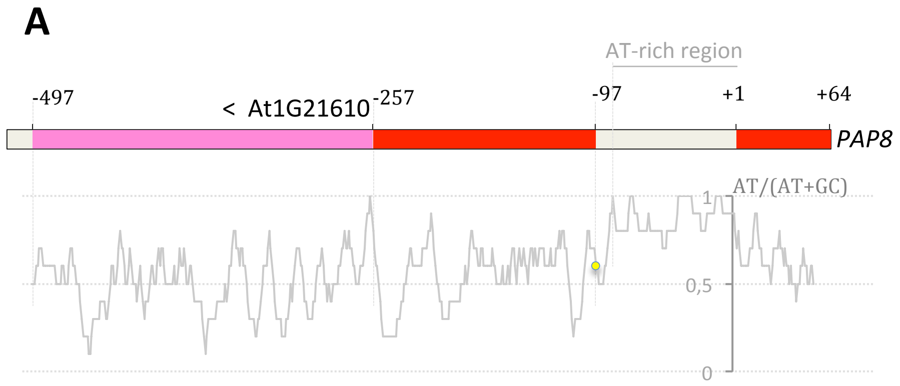

B

TF Family	occ(-497-97)	occ(-97+1)
AP2/ERF	103	6
ARF	4	0
AT-Hook	2	20
bHLH	4	0
bZIP	10	5
C2H2	1	1
C3H	6	3
Dehydrin	17	0
DOF	28	39
EIN3	1	0
GATA	38	1
HD-ZIP	38	21
MYB	17	9
NAC	3	1
NF	17	2
SANT	27	6
Trihelix	18	0
WRKY	38	0
ZF-HD	7	21

C >Promoter_PAP8^{-497}.Selected_Binding_Sites_PlantPan3.0

```
-497 CGGTGCAATTCGAAACTCAAGGTTAGGGTTAGCATTAGGAGGCGGGTCGGGAACCGAAGCCGATAAACCATTGACCTTACCAGCATCCCTCATAAGCTTC -398
                                                                            <----------->        <<<<<<
                                                                            WRKY  >>>>>          m0271_bZIP
                                                                                  m0271_bZIP
-397 TTCCACGAAACATACGTCGTATCCCCTGGCCGAAGCTCCACCTTGAGTAATTTCCGATCACCGGCCGTTAAAACCTTCGGCGACGCTCTCAACAATTCGC -298
                      >>>>>>>>                                                      <<<<<          >>>>>
                      m0410_bHLH                                                    m0271_bZIP     m0271_bZIP
                       <----->                                                                           <--------
                       bZIP                                                                              AP2/ERF
-297 CGCCAATAGAACCACCACTCATCTCATTAACTTCCGACATtaataattcgggtcgggtcgggtcggatcagtttgatccactatatactaacccctgggt -198
           ------->                <--------------------->
           AP2/ERF                 HD-ZIP/ AP2/ERF
           >>>>>                      <<<<<<<<<<<<<<<<
           m0271_bZIP                 m0805_bHLH
                                          >>>>>>>>>>>
                                          B3/ARF
                                            >>>>>
                                            m0271_bZIP
-197 tcgagacggattgatctaaacagcaatcaagagagtggaatcgatgaatcgatgtagagaaactgaaactgagaagaaaaagttgcgcgggataccaaaa -98
              >>>>>                                                                                  TIS<
              m0271_bZIP
              <<<<<<<<
              m0410_bHLH
-97 atgacgctcttaattatttcctaatttatttttgttgttttattcactaaaaaggattattattatattatatagtttttcttttttttttaattgtatt +03
           <------->                                                                                 >TIS
           bZIP
           <----------->
           HD-ZIP
+04 tttcctcgaaatatctaatccacagatagatagaacactctgtgagctttatccgcttc +63
```

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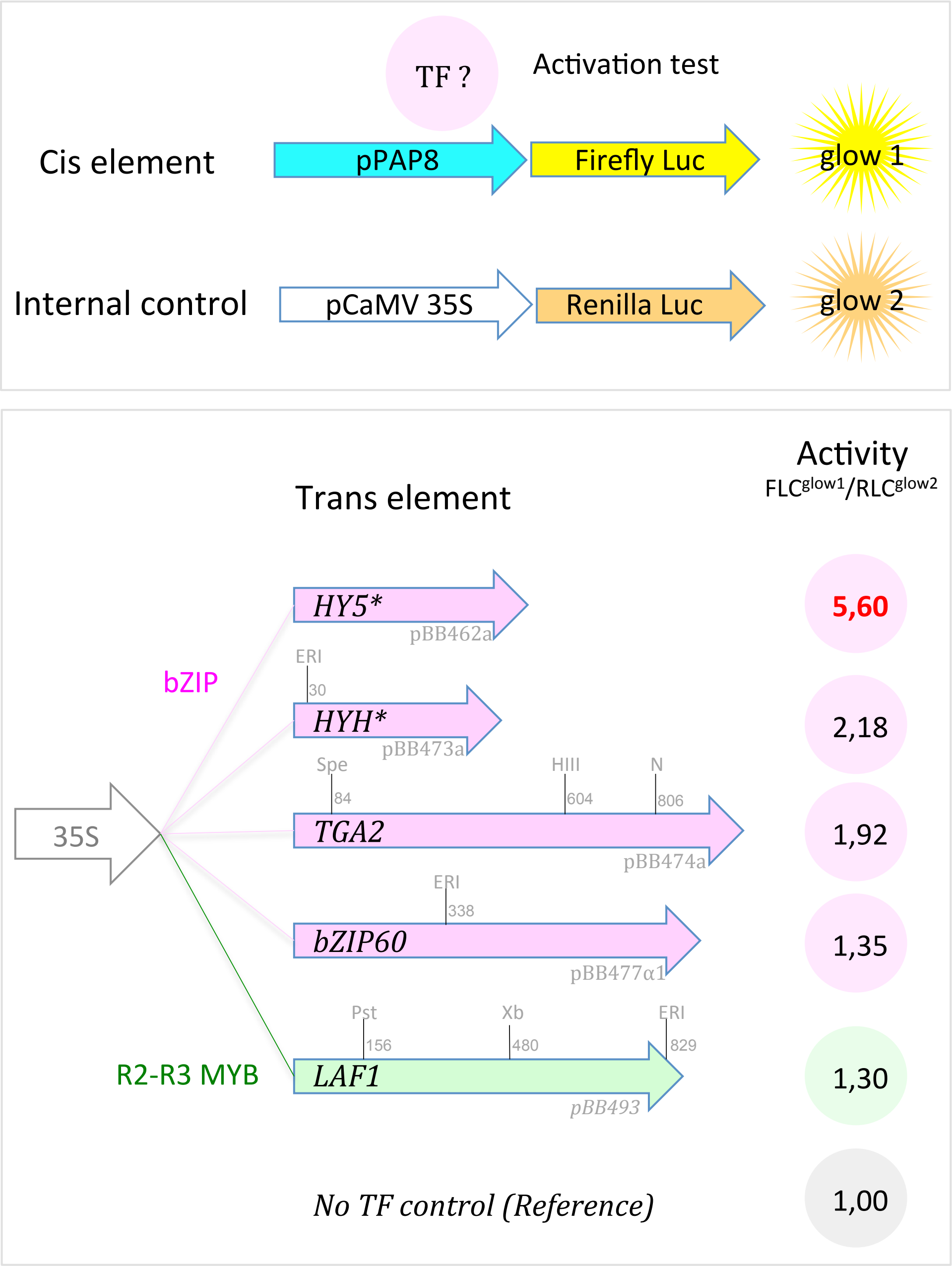

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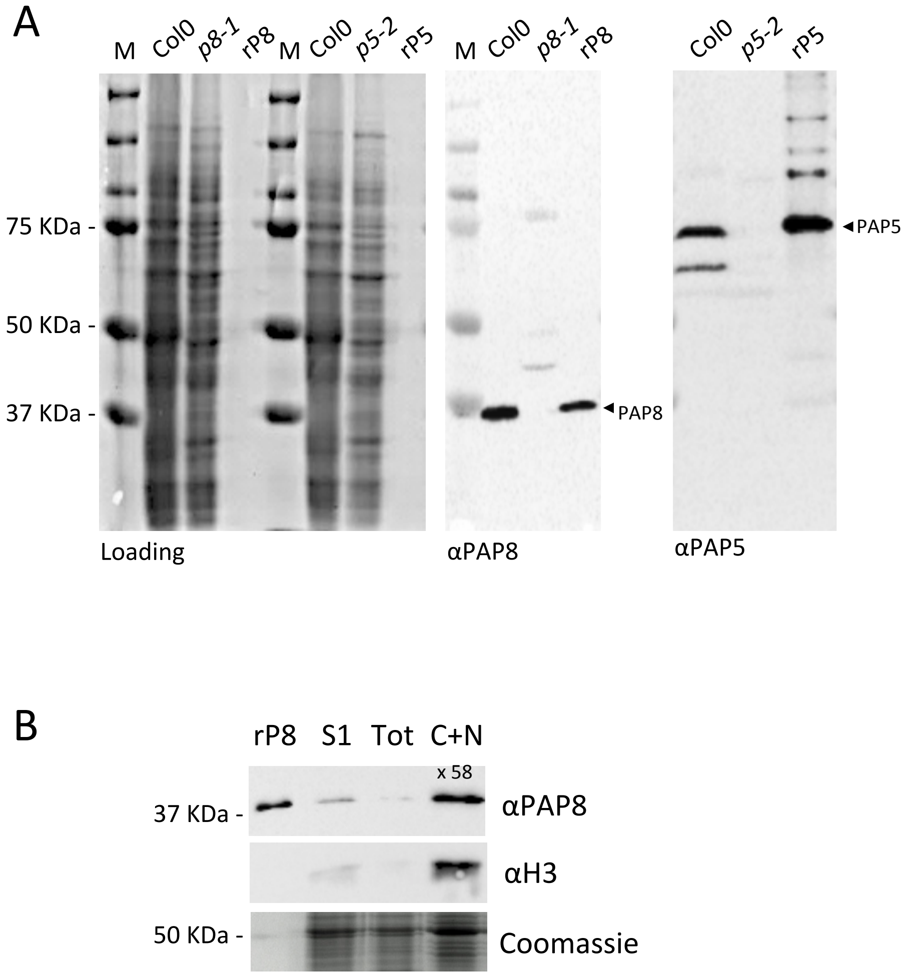

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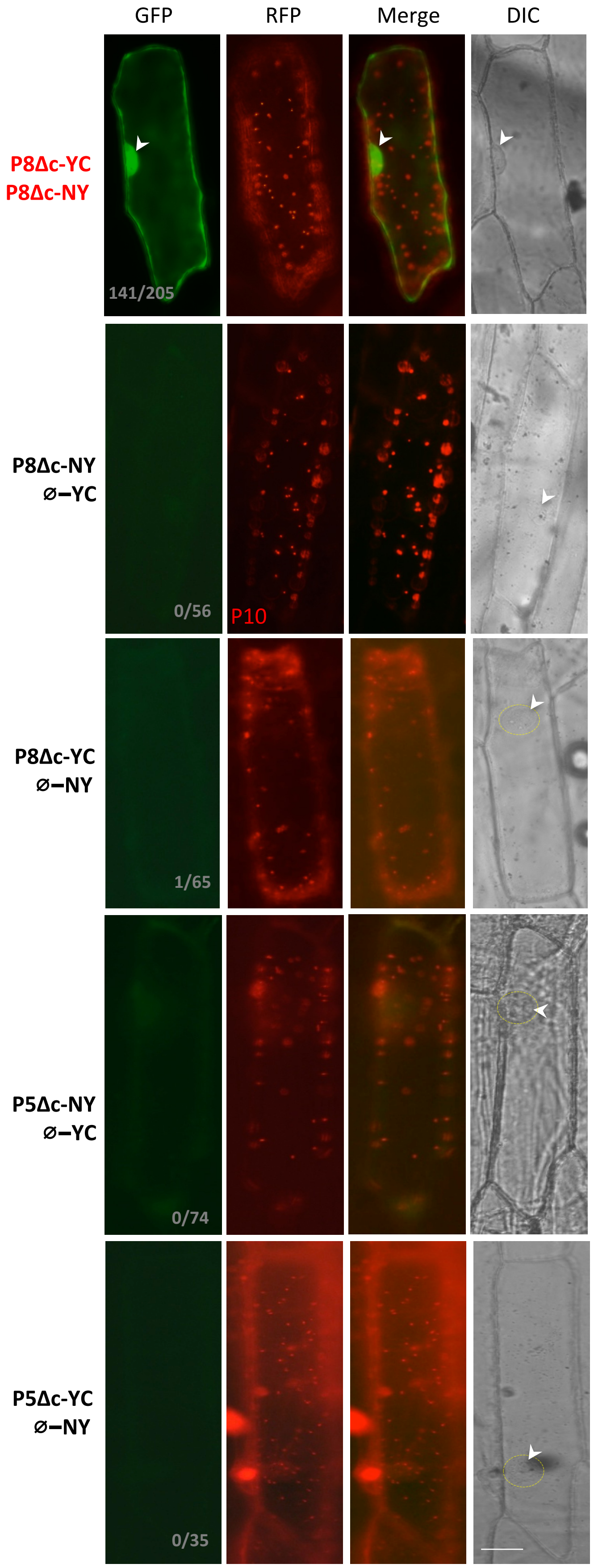

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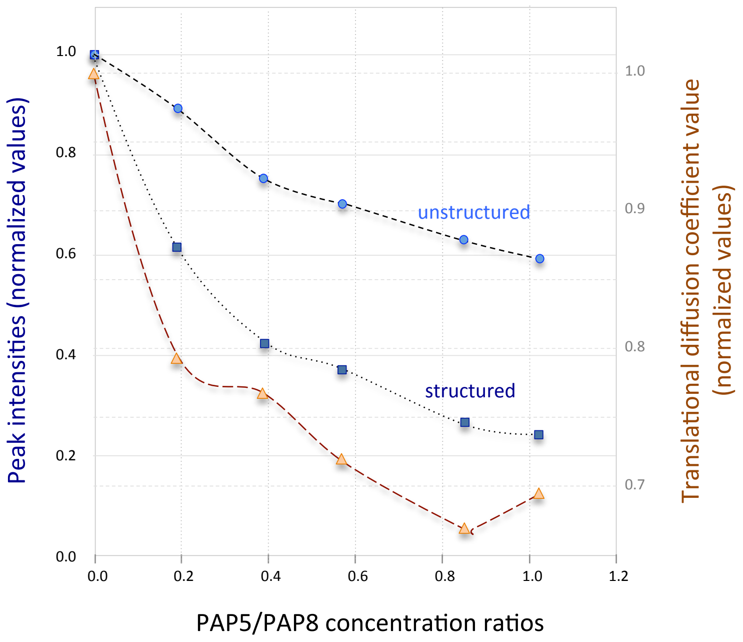

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Appendix Table S1

#	transgene	Plamsid id	bR	Plant R	genotype	Cloning Informations				
						fwd primer id	sequence (5'>3')	rev primer id	sequence (5'>3')	Comments/Reference
A	*Functional complementation experiment*									
1	pPAP8::PAP8	pBB389	spec	Hygro	*p8-1 or hy5-1*	oPAP8orf_FXN	ctcgagccATGGCGTCTTCCGCCGCTTCTCC	oPAP8_RXba	tctagaTTAGAACCAATTTGAGACACTGAAGTCTCG	All binary vectors in this study derive from pArt27, Gleave *et al.*, 1992
2	pPAP8::PAP8^{NLSm5}	pAi10			*p8-1*	oNLSP8mF	GGGAGGAGGAGGAGGGGATGGGGGGGATGACTTGC	oNLSP8mR	GCAAGTCATCCCCCCCATCCCCTCCTCCTCCTCCC	
3	pPAP8::PAP8$^{\Delta nls}$	pAi14				recloned from pKP17 and pKP19 using oPAP8_Rxba				
4	pPAP8:PAP8$^{\Delta ctp}$	pAi15								
5	pPAP8^{-257}::PAP8	pAi11				see pBB346, fc1: tested positive in functional complementation see legend				
6	pPAP8^{-97}::PAP8	pAi16				see pBB380, fc2: tested positive in functional complementation see legend				
7	p35S::PBG	pRB1637		Kan		PhyB KpnI SmaI in pEZS-NL then NotI in pArt27 NotI				Quail lab
B	*Promoter deletion experiment*									
8	pPAP8::GUS (-1133)	pBB304	Spec	Hygro	Col-0	opPAP8_FSacI	gagctccgtttcaatctctactggatgc	oP8_RNco	5’-ccatgggaagcggataaagctcacagag-3’	Liebers *et al.*, 2018
9	pPAP8::GUS (-909)	pBB344				oP8_F257S	gagctccattgcaactatgtgaacc			
10	pPAP8::GUS (-729)	pBB345				oP8_F729S	gagctcgtcagagagcaataacaacag			
11	pPAP8::GUS (-497)	pBB349				oP8_F497S	gagctcggtgcaattcgaaactc			
12	pPAP8::GUS (-257)	pBB346				oP8_F257S	gagctctaataattcgggtcgggtcg			
13	pPAP8::GUS (-97)	pBB380				oP8_F97_S	gagctcatgacgctcttaattatttcc			
14	pPAP8::GUS (+1)	pBB381				oP8_F1_S	gagctcatttttcctcgaaatatctaatcc			
15	pPAP8::GUS (-97m3)	pBB468				oP8_F97mx3	gagctcataaaactcttaattatttcc			
16	pPAP8::GUS (Δ)	pBB328				pBB304 *EcoR*I *Hind*III Klenow fill in religated				
C	*trans-activation experiment*									
17	p35S::HY5	pBB462	carb	-	*transient expression in onion epidermal cells*	oHY5_FXho	ctcgagATGCAGGAACAAGCGACTAGCTC	oHY5_RXba	tctagaTTAAAGGCTTGCATCAGCATTAGAACC	
18	p35S::HYH	pBB473				oHYH_FXho	ctcgagATGTCTCTCCAACGACCCAATGGGAATTCGAGTTCG	oHYH_RXba	tctagaTTAGTGATTGTCATCAGTTTTAGGC	
19	p35S::TGA2	pBB474				oTGA2_FXho	ctcgagATGGCTGATACCAGTCCGAG	oTGA2_RXba	tctagaTtACTCTCTGGGTCGAGCAAGC	
20	p35S::bZIP60	pBB477				obZIP60_F_XN	ctcgagccATGGCGGAGGAATTTGGAAGC	obZIP60_R_Xba	tctagaTTACGCCGCAAGGGTTAAGATTTGG	
21	p35S::LAF1	pBB493				oLAF1_FXho	ctcgagATGGCGAAGACGAAATATGG	oLAF1_RXba	tctagaTTACGTCGTTGTTGATGGAG	
22	pPAP8::LUC (-1133)	pBB456				The different promoters from pBB304/380/468 were cloned in pLUC* using *Sac*I/*Nco*I sites				*Blanvillain *et al.*, 2011
23	pPAP8::LUC (-97)	pBB457								
24	pPAP8::LUC (-97m3)	pBB458								
25	**pKar6/pRLC***									
D	*Sub-cellular localisation experiment and complementation tests*									
26	pPAP8::0	pKP04	Spec	Hygro	cloning	oNdXNX1	catgcctcgagccatggt	oNdXNX2	ctagaccatggctcgagg	
27	p35S::PAP8ΔcTP-GFP	pKP15	carb	-	onion cells					
28	p35S::PAP8Δnls-GFP	pKP13								
29	p35S::PAP8ΔΔ-GFP	pKP14								
30	p35S::PAP8-GFP	pKP16				oPAP8orf_FXN		oPAP8_RBHI	ggatccaagaaccaatttgagacactgaagtctcg	
31	p35S::PAP8-GFP	pKP34	spec	Hygro	wt & *p8-1*					
32	pPAP8::PAP8-GFP	pKP20								
33	p35S::PAP8ΔcTP-GFP	pKP33				oPAP8ΔcTP_FXho	ctcgagatggctgatggaggtggagcgg			
34	pPAP8::PAP8Δctp-GFP	pKP19								
35	p35S::PAP8Δnls-GFP	pKP31				oPAP8orf_FXN		oPAP8ΔNLS_PmlI	cacgtgcggaactgtcaccagaac	
36	pPAP8::PAP8Δnls-GFP	pKP17								
37	p35S::PAP8ΔΔ-GFP	pKP32				oPAP8DcTP_FXho		oPAP8ΔNLS_PmlI		
38	pPAP8::PAP8ΔΔ-GFP	pKP18								
39	p35S::PAP8NLSm5-GFP	pAi09	carb	-	*onion cells*					
40	p35S::PAP10-RFP	pBB301				oPAP10orf_xho	ctcgagATGGCTCTTGTTCAATCCAGAAC	oPAP10orf_BH	GGATCCCCCCATCTCGTTGTCAATGATATCGTGC	Pfalz and Pfannschmidt, 2015
41	pRecA-RFP					plastid marker				Cerruti *et al.*, 1992
E	*Split YFP experiment*									
42	p35S::PAP8ΔcTP-YC	pRT12	carb	-	*onion cells*					
43	p35S::PAP8ΔcTP-NY	pSC01				GFP replaced by NY-YFP in pKP15				
44	p35S::PAP5ΔcTP-YC	pRT13				oP5DcTP_FX	ctcgagATGATGACAGACAGTGGAAAGTCCAG	oP5_RBH	GGATCCCAGGATCAGTCTCCTCTTC	
45	p35S::PAP5ΔcTP-NY	pBB526								
46	p35S::YC	pBB336								
47	p35S::NY	pBB335								
F	*Protein Production*									
40	HY5-H6	pBB543	carb	-	*for expression in Rosetta2*	oHY5fl_Fnco	ccatggcgcaggaacaagcgactagctc	oHY5_Rnot	gcggccgcaaggcttgcatcagcattagaacc	*Nco*I *Not*I in pEt21d
41	PAP8Δctp-H6	pAG21d				oPap8_Fnco	ccatgggcgctgatggaggtggagcggacg	oPap8_Rnot	gcggccgcgaaccaatttgagacactgaagtctcg	
42	H6-MBP-PAP5Δctp-H6	pAG08	kan			oPAP5_FNco	ccatgggcacagacagtggaaagtccag	oPAP5_Rnot	gcggccgcaggatcagtctcctcttcaaagtcc	*Nco*I *Not*I in pET-M41
43	MBP	pET-M40								

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Position	Matrix ID	Family	Strand	Similar Score	Hit Sequence	TF ID or Motif name	Gene name
-492	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0.8	GCAAT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;	
-489	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	-	0.8	ATTCG	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;	
-485	TF_motif_seq_0267	Trihelix	-	0.8	GAAAC	AT5G01380	
-485	TF_motif_seq_0261	(Motif sequence only)	+	0.8	GAAAC	SURECOREATSULTR11	
-484	TFmatrixID_1238	MYB-related	+	0.96	aaactcaaggtTAGGGttagc	AT1G72740	
-481	TF_motif_seq_0275	(Motif sequence only)	-	0.8	CTCAA	WBOXATNPR1	
-478	TF_motif_seq_0239	Dof	+	1	AAGGT	AT1G29160;AT1G64620;AT2G37590;AT3G21270;AT3G45610;AT3G47500;AT4G38000;AT5G39660;AT5G60200;AT5G60850;AT5G62940;AT2G46590;AT1G07640;AT1G21340;AT1G26790;AT1G47655;AT1G51700;AT1G69570;AT2G28510;AT2G28810;AT2G34140;AT3G50410;AT3G55370;AT3G61850;AT4G00940;AT4G21050;AT4G21080;AT4G24060;	
-478	TFmatrixID_1150	Myb/SANT; MYB	-	0.89	aaggTTAGGgtta	AT1G68320	
-478	TFmatrixID_1160	Myb/SANT; MYB	+	0.86	aaggTTAGGgtta	AT1G25340	
-478	TFmatrixID_1254	Myb/SANT; MYB-related	-	0.95	aaggtTAGGGttagcatta	AT5G67580	
-477	TFmatrixID_1259	MYB-related	-	0.93	aggtTAGGGttagca	AT1G72740	
-477	TFmatrixID_1271	Myb/SANT; MYB-related	+	0.93	aggtTAGGGttagcattag	AT5G67580	
-477	TF_motif_seq_0366	(Motif sequence only)	-	0.86	agGTTAG	MYBATRD22	
-476	TFmatrixID_1555	MYB	-	0.88	ggTTAGGg	AT3G01530	
-475	TF_motif_seq_0267	Trihelix	+	0.8	GTTAG	AT5G01380	
-474	TFmatrixID_0306	MADF; Trihelix	-	1	ttagGGTTAg	AT3G25990	
-474	TFmatrixID_0363	Myb/SANT; MYB-related	+	0.97	tTAGGGtt	AT3G49850;AT5G67580	
-474	TFmatrixID_1531	Myb/SANT; MYB-related	+	0.98	tTAGGGtt	AT5G67580	
-471	TF_motif_seq_0366	(Motif sequence only)	-	0.86	ggGTTAG	MYBATRD22	
-469	TF_motif_seq_0267	Trihelix	+	0.8	GTTAG	AT5G01380	
-463	TF_motif_seq_0241	ZF-HD	+	1	ATTAG	AT1G75240	
-463	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	-	0.8	ATTAG	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;	
-458	TF_motif_seq_0261	(Motif sequence only)	+	0.8	GAGGC	SURECOREATSULTR11	
-458	TF_motif_seq_0263	(Motif sequence only)	-	0.8	GAGGC	SORLIP1AT	
-456	TF_motif_seq_0258	Dehydrin	-	0.8	GGCGG	U01377	
-455	TF_motif_seq_0331	TCP	+	0.95	gCGGGT	AT3G27010	
-454	TF_motif_seq_0251	TCP	-	1	CGGGT	AT3G27010	
-453	TF_motif_seq_0265	(Motif sequence only)	+	0.8	GGGTC	SORLIP2AT	
-451	TF_motif_seq_0258	Dehydrin	-	1	GTCGG	U01377	
-451	TF_motif_seq_0292	AP2; ERF;ERF	-	0.95	GTCGGg	AT1G12610;AT1G63030;AT1G75490;AT3G57600;AT4G25470;AT4G25480;AT4G25490;AT5G05410;AT5G18450;AT5G51990;AT2G38340;AT3G11020	
-451	TFmatrixID_1208	Myb/SANT; MYB	+	0.92	gtcgggAACCGaagc	AT2G32460	
-447	TF_motif_seq_0267	Trihelix	-	0.8	GGAAC	AT5G01380	
-445	TF_motif_seq_0248	(Motif sequence only)	+	0.8	AACCG	MYBCOREATCYCB1	
-443	TF_motif_seq_0258	Dehydrin	+	0.8	CCGAA	U01377	
-439	TFmatrixID_1264	Myb/SANT	+	0.64	agccgaTAAACcattgaccttac	AT5G59430	
-438	TFmatrixID_0131	AT-Hook	+	1	gccgATAAA	AT1G19485;AT1G48610	
-437	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0.8	CCGAT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;	
-437	TF_motif_seq_0258	Dehydrin	+	0.8	CCGAT	U01377	
-437	TF_motif_seq_0248	(Motif sequence only)	-	0.8	CCGAT	MYBCOREATCYCB1	
-436	TF_motif_seq_0237	GATA; tify	+	1	CGATA	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620	
-435	TF_motif_seq_0243	GATA; tify	+	1	GATAA	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620	
-435	TF_motif_seq_0321	(Motif sequence only)	+	1	GATAAa	GT1CONSENSUS	
-433	TFmatrixID_1491	WRKY	-	0.84	taaaccaTTGACcttaccag	AT4G04450	
-433	TFmatrixID_1500	WRKY	+	0.88	taaaccaTTGACct	AT4G01720	
-432	TF_motif_seq_0341	(Motif sequence only)	+	1	aAACCA	MYB1AT	
-431	TFmatrixID_1733	WRKY	+	0.89	aaccaTTGACctt	AT2G04880	
-431	TFmatrixID_1736	WRKY	-	0.88	aaccaTTGACctt	AT2G04880	
-430	TFmatrixID_0461	WRKY	-	0.93	accaTTGACc	AT1G18860;AT1G29280;AT1G62300;AT1G64000;AT1G66550;AT1G66560;AT1G68150;AT1G80590;AT2G34830;AT2G40740;AT2G40750;AT2G44745;AT2G46400;AT3G01970;AT3G04670;AT3G56400;AT3G58710;AT3G62340;AT4G04450;AT4G11070;AT4G22070;AT4G23810;AT4G24240;AT4G39410;AT5G15130;AT5G22570;AT5G24110;AT5G26170;	
-430	TFmatrixID_1443	WRKY	-	0.84	accaTTGACctta	AT4G01250	
-430	TFmatrixID_1445	WRKY	-	0.81	accaTTGACcttacc	AT5G46350	
-430	TFmatrixID_1451	WRKY	+	0.82	accaTTGACctta	AT4G01250	
-430	TFmatrixID_1462	WRKY	-	0.83	accaTTGACctta	AT1G30650	
-430	TFmatrixID_1478	WRKY	+	0.93	accaTTGACctta	AT4G26640	
-430	TFmatrixID_1484	WRKY	+	0.87	accaTTGACcttac	AT2G46130	
-430	TFmatrixID_1734	WRKY	-	0.89	accaTTGACctta	AT2G04880	
-430	TFmatrixID_1735	WRKY	-	0.92	accaTTGACctta	AT2G04880	
-430	TFmatrixID_1737	WRKY	-	0.89	accaTTGACctta	AT2G04880	
-430	TFmatrixID_1738	WRKY	+	0.88	accaTTGACctta	AT2G04880	
-430	TFmatrixID_1739	WRKY	+	0.94	accaTTGACctta	AT2G04880	
-430	TFmatrixID_1740	WRKY	-	0.91	accaTTGACctta	AT2G04880	
-429	TFmatrixID_0446	WRKY	-	0.98	ccaTTGACct	AT1G18860;AT1G29280;AT1G29860;AT1G55600;AT1G62300;AT1G64000;AT1G68150;AT1G69810;AT2G21900;AT2G23320;AT2G34830;AT2G40740;AT2G44745;AT3G01970;AT3G04670;AT3G58710;AT3G62340;AT4G04450;AT4G11070;AT4G18170;AT4G22070;AT4G23810;AT4G24240;AT4G39410;AT5G15130;AT5G22570;AT5G26170;AT5G28650;	
-429	TFmatrixID_0448	WRKY	-	0.97	ccaTTGACctt	AT1G18860;AT1G29280;AT1G29860;AT1G55600;AT1G62300;AT1G64000;AT1G68150;AT1G69810;AT2G21900;AT2G25000;AT2G34830;AT2G44745;AT2G46400;AT3G01970;AT3G04670;AT3G58710;AT3G62340;AT4G04450;AT4G11070;AT4G18170;AT4G22070;	
-429	TFmatrixID_0455	WRKY	-	0.92	ccaTTGACctt	AT1G18860;AT1G29280;AT1G29860;AT1G55600;AT1G62300;AT1G64000;AT1G66550;AT1G66560;AT1G68150;AT1G69810;AT2G21900;AT2G34830;AT2G40740;AT2G44745;AT2G46400;AT3G01970;AT3G04670;AT3G58710;AT3G62340;AT4G01720;AT4G04450;AT4G11070;AT4G18170;AT4G22070;AT4G23810;AT4G24240;AT4G39410;AT5G15130;	
-429	TFmatrixID_0457	WRKY	-	0.97	ccaTTGACct	AT1G18860;AT1G29280;AT1G29860;AT1G55600;AT1G62300;AT1G64000;AT1G66560;AT1G68150;AT1G69810;AT2G21900;AT2G34830;AT2G40740;AT2G44745;AT2G46400;AT3G01970;AT3G04670;AT3G56400;AT3G58710;AT3G62340;AT4G04450;AT4G11070;AT4G18170;AT4G22070;AT4G23810;AT4G24240;AT4G31550;AT4G39410;AT5G15130;	
-429	TFmatrixID_0629	WRKY	+	0.92	ccaTTGACct	AT2G44745	
-429	TFmatrixID_0631	WRKY	+	0.9	ccaTTGACct	AT5G22570	
-429	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0.8	CCATT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;	
-429	TFmatrixID_1481	WRKY	-	0.86	ccaTTGACcttacca	AT2G46130	
-429	TFmatrixID_1742	WRKY	-	0.9	ccaTTGACcttac	AT2G04880	
-429	TF_motif_seq_0248	(Motif sequence only)	-	0.8	CCATT	MYBCOREATCYCB1	
-428	TFmatrixID_0382	NAC; NAM	-	1	caTTGACct	AT1G01720;AT1G52880;AT1G52890;AT1G69490;AT3G04070;AT3G15500;AT3G15510;	
-428	TFmatrixID_0458	WRKY	-	1	caTTGACctt	AT1G18860;AT1G29280;AT1G29860;AT1G55600;AT1G62300;AT1G64000;AT1G68150;AT1G69810;AT2G21900;AT2G34830;AT2G40740;AT2G44745;AT2G46400;AT3G01970;AT3G04670;AT3G58710;AT3G62340;AT4G04450;AT4G11070;AT4G18170;AT4G22070;AT4G24240;AT4G31800;AT4G39410;AT5G15130;AT5G26170;AT5G28650;AT5G41570;	
-428	TFmatrixID_0463	WRKY	-	1	caTTGACctt	AT1G18860;AT1G29280;AT1G29860;AT1G55600;AT1G62300;AT1G64000;AT1G66550;AT1G66560;AT1G68150;AT1G69810;AT1G80590;AT2G21900;AT2G34830;AT2G40740;AT2G40750;AT2G44745;AT2G46400;AT3G01970;AT3G04670;AT3G56400;AT3G58710;AT3G62340;AT4G04450;AT4G11070;AT4G18170;AT4G22070;AT4G23810;AT4G24240;	

-428	TFmatrixID_0466	WRKY	-	0.99	caTTGACctt	AT1G18860;AT1G29280;AT1G29860;AT1G55600;AT1G62300;AT1G64000;AT1G68150;AT1G69810;AT2G21900;AT2G34830;AT2G44745;AT3G01970;AT3G04670;AT3G58710;AT3G62340;AT4G04450;AT4G18170;AT4G22070;AT4G24240;AT4G39410;AT5G15130;
-428	TFmatrixID_0468	WRKY	-	0.99	caTTGACct	AT1G18860;AT1G29280;AT1G29860;AT1G55600;AT1G62300;AT1G64000;AT1G66550;AT1G66560;AT1G68150;AT1G69810;AT1G80590;AT2G21900;AT2G34830;AT2G40740;AT2G40750;AT2G44745;AT2G46400;AT3G01970;AT3G04670;AT3G56400;AT3G58710;AT3G62340;AT4G04450;AT4G11070;AT4G18170;AT4G22070;AT4G23810;AT4G24240;
-428	TFmatrixID_0630	WRKY	-	0.96	caTTGACctt	AT4G31800
-428	TFmatrixID_1444	WRKY	-	0.89	caTTGACctta	AT2G23320
-428	TFmatrixID_1459	WRKY	-	0.85	caTTGACctta	AT1G29860
-428	TFmatrixID_1480	WRKY	-	0.84	caTTGACctta	AT2G30590
-428	TFmatrixID_1502	WRKY	+	0.86	caTTGACctta	AT2G46400
-427	TFmatrixID_0445	WRKY	-	1	aTTGACct	AT1G18860;AT1G29280;AT1G29860;AT1G55600;AT1G62300;AT1G64000;AT1G68150;AT1G69810;AT1G80840;AT2G21900;AT2G34830;AT2G44745;AT3G01970;AT3G04670;AT3G58710;AT3G62340;AT4G04450;AT4G18170;AT4G22070;AT4G24240;AT4G39410;
-427	TFmatrixID_0465	WRKY	-	0.98	aTTGACct	AT1G13960;AT2G03340;AT2G37260;AT3G01080;AT4G12020;AT4G26440;AT4G26640;AT4G30935;AT5G07100;AT5G56270
-427	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	-	0.8	ATTGA	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-426	TFmatrixID_0534	WRKY	-	0.88	TTGACcttacc	AT1G13960;AT2G03340;AT2G04880;AT2G37260;AT3G01080;AT4G12020;AT4G26440;AT4G26640;AT4G30935;AT5G07100
-426	TF_motif_seq_0339	WRKY	+	1	TTGACc	AT1G13960;AT1G18860;AT1G29280;AT1G29860;AT1G30650;AT1G55600;AT1G62300;AT1G64000;AT1G66550;AT1G68150;AT1G69310;AT1G69810;AT1G80590;AT1G80840;AT2G03340;AT2G23320;AT2G24570;AT2G25000;AT2G30250;AT2G30590;AT2G34830;AT2G37260;AT2G38470;AT2G40740;AT2G40750;AT2G44745;AT2G46130;AT2G46400;AT2G47260;AT3G01080;AT3G01970;AT3G04670;AT3G56400;AT3G58710;AT4G01250;AT4G01720;AT4G04450;AT4G12020;AT4G18170;AT4G22070;AT4G23810;AT4G24240;AT4G26440;AT4G26640;AT4G30935;AT4G31550;AT4G31800;AT4G39410;AT5G07100;
-426	TF_motif_seq_0275	(Motif sequence only)	+	1	TTGAC	WBOXATNPR1
-425	TF_motif_seq_0246	Homeodomain; TALE	+	1	TGACC	AT1G23380;AT1G62360;AT1G70510;AT4G08150
-425	TF_motif_seq_0270	WRKY	+	1	TGACC	AT1G13960;AT1G18860;AT1G29280;AT1G29860;AT1G30650;AT1G55600;AT1G62300;AT1G64000;AT1G66550;AT1G68150;AT1G69310;AT1G69810;AT1G80590;AT1G80840;AT2G03340;AT2G23320;AT2G24570;AT2G25000;AT2G30250;AT2G30590;AT2G34830;AT2G37260;AT2G38470;AT2G40740;AT2G40750;AT2G44745;AT2G46130;AT2G46400;AT2G47260;AT3G01080;AT3G01970;AT3G04670;AT3G56400;AT3G58710;AT4G01250;AT4G01720;AT4G04450;AT4G12020;AT4G18170;AT4G22070;AT4G23810;AT4G24240;AT4G26440;AT4G26640;AT4G30935;AT4G31550;AT4G31800;AT4G39410;AT5G07100;
-425	TF_motif_seq_0271	bZIP	+	0.8	TGACC	AT1G77920;AT3G12250;AT5G06950;AT5G06960;AT5G10030;AT5G65210;AT1G22070
-425	TF_motif_seq_0450	(Motif sequence only)	+	0.75	TGACCtta	PALINDROMICCBOXGM
-423	TF_motif_seq_0239	Dof	-	1	ACCTT	AT1G29160;AT1G64620;AT2G37590;AT3G21270;AT3G45610;AT3G47500;AT4G38000;AT5G39660;AT5G60200;AT5G60850;AT5G62940;AT2G46590;AT1G07640;AT1G21340;AT1G26790;AT1G47655;AT1G51700;AT1G69570;AT2G28510;AT2G28810;AT2G34140;AT3G50410;AT3G55370;AT3G61850;AT4G00940;AT4G21050;AT4G21080;AT4G24060;
-421	TF_motif_seq_0267	Trihelix	+	0.8	CTTAC	AT5G01380
-413	TF_motif_seq_0237	GATA; tify	-	1	CATCC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-409	TF_motif_seq_0271	bZIP	-	0.8	CCTCA	AT1G77920;AT3G12250;AT5G06950;AT5G06960;AT5G10030;AT5G65210;AT1G22070
-408	TF_motif_seq_0188	(Motif sequence only)	+	0.86	ctcataagcttcttCCACG	UPRMOTIFIIAT
-405	TF_motif_seq_0010	HSF	-	0.88	ataagCTTCT	AT3G24520;AT1G32330;AT1G46264;AT1G67970;AT2G26150;AT2G41690;AT3G02990;AT3G22830;AT3G51910;AT3G63350;AT4G11660;AT4G13980;AT4G17750;AT4G18880;AT5G03720;AT5G16820;AT5G43840;AT5G45710;AT5G54070;AT5G62020
-395	TF_motif_seq_0263	(Motif sequence only)	+	0.8	TCCAC	SORLIP1AT
-393	TF_motif_seq_0249	(Motif sequence only)	-	0.8	CACGA	ABRELATERD1
-390	TF_motif_seq_0267	Trihelix	-	0.8	GAAAC	AT5G01380
-390	TF_motif_seq_0261	(Motif sequence only)	+	0.8	GAAAC	SURECOREATSULTR11
-389	TF_motif_seq_0343	(Motif sequence only)	+	0.86	AAACAta	ANAERO1CONSENSUS
-386	TF_motif_seq_0120	(Motif sequence only)	+	0.77	CATACgtcgtatc	JASE2ATOPR1
-385	TF_motif_seq_0410	bHLH	+	0.75	ATACGtcg	AT1G32640
-384	TF_motif_seq_0240	bZIP	-	1	TACGT	AT3G54620;AT4G02640
-384	TFmatrixID_1353	NAC; NAM	-	1	TACGT	AT1G01720
-384	TF_motif_seq_0249	(Motif sequence only)	-	0.8	TACGT	ABRELATERD1
-383	TFmatrixID_0621	AP2	+	0.85	acgTCGTAtc	AT2G28550
-383	TFmatrixID_0624	AP2	+	0.84	acgTCGTAtc	AT5G60120
-383	TF_motif_seq_0240	bZIP	+	1	ACGTC	AT3G54620;AT4G02640
-383	TFmatrixID_1636	Myb/SANT	-	0.9	acgtcGTATCccct	AT3G46640
-383	TFmatrixID_1644	Myb/SANT	-	0.92	acgtcGTATCccct	AT3G46640
-383	TF_motif_seq_0009	(Motif sequence only)	+	0.7	ACGTCgtatc	LS7ATPR1
-383	TF_motif_seq_0249	(Motif sequence only)	+	0.8	ACGTC	ABRELATERD1
-382	TF_motif_seq_0271	bZIP	-	0.8	CGTCG	AT1G77920;AT3G12250;AT5G06950;AT5G06960;AT5G10030;AT5G65210;AT1G22070
-381	TF_motif_seq_0258	Dehydrin	-	0.8	GTCGT	U01377
-378	TF_motif_seq_0243	GATA; tify	-	1	GTATC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-378	TF_motif_seq_0267	Trihelix	-	0.8	GTATC	AT5G01380
-378	TF_motif_seq_0261	(Motif sequence only)	-	0.8	GTATC	SURECOREATSULTR11
-377	TF_motif_seq_0237	GATA; tify	-	1	TATCC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-371	TF_motif_seq_0263	(Motif sequence only)	-	0.8	CTGGC	SORLIP1AT
-370	TF_motif_seq_0265	(Motif sequence only)	+	0.8	TGGCC	SORLIP2AT
-369	TF_motif_seq_0265	(Motif sequence only)	-	0.8	GGCCG	SORLIP2AT
-367	TF_motif_seq_0258	Dehydrin	+	0.8	CCGAA	U01377
-360	TF_motif_seq_0263	(Motif sequence only)	+	0.8	TCCAC	SORLIP1AT
-358	TF_motif_seq_0249	(Motif sequence only)	-	0.8	CACCT	ABRELATERD1
-357	TF_motif_seq_0239	Dof	-	1	ACCTT	AT1G29160;AT1G64620;AT2G37590;AT3G21270;AT3G45610;AT3G47500;AT4G38000;AT5G39660;AT5G60200;AT5G60850;AT5G62940;AT2G46590;AT1G07640;AT1G21340;AT1G26790;AT1G47655;AT1G51700;AT1G69570;AT2G28510;AT2G28810;AT2G34140;AT3G50410;AT3G55370;AT3G61850;AT4G00940;AT4G21050;AT4G21080;AT4G24060;
-354	TFmatrixID_0384	NAC; NAM	-	0.89	ttgAGTAAt	AT1G33060;AT3G49530;AT4G35580;AT5G24590
-354	TF_motif_seq_0275	(Motif sequence only)	+	0.8	TTGAG	WBOXATNPR1
-350	TF_motif_seq_0241	ZF-HD	-	1	GTAAT	AT1G75240
-350	TF_motif_seq_0267	Trihelix	-	0.8	GTAAT	AT5G01380
-347	TF_motif_seq_0321	(Motif sequence only)	-	1	aTTTCC	GT1CONSENSUS
-346	TFmatrixID_0940	GATA	-	0.89	tttcCGATCac	AT4G36620
-346	TFmatrixID_0942	GATA	-	0.9	tttcCGATCac	AT4G36620
-343	TFmatrixID_0262	GATA	-	1	ccGATCAcc	AT3G06740;AT3G16870;AT4G16141;AT4G26150;AT5G26930;AT5G49300;AT5G56860
-343	TFmatrixID_0268	GATA	+	1	cCGATCaccg	AT4G17570
-343	TFmatrixID_0272	GATA	+	1	cCGATCacc	AT5G47140
-343	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0.8	CCGAT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-343	TF_motif_seq_0258	Dehydrin	+	0.8	CCGAT	U01377
-343	TF_motif_seq_0248	(Motif sequence only)	-	0.8	CCGAT	MYBCOREATCYCB1
-343	TF_motif_seq_0435	(Motif sequence only)	-	0.75	ccgATCAC	PIATGAPB
-342	TF_motif_seq_0237	GATA; tify	+	1	CGATC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-341	TF_motif_seq_0237	GATA; tify	-	1	GATCA	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-340	TFmatrixID_0994	C3H	+	0.83	aTCACCg	AT1G70910
-339	TFmatrixID_1152	MYB	+	0.9	tcaccggCCGTTa	AT4G32730
-338	TFmatrixID_1432	MADF; Trihelix	-	0.91	caccggcCGTTAaaa	AT3G10030

-337	TFmatrixID_1171	Myb/SANT; MYB	-	0.91	accggcCGTTAaaac	AT5G17800
-337	TFmatrixID_1434	MADF; Trihelix	-	0.9	accggcCGTTAaaa	AT3G10030
-337	TF_motif_seq_0248	(Motif sequence only)	+	0.8	ACCGG	MYBCOREATCYCB1
-336	TFmatrixID_0355	Myb/SANT	+	1	ccggCCGTTa	AT3G11440;AT5G06100
-336	TFmatrixID_0416	Storekeeper	+	0.96	cCGGCCgt	AT2G25650;AT4G00270
-336	TFmatrixID_0416	Storekeeper	-	0.98	ccGGCCGt	AT2G25650;AT4G00270
-336	TF_motif_seq_0258	Dehydrin	+	0.8	CCGGC	U01377
-336	TFmatrixID_1201	Myb/SANT; MYB	-	0.89	ccggcCGTTAaaacctt	AT1G69560
-336	TFmatrixID_1223	Myb/SANT; MYB	+	0.92	ccggCCGTTaaaaccttcg	AT3G09230
-335	TFmatrixID_1166	Myb/SANT; MYB	+	0.89	cggcCGTTAaa	AT5G58850
-335	TFmatrixID_1516	Myb/SANT; MYB	+	1	cggCCGTTa	AT5G67300
-335	TFmatrixID_1518	Myb/SANT	-	1	cggCCGTTa	AT3G11440
-335	TFmatrixID_1549	Myb/SANT	+	1	cggCCGTTa	AT2G23290
-335	TF_motif_seq_0265	(Motif sequence only)	+	0.8	CGGCC	SORLIP2AT
-334	TFmatrixID_0330	Myb/SANT	+	0.95	ggCCGTTa	AT2G23290;AT4G37260
-334	TFmatrixID_0350	Myb/SANT; MYB	+	0.9	ggcCGTTAaaa	AT4G18770
-334	TF_motif_seq_0265	(Motif sequence only)	-	0.8	GGCCG	SORLIP2AT
-333	TFmatrixID_0241	Dof	-	0.93	gcCGTTAaaa	AT5G60850
-333	TFmatrixID_0590	MYB	-	0.91	gCCGTTaaaa	AT1G17950
-333	TFmatrixID_1014	EIN3; EIL	+	0.95	gCCGTTa	AT3G20770
-332	TF_motif_seq_0313	(Others)	+	1	CCGTTa	D14712
-332	TF_motif_seq_0248	(Motif sequence only)	-	1	CCGTT	MYBCOREATCYCB1
-332	TF_motif_seq_0342	(Motif sequence only)	-	1	CCGTTa	MYB2CONSENSUSAT
-331	TF_motif_seq_0271	bZIP	-	0.8	CGTTA	AT1G77920;AT3G12250;AT5G06950;AT5G06960;AT5G10030;AT5G65210;AT1G22070
-330	TF_motif_seq_0267	Trihelix	+	0.8	GTTAA	AT5G01380
-330	TF_motif_seq_0275	(Motif sequence only)	-	0.8	GTTAA	WBOXATNPR1
-324	TF_motif_seq_0239	Dof	-	1	ACCTT	AT1G29160;AT1G64620;AT2G37590;AT3G21270;AT3G45610;AT3G47500;AT4G38000;AT5G39660;AT5G60200;AT5G60850;AT5G62940;AT2G46590;AT1G07640;AT1G21340;AT1G26790;AT1G47655;AT1G51700;AT1G69570;AT2G28510;AT2G28810;AT2G34140;AT3G50410;AT3G55370;AT3G61850;AT4G00940;AT4G21050;AT4G21080;AT4G24060;
-321	TF_motif_seq_0258	Dehydrin	-	0.8	TTCGG	U01377
-317	TF_motif_seq_0258	Dehydrin	+	0.8	GCGAC	U01377
-317	TFmatrixID_1165	Myb/SANT; MYB	-	0.93	gcgaCGCTCtcaa	AT2G02820
-317	TF_motif_seq_0261	(Motif sequence only)	+	0.8	GCGAC	SURECOREATSULTR11
-317	TF_motif_seq_0263	(Motif sequence only)	+	0.8	GCGAC	SORLIP1AT
-316	TF_motif_seq_0271	bZIP	+	0.8	CGACG	AT1G77920;AT3G12250;AT5G06950;AT5G06960;AT5G10030;AT5G65210;AT1G22070
-311	TFmatrixID_0706	AP2; ERF	-	0.94	ctctcaacaattCGCCGccaa	AT3G20310
-311	TF_motif_seq_0261	(Motif sequence only)	-	0.8	CTCTC	SURECOREATSULTR11
-309	TF_motif_seq_0275	(Motif sequence only)	-	0.8	CTCAA	WBOXATNPR1
-308	TFmatrixID_0991	C3H Zinc finger	+	1	TCAACa	AT5G58620
-308	TFmatrixID_0992	C3H	-	1	tCAACAa	AT5G42820
-307	TF_motif_seq_0255	AP2; RAV; B3	+	1	CAACA	AT1G25560;AT1G13260
-306	TFmatrixID_0675	AP2; ERF	-	0.95	aacaattCGCCGccaataga	AT3G15210
-306	TFmatrixID_0715	AP2; ERF	-	0.95	aacaattCGCCGccaataga	AT1G28370
-306	TFmatrixID_0748	AP2; ERF	+	0.97	aacaattcgCCGCCaatagaaccaccac	AT3G23240
-305	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0.8	ACAAT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-305	TFmatrixID_0676	AP2	+	0.93	acaattCGCCGccaatagaac	AT5G64750
-305	TFmatrixID_0688	AP2; ERF	-	0.97	acaattCGCCGccaatag	AT1G53170
-305	TFmatrixID_0709	AP2; ERF	-	0.9	acaattCGCCGccaataga	AT4G34410
-304	TFmatrixID_0740	AP2; ERF	+	0.94	caattCGCCGccaatag	AT5G44210
-303	TFmatrixID_0685	AP2; ERF	-	0.94	aattcGCCGCcaatagaacca	AT1G53910
-303	TFmatrixID_1013	E2F/DP	+	0.83	aattcgcCGCCAata	AT1G47870
-302	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	-	0.8	ATTCG	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-302	TFmatrixID_0735	AP2	-	0.96	attCGCCGccaatagaacca	AT1G03800
-302	TFmatrixID_0738	AP2; ERF	+	0.96	attcgCCGCCaatag	AT2G44840
-302	TFmatrixID_1007	E2F/DP	-	0.86	attcgcCGCCAata	AT2G36010
-302	TFmatrixID_1008	E2F/DP	-	0.75	attcgCCGCCaatagaacca	AT5G14960
-302	TFmatrixID_1009	E2F/DP	+	0.86	attcgcCGCCAata	AT2G36010
-302	TF_motif_seq_0458	(Motif sequence only)	+	1	aTTCGCcg	E2FCONSENSUS
-301	TFmatrixID_0039	AP2; ERF	+	0.99	ttcGCCGCca	AT3G23240
-301	TFmatrixID_0102	AP2; ERF	+	1	ttcGCCGCca	AT1G04370;AT1G53910;AT3G23220;AT4G18450;AT4G34410;AT5G07310;AT5G47220;AT5G50080;AT5G61590;AT5G61890;AT5G64750
-301	TFmatrixID_0103	AP2; ERF	+	1	ttCGCCGcca	AT1G04370;AT1G28360;AT1G53910;AT2G47520;AT3G61630;AT4G18450;AT4G34410;AT5G07310;AT5G44210;AT5G47230;AT5G50080;AT5G61590;AT5G61600;AT5G61890;
-301	TFmatrixID_0113	AP2; ERF	+	1	ttcGCCGCca	AT1G04370;AT1G22190;AT1G36060;AT1G53910;AT2G20880;AT2G40220;AT2G46310;AT2G47520;AT3G16770;AT3G23220;AT3G61630;AT4G11140;AT4G18450;AT4G28140;AT4G34410;AT5G07310;AT5G44210;AT5G50080;AT5G61890;AT5G64750
-301	TFmatrixID_0598	AP2; ERF	+	0.98	ttcGCCGCca	AT3G16770
-301	TFmatrixID_0606	AP2; ERF	+	0.95	ttCGCCGcca	AT4G34410
-300	TFmatrixID_0056	AP2; ERF	+	1	tCGCCGcca	AT1G22985;AT1G71130;AT3G61630;AT4G11140
-300	TFmatrixID_0059	AP2; ERF	+	1	tCGCCGccaa	AT1G03800;AT1G12980;AT1G24590;AT1G28360;AT1G28370;AT1G72360;AT5G44210;
-300	TFmatrixID_0078	AP2; ERF	+	1	tcGCCGCc	AT2G46310;AT3G23220;AT3G23230;AT3G61630;AT4G11140;AT4G18450;AT4G34410;
-300	TFmatrixID_0079	AP2; ERF	+	0.99	tcGCCGCcaa	AT1G04370;AT3G23220;AT3G23240;AT4G18450
-300	TFmatrixID_0082	AP2; ERF	+	1	tCGCCGcca	AT1G04370;AT1G53910;AT3G23220;AT3G61630;AT4G17500;AT4G18450;AT4G34410;AT5G07310;AT5G50080;AT5G61590;AT5G61890;AT5G64750
-300	TFmatrixID_0092	AP2; ERF	+	1	tcgCCGCCa	AT5G07580;AT5G61590;AT5G61600
-300	TFmatrixID_0100	AP2; ERF	+	1	tCGCCGccaa	AT1G28360;AT1G36060;AT1G53910;AT2G46310;AT2G47520;AT3G16770;AT3G57600;AT3G61630;AT4G11140;AT4G34410;AT5G07310;AT5G13330;AT5G44210;AT5G50080;
-300	TFmatrixID_0101	AP2; ERF	+	1	tcGCCGCcaa	AT1G04370;AT1G12890;AT1G24590;AT1G28160;AT3G23220;AT4G18450;AT5G13910;AT5G43410;AT5G44210;AT5G61600
-300	TFmatrixID_0107	AP2; ERF	+	1	tCGCCGcca	AT1G53910;AT2G46310;AT3G61630;AT4G11140;AT4G34410;AT5G53290
-300	TFmatrixID_0599	AP2; ERF	+	0.97	tcGCCGCcaa	AT3G16770
-300	TFmatrixID_0600	AP2; ERF	+	0.96	tCGCCGccaa	AT3G16770
-300	TFmatrixID_0602	AP2; ERF	+	0.96	tcGCCGCcaa	AT1G43160
-300	TFmatrixID_0607	AP2; ERF	+	0.98	tcGCCGCcaa	AT4G34410
-300	TFmatrixID_0608	AP2; ERF	+	0.94	tCGCCGccaa	AT4G34410
-300	TFmatrixID_1558	AP2	-	1	tcGCCGCca	AT1G04370
-299	TFmatrixID_0053	AP2; ERF	+	1	CGCCGcca	AT1G03800;AT1G12890;AT1G12980;AT1G24590;AT1G28160;AT1G28360;AT3G16770;AT5G07310;AT5G13910;AT5G18560;AT5G44210;AT5G50080;AT5G61890;AT5G64750
-299	TFmatrixID_0061	AP2; ERF	+	1	CGCCGcca	AT1G03800;AT1G12980;AT1G24590;AT1G28360;AT1G50640;AT1G80580;AT4G11140;AT5G13910;AT5G18560;AT5G44210;AT5G50080;AT5G64750
-299	TFmatrixID_0062	AP2; ERF	+	1	CGCCGccaat	AT1G03800;AT1G12980;AT1G24590;AT1G28360;AT1G53170;AT4G34410;AT5G13910;AT5G18560;AT5G44210;AT5G50080;AT5G64750
-299	TFmatrixID_0071	AP2; ERF	+	1	cgCCGCCa	AT1G04370;AT2G44840;AT3G23220;AT4G34410;AT5G61590;AT5G61600;AT5G61890
-299	TFmatrixID_0077	AP2; ERF	+	1	cGCCGCcaat	AT1G12980;AT1G24590;AT1G28360;AT3G20310;AT4G34410;AT5G44210;AT5G61590;
-299	TFmatrixID_0110	AP2; ERF	+	1	CGCCGcca	AT1G24590;AT1G28360;AT5G44210;AT5G61600
-299	TFmatrixID_0122	AP2; ERF	+	1	cGCCGCca	AT1G12980;AT1G22190;AT1G24590;AT1G28160;AT1G28360;AT1G36060;AT1G53910;AT3G16770;AT5G13910;AT5G50080
-299	TFmatrixID_0512	AP2; ERF	+	1	cGCCGCca	AT1G04370;AT3G23220;AT3G23240;AT4G18450
-299	TFmatrixID_0689	AP2; ERF	+	1	CGCCGc	AT1G43160
-299	TFmatrixID_0720	AP2; ERF	-	1	cgCCGCCa	AT3G23240
-299	TFmatrixID_1550	AP2; ERF	+	1	cGCCGCca	AT3G16770
-298	TFmatrixID_1535	AP2; ERF	-	1	GCCGCcaata	AT1G53910
-298	TF_motif_seq_0263	(Motif sequence only)	+	0.8	GCCGC	SORLIP1AT
-298	TF_motif_seq_0318	(Motif sequence only)	+	1	GCCGCc	GCCCORE
-297	TF_motif_seq_0258	Dehydrin	+	0.8	CCGCC	U01377
-297	TF_motif_seq_0458	(Motif sequence only)	-	1	ccGCCAAt	E2FCONSENSUS
-296	TF_motif_seq_0271	bZIP	-	0.8	CGCCA	AT1G77920;AT3G12250;AT5G06950;AT5G06960;AT5G10030;AT5G65210;AT1G22070
-295	TF_motif_seq_0263	(Motif sequence only)	+	0.8	GCCAA	SORLIP1AT
-295	TF_motif_seq_0275	(Motif sequence only)	-	0.8	GCCAA	WBOXATNPR1

-294	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	1	CCAAT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-291	TFmatrixID_1214	MYB	+	0.95	atagaaCCACCact	AT4G01680
-290	TF_motif_seq_0254	AP2; ERF	-	0.8	TAGAA	AT3G14230
-289	TFmatrixID_0589	MYB	+	0.97	agAACCAcca	AT5G12870
-288	TF_motif_seq_0341	(Motif sequence only)	+	0.95	gAACCA	MYB1AT
-286	TF_motif_seq_0263	(Motif sequence only)	+	0.8	ACCAC	SORLIP1AT
-283	TF_motif_seq_0263	(Motif sequence only)	+	0.8	ACCAC	SORLIP1AT
-282	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0.8	CCACT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-280	TF_motif_seq_0288	(Motif sequence only)	+	1	ACTCAt	PREATPRODH
-278	TF_motif_seq_0390	(Motif sequence only)	+	0.86	TCATCtc	ANAERO3CONSENSUS
-277	TF_motif_seq_0237	GATA; tify	-	1	CATCT	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-277	TFmatrixID_0680	AP2; ERF	+	0.93	catctcattaacttCCGACat	AT1G12630
-276	TF_motif_seq_0254	AP2; ERF	+	0.8	ATCTC	AT3G14230
-276	TF_motif_seq_0261	(Motif sequence only)	-	0.8	ATCTC	SURECOREATSULTR11
-273	TFmatrixID_0280	Homeodomain; HD-ZIP	-	0.95	tcATTAActt	AT1G05230;AT1G17920;AT1G73360;AT1G79840;AT3G03260;AT3G61150;AT5G46880
-273	TFmatrixID_1064	Homeodomain; HD-ZIP	+	0.9	tcATTAActtc	AT4G00730
-273	TFmatrixID_1068	Homeodomain; HD-ZIP	+	0.91	tcATTAActtc	AT4G00730
-273	TFmatrixID_1070	HD-ZIP	-	0.94	tcATTAActtc	AT5G52170
-273	TFmatrixID_1074	Homeodomain; HD-ZIP	-	0.9	tcATTAActtc	AT3G61150
-273	TFmatrixID_1082	Homeodomain; HD-ZIP	+	0.93	tcATTAActtc	AT1G73360
-273	TFmatrixID_1084	Homeodomain; HD-ZIP	-	0.92	tcATTAActtc	AT3G61150
-273	TFmatrixID_1616	AP2; ERF	+	0.86	tcattaacttCCGACattaataa	AT1G12610
-273	TFmatrixID_1625	AP2; ERF	+	0.88	tcattaacttcCGACAttaataa	AT1G63030
-272	TFmatrixID_0776	AP2; ERF	-	0.86	cattaacttCCGACatt	AT4G16750
-272	TFmatrixID_1618	AP2; ERF	-	0.92	cattaacttcCGACAttaataat	AT1G12610
-271	TF_motif_seq_0241	ZF-HD	+	1	ATTAA	AT1G75240
-271	TFmatrixID_1611	AP2; ERF	-	0.9	attaacttcCGACAttaataat	AT1G12610
-271	TFmatrixID_1612	AP2; ERF	-	0.88	attaacttcCGACAttaataatt	AT1G12610
-271	TFmatrixID_1613	AP2; ERF	-	0.88	attaacttcCGACAttaataat	AT1G12610
-271	TFmatrixID_1614	AP2; ERF	-	0.9	attaacttcCGACAttaataat	AT1G12610
-271	TFmatrixID_1615	AP2; ERF	-	0.87	attaacttcCGACAttaataatt	AT1G12610
-271	TFmatrixID_1617	AP2; ERF	-	0.9	attaacttcCGACAttaataat	AT1G12610
-271	TFmatrixID_1619	AP2; ERF	-	0.87	attaacttcCGACAttaataat	AT1G12610
-271	TFmatrixID_1620	AP2; ERF	-	0.91	attaacttcCGACAttaataat	AT1G63030
-271	TFmatrixID_1621	AP2; ERF	-	0.89	attaacttcCGACAttaataat	AT1G63030
-271	TFmatrixID_1622	AP2; ERF	+	0.91	attaacttcCGACAttaataat	AT1G63030
-271	TFmatrixID_1623	AP2; ERF	-	0.91	attaacttcCGACAttaataat	AT1G63030
-271	TFmatrixID_1624	AP2; ERF	-	0.89	attaacttcCGACAttaataat	AT1G63030
-271	TFmatrixID_1626	AP2; ERF	-	0.91	attaacttcCGACAttaataat	AT1G63030
-271	TFmatrixID_1627	AP2; ERF	-	0.88	attaacttcCGACAttaataat	AT1G63030
-270	TF_motif_seq_0267	Trihelix	-	0.8	TTAAC	AT5G01380
-270	TF_motif_seq_0275	(Motif sequence only)	+	0.8	TTAAC	WBOXATNPR1
-269	TFmatrixID_0665	AP2; ERF	-	0.95	taacttCCGACatta	AT4G25490
-269	TFmatrixID_0682	AP2; ERF	-	0.92	taacttCCGACatta	AT5G52020
-269	TFmatrixID_0697	AP2; ERF	-	0.93	taacttCCGACatt	AT5G52020
-269	TFmatrixID_0711	AP2; ERF	+	0.95	taacttCCGACatta	AT4G25470
-269	TFmatrixID_0727	AP2; ERF	-	0.91	taacttCCGACatta	AT1G12610
-269	TFmatrixID_0773	AP2; ERF	-	0.91	taacttcCGACAtta	AT1G63030
-269	TFmatrixID_0778	AP2; ERF	+	0.95	taacttCCGACat	AT1G12610
-268	TFmatrixID_0670	AP2; ERF	-	0.93	aacttCCGACattaat	AT1G12630
-268	TFmatrixID_0695	AP2; ERF	-	0.86	aacttCCGACatt	AT2G44940
-268	TFmatrixID_0736	AP2; ERF	+	0.9	aacttCCGACattaa	AT5G25810
-268	TFmatrixID_0805	bHLH	-	0.87	aacttCCGACatt	AT2G31220
-267	TFmatrixID_0652	AP2; ERF	-	0.91	acttCCGACatt	AT1G77200
-267	TFmatrixID_0667	AP2; ERF	-	0.95	acttCCGACatta	AT5G51990
-267	TFmatrixID_0669	AP2; ERF	-	0.96	acttCCGACatta	AT4G25470
-266	TFmatrixID_0020	AP2; ERF	+	0.89	cttCCGACat	AT1G77200
-266	TFmatrixID_0040	B3; ARF	-	0.98	cttCCGACat	AT2G33860
-266	TFmatrixID_0109	AP2; ERF	+	0.91	cttCCGACat	AT1G12610;AT4G25490;AT5G51990
-266	TFmatrixID_0655	AP2; ERF	-	0.96	cttCCGACatta	AT5G51990
-266	TFmatrixID_0683	AP2; ERF	-	0.95	cttCCGACatt	AT4G25480
-266	TFmatrixID_0691	AP2; ERF	+	0.89	cttCCGACattaat	AT1G77200
-266	TFmatrixID_0747	AP2; ERF	-	0.86	cttCCGACattaat	AT3G60490
-265	TFmatrixID_0032	AP2; ERF	-	0.93	ttcCGACAtt	AT1G12610
-265	TFmatrixID_0088	AP2; ERF	+	0.92	ttCCGACa	AT1G01250;AT1G12630;AT1G77200;AT2G25820;AT2G35700;AT2G44940;AT3G16280;AT3G60490;AT4G25490;AT4G32800;AT5G11590;AT5G25810;AT5G51990
-265	TFmatrixID_0785	ARF	+	0.99	ttcCGACAtt	AT5G62000
-264	TFmatrixID_0084	AP2; ERF	+	0.97	tCCGACat	AT2G35700;AT2G44940;AT3G16280;AT3G60490;AT4G25470;AT4G25490;AT5G11590;
-264	TFmatrixID_0156	B3; ARF	+	1	tcCGACAtt	AT1G19220;AT1G19850;AT1G30330;AT5G20730;AT5G37020;AT5G60450
-264	TF_motif_seq_0292	AP2; ERF;ERF	+	0.95	tCCGAC	AT1G12610;AT1G63030;AT1G75490;AT3G57600;AT4G25470;AT4G25480;AT4G25490;AT5G05410;AT5G18450;AT5G51990;AT2G38340;AT3G11020
-264	TF_motif_seq_0349	(Others)	+	0.86	TCCGAca	X67670;X67671
-264	TFmatrixID_0784	B3; ARF	+	0.95	tcCGACAtta	AT1G19850
-263	TF_motif_seq_0258	Dehydrin	+	1	CCGAC	U01377
-262	TF_motif_seq_0271	bZIP	-	0.8	CGACA	AT1G77920;AT3G12250;AT5G06950;AT5G06960;AT5G10030;AT5G65210;AT1G22070
-261	TFmatrixID_0290	Homeodomain; HD-ZIP	-	0.98	gacATTAAta	AT1G05230;AT1G17920;AT2G32370;AT3G61150;AT4G21750;AT5G46880
-260	TFmatrixID_0280	Homeodomain; HD-ZIP	-	0.95	acATTAAtaa	AT1G05230;AT1G17920;AT1G73360;AT1G79840;AT3G03260;AT3G61150;AT5G46880
-260	TFmatrixID_0288	Homeodomain; HD-ZIP	+	0.96	acaTTAATaat	AT1G05230;AT1G17920;AT3G61150;AT4G00730;AT5G46880
-260	TFmatrixID_1067	HD-ZIP	-	0.89	acattaATAATtcgg	AT5G66700
-260	TFmatrixID_1068	Homeodomain; HD-ZIP	+	0.9	acATTAAtaat	AT4G00730
-260	TFmatrixID_1074	Homeodomain; HD-ZIP	-	0.9	acATTAAtaat	AT3G61150
-259	TFmatrixID_0144	AT-Hook	-	0.9	catTAATAattc	AT4G21895;AT5G62260
-259	TFmatrixID_1058	bZIP; Homeodomain; HD-ZIP	-	0.85	cattaATAATtcg	AT5G03790
-258	TFmatrixID_0058	Homeodomain; bZIP; HD-ZIP	-	0.94	attaATAATtcggg	AT3G01470
-258	TFmatrixID_0540	Homeodomain; HD-ZIP; bZIP	+	0.91	attAATAAttcggg	AT1G69780;AT3G01220;AT3G01470;AT5G15150
-258	TF_motif_seq_0241	ZF-HD	+	1	ATTAA	AT1G75240
-258	TFmatrixID_1060	bZIP; Homeodomain; HD-ZIP	-	0.9	attAATAAttcgg	AT5G03790
-258	TFmatrixID_1088	Homeodomain; bZIP; HD-ZIP	+	0.95	attAATAAttcggg	AT3G01470
-257	TFmatrixID_0026	bZIP; Homeodomain; HD-ZIP	-	0.94	ttaATAATtc	AT5G03790
-257	TFmatrixID_0281	Homeodomain; HD-ZIP	-	0.98	ttAATAAtt	AT1G26960;AT1G69780;AT2G22430;AT3G01220;AT5G15150
-257	TFmatrixID_0517	Homeodomain; HD-ZIP; bZIP	+	0.93	ttAATAAttcgg	AT1G69780;AT3G01220;AT3G01470;AT5G15150
-257	TF_motif_seq_0241	ZF-HD	-	1	TTAAT	AT1G75240
-257	TFmatrixID_1057	Homeodomain; bZIP; HD-ZIP	+	0.97	ttAATAAttcg	AT5G65310
-257	TFmatrixID_1062	HD-ZIP	+	0.94	ttAATAAttcg	AT5G66700
-257	TFmatrixID_1073	Homeodomain; HD-ZIP	+	0.99	ttAATAAttcg	AT1G69780
-257	TFmatrixID_1078	Homeodomain; HD-ZIP	-	0.96	ttaATAATtcg	AT3G01220
-257	TFmatrixID_1086	Homeodomain; HD-ZIP	+	0.96	ttAATAAttcg	AT1G69780
-257	TFmatrixID_1087	Homeodomain; HD-ZIP	+	0.93	ttAATAAttcg	AT2G22430
-257	TFmatrixID_1089	Homeodomain; bZIP; HD-ZIP	+	0.97	ttAATAAttcg	AT3G01470
-257	TFmatrixID_1090	Homeodomain; HD-ZIP	+	0.98	ttAATAAttcg	AT3G01220
-256	TFmatrixID_0047	bZIP; Homeodomain; HD-ZIP	-	0.91	taATAATtcg	AT1G52150
-256	TFmatrixID_0116	Homeodomain; bZIP; HD-ZIP	-	0.92	tAATAAttc	AT5G65310
-256	TFmatrixID_0292	Homeodomain; HD-ZIP	-	1	taATAATt	AT1G26960;AT1G69780;AT3G01220;AT4G40060;AT5G15150
-256	TFmatrixID_0790	ARID	-	1	tAATAA	AT3G13350
-255	TFmatrixID_0471	Homeodomain; HD-ZIP; bZIP	+	0.99	aATAATtc	AT1G69780;AT3G01220;AT3G01470;AT5G15150
-254	TF_motif_seq_0241	ZF-HD	-	1	ATAAT	AT1G75240
-254	TFmatrixID_1509	ZF-HD	-	0.94	ATAATtcgggt	AT1G14687

-251	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	-	0.8	ATTCG	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-251	TF_motif_seq_0410	bHLH	+	0.75	ATTCGggt	AT1G32640
-250	TF_motif_seq_0258	Dehydrin	-	0.8	TTCGG	U01377
-249	TF_motif_seq_0331	TCP	+	1	tCGGGT	AT3G27010
-248	TF_motif_seq_0251	TCP	-	1	CGGGT	AT3G27010
-247	TF_motif_seq_0265	(Motif sequence only)	+	0.8	GGGTC	SORLIP2AT
-245	TF_motif_seq_0258	Dehydrin	-	1	GTCGG	U01377
-245	TF_motif_seq_0292	AP2; ERF;ERF	-	0.95	GTCGGg	AT1G12610;AT1G63030;AT1G75490;AT3G57600;AT4G25470;AT4G25480;AT4G25490;AT5G05410;AT5G18450;AT5G51990;AT2G38340;AT3G11020
-244	TF_motif_seq_0331	TCP	+	1	tCGGGT	AT3G27010
-243	TF_motif_seq_0251	TCP	-	1	CGGGT	AT3G27010
-242	TF_motif_seq_0265	(Motif sequence only)	+	0.8	GGGTC	SORLIP2AT
-240	TF_motif_seq_0258	Dehydrin	-	1	GTCGG	U01377
-240	TF_motif_seq_0292	AP2; ERF;ERF	-	0.95	GTCGGg	AT1G12610;AT1G63030;AT1G75490;AT3G57600;AT4G25470;AT4G25480;AT4G25490;AT5G05410;AT5G18450;AT5G51990;AT2G38340;AT3G11020
-239	TF_motif_seq_0331	TCP	+	1	tCGGGT	AT3G27010
-238	TF_motif_seq_0251	TCP	-	1	CGGGT	AT3G27010
-237	TF_motif_seq_0265	(Motif sequence only)	+	0.8	GGGTC	SORLIP2AT
-235	TF_motif_seq_0258	Dehydrin	-	1	GTCGG	U01377
-235	TF_motif_seq_0292	AP2; ERF;ERF	-	0.95	GTCGGa	AT1G12610;AT1G63030;AT1G75490;AT3G57600;AT4G25470;AT4G25480;AT4G25490;AT5G05410;AT5G18450;AT5G51990;AT2G38340;AT3G11020
-235	TFmatrixID_0944	GATA	+	0.88	gtcGGATC	AT2G18380
-234	TFmatrixID_0015	MYB; ARR-B	+	0.89	tcGGATCagt	AT1G67710
-234	TFmatrixID_0018	Myb/SANT; MYB; ARR-B	+	0.91	tcGGATCagt	AT2G01760
-232	TF_motif_seq_0237	GATA; tify	+	1	GGATC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-231	TF_motif_seq_0237	GATA; tify	-	1	GATCA	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-228	TF_motif_seq_0248	(Motif sequence only)	-	0.8	CAGTT	MYBCOREATCYCB1
-225	TF_motif_seq_0399	(Motif sequence only)	+	0.84	TTTGAtc	WBBOXPCWRKY1
-224	TF_motif_seq_0254	AP2; ERF	-	0.8	TTGAT	AT3G14230
-224	TF_motif_seq_0275	(Motif sequence only)	+	0.8	TTGAT	WBOXATNPR1
-223	TF_motif_seq_0237	GATA; tify	+	1	TGATC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-222	TF_motif_seq_0237	GATA; tify	-	1	GATCC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-221	TF_motif_seq_0254	AP2; ERF	+	0.8	ATCCA	AT3G14230
-220	TFmatrixID_0793	ARID; Sox	-	0.83	tccactATATActaac	AT1G04880
-220	TF_motif_seq_0263	(Motif sequence only)	+	0.8	TCCAC	SORLIP1AT
-219	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0.8	CCACT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-219	TFmatrixID_0788	ARID; Sox	+	0.87	ccacTATATactaac	AT1G04880
-218	TF_motif_seq_0133	(Motif sequence only)	+	0.71	CACTAtatactaac	14BPATERD1
-216	TF_motif_seq_0434	(Motif sequence only)	-	0.83	ctaTATAC	P1BS
-215	TF_motif_seq_0254	AP2; ERF	-	0.8	TATAT	AT3G14230
-214	TF_motif_seq_0254	AP2; ERF	+	0.8	ATATA	AT3G14230
-211	TF_motif_seq_0373	(Motif sequence only)	-	0.86	taCTAAC	MYB1LEPR
-209	TF_motif_seq_0267	Trihelix	-	0.8	CTAAC	AT5G01380
-209	TF_motif_seq_0366	(Motif sequence only)	+	0.86	CTAACcc	MYBATRD22
-194	TF_motif_seq_0261	(Motif sequence only)	+	1	GAGAC	SURECOREATSULTR11
-193	TF_motif_seq_0271	bZIP	+	0.8	AGACG	AT1G77920;AT3G12250;AT5G06950;AT5G06960;AT5G10030;AT5G65210;AT1G22070
-193	TF_motif_seq_0410	bHLH	-	0.75	agaCGGAT	AT1G32640
-192	TF_motif_seq_0258	Dehydrin	-	0.8	GACGG	U01377
-192	TF_motif_seq_0248	(Motif sequence only)	+	0.8	GACGG	MYBCOREATCYCB1
-189	TF_motif_seq_0237	GATA; tify	+	1	GGATT	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-189	TF_motif_seq_0252	Myb/SANT; MYB; ARR-B;MYB;ARR-B	+	1	GGATT	AT2G01760;AT3G16857;AT4G16110;AT4G18020;AT4G31920;AT5G58080;AT1G67710;AT1G49190;AT2G25180;AT5G49240
-189	TFmatrixID_0932	GATA	+	0.9	ggattGATCTaaaca	AT3G60530
-189	TF_motif_seq_0268	(Motif sequence only)	+	1	GGATT	ARR1AT
-188	TFmatrixID_0265	GATA; tify	-	0.96	gattGATCTa	AT2G45050;AT3G45170;AT3G51080;AT5G25830;AT5G66320
-188	TFmatrixID_0270	GATA; tify	-	1	gattGATCTa	AT2G28340;AT2G45050;AT4G34680;AT5G25830;AT5G66320
-187	TFmatrixID_0042	GATA; tify	-	0.95	attGATCTaa	AT5G25830
-187	TFmatrixID_0264	GATA; tify	-	1	attGATCTaa	AT2G45050;AT3G24050;AT5G25830;AT5G66320
-187	TFmatrixID_0267	GATA; tify	-	0.99	attGATCTaa	AT2G28340;AT2G45050;AT3G60530;AT5G25830;AT5G66320
-187	TFmatrixID_0271	GATA; tify	+	0.97	attGATCTaa	AT2G45050;AT3G45170;AT4G36240;AT5G25830;AT5G66320
-187	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	-	0.8	ATTGA	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-186	TFmatrixID_0263	GATA	-	1	ttGATCT	AT3G21175;AT4G24470
-186	TFmatrixID_0266	GATA; tify	+	0.99	ttGATCTaa	AT2G28340;AT2G45050;AT3G54810;AT5G25830;AT5G66320
-186	TF_motif_seq_0254	AP2; ERF	-	0.8	TTGAT	AT3G14230
-186	TFmatrixID_0934	GATA; tify	+	0.9	ttGATCTaaacagca	AT5G25830
-186	TF_motif_seq_0275	(Motif sequence only)	+	0.8	TTGAT	WBOXATNPR1
-185	TF_motif_seq_0237	GATA; tify	+	1	TGATC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-184	TF_motif_seq_0237	GATA; tify	-	1	GATCT	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-183	TF_motif_seq_0254	AP2; ERF	+	1	ATCTA	AT3G14230
-178	TF_motif_seq_0248	(Motif sequence only)	+	0.8	AACAG	MYBCOREATCYCB1
-176	TFmatrixID_0627	Homeodomain; bZIP; HD-ZIP; WOX	+	0.95	cagCAATCaa	AT4G35550
-174	TFmatrixID_0283	Homeodomain; HD-ZIP	-	0.97	gcAATCAaga	AT2G22800;AT2G44910;AT4G16780;AT4G37790;AT5G06710;AT5G47370
-174	TFmatrixID_0284	Homeodomain; HD-ZIP	-	0.95	gcAATCAaga	AT2G46680
-174	TFmatrixID_0286	Homeodomain; HD-ZIP	-	1	gcAATCAa	AT2G22800;AT3G60390;AT4G16780;AT4G37790;AT5G06710;AT5G47370
-174	TFmatrixID_0291	Homeodomain; bZIP; HD-ZIP; WOX	-	0.92	gcAATCAa	AT4G35550
-174	TFmatrixID_0299	Homeodomain; WOX	-	0.99	gcAATCAa	AT1G20700;AT1G20710
-174	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0.8	GCAAT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-172	TF_motif_seq_0237	GATA; tify	-	1	AATCA	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
-172	TF_motif_seq_0268	(Motif sequence only)	-	1	AATCA	ARR1AT
-171	TF_motif_seq_0254	AP2; ERF	+	0.8	ATCAA	AT3G14230
-171	TF_motif_seq_0275	(Motif sequence only)	-	0.8	ATCAA	WBOXATNPR1
-166	TF_motif_seq_0261	(Motif sequence only)	+	0.8	GAGAG	SURECOREATSULTR11
-163	TFmatrixID_0358	Myb/SANT	+	0.99	agtgGAATCg	AT5G18240
-163	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	-	0.8	AGTGG	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
-162	TFmatrixID_0758	AP2; ERF	+	0.86	gtgGAATCgatgaatcg	AT1G68550
-162	TF_motif_seq_0263	(Motif sequence only)	-	0.8	GTGGA	SORLIP1AT
-160	TFmatrixID_1028	Myb/SANT; G2-like	-	0.86	gGAATCgatgaatcg	AT1G49560
-160	TFmatrixID_1047	Myb/SANT	-	0.86	gGAATCgatgaatc	AT2G03500

-158	TF_motif_seq_0237	GATA; tify	-	1	AATCG	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620	
-158	TF_motif_seq_0268	(Motif sequence only)	-	1	AATCG	ARR1AT	
-157	TF_motif_seq_0254	AP2; ERF	+	0.8	ATCGA	AT3G14230	
-156	TF_motif_seq_0254	AP2; ERF	-	0.8	TCGAT	AT3G14230	
-155	TF_motif_seq_0237	GATA; tify	+	1	CGATG	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620	
-150	TF_motif_seq_0237	GATA; tify	-	1	AATCG	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620	
-150	TF_motif_seq_0268	(Motif sequence only)	-	1	AATCG	ARR1AT	
-149	TF_motif_seq_0254	AP2; ERF	+	0.8	ATCGA	AT3G14230	
-148	TFmatrixID_0604	B3	-	0.96	tcgaTGTAGa	AT4G31610	
-148	TF_motif_seq_0254	AP2; ERF	-	0.8	TCGAT	AT3G14230	
-148	TF_motif_seq_0052	(Motif sequence only)	-	0.7	tcgatGTAGA	LS5ATPR1	
-147	TF_motif_seq_0237	GATA; tify	+	1	CGATG	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620	
-145	TF_motif_seq_0254	AP2; ERF	+	0.8	ATGTA	AT3G14230	
-142	TF_motif_seq_0254	AP2; ERF	-	0.8	TAGAG	AT3G14230	
-140	TF_motif_seq_0261	(Motif sequence only)	+	0.8	GAGAA	SURECOREATSULTR11	
-138	TF_motif_seq_0267	Trihelix	-	0.8	GAAAC	AT5G01380	
-138	TF_motif_seq_0261	(Motif sequence only)	+	0.8	GAAAC	SURECOREATSULTR11	
-137	TFmatrixID_0968	C2H2	-	0.98	aAACTGaaact	AT1G13400	
-136	TF_motif_seq_0248	(Motif sequence only)	+	0.8	AACTG	MYBCOREATCYCB1	
-135	TFmatrixID_0912	Dof	-	0.85	actgaaactgagaagaAAAAGttgcgc	AT1G69570	
-133	TFmatrixID_0918	Dof	+	0.92	tgaaactgagaagaAAAAGtt	AT1G69570	
-132	TF_motif_seq_0267	Trihelix	-	0.8	GAAAC	AT5G01380	
-132	TF_motif_seq_0261	(Motif sequence only)	+	0.8	GAAAC	SURECOREATSULTR11	
-130	TF_motif_seq_0248	(Motif sequence only)	+	0.8	AACTG	MYBCOREATCYCB1	
-129	TFmatrixID_0900	Dof	-	0.94	actgagaagaAAAAGttgc	AT3G45610	
-127	TFmatrixID_0903	Dof	-	0.93	tgagaagaAAAAGttgcgc	AT5G02460	
-127	TFmatrixID_0922	Dof	+	0.93	tgagaagaAAAAGttgcgcgg	AT1G51700	
-126	TFmatrixID_0914	Dof	+	0.98	gagaagaAAAAGttg	AT2G37590	
-126	TF_motif_seq_0261	(Motif sequence only)	+	0.8	GAGAA	SURECOREATSULTR11	
-125	TFmatrixID_0890	Dof	-	0.96	agaagaAAAAGttgc	AT2G28810	
-124	TFmatrixID_0986	C3H Zinc finger	+	0.97	gaagaAAAAGttgc	AT3G12130	
-122	TFmatrixID_0238	Dof	+	1	agaAAAAGt	AT4G38000	
-121	TFmatrixID_0031	Dof	+	0.98	gaAAAAGttg	AT2G46590	
-121	TFmatrixID_0233	Dof	+	1	gaAAAAGttg	AT1G64620	
-121	TFmatrixID_0235	Dof	+	1	gaAAAAGt	AT3G21270	
-121	TFmatrixID_0239	Dof	+	0.99	gaAAAAGttg	AT5G39660	
-121	TFmatrixID_0240	Dof	+	1	gaAAAAG	AT5G60200	
-121	TFmatrixID_0243	Dof	+	1	gaAAAAGt	AT5G62940	
-121	TFmatrixID_0896	Dof	+	0.97	gaAAAAGttgc	AT1G64620	
-121	TFmatrixID_0905	Dof	+	0.96	gaAAAAGttgc	AT2G46590	
-121	TFmatrixID_0911	Dof	+	0.95	gaAAAAGttgcgc	AT2G46590	
-121	TFmatrixID_0917	Dof	+	0.98	gaAAAAGttgc	AT3G52440	
-121	TFmatrixID_0920	Dof	+	0.98	gaAAAAGttgc	AT4G38000	
-121	TFmatrixID_0985	C3H Zinc finger	+	0.97	gaAAAAGttgc	AT5G63260	
-121	TFmatrixID_0988	C3H Zinc finger	+	0.96	gaAAAAGttgc	AT5G63260	
-121	TF_motif_seq_0321	(Motif sequence only)	+	1	GAAAAa	GT1CONSENSUS	
-120	TFmatrixID_0234	Dof	+	1	aAAAAGt	AT2G37590	
-120	TFmatrixID_0237	Dof	+	0.99	aAAAAGttg	AT3G47500	
-120	TFmatrixID_1544	Dof	+	1	aAAAAGttg	AT1G64620	
-118	TF_motif_seq_0239	Dof	+	1	AAAGT	AT1G29160;AT1G64620;AT2G37590;AT3G21270;AT3G45610;AT3G47500;AT4G38000;AT5G39660;AT5G60200;AT5G60850;AT5G62940;AT2G46590;AT1G07640;AT1G21340;AT1G26790;AT1G47655;AT1G51700;AT1G69570;AT2G28510;AT2G28810;AT2G34140;AT3G50410;AT3G55370;AT3G61850;AT4G00940;AT4G21050;AT4G21080;AT4G24060;	
-115	TF_motif_seq_0267	Trihelix	+	0.8	GTTGC	AT5G01380	
-115	TF_motif_seq_0263	(Motif sequence only)	-	0.8	GTTGC	SORLIP1AT	
-112	TF_motif_seq_0285	CG-1; CAMTA;CAMTA	+	1	GCGCGg	AT2G22300;AT5G64220;AT1G67310;AT3G16940;AT5G09410	
-112	TF_motif_seq_0285	CG-1; CAMTA;CAMTA	-	1	gCGCGG	AT2G22300;AT5G64220;AT1G67310;AT3G16940;AT5G09410	
-112	TF_motif_seq_0340	(Motif sequence only)	+	1	GCGCGg	CGCGBOXAT	
-112	TF_motif_seq_0340	(Motif sequence only)	-	1	gCGCGG	CGCGBOXAT	
-111	TF_motif_seq_0510	(Motif sequence only)	-	0.85	cgCGGGAta	E2FAT	
-110	TFmatrixID_0339	Myb/SANT	+	0.93	gcgGGATAcca	AT1G74840	
-107	TF_motif_seq_0237	GATA; tify	+	1	GGATA	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620	
-106	TF_motif_seq_0243	GATA; tify	+	1	GATAC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620	
-106	TF_motif_seq_0267	Trihelix	+	0.8	GATAC	AT5G01380	
-106	TF_motif_seq_0261	(Motif sequence only)	+	0.8	GATAC	SURECOREATSULTR11	
-102	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0.8	CCAAA	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;	
-100	TFmatrixID_1557	bZIP	-	0,91	ctcaTGACGctc	AT1G08320	TGA9
-98	TFmatrixID_0199	bZIP	-	0,97	caTGACGctc	AT1G08320;AT1G68640;AT5G06839;AT5G65210	TGA1; (TGA9; PAN; BZIP65)
-98	TFmatrixID_1504	ZF-HD	-	0,9	catgacgctctTAATTatttcc	AT5G39760	HB23
-97	TF_motif_seq_0014	bZIP	+	0,7	ATGACgctct	AT5G06950	TGA2; AHBP-1B
-97	TF_motif_seq_0275	(Motif sequence only)	+	0,8	ATGAC	WBOXATNPR1	
-97	TFmatrixID_0196	bZIP	-	0,88	aTGACGct	AT1G08320;AT1G68640;AT5G06839;AT5G06960	TGA5/OBF5; (TGA9; PAN; BZIP65)
-97	TFmatrixID_1165	Myb/SANT; MYB	-	0,94	atgaCGCTCttaa	AT2G02820	MYB88
-96	TF_motif_seq_0080	AP2; ERF	-	0,73	tgacgcTCTTA	AT3G16770	RAP2.3/ERF72
-96	TF_motif_seq_0246	Homeodomain; TALE	+	1	TGACG	AT1G23380;AT1G62360;AT1G70510;AT4G08150	KNAT6; 2; 1…
-96	TF_motif_seq_0271	bZIP	+	1	TGACG	AT1G77920;AT3G12250;AT5G06950;AT5G06960;AT5G10030;AT5G65210;AT1G22070	TGA7; TGA6/BZIP45; TGA2/AHBP-
-96	TFmatrixID_1513	ZF-HD	+	0,94	tgacgctctTAATTa	AT3G28920	
-92	TFmatrixID_1504	ZF-HD	+	0,89	gctcttAATTAtttcctaattt	AT5G39760	
-91	TFmatrixID_1505	ZF-HD	+	0,96	ctctTAATTatttcc	AT5G65410	
-91	TFmatrixID_1511	ZF-HD	-	0,93	ctctTAATTatttcc	AT2G18350	
-91	TFmatrixID_1514	ZF-HD	-	0,94	ctctTAATTatttcc	AT2G18350	
-90	TFmatrixID_0058	Homeodomain; bZIP; HD-ZIP	+	0,94	tcttaATTATttcc	AT3G01470	
-90	TFmatrixID_0412	Sox; YABBY	+	1	tctTAATTat	AT1G23420	
-90	TFmatrixID_0540	Homeodomain; HD-ZIP; bZIP	-	0,91	tcttaaTTATTtcc	AT1G69780;AT3G01220;AT3G01470;AT5G15150	
-90	TFmatrixID_1069	WOX	+	0,93	tcTTAATtatt	AT3G03660	
-90	TFmatrixID_1088	Homeodomain; bZIP; HD-ZIP	-	0,95	tcttaaTTATTtcc	AT3G01470	
-90	TFmatrixID_1506	ZF-HD	-	0,99	tctTAATTatt	AT5G65410	
-90	TFmatrixID_1508	ZF-HD	-	0,98	tctTAATTatt	AT5G39760	
-89	TFmatrixID_0002	AT-Hook	+	0,97	ctTAATTatt	AT1G63480	
-89	TFmatrixID_0517	Homeodomain; HD-ZIP; bZIP	-	0,93	cttaaTTATTtc	AT1G69780;AT3G01220;AT3G01470;AT5G15150	HAT5
-89	TFmatrixID_0628	Homeodomain; bZIP; HD-ZIP; WOX	+	0,96	ctTAATTatt	AT4G35550	
-89	TFmatrixID_0628	Homeodomain; bZIP; HD-ZIP; WOX	-	0,96	cttAATTAtt	AT4G35550	
-89	TFmatrixID_1060	bZIP; Homeodomain; HD-ZIP	+	0,92	cttaaTTATTtcc	AT5G03790	
-89	TFmatrixID_1507	ZF-HD	-	0,96	cTTAATtatttccta	AT3G28920	
-89	TFmatrixID_1510	ZF-HD	-	0,98	cTTAATtattt	AT1G75240	
-89	TFmatrixID_1512	ZF-HD	-	0,98	cTTAATtatttccta	AT1G75240	
-88	TF_motif_seq_0241	ZF-HD	-	1	TTAAT	AT1G75240	
-88	TFmatrixID_0047	bZIP; Homeodomain; HD-ZIP	+	0,92	ttaATTATtt	AT1G52150	
-88	TFmatrixID_0412	Sox; YABBY	-	1	ttAATTAttt	AT1G23420	
-88	TFmatrixID_1057	Homeodomain; bZIP; HD-ZIP	-	0,96	ttaaTTATTtc	AT5G65310	
-88	TFmatrixID_1058	bZIP; Homeodomain; HD-ZIP	+	0,87	ttaATTATttcct	AT5G03790	

-88	TFmatrixID_1062	HD-ZIP	-	0,95	ttaaTTATTtc	AT5G66700	
-88	TFmatrixID_1073	Homeodomain; HD-ZIP	-	0,98	ttaaTTATTtc	AT1G69780	
-88	TFmatrixID_1078	Homeodomain; HD-ZIP	+	0,96	ttaATTATttc	AT3G01220	
-88	TFmatrixID_1086	Homeodomain; HD-ZIP	-	0,97	ttaaTTATTtc	AT1G69780	
-88	TFmatrixID_1087	Homeodomain; HD-ZIP	-	0,93	ttaaTTATTtc	AT2G22430	
-88	TFmatrixID_1089	Homeodomain; bZIP; HD-ZIP	-	0,98	ttaaTTATTtc	AT3G01470	
-88	TFmatrixID_1090	Homeodomain; HD-ZIP	-	0,98	ttaaTTATTtc	AT3G01220	
-87	TFmatrixID_0001	AT-Hook	+	0,99	tAATTAtttc	AT1G63480	
-87	TFmatrixID_0026	bZIP; Homeodomain; HD-ZIP	+	0,94	taATTATttc	AT5G03790	ATHB51
-87	TFmatrixID_0116	Homeodomain; bZIP; HD-ZIP	+	0,92	taaTTATTt	AT5G65310	
-87	TFmatrixID_0471	Homeodomain; HD-ZIP; bZIP	-	0,99	taATTATt	AT1G69780;AT3G01220;AT3G01470;AT5G15150	
-87	TFmatrixID_1513	ZF-HD	-	0,95	tAATTAtttcctaat	AT3G28920	
-86	TFmatrixID_0292	Homeodomain; HD-ZIP	+	0,95	aATTATtt	AT1G26960;AT1G69780;AT3G01220;AT4G40060;AT5G15150	
-85	TF_motif_seq_0241	ZF-HD	+	1	ATTAT	AT1G75240	
-85	TFmatrixID_0146	AT-Hook	-	0,99	ATTATttcc	AT4G21895;AT5G62260	
-83	TFmatrixID_1170	Myb/SANT; MYB	+	0,86	tatttCCTAAtttatt	AT3G53200	
-82	TF_motif_seq_0321	(Motif sequence only)	-	1	aTTTCC	GT1CONSENSUS	
-82	TFmatrixID_1151	MYB	+	0,86	atttCCTAAtttat	AT3G01530	
-82	TFmatrixID_1179	Myb/SANT; MYB	-	0,86	atttCCTAAtttatt	AT3G53200	
-81	TFmatrixID_1216	Myb/SANT; MYB	-	0,94	tttCCTAAtttattt	AT1G68320	
-80	TFmatrixID_1218	Myb/SANT; MYB	-	0,94	ttCCTAAtttatttt	AT1G25340	
-80	TFmatrixID_1376	AP2; B3; RAV	+	0,94	ttcctaatttattttTGTTGt	AT1G13260	
-79	TFmatrixID_1555	MYB	+	0,89	tCCTAAtt	AT3G01530	MYB57
-77	TF_motif_seq_0067	HB-PHD	+	0,73	CTAATttattt	AT4G29940	
-77	TF_motif_seq_0241	ZF-HD	-	1	CTAAT	AT1G75240	
-77	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0,8	CTAAT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;	
-76	TFmatrixID_0009	AT-Hook	+	1	taatTTATTt	AT4G35390	
-76	TFmatrixID_1375	AP2; B3; RAV	+	0,96	taatttattttTGTTGt	AT1G13260	
-74	TF_motif_seq_0254	AP2; ERF	+	0,8	ATTTA	AT3G14230	
-74	TFmatrixID_0142	AT-Hook	-	1	attTATTT	AT4G21895;AT5G62260	
-73	TFmatrixID_0131	AT-Hook	-	1	TTTATtttt	AT1G19485;AT1G48610	
-73	TFmatrixID_0136	AT-Hook	-	1	TTTATttt	AT4G21895;AT5G62260	
-73	TFmatrixID_0138	AT-Hook	-	1	ttTATTTt	AT4G21895;AT5G62260	
-70	TFmatrixID_1221	MYB	+	0,99	atttTTGTTgt	AT5G40330	MYB23
-69	TFmatrixID_0089	AP2; B3; RAV	-	0,96	ttttTGTTGttt	AT1G13260	
-67	TFmatrixID_0127	AP2; B3; RAV	-	0,93	ttTGTTGt	AT3G25730	
-66	TFmatrixID_0992	C3H	+	0,83	tTGTTGt	AT5G42820	
-65	TF_motif_seq_0255	AP2; RAV; B3	-	1	TGTTG	AT1G25560;AT1G13260	
-64	TF_motif_seq_0343	(Motif sequence only)	-	0,86	gtTGTTT	ANAERO1CONSENSUS	
-61	TFmatrixID_0222	CSD	-	0,97	gtTTTATt	AT2G21060;AT4G38680	
-59	TFmatrixID_0131	AT-Hook	-	1	TTTATtcac	AT1G19485;AT1G48610	
-59	TFmatrixID_0953	C2H2	-	0,99	tttatTCACTa	AT5G04390	
-56	TFmatrixID_0908	Dof	+	0,92	attcactaAAAAGgattat	AT1G64620	
-55	TF_motif_seq_0275	(Motif sequence only)	+	0,8	TTCAC	WBOXATNPR1	
-54	TFmatrixID_0924	Dof	+	0,94	tcactaAAAAGgattatta	AT4G21030	
-50	TFmatrixID_0891	Dof	+	0,93	taAAAAGgattatt	AT4G21080	
-48	TFmatrixID_1509	ZF-HD	+	0,86	aaaaggATTAT	AT1G14687	
-47	TF_motif_seq_0239	Dof	+	1	AAAGG	AT1G29160;AT1G64620;AT2G37590;AT3G21270;AT3G45610;AT3G47500;AT4G38000;AT5G39660;AT5G60200;AT5G60850;AT5G62940;AT2G46590;AT1G07640;AT1G21340;AT1G26790;AT1G47655;AT1G51700;AT1G69570;AT2G28510;AT2G28810;AT2G34140;AT3G50410;AT3G55370;AT3G61850;AT4G00940;AT4G21050;AT4G21080;AT4G24060;	
-47	TF_motif_seq_0248	(Motif sequence only)	+	0,8	AAAGG	MYBCOREATCYCB1	
-46	TF_motif_seq_0239	Dof	+	1	AAGGA	AT1G29160;AT1G64620;AT2G37590;AT3G21270;AT3G45610;AT3G47500;AT4G38000;AT5G39660;AT5G60200;AT5G60850;AT5G62940;AT2G46590;AT1G07640;AT1G21340;AT1G26790;AT1G47655;AT1G51700;AT1G69570;AT2G28510;AT2G28810;AT2G34140;AT3G50410;AT3G55370;AT3G61850;AT4G00940;AT4G21050;AT4G21080;AT4G24060;	
-44	TF_motif_seq_0237	GATA; tify	+	1	GGATT	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620	
-44	TF_motif_seq_0252	Myb/SANT; MYB; ARR-B;MYB;ARR-B	+	1	GGATT	AT2G01760;AT3G16857;AT4G16110;AT4G18020;AT4G31920;AT5G58080;AT1G67710;AT1G49190;AT2G25180;AT5G49240	
-44	TF_motif_seq_0268	(Motif sequence only)	+	1	GGATT	ARR1AT	
-43	TFmatrixID_0006	AT-Hook	+	0,95	gATTATtatt	AT4G14465	
-42	TF_motif_seq_0241	ZF-HD	+	1	ATTAT	AT1G75240	
-41	TFmatrixID_0790	ARID	+	1	TTATTa	AT3G13350	
-40	TFmatrixID_0006	AT-Hook	+	0,96	tATTATtata	AT4G14465	
-39	TF_motif_seq_0241	ZF-HD	+	1	ATTAT	AT1G75240	
-39	TFmatrixID_0793	ARID; Sox	+	0,83	attatTATATtatata	AT1G04880	
-38	TFmatrixID_0130	AT-Hook	-	0,98	ttatTATATt	AT1G19485;AT1G48610;AT4G17950	
-38	TFmatrixID_0788	ARID; Sox	+	0,94	ttatTATATtatata	AT1G04880	
-38	TFmatrixID_0790	ARID	+	1	TTATTa	AT3G13350	
-38	TFmatrixID_0915	Dof	+	0,91	ttattatattatatagtttttCTTTTtt	AT4G38000	
-37	TFmatrixID_0004	AT-Hook	-	0,9	tattATATTa	AT4G14465	
-37	TFmatrixID_0006	AT-Hook	+	0,97	tATTATatta	AT4G14465	
-37	TFmatrixID_0008	AT-Hook	-	0,94	tattATATTa	AT4G35390	
-37	TFmatrixID_0139	AT-Hook	+	0,98	tattaTATTA	AT4G21895;AT5G62260	
-37	TFmatrixID_0282	Homeodomain	+	1	tattaTATTAtat	AT2G36610	
-36	TF_motif_seq_0241	ZF-HD	+	1	ATTAT	AT1G75240	
-36	TFmatrixID_0146	AT-Hook	-	0,99	ATTATatta	AT4G21895;AT5G62260	
-34	TF_motif_seq_0254	AP2; ERF	-	0,8	TATAT	AT3G14230	
-34	TFmatrixID_0644	B3	+	0,78	tatattatatagtttttcTTTTTttttta	AT3G18990	
-34	TFmatrixID_0788	ARID; Sox	-	1	tatattATATAgttt	AT1G04880	
-34	TFmatrixID_0793	ARID; Sox	+	1	tatatTATATagtttt	AT1G04880	
-33	TFmatrixID_0130	AT-Hook	-	0,98	atatTATATa	AT1G19485;AT1G48610;AT4G17950	
-33	TFmatrixID_0644	B3	+	0,79	atattatatagtttttctTTTTTttttaa	AT3G18990	
-33	TFmatrixID_0894	Dof	+	0,93	atattatatagtttttCTTTTtttttaa	AT5G66940	
-32	TFmatrixID_0644	B3	+	0,81	tattatatagtttttcttTTTTTtttaat	AT3G18990	
-32	TFmatrixID_0895	Dof	+	0,95	tattatatagtttttCTTTTt	AT3G50410	
-31	TF_motif_seq_0241	ZF-HD	+	1	ATTAT	AT1G75240	
-31	TFmatrixID_0146	AT-Hook	-	0,99	ATTATatag	AT4G21895;AT5G62260	
-31	TFmatrixID_0644	B3	+	0,8	attatatagtttttctttTTTTTttaatt	AT3G18990	
-31	TFmatrixID_0888	Dof	-	0,9	attatatagtttttCTTTTtt	AT5G02460	
-31	TFmatrixID_0893	Dof	+	0,93	attatatagtttttCTTTTtt	AT2G28810	
-30	TFmatrixID_0644	B3	+	0,79	ttatatagtttttcttttTTTTTtaattg	AT3G18990	
-29	TF_motif_seq_0254	AP2; ERF	-	0,8	TATAT	AT3G14230	
-29	TFmatrixID_0644	B3	+	0,79	tatatagtttttcttttTTTTTaattgt	AT3G18990	
-29	TFmatrixID_0919	Dof	+	0,96	tatatagtttttCTTTTtt	AT3G55370	
-28	TF_motif_seq_0254	AP2; ERF	+	0,8	ATATA	AT3G14230	
-26	TFmatrixID_0909	Dof	-	0,97	atagtttttCTTTTtttttta	AT1G51700	
-26	TFmatrixID_1371	(Others)	-	0,95	atagtttttCTTTTt	AT3G21890	
-25	TF_motif_seq_0254	AP2; ERF	-	0,8	TAGTT	AT3G14230	
-25	TFmatrixID_0897	Dof	+	0,96	tagtttttCTTTTtt	AT2G37590	
-25	TFmatrixID_0899	Dof	+	0,98	tagtttttCTTTTtt	AT3G45610	
-25	TFmatrixID_0902	Dof	+	0,95	tagtttttCTTTTtttttttaa	AT5G66940	
-25	TFmatrixID_0921	Dof	+	0,92	tagtttttCTTTTtt	AT1G29160	
-25	TFmatrixID_0922	Dof	-	0,95	tagtttttCTTTTtttttttaa	AT1G51700	
-25	TFmatrixID_0924	Dof	-	0,93	tagtttttCTTTTtttttt	AT4G21030	
-24	TFmatrixID_0892	Dof	+	0,95	agtttttCTTTTtttttttaat	AT3G52440	
-24	TFmatrixID_0907	Dof	-	0,96	agtttttCTTTTtt	AT5G60850	
-24	TFmatrixID_0916	Dof	+	0,96	agtttttCTTTTttt	AT1G47655	
-23	TFmatrixID_0476	AT-Hook	-	0,97	gTTTTTcttttttttt	AT1G48610	
-23	TFmatrixID_0503	MADS box; MIKC	-	0,9	gttTTTCTtttttttttaatt	AT4G22950;AT5G10140;AT5G65050;AT5G65070;AT5G65080;AT1G77080;AT2G45650;AT3G57390;AT4G11880	FLC

-23	TFmatrixID_0648	B3	+	0,89	gttttcTTTTTtttttaa	AT3G18990
-23	TFmatrixID_0889	Dof	-	0,97	gtttttCTTTTtttttaatt	AT5G62940
-23	TFmatrixID_0903	Dof	+	0,96	gtttttCTTTTtttttaa	AT5G02460
-23	TFmatrixID_0906	Dof	-	0,97	gtttttCTTTTtttttaa	AT5G60850
-23	TFmatrixID_0908	Dof	-	0,97	gtttttCTTTTtttttaa	AT1G64620
-23	TFmatrixID_0910	Dof	-	0,94	gtttttCTTTTtttttaatt	AT1G29160
-23	TFmatrixID_0911	Dof	-	0,95	gtttttCTTTTtt	AT2G46590
-23	TFmatrixID_0912	Dof	+	0,93	gtttttCTTTTttttttaattgtattt	AT1G69570
-23	TFmatrixID_0913	Dof	-	0,92	gtttttCTTTTtttttaa	AT3G47500
-23	TFmatrixID_1377	B3	-	0,92	gtttttcTTTTTtttttaatt	AT1G49480
-22	TF_motif_seq_0321	(Motif sequence only)	-	1	tTTTTC	GT1CONSENSUS
-22	TFmatrixID_0648	B3	+	0,88	tttttctTTTTTttttaat	AT3G18990
-22	TFmatrixID_1331	NAC	-	0,91	tttttCTTTTttttttaattg	AT4G01540
-22	TFmatrixID_1377	B3	-	0,91	tttttctTTTTTttttaattg	AT1G49480
-21	TFmatrixID_0648	B3	+	0,89	ttttcttTTTTTtttaatt	AT3G18990
-21	TFmatrixID_0890	Dof	+	0,99	ttttCTTTTtttttt	AT2G28810
-21	TFmatrixID_0896	Dof	-	0,98	ttttCTTTTtt	AT1G64620
-21	TFmatrixID_0900	Dof	+	0,97	ttttCTTTTttttttaatt	AT3G45610
-21	TFmatrixID_0901	Dof	+	0,92	ttttCTTTTttttttaattgt	AT3G55370
-21	TFmatrixID_0904	Dof	+	0,9	ttttCTTTTttttttaat	AT3G47500
-21	TFmatrixID_0905	Dof	-	0,96	ttttCTTTTtt	AT2G46590
-21	TFmatrixID_0920	Dof	-	0,95	ttttCTTTTtt	AT4G38000
-21	TFmatrixID_0986	C3H Zinc finger	-	0,99	ttttCTTTTttttt	AT3G12130
-21	TFmatrixID_0988	C3H Zinc finger	-	0,95	ttttCTTTTtt	AT5G63260
-21	TFmatrixID_1377	B3	-	0,88	ttttcttTTTTTtttaattgt	AT1G49480
-21	TFmatrixID_1378	B3	-	0,93	ttttcTTTTTttttt	AT1G49480
-20	TFmatrixID_0648	B3	+	0,92	tttctttTTTTTttaattg	AT3G18990
-20	TFmatrixID_0914	Dof	-	0,95	tttCTTTTtttttta	AT2G37590
-20	TFmatrixID_1377	B3	-	0,85	tttctttTTTTTttaattgta	AT1G49480
-19	TFmatrixID_0648	B3	+	0,92	ttcttttTTTTTtaattgt	AT3G18990
-19	TFmatrixID_0918	Dof	-	0,94	ttCTTTTttttttaattgtat	AT1G69570
-19	TFmatrixID_1378	B3	-	0,94	ttcttTTTTTtttaa	AT1G49480
-18	TF_motif_seq_0239	Dof	-	1	TCTTT	AT1G29160;AT1G64620;AT2G37590;AT3G21270;AT3G45610;AT3G47500;AT4G38000;AT5G39660;AT5G60200;AT5G60850;AT5G62940;AT2G46590;AT1G07640;AT1G21340;AT1G26790;AT1G47655;AT1G51700;AT1G69570;AT2G28510;AT2G28810;AT2G34140;AT3G50410;AT3G55370;AT3G61850;AT4G00940;AT4G21050;AT4G21080;AT4G24060;
-18	TFmatrixID_1378	B3	-	0,93	tctttTTTTTttaat	AT1G49480
-10	TFmatrixID_0792	ARID	-	0,89	tttTAATTgtatttt	AT2G17410
-8	TF_motif_seq_0241	ZF-HD	-	1	TTAAT	AT1G75240
-5	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	-	0,8	ATTGT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
2	TF_motif_seq_0321	(Motif sequence only)	-	1	tTTTTC	GT1CONSENSUS
3	TF_motif_seq_0321	(Motif sequence only)	-	1	tTTTCC	GT1CONSENSUS
7	TFmatrixID_1230	Myb/SANT	+	0,98	cctcgaAATATctaa	AT3G10113
8	TFmatrixID_1231	MYB-related	+	0,98	ctcgaAATATctaa	AT5G17300
8	TFmatrixID_1241	Myb/SANT; MYB-related	-	0,97	ctcgaaATATCt	AT5G52660
8	TFmatrixID_1247	Myb/SANT; MYB-related	-	0,97	ctcgaaATATCt	AT3G09600
9	TFmatrixID_1232	Myb/SANT; MYB-related	+	0,97	tcgaAATATct	AT1G18330
9	TFmatrixID_1236	Myb/SANT; MYB-related	-	0,97	tcgaaATATCt	AT3G09600
9	TFmatrixID_1242	Myb/SANT; MYB-related	-	0,99	tcgaaATATCt	AT1G01060
9	TFmatrixID_1243	Myb/SANT; MYB-related	-	0,98	tcgaaATATCt	AT4G01280
9	TFmatrixID_1249	Myb/SANT; MYB-related	-	0,96	tcgaaATATCt	AT4G01280
9	TFmatrixID_1258	Myb/SANT; MYB-related	-	0,96	tcgaaATATCt	AT5G52660
9	TFmatrixID_1261	Myb/SANT; MYB-related	-	0,97	tcgaaATATCt	AT5G02840
10	TFmatrixID_1229	Myb/SANT; MYB-related	+	0,96	cgaAATATctaa	AT1G18330
10	TFmatrixID_1237	Myb/SANT; MYB-related	-	0,98	cgaaATATCt	AT1G01060
10	TFmatrixID_1244	MYB-related	-	1	cgaaATATCt	AT5G17300
10	TFmatrixID_1255	Myb/SANT; MYB-related	-	0,95	cgaAATATct	AT5G02840
10	TFmatrixID_1366	(Others)	+	0,99	cgaaATATCt	AT2G28920
11	TFmatrixID_0029	MYB-related	+	0,98	gaaATATCta	AT2G46830
11	TFmatrixID_0334	Myb/SANT; MYB-related	+	1	gaaATATCt	AT1G18330;AT3G10113
11	TFmatrixID_0609	MYB-related	+	0,97	gaaATATCta	AT5G17300
11	TFmatrixID_1517	Myb/SANT; MYB-related	-	1	gaaATATCta	AT1G18330
11	TFmatrixID_1521	Myb/SANT; MYB-related	+	1	gaaATATCta	AT3G09600
11	TFmatrixID_1522	Myb/SANT; MYB-related	+	1	gaaATATCta	AT4G01280
12	TFmatrixID_0320	Myb/SANT; MYB-related	-	1	aaATATCta	AT1G01520;AT3G09600;AT4G01280;AT5G02840;AT5G52660
12	TFmatrixID_0364	Myb/SANT; MYB-related	+	1	aaATATCt	AT3G09600;AT4G01280
12	TFmatrixID_0369	Myb/SANT; MYB-related	+	1	aaATATCta	AT1G01060;AT5G37260
12	TFmatrixID_0610	MYB-related	+	1	aaATATCtaa	AT5G17300
13	TFmatrixID_1525	Myb/SANT; MYB-related	+	1	aATATCta	AT5G52660
14	TF_motif_seq_0243	GATA; tify	-	1	ATATC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
15	TF_motif_seq_0237	GATA; tify	-	1	TATCT	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
16	TF_motif_seq_0254	AP2; ERF	+	1	ATCTA	AT3G14230
18	TF_motif_seq_0241	ZF-HD	-	1	CTAAT	AT1G75240
18	TF_motif_seq_0257	NF-YB;NF-YA;NF-YC	+	0,8	CTAAT	AT1G09030;AT1G17590;AT1G21970;AT1G30500;AT1G54160;AT1G54830;AT1G56170;AT1G72830;AT2G38880;AT2G47810;AT3G05690;AT3G14020;AT3G20910;AT3G53340;AT4G14540;AT5G06510;AT5G12840;AT5G27910;AT5G38140;AT5G47640;AT5G47670;
20	TF_motif_seq_0237	GATA; tify	-	1	AATCC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
20	TF_motif_seq_0252	Myb/SANT; MYB; ARR-B;MYB;ARR-B	-	1	AATCC	AT2G01760;AT3G16857;AT4G16110;AT4G18020;AT4G31920;AT5G58080;AT1G67710;AT1G49190;AT2G25180;AT5G49240
20	TF_motif_seq_0268	(Motif sequence only)	-	1	AATCC	ARR1AT
21	TF_motif_seq_0254	AP2; ERF	+	0,8	ATCCA	AT3G14230
22	TF_motif_seq_0263	(Motif sequence only)	+	0,8	TCCAC	SORLIP1AT
26	TF_motif_seq_0254	AP2; ERF	-	0,8	CAGAT	AT3G14230
27	TF_motif_seq_0237	GATA; tify	+	1	AGATA	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
28	TF_motif_seq_0243	GATA; tify	+	1	GATAG	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
30	TF_motif_seq_0254	AP2; ERF	-	1	TAGAT	AT3G14230
31	TF_motif_seq_0237	GATA; tify	+	1	AGATA	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
32	TF_motif_seq_0243	GATA; tify	+	1	GATAG	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
34	TFmatrixID_0214	C2H2	+	0,98	tagaACACTctgt	AT2G28710;AT2G37430;AT3G46070;AT3G46080;AT3G46090
34	TF_motif_seq_0254	AP2; ERF	-	0,8	TAGAA	AT3G14230
35	TF_motif_seq_0010	HSF	+	0,88	AGAACactct	AT3G24520;AT1G32330;AT1G46264;AT1G67970;AT2G26150;AT2G41690;AT3G02990;AT3G22830;AT3G51910;AT3G63350;AT4G11660;AT4G13980;AT4G17750;AT4G18880;AT5G03720;AT5G16820;AT5G43840;AT5G45710;AT5G54070;AT5G62020
37	TFmatrixID_0211	C2H2	+	1	aACACTc	AT1G27730;AT3G49930;AT3G60580;AT5G04340;AT5G43170
37	TFmatrixID_0213	C2H2	+	1	aACACTc	AT1G02030;AT2G45120;AT3G19580;AT3G49930;AT3G60580;AT5G04340;AT5G43170
45	TFmatrixID_1233	Myb/SANT; MYB-related	+	0,92	gtgagctTTATCcgct	AT5G56840
46	TFmatrixID_1239	Myb/SANT	+	0,93	tgagctTTATCcgct	AT5G47390
48	TFmatrixID_1050	Storekeeper	+	0,92	agctTTATCcgct	AT4G00250
48	TFmatrixID_1240	Myb/SANT	+	0,92	agctTTATCcgctt	AT1G19000

48	TFmatrixID_1245	Myb/SANT	-	0,92	agcttTATCCgctt	AT1G19000
48	TFmatrixID_1250	Myb/SANT; MYB-related	+	0,9	agctTTATCCgcttc	AT5G56840
48	TFmatrixID_1253	Myb/SANT; MYB-related	-	0,91	agcttTATCCgcttc	AT5G61620
48	TFmatrixID_1265	Myb/SANT	+	0,93	agcttTATCCgctt	AT1G74840
48	TFmatrixID_1266	Myb/SANT	-	0,91	agctTTATCcgctt	AT5G47390
49	TFmatrixID_0353	Myb/SANT	+	0,96	gctTTATCcg	AT5G04760
49	TF_motif_seq_0239	Dof	-	1	GCTTT	AT1G29160;AT1G64620;AT2G37590;AT3G21270;AT3G45610;AT3G47500;AT4G38000;AT5G39660;AT5G60200;AT5G60850;AT5G62940;AT2G46590;AT1G07640;AT1G21340;AT1G26790;AT1G47655;AT1G51700;AT1G69570;AT2G28510;AT2G28810;AT2G34140;AT3G50410;AT3G55370;AT3G61850;AT4G00940;AT4G21050;AT4G21080;AT4G24060;
50	TFmatrixID_0326	Myb/SANT	+	0,98	cttTATCCgc	AT1G70000
50	TFmatrixID_0331	Myb/SANT	+	1	cttTATCCgc	AT3G16350
50	TFmatrixID_0339	Myb/SANT	-	0,91	cttTATCCgct	AT1G74840
50	TFmatrixID_0356	Myb/SANT	+	1	ctTTATCcg	AT5G08520
50	TFmatrixID_0361	Myb/SANT	+	0,98	ctTTATCcgc	AT1G70000;AT3G16350;AT5G47390
50	TFmatrixID_0372	Myb/SANT	+	1	cttTATCCg	AT1G70000;AT3G16350
50	TFmatrixID_1246	Myb/SANT; MYB-related	+	0,92	ctTTATCcgct	AT5G61620
50	TFmatrixID_1248	Myb/SANT	-	0,94	cttTATCCgct	AT1G74840
50	TFmatrixID_1515	Myb/SANT; MYB-related	-	1	ctTTATCcg	AT4G09450
50	TFmatrixID_1530	Myb/SANT; MYB	-	0,99	ctTTATCcgc	AT3G11280
51	TFmatrixID_0131	AT-Hook	-	1	TTTATccgc	AT1G19485;AT1G48610
51	TFmatrixID_0319	Myb/SANT	-	1	ttTATCCgct	AT3G16350
51	TFmatrixID_0328	Myb/SANT	-	0,99	ttTATCCg	AT1G70000;AT3G16350
51	TFmatrixID_0335	Myb/SANT	-	0,99	ttTATCCgct	AT1G19000
51	TFmatrixID_1524	Myb/SANT	+	0,99	ttTATCCgct	AT3G16350
51	TF_motif_seq_0321	(Motif sequence only)	-	1	tTTATC	GT1CONSENSUS
52	TF_motif_seq_0243	GATA; tify	-	1	TTATC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
52	TF_motif_seq_0336	(Motif sequence only)	+	1	TTATCc	SREATMSD
53	TF_motif_seq_0237	GATA; tify	-	1	TATCC	AT1G51600;AT2G45050;AT3G06740;AT3G16870;AT3G21175;AT3G24050;AT3G54810;AT3G60530;AT4G17570;AT4G24470;AT4G26150;AT4G32890;AT4G34680;AT5G25830;AT5G26930;AT5G56860;AT5G66320;AT2G18380;AT3G50870;AT4G36620
56	TF_motif_seq_0248	(Motif sequence only)	-	0,8	CCGCT	MYBCOREATCYCB1