

Supplementary 1

1. MaPR-10 molecular weight (mW) and theoretical isoelectric point (pI).

Num	Accession Numbers	mW (Da)	Theoretical pI
1	Ma08_p34150.1	17404.89	5.41
2	Ma01_p19550.1	17601.25	5.37
3	Ma08_p34160.1	20596.50	5.91
4	Ma03_p08150.1	17131.56	5.23
5	Ma03_p08160.1	17149.61	5.42
6	Ma09_p15840.1	17178.51	4.84
7	Ma03_p08140.1	17115.58	5.20
8	Ma03_p10130.1	16682.80	4.66
9	Ma04_p33910.1	22445.64	5.66
10	Ma09_p17720.1	15931.18	5.34

Supplementary 2

1. MaPR-10 signal peptide prediction.

Num	Accession Numbers	Signal Peptide (Sec/SPI)	Other
1	Ma08_p34150.1	0.0014	0.9986
2	Ma01_p19550.1	0.0045	0.9955
3	Ma08_p34160.1	0.0015	0.9985
4	Ma03_p08150.1	0.0011	0.9989
5	Ma03_p08160.1	0.0013	0.9987
6	Ma09_p15840.1	0.0013	0.9987
7	Ma03_p08140.1	0.0011	0.9989
8	Ma03_p10130.1	0.0006	0.9994
9	Ma04_p33910.1	0.0008	0.9992
10	Ma09_p17720.1	0.0006	0.9994

Supplementary 3

1. MaPR-10 protein characteristics.

Num	Accession Numbers	Residues Charge (%)		Polar residues (%)	Hydrophobic residues (%)	Aliphatic index	Grand Average of Hydropathicity (GRAVY)
		Negative	Positive				
1	Ma08_p34150.1	14.37	14.37	20.00	51.25	78.63	-0.096
2	Ma01_p19550.1	15.00	14.37	19.38	51.25	84.75	-0.061
3	Ma08_p34160.1	13.37	16.04	22.99	47.59	87.11	-0.209
4	Ma03_p08150.1	13.13	11.88	20.63	54.37	90.25	-0.005
5	Ma03_p08160.1	12.50	11.88	20.00	55.63	88.88	0.023
6	Ma09_p15840.1	13.75	10.63	21.25	54.37	95.00	0.111
7	Ma03_p08140.1	13.13	11.88	20.00	55.00	90.25	0.036
8	Ma03_p10130.1	16.67	11.33	25.33	46.67	81.87	-0.338
9	Ma04_p33910.1	13.11	13.11	19.90	53.88	94.56	-0.080
10	Ma09_p17720.1	11.34	15.06	22.70	51.10	92.62	-0.245

Supplementary 4

1. MaPR-10 protein sequence similarities and identities (SIAS).

1a. MaPR-10 protein sequence identity.

Ma08_p34 150.1	100%						
Ma01_p19 550.1	66.87%	100%					
Ma08_p34 160.1	3.75%	2.5%	100%				
Ma03_p08 150.1	28.12%	28.74%	5%	100%			
Ma03_p08 160.1	26.25%	28.12%	6.25%	80.62%	100%		
Ma09_p15 840.1	26.25%	27.5%	5%	86.25%	80%	100%	

Ma03_p08 140.1	27.5%	28.12%	5%	98.12%	79.37%	86.25%	100%			
Ma03_p10 130.1	10.06%	11.4%	9.39%	10.73%	10.73%	11.4%	11.4%	100%		
Ma04_p33 910.1	5%	5%	7.48%	6.87%	7.5%	6.87%	6.87%	10.06%	100%	
Ma09_p17 720.1	12.05%	9.92%	4.25%	6.38%	7.09%	7.8%	6.38%	39%	8.51%	100%
	Ma08_p34 150.1	Ma01_p19 550.1	Ma08_p34 160.1	Ma03_p08 150.1	Ma03_p08 160.1	Ma09_p15 840.1	Ma03_p08 140.1	Ma03_p10 130.1	Ma04_p33 910.1	Ma09_p17 720.1

Identity Stats

Min = 2.5

Max = 98.12

Mean = 23.5048888888889

1b. MaPR-10 protein sequence similarity.

Ma08_p34 150.1	100%							
Ma01_p19 550.1	75.62%	100%						
Ma08_p34 160.1	11.25%	11.25%	100%					
Ma03_p08 150.1	40.62%	42.5%	13.12%	100%				
Ma03_p08 160.1	41.87%	45%	15%	85.62%	100%			
Ma09_p15 840.1	40.62%	43.75%	13.75%	91.87%	86.25%	100%		
Ma03_p08 140.1	39.37%	41.25%	13.12%	98.75%	85%	91.25%	100%	

Ma03_p10 130.1	20.8%	24.83%	16.77%	20.13%	20.13%	19.46%	20.13%	100%		
Ma04_p33 910.1	10.62%	11.25%	14.43%	10.62%	11.87%	11.87%	10.62%	16.77%	100%	
Ma09_p17 720.1	17.73%	18.43%	9.92%	12.05%	14.18%	13.47%	12.05%	46.8%	18.43%	100%
	Ma08_p34 150.1	Ma01_p19 550.1	Ma08_p34 160.1	Ma03_p08 150.1	Ma03_p08 160.1	Ma09_p15 840.1	Ma03_p08 140.1	Ma03_p10 130.1	Ma04_p33 910.1	Ma09_p17 720.1

Identity Stats

Min = 9.92

Max = 98.75

Mean = 32.5257858254032

Supplementary 5: Cis-acting elements in MaPR-10s

	Ma08_p34150.1	Ma01_p19550.1	Ma08_p34160.1	Ma03_p08150.1	Ma03_p08160.1	Ma09_p15840.1	Ma03_p08140.1	Ma03_p10130.1	Ma04_p33910.1	Ma09_p17720.1	Total	Function relatedness
-10EPHVSBD	/	/	/	/	/	/	/	/	0	0	8	Light
BOXCPSA51	0	0	0	0	/	/	0	0	0	/	3	
GT1CORE	0	0	/	0	0	0	0	0	/	/	3	
ASF1MOTIFCAMV	0	/	/	/	/	/	/	0	/	/	8	
SORLIP1AT	/	0	0	/	/	/	/	/	/	/	8	
CIACADIANLELHC	/	0	/	/	0	0	0	0	/	/	5	
SORLIP5AT	0	0	/	0	0	0	0	0	0	0	1	
CGCGBOXAT	0	0	0	/	0	0	/	0	/	0	2	
TBOXATGAPB	/	0	/	0	/	0	0	/	/	0	7	
BOXHPCCH5	0	0	/	0	0	0	/	0	/	0	2	
IBOX	0	0	/	0	/	/	0	/	0	/	5	
LRENPCABE	0	0	0	0	0	0	/	0	0	0	1	
AT1BOX	0	0	0	0	0	/	0	0	0	0	1	
MNF12MPPC1	0	/	0	0	0	0	0	0	0	0	1	
SORLIP2AT	0	0	0	0	0	0	0	0	/	0	1	
HDZIP2ATATHB2	0	0	0	/	0	0	0	0	0	0	1	
IBOXCORENT	0	0	/	0	/	/	0	/	0	0	4	
BOXCPSA51	0	0	0	0	0	/	0	0	0	/	2	
DRECRTCOREAT	/	/	/	0	0	0	/	/	/	0	6	
GATABOX	/	/	/	/	/	/	/	/	/	/	10	
INRNTP5ADB	/	/	/	/	/	/	/	/	/	/	10	
GT1CONSENSUS	/	/	/	/	/	/	/	/	/	/	10	
IBOXCORE	/	/	/	/	/	/	/	/	/	/	10	
INRNTP5ADB	/	/	/	/	/	/	/	/	/	/	10	
REALPHALGLHCB21	0	0	0	/	/	/	0	0	0	/	5	
CCA1ATHCB1	/	/	0	0	0	/	0	0	0	0	3	
LTRECOREATCOR15	/	/	/	/	/	/	/	/	/	0	9	
BOXINTPATPB	0	0	/	/	/	/	/	/	0	/	7	
PRECONSCRHSP70A	0	/	/	/	/	0	/	/	/	/	8	
TELOBOXATEEF1AA1	0	0	0	0	/	0	/	0	/	0	3	
S1FSORPL21	0	0	0	0	/	0	0	0	0	0	1	
S1FBOXSORP51L21	/	0	/	/	/	0	/	/	/	/	8	
ABRELATERD1	0	0	0	/	/	/	/	0	/	/	6	
ACGTATERD1	/	/	/	/	/	/	/	/	/	/	10	
CPBCSPOR	0	0	0	0	0	0	0	0	0	/	2	
MYCCONSENSUSAT	/	/	/	/	/	/	/	/	/	/	10	
MYCATRD22	/	/	0	/	0	/	0	0	/	/	6	
DPBFCOREDCD3	/	/	/	/	/	/	/	/	/	/	9	
LTRECOREATCOR15	/	/	/	/	/	/	/	/	/	0	9	
ACGTABREMOTIFAZOSEM	0	0	0	0	0	0	/	0	/	0	2	
PROXBNNAPA	0	0	0	0	0	/	0	0	0	0	1	ABA
MYB1AT	0	/	0	/	/	0	/	0	/	/	6	
MYB2CONSENSUSAT	0	/	/	0	/	0	0	0	/	/	6	
DRE2COREZMRAB17	0	/	/	0	0	0	0	/	0	0	3	
ATHB6COREAT	/	0	0	0	0	0	0	0	0	/	2	
MYBATRD22	0	/	0	0	0	0	0	/	0	0	2	
ACGTABREMOTIFAZOSEM	0	0	0	0	0	0	0	0	/	0	1	
ABREMOTIFAZOSEM	0	0	0	0	0	0	0	0	/	0	1	
ABREZMRAB28	0	0	0	0	0	0	0	0	/	0	1	
CGCGBOXAT	0	0	0	0	0	0	/	0	/	0	2	
PYRIMIDINEBOXHVEPB1	0	/	0	0	0	0	/	0	0	/	3	
CAREOSREP1	0	0	/	0	/	/	/	0	0	0	4	GA
WRK7105	/	/	/	/	/	/	/	/	/	/	10	
PYRIMIDINEBOXSAM1A	/	/	/	/	/	/	/	/	/	/	10	
GAREAT	0	0	/	0	0	0	0	/	/	/	4	
GADOWNAT	0	0	0	0	0	0	0	0	/	0	1	
GAREAT	0	0	/	0	0	0	0	0	/	0	2	
GAREZOSREP1	0	0	/	0	/	0	0	0	0	0	2	
TATCCAOSAMY	0	0	0	0	0	/	0	/	0	/	3	
TATCCACHVAL21	0	0	0	0	0	/	0	0	0	/	2	
PYRIMIDINEBOXHVEPB1	0	/	0	0	0	0	/	0	0	/	3	
LECPLEACS2	/	0	/	0	0	0	0	0	0	0	2	Ethylene
GCCCORE	0	0	0	0	0	0	/	0	/	0	2	
RAV1AAT	/	/	/	/	/	/	/	/	0	/	9	
CGCGBOXAT	0	0	0	0	0	0	/	0	/	0	2	
AGCBONNPGLB	0	0	0	0	0	0	/	0	0	0	1	
ERLEE4	0	0	0	/	0	0	0	0	0	0	1	Auxin
ASF1MOTIFCAMV	0	/	/	/	/	/	/	0	/	/	8	
AWFAT	0	/	0	0	/	0	0	0	/	0	3	
AUXREPSIAA4	0	0	0	0	0	0	0	0	/	0	1	
NTBFL1ARROLB	/	/	/	/	/	/	/	/	/	0	9	
CATATGMSAUR	0	0	/	/	0	/	0	0	0	/	3	
ACGTOSGLUB1	0	0	0	0	0	0	0	0	0	/	1	
AUXRETGA1GMGH3	0	0	/	0	0	0	0	0	0	0	1	
WBOXATNPR1	/	/	/	/	/	/	/	/	/	/	10	
ELRECOREPCRP1	/	/	0	/	/	/	/	0	0	/	6	SA
ASF1MOTIFCAMV	0	/	/	/	/	/	/	0	/	/	8	
PALINDROMICCBXGGM	0	0	0	0	0	0	0	0	/	0	1	Cytokinin
CPBCSPOR	0	0	0	0	0	/	0	0	0	/	2	
T/GBOXATPIN2	0	0	0	0	0	0	/	0	0	0	1	MeJA
GCCCORE	0	0	0	0	0	0	/	0	/	0	2	
CAATBOX1	/	/	/	/	/	/	/	/	/	/	10	Seed
RYREPEATLEGUMINBOX	0	0	/	0	0	/	/	0	0	0	3	
ZSSEEDPROTANAPA	0	0	0	0	0	/	0	0	0	0	1	
SEF3MOTIFGM	0	0	0	/	/	/	/	/	0	0	4	
RYREPEATGMGY2	0	0	0	0	0	/	0	0	0	0	1	
SEF1MOTIF	0	/	0	/	/	0	0	0	0	0	3	
ACGTCTBOX	0	/	0	0	0	0	0	0	/	0	2	
RYREPEATBNNAPA	0	0	/	/	/	/	/	0	0	/	6	
PROXBNNAPA	0	0	0	0	0	/	0	0	0	0	1	
SEF4MOTIFGM75	/	0	/	/	/	/	/	/	/	/	9	
CERGLUBOX3PSLEGA	0	/	0	0	0	0	0	0	0	0	1	
NAPINMOTIFBN	0	0	0	0	0	0	0	0	0	/	1	Water-related
ACGTABOX	/	0	0	0	0	0	0	0	0	0	1	
CERGLUBOX2PSLEGA	0	0	0	0	0	0	0	0	0	/	1	
CANBNNAPA	0	0	0	0	/	0	0	0	0	0	1	
AMYBOX2	0	0	0	0	0	0	0	0	/	0	1	
AMYBOX1	0	0	/	0	/	0	0	0	/	0	3	
TGACCTVIMAMY	0	/	/	/	0	/	0	0	/	0	4	
CARGCWGAT	/	/	/	/	/	/	/	/	/	/	9	
DPBFCOREDCD3	/	0	0	0	/	0	0	0	/	/	9	
CACGTGMOTIF	0	0	0	0	/	0	0	0	0	0	1	
AACACOREOSGLUB1	0	0	/	/	0	/	0	/	0	0	4	
GCN4OSGLUB1	0	0	0	0	0	/	0	0	0	0	1	
PROLAMINBOXOSGLUB1	0	0	0	0	0	0	0	0	0	/	1	
(-)300ELEMENT	0	0	0	/	/	0	/	0	0	/	4	
EMHVCHORD	0	0	0	/	0	0	0	0	0	0	1	
(-)300CORE	0	0	0	/	0	0	0	0	0	0	1	
MYB2AT	0	0	/	0	0	0	0	/	0	/	3	
ABRELATERD1	0	0	0	/	/	/	/	0	/	/	6	
MYBATRD22	0	/	0	0	0	0	0	/	0	0	2	
ACGTATERD1	/	/	/	/	/	/	/	/	/	/	10	
ACGTABREMOTIFAZOSEM	0	0	0	0	0	0	0	/	0	0	2	
MYB2CONSENSUSAT	0	/	/	0	0	0	/	/	/	/	6	
DRECRTCOREAT	/	/	/	0	0	0	/	/	/	0	7	
CBFHV	/	/	/	0	/	0	/	/	/	/	8	
MYBCORE	/	/	/	/	/	0	0	/	/	/	8	
MYCATRD22	/	/	0	/	0	/	0	0	/	/	6	

MJBMB, 2022, 2, 1 – 11: FUNCTIONAL PREDICTION OF PATHOGENESIS-RELATED 10 IN *Musa acuminata* DH PAHANG (MaPR-10) FOR TARGETED BANANA ADAPTATION AGAINST STRESSES

MYB1AT	0	/	0	/	/	/	0	/	0	/	6	
DREZCOREZMRAB17	0	/	/	0	0	0	0	/	0	0	3	
MYCATERD1	/	/	0	/	/	/	0	0	/	/	7	
LTRECOREATCOR15	/	/	/	/	/	/	/	/	/	0	9	
MYCSENSUSAT	/	/	/	/	/	/	/	/	/	/	10	
PREATPRODH	0	0	0	/	0	0	0	0	0	0	1	
SREATMSD	0	0	0	0	0	/	0	/	0	0	2	
TATCCAYMOTIFOSRAMY3D	0	0	0	0	0	/	0	/	0	0	3	
ACGTABOX	/	0	0	0	0	0	0	0	0	0	1	
PYRIMIDINEBOXOSRAMY1A	/	/	/	/	/	/	/	/	/	/	10	Sugar
WBOXHVUSJ1	/	/	/	/	/	/	/	/	/	/	10	
TATCCASAMV	0	0	0	0	0	/	0	/	0	/	3	
CGACGOSAMV3	/	/	/	0	0	/	0	0	/	/	6	
ACGTBOX	0	/	0	0	0	0	0	0	/	0	2	
MYBCOREATCYCB1	/	0	/	/	/	/	0	0	/	0	5	
E2FANTRNR	0	0	0	0	0	0	/	0	0	0	1	
E2FCONSENSUS	0	/	0	0	/	/	/	0	/	0	5	Cell cycle
E2F1OSPNA	0	0	0	0	0	0	/	0	0	0	1	
MARTBOX	0	/	/	/	/	/	/	0	0	/	7	
MARARS	0	/	0	/	0	/	0	0	0	0	3	
LTRECOREATCOR15	/	/	/	/	/	/	/	/	/	0	9	
CRDREHVCBF2	0	0	0	0	0	0	0	0	/	0	1	
LTREATLT78	0	0	/	0	0	0	0	0	0	0	1	
DRECRTCOREAT	/	/	/	0	0	0	/	/	/	0	6	
MYCSENSUSAT	/	/	/	/	/	/	/	/	/	/	10	
CBPHV	0	/	/	0	/	0	/	/	/	0	7	
ACGTBOX	0	/	0	0	0	0	0	0	/	0	2	
CTRMCAHV355	/	0	/	0	0	/	0	0	/	0	4	
SVADCORENHAN	0	0	0	0	/	0	0	0	/	0	2	
PALBOXAPC	0	0	0	0	0	0	0	0	/	/	3	
PALBOXPPC	0	1	0	0	0	0	0	0	0	0	1	
PALBOXLPC	0	1	0	0	0	0	0	0	0	0	1	
WBOXNXTCHN48	/	0	/	0	/	0	/	/	/	0	6	
WBOXPCWRKY1	/	/	0	/	/	/	0	0	/	0	6	
AGMOTIFNTMYB2	0	0	0	0	0	0	0	0	0	/	1	
BOXLCOREDCPAL	/	/	0	/	/	/	/	0	/	/	8	
ACIPVPAL2	0	0	0	0	/	0	/	0	0	0	2	
BS1EGCCR	0	0	0	0	0	/	0	0	0	0	1	
XYLAT	0	0	/	0	0	0	0	/	/	0	3	
RGATAOS	0	0	0	0	0	0	0	0	0	0	1	
AMMORESIVUCRNIA1	0	0	0	0	0	0	0	/	0	0	1	
BHD1OS	/	/	/	/	/	/	/	/	/	/	10	
GT1GMSCAM4	/	/	/	/	/	/	/	/	/	/	10	
WRKY71OS	/	/	/	/	/	/	/	/	/	/	10	
OSE1ROOTNODULE	0	/	/	/	/	/	/	/	0	/	8	
SEBFCONSSTPR10A	0	/	0	/	0	0	/	/	/	0	5	
ROOTMOTIFTAPOX1	/	/	/	/	/	/	/	/	/	/	10	
OSE2ROOTNODULE	/	/	/	/	/	/	/	/	/	/	10	
SP8BFBSP8BIB	0	0	0	/	/	/	0	0	0	0	3	
RHERPATEXPA7	0	/	/	/	/	/	/	0	/	0	7	
ANAEROZCONSENSUS	0	0	/	0	0	/	0	/	/	/	5	
ANAERO1CONSENSUS	/	0	/	/	/	/	/	/	/	/	9	
LTRE1HVBTL49	0	0	0	/	/	/	/	0	0	0	4	
ANAERO3CONSENSUS	/	/	0	/	/	/	/	0	0	0	6	
POLLEN1LELAT52	/	/	/	/	/	/	/	/	/	/	10	
POLLEN2LELAT52	/	0	0	0	0	0	0	0	0	0	1	
GTGAN1G10	/	/	/	/	/	/	/	/	/	/	10	
GELEMENTM2M13	0	0	0	0	/	0	0	0	0	0	1	
NTBFB1ARROL9	/	0	/	0	/	0	/	0	/	0	9	
ACGTOSGLUB1	0	0	0	0	0	0	0	0	0	/	1	
DOFCOREZM	/	/	/	/	/	/	/	/	/	/	10	
WBOXNTERF3	/	/	/	/	/	/	/	/	/	/	10	
AGMOTIFNTMYB2	0	0	0	0	0	0	0	0	0	/	1	
NODCON2GM	/	/	/	/	/	/	/	/	/	/	10	
NODCON1GM	0	/	/	/	/	/	/	/	0	/	8	
RBCSCONSENSUS	/	/	/	0	0	0	0	0	/	0	4	
SITEIATCYTC	0	/	0	/	/	/	/	0	/	0	6	
RAV1AAT	/	/	/	/	/	/	/	0	0	/	9	
RAV1BAT	0	/	0	0	/	0	0	0	/	0	3	
UP2ATMSD	0	0	0	0	/	0	/	0	/	0	3	
SREATMSD	0	0	0	0	0	/	0	/	0	0	2	
MYBPLANT	0	/	0	/	/	/	/	0	0	/	6	
MYBPSM	/	/	0	/	/	/	/	0	/	/	8	
EVENINGAT	0	/	0	0	0	0	0	0	0	0	2	
CIACADIANLELHC	/	0	/	/	0	0	0	/	/	/	5	
CGCGBOXAT	0	0	0	0	0	0	/	0	/	0	2	
ABRERATCAL	0	0	0	0	0	/	/	0	0	0	2	
MYB5T1	/	0	0	0	/	/	/	0	/	0	6	
MYB26PS	0	0	0	0	/	0	0	0	0	/	2	
TAAAGSTK1	/	/	/	/	/	/	/	/	/	/	10	Guard cell
CACTFPPCA1	/	/	/	/	/	/	/	/	/	/	10	Mesophyll specific
TGTACACMCUCUMISIN	0	0	0	0	0	0	/	0	0	0	2	Fruit specific
L1BOXATPDF1	0	0	/	0	0	0	0	0	0	0	1	Trichome development
ARR1AT	/	/	/	/	/	/	/	/	/	/	10	Response regulator
GT1GMSCAM4	/	/	/	/	/	/	/	/	/	/	10	Salt induced
AMMORESIVUCRNIA1	0	0	0	0	0	0	0	0	/	0	1	Ammonium responsiveness
CAATBOX1	/	/	/	/	/	/	/	/	/	/	10	Heat stress
CLURECORECR	/	/	/	/	/	/	/	/	/	/	10	Copper response
CLURECORECR	/	/	/	/	/	/	/	/	/	/	10	Hypoxic
EFCRCRH1	/	/	0	/	/	/	/	/	/	/	9	Carbon dioxide responsiveness
SURECREATSULT11	/	/	/	0	/	/	/	0	/	/	8	Sulphur responsiveness
SURE1STPAT21	0	0	0	/	0	0	0	/	0	0	2	Sucrose
MYBCORE	/	/	/	/	/	0	0	/	/	/	8	Flavonoid biosynthesis
PIBS	0	0	0	/	0	0	0	0	0	0	1	Phosphate responsiveness
EPHVCORD	0	0	0	/	0	0	0	0	0	0	1	Nitrogen response

Type of CAREs	Number of MaPR-10 genes	
10pewpab1	8	Light-related
boxcpas1	3	
gt1core	3	
ad1motifcamv	8	
scrip1at	8	
caacahar1ehc	5	
scrip1at	1	
cgqgboxat	2	
tbocatgapb	7	
boxipcch	2	
box	5	
irenpabe	1	
at1box	1	
mrf1zmppc1	1	
scrip1at	1	
hdap1atathb2	1	
ibocorent	4	
boxcpas1	2	
directcoreat	6	
gatabox	10	
invrtpsadb	10	
gt1consensus	10	
ibocore	10	
invrtpsadb	10	
realp1alghcb21	5	
cca1athcb1	3	
ltrecoreatcor15	9	
boxintpatpb	7	
preconscrip70a	8	
tebbowatet1aa1	3	
sl1cor21	8	
sl1boxcorps101	6	
abrelaterd1	10	
acgtaterd1	2	Seed-related
cpbcspor	10	
caatbox1	3	
ryrepeatlegumibox	1	
2sseedprdtbanapa	4	
self1motifgm	1	
ryrepeatgmgy2	3	
self1motif	2	
acgtcbox	6	
ryrepeat1annapa	1	
probbnnapa	9	
self4motifgm7s	1	
ceroglubox3pslega	1	
napiinnotifbn	1	
acgtabox	1	
ceroglubox3pslega	1	
carbnnapa	1	
amybox2	3	
amybox1	4	
tgacgtvmany	9	
cargcwgat	9	
dpbfcoredcic3	1	ABA-related
caacgtmotif	4	
aacacoreosglub1	1	
gcndosglub1	1	
prolaminkoxosglub1	4	
l130delement	1	
emichord	1	
l1300core	10	
mycconsensusat	6	
dpbfcoredcic3	9	
ltrecoreatcor15	2	
acgtabremotifa2oem	1	
probbnnapa	6	
myb1at	6	
myb2consensusat	3	
dre2corezmrab17	2	Water-related
athbcoreat	2	
mybatrd22	1	
acgtabremotifa2oem	1	
abremotifa2oem	1	
abrebmrab28	2	
cgqgboxat	3	
pyrimidineboxhwpb1	3	
myb1at	3	
abrelaterd1	6	
mybatrd22	2	
acgtaterd1	10	
acgtabremotifa2oem	2	
myb2consensusat	6	
directcoreat	6	
cdffv	7	
mybcore	8	
mycatrd22	6	
myb1at	6	
dre2corezmrab17	3	
mycatrd1	7	
ltrecoreatcor15	9	
mycconsensusat	10	
preatprodh	1	

