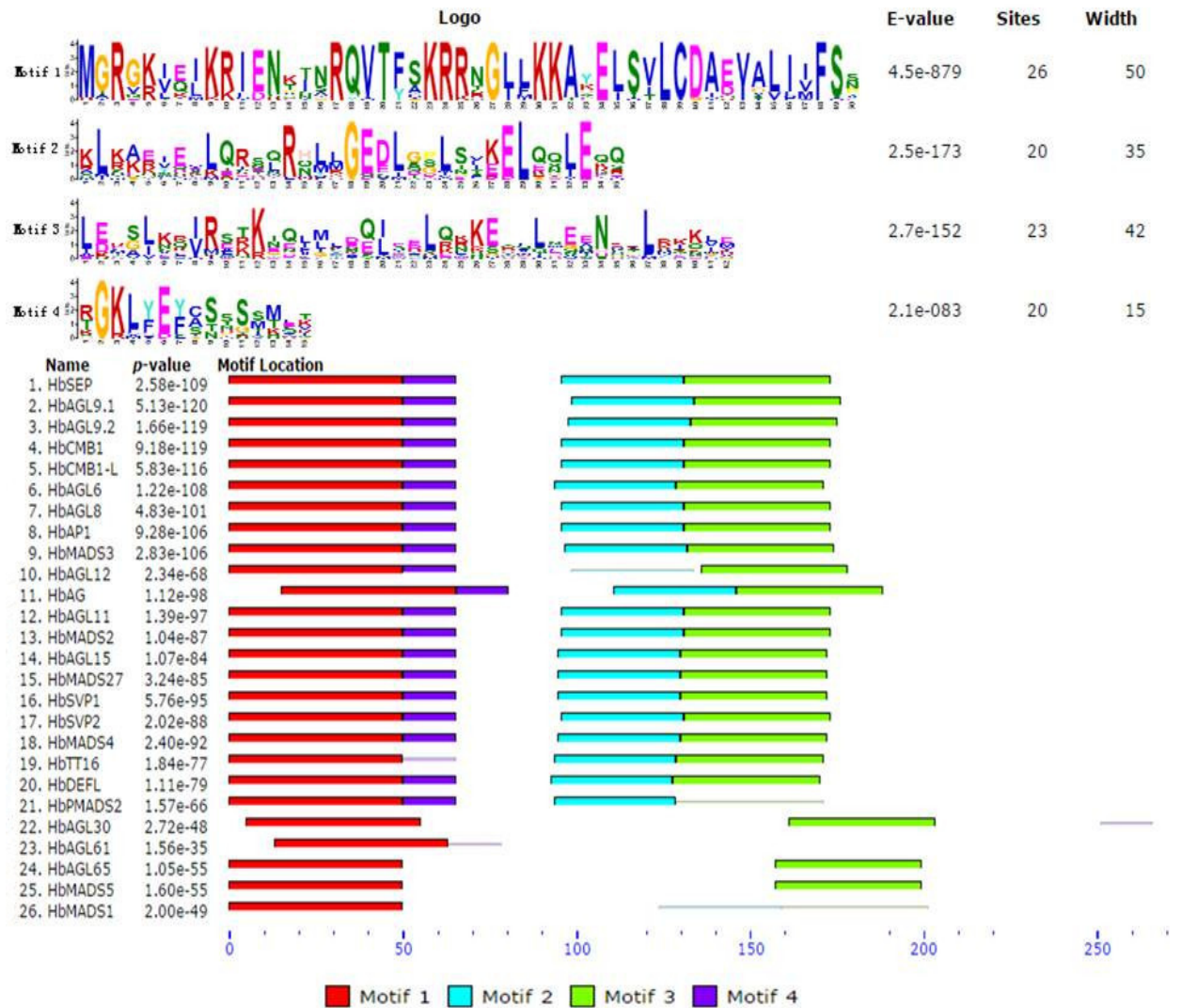


## Supplementary Materials

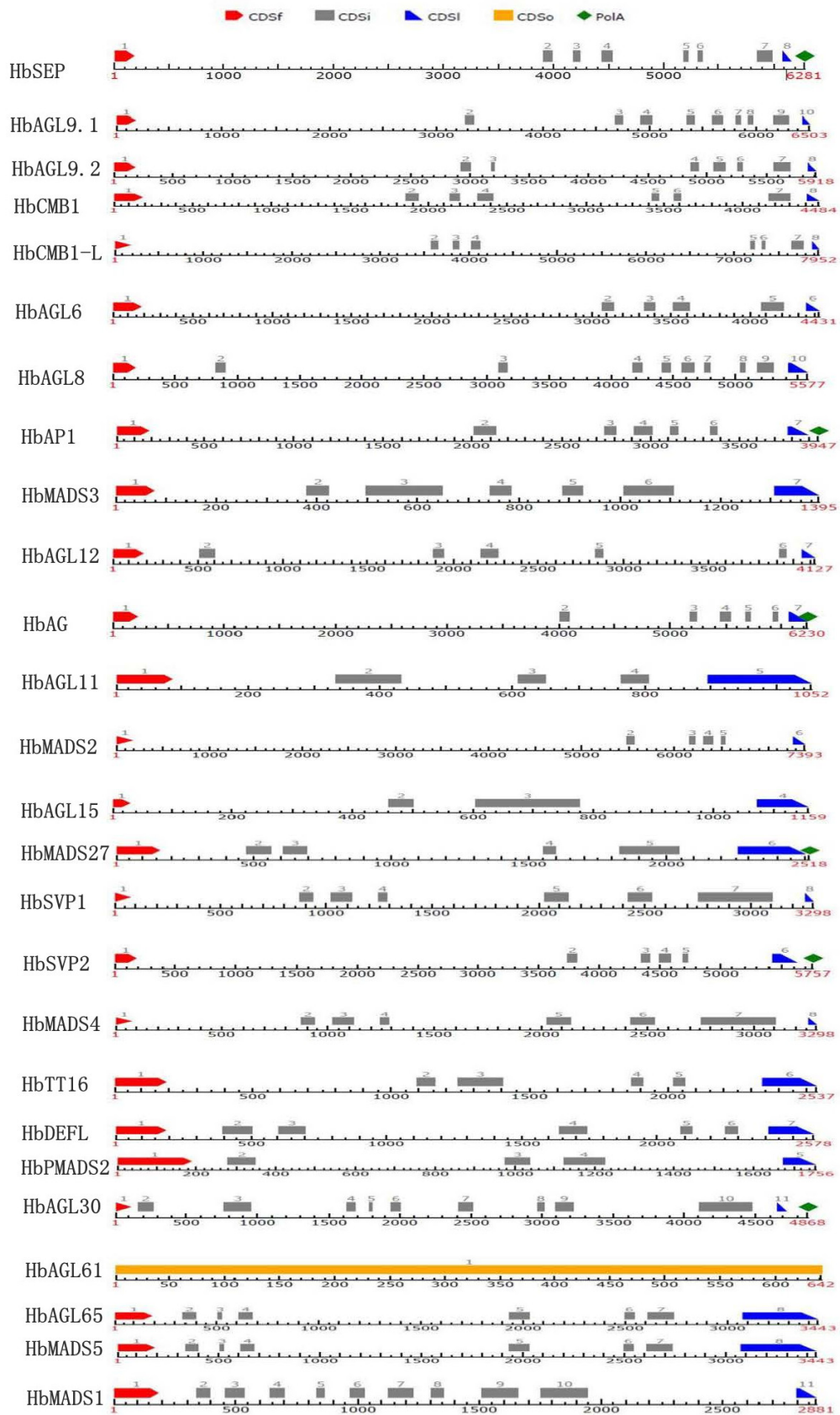
Figure S1: Tissue samples of rubber tree flowers. Figure S2: The conserved domain logo and motif composition of HbMADS-box genes. Figure S3: Exon-intron structures of HbMads-box genes. Figure S4: Expression profiles of the floral-enriched HbMad-box genes under cold stress. Figure S5: Expression profiles of the floral-enriched HbMad-box genes under high temperature stress. Figure S6: Expression profiles of the floral-enriched HbMad-box genes under drought stress. Figure S7: Expression profiles of the floral-enriched HbMad-box genes under salt stress. Figure S8: Expression profiles of the floral-enriched HbMad-box genes responding to ABA treatment. Figure S9: Expression profiles of the floral-enriched HbMad-box genes responding to GA3 treatment. Table S1: List of primer sequences used for HbMad-box TFs amplification. Table S2: List of primer sequences used for qRT-PCR analysis. Table S3: Sequence features of AtMADSs in *A. thaliana*. Gene IDs, protein length, pI and molecular weight of corresponding AtMADSs in *A.thaliana* are shown. Table S4: Percent identity matrix of HbMad-box TFs proteins. Table S5: Statistics of exon and intron number distribution among HbMad-box TFs.



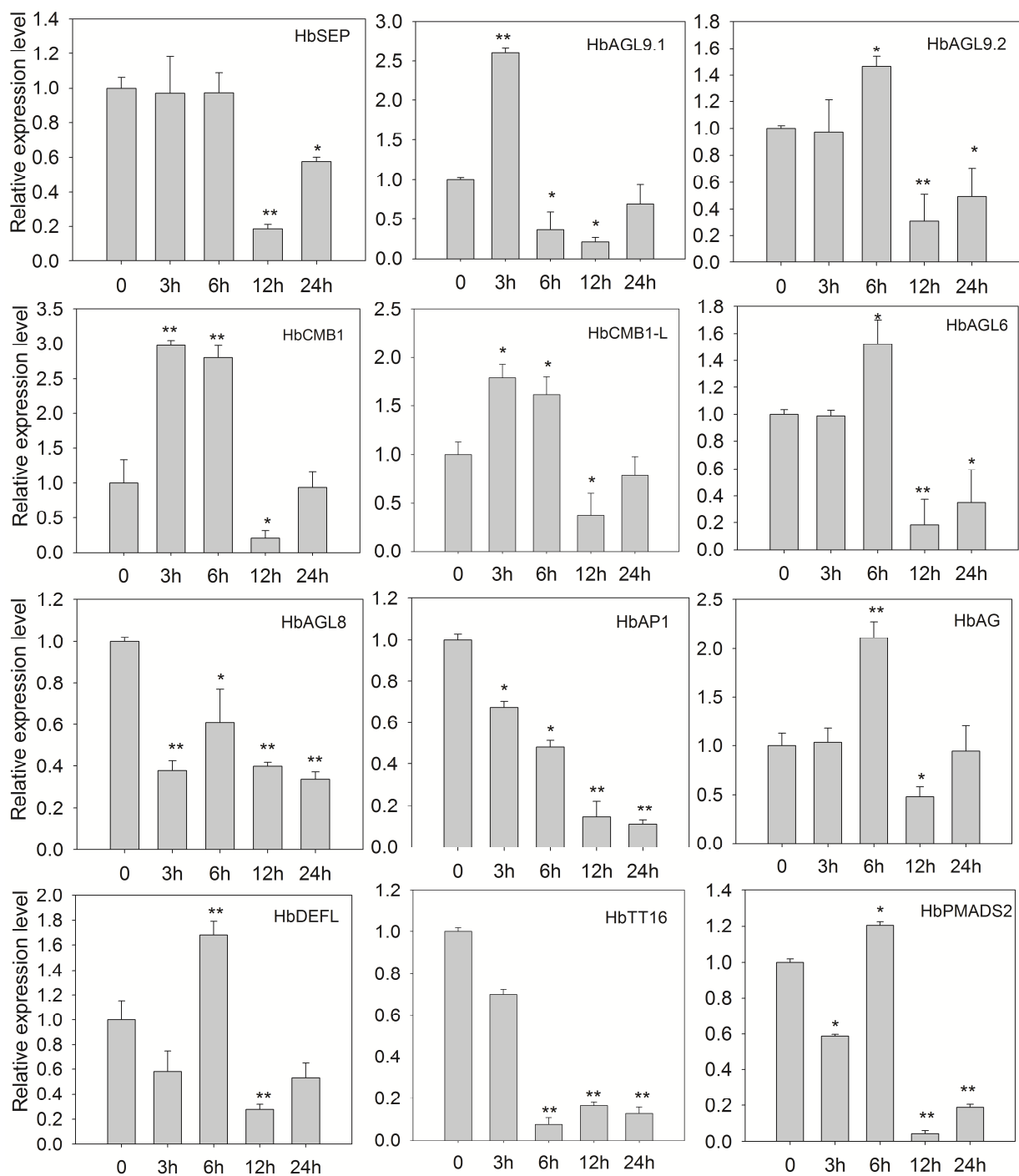
**Figure S1.** Tissue samples of rubber tree flowers. a: inflorescence; b: female flower; c: male flower; d: fruit.



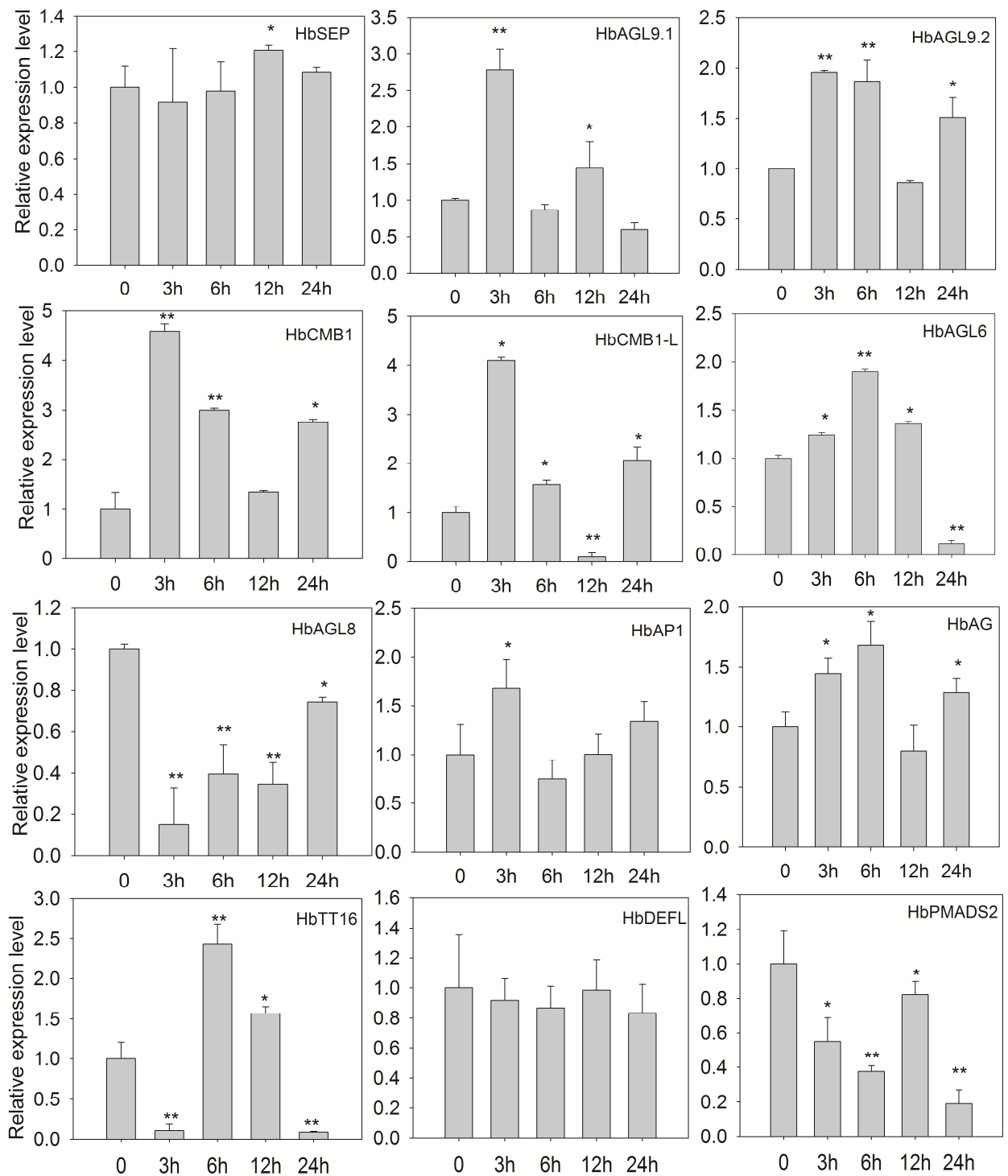
**Figure S2.** The conserved domain logo and motif composition of HbMADS-box genes. Motif 1 and Motif 3 present M-box, Motif 2 and Motif 4 present K-box.



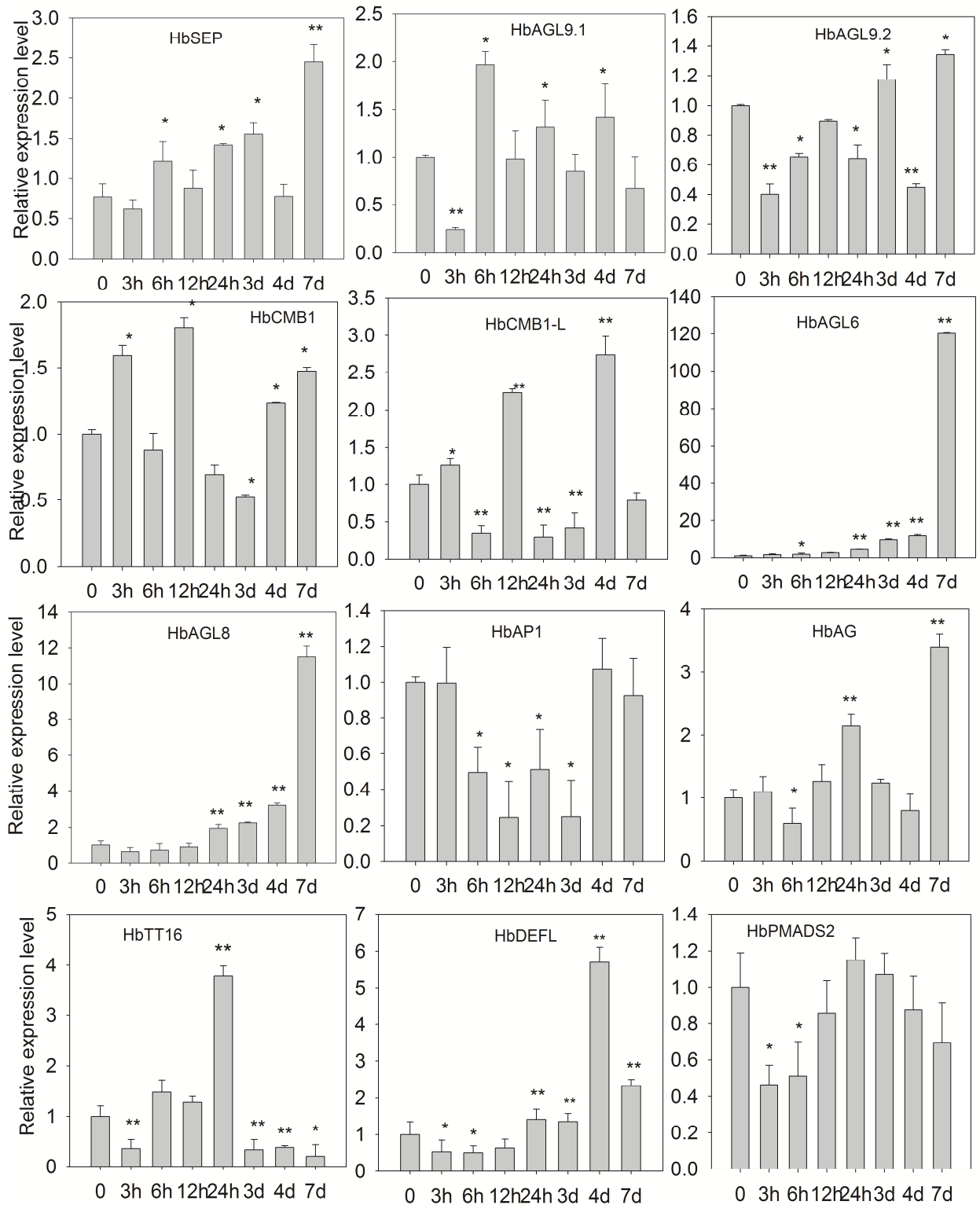
**Figure S3.** Exon-intron structures of HbMads-box genes. CDSf: the first exons (starting with start codon) are represented by red boxes; CDSi: internal exons are represented by grey boxes; CDSl: the last exons (ending with stop codon) are represented by blue boxes; CDSo: gene contains the one coding exon are represented by yellow boxes; PolA: terminal polyA signal are represented by green boxes. Scales show the length of each gene's exons and introns in bp.



**Figure S4.** Expression profiles of the floral organ specific HbMad-box genes under cold stress. Leaves of seedlings were sampled at 0, 3, 6, 12, and 24 h after cold (5°C) stress treatment. Relative expression level of each HbMad-box gene was normalized with 18S rRNA gene. Data are means  $\pm$  SD of three biological replicates.

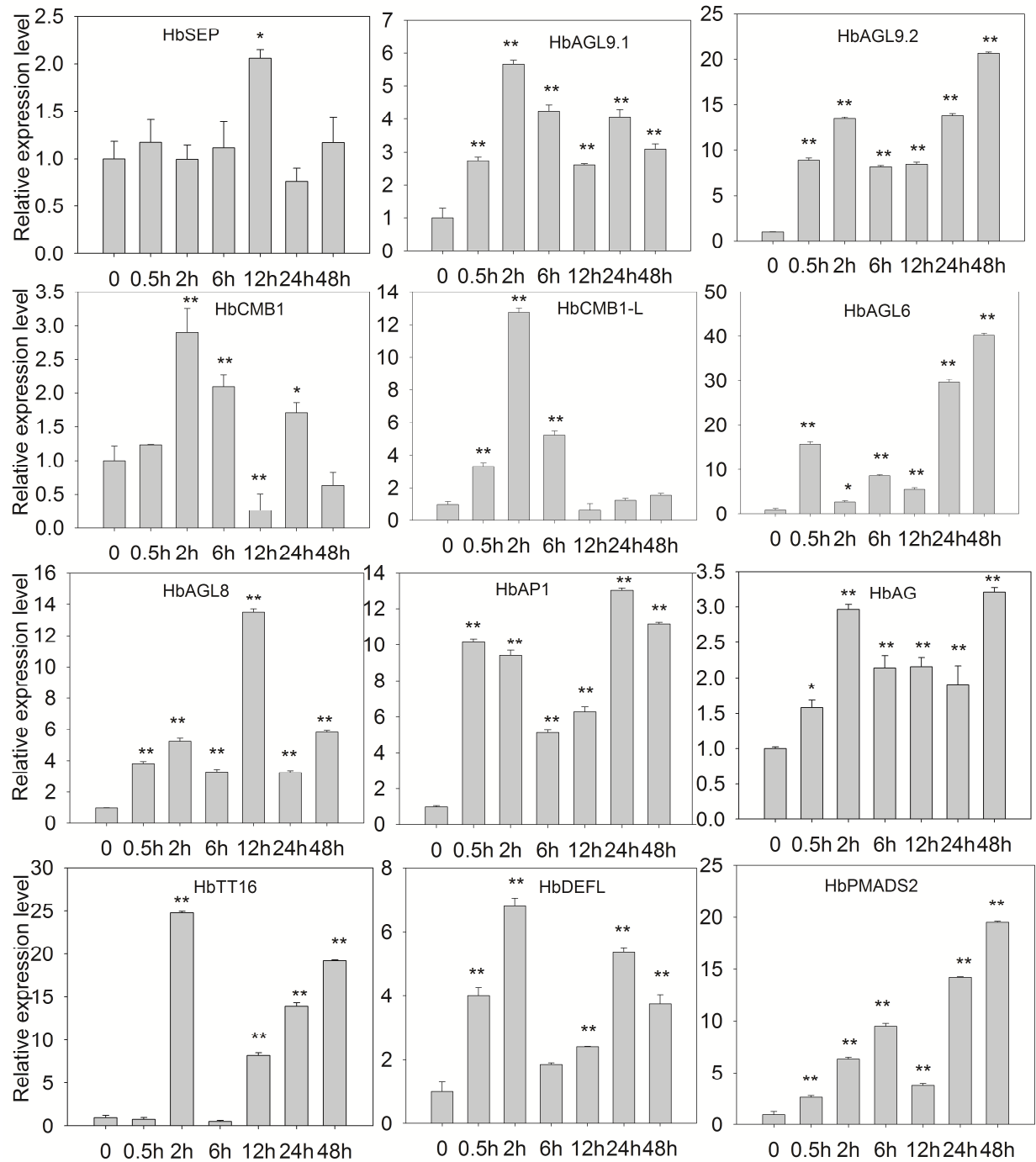


**Figure S5.** Expression profiles of the floral-enriched HbMad-box genes under high temperature stress. Leaves of seedlings were sampled at 0, 3, 6, 12, and 24 h after high temperature (40°C) stress treatment. Relative expression level of each HbMad-box gene was normalized with 18S rRNA gene. Data are means  $\pm$  SD of three biological replicates.

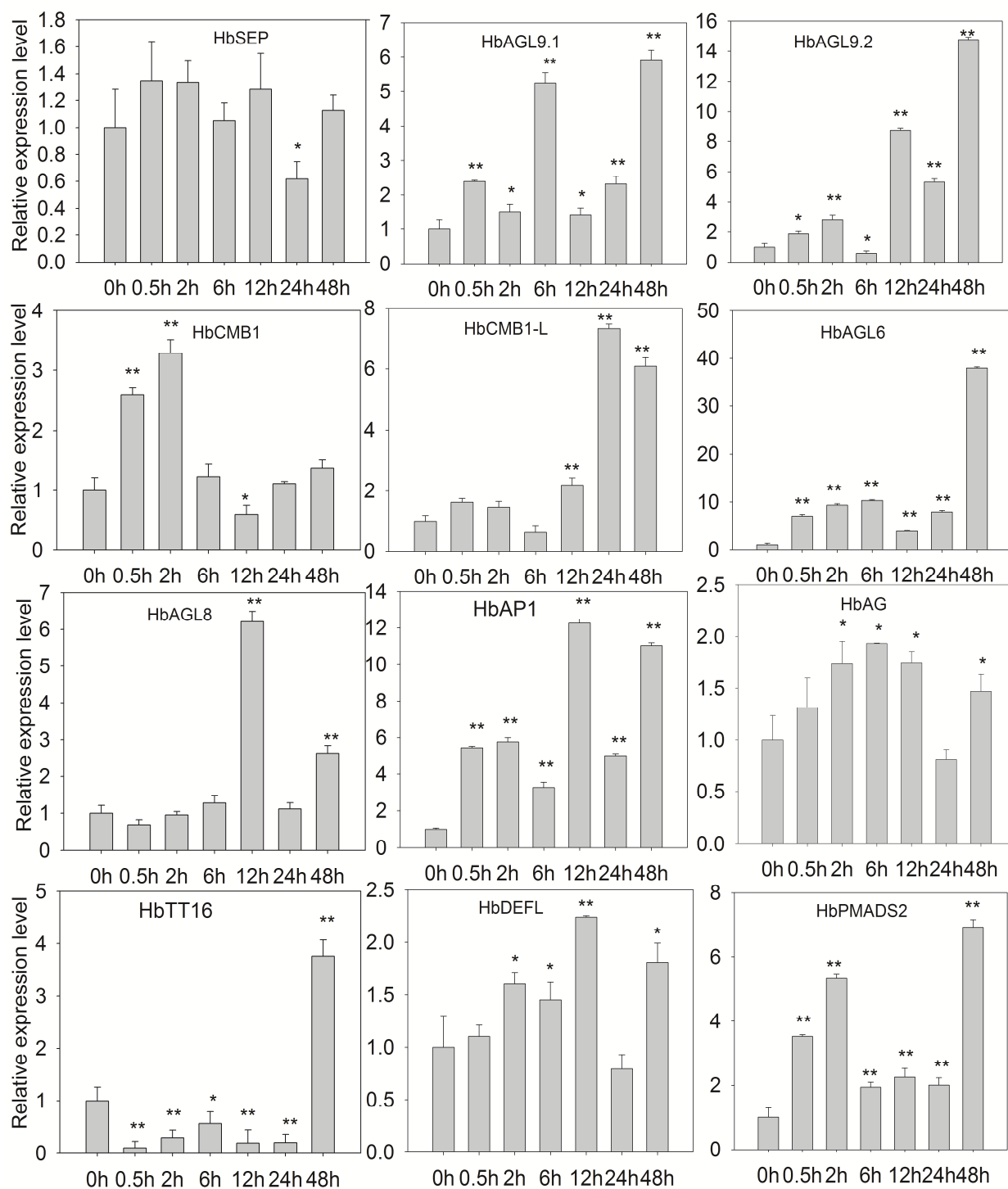


**Figure S6.** Expression profiles of the floral-enriched HbMad-box genes under drought stress. Leaves of seedlings were sampled at 0 h, 3 h, 6 h, 12 h, 24 h, 3 days, 4 days, and 7 days after drought stress treatment. Relative expression level of each HbMad-box gene was normalized with 18S rRNA gene. Data are means  $\pm$  SD of three biological replicates.



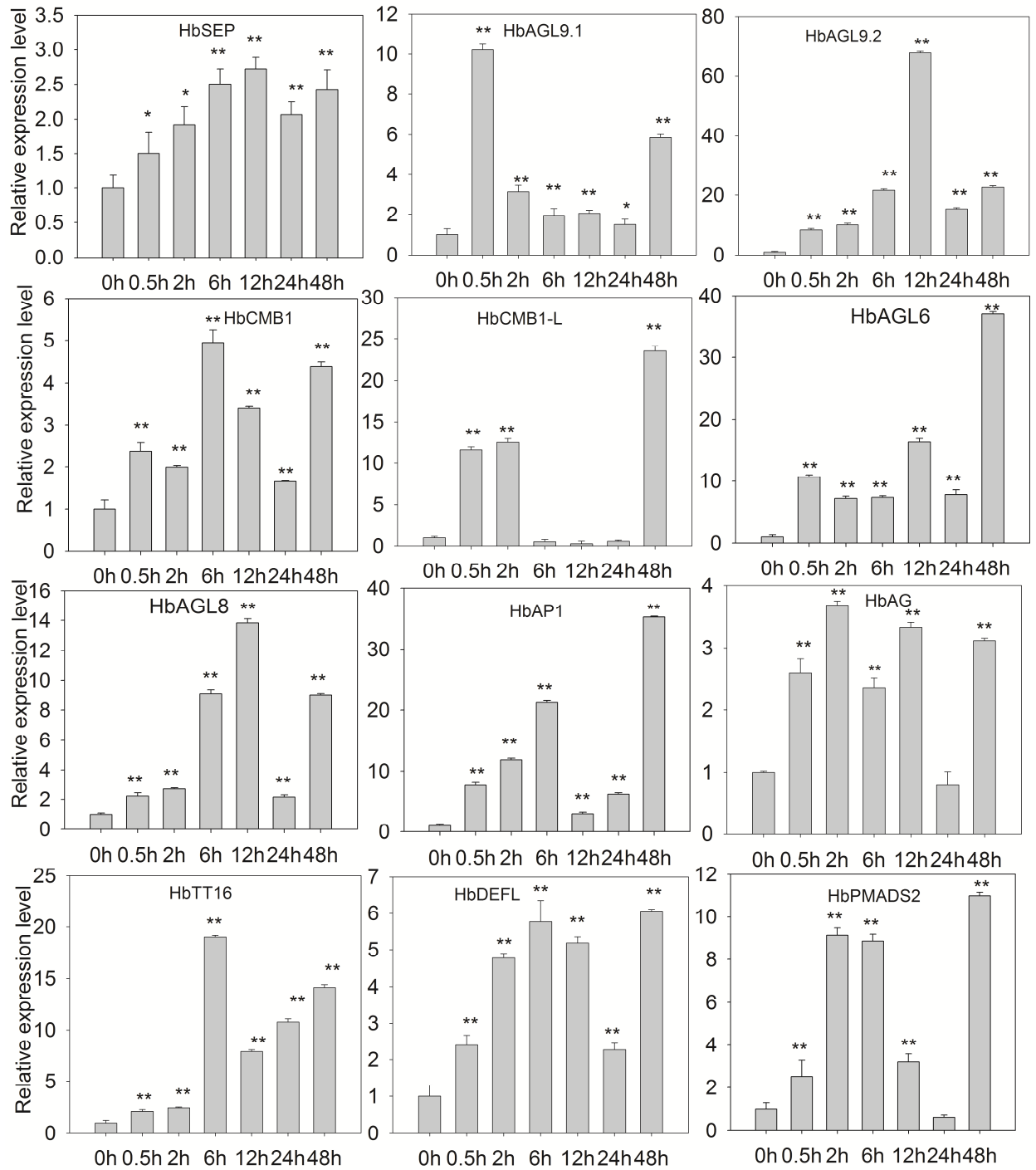


**Figure S7.** Expression profiles of the floral-enriched HbMad-box genes under salt stress. Leaves of seedlings were sampled at 0, 0.5, 2, 6, 12, 24, and 48 h after salt stress (1 M NaCl) treatment. Relative expression level of each HbMad-box gene was normalized with 18S rRNA gene. Data are means  $\pm$  SD of three biological replicates.



**Figure S8.** Expression profiles of the floral-enriched HbMad-box genes responding to ABA treatment. Leaves of seedlings were sampled at 0, 0.5, 2, 6, 12, 24, and 48 h after ABA treatment. Relative expression level of each HbMad-box gene was normalized with 18S rRNA gene. Data are means  $\pm$  SD of three biological replicates.





**Figure S9.** Expression profiles of the floral-enriched HbMad-box genes responding to GA3 treatment. Leaves of seedlings were sampled at 0, 0.5, 2, 6, 12, 24, and 48 h after GA3 treatment. Relative expression level of each HbMad-box gene was normalized with 18S rRNA gene. Data are means  $\pm$  SD of three biological replicates.

**Table S1.** List of primer sequences used for HbMad-box TFs amplification.

<b>Gene</b>	<b>Forward primer (5'-3')</b>	<b>Reverse primer (5'-3')</b>
<i>HbSEP</i>	ATGGGGAGGGGAAGAGTGGA	TCAAAGCATCCATCCAGG
<i>HbAGL9.1</i>	ATGGGGAGAGGTAGGGTTGA	TCAGGGTAACCATTCTGGCATGTA
<i>HbAGL9.2</i>	ATGGGAAGAGGTAGGGTTGA	AGTCTTCTTGTCAGGGTAACCATCC
<i>HbCMB1</i>	ATGGGGAGAGGGAAAGTGGAGTT	CTATTCATTGACATGACGAAGC
<i>HbCMB1-L</i>	ATGGGTAGAGGAAGGGTAGAGC	TTAAAGCATCCACCCAGGCAAG
<i>HbAGL6</i>	ATGGGAAGAGGAAGAGTGAG	TTAAAGGATCCATCCCTGCAT
<i>HbAGL8</i>	ATGGGAAGAGGTAGGGTT	CTATTCATTGACATGACGAAGC
<i>HbAP1</i>	ATGGGGCGAGGTAGGGTTCAGTTGA	TCATGTGGTGAAGCATCCAAGGT
<i>HbAGL12</i>	ATGGCTCGAGGAAAGGTTTCAGAT	CAACCCCATCAAACACTATTTCTAA
<i>HbAG</i>	ATGGCATACCAGAGCGAG	TTAAACTAACTGAAGGGACATCTG
<i>HbAGL11</i>	ATGGGAAGAGGAAAGATCGAGAT	TTACCCAAGATGGAGAATCTTG
<i>HbAGL15</i>	ATGGGTAGAGGGAAGATTGAAA	TCACAGCAAGACTAATTGGCTCCAT
<i>HbSVP1</i>	ATGACAAGGCAGAAAATCCAGA	TCAATCTGGGAAGGGTAA
<i>HbSVP2</i>	ATGGCTAGGGAGAAGATTCAG	TTATCCGTTGTACGGTAACCCCA
<i>HbTT16</i>	ATGGGTCGTGGCAAGATA	TTAAACATTGGAACCTTG
<i>HbDEFL</i>	ATGGGTCGTGGAAAGATCG	TTAAGCTAGGCGGAGTTCA
<i>HbPMADS2</i>	ATGGGAAGAGGAAAGATTGAGA	TTACATCCTCTCCTGCAAAT
<i>HbAGL30</i>	ATGCAACCCTATATGATGG	TCAGGAAATTCTGTAATATTC
<i>HbAGL61</i>	ATGGATGGAACGACCGACC	TTAAAGAAACCCATTATTCAAACC
<i>HbAGL65</i>	ATGGGAAGGGTGAAGCTAAAG	TTACAACCTTACAAGGTACTGGGAC

**Table S2.** List of primer sequences used for qRT-PCR analysis.

<b>Gene</b>	<b>Forward primer (5'-3')</b>	<b>Reverse primer (5'-3')</b>
<i>HbSEP</i>	GAAGGTGGTGAGCAAAGCAT	TGTGGCAGTCATCTGGTCTG
<i>HbAGL9.1</i>	GGGTAACCATTCTGGCATGT	CAGGGAGATGGCTTCTTTCA
<i>HbAGL9.2</i>	ACCTCGGCATCACAAAGAAC	GGAAGGAGAGAAATGGGAAGA
<i>HbCMB1</i>	TGGTAGTTGCTCTGTGTCTCG	TGTGATGCTGAGGTTGCTCT
<i>HbCMB1-L</i>	TGCAAGGGATCGACTAAACC	GGAAACTGATGCAACCCTTC
<i>HbAGL6</i>	TGAGGAGTGAAGCAACAACG	TGATGCTGAAGTTGCCCTTA
<i>HbAGL8</i>	GGGCAGAATCAAACCTCCTT	AGCCTCCTCATCTTCGTTCA
<i>HbAP1</i>	ATGCTGAGGTCGCTTTGATT	TGCTGTGAGTTGCCTCTCTG
<i>HbMADS3</i>	CGGTCAAGGAGAAGGAGAAG	GCATTGGTGGTGGTAGAACA
<i>HbAGL12</i>	GGGGTTAGCTGGGAAGAAAG	GCAAATCCACCCTGATCTCT
<i>HbAG</i>	GGAGAATGGGTAGGGGAAAG	AGAGCAACCTCAGCATCACA
<i>HbAGL11</i>	CAAGAGGATAGAGAACACGACGA	CAGCATCACAAAGGACTGACAA
<i>HbMADS2</i>	CATAGAGAACGCCACAAGCA	GAGAAGACGATAAGGGCAACC
<i>HbAGL15</i>	GGTTTCTTCCCGTCAACAGA	CGAATCTCCTTTCTCCATCG
<i>HbSVP1</i>	TGCCTTGCTGTATGGTTGTC	TCCTTGTGCCTTCTGCTTCT
<i>HbSVP2</i>	GGTCCTCCACACGACTATGAA	TCAAACCAGACAACGCAAAG
<i>HbTT16</i>	TGGCAATATGTACCGTTGGA	TCTCCACAAAAGGGGAATTG
<i>HbDEFL</i>	CTTCTTCCTGCGGGTGTCT	TGATGTGAGCTTCGATGAGC
<i>HbPMADS2</i>	CGACAACATGCAGATTGAGC	TGTCACGAATAGTGGCAAGG
<i>HbAGL30</i>	TCTTCATCAGGACCATGTGC	CCCAAACGAAGCTACCACTC
<i>HbAGL61</i>	ATTGCTGCCGATTTCCAGTA	TTTCTCCGAACATGGGAAAG
<i>HbAGL65</i>	TAGGTCACTTGCCGATTGCT	TAGTTGTGGTGCTGGGATGA
<i>HbMADS1</i>	TCGTCCTCCAAACCACTTCT	TTCGTCAGAGAGAGCCACAA
<i>18S RNA</i>	GCTCGAAGACGATCAGATACC	TTCAGCCTTGCGACCATAC

**Table S3.** Sequence features of AtMADSs in *A. thaliana*

	<b>Name</b>	<b>Gene ID</b>	<b>Len (AA)</b>	<b>pI</b>	<b>Mw (KDa)</b>
HbSEP	AtSEP2	821151	250	8.64	28.58
HbAGL9.1	AtSEP3	839040	251	8.27	29.07
HbAGL9.2	AtSEP3	839040	251	8.27	29.07
HbCMB1	AtSHP2	818883	248	9.4	28.38
HbCMB1-L	AtSHP2	818883	248	9.4	28.38
HbAGL6	AtAGL6	819173	252	7.6	28.74
HbAGL8	AtAGL8	836212	242	9.36	27.54
HbAP1	AtAP1	843244	276	9.64	31.93
HbMADS3	AtAGL79	822726	249	9.56	28.08
HbAGL12	AtAGL12	843497	211	6.76	23.92
HbAG	AtAG	827631	125	6.84	14.36
HbAGL11	AtSTK	826586	256	9.64	29.48
HbMADS2	AtAGL19	828394	219	9.35	25.05
HbAGL15	AtAGL15	831224	268	8.58	30.33
HbMADS27	AtAGL44	815907	234	9.69	26.8
HbSVP2	AtAGL24	828556	220	8.35	25.06
HbSVP1	AtSVP	816787	240	5.44	26.89
HbMADS4	AtSVP	816787	240	5.44	26.89
HbTT16	AtTT16	832390	252	6.14	29.69
HbDEFL	AtAP3	824601	232	8.71	27.34
HbPMADS2	AtPI	832146	208	9.06	24.05
HbMADS1	AtGOA	839999	215	9.4	25.17
HbAGL30	AtAGL30	814835	386	6.43	43.9
HbAGL61	AtAGL61	817021	264	9.58	30.26
HbAGL65	AtAGL65	838457	389	6.05	44.98
HbMADS5	AtAGL94	843289	344	6.67	39.22

**Table S4.** Percent identity matrix of HbMad-box TFs proteins.

	HbSEP	HbAGL9.1	HbAGL9.2	HbCMB1	HbCMB1-L	HbAGL6	HbAGL8	HbAP1	HbMADS3	HbAGL12	HbAG	HbAGL11	HbMADS2	HbAGL15	HbMADS27	HbSVP1	HbSVP2	HbMADS4	HbTT16	HbDEFL	HbPMADS2	HbAGL30	HbAGL61	HbAGL65	HbMADS5	HbMADS1
HbSEP	100																									
HbAGL9.1	61.79	100																								
HbAGL9.2	63.67	92.59	100																							
HbCMB1	70.37	62.04	63.11	100																						
HbCMB1-L	64.75	58.3	59.84	67.21	100																					
HbAGL6	52.44	52.8	55.06	53.66	52.24	100																				
HbAGL8	41.34	41.18	40.55	42.69	43.53	40.71	100																			
HbAP1	41.87	40.57	41.53	41.56	45.12	45.34	59.13	100																		
HbMADS3	42.17	40.57	42.45	42.34	45.16	42.68	56.47	64.34	100																	
HbAGL12	33.47	32.65	32.1	32.39	33.6	30.12	29.57	29.67	27.98	100																
HbAG	33.59	34.5	36.96	38.37	36.43	35.91	33.21	31.64	32.68	33.33	100															
HbAGL11	36.89	38.68	38.75	41.98	37.04	38.52	30.95	37.04	36.25	33.48	65.15	100														
HbMADS2	36.89	37.45	37.08	37.68	37.45	38.52	35.97	35.63	32.78	34.23	35.68	38.22	100													
HbAGL15	33.98	35.04	35.27	36.72	34.38	35.29	33.85	32.03	30.89	25	31	32.03	35.94	100												
HbMADS27	33.47	36.21	33.2	35.92	34.96	35.1	32.94	34.98	34.85	31.56	36.22	38.08	35.56	36.72	100											
HbSVP1	31.28	30.86	29.58	31.82	31.4	30.86	31.35	31.12	31.38	30.88	31.95	34.23	38.81	34.11	37.24	100										
HbSVP2	31.15	30.45	29.17	32.1	28.1	29.92	34.39	33.47	32.22	28.02	33.2	34.8	37.44	35.77	39.42	60.79	100									
HbMADS4	31.28	30.45	29.17	31.4	31.82	30.45	30.95	30.71	30.96	30.88	31.54	34.23	38.81	34.5	37.24	98.57	59.91	100								
HbTT16	33.61	31.73	35.27	32.51	30.45	33.2	32.41	35.12	32.1	32.23	30.56	34.87	37.92	29.84	33.61	31.22	30.51	30.8	100							
HbDEFL	28.81	30.04	31.67	29.75	30.99	33.47	27.38	26.56	27.2	2489	29.92	31.88	28.63	30.59	28.99	28.32	30.3	28.32	32.91	100						
HbPMADS2	30.74	29.1	29.88	30.45	27.98	30.58	27.67	31.82	27.92	28.18	27.39	31.53	31.65	25.1	27.31	28.57	29.96	28.11	34.19	33.33	100					
HbAGL30	15.63	14.29	15.55	16.17	16.17	14.82	16.44	14.78	13.67	14.21	13.91	13.75	14.29	18.87	16.98	17.25	17.52	17.25	15.59	14.56	14.03	100				
HbAGL61	22.66	22.27	23.32	21.96	20.78	23.44	18.11	20.78	21.83	19.27	21.16	22.88	21.55	21.27	20.32	22.22	24.9	22.67	19.28	19.83	18.34	14.51	100			
HbAGL65	21.43	21.96	21.18	23.23	23.9	26.07	21.74	24.21	21.51	21.95	22.22	24.6	25.61	22.96	23.39	24.39	18.95	23.17	25.9	22	21.86	40.32	20.38	100		
HbMADS5	18.16	17.88	17.04	18.99	17.08	16.43	16.48	18.72	16.2	15.08	14.48	18.06	17.6	20.67	17.6	16.76	15.92	17.04	18.11	16.76	14.76	50.53	14.25	64.8	100	
HbMADS1	22.19	24.01	21.99	24.92	23.71	23.4	24.24	25.23	24.92	18.54	21.8	22.8	22.73	22.19	21.58	19.76	21.88	19.76	21.52	20.06	19.76	21.81	16.03	23.49	22.78	100

**Table S5.** Statistics of exon and intron number distribution among HbMad-box TFs.

	<b>Exons</b>	<b>Introns</b>	<b>Group</b>		<b>Number</b>
HbSEP	8	7	The first group	The first group	8
HbAGL9.1	10	9	The fourth group	The second group	5
HbAGL9.2	8	7	The first group	The third group	5
HbCMB1	8	7	The first group	The fourth group	2
HbCMB1-L	8	7	The first group	The fifth group	2
HbAGL6	6	5	The second group	The sixth group	2
HbAGL8	10	9	The fourth group	The seventh group	1
HbAP1	7	6	The third group	The eighth group	1
HbMADS3	7	6	The third group		
HbAGL12	7	6	The third group		
HbAG	7	6	The third group		
HbAGL11	5	4	The fifth group		
HbMADS2	6	5	The second group		
HbAGL15	4	3	The seventh group		
HbMADS27	6	5	The second group		
HbSVP1	8	7	The first group		
HbSVP2	6	5	The second group		
HbMADS4	8	7	The first group		
HbTT16	6	5	The second group		
HbDEFL	7	6	The third group		
HbPMADS2	5	4	The fifth group		
HbAGL30	11	10	The sixth group		
HbAGL61	1	0	The eighth group		
HbAGL65	8	7	The first group		
HbMADS5	8	7	The first group		
HbMADS1	11	10	The sixth group		