Table 1 Suppl1. A list of primers of candidate *HvWRKY* genes for quantitative real-time PCR analysis (Tm - melting temperature).

Gene name	NCBI accession number	Primers	Sequence (5'-3')	Tm
HvWRKY_IIc2	AK363451	forward	CAGTCCCAGCACCATCTAC	60
		reverse	AGCGGCGTACACCATTGAG	60
HvWRKY_III11	DQ863116	forward	AGATACAGAACTCCAAGCACTCC	68
		reverse	TACGTGTCCGGGTCTTCGTC	64
HvWRKY_IIb2	AK364800	forward	GACCTCACCATTAACCTCCTTTC	66
		reverse	CTGCCGTTACTGTCCTCATC	62
HvWRKY_IId4	DQ863122	forward	AGCATGAGCAGAAGCCTGTC	62
		reverse	ACGTCGGGTACTGCTCGAAC	64
HvWRKY_III23	DQ863112	forward	GTTCCGAGCAAAGAGAGATGG	64
		reverse	CTTCACCAGCTCCTTGATGT	60
HvWRKY_I8	*DQ863125*	forward	CTTGCCCTCCTGTATCTG	58
		reverse	CTAAAGAAATGGTGCCTTGT	58
HvWRKY_IIa5	DQ863131	forward	TCCTCCAAGAAAAGCCACGAG	64
		reverse	CAGGTCGGAGTACTTTACCAC	64
HvWRKY_IIc19	DQ840418	forward	AGGGTGCAGCGTGAAGAAG	60
		reverse	TCCTGGCTGGCGTAGTAGAC	64

Table 2 Suppl1. Composition of amino acid sequences of conserved motifs identified in HvWRKYs using *MEME*.

Motif	Amino acid sequence composition of motif	site	width	E-value	Molecular function
1	[PI]LDDGYRWRKYGQKV[IV]K[GN][SN]P[HN]PRSYY[RK]	98	28	$2.4e^{-1994}$	WRKY DNA-binding domain
2	CP[VA][KR]K[QH]V[EQ]R[SA]X[DE]DPXX[VL][IV][TV]	98	19	$1.0e^{-705}$	-
3	TYEGEHNHPXPAA[RA]	59	14	$2.4e^{-279}$	-
4	[GA]E[RK][RK][VA]REPR[VIF]A[FV][QR]T[RKT]SEV[DE]	32	19	$4.0e^{-163}$	-
5	[TV]Y[HY][GN][ED]HTCAQ	26	10	$8.5e^{-070}$	-
6	[MD][ET][DAG][TA][AT]ATLA[TAS]ELD[GR]LLAMARELEARVDGDQGAPG[AD]AR[EQ]LC[AS][AE]LA[AE]SVDRA[VIM]RLAG	4	55	$9.3e^{-058}$	-
7	[RK]CHCSK[RK]RKLR[VI][KR]R[TS][ITV][KR]VPA[IV]S[NS]K[IAV]AD	8	27	$4.1e^{-057}$	zinc domain
8	[KAN]D[DH][EK][LV][AE]A[LMT][EKQ][AS]E[LM][GR][RE][VM][GNRS]EEN[REK]RL[KGR][TDE][ML]L	19	26	$1.2e^{-039}$	-
9	[PI]LDDG[YF]SWRKYGQK[DA][IV]K[GN]	8	18	$1.5e^{-039}$	WRKY DNA-binding domain
10	K[VR][RS]TQVRV[AS]S[MV][QT]DV	12	14	$1.9e^{-032}$	-
11	Y[KR]GTHNHP[RK]P[PQ][NKP]PR	12	14	$2.0e^{-032}$	-
12	L[VAT][ED][QT][MI]A[AK][AT][LI]T[RS]DP[GS]F[KT]AAL[AV][AS]A[IL][ST][GS][RY][IM]	8	27	$1.8e^{-029}$	-
13	LQHQQHGFFPAGADVYGRMCVPPTTAAAPAVPHRSSEYGGMVSYADLLPDAVMGYQQGHR	2	60	$1.4e^{-016}$	-
14	[AL]VV[ED][ED]LXKG[QR][EQ]LAAQLQALLRLSP	11	24	$4.2e^{-013}$	-
15	E[HR][MT]TLQ[KEI]Q[YCN][DG][IV]KKE	4	14	$6.0e^{-013}$	-

Table 3 Suppl1. Analysis of variance (df and mean squares) for the gene expression of eight *HvWRKY* genes (** indicates significance at $P \leq 0.01$).

Source	df	*HvWRKY_IIc2*	*HvWRKY_III11*	*HvWRKY_IIb2*	*HvWRKY_IId4*	*HvWRKY_III23*	*HvWRKY_I8*	*HvWRKY_IIa5*	*HvWRKY_IIc19*
Treatment	3	14.15**	195.96 **	16.86**	428.46**	85.87**	0.32**	1.61**	2.45**
Error	8	0.08	0.090	0.07	0.99	.17	0.003	0.019	0.004