

**Table S1. The accession numbers and samples information of RNA-seq data used in this study**

	Accession number	Tissue	Treatment
<b>Abiotic stresses</b>	SRR2989984	Leaf	drought
	SRR2989985	Leaf	control
	SRR5967006	Leaf	Leaf_salt
	SRR5966999	epidermal bladder cells	control
	SRR5966989	epidermal bladder cells	salt
	SRR5966995	leaf with epidermal bladder cells	control
	SRR5966985	leaf with epidermal bladder cells	salt
	SRR5572173	Leaf	control
	SRR5572148	Leaf	heat
	SRR5572172	Root	control
	SRR5572144	<b>Root</b>	heat
	<b>Different tissues</b>	SRR5974425	Stem
SRR5974426		Seed	—
SRR5974427		Inflorescence	—
SRR5974428		Seedling	—
SRR5974435		Leaf	—

**Table S2. The primers were used for semi-quantitative RT-PCR analysis**

Genes	Forward primers(5'to3')	Reverse primers(5'to3')	Tm (°C)	Product size
<b>Actin</b>	TATGGTCAAGGCTGGATT	CACTGGGTGTTCTTCTGG	50	265
<b>CqHsf4</b>	GCCTCCAAATCCTACACC	AGATGACAGCAGCAACGA	52	213
<b>CqHsf5</b>	TCCAGCACCATTCTTAC	TCGTCATCGGTTGAGTTT	50	399
<b>CqHsf9</b>	TGGGTCGTCATTCTGGTG	TTTGGGTTTGGGTTTCCT	55	200
<b>CqHsf10</b>	GGACAGAGGGAATATGTAG	AAAGTTCGTGGTAAGGAG	48	290

**Table S3. Conserved functional domains of CqHsfs**

Subfamily	Gene	DBD	HR-A/B	RD	NLS	NES	AHA	AHA2	AHA1	AHA3	AHA4
C	CqHsf2	1	1	0	1	1	1	0	0	0	0
	CqHsf5	1	1	0	1	1	0	1	1	0	0
B	CqHsf3	1	1	1	1	1	0	0	0	0	0
	CqHsf4	1	1	1	1	1	0	0	0	0	0
	CqHsf6	1	1	1	1	0	0	0	0	0	0
	CqHsf8	1	1	1	1	0	0	0	0	0	0
	CqHsf9	1	1	1	1	0	0	0	0	0	0
	CqHsf10	1	1	1	1	0	0	0	0	0	0
	CqHsf11	1	1	1	1	0	0	0	0	0	0
	CqHsf17	1	1	1	1	0	0	0	0	0	0
	CqHsf22	1	1	1	1	0	0	0	0	0	0
	A1	CqHsf7	1	1	0	1	1	0	1	0	0
CqHsf16		1	1	0	1	1	0	1	0	0	0
CqHsf20		1	1	0	1	1	0	0	0	0	0
A2	CqHsf2	1	1	0	1	1	1	0	0	0	0
	CqHsf18	1	1	0	1	1	1	0	0	0	0
	CqHsf21	1	1	0	1	1	1	0	0	0	0
A3	CqHsf1	1	1	0	1	1	1	0	0	0	0
	CqHsf19	1	1	0	1	0	0	1	1	1	1
A4	CqHsf13	1	1	0	1	1	1	0	0	0	0
	CqHsf14	1	1	0	1	1	1	0	0	0	0
	CqHsf15	1	1	0	1	1	0	1	1	0	0
	CqHsf23	1	1	0	1	0	0	1	1	0	0