

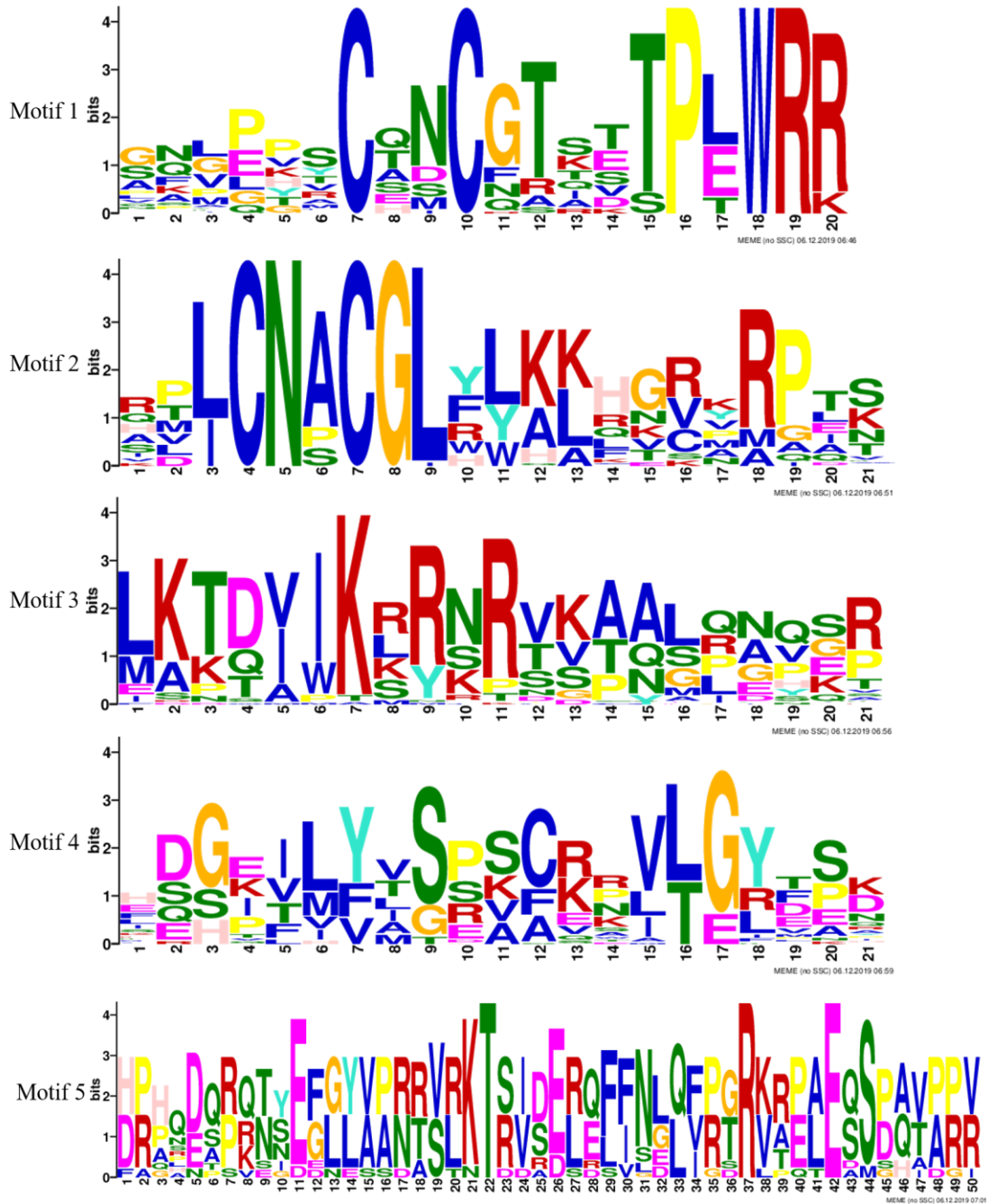
**Table S1 qRT-PCR primers of *A. oryzae* GATA gene expression in response to abiotic stress.**

Genes	Primer sequence 5'→3'	product size (bp)
AoAreA	F: ACTTTTACCACCCACCACCC; R: CTGAAGTAGGCCGTCATGGG	144
AoSnf5	F: TCCGCGAGTCCGTCAATATG; R: TATTGCTGCTGTTCCCTCGCT	103
AoLreB	F: GCTCAGGAAATGGTGGCTCT; R: ACTTCTCGTCCAATGCTGGG	113
AoLreA	F: GCAGGGAGGCAATGATGAGT; R: TCCCGCTACACCAGAAACAC	106
AoSreA	F: TCGGTAAAGAATGGCACCCC; R: ATTCTCGTCTCGTCGCCAAA	108
AoNsdD	F: CATCCACGAGGCGTTAGGAA; R: ACAGGAGATGTGAATGCGGT	101
AoAreB	F: CTCCCGTGTGCCAAAATTGC; R: GCTTATCGGACGGGGTCTTC	125
GADPH	F: GAAGGGGAACCCTCATTTCATC; R: TGGCAATGTAGGCAGTCAGG	140
AoCreA	F: CGGTCACATGCGTTCCAATC; R: TGGTGATTACGTGGACCAGC	150

F: Forward primer, R: Reverse primer

**Table S2 The detailed information of the proteins in the PPI network.**

Predicted Functional Partners	Information of Predicted Functional Partners
The protein in PPI network of <i>AoAreA</i>	
creA	DNA-binding protein creA
pacC	PH-response transcription factor pacC/RIM101
CADAORAP00007152	Glutathione S-transferase
blrA	BRLA predicted protein
CADAORAP00008916	Ammonia protein
CADAORAP00011087	Predicted protein
CADAORAP00010185	Zn-finger
CADAORAP00008991	Zn-finger
CADAORAP00008641	Predicted protein
CADAORAP00008102	Predicted protein
The protein in PPI network of <i>AoSreA</i>	
CADAORAP00011087	Predicted protein
CADAORAP00010185	Zn-finger
CADAORAP00008991	Zn-finger
CADAORAP00008641	Predicted protein
creA	DNA-binding protein creA
CADAORAP00008102	Predicted protein
CADAORAP00007597	Predicted protein
CADAORAP00007465	Predicted protein
CADAORAP00003985	Predicted protein
CADAORAP00003882	Predicted protein



**Figure S1.** The five structural motifs in *A. oryzae* GATA TF proteins.

	N-terminal ZnF_GATA domain	cysteine-rich region (CRR)
SreA-N	CSNCGTKSTPLWRRSPTGAMICNACGLYLKARNVAR	GSCPGGGNCNGTGGAEGCDGCPAYNN
SreB-N	CSNCGTKSTPLWRRSPTGAMICNACGLYLKARNVDR	GSCPGGGNCNGTGGAEGCDGCPAYNN
	C-terminal ZnF_GATA domain	conserved C-terminus (CCT)
SreA-C	CQNCGTTVTPLWRRDENGHPICNACGLYKLGHCYRPTTMKKTI IKRR	RRALQREAEEMREMLRAKERELAEI
SreB-C	CQNCGTTVTPLWRRDENGHPICNACGLYKLGHCYRPTTMKKTI IKRR	RRALQREAEEDMREALKAKERELAAI

**Figure S2.** The predicted amino acid sequence of AoSreA aligned with SreB. AoSreA and SreB contained several conserved domains including two ZnF\_GATA (N-terminal and C-terminal) separated

by a cysteine-rich region (CRR) and a conserved C-terminus (CCT) with a predicted coiled-coil domain.