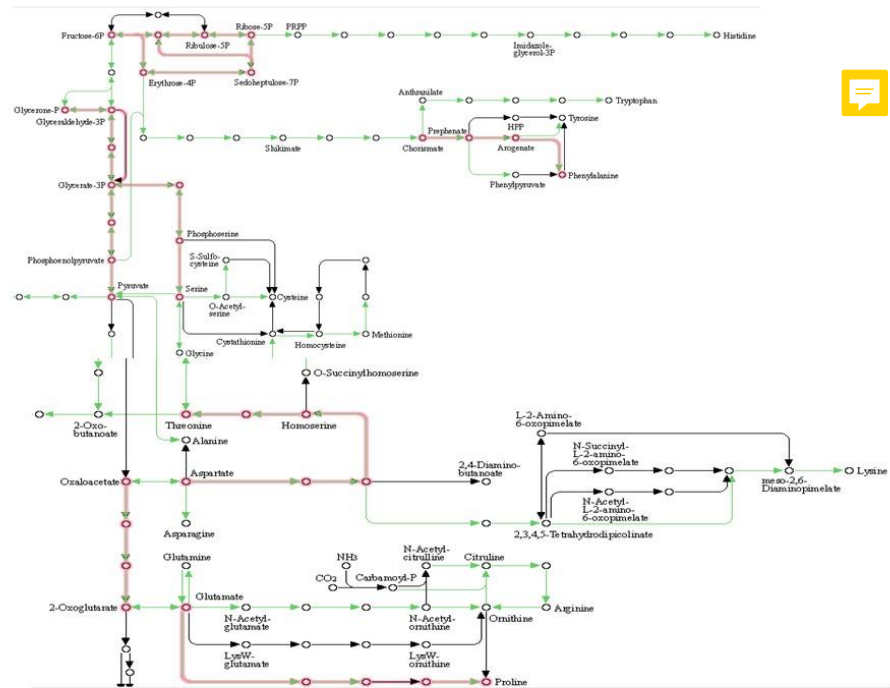
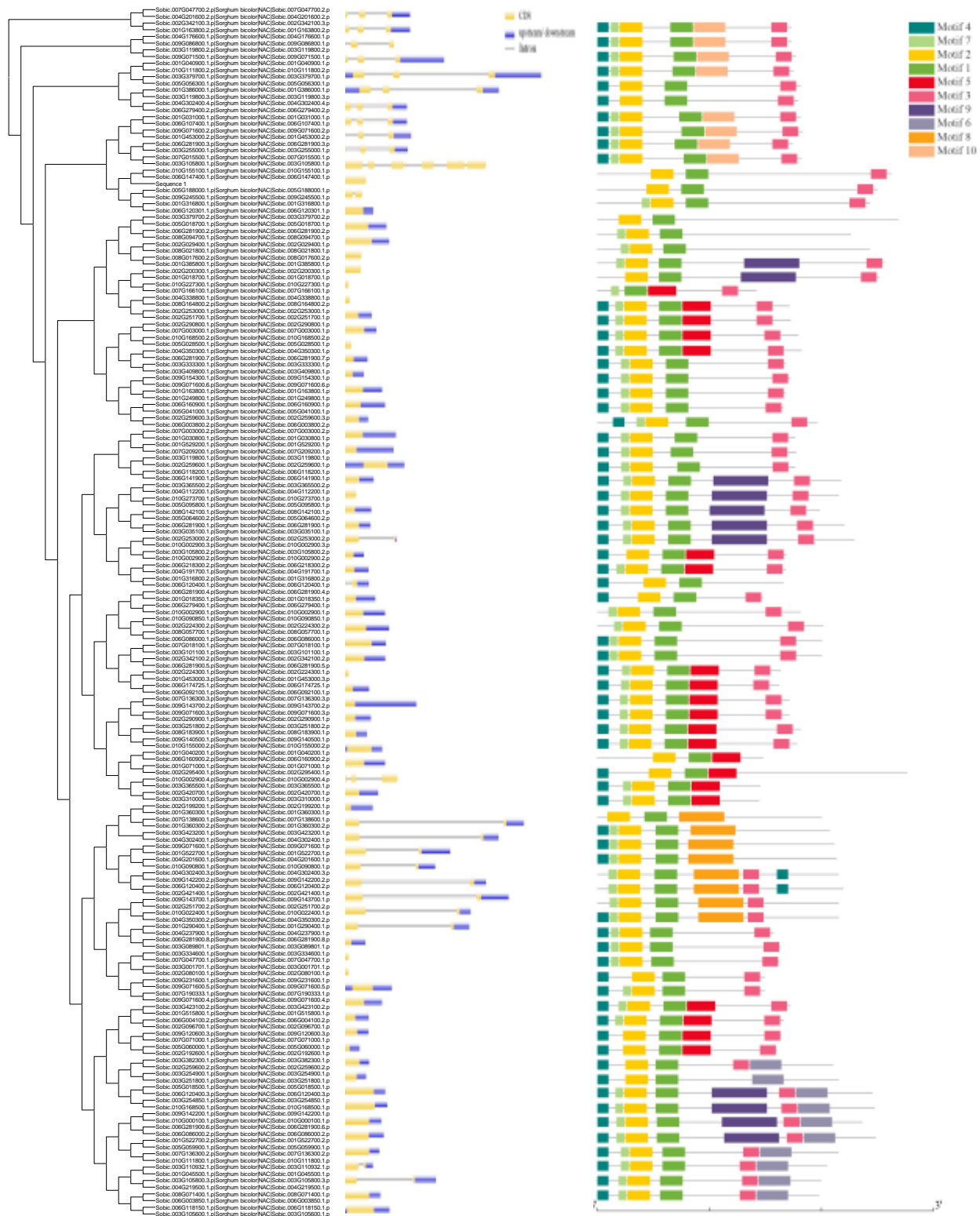


**Table S1.** Assembly statistics of unigenes in *Sorghum bicolor*.

	Assembled transcripts	Clustered transcripts
Number of transcripts identified	171,896	125,457
Maximum contig length	13,459	13,459
Minimum contig length	350	350
Average contig length	1,145±1011.2	1,121
Median contig length	821.8	1436
Total contigs length	223,458,498	167,467,734
Total number of non-ATGC characters	0	0
Contigs ≥ 200 bp	174,698	121,563
Contigs ≥ 500 bp	132,459	97,462
Contigs ≥ 1 Kbp	79,164	48,627
Contigs ≥ 10 Kbp	28	19
N50 value	1845	1807

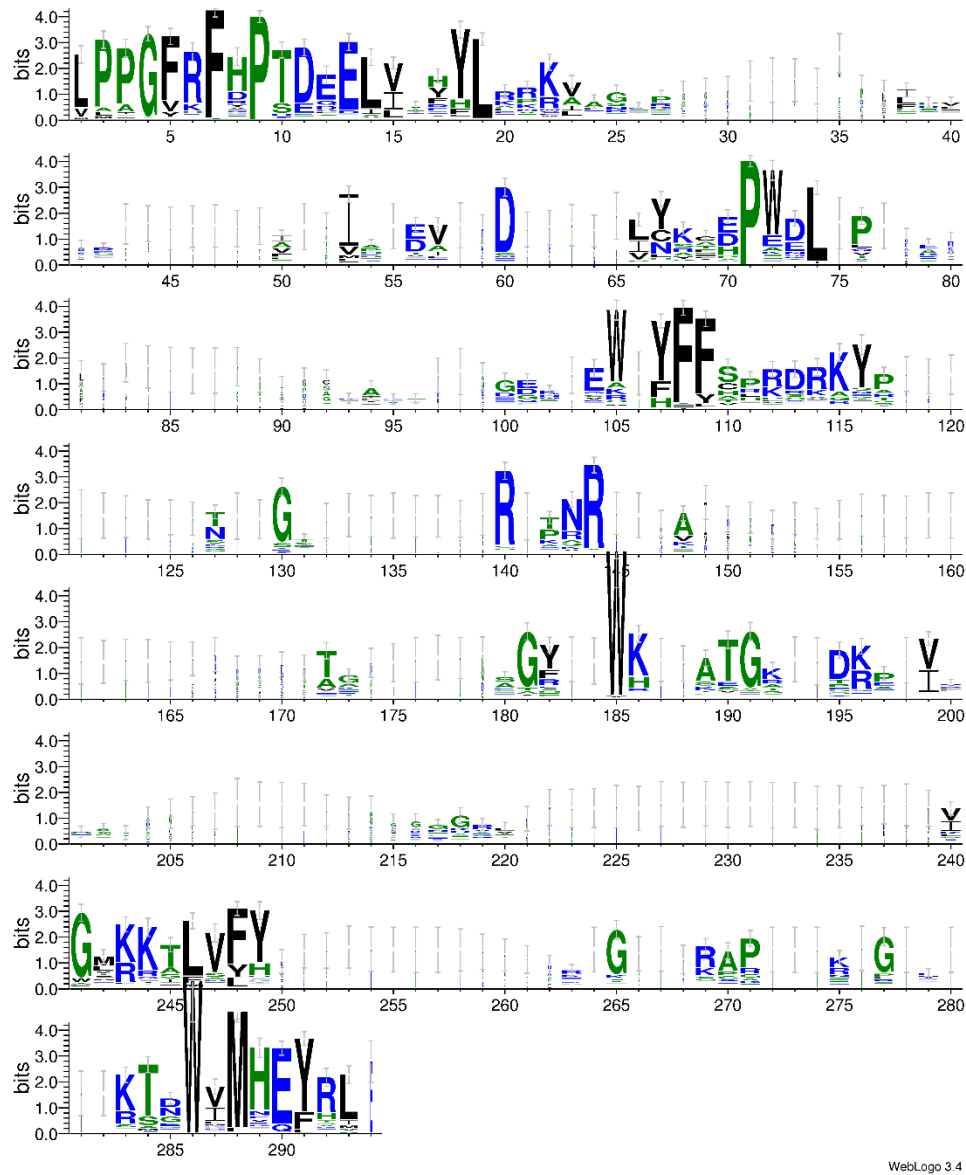


**Figure S1.** KEGG pathways of stress responsive metabolites. Pink represents highly upregulated metabolite biosynthetic pathways of the tolerant genotype and green represents those of the susceptible genotype.

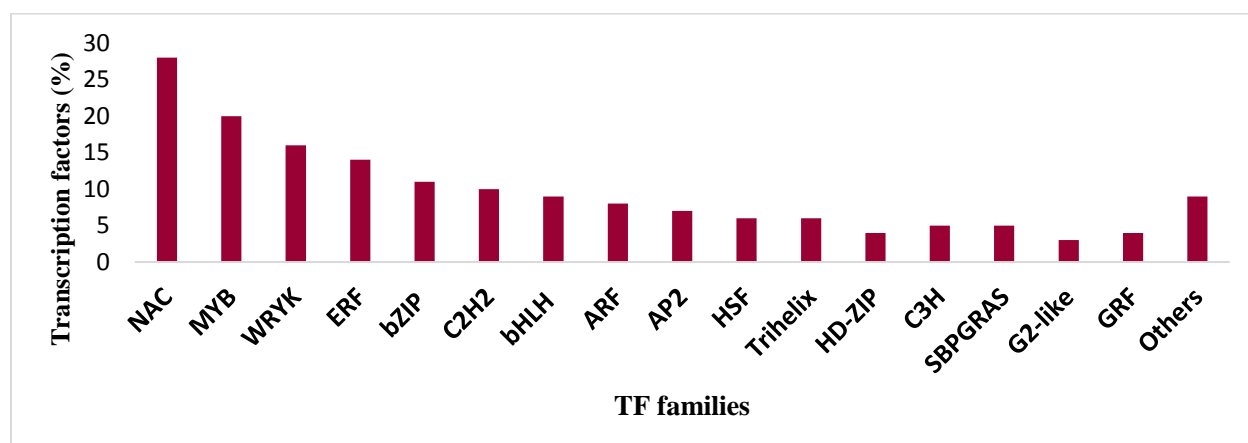
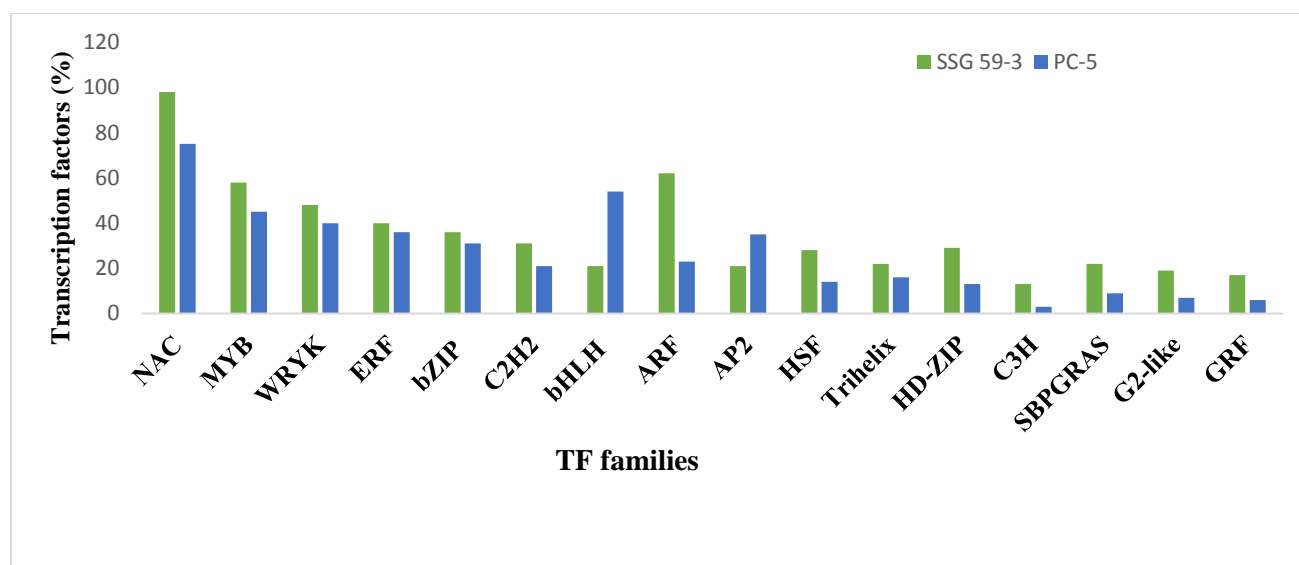


**Figure S2.** Phylogenetic relationships, gene structures, and conserved motifs of SbSNAC1 TFs. (A) Phylogenetic tree of *SbSNAC1* proteins from soybean constructed using the ML method.

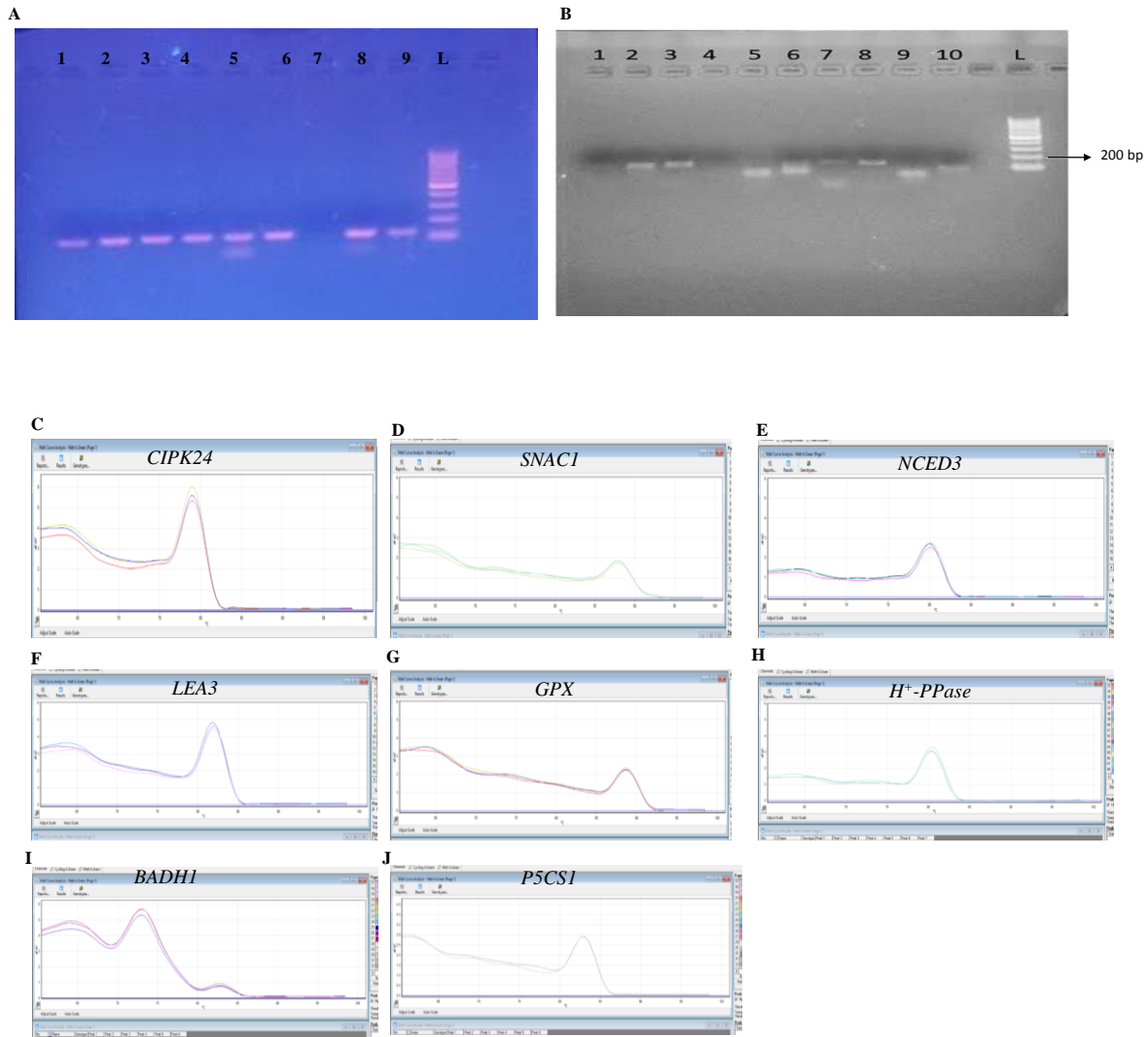
(B) Exon/intron organization of *SbSNAC1* genes. Yellow boxes represent exons and black lines represent introns. The upstream/ downstream regions of *SbSNAC1* genes are indicated by blue boxes. (C) Distribution of conserved motifs in *SbSNAC1* genes.



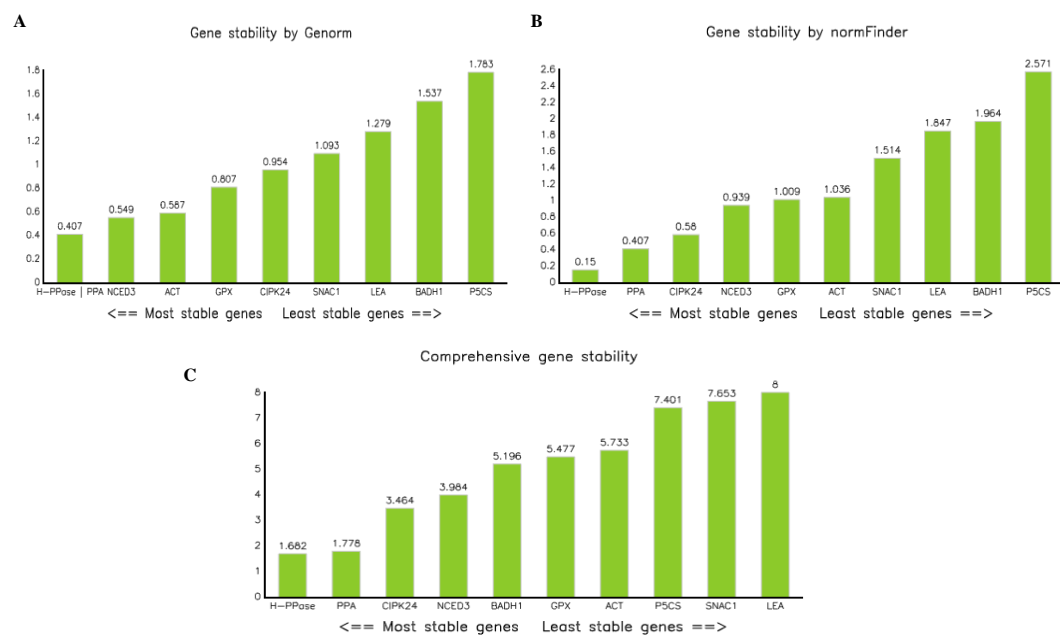
**Figure S3.** The DNA binding domain (DBD) alignment of *SbSNAC1* TFs.



**Figure S4.** (A) Comparisons of differentially expressed transcription factors in both the tolerant and the sensitive genotype under salt stress; (B) differentially expressed transcription factor families in sorghum genotypes under salt stress.



**Figure S5.** Agarose gel: (A) mRNA of salt stress-responsive genes ((1: *GPX*; 2: *LEA3*; 3: *CIPK24*; 4: *NCED3*; 5: *SNAC1*; 6: *H<sup>+</sup>-PPase*; 7: *Act*; 8: *BADH1*; 9: *P5CS1*; L: ladder), (B) PCR products of the expected sizes ( $\leq 200$ bp; 1: *Act*; 2: *LEA3*; 3: *CIPK24*; 4: *NCED3*; 5: *SNAC1*; 6: *H<sup>+</sup>-PPase*; 7: *GPX*; 8: *PP2A*; 9: *BADH1*; 10: *P5CS1*; L: ladder); (C–J) melt/dissociation curve of salt stress-responsive genes under saline conditions .



**Figure S6.** Expression stability and ranking of the salt responsive genes using: (A) geNorm, (B) NormFinder, and (C) comprehensive gene stability in *Sorghum bicolor* samples.