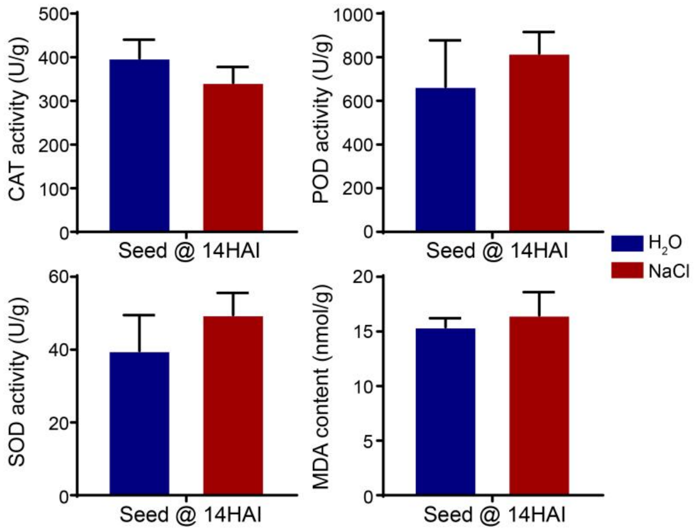

**Figure S1** Physiological changes in germinating seeds induced by salt stress compared to control conditions. Quantitative detection of CAT, POD, and SOD activities and MDA content in seeds at 18 hours after control and salt stress treatment. Data are presented as mean ± SD of three biological replicates.

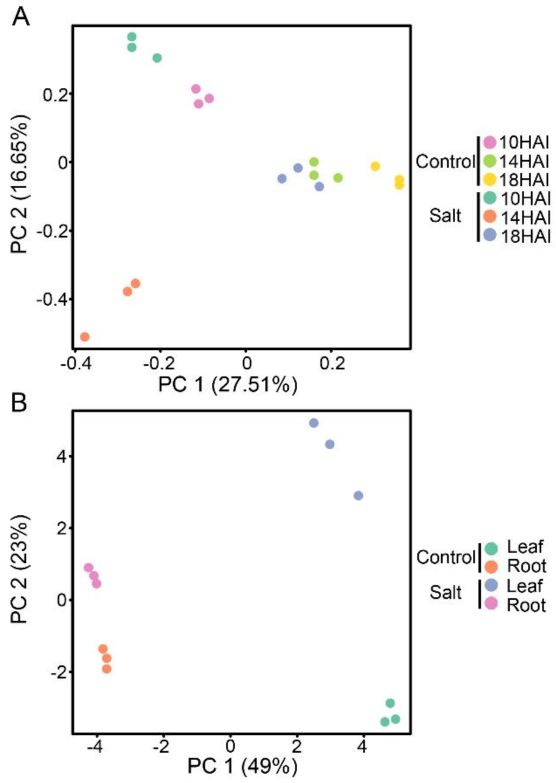

**Figure S2** Principle component analysis (PCA) of all sequenced samples. **(A)** PCA of the transcriptomes of samples from embryo under the indicated times after imbibition. **(B)** PCA of the transcriptomes of samples from leaf and root at seedling stage. PCA plots were generated by plotMDS function wrapped in edgeR package.

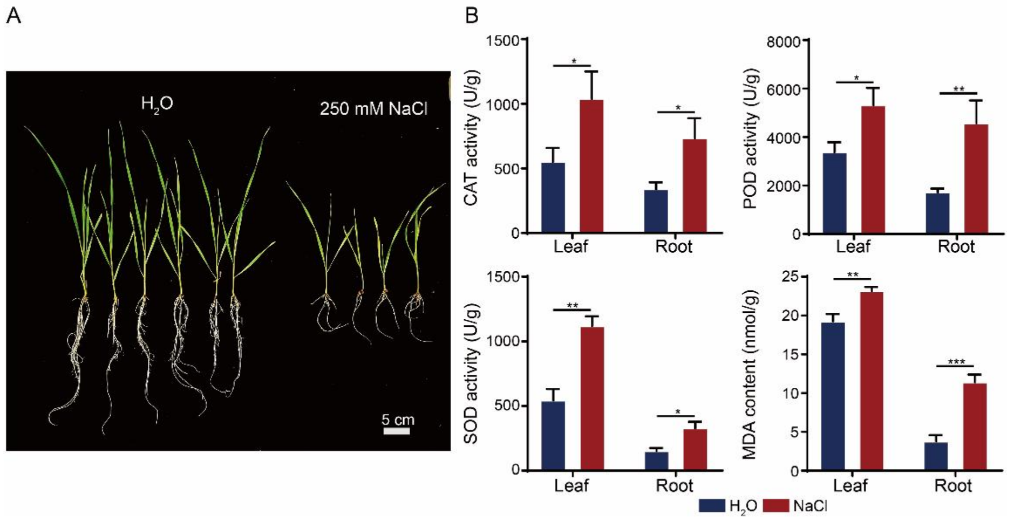

**Figure S3** Effect of salt stress on wheat seedling growth. **(A)** Phenotypic response of wheat seedlings to salt stress. Fourteen-day-old seedlings were treated with 250 mM NaCl for 7 days under normal and salt stress conditions. Scale bar represents 5 cm. **(B)** Quantitative analysis of antioxidant enzyme activities and oxidative stress markers in salt-stressed wheat seeds and seedlings. Seedlings (14 days old) were treated with 250 mM NaCl for 7 days. The following enzymes and markers were assessed: catalase (CAT), peroxidase (POD), superoxide dismutase (SOD), and malondialdehyde (MDA). Error bars represent the SD of the mean. Significance was determined by Student's t-test: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$.

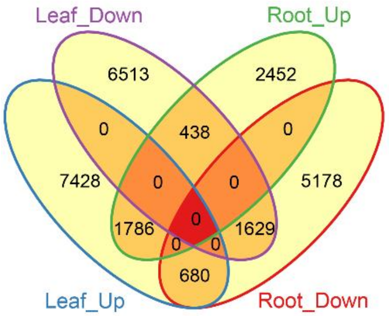

**Figure S4** Comparative transcriptomic profiling of salt stress-responsive genes in leaf and root tissues. Up: upregulated genes; Down: downregulated genes.

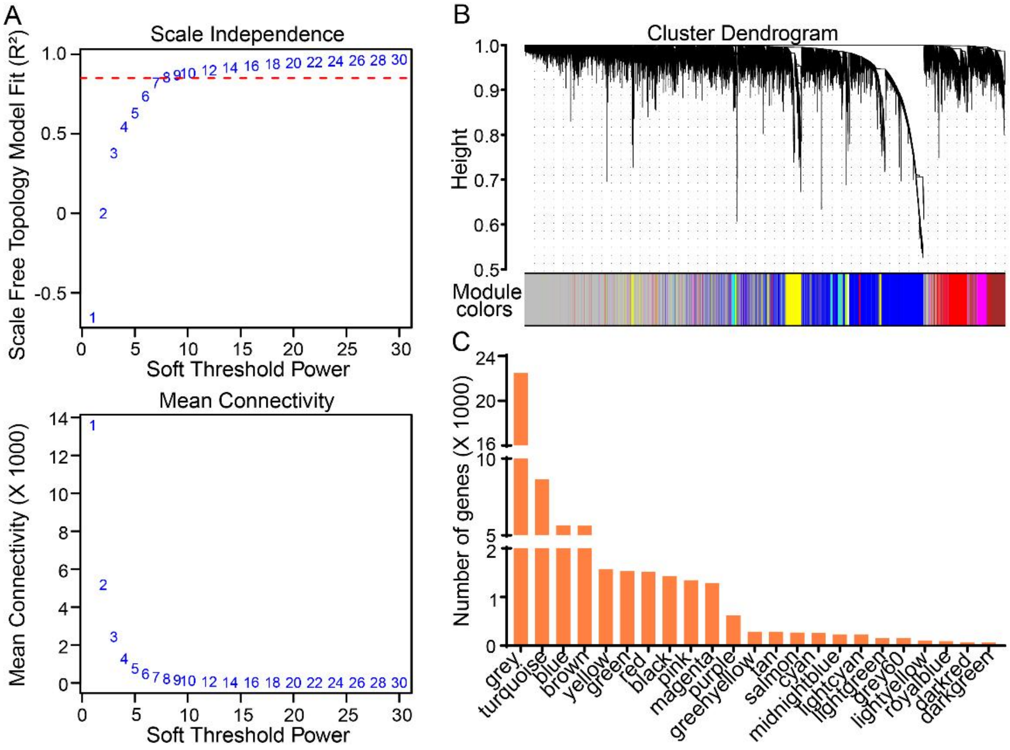

**Figure S5** Statistical results of WGCNA. **(A)** Screening of the optimal soft threshold. The soft threshold was determined by the scale-free network index (left panel). $R^2$ was set to 0.85, and the best soft threshold was 8. The soft threshold was determined by network connectivity. The average value of the gene adjacency coefficient in the gene network corresponding to different soft thresholds reflects the average network connection level. Network connectivity was better when the soft threshold was 8. **(B)** Cluster dendrogram and module colors of 53,936 genes. Modules were identified by the dynamic tree cut and the merged modules with similar expression pattern. **(C)** Bar plot showing the number of genes in each module.

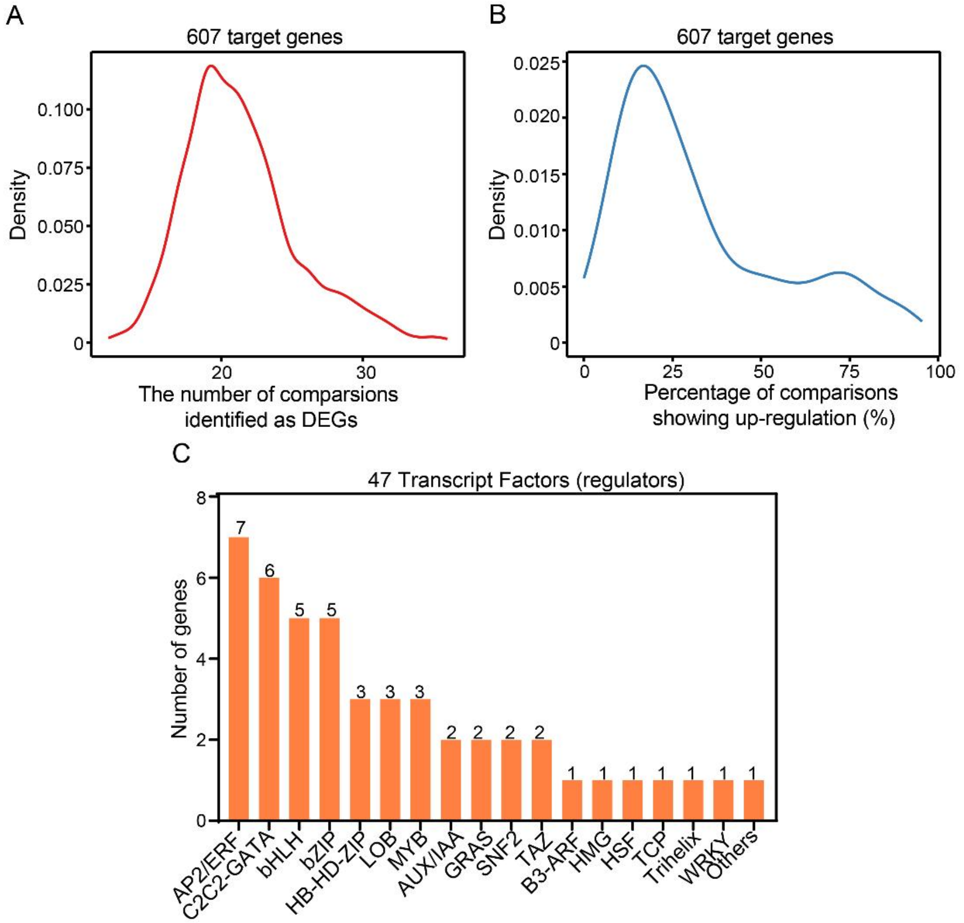

**Figure S6** Statistical results of the 607 core DEGs. **(A)** Density distribution of the number of comparisons showing differential expression for the 607 core DEGs. **(B)** Density distribution of the proportion of comparisons indicating upregulation for 607 core DEGs. **(C)** The number of transcription factors (regulators) belonging to different families in 607 core DEGs. The figures indicate the number of genes in corresponding families.