Figure S1 Enrichment analysis of the top 20 KEGG pathways in the four comparison groups under the reference transcriptome. (a) Top 20 pathways in TIR vs. STR; (b) Top 20 pathways in TIR vs. YBZ; (c) Top 20 pathways in TIR vs. TL; (d) Top 20 pathways in STR vs. YBZ; (e) Top 20 pathways in STR vs. TL; (f) Top 20 pathways in YBZ vs. TL. Rich factor is number of DEGs enriched into the pathway/total genes enriched into the pathway. P value $<$ 0.05.

Table S1: Water quality parameters of the sampling sites and biological parameters.

Table S2: De novo transcriptome analysis flow.

Table S3: Primer for qRT-PCR validation.

Table S4: Summary of Illumina RNA-seq data.

Table S5: The distribution of annotated species in NR.

Table S6: Detailed data of Figure 3b.

Table S7: Detailed data of Figure 4.

Table S8: Detailed data of Figure 5.

Table S9: General information for the modules of WGCNA.

Table S10: DEG-related functional information.

Table S11: Sequences of DEGs related to saline–alkaline tolerance.

Table S12: Reference genome comparison results.

Table S13: Research related to saline–alkaline adaptation.