

Supporting information

Additional supporting information may be found in the online version of this article:

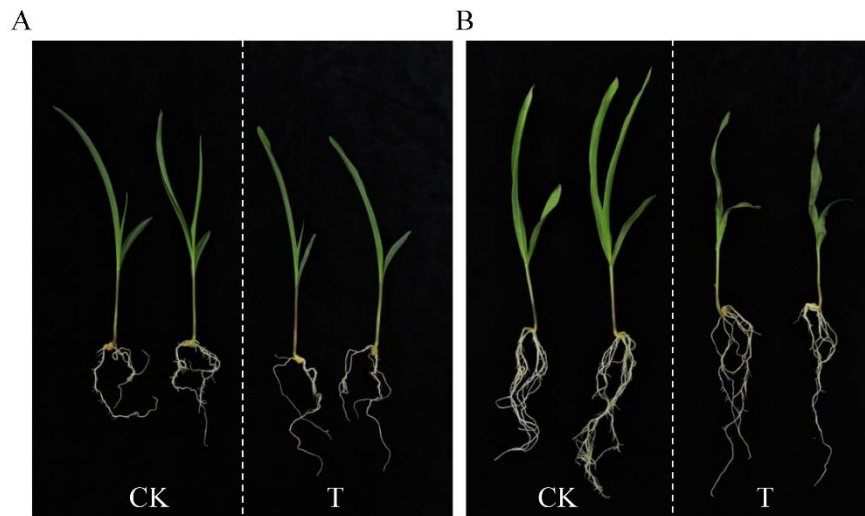


Figure. S1 Phenotypes in maize lines L2010-3 and BML1234 at 72 hours under 150 mM NaCl treatment. (A) the salt-tolerant line L2010-3. (B) the salt-sensitive BML1234.

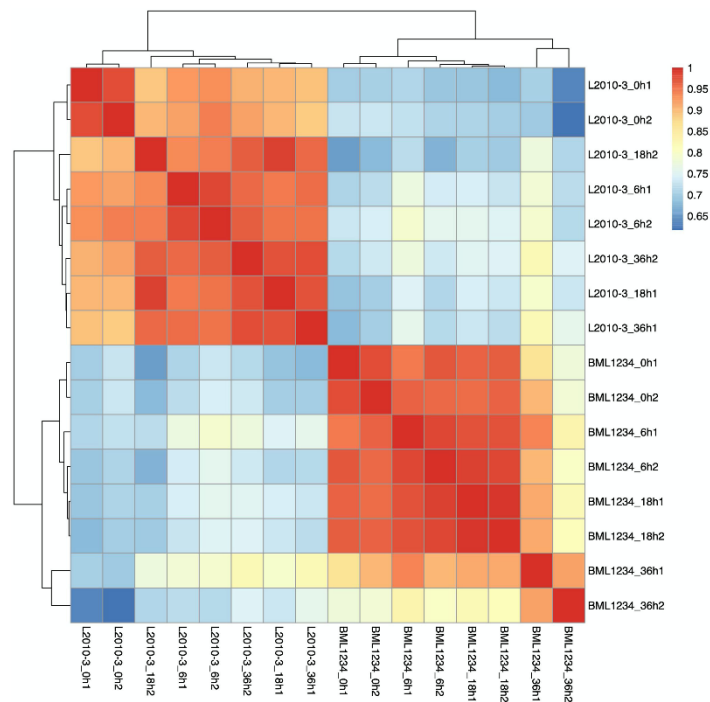


Figure. S2 Spearman's correlation analysis between biological replicates for RNA-seq at three stages. Color levels correspond to the degree of correlation in each replicate.

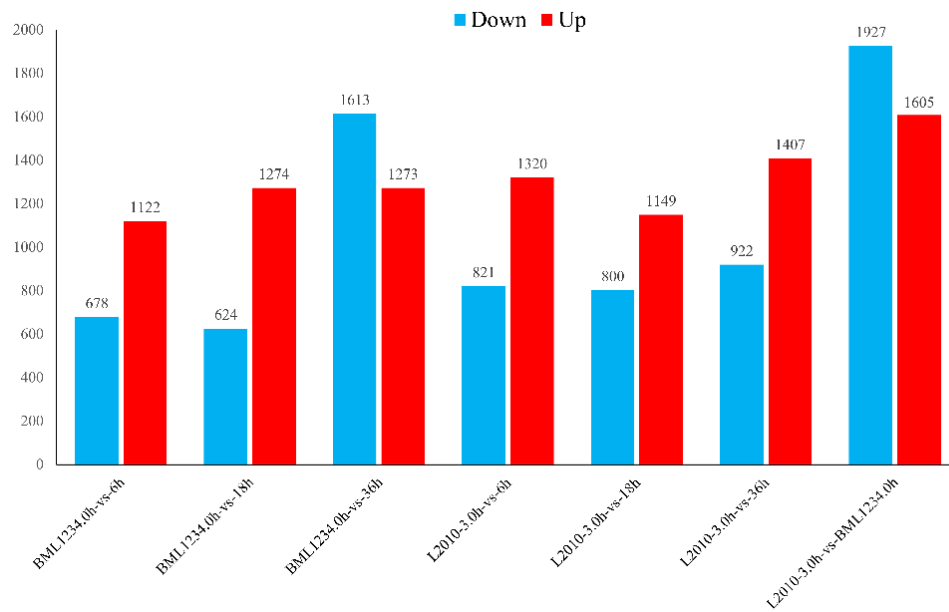


Figure. S3 Numbers of DEGs in the salt-tolerant line (L2010-3) and salt-sensitive line (BML1234) under normal condition (0 h) and salt treatment (from 6 to 36 h).

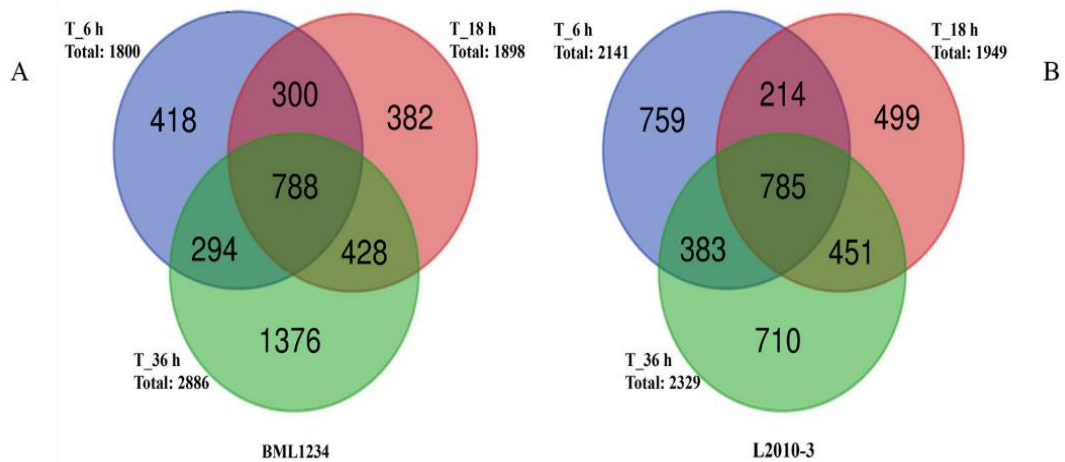


Figure. S4 Venn diagrams of genes differentially expressed at the three stages in the salt-sensitive line BML1234 and the salt-tolerant line L2010-3.

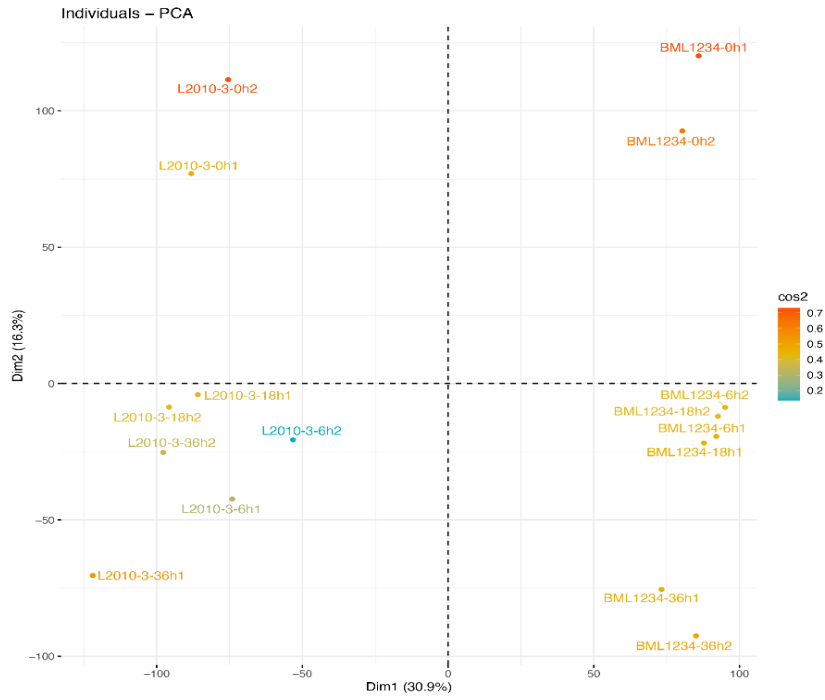


Figure. S5 Principal Component Analysis (PCA) diagram for the 16 libraries.

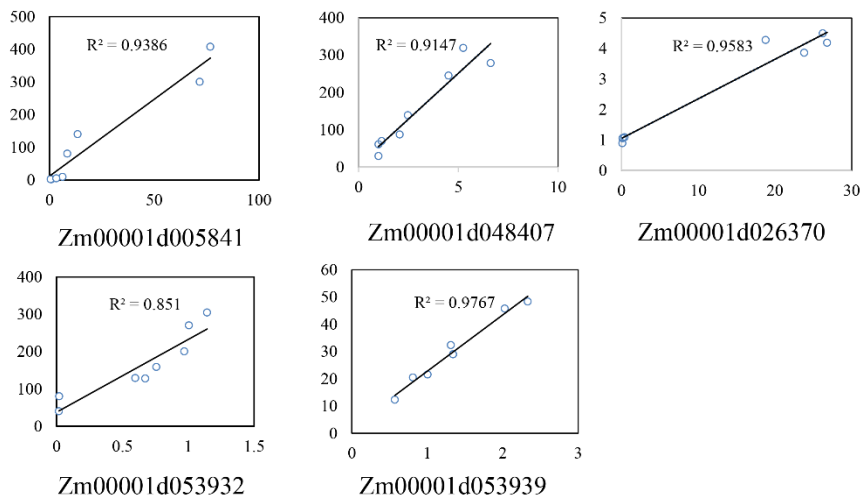


Figure. S6 Correlation analysis between RNA-seq and qPCR data.