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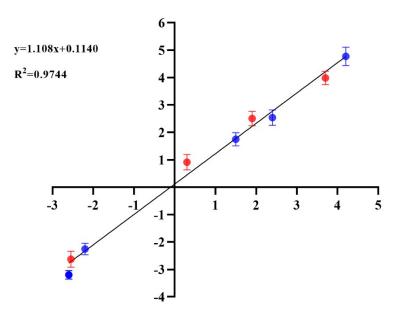


Fig. S1 Correlation analysis of the gene expression levels between qPCR and transcriptome data for nine selected genes. The nine analyzed genes and primers are listed in Table S1. Each point represents a value of fold-change of the expression level of acid–stress treatment compared with the control group.