Article

Transcriptome profiling of maize (*Zea mays* L.) leaves reveals key cold-responsive genes, transcription factors, and metabolic pathways regulating cold stress tolerance at the seedling stage

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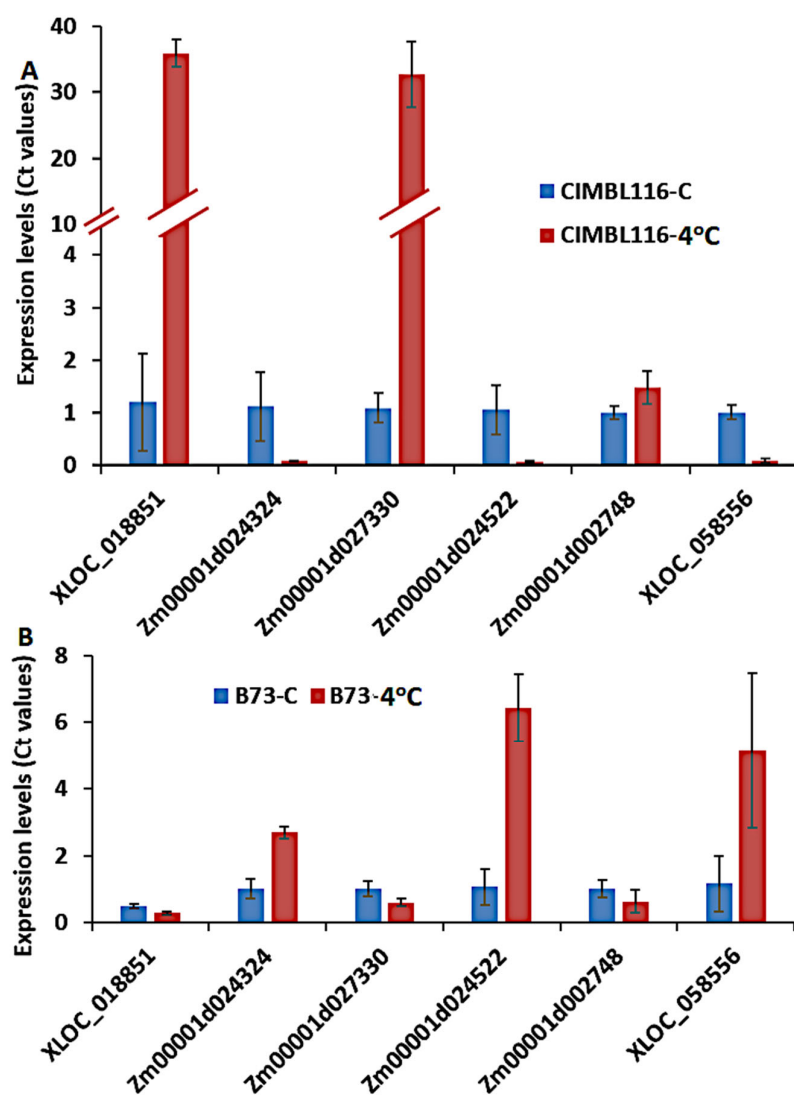
Figure S3. Validation of expression pattern of six genes identified by RNA-Seq by Ct values obtained from qRT-PCR. (**A**) Expression patterns of six genes in the cold-tolerant line (CIMBL116) before and after cold treatment. (**B**) Expression patterns of six genes in the cold-sensitive line (B73) before and after cold treatment. Error bars represent the standard deviation while blue and dark red color represents control and treatment at 4°C.