

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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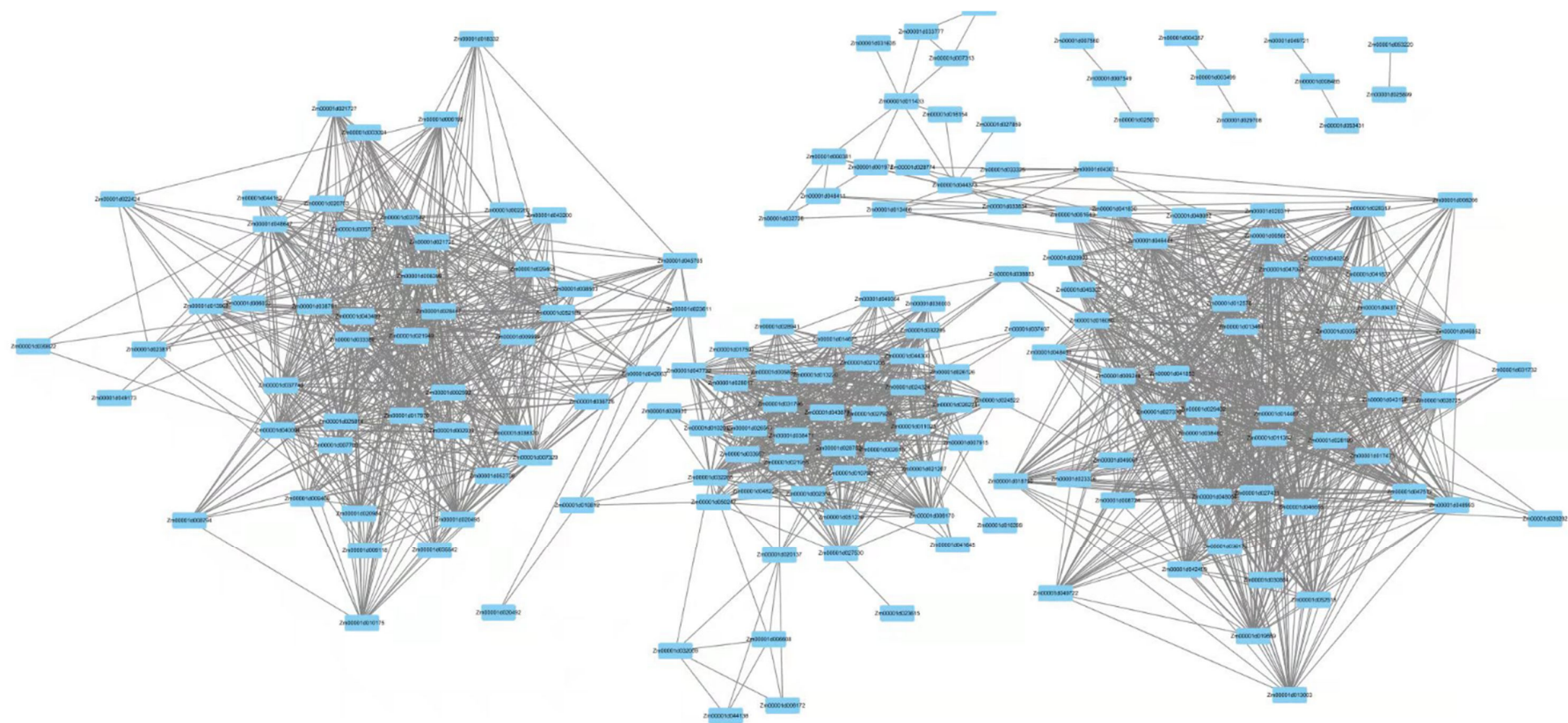
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**Figure S2.** Co-expression network analysis of our DEGs from 24-tolerant and 22-sensitive maize inbred lines under cold stress conditions. The blue rectangle contains the Gene ID of the DEGs. For details about the critical genes, genes they regulate and expression pattern see supplementary material table S8.