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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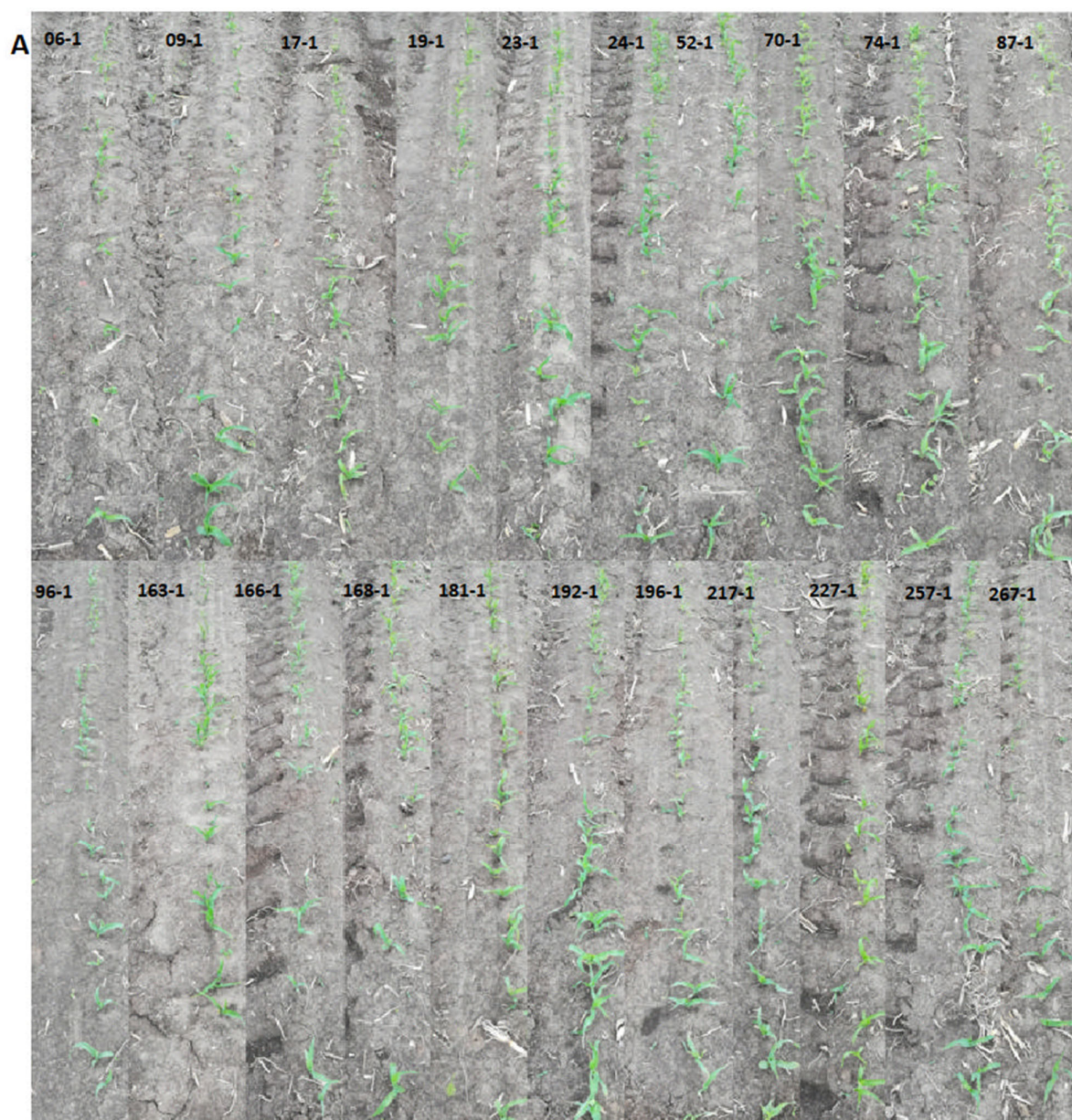
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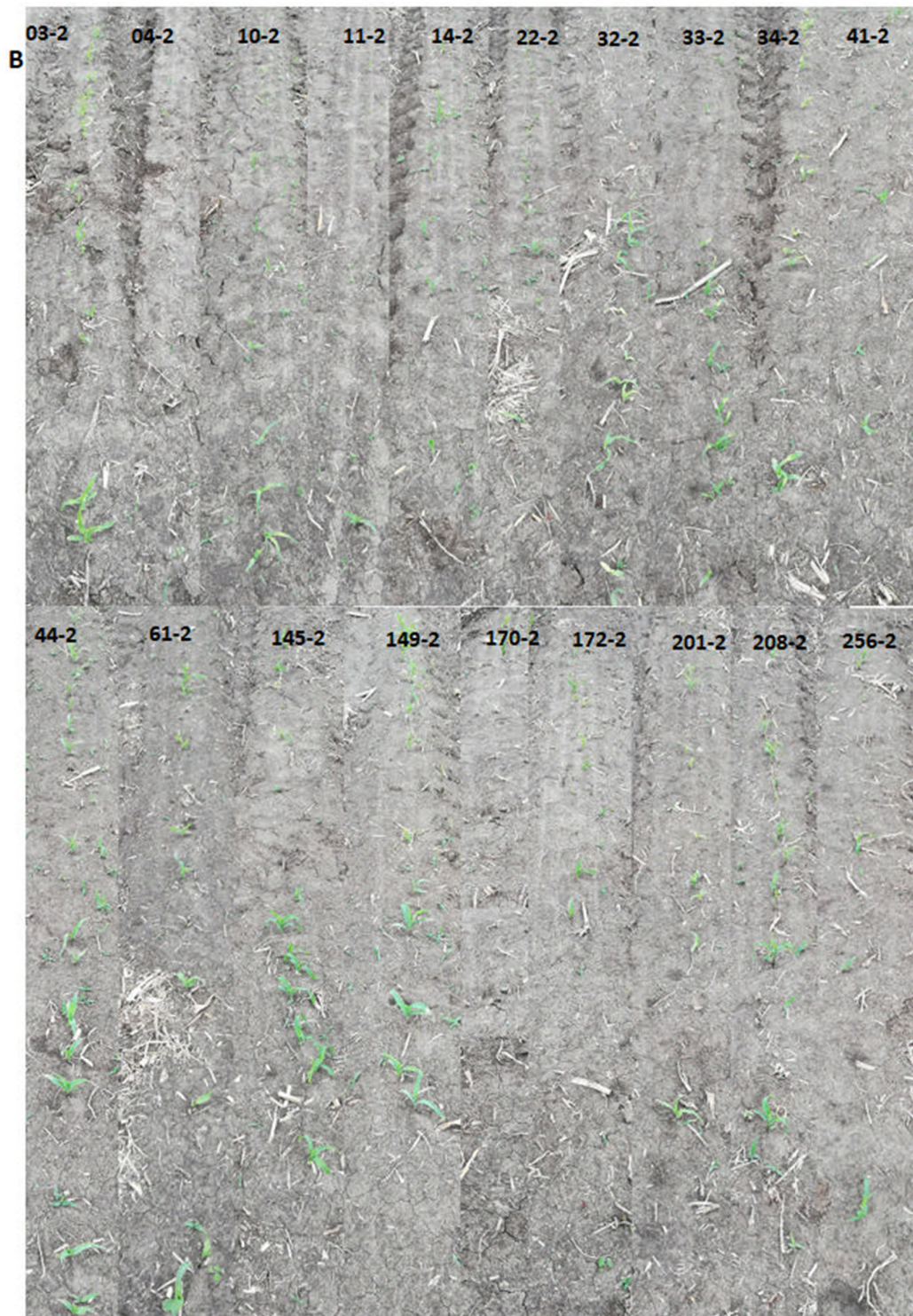
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Figure S1. Phenotypic analysis of maize population under cold stress conditions (**A**) Tolerant lines (-1) maintained fully expanded green leaves, intact plant architecture, and high survival rates under cold stress (**B**) Sensitive lines (-2) displayed shriveled, curled, and yellowish coloured spots on the leaves under cold stress.