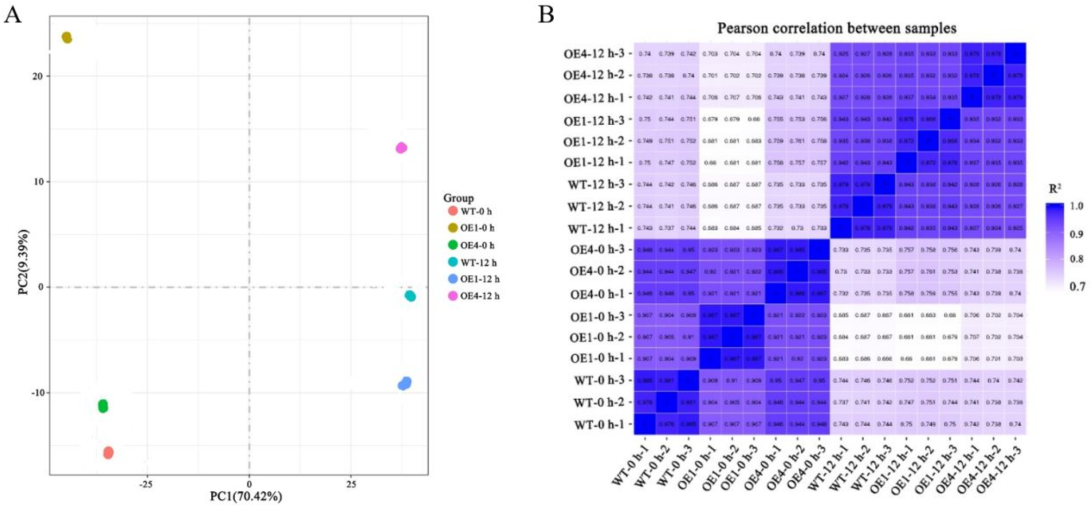

Figure S3. Principal component analysis (PCA) and correlation analysis of transcriptome data. (A) At 0h and 12h post-cold treatment, differentially expressed genes (DEGs) primarily clustered within PC1. Significant DEGs distinguishing WT from OE1/OE4 lines were concentrated in PC2. Biological triplicates showed tight clustering within each group. (B) Distinct gene expression patterns were observed among OE1, OE4, and WT groups at 0h and 12h post-treatment. Results were consistent with PCA analysis, with biological replicates clustering tightly within groups, confirming data reliability for downstream analysis.