



Article

Cold Response Transcriptome Analysis of the Alternative Splicing Events Induced by the Cold Stress in *D. catenatum*

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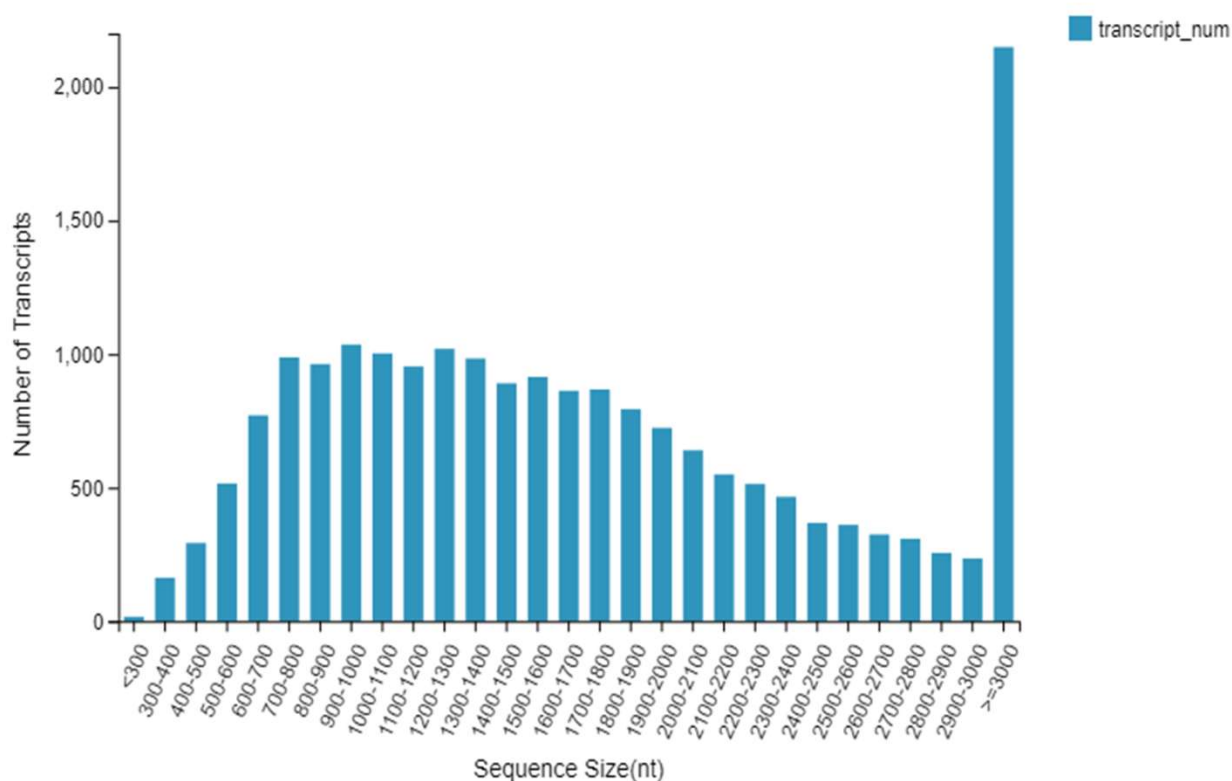


Figure S1. Distribution of transcripts lengths in *D. catenatum* transcriptome.

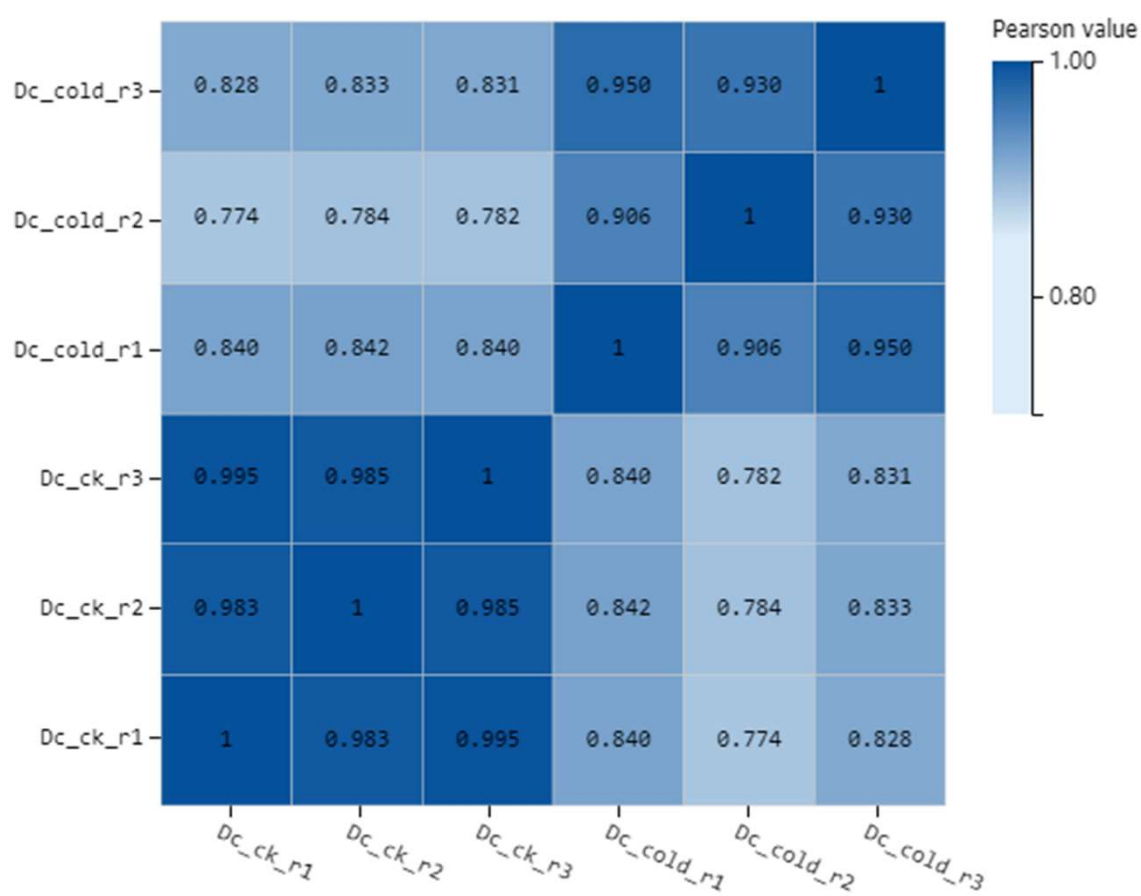


Figure S2. Heatmap of Pearson correlation analysis among different samples.

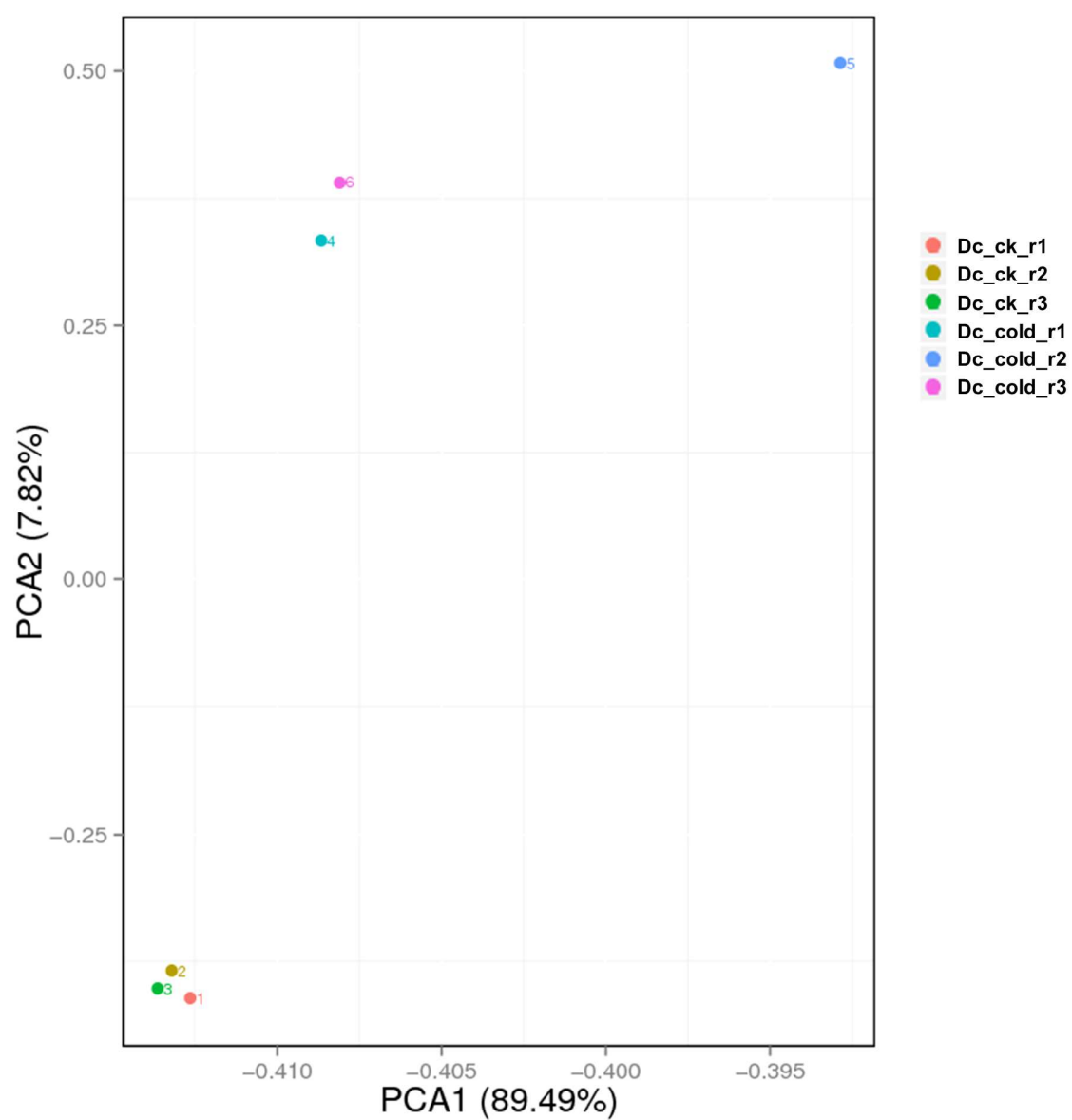


Figure S3. Principal component analysis (PCA) factorial maps of transcriptome data.

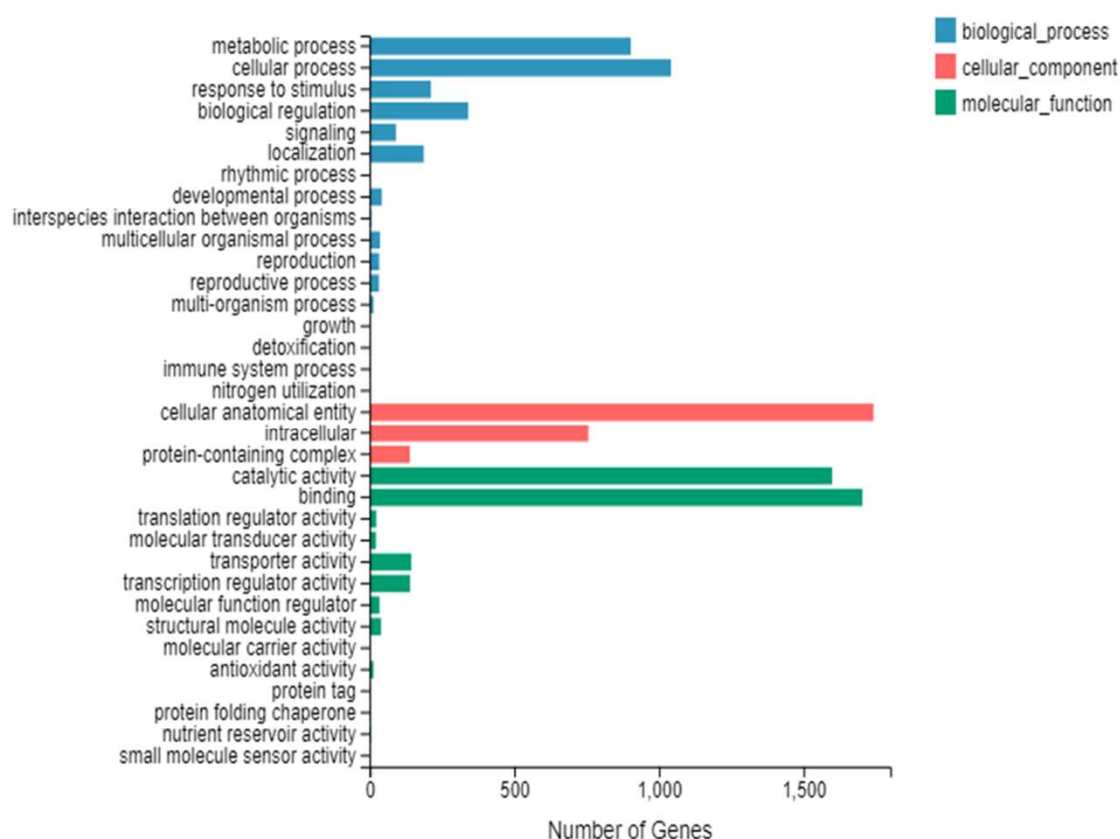


Figure S4. GO annotation of differentially expressed genes in *D. catenatum* in response to cold.

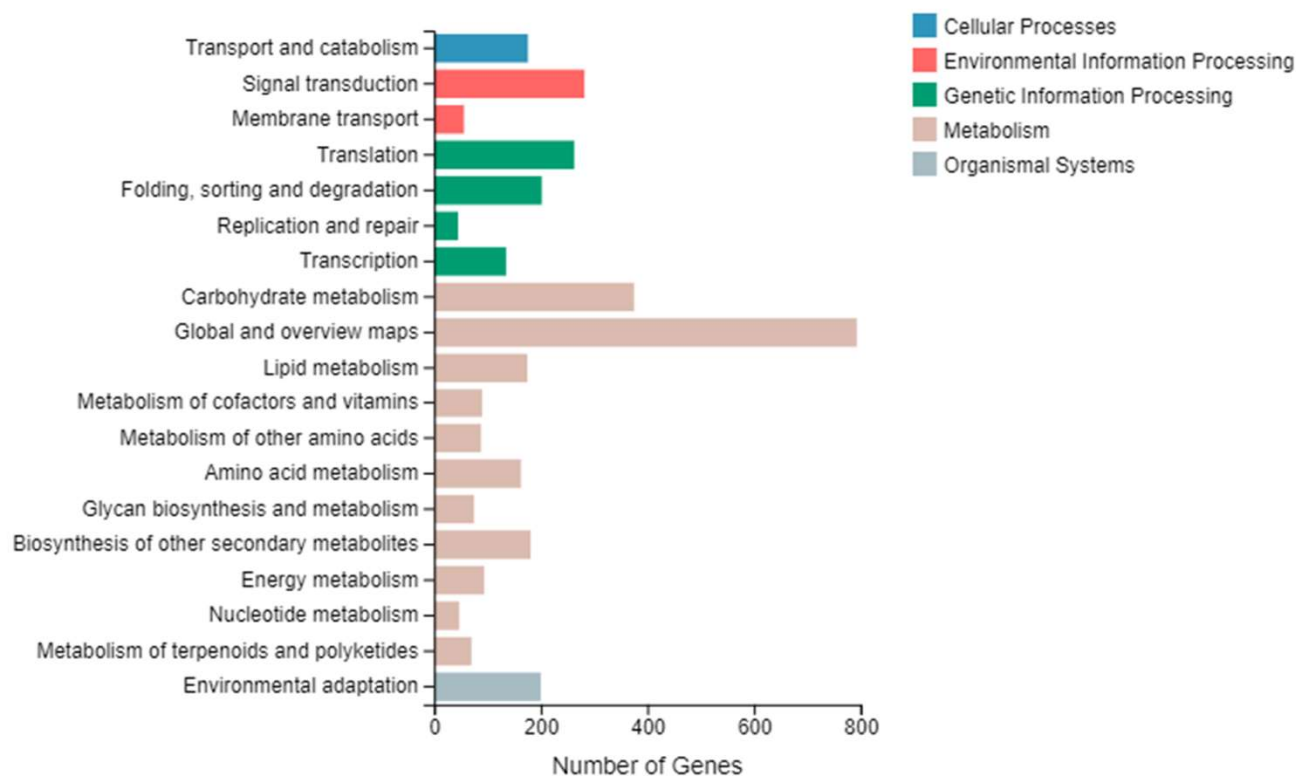
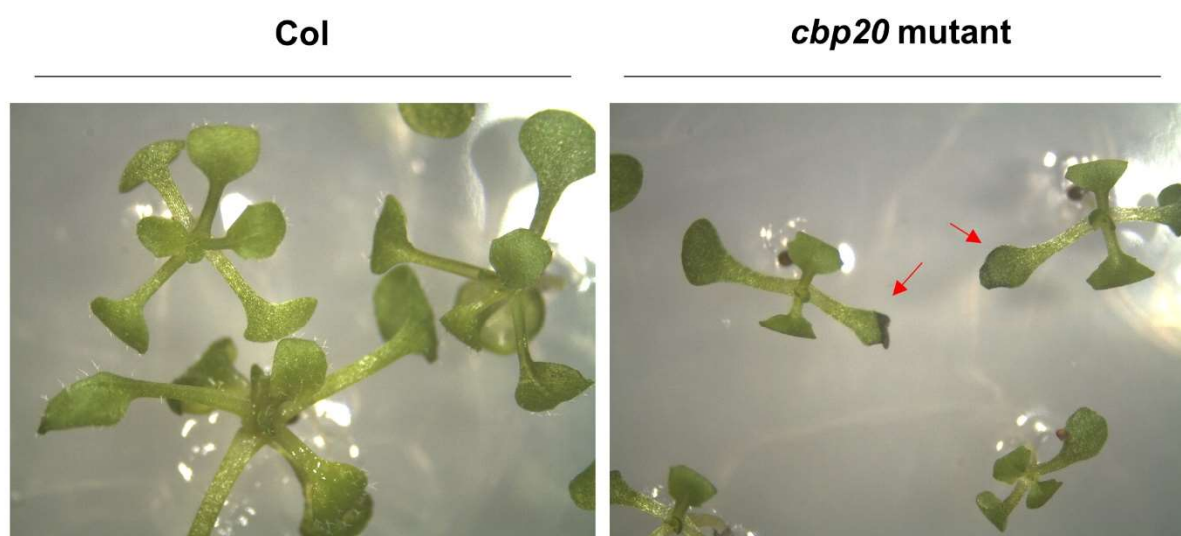


Figure S5. KEGG pathway annotation for differentially expressed genes in *D. catenatum* in response to cold.



Cold stress in *Arabidopsis*

Figure S6. Phenotypes of wild type (Col-0) and *cbp20* mutant *Arabidopsis* in response to cold. The plants were treated at 4°C for 20 d under a 16-h light/8-h dark photoperiod condition.

A



B

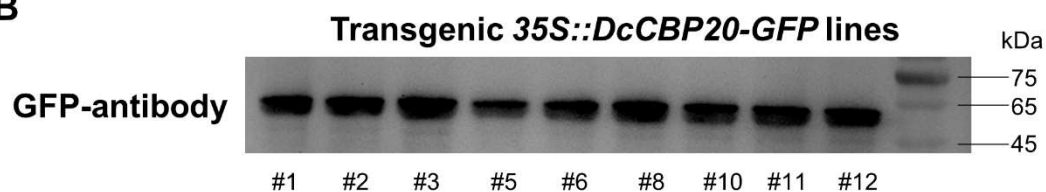


Figure S7. Generation of transgenic *Arabidopsis* overexpression of *DcCBP20*. **(A)** Phenotypes of the *DcCBP20* overexpressed *Arabidopsis*. **(B)** Identification of transgenic lines using western blot. The GFP antibody was used to detect the *DcCBP20*-GFP protein.

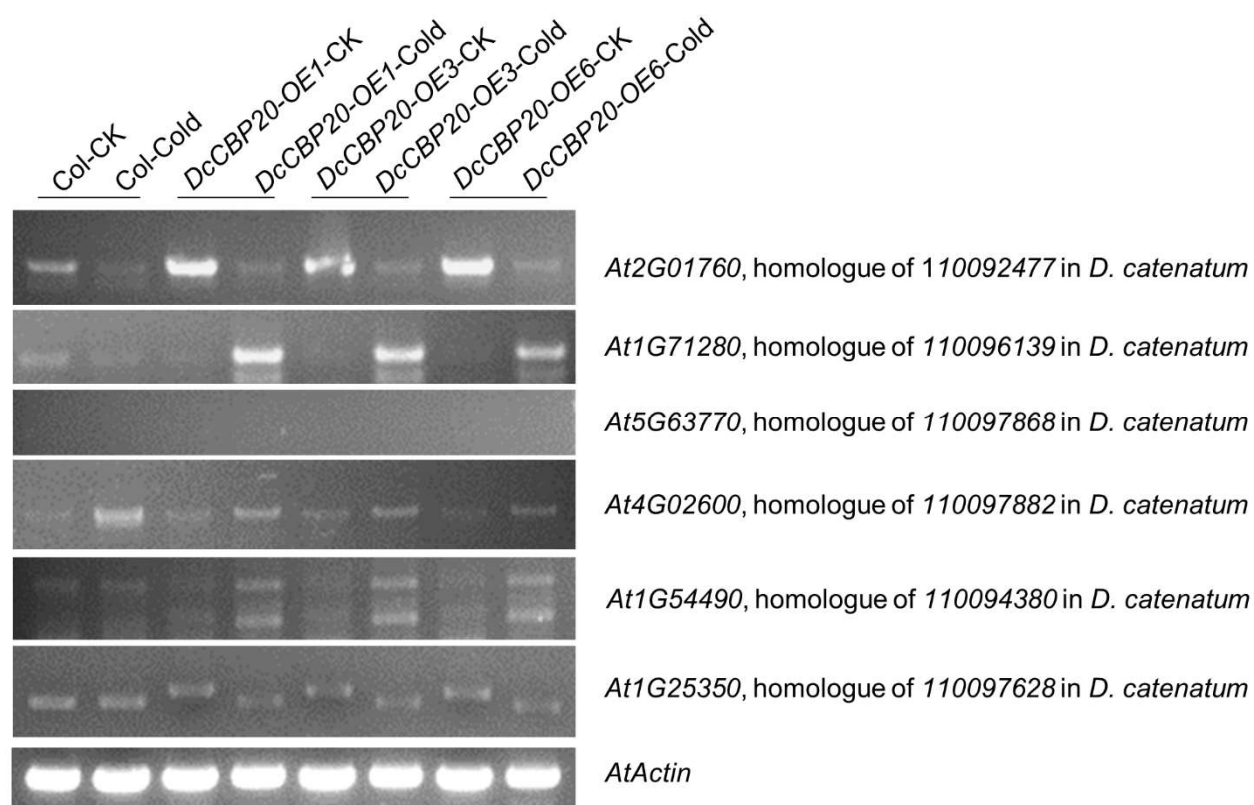


Figure S8. The splicing isoforms of the PCR products using specific primers in cDNA of *DcCBP20* transgenic *Arabidopsis* detected by RT-PCR. RT-PCR products were detected using 1.5% agarose gels.