

Transcriptome analysis of pecan (*Carya illinoensis*) differentially expressed genes in response to drought stress

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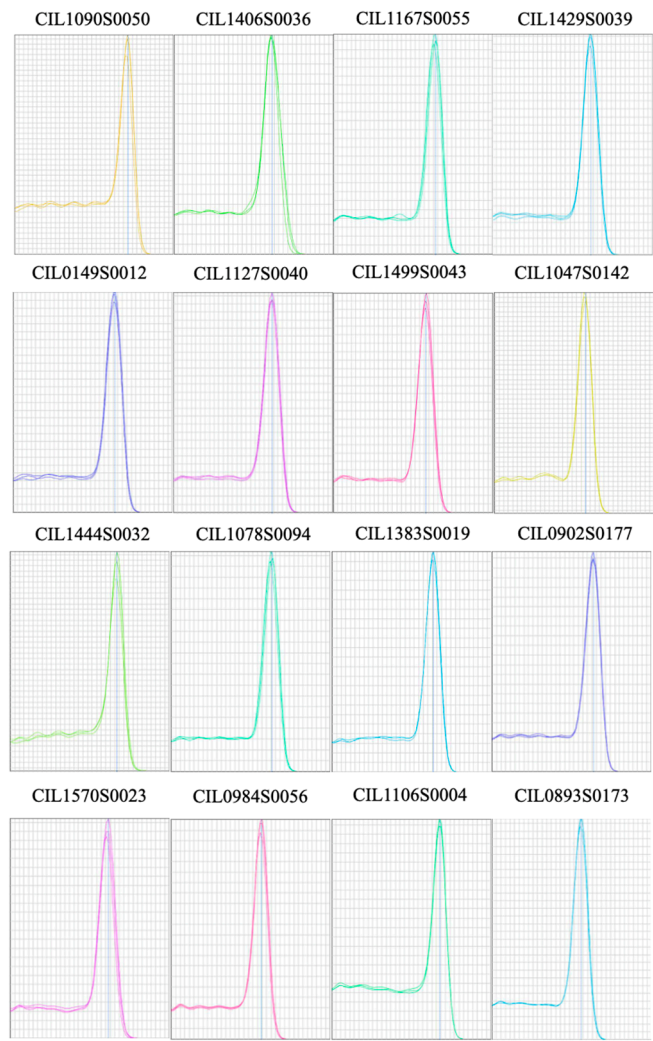
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18 **Supplementary Data**

19 Supplementary data are available online.

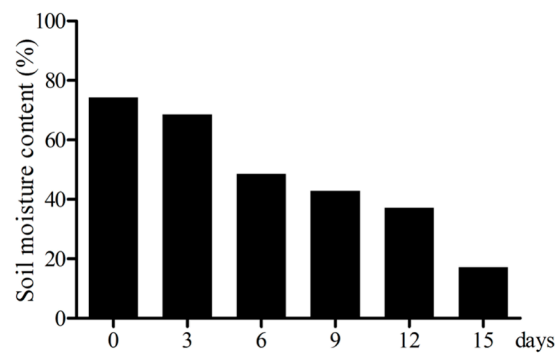
20 **Figure S1**



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22 **Figure S1.** Melt curves of 16 selected genes.

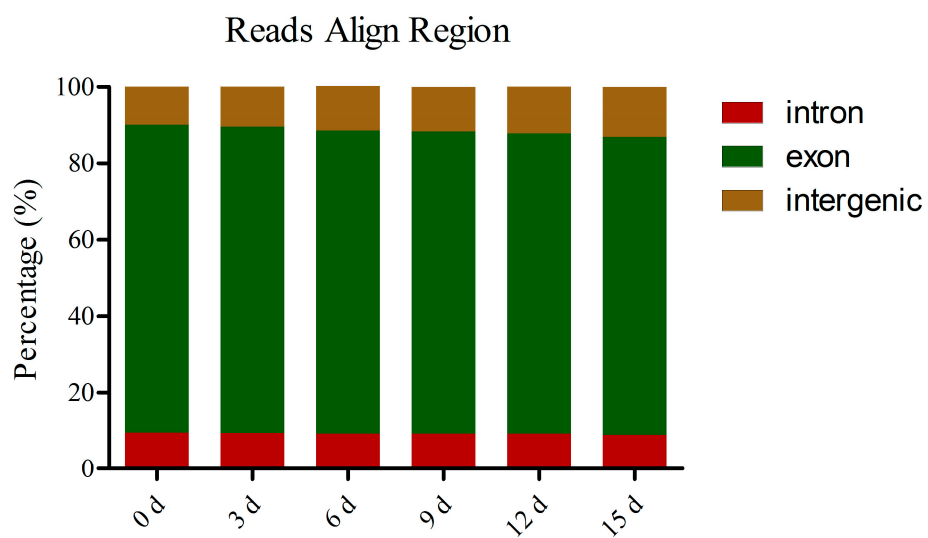
23 **Figure S2**



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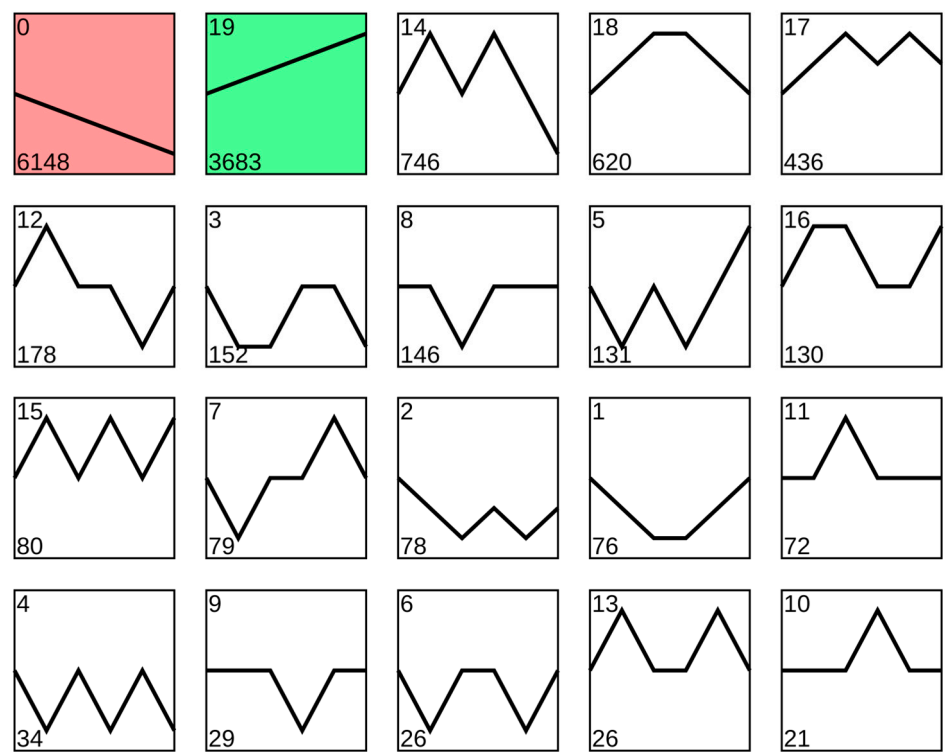
25 **Figure S2.** Soil moisture content after drought treatment of pecan.

26 **Figure S3**



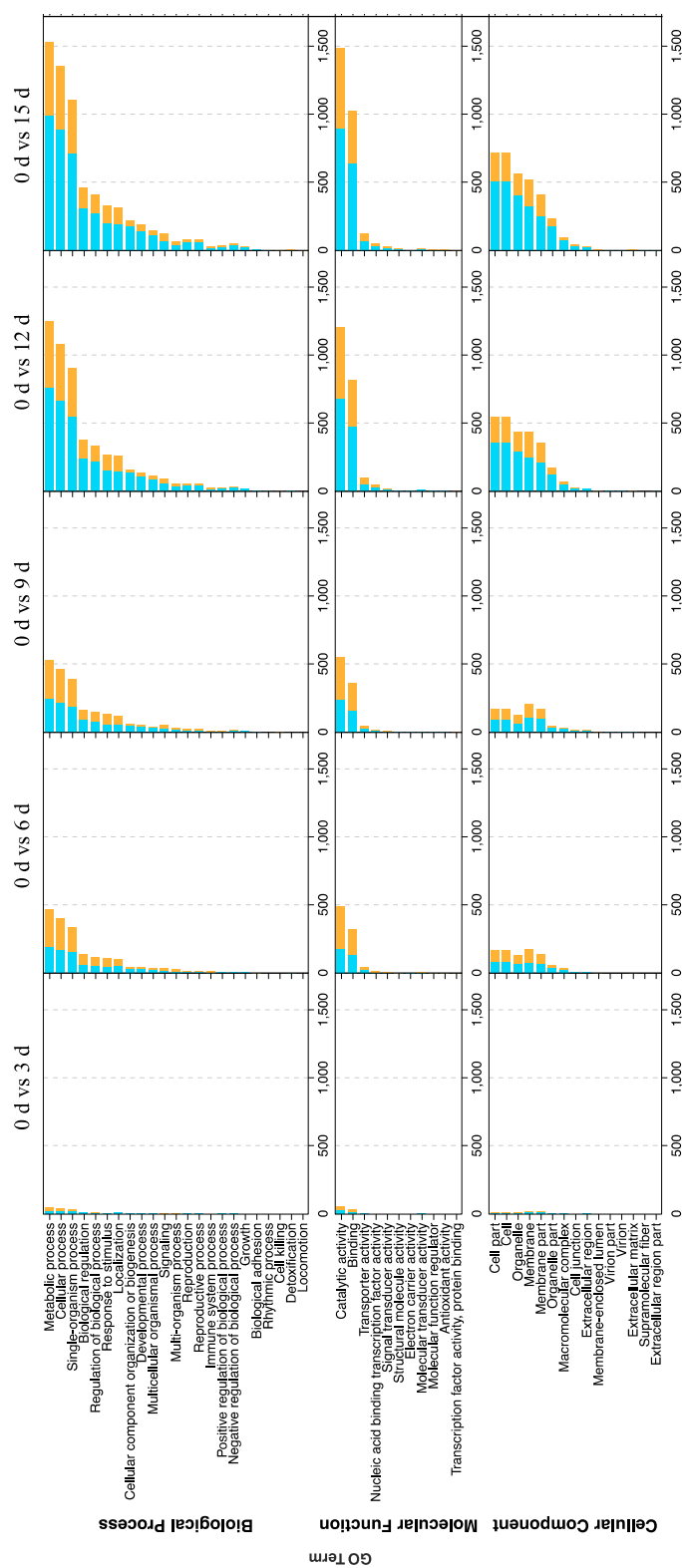
27 **Figure S3.** Distribution of reads in different regions of pecan genome.

28 **Figure S4**



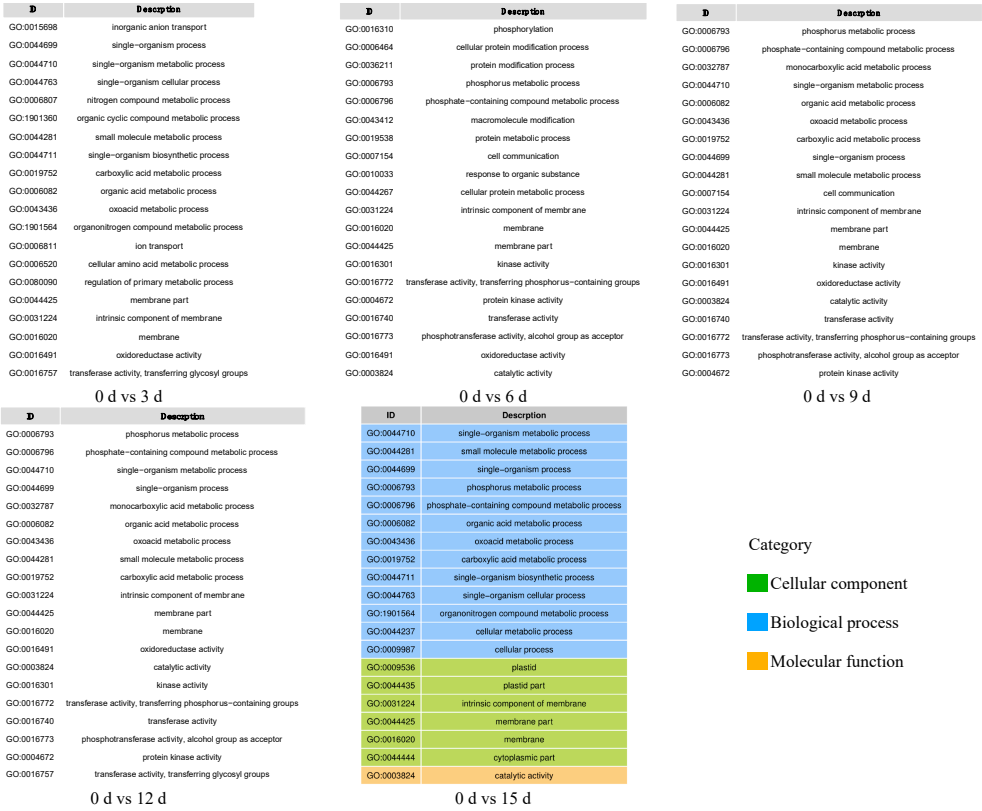
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30 **Figure S4.** Expression patterns of DEGs under drought stress in pecan. The DEGs in
31 each cluster were listed in Supplementary Table S4.



34 **Figure S5.** GO classification of differentially expressed genes. The blue boxes
 35 indicated down-regulated genes, and the yellow boxes indicated up-regulated genes.

36 **Figure S6**

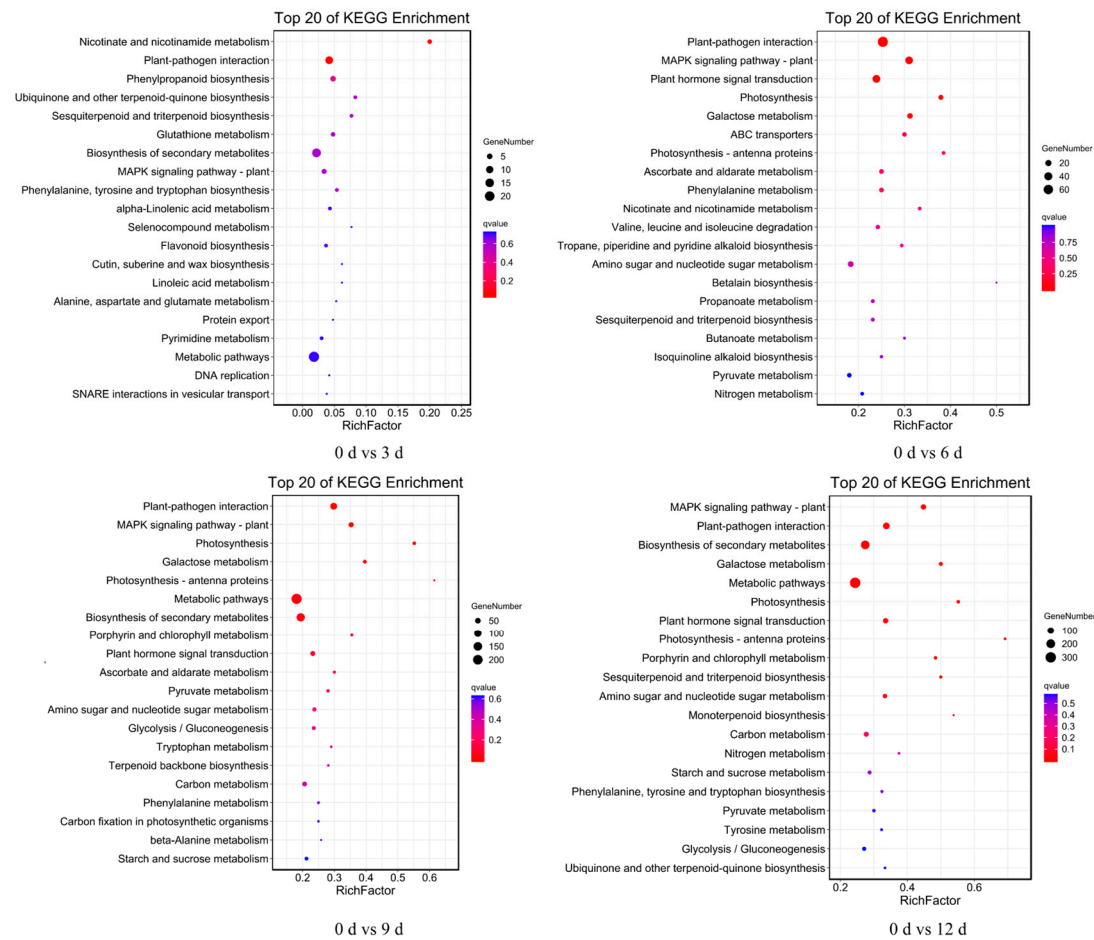


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38 **Figure S6.** GO enrichment analysis of the DEGs in pecan under drought treatment.

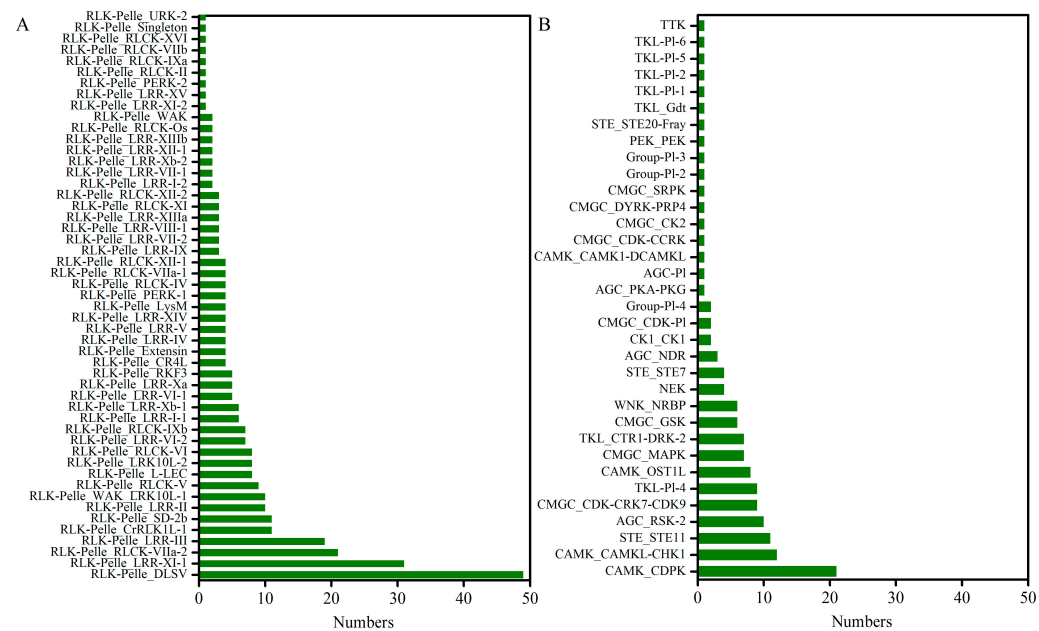
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40 **Figure S7**



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42 **Figure S7.** The top 20 enriched pathways under drought treatment for 3, 6, 9 and 12 d
43 compared to that in control. The rich factor represented the ratio of the number of
44 DEGs in the pathway.

46 **Figure S8**



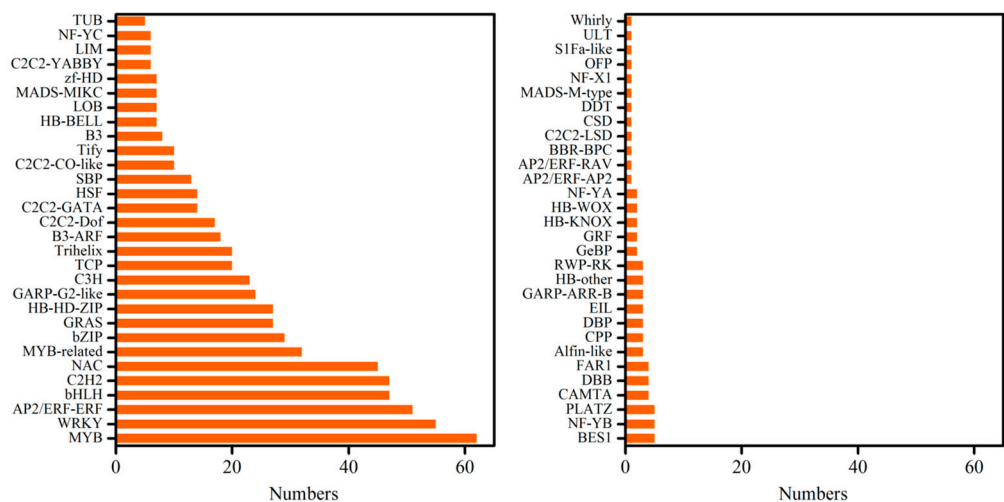
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48 **Figure S8.** Classification of differentially expressed protein kinase genes involved in
49 the pecan response to drought. All differentially expressed PK genes were identified
50 and classified into different families. (A) PK families in the RLK group. (B) PK
51 families in the non-RLK group.

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54 **Figure S9**



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56 **Figure S9.** Classification of differentially expressed transcription factor genes
57 involved in pecan response to drought. All differentially expressed TF genes were
58 identified and classified into different families.

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