Supplementary Materials

Co-Expression Network Analysis Suggests PacC Transcriptional Factor Involved in *Botryosphaeria dothidea* Pathogenicity in Chinese Hickory

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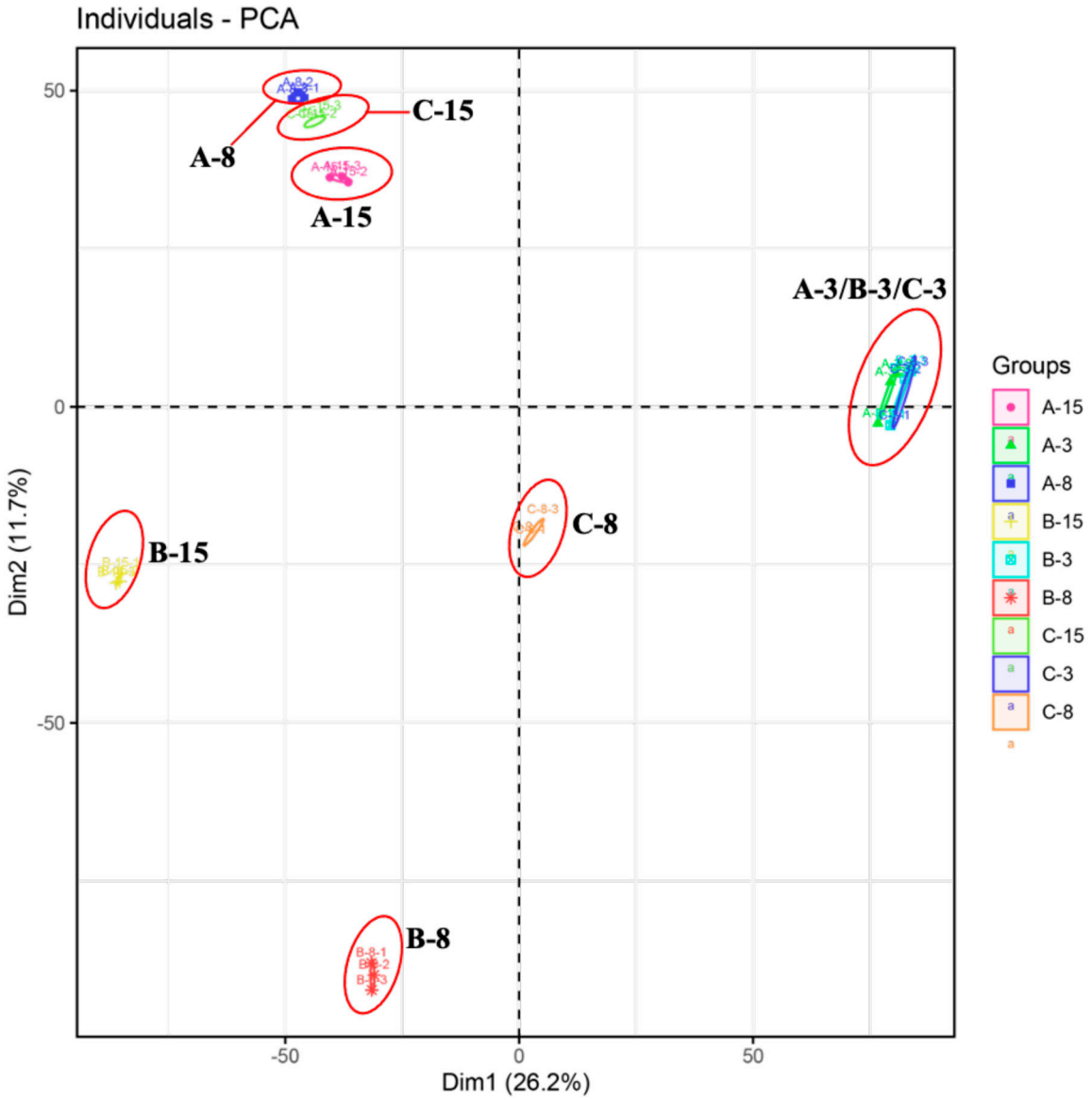

Figure S1. Principal component analysis (PCA) of RNA-seq data samples.

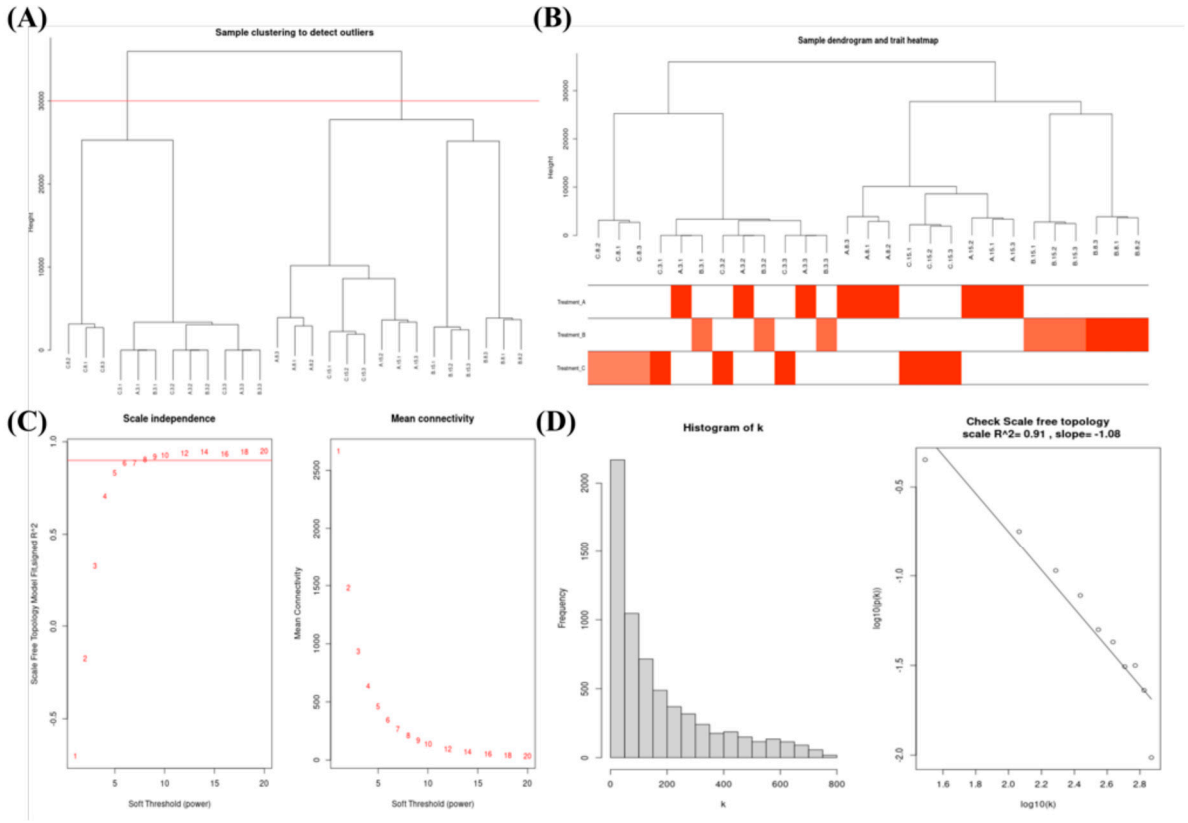

Figure S2. Investigation of DEGs before co-expression network construction. (A) A dendrogram of all samples; (B) measurement of temperature conditions of each sample; threshold determination of co-expression network of soft threshold (β value) (C); and free topology scale (D).

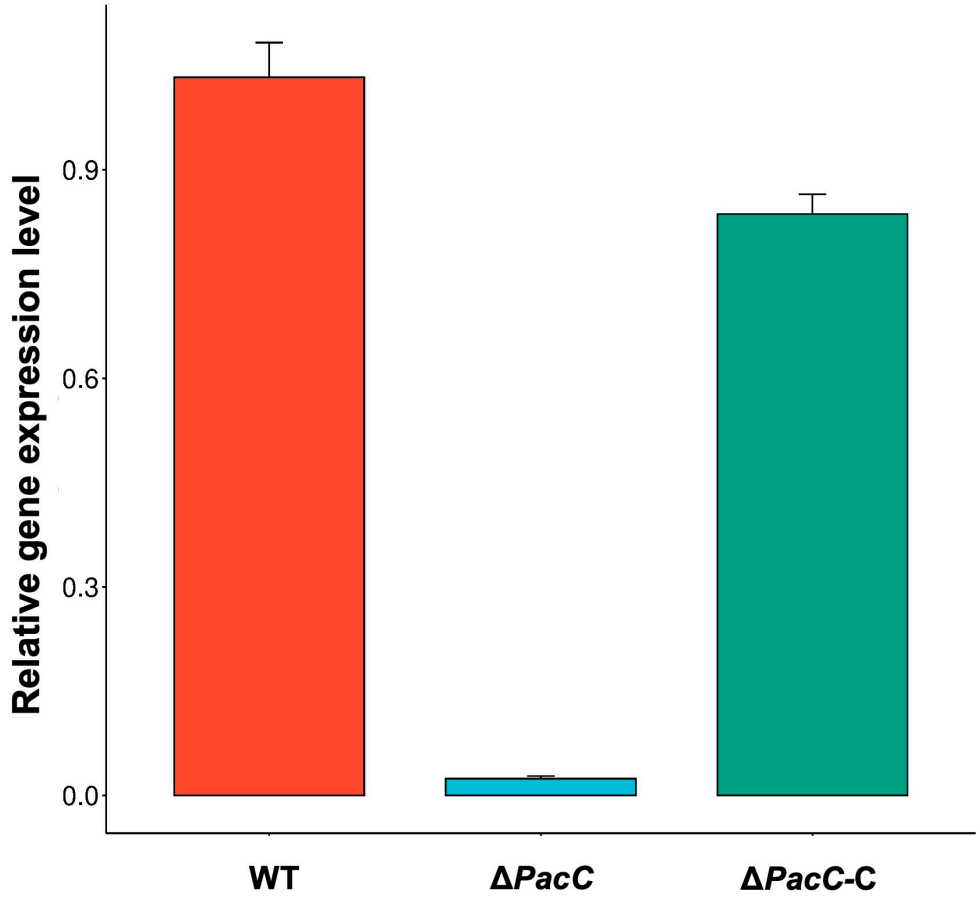

Figure S3. Quantitative real-time PCR verification of expression of PacC gene in wild-type strain (BDLA16-7), *PacC* mutant strain (Δ*PacC*) and complemented the strain (Δ*PacC*-C).