

Supplementary Information

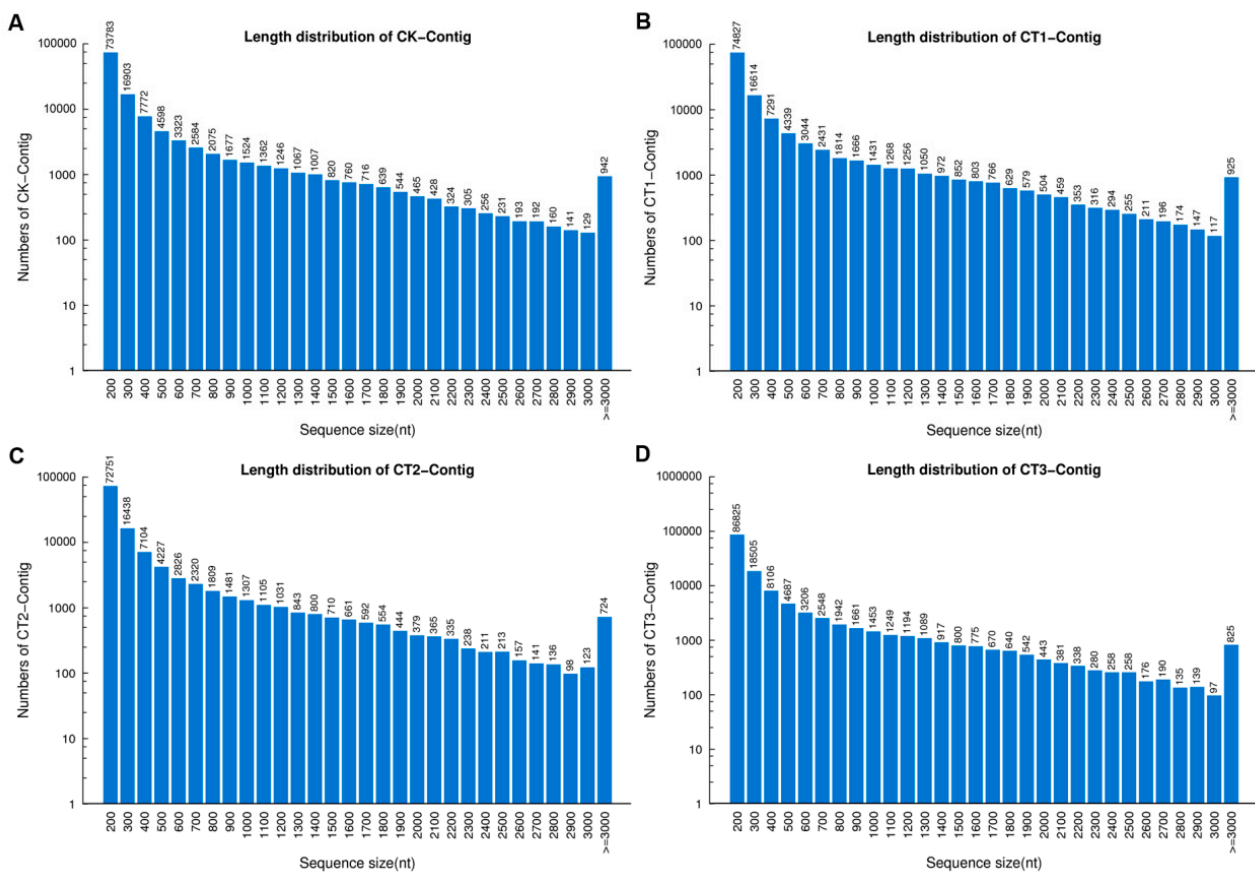


Figure S1. Length distribution of the contigs. The length distribution of contigs of CK sample (A); CT1 sample (B); CT2 sample (C); and CT3 sample (D).

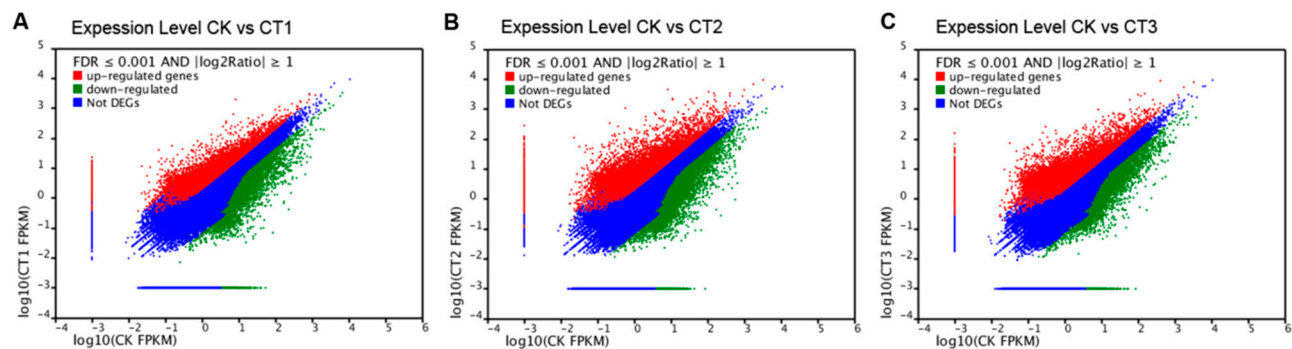


Figure S2. Distribution of differentially expressed genes (DEGs) in cold-treated (CT) samples compared with control sample (CK). We use “FDR (False Discovery Rate) ≤ 0.001 and the absolute value of $\log_2\text{Ratio} \geq 1$ ” as the threshold to judge the significance of gene expression difference. Control plants were grown at 20 °C. CT1 (A); CT2 (B); CT3 (C), plants were treated under low temperature for 4, 0 and -10 °C, respectively.

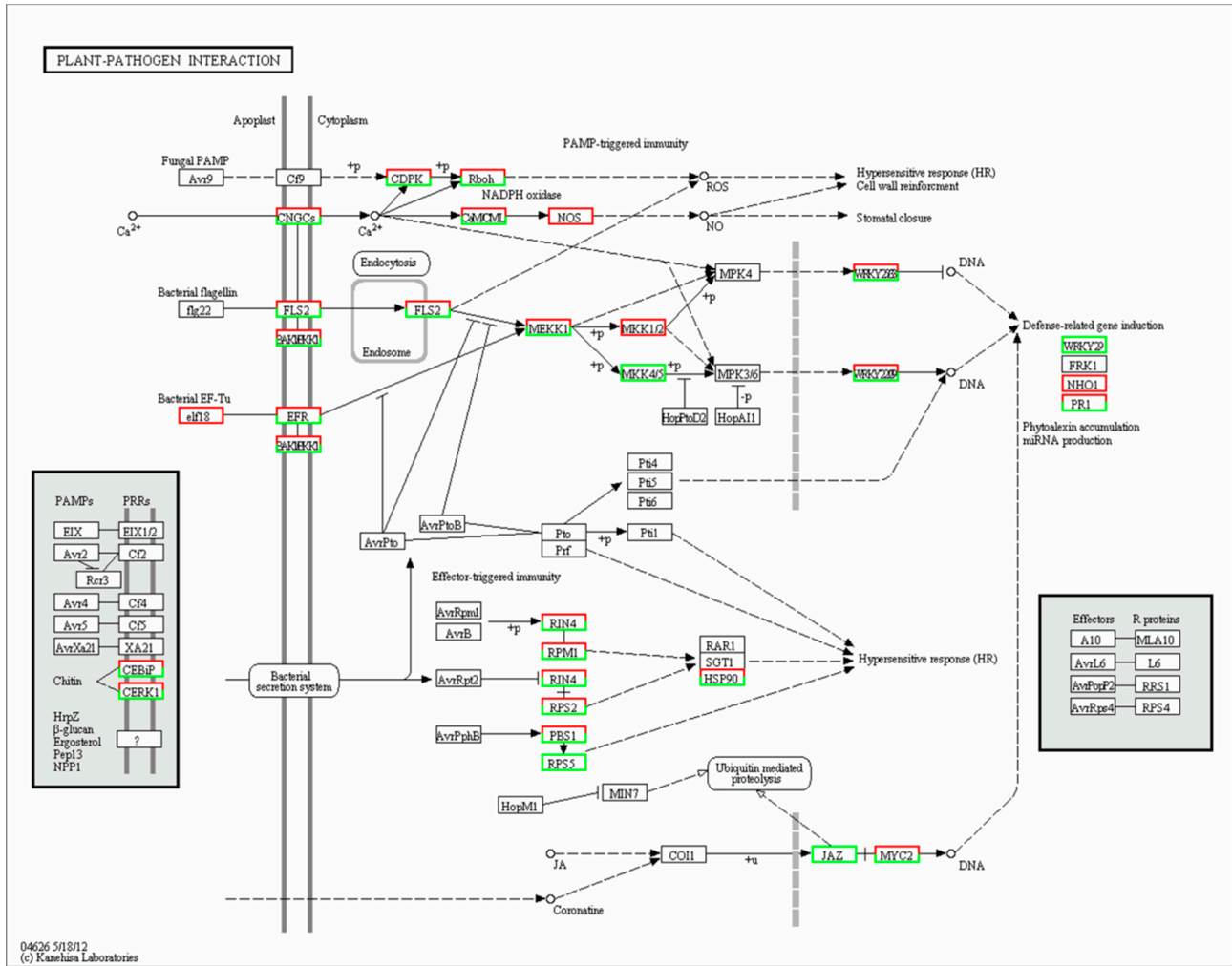


Figure S3. Detailed information of plant-pathogen interaction pathway in KEGG database. In the figure, up-regulated genes are marked with red borders while down-regulated genes are marked with green borders. Non-change genes are marked with black borders.

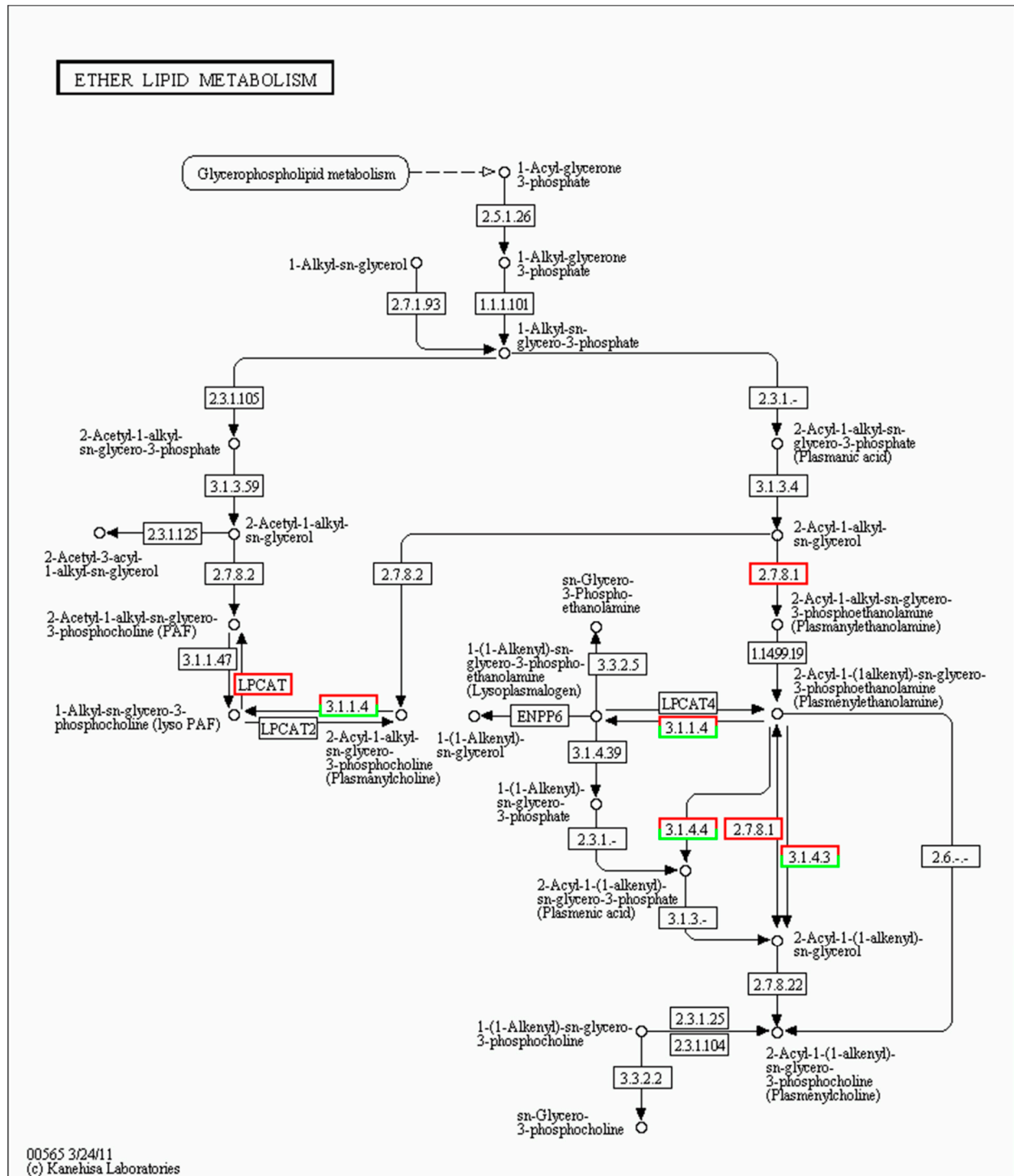


Figure S4. Detailed information of ether lipid metabolism pathway in KEGG database. In the figure, up-regulated genes are marked with red borders while down-regulated genes are marked with green borders. Non-change genes are marked with black borders.

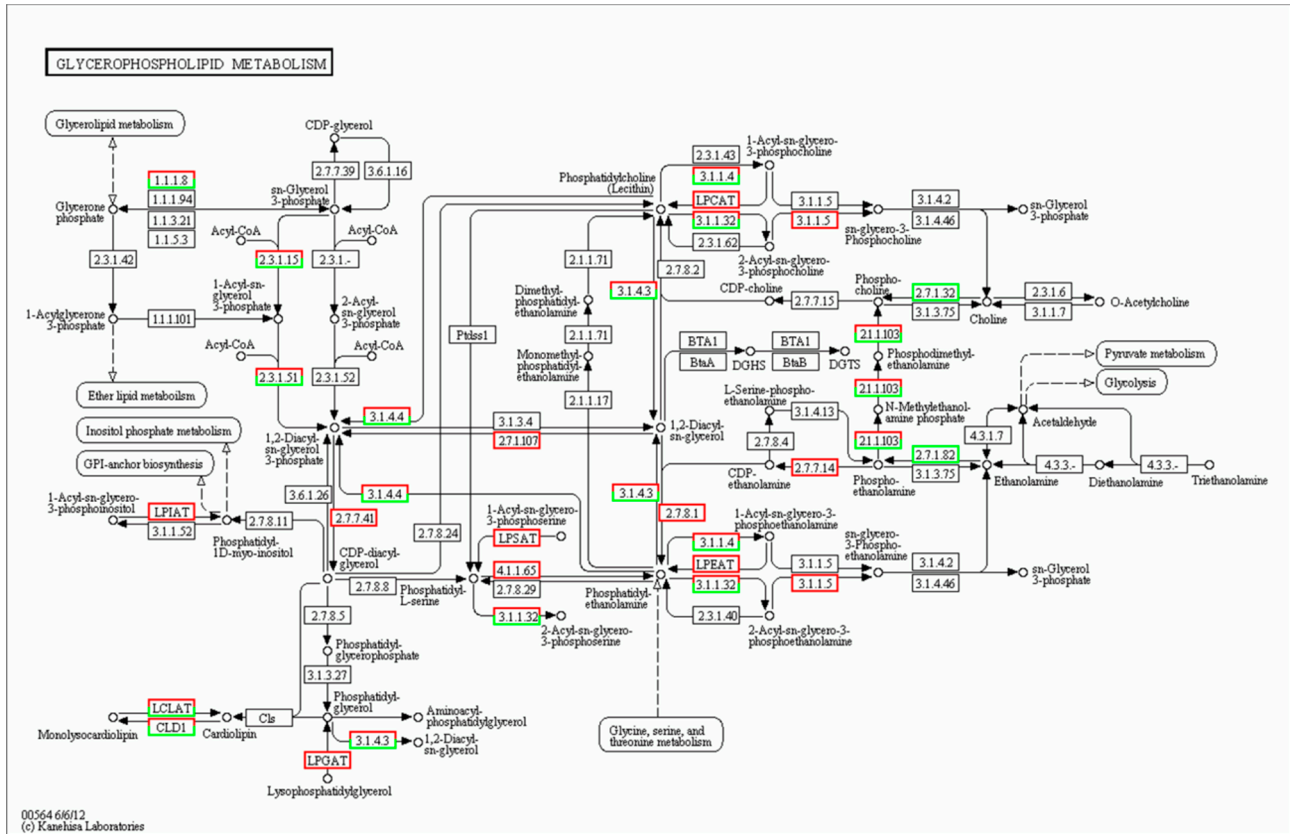


Figure S5. Detailed information of glycerophospholipid metabolism pathway in KEGG database. In the figure, up-regulated genes are marked with red borders while down-regulated genes are marked with green borders. Non-change genes are marked with black borders.