

Figure S3. Correlation analysis between qRT-PCR and RNA-seq. The analysis between qRT-PCR and RNA-seq Results for random subset of 16 genes (a-p).

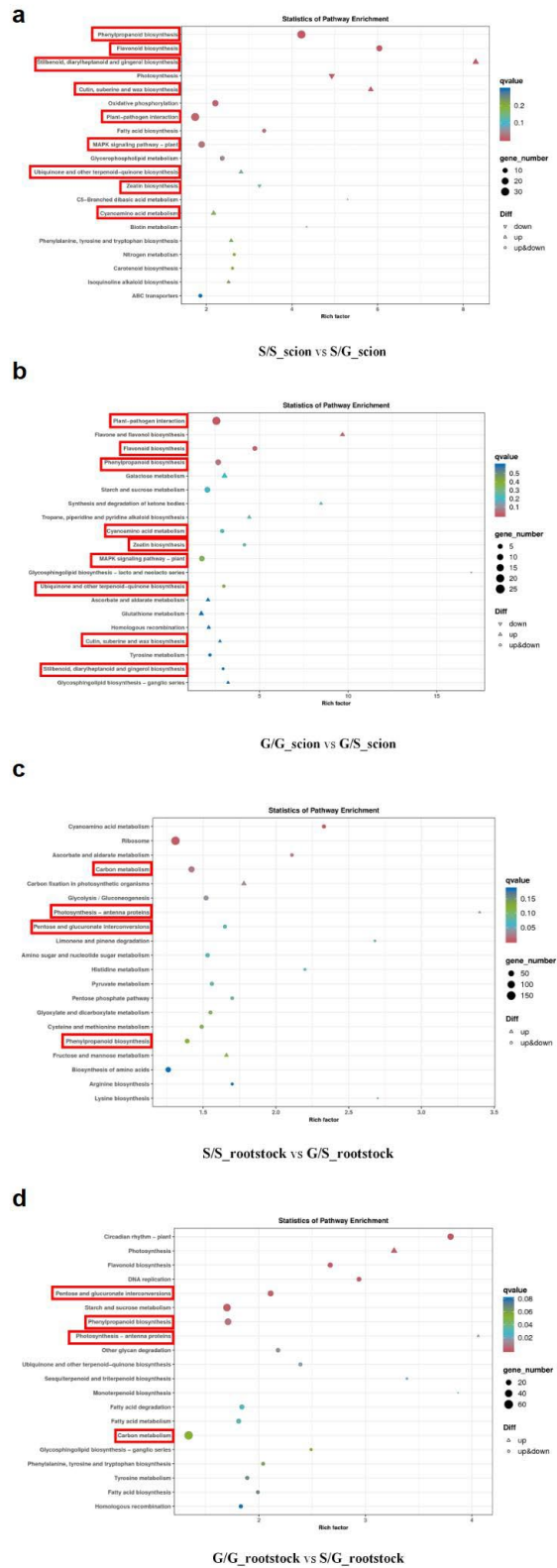


Figure S4. Enrichment analysis on KEGG pathways. (a–d) The top 20 pathway with highest level were exhibited according to the amount and enrichment level of DEGs annotated in the comparing groups.

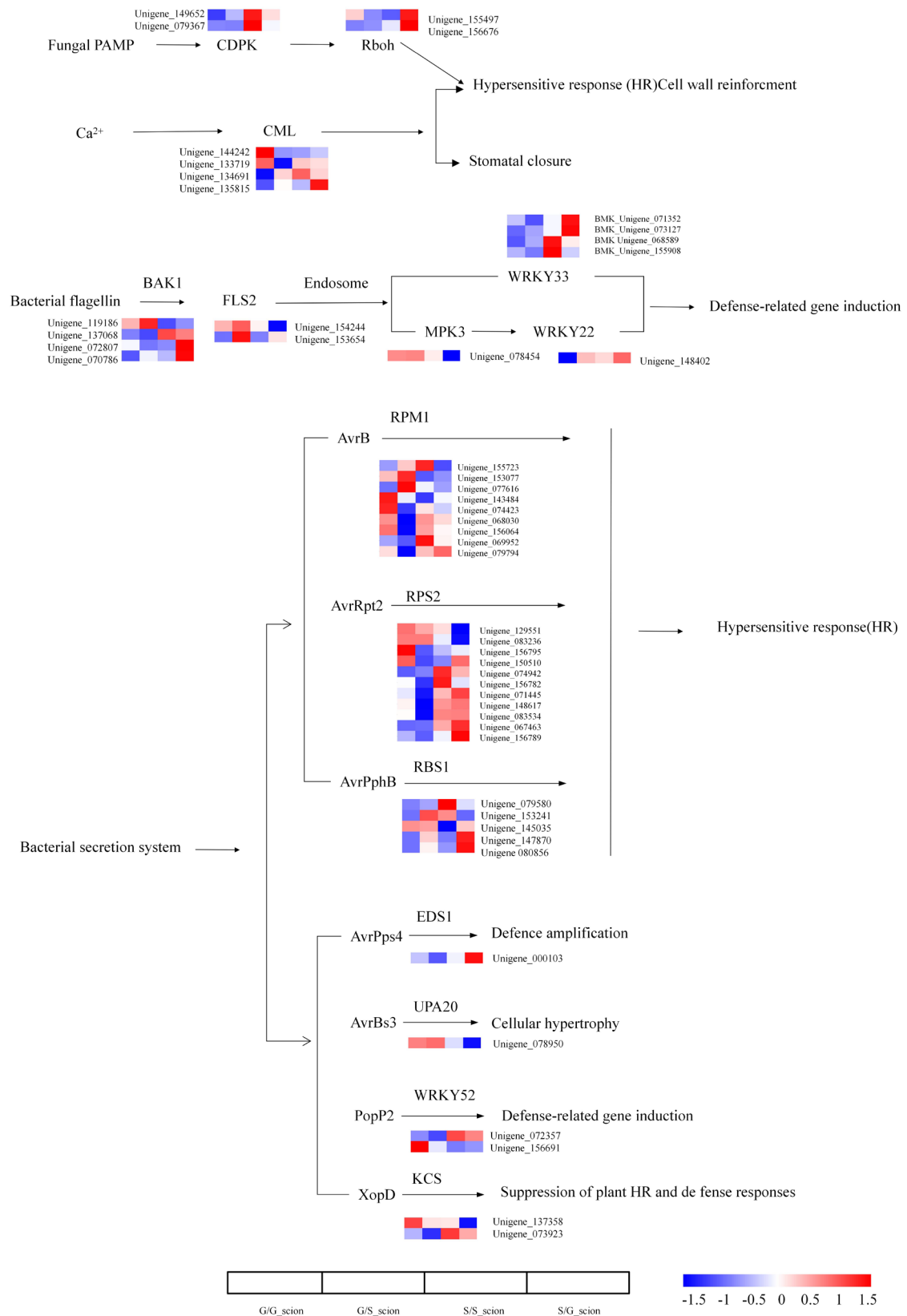


Figure S7. Analysis of differentially expressed genes in the pathways of plant-pathogen interaction. The color scale represents log₂-transformed FPKM (fragments per kilobase of exon per million mapped reads) values. Red represents high expression, and blue represents low expression.

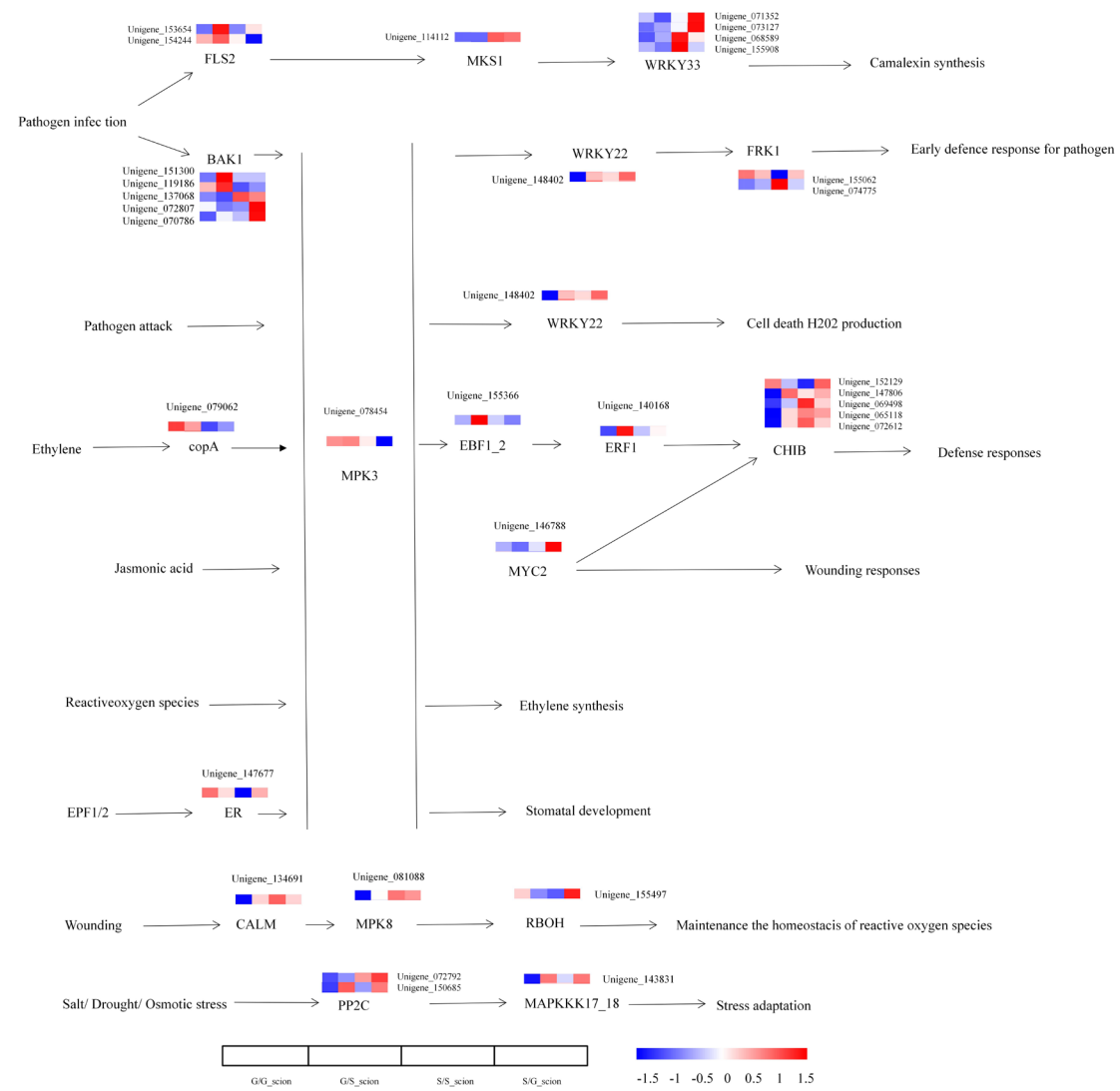


Figure S8. Analysis of differentially expressed genes in the pathways of MAPK signaling. The color scale represents \log^2 -transformed FPKM (fragments per kilobase of exon per million mapped reads) values. Red represents high expression, and blue represents low expression.

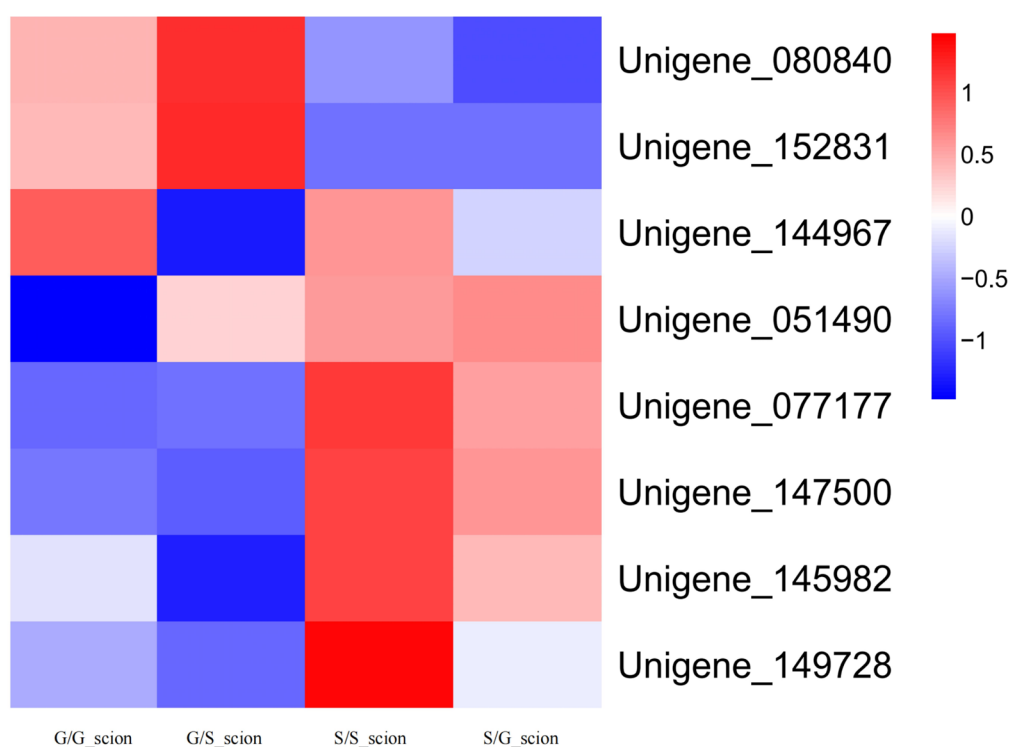


Figure S9. Analysis of differentially expressed genes in the pathways of Zeatin biosynthesis. The color scale represents log²-transformed FPKM (fragments per kilobase of exon per million mapped reads) values. Red represents high expression, and blue represents low expression.