



Figure S6. Schematic diagram of relationships between differentially expressed genes (DEGs) enriched in plant-pathogen interaction pathways as identified by KEGG analysis. All genes encoding genes/transcription factors revealed by RNA-sequencing data are highlighted by a gray box and those genes that were also validated by qRT-PCR are highlighted by a green box. Those that showed no change by either RNA-sequencing or qRT-PCR assay are enclosed by white boxes.