

Figure S1. Identification of *MdWRKY87*-OE lines.

Quantitative RT-PCR analysis of *MdWRKY87* expression levels in WT and transgenic lines. The mean values ± SEM are shown for three biological replicates.



Figure S2. The number of differentially expressed genes (DEGs) in **WT and transgenic lines.**



Figure S3. Gene ontology (GO) enrichment analysis for DEGs based on biological process, cellular component and molecular function.



Figure S4. The expression levels of overlapping transcription factor genes and transcriptional regulator genes involved in the top 4 GO terms.