

and green shading indicates 50% to 75% identity. Alignment was conducted by the DNAMAN5. *CaWRKY40b* has 59.46% sequence identity with *CaWRKY40*.

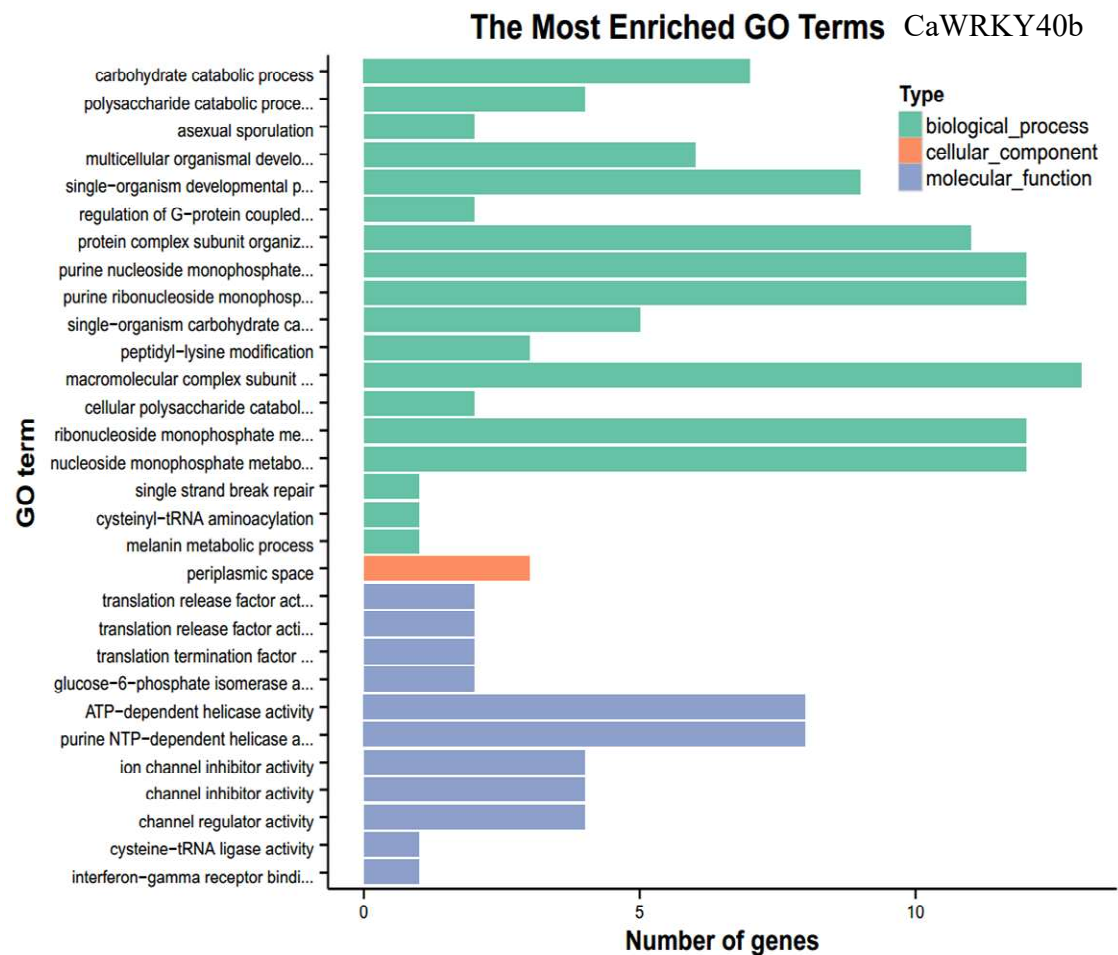


Figure S2. The gene ontology analysis of the direct transcriptional target genes of *CaWRKY40b* from ChIP-seq.

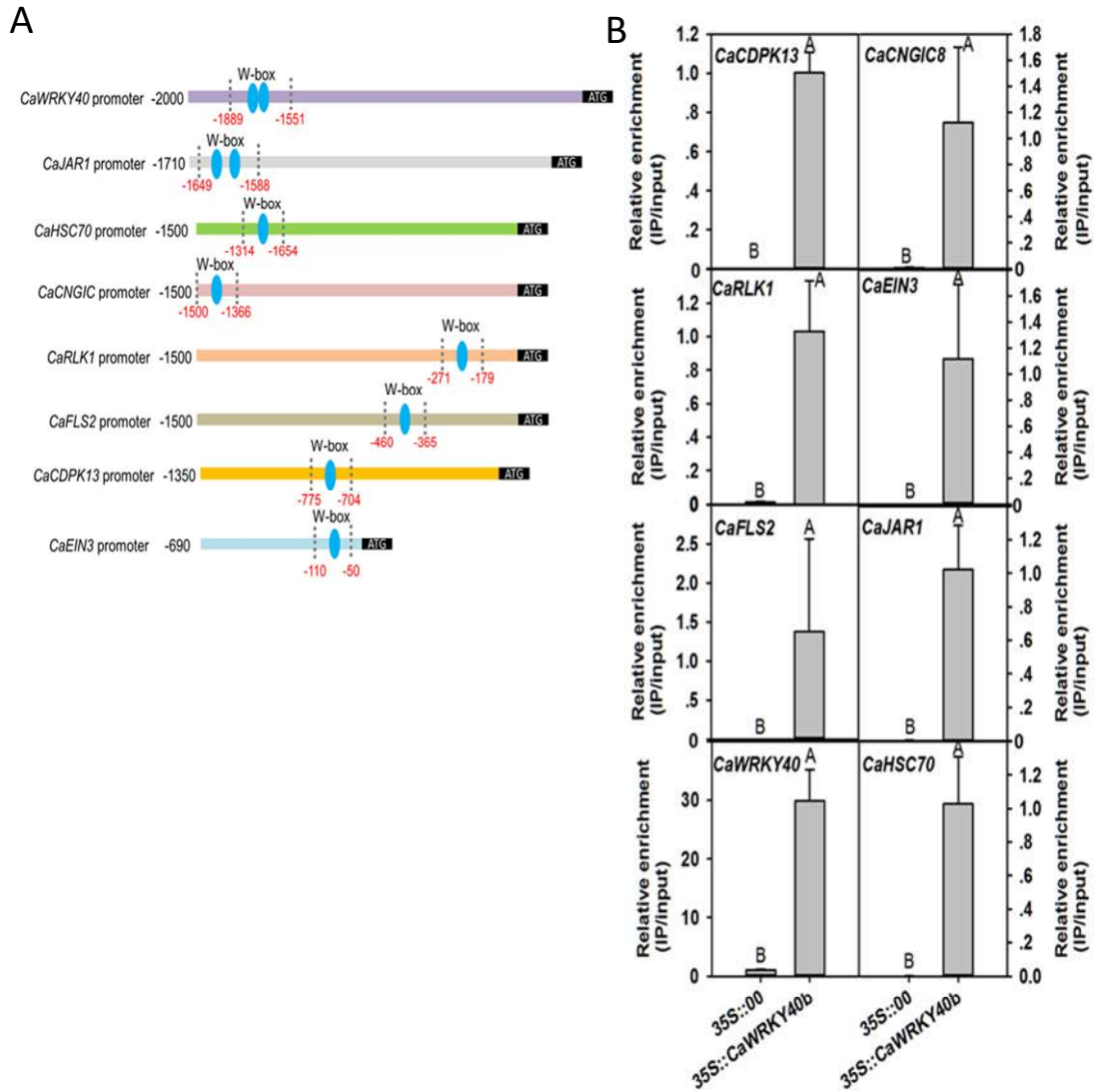


Figure S3. Confirmation of the specific binding between *CaWRKY40b* and the promoters of its possible target genes identified by ChIP-seq and RT-PCR. (A) *CaWRKY40b* binds to the promoters of *CaWRKY40* and *CaJAR1* harboring two W boxes each at their binding sites, *CaWRKY40b* also binds to the promoters of *CaHSC70*, *CaCNGIC8*, *CaRLK1*, *CaFLS2*, *CaCDPK13*, and *CaEIN3* that possess one W box each at their binding sites. (B) GV3101 cells containing 35S::CaWRKY40b-HA infiltrated into pepper leaves, with GV3101 cells containing 35S::00 as mock treatment. The *CaWRKY40b*-HA overexpressed and mock leaves were harvested at 48 hpi for chromatin preparation. Chromatin was isolated from infiltrated pepper leaves crosslinked with 1% formaldehyde, sheared, and immune-precipitated with an anti-HA antibody. Relative enrichment levels of samples of *CaWRKY40b* were set to 1, normalized by input. Data represent the means \pm SD of three independent biological replicates. Capital and lowercase letters above the bars indicate significantly different means ($p < 0.01$) and significantly different means ($p < 0.05$), respectively, as analyzed by Fisher's protected LSD test.