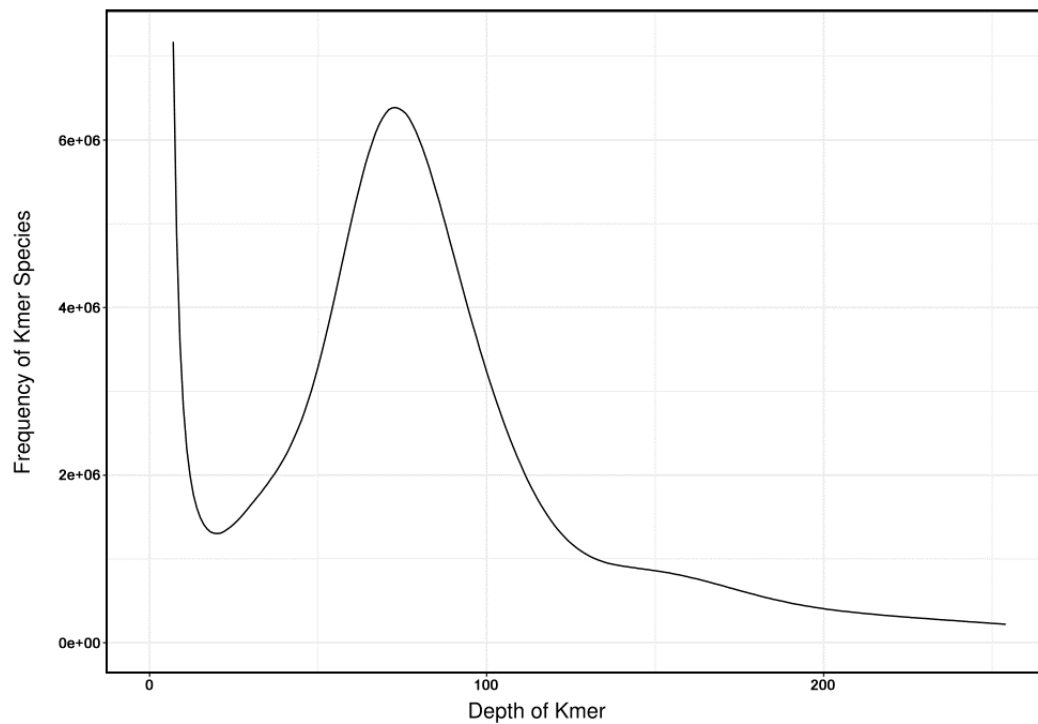
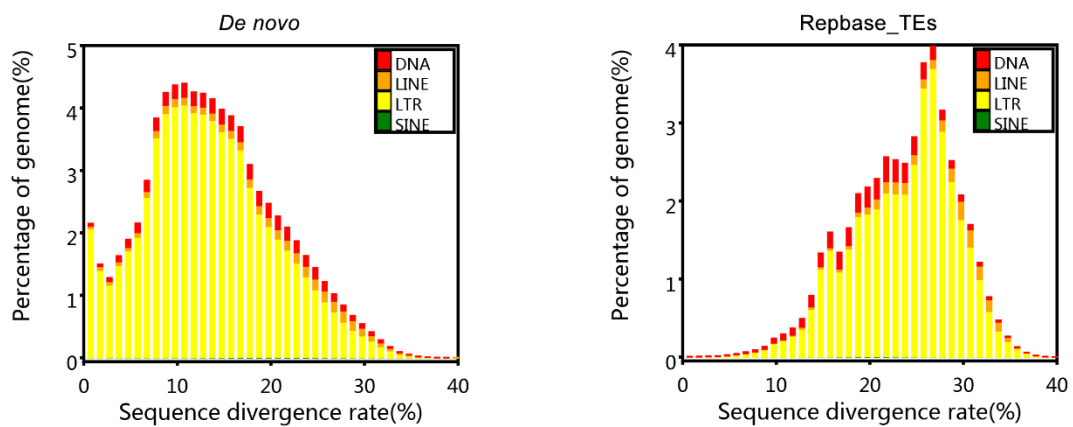


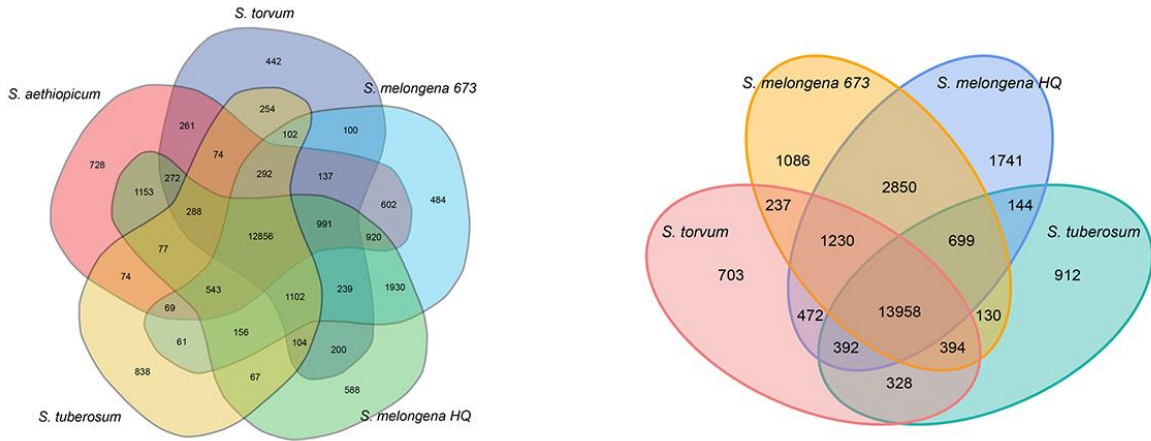
Supplementary Figures



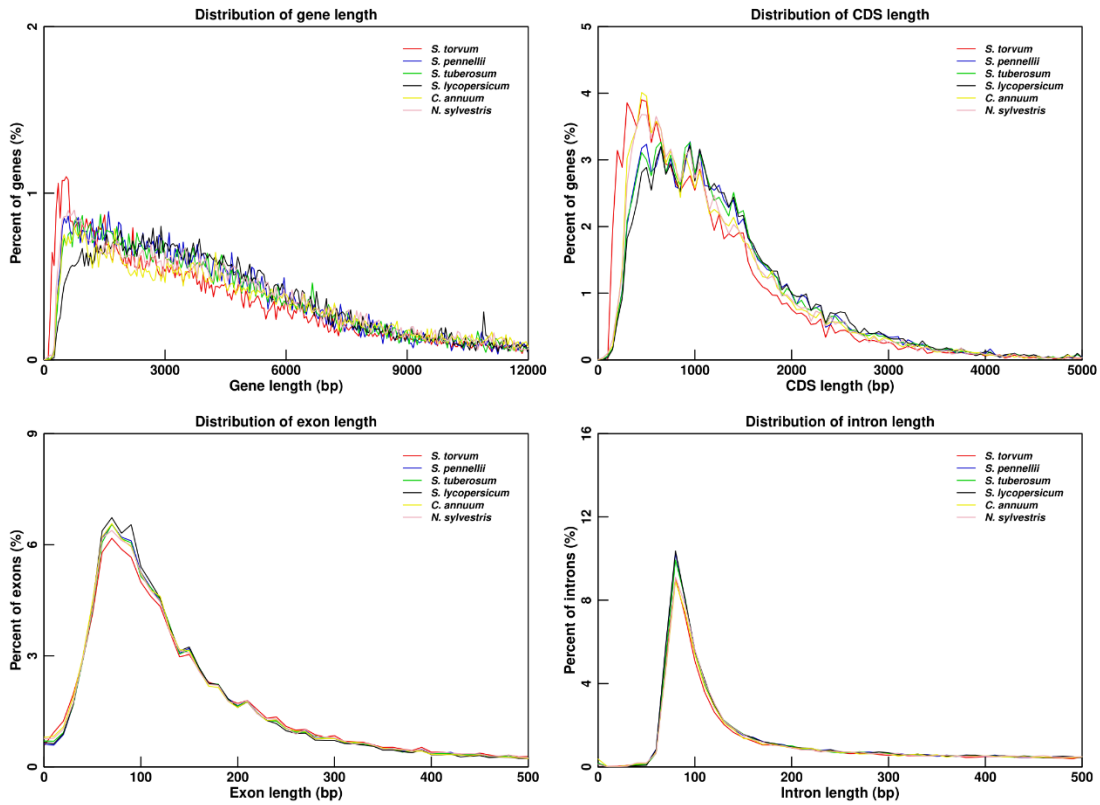
Supplementary Figure 1 K-mer analysis for estimating the genome feature of *Solanum torvum*.



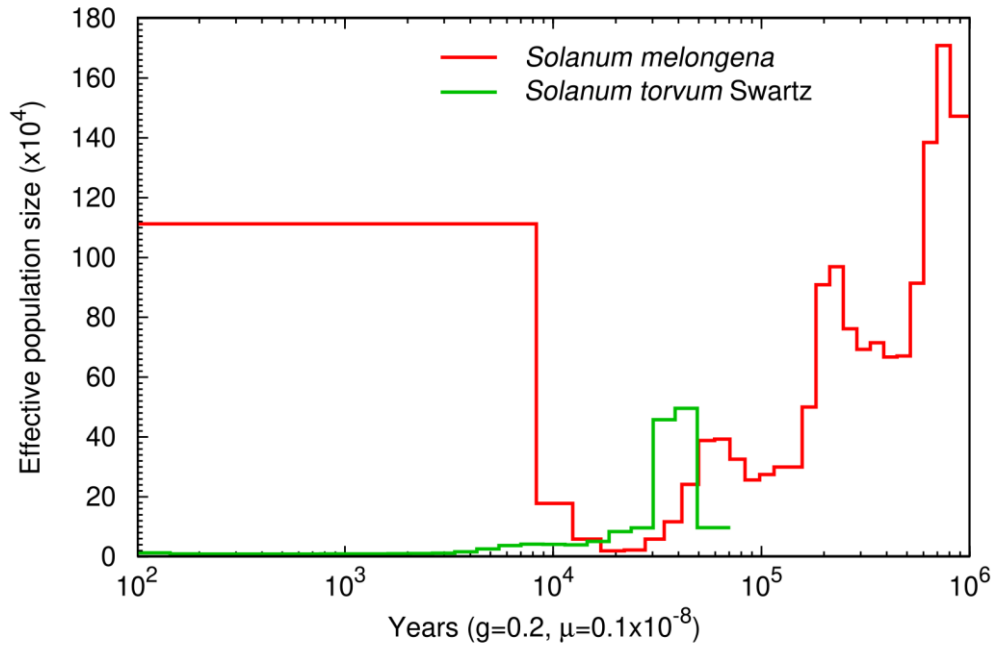
Supplementary Figure 2 Repetitive sequences predicted by *De novo* and based on RepBase in *Solanum torvum*.



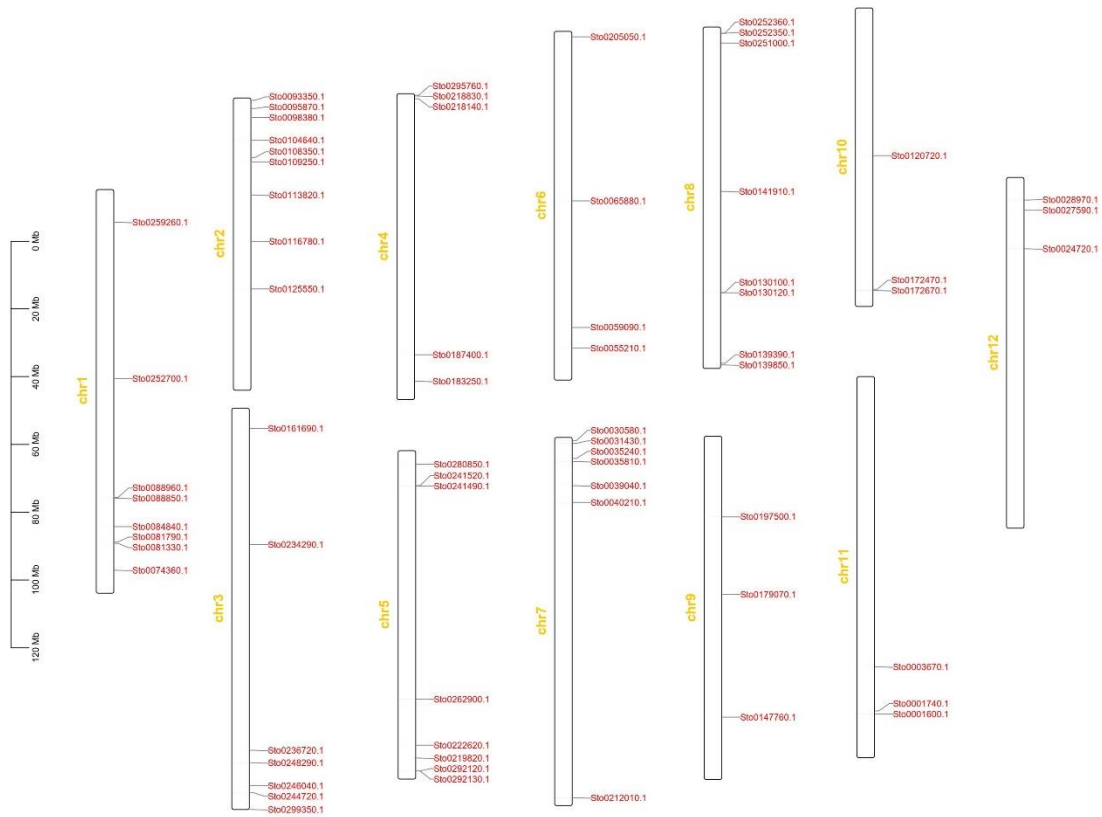
Supplementary Figure 3 Number of shared and unique gene orthologs in *Solanum* species.



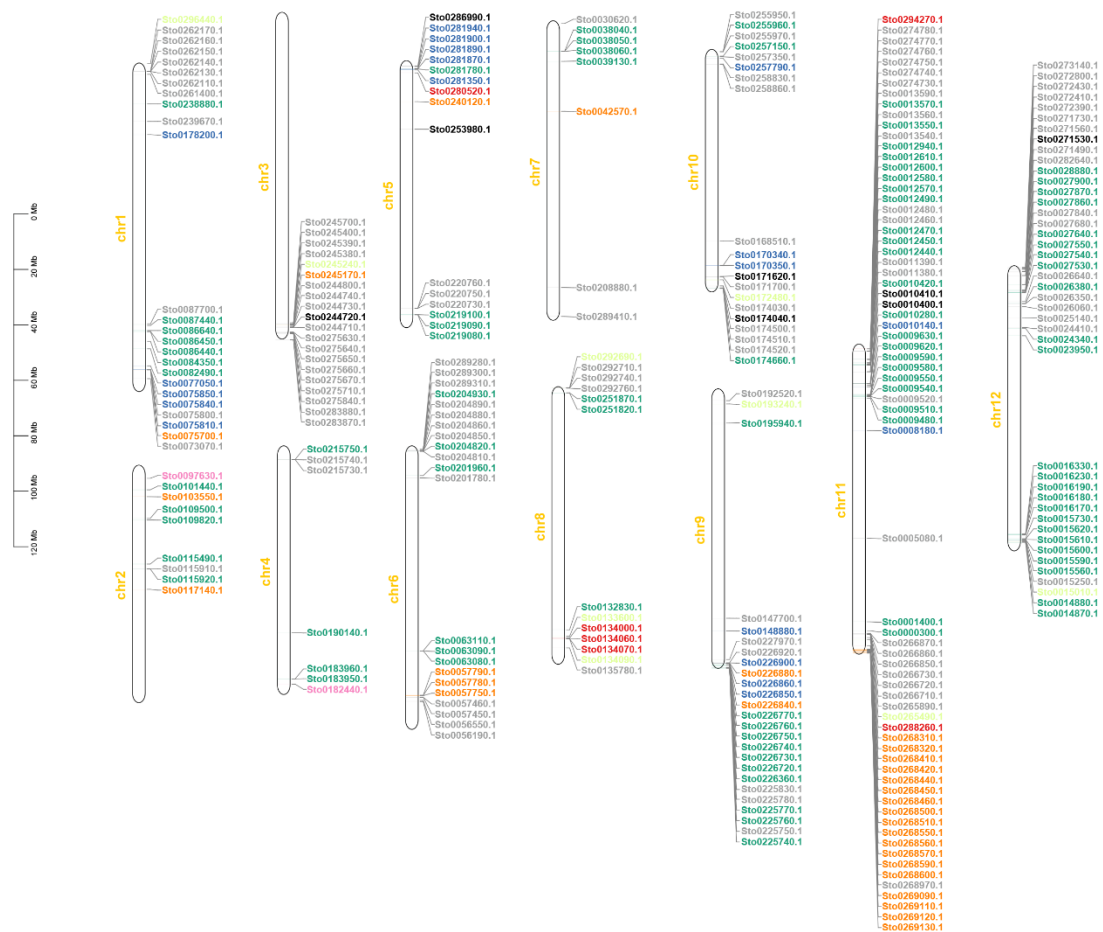
Supplementary Figure 4 Quality of gene annotation shown with gene length, CDS length, exon length and intron length in *Solanum torvum* genome, respectively.



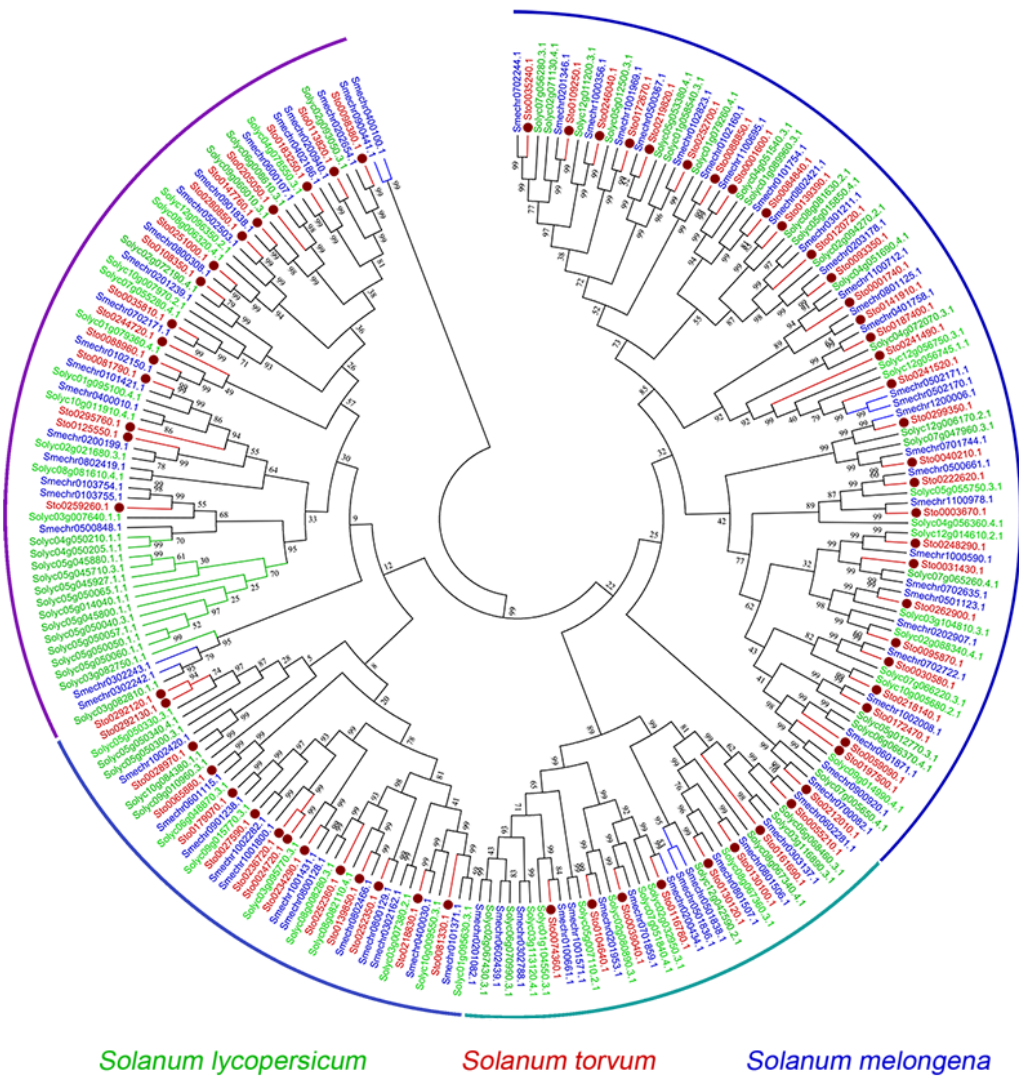
Supplementary Figure 5 Demographic N_e history of *Solanum melongena* and *Solanum torvum* inferred by PSMC analysis.



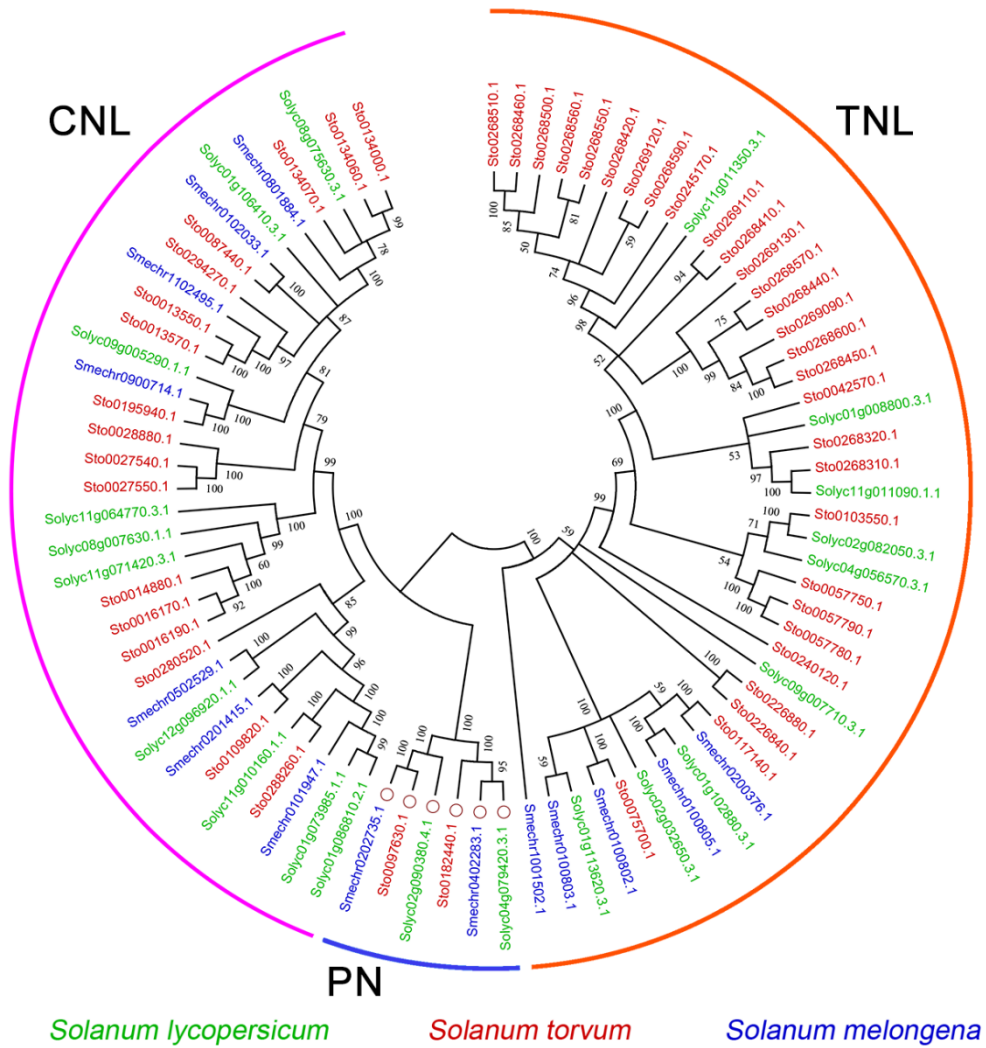
Supplementary Figure 6 The WRKY genes on *Solanum torvum* chromosomes.



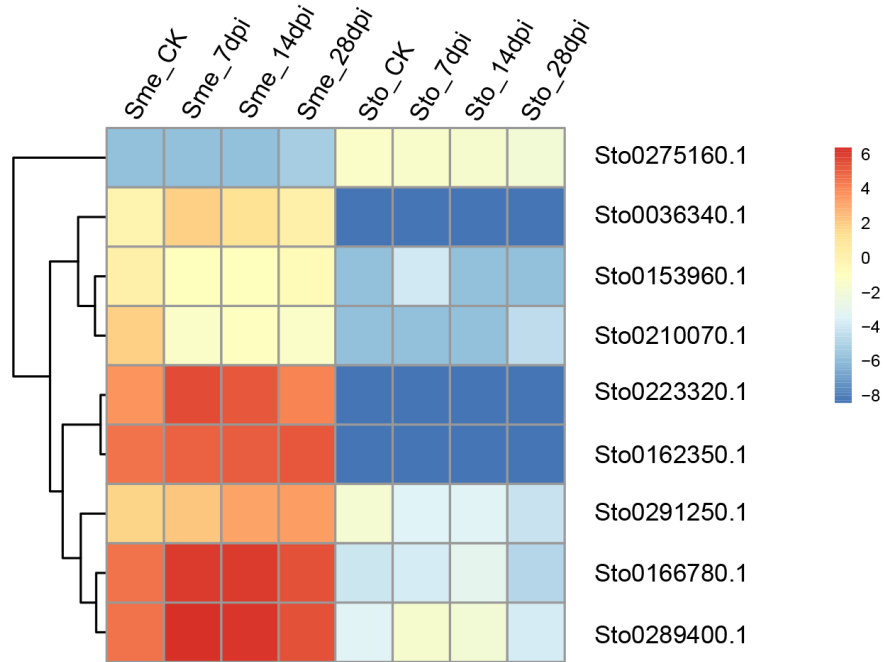
Supplementary Figure 7 The NBS-LRR genes on *Solanum torvum* chromosomes.



Supplementary Figure 8 Phylogenetic tree of the WRKYs in three species of *Solanaceae*.



Supplementary Figure 9 Phylogenetic tree of the *NBS-LRR* genes in three species of *Solanaceae*.



Supplementary Figure 10 The expression patterns of chlorogenic acid (CGA) related genes in *S. torvum* and *S. melongena* after RKN infection.