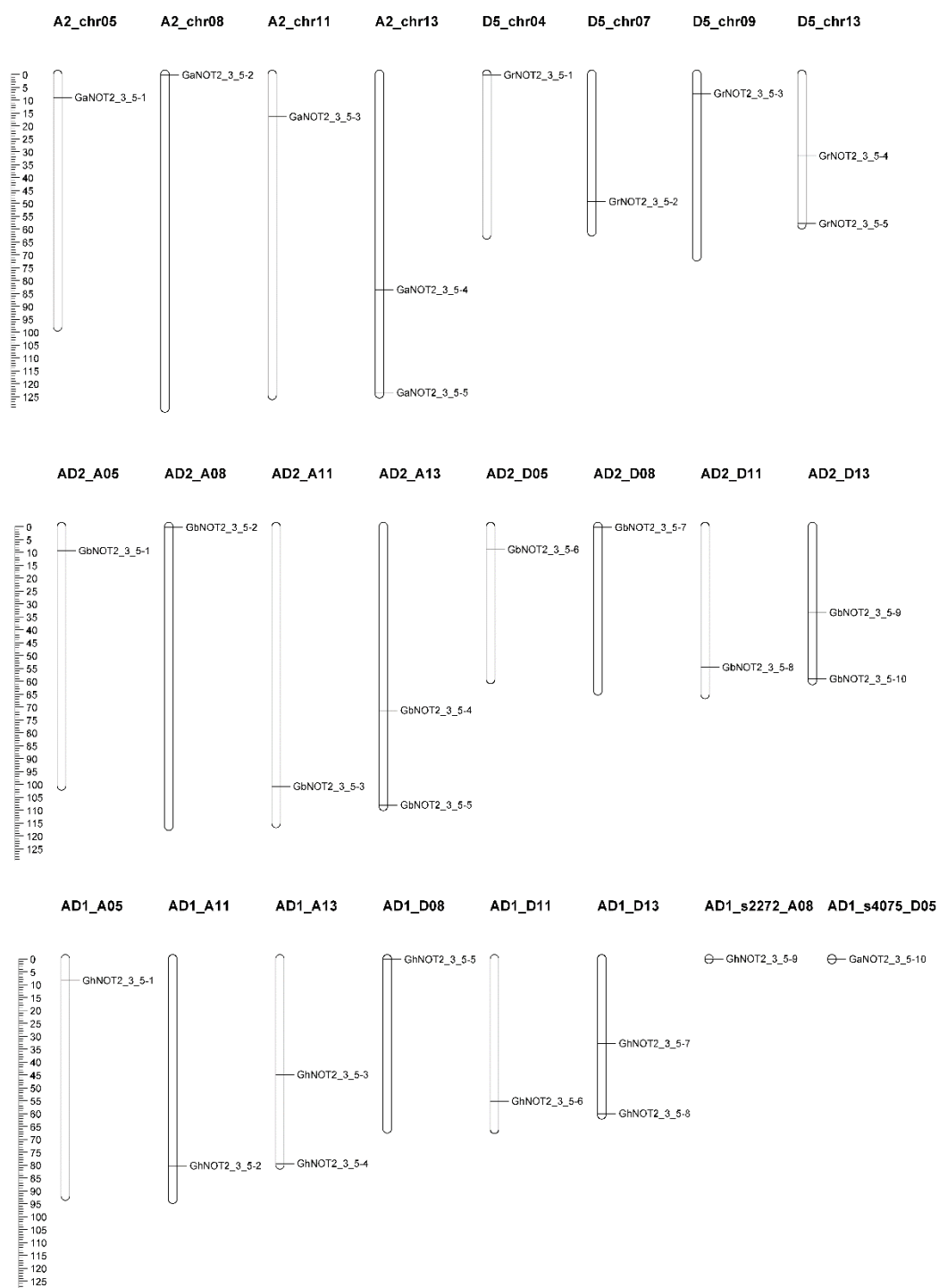
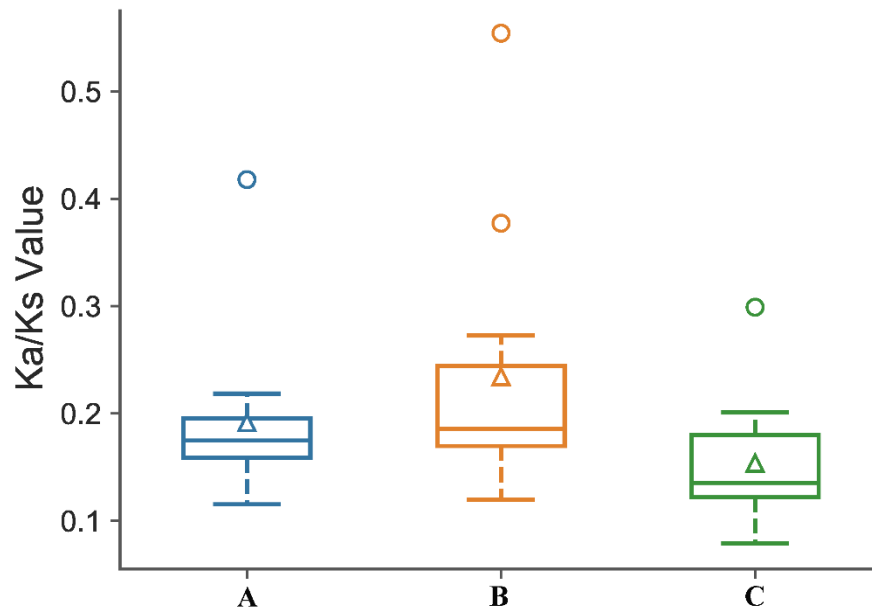


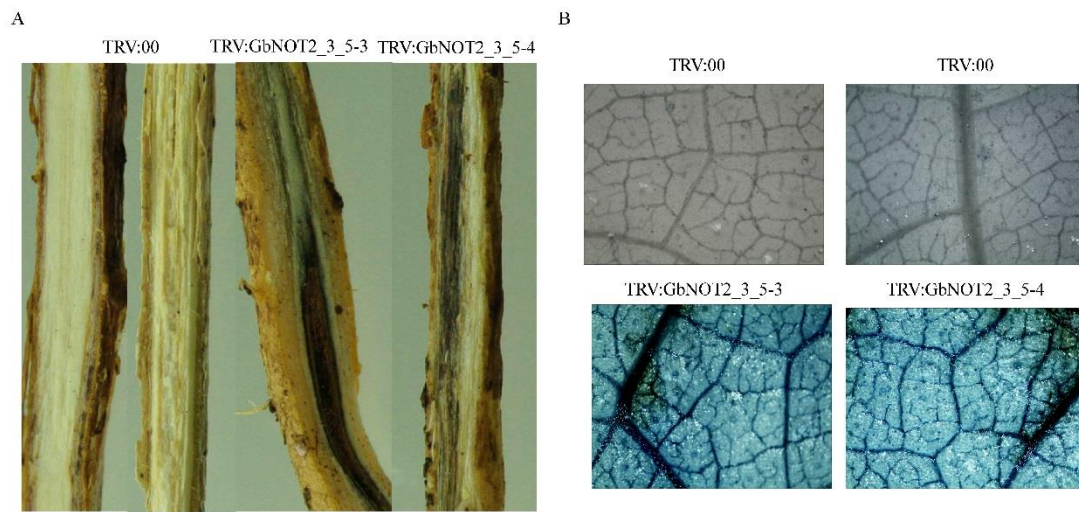
**Figure S1:** Conserved domain-sequence and amino residues analysis of NOT2\_3\_5 domain proteins. A: Conserved domain-sequence analysis. NOT2\_3\_5 domain were located in the C-terminal. B: Conserved amino residues analysis. The conservation degrees of amino acid residue from each class of NOT2\_3\_5 domains were very high.



**Figure S2:** Chromosome Location of *NOT2\_3\_5* genes from four cotton species. Abbreviated A2, D5, AD1, AD2 represented *G. arboreum*, *G. raimondii*, *G. hirsutum* and *G. barbadense*, respectively.



**Figure S3:** Distribution of Ka/Ks ratios of NOT2\_3\_5 gene pairs in tetraploid cotton. A: Ka/Ks ratios between A and D sub-genomes of *G. hirsutum*. B: Ka/Ks ratios between *G. hirsutum* and *G. barbadense*. C: Ka/Ks ratios between A and D sub-genomes of *G. barbadense*.



**Figure S4:** The stems and leaves of silencing *GbNOT2\_3\_5* genes plants showed more severe symptoms after infection of *V. dahlia*. A: The stems from silencing *GbNOT2\_3\_5* genes plants and control. B: Trypan blue array of leaves from silencing *GbNOT2\_3\_5* genes plants and control.