

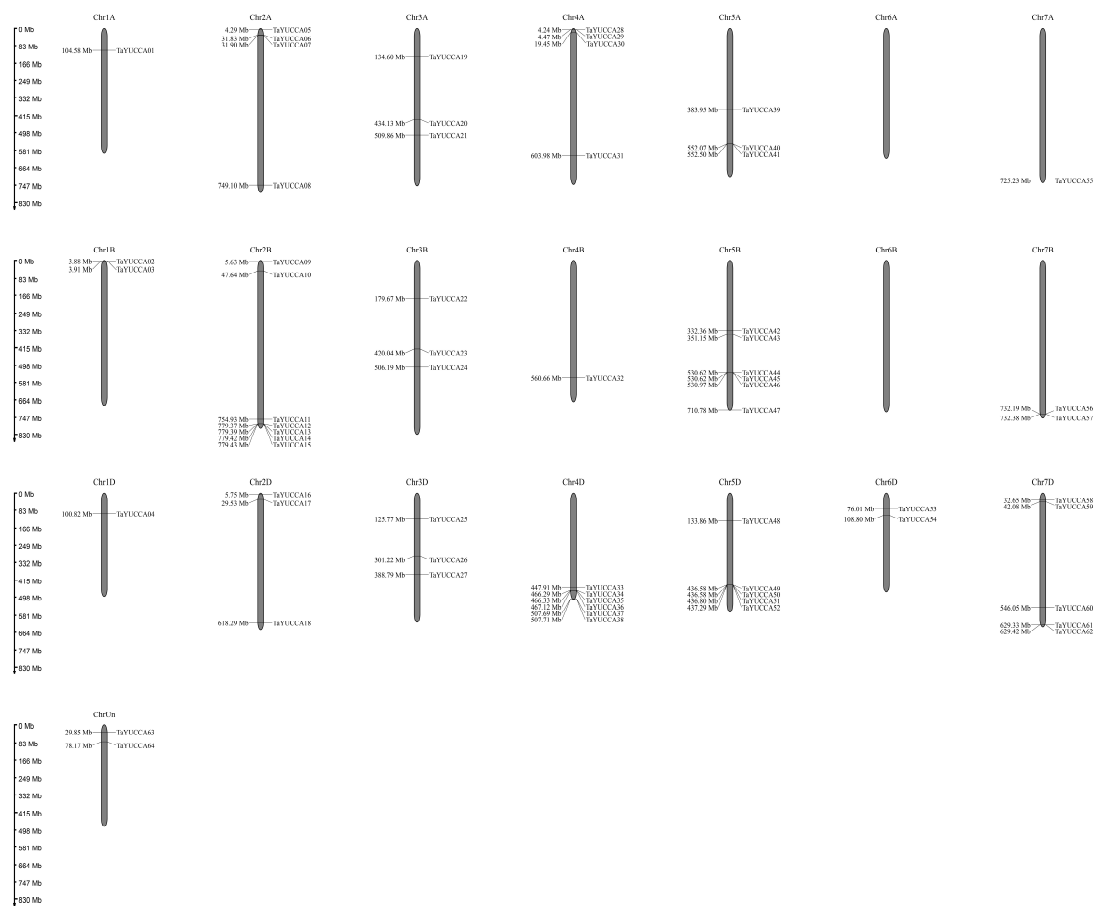


Figure S1. Chromosomal distribution of *TaYUCCAs* in wheat.

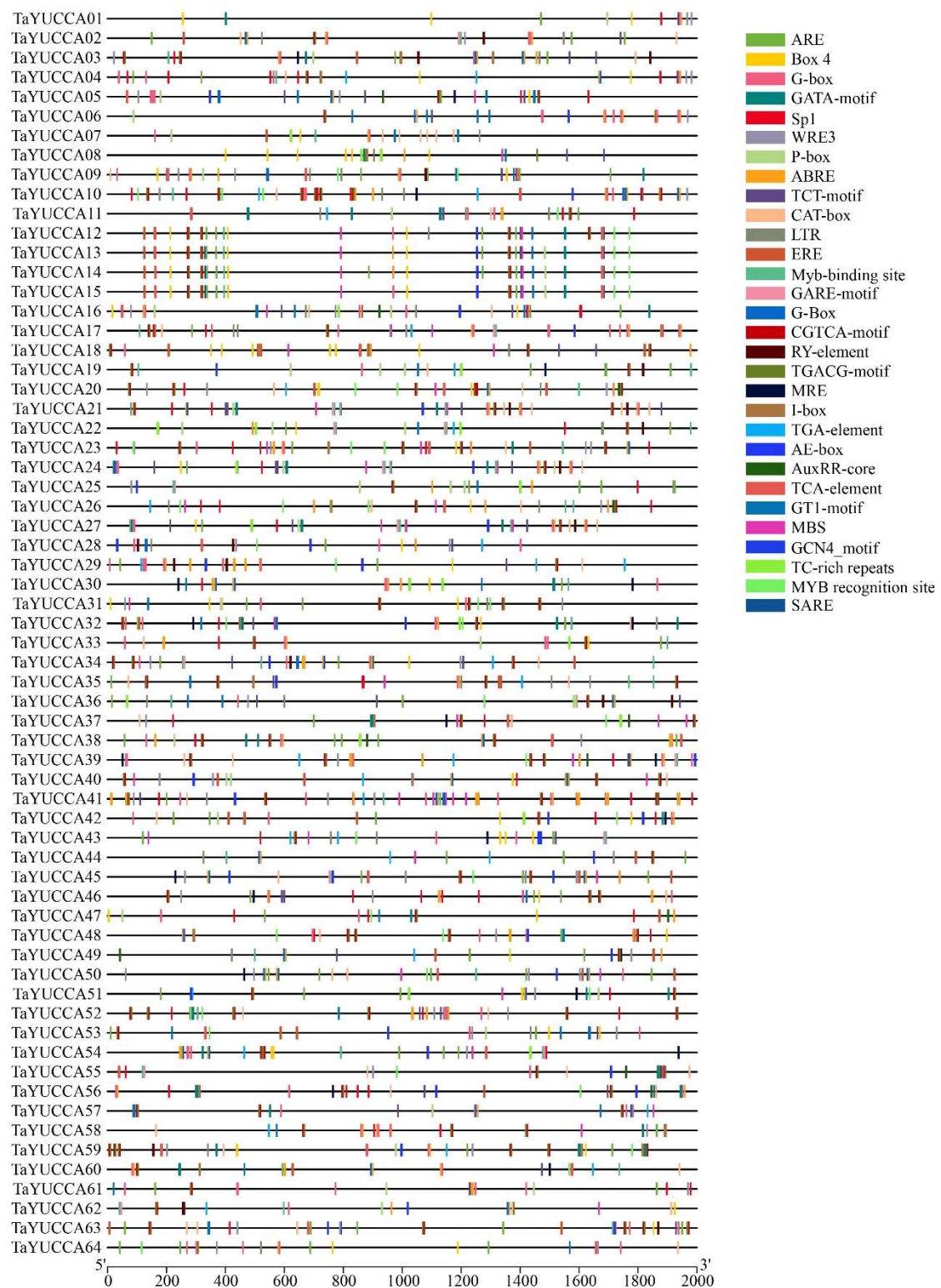


Figure S2. Distribution of *cis*-acting elements in the promoter regions of *TaYUCCAs*.

The figure illustrates the distribution of *cis*-acting elements within the 2000 bp upstream promoter regions of *TaYUCCAs*. Different colored boxes represent distinct types of *cis*-acting elements.

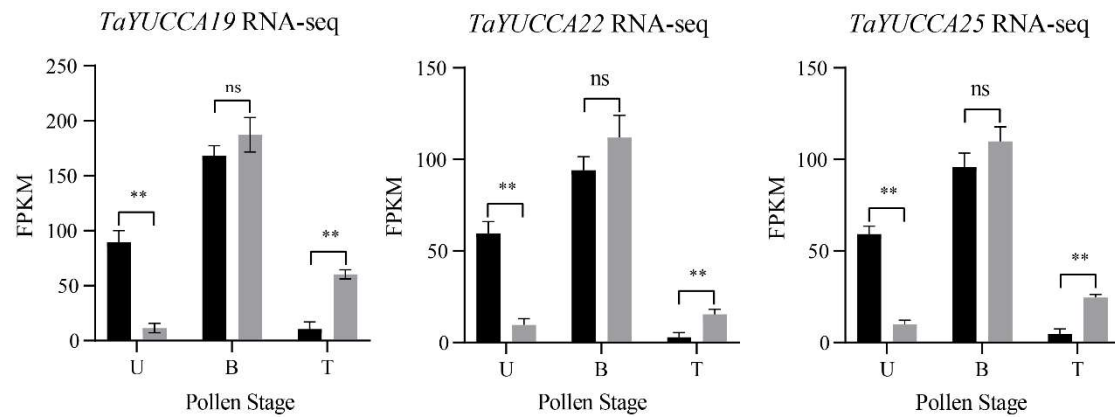


Figure S3. Differential expression analysis of *TaYUCCA19*, *TaYUCCA22* and *TaYUCCA25* based on FPKM values.

The figure shows the differences in FPKM expression levels of *TaYUCCA19*, *TaYUCCA22* and *TaYUCCA25* between YSF and YSS. "***" indicates extremely significant differences determined by Student's t-test ($P \leq 0.01$).

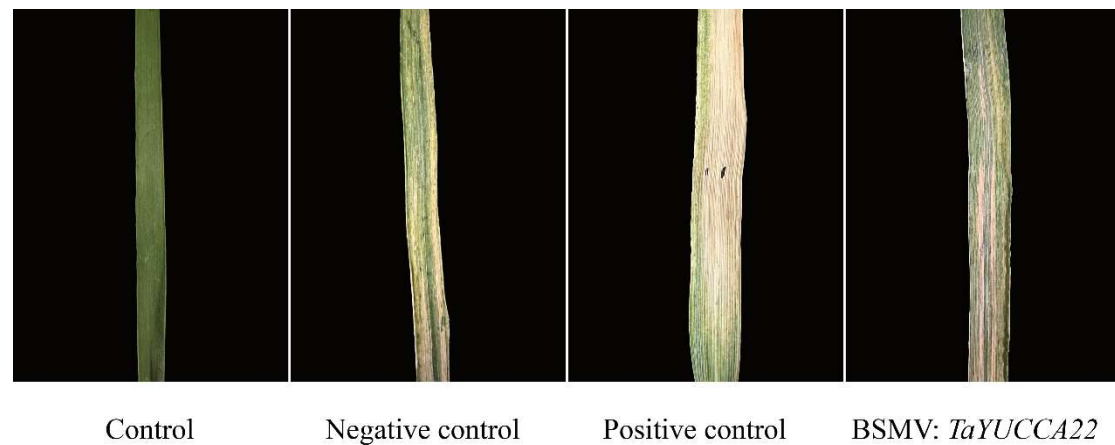


Figure S4. Phenotypes of leaves under different treatment combinations after BSMV-VIGS.

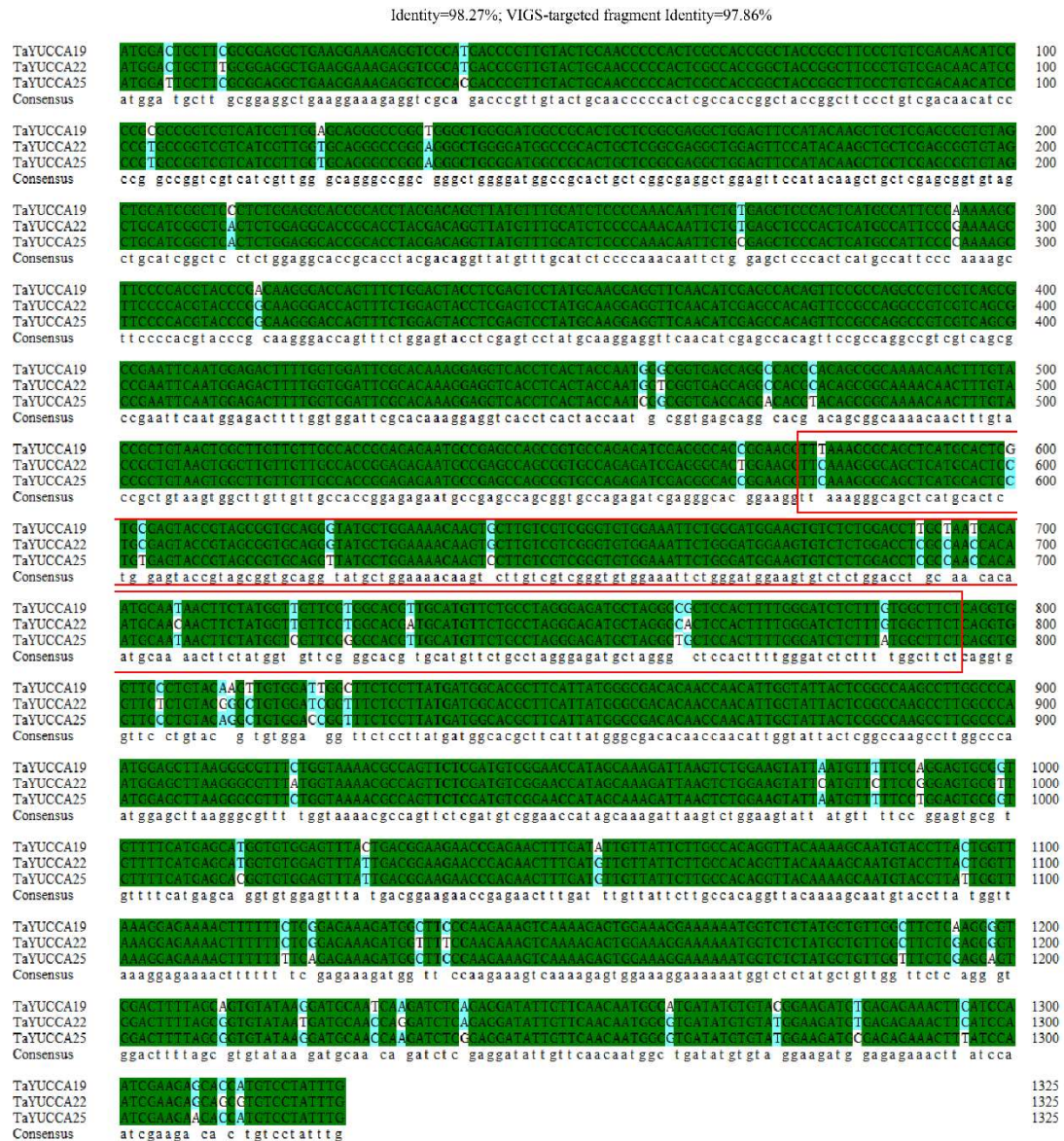


Figure S5. Multiple sequence alignment of *TaYUCCA19*, *TaYUCCA22*, and *TaYUCCA25*. The overall sequence identity among the three genes is 98.27%, and the VIGS-targeted fragment shows an identity of 97.86%. The VIGS-targeted fragment is highlighted with a red box.