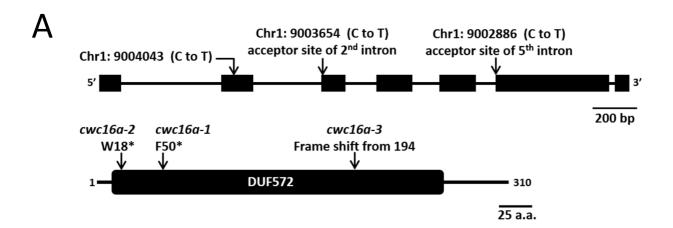
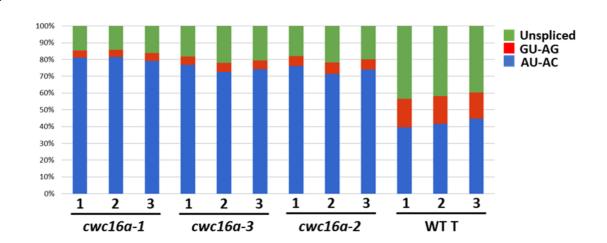
CWC16a - At1g25682

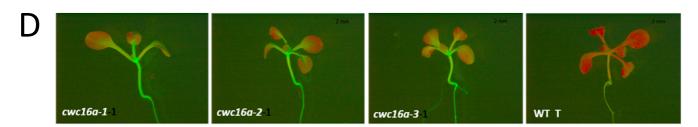


B









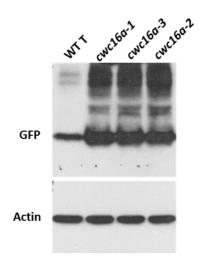


Figure S8: CWC16

- A. Top: Intron-exon structure of the *CWC16a* gene (At1g25682) and position of the nucleotide changes in the *cwc16a-1* mutant (Kanno et al., 2017a) and in two new mutants, *cwc16a-2* and *cwc16a-3* (identified in this study). The domain structure of the CWC16a protein (310 amino acids) and the positions of the premature termination codons (asterisks) resulting from the *cwc16a-1* and *cwc16a-2* mutations and the frame shift resulting from the *cwc16a-3* mutation are shown below.
- B. Expected positions of T-DNA insertions in five putative *cwc16b* alleles examined for this study. For two lines, SALK-009736C and SALK_132471, the T-DNA was found integrated as expected (https://www.arabidopsis.org/) using the primers shown in Table S1. However, we were unable to demonstrate that *CWC16b* transcripts were eliminated in these two lines. For three lines, however, SALK_152264, SALK_527_G04 and SALK_053475, the T-DNA could not be detected at the expected insertion siteusing the primers shown in Table S1.
- C. Quantification of the three *GFP* splice variants in triplicate RNA-seq data from the *cwc16a* mutants. The percentage of the translatable AU-AC transcript increases from ~40% in the WT T line to 70-80% in the three *cwc16a* mutants. This increase, which occurs at the expense of the GU-AG and unspliced transcripts, presumably accounts in large part for the hyper-GFP phenotype of *cwc16a* mutants.
- D. Top: GFP fluorescence in seedlings with the indicated genotypes. The *cwc16a* mutants all have a hyper-GFP phenotype relative to the WT T line. Bottom: GFP Western blot confirming elevated levels of GFP protein relative to the WT T line in the three *cwc16a* mutants.

Kanno, T., W. D. Lin, J. L. Fu, A. J. M. Matzke, and M. Matzke, 2017a A genetic screen implicates a CWC16/Yju2/CCDC130 protein and SMU1 in alternative splicing in *Arabidopsis thaliana*. RNA 23(7): 1068–1079. https://doi.org/10.1261/rna.060517.116