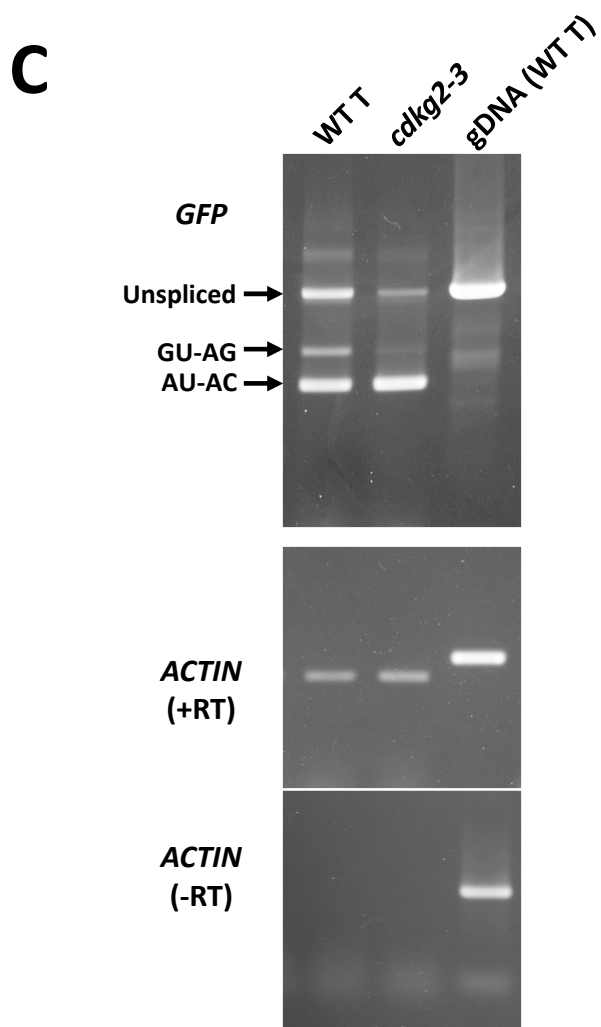
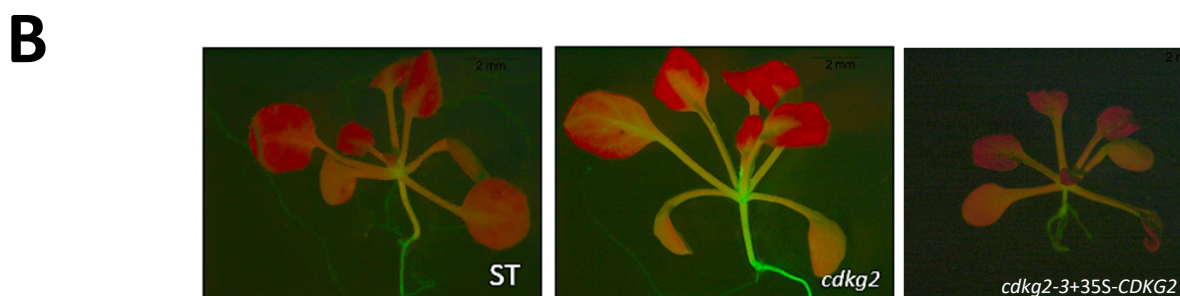
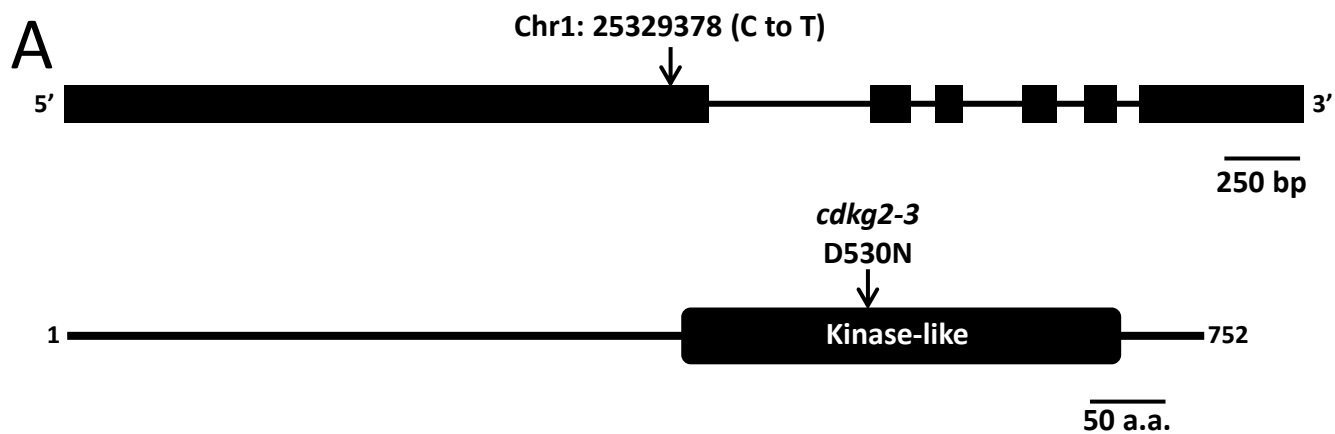


# CDKG2 –At1g67580



### Figure S3: CDKG2

- A. Top: Intron-exon structure of the *CDKG2* gene (At1g67580) and position of the nucleotide change in the *cdkg2-3* mutant. Bottom: Domain structure of the CDKG2 protein (752 amino acids) and the position of the amino acid substitution (D530N) in the highly conserved kinase domain.
- B. GFP fluorescence in seedlings with the indicated genotypes. The *cdkg2-3* mutant shows a hyper-GFP relative to the WT T line. A complemented *cdkg2-3* mutant, labeled with '+35S-*CDKG2*' (35S denotes the 35S promoter of cauliflower mosaic virus), shows a return to more WT T levels of GFP.
- C. Semi-quantitative RT-PCR indicating levels of the three *GFP* splice variants in the *cdkg2-3* mutant. The level of the translatable AU-AC transcript increase substantially in the *cdkg2-3* mutant at the expense of the unspliced and GU-AG transcripts, suggesting enhanced splicing efficiency of the non-canonical splice sites in *GFP* pre-mRNA. Actin, with and without reverse transcriptase (RT), was used as a constitutively expressed control. gDNA, genomic DNA control