genes

MDPI

Article

Ectopic Expression of MADS-Box Transcription Factor *VvAGL12* from Grape Promotes Early Flowering, Plant Growth, and Production by Regulating Cell-Wall Architecture in *Arabidopsis*

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Supplementary Materials:

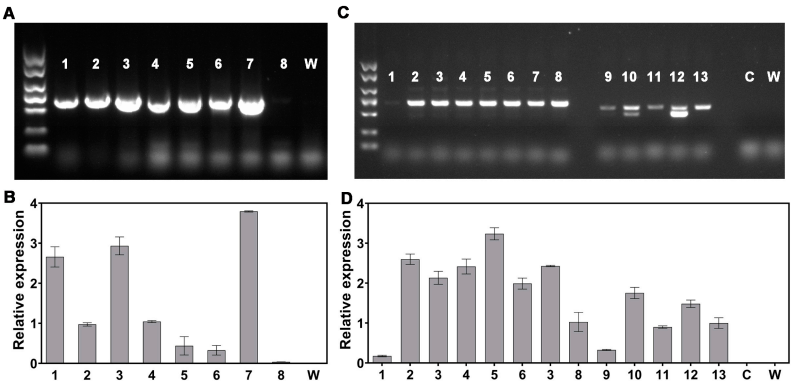

Figure S1: Molecular confirmation of *VvAGL12* transgenic *Arabidopsis*. (A) Identification of 8 overexpression of *VvAGL12* lines via PCR. (B) Evaluation of expression levels in eight *VvAGL12* overexpressing lines. (C) Identification of 13 lines with complementary mutant *agl12* by PCR. (D) Evaluation of expression levels in 13 complementary lines. The numbers represent the transgenic lines, W represents the wild-type, and C represents the water control.

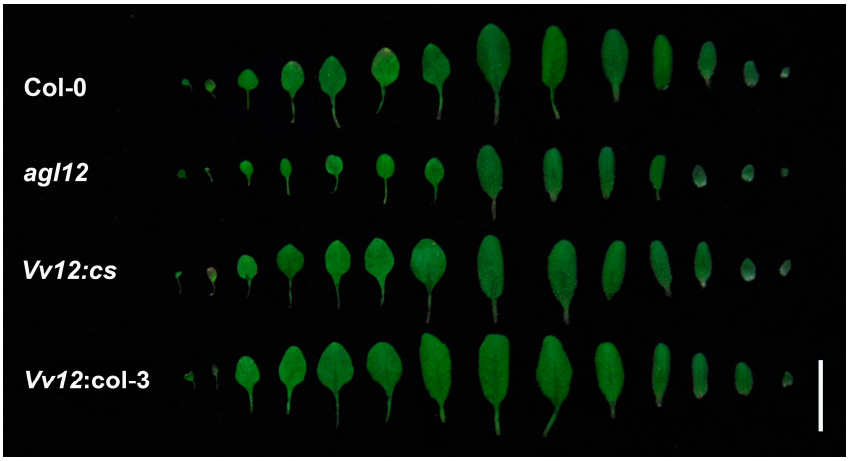

Figure S2: Phenotype of rosette leaves in four lines (Col-0, *agl12*, *Vv12:cs*, and *Vv12*:col) at reproductive growth stage. Col-0 was a wild-type *Arabidopsis*, *agl12* was a mutant of AGL12, *Vv12: cs* was the *VvAGL12* complementary *Arabidopsis* mutant *agl12*, and *Vv12*: col was overexpressed *VvAGL12* in the wild-type.

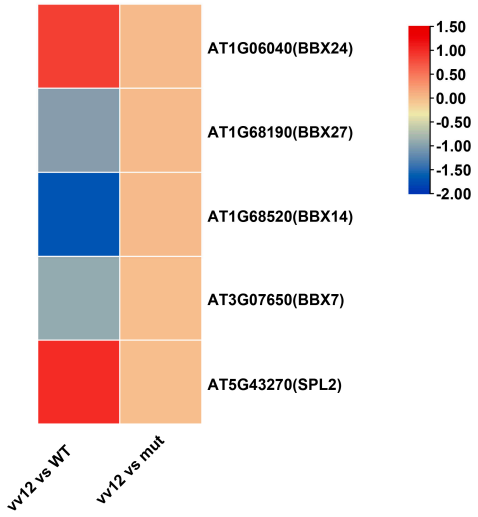

Figure S3: The Fold changes in flowering genes induced by introducing *VvAGL12* in wild-type plants.

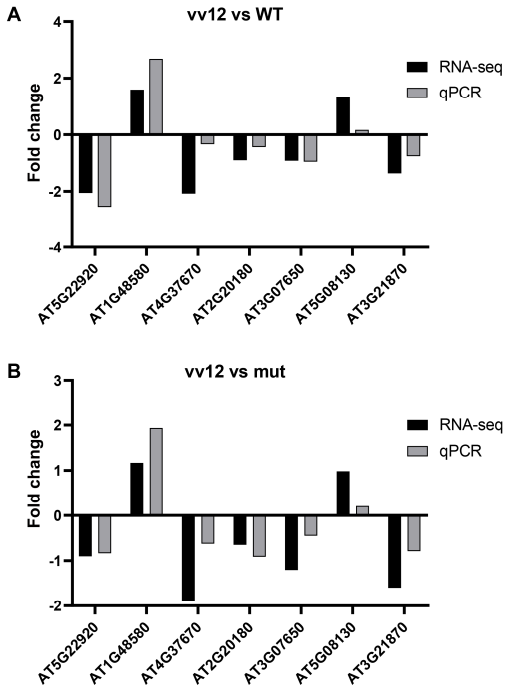

Figure S4: Validation of transcriptome data using real-time quantitative PCR. (A) Comparison between transcriptome and real-time quantitative PCR data in vv12 vs WT. (B) Comparison between transcriptome and real-time quantitative PCR data in vv12 vs Mut.