Supplemental Materials

Figure Legends

Supplemental Figure 1. RT-PCR analysis of transgene expression.

(A) Expression of *FHY3p::FHY3*. Lane 1: No-0 wild type; lane 2: *fhy3-4* mutant; lane 3 and lane 4: *FHY3p::FHY3/fhy3-4* transgenic lines A3 and F2, respectively. (B) Expression of *FAR1p::FAR1*. Lane 1: No-0 wild type; lane 2: *far1-2* mutant; lane 3 and lane 4: *FAR1p::FAR1/far1-2* transgenic lines B2 and E2, respectively. (C) Expression of *FAR1p::FHY3*. Lane 1: No-0 wild type; lane 2: *far1-2* mutant; lane 3 and lane 4: *FAR1p::FHY3/far1-2* transgenic lines C3 and G3, respectively. (D) Expression of *FAR1p::FHY3*. Lane 1: No-0 wild type; lane 2: *fhy3-4* mutant; lane 3 and lane 4: *FAR1p::FHY3/fhy3-4* transgenic lines #9 and #11, respectively. (E) Expression of *FHY3p::FAR1*. Lane 1: No-0 wild type; lane 2: *far1-2* mutant; lane 3 and lane 4: *FHY3p::FAR1/far1-2* transgenic lines #11 and #22, respectively. (F) Expression of *FHY3p::FAR1*. Lane 1: No-0 wild type; lane 2: *fhy3-4* mutant; lane 3 and lane 4: *FHY3p::FAR1/fhy3-4* transgenic lines A2 and A3, respectively. For RT-PCR, 32 PCR cycles were used for transgenes driven by the *FAR1* promoter and 30 PCR cycles were used for transgenes driven by the *FHY3* promoter. RT-PCR of an *ubiquitin* gene is shown below as a positive control.

Supplemental Figure 2. Amino acid alignment of Arabidopsis FHY3 and FAR1 with the maize MURA and *Jittery* transposases.

For clarity, the less conserved extremities of the alignment were trimmed off. The predicted WRKY-GCM1 zinc finger domain is underlined with a single solid line, with the conserved cysteines and histidines of the CCHH motif indicated by asterisks. The dashed line under the alignment indicates the putative core transposase domain of MULE transposases. The diamonds indicate the conserved D288 and E323 residues in FHY3. The C-terminal region of the proteins is characterized by a predicted SWIM zinc-finger domain (double-line under the alignment) with a conserved CCCH motif highlighted by '#'.

Supplemental Figure 3. RT-PCR analysis of *FHY3* transgene expression.

(A) *FHY3* expression in the zinc finger domain mutant transgenic plants. Lane 1: No-0 wild type; lane 2: *fhy3-4* mutant; lane 3 and lane 4: *FHY3p::Bm1/fhy3-4* transgenic lines B6 and C5, respectively; lane 5 and lane 6: *FHY3p::Bm11/fhy3-4* transgenic lines B7 and E7, respectively; lane 7 and lane 8: *FHYp::Bm13/fhy3-4* transgenic lines A2 and C4, respectively; lane 9 and lane 10: *FHY3p::Bm14/fhy3-4* transgenic lines D1 and D2, respectively. (B) *FHY3* expression in the putative transposase catalytic domain mutant transgenic plants. Lane 1: No-0 wild type; lane 2: *fhy3-4* mutants; lane 3 and lane 4: *FHY3p::D288A-YFP/fhy3-4* transgenic lines #4 and #16, respectively; lane 5 and lane 6: *FHY3p::E323A-YFP/fhy3-4* transgenic lines #8 and #21, respectively. (C) *FHY3* expression in the SWIM domain mutant transgenic plants. Lane 1: No-0 wild type; lane 2: *fhy3-4* mutants; lane 3 and lane 4: *FHY3p::C579A-YFP/fhy3-4* transgenic lines E1 and E4, respectively; lane 5 and lane 6: *FHY3p::H591A-YFP/fhy3-4* transgenic lines #30 and #34, respectively. RT-PCR of an *Ubiquitin* gene is shown below as a positive control.

Supplemental Figure 4. *FHY3-YFP* rescues *fhy3-4* mutant phenotype.

(A) Representative images showing that *FHY3p::FHY3-YFP* completely restores the *fhy3-4* mutant phenotype. Bar: 2 mm. (B) *FHY3* gene expression. Lane 1: No-0 wild type; lane 2: *fhy3-4* mutant; lane 3 and lane 4: *FHY3p::FHY3-YFP/fhy3-4* transgenic lines #9 and #10, respectively. RT-PCR of an *Ubiquitin* gene is shown below as a positive control. For (A) and (B), seedlings were grown in continuous FR for 4 d.