Figure S1. (A) The *PECT1* mRNA levels in whole seedlings and SAM-enriched samples at 23°C (ZT8) under SD conditions. **(B)** Morphology of *pFD::amiR-PECT1* plants grown under 23°C LD conditions. Asterisks represent significant differences derived from one-way ANOVA followed by Dunnett's multiple comparison tests (*: $P \leq 0.05$, **: $P \leq 0.01$).
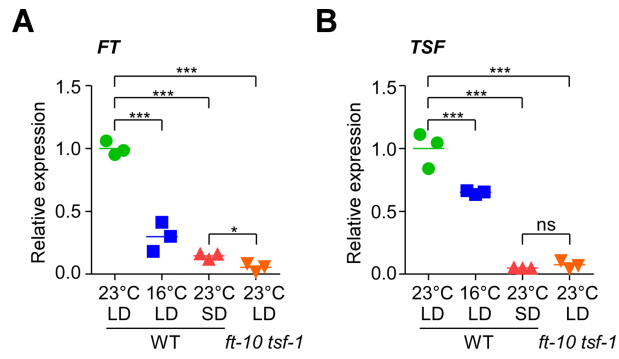
Figure S2. *FT* **(A)** and *TSF* **(B)** mRNA levels under different conditions (23°C LD, 16°C LD, and 23°C SD). Asterisks represent significant differences from Student's *t*-tests (ns: non-significant, *: $P \leq 0.05$, ***: $P \leq 0.001$).
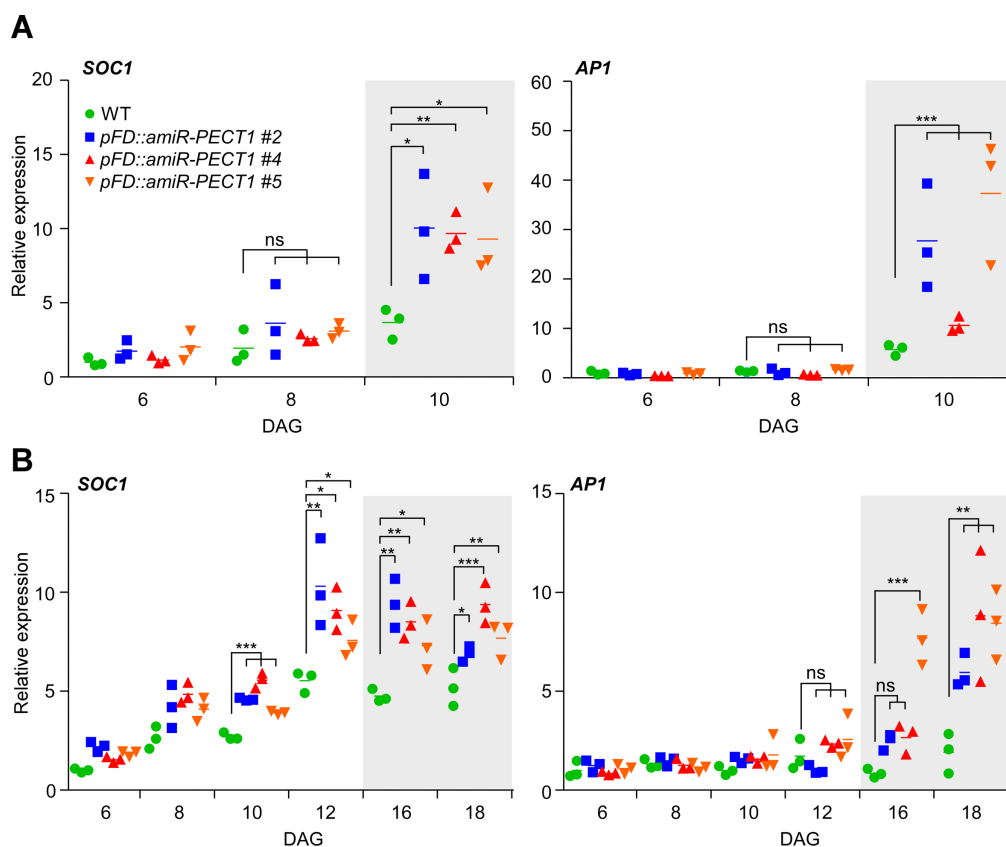
Figure S3. Time course of *SOC1* and *AP1* mRNA levels in *pFD::amiR-PECT1* plants under 23°C LD (ZT16) **(A)** and 23°C SD (ZT8) **(B)** conditions. Asterisks represent significant differences from one-way ANOVA followed by Dunnett's multiple comparison tests (ns: non-significant, *: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$).
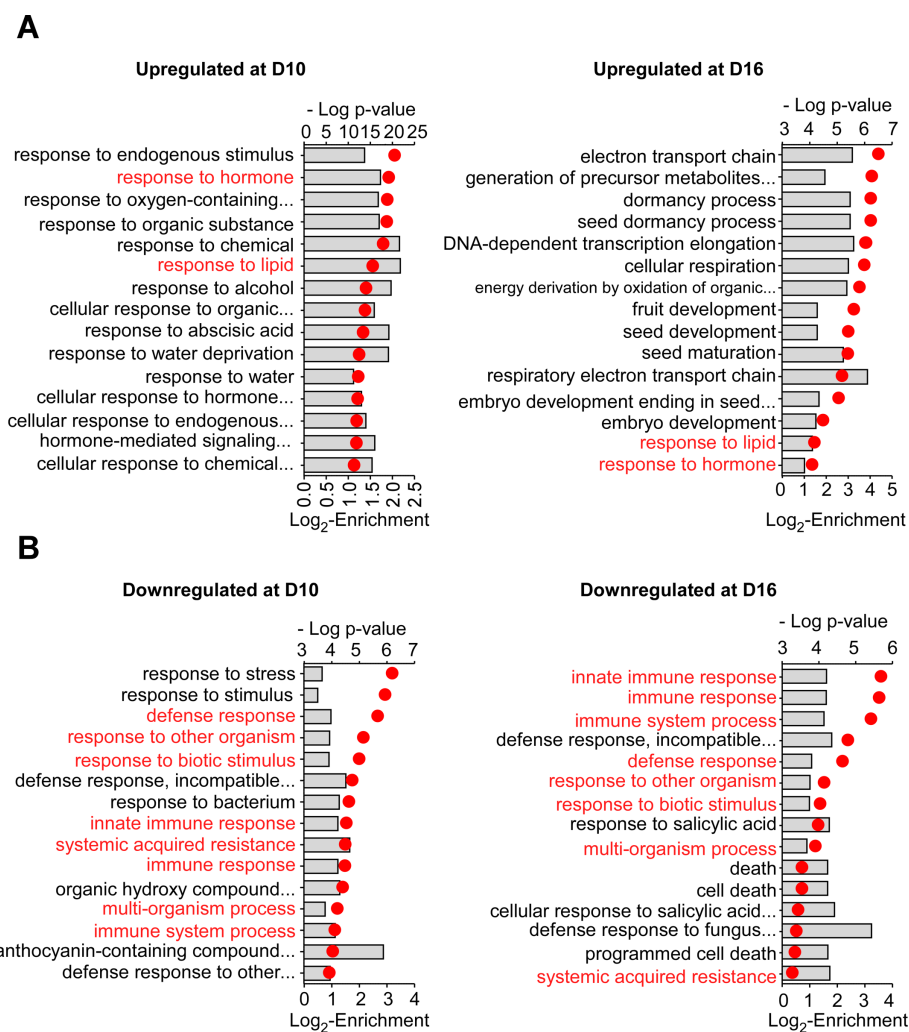
Figure S4. Top 15 GO terms enriched among the genes that were upregulated **(A)** and downregulated **(B)** in the SAM-enriched sample of 10- and 16-day-old *pFD::amiR-PECT1* plants (line #5). Y-axis represents GO terms; the primary X-axis represents $\log_2$ enrichment (grey bars), whereas the secondary X-axis shows the negative log of *P* values (red filled circles). Red color indicates GO terms present at both 10 and 16 days after germination.
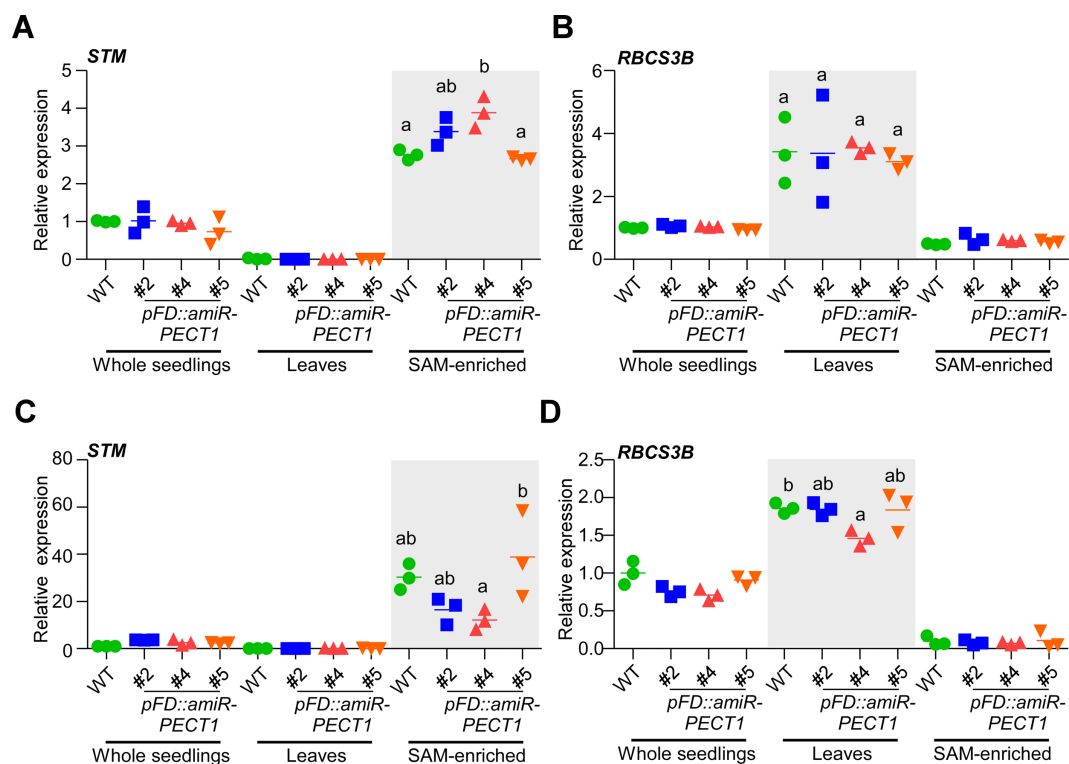
Figure S5. The mRNA levels of marker genes *STM* and *RBCS3B* in the samples from Fig. 3A and C **(A–B)** and Fig. S6 **(C–D)**. Letters indicate significant difference from one-way ANOVA followed by Duncan's multiple range tests ($P \leq 0.01$).
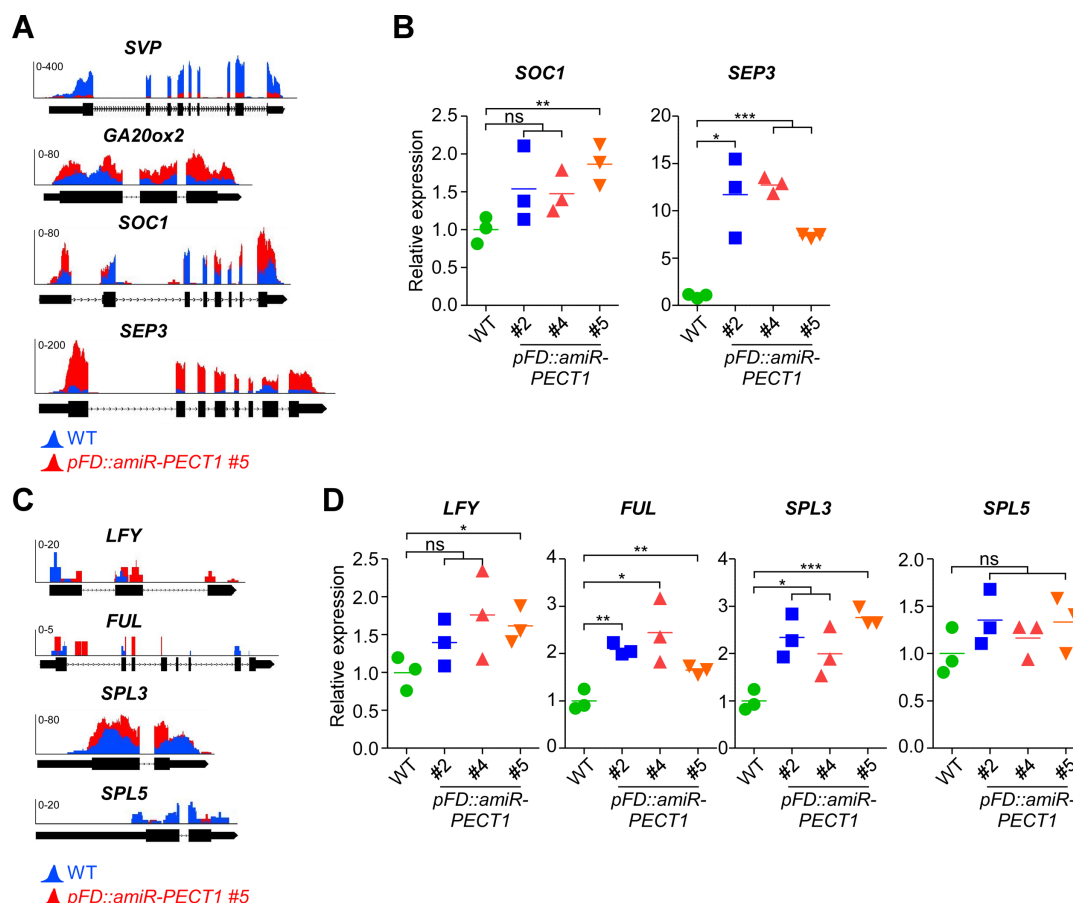
Figure S6. (A) The RNA-seq peak map of *SVP*, *GA20ox2*, *SOC1*, and *SEP3* in the SAM-enriched samples of 10-day-old WT (blue) and *pFD::amiR-PECT1* plants (line #5) (red). **(B)** The mRNA levels of *SOC1* and *SEP3* in the SAM-enriched samples of *pFD::amiR-PECT1* plants under 23°C SD conditions (ZT8). **(C)** The RNA-seq peak map of GA-downstream target genes, *LFY*, *FUL*, *SPL3*, and *SPL5*, in the SAM-enriched samples of 10-day-old WT (blue) and *pFD::amiR-PECT1* plants (line #5) (red). **(D)** The mRNA levels of *LFY*, *FUL*, *SPL3*, and *SPL5* in the SAM-enriched samples of *pFD::amiR-PECT1* plants under 23°C SD conditions (ZT8). Asterisks represent significant differences derived from Student's *t*-tests (ns: non-significant, *: $P \le 0.05$, **: $P \le 0.01$, ***: $P \le 0.001$).

Figure S7. The mRNA levels of *SOC1* and *SEP3* in *pFD::amiR-PECT1 ft-10 tsf-1* seedlings under 23°C SD conditions (ZT8). Asterisks represent significant differences derived from Student's *t*-tests (ns: non-significant, *: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$).
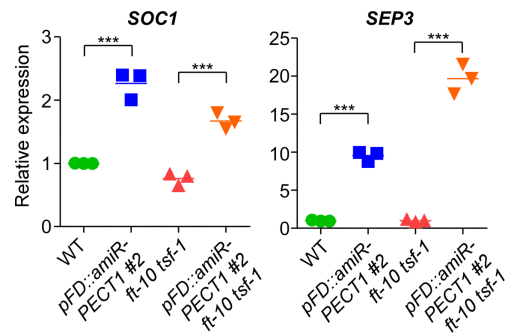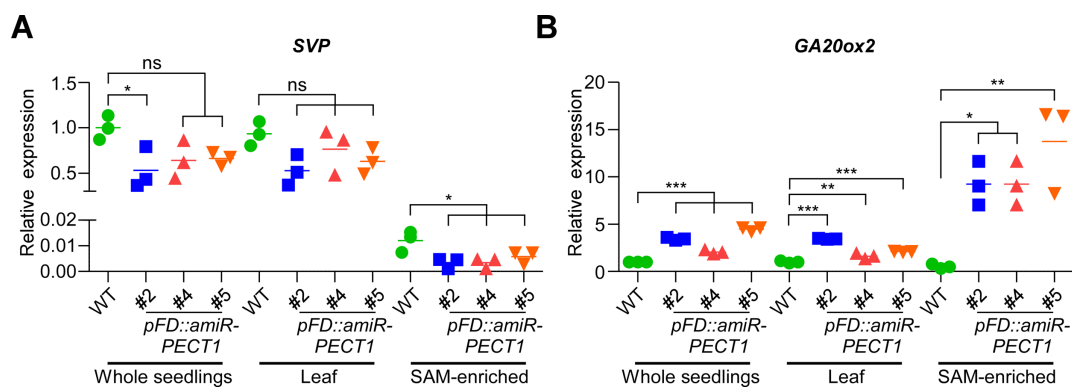
Figure S8. The mRNA levels of *SVP* **(A)** and *GA20ox2* **(B)** in whole seedlings, leaves, and SAM-enriched samples of *pFD::amiR-PECT1* plants at 23°C (ZT16) under LD conditions. Asterisks represent significant differences derived from one-way ANOVA followed by Dunnett's multiple comparison tests (ns: non-significant, *: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$).
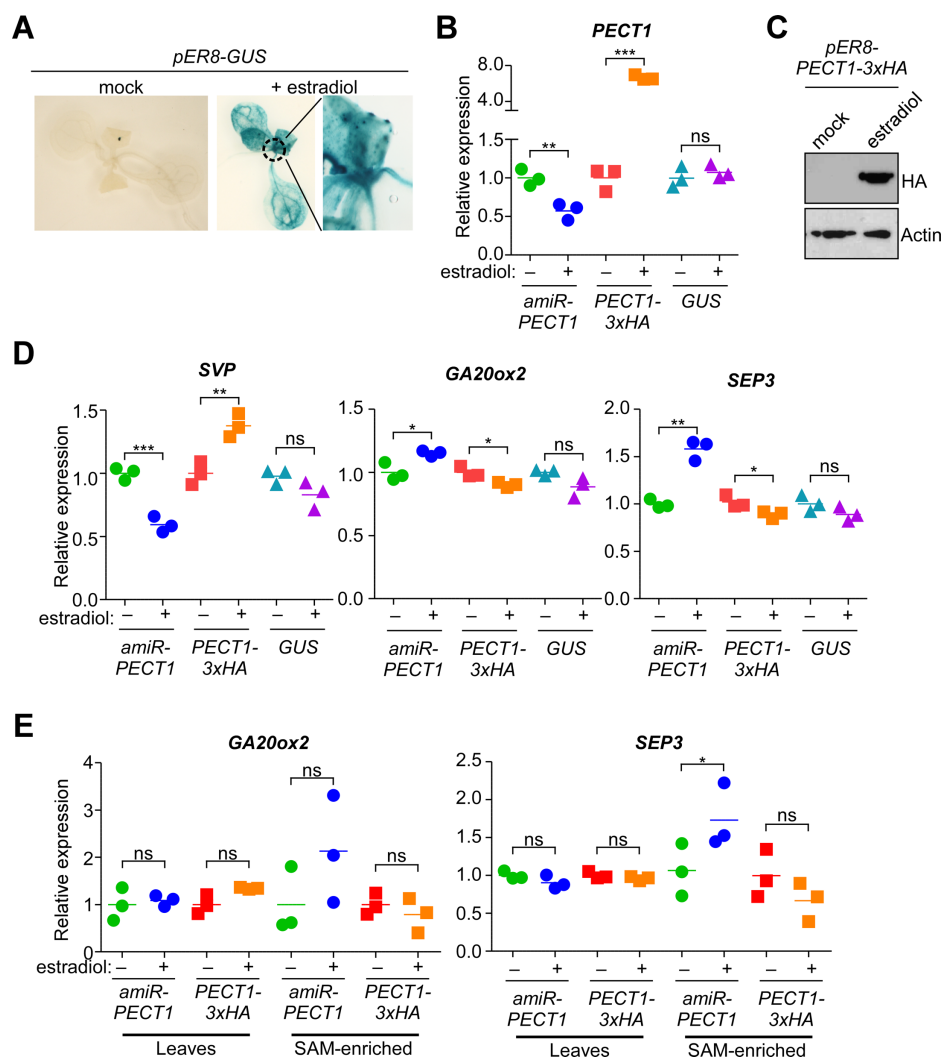
Figure S9. (A) GUS histochemical analyses of *pER8::GUS* plants upon estradiol treatment. **(B)** The mRNA levels of *PECT1* in *pER8::amiR-PECT1*, *pER8::PECT1:3×HA*, and *pER8::GUS* seedlings upon estradiol treatment. **(C)** The levels of PECT1:3×HA protein in *pER8::PECT1:3×HA* plants upon estradiol treatment. **(D–E)** The mRNA levels of *SVP*, *GA2ox2*, and *SEP3* in whole seedlings **(D)** and in SAM-enriched and leaf samples **(E)** of *pER8::amiR-PECT1*, *pER8::PECT1:3×HA*, and *pER8::GUS* seedlings upon estradiol treatment under 23°C SD conditions (ZT8). Asterisks represent significant differences derived from Student's *t*-tests (ns: non-significant, *: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$).
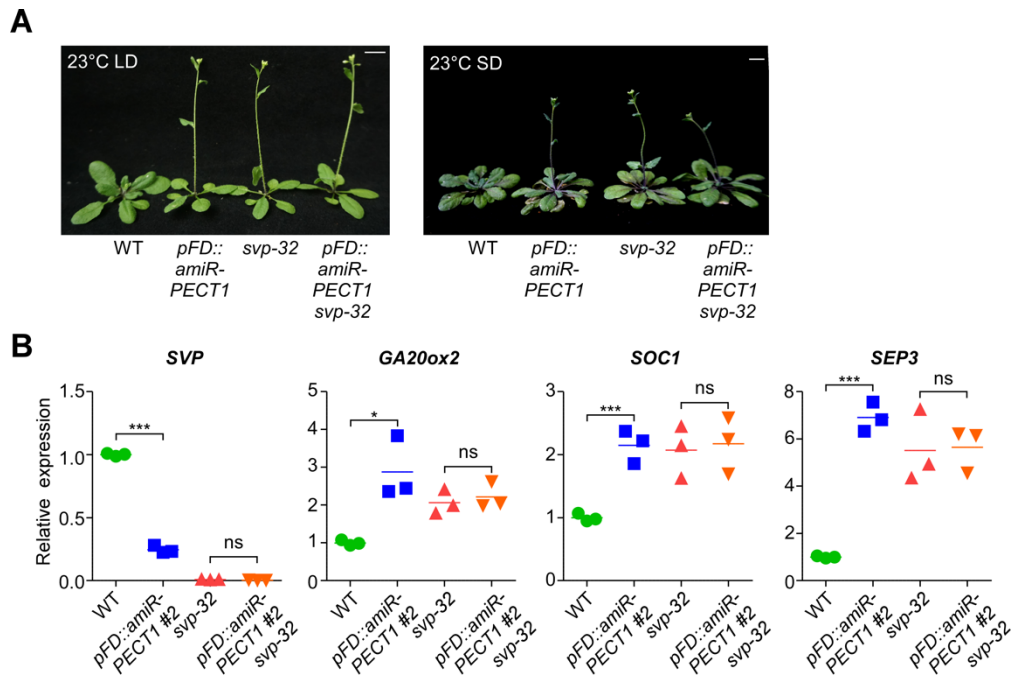
Figure S10. The morphology **(A)** and mRNA levels of *SVP*, *GA20ox2*, *SOC1*, and *SEP3* in the SAM-enriched samples **(B)** of *pFD::amiR-PECT1 svp-32* plants under 23°C SD conditions (ZT8). Asterisks represent significant differences derived from Student's *t*-tests (ns: non-significant, *: $P \leq 0.05$, ***: $P \leq 0.001$).
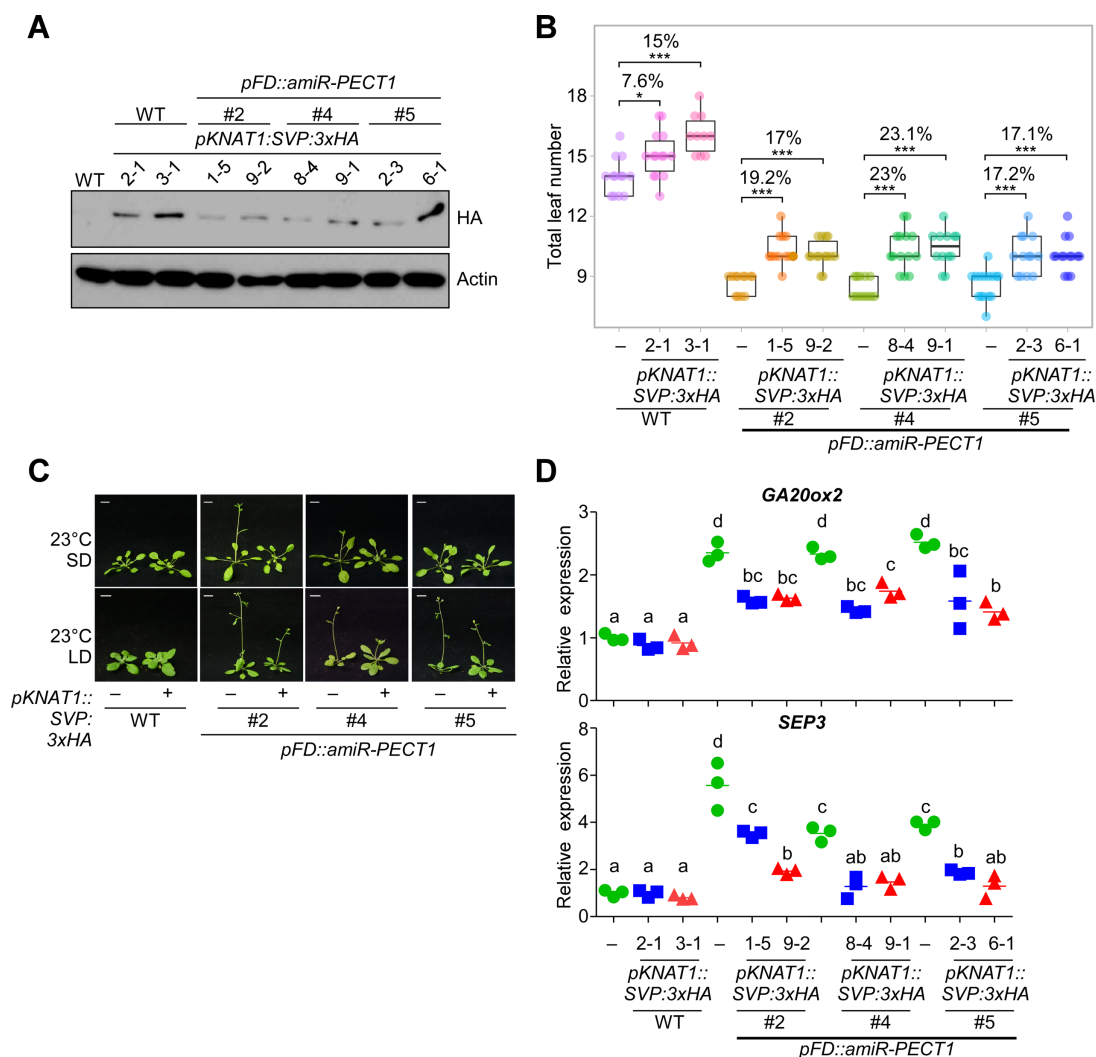
Figure S11. (A) Confirmation of SVP-3×HA protein expression in *pKNAT1::SVP:3×HA* transgenic lines. **(B)** Total leaf number at flowering of *pKNAT1::SVP:3×HA pFD::amiR-PECT1* plants under 23°C LD conditions. **(C)** Morphology of *pKNAT1::SVP:3×HA* transgenic lines under 23°C SD and LD conditions. **(D)** The mRNA levels of *GA20ox2* and *SEP3* in the SAM-enriched samples of *pKNAT1::SVP:3×HA* transgenic lines under 23°C SD conditions. Asterisks represent significant differences derived from Student's *t*-tests (*: $P \leq 0.05$, ***: $P \leq 0.001$), and different lowercase letters represent significant differences derived from one-way ANOVA followed by Duncan's multiple range tests ($P \leq 0.01$).
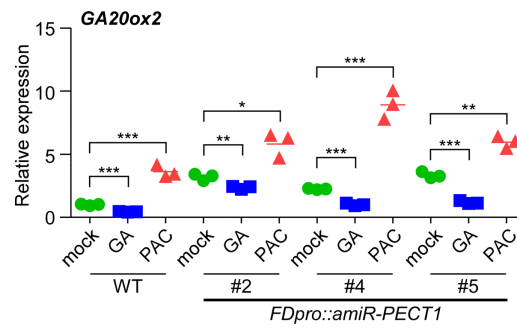
Figure S12. The mRNA levels of *GA20ox2* in *pFD::amiR-PECT1* plants under 23°C SD conditions upon 50 µM GA_3 and 5 µM paclobutrazol (PAC) treatment. Asterisks represent significant differences derived from one-way ANOVA followed by Dunnett's multiple comparison tests (*: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$).

Table S1. Flowering times of mutants and transgenic lines used in this study.

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Table S2. List of DEGs (fold change > 2 and *P*-value < 0.01) of *pFD::amiR-PECT1* SAM-enriched samples under 23°C SD conditions (ZT8; 10 and 16 days after germination).

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Table S3. Primers used in this study.

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Table S4. Selected monitoring conditions for GAs and deuterium isotope-labeled GAs.

Analytes	Molecular ions	Fragment ions	Retention time (min)	Collision energy (eV)
GA$_3$	345	239	0.5	14
GA$_4$	331	257	0.7	10
[^{2}H$_2$]-GA$_4$	333	259	0.7	10
GA$_5$	329	145	0.2	15