Supplemental Figure 1: *ath1-1* phenotypes are comparable to those of *ath1-3*.

(A) Part of a mature inflorescence; arrows indicate stamens that remained attached to the base of developing siliques (compare with *ath1-3* in Figure 1).

(B) Displaced shoot apex (arrow) in a two week-old seedling grown in the dark on medium supplemented with 1% sucrose (compare with *ath1-3* in Figure 4). Size bars: 1 mm (A), 100 *μ*m (B).
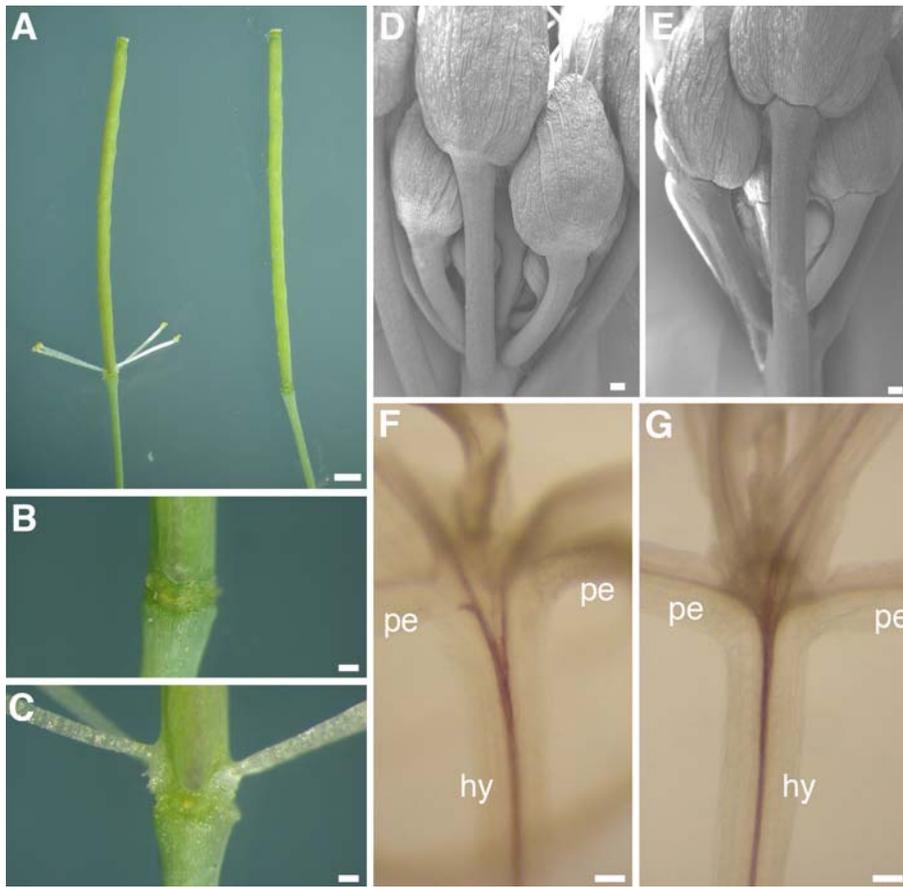
Supplemental Figure 2: Complementation of *ath1-3.*
(A) Developing siliques of *ath1-3* (left), with stamens still attached, and of complemented line (*ath1-3 ATH1:ATH1,* on the right), with stamen dehiscence restored. (B,C) Close-up of the base of the silique in *ath1-3* (C) and in *ath1-3 ATH1:ATH1* (B). (D,E) Scanning electron micrograph showing the basal boundaries of sepals in *ath1-3* (D) and in *ath1-3 ATH1:ATH1* (E). (F,G) Vascular strands in the shoot apex of two week-old *ath1-3* (F) and *ath1-3 ATH1:ATH1* (G) seedlings; hy: hypocotyls; pe: petiole. Size bars: 1 mm (A), 100 *µ*m (D-G).
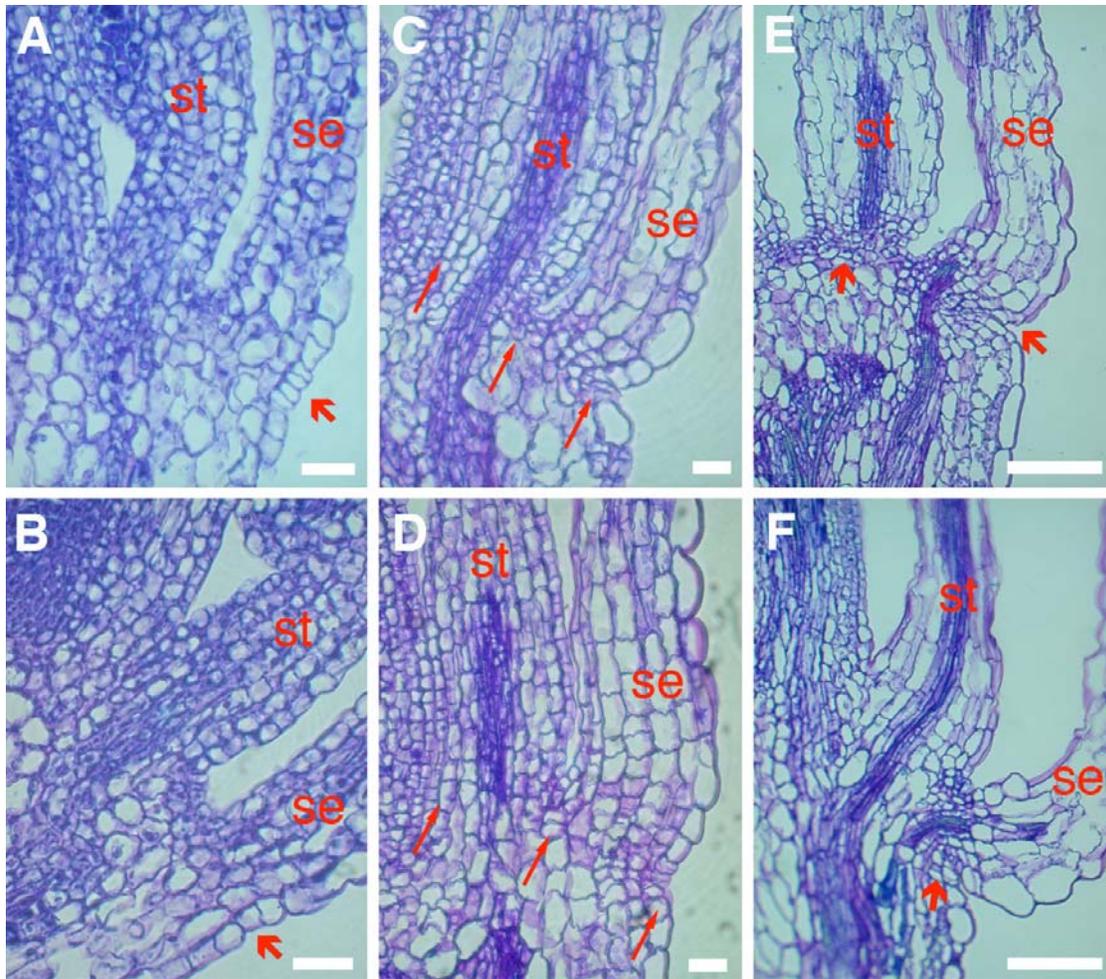
Supplemental Figure 3: Development of the basal region of stamens and sepals in the wild type and in *ath1-3*. st: stamen; se: sepal.

(A,B) Sections through stage 8 wild-type (A) and *ath1-3* (B) buds. Arrows indicate the boundary between sepal and pedicel. Note the row of small cells visible in the wild-type but absent in the mutant.

(C,D) Sections through stage 11 wild-type (C) and *ath1-3* (D) buds. Arrows indicate the limits between adjacent organs, at their junction with the pedicel. Note that, compared to the wild type, the junction with the pedicel in *ath1-3* is less constricted and the region between the sepal and the stamen has larger cells .

(E,F) Sections through stage 13 wild-type (E) and *ath1-3* (F) flowers. Note that although the abscission zone (arrows) has developed at the base of the sepal in *ath1-3* flowers, it is absent from the stamen; the base of the stamen is also partially fused with the carpel. Size bars: 20 *μ*m (A-D) and 100 *μ*m (E,F).
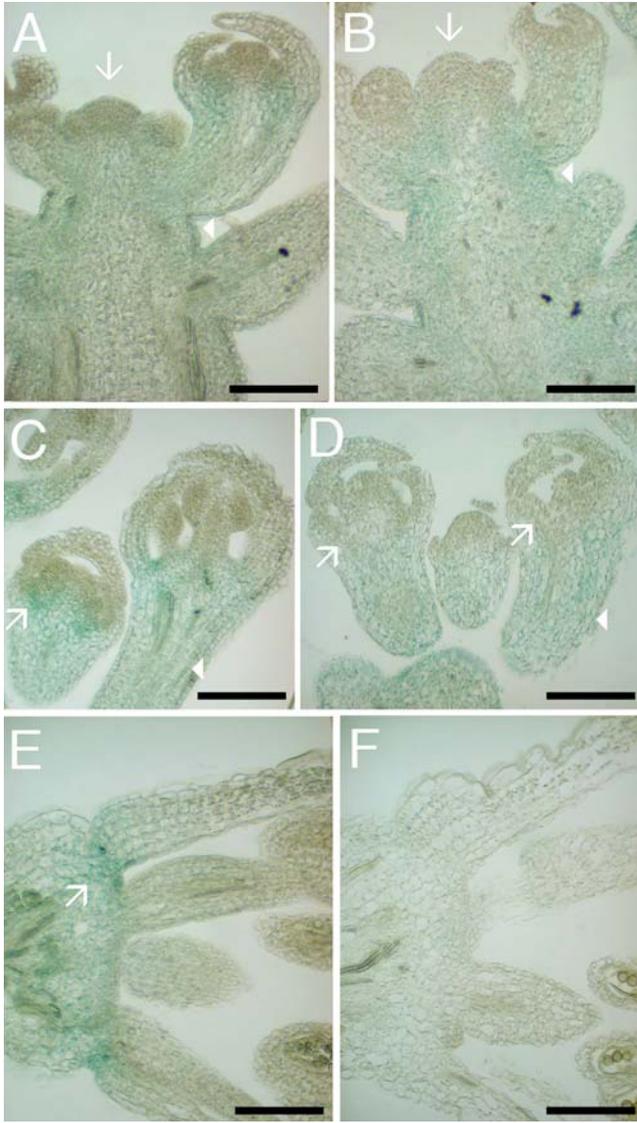
Supplemental Figure 4: Sections through GUS-stained wild-type *BP:GUS* and *ath1-3 BP:GUS* inflorescences.

(A,B) Sections through the inflorescence apex of wild-type (A) and *ath1-3* (B). Note that in *ath1-3*, BP:GUS expression is not detectable in the inflorescence meristem (arrows), while it is expressed at wild-type levels in the subtending stem (arrowheads).

(C,D) Sections through early (stage 6-7 buds of the wild type (C) and *ath1-3* (D); note that *BP:GUS* expression at the base of developing stamens (arrow) is lower in *ath1-3*, whereas expression in the pedicel (arrowheads) is comparable to the wild type.

(E,F) Sections through late (stage 10-11) floral buds; note that the expression at the base of the flower (arrow in E) is absent in *ath1-3.* Size bars: 100 *μm*.
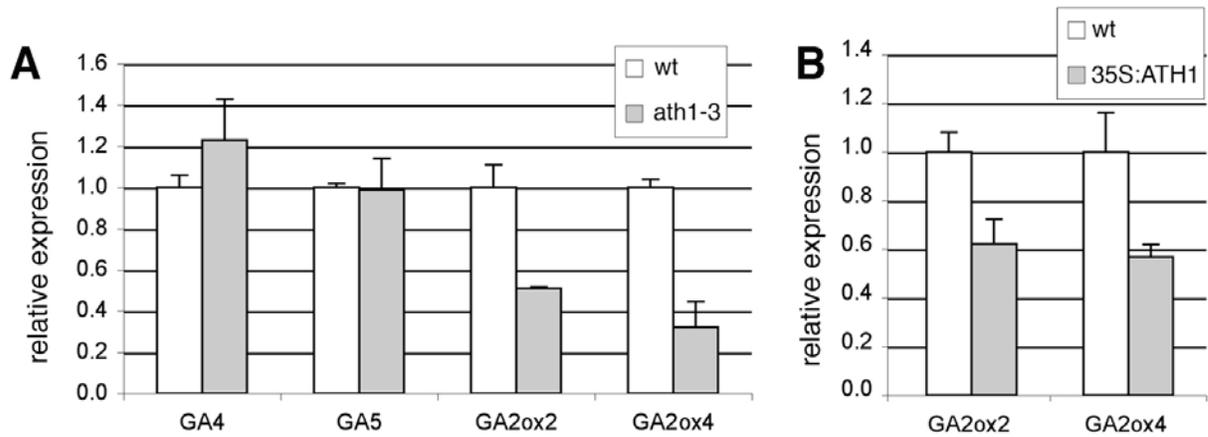
Supplemental Figure 5: Expression of gibberellin homeostasis genes in the wild type, *ath1-3* and *35S:ATH1*, measured by quantitative RT-PCR. The vertical axes show expression levels relative to the average of the wild type; the bars show the average and standard deviation for three to five independent RNA extractions. (A) Expression of *GA4, GA5, GA2ox2* and *GA2ox4* in 2 week-old wild-type and *ath1-3* seedlings (whole rosettes). (B) Expression of *GA2ox2* and *GA2ox4* in wild-type and *35S:ATH1* inflorescences.

Supplemental Figure 6: External gibberellin treatment did not restore inflorescence stem growth in *35S:ATH1* plants.
(A) *35S:ATH1* plants treated for seven days with 100 *μ*M GA3; note the multiple axillary inflorescence stems clustered together on the rosette.
(B) Untreated *35S:ATH1* control plants.

Supplemental Table 1: oligonucleotides used for QRT-PCR

APT for	TCCCAGAATCGCTAAGATTGCC
APT rev	CCTTTCCCTTAAGCTCTG
GA4 for	CCA ACA TCA CCT CAA CTA CTG
GA4 rev	CTC TTT CCA TGT CAC CGA TTG
GA5 for	ACATGGGTTTCAGCCATTTGGGAAGGTGTA
GA5 rev	AGATGGGTTTGGTGAGCCAATCTGAAAAGG
ATH1 for	AGG CGG GTT TCG GAT CTA CAT
ATH1 rev	TTA TTT ATG CAT TGC TTG GCT
GA2ox2 F	GTG TCG TAC AAG GTG TTG GAG A
GA2ox2 R	CCA AGT CTA TAA TCA CCA AGC
GA2ox4 for	CTGAGAGTGAATCATTATCCACCG
GA2ox4 rev	TACGCACGTTTCTTGTACTCGC