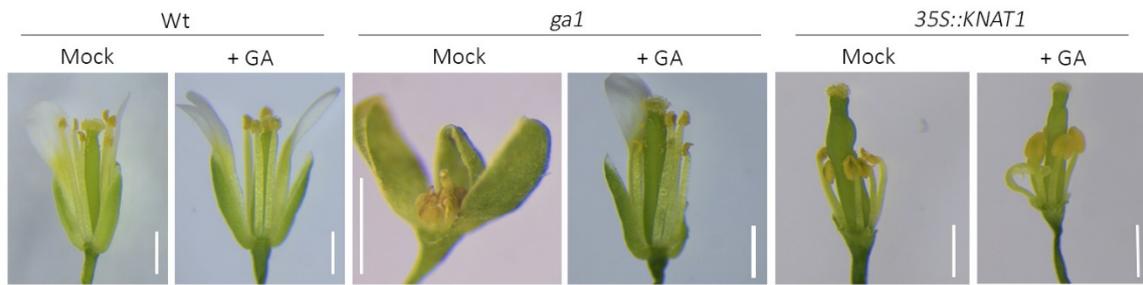


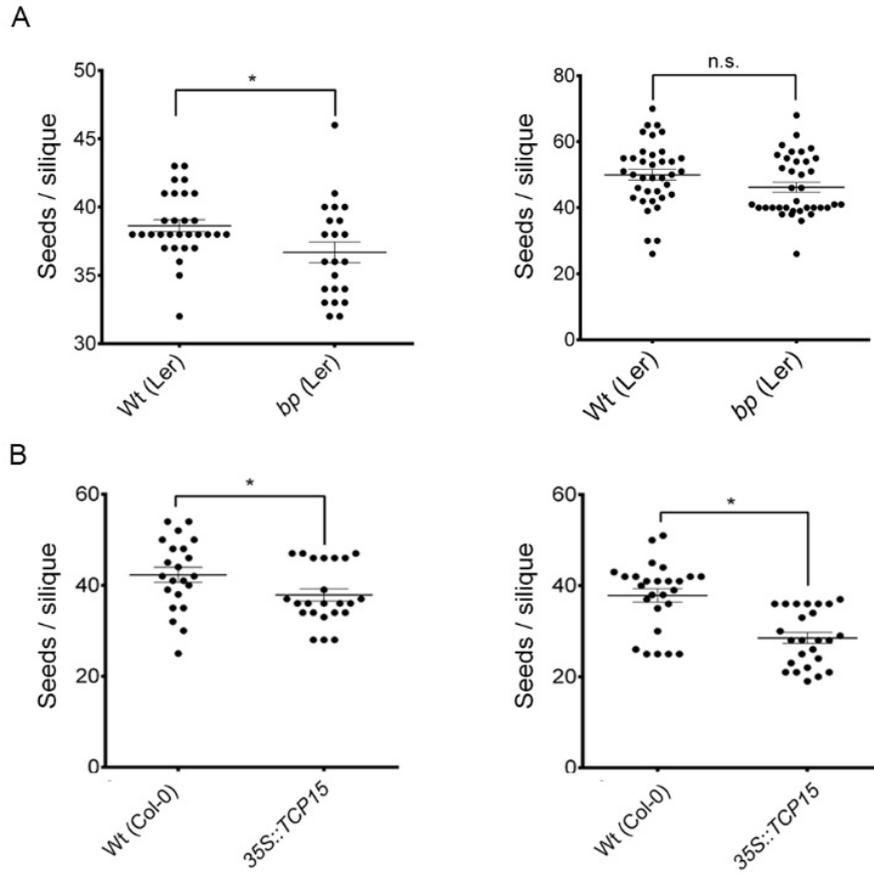
Supplemental Figure S1. Expression levels of class I *KNOX* genes in stamens from *bp-1* flowers. Relative *STM*, *KNAT1* and *KNAT2* transcript levels in stamens from stage 13 wild-type and *bp-1* flowers were determined by RT-qPCR. The bars indicate the mean \pm SE of three biological replicates. Asterisks indicate significant differences with wild-type ($P < 0.05$; Student's *t*-test).



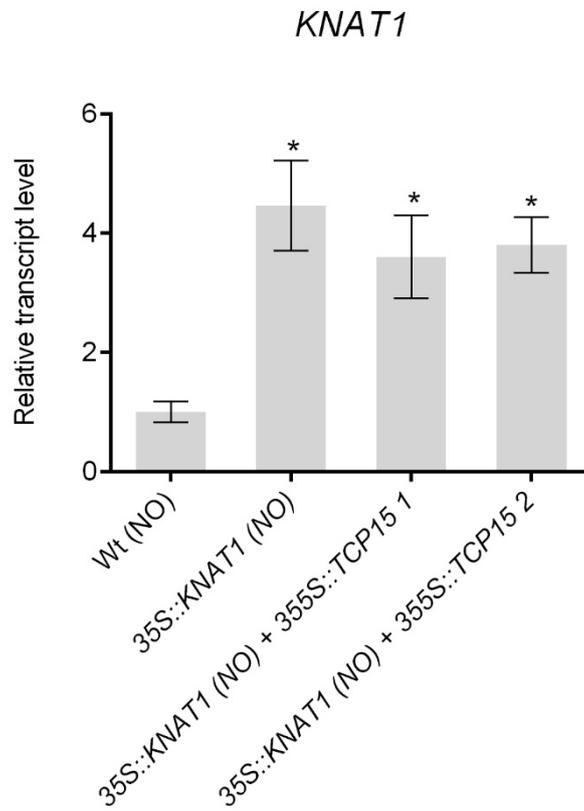
Supplemental Figure S2. Flowers of wild-type, *35S::KNAT1* and *gal* plants after treatment with either gibberellin (GA₃) or mock solution. Outer organs were removed for visualization of the stamens. Bars: 1 mm.



Supplemental Figure S3. Histochemical analysis of *KNAT1* and *TCP15* expression in stamen filaments. GUS histochemical staining was performed on flowers from plants carrying *pTCP15::GUS* or *pKNAT1::GUS* constructs. Arrowheads indicate the vascular system of stamen filaments. Bars: 1 mm.



Supplemental Figure S4. Seed production in siliques from *bp-1* and *35S::TCP15* plants. The number of seeds per silique was analyzed in *bp-1* (A), *35S::TCP15* plants (B), and the corresponding wild-type lines. The results of two independent experiments (mean \pm SE; n = 22–37 siliques) with plants grown at different times are shown. For *35S::TCP15* plants, the experiments were performed with two different lines. Asterisks indicate significant differences with wild-type (P < 0.05; Student's *t*-test).



Supplemental Figure S5. *KNAT1* expression levels in wild-type, *35S::KNAT1* and *35S::KNAT1 35S::TCP15* plants. The bars indicate the mean±SE of three biological replicates. Asterisks indicate significant differences with wild-type plants ($P < 0.05$; Student's *t*-test).