

Expanded View Figures

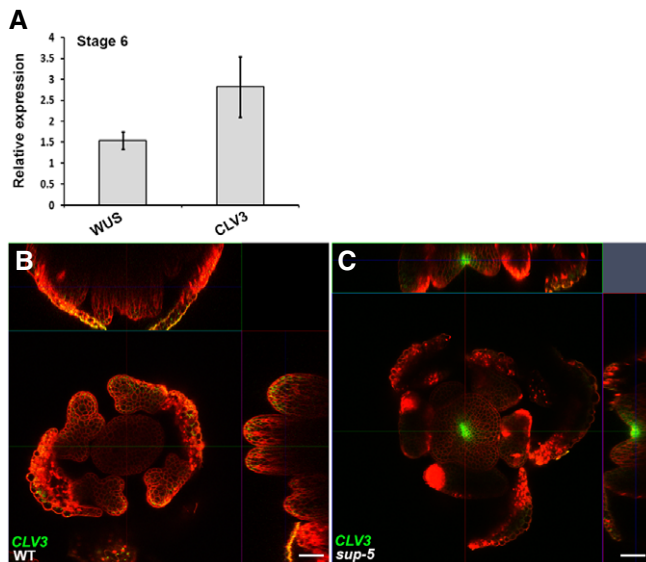


Figure EV1. WUS and CLV3 are increased at stage 6 floral buds in *sup-5*.

- A** Expression of *WUS* and *CLV3* (in floral buds of approximately stage 6) 5 days after treatment of *ap1 cal p35S::API-GR sup-5* inflorescences with 1 μ M DEX. The relative values to equally treated *ap1 cal p35S::API-GR* plants are shown. Error bars indicate standard errors from qRT-PCR experiments of four biological repeats. $P = 0.028$ and 0.031 for *WUS* and *CLV3* based on a Student's *t*-test, respectively.
- B, C** The *pCLV3::GFP-ER* (green) can be detected in a *sup-5* floral bud (**C**) but not in WT (**B**) at a floral stage later than 6. Scale bars, 20 μ m.

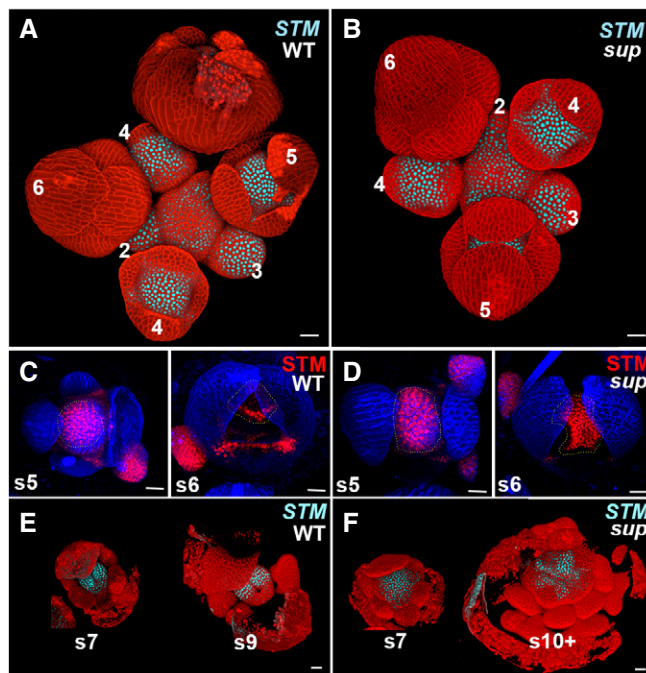


Figure EV2. STM expression is expanded in *sup* floral buds.

- A, B** The expression of *pSTM::CFP-N7* (light blue) in WT and *sup-5* inflorescence. In both WT and *sup-5*, the STM-VENUS fusion protein was highly expressed in the center of floral buds younger than stage 5 as well as in the boundary regions of sepals.
- C, D** A stem cell marker *pSTM::STM-VENUS* (red) in WT (**C**) and *sup-5* (**D**) floral buds at the stages 5 and 6. From late stage 5 (s5), STM was reduced in the regions with developing stamens. The STM expression domain in FM centers is relatively larger in *sup-5* ($1,680 \pm 167 \mu\text{m}^2$, $n = 15$) than that in WT ($1,150 \pm 160 \mu\text{m}^2$, $n = 16$). $P < 0.05$ based on a Student's *t*-test. Dashed lines mark the FM regions and whorl 3/4 boundary regions with STM-VENUS.
- E, F** The expression of *pSTM::CFP-N7* (light blue) only remains expressed at the carpel margins/placenta region in the WT at stage 7 (s7) and greatly diminished at stage 9 (s9) (**E**). Conversely, in *sup-5*, STM is expressed in a larger domain, which encompasses the FM that keeps proliferating as well as in emerging extra stamen primordia up to stage later than 10 (s10+) (**F**).
- Data information: Scale bars, 20 μ m.

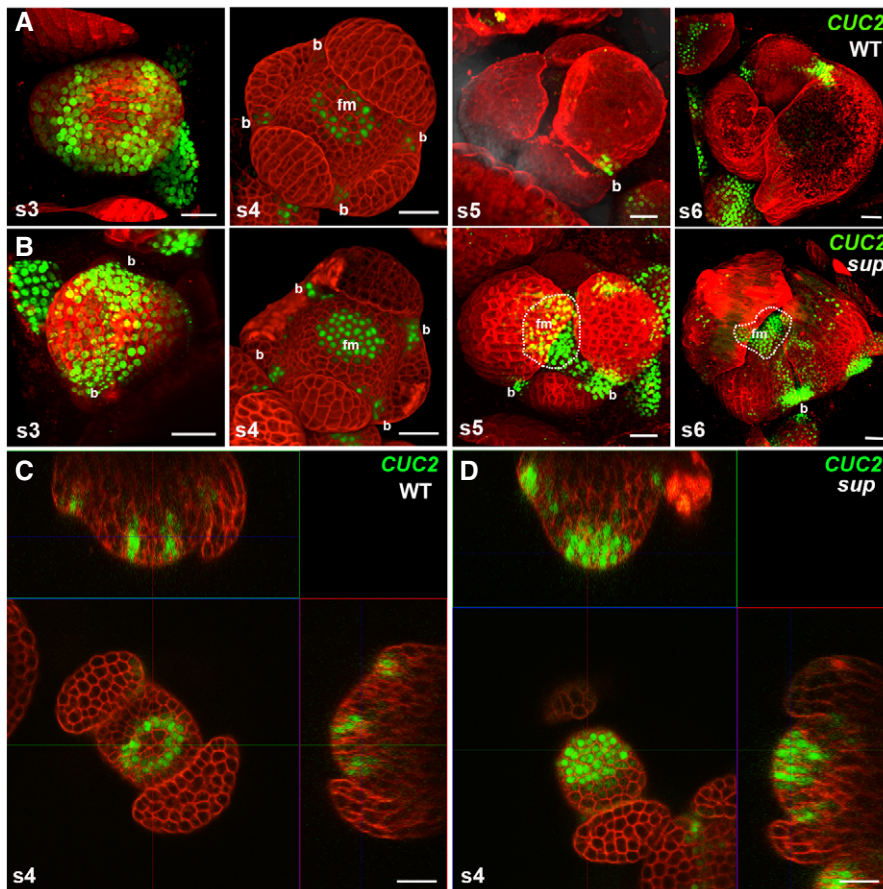


Figure EV3. *pCUC2::3xVENUS-N7* expression is expanded in the epidermal cells of *sup* mutants.

- A** *pCUC2::3xVENUS-N7* in WT floral buds at stages 3–6. *CUC2* was highly expressed in the floral buds of stage 3, and its expression started to be constrained to the boundary regions between the sepals after stage 3. At stage 5 and stage 6 floral buds, *CUC2* was only detected in the small boundary regions at the bottom of the sepals.
- B** *pCUC2::3xVENUS-N7* in *sup-5* floral buds at stages 3–6. At stage 3, the *CUC2* expression pattern was similar to that in WT. From stage 4, the *CUC2* expression pattern in *sup-5* started to show differences from that of WT. *CUC2* expression was detected in FM region of at stage 4. At stages 5 and 6, the *CUC2* expression was still relatively high but was more concentrated at the bottom of the developing sepals as well as in the broad FM regions. Dashed lines mark the regions with *CUC2*-3xVENUS-N7 in the flower center. “b” indicates the boundary region between sepals; “fm” indicates the floral meristem region in the center.
- C** A cross section of a stage 4 WT floral bud showing a ring of *CUC2*-3xVENUS-N7 signal at the whorl 3/4 boundary.
- D** A cross section of a stage 4 *sup-5* floral bud showing the additional signal of *CUC2*-3xVENUS-N7 in the FM center.

Data information: Scale bars, 20 μ m.

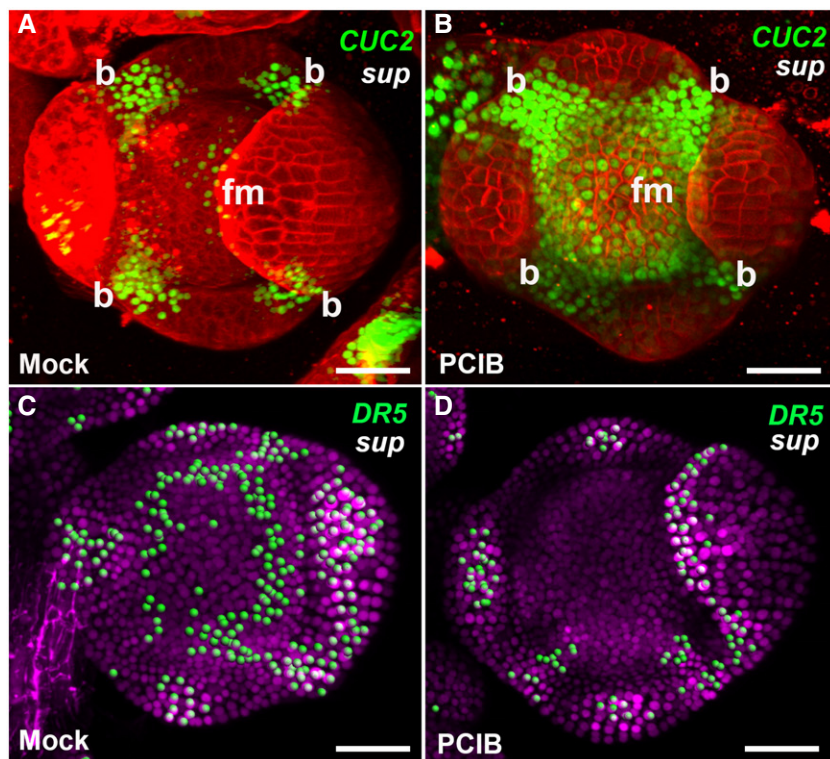


Figure EV4. PCB treatments induced *CUC2* expression but repressed *DR5* activity in *sup-5*.

A, B The expression of *pCUC2::CUC2-3xVENUS-N7* was induced in stage 4 floral buds of *sup-5* plants 4–6 h after treatment with PCB (B) but after a mock treatment (A).
C, D The expression of *pDR5rev::3xVENUS-N7* was reduced in stage 4 floral buds of *sup-5* plants 4–6 h after treatment with PCB (D) but not after a mock treatment (C).

Data information: Scale bars, 20 μ m.

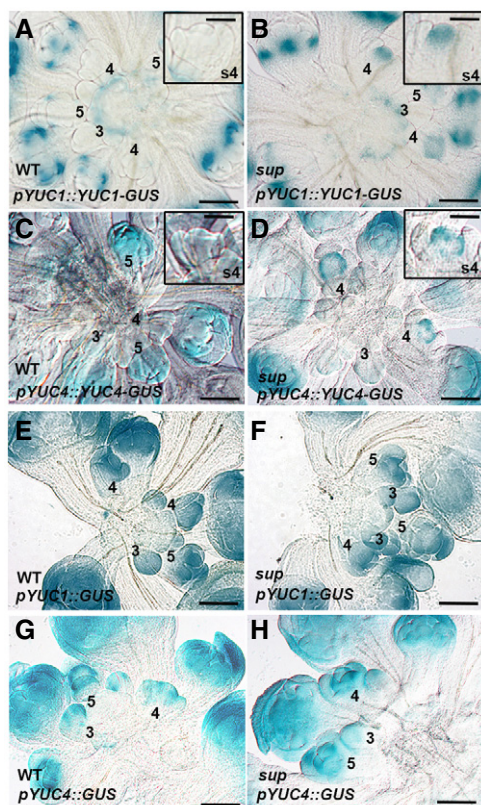


Figure EV5. The up-regulation of *YUC1* and *YUC4* GUS reporter lines in young *sup* floral buds.

A, B GUS staining of *YUC1* full-length reporter *pYUC1::YUC1-GUS* in WT (A) and *sup-5* (B) inflorescences. The expression of *pYUC1::YUC1-GUS* is weak at floral buds earlier than stage 5. At stage 5, GUS starts to be highly expressed at the sepals, especially at the bottom of sepals at the later stages. In *sup-5*, *pYUC1::YUC1-GUS* is expressed highly at the SUP expression domain as well as the FM region at the stage 4. Floral buds at stage 4 with GUS staining are shown as insets.
C, D GUS staining of *YUC4* full-length reporter *pYUC4::YUC4-GUS* in WT (C) and *sup-5* (D) inflorescences. In WT, the expression of *pYUC4::YUC4-GUS* is weak at the floral buds at earlier than stage 5. From stage 5, GUS is almost expressed in the whole floral buds (C). In *sup-5*, *pYUC4::YUC4-GUS* is highly expressed at the SUP expression domain at the floral buds of stage 4. Floral buds at stage 4 with GUS staining are shown as insets.
E, F GUS staining of *YUC1* promoter reporter *pYUC1::GUS* was detected in almost all WT (E) and *sup-5* (F) young floral buds.
G, H GUS staining of *YUC4* promoter reporter *pYUC4::GUS* was detected in almost all WT (G) and *sup-5* (H) young floral buds.

Data information: Scale bars, 0.02 mm.