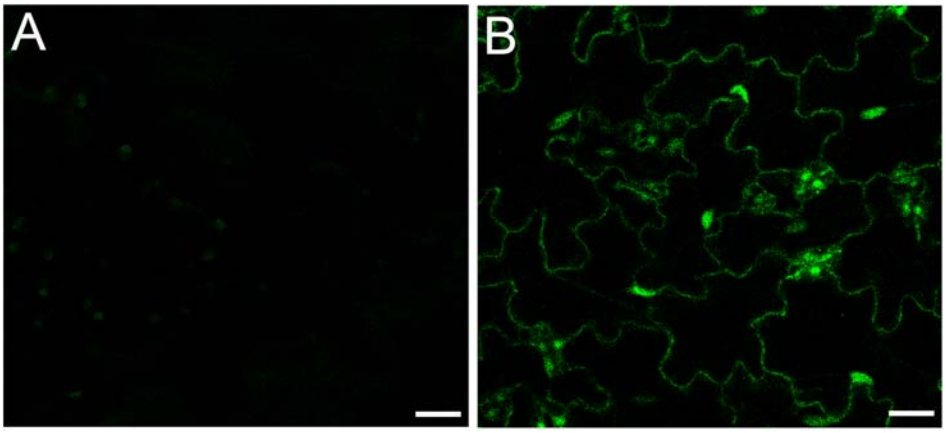
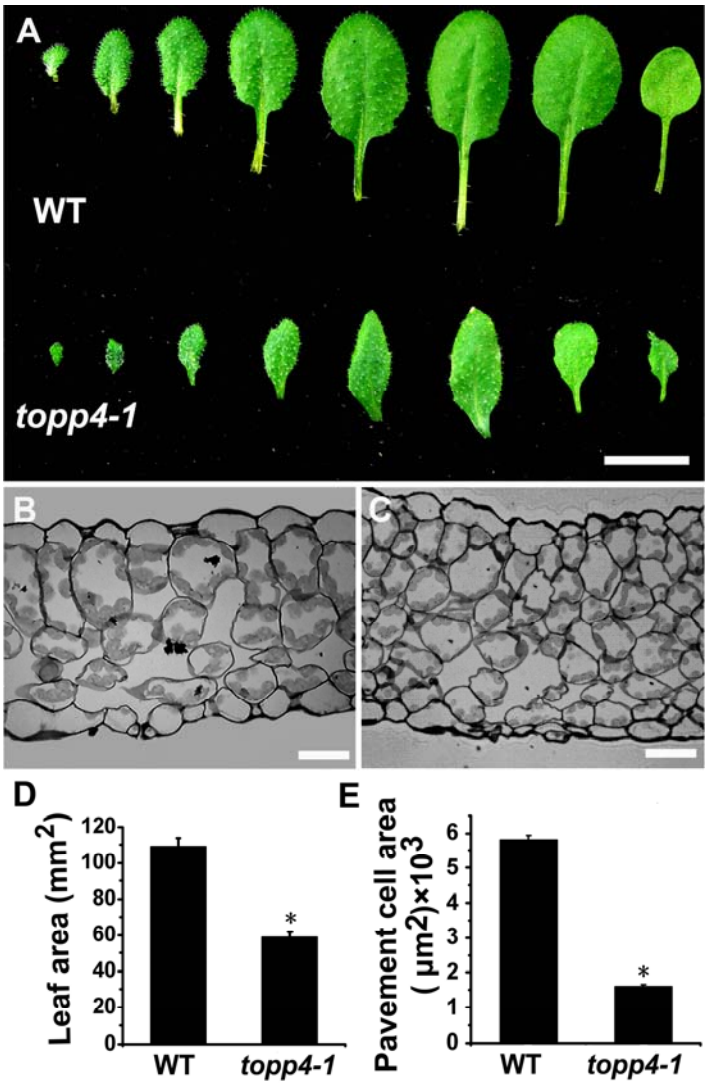
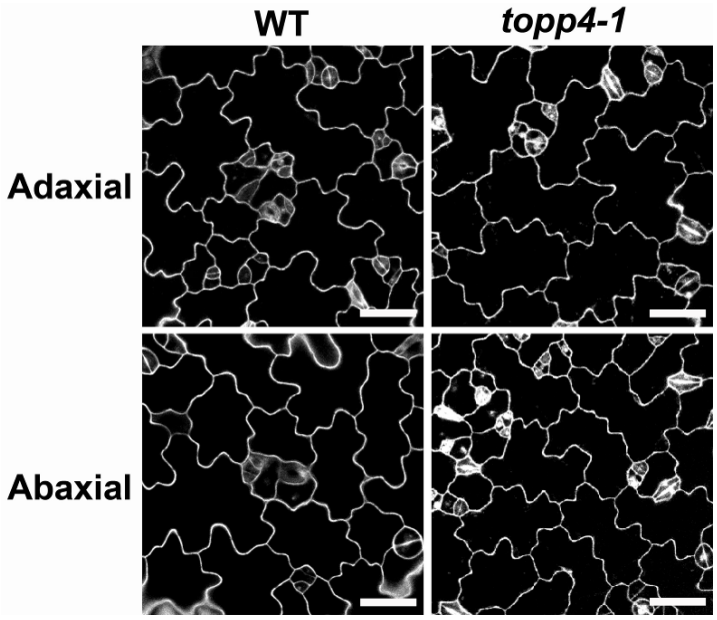
**Supplemental Data**



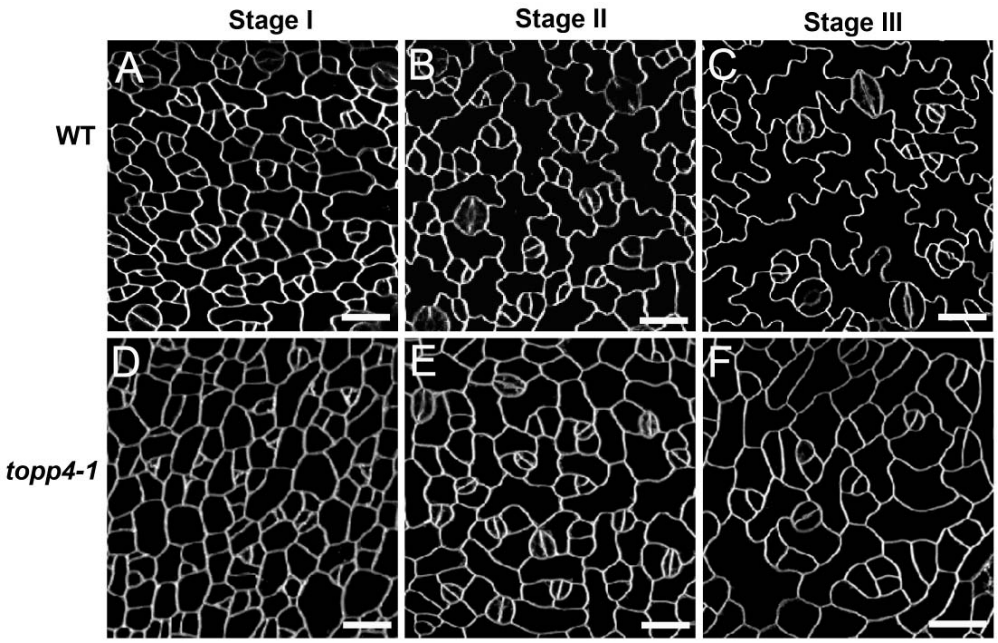

**Supplemental Figure S1.** Tissue-specific expression of TOPP4 protein. We found that TOPP4 is expressed in leaf PCs using the *TOPP4:TOPP4-GFP* transgenic line. (A) Wild-type control, (B) *TOPP4:TOPP4-GFP* transgenic line. Scale bar = 40 μm.



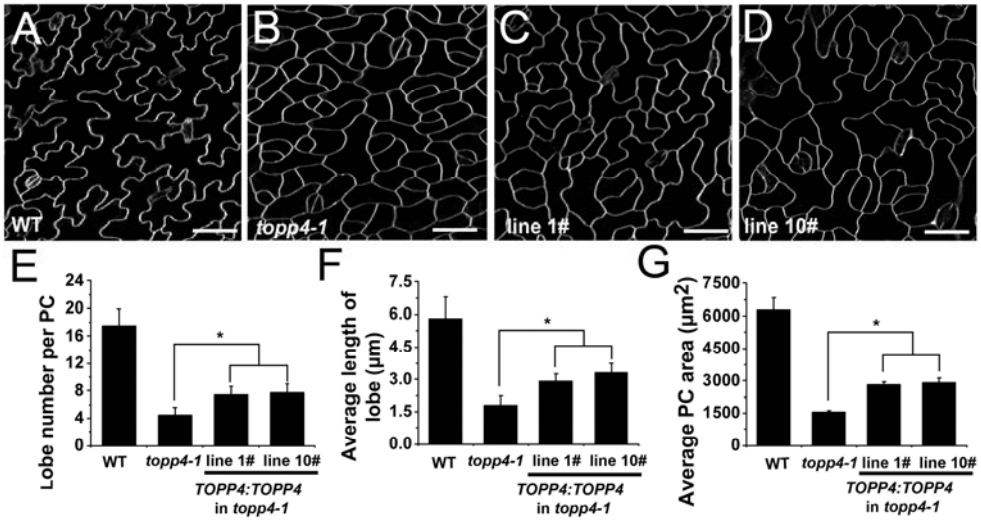

**Supplemental Figure S2.** The rosette leaf phenotypes of *topp4-1*.
(A) The rosette leaves excised from 21-day-old wild-type plants and *topp4-1* mutants. Scale bar = 1 cm.
(B) and (C) Semi-thin transverse sections of the third leaves showed that more cells were formed in *topp4-1* compared to wild type. Scale bars = 10 μm.
(D) Quantitative analyses of the third leaf area.
(E) Quantitative analyses of the PC area. Asterisks in (D) and (E) represent statistic difference from wild type based on Student's *t* test with $P < 0.01$. Error bars represent SE (n = 100).




**Supplemental Figure S3.** The cotyledon PCs show normal shape in *topp4-1*. Scale bars = 50 μm.




**Supplemental Figure S4.** Effect of *TOPP4* mutation on PC development at different stages.
(A) –(C) Wild-type PCs on the adaxial leaf side.
(D) –(F) The *topp4-1* PCs on the adaxial leaf side. Scale bars = 50 μm.



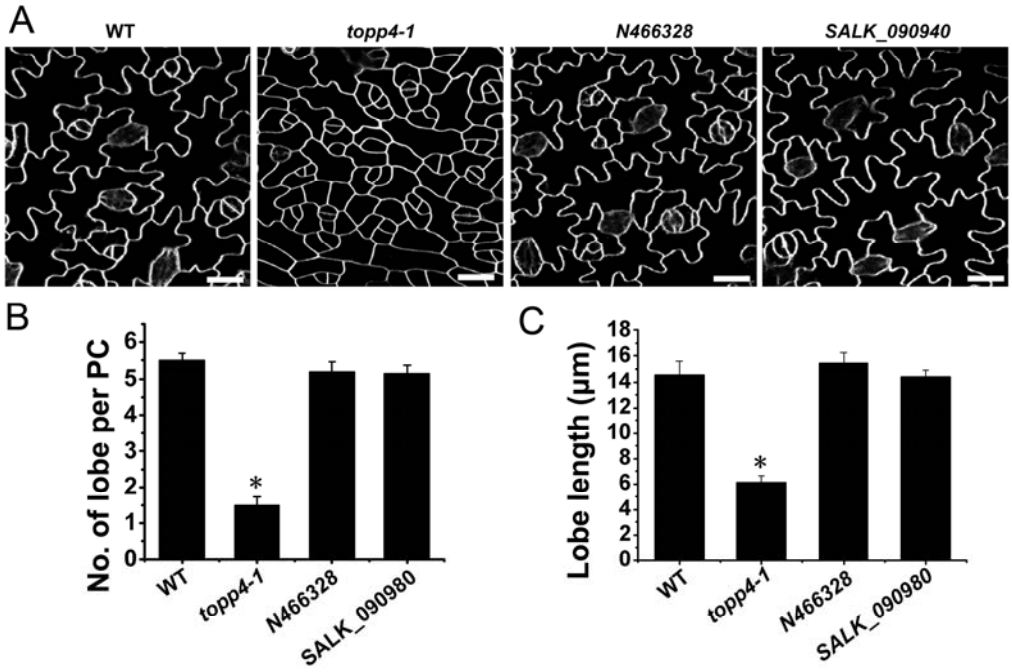

**Supplemental Figure S5.** Transformed *TOPP4:TOPP4* into the *topp4-1* mutant slightly rescues the mutant phenotype.

(A)–(D) The *topp4-1* mutant was transformed with *TOPP4* driven by its native promoter. The adaxial sides of the third leaves in two transgenic lines (1# and 10#) displayed shallower lobe PCs compared to wild type.

(E) and (F) Quantitative analyses of lobe number (E) and lobe length (F) in wild type, *topp4-1*, and line 1# and 10#.

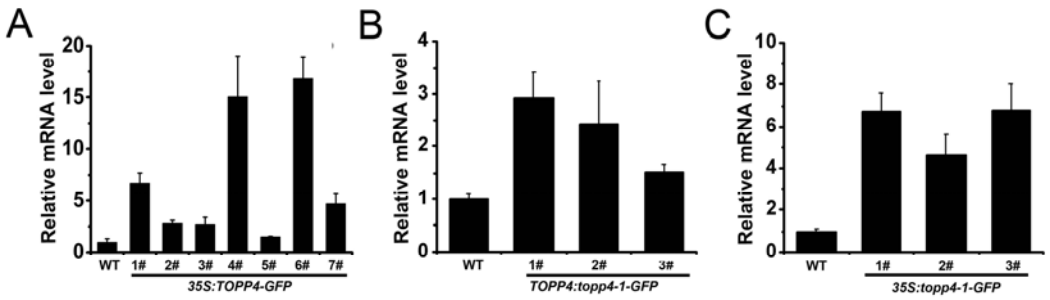
(G) Quantitative analyses of the PC area in wild type, *topp4-1*, and line 1# and 10#.

Asterisks in (E)−(G) represent statistic differences from the *topp4-1* mutant based on Student's *t* test with $P < 0.05$. Error bars represent SE (n = 100).

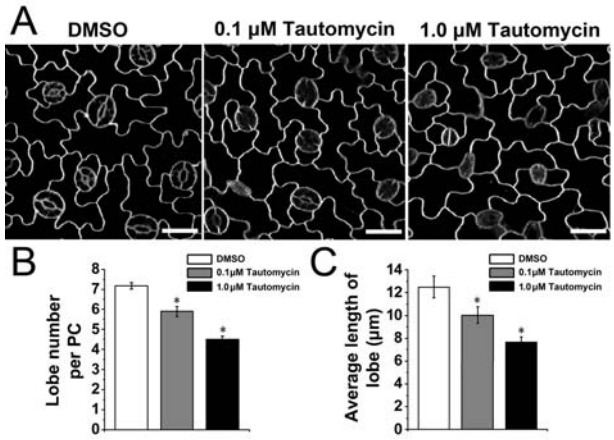



**Supplemental Figure S6.** Phenotype analysis of two T-DNA insertion alleles of *TOPP4*. (A) PCs on the adaxial leaf side in wild type, *topp4-1* and two T-DNA insertion lines of *TOPP4*. Scale bars = 25 μm.

(B) and (C) Quantitative analyses of the lobe number (E) and lobe length (F) in wild type, *topp4-1* and two T-DNA insertion lines of *TOPP4*. Asterisk represents statistic difference from wild type based on Student's *t* test with $P < 0.01$. Error bars represent SE (n = 100).

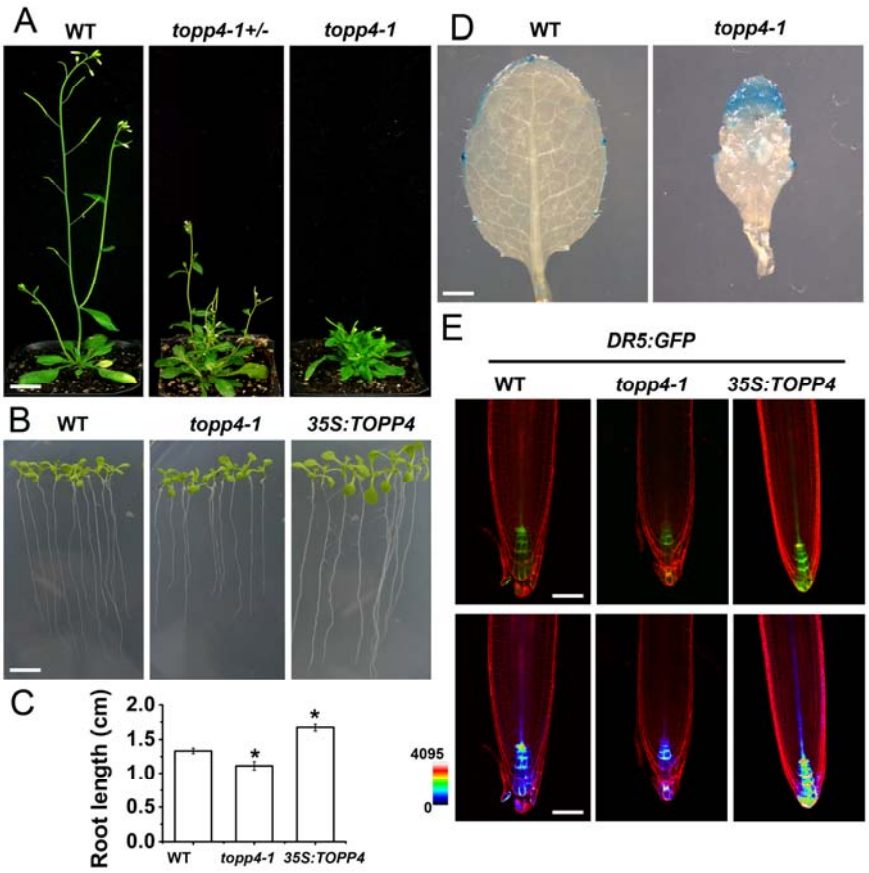



**Supplemental Figure S7.** The *TOPP4/topp4-1* expression levels of the *35S:TOPP4*, *TOPP4:topp4-1-GFP*, or *35S:topp4-1-GFP* transgenic plants.
(A)The relative expression levels of the *TOPP4* in seven *35S:TOPP4* transgenic lines.
(B)The relative expression levels of the *topp4-1/TOPP4* in three *TOPP4:topp4-1-GFP* transgenic lines.
(C) The relative expression levels of the *topp4-1/TOPP4* in three *35S:topp4-1-GFP* transgenic lines. The expression level of *TOPP4* in wild type in (A)−(C) was set to 1.0.

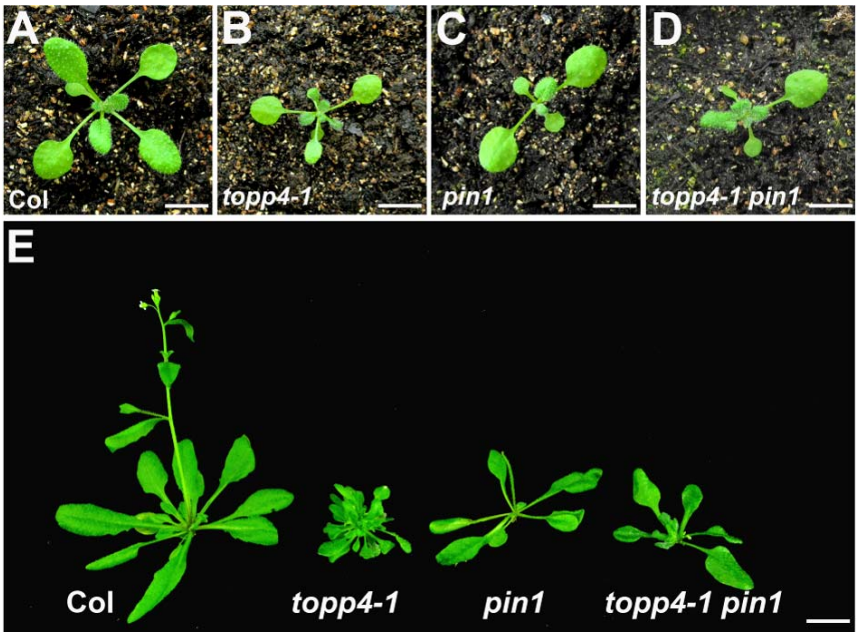



**Supplemental Figure S8.** Inhibition of PP1 partially repressed interdigitated growth of PCs.

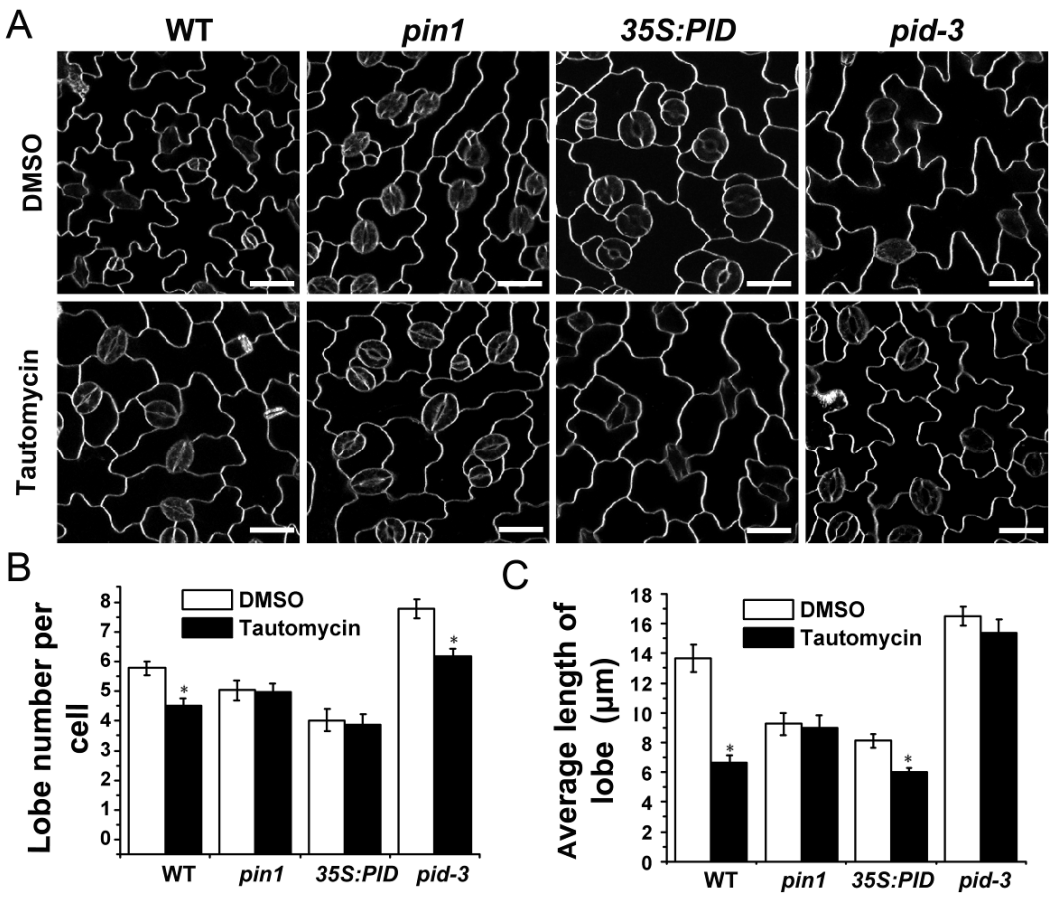
**(A)** The PC shape of adaxial sides of the third leaves. Scale bars = 25 μm.
**(B)** and **(C)** Quantitative analyses of lobe number (B) and lobe length (C) of PC. Asterisks represent statistic differences from the control based on Student's *t* test with $P < 0.01$. Error bars represent SE (n = 100).




**Supplemental Figure S9.** The *topp4-1* mutant shows auxin-related defects.
(A) Morphology of 6-week-old wild-type, heterozygous *topp4-1*+/- and homozygous *topp4-1* seedlings. The homozygous *topp4-1* showed a lack of apical dominance and more lateral branching than wild type. Scale bar = 1.5 cm.
(B) and (C) Length of primary root on 1/2 MS medium. Scale bar = 0.5 cm. Asterisk represents statistic difference from wild type based on Student's *t* test with $P < 0.05$. Error bars represent SE (n = 30).
(D) The expression of the DR5-GUS signal in leaves of wild-type and *topp4-1* plants. Scale bar = 0.2 cm.
(E) The expression of the DR5-GFP signal in roots of wild-type, *topp4-1* and *35S:TOPP4* plants. Scale bars = 50 μm.



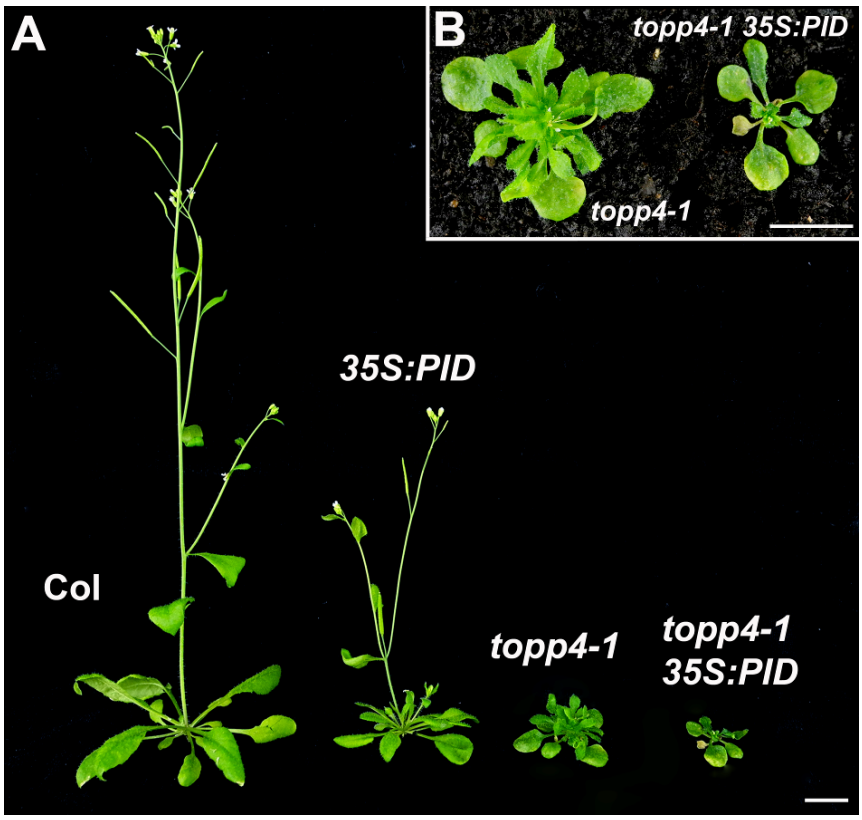

**Supplemental Figure S10.** The phenotype of *topp4-1 pin1* double mutants.
(A)–(D) The leaf phenotype of 21-day-old seedlings of wild-type (A), *topp4-1* (B), *pin1* (C) and *topp4-1 pin1* (D) plants. Scale bars = 1 cm.
(E) The phenotype of 6-week-old seedlings of wild-type, *topp4-1*, *pin1* and *topp4-1 pin1* plants. Scale bar = 0.5 cm.




**Supplemental Figure S11.** Effect of tautomycin on PC shape in wild-type, *pin1*, *35S:PID* and *pid-3* plants.

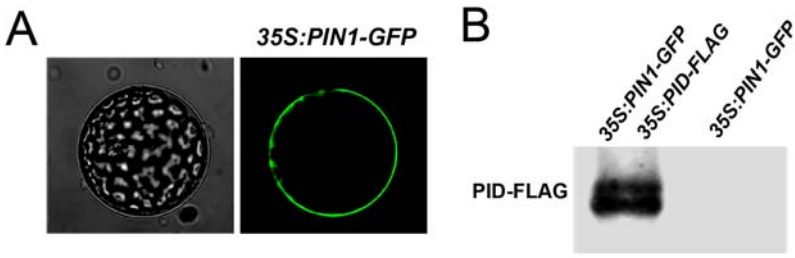
(A) PCs on the adaxial side in wild-type, *pin1*, *35S:PID*, and *pid-3* plants treated with 1.0 μm tautomycin.

(B) Quantitative analyses of lobe number (B) and lobe length (C) of PCs in wild-type, *pin1*, *35S:PID*, and *pid-3* plants treated with 1.0 μm tautomycin. Asterisk represents statistic difference from control based on Student's *t* test with $P < 0.01$. Error bars represent SE (n = 100).

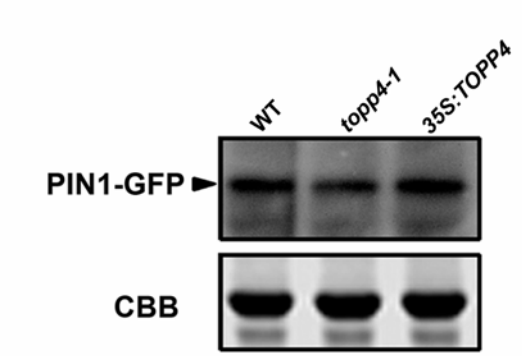



**Supplemental Figure S12.** The phenotype of *topp4-1 35S:PID* double mutants.
(A) Seven-week-old plants.
(B) Larger image of *topp4-1* and *topp4-1 35S:PID* plants. Scale bars = 0.5 cm.

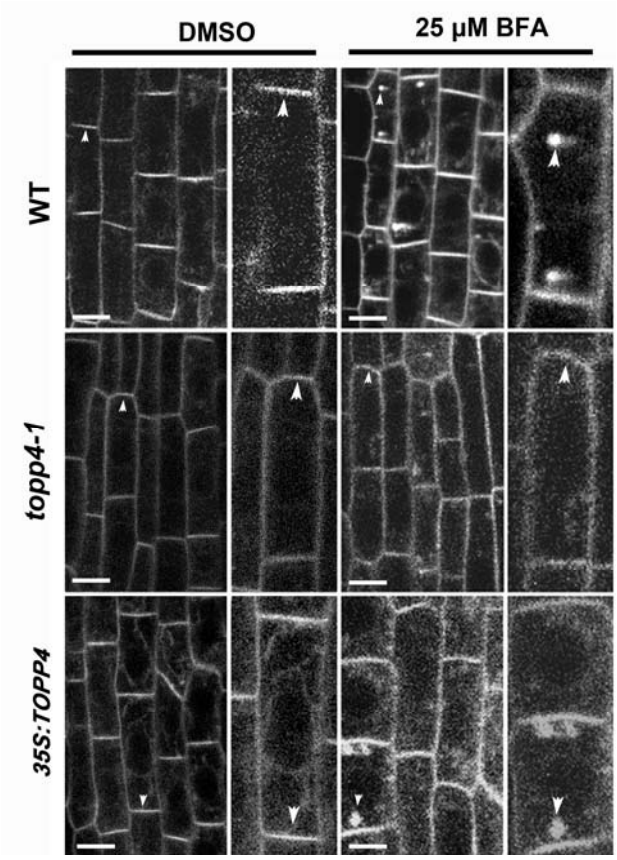

**Supplemental Figure S13.** The phenotype of two-month-old *topp4-1 pid-3* double mutants. Scale bar = 2 cm.



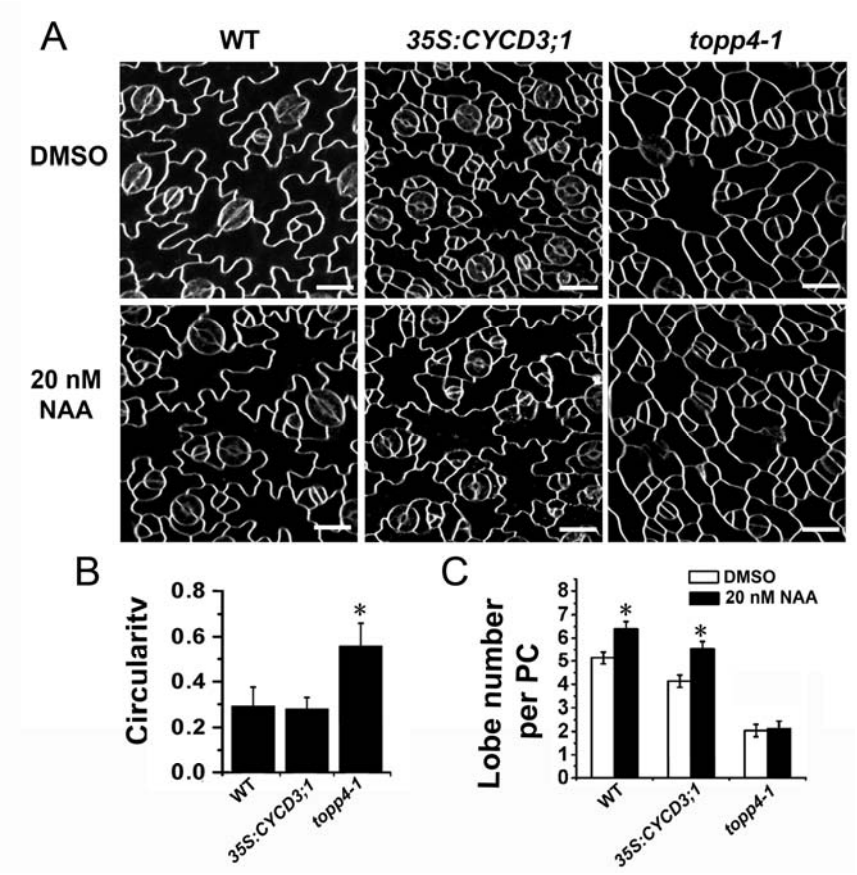

**Supplemental Figure S14.** Transient expression of *35S:PIN1-GFP* and *35S:PID-FLAG* in *Arabidopsis* protoplasts.
(A) Transient expression of *35S:PIN1-GFP* in *Arabidopsis* leaf protoplasts showed that PIN1-GFP is localized predominantly to the plasma membrane.
(B) Western blot demonstrating the PID-FLAG expression in protoplast extracts transfected with *35S:PIN1-GFP* and *35S:PID-FLAG* or without *35S:PID-FLAG* using anti-FLAG antibody.




**Supplemental Figure S15.** Immunoblot analyses of PIN1-GFP in wild-type, *topp4-1*, and *35S:TOPP4* plants expressing *PIN1:PIN1-GFP*.




**Supplemental Figure S16.** PIN1 internalization in root cells after BFA treatment. Arrowheads represent the most pronounced localization of PIN1 at the apical/basal cell side or in BFA bodies. Scale bars = 10 µm.

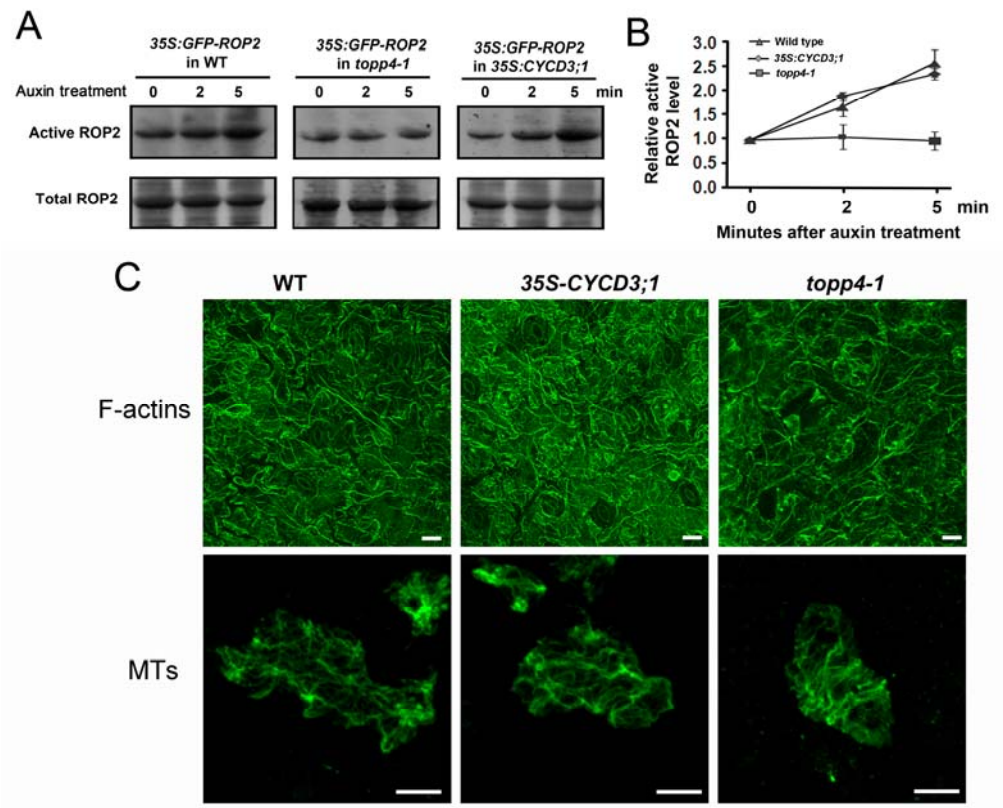



**Supplemental Figure S17.** The effect of exogenous auxin on the PC lobe formation in *35S:CYCD3;1*.

**(A)** PCs on the adaxial leaf side in wild-type, *35S:CYCD3;1* and *topp4-1* plants treated with DMSO or 20 nM NAA. Scale bars = 20 μm.

**(B)** The circularity values of PCs in wild-type, *35S:CYCD3;1* and *topp4-1* plants.

**(C)** Analyses of lobe number per PC in wild-type, *35S:CYCD3;1* and *topp4-1* plants treated with DMSO or 20 nM NAA. Asterisks in (B) and (C) represent statistic differences from wild type based on Student's *t* test with $P < 0.01$. Error bars represent SE (n = 100).




**Supplemental Figure S18.** The effect of auxin on ROP2 activity and the organization of cortical MTs and F-actins in *35S:CYCD3;1*.

**(A)** Measurements of GTP-bound ROP2 activity in wild-type, *35S:CYCD3;1* and *topp4-1* protoplasts transiently expressing *35S:GFP-ROP2*.

**(B)** Quantitative analyses of the relative active ROP2 activity. Error bars represent SE (n = 3).

**(C)** The organization of cortical MTs and F-Actins in the PCs of wild-type, *35S:CYCD3;1* and *topp4-1*. Scale bar= 20 μm.

**Supplemental Table S1.** Primers used for plasmid construction and qRT-PCR.

| Primer Name | Sequence |
|---|---|
| *pid-3*-F | TTAGCTAATGAGTATTTATTTTG |
| *pid-3*-R | AAGATTCAACGGCTGCG |
| *pin1*-F | CAAAAACACCCCCAAAATTTC |
| *pin1*-R | AATCATCACAGCCACTGATCC |
| *topp4-1*-F | ATGGCGACGACGACGAC |
| *topp4-1*-R | TCCTCCTCCAATCTTTGTG |
| *pA7:PIN1*-F | GCGTCGACATGATTACGGCGGCGGAC |
| *pA7:PIN1*-R | CGGGATCCTAGACCCAAGAGAATGTAG |
| *pA7:RIC1*-F | GTCGACATGGCGACGACAATGAAG |
| *pA7:RIC1*-R | GGATCCGATAATATCGTTACAGG |
| *pA7:RIC4*-F | GTCGACATGAGAGATAGAATGGAG |
| *pA7:RIC4*-R | GGATCCTAAAGTTGGATGAAGATG |
| *ROP2*-RT-F | CTGGTGTTCCCATTATCCTTG |
| *ROP2*-RT-R | CCTCTCCCTGGTTTGTAGTA |
| *ROP4*-RT-F | CACTTTCCCTACGGACTATG |
| *ROP4*-RT-R | CACGGTAACTCAACGGTCTT |
| *ROP6*-RT-F | CCACGGATTATGTGCCAACTG |
| *ROP6*-RT-R | ATCTGCACCGCGATAGCTCA |