

Fig. S1. Fine scale mapping of the *NOP* locus. 990 *ptl nop-1* mutant F2 plants from a cross between *ptl-3 pmd-1d nop-1 er* (in *Ler* background) and *ptl-1 PMD NOP ER* (in *Col* background) were scored for DNA markers on chromosome 2 lying between F13M22 and T16B24. The strand diagrams show the deduced two chromosomes of 43 plants with recombination detected in this interval (black represents the *Ler* derived strand; red represents the *Col*-derived strand). The *NOP* locus must lie between DNA markers F16M14-C1 and F16M14-C5.

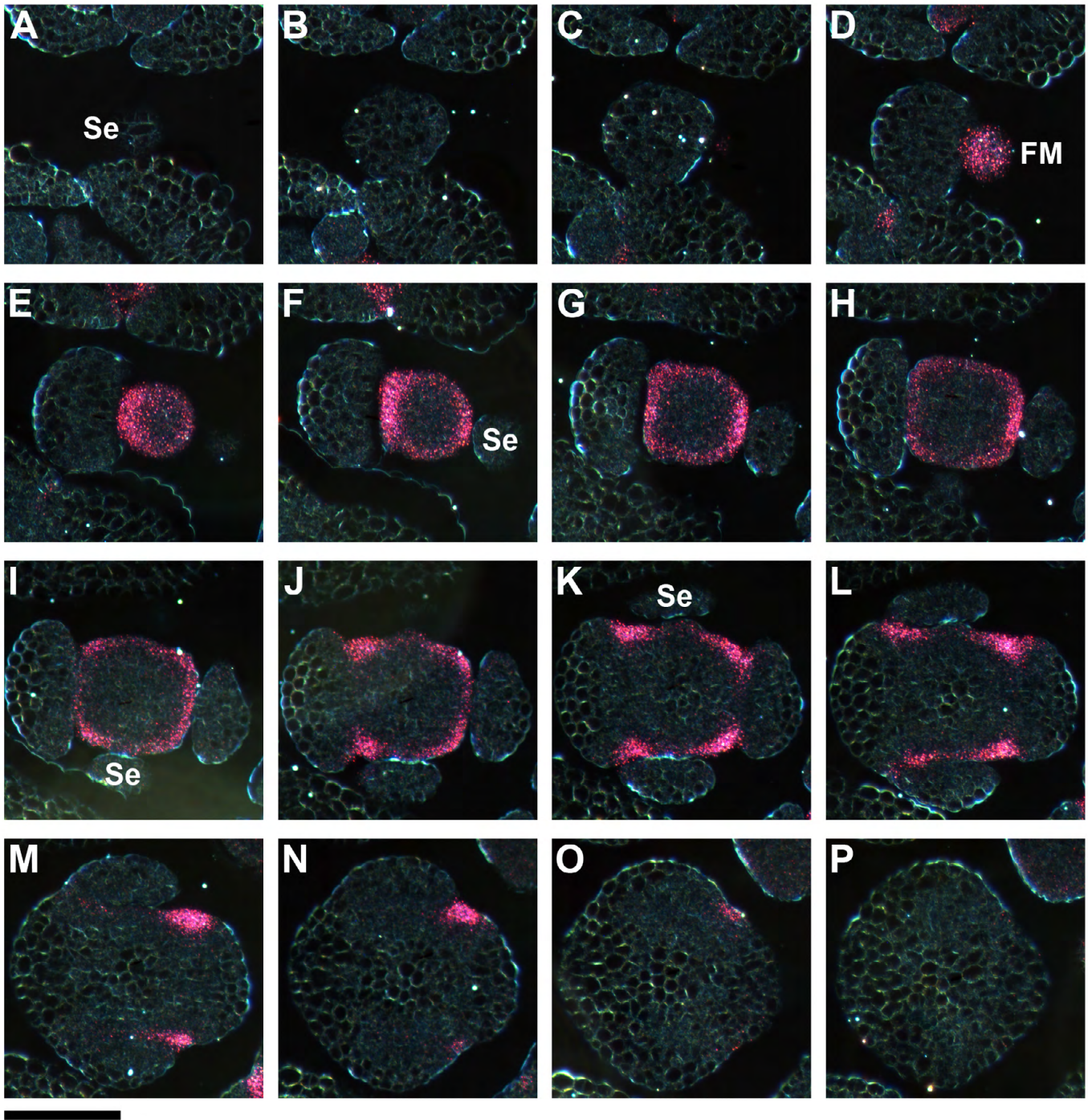


Fig. S2. pAUX1:GUS expression in serial transverse sections of a wild-type stage 4 bud. (A-P) Strong *AUX1* expression occurs in the epidermis of the floral meristematic dome (FM) and the inter-sepal zones (Se, sepals). (L) This panel is shown in Fig. 2. Scale bar: 50 μ m.

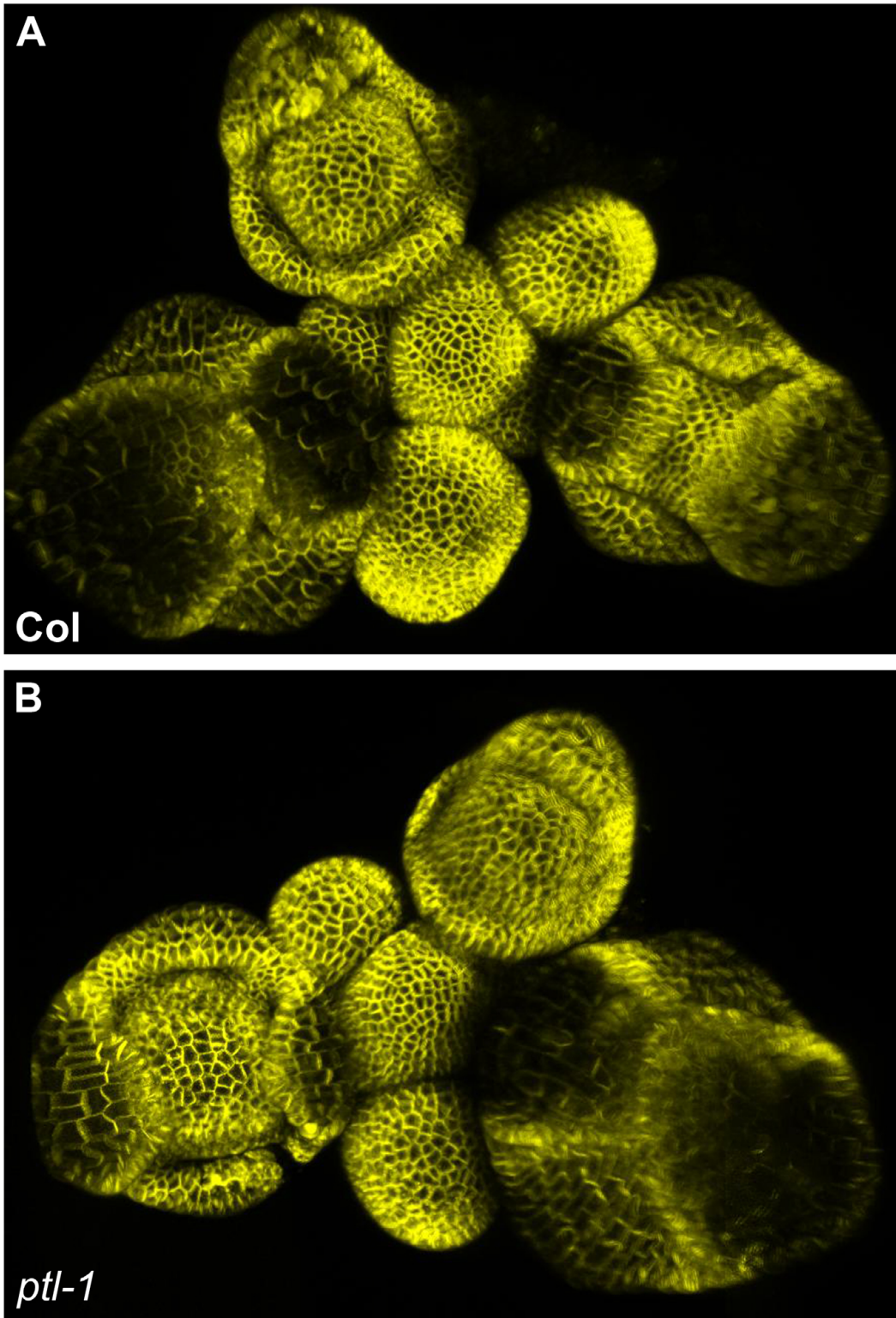


Fig. S3. pPIN1:PIN1-GFP expression in wild type and *ptl-1* mutant inflorescences. (A) Columbia wild type inflorescence. (B) *ptl-1* mutant inflorescence.

Table S1. DNA primers used

(A) For allele identification

| Gene | Primer | Sequence | Restriction enzyme | Product size (bp) | |
|------|--------------|---------------------------------|--------------------|-------------------|----------|
| | | | | | |
| AUX1 | A25F | 5'-TCTTTCTTGTAGAATGCGGCG-3' | Sau3AI | AUX1 | aux1-7 |
| | A26R | 5'-TCAAAGACGGTGGTGTAAAGC-3' | | 246 | 84, 162 |
| | A48F+600 | 5'-CATTTAATTGCACTTTCCTCTTGTT-3' | ApaI | AUX1 | aux1-21 |
| | A49R+1043 | 5'-CATATACTGTCACTCAATGCAAAG-3' | | 443 | 220, 223 |
| | A18F | 5'-AGCTTTGGATTTTGTCCATTAC-3' | TaqI | AUX1 | aux1-n1 |
| | A50+3206R | 5'-ACTTGACGAACAAAGTTGGTTACA-3' | | 250 | 39, 211 |
| AXR4 | axr4-144F | 5'-AAACACGCTCCTTGAATGATG-3' | - | AXR4 | axr4-1,2 |
| | axr4-2147R | 5'-TCCCAAAGAAAAATCTCAAAA-3' | | 2,291 | - |
| LAX1 | lx1-1 | 5'-ATATGGTTGCAGGTGGCACA-3' | - | LAX1 | lax1-1 |
| | lx1-2 | 5'-GTAACCGGCAAAAGCTGCA-3' | | 1,193 | - |
| LAX2 | lx2-3 | 5'-ACAGCTGGGGATGCTCTCA-3' | - | LAX2 | lax2-1 |
| | lx2-4 | 5'-TCAGCACGTAGAGTGTGCA-3' | | 1,193 | - |
| LAX3 | lx3-1 | 5'-TACTTCACCGGAGCCACCA-3' | - | LAX3 | lax3-1 |
| | lx3-2R | 5'-ACTTAGAAATGGAGAGGGAAGA-3' | | 1,043 | - |
| PTL | ptl-30F P1 | 5'-TCTCTTTCGGCTGAATATAAATCTG-3' | HaeIII | PTL | ptl-1 |
| | ptl+498R P1 | 5'-ATTAGGGTAAAATCGAGAGAGGAGA-3' | | 138, 390 | 528 |
| | ptl+1624 P3 | 5'-GAAGAAATGCAGAGAGAAGTTTGAG-3' | - | PTL | ptl-3 |
| | ptl+2315R P3 | 5'-ATTGTTTCGGATCTCATTATTACCA-3' | | 691 | 599 |
| RBE | rbe+74F | 5'-CTTTATTTGGCCGTTTAGGG-3' | - | RBE | rbe-2 |
| | rbe+1105R | 5'-GGAGTTCACATGGAATACCAGAC-3' | | 1,031 | 959 |
| | Lbb1.3 | 5'-ATTTTGCCGATTCGGAAC-3' | | | |

(B) For insert generation

| Construct | Primer | Sequence* | Substrate | Size (bp) |
|-------------------|--------------|---------------------------------------|-----------|-----------|
| pPTL(FI313):iaaH | iaah-bamhi-F | 5'-ttaggatccATGGTGGCCATTACCTCGTTA-3' | TOPO-iaaH | 1,404 |
| | iaah-xbai-R | 5'-atgtctagaTTAATTGGGTAAACCGGC AAA-3' | | |
| pPTL(FI313):AUX1 | aux1-bamhi-F | 5'-agcggatccATGTCGGAAGGAGTAGAAGCG-3' | F16M14 | 4,188 |
| | aux1-ncoi-R | 5'-tgccatggTCAAAGACGGTGGTGTAAAGC-3' | | |
| pAUX1(3.67bp):GUS | A33F-3770 | 5'-TGTTTCATAGTGCGCATGTTTC-3' | F16M14 | 3,770 |
| | Am32R+7 | 5'-CCGggATcTTTTAGCTTCTAGATCTGAG-3' | | |

*Lower case represents added restriction sites

(C) For confirmation of inserts in T1 plants

| Construct | Primer | Sequence |
|-------------------|---------------|-----------------------------------|
| pPTL(FI313):iaaH | ptl-30F P1 | 5'-TCTCTTTTCGGCTGAATATAAAATCTG-3' |
| | 3'OCSR | 5'-CATGCGATCATAGGCGTCTC-3' |
| pPTL(FI313):AUX1 | ptl-30F P1 | 5'-TCTCTTTTCGGCTGAATATAAAATCTG-3' |
| | A49R+1043 | 5'-CATATACTGTACCTCAATGCAAAG-3' |
| pAUX1(3.67bp):GUS | A01F-525 | 5'-AAAGGAGGAGTAGGGGTGA-3' |
| | GUS84R | 5'-ACAGTTTTTCGCGATCCAGAC-3' |
| | | |

Table S2. Mean number of floral organs per flower in single and double mutant combinations of *ptl-3* and *nop-1* (*aux1-n1*) or *nop-2* (*aux1-n2*)

| | Mean number of organs per flower \pm s.e.m. | | | |
|--------------------------------|---|-----------------|-----------------|-----------------|
| | Sepals | Petals | Stamens | Carpels |
| Ler n=72 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>nop-1</i> n=72 | 4.00 \pm 0.00 | 3.93 \pm 0.03 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>nop-2</i> n=72 | 4.00 \pm 0.00 | 3.82 \pm 0.05 | 5.86 \pm 0.06 | 2.00 \pm 0.06 |
| <i>ptl-3</i> n=48 | 4.01 \pm 0.01 | 6.29 \pm 0.18 | 6.01 \pm 0.01 | 2.00 \pm 0.01 |
| <i>ptl-3 nop-1</i> n=72 | 4.00 \pm 0.00 | 0.44 \pm 0.09 | 5.97 \pm 0.03 | 2.00 \pm 0.03 |
| <i>ptl-3 nop-2</i> n=72 | 3.89 \pm 0.05 | 0.11 \pm 0.04 | 5.83 \pm 0.07 | 2.00 \pm 0.07 |

The first six flowers of the indicated number of plants (*n*) were scored.

Table S3. Mean number of floral organs per flower in single and double mutant combinations of *ptl-1* and *aux1-7* or *aux1-21*

| | Mean number organs per flower \pm s.e.m. | | | |
|----------------------------------|--|-----------------|-----------------|-----------------|
| | Sepals | Petals | Stamens | Carpels |
| Col n=60 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>aux1-7</i> n=60 | 4.00 \pm 0.00 | 3.93 \pm 0.03 | 5.88 \pm 0.06 | 2.00 \pm 0.00 |
| <i>aux1-21</i> n=72 | 3.92 \pm 0.04 | 3.79 \pm 0.05 | 5.81 \pm 0.07 | 2.00 \pm 0.00 |
| <i>ptl-1</i> n=60 | 4.00 \pm 0.00 | 2.30 \pm 0.11 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>ptl-1 aux1-7</i> n=72 | 4.00 \pm 0.00 | 0.11 \pm 0.04 | 5.82 \pm 0.06 | 2.00 \pm 0.00 |
| <i>ptl-1 aux1-21</i> n=72 | 3.89 \pm 0.04 | 0.00 \pm 0.00 | 5.85 \pm 0.06 | 2.00 \pm 0.00 |

The first six flowers of the indicated number of plants (*n*) were scored.

Table S4. Mean number of floral organs per flower in single and multiple mutant combinations of *aux1-21*, *lax1-1*, *lax2-1* and *lax3-1*

| | Mean number organs per flower \pm s.e.m. | | | |
|---|--|-----------------|-----------------|-----------------|
| | Sepals | Petals | Stamens | Carpels |
| Col n=72 | 4.00 \pm 0.00 | 3.99 \pm 0.01 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>aux1-21</i> n=119 | 4.00 \pm 0.00 | 3.98 \pm 0.01 | 5.79 \pm 0.05 | 2.00 \pm 0.00 |
| <i>lax1</i> n=84 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 5.86 \pm 0.05 | 2.00 \pm 0.00 |
| <i>lax2</i> n=72 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>lax3</i> n=72 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>aux1-21 lax1</i> n=95 | 4.00 \pm 0.00 | 3.72 \pm 0.06 | 4.84 \pm 0.12 | 2.00 \pm 0.00 |
| <i>aux1-21 lax2</i> n=71 | 4.00 \pm 0.00 | 3.94 \pm 0.03 | 5.63 \pm 0.08 | 2.00 \pm 0.00 |
| <i>aux1-21 lax3</i> n=72 | 4.00 \pm 0.00 | 3.97 \pm 0.02 | 5.51 \pm 0.09 | 2.00 \pm 0.00 |
| <i>aux1-21 lax2 lax3</i> n=72 | 4.00 \pm 0.00 | 3.96 \pm 0.03 | 5.63 \pm 0.09 | 2.00 \pm 0.00 |
| <i>aux1-21 lax1 lax2</i> n=59 | 4.00 \pm 0.00 | 3.63 \pm 0.10 | 4.17 \pm 0.18 | 2.00 \pm 0.00 |
| <i>aux1-21 lax1 lax3</i> n=54 | 4.00 \pm 0.00 | 3.70 \pm 0.07 | 4.53 \pm 0.16 | 2.00 \pm 0.00 |
| <i>aux1-21 lax ;lax2 lax3</i> n=60 | 3.90 \pm 0.06 | 3.65 \pm 0.09 | 4.34 \pm 0.17 | 2.00 \pm 0.00 |

The first six flowers of the indicated number of plants (*n*) were scored.

Table S5. Restoration of petals in *ptl* mutant plants by a pPTL:iaaH transgene

| Genotype | Construct | Number of independent lines | Mean number of organs per flower \pm s.e.m. | | | |
|--------------|------------------|-----------------------------|---|-----------------|-----------------|-----------------|
| | | | Sepals | Petals | Stamens | Carpels |
| Col | Nil | 10 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| Col | pPTL(FI313):iaaH | 10 | 4.00 \pm 0.00 | 4.01 \pm 0.01 | 5.96 \pm 0.02 | 2.00 \pm 0.00 |
| <i>ptl-1</i> | Nil | 10 | 4.00 \pm 0.00 | 1.45 \pm 0.11 | 5.99 \pm 0.01 | 2.00 \pm 0.00 |
| <i>ptl-1</i> | pPTL(FI313):iaaH | 7 | 4.00 \pm 0.00 | 3.33 \pm 0.10 | 5.93 \pm 0.04 | 2.00 \pm 0.00 |

The mean number of floral organs per flower in flowers 1-12 of T1 plants carrying the pPTL(FI313):iaaH transgene in either Col or *ptl-1* are shown. Controls without the transgene are also shown.

Table S6. Restoration of petals in *ptl aux1* mutant plants by a pPTL:AUX1 transgene

| Genotype | Construct | Number of independent lines | Mean number organs per flower \pm s.e.m | | | |
|----------------------|------------------|-----------------------------|---|-----------------|-----------------|-----------------|
| | | | Sepals | Petals | Stamens | Carpels |
| Col | Nil | 10 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| Col | pPTL(FI313):AUX1 | 7 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>ptl-1</i> | Nil | 10 | 4.00 \pm 0.00 | 1.45 \pm 0.11 | 5.99 \pm 0.01 | 2.00 \pm 0.00 |
| <i>ptl-1 aux1-7</i> | Nil | 10 | 4.00 \pm 0.00 | 0.07 \pm 0.02 | 5.99 \pm 0.01 | 2.00 \pm 0.00 |
| <i>ptl-1 aux1-7</i> | pPTL(FI313):AUX1 | 9 | 4.02 \pm 0.01 | 0.99 \pm 0.10 | 5.99 \pm 0.01 | 2.00 \pm 0.00 |
| Ler | Nil | 10 | 4.02 \pm 0.01 | 4.01 \pm 0.01 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| Ler | pPTL(FI313):AUX1 | 7 | 4.01 \pm 0.01 | 4.01 \pm 0.01 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>ptl-3</i> | Nil | 10 | 4.02 \pm 0.01 | 5.36 \pm 0.15 | 5.95 \pm 0.03 | 2.00 \pm 0.00 |
| <i>ptl-3 aux1-n1</i> | Nil | 10 | 4.01 \pm 0.01 | 0.23 \pm 0.04 | 5.93 \pm 0.03 | 2.00 \pm 0.00 |
| <i>ptl-3 aux1-n1</i> | pPTL(FI313):AUX1 | 12 | 4.01 \pm 0.01 | 2.05 \pm 0.15 | 5.97 \pm 0.02 | 2.00 \pm 0.00 |

The mean number of floral organs per flower in flowers 1-12 of T1 plants carrying the pPTL(FI313):AUX1 transgene in either Col or *ptl-1 aux1-7*, and in either Ler or *ptl-3 aux1-n1*, are shown. Controls without the transgene are also shown.

Table S7. Mean number of floral organs per flower in single and double mutant combinations of *ptl-1* and *axr4-1* or *axr4-2*

| | Mean number organs per flower \pm s.e.m. | | | |
|---------------------------------|--|-----------------|-----------------|-----------------|
| | Sepals | Petals | Stamens | Carpels |
| <i>Col</i> n=72 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>ptl-1</i> n=54 | 4.00 \pm 0.00 | 2.31 \pm 0.13 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>axr4-1</i> n=72 | 4.00 \pm 0.00 | 3.90 \pm 0.04 | 5.26 \pm 0.10 | 2.00 \pm 0.00 |
| <i>axr4-2</i> n=72 | 4.00 \pm 0.00 | 3.93 \pm 0.03 | 5.76 \pm 0.06 | 2.00 \pm 0.00 |
| <i>ptl-1 axr4-1</i> n=72 | 4.00 \pm 0.00 | 0.11 \pm 0.04 | 5.57 \pm 0.09 | 2.00 \pm 0.00 |
| <i>ptl-1 axr4-2</i> n=63 | 4.00 \pm 0.00 | 0.16 \pm 0.05 | 5.51 \pm 0.11 | 2.00 \pm 0.00 |

The first six flowers of the indicated number of plants (*n*) were scored

Table S8. Mean number of floral organs per flower in single and double mutant combinations of *ptl-1* and *rbe-2*, or *aux1-7* and *rbe-2*

| | Mean number organs per flower \pm s.e.m. | | | |
|---|--|-----------------|-----------------|-----------------|
| | Sepals | Petals | Stamens | Carpels |
| Col <i>n</i>=72 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>ptl-1</i> <i>n</i>=54 | 4.00 \pm 0.00 | 2.31 \pm 0.13 | 6.00 \pm 0.00 | 2.00 \pm 0.00 |
| <i>rbe-2</i> <i>n</i>=54 | 4.00 \pm 0.00 | 2.02 \pm 0.10 | 5.96 \pm 0.03 | 2.00 \pm 0.00 |
| <i>ptl-1 rbe-2</i> <i>n</i>=66 | 4.00 \pm 0.00 | 2.22 \pm 0.08 | 5.98 \pm 0.02 | 2.00 \pm 0.00 |
| <i>aux1-7</i> <i>n</i>=168 | 4.00 \pm 0.00 | 3.96 \pm 0.02 | 5.83 \pm 0.04 | 2.00 \pm 0.00 |
| <i>aux1-7 rbe-2</i> <i>n</i>=118 | 4.00 \pm 0.00 | 0.22 \pm 0.04 | 5.88 \pm 0.04 | 2.00 \pm 0.00 |

The first six flowers of the indicated number of plants (*n*) were scored.

Table S9. Mean number of floral organs per flower in mutant combinations of *ptl* with *pin1*, *pid* or *pin1 aux1*

| Genotype All <i>pmd-1d</i> except Col strains* | Number of flowers | Mean number organs per flower \pm s.e.m. | | |
|---|-------------------------|--|-----------------|-----------------|
| | | Sepals | Petals | Stamens |
| <i>PIN-FORMED1</i> | | | | |
| Ler | 95 | 4.00 \pm 0.00 | 4.00 \pm 0.00 | 5.91 \pm 0.00 |
| <i>ptl-3</i> | 85 | 4.01 \pm 0.01 | 5.22 \pm 0.14 | 5.99 \pm 0.01 |
| <i>pin1-3</i> | 28 | 8.11 \pm 0.78 | 7.39 \pm 0.77 | 0.18 \pm 0.16 |
| <i>ptl-3 pin1-3</i> | 16 | 8.19 \pm 1.32 | 1.13 \pm 0.41 | 1.31 \pm 0.53 |
| <i>pin1-5</i> | 37 | 5.45 \pm 0.13 | 6.43 \pm 0.26 | 0.89 \pm 0.15 |
| <i>ptl-3 pin1-5</i> | 30 | 5.33 \pm 0.14 | 2.83 \pm 0.18 | 2.43 \pm 0.27 |
| <i>PINOID</i> | | | | |
| <i>pid-1</i> | 43 | 4.51 \pm 0.15 | 6.51 \pm 0.27 | 2.65 \pm 0.28 |
| <i>ptl-3 pid-1</i> | 86 | 4.29 \pm 0.10 | 1.28 \pm 0.15 | 4.18 \pm 0.13 |
| Col* | 25 | 4.00 \pm 0.00 | 4.03 \pm 0.03 | 5.93 \pm 0.05 |
| <i>ptl-1*</i> | 25 | 4.00 \pm 0.00 | 2.60 \pm 0.20 | 6.00 \pm 0.00 |
| <i>pid-3*</i> | 81 | 5.22 \pm 0.21 | 7.47 \pm 0.52 | 3.01 \pm 0.35 |
| <i>ptl-1 pid-3*</i> | 69 | 4.53 \pm 0.18 | 2.20 \pm 0.31 | 5.10 \pm 0.31 |
| <i>AUXIN1 PIN-FORMED1</i> | | | | |
| <i>aux-n1</i> | 80 | 4.00 \pm 0.00 | 3.95 \pm 0.02 | 5.51 \pm 0.08 |
| <i>aux1-n1 pin1-3</i> | 11 | 6.00 \pm 0.50 | 7.55 \pm 0.41 | 0.27 \pm 0.19 |
| <i>aux1-n1 ptl-3</i> | 60 | 4.02 \pm 0.02 | 0.78 \pm 0.10 | 5.67 \pm 0.07 |
| <i>aux1-n1 pin1-3 ptl-3</i> | 12 | 6.25 \pm 0.30 | 0.42 \pm 0.19 | 0.67 \pm 0.19 |
| <i>aux1-n1 pin1-5</i> | 45 | 4.18 \pm 0.11 | 5.09 \pm 0.21 | 0.71 \pm 0.13 |
| <i>aux1-n1 pin1-5 ptl-3</i> | 31 | 4.48 \pm 0.20 | 0.06 \pm 0.04 | 1.00 \pm 0.18 |

*PMD

Fourth whorl organs were severely disrupted in many genotypes; numbers were not scored.

Table S10. Deduced genes lying between DNA markers F16M14-C1 and F16M14-C5.

| Location | Locus | Gene Model | Description |
|-------------------|-----------|---------------|--|
| 15972993-15977180 | AT2G38120 | <i>AUX1</i> | Auxin influx transporter. |
| 15978512-15980749 | AT2G38130 | <i>ATMAK3</i> | <i>Arabidopsis</i> homolog of the yeast protein MAK3, a component of the N-terminal acetyltransferase complex C. |
| 15980883-15981612 | AT2G38140 | <i>PSRP4</i> | Plastid-specific ribosomal protein 4 (PSRP4) mRNA. |
| 15981700-15982917 | AT2G38150 | AT2G38150 | Putative transferase involved in transferring glycosyl groups. |
| 15986643-15988522 | AT2G38160 | AT2G38160 | Unknown protein (best <i>Arabidopsis</i> protein match is AT2G40070 (also an unknown protein)). |
| 15989083-15993276 | AT2G38170 | <i>CAX1</i> | High affinity vacuolar calcium antiporter. |
| 15997114-15998906 | AT2G38180 | AT2G38180 | GDSL-motif lipase/hydrolase family protein. |

Table S11. DNA primers used for positional cloning of *NOP*

| Primer Name | Coordinates (kbp) | Sequence | Type | Notes |
|----------------|-------------------|-----------------------------------|------|---|
| CIW2 F | 1,194,606 | 5'-CCCAAAGTTAATTATACTGT-3' | SSLP | 15 bp deletion in Ler |
| CIW2 R | 1,194,710 | 5'-CCGGGTTAATAATAAATGT-3' | | |
| CIW3 F | 6,402,846 | 5'-GAAACTCAATGAAATCCACTT-3' | SSLP | 30 bp deletion in Ler |
| CIW3 R | 6,403,081 | 5'-TGAACCTGTTGTGAGCTTTGA-3' | | |
| F13M22 F | 15,769,483 | 5'-TTCTTCTTGCTTAGCATGTTCTTG-3' | SSLP | 12 bp deletion in Ler |
| F13M22 R | 15,769,678 | 5'-CCCCTCCATTAGGATG-3' | | |
| T8P21 F | 15,829,952 | 5'-AACTTGGATTTATTGACATGATGTTT-3' | SSLP | 9 bp deletion in Ler |
| T8P21 R | 15,830,155 | 5'-CAGTAACATTGAAAAACAAAAGAC-3' | | |
| F16M14 - C1 F | 15,960,540 | 5'-ATGTTGGAAGCTGAGCCTGT-3' | CAPS | <i>HincII</i> cleavage site lost in Ler |
| F16M14 - C1 R | 15,960,789 | 5'-GGCAACTGTAGCCATTTGAA-3' | | |
| F16M14 - III F | 15,989,704 | 5'-CAATGAACGTGAAGACCAAATG-3' | SSLP | 10 bp deletion in Ler |
| F16M14 - III R | 15,989,908 | 5'-CGCCAAAACCGAAAAATAAC-3' | | |
| F16M14 - C5 F | 16,000,894 | 5'-TGTTGTCTTTGTATACTTCACATTGAT-3' | CAPS | <i>TspRI</i> cleavage site lost in Ler |
| F16M14 - C5 R | 16,001,135 | 5'-CTTCATCGACCACAAGCTGA-3' | | |
| T19C21 F | 16,102,876 | 5'-TGAATGCCTTTGCTCACAGT-3' | SSLP | 19 bp deletion in Ler |
| T19C21 R | 16,103,085 | 5'-GCCAGTCTTCCAATGCCTA-3' | | |
| NGA168 F | 16,291,841 | 5'-TCGTCTACTGCACTGCCG-3' | SSLP | 16 bp deletion in Ler |
| NGA168 R | 16,291,991 | 5'-GAGGACATGTATAGGAGCCTCG-3' | | |
| T16B24 F | 16,422,953 | 5'-TTGACACTTTCGCGTAGAAC-3' | SSLP | 14 bp deletion in Ler |
| T16B24 R | 16,423,101 | 5'-AAC AAGCTATTGGTGATGAACG-3' | | |