PNAS

Supporting Information for

Genetic robustness control of auxin output in priming organ initiation

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Figures S1 to S22

Table S1

SUPPLEMENTAL FIGURES

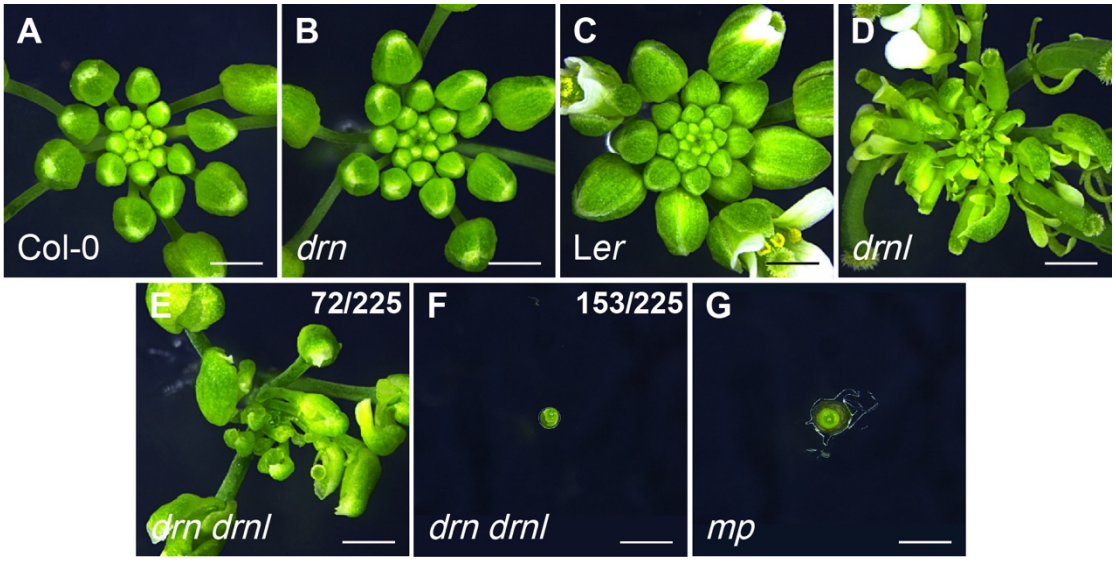


Fig. S1. The *drn drnl* and *mp* mutants have severe defects in lateral organ initiation. Top views of the inflorescences of six-week-old Col-0 (*A*), *drn* (*B*), L*er* (*C*), *drnl* (*D*), *mp* (*G*) and *drn drnl* (*E*, *F*) plants. The number of *drn drnl* mutants with different phenotypes are indicated (*E*, *F*); n ≥ 12 shoot apexes per genotype were observed with similar results. Scale bars, 1 mm.

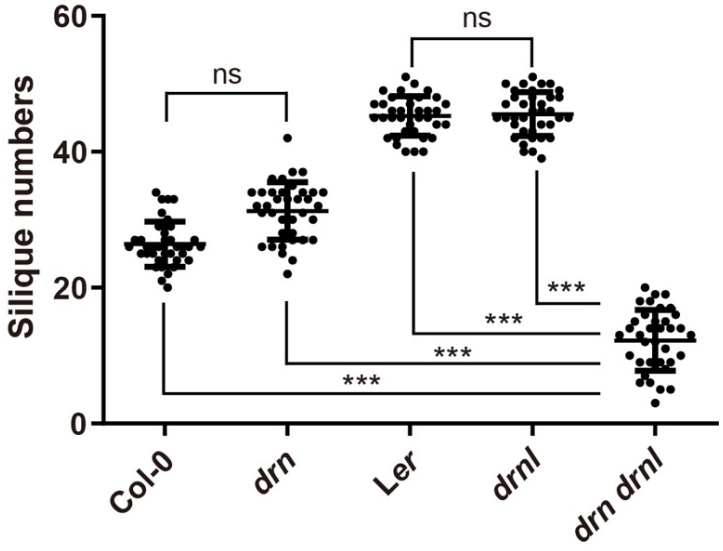


Fig. S2. Measurement of silique numbers in *drn drnl* double mutants. The silique numbers of the *drn* and *drnl* single mutants showed no difference from their respective wild-type plants (*drn* vs Col-0 and *drnl* vs L*er*) but were significantly decreased in the *drn drnl* double mutant. N = 37 for each genotype, two-tailed Student's *t* tests, ***P < 0.001; ns, no significant difference. Six-week-old plants were used for the measurement.

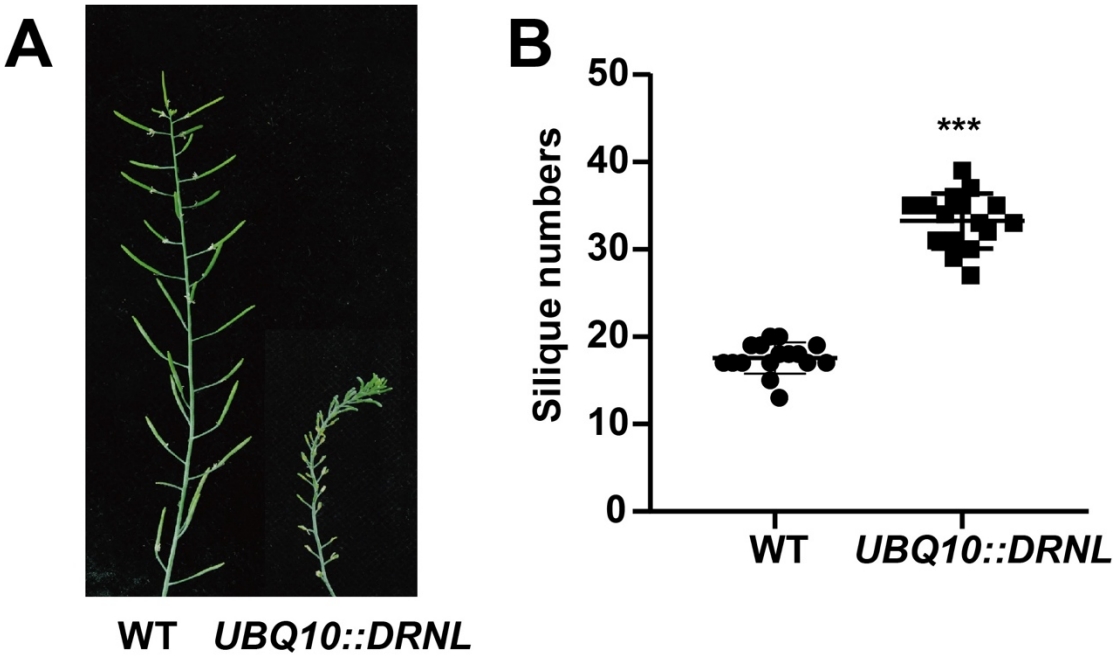


Fig. S3. Overexpression of *DRNL* increased the number of siliques in the wild type. (*A*) The inflorescences of six-week-old WT and *UBQ10::DRNL* plants. (*B*) Measurement of silique numbers in WT and *UBQ10::DRNL* plants. N = 17 for each genotype, two-tailed Student's *t* tests, ***P < 0.001.

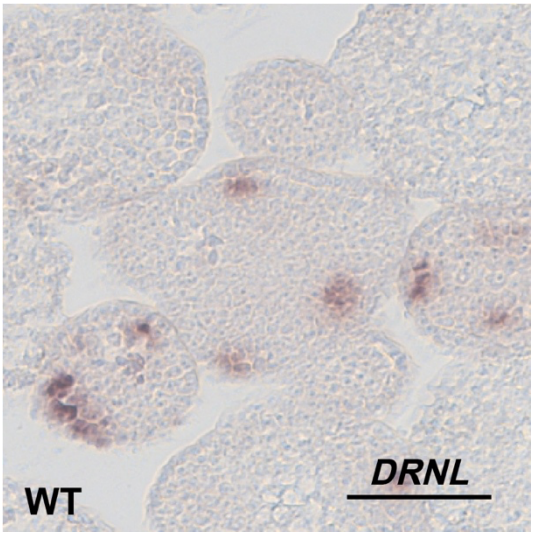


Fig. S4. Top view of *DRNL* expression patterns in the SAM. *DRNL* expression was detected in the inflorescences of wild-type plants by RNA *in situ* hybridization. n ≥ 13 shoot apexes were observed with similar results. Scale bars, 50 μm.

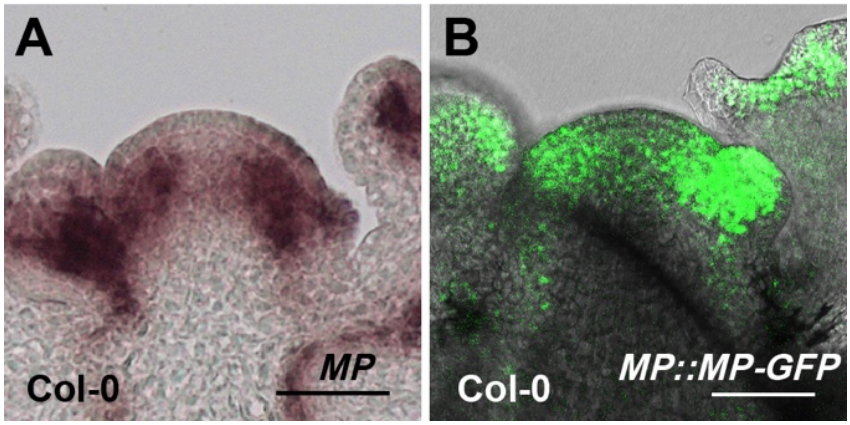


Fig. S5. *MP* distribution patterns in the SAM. (*A*) *MP* transcripts were detected by RNA *in situ* hybridization; n = 10 shoot apexes were observed with similar results. Scale bars, 50 μm. (*B*) MP protein distribution patterns in *MP::MP-GFP*/*mp* rescued plants. n = 29 shoot apexes were observed with similar results. Scale bars, 50 μm.

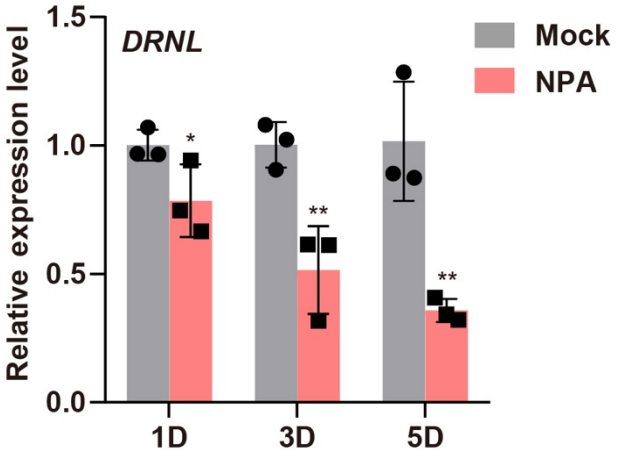


Fig. S6. The expression levels of *DRNL* with NPA treatment. Detection of *DRNL* expression levels in the SAM under NPA treatment after 1 day (1D), 3 days (3D) and 5 days (5D) using qRT–PCR. The data are shown as the mean ± s.d. ; n = 3 biological replicates, two-tailed Student's *t* tests, *P < 0.05, **P < 0.01.

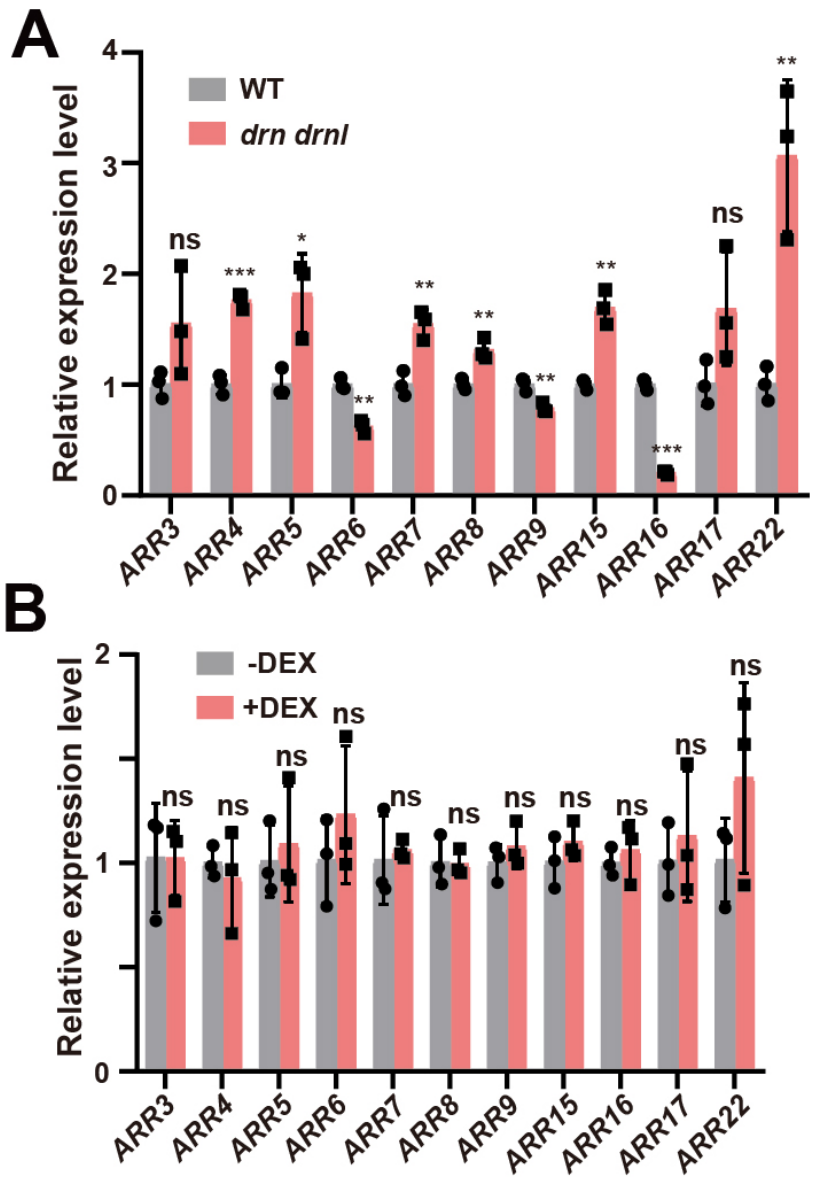


Fig. S7. A-type *ARRs* were not under direct control by DRNL. Expression levels of A-type *ARRs* in *drn drnl* double mutants (*A*) and *UBQ10::DRNL-GR* inflorescences with DEX induction in the presence of cycloheximide (*B*) were measured by qRT–PCR. The data are shown as the mean ± s.d. ; n = 3 biological replicates, two-tailed Student's *t* tests, *P < 0.05, **P < 0.01, ***P < 0.001; ns, no significant difference.

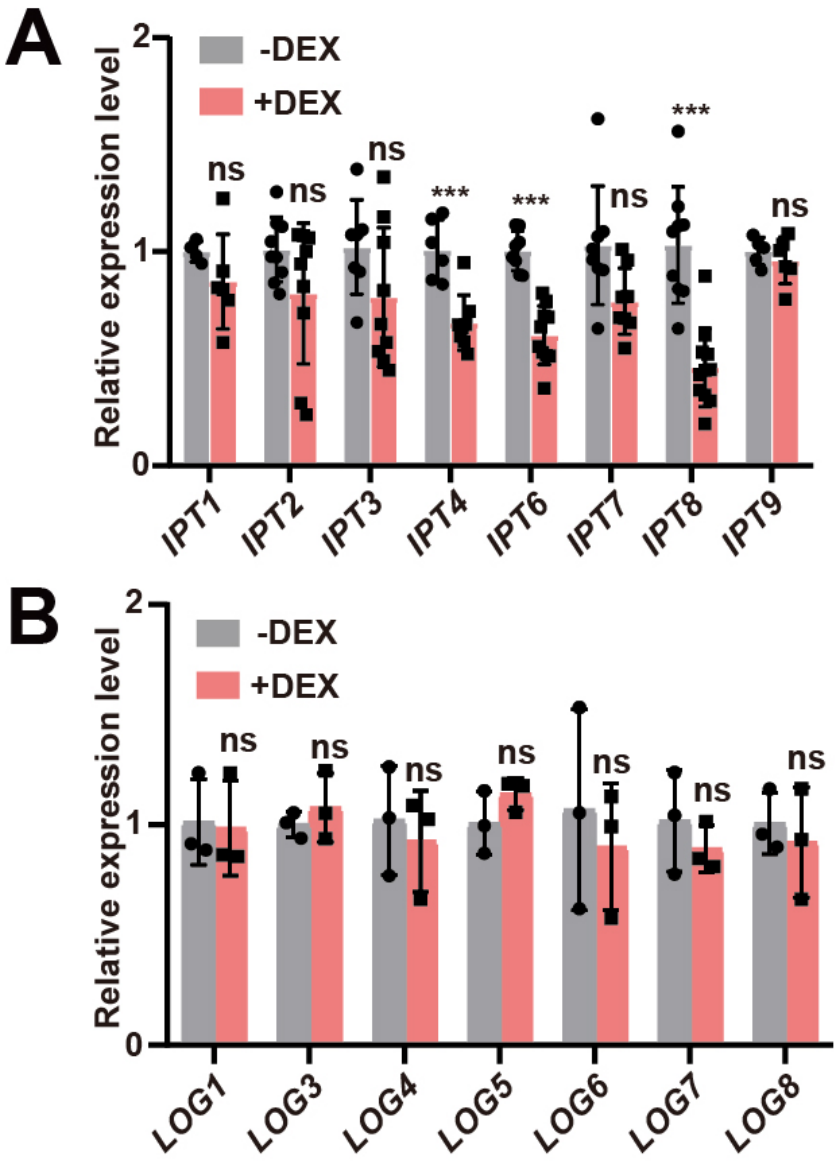


Fig. S8. The expression levels of *IPTs* and *LOGs* in *UBQ10::DRNL-GR* plants with DEX induction. Expression levels of *IPTs* (*A*) and *LOGs* (*B*) in the inflorescences of *UBQ10::DRNL-GR* transgenic plants with or without DEX induction in the presence of cycloheximide were measured by qRT–PCR. The data are shown as the mean ± s.d. ; n ≥ 3 biological replicates, two-tailed Student's *t* tests, ***P < 0.001; ns, no significant difference.

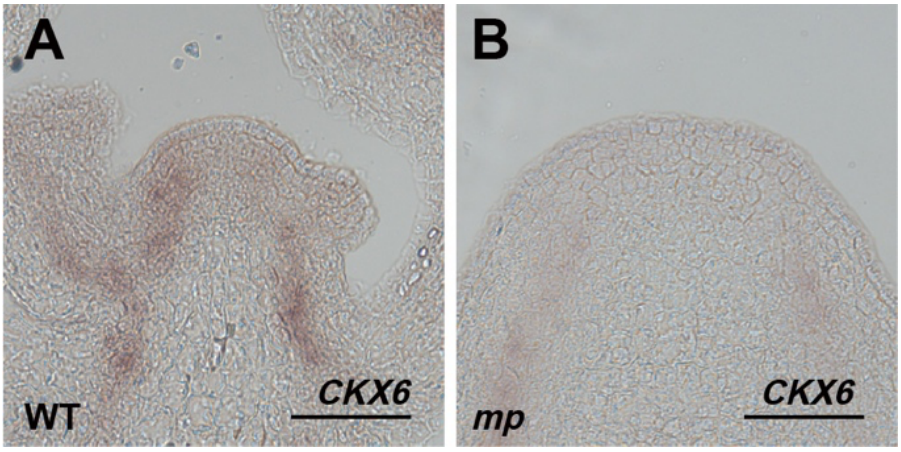


Fig. S9. The expression patterns of *CKX6* in the wild type and *mp* mutant. *CKX6* expression patterns in the SAM of WT (*A*) and *mp* (*B*) were detected by RNA *in situ* hybridization; n ≥ 7 shoot apexes per genotype were observed with similar results. Scale bars, 50 μm.

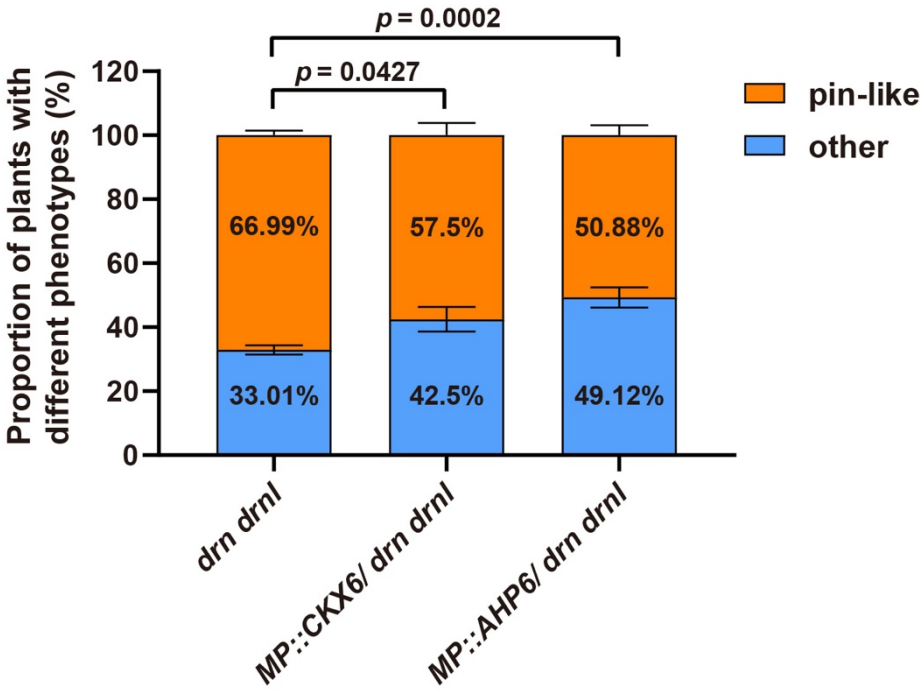


Fig. S10. Expression of either *AHP6* or *CKX6* partially rescues the organ initiation defects in *drn drnl* mutants. The proportion of "pin-like" phenotypes in *drn drnl* mutants was partially restored by the expression of *AHP6* or *CKX6* under the control of a 4.1 kb *MP* promoter. *drn drnl*, n = 3 replicates, with each replicate having more than 95 plants. *MP::CKX6/drn drnl*, n = 3 replicates, with each replicate having more than 52 plants. *MP::AHP6/drn drnl*, n = 3 replicates, with each replicate having more than 68 plants. Bars depict SD; Statistics, Chi-square test.

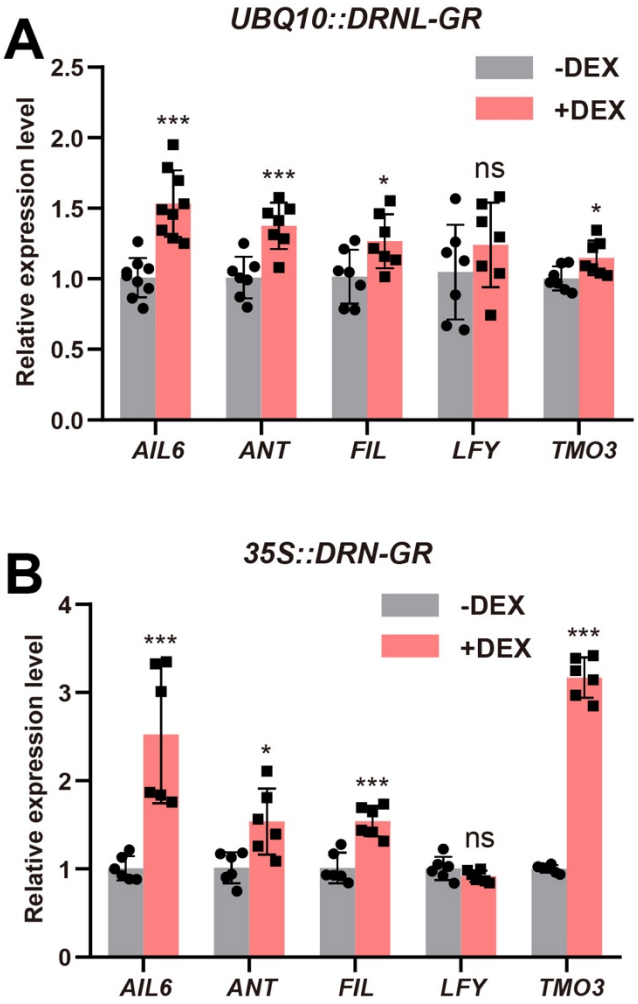


Fig. S11. DRNL and DRN directly activate the expression of *AIL6, ANT, FIL* and *TMO3*. Detection of *AIL6, ANT, FIL*, *LFY* and *TMO3* expression levels in the inflorescences of *UBQ10::DRNL-GR* (*A*) and *35S::DRN-GR* (*B*) transgenic plants with or without DEX induction in the presence of cycloheximide. The data are shown as the mean ± s.d. ; n ≥ 6 biological replicates, two-tailed Student's *t* tests, *P < 0.05, ***P < 0.001; ns, no significant difference.

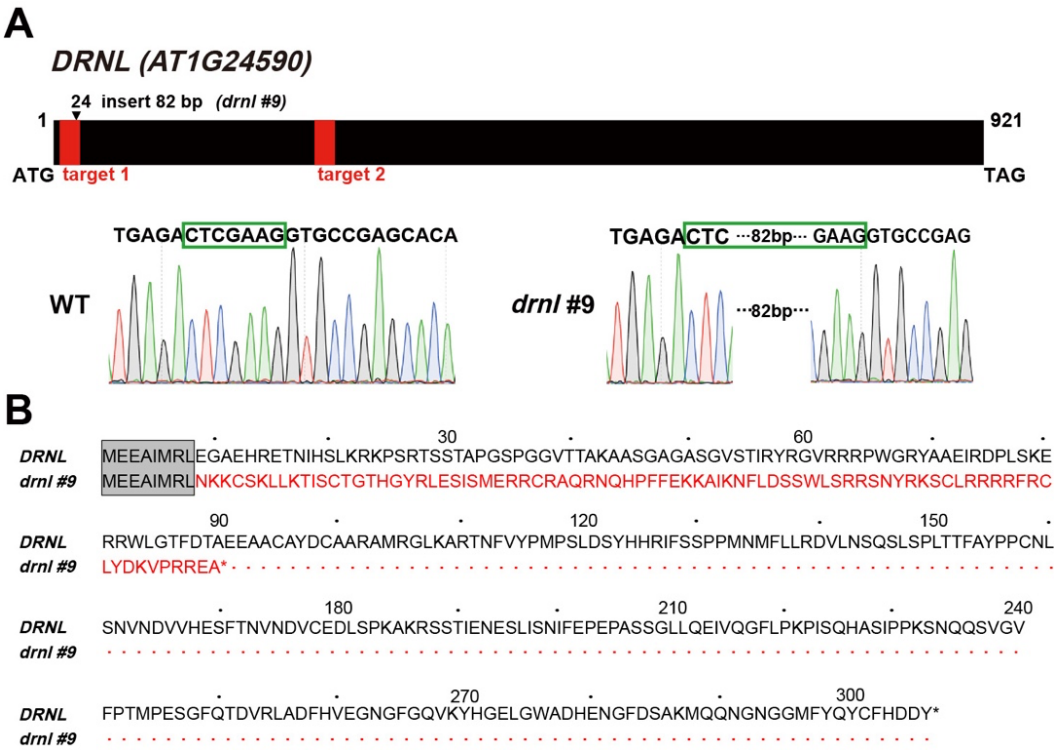


Fig. S12. Generation of the *drnl* mutant in the Col-0 background. (*A*) The *drnl* #9 mutant in the Col-0 background was generated by CRISPR/Cas9 with 82 bp inserted in the first CRISPR/Cas9 target region (upper panel). Arrows indicate the insertion site of 82 bp in *drnl #9*. The two 20-bp sgRNA targets are shown in red. The bottom panel shows the sequencing of the target region in *drnl #9*. (*B*) Comparison of the translated amino acid sequences of the WT and *drnl #9*.

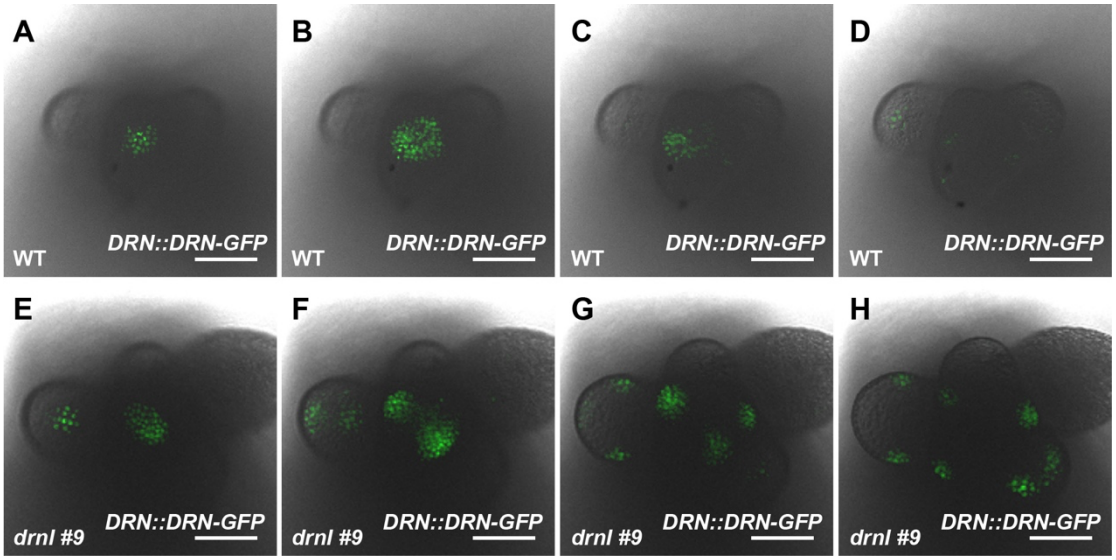


Fig. S13. DRN protein distribution patterns in the *drnl* #9 SAM. Top view of *DRN::DRN-GFP* in WT Col-0 (*A-D*) and *drnl* #9 mutant (*E-H*) inflorescences by the serial optical transverse sections imaged using an Olympus FV3000 confocal microscope; n ≥ 16 shoot apexes per genotype were observed with similar results. Scale bars, 50 μm.

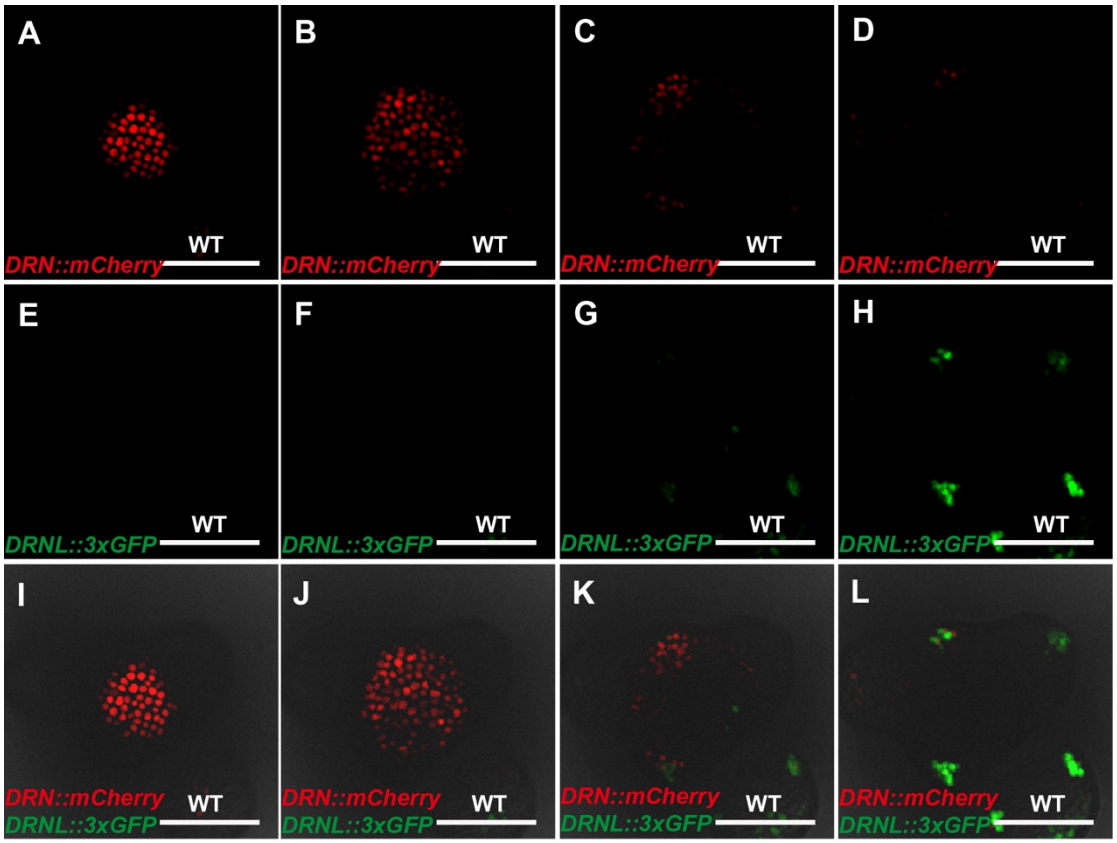


Fig. S14. Top view of *DRN::mCherry* and *DRNL::3×GFP* in the WT. Separate images from each channel of Fig. 5 E-H are shown, including *DRN::mCherry* (*A-D*), *DRNL::3×GFP* (*E-H*) and merged images (*I-L*); n ≥ 20 shoot apexes per genotype were observed with similar results Scale bars, 50 μm.

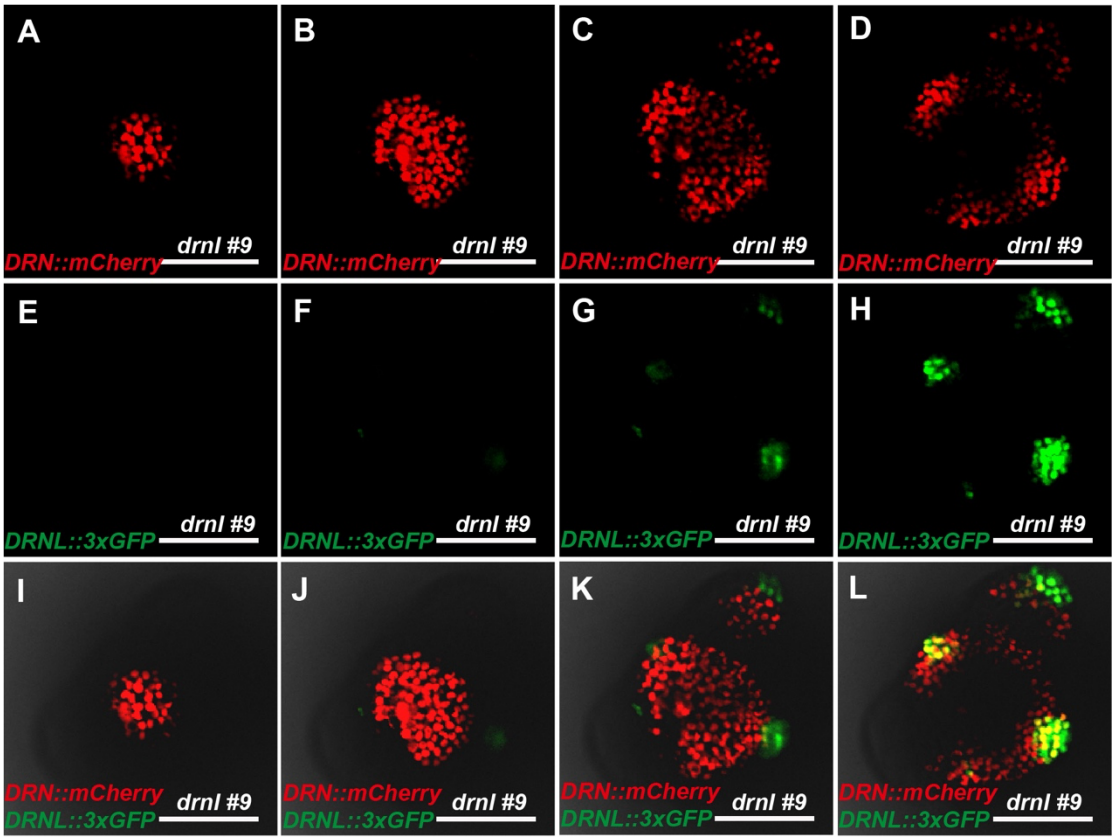


Fig. S15. Top view of *DRN::mCherry* and *DRNL::3×GFP* in the *drnl #9*. Separate images from each channel of Fig. 5 I-L are shown, including *DRN::mCherry* (*A-D*), *DRNL::3×GFP* (*E-H*) and merged images (*I-L*); n ≥ 30 shoot apexes per genotype were observed with similar results. Scale bars, 50 μm.

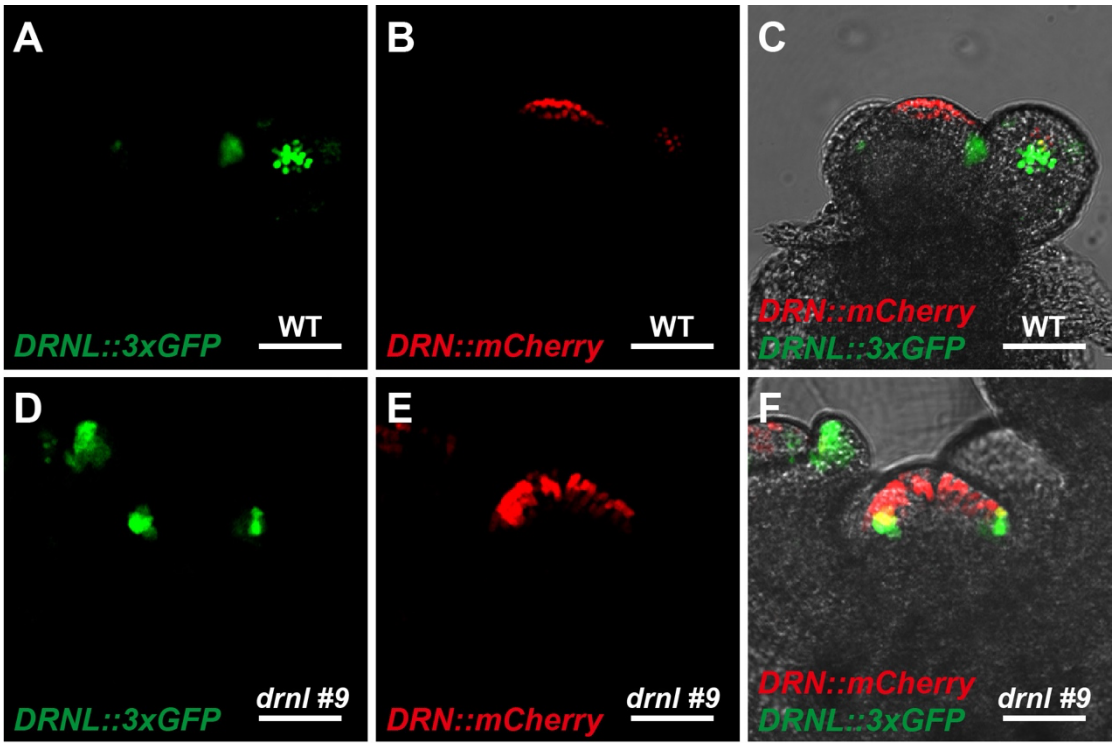


Fig. S16. The expression patterns of *DRNL* and *DRN* in the SAM of wild-type and *drnl #9* plants. *DRNL* (*A*, *D*) and *DRN* (*B*, *E*) expression was detected by *DRNL::3×GFP* and *DRN::mCherry* in the WT (*A*-*C*) and *drnl #9* (*D*-*F*) apexes. (*C*) Merged images of (*A*, *B*). (*F*) Merged images of (*D*, *E*). n ≥ 12 shoot apexes per genotype were observed with similar results. Scale bars, 50 μm.

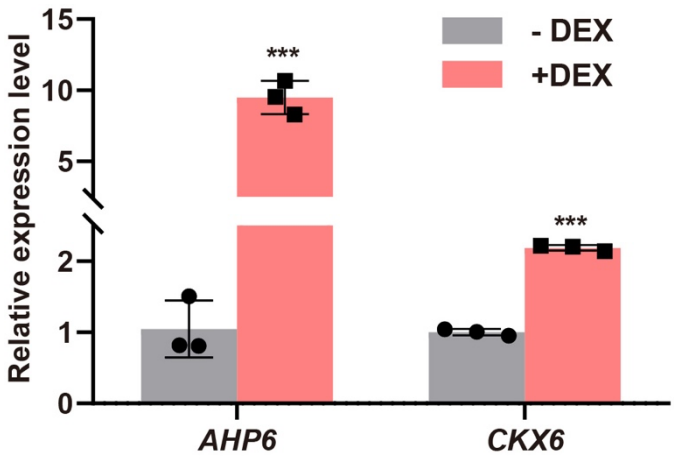


Fig. S17. DRN directly activates the expression of *AHP6* and *CKX6*. Detection of *AHP6* and *CKX6* expression levels in the inflorescences of *35S::DRN-GR* transgenic plants with or without DEX induction in the presence of cycloheximide. The data are shown as the mean ± s.d. ; n = 3 biological replicates, two-tailed Student's *t* tests, ***P < 0.001.

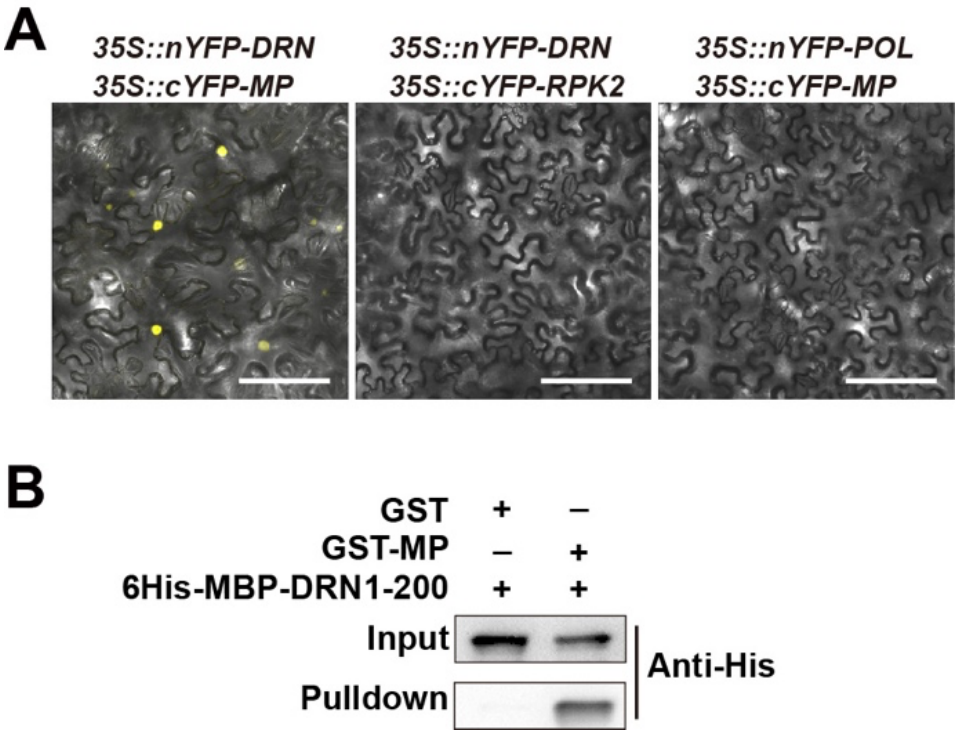


Fig. S18. DRN interacts with MP *in vivo* and *in vitro*. (*A*) BiFC experiments showing that MP interacts with DRN in tobacco leaves. *35S::cYFP-RPK2* and *35S::nYFP-POL* were used as negative controls, n ≥ 7 for each of three independent experiments; Scale bars, 50 μm. (*B*) Pull-down assays show that MP physically interacts with DRN *in vitro*. Two independent experiments were performed with similar results.

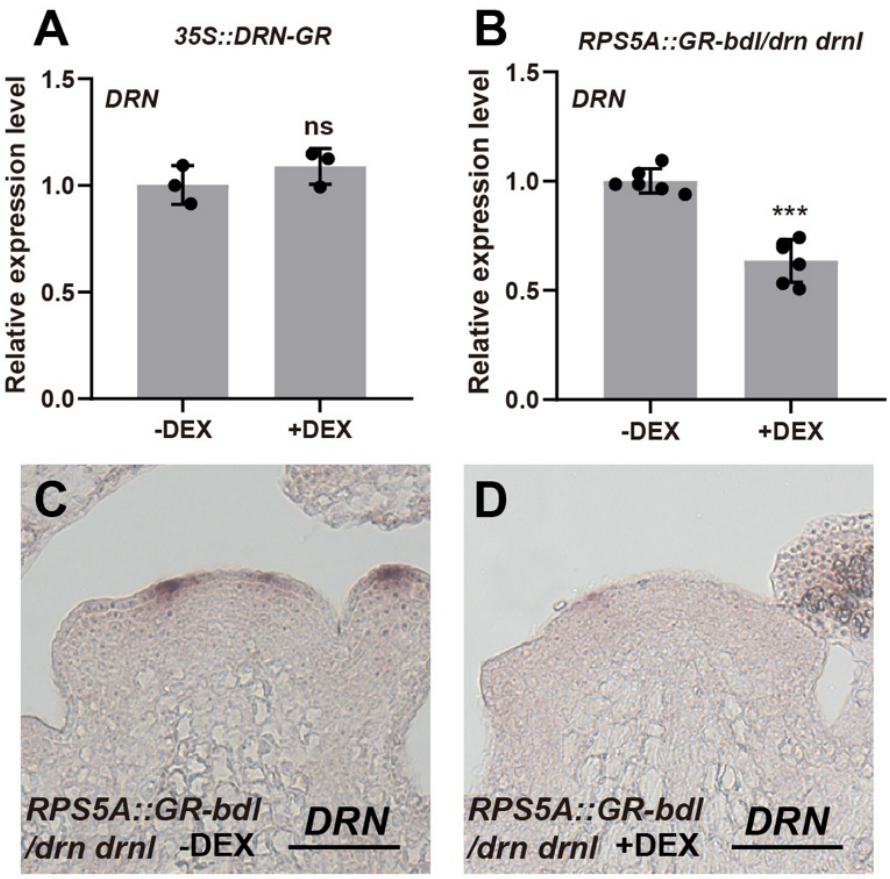


Fig. S19. DRN transcription in the *drnl* mutant was activated by auxin signaling. (*A*) The expression levels of *DRN* in the SAM of *35S::DRN-GR* with or without DEX induction. The data are shown as the mean ± s.d. ; n = 3 biological replicates; two-tailed Student's *t* tests, ns, no significant difference. (*B*) The expression levels of *DRN* in the SAM of *RPS5A::GR-bdl/drn drnl* plants with or without DEX induction. The primers were designed upstream of the inserted *dSpm* element in *drn* plants. The data are shown as the mean ± s.d. ; n ≥ 5 biological replicates; two-tailed Student's *t* tests, ***P < 0.001. (*C*, *D*) *DRN* expression patterns in the SAM of *RPS5A::GR-bdl/drn drnl* plants with (*D*) or without (*C*) DEX induction detected by RNA *in situ* hybridization; n ≥ 24 shoot apexes for each treatment with similar results. Scale bars, 50 μm.

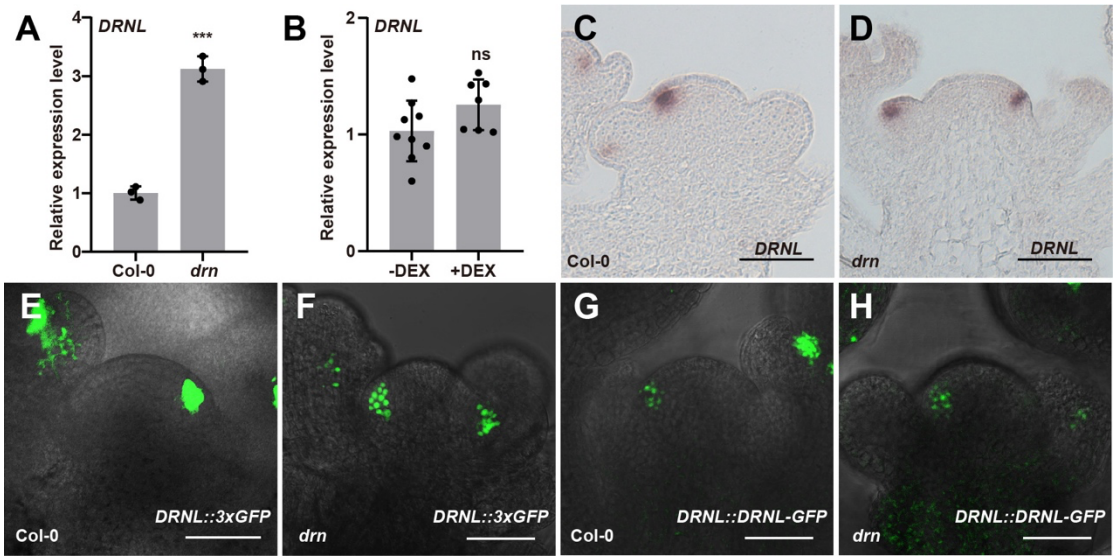
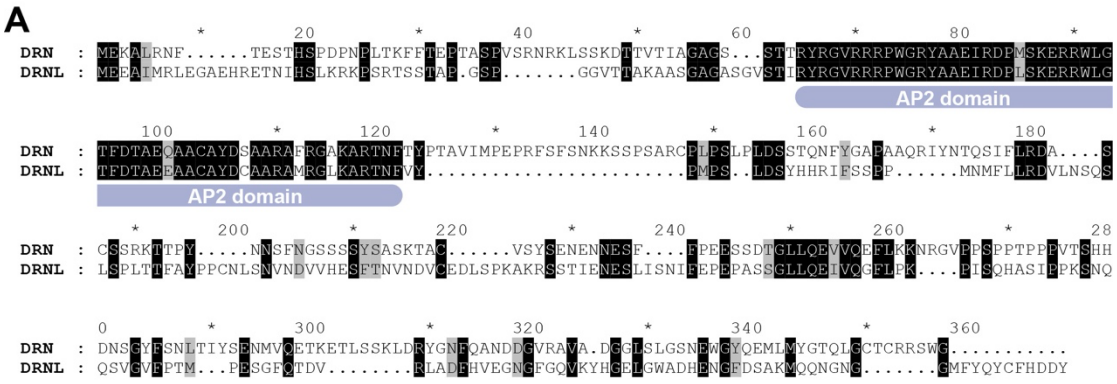


Fig. S20. DRN regulates *DRNL* expression indirectly in the SAM. (*A*** and ***B***) Detection of *DRNL* expression levels in the inflorescences of *drn* mutants (*A*) and *35S::DRN-GR* plants with or without DEX induction in the presence of cycloheximide (*B*). The data are shown as the mean ± s.d. ; n ≥ 3 biological replicates, two-tailed Student's *t* tests, ***P < 0.001; ns, no significant difference. (*C* and *D*) *DRNL* expression patterns in the SAM of Col-0 (*C*) and *drn* (*D*) using RNA *in situ* hybridization; n ≥ 18 shoot apexes per genotype were observed with similar results. Scale bars, 50 μm. (*E* and *F*) *DRNL* expression patterns in the SAM using *DRN::3×GFP* transgenic plants in the Col-0 (*E*) and *drn* (*F*) backgrounds; n ≥ 14 shoot apexes per genotype were observed with similar results. Scale bars, 50 μm. (*G* and *H*) DRNL protein distributions in the SAM using *DRNL::DRNL-GFP* transgenic plants in the Col-0 (*G*) and *drn* (*H*) backgrounds; n ≥ 18 shoot apexes per genotype were observed with similar results. Scale bars, 50 μm.



B

Gene ID	Symbol	Scientific Name	Common Name	Gene type	Chromosome	Gene Age	Branch	Interval
AT1G12980	ESR1	arabidopsis_thaliana	Arabidopsis thaliana	protein_coding	1	306	8	181-341

Gene ID	Symbol	Scientific Name	Common Name	Gene type	Chromosome	Gene Age	Branch	Interval
AT1G24590	ESR2	arabidopsis_thaliana	Arabidopsis thaliana	protein_coding	1	113	11	110-117

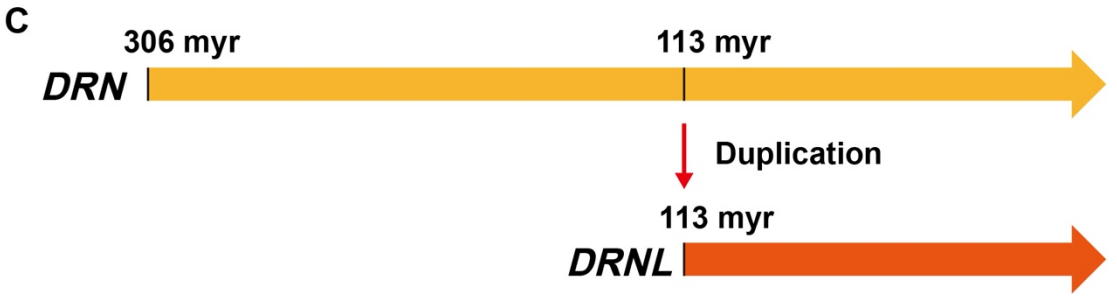


Fig. S21. The predicted gene ages of *DRN* and *DRNL*. (*A*) Schematic comparison of amino acid sequences between DRN and DRNL with the location of the AP2 domain. (*B* and *C*) The gene ages of *DRN* and *DRNL* (*C*) were predicted by GenOrigin (*B*) (http://genorigin.chenzxlab.cn/).

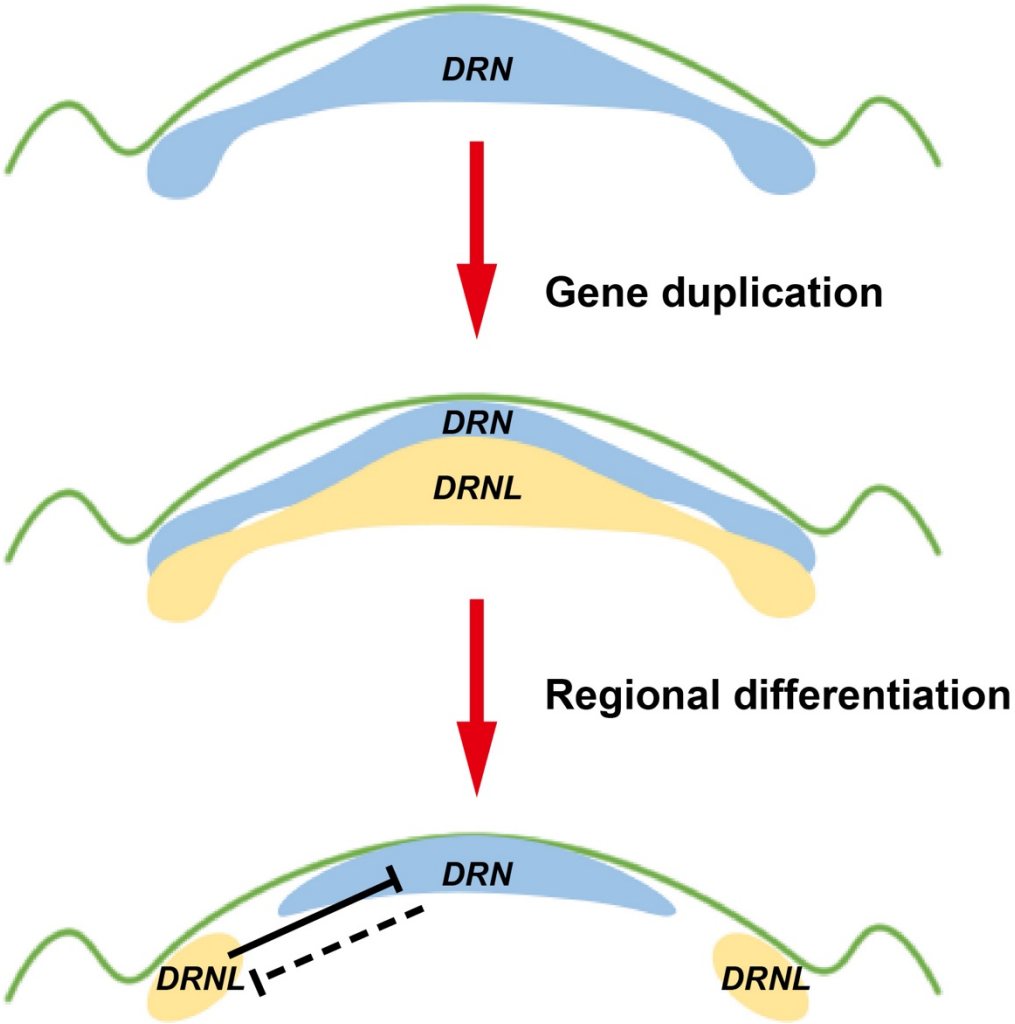


Fig. S22. Hypothetical evolutionary relationships between *DRN* and *DRNL*. *DRNL* originated from a gene duplication event from the *DRN* and shows redundant functions immediately following the duplication. During evolution, the expression of *DRN* in organ initiation cells is repressed directly by DRNL, which promotes the functional diversity and differentiation of paralogous genes. However, in the case of any disturbance in the DRNL, *DRN* is ectopically activated in the primordia and fully restores the functional deficiency to ensure a robust output of auxin during organ initiation.

Table S1 | Oligonucleotides used in this study (5'→3').

Real-time PCR	
Gene	**Sequence**
IPT1-F	ACGTTAGCGAAGAGACAAGTG
IPT1-R	TCACAATCTTTACGCTTGGCTC
IPT2-F	TGCTTCAGAGATCATCAGGTG
IPT2-R	TTCTGCTTCTTGAACTTCTCTG
IPT3-F	TTGAGTTAGCTTGTAGGCAGAG
IPT3-R	ACACAGTATCTGTGCTTGGTC
IPT4-F	TCACGAAGATCAACAAGCTGAG
IPT4-R	TCCTGACAATCTTCACACACG
IPT5-F	ACGGAGAGACTTCTTGAAACG
IPT5-R	TGGTCATCGCTGTAACTAAGG
IPT6-F	AGGAGTTCGACCGATACTTTAG
IPT6-R	TCTCCCATTCTTTCCTTCTCC
IPT7-F	CGTCTAGGCCCTTGTAAAGTTGA
IPT7-R	GTCTCGCCATCGACCTAGCA
IPT8-F	TATGACGAAGCTGTCCAAGAG
IPT8-R	TCACCAAGAAGCGTTTCACAAC
IPT9-F	TCGTGCCATTGGGTACAGAC
IPT9-R	TATCTCCACCATCTCTGCTTC
LOG1-F	ATGGAGATAGAATCAAAGTTCAAGA
LOG1-R	TCATCTTGAGATTTCACAAGTGGGA
LOG2-F	ATGGAAGAGACAAAATCAAGATTCA
LOG2-R	CTAAAACGAGTCGCCTTCCAAAGTG
LOG3-F	ATGGAAATCAAAGGTGAATCGATGC
LOG3-R	TCACTCTTCAGAGGAGTAACCAATC
LOG4-F	ATGGAGGTCAACAATGAAACCATGC
LOG4-R	TCAGTCTTCAGAAGAGTAGTCAATC

LOG5-F	ATGGAAATAGTGAAGTCGAGGTTCA
LOG5-R	CTAAAGGGCAATCTCAGTCTGCATG
LOG6-F	ATGGAGAATGAAGAGGGAAAAAGAG
LOG6-R	CTAACCAGCTTTAGACATAACTTGA
LOG7-F	ATGGAAGAGACAAAATCGAGATTCA
LOG7-R	GTTTGGTATATACGCGGTTAGCAGT
LOG8-F	ATGGAAGATAATCAGCGAAGCAGAT
LOG8-R	TTATTGCGGCTTGTTTTCTTGTCCC
LOG9-F	CATATCTGGTGAGACTGTTGGAGAG
LOG9-R	GGCTTGTTCTCATTTAGTAGTGGGT
AHK2-F	GAGCTTTTTGACATCGGG
AHK2-R	TTCTCACTCAACCAGACGAG
AHK3-F	GTGACCAGGCCAAGAACTTA
AHK3-R	CTTCCCTGTCCAAAGCAA
AHK4-F	GGCACTCAACAATCATCAAG
AHK4-R	TCTTTCTCGGCTTTTCTGAC
AHP1-F	TAGGAGCACAGAGAGTTAAGA
AHP1-R	GCACAAAGAAAGAAGTTCAC
AHP2-F	AAAAATCCTCTCCCAATCTCC
AHP2-R	CTTTGTCTTTAACGCCTTGTA
AHP3-F	AGCTGCAAGATGAATGTAGTC
AHP3-R	CACTTGAGGGATTCTACCAC
AHP4-F	TGTTGAAGAAGTTTCCGCATTA
AHP4-R	AAGCATCCTTCCGCATTT
AHP5-F	CAGGTGGATTCAGGTGTTCA
AHP5-R	ATTTTTCACCCTCCTTGCAC
AHP6-F	CCGCAACCTTAGATTATTGTTGAT
AHP6-R	CCCTACGAGCACCAATGC
ARR1-F	TGGCTACGGATACAGCAACAATG

ARR1-R	ATGTTATCGATGGAGTATGCGTC
ARR2-F	TCAGGACGCAGCAACTGCAAC
ARR2-R	TGGAGGACAAGTCACTGTCTC
ARR3-F	TCTCAGCCACATCCTCGATGG
ARR3-R	TCCACAAGCGAAGTTGCAGAC
ARR4-F	TGGAGATCTTTTCCACCTCGC
ARR4-R	TCATCTTCTGCCGTCGAATCG
ARR5-F	AGCTCAAAGATTCACACACATGC
ARR5-R	TCTCCTCTCTAATGAATCCAAGTC
ARR6-F	TCCGATGCAAATTCCGTGACTG
ARR6-R	AACCCACTGAATTCAATCAGCG
ARR7-F	TGAGGTCATGAGGATGGAGATTC
ARR7-R	CAAGATACTGCAAAGCCCTAGTTC
ARR8-F	TCGGTCTGAAGGAGGACTAACG
ARR8-R	TGCAGTCCGTTGTTGTTTGCTTC
ARR9-F	AATGGAGTCCCCACTGCAGTAG
ARR9-R	TTGTTGATACTCAATGTTTGCTCCT
ARR10-F	TGCGTTCTGCGACTCAGCTAG
ARR10-R	TGAGTTGTTTGCAGGCTGCTG
ARR11-F	TCTCCAGCAACAACCATTGCCAAG
ARR11-R	TCTGTGTTGAACTCCTGCAGC
ARR12-F	ACTCCACGATGAAGCAGGTGTG
ARR12-R	TCTCTCATATGCATGTTCTGAGTG
ARR13-F	ATGCAACTACACAGCCAAATCTTG
ARR13-R	TGTTCACGAAGGTCCAGTCACC
ARR14-F	TTCATGGTCTATCTTCCTCAGC
ARR14-R	ACAGTTGCAGAGCCTTCTCTTC
ARR15-F	TCAGCACTCAGAGAAATCCCA
ARR15-R	TTCCTTCTTCAGCTTCACCA

ARR16-F	ATGAACAGTTCAGGAGGTTCTTG
ARR16-R	TGCAACAAGAGATCTTGAGCAAC
ARR17-F	AAGGGCTGTGGAAGTGGAAG
ARR17-R	GCCCGTTTTCTGCAGTTGTC
ARR18-F	TGAGATGATGAAACAGGAGGAG
ARR18-R	TGCAACTGGTAGAGAAAGAG
ARR19-F	ACCAGATCATAACCAATCCTCCG
ARR19-R	AGAGGCTTGAAGAAGTTCTTC
ARR20-F	AGATGTCACTCTTGCAGCCTC
ARR20-R	ACGTGTCTAGATTCTTGCTTGG
ARR21-F	TGGATCTGGATCAAACTTGACGC
ARR21-R	TGTCCAAACCCAAGAACTTGAG
ARR22-F	TCTTGATGCAATGCCTACCTTC
ARR22-R	TCTTCACTTCTATCGACTTGG
CKX1-F	AGCTTCGACGATGTCCACAA
CKX1-R	GTCCTTGAAGCGAGTGACCA
CKX2-F	GGCCAAGGCCACTCCTTAAA
CKX2-R	CCTTTCTCCGCCGTCTTCTT
CKX3-F	GACGAAACTTCTCAATACAC
CKX3-R	GTTGCGATTCATAGGATA
CKX4-F	ATAAAGGCTCAACCAGCCCC
CKX4-R	ACGTCATGTTCACGACGACA
CKX5-F	CGCATCGGAGCCATAGATGT
CKX5-R	TCGGCCGATGATGGATGAAG
CKX6-F	ATGTGTCTGGTGGTGAGCTG
CKX6-R	GGCCGCTTATTCCAGCATTG
CKX7-F	GTTTGTCAACGGTGCTGACC
CKX7-R	GAAGACCGAGTTCGAGGCAA
DRNL-F	CGTTTAGCTGACTTCCATGTC

DRNL-R	CCGTTCTGCTGCATCTTAGC
DRN-F	TGTACGGAACTCAGTTAGGC
DRN-R	ACATTGGGAAAGGTAGCAAC
AHP6-F	CCGCAACCTTAGATTATTGTTGAT
AHP6-R	CCCTACGAGCACCAATGC
AIL6-F	AGCAGCAGCAGCAACAGAACTT
AIL6-R	AGAGGAAGAACTCAGCCGGATTT
ANT-F	AGATCCCAACGGATTCAAACAGC
ANT-R	CTTTAGGAGGATATAGGAGAGGG
FIL-F	CAGCAACCCAACAATCAAGAAG
FIL-R	GATTGATTGATGGGTATTTGAC
LFY-F	ATGGATCCTGAAGGTTTCACGA
LFY-R	CTCTAAACCACCAAGTCGCAT
TMO3-F	CCGAGGAGTGAGACAGCGTCC
TMO3-R	GCTTCTTCCGCCGTGTTGTAAGTACC
DRN-F (3'UTR)	GTACGGAACTCAGTTAGGCT
DRN-R (3'UTR)	CCAACATTGGGAAAGGTAGC
DRN-F (Upstream of *dSpm* element)	ATGGAAAAAGCCTTGAGAAAC
DRN-R (Upstream of *dSpm* element)	TTTGAAGACAGTTTGCGGTTG

***in situ* hybridization**	
Gene	**Sequence**
AHP6-F	ATGTTGGGGTTGGGTGTGGAC
AHP6-R	GTAATACGACTCACTATAGGGCGACATTGGATATCTGAC TCCTG
CKX6-F	GAGCTATCTACATGCAAGCC

CKX6-R	AATTAACCCTCACTAAAGGGACATGGTTGGTGCTGGTTCCA
DRN-F	ATGGAAAAAGCCTTGAGAAAC
DRN-R	GTAATACGACTCACTATAGGGCGCTATCCCCACGATCTTCGGC
DRNL-F	ATGGAAGAAGCAATCATGAGA
DRNL-R	GTAATACGACTCACTATAGGGCGCTAATAATCATCATGAAAGC
MP-F	TATCCGAACCTTCCATCTCAG
MP-R	GTAATACGACTCACTATAGGGCGGCGACAATATCCTTATGCACC
DRN-F (Upstream of *dSpm* element)	ATGGAAAAAGCCTTGAGAAACTTCACCGAATCTACCCACT
DRN-F (Upstream of *dSpm* element)	GTAATACGACTCACTATAGGGCGTGCTCCACGAAAGGCACGA

Plasmid construction	
DRNL promoter-F	TCGTATCCAAGGTTGAATGTTGG
DRNL promoter-R	GGTTGACCTAAGGGAAATTTTTA
MP promoter-F	TAGAGAGAGGACGTGTGTGA
MP promoter-R	CATCATACAGAGAGATTTTT
P16 promoter-F	ACGCGTCGACTGGAACCATCTTTTGGGTTC
P16 promoter-R	CCGGAATTCCCACGCCGTCGTAGATGAGA
DRNL CDS-F	ATGGAAGAAGCAATCATGAG
DRNL CDS-R	ATAATCATCATGAAAGCAAT
DRN CDS-F	ATGGAAAAAGCCTTGAGAAA
DRN CDS-R	CTATCCCCACGATCTTCGGC
MP CDS-F	ATGATGGCTTCATTGTCTTG
MP CDS-R	TTATGAAACAGAAGTCTTAA

AHP6 genome sequence-F	ATGTTGGGGTTGGGTGTGGA
AHP6 genome sequence-R	TTACATTGGATATCTGACTC
CKX6 genome sequence-F	ATGAGCTATCTACATGCAAG
CKX6 genome sequence-R	TCATGAGTATGAGACTGCCT
POL CDS-F	ATGGGAAACGGGACTTCCCGTG
POL CDS-R	TTATCTATTGAATTTTTG
RPK2 CDS-F	ATGACTTCTTTGCCTTCT
RPK2 CDS-R	CTAACACGACGGAGGTTG

CRISPR-Cas9	
DRNL-CRISPER-DT1-BsF	ATATATGGTCTCGATTGAAGCAATCATGAGACTCGAGTT
DRNL-CRISPER-DT1-F0	TGAAGCAATCATGAGACTCGAGTTTTAGAGCTAGAAATAGC
DRNL-CRISPER-DT2-R0	AACCATGGCCTACGCCTCACGCCAATCTCTTAGTCGACTCTAC
DRNL-CRISPER-DT2-BsR	ATTATTGGTCTCGAAACCATGGCCTACGCCTCACGCC

ChIP	
AHP6 S1-F	TGAATAGGGTACTCGAGCAC
AHP6 S1-R	ACGGAACAAACAACTAGCTAG
AHP6 S2-F	TATACTTTCTGGTTCCAGGAG
AHP6 S2-R	TACCAACACCTCTGGTTACGTG
AHP6 S3-F	ACGTAACCAGAGGTGTTGGTAC
AHP6 S3-R	AAGGCCTTTCTCTTTCTCGATC

AHP6 S4-F	ACCAGCTGGTCTGACAGGGTAC
AHP6 S4-R	ACATGAGATGAGGTGACCCAC
AHP6 S5-F	TGTGGGTCACCTCATCTCATG
AHP6 S5-R	CCACAACGGCACACCCGTCTTG
CKX6 S1-F	TCTGTTATCCACCTGCCCGA
CKX6 S1-R	TCCCATTGCAGCTAGCTGAC
CKX6 S2-F	GTGGGTGTAACTGTTATC
CKX6 S2-R	TATAGTTGAGGCCTCTCCCT
CKX6 S3-F	TGGTTGCCTCGGCCATTCAG
CKX6 S3-R	GCTCATAAGGCCTCTTGATTTCT
CKX6 S4-F	TGAACATGTCCATCACGCCT
CKX6 S4-R	TTGAGGCGATGTCGCTTACC
CKX6 S5-F	TCTAACCAAACATGCGAGAGTGA
CKX6 S5-R	ACCACACAAATGAGCAGCAG
DRN S1-F	AACGCAGGGGTTTTAATTGC
DRN S1-R	CTGGAGTATCTTTCAAAAGC
DRN S2-F	AAACGTAAGCATCGGGCGAT
DRN S2-R	GGAACAAAAGATATGCATAGC
DRN S3-F	CTTCTCGATATCACCGAT
DRN S3-R	CGACCAACAGTCATTTC
DRN S4-F	AGCAATAAGAACGTGGT
DRN S4-R	GGAAACTTTTGAGTTGCAC
DRN S5-F	GTGCAACTCAAAAGTTTCC
DRN S5-R	CCATTTTTGGTTTCTAGGG
DRN S6-F	ATGGAAAAAGCCTTGAGAAACTTCACCG
DRN S6-R	TGCCAGCTCCGGCGATGGTTA

EMSA

AHP6-F	GCAGAGTCACGCGGGGTAACCGGCTGGCGGCTGTAGCC GGTCACAGAGTGTATTAA
AHP6-R	TTAATACACTCTGTGACCGGCTACAGCCGCCAGCCGGTT ACCCCGCGTGACTCTGC
AHP6-mutant probe-F	GCAGAGTCACGCGGGGTAACCGGCTGGAGGATGTAGCC GGTCACAGAGTGTATTAA
AHP6-mutant probe-R	TTAATACACTCTGTGACCGGCTACATCCTCCAGCCGGTT ACCCCGCGTGACTCTGC
CKX6-for DRNL binding-F	GAAATCGATACCAGTTGATCCCTTTGGCGGTCTTACATC CCAAATCGGTAAGCGA
CKX6-for DRNL binding-R	TCGCTTACCGATTTGGGATGTAAGACCGCCAAAGGGATC AACTGGTATCGATTTC
CKX6-probe1-for MP binding-F	ATATAAAGCTAATCTTTTATCATAATGTCTGATCAAAAGAA TTTAAGAAAAGAA
CKX6-probe1-for MP binding-R	TTCTTTTCTTAAATTCTTTTGATCAGACATTATGATAAAAG ATTAGCTTTATAT
CKX6-probe2-for MP binding-F	AAAGAAGAGATGATTCATTTAGTTTTGTCAGCTAGCTGCA ATGGGAGGCCTTAA
CKX6-probe2-for MP binding-R	TTAAGGCCTCCCATTGCAGCTAGCTGACAAAACTAAATG AATCATCTCTTCTTT
CKX6-probe3-for MP binding-F	AAGTAAAAGTGTTATGGTATGATCTTGTCTGCCTTTTCTTT GAAAAAGCCAAGA
CKX6-probe3-for MP binding-R	TCTTGGCTTTTTCAAAGAAAAGGCAGACAAGATCATACCA TAACACTTTTACTT
CKX6-mutant probe1-for MP binding-F	ATATAAAGCTAATCTTTTATCATAATGGCTGATCAAAAGAA TTTAAGAAAAGAA
CKX6-mutant probe1-for MP binding-R	TTCTTTTCTTAAATTCTTTTGATCAGCCATTATGATAAAAG ATTAGCTTTATAT

CKX6-mutant probe2-for MP binding-F	AAAGAAGAGATGATTCATTTAGTTTTGGCAGCTAGCTGCAATGGGAGGCCTTAA
CKX6-mutant probe2-for MP binding-R	TTAAGGCCTCCCATTGCAGCTAGCTGCCAAAACTAAATGAATCATCTCTTCTTT
CKX6-mutant probe3-for MP binding-F	AAGTAAAAGTGTTATGGTATGATCTTGGCTGCCTTTTCTTTGAAAAAGCCAAGA
CKX6-mutant probe3-for MP binding-R	TCTTGGCTTTTTCAAAGAAAAGGCAGCCAAGATCATACCATAACACTTTTACTT
DRN-F	AGAAAAGCATTTATACTCTTCGCCATATATTTCAAACTTCACA
DRN-R	TGTGAAGTTTGAAATATATGGCGAAGAGTATAAATGCTTTTCT