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Supplementary Information for

Robust control of floral meristem determinacy by position-specific multifunctions of KNUCKLES

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This PDF file includes:

SI Materials and Methods

Plant Materials and Growth Condition

All *Arabidopsis thaliana* plants are Landsberg *erecta* (L*er*) background, except for *pWUS:WUS-linker-GFP wus-101* (GABI-Kat line GK870H12, Columbia background). All plants are grown at 22°C under continuous light.

DEX (D4902, Sigma-Aldrich) and CHX (01810, Sigma-Aldrich) treatments were performed as described previously (1). 1 μM DEX solution was used for for *ap1 cal 35S:AP1-GR*, 10 μM DEX for *ap1 cal 35S:KNU-GR-myc*, and 10 μM CHX for *ap1 cal 35S:KNU-GR-myc*. The initial time of DEX or CHX treatment was defined as Day 0 or 0 h.

Vector Construction

For *pCLV3:KNU* vector*,* construction process was as follows: The 3156-bp promoter fragment upstream of the start codon of *CLV3* was amplified and cloned into pCR8 TOPO cloning vector (Invitrogen). Then 2208-bp fragment downstream of *CLV3* stop codon was introduced after the promoter fragment. KNU full-length coding sequence was later inserted into the Sac I site created at the 3' end of *CLV3* promoter fragment. Finally, the cloned fragment in pCR8 was recombined into CD3-694 vector by LR recombinase (Invitrogen).

To generate *pCLV3:KNU-GFP, pCLV3:KNU-NLS* and *pCLV3:KNU-GFP-NLS,* the coding sequences of GFP, SV40 NLS, and GFP-NLS were introduced at the 3' end of *KNU* coding sequence in pCR8-*pCLV3:KNU* vector respectively and recombined into CD3-694 vector.

To generate *pWUS:WUS-myc*, 4058-bp *WUS* genomic fragment including 2489-bp *WUS* promoter sequence upstream of start codon was cloned into pENTR-D (Invitrogen). Then, SfoI site was introduced before the stop codon. Subsequently, the 1220-bp sequence downstream of *WUS* stop codon was added to generate the pENTR-D-*pWUS:WUS*. Later, *myc* fragment was introduced into the SfoI site. Finally, the pENTR-D based construct was recombined into the binary vector pKGW by LR

recombinase (Invitrogen).

In order to obtain *pWUS:KNU*, the intermediate pENTR-D vector containing 2489-bp *WUS* promoter sequence followed by 1220-bp sequence downstream of *WUS* stop codon was first created. Then *KNU* CDS was cloned after the 2489-bp *WUS* promoter sequence to generate pENTR-D-*pWUS:KNU*. Finally, pENTR-D based constructs were recombined into the binary pBGW vector.

For the construction of *pGIR1:KNU* or *pGIR1:KNU-eGFP*, the 2242-bp promoter fragment upstream of *GIR1* start codon was cloned into pCR8 vector. Then *KNU* or *KNU-eGFP* coding sequences were added after the *GIR1* promoter fragment. To generate *pAtML1:KNU* or *pAtML1:KNU-eGFP*, the 3616-bp promoter fragment upstream of *AtML1* start codon followed by 957-bp fragment downstream of *AtML1* stop codon was cloned into pCR8 vector. Subsequently, *KNU* or *KNU-eGFP* coding sequences were inserted into the SfoI site at the end of the *AtML1* promoter fragment. For *pMCT1:KNU* or *pMCT1:KNU-eGFP*, 2396-bp *MCT1* promoter fragment upstream of start codon was cloned into pCR8 vector, and *KNU* or *KNU-eGFP* coding sequences were added after *MCT1* promoter fragment. To generate the *pCLV1:KNU* or *pCLV1:KNU-eGFP*, 5704-bp *CLV1* promoter upstream of start codon and 1063-bp fragment downstream of stop codon was introduced to pCR8 vector. Then *KNU* or *KNU-eGFP* were cloned to the 3' end of *CLV1* promoter fragment. Finally, the fused fragments in pCR8 were introduced to pBGW.

To generate amiRNA for silencing *KNU*, the amiRNAs (21-nt) were designed by the Web MicroRNA Designer (WMD3, http://wmd3.weigelworld.org./cgi-bin/webapp.cgi). Pre-amiRNA was assembled by several rounds of PCR using primers listed in *SI Appendix,* Table S2. The final PCR fragments were driven under aforementioned *CLV3* or *WUS* promoters in pCR8 or pENTR-D, and later recombined into the binary CD3-694 or pBGW vectors respectively.

RNA Extraction and Expression Analyses

The total RNA was isolated from inflorescence tissues using RNA isolater Total RNA Extraction Reagent (Vazyme). The HiScript II Q RT SuperMix for qPCR kit (Vazyme) was used to synthesize cDNA. ChamQ Universal SYBR qPCR Master Mix was used for quantitative real-time PCR (Vazyme), and the assays were performed in triplicate using the Step One Plus real-time PCR system (Applied Biosystems). The gene *Tip41-like* (AT4G34270) was used as the internal reference gene. Except for expression assays of *MIR394B* and *LCR* (performed with two biological replicates), all gene expression assays were carried out for three biological replicates.

Chromatin Immunoprecipitation Assay

Chromatin immunoprecipitation (ChIP) experiments were performed according to previous description (1) using a ChIP Assay Kit (17-295, Millipore). To estimate the H3K27me3 enrichment, cleared chromatin solution was incubated with anti-H3K27me3 antibody (07-449, Millipore) in a ratio of 1:200 (v/v). To monitor the Pol II enrichment on *CLV3* locus, Pol II antibody (ab817, Abcam) was used for immunoprecipitation in a ratio of 1:200 (v/v). To check the enrichment of KNU on *CLV3* and *CLV1*, the chromatin complexes from *ap1 cal 35S:KNU-GR-myc* inflorescence tissues was pre-cleared with protein-A agarose beads (16-157, Millipore), and then incubated with anti–c-Myc-Agarosebeads (A7470, Sigma-Aldrich) in a ratio of 1:20 (v/v). To estimate the enrichment of KNU on *CLV3* locus, the chromatin complexes from *pCLV3:KNU-GFP* and *pCLV3:KNU-GFP-NLS* inflorescence tissues was pre-cleared with protein-G agarose beads (16-201, Millipore), and incubated with GFP-Trap Agarose (gta-20, ChromoTek) in a ratio of 1:20 (v/v) overnight. Agarose beads without antibody were added to same solution as control. DNA fragments was purified using PCR Purification Kit (#K0702, Thermo). On *CLV3* locus, nine primer pairs for ChIP assays were designed and eventually six pairs were chosen as representatives. The other three pairs with negative KNU enrichment were only presented in supplemental figures. The enrichment rate for H3K27me3 level on *CLV3* locus was presented as the ratio of bound DNA after IP to the input DNA before IP. The enrichment rate of other ChIP experiments were shown as antibody-bound

DNA to no antibody control. *Mu-like* transposons was taken for the negative control locus and the relative enrichment rate was set to 1 for all ChIP experiments. Except for KNU binding on *BAM* genes (performed with two biological replicates), three independent biological replicates were performed and each ran in triplicate (technical replicates) for all ChIP assays.

Electrophoretic Mobility Shift Assay

The electrophoretic mobility shift assays were carried out according to previous procedures (1). The CDS of *WUS* and *KNU* were individually cloned into the multiple cloning sites and fused with *MBP* in pMAL-c5G vector (NEB). The MBP-tagged proteins were expressed in Transetta (DE3) Chemically Competent Cells (TransGen Biotech) and purified using Amylose Resin (#E8021V, NEB). The DNA-protein binding reactions, and detection of biotin-labeled probes were performed by using the EMSA kit (20148, Thermo).

Size-Exclusion Chromatography (SEC)

Full-length *KNU* CDS was cloned into the expression vector pMAT9s containing an N-terminal 6×His-tag followed by maltose binding protein (MBP) and a SARS-Mpro cleavage site. The recombinant *KNU* was expressed in BL21 CodonPlus (DE3)-RIL *Escherichia coli* cells (Stratagene) and induced with 0.3 mM IPTG at 18°C for 20 h. The resulting MBP-fusion protein was purified by an MBPtrap HP affinity column (GE Healthcare), followed by a HitrapQ anion exchange column (GE Heathcare) in 50 mM Tris-HCl (pH 8.0) using a 50-300 mM NaCl gradient elution. MBP-KNU was further purified using a Superdex 200 Increase 10/300 GL column (GE Heathcare) equilibrated in 20 mM Tris-HCl (pH 8.0), 150 mM NaCl, 0.1 mM Tris (2-carboxyethyl) phosphine (TCEP) and the protein purity was examined by SDS-PAGE. Duplex DNAs were annealed using complementary single-strand HPLC purified DNAs (GenScript). Lyophilized oligonucleotides were dissolved in 20 mM Tris-HCl (pH 8.0), 150 mM NaCl, 0.1 mM TCEP and mixed 1:1 with the complementary strand at a final concentration of 500 μM. The reaction mixture was heated to 95 °C for 5 min and naturally cool to

room temperature.The SEC was performed at 4 °C using a Superdex 200 Increase 10/300 GL column (GE Healthcare) pre-equilibrated in 20 mM Tris-HCl (pH 8.0), 150 mM NaCl, 0.1 mM TCEP. The KNU protein (0.8 mg/mL) was mixed with a solution of annealed, blunt-ended P3-2 dsDNA (55-bp) at a molar ratio of 1:0.6 (protein:dsDNA) and incubated on ice for about 30 min. The ~100 µL volume of mixture was then injected and eluted one column volume at a flow rate of 0.5 mL/min.

Sectioning and Confocal Microscopy Imaging

For floral section, inflorescence tissues were embedded in 5% liquid LM agarose (CA1351, Coolaber) at 40°C and then placed on ice for 10 min. Sections of 80 µm thickness were produced using a vibratome (VT1000S, Leica). Then the obtained floral sections were placed onto microscope slides mounted with 0.1% MES or 1 µg/mL FM4-64 (T13320, Thermo) solution. Floral sections were snapped with Zeiss LSM880 confocal microscope. For GFP-only floral tissues, the excitation wavelength was 488 nm, and the detection wavelength was between 493 and 594 nm. For the observation of floral tissues expressing both GFP and VENUS, GFP was stimulated at 488 nm and detected with a spectrum from 493 to 518 nm, and VENUS was stimulated at 514 nm and detected with a spectrum from 519 to 620 nm. For FM4-64 observation, it was excited at 514 nm and the detection wavelength was between 592 and 758 nm.

Co-IP Assays

The floral buds at stage 6 from transgenic line *ap1 cal 35S:AP1-GR pKNU:KNU-VENUS pWUS:WUS-myc* were collected for protein extraction and *ap1 cal 35S:AP1-GR* or *ap1 cal 35S:AP1-GR pKNU:KNU-VENUS* was used as a negative control. Co-IP experiments was operated as described previously (1). In Western blot analysis, KNU-VENUS and WUS-myc were immunoblotted with anti-GFP antibody (2856, Cell Signaling Technology) and anti-myc antibody (A00173, GenScript) respectively. Three independent experiments were performed, and similar results were obtained, and representative data were exhibited.

Yeast One-Hybrid Assays

The experimental procedures was conducted followed the manufacturer's instructions (Clontech). Three tandem repeated CLV3-P3 fragments were cloned into the pABAi vector (Clontech). The resulting constructs were linearized with BstBI and transformed into the Y1H Gold yeast strain (Weidi Biotech). The full coding sequence of *KNU* was fused with the GAL4 activation domain in vector pGADT7, forming AD-KNU. The plasmid containing AD-KNU was subsequently transformed into the Y1HGold strain containing the pABAi-CLV3-P3 constructs. The validated interaction between WUS-W2 and KNU was used as a positive control (1), and the empty pGADT7 was used as a negative control. The DNA-protein interaction in yeast was selected by SD/-Ura agar plates containing 150 ng/mL aureobasidin A (AbA).

Yeast Two-Hybrid Assays

To obtain yeast two-hybrid assays vectors, the full length KNU and series truncated KNU were individually cloned into pGADT7 (Clontech). The full length WUS and series truncated WUS were individually cloned into pGBKT7 (Clontech). The full length CLV3 was also cloned into pGBKT7. The yeast two hybrid assays were performed using the Yeastmaker Yeast Transformation System 2 (Clonetech) according to the manufacturer's instructions.

Yeast Three-Hybrid Assays

The vectors of pBridge (Clontech) and pGADT7 (Clontech) were used for yeast three-hybrid assays. The full length WUS and KNU were cloned into MCS I and MCS II of pBridge respectively. The full length WUS, STM and HAM1 were cloned into pGADT7 vector respectively. The pGADT7 vectors were co-transformed with pBridge vectors into the yeast strain AH109 in designed combinations, and screened on SD/-Leu/-Trp/-Met agar plates. The interactions among three proteins were evaluated on SD/-Leu/-Trp/-Met/-His agar plates complemented with 3-AT .

Protein Extraction and Expression Analyses in Yeast

Protein extraction experiments were performed according to previous method (2). Yeast cells were collected at OD600 = 1.0 and then treated with 2.0 M LiAC solution for 1 min, then replacing with 0.4 M NaOH for 5 min. Subsequently, cells were resuspended in SDS-PAGE loading buffer and boiled for 10 min. For relative level of protein expression, BD-WUS was immunoblotted with anti-BD antibody (ABP57232, Abbkine), and AD-HA-STM or HA-KNU was immunoblotted with anti-HA antibody (26D11, Abmart) by Western blot.

Bimolecular Fluorescence Complementation Assay

The full-length coding sequences of KNU and WUS were cloned into pGreen vectors and transformed into Agrobacterium. The Agrobacteria were co-infiltrated into tobacco (*Nicotiana benthamiana*) leaves of 4-week-old plants as described previously (3). The infected tobacco leaves were cultured for 48-72 h before observation. For DAPI staining, leaves were immersed in 5 μg/mL DAPI solution. Leica TCS SP8-MaiTai M confocal microscopy was used for imaging.

Bimolecular Luciferase Complementation Assays

Bimolecular luciferase complementation (BiLC) assays were performed as previous description (4). The full length *WUS* CDS was cloned into JW771. The full length CDS of *WUS, HAM1* and *STM* were cloned into JW772 respectively. The full length *KNU* CDS was cloned into pGreen vector. The constructs were transformed into Agrobacterium subsequently. To test the WUS-WUS interaction, WUS-HAM1 interaction or WUS-STM interaction, Agrobacterium cells were resuspend at OD_{600}=0.8 and different combinations were co-infiltrated into tobacco leaves of 4-week-old plants. To monitor the disruptive effects of KNU for WUS-WUS, WUS-HAM1 or WUS-STM interactions, increasing amounts of Agrobacterium cells transformed with *35S:KNU* (OD_{600}=0.2 and 0.4) were incorporated and Agrobacterium cells transformed with empty pGreen vector served as control (OD_{600}=0.4). The infected tobacco leaves were cultured for 72 h before observation. The LUC activity was monitored with an imaging system (ChemiDOC^{TM} XRS+, Bio-Rad)

after luciferin was infiltrated for 10 min.

Statistical Analyses

The statistical difference between two groups were evaluated by Student's t-tests using SPSS software (version 21, IBM). The *P*-value < 0.05 represents significant difference. *P*-values < 0.05 are represented by an asterisk (*) and *P*-values < 0.01 are represented by two asterisk (**). Detailed results of statistical analyses are available in *SI Appendix,* Table S3.

Accession Numbers

All genes information in this study were obtained in the *Arabidopsis* Genome Initiative according to accession numbers as follows: *KNU* (AT5G14010), *WUS* (AT2G17950), *CLV1* (AT1G75820), *CLV2* (AT1G65380), *CLV3* (AT2G27250), *GIR1* (AT5G06270), *AtML1* (AT4G21750), *MCT1* (AT1G37140), *STM* (AT1G62360), *HAM1* (AT2G45160), *CRN* (AT5G13290), *RPK2* (AT3G02130), *BAM1* (AT5G65700), *BAM2* (AT3G49670), *BAM3* (AT4G20270), *CIK1* (AT1G60800), *CIK2* (AT2G23950), *CIK3* (AT4G30520), *CIK4* (AT5G45780), *CLE6* (AT2G31085), *CLE9* (AT1G26600), *CLE10* (AT1G69320), *CLE11* (AT1G49005), *CLE12* (AT1G68795), *CLE13* (AT1G73965), *CLE18* (AT1G66145), *CLE19* (AT3G24225), *CLE20* (AT1G05065), *CLE21* (AT5G64800), *CLE22* (AT5G12235), *CLE45* (AT1G69588), *AP1* (AT1G69120), *CAL* (AT1G26310), *MIR394B* (AT1G76135), *LCR* (AT1G27340).

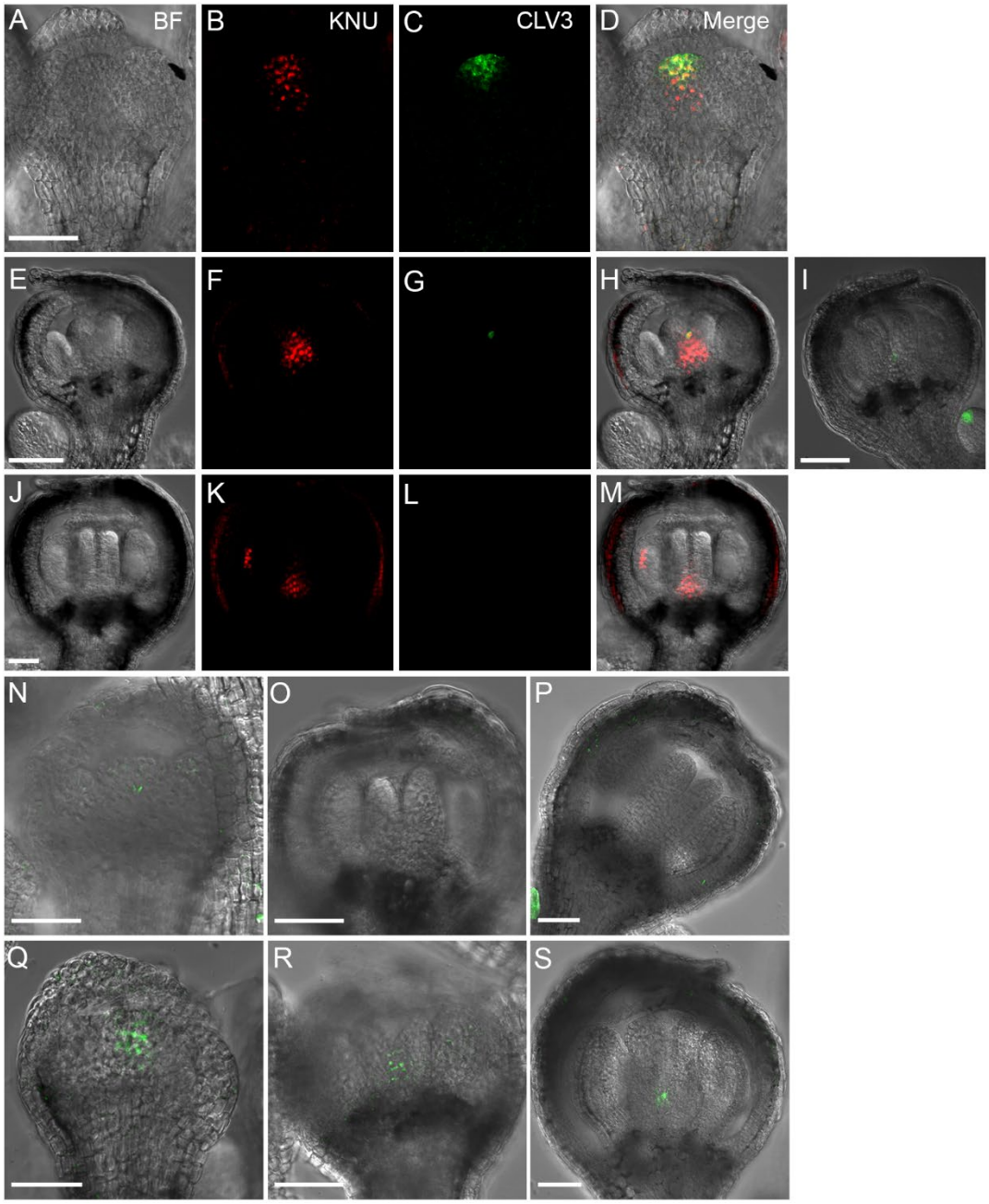

Fig. S1. Expression patterns of *KNU*, *CLV3* and *WUS* in floral buds. (*A*-*M*) Expression patterns of *KNU* and *CLV3* in floral buds from plant doubly transgenic for *pKNU:KNU-VENUS* (red) and *pCLV3:GFP-ER* (green). (*A*–*D*) stage 6 floral bud, (*E*-*I*) stage 7 floral bud, and (*J*–*M*) stage 8 floral bud. (*N*-*S*) *WUS* expressions in early floral buds. (*N*-*P*) WUS activity in flower buds in stage 6 (*N*), stage 7 (*O*) and stage 8 (*P*) of *pWUS:WUS-linker-GFP*. (*Q*-*S*) WUS activity in flower buds in stage 6 (*Q*), stage 7 (*R*) and stage 8 (*S*) of *knu-2 pWUS:WUS-linker-GFP*. (Scale bars: 50 μm).

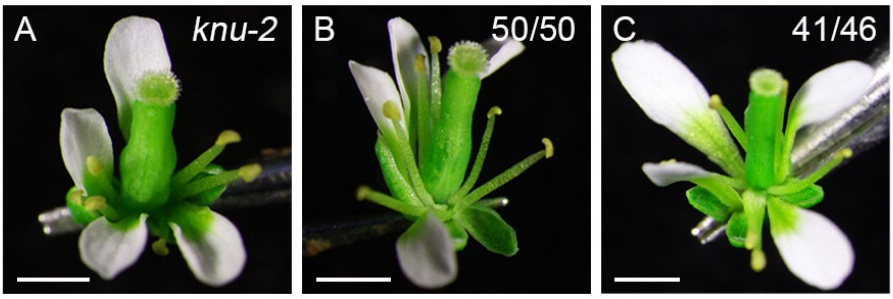

Fig. S2. The indeterminate phenotype of *knu-2* is rescued by induced KNU in *35S:KNU-GR knu-2* lines. (*A*) Flower phenotype of *knu-2*. (*B-C*) Flower phenotypes of *35S:KNU-GR knu-2* with one time (*B*) and 3 times (*C*) of DEX treatments. (Scale bars: 1 mm). Numbers indicate the ratio of flowers with little rescue (*B*) and full rescue (*C*).

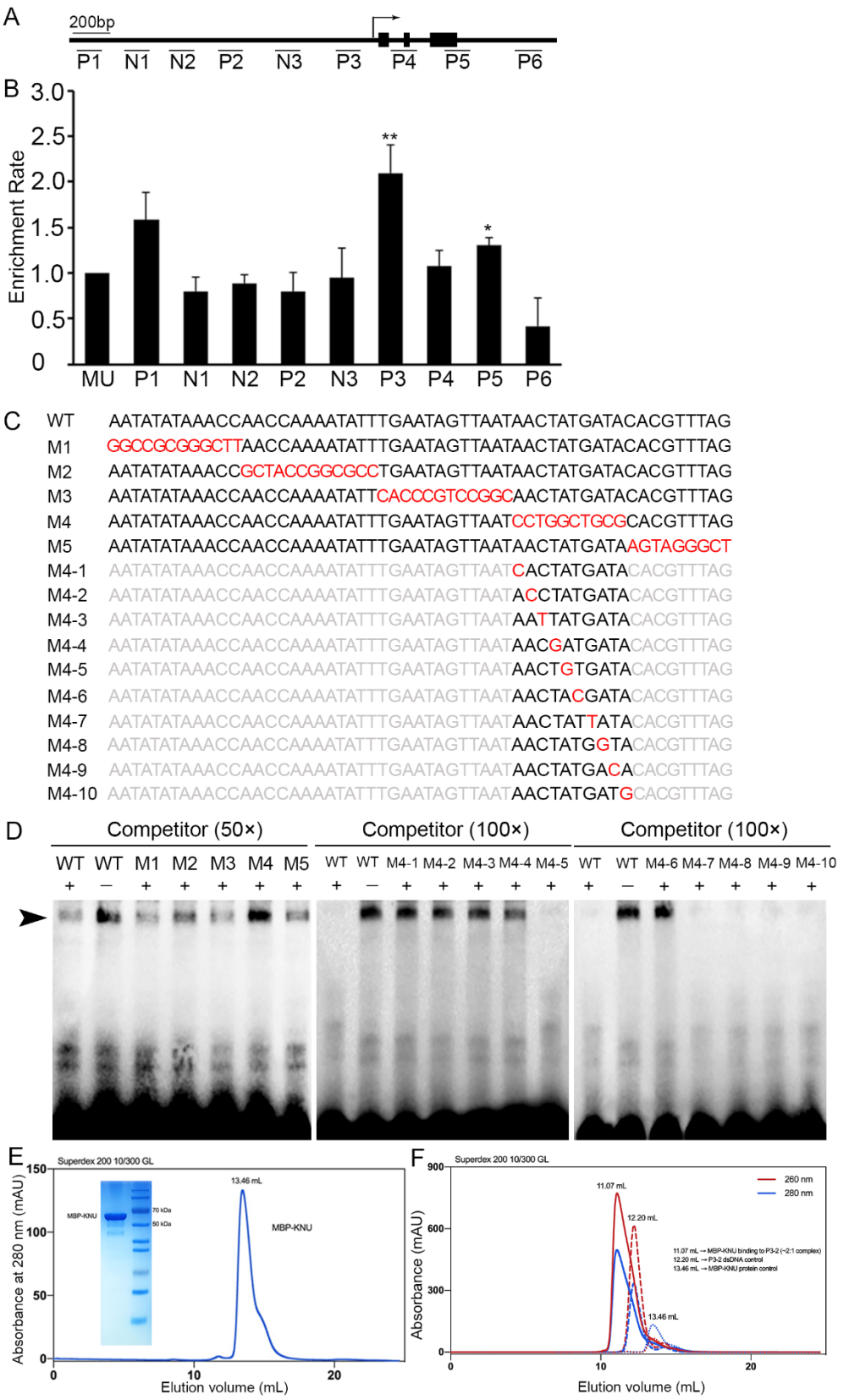
A
200bp
P1 N1 N2 P2 N3 P3 P4 P5 P6
B
Enrichment Rate
3.0
2.5
2.0
1.5
1.0
0.5
0
**
*
MU P1 N1 N2 P2 N3 P3 P4 P5 P6
C
WT AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATGATACACGTTTAG
M1 GGCCGCGGGCTTAACCAAAATATTTGAATAGTTAATAACTATGATACACGTTTAG
M2 AATATATAAACCGCTACCGGCGCCTGAATAGTTAATAACTATGATACACGTTTAG
M3 AATATATAAACCAACCAAAATATTCACCCGTCCGGCAACTATGATACACGTTTAG
M4 AATATATAAACCAACCAAAATATTTGAATAGTTAATCCTGGCTGCGCACGTTTAG
M5 AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATGATAAGTAGGGCT
M4-1 AATATATAAACCAACCAAAATATTTGAATAGTTAATCACTATGATACACGTTTAG
M4-2 AATATATAAACCAACCAAAATATTTGAATAGTTAATACCTATGATACACGTTTAG
M4-3 AATATATAAACCAACCAAAATATTTGAATAGTTAATAATTATGATACACGTTTAG
M4-4 AATATATAAACCAACCAAAATATTTGAATAGTTAATAACGATGATACACGTTTAG
M4-5 AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTGTGATACACGTTTAG
M4-6 AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTACGATACACGTTTAG
M4-7 AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATTATACACGTTTAG
M4-8 AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATGGTACACGTTTAG
M4-9 AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATGACACACGTTTAG
M4-10 AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATGATGCACGTTTAG
D
Competitor (50×)
Competitor (100×)
Competitor (100×)
WT WT M1 M2 M3 M4 M5
WT WT M4-1 M4-2 M4-3 M4-4 M4-5
WT WT M4-6 M4-7 M4-8 M4-9 M4-10
E
Superdex 200 10/300 GL
MBP-KNU
70 kDa
50 kDa
13.46 mL
MBP-KNU
Absorbance at 280 nm (mAU)
Elution volume (mL)
F
Superdex 200 10/300 GL
260 nm
280 nm
11.07 mL
12.20 mL
13.46 mL
11.07 mL → MBP-KNU binding to P3-2 (~2:1 complex)
12.20 mL → P3-2 dsDNA control
13.46 mL → MBP-KNU protein control
Absorbance (mAU)
Elution volume (mL)

Fig. S3. KNU directly binds to *CLV3* promoter. (*A*) Schematic diagram of *CLV3* locus and originally designed 9 primer sets used for ChIP assays. (*B*) ChIP assay using *ap1 cal 35S:KNU-GR-myc* inflorescences. Nuclear proteins were immuno-precipitated with anti-c-Myc agarose beads, and the enriched DNA was used for q-PCR assays. The y-axis shows relative enrichment compared with no antibody (negative control). MU served as a negative control locus, and the values of MU were calibrated to 1. Error bars represent SD of three biological replicates. Asterisks indicate significant differences between MU and different primer sets on *CLV3* (*$P < 0.05$ and **$P < 0.01$, Student's *t*-test). N1-N3 primer sets showing no enrichment and were omitted in main figures, and P1-P6 were used as representative primer sets in the main figures. (*C*) Sequences of WT and mutated competitors of P3-2 oligonucleotides (from –210-bp to –156bp upstream of ATG start codon) used for the EMSAs. The red letters represent mutated oligonucleotides. (*D*) The binding of KNU to WT P3-2 is not affect by M4, and is slightly weakened by single nucleotide mutant competitor probes including M4-1, M4-2, M4-3, M4-4 and M4-6. The black arrow indicates DNA-protein complex. Non-labeled oligo-nucleotides were used as competitors. (*E* and *F*) Interaction of KNU with P3-2 dsDNA in vitro. (*E*) The purity of recombinant MBP-tagged KNU (MBP-KNU) as demonstrated by SDS-PAGE (left) and analytical size-exclusion chromatography (right). MBP-KNU (100 µL) at 1 mg/ml was applied to a Superdex 200 Increase 10/300 GL column. (*F*) Size-exclusion chromatographic profiles of individual MBP-KNU (150 µM) (dotted line), dsDNA (75 µM) (dashed line), and their mixture (solid line). Samples were detected by examining the absorbance at 280 nm (blue lines) and 260 nm (red lines).

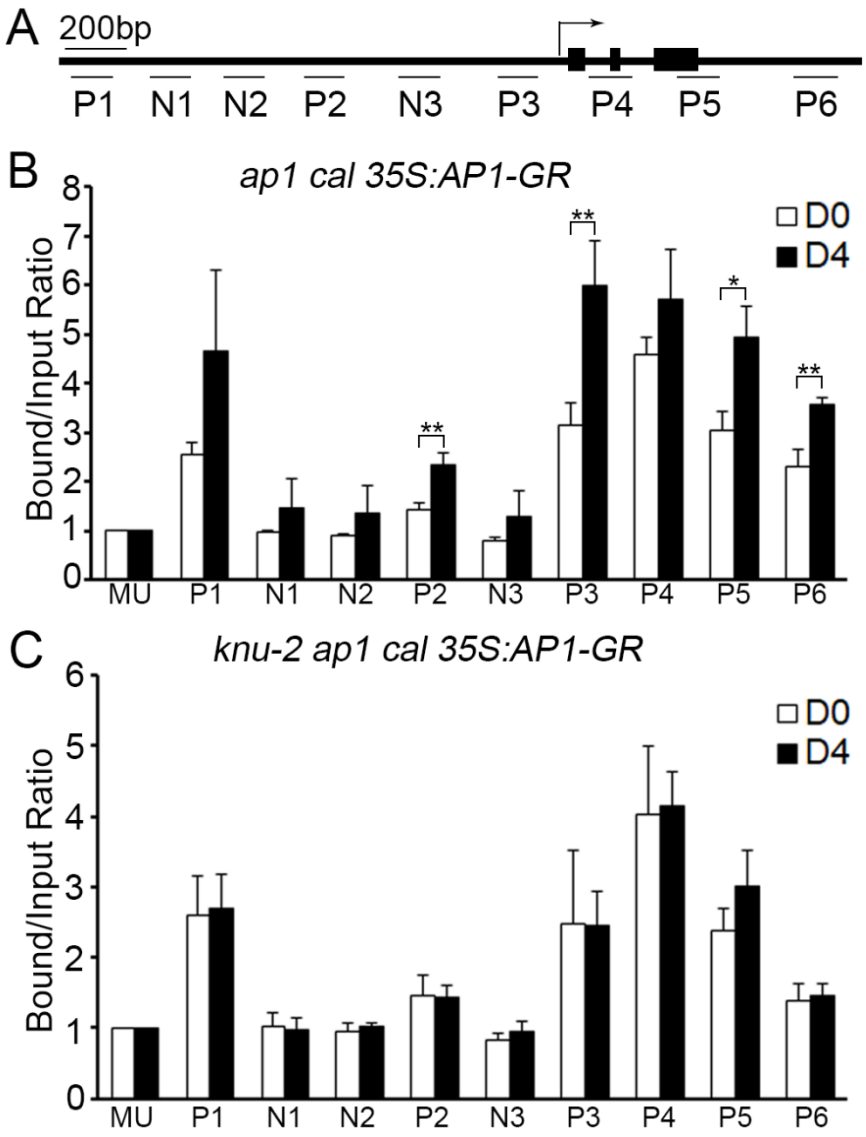

Fig. S4. H3K27me3 deposition on *CLV3* is KNU-dependent. (*A*) Schematic diagram of *CLV3* locus and primer sets used for ChIP assays. (*B* and *C*) Analysis of H3K27me3 enrichment on *CLV3* by ChIP assays using *ap1 cal 35S:AP1-GR* inflorescences (*B*) and *knu-2 ap1 cal 35S:AP1-GR* (*C*) in day 0 (D0) and day 4 (D4) after treatment with DEX. MU served as negative control locus and the values of MU were calibrated to 1. Error bars represent SD of three biological replicates. Asterisks indicate significant differences between D0 and D4 at certain primer sets on *CLV3* (*$P < 0.05$ and **$P < 0.01$, Student's *t* test).

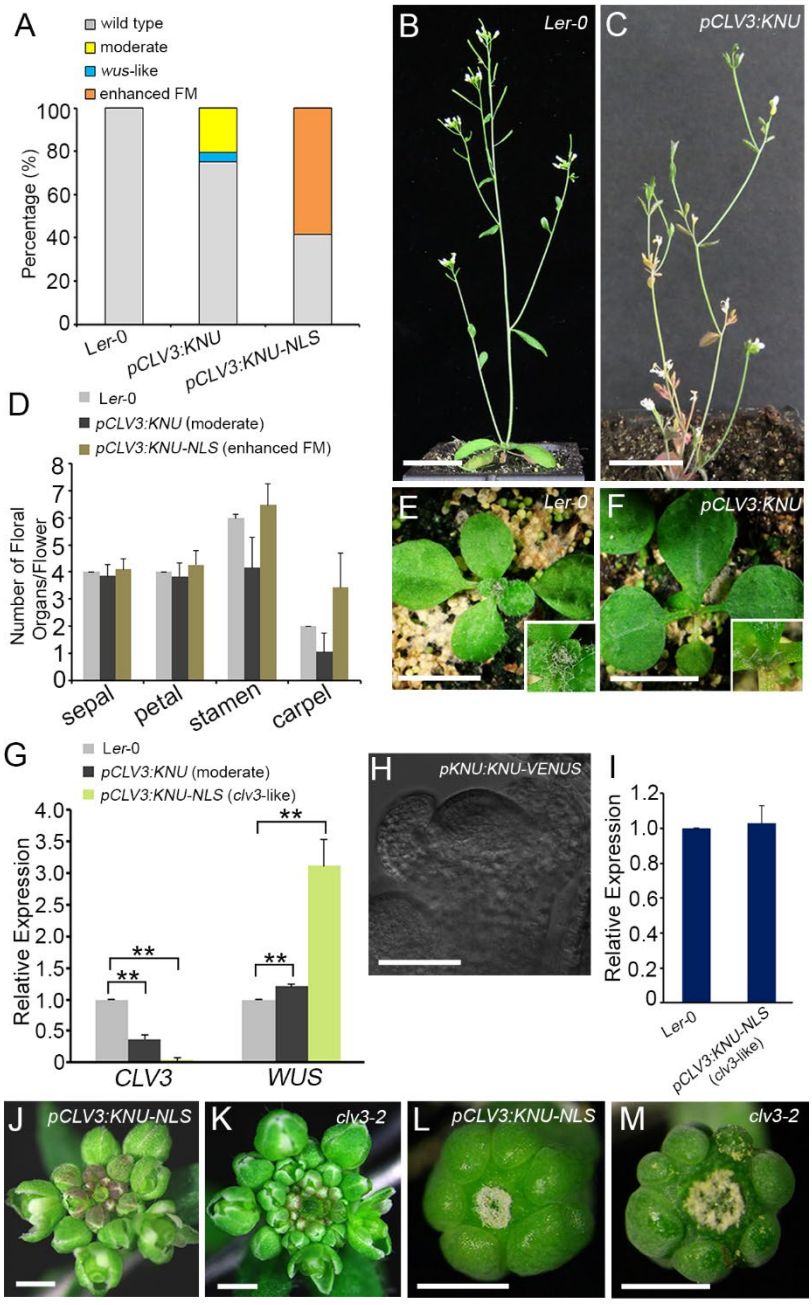
A
wild type
moderate
wus-like
enhanced FM
Percentage (%)
100
80
60
40
20
0
Ler-0
pCLV3:KNU
pCLV3:KNU-NLS
B
Ler-0
C
pCLV3:KNU
D
Ler-0
pCLV3:KNU (moderate)
pCLV3:KNU-NLS (enhanced FM)
Number of Floral Organs/Flower
8
7
6
5
4
3
2
1
0
sepal
petal
stamen
carpel
E
Ler-0
F
pCLV3:KNU
G
Ler-0
pCLV3:KNU (moderate)
pCLV3:KNU-NLS (clv3-like)
Relative Expression
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0
**
**
**
**
CLV3
WUS
H
pKNU:KNU-VENUS
I
Relative Expression
1.2
1.0
0.8
0.6
0.4
0.2
0
Ler-0
pCLV3:KNU-NLS (clv3-like)
J
pCLV3:KNU-NLS
K
clv3-2
L
pCLV3:KNU-NLS
M
clv3-2

Fig. S5. KNU represses *CLV3* in *pCLV3:KNU* and *pCLV3:KNU-NLS*. (*A*) Phenotypic analysis of L*er*-0 (*n* = 100), *pCLV3:KNU* (*n* = 113) and *pCLV3:KNU-NLS* (*n* = 228) T1 plants. (*B* and *C*) Phenotypes of L*er*-0 (*B*) and *pCLV3:KNU* lines of moderate phenotype (*C*). (*D*) Average numbers of floral organs in *Ler-0*, *pCLV3:KNU* lines of moderate phenotype and *pCLV3:KNU-NLS* enhanced FM lines. Floral organs from 100 random flowers were used for analysis. (*E* and *F*) The seedling phenotypes of L*er*-0 (*E*) and *pCLV3:KNU* (*wus*-like)lines (*F*). (*G*) Levels of *CLV3* and *WUS* mRNA in inflorescence samples from L*er*-0, *pCLV3:KNU* moderate lines and *pCLV3:KNU-NLS* (*clv3*-like)lines. (*H*) The activity of KNU was not detected in stage 3 bud of *pKNU:KNU-VENUS* plants. (*I*) Levels of endogenous *KNU* mRNA in inflorescence samples (with floral buds no later than stage 7) from L*er*-0 and *pCLV3:KNU-NLS* (*clv3*-like) lines. Transcript levels are quantified by q-PCR in (*G* and *I*). For q-PCR, *Tip41-like* served as the internal control. Error bars represent SD of three biological replicates. Asterisks indicate significant differences between L*er*-0 and transgenic lines (*$P < 0.05$ and **$P < 0.01$, Student's *t* test). (*J* and *K*) The inflorescence phenotypes of *pCLV3:KNU-NLS* (*clv3*-like)lines (*J*) and *clv3-2* (*K*). (*L* and *M*) The silique phenotypes of *pCLV3:KNU-NLS* (*clv3*-like)lines (*L*) and *clv3-2* (*M*). (Scale bars: 2 cm in *B* and *C*; 1 cm in *E* and *F*; 50 μm in *H*; 1 mm in *J*–*M*).

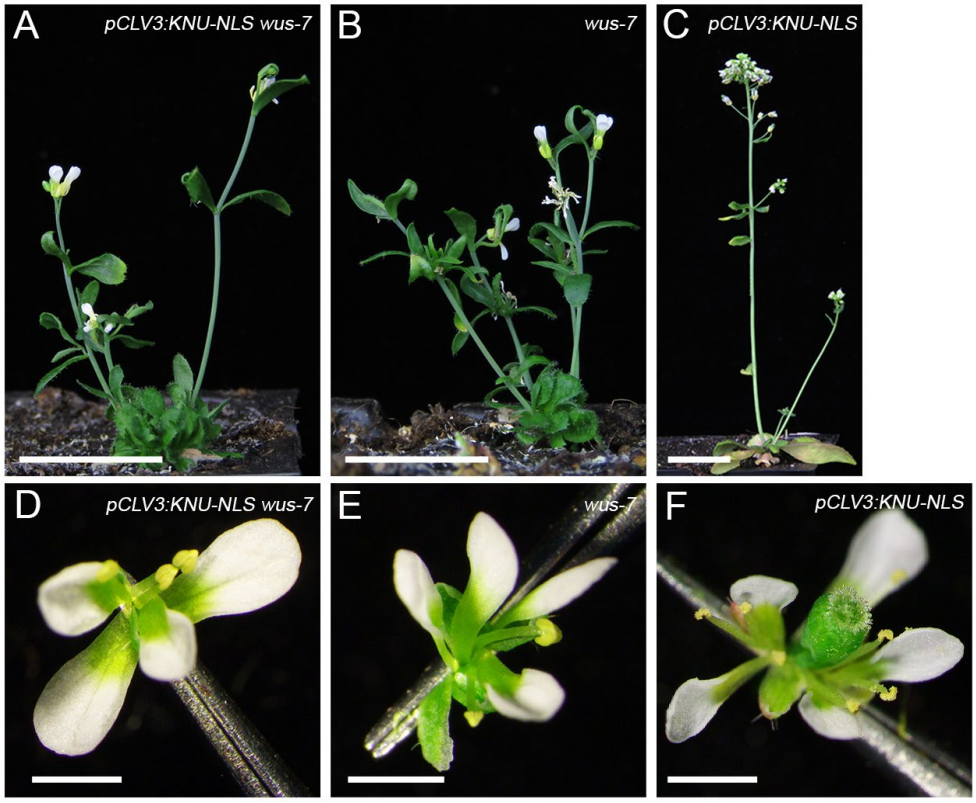

Fig. S6. KNU represses *CLV3* through *CLV-WUS* pathway. (*A-C*) Plant phenotypes of *wus-7 pCLV3:KNU-NLS* (*clv3*-like) (*A*), *wus-7* (*B*) and *pCLV3:KNU-NLS* (*clv3*-like)(*C*). (*D-F*) Flower phenotypes of *wus-7 pCLV3:KNU-NLS* (*clv3*-like)(*D*), *wus-7* (*E*) and *pCLV3:KNU-NLS* (*clv3*-like)(*F*). (Scale bars: 2 cm in *A-C*; 1 mm in *D–F*).

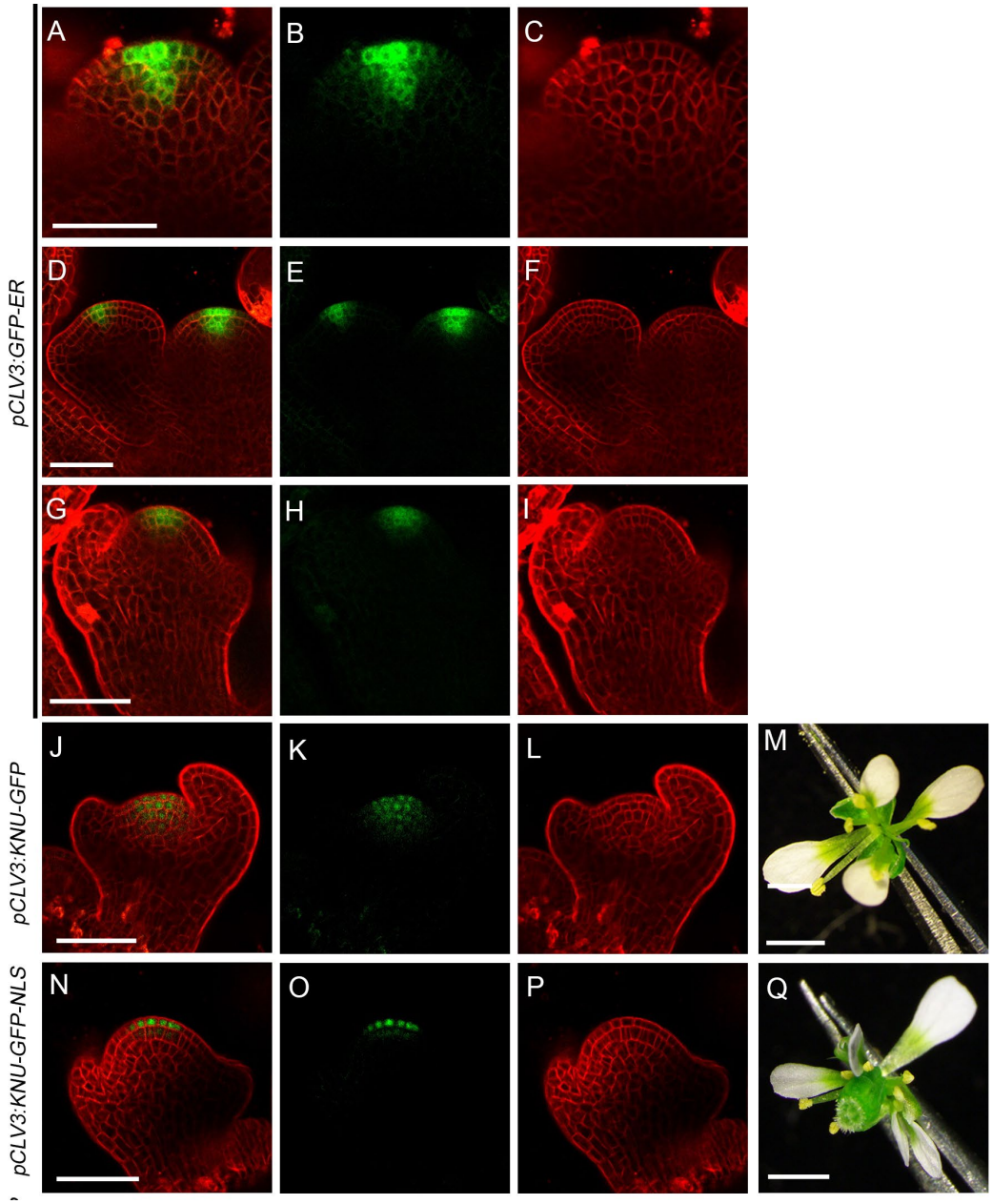

Fig. S7. KNU represses *CLV3* in FM. (*A-I*) GFP signals in SAM (*A-F*) and stage 3-4 floral bud (*G-I*) of *pCLV3:GFP-ER* plants. (*J-L*) GFP signals in stage 3-4 floral bud of *pCLV3:KNU-GFP* plants. (*M*) Flower phenotype of *pCLV3:KNU-GFP*. (*N-P*) GFP signals in stage 3-4 floral bud of *pCLV3:KNU-GFP-NLS* (enhanced FM). (*Q*) Flower phenotype of *pCLV3:KNU-GFP-NLS* (enhanced FM). (Scale bars: 50 μm in *A-L*, *N-P*; 1 mm in *M* and *Q*).

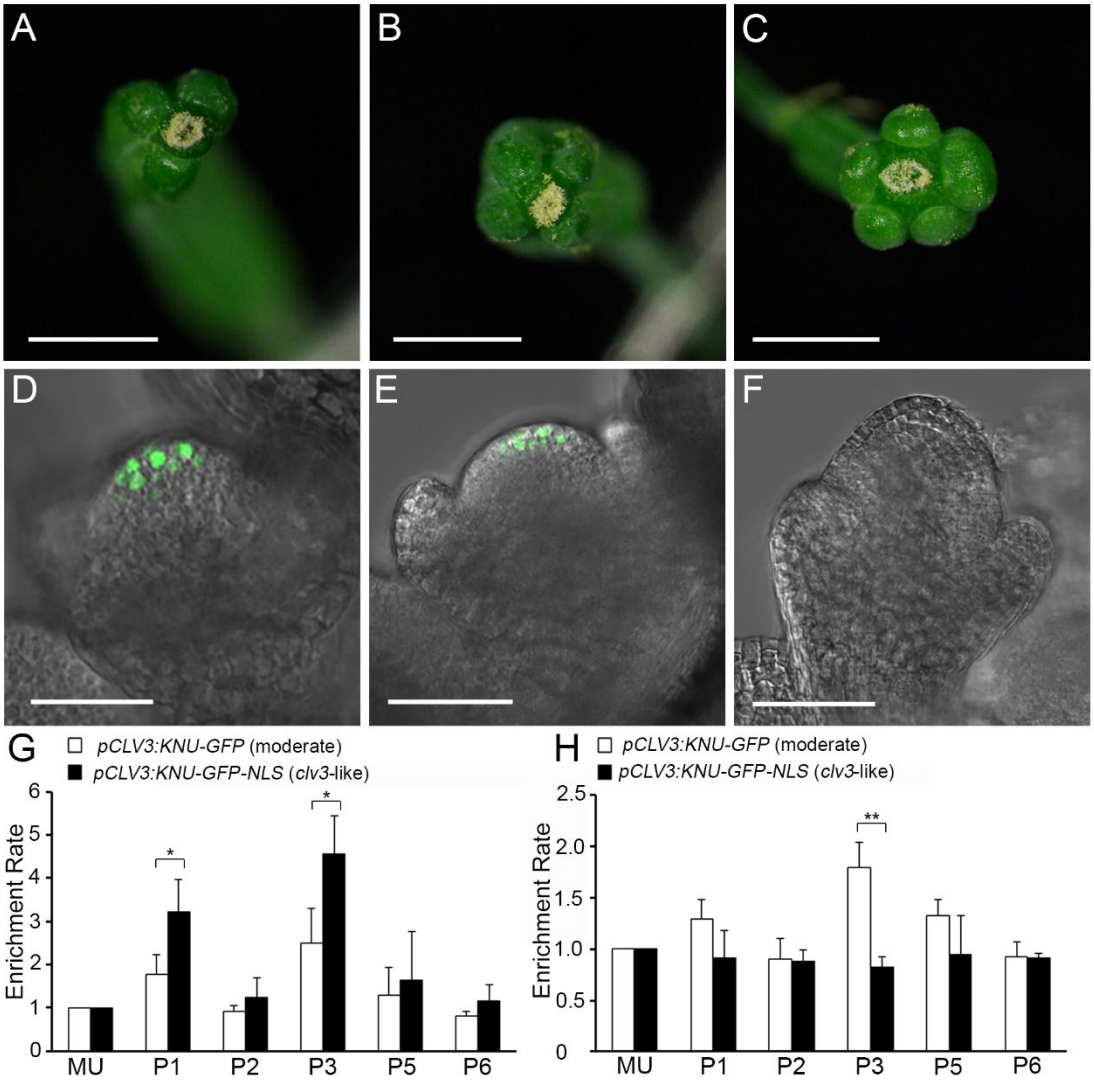

Fig. S8. KNU represses of *CLV3* promoter activity. (*A*-*C*) Siliques of *pCLV3:KNU-GFP-NLS* showing different extent of FM indeterminacy. (*D*-*F*) GFP signals in stage 3-4 floral buds corresponding to siliques in (*A*-*C*). (*G* and *H*) ChIP assays for KNU (*G*) and Pol II (*H*) binding on *CLV3* by using inflorescences from *pCLV3:KNU-GFP* moderate lines and *pCLV3:KNU-GFP-NLS* (*clv3*-like) lines. Nuclear proteins were immuno-precipitated with GFP-trap in (*G*) and anti-pol II antibody in (*H*). MU served as negative control locus and the values of MU were calibrated to 1. Error bars represent SD of three biological replicates. Asterisks indicate significant differences between the two different lines at certain primer sets on *CLV3* (*$P < 0.05$ and ** $P < 0.01$, Student's *t* test). (Scale bars: 1 mm in *A*-*C*; 50 μm in *D*-*F*).

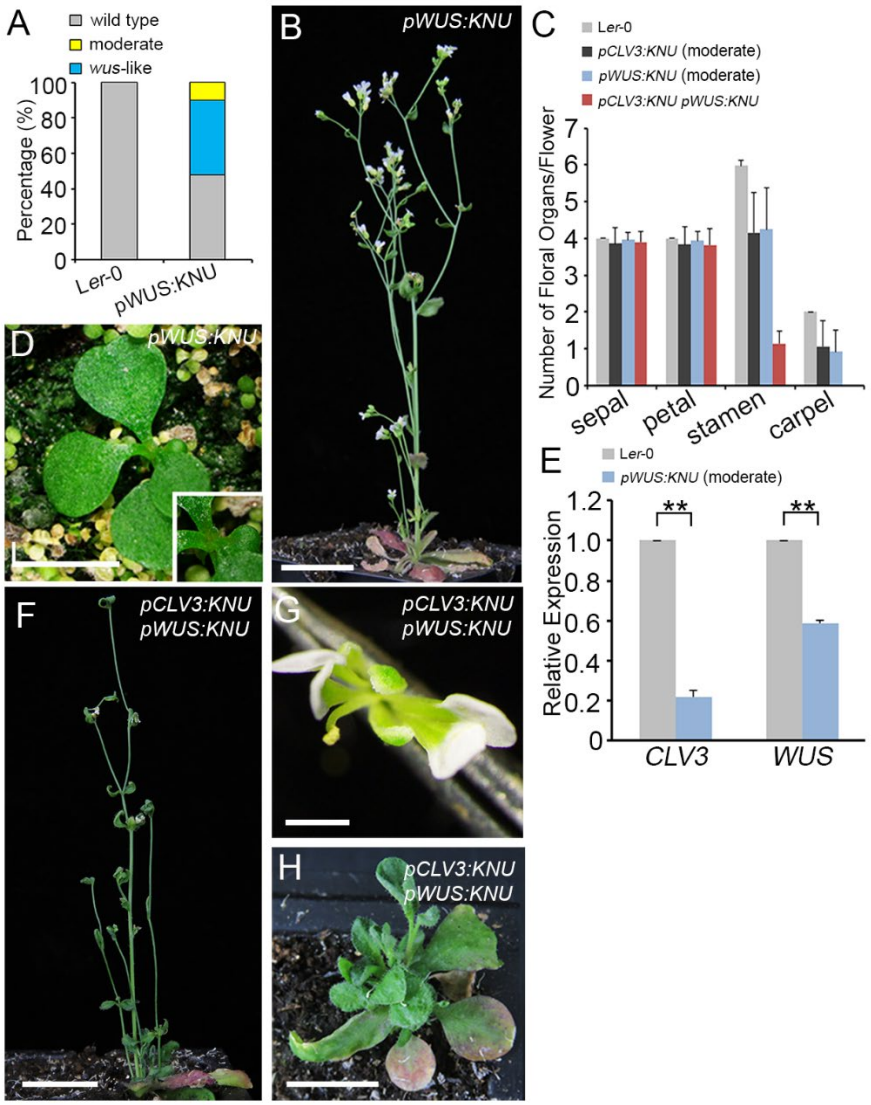

Fig. S9. KNU represses *CLV3* and *WUS* in FM synergistically. (*A*) Phenotypic analysis of L*er*-0 (*n* = 100) and *pWUS:KNU* (*n* = 138). (*B*) Plant of *pWUS:KNU* with moderate phenotype. (*C*) Average number of floral organs in *Ler-0* (*n* = 100), *pCLV3:KNU* (*n* = 100) with moderate phenotype, *pWUS:KNU* (*n* = 100) with moderate phenotype and *pCLV3:KNU pWUS:KNU* (*n* = 100). (*D*) Phenotype of *pWUS:KNU* (*wus*-like) seedling . (*E*) *CLV3* and *WUS* mRNA levels in inflorescences of L*er*-0 and *pWUS:KNU* with moderate phenotype. Transcript levels are quantified by q-PCR. *Tip41-like* served as the internal control. Error bars represent SD of three biological replicates. Asterisks indicate significant differences between L*er*-0 and *pWUS:KNU* (**$P < 0.01$, Student's *t* test). (*F* and *H*) Phenotypes of *pCLV3:KNU pWUS:KNU* plants. (*G*) Flower of *pCLV3:KNU pWUS:KNU*. (Scale bars: 2 cm in *B* and *F*; 1 cm in *D* and *H* and 1 mm in *G*).

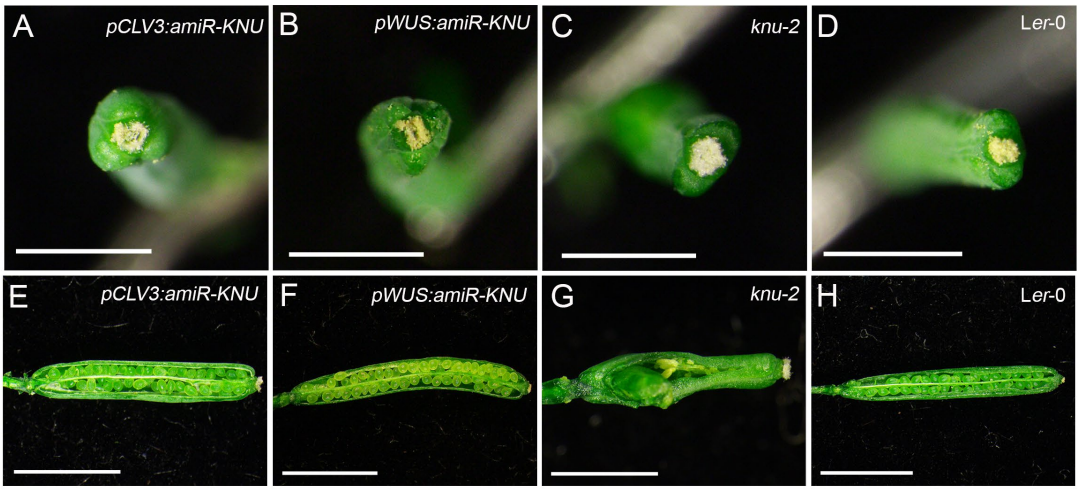

Fig. S10. Silique phenotypes of *pCLV3:amiR-KNU* (*A* and *E*), *pWUS:amiR-KNU* (*B* and *F*), *knu-2* (*C* and *G*) and L*er*-0 (*D* and *H*). (Scale bars: 1 cm).

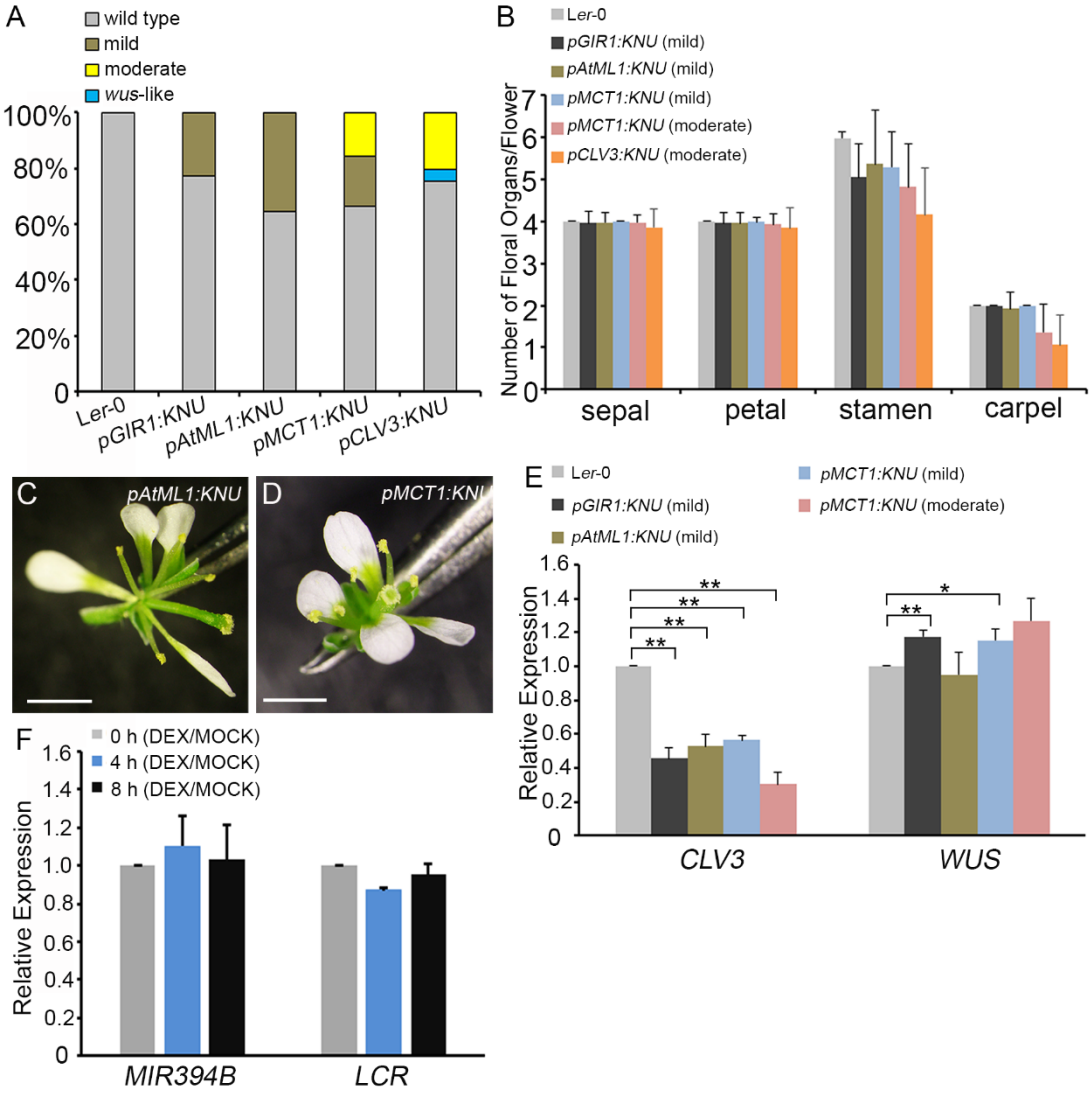
A
wild type
mild
moderate
wus-like
100%
80%
60%
40%
20%
0
Ler-0
pGIR1:KNU
pAtML1:KNU
pMCT1:KNU
pCLV3:KNU
B
Ler-0
pGIR1:KNU (mild)
pAtML1:KNU (mild)
pMCT1:KNU (mild)
pMCT1:KNU (moderate)
pCLV3:KNU (moderate)
Number of Floral Organs/Flower
sepal
petal
stamen
carpel
C
pAtML1:KNU
D
pMCT1:KNU
E
Ler-0
pGIR1:KNU (mild)
pAtML1:KNU (mild)
pMCT1:KNU (mild)
pMCT1:KNU (moderate)
Relative Expression
CLV3
WUS
F
0 h (DEX/MOCK)
4 h (DEX/MOCK)
8 h (DEX/MOCK)
Relative Expression
MIR394B
LCR

Fig. S11. KNU regulates FM determinacy in different stem cell layers independent of *miR394* signaling. (*A*) Phenotypic analysis of L*er*-0 (*n* = 100), *pGIR1:KNU* (*n* = 101), *pAtML1:KNU* (*n* = 87), *pMCT1:KNU* (*n* = 122) and *pCLV3:KNU* (*n* = 113). (*B*) Average number of floral organs in *Ler-0*, *pGIR1:KNU* lines of mild phenotype, *pAtML1:KNU* lines of mild phenotype, *pMCT1:KNU* lines of mild phenotype, *pMCT1:KNU* lines of moderate phenotype and *pCLV3:KNU* lines of moderate phenotype. Random 100 flowers each were used for analysis. (*C* and *D*) Flower phenotypes of *pAtML1:KNU* (*C*) and *pMCT1:KNU* (*D*). (*E*) *CLV3* and *WUS* mRNA levels in inflorescence from L*er*-0, *pGIR1:KNU*, *pAtML1:KNU* and *pMCT1:KNU*. Transcript levels are quantified by q-PCR.. Asterisks indicate significant differences between L*er*-0 and different transgenic lines (*$P < 0.05$ and **$P < 0.01$, Student's *t* test). (*F*) *MIR394B* and *LCR* mRNA levels in *ap1 cal 35S:KNU-GR-myc* inflorescences after single DEX treatment. Gene transcript levels are quantified by q-PCR. For q-PCR analysis (*E* and *F*), *Tip41-like* served as the internal control. Error bars represent SD of three biological replicates for (*E*) and two biological replicates for (*F*). (Scale Bars: 1 mm).

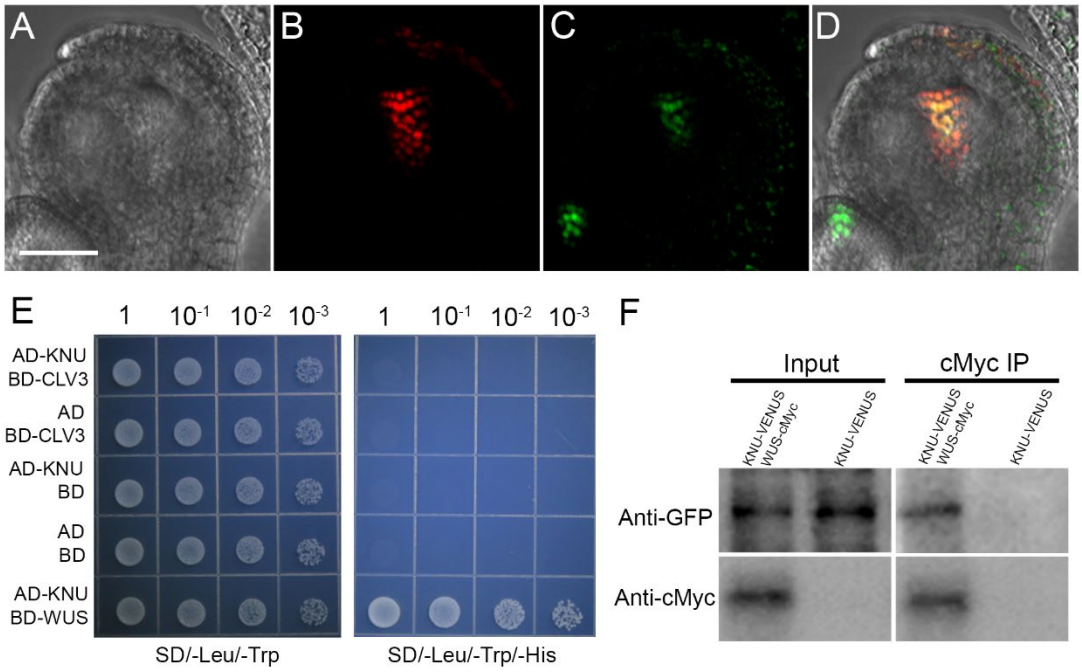

Fig. S12. KNU physically interacts with WUS but not CLV3. (*A-D*) Expression patterns of *KNU* and *WUS* in stage 6 floral bud from plant doubly transgenic for *pKNU:KNU-VENUS* (red) and *pWUS:WUS-linker-GFP* (green). (Scale bars: 50 µm). (*E*) Y2H assay using full-length KNU and CLV3. Transformed yeast cells were grown on SD/-Leu/-Trp and SD/-Leu/-Trp/-His supplemented with 2 mM 3-AT. AD-KNU/BD-WUS serves as positive control. AD or BD refers to empty vector only. (*F*) Co-IP assay. Nuclear extracts were incubated with anti-c-Myc agarose beads. In Western blot analysis, KNU-VENUS and WUS-cMyc was immunoblotted with anti-GFP and anti-cMyc, respectively. Test and control represent samples from stage 6-7 flower buds of *ap1 cal 35S:AP1-GR pKNU:KNU-VENUS pWUS:WUS-myc* (*KNU-VENUS WUS-cMyc*) and *ap1 cal 35S:AP1-GR pKNU:KNU-VENUS* (*KNU-VENUS*), respectively. IP represents immunoprecipitation.

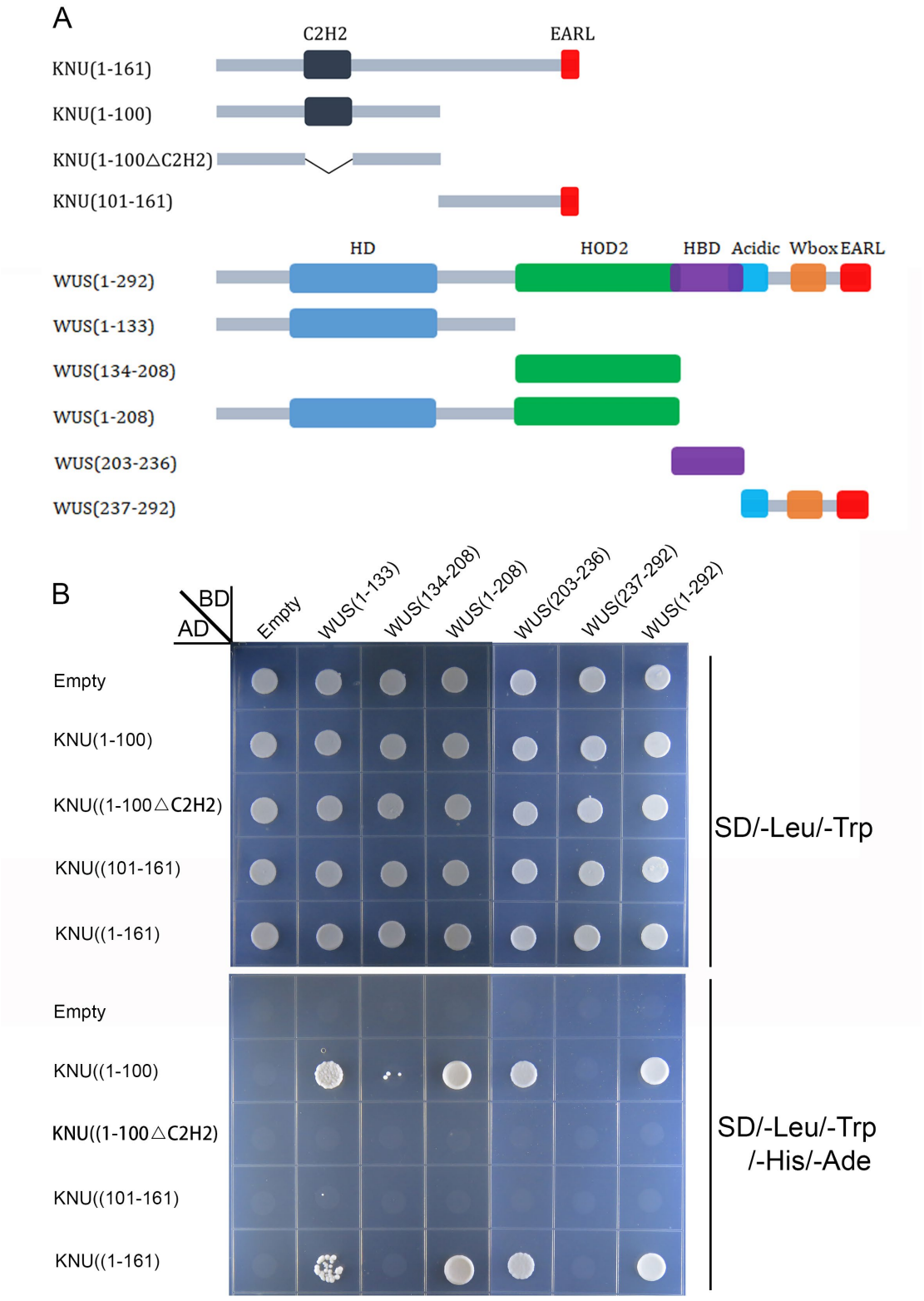
A
C2H2
EARL
KNU(1-161)
KNU(1-100)
KNU(1-100△C2H2)
KNU(101-161)
HD
HOD2
HBD
Acidic
Wbox
EARL
WUS(1-292)
WUS(1-133)
WUS(134-208)
WUS(1-208)
WUS(203-236)
WUS(237-292)
B
BD
AD
Empty
WUS(1-133)
WUS(134-208)
WUS(1-208)
WUS(203-236)
WUS(237-292)
WUS(1-292)
Empty
KNU(1-100)
KNU((1-100△C2H2)
KNU((101-161)
KNU((1-161)
SD/-Leu/-Trp
Empty
KNU((1-100)
KNU((1-100△C2H2)
KNU((101-161)
KNU((1-161)
SD/-Leu/-Trp
/-His/-Ade

Fig. S13. Y2H assay for different domains of KNU and WUS. (*A*) Schematic diagrams of full length and truncated forms of protein KNU and WUS. For KNU, C2H2 and EARL indicate C2H2 domain (amino acids 40-60) and EAR-like motif (amino acids 155-161) respectively. For WUS, HD indicates homeodomain (amino acids 34-99), HOD2 indicates the second homodimerization interaction domains (amino acids 134-208), HBD indicates HAM binding domain (amino acids 203-236), Acidic indicates acidic domain, Wbox indicates WUS box and EARL indicates EAR-like motif. (*B*) Y2H assays. Transformed yeast cells were grown on SD/–Leu/–Trp (top panel) and SD/-Leu/-Trp/-His/-Ade/ (bottom panel) media. Empty refers to the AD or BD only.

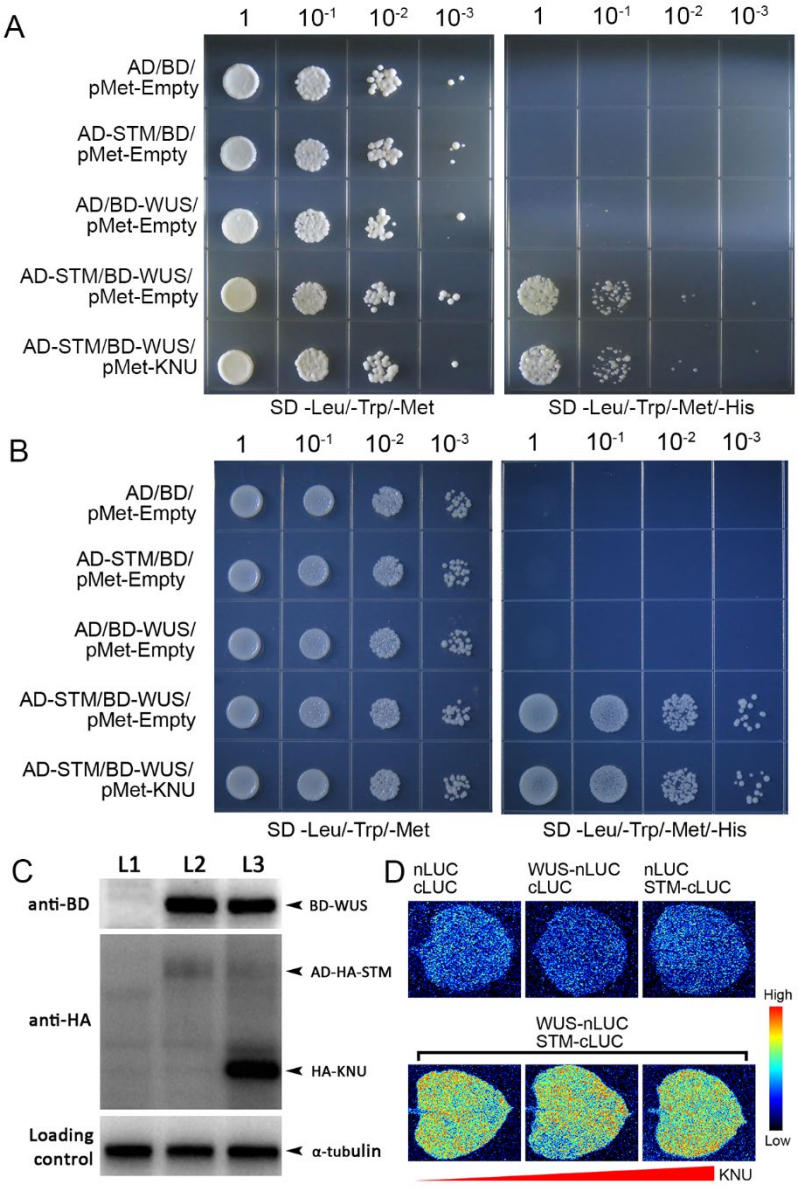

Fig. S14. KNU does not affect WUS-STM interaction. (*A* and *B*) Y3H assay. Transformed yeast cells were grown on SD/-Leu/-Trp/-Met and SD/-Leu/-Trp/-Met/-His medium supplemented with 20 mM 3-AT. (*C*) Protein expression of WUS, STM and KNU in yeast cells for Y3H assay. Protein for Western blot analysis were extracted from AH109 (L1), AH109 transformed with AD-STM/BD-WUS/pMet-Empty (L2), and AH109 transformed with AD-STM/BD-WUS/pMet-KNU (L3). α-tubulin serves as a loading control. (*D*) BiLC assays. nLUC and cLUC refer to the N-terminal and C-terminal of luciferase. WUS-nLUC indicates WUS-nLUC fusion and STM-cLUC indicates STM-cLUC fusion. The color column on the right presents the range of luminescence intensity.

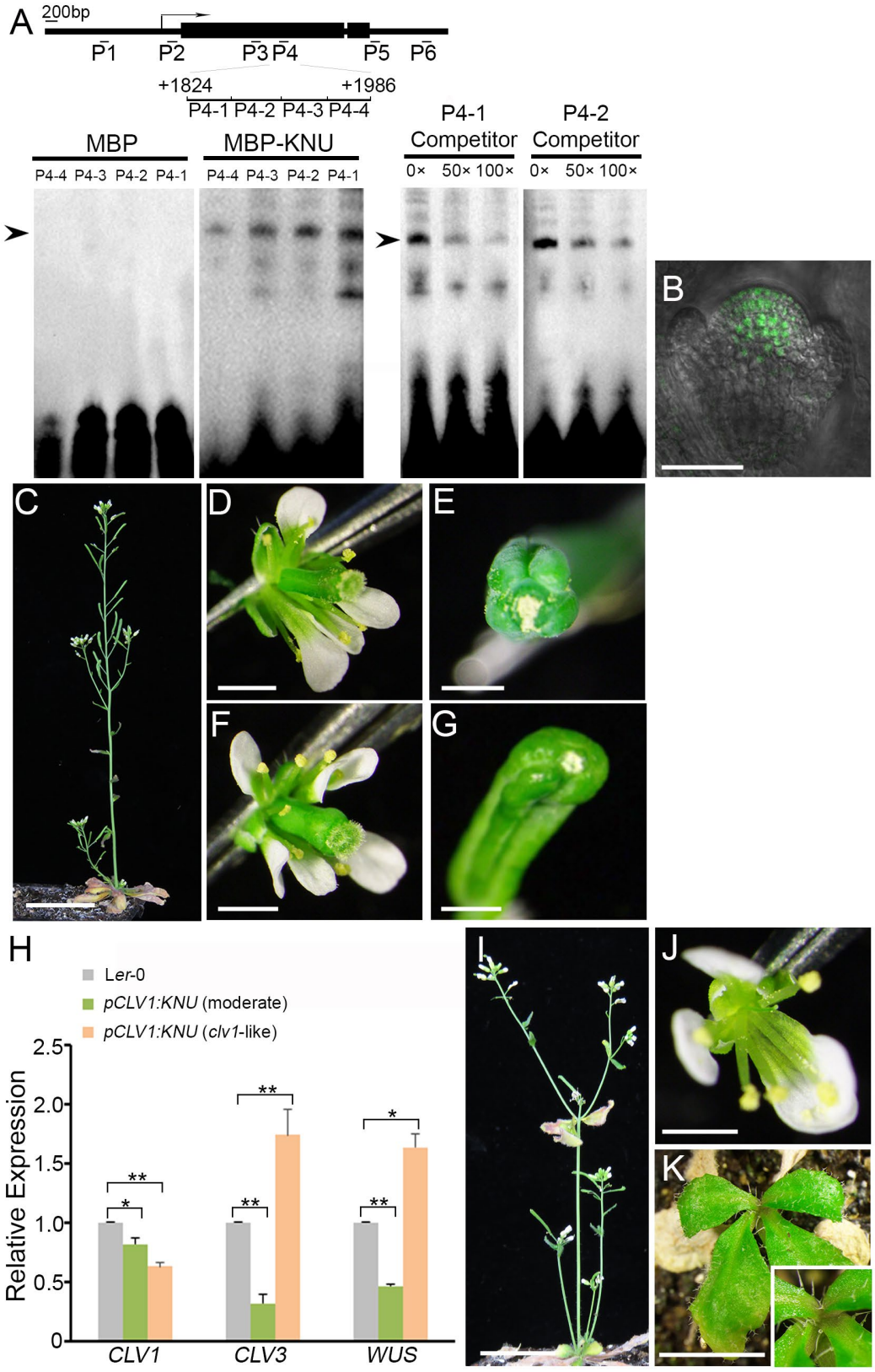
A
200bp
P1
P2
P3
P4
P5
P6
+1824
+1986
P4-1 P4-2 P4-3 P4-4
MBP
MBP-KNU
P4-4 P4-3 P4-2 P4-1
P4-4 P4-3 P4-2 P4-1
P4-1 Competitor
P4-2 Competitor
0× 50× 100×
0× 50× 100×
B
C
D
E
F
G
H
Ler-0
pCLV1:KNU (moderate)
pCLV1:KNU (clv1-like)
Relative Expression
2.5
2.0
1.5
1.0
0.5
0
CLV1
CLV3
WUS
I
J
K

Fig. S15. KNU directly represses *CLV1*. (*A*) EMSAs confirm that KNU binds to the P4-1 and P4-2 fragments. The black arrow indicates DNA-protein complex. Non-labeled oligo-nucleotides were used as competitors. MBP was used as a negative control. (*B*) GFP signal in the stage 3-4 floral buds of *pCLV1:KNU-GFP*. (*C*-*E*) Phenotypes of plant (*C*), flower (*D*) and silique (*E*) of *pCLV1:KNU* (*clv1*-like). (*F* and *G*) Phenotypes of flower (*F*) and silique (*G*) of *clv1-1*. (*H*) *CLV1*, *CLV3* and *WUS* mRNA levels in inflorescences of L*er*-0 and *pCLV1:KNU*. Transcript levels are quantified by q-PCR. *Tip41-like* served as the internal control. Error bars represent SD of three biological replicates. Asterisks indicate significant differences between L*er*-0 and *pCLV1:KNU* (* $P < 0.05$ and ** $P < 0.01$, Student's *t* test). (*I* and *J*) Phenotypes of plant (*I*) and flower (*J*) from *pCLV1:KNU* with moderate phenotype. (*K*) Phenotype of *pCLV1:KNU* (*wus*-like). (Scale bars: 50 μm in *B*; 2 cm in *C* and *I*; 1 mm in *D*-*G* and *J*; 1 cm in *K*).

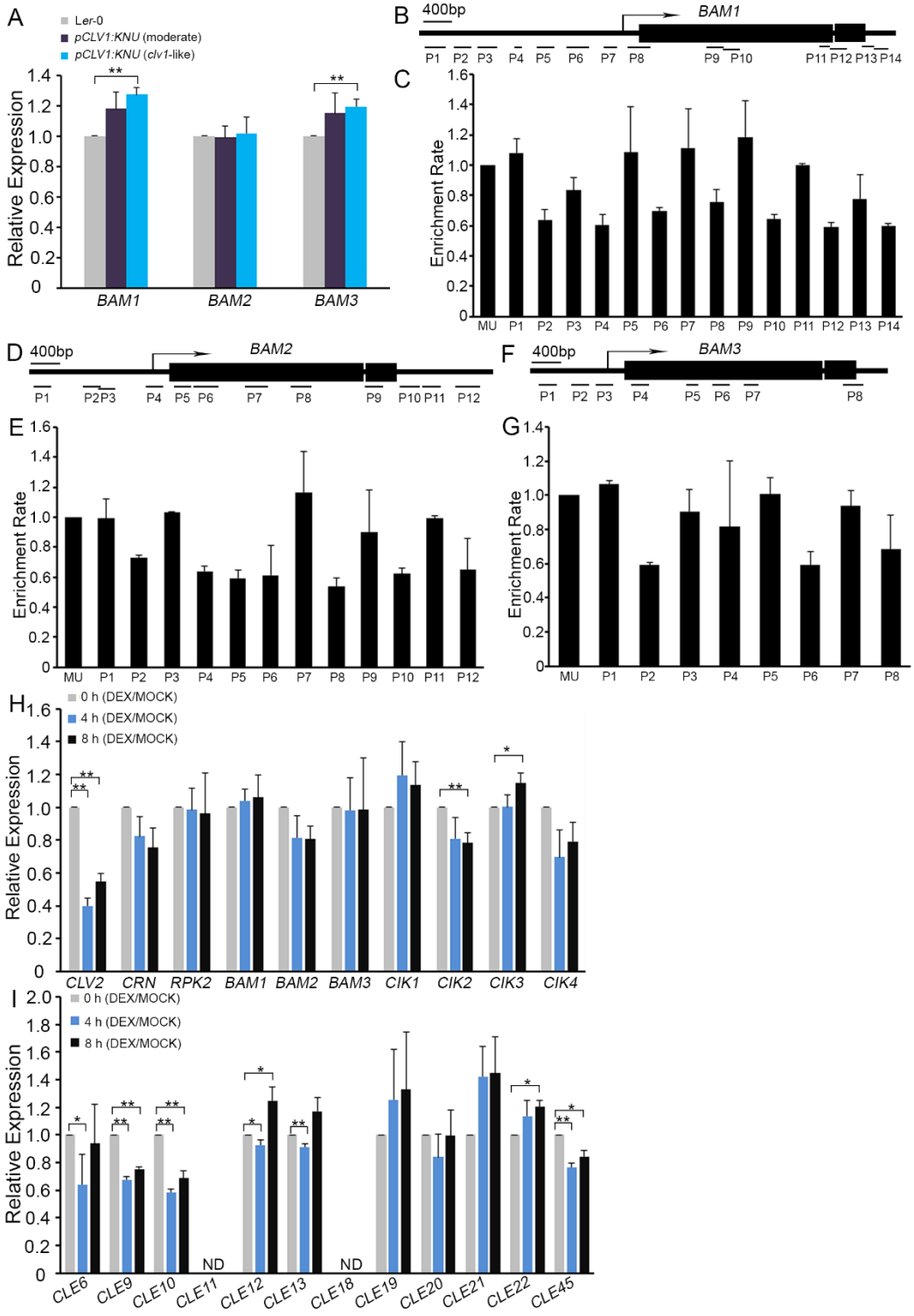
A
Ler-0
pCLV1:KNU (moderate)
pCLV1:KNU (clv1-like)
Relative Expression
BAM1
BAM2
BAM3
B
400bp
BAM1
P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12 P13 P14
C
Enrichment Rate
MU P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12 P13 P14
D
400bp
BAM2
P1 P2P3 P4 P5 P6 P7 P8 P9 P10 P11 P12
E
Enrichment Rate
MU P1 P2 P3 P4 P5 P6 P7 P8 P9 P10 P11 P12
F
400bp
BAM3
P1 P2 P3 P4 P5 P6 P7 P8
G
Enrichment Rate
MU P1 P2 P3 P4 P5 P6 P7 P8
H
0 h (DEX/MOCK)
4 h (DEX/MOCK)
8 h (DEX/MOCK)
Relative Expression
CLV2 CRN RPK2 BAM1 BAM2 BAM3 CIK1 CIK2 CIK3 CIK4
I
0 h (DEX/MOCK)
4 h (DEX/MOCK)
8 h (DEX/MOCK)
Relative Expression
ND
ND
CLE6 CLE9 CLE10 CLE11 CLE12 CLE13 CLE18 CLE19 CLE20 CLE21 CLE22 CLE45

Fig. S16. The compensation mechanisms in *pCLV1:KNU* and *ap1 cal 35S:KNU-GR-myc*. (*A*) Transcript levels of *BAMs* in inflorescences of L*er*-0 and *pCLV1:KNU*. Gene transcript levels are quantified by q-PCR. (*B*-*G*) KNU does not directly binds to *BAMs* locus in plants. (*B*, *D* and *F*) Schematic diagrams of *BAM1* (*B*)*, BAM2* (*D*) and *BAM3* (*F*) loci, and primer sets used for ChIP assays. (*C*, *E* and *G*) ChIP assays for KNU binding to *BAM1* (*C*)*, BAM2* (*E*) and *BAM3* (*G*) using *ap1 cal 35S:KNU-GR-myc* inflorescences. Nuclear proteins were immuno-precipitated with anti-c-Myc agarose beads, and the enriched DNA was used for q-PCR assays. The y-axis shows relative enrichment compared with no antibody (negative control). MU served as a negative control locus, and the values of MU were calibrated to 1. Error bars represent SD of two biological replicates. (*H* and *I*) Transcript levels of compensatory *CLV*-like signaling components (*H*) and *CLEs* (*I*) in *ap1 cal 35S:KNU-GR-myc* inflorescences after single DEX treatment. Gene transcript levels are quantified by q-PCR. ND indicates none detected. For q-PCR analysis in (*A*, *H* and *I*), *Tip41-like* served as the internal control. Error bars represent SD of three biological replicates. Asterisks mean significant differences between different time points (*$P < 0.05$ and **$P < 0.01$, Student's *t* test).

Table S1. Phenotypic statistics.

Figure S2. Phenotypic analysis of *35S:KNU-GR knu-2* T1 plants.		
	Phenotype of flower	
	not fully rescue	fully rescue
plants	proportion	proportion
35S:KNU-GR knu-2	50/50	41/46

Figure S5A. Phenotypic analysis of L*er*-0, *pCLV3:KNU, pCLV3:KNU-NLS*, *pCLV3:KNU-GFP* and *pCLV3:KNU-GFP-NLS* T1 plants.									
	Phenotype								
	wild type		moderate repression		*wus*-like		enhanced FM		
plants	lines	percentage	lines	percentage	lines	percentage	lines	percentage	total
L*er*-0	100	100%	0	0%	0	0%	0	0%	100
pCLV3:KNU	85	75.2%	23	20.4%	5	4.4%	0	0%	113
pCLV3:KNU-NLS	95	41.7%	0	0%	0	0%	133	58.3%	228
pCLV3:KNU-GFP	69	75.8%	18	19.8%	4	4.4%	0	0%	91
pCLV3:KNU-GFP-NLS	30	41.1%	0	0%	0	0%	43	58.9%	73

Figure S5D. Average numbers of floral organs in L*er*-0, *pCLV3:KNU* lines of moderate repression phenotype and *pCLV3:KNU-NLS* enhanced FM lines.								
	sepal		petal		stamen		carpel	
	numbers (average)	SD	numbers (average)	SD	numbers (average)	SD	numbers (average)	SD
L*er*-0	4.00	0.00	4.00	0.00	5.98	0.14	2.00	0.00
pCLV3:KNU (moderate repression)	3.86	0.43	3.84	0.49	4.16	1.10	1.06	0.71
pCLV3:KNU-NLS (enhanced FM)	4.10	0.39	4.27	0.53	6.47	0.77	3.43	1.28

Figure S9A. Phenotypic analysis of L*er*-0 and *pWUS:KNU*T1 plants.

	Phenotype								
	wild type		moderate repression		*wus*-like		enhanced FM		
plants	lines	percentage	lines	percentage	lines	percentage	lines	percentage	total
L*er*-0	100	100%	0	0%	0	0%	0	0%	100
pWUS:KNU	66	47.8%	14	10.2%	58	42.0%	0	0%	138

Figure S9C. Average numbers of floral organs in L*er*-0, *pCLV3:KNU* with moderate repression *,* *pWUS:KNU* with moderate repression and *pCLV3:KNU pWUS:KNU* lines.

	sepal		petal		stamen		carpel	
	numbers (average)	SD	numbers (average)	SD	numbers (average)	SD	numbers (average)	SD
L*er*-0	4.00	0.00	4.00	0.00	5.98	0.14	2.00	0.00
pCLV3:KNU (moderate repression)	3.86	0.43	3.84	0.49	4.16	1.10	1.06	0.71
pWUS:KNU (moderate repression)	3.96	0.20	3.94	0.24	4.25	1.12	0.92	0.58
pCLV3:KNU pWUS:KNU	3.90	0.30	3.82	0.44	1.14	0.35	0.00	0.00

Figure S11A. Phenotypic analysis of L*er*-0, *pGIR1:KNU*, *pAtML1:KNU* and *pMCT1:KNU* T1 plants.

	Phenotype								
	wild type		mild repression		moderate repression		*wus*-like		
plants	line	percentage	line	percentage	line	percentage	lines	percentage	total
L*er*-0	100	100%	0	0%	0	0%	0	0%	100
pGIR1:KNU	78	77.2%	23	22.8%	0	0%	0	0%	101
pAtML1:KNU	56	64.4%	31	35.6%	0	0%	0	0%	87
pMCT1:KNU	81	66.4%	22	18.0%	19	15.6%	0	0%	122
pCLV3:KNU	85	75.2%	0	0.0%	23	20.4%	5	4.4%	113

Figure S11B. Average numbers of floral organs in L*er*-0, *pGIR1:KNU* (mild repression), *pAtML1:KNU* (mild repression), *pMCT1:KNU* (mild repression), *pMCT1:KNU* (moderate repression) and *pCLV3:KNU* lines of moderate repression.

	sepal		petal		stamen		carpel	
	numbers (average)	SD	numbers (average)	SD	numbers (average)	SD	numbers (average)	SD
L*er*-0	4.00	0.00	4.00	0.00	5.98	0.14	2.00	0.00
pGIR1:KNU (mild repression)	3.95	0.30	3.96	0.24	5.04	0.80	2.00	0.00
pAtML1:KNU (mild repression)	3.97	0.22	3.96	0.24	5.36	1.29	1.92	0.39
pMCT1:KNU (mild repression)	4.00	0.00	3.99	0.10	5.29	0.83	2.00	0.00
pMCT1:KNU (moderate repression)	3.97	0.17	3.93	0.26	4.81	1.02	1.36	0.67
pCLV3:KNU (moderate repression)	3.86	0.43	3.84	0.49	4.16	1.10	1.06	0.71

Phenotypic analysis of L*er*-0 and *pCLV1:KNU* T1 plants.

	Phenotype								
	wild type		moderate repression		*wus*-like		*clv*-like		
plants	lines	percentage	lines	percentage	lines	percentage	lines	percentage	total
L*er*-0	100	100%	0	0%	0	0%	0	0%	100
pCLV1:KNU	46	50.5%	19	20.9%	12	13.2%	14	15.4%	91

Table S2. Primer sequences.

1. Vectors construction		
Primer Name	Sequence 5’ to 3’	Vector
pCLV3(pCR8)-F	GAATCTAGTGAAGGCACACTGCT	*pCLV3:KNU, pCLV3:KNU-GFP, pCLV3:KNU-NLS, pCLV3:KNU-GFP-NLS*
pCLV3(pCR8)-R	GAGCTCTTTTAGAGAGAAAGTGACTGAGTGA	
3'UTR-CLV3(pCR8)-F	TTCTCTCTAAAAGAGCTCCCTAATCTCTTGTTGCTTTAAATT	
3'UTR-CLV3(pCR8)-R	GTCGAATTCGCCCTTATCCACTTTGTCTATCTCACTCG	
pWUS(pENTR-D)-F	CACCCTGAATATAAGGCTCGGATCGTA	*pWUS:WUSg-myc, pWUS:KNU*
pWUS:WUSg(pENTR-D)-R	GGATCCGTTCAGACGTAGCTCAAGAGAAGC	
pWUS(pENTR-D)-R	GGCGCCGTGTGTTTGATTCGACTTTTGTT	
3'UTR-WUS(pENTR-D)-F	AATCAAACACACGGCGCCCTCTTACGCCGGTGTCGCT	
3'UTR-WUS(pENTR-D)-R	GCGCCCCCCCTTGGGTTCAAGGTTTTTCACTATAATC	
RNAi(KNU)-I	GATAACGGATCGTAGACATCCATTCTCTCTTTTGTATTCC	RNAi
RNAi(KNU)-II	GAATGGATGTCTACGATCCGTTATCAAAGAGAATCAATGA	
RNAi(KNU)-III	GAATAGATGTCTACGTTCCGTTTTCACAGGTCGTGATATG	
RNAi(KNU)-IV	GAAAACGGAACGTAGACATCTATTCTACATATATATTCCT	
RNAi-A	CTGCAAGGCGATTAAGTTGGGTAAC	
RNAi-B	GCGGATAACAATTTCACACAGGAAACAG	
pGIR1(pCR8)-F	ATTGCTTTCGGTGTGAGGCTA	*pGIR1:KNU, pGIR1:KNU-eGFP*
pGIR1(pCR8)-R	GGCGCCCTAAATTGGATTAAGTTTGGTTCAG	
pAtML1(pCR8)-F	TATGCAAATGCAGGGTCGTG	*pAtML1:KNU, pAtML1:KNU-eGFP*
pAtML1(pCR8)-R	GGCGCCGATGATGATGGATGCCTATCAATTT	
3'UTR-AtML1(pCR8)-F	TCCATCATCATCGGCGCCTCGATGTTTTCGGGTAAGCT	
3'UTR-AtML1(pCR8)-R	GTCGAATTCGCCCTTAAGATTTTTCATTTTTTATGTGTTC	
pMCT1(pCR8)-F	AATCATCATTCAACCGCCAGTA	*pMCT1:KNU or pMCT1:KNU-eGFP*
pMCT1(pCR8)-R	GGCGCCGGAAGCTAAAGAAACTAGGAAGAGA	
pCLV1(pCR8)-F	GAAGAAATCTGCTTGAAATCAACCA	*pCLV1:KNU or pCLV1:KNU-eGFP*
pCLV1(pCR8)-R	GGATCCTTTTTTAGTGTCCTCTCAGTGAGAAAGA	
3'UTR-CLV1(pCR8)-F	GAGGACACTAAAAAAGGATCCCCCAAGCAAGATAAATATGAAAA	
3'UTR-CLV1(pCR8)-R	GAATTCGCCCTTGATATGTTGTAAAATCGGATAGTGA	
NLS	CCAAAAAAGAAGAGAAAGGTA	
myc	GGTGAACAAAAGTTGATTTCTGAAGAAGATTTGAACGGTGAACAAAAGCTAATCTCCGAGGAAGACTTGAACGGTGAACAAAATTAATCTCAGAAGAAGACTTGAAC	

2. qRT-PCR assays	
Primer Name	Sequence 5’ to 3’
Tip41-like-F	GTGAAAACTGTTGGAGAGAAGCAA
Tip41-like-R	TCAACTGGATACCCTTTCGCA

Primer Name	Sequence 5’ to 3’
WUS(qRT)-F	GCAAGCTCAGGTACTGAATGTGGTG
WUS(qRT)-R	GACCAAACAGAGGCTTTGCTCTATCG
CLV3(qRT)-F	GAAAGTGAATGGGTTGGAGC
CLV3(qRT)-R	CTGAAAGTTGTTTCTTGGCTGTC
CLV1(qRT)-F	GAGTACATGCCTAATGGAAGCC
CLV1(qRT)-R	GATCAATGGTGAACAATCATGG
CLV2(qRT)-F	CCTCTAGCTCAATCTCAGCTTC
CLV2(qRT)-R	GGTCGGATTCTGACAAGCTAGAC
CRN(qRT)-F	TCAGTTGCTTGGCTCTGACCT
CRN(qRT)-R	GTTCCTATGCCTTAACCCAGC
RPK2(qRT)-F	CTTCAGTGATCAAATGGCGTT
RPK2(qRT)-R	CAGGGTCCGATACCGTTTTCT
BAM1(qRT)-F	AAGCTGTTGAGAGGCCGACTAT
BAM1(qRT)-R	AGTAGATCCGGCGGACTTTGA
BAM2(qRT)-F	ATTGTGTGCTCAAAGTAATCGATCT
BAM2(qRT)-R	CTGATTCCGCCGCTTGCTG
BAM3(qRT)-F	AACAACGCAAGATCCCGAGGT
BAM3(qRT)-R	GACAATCCCTCGTCCGCCTT
CIK1(qRT)-F	TTGTGGTGTGGAGATTAGGAT
CIK1(qRT)-R	CTCCAGCTACAAGGATCAACT
CIK2(qRT)-F	ACGATAGAATAGAAGTTGGAGA
CIK2(qRT)-R	GTAGAGGTAATAGTCCTGTAAGAC
CIK3(qRT)-F	CTCATCGTCCTAAAATGTCTGAA
CIK3(qRT)-R	TCAAGCCTTGAGACAGAAGTAGTAG
CIK4(qRT)-F	CTTTGATGAAGTTTCTGTTTTTAGGA
CIK4(qRT)-R	TTCTTCACTGACATTAACGCAGC
CLE6(qRT)-F	ACCATGGGCGATATGGATAG
CLE6(qRT)-R	GGAGAAACCCTTTCGGAATC
CLE9(qRT)-F	GTTCCGAGGTTTAACCACCA
CLE9(qRT)-R	CGACTGCTACGGTGGATTCT
CLE10(qRT)-F	ACTGGACCAACCGAACTCAC
CLE10(qRT)-R	ATGCACATAGAGCGTGCGTATG
CLE11(qRT)-F	TCTTTTGCTTTTACGACTTCTTACA
CLE11(qRT)-R	CACCCGTTCCTCATCATTGTA
CLE12(qRT)-F	GAGCCATCATTGTTGAAGCA
CLE12(qRT)-R	ACGATGGTTATGTCGGCTGT
CLE13(qRT)-F	AAACCCATAAACCCTTTTCCTT
CLE13(qRT)-R	ATATCTCGGGTCAATCTCGGA
CLE18(qRT)-F	TCGTTGATTGGAGTAGACAGACA
CLE18(qRT)-R	GCAGGCTCAGGAGAGTTATGTAT
CLE19(qRT)-F	CAATGCGGAGTTTGCTGATGA

Primer Name	Sequence 5’ to 3’
CLE19(qRT)-R	TGGATTTGGACCAGTGGGAA
CLE20(qRT)-F	CGCTTCTCATCCAAACCTTC
CLE20(qRT)-R	CCCGTCTTAACCTTCCGTTT
CLE21(qRT)-F	TGTGATCACGGAGATGTCAAA
CLE21(qRT)-R	GATTTGGACCTGTGGGGATA
CLE22(qRT)-F	CTGCGTCATCAAGAGGATCA
CLE22(qRT)-R	GCAATGGATTAGGACCTGTGA
CLE45(qRT)-F	CACAAGCAGAAAAAGCAGGA
CLE45(qRT)-R	ACGCGTCGGTTTTTATTGAG
MIR394B(qRT)-F	CTTACAGAGATCTTTGGCATTCT
MIR394B(qRT)-R	CTAACAGATCTCTATTGGCAGTATG
LCR(qRT)-F	CATCCGATTATCCCAGCACTA
LCR(qRT)-R	AAGACTTGGTAAGCGGGTTGC
KNU(endogenous-qRT)-F	CGCTTCAGGAACAGCCGAC
KNU(endogenous-qRT)-R	AAAGAGTCATCTGAACAAAAAACAA

3. ChIP assays	
Primer Name	Sequence 5’ to 3’
MU(ChIP)-F	GATTTACAAGGAATCTGTTGGTGGT
MU(ChIP)-F	CATAACATAGGTTTAGAGCATCTGC
CLV3-P1-F	CCTGATCGATATGGCAGTAG
CLV3-P1-R	CTACTTGAGTTGAGAGCTGC
CLV3-P2-F	ACTCCAGGTATCATTCTCTC
CLV3-P2-R	TATGGATGATACCTTAATCGG
CLV3-P3-F	GTACCATATACCTTTTCTATGC
CLV3-P3-R	CTTTGGTAATGAAATGAGAAGG
CLV3-P4-F	CTCACTCTCTCTTTCACTCCTCTAT
CLV3-P4-R	ACATAACACATGAATATTGAGAGGC
CLV3-P5-F	GAAACAACTTTCAGCTCCCTTG
CLV3-P5-R	CAAGCTTACCAAACGAAACAG
CLV3-P6-F	AAGCAATGTACCGTTGGGAAAA
CLV3-P6-R	TTAATTTATCCTTCCCACCACATCA
CLV3-N1-F	CAATCAGTCTCTTGTCGCTTAAC
CLV3-N1-R	ATGTCGTCGAATCGTTACCG
CLV3-N2-F	TTCGTGGACTTGGAGTTGATG
CLV3-N2-R	ATGGATAATCCGGAATTCGATT
CLV3-N3-F	TATTATTTCACACATTTCTTAGAAGA
CLV3-N3-R	TCAATGGTGTTTCTATATTACTACC
CLV1-P1-F	TCCCTAATGTTTTCAAGAGAGTCAC
CLV1-P1-R	CTTTAACTTCCAAGTCAACGCTCT
CLV1-P2-F	ATTCGCTCACAAAGTCTTACGGT

Primer Name	Sequence 5’ to 3’
CLV1-P2-R	TAAGATAGCGTGAGTGTTATGCGAT
CLV1-P3-F	GACTTATCCCCAAGGACTTATGC
CLV1-P3-R	TCGTAACTAACGGTAGATTGAAAAG
CLV1-P4-F	AAACACTTACCTCTGTCTCCCTCAC
CLV1-P4-R	CATCTGACGAATCGCTACACTGA
CLV1-P5-F	AAAATAAGATGCGAAATGTGGTG
CLV1-P5-R	TAAAGCCATCAAGCAATAAGCAT
CLV1-P6-F	TTTAAATCACAAAACTTTCAAGGC
CLV1-P6-R	AATCGATTTTGAATTTTGAGAGC
BAM1-P1-F	CTCTCTAATTCTCTCTGTTTTCCC
BAM1-P1-R	TGGTTTGAAAAAAAAAAGTTGC
BAM1-P2-F	TTATTACATGATTTCAAAACAAGC
BAM1-P2-R	TTGATTCAAATCTCTTTACTCACC
BAM1-P3-F	GGATACAACGTGATTCCATCG
BAM1-P3-R	ACGTGTGAAGGGAGCTTTATG
BAM1-P4-F	TTATAGATGAAACGAGAATGCAG
BAM1-P4-R	CATGATCGTAATCGTGTGTCC
BAM1-P5-F	CCATGGTCAAGAATGTATTCAGTC
BAM1-P5-R	AGCAAAATCTGTTGAGAAGAGC
BAM1-P6-F	CTATTTTATTTACAGACACATGGG
BAM1-P6-R	AGATCGTTATTGGTAATCTAATCC
BAM1-P7-F	ATGTTTCAAGAACAACATGACTCC
BAM1-P7-R	TGATAAAACAGTAAAAATAGCCTG
BAM1-P8-F	AATTCACACCTTCCTCATCTTC
BAM1-P8-R	AGGTTTTGAGTGAGAGGAGAGC
BAM1-P9-F	TTCACCGGAGAGATTCCAGC
BAM1-P9-R	TGTTACCGGAGCACATGTTC
BAM1-P10-F	ACTTTACCGCCGAACATGTG
BAM1-P10-R	CAAGATTAACAGAGACACCTCC
BAM1-P11-F	ATCGTTCACAGAGATGTCAAAT
BAM1-P11-R	TATGTAGCCGTAAGAGCCAGC
BAM1-P12-F	CGGTACTTCTGAATGTATGTCTGC
BAM1-P12-R	CCGGTGACGAGTTCCAAAAG
BAM1-P13-F	TTCGCCGAAGTCTGGTGTTC
BAM1-P13-R	AGCACAAACCGTACTAAGAGGG
BAM1-P14-F	TCCCTCTTAGTACGGTTTGTGC
BAM1-P14-R	ATTACACATTTCACTCTTTTCAAG
BAM2-P1-F	GCTTTTACAGCGTGTCTTTCTG
BAM2-P1-R	TGCTACTACAATCATAAAGAATTC
BAM2-P2-F	ATGTTTGTTCACTGAGCAAACC
BAM2-P2-R	TCAACAATAATGGTTTCCCGAC

Primer Name	Sequence 5’ to 3’
BAM2-P3-F	TAAAATACATGTCGGGAAACCA
BAM2-P3-R	ACTGATAATGACGAGAACAACC
BAM2-P4-F	CATGTTTCATTAAATCCACCAC
BAM2-P4-R	GATTGTGTGTGTGTTTTTTATGAG
BAM2-P5-F	ACTCAAATCCTCCTTCACCATC
BAM2-P5-R	TCTGATTAGCAGCGAGTGATAG
BAM2-P6-F	GTCTTCAACGGTTCATTTCC
BAM2-P6-R	AAAAGCGTTGTAATATCCGATG
BAM2-P7-F	AGTGATTCTTGATCTCTCTTCG
BAM2-P7-R	GACTCCTCCTCCGCTTATTG
BAM2-P8-F	TTGGTTCCATACCTGTGACG
BAM2-P8-R	AAGAGCAATCCAAGGACGAG
BAM2-P9-F	TTGTTTGTTCCTTGTTGAGC
BAM2-P9-R	AGATCGATTACTTTGAGCACAC
BAM2-P10-F	GAGTTAATTACTTAATTAGCCCGTTG
BAM2-P10-R	CTGCATGTATATATATGCTGATATGC
BAM2-P11-F	ACTTTTGCCCCTTATATTCTTAAG
BAM2-P11-R	ATGGAATGTCTTGTTGTGACAC
BAM2-P12-F	TCCCTCTCATTAATTACAAGCC
BAM2-P12-R	TAGTTTCTTGATAACTAACTCCTGAC
BAM3-P1-F	TAAAAAGTTATCAACGAAAACGTCT
BAM3-P1-R	CCCTAACAACTCTTCCCAAAA
BAM3-P2-F	AAACTATTTTCCTTTAGATTGCA
BAM3-P2-R	CTTTTTCTTTAATGGAGAAAACTA
BAM3-P3-F	AATCCAAAAGACGAAGAATGC
BAM3-P3-R	GTTCTGGAGTTGCTCTGCTTA
BAM3-P4-F	ACAAGCAAATGTCCTTATCTCTCTA
BAM3-P4-R	CGGAGAAACTGTTAGAAGAAATG
BAM3-P5-F	AGCTTACAGGCTCTGTTCCTC
BAM3-P5-R	AGCTTTTGAAGTCCAGATAGCT
BAM3-P6-F	CTTCTTGTTCGGTCCTCTCCC
BAM3-P6-R	TCTTCGGGGATTTCTCCAGTC
BAM3-P7-F	TTGAGTCACAACCAGATTTCC
BAM3-P7-R	TGTTGTGTGAGAAATCTGCTG
BAM3-P8-F	CAAACTGTAACAGACAAGGTGTG
BAM3-P8-R	AAACTCTATGAAACACATAAAACAG

4. EMSA assays	
Probe Name	Sequence 5’ to 3’
CLV3(-1080)-F	GGCTCATATAATCCATTCAATTTATG
CLV3(-1080)-R	CATAAATTGAATGGATTATATGAGCC

Probe Name	Sequence 5’ to 3’
CLV3(+970)-F	TTGTCAATGCAAATAATTAATGGATGTG
CLV3(+970)-R	CACATCCATTAATTATTTGCATTGACAA
P3-1-CLV3-F	GTACCATATACCTTTTCTATGCCCACTATATATACTTACTACACAT
P3-1-CLV3-R	ATGTGTAGTAAGTATATATAGTGGGCATAGAAAAGGTATATGGTAC
P3-2-CLV3-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATGATACACGTTTAG
P3-2-CLV3-R	CTAAACGTGTATCATAGTTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
P3-3-CLV3-F	GACAAATAAAATTAAAAAATAGGAGATCCCATTTCTCGCCCTTGTAGGC
P3-3-CLV3-R	GCCTACAAGGGCGAGAAATGGGATCTCCTATTTTTTAATTTTATTTGTC
P3-4-CLV3-F	TTACGCTATAAATTGGACTGTCCCCTTCTCATTTCATTACCAAAG
P3-4-CLV3-R	CTTTGGTAATGAAATGAGAAGGGGACAGTCCAATTTATAGCGTAA
M1(P3-2)-F	GGCCGCGGGCTTAACCAAAATATTTGAATAGTTAATAACTATGATACACGTTTAG
M1(P3-2)-R	CTAAACGTGTATCATAGTTATTAACTATTCAAATATTTTGGTTAAGCCCGCGGCC
M2(P3-2)-F	AATATATAAACCGCTACCGGCGCCTGAATAGTTAATAACTATGATACACGTTTAG
M2(P3-2)-R	CTAAACGTGTATCATAGTTATTAACTATTCAGGCGCCGGTAGCGGTTTATATATT
M3(P3-2)-F	AATATATAAACCAACCAAAATATTCACCCGTCCGGCAACTATGATACACGTTTAG
M3(P3-2)-R	CTAAACGTGTATCATAGTTGCCGGACGGGTGAATATTTTGGTTGGTTTATATATT
M4(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATCCTGGCTGCGCACGTTTAG
M4(P3-2)-R	CTAAACGTGCGCAGCCAGGATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M5(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATGATAAGTAGGGCT
M5(P3-2)-R	AGCCCTACTTATCATAGTTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M4-1(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATCACTATGATACACGTTTAG
M4-1(P3-2)-R	CTAAACGTGTATCATAGTGATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M4-2(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATACCTATGATACACGTTTAG
M4-2(P3-2)-R	CTAAACGTGTATCATAGGTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M4-3(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATAATTATGATACACGTTTAG
M4-3(P3-2)-R	CTAAACGTGTATCATAATTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M4-4(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATAACGATGATACACGTTTAG
M4-4(P3-2)-R	CTAAACGTGTATCATCGTTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M4-5(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTGTGATACACGTTTAG
M4-5(P3-2)-R	CTAAACGTGTATCACAGTTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M4-6(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTACGATACACGTTTAG
M4-6(P3-2)-R	CTAAACGTGTATCGTAGTTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M4-7(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATCATACACGTTTAG
M4-7(P3-2)-R	CTAAACGTGTATGATAGTTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M4-8(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATGGTACACGTTTAG
M4-8(P3-2)-R	CTAAACGTGTACCATAGTTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M4-9(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATGACACACGTTTAG
M4-9(P3-2)-R	CTAAACGTGTGTCATAGTTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
M4-10(P3-2)-F	AATATATAAACCAACCAAAATATTTGAATAGTTAATAACTATGATGCACGTTTAG
M4-10(P3-2)-R	CTAAACGTGCATCATAGTTATTAACTATTCAAATATTTTGGTTGGTTTATATATT
P4-1-CLV1-F	AAACACTTACCTCTGTCTCCCTCACCGTGTCTCTTGTCCAACACG

Probe Name	Sequence 5’ to 3’
P4-1-CLV1-R	CGTGTTGGACAAGAGACACGGTGAGGGAGACAGAGGTAAGTGTTT
P4-2-CLV1-F	GCCAGGACAAACCTCCGATCACAATCACACGGCGTTGTT
P4-2-CLV1-R	AACAACGCCGTGTGATTGTGATCGGAGGTTTGTCCTGGC
P4-3-CLV1-F	CTCACCGTCAAGGATCGTAATCACGGTTATCGCAGCGATCACCGGT
P4-3-CLV1-R	ACCGGTGATCGCTGCGATAACCGTGATTACGATCCTTGACGGTGAG
P4-4-CLV1-F	TTGATCCTAATCAGTGTAGCGATTCGTCAGATG
P4-4-CLV1-R	CATCTGACGAATCGCTACACTGATTAGGATCAA

Table S3. Statistical Analysis.

Figure. 2A (q-PCR)						
		t-test for Equality of Means (Confidence Interval Percentage is 95%)				
		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
0h	DEX vs Mock	0.181	2	0.873	>0.05	ns
	DEX+CHX vs CHX	0.386	4	0.719	>0.05	ns
4h	DEX vs Mock	5.839	4	4.29E-03	<0.01	**
	DEX+CHX vs CHX	5.452	4	5.50E-03	<0.01	**
8h	DEX vs Mock	5.733	4	4.58E-03	<0.01	**
	DEX+CHX vs CHX	7.181	4	1.99E-03	<0.01	**
12h	DEX vs Mock	4.104	4	0.015	<0.05	*
	DEX+CHX vs CHX	4.396	4	0.012	<0.05	*

Figure. 2C (ChIP-qPCR)						
		t-test for Equality of Means (Confidence Interval Percentage is 95%)				
anti-myc vs no antibody		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
P1	vs MU	-3.335	2	0.079	>0.05	ns
P2		1.723	2	0.227	>0.05	ns
P3		-6.051	4	3.76E-03	<0.01	**
P4		-0.754	4	0.493	>0.05	ns
P5		-6.329	2	0.024	<0.05	*
P6		3.321	2	0.08	>0.05	ns

Figure. 6B (ChIP-qPCR)						
		t-test for Equality of Means (Confidence Interval Percentage is 95%)				
anti-myc/no antibody		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
pWUS:eGFP-WUS vs *pCLV3:KNU pWUS:eGFP-WUS*	P1	1.156	4	0.312	>0.05	ns
	P2	5.073	4	7.00E-03	<0.01	**
	P3	3.787	4	0.019	<0.05	*
	P5	0.547	4	0.613	>0.05	ns
	P6	5.866	2	0.026	<0.05	*

Figure. 7A (q-PCR)						
		t-test for Equality of Means (Confidence Interval Percentage is 95%)				
		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
0h	DEX vs Mock	-1.127	2	0.377	>0.05	ns
	DEX+CHX vs CHX	0.791	2	0.508	>0.05	ns
4h	DEX vs Mock	19.085	4	4.40E-05	<0.01	**
	DEX+CHX vs CHX	10.712	4	4.30E-04	<0.01	**
8h	DEX vs Mock	10.531	4	4.60E-04	<0.01	**
	DEX+CHX vs CHX	12.077	4	2.70E-04	<0.01	**
12h	DEX vs Mock	9.023	4	8.35E-04	<0.01	**
	DEX+CHX vs CHX	10.568	4	4.54E-04	<0.01	**

Figure. 7C (ChIP-qPCR)						
		t-test for Equality of Means (Confidence Interval Percentage is 95%)				
anti-myc vs no antibody		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
P1	vs MU	-1.334	2	0.314	>0.05	ns
P2		-2.363	4	0.077	>0.05	ns
P3		-2.337	2	0.144	>0.05	ns
P4		-10.522	2	9.00E-03	<0.01	**
P5		-0.98	2	0.43	>0.05	ns
P6		0.367	4	0.732	>0.05	ns

Figure. S3B (ChIP-qPCR)						
		t-test for Equality of Means (Confidence Interval Percentage is 95%)				
anti-myc vs no antibody		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
P1	vs MU	-3.335	2	0.079	>0.05	ns
N1		2.267	2	0.152	>0.05	ns
N2		2.234	4	0.089	>0.05	ns
P2		1.723	2	0.227	>0.05	ns
N3		0.227	2	0.808	>0.05	ns
P3		-6.051	4	3.76E-03	<0.01	**
P4		-0.754	4	0.493	>0.05	ns
P5		-6.329	2	0.024	<0.05	*
P6		3.321	2	0.08	>0.05	ns

Figure. S4B (ChIP-qPCR)						
		t-test for Equality of Means (Confidence Interval Percentage is 95%)				
anti-H3K27me3/input		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
ap1 cal 35S:AP1-GR(D4 vs D0)	P1	-2.227	2	0.151	>0.05	ns
	N1	-1.439	4	0.224	>0.05	ns
	N2	-1.424	4	0.227	>0.05	ns
	P2	-6.197	4	3.45E-03	<0.01	**
	N3	-1.605	4	0.184	>0.05	ns
	P3	-4.826	4	8.49E-03	<0.01	**
	P4	-1.798	4	0.147	>0.05	ns
	P5	-4.42	4	0.012	<0.05	*
	P6	-5.913	4	4.10E-03	<0.01	**

Figure. S4C (ChIP-qPCR)						
		t-test for Equality of Means (Confidence Interval Percentage is 95%)				
anti-H3K27me3/input		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
knu-2 ap1 cal 35S:AP1-GR(D4 vs D0)	P1	-0.236	4	0.825	>0.05	ns
	N1	0.318	4	0.766	>0.05	ns
	N2	-0.917	4	0.411	>0.05	ns
	P2	0.018	4	0.987	>0.05	ns
	N3	-1.023	4	0.364	>0.05	ns
	P3	0.024	4	0.982	>0.05	ns
	P4	-0.215	4	0.840	>0.05	ns
	P5	-1.755	4	0.154	>0.05	ns
	P6	-0.496	4	0.646	>0.05	ns

Figure. S5G (q-PCR)							
			t-test for Equality of Means (Confidence Interval Percentage is 95%)				
			t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
CLV3	*pCLV3:KNU*	vs WT	16.248	4	8.40E-05	<0.01	**
	pCLV3:KNU-NLS		50.423	2	3.93E-04	<0.01	**
WUS	*pCLV3:KNU*		-13.227	2	5.67E-03	<0.01	**
	pCLV3:KNU-NLS		-8.699	4	9.61E-04	<0.01	**

Figure. S5I (q-PCR)							
			t-test for Equality of Means (Confidence Interval Percentage is 95%)				
			t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
KNU	*pCLV3:KNU-NLS*	vs WT	-0.498	2	0.668	>0.05	ns

Figure. S8G (ChIP-qPCR)						
		t-test for Equality of Means (Confidence Interval Percentage is 95%)				
anti-GFP/no antibody		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
pCLV3:KNU-GFP vs *pCLV3:KNU-GFP-NLS*	P1	-2.83	4	0.047	<0.05	*
	P2	-1.142	4	0.317	>0.05	ns
	P3	-2.941	4	0.042	<0.05	*
	P5	-0.473	4	0.661	>0.05	ns
	P6	-1.493	4	0.21	>0.05	ns

Figure. S8H (ChIP-qPCR)						
		t-test for Equality of Means (Confidence Interval Percentage is 95%)				
anti-pol II/no antibody		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
pCLV3:KNU-GFP vs *pCLV3:KNU-GFP-NLS*	P1	0.628	4	0.564	>0.05	ns
	P2	0.147	4	0.89	>0.05	ns
	P3	6.321	4	3.00E-03	<0.01	**
	P5	1.624	4	0.18	>0.05	ns
	P6	0.106	4	0.921	>0.05	ns

Figure. S9E (q-PCR)							
			t-test for Equality of Means (Confidence Interval Percentage is 95%)				
			t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
CLV3	*pWUS:KNU*	vs WT	43.892	2	5.19E-04	<0.01	**
WUS			43.289	2	5.33E-04	<0.01	**

Figure. S11E (q-PCR)							
			t-test for Equality of Means (Confidence Interval Percentage is 95%)				
			t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
CLV3	*pGIR1:KNU*	vs WT	14.689	4	1.25E-04	<0.01	**
	pAtML1:KNU		11.064	4	3.79E-04	<0.01	**
	pMCT1:KNU(mild)		24.565	2	1.65E-03	<0.01	**
	pMCT1:KNU(moderate)		17.161	4	6.80E-05	<0.01	**
WUS	*pGIR1:KNU*		-8.096	4	1.27E-03	<0.01	**
	pAtML1:KNU		0.651	2	0.582	>0.05	ns
	pMCT1:KNU(mild)		-4.036	4	0.016	<0.05	*
	pMCT1:KNU(moderate)		-3.438	2	0.075	>0.05	ns

Figure. S15H (q-PCR)							
			t-test for Equality of Means (Confidence Interval Percentage is 95%)				
			t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
CLV1	*pCLV1:KNU (repressed)*	vs WT	6.174	2	0.025	<0.05	*
	pCLV1:KNU (enhanced)		19.288	4	4.30E-05	<0.01	**
CLV3	*pCLV1:KNU (repressed)*		15.124	2	4.34E-03	<0.01	**
	pCLV1:KNU (enhanced)		-5.944	4	4.02E-03	<0.01	**
WUS	*pCLV1:KNU (repressed)*		52.44	2	3.63E-04	<0.01	**
	pCLV1:KNU (enhanced)		-9.837	2	0.011	<0.05	*

Figure. S16A (q-PCR)							
			t-test for Equality of Means (Confidence Interval Percentage is 95%)				
			t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
BAM1	*pCLV1:KNU(moderate)*	vs WT	-2.744	2	0.111	>0.05	ns
BAM2			0.195	2	0.863	>0.05	ns
BAM3			-1.998	2	0.184	>0.05	ns
BAM1	*pCLV1:KNU(clv-like)*		-10.886	2	0.008	<0.01	**
BAM2			-0.268	4	0.802	>0.05	ns
BAM3			-7.063	4	0.002	<0.01	**

Figure. S16H (q-PCR)							
			t-test for Equality of Means (Confidence Interval Percentage is 95%)				
	DEX/Mock		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
CLV2	4h	vs 0h	20.376	2	2.40E-03	<0.01	**
	8h		17.13	2	3.39E-03	<0.01	**
CRN	4h		2.594	4	0.06	>0.05	ns
	8h		3.55	2	0.071	>0.05	ns
RPK2	4h		0.213	2	0.851	>0.05	ns
	8h		0.275	2	0.809	>0.05	ns
BAM1	4h		-0.946	4	0.398	>0.05	ns
	8h		-0.812	4	0.462	>0.05	ns
BAM2	4h		2.359	2	0.142	>0.05	ns
	8h		4.056	2	0.056	>0.05	ns
BAM3	4h		0.163	2	0.886	>0.05	ns
	8h		0.079	2	0.944	>0.05	ns
CIK1	4h		-1.643	4	0.176	>0.05	ns
	8h		-1.728	4	0.159	>0.05	ns
CIK2	4h		2.54	4	0.064	>0.05	ns
	8h		5.926	4	4.00E-03	<0.01	**
CIK3	4h		-0.085	4	0.936	>0.05	ns
	8h		-4.371	4	0.012	<0.05	*
CIK4	4h		3.181	2	0.086	>0.05	ns
	8h		3.136	2	0.088	>0.05	ns

Figure. S16I (q-PCR)							
			t-test for Equality of Means (Confidence Interval Percentage is 95%)				
	DEX/Mock		t	df (Degrees of freedom)	Sig.(2-tailed)	comparative results	Symbol
CLE6	4h	vs 0h	2.844	4	0.047	<0.05	*
	8h		0.379	2	0.741	>0.05	ns
CLE9	4h		29.222	2	1.17E-03	<0.01	**
	8h		24.041	2	1.73E-03	<0.01	**
CLE10	4h		27.118	2	1.36E-03	<0.01	**
	8h		10.209	2	9.46E-03	<0.01	**
CLE12	4h		3.354	4	0.028	<0.05	*
	8h		-4.33	4	0.012	<0.05	*
CLE13	4h		5.745	4	4.55E-03	<0.01	**
	8h		-2.908	2	0.101	>0.05	ns
CLE19	4h		-1.224	2	0.346	>0.05	ns
	8h		-1.376	4	0.241	>0.05	ns
CLE20	4h		1.692	2	0.233	>0.05	ns
	8h		0.047	2	0.967	>0.05	ns
CLE21	4h		-3.279	2	0.082	>0.05	ns
	8h		-2.987	2	0.096	>0.05	ns
CLE22	4h		-1.987	4	0.118	>0.05	ns
	8h		-8.7	2	0.013	<0.05	*
CLE45	4h		12.14	4	2.64E-04	<0.01	**
	8h		5.741	2	0.029	<0.05	*

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