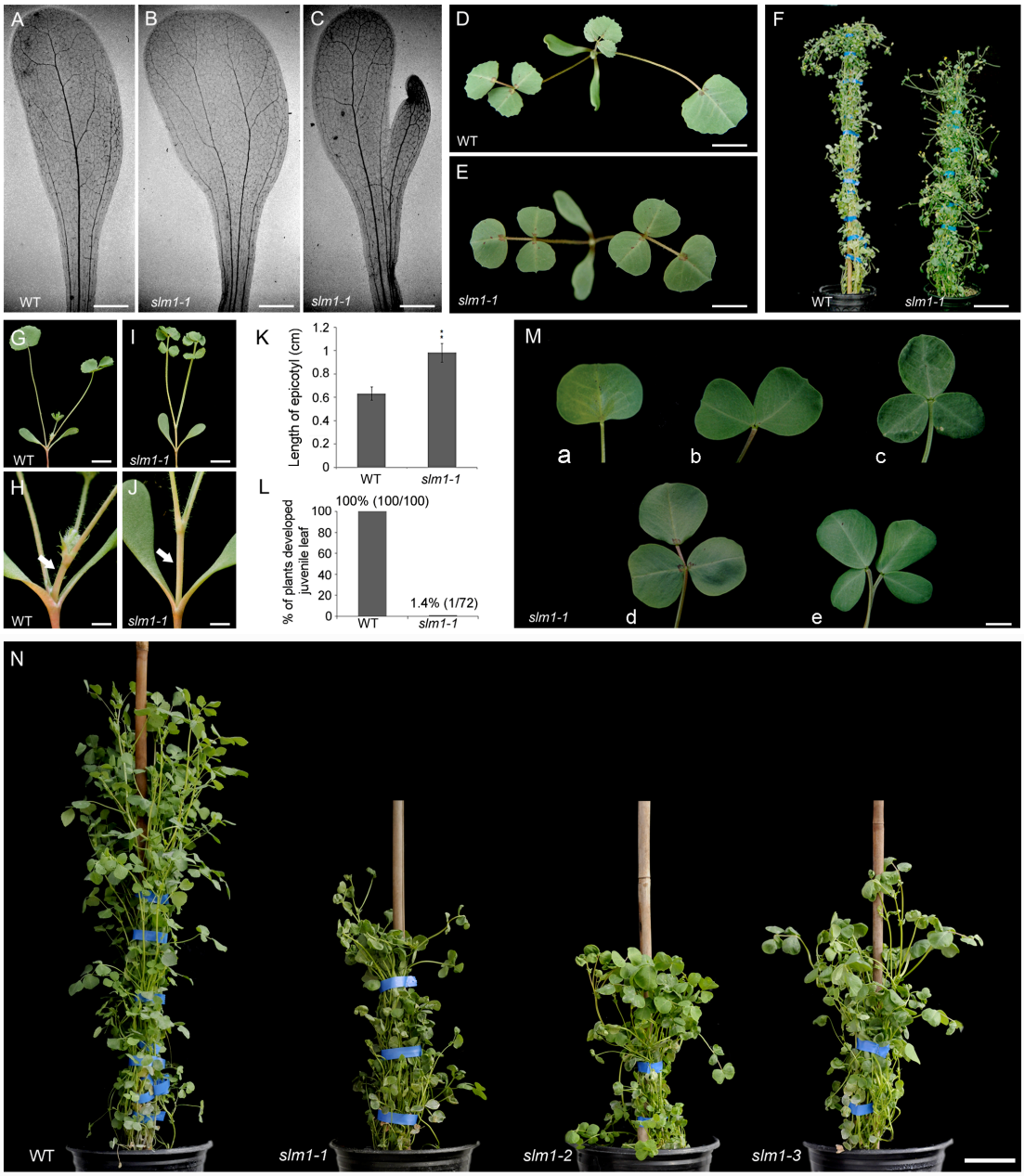


Supplemental Figure 1. Developmental Defects in the *slm1-1* Mutant of *M. truncatula*.

(A) to **(C)** Vein patterns of cotyledons in the wild type (WT; **A**) and *slm1-1* (**B, C**).

(D) and **(E)** Ten-day-old plants of the wild type (**D**) and *slm1-1* (**E**). In the wild type, a simple leaf (juvenile leaf) developed first, followed by two adult leaves (**D**). Note that the first true leaf did not develop, but two adult leaves were produced in the *slm1-1* mutant (**E**).

(F) Three-month-old plants at the reproductive stage of the wild type (left) and *slm1-1* (right).

(G) to **(J)** Length of epicotyls of the wild type (**G, H**) and *slm1-1* (**I, J**). Arrows indicate epicotyls.

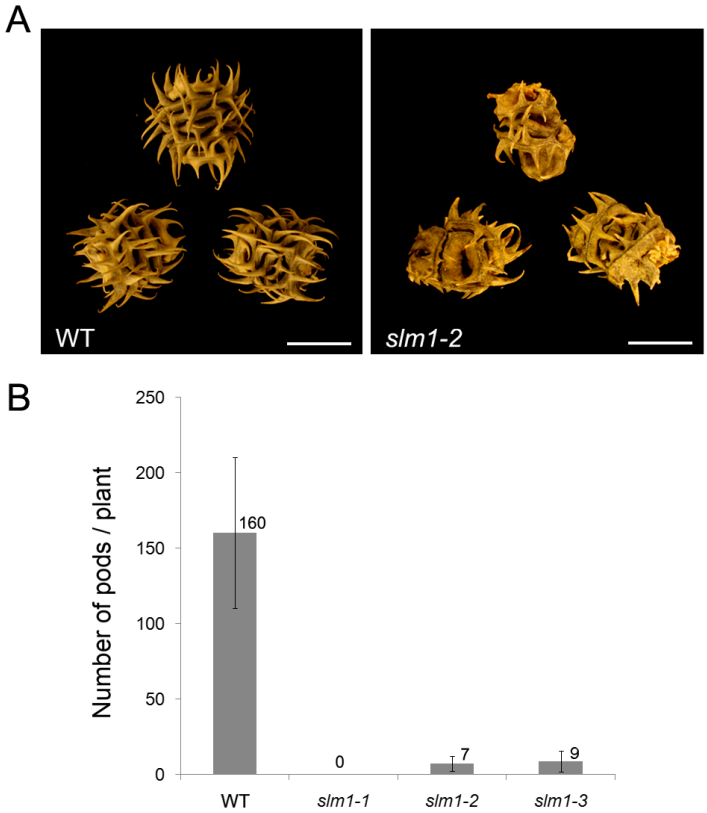
(K) Length of epicotyls of the wild type and *slm1-1*. Asterisks indicate that the differences between the wild type and *slm1* are statistically significant at $P < 0.01$. Means ± SE are shown (n=20).

(L) Percentage of first leaf initiation in the wild type and *slm1-1*.

(M) Phenotypic variation of adult leaves of *slm1-1*. a: a simple leaf with a single leaflet; b: two terminal leaflets developed on a single petiole; c: three terminal leaflets developed on a single petiole; d: one terminal leaflet and two lateral leaflets developed in a trifoliate form; e: two petioles fused together; two terminal leaflets developed on the distal end of each petiole, respectively; no lateral leaflets were produced.

(N) Fifty-day-old plants at the vegetative stage in the wild type, *slm1-1*, *slm1-2,* and *slm1-3*.

Bars = 10 cm in (**F**), 5 cm in (**N**), 5 mm in (**D**), (**E**), (**G**) to (**J**) and (**M**), and 2 mm in (**A**) to (**C**).

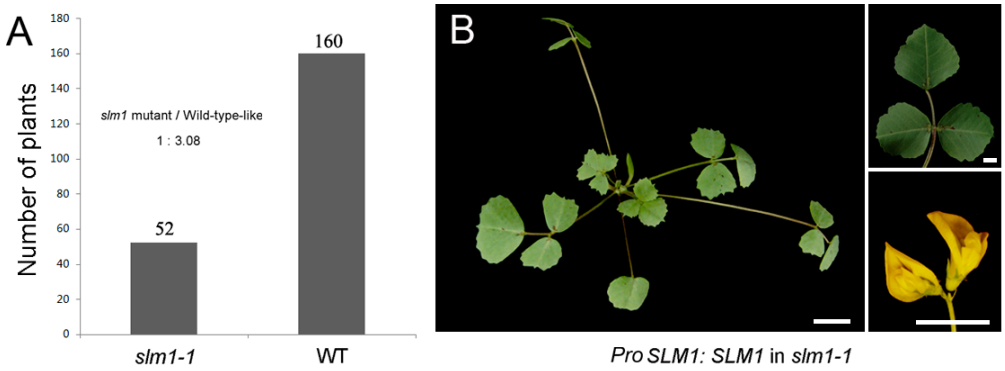


Supplemental Figure 2. Loss-of-function in *SLM1* Leads to Defects in Fertility.

(A) Seed pods of the wild type (left) and *slm1-2* (right).

(B) Seed pod production in the wild type and *slm1* alleles. Error bars represent SE (n =10).

Bars = 5 mm.

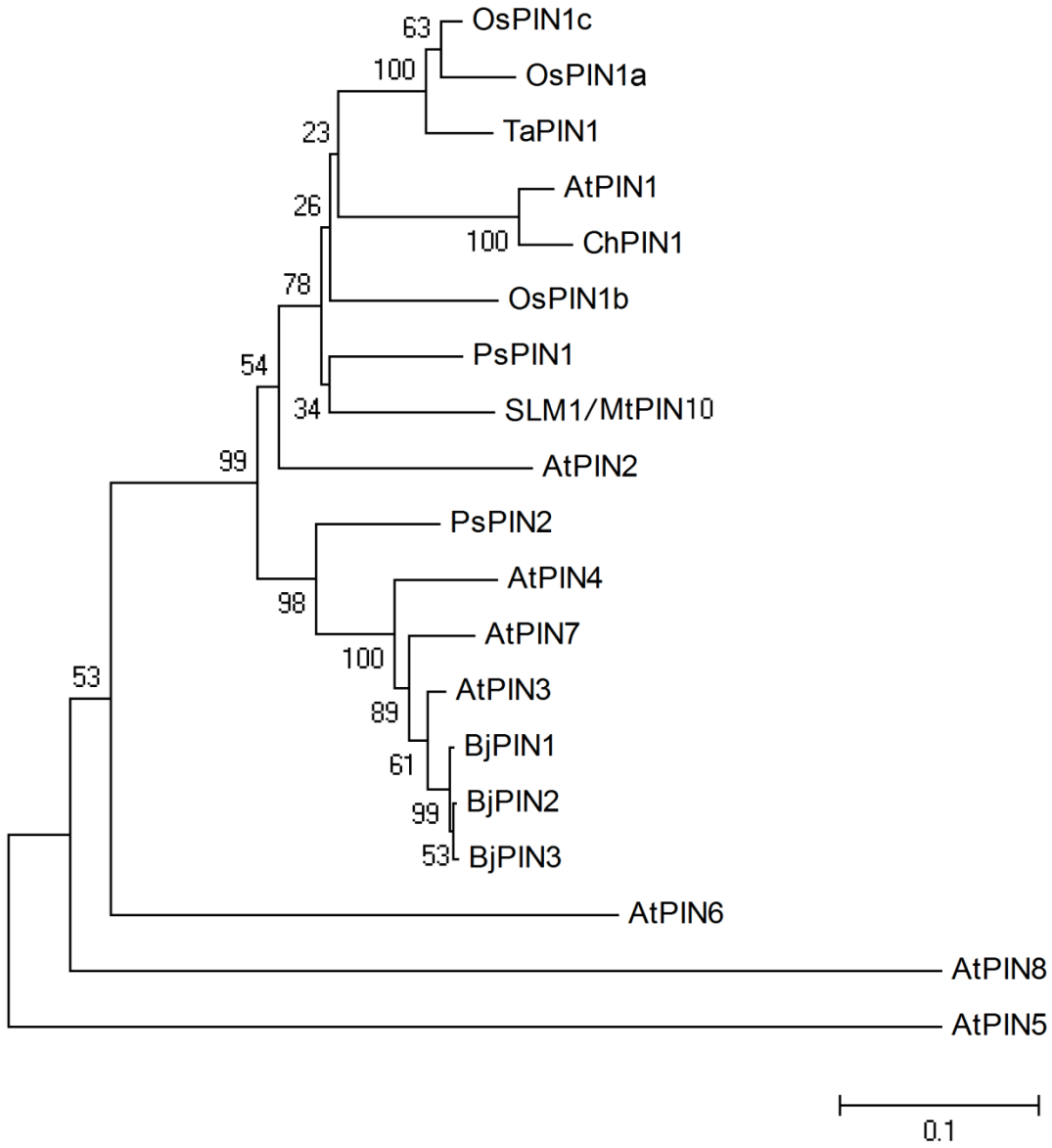


Supplemental Figure 3. Genetic Segregation Analysis and Genetic Complementation of the *slm1-1* Mutant.

(A) Number of wild-type-like and mutant plants obtained from a backcross F_2 population.

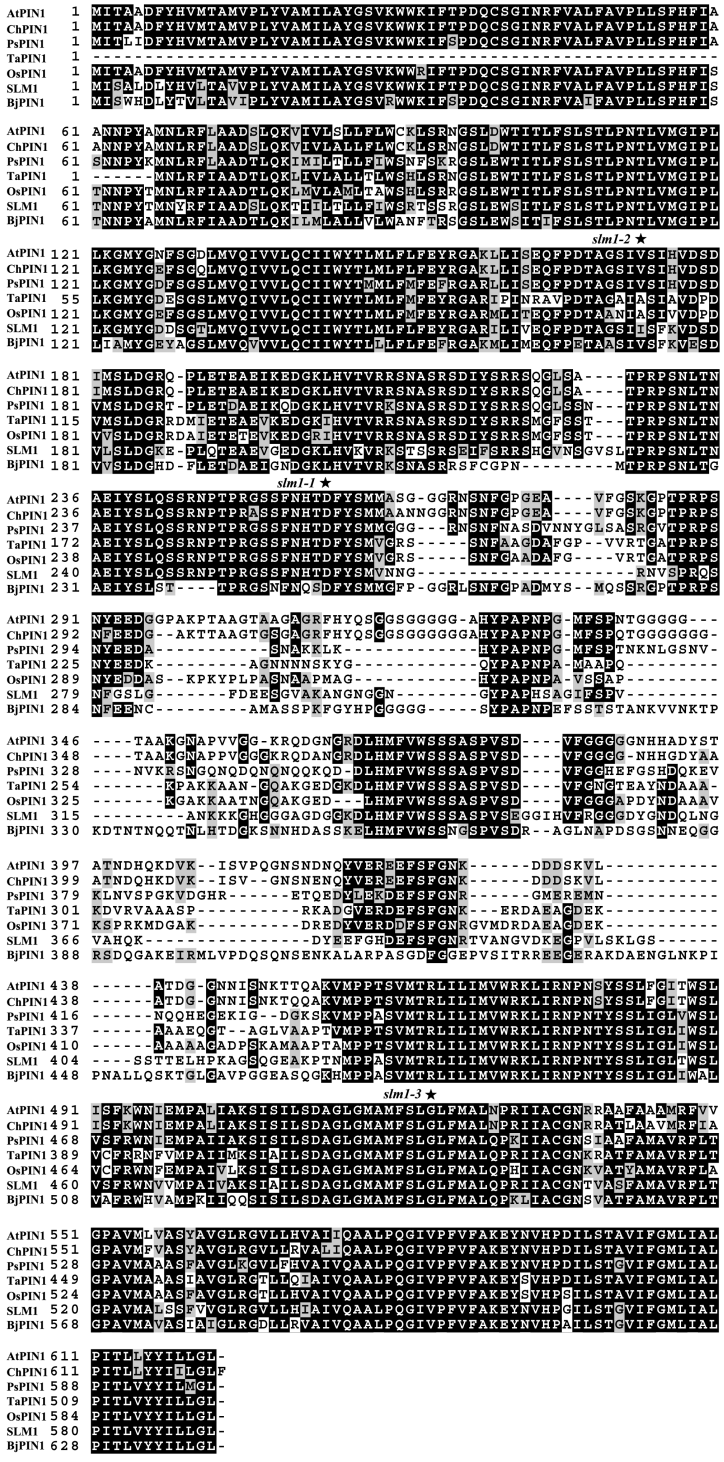
(B) A representative *slm1-1* line transformed with the *SLM1* genomic sequence (*ProSLM1:SLM1*) showed normal wild-type-like leaves and flowers.

Bars = 5 mm.

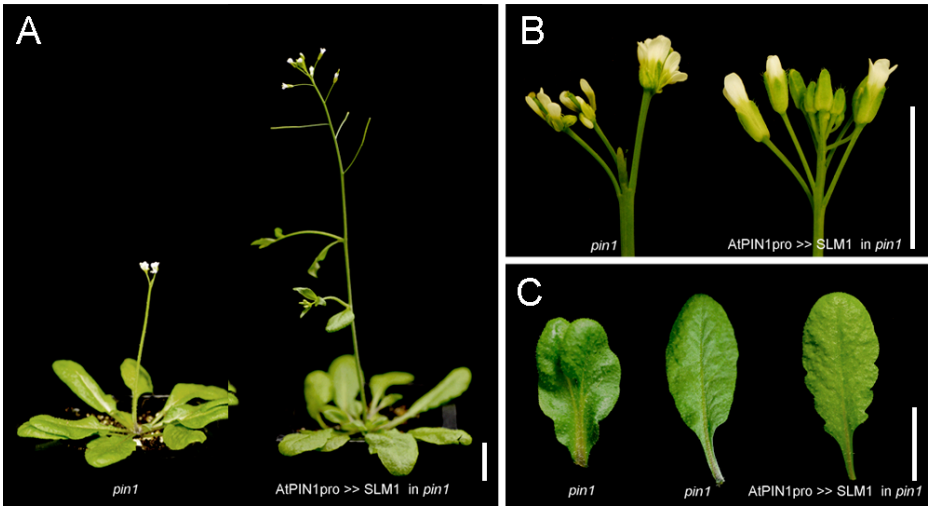


Supplemental Figure 4. Phylogenetic Analysis of SLM1/Mt PIN10 and PIN.

At PIN1 to At PIN8 from *Arabidopsis thaliana* (At); Ch PIN1 from *Cardamine hirsuta* (Ch); Ps PIN1 and Ps PIN2 from *Pisum sativum* (Ps); Ta PIN1 from *Triticum aestivu*m (Ta); Os PIN1a, Os PIN1b, and Os PIN1c from *Oryza sativa* (Os); Bj PIN1 to Bj PIN3 from *Brassica juncea* (Bj). The scale bar indicates the genetic distance based on branch length.



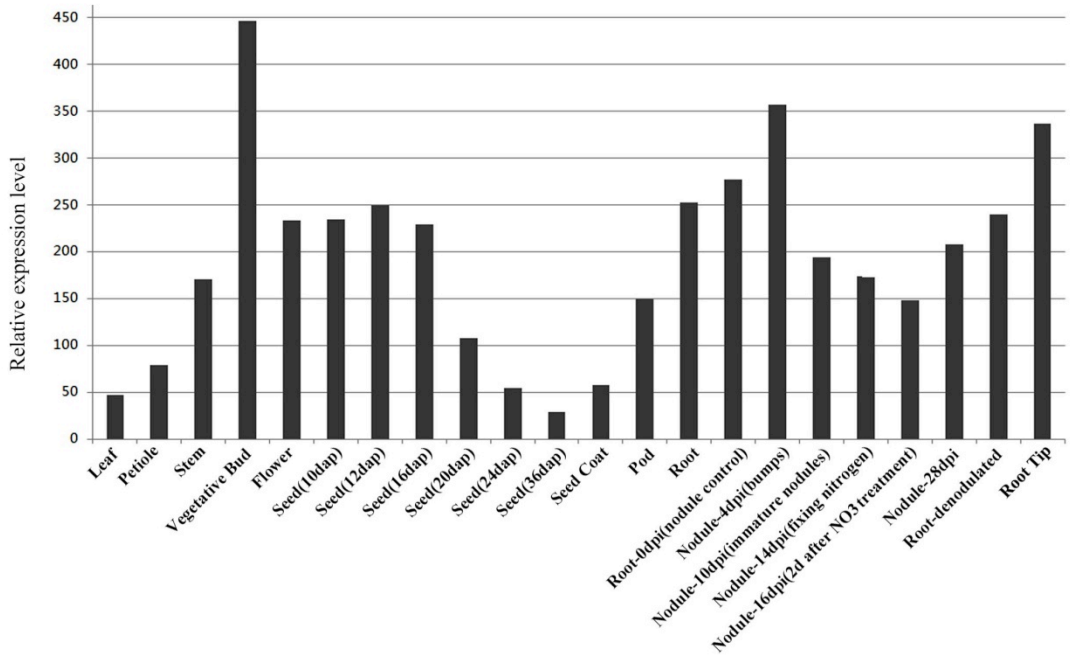
Supplemental Figure 5. Alignment of Amino Acid Sequences of At PIN1, Ch PIN1, Ps PIN1, Ta PIN1, Os PIN1, Bj PIN1, and SLM1. The conserved regions are marked by shaded boxes. Numbers on the sides indicate amino acid positions. The positions of mutation in *slm1-1* to *slm1-3* are indicated by asterisks on the amino acid sequences.



Supplemental Figure 6. Genetic Complementation of the *Arabidopsis pin1* Mutant.

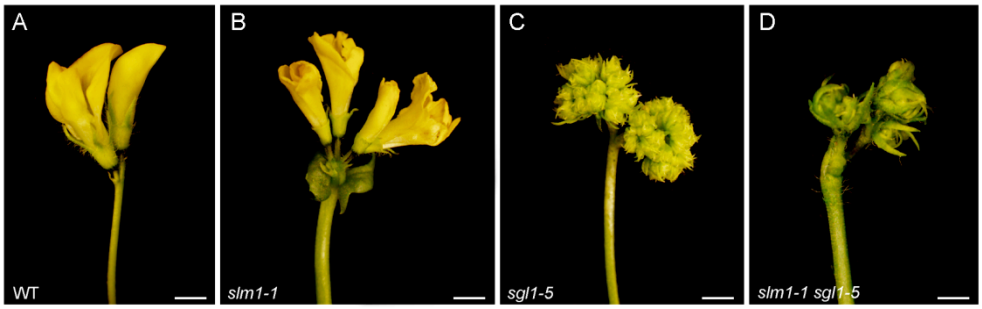
The *Arabidopsis pin1* mutant was fully rescued by the *SLM1* CDS driven by the *Arabidopsis PIN1* promoter. The *Arabidopsis* mutant and complemented plants (**A**), flowers (**B**) and leaves (**C**) are shown.

Bars = 5 mm.



Supplemental Figure 7. Expression Profiling of the *SLM1* Transcript.

The data for *SLM1* (TC142052; probe set *Mtr.47942.1.S1*) are accessible at http://bioinfo.noble.org/gene-atlas/.



Supplemental Figure 8. Flower Phenotype of the Seventy-day-old Plants of Wild type and the Mutants Analyzed.

(A) Flowers of the wild type.
(B) Flowers of *slm1-1*.
(C) Flowers of *sgl1-5*.
(D) Flowers of *slm1-1 sgl1-5*.
Bars = 2 mm.

Supplemental Table 1. Primers Used in This Study.

Primer	Sequence	Application
cSLM1-F	Forward-catgccatggaaatgataagtgctttagac	For cloning of the *SLM1* full length CDS
cSLM1-R	Reverse-gtcgggttacctcaaagtcccaataaaatgtag	
gSLM1-F	Forward-cacctagtatgatgtttgcggaatg	For cloning of the *SLM1* promoter and genomic sequences
gSLM1-R	Reverse-gctcgtggcctctaccatagctag	
pSLM1-F	Forward-cacctagtatgatgtttgcggaatg	For cloning of the *SLM1* promoter
pSLM1-R	Reverse-gctcgtggcctctaccatagcta	
pAtPIN1-F	Forward-ccggaattctaaattattccattggcgttgtcgc	For cloning of the *AtPIN1* promoter
pAtPIN1-R	Reverse-catgccatggcttttgttcgccggagaagagagag	
prbSGL1-F	Forward-ttaccatggatcccgacgcattca	For cloning of the *SGL1* cDNA as probe for in situ hybridization
prbSGL1-R	Reverse-ttggtggtatcgccggaaagaaga	
prbSLM1-F	Forward-tgcttcacctgtttctgaaggtgg	For cloning of the *SLM1* cDNA as probe for in situ hybridization
prbSLM1-R	Reverse-ggaagagcagcctgtacaatagca	
DR5GUS-F	Forward-caccctgcaggtcgacggtatcgca	For cloning of the *DR5:GUS*
DR5GUS-R	Reverse-cgcgcgataatttatcctagtttgc	
qMtKNOX1-F	Forward-caaggttagaagaagcatgtgcaa	For qRT-PCR analysis of *MtKNOX1*
qMtKNOX1-R	Reverse-caacctgatccaactgcatctc	
qMtKNOX2-F	Forward-gagttgcattacaaatggccatat	For qRT-PCR analysis of *MtKNOX2*
qMtKNOX2-R	Reverse-acctgttgactcagccaatgct	
qMtKNOX6-F	Forward-ttggtggagcaggcattaca	For qRT-PCR analysis of *MtKNOX6*
qMtKNOX6-R	Reverse-aagggcttgcttttgggatt	
qSGL1-F	Forward-gatgaacagcctttcccagatt	For qRT-PCR analysis of *SGL1*
qSGL1-R	Reverse-gatgccgtaacgctctccaa	
qPALM1-F	Forward-ctcatccttcatcaccattcataaa	For qRT-PCR analysis of *PALM1*
qPALM1-R	Reverse-gcacaatccagcattagcaaca	