

Supplemental Figure 1. Developmental Defects in the slml-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 slml-l (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 slml-l 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 slml-l (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 \pm 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 aestivum* (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.

AtPIN1 1 ChPIN1 1 PsPIN1 1	MITA <mark>A</mark> DFYHVMTAMVPLYVAMILAYGSVKWWKIFTPDQCSGINRFVALFAVPLLSFHFIA MITA <mark>A</mark> DFYHVMTAMVPLYVAMILAYGSVKWWKIFTPDQCSGINRFVALFAVPLLSFHFIA MIT <mark>LI</mark> DFYHVMTAMVPLYVAMILAYGSVKWWKIFI <mark>S</mark> PDQCSGINRFVALFAVPLLSFHFIA
TaPINI 1 OsPINI 1 SLMI 1 BjPINI 1	MITAADFYHVMTAMVPLYVAMILAYGSVKWW <mark>R</mark> IFTPDQCSGINRFVALFAVPLLSFHFIS MISALDHYHVHTAVVPLYVAMILAYGSVKWWKIFTPDQCSGINRFVALFAVPLLSFHFIS MI <mark>SWHDLYHVH</mark> TAVVPLYVAMILAYGSVRWWKIFSPDQCSGINRFVAHFAVPLLSFHFIS
AtPIN1 61 ChPIN1 61 PsPIN1 61 TaPIN1 1	ANNPYAMNLRFHAADSLQKWIVLSLLFLWCKLSRNGSLDWTITLFSLSTLPNTLVMGIPL ANNPYAMNLRFHAADSLQKWIVLALLFLWCKLSRNGSLDWTITLFSLSTLPNTLVMGIPL SNNPYKMNLRFHAADTLQKHMTLGLLFHWSNSSKRGSLEWTITLFSLSTLPNTLVMGIPL
OsPIN1 61 SLM1 61 BjPIN1 61	TNNPYTMNLRFIAADTLOKUMULAMLTAWSHLSRRGSLEWTITLFSLSTLPNTLVMGIPL TNNPYTMNMRFIAADSLOKTITLFLFINSRTSSRGSLEWSITLFSLSTLPNTLVMGIPL TNNPYAMNLRFIAADTLOKILMLALLVLWANFTRSSLEWSITHFSLSTLPNTLVMGIPL
AtPIN1 121 ChPIN1 121 PsPIN1 121 TaPIN1 55 OsPIN1 121 SLM1 121 BjPIN1 121	LKGMYGNFSGDLMVQIVVLQCIIWYTLMLFLFEYRGAKLLISEQFPDTAGSIVSIHVDSD LKGMYGEFSGQLMVQIVVLQCIIWYTLMLFLFEYRGAKLLISEQFPDTAGSIVSIHVDSD LKGMYGDESGSLMVQIVVLQCIIWYTMLFMFERGARLLISEQFPDTAGSIVSIHVDSD LKGMYGDESGSLMVQIVVLQCIIWYTMLFMFEYRGARTDINRAVPDTAGAIASIVVS LKGMYGDESGSLMVQIVVLQCIIWYTLMLFMFEYRGARTDINRAVPDTAGAIASIV LKGMYGDEGGLMVQIVVLQCIIWYTLMLFMFEYRGARTLIVGPPDTAANIASIVVDD LKGMYGDEGGLMVQIVVLQCIIWYTLMLFMFEYRGARTLIVGPPDTAGSIS LKGMYGDSGTLMVQIVVLQCIIWYTLMLFMFEYRGARTLIVGPPDTAGSIS
AtPINI 181 ChPINI 181 PsPINI 181 TaPINI 115 OsPINI 181 SLMI 181 BjPINI 181	IMSLDGRQ - PLETEAEIKEDGKLHVTVRRSNASRSDIYSRRSQGLSATPRPSNLTN IMSLDGRQ - PLETEAEIKEDGKLHVTVRSNASRSDIYSRRSQGLSA FPRPSNLTN VMSLDGRF - PLETDAEIKQDGKLHVTVRSNASRSDIYSRRSQGLSSN FPRPSNLTN VMSLDGRRDMIETEAEVKEDGKIHVTVRSNASRSDIYSRRSMGFSST FPRPSNLTN VVSLDGRRDAIETETEVKEDGRIHVTVRSNASRSDIYSRRSMGFSST FPRPSNLTN VLSLDGRE - PLQTEAEVGEDGKLHVTVRSNASRSDIYSRRSMGFSST FPRPSNLTN VVSLDGRDAIETETEVKEDGRIHVTVRSNASRSDIYSRRSMGFSST FPRPSNLTN VVSLDGHD - FLETDAEIGNDGKLHVTVRSNASRSDIYSRRSMGFSST MTPRPSNLTG VMSLDGHD - FLETDAEIGNDGKLHVTVRSNASRSDIYSRRSMGFSST MTPRPSNLTG
AtPIN1 236 ChPIN1 236 PsPIN1 237 TaPIN1 172 OsPIN1 238 SLM1 240 BjPIN1 231	$\label{eq:scalar} \begin{array}{l} \texttt{AEIYSLOSSRNPTPRGSSFRHTDFYSMMASG-GGRNSNFGPGEAVFGGKGPTPRPS}\\ \texttt{AEIYSLOSSRNPTPR}\\ \texttt{AEIYSLOSSRNPTPR}\\ \texttt{AEIYSLOSSRNPTPR}\\ \texttt{AEIYSLOSSRNPTPRGSFRHTDFYSMMGGCRNSNFADSDVNVCISABRGVTPRPS}\\ \texttt{AEIYSLOSSRNPTPRGSFRHTDFYSMWGCSSNFAAGDAFGP-VVTGATPRPS}\\ \texttt{AEIYSLOSSRNPTPRGSFRHTDFYSMVGRSSNFAAGDAFGP-VVTGATPRPS}\\ \texttt{AEIYSLOSSRNPTPRGSFRHTDFYSMVGRSSNFAADAFGVTGAPPRPS}\\ \texttt{AEIYSLOSSRNPTPRGSFRHTDFYSMVGRSSNFAADAFGVTGAPPRPS}\\ \texttt{AEIYSLOSSRNPTPRGSFRHTDFYSMVGRSSNFAADAFGVTGAPPRPS}\\ \texttt{AEIYSLOSSRNPTPRGSFRHTDFYSMVGRSSNFAADAFGVTGAPPRPS}\\ \texttt{AEIYSLOSSRNPTPRGSFRHTDFYSMVGRSSNFAADAFGVTGAPPRPS}\\ \texttt{AEIYSLOSSRNPTPRGSFRHTDFYSMVGRSSNFAADAFGVTGAPPRPS}\\ \texttt{AEIYSLOSSRNPTPRGSFRHTDFYSMVGRSSNFAADAFGVTGAPPRPS}\\ \texttt{AEIYSLSTTPRGSNFNOSDFYSMVGFP-GGRLSNFGPADMYSMOSSRGPTPRPS}\\ \texttt{AEIYSLSTTPRGSNFNOSDFYSMVGFP-GGRLSNFGPADMYSMOSSRGPTPRPS}\\ \texttt{AEIYSLSTTPRGSNFNOSDFYSMVGFP-GGRLSNFGPADMYSMOSSRGPTPRPS}\\ \texttt{AEIYSLSTTPRGSNFNOSDFYSMVGFP-GGRLSNFGPADMYSMOSSRGPTPRPS}\\ \texttt{AEIYSLSTTPRGSNFNOSDFYSMVGFP-GGRLSNFGPADMYSMOSSRGPTPRPS}\\ \texttt{AEIYSLSTMOSSRGPTPRPS}\\ \texttt{AEIYSLSTMOSSRGPTPRS}\\ AEIYSLST$
AtPIN1 2 9 1 ChPIN1 2 9 2 PsPIN1 2 9 4 TaPIN1 2 2 5 OsPIN1 2 8 9 SLM1 2 7 9 BjPIN1 2 8 4	NYBEDGGPAKPTAAGTÄAGÄGRFHYQSCCSGGGGG-AHYPAPNPG-MFSPNTGGGGG NFBEDGAKTTAAGTGGAÄRFHYQSCCSGGGGGAHYPAPNPG-MFSPNTGGGGG NYBEDASNÄRKLK
AtPIN1 346 ChPIN1 348 PsPIN1 328 TaPIN1 254 OsPIN1 325 SLM1 315 BjPIN1 330	TAAMGNAPVVGG-KRQDGNGRDLHMFVWSSSASPVSDVFGGGGGNHHADYST TAAMGNAPVGGGKRQDANGRDLHMFVWSSSASPVSDVFGGG-NHHGDYAA NVKRSNGQNQONQOQXOD-DLHHFVWSSSASPVSDVFGGHEFGSHDOKEV
AtPIN1 397 ChPIN1 399 PsPIN1 379 TaPIN1 301 OsPIN1 371 SLM1 366 BjPIN1 388	ATNDHQKDVKISVPQGNSNDNQ <mark>VVER</mark> EFSFGNKDDDSKVL- ATNDQHKDVKISV-GNSNENQ <mark>VVER</mark> EFSFGNKDDDSKVL- KLNVSFGVDGHRBTQEDUIERDFSFGNKGMEREMM KDVRVAASPRKADGVERDFSFGNKERDAEAGDEK- KSPRKMDGAKDREDVVERDDFSFGNRGVMDRDAEAGDEK- VAHQKDREFGUDEFSFGNRTVANVDREGFVLSKLGS- RSDQGAKEIRMLVPDQSQNSENKALARPASGDFGGBPVSITRREEGERAKDAENGLNKPI
AtPIN1 4 3 8 ChPIN1 4 3 8 PsPIN1 4 1 6 TaPIN1 3 3 7 OsPIN1 4 1 0 SLM1 4 0 4 BjPIN1 4 4 8	ATDG-GNNISNKTTQAKVMPPTSVMTRLILIMVWRKLIRNPNSYSSLFGITWSL ATDG-GNNISNKTTQAKVMPPTSVMTRLILIMVWRKLIRNPNSYSSLFGITWSL QUHEGEKIGDGRSKVMPPTSVMTRLILIMVWRKLIRNPNTYSSLIGITWSL
AtPIN1 4 9 1 ChPIN1 4 9 1 PsPIN1 4 6 8 TaPIN1 3 8 9 OsPIN1 4 6 4 SLM1 4 6 0 BjPIN1 5 0 8	ISFKWNIEMPALIAKSISILSDAGLGMAMFSLGLFMALNPRIIACGNRRAAFAAAMRFVV ISFKWNIEMPALIAKSISILSDAGLGMAMFSLGLFMALNPRIIACGNRRATEAAMRFIA VSFRWIEMPATIAKSISILSDAGLGMAMFSLGLFMALQPRIIACGNKRATEAMAVRFIT VCFRWIFMYATAIIMKSIAILSDAGLGMAMFSLGLFMALQPRIIACGNKRATEAMAVRFIT VCFRWIFEMPAIVLKSISILSDAGLGMAMFSLGLFMALQPEIIACGNKVATWAMAVRFIT VSFRWIFVMPAIMAKSIAILSDAGLGMAMFSLGLFMALQPEIIACGNKVATWAMAVRFIT VSFRWIFVMPAIMAKSIAILSDAGLGMAMFSLGLFMALQPEIIACGNKVATWAMAVRFIT VSFRWIFVMPAIMAKSIAILSDAGLGMAMFSLGLFMALQPEIIACGNKVATWAMAVRFIT
AtPIN1 551 ChPIN1 551 PsPIN1 528 TaPIN1 449 OsPIN1 524 SLM1 520 BjPIN1 568	GPAVMLVASYAVGLRGVLLHVAIDOALPOGIVPFVFAKEYNVHPDILSTAVIFGMLIAL GPAVMFVASYAVGLRGVLERVAIDOALPOGIVPFVFAKEYNVHPDILSTAVIFGMLIAL GPAVMAAASTAVGLRGVLEHVAIVQAALPOGIVPFVFAKEYNVHPDILSTAVIFGMLIAL GPAVMAASTAVGLRGTLLGTAIVQAALPOGIVPFVFAKEYSVHPSILSTAVIFGMLIAL GPAVMAASTAVGLRGTLEHVAIVQAALPOGIVPFVFAKEYSVHPSILSTAVIFGMLIAL GPAVMAASTAVGLRGTLEHVAIVQAALPOGIVPFVFAKEYSVHPSILSTAVIFGMLIAL GPAVMAASTAVGLRGTLEHVAIVQAALPOGIVPFVFAKEYNVHPSILSTGVIFGMLIAL GPAVMAYASIANGLRGTLEHVAIVQAALPOGIVPFVFAKEYNVHPSILSTGVIFGMLIAL
AtPIN1 611 ChPIN1 611 PsPIN1 588 TaPIN1 509 OsPIN1 584 SLM1 580 BiPIN1 628	PITLMYYILLGL PITLMYYILLGL PITLVYYILLGL PITLVYYILLGL PITLVYYILLGL PITLVYYILLGL PITLVYYILLGL

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.

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
gSLM1-R	Reverse-gctcgtggcctctaccatagctag	genomic sequences
pSLM1-F	Forward-cacctagtatgatgtttgcggaatg	For cloning of the SLM1 promoter
pSLM1-R	Reverse-gctcgtggcctctaccatagcta	
pAtPIN1-F	Forward-ccggaattctaaattattccattggcgttgtcgc	For cloning of the <i>AtPIN1</i> promoter
pAtPIN1-R	Reverse-catgccatggcttttgttcgccggagaagagagag	
prbSGL1-F	Forward-ttaccatggatcccgacgcattca	For cloning of the <i>SGL1</i> cDNA as probe for in situ hybridization
prbSGL1-R	Reverse-ttggtggtatcgccggaaagaaga	
prbSLM1-F	Forward-tgcttcacctgtttctgaaggtgg	For cloning of the <i>SLM1</i> cDNA as probe for in situ hybridization
prbSLM1-R	Reverse-ggaagagcagcctgtacaatagca	
DR5GUS-F	Forward-caccctgcaggtcgacggtatcgca	For cloning of the <i>DR5:GUS</i>
DR5GUS-R	Reverse-cgcgcgataatttatcctagtttgc	
qMtKNOX1-F	Forward-caaggttagaagaagcatgtgcaa	For qRT-PCR analysis of <i>MtKNOX1</i>
qMtKNOX1-R	Reverse-caacetgatecaactgcatete	
qMtKNOX2-F	Forward-gagttgcattacaaatggccatat	For qRT-PCR analysis of <i>MtKNOX2</i>
qMtKNOX2-R	Reverse-acctgttgactcagccaatgct	
qMtKNOX6-F	Forward-ttggtggagcaggcattaca	For qRT-PCR analysis of <i>MtKNOX6</i>
qMtKNOX6-R	Reverse-aagggcttgcttttgggatt	
qSGL1-F	Forward-gatgaacagcctttcccagatt	For qRT-PCR analysis of SGL1
qSGL1-R	Reverse-gatgccgtaacgctctccaa	
qPALM1-F	Forward-etcatectteatcaceatteataaa	For qRT-PCR analysis of PALM1
qPALM1-R	Reverse-gcacaatccagcattagcaaca	

Supplemental Table 1. Primers Used in This Study.