

Supplemental Figure 1: Whole-plant phenotypes and plastochron measurements of *slomo* **mutants.** (A-D) Phenotypes of 40-day-old Ler wild-type (A), *slomo-1* mutant (B), Col-0 wild-type (C) and *slomo-3* mutant plants (D). White arrows indicate the youngest lateral inflorescences, highlighting their delayed development in *slomo* mutants. Scale bar in (A) represents 5 cm and applies to all four images. (E) Rate of flower initiation in *slomo-2* mutants compared to Ler wild-type plants. Measurements were done as in Fig. 1G,H.

(F) Leaf formation in short-day-grown *slomo-1* mutants compared to Ler wild-type plants. *slomo-1* mutants form fewer leaves overall before flowering at the same time, as indicated by the leveling off of the leaf number after day 54.

(G) Rate of flower formation in F1 plants from a complementation cross of *slomo-1* and *slomo-2* (right bar) compared to wild type and homozygous *slomo-1* and *slomo-2* mutants.

(H) Rate of flower formation in *slomo-1/+* heterozygous plants compared to homozygous genotypes. Measurements were done as in Fig. 3.

Values are mean \pm SEM from eight (E), nine (F) or at least ten (G,H) plants per genotype. **: different from wild type at p<0.01.



Supplemental Figure 2: Molecular nature of *slomo* mutant alleles.

(A) Schematic representation of *SLOMO* gene structure. Red/white arrow indicates the transcribed region, with red squares representing exons and white squares introns. P1 and P2 show the positions of the oligonucleotides used for the RT-PCRs (*SLOMO* 5' region) in (E).

(B,C) Detail of the exon-exon junction in the spliced cDNA from the wild type (B) and the *slomo-2* mutant (C). The mutated base of the conserved GT-dinucleotide of the splice donor site is indicated, as are the four additional bases leading to a premature stop codon in the mutant cDNA sequenced from *slomo-2* plants. (D) Schematic representation of the SLOMO protein. Orange square shows the position of the F-box domain and grey squares show the predicted leucine-rich repeats. Positions of the mutations encoded by the *slomo-1* and *slomo-2* mutant alleles are shown (arrows).

(E) RT-PCR on total RNA from Col-0 wild-type and *slomo-3* mutant plants. *slomo-3* mutants do not form full-length *SLOMO* mRNA, although the 3' region downstream of the T-DNA insertion site is still being transcribed. *PDF2* is a constitutively transcribed control gene (AT1G13320; Czechowski et al., 2005). The figure shows one of two technical replicate PCRs performed on one biological replicate of the RNA. Both technical replicates gave the same result

(F) Complementation of the *slomo-3* mutant phenotype by a genomic rescue construct (yellow bar). Measurements were taken as in Fig. 3. Values are mean \pm SEM from at least 18 plants per genotype.

Supplemental Data. Lohmann et al. (2010). Plant Cell 10.1105/tpc.109.071498

At Sl Vv	SLOMO SLOMO SLOMO SLOMO SLOMO	1 1 1 1	MRIWCFSCFTDEDEDEEDDNGGRVKKQSLATAMDNSNGDGDFVNFGENERAPRVPRWRLR MRIWCCLCFGEEEDNKKGYKSMRDPILGNNGDESPDENSAFDWRNVFEGV				
Os Pp			MRWTMPPHSWDHDAAGSSRAATHVPPLRCR				
At Sl Vv Os Pp	SLOMO SLOMO SLOMO SLOMO SLOMO	61 51 31 1	LCAEESEAAWAELDRFWTSEIPLNQLVQGESSSNVVAEAEDCTMEEADHDSYHKRAKVYS NVAAVVSPQACAVGDLGVPKNEEIDFDSNWTSSTVEVKNESYSGEKMLDVNLNLGLSGEA MFVATYYGSCFCCRGCTY DIWHGDNDAGCALEGAEEGDEEDEEGDEDGDRDLQSKRPKVRGFCEESPQ				
At	SLOMO	121	GLAECRSVSGVSSDAGNSVSSVERTVSFGIASSSRTDTDMFCQNFILNYNRKDGKKDDGD				
Sl	SLOMO	111	SSSTVLKEDSDPFTCSKRPKVNSFSLDWDNHLLQETSYLCPMNEGGGDVSLSNLLGATDD				
Vv	SLOMO	19	AITAMPLEAGNSSSSTDRDYNVSQSPIPFNNEILRLTSMSNDSDDENPLDSNDGRDEEGD				
Os	SLOMO	81	HSGVNASFFGLESTHFPGSDEHGHFKLSHCPENELDFGLSLFPNDGVNENPGDGNVGDVE				
Pp	SLOMO	1	MDSDLVGGDEDDGGR				
At	SLOMO	181	DNGSSDTEDFEVHIDLTDDLLHMVFSFLNHVDLCRSAMVCRQWRVASAHEDFWRVLNFEN				
Sl	SLOMO	171	EGKDSKMEDLDVRMDLTDDLLHMVFSFLDHIDLCRAASVCSQWRAASSHEDFWRYLNFEN				
Vv	SLOMO	79	GFSTSKMEDLEVRMDLTDDLLHMVFSFLDHINLCRAAIVCKQWRAGSSHEDFWRCLNFEN				
Os	SLOMO	141	ISGGENSEDVEIRMDLSDDLLHLIFSFLGQRDLCKAGASCKQWRSASMHEDFWKCLKFEN				
Pp	SLOMO	16	QHNLVDAEDGEARMDLTDDLLHKVFSFLKDVDLCQAAKVCRQWRVASAHEDFWKSLNFES				
At	SLOMO	241	IRISMEQFENMCSRYPNATEVNVYGAPAVNALAMKAATT-LRNLEVLTIGKGHISESFFQ				
Sl	SLOMO	231	KQISSNQFEDMCRRYPNATTINLYGTPNIHPLAMKAVSS-LRNLETLSLGRGQLGETFFQ				
Vv	SLOMO	139	RNISEEQFEDMCRRYPNATEVNIFGAPSIHSLVMTAMSS-LRNLETLTLGKGTLGDTFFQ				
Os	SLOMO	201	TRISLONFVDICHRYQNVTYLNLSGVPHAELLVMEAITC-LRHLKTLIMGKGQLGEAFFQ				
Pp	SLOMO	76	RQVTHQQVTVLCARYPKATELNLKGCPCVDEVVVQQAMLSLRNLEVLTLGRGFFSDGFFY				
At	SLOMO	300	ALGECNMLRSVTVSDAILGNG-AQEIHLSHDRLRELKITKCRVMRLSIRCPQLRSLSLKR				
Sl	SLOMO	290	ALTDCHVLRSLTINDATLGNG-IQEIPISHDSLRLLQLVKCRVLRVSIRCPQLETLSLKR				
Vv	SLOMO	198	ALADCYMLKRLLVNDATLGNG-IQEIPIYHDRLHHLQITKCRVLRISVRCPQLETLSLKR				
Os	SLOMO	260	LLSECPLLTTLTVSDASLGSG-IQEVTVNHDGLRELQILKCRALRISVRCSQLQILSLRR				
Pp	SLOMO	136	LLSGCESLQNLSITDATLGSGGAQEIQLKHESLRSLQILKCRVLRIA				
At	SLOMO	359	SNMSQAMLNCPLLQLLDIASCHKLLDAAIRSAAISCPQLESLDVSNCSCVSDETLREIAQ				
Sl	SLOMO	349	SSMPHAVLNCPLLHDLDIASCHKLSDAAIRSAATACPLLESLDMSNCSCVSDETLRDIAQ				
Vv	SLOMO	257	SSMAHAVLNCPLLHDLDIGSCHKLTDAAIRSAAT <mark>S</mark> CPLLESLDMSNCSCVSDDTLREIAL				
Os	SLOMO	319	TGMAHVSLNCPQLVELDFQSCHKLSDNAIRQAATACPLLASLDMSSCSCVTDETLREIAN				
Pp	SLOMO	196	TGMASAMLYCPRLLKLDVSSCHKLSDAGVRAAATACPLLTYLDISNCSYVSDETLREISL				
At	SLOMO	419	ACANLHILNASYCPNISLESVHLPMLTVLKLHSCEGITSASMTWIANSPALEVLELDNCN				
Sl	SLOMO	409	TCGHLRVLDASYCPNISLESVRLVMLTVLKLHSCEGITSASMAAIAHSYMLEVLELDNCS				
Vv	SLOMO	317	TCANLHILDASYCPNISLESVRLSMLTVLKLHSCEGITSASMAAISHSYMLEVLELDNCS				
Os	SLOMO	379	SCPNLSVLDASNCPNISEESVRLPMLVDLRLLSCEGITSASMAAIAYSRLLEALQLDNCS				
Pp	SLOMO	256	ACTHLRSLDASYCPNISLEGVRMPVLTDLKLVNCEGINSSSMAAISFCVMLEVLAMDYCW				
At	SLOMO	479	LLTTVSLHLSRLQSISLVHCRKFTDLNLQSIMLSSITVSNCPALRRITITSNAL				
Sl	SLOMO	469	LLTSVSLDLPRLQSIRLVHCRKFIDLNLHCGMLSSITVSNCPLLQRINITSSAL				
Vv	SLOMO	377	LLTSVSLELPRLQNIRLVHCRKFVDLNLRSIMLSSMTVSNCPALHRINVTSNSL				
Os	SLOMO	439	LLTSVSLDLPHLKNISLVHLRKFAELTLRSPVLSYIKVSRCSVLHRVSITSNAL				
Pp	SLOMO	316	LLTSVTLDLPRLRSITFINWPALWTLHRFGELTLRSPALTLLNISHCPALSRIDIASSF				
At	SLOMO	533	RRL <mark>A</mark> LQKQEN <mark>LTTLVLQCHSLQEVDLSDCESLSNSVC</mark> KIFSD <mark>D</mark> GGCPMLKSLILDNCESL				
Sl	SLOMO	523	KKLVLQKQESLTTIALQCPNLLEVDLTECESLTNSVCEVFSDGGGCPVLKSLVLDNCESL				
Vv	SLOMO	431	QKLVLQKQASLTTLALQCQYLQEVDLTDCESLTNSICDVFSD <mark>D</mark> GGCPMLKSLVLDNCECL				

Os	SLOMO	493	QKLVLQKQESLSSL <mark>SLLCNNLIDVDLSDCESLTNAVCEVFSDGGGCPLLRSLILDNCESL</mark>
Pp	SLOMO	376	EKLCLKNQMGLSSLALQCPWLREVDLTDCESLTDSVCDVFGDGGGCPKLDLLTLDNCDGL
At	SLOMO	593	TAVRFCNSSLASLSLVGCRAVTSLELKCPRIEQICLDGCDHLETAFFQPVALRSLNLGIC
Sl	SLOMO	583	TLVAFCSTSLVSLSLCGCRALISLALRCPYLEQVSLDGCDHLEVASFCPVGLRSLNLGIC
Vv	SLOMO	491	TAVGFRSTSLVSLSLVGCRAITSLELVCPYLEQVHLDGCDHLERASFRPVGLRSLNLGIC
Os	SLOMO	553	STVELNSSSMVNLSLAGCRSMTLLKLSCPNLQNVNLDGCDHLERASFCPVGLESLNLGIC
Pp	SLOMO	436	VKVKLMASSLRALSLVGCRNMISLELSCPILQSLQLDGRNRLVAASFSPVGLVSLNLGIC
At Sl Vv Os Pp	SLOMO SLOMO SLOMO SLOMO SLOMO	653 643 551 613 496	↓ PKLSVINIEAPYMVSLELKGCGVLSEASIMCPLLTSLDASFCSQLRDDCLSATTASCPLI PKMNMLHIEAPQMASLELKGCGVLSEASINCPLLTSFDASFCSQLKDDCLSATTSSCPLI PKLSALHIEAPSMVQLELKGCGCLSEASINCPMLTSLDASFCSKLKDDCLSATAASCPFI PKLSDLHIEAPKMSLLELKGCGVLSQASINCPRLTSLDASFCRKLMDDSLSQTAEACPLI PHLTTLEIEAAQMITLDLRGCGGLSQASIRCSNLSSLDASYCSRLGDDCLAATTASCSAI
At	SLOMO	713	ESLVLMSCPSIGSDGLSSLNGLPNLTVLDLSYTFLMNLEPVFKSCIQLKVLKLQACKYLT
Sl	SLOMO	703	ESLVLMSCPSVGCDGLLSLQSLPNLTYLDLSYTFLVTLQPVYESCLQLKVLKLQACKYLT
Vv	SLOMO	611	ESLILMSCPSVGYEGLSSLRLLPHLTILDLSYTFLMNLQPVFESCLQLKVLKLQACKYLT
Os	SLOMO	673	ENLILSSCVSIDLNGLSSLHCLHKLALLDLSYTFLTNLKPVFDSCPQLKILKLSACKYLS
Pp	SLOMO	556	QTLVLAACPKVGPAGLLALKKLPRLTMLDLSYTFLTDLSPVFEACPYLKVLRLSACKYLG
At	SLOMO	773	DSSLEPLYKEGALPALEELDLSYGTLCQTAIDDLLACCTHLTHLSLNGCVNMHDLDWGST
Sl	SLOMO	763	DTSLEPLYKENALPALCELDLSYGTLCQSAIEELLACCTHLSHVSLNGCINMHDLNWGFS
Vv	SLOMO	671	DSSLEALYKEGALPALCELDLSYGALCQSAIEELLACCTHLTHVSLNGCINMHDLNWGFS
Os	SLOMO	733	DSSLDALYREGALPMLVELDLSYSSIGQTAIEELLSCCTNLVNVNLNGCTNIHQLVCGSD
Pp	SLOMO	616	DTALNALHGGKVLPQLQELDMSYGSLGRAAIEGVLALCPHLTQVSLNGCLHVTDQLWSRL
At	SLOMO	833	SVHLFDYFGVYSSSDNTQEPAETANRLLQNLNCVGCPNIRKVLIPPAARFYHLST
Sl	SLOMO	823	GDQLSQIPSVS-IPHVSSLGEQQLSNBQPKRLLENLNCVGCPNIKKVLIP-MAQGFLLSS
Vv	SLOMO	731	SGPISELPSIYNTSSLSSHGDDHELIEQPNRLLQNLNCVGCQNIKKVLIPPMARCTHLSS
Os	SLOMO	793	DCSSGDMPVDVCPPD-SAPVRSEEISERSDRLLEVLNCTGCPNIKKVIIPSMTTYLRLSK
Pp	SLOMO	676	ATPP
At	SLOMO	888	LNLSLSVNLKEVDLTCSNLVLLNLSNCCSLEVLKLGCPRLASLFLQSCNMDE-AGVEAAI
Sl	SLOMO	881	LNLSLSGNLKEVDIACYNLCVLNLSNCCSLESLQLECPRLSSLFLQSCNVDE-ESVEAAV
Vv	SLOMO	791	LNLSLSANLKEVDVACYNLCFLNLSNCSSLEILKLECPRLTSLFLQSCNITV-EAVEAAI
Os	SLOMO	852	INLNLSTNLKEVDLTCSNLYTLNLSNCSSLEVLKLDCPRLTNLQLACTMLQDEELESAI
Pp	SLOMO	680	FPIELMASEDTGMEDVSSSDNHQCSALVVLQLNCPRLITLSLQSCGIAA-EMLEDAL
At	SLOMO	947	SGCSSLETLDLRFCPKISSVSMSKFRTVCPSLKRVFSSPNLLQD
Sl	SLOMO	940	SRCMMLETLDVRFCPKICPLNMTRLRVACPSLKRIFSS
Vv	SLOMO	850	SQCNMLETLDIRFCPKISNASMKTLRAVCPSLKRIFSSL
Os	SLOMO	912	SRCSALEILNVHSCPKINVLDFSRLRVVCPSLKRIQSSLIT
Pp	SLOMO	736	RGCSLLETLDVRHCTKVSASVLARIRCICPGLKRLYSTSSA

Supplemental Figure 3: Sequence alignment of SLOMO and related proteins from other plant species.

Identical amino acids are highlighted in black, similar ones in gray. Asterisks indicate the position of the F-box. The glycine highlighted in red (arrow) is the one mutated to glutamate in the *slomo-1* allele.



Supplemental Figure 4: *slomo* mutants show normal auxin sensitivity, but form more lateral roots and longer hypocotyls.

(A) Quantification of root length of Col-0 and *slomo-3* mutants after growth on medium with increasing concentrations of the auxin NAA.

(B) *slomo-3* mutants grown on medium without external auxin form more lateral roots overall and have a higher density of lateral roots than Col-0 wild-type plants.

(C) Hypocotyl lengths of *slomo* mutants compared to wild-type strains after growth in long-day conditions. Values are mean \pm SEM from at least 16 plants per genotype. **: significantly different from wild type at p<0.01 (Student's t-test).



Supplemental Figure 5: The pattern and levels of *ProDR5* promoter activity are unchanged in *slomo* mutants.

(A,B) Projected z-stacks of confocal micrographs of the inflorescence meristem from wild-type (A) or *slomo-3* (B) plants expressing the auxin-responsive *ProDR5:VENUS* reporter (Heisler et al., 2005). Arrowheads indicate the position where the next primordium will be initiated. The asterisk in (A) indicates slight damage to the meristem during preparation. YFP-fluorescence is shown in green, while red represents fluorescence of the membrane dye FM4-64. Scale bars are 50 μ m.





Supplemental Figure 6: Genetic interactions between SLOMO and miR156.

(A-D) Whole-plant phenotypes of 30-day-old plants.

- (A) Col-0 wild type.
- (B) slomo-3 mutant showing slightly delayed development of lateral inflorescences.
- (C) Pro35S:miR156b overexpressing plant with reduced apical dominance.
- (D) slomo-3 Pro35S:miR156b plant with intermediate phenotype in terms of apical dominance.

(E) Quantification of the rate of flower formation in the indicated genotypes. Values are mean \pm SEM from at least nine plants per genotype.

Scale bar in (A) represents 4 cm and applies to all four images (A-D).

Marker	Chromosome	Approximate location (kb)	BAC	Forward primer (5'-3')	Reverse primer (5'-3')	Annealing temperature (°C)	Length of product from Ler allele (bp)	Length of product from Col allele (bp)
AL049915	4	15,818	T16I18	CGGCTATGAGTATCAAAGGAA	GACGATGAGAACGACACC	55	271	235
CER451516	4	15,955	F26P21	GGGTTCACTTTTAAAGTTTCAA	AAACCCCAAAACCATCTG	55	137	150
CER449763	4	16,241	F17I5	TAATTATGGTGGGCTCTCTGC	GCCACCACAATCATTTCTCA	55	177	193
TWC10	4	17,376	AP21	CAGATAAATATCTCCCGTTATATAG	GGACATGCAAGATGGTGGACG	46	141	153

Supplemental Table 1: Markers used for mapping the *SLOMO* gene.

The *SLOMO* coding region (including introns) is located between 16,015,971 bp and 16,020,697 bp on chromosome 4.

kb: kilobase-pair; bp: base-pair; Ler: Landsberg erecta; Col: Columbia

Primer name	Sequence (5' - 3')	Restriction enzyme	Remarks	
slomo- 1_dCAPS_for	CATTCTTCCAACCTGTGAGTGTTAC	Apal L cuts product		
slomo- 1_dCAPS_rev	TAATGGATGCTTCAGACAGTGCA	from wild-type allele		
slomo- 2_dCAPS_for	TCAACCTGCAGATATTGTGATGAG	XmnI, cuts product		
slomo- 2_dCAPS_rev	СААТААСААААССАТСАТААСТААGAACATA	from mutant allele		
slomo-3_RT- PCR_for	TCAGTTGGTTCAGGGTGAGAGT		3-primer PCR to	
slomo- 3_3xgeno_rev	CCACCGACGAAACAGAATTTCC		genotype slomo-3 allele; product from mutant allele longer than from wild-type allele	
Salk_Lba	TGGTTCACGTAGTGGGCCATCG			
1642 dCAPS F				
HinfI	GGIGAAGIIGAAGIGAAAAAGAICGIIC	HinfI, cuts product		
1642 dCAPS R HinfI	CTTGGAAGTCAAACCAACGAAGGAA	from mutant anele		
pid-1_dCAPS_for	CCGGCGATGTTACGAGAATCAG	BclI, cuts product		
pid-1_dCAPS_rev	TCTCTGCGTAAGCGAAATCTGATGATC	from mutant allele		
pid-2_dCAPS_for	CCGTTCGTTGCGCCGACTAATG	Dalli auto meduat		
pid-2_dCAPS_rev	CTTTAACCTCCGCCGCACCTCGCCGAGATC	from mutant allele		
pin1_geno_for	CCCAAAATTTCTCTATGTCCTTCGA		3-primer PCR to genotype pin1	
pin1_geno_rev	AAACTACCTGGATAATGGCAACATG		(GK_051A10) allele; product from wild-type allele longer than from mutant allele	
08409	ATATTGACCATCATACTCATTGC			
slomo-3_RT-	TCAGTTCGTTCACCCTGACACT			
PCR_for			test for expression of full-length mRNA in	
slomo-3_RT- PCR_rev	TCATCCTTTTTCCCATCTTTCC		slomo-3 mutants	

Supplemental Table 2: Oligonucleotides for PCR-genotyping and RT-PCR

Primers for RT-PCR against the constitutively expressed *PDF2* have been described before (Anastasiou et al., 2007).

SUPPLEMENTAL METHODS

Molecular cloning and plant transformation

To generate the *ProSLOMO:GUS* and the *ProSLOMO:vYFPer* reporters, a 1.8 kbfragment of the *SLOMO* 5' genomic region up to the start codon was amplified using T3-primer and oligo pSLOMO_rev_KpnI (5' – CATGGTACCCCTAAGCCCACCT – 3') on pDL22 as template. The resulting product was digested with *SacI* and *KpnI* and subcloned into pBlueML2AP:NLSGUS and pBlueML2AP:vYFPer to give plasmids pDL24 and pDL25, respectively. From there, the *ProSLOMO:GUS* and *ProSLOMO:vYFPer* fragments were subcloned via *AscI*-sites into pBarMAP.

To generate the *SLOMO* rescue construct used in Supplemental Figure 2F, nucleotides 88794 to 96725 of BAC F4I10 (GenBank ID: 4455321) were subcloned into pBlueML2AP to give plasmid pDL22. From there, the insert was subcloned as an *AscI*-fragment into pML997.

Plants were transformed using 'floral dip' (Clough and Bent, 1998).

SUPPLEMENTAL REFERENCES

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