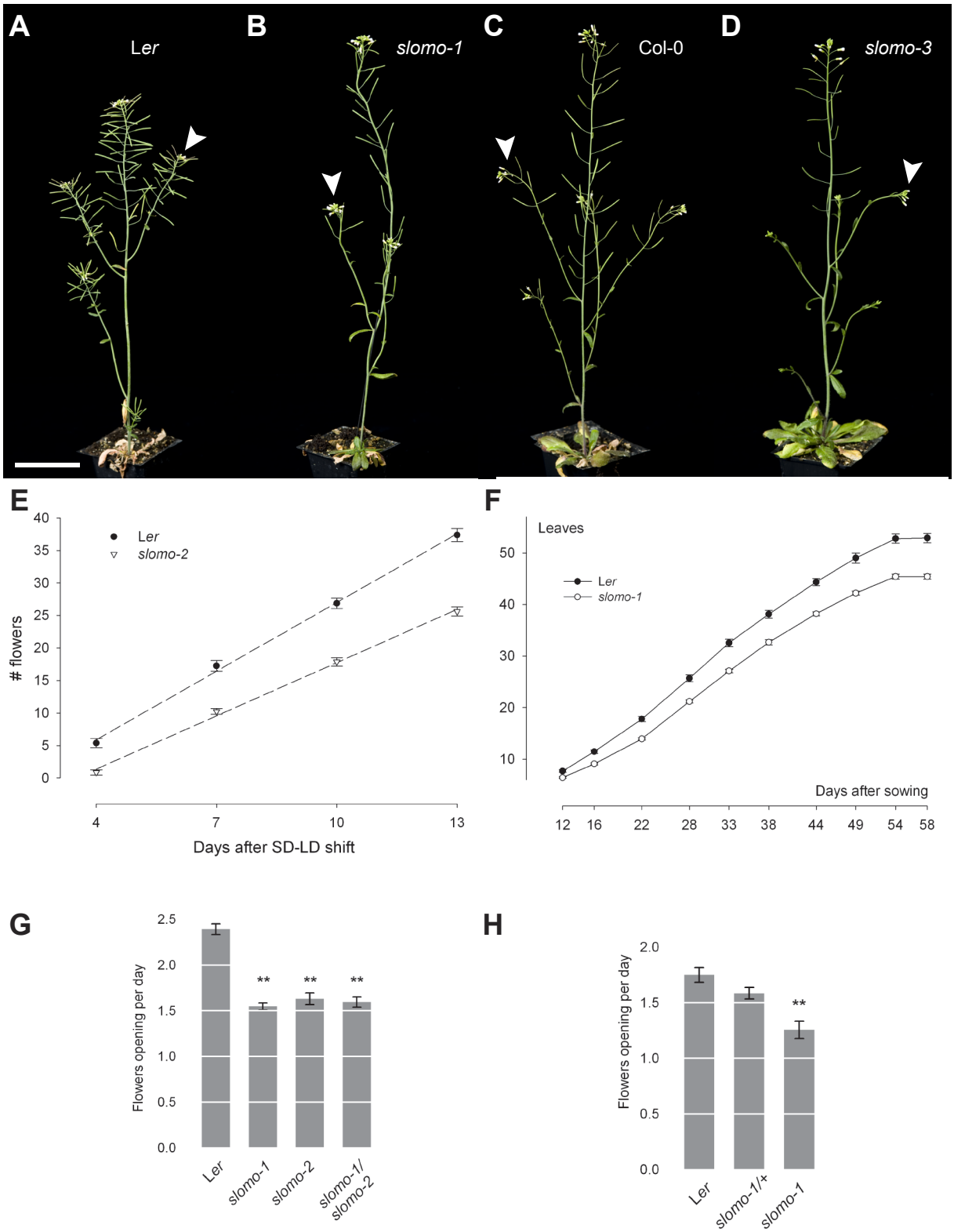
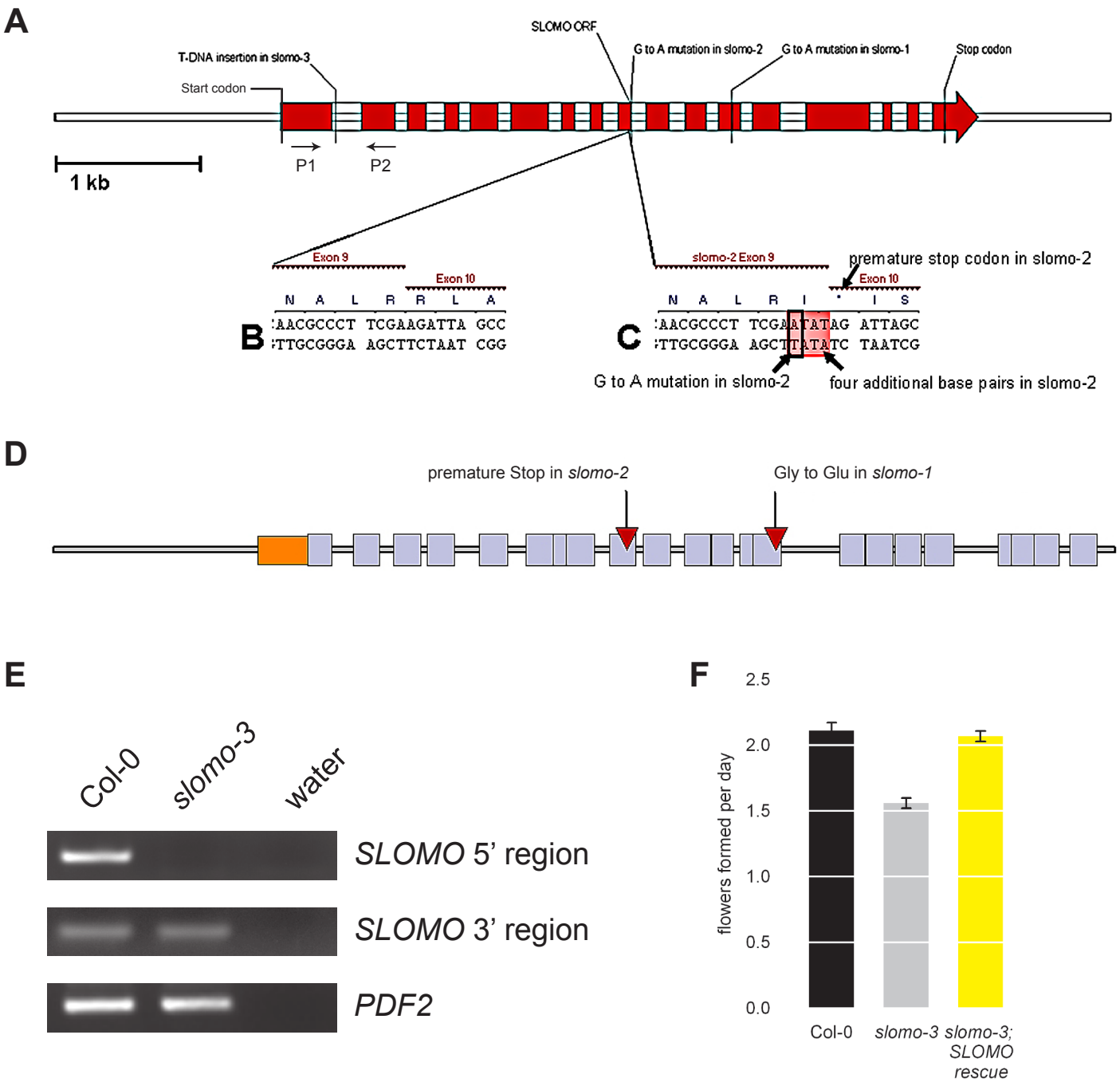
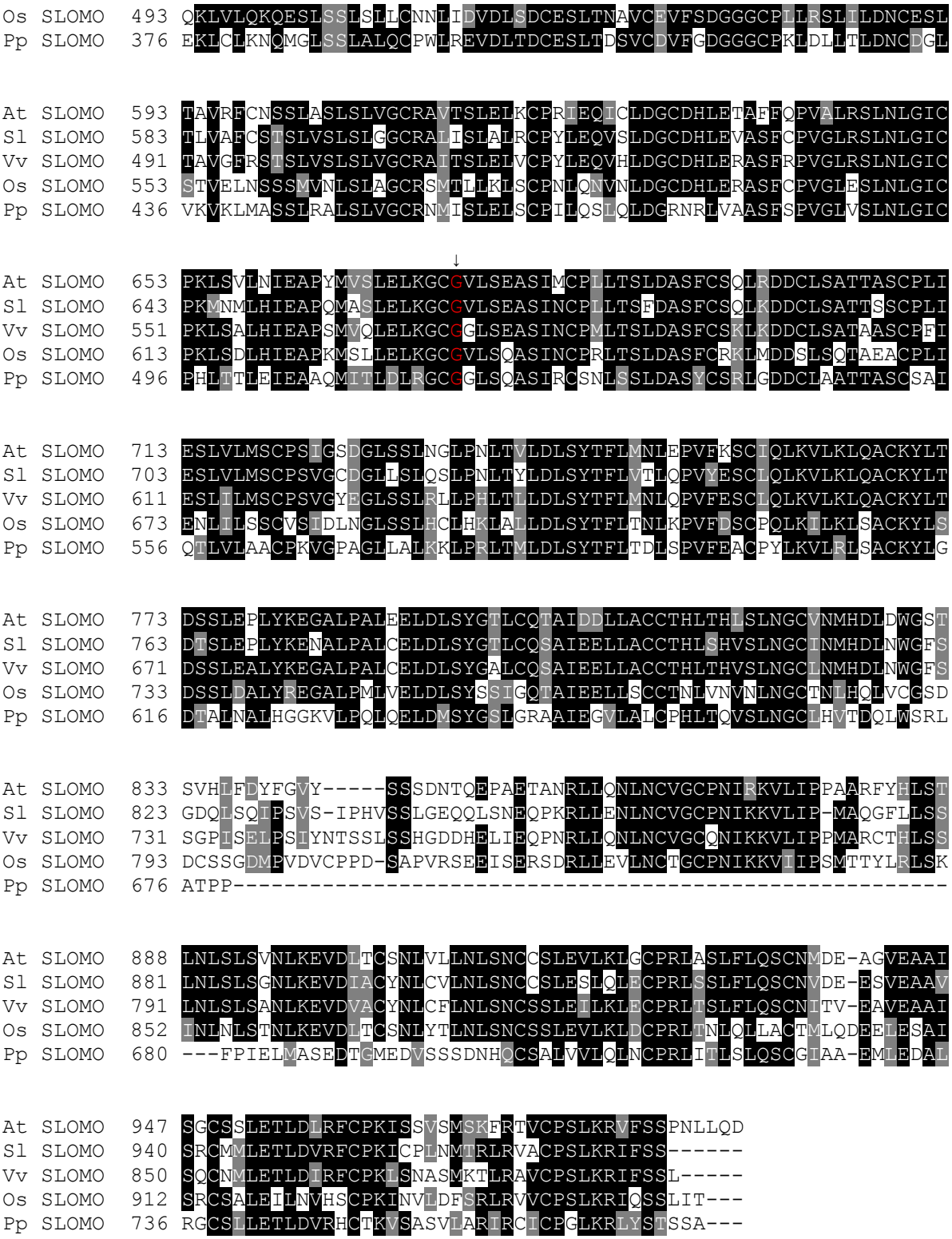


Supplemental Figure 1: Whole-plant phenotypes and plastochron measurements of *slomo* mutants.
(A-D) Phenotypes of 40-day-old L*er* wild-type (A), *slomo-1* mutant (B), Col-0 wild-type (C) and *slomo-3* mutant plants (D). White arrows indicate the youngest lateral inflorescences, highlighting their delayed 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 L*er* wild-type plants. Measurements were done as in Fig. 1G,H.
(F) Leaf formation in short-day-grown *slomo-1* mutants compared to L*er* 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 ± SEM from eight (E), nine (F) or at least ten (G,H) plants per genotype. **: different from wild type at $p<0.01$.



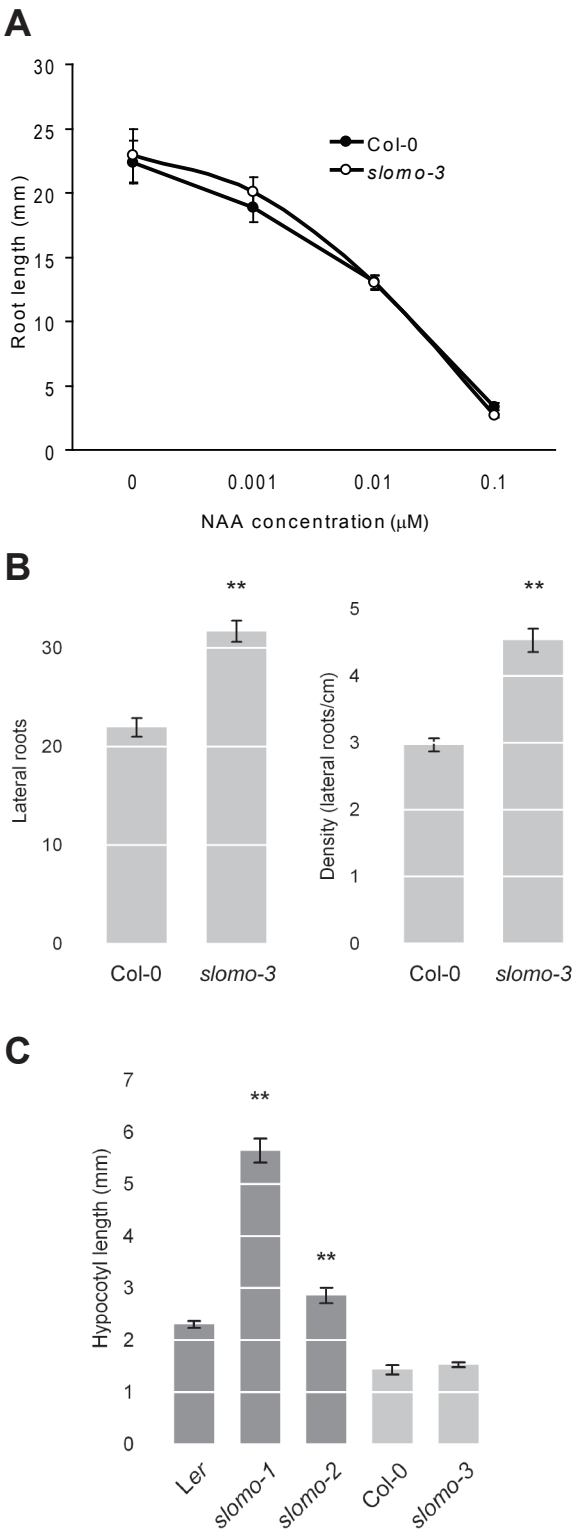
Supplemental Figure 2: Molecular nature of *slomo* mutant alleles.
(A) Schematic representation of *SLOMO* gene structure. Red/white arrow indicates the transcribed region, with red squares representing exons and white squares introns. P1 and P2 show the positions of the oligonucleotides used for the 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 ± SEM from at least 18 plants per genotype.


At SLOMO 1 MRIWCFSCFTDEDEDEEDDNGGRVKKQSLATAMDNSNGDGDFVNFGENERAPRVPRWRLR
Sl SLOMO 1 MRIWCCLCFGEEEDNKKGYKS----------MRDPILGNNGDESPDENSAFDWRNVFEGV
Vv SLOMO 1 ----------
Os SLOMO 1 ----------MRWTMPPHSWDHDAAGSSRAATHVPPLRCR
Pp SLOMO 1 ----------
At SLOMO 61 LCAEESEAAWAELDRFWTSEIPLNQLVQGESSSNVVAEAEDCTMEEADHDSYHKRAKVYS
Sl SLOMO 51 NVAAVVSPQAGAVGDLGVPKNEEIDFDSNWTSSTVEVKNESYSGEKMLDVNLNLGLSGEA
Vv SLOMO 1 ----------MFVATYYGSCFCGRGCTY
Os SLOMO 31 DIWHGDNDAGGAIEGAEEGDEEDEEGD----------EDGDRDLQSKRPKVRGFGEESPQ
Pp SLOMO 1 ----------
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 TRISLQNFVDICHRYQNVTYLNLSGVPHAELLVMEAITC-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 LLSGCESLQNLSITDATLGSGGAQEIQLKHESLRSLQILKCRVLRIAIRCLFLETLSLKR
At SLOMO 359 SNMSQAMLNCPLLQLLDIASCHKLLDAAIRSAAISCPQLESLDVSNCSCVSDETLREIAQ
Sl SLOMO 349 SSMPHAVLNCPLLHDLDIASCHKLSDAAIRSAATACPLLESLDMSNCSCVSDETLRDIAQ
Vv SLOMO 257 SSMAHAVLNCPLLHDLDIGSCHKLTDAAIRSAATSCPLLESLDMSNCSCVSDDTLREIAL
Os SLOMO 319 TGMAHVSLNCPQLVELDFQSCHKLSDNAIRQAATACPLLASLDMSSCSCVTDETLREIAN
Pp SLOMO 196 TGMASAMLYCPRLLKLDVSSCHKLSDAGVRAAATACPLLTYLDISNCSYVSDETLREISL
At SLOMO 419 ACANLHILNASYCPNISLESVHLPMLTVLKLHSCEGITSASMTWIANSPALEVLELDNCN
Sl SLOMO 409 TCGHLRVLDASYCPNISLESVRLVMLTVLKLHSCEGITSASMAAIAHSYMLEVLELDNCS
Vv SLOMO 317 TCANLHILDASYCPNISLESVRLSMLTVLKLHSCEGITSASMAAISHSYMLEVLELDNCS
Os SLOMO 379 SCPNLSVLDASNCPNISFESVRLPMLVDLRLLSCEGITSASMAAIAYSRLLEALQLDNCS
Pp SLOMO 256 ACTHLRSLDASYCPNISLEGVRMPVLTDLKLVNCEGINSSSMAALSFCVMLEVLAMDYCW
At SLOMO 479 LLTTVSLHLSRLQSISLV------HCRKFTDLNLQSIMLSSITVSNCPALRRITITSNAL
Sl SLOMO 469 LLTSVSLDLPRLQSIRLV------HCRKFIDLNLHCGMLSSITVSNCPLLQRINITSSAL
Vv SLOMO 377 LLTSVSLELPRLQNIRLV------HCRKFVDLNLRSIMLSSMTVSNCPALHRINVTSNSL
Os SLOMO 439 LLTSVSLDLPHLKNISLV------HLRKFAELTLRSPVLSYIKVSRCSVLHRVSITSNAL
Pp SLOMO 316 LLTSVTLDLPRLRSITFLNWPALWTLHRFGELTLRSPALTLLNLSHCPALSRIDIASSSF
At SLOMO 533 RRLALQKQENLTTLVLQCHSLQEVDLSDCESLSNSVCKIFSDDGGCPMLKSLILDNCESL
Sl SLOMO 523 KKLVLQKQESLTTIALQCPNLLEVDLTECESLTNSVCEVFSDGGGCPVLKSLVLDNCESL
Vv SLOMO 431 QKLVLQKQASLTTLALQCQYLQEVDLTDCESLTNSICDVFSDDGGCPMLKSLVLDNCECL

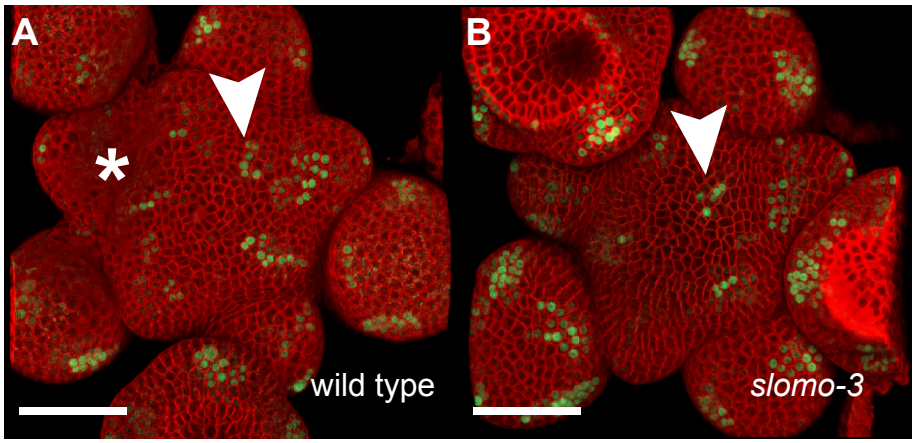


Supplemental Figure 3: Sequence alignment of SLOMO and related proteins from other plant species.

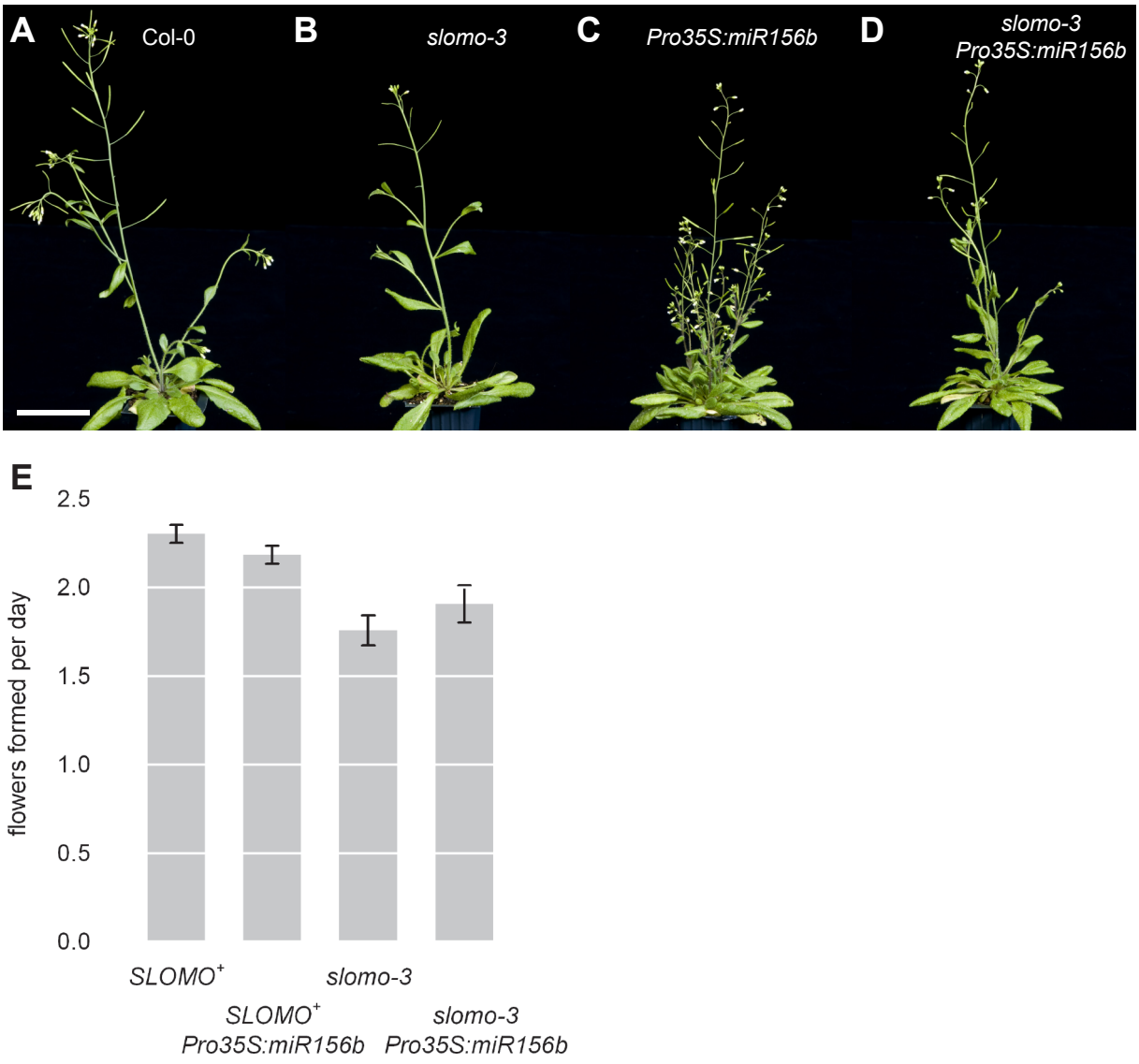
Identical amino acids are highlighted in black, similar ones in gray. Asterisks indicate the position of the F-box. The glycine highlighted in red (arrow) is the one mutated to glutamate in the *slomo-1* allele.



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 ± 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 μm.



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 ± SEM from at least nine plants per genotype.
Scale bar in (A) represents 4 cm and applies to all four images (A-D).

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

Marker	Chromosome	Approximate location (kb)	BAC	Forward primer (5'-3')	Reverse primer (5'-3')	Annealing temperature (°C)	Length of product from L*er* 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

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; L*er*: Landsberg *erecta*; Col: Columbia

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

Primer name	Sequence (5' - 3')	Restriction enzyme	Remarks
slomo-1_dCAPS_for	CATTCTTCCAACCTGTGAGTGTTAC	ApaLI, cuts product from wild-type allele	
slomo-1_dCAPS_rev	TAATGGATGCTTCAGACAGTGCA		
slomo-2_dCAPS_for	TCAACCTGCAGATATTGTGATGAG	XmnI, cuts product from mutant allele	
slomo-2_dCAPS_rev	CAATAACAAAACCATCATAACTAAGAACATA		
slomo-3_RT-PCR_for	TCAGTTGGTTCAGGGTGAGAGT		3-primer PCR to genotype slomo-3 allele; product from mutant allele longer than from wild-type allele
slomo-3_3xgeno_rev	CCACCGACGAAACAGAATTTCC		
Salk_Lba	TGGTTCACGTAGTGGGCCATCG		
1642 dCAPS F HinfI	GGTGAAGTTGAAGTGAAAAAGATCGTTC	HinfI, cuts product from mutant allele	
1642 dCAPS R HinfI	CTTGGAAGTCAAACCAACGAAGGAA		
pid-1_dCAPS_for	CCGGCGATGTTACGAGAATCAG	BclI, cuts product from mutant allele	
pid-1_dCAPS_rev	TCTCTGCGTAAGCGAAATCTGATGATC		
pid-2_dCAPS_for	CCGTTCGTTGCGCCGACTAATG	BglII, cuts product from mutant allele	
pid-2_dCAPS_rev	CTTTAACCTCCGCCGCACCTCGCCGAGATC		
pin1_geno_for	CCCAAAATTTCTCTATGTCCTTCGA		3-primer PCR to genotype pin1 (GK_051A10) allele; product from wild-type allele longer than from mutant allele
pin1_geno_rev	AAACTACCTGGATAATGGCAACATG		
o8409	ATATTGACCATCATACTCATTGC		
slomo-3_RT-PCR_for	TCAGTTGGTTCAGGGTGAGAGT		test for expression of full-length mRNA in slomo-3 mutants
slomo-3_RT-PCR_rev	TCATCCTTTTTCCCATCTTTCC		

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 kb-fragment 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 *Sac*I and *Kpn*I 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 *Asc*I-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 *Asc*I-fragment into pML997.

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

SUPPLEMENTAL REFERENCES

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