

Fig. S1. Examples of the most severe indeterminacy phenotypes in *vip3-1* siliques.

Representative images of the most severe phenotypes in *vip3-1* flowers, displaying an inflorescence stem with siliques and flowers, emerging from a silique. Scale bar: 1 cm.

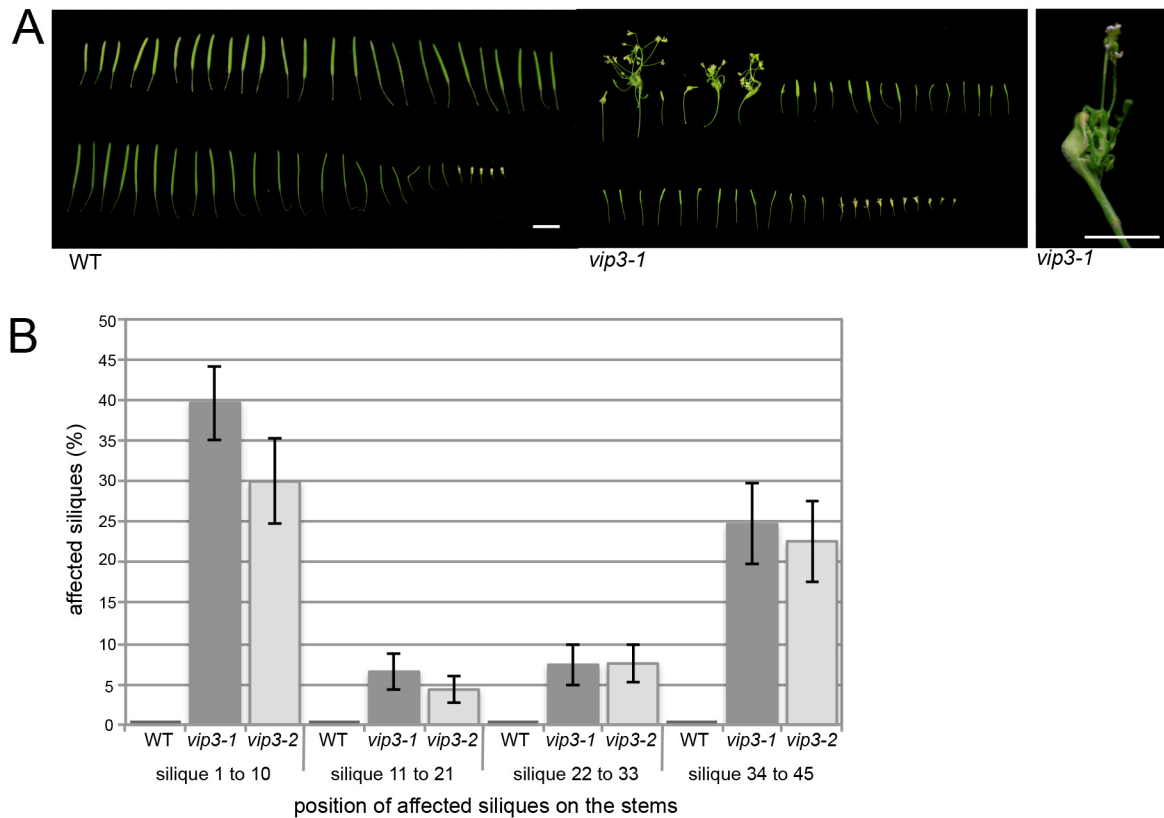


Fig. S2. *vip3* phenotype in short day then continuous light 21°C.

(A) Phenotype of WT (left panel) and *vip3-1* (middle panel) siliques, from plants grown in short day 21°C followed by continuous light 21°C conditions, harvested in a sequence of initiation along the stem. Scale bar : 1 cm. Right panel shows representative silique of the *vip3* displaying the indeterminacy phenotype. Scale bar : 5 mm. (B) Distribution (%) of affected siliques along the stems of the wild type (N=13), *vip3-1* (N=32) and *vip3-2* (N=21) grown in short day 21°C followed by continuous light 21°C condition (on average, 19% of *vip3-1* and 17% of *vip3-2* siliques displayed visible indeterminacy defects in these conditions).

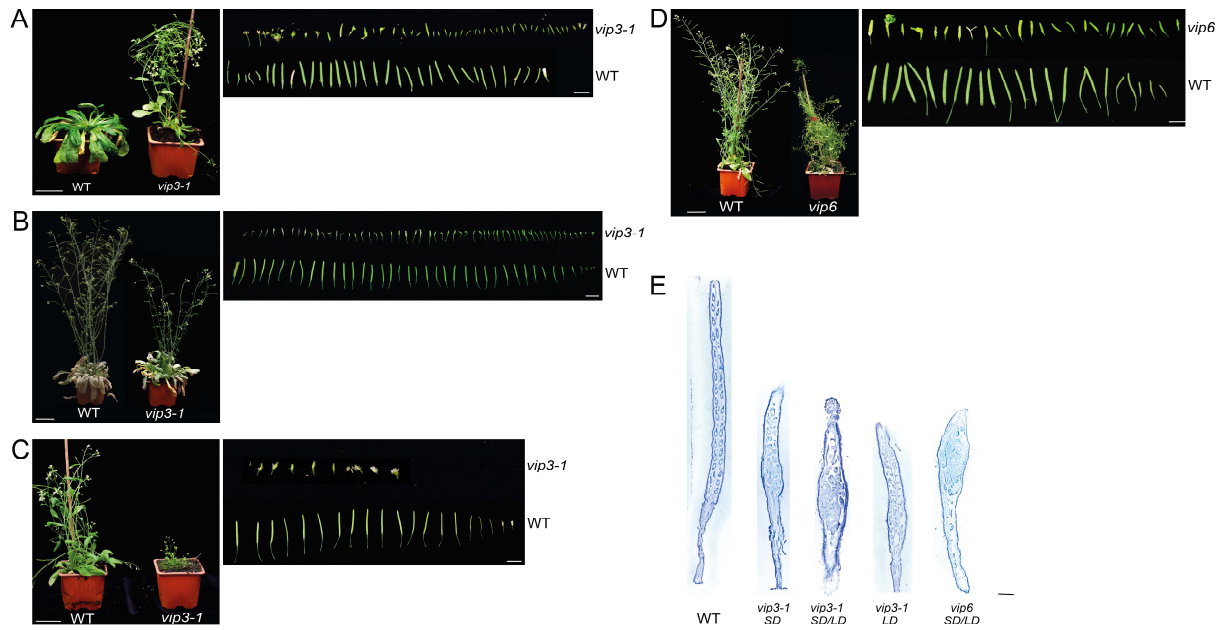


Fig. S3. Indeterminacy phenotype in different growth conditions and in different mutants of the Paf1 complex.

(A-C) Phenotypes of WT and *vip3-1* mutants grown in short day conditions (A, N=9 plants), in short then long day conditions (B, N=22 plants), and in long day conditions (C, N=22 plants). (D) Phenotype of WT and *vip6* mutant grown in short day 21°C followed by continuous light 16°C conditions displaying the indeterminacy phenotype (N=19 plants). For each condition, left panels display wild-type and *vip* adult plants, and right panels the siliques harvested in the order of their initiation along the stem. (E) Representative sections in young siliques, stained with toluidine blue, of *vip3-1*, in each culture condition, and *vip6* mutant, displaying the indeterminacy phenotype. Scale bars : 3 cm (A-D, left panels); 1 cm (A-D, right panels); 500 μ m (E).

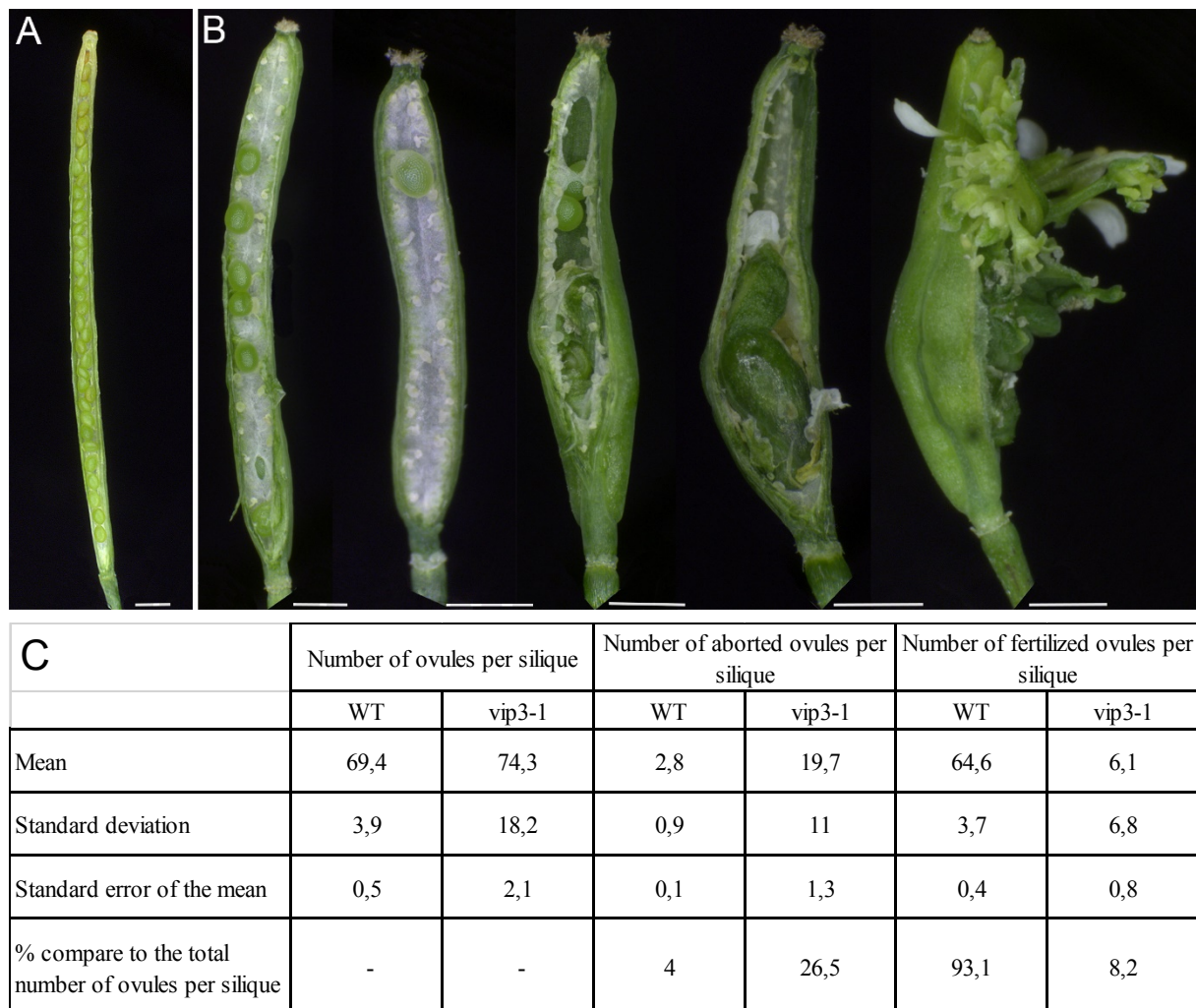
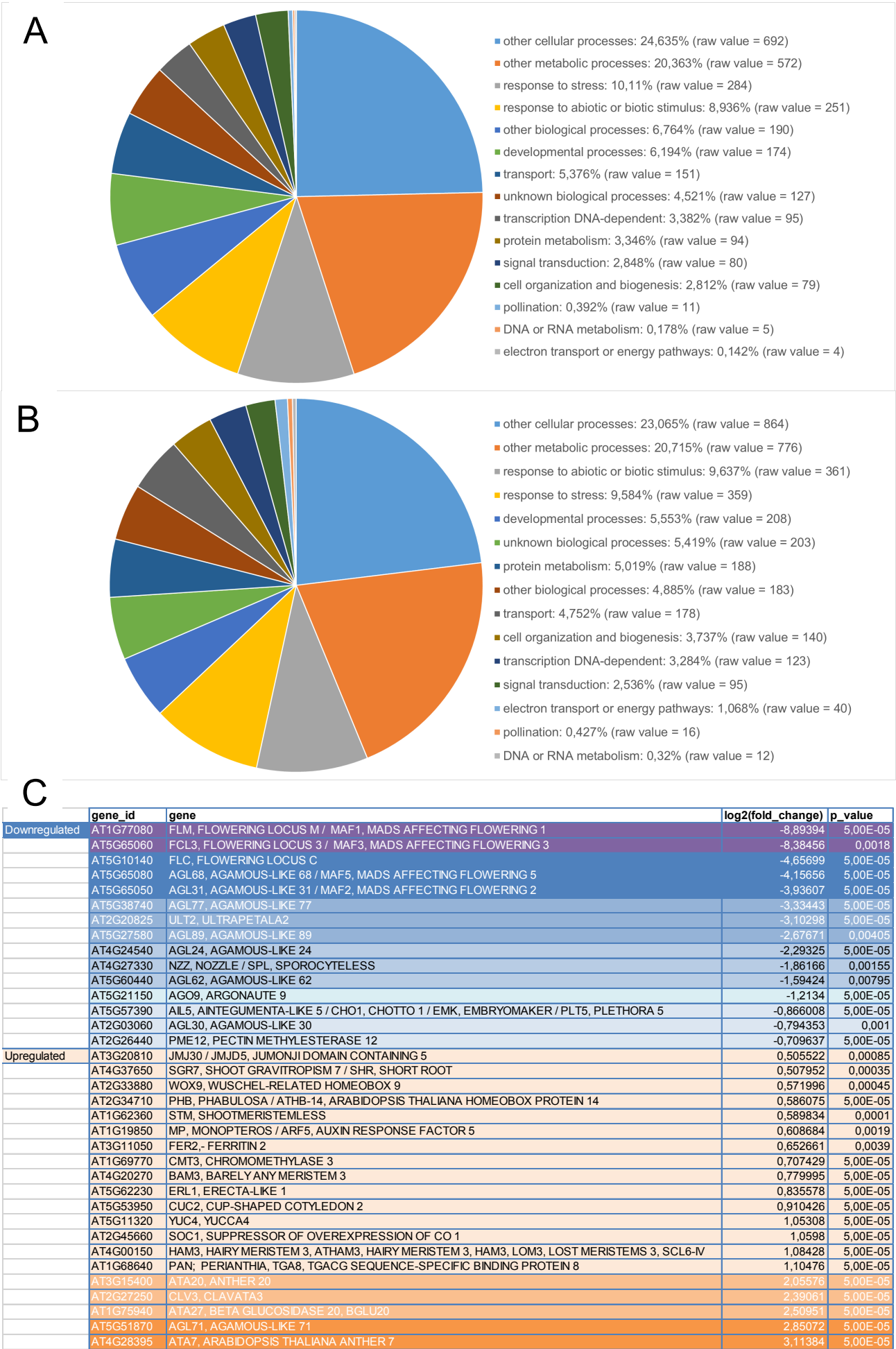


Fig. S4. Proportion of aborted ovules and seeds in *vip3-1*.

(A-B) illustrates the range of phenotypes observed in *vip3-1* (B) compared to Col0 (A) (grown in short day and then in continuous light 16°C). *vip3-1* displays a strong and highly variable reduction of seed set in siliques showing no indeterminacy. In silique showing indeterminacy no or very few seeds usually develop. Bars = 500 μ m. (C) Number of aborted ovules and seeds in *vip3-1* (N=73 siliques) and WT (N=70 siliques). The standard deviation reflects the variability of the original distribution. The standard error of the mean indicates the precision of estimated means (95% confidence interval).



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	gene_id	gene	log2(fold_change)	p_value
Downregulated	AT2G14610	PR1; pathogenesis-related protein 1	-5.18392	5.00E-05
	AT5G59220	HAI1; PP2C protein (Clade A protein phosphatases type 2C)	-1.72227	5.00E-05
	AT4G34760	SAUR-like auxin-responsive protein family	-1.13968	5.00E-05
	AT1G08320	TGA9; bZIP transcription factor family protein	-0.969944	0.00355
	AT1G67710	ARR11; response regulator 11	-0.934393	0.00065
	AT3G23030	IAA2; indole-3-acetic acid inducible 2	-0.884945	0.0009
	AT4G34000	ABF3; abscisic acid responsive elements-binding factor 3	-0.857165	5.00E-05
	AT5G54510	DFL1; Auxin-responsive GH3 family protein	-0.799458	5.00E-05
	AT5G57560	TCH4; Xyloglucan endotransglucosylase/hydrolase family protein	-0.672642	5.00E-05
	AT3G23050	IAA7; indole-3-acetic acid 7	-0.628497	0.00325
	AT1G03430	AHP5; histidine-containing phosphotransfer factor 5	-0.590316	0.0007
	AT4G34750	SAUR-like auxin-responsive protein family	-0.579414	0.00535
Upregulated	AT1G80100	AHP6; histidine phosphotransfer protein 6	0.514231	0.0006
	AT2G22670	IAA8; indoleacetic acid-induced protein 8	0.537947	0.00075
	AT3G63010	GID1B; alpha/beta-Hydrolases superfamily protein	0.572849	0.00025
	AT1G28130	GH3.17; Auxin-responsive GH3 family protein	0.575311	5.00E-05
	AT5G46570	BSK2; BR-signaling kinase 2	0.576718	5.00E-05
	AT1G19850	MP; Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-like protein	0.608684	0.0019
	AT1G51950	IAA18; indole-3-acetic acid inducible 18	0.628133	5.00E-05
	AT5G46790	PYL1; PYR1-like 1	0.646811	5.00E-05
	AT2G38120	AUX1; Transmembrane amino acid transporter family protein	0.691917	5.00E-05
	AT2G01570	RGA1; GRAS family transcription factor family protein	0.759926	5.00E-05
	AT1G45249	ABF2; abscisic acid responsive elements-binding factor 2	0.794846	5.00E-05
	AT1G19050	ARR7; response regulator 7	0.811842	5.00E-05
	AT2G38310	PYL4; PYR1-like 4	0.856148	5.00E-05
	AT4G27260	WES1; Auxin-responsive GH3 family protein	0.864813	5.00E-05
	AT1G72450	JAZ6; jasmonate-zim-domain protein 6	0.885443	5.00E-05
	AT1G17380	JAZ5; jasmonate-zim-domain protein 5	0.960683	5.00E-05
	AT4G33950	OST1; Protein kinase superfamily protein	1.02011	5.00E-05
	AT5G13220	JAZ10; jasmonate-zim-domain protein 10	1.03421	5.00E-05
	AT1G19180	JAZ1; jasmonate-zim-domain protein 1	1.04499	5.00E-05
	AT5G11320	YUC4, YUCCA4	1.05308	5.00E-05
	AT2G41310	RR3; response regulator 3	1.11732	5.00E-05
	AT1G77920	TGA7; bZIP transcription factor family protein	1.15091	0.00385
	AT5G17490	RGL3; RGA-like protein 3	1.15216	5.00E-05
	AT3G11410	PP2CA; protein phosphatase 2CA	1.21844	5.00E-05
	AT4G14550	IAA14; indole-3-acetic acid inducible 14	1.31153	0.0009
	AT1G04250	AXR3; AUX/IAA transcriptional regulator family protein	1.58048	0.0001
	AT3G21510	AHP1; histidine-containing phosphotransmitter 1	1.80767	0.00015
	AT1G77690	LAX3; like AUX1 3	2.1705	5.00E-05
	AT4G00880	SAUR-like auxin-responsive protein family	2.62316	5.00E-05
	AT5G13380	Auxin-responsive GH3 family protein	3.54665	5.00E-05
	AT2G46690	SAUR-like auxin-responsive protein family	3.63345	5.00E-05

Fig. S5. Differential gene expression in *vip3-1* vs. wild-type shoot apices.

(A, B) Gene ontology analysis: categories of genes involved in biological processes that are up-regulated (A) and down-regulated (B) in *vip3-1*. (C, D) Short list of genes involved in flowering and flower development (C) and signaling (D) pathways that are misexpressed in *vip3-1*. Genes that are down-regulated are highlighted in blue, and those that are up-regulated are highlighted in orange.

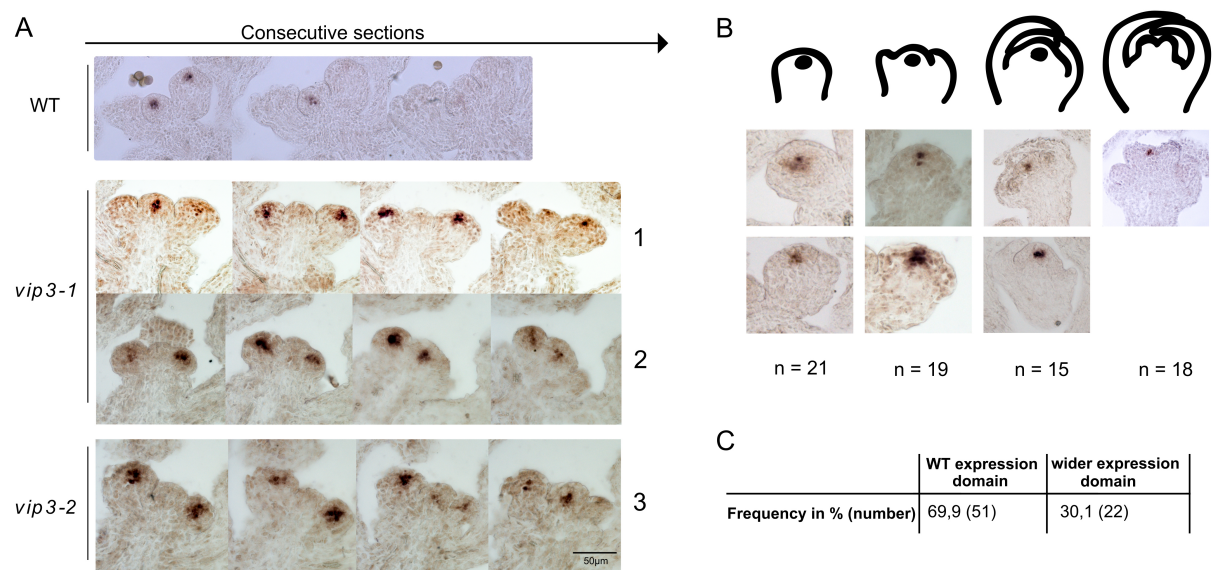


Fig. S6. Expression patterns of *WUS* in *vip3* flowers.

(A, B) *In situ* hybridization of *WUS* transcripts in wild-type (A, upper panel) and *vip3-1* (A, lower panel and B). (A) Consecutive sections on WT and 3 independent *vip3* (1-2: *vip3-1*; 3: *vip3-2*) apices showing an expansion of *WUS* expression domain in *vip3-1* floral meristems, when compared to wild type. (B) Representative patterns of *WUS* expression domain in *vip3-1* flower buds at four different developmental stages (as represented by schematic drawings). Plants were grown in short day then continuous light 16°C conditions (as in Fig. 1). Scale bar: 50 µm. (C) Number of flower meristems displaying a wild-type *WUS* expression domain and an enlarged *WUS* expression domain in *vip3-1*.

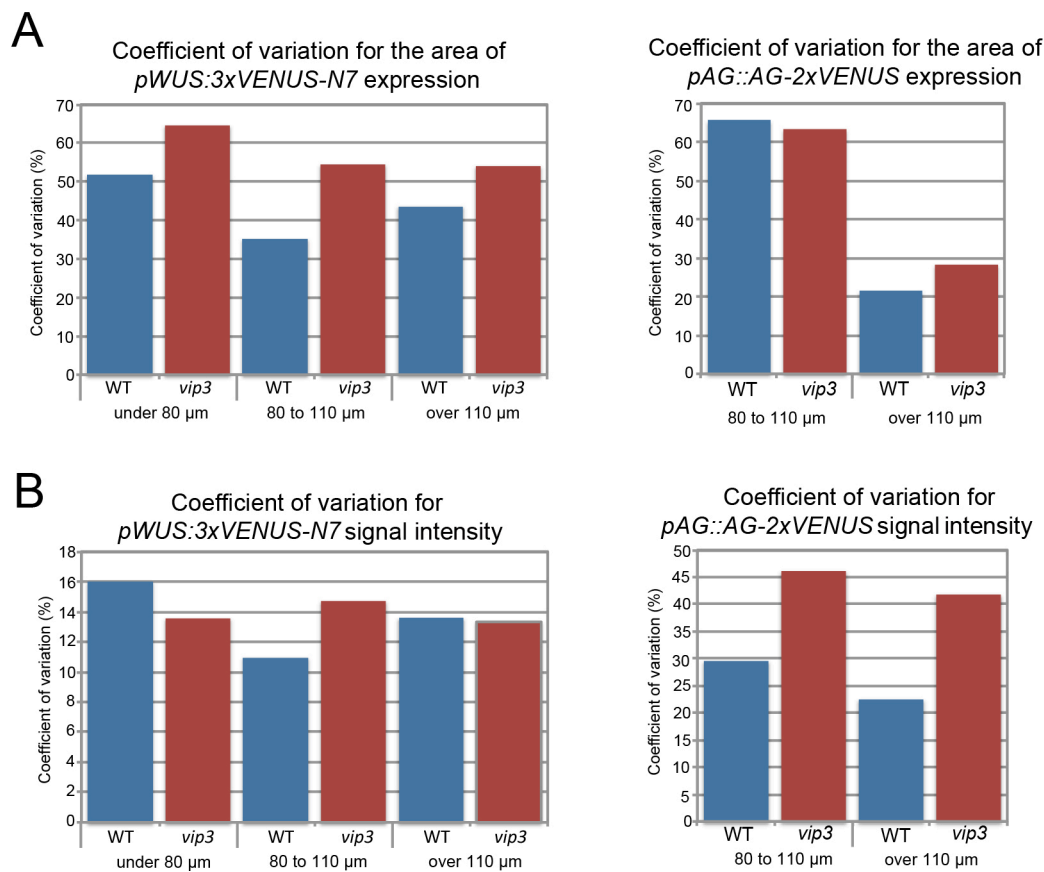


Fig. S7. Coefficient of variation for *WUS* and *AG* expression area and average intensity in *vip3* flowers

(A) Histograms displaying the coefficients of variation (%) for the area of *pWUS::3xVENUS-N7* (left) and *pAG::AG-2xVENUS* (right) expression in wild-type and *vip3-1* flowers. (B) Histograms displaying the coefficients of variation for the average fluorescence signal intensity of *pWUS::3xVENUS-N7* (left) and *pAG::AG-2xVENUS* (right) expression in wild-type and *vip3-1* flowers.

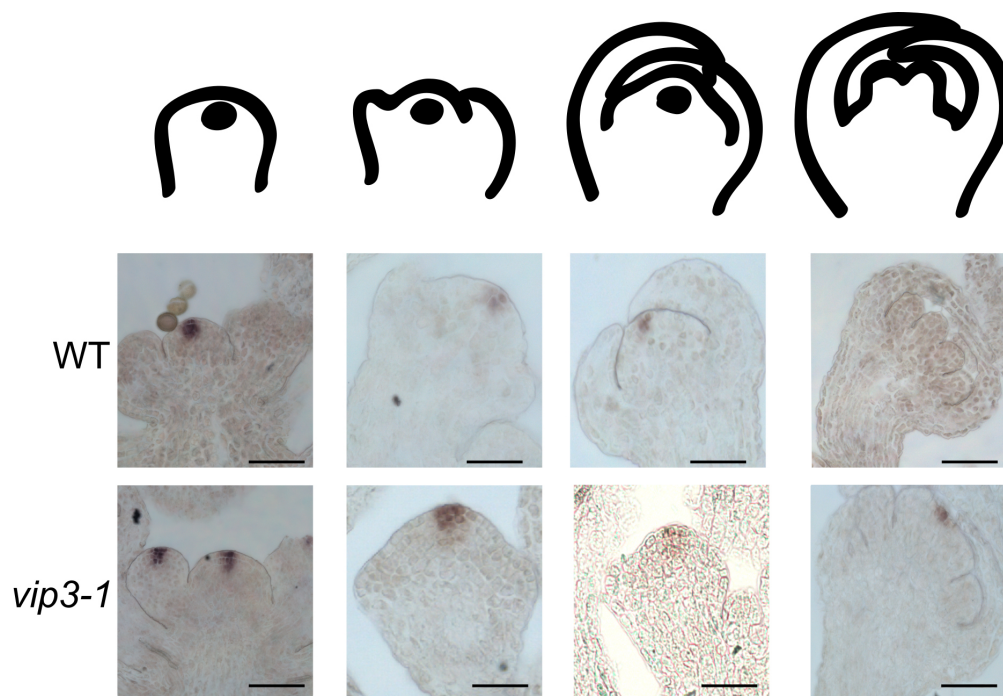


Figure S8. Expression patterns of *CLV3* in *vip3-1* flowers

In situ hybridization of *CLV3* transcripts in wild-type (A) and *vip3-1* (B). Plants were grown in short day then continuous light 16°C conditions (as in Figure 1). Scale bar = 50 μ m.

Table S1. List of primers

Name	Sequence
Genotyping primers	
LBb1.3	ATTTTGCCGATTTCGGAAC
<i>vip3-1</i> F	GACTGCAAGTACCACTTTCGC
<i>vip3-1</i> R	TAATGGGAAACGACTTGCTTG
<i>vip3-2</i> F	CTGACTGGATCTCTTGACGAGACG
<i>vip3-2</i> R	GATACTCAGCAATTCCATATAGTACCCAAGC
Primers for <i>in situ</i> probes	
<i>WUS_in_situ_F</i>	CAACAAGTCCGGCTCTGGTG
<i>WUS_in_situ_RT7</i>	TGTAATACGACTCACTATAGGGCGGGAAGAGAGGAAGCGTACGTCG
<i>AG_in_situ_F</i>	ACGGCGTACCAATCGGAGCT
<i>AG_in_situ_RT7</i>	TGTAATACGACTCACTATAGGGCGTTGCAATGCCGCGACTTGG
<i>CLV3_in_situ_F</i>	ATGTCCGGTCCAGTTCAACAAC
<i>CLV3_in_situ_RT7</i>	TGTAATACGACTCACTATAGGGCGGTCAGGTCCCGAAGGAACA
Primers for <i>pAG::AG-2xVenus</i> construction	
<i>pPD381</i>	GTCCCCGGGAGTGATCCCTTCTCCAACACA
<i>pPD413</i>	AGTCCCCGGGTAAGTGGAGAGCGGTTTGGT
<i>pPD441</i>	AGTGGATCCGCAGCTGCCGCAGCTGCGATGGTGAGCAAGGGCGAG
<i>pPD442</i>	GTCTCTAGACTAGATAGATCTCTTGACAGCTC