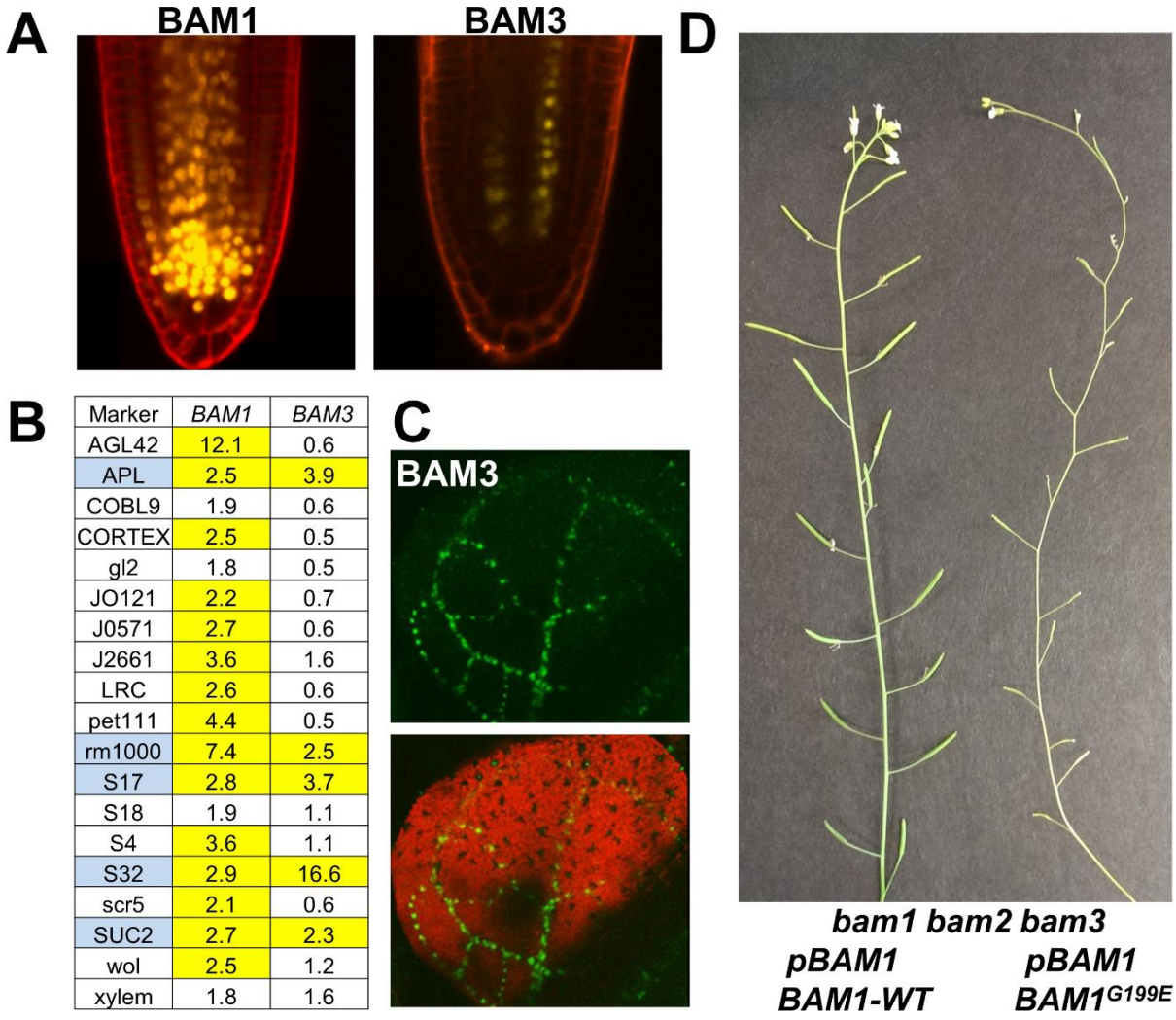
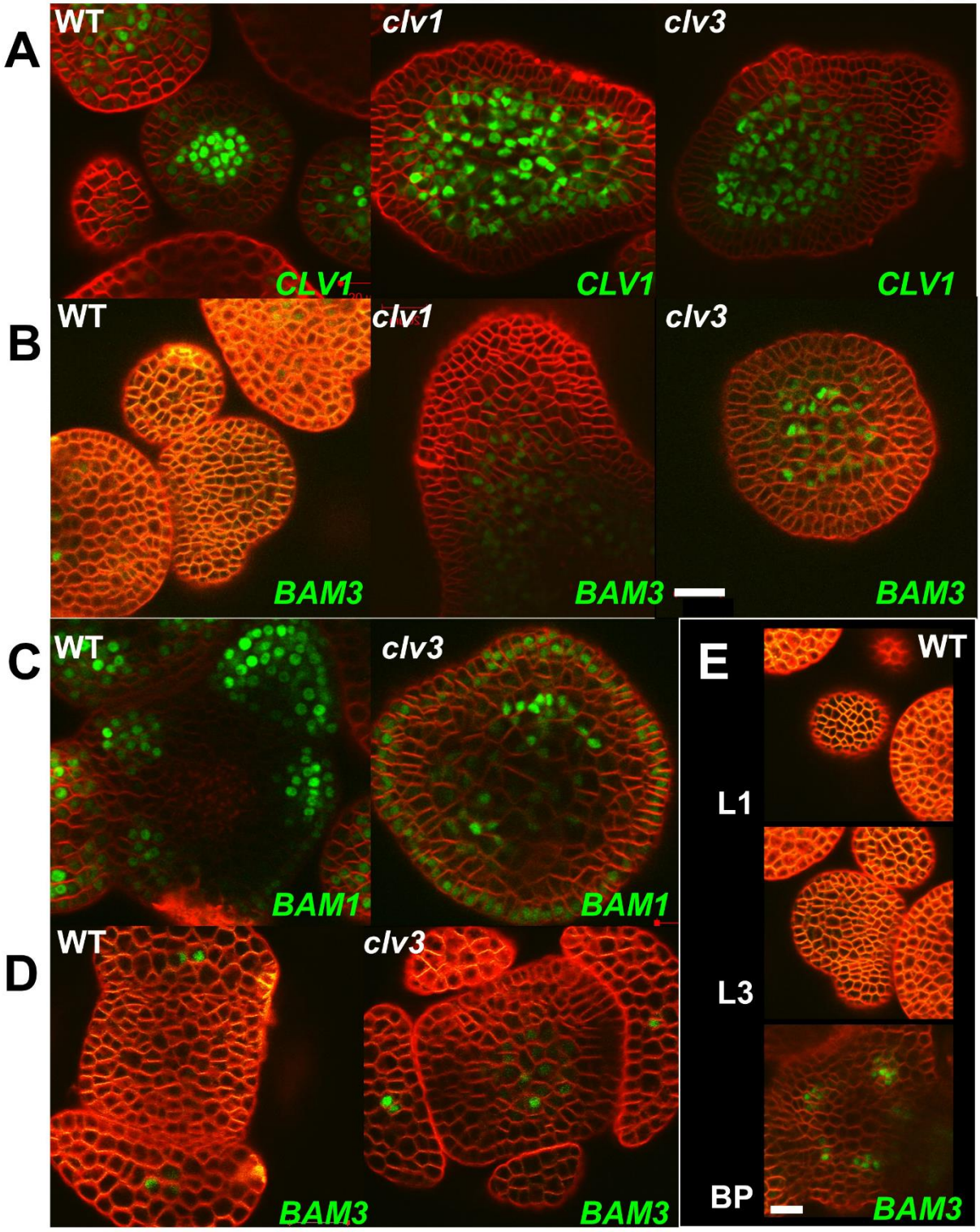


Marker	*BAM1*	*BAM3*
AGL42	12.1	0.6
APL	2.5	3.9
COBL9	1.9	0.6
CORTEX	2.5	0.5
gl2	1.8	0.5
JO121	2.2	0.7
J0571	2.7	0.6
J2661	3.6	1.6
LRC	2.6	0.6
pet111	4.4	0.5
rm1000	7.4	2.5
S17	2.8	3.7
S18	1.9	1.1
S4	3.6	1.1
S32	2.9	16.6
scr5	2.1	0.6
SUC2	2.7	2.3
wol	2.5	1.2
xylem	1.8	1.6

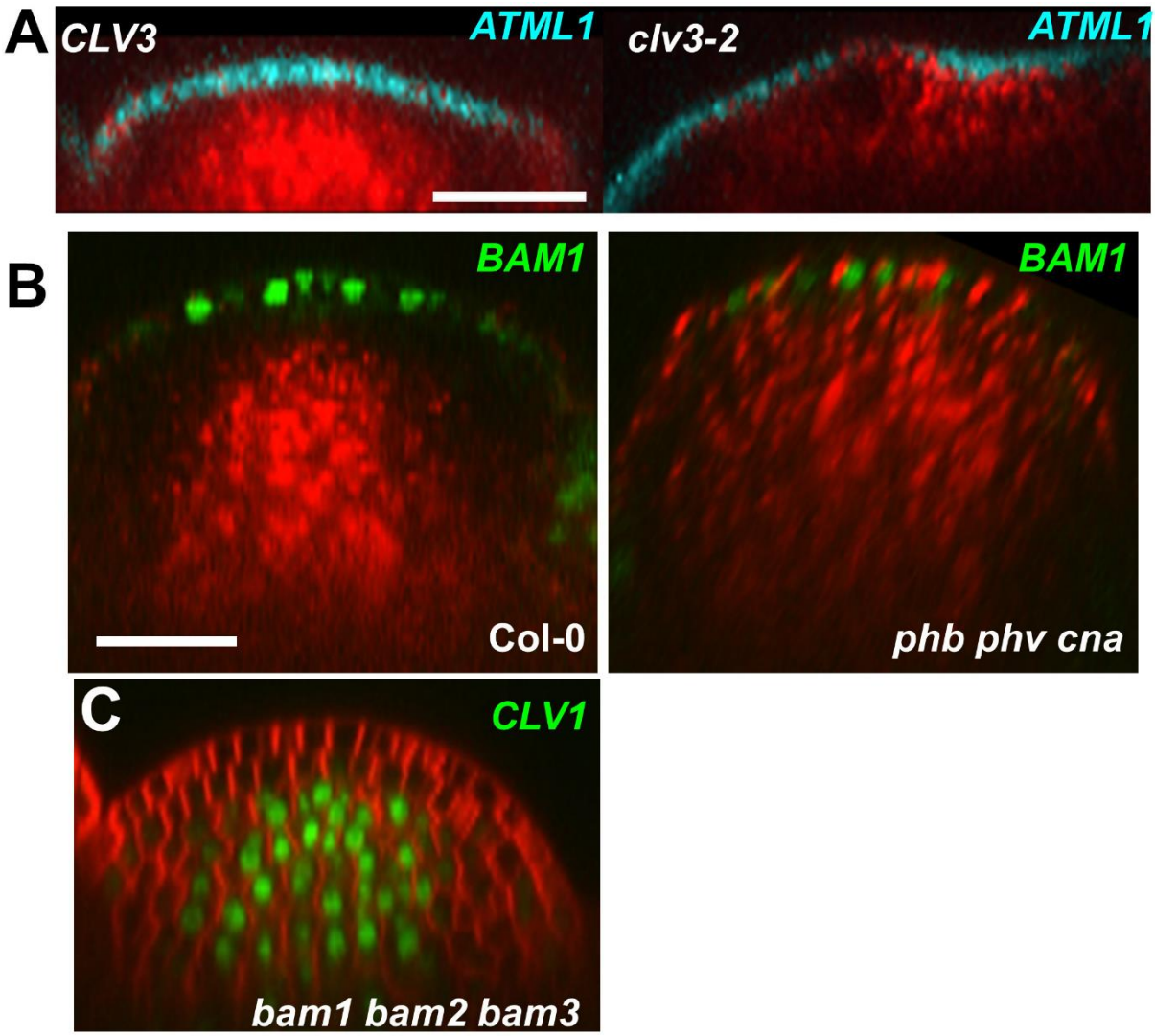
Supplementary Figure 1. *BAM1* and *BAM3* promoters replicate previous expression data in roots and vasculature, and complement *bam* mutants.

A. *pBAM1::2YN7* (left), and *pBAM3::2YN7* (right), expression in root tips. Yellow, nuclear 2YN7 signal; Red, propidium iodide staining. B. Collected cell type-specific enrichment of *BAM1* and *BAM3* from the Brady et al root cell profiling data set (Brady et al 2007). Marker column: marker cell line profiled, phloem-associated cell types in blue. Note the restriction of *BAM3* expression to phloem lineage cells, and the broader enrichment of *BAM1*-derived RNAs. We noticed in the Brady set that markers for one phloem cell type (e.g. *SUC2*) are frequently scored as enriched in other phloem cell types, suggesting possible cross contamination of closely associated cell types. C. Expression of *BAM3* is restricted to vascular tissues in leaf tissue as well. D. Expression of wild type *BAM1* (left), but not *BAM1* defective in CLE-peptide binding (right, see Shinohara et al., 2012), from the *BAM1* promoter complements fertility defects in the *bam1 bam2 bam3* triple mutant.



Supplementary Figure 2. *BAM3* and *BAM1* are repressed in the SAM and FM by the CLV signaling pathway. All cross sections represent 2YN7 reporter activity in L3 cells. Each image reflects a scan of L3 cell layer from the top of the SAM down. L3 cells expressing 2YN7 activity or not were identified by counting cell layers in cross sections in SAMs (A, B, C), or FMs (D). Genotypes in

white, reporter in green. Note for *BAM1* (C), the lack of signal in the center L3 cells, but enrichment of signal in bisected abaxial primordia on the flanks of the SAM. E) Serial sections of SAM for wild type (WT) plant expressing the *BAM3* 2YN7 reporter. Sections depict the L1 tissue layer, the L3 tissue layer and a deeper section below primordia emergence (BP). Red signal, FM4-64 membrane staining. Solid white scale bars, 20 μM.

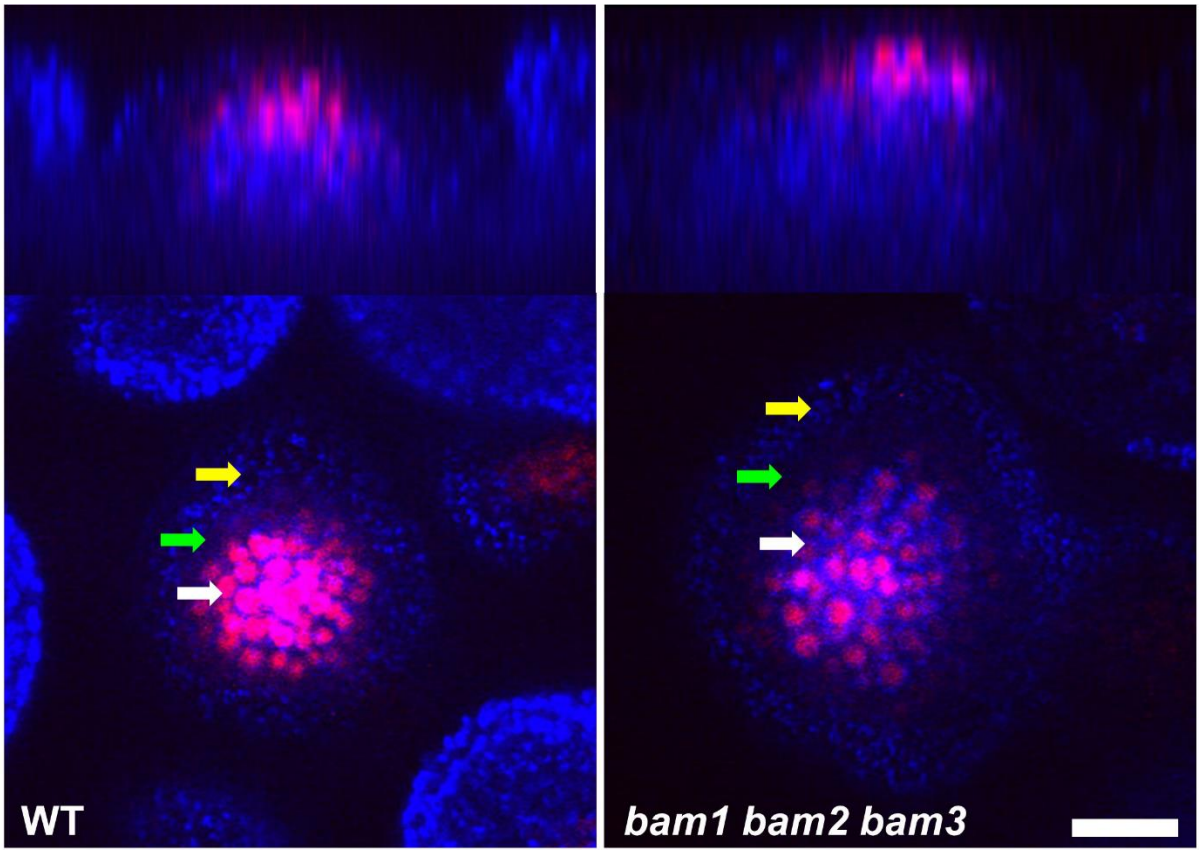


Supplementary Figure 3. Repression of BAM1 by CLV signaling is specific and non-reciprocal.

Plant genotypes in white lettering. Reporters in colored lettering. A. Unlike *BAM1*, the L1 marker *ATML1::mTFP1-ER* (blue) is not ectopically expressed in the RM of *clv3* mutants indicating that the RM is not globally re-specified as L1 tissue in *clv3* mutants. Red, chlorophyll autofluorescence. Both lines in La-*er* background. B. *BAM1* (green) is not ectopically expressed in the RM of *phb phv cna* mutants, a mutant superficially similar to *clv* class mutants in phenotype. C. *bam1 bam2 bam3* mutants display normal *CLV1* expression (green) in the RM, with no ectopic expression in the L1.

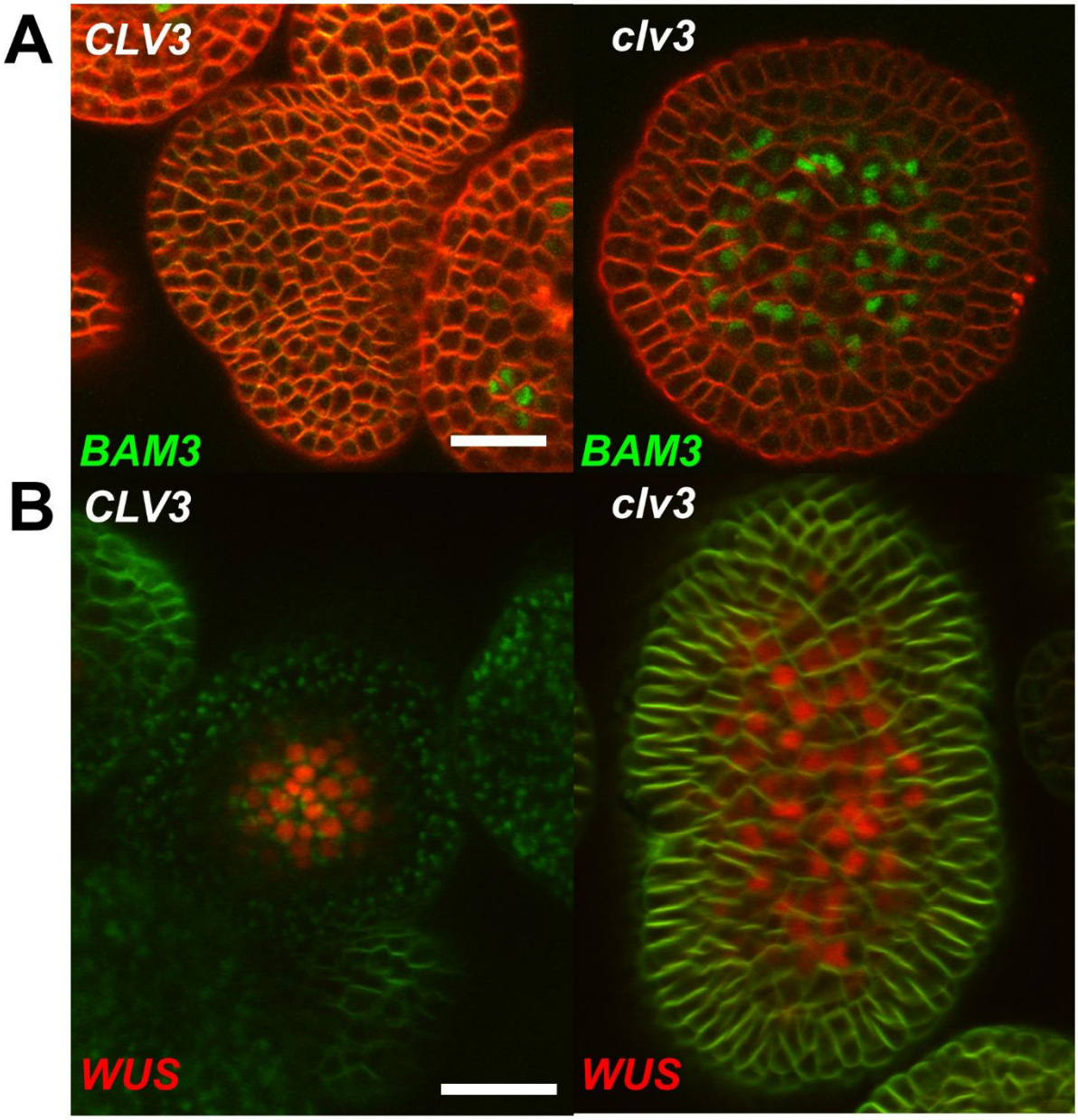
Supplementary Figure 4. Phenotypes of *bam1 bam2 bam3* and *bam1 bam2 bam3 clv1* null mutant plants in the mixed La-*er*/Col-0 background.

Inset, arrow denotes massive over-proliferation of tissue in the center of *bam1 bam2 bam3 clv1* (*b123clv1*) plants (white arrow). Main figure, *b123clv1* plants (white arrow), are highly stunted and rarely flower in the La-*er*/Col-0 background. Right, inflorescence phenotypes of *bam1 bam2 bam3* (top) and *bam1 bam2 bam3 clv1* (middle). Bottom: A Rare example of silique formation in *bam1 bam2 bam3 clv1* plants that contains 12 partially fused carpels and over proliferating internal tissues visible in the unfused top of the silique.



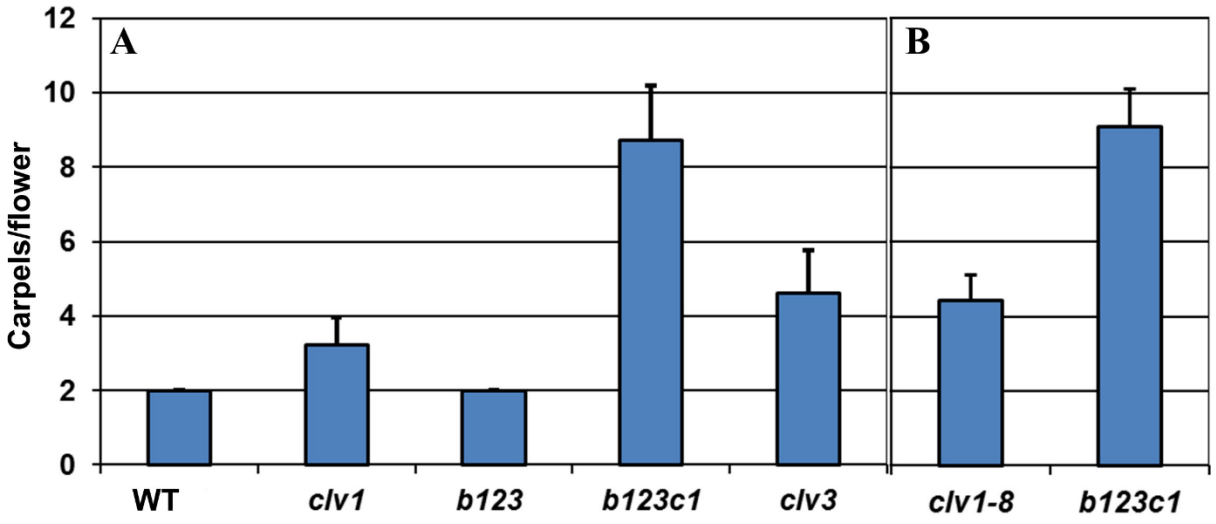
Supplementary Figure 5. Expression pattern of *WUS* in *bam1 bam2 bam3* SAMs is unaltered.

Expression of p*WUS::dsRed-N7* (Red) in Col-0 null allele *bam1 bam2 bam3* inflorescence meristem (right), or wild type (WT, left). Top, side view showing central location of *WUS* domain. Bottom, L3 expression of *WUS* reporter. Blue, chlorophyll autofluorescence. Solid white scale bar, 20 μM. Arrows denote cell layers of the SAM. The wild type patterning of *WUS* expression is maintained in the *bam1 bam2 bam3* inflorescence meristem. Yellow arrow, L1 layer containing chloroplasts (blue), but no *WUS* dsRed signal (red). Green arrow, L2 layer which lacks chloroplasts (Nimchuk et al., 2011) and *WUS* dsRed signal. White arrow, L3 cells containing both chloroplasts and *WUS* dsRed signal in both genotypes. The wild type pattern of *WUS* expression in *bam1 bam2 bam3* mutants also correlates with lack of alterations in carpel number in the Col-0 background triple mutant (Fig. 4).



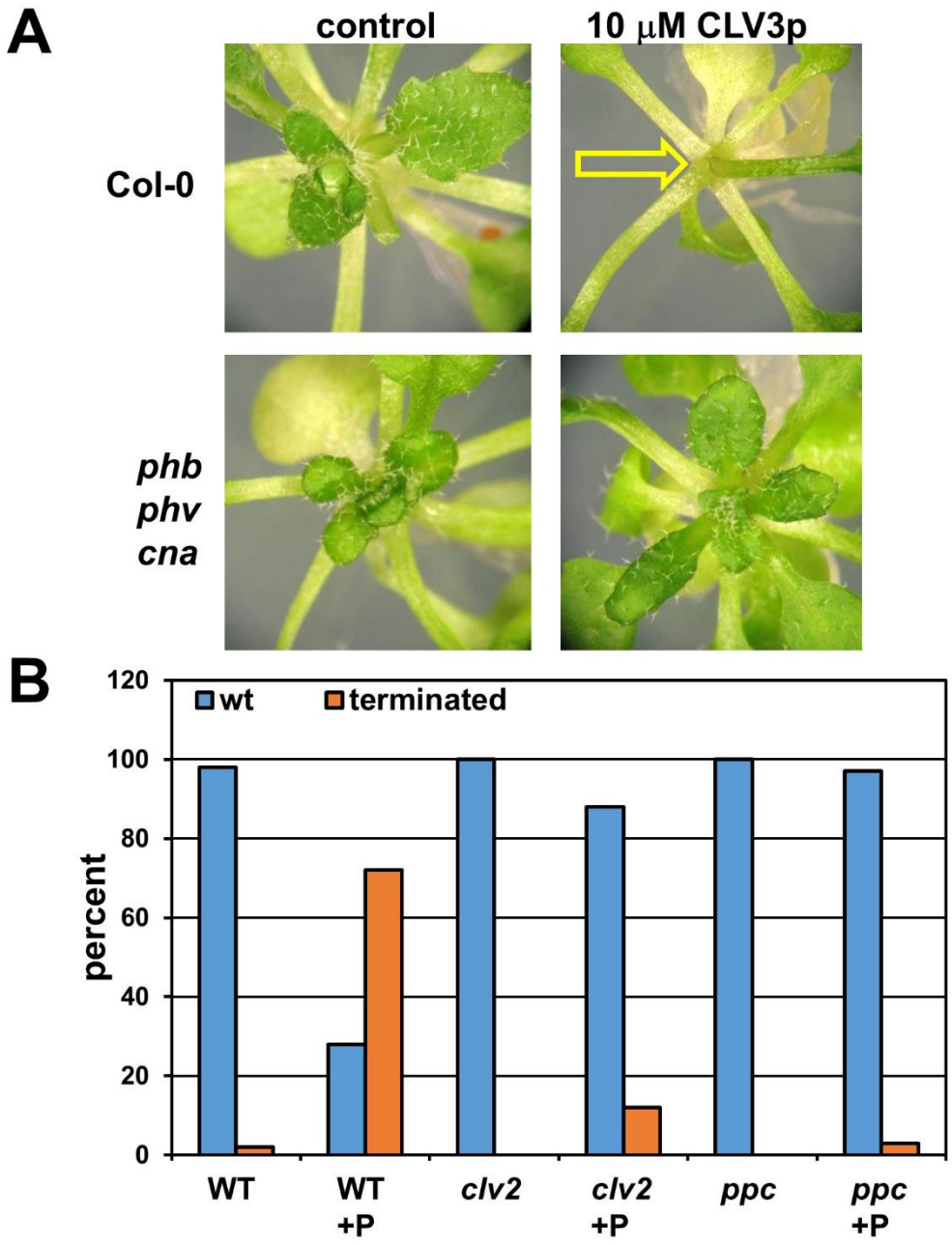
Supplementary Figure 6. Differential dynamics in CLV1 target genes.

A, B: Expression of *BAM3* (A), or *WUS* (B) in L3 cells of the SAM. Note the absence of signal in the L3 cells of wild type *CLV3* plants for the *BAM3* reporter (Green), compared to the robust signal for the *WUS* transcriptional reporter (Red). The SAM plants as in Supp. Fig. 2 were used here for the *BAM3* reporter.



Supplementary Figure 7. *CLV1*-clade quadruple mutants display stronger phenotypes than dominant negative *clv1* or *clv3* mutants.

X axis, carpel numbers per flower. A. *bam1 bam2 bam3 clv1* (*b123c1*) plants have greater carpel number than null *clv3* plants (*clv3-9*). A one-way ANOVA was carried out for the data set, and comparisons were performed with a SPSS Tukey HSD test at $P<0.05$ level. Only wild-type (WT) and *bam1 bam2 bam3* (*b123*) carpel counts were not statistically different for. B. *bam1 bam2 bam3 clv1* plants are phenotypically stronger than the dominant negative *clv1-8* allele. N=60, 10 siliques/plant were counted for A and B. All alleles are in the Col-0 background. Error bars, standard deviation.



Supplementary Figure 8. Suppression of CLV3p-induced SAM termination can be bypassed.

A. *phb phv cna* plants are resistant to CLV3p induced SAM termination. Yellow arrow, terminated SAM in wild type Col-0 plants grown on 10 μM CLV3p B5 plate media. B. Quantification of CLV3p induced termination. X axis, percentage terminated. Blue bars, plants displaying wild type growth. Red bars, terminated SAM growth. -, B5 media-grown plants. +, 10 μM CLV3p B5 media-grown plants. WT, Col-0. *clv2*, *clv2-101* Col-0 null control for peptide termination. *ppc*: *phb phv cna* triple mutant. N=50-100 plants per treatment.