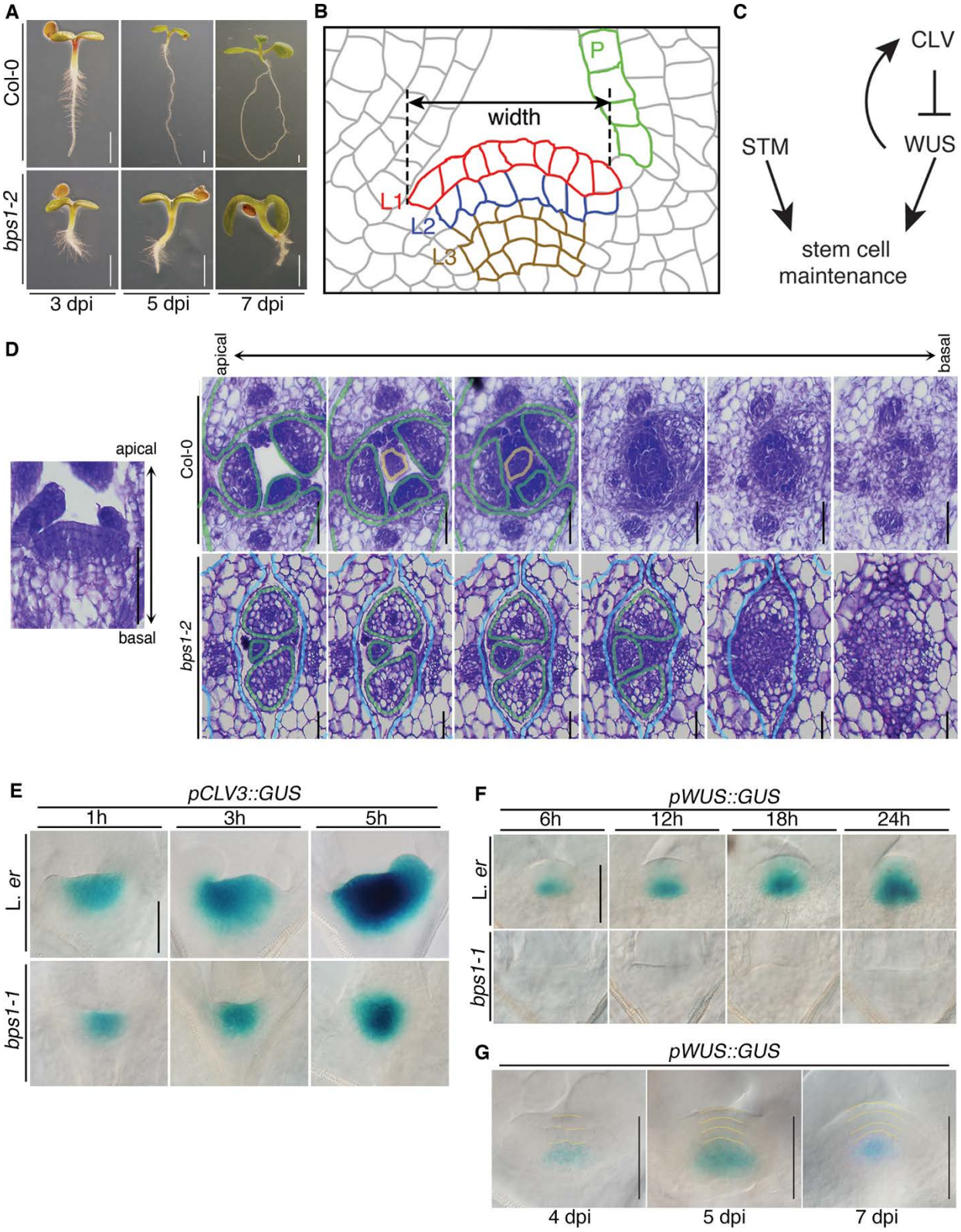
SUPPLEMENTAL DATA



Supplemental Figure S1. The *bps* signal disrupts shoot apical meristem maintenance.

A, Early seedling development in the wild type (Col-0, top) and *bps1-2* mutants shows the *bps1* defects in shoot and root growth.

B, Diagram of the shoot apical meristem, with a black double headed arrow depicting the SAM width measurement. The L1 cells are outlined in red, the L2 cells in blue, and the cells outlined in brown combine the L3, organizing center, and the rib meristem. The position of cells selected for measurement of primordium size indicated by green P.

C, Model for STM, CLV, and WUS functions in SAM maintenance.

D, Longitudinal and serial cross-sections of shoot apices of 7 day wild type (Col-0) and *bps1-2* mutant. Fixed and wax-embedded tissue was sectioned across the transverse plane, and representative serial sections are shown. Leaves and leaf primordia are outlined in green, the meristem is outlined in yellow, and cotyledons are outlined in blue.

E, *pCLV3::GUS* staining controls in 5 dpi wild type and *bps1* mutants. To ensure the fidelity of our GUS staining observations, we compared three staining times; comparison between these samples confirmed that *pCLV3::GUS* expression domain was smaller in *bps1* mutants, but that within the expression domains, staining levels were very similar.

F, *pWUS::GUS* staining controls in 5 dpi wild type and *bps1* mutants. To ensure the fidelity of our GUS staining observations, we compared X-GLUC stain solution incubation times (6, 12, 18, and 24h). These analyses confirmed that no *pWUS::GUS* staining could be detected in *bps1* mutants.

G, *pWUS::GUS* expression domains in 4-7 dpi wild-type seedlings. Yellow lines outline layers 1 and 2 of the SAM. In the 4 dpi seedlings, *pWUS::GUS* expression in L3 and underlying cells, resembling the embryonic expression pattern. By 5 dpi, and also observed in 7 dpi, the *pWUS::GUS* expression domain is in the OC, below the L3.

Scale bars 1 mm (A), and 50 μm (D-G)

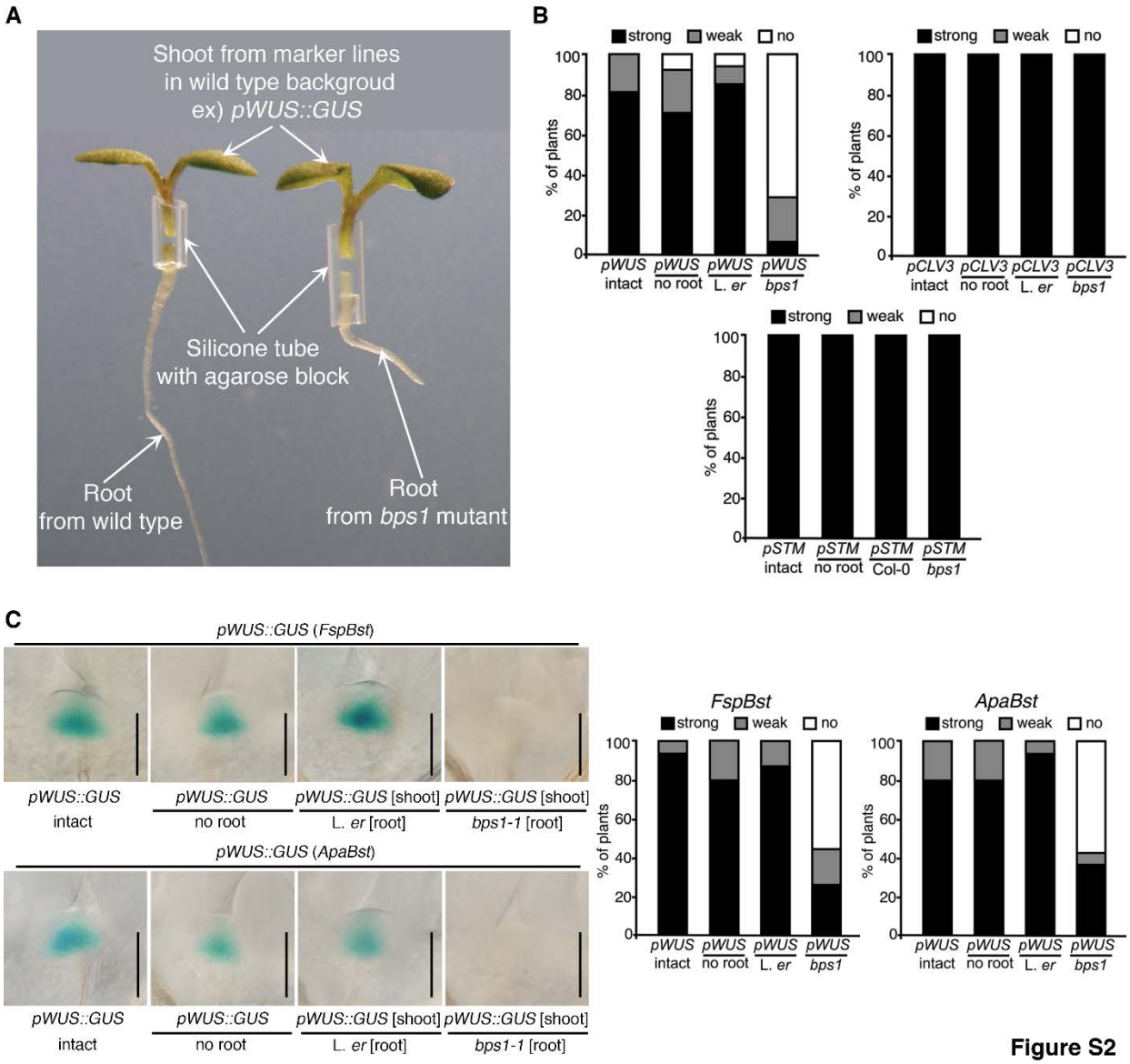


Figure S2

Supplemental Figure S2. Transient micrograft establishment and analysis.

A, Transient micrograft experimental setup. Shoots (scion) of wild-type seedlings were inserted into silicone collars that contained agarose (0.8% agarose). Controls entailed wild-type scions either simply inserted into the agarose-filled tubing or having a wild-type root inserted into the tubing's other end, and were compared to wild-type scions coupled to a *bps1* root. Note that approximately 0.3 mm of agarose-containing space was left between rootstock and scion. These transient grafts were maintained for 24h in sealed Petri plates and then analyzed.

B, Quantitative analysis of SAM GUS marker expression following transient grafting. Each shoot from a transient micrograft experiment was classified as giving strong, weak, or no GUS expression, as described in methods. The *pWUS::GUS* analysis included 48 scions for each

analysis (intact, no root, wild-type (L.*er*) root, and *bps1* root) for each of three independent experiments. Both *pCLV3::GUS* and *pSTM::GUS* included 16 scions for each of the four analyses.

C, Transient micrograft analysis with two additional, independently produced *pWUS::GUS* transgenic lines (*FspBst* and *ApaBst*). Expression of both *pWUS::GUS* was abolished in wild-type scions transiently micrografted to the *bps1* root for 24h. Both *pWUS::GUS* lines included 16 scions for each of the four analyses.

Scale bars, 50 μm.

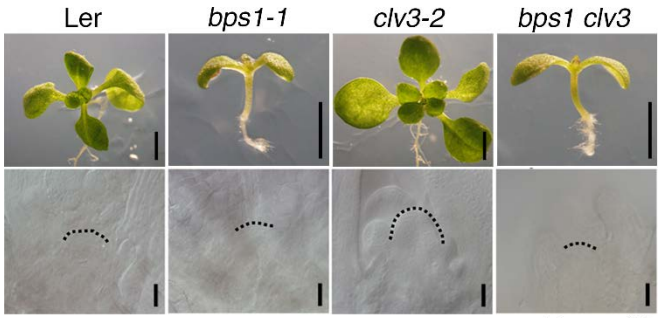


Figure S3

Supplemental Figure S3. Seedling and SAM phenotypes of 12d *bps1 clv3* seedlings reveal SAM arrest in *bps1 clv3* double mutants.

Seedling images (top row) and SAM images (bottom row) of 12 dpi L. *er*, *bps1-1*, *clv3-2*, and *bps1 clv3*. Seed germination and plant growth were on GM.

Scale bars 2 mm (top row), and 50 μm (bottom row).

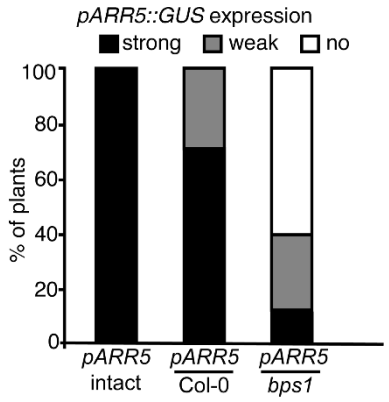


Figure S4

Supplemental Figure S4. Quantitative analysis of *pARR5::GUS* by transient grafting assay. Quantitative analysis of *pARR5::GUS* marker expression following transient grafting. Each shoot from a transient micrograft experiment was classified as giving strong, weak, or no GUS expression. The *pARR5::GUS* included 16 scions for each of the three analyses (intact, wild-type (Col-0) root, and *bps1-2* root).

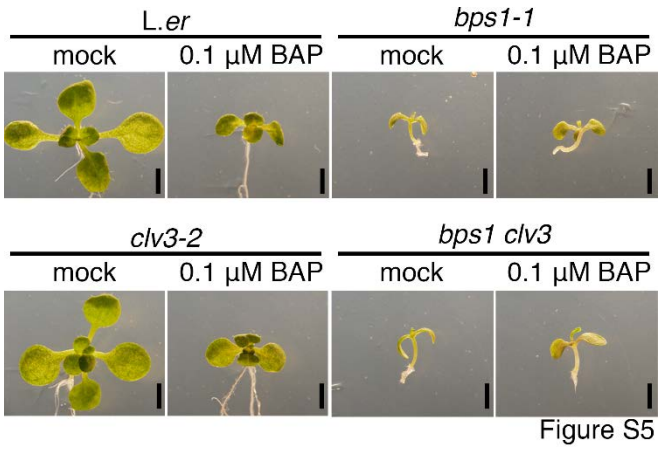
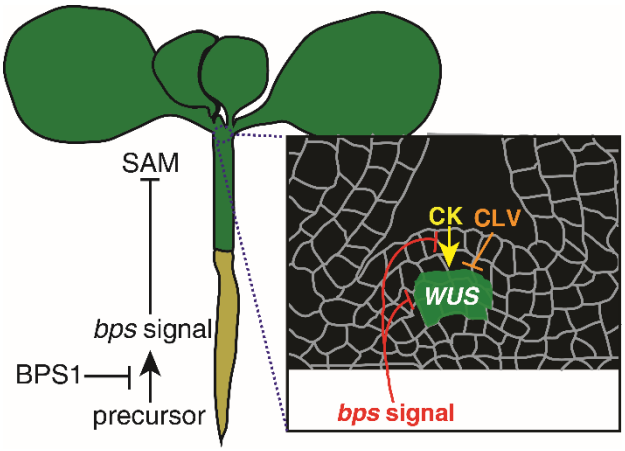


Figure S5

Supplemental Figure S5. CK-treated 12d *bps1 clv3* seedlings.

12 dpi L. *er*, *bps1-1*, *clv3-2*, and *bps1 clv3* seedlings, mock-treated and grown on medium containing CK (0.1 µM BAP). Seed germination and plant growth were on GM without or with 0.1 µM BAP until 12 dpi.

Scale bars, 2 mm.



Supplemental Figure S6. Model for mechanism by which the root-derived *bps* signal arrests SAM maintenance.

BPS1 is a negative regulator whose normal function is to prevent (or modulate) synthesis of the *bps* signal. *bps1* mutants arrest shoot growth due to excess generation of the *bps* signal, which is mainly synthesized in roots and moved to shoots. The root-derived *bps* signal leads to repression of *WUS* expression and reduced CK responses in SAM.

Supplemental Table S1. Expression in wild-type shoots transiently grafted to Col-0 and *bps1-2* roots.

Target	ID	Grafted to roots	Mean Cq	Normalized expression	Fold change	P-value[a]
ACT2	AT3G18780	*bps1-2*	22.02			0.997865
ACT2		Col-0	22.23			
AHK2	AT5G37550	*bps1-2*	32.12	0.83205	-1.20185	0.068409
AHK2		Col-0	32.07	1.00000	1.00000	
AHK3	AT1G27320	*bps1-2*	34.28	1.08717	1.08717	0.140876
AHK3		Col-0	34.61	1.00000	1.00000	
AHK4	AT2G01830	*bps1-2*	34.86	0.59182	-1.68969	0.000596
AHK4		Col-0	34.32	1.00000	1.00000	
AHP1	AT3G21510	*bps1-2*	29.10	1.46899	1.46899	0.006378
AHP1		Col-0	29.87	1.00000	1.00000	
AHP2	AT3G29350	*bps1-2*	26.44	0.81675	-1.22436	0.043030
AHP2		Col-0	26.36	1.00000	1.00000	
AHP3	AT5G39340	*bps1-2*	25.28	1.16566	1.16566	0.152592
AHP3		Col-0	25.71	1.00000	1.00000	
AHP4	AT3G16360	*bps1-2*	23.49	1.19399	1.19399	0.053662
AHP4		Col-0	23.95	1.00000	1.00000	
AHP5	AT1G03430	*bps1-2*	25.82	1.18911	1.18911	0.161430
AHP5		Col-0	26.28	1.00000	1.00000	
AHP6	AT1G80100	*bps1-2*	37.42	0.63210	-1.58203	0.010271
AHP6		Col-0	36.97	1.00000	1.00000	
CLV3	AT2G27250	*bps1-2*	35.69	1.26012	1.26012	0.393719
CLV3		Col-0	36.24	1.00000	1.00000	
STM	AT2G62360	*bps1-2*	28.32	1.08902	1.08902	0.597939
STM		Col-0	28.65	1.00000	1.00000	
WUS	AT2G17950	*bps1-2*	38.09	0.18694	-5.34924	0.000241
WUS		Col-0	35.88	1.00000	1.00000	

[a]P-value based on Student's T-test.

Supplemental Table S2. qRT-PCR primers.

Gene name	ID	Primer name	Sequence
ACT2	AT3G18780	qACT2F	tccctcagcacattcctgcagat
		qACT2R	aacgattcctggacctgcctcatc
AHK2	AT5G37550	AHK2f	tggcaagaagaggcaaccgaac
		AHK2r	gcagctttgccactctcaacgc
AHK3	AT1G27320	AHK3f	tgggatcgaggacaagtctggtc
		AHK3r	ccaccacaagcttcctccacc
AHK4	AT2G01830	AHK4f	cagcaacagcttcagcattcagtg
		AHK4r	ccatccactgataaatcccactgc
AHP1	AT3G21510	AHP1f	aggtagcagctccagtatagg
		AHP1r	caaaatccgagttcgacggc
AHP2	AT3G29350	AHP2f	tctcatggacgctctcattgctca
		AHP2r	atgcacactagcacctacctgact
AHP3	AT5G39340	AHP3f	gatttcaccattagtctctatcacca
		AHP3r	cacagtcttcaaagaagagagtaacaa
AHP4	AT3G16360	AHP4f	gaccaagctttggaaagaggatca
		AHP42r	ttgctggaaagtcctcaagcatcc
AHP5	AT1G03430	AHP5f	caggtggattcaggtgttca
		AHP5r	atttttcaccctccttgcac
AHP6	AT1G80100	AHP6f	ccgcaaccttagattgttgat
		AHP6r	ccctacgagcaccaatgc
CLV3	AT2G27250	qRT-CLV3-F-1	gactttccaaccgcaagatgat
		qRT-CLV3-R	ttcatgtagtcctaaacccttcg
STM	AT2G62360	qRT-STM-F	tcatggctcatcctcactacc
		qRT-STM-R	cctgttggtcccatagatgc
WUS	AT2G17950	WUS-qrt-2f	aaccaagaccatcatctctatcatc
		WUS-qrt-2r	ccatcctccacctacgttgt