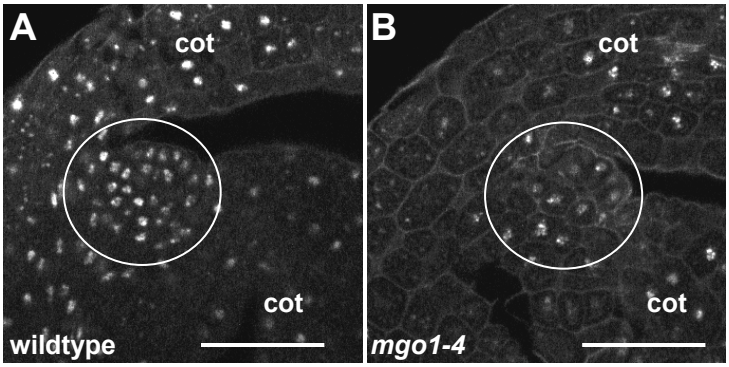
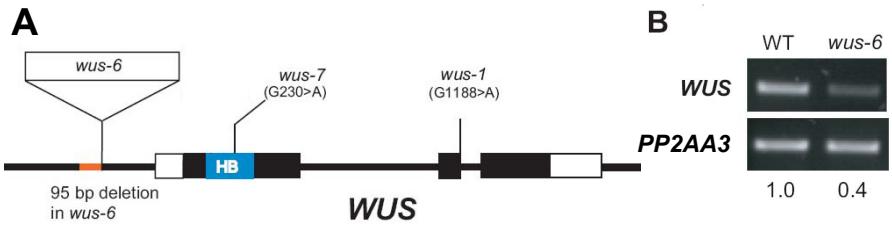


Supplemental Figure 1. Embryo Shoot Apices of *mgo1* mutants

(A-B) Confocal micrographs of shoot apices (circled) of wildtype (A) and *mgo1-4* (B) mature embryos. The mutant apices consist of fewer and larger cells. Samples were stained with propidium iodine. cot, cotyledons.

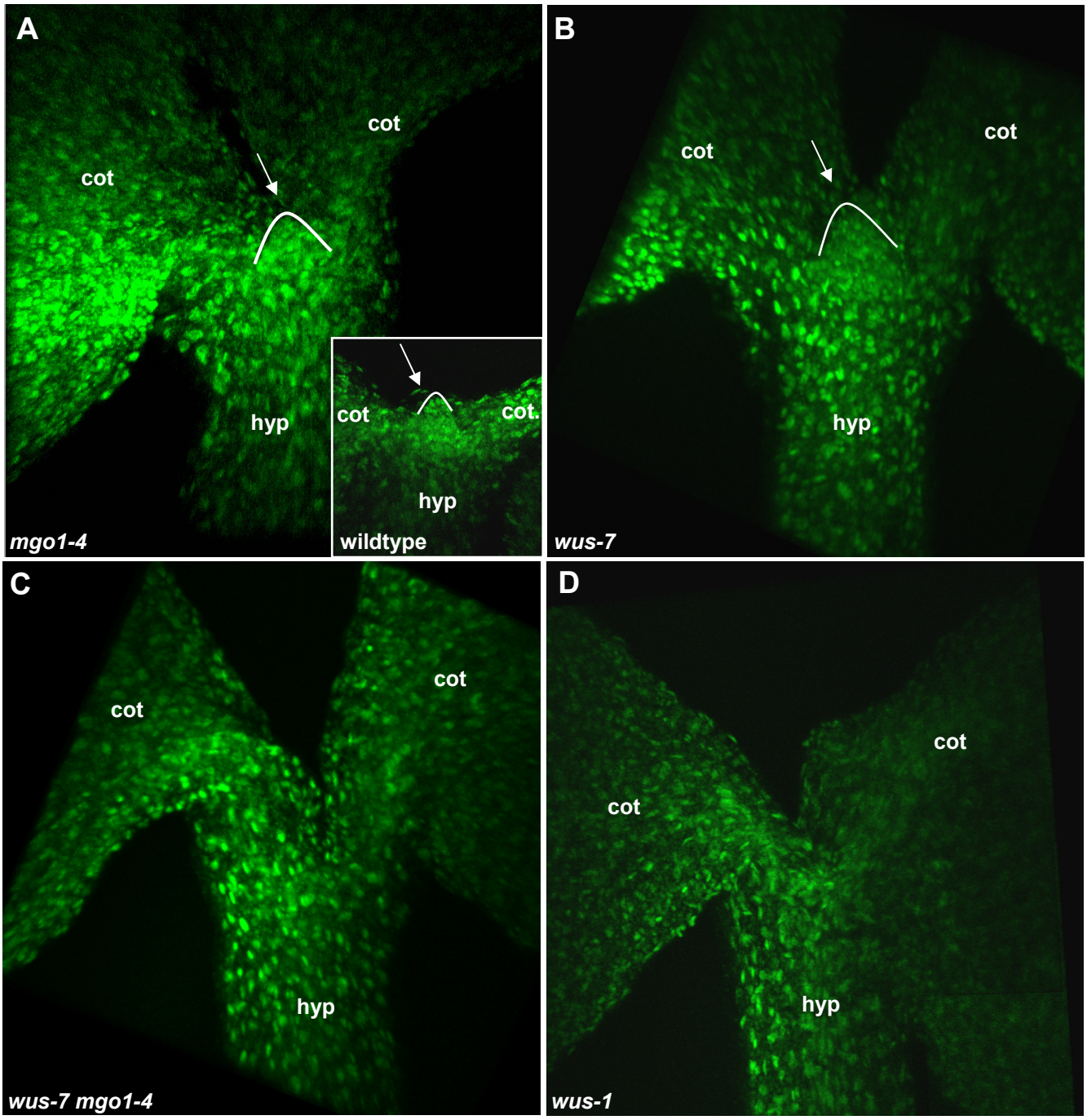
Scale bar: 50µm



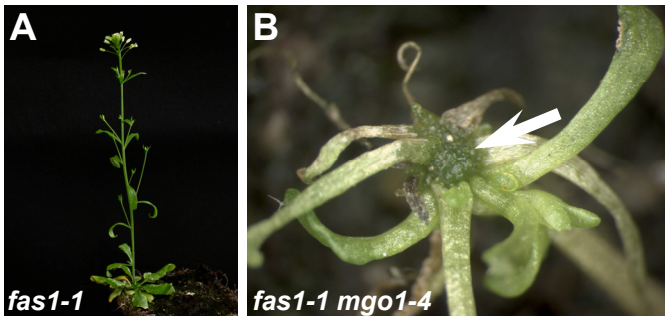
Supplemental Figure 2. Mutations in the *WUS* gene

(A) Genomic structure of the *WUS* gene and location of mutations. *wus-6* represents a T-DNA insertion in the *WUS* promoter 343 bp upstream of the *WUS* start (from Hamada et al., 2000). The insertion also generated a 95 bp deletion (red). *wus-7* mutations lead to nucleotide transitions in the homeobox (HB in blue) as indicated. *wus-1* carries a mutation in the 5' splicing site of the second intron. Boxes represent exons, including untranslated regions (white) and the coding region (black).

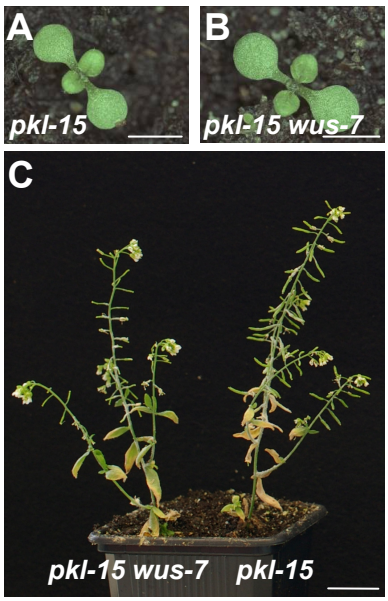
(B) RT-PCR analysis of *WUS* gene mRNA from inflorescences of wild type (WT) and *wus-6* mutants. *WUS* transcript level is reduced in the mutant to 0.4 of the wildtype level. The constitutively expressed *PP2AA3* gene was amplified as a control.



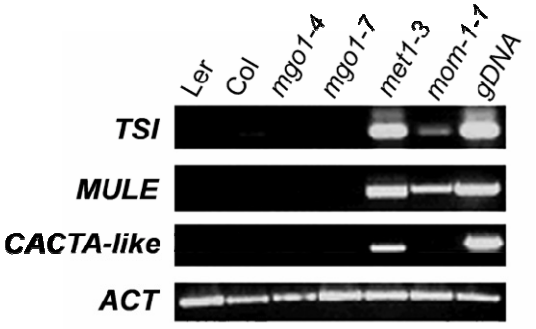
Supplemental Figure 3. Comparison of shoot apices of *wus-1* and *wus-7 mgo1-4*
3-day-old seedlings after DAPI staining of nuclei. Meristem region and emerging primordia appear brighter (arrow and outlined), due to the smaller cells and the higher densitiy of nuclei. cot, cotyledons, hyp, hypocotyls



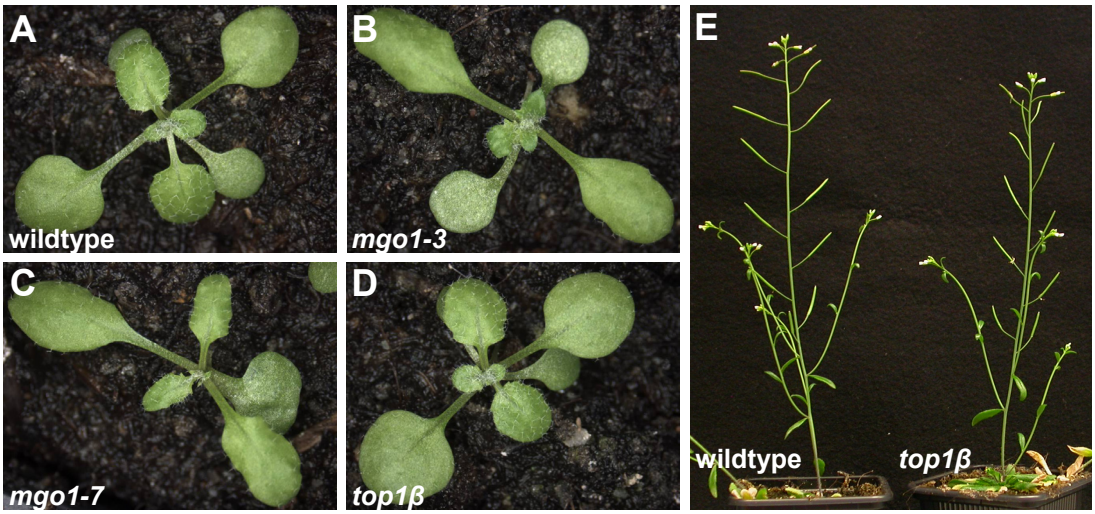
Supplemental Figure 4. ***mgo1-4 fas1-1*** **double mutant**
(A) Flowering *fas1-1* single mutant.
(B) *fas1-1 mgo1-4* double mutants of the same age exhibit narrow lateral organs and a disorganized apex of proliferating cells (arrow). Compared also to *mgo1-4* single mutant in Fig. 5C.



Supplemental Figure 5. ***wus-7 pkl-15*** **double mutant**
(A-B) Phenotype of 10-day-old seedlings. In *pkl-15* (A) and *pkl-15 wus-7* (B) seedlings the first leaves have been formed. Compare also to *wus-7* single mutant in Fig. 4B.
(C) Comparison of 45-day-old plants. *pkl-15 wus-7* plants display an additive phenotype. Compare also to *wus-7* single mutant in Fig. 4F.
Scale bars: (A-B) 2,5mm, (C) 2 cm



Supplemental Figure 6. Heterochromatic gene expression in *mgo1* mutants
No derepression was observed in *mgo1* mutant alleles by RT-PCR of heterochromatic gene transcripts. cDNA from mutants impaired in transcriptional gene silencing (*met1-3, mom1-1*) was used as positive control.



Supplemental Figure 7. Phenotype of the *top1β* mutant

(A-D) 18-day-old seedlings. *mgo1* mutants (B, C) display pointed leaves, whereas *top1β* mutants (D) are indistinguishable from wildtype.

(E) Flowering wildtype and *top1β* plants are indistinguishable.

SUPPLEMENTAL TABLES

Supplemental Table 1. *CYCB1;1:GUS* expression in *mgo1* primary roots (5d).

Genotype	Number of GUS positive cells	n
wildtype	110,3 ±7,2	6
mgo1-4	38,0 ±8,8	6

Supplemental Table 2. Shoot meristem defects in *wus fas* plants.

Genotype of mother plant	n	Seedling phenotypes in %			
		no SAM	filam.	*fas1* like leaves	wildtype
fas1-1	23	0	0	100	0
wus-7/+	24	0	0	0	100
fas1-1 wus-7/+	47	4,3	17	78,7	0
wus-1/+	59	20,3	0	0	79,7

Primary shoot meristems were analyzed in 11-day-old seedlings.

no SAM, no shoot meristem; filam., filament instead of a shoot meristem.

Supplemental Table 3. Plant materials.

Allele	Ecotype	Reference
pkl-15 (gym-5)	L*er*	(Eshed et al., 1999)
syd-2	L*er*	(Wagner and Meyerowitz, 2002)
pAG-I:GUS	L*er*	(Sieburth and Meyerowitz, 1997)
clf-2	L*er*	(Goodrich et al., 1997)
lhp1-3	Col	CS3796 ABRC
ag-1	L*er*	(Bowman et al., 1989)
pBP:GUS	Col	(Ori et al., 2000)
WUS:GUS	L*er*	(Gross-Hardt et al., 2002)
CLV3:GUS	L*er*	(Gross-Hardt et al., 2002)
fas1-1	Enkheim	(Kaya et al., 2001)
fas2-2	Nossen	(Kaya et al., 2001)

wus-1	L*er*	(Laux et al., 1996)
wus-6/jam	L*er*	(Hamada et al., 2000)
CycB1;1:GUS	L*er*	(de Almeida Engler et al., 1999)

Supplemental Table 4. Sequences of oligonucleotides used for RT-PCR.

Gene	Forward Primer	Reverse Primer	anneal
PP2AA3	CGTTACTGCCAGCCATTGTAGAA	CCGCAGGTAAGAGTTTGGAACAT	60
WUS	CTGCTAATTCCGTCAACGTT	CATACTTCCAGATGGCACCA	60
MGO1	TCAGCGTACTGTATCAAAGACACATG	GGGAGGAAGATGAATAGAAGAAAGGC	58
ACT7	GGTGAGGATATTCAGCCACTTGTCTG	TGTGAGATCCCGACCCGCAAGATC	55

Supplemental Table 5. Sequences of oligonucleotides used for qRT-PCR.

Gene	Forward Primer	Reverse Primer	anneal
AT2G28390	AACTCTATGCAGCATTTGATCCACT	TGATTGCATATCTTTATCGCCATC	60
AT4G34270	GAACTGGCTGACAATGGAGTG	ATCAACTCTCAGCCAAAATCG	60
ATt4G26410	GAGCTGAAGTGGCTTCCATGAC	GGTCCGACATACCCATGATCC	60
WUS	CTGCTAATTCCGTCAACGTT	CATACTTCCAGATGGCACCA	60