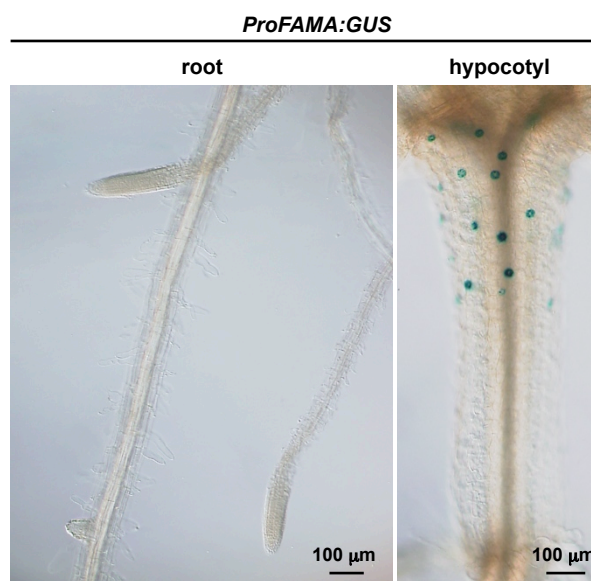


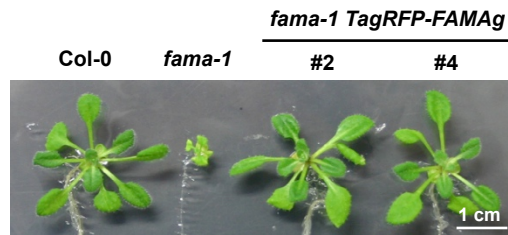


Supplemental Figure 1. *FAMA* Co-Expression Network Predicted by ATTED-II.

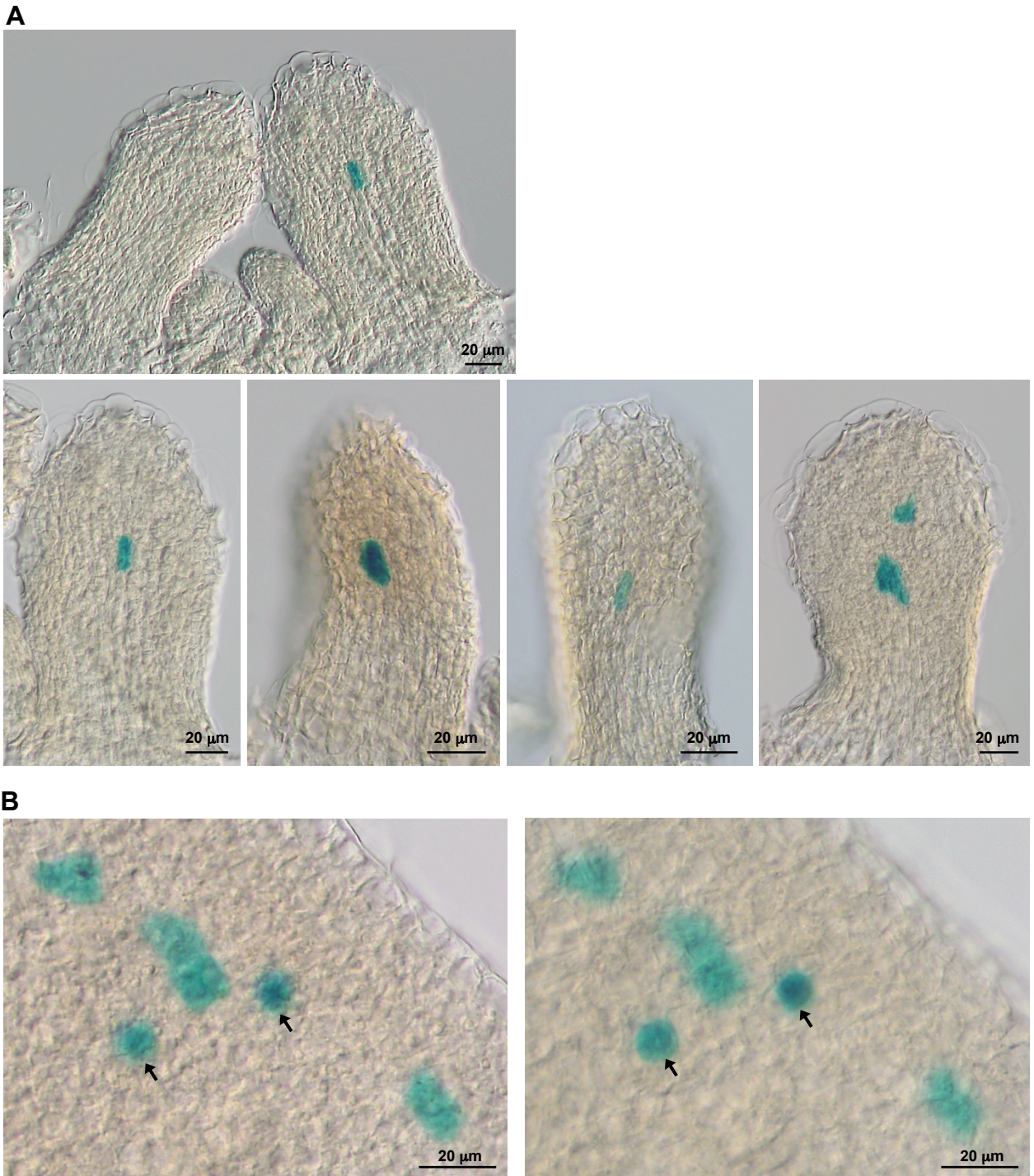
FAMA (At3g24140, a yellow shading octagon) was used as a query in the ATTED-II database (<http://atted.jp>). The output data show 20 genes were co-expressed with *FAMA*. *ESM1* (*EPITHIOSPECIFIER MODIFIER1*) encodes a protein in the myrosinase-glucosinolate system. Octagons indicate transcription factors and ovals indicate genes except transcription factors.



Supplemental Figure 2. *FAMA* Expression Pattern in Wild-Type Plants. GUS staining of Col-0 expressing *ProFAMA:GUS*.



Supplemental Figure 3. *ProFAMA:TagRFP-FAMAg* Expression Rescues *fama-1* Dwarfism. Col-0, *fama-1*, and two independent *fama-1* transgenic lines expressing *ProFAMA:TagRFP-FAMAg*.



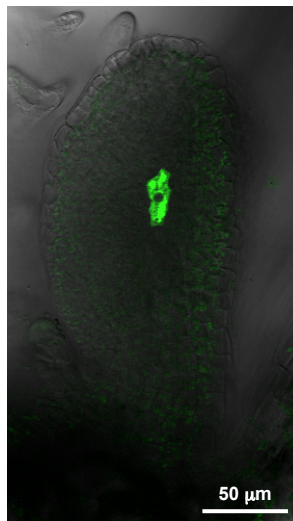
Supplemental Figure 4. *ProFAMA:GUS* Expression Pattern in Early Developmental Stages of Leaves.

GUS staining of leaf primordia of Col-0 expressing *ProFAMA:GUS*.

(A) Typical images showing the first GUS-positive cell at the middle point in early leaf primordia. The first GUS-positive cell is detected in one (right leaf) of a pair of rosette leaves but not yet in the other (left leaf) in the upper panel.

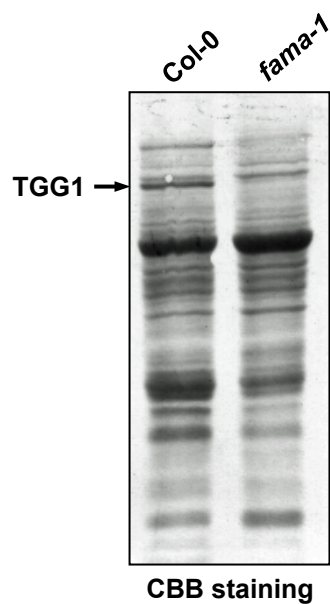
(B) Leaf primordia at a later stage than those shown in **(A)**. In addition to the leaf inner tissue layers (focused in left panel), GUS signals appear in epidermal stomatal-lineage cells (focused in right panel). Arrows indicate stomatal-lineage cells.

ProTGG2:VENUS-2sc

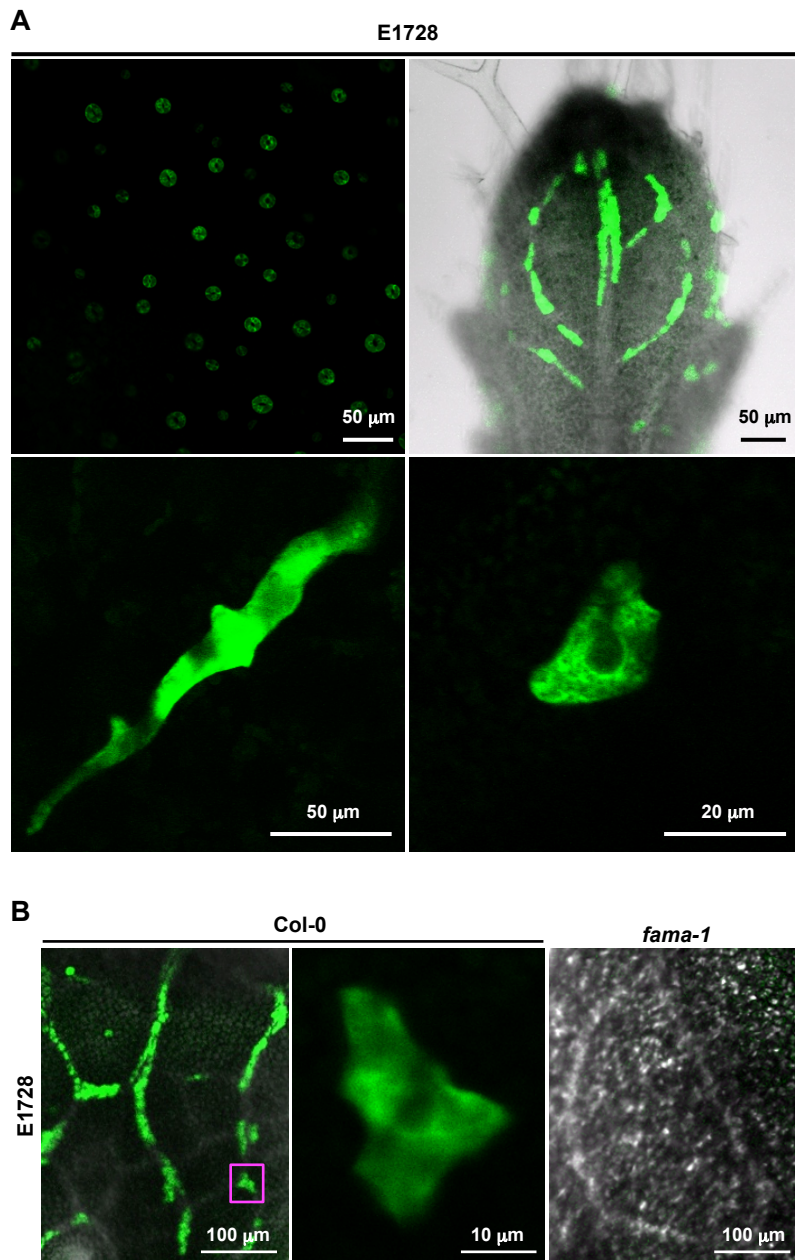


Supplemental Figure 5. *ProTGG2:VENUS-2sc* Expression Pattern in a first true leaf primordium at 3.5 days after germination.

Merged overlays of the fluorescent images (green) and the bright-field images of leaf inner tissue primordia expressing *ProTGG2:VENUS-2sc*. *VENUS-2sc* localizes to the ER and vacuoles.



Supplemental Figure 6. The *fama*-Deficient Mutant Lacks Endogenous TGG1 Protein. Rosette leaves of Col-0 and *fama-1* were subjected to SDS-PAGE and electroblotted onto a PVDF membrane. The membrane was stained with CBB.

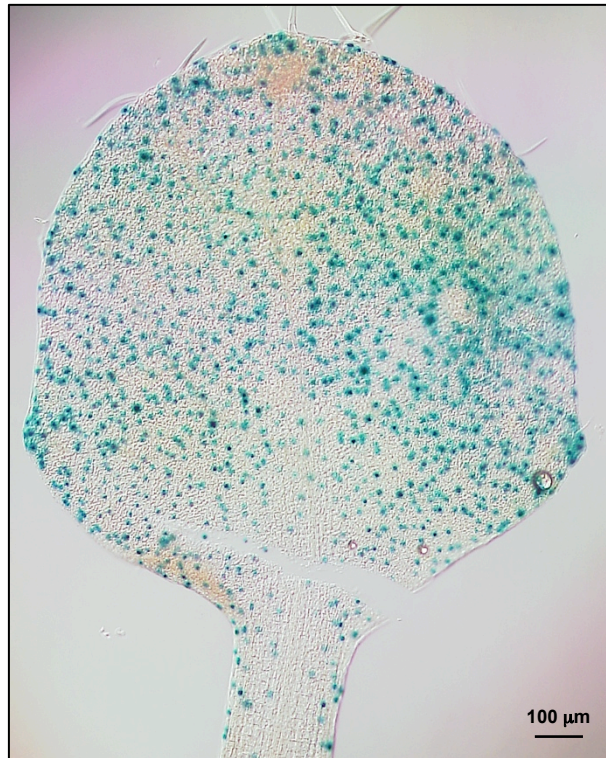


Supplemental Figure 7. Myosin Cell Development in Leaf Primordia of *fama* Loss-of-Function Mutants.

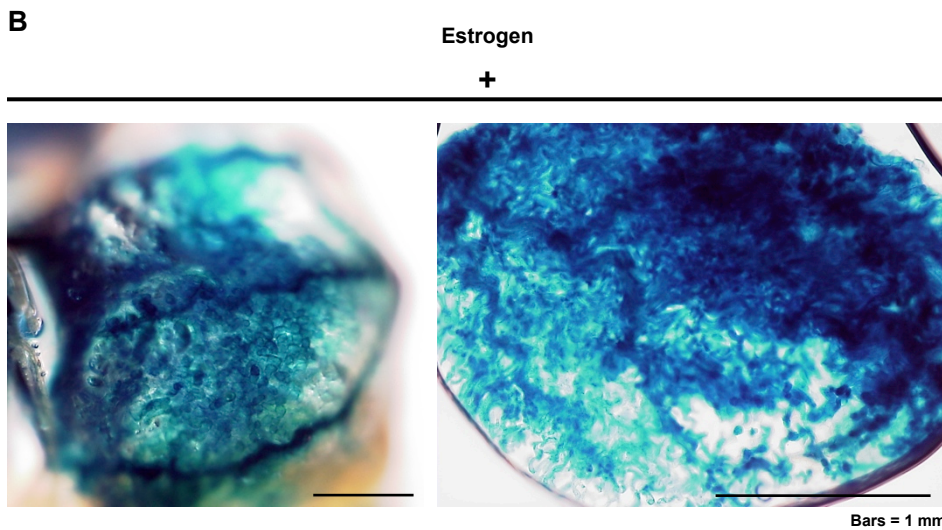
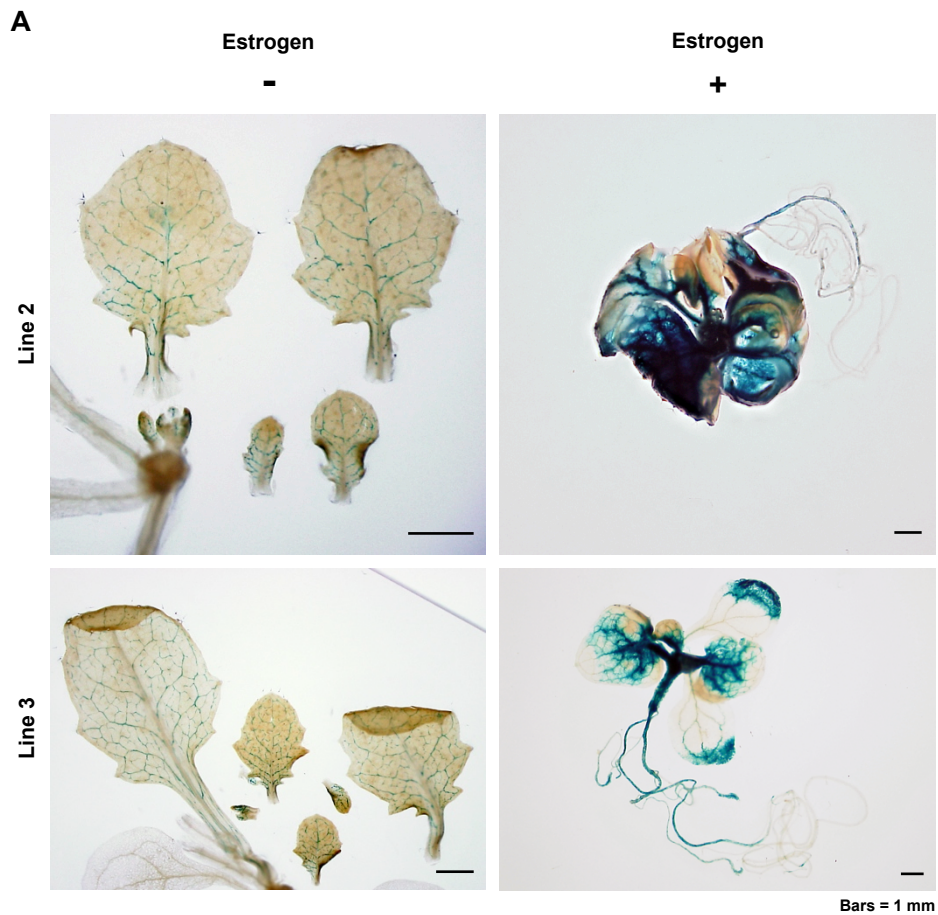
(A) *GFP* Expression Pattern in Leaf Primordia of the E1728 Line. Confocal images of the epidermis (upper left panel) and the inner tissue (upper right and lower panels) in leaf primordia of E1728.

(B) Merged overlays of fluorescent images (green) and bright-field images of the rosette leaf inner tissue of Col-0 and *fama-1* plants expressing E1728. The boxed area in the left panel is enlarged in the middle panel.

fama-1 ProFAMA:GUS



Supplemental Figure 8. *FAMA* Expression Pattern in the *fama*-Deficient Mutant. GUS staining of rosette leaves of *fama-1* expressing *ProFAMA:GUS*.

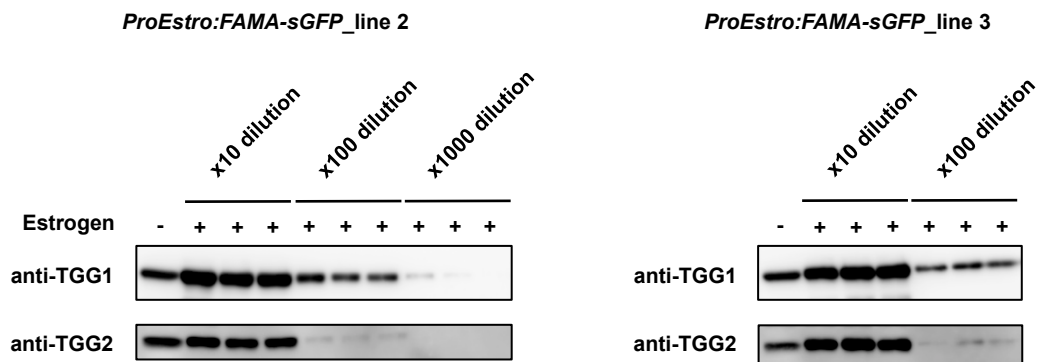


Supplemental Figure 9. Development of Myrosin Cells in *FAMA-sGFP* Overexpression Lines.

Transgenic plants expressing *FAMA-sGFP* under the estrogen-inducible promoter (*ProEstro:FAMA-sGFP*) were generated. The 8-day-old plants were transplanted onto inductive medium containing no estrogen (-Estrogen) or 10 μ M estrogen (+Estrogen) and incubated for two weeks.

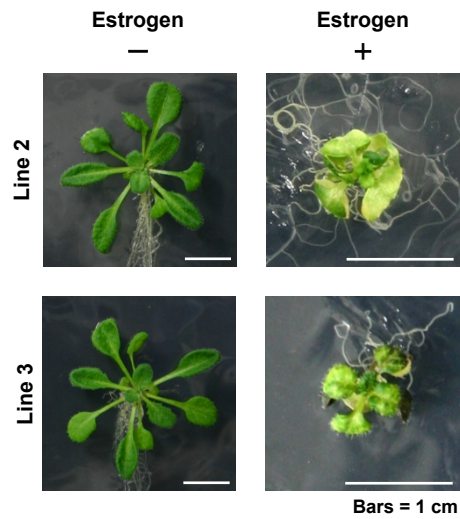
(A) GUS staining of *ProEstro:FAMA-sGFP* plants (independent lines #2 and #3) expressing *MYR001:GUS*.

(B) Enlarged images of GUS-stained leaves of *ProEstro:FAMA-sGFP* plants.



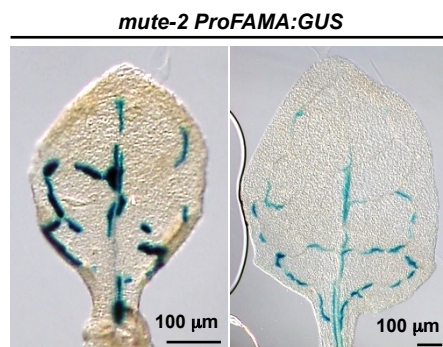
Supplemental Figure 10. Accumulation Levels of TGG1 and TGG2 in *FAMA-sGFP* Overexpression Lines.

The 8-day-old *ProEstro:FAMA-sGFP* plants were transplanted onto inductive medium containing no estrogen (-Estrogen) or 10 μ M estrogen (+Estrogen) and incubated for two weeks. Dilution series were prepared from three sets of rosette leaf extracts derived from independent *ProEstro:FAMA-sGFP* plants. Samples were subjected to immunoblotting with anti-TGG1 and anti-TGG2 antibodies. Signal intensities of the immunoblot band ($\times 100$ dilution) were quantified by densitometry. See also Figure 5B.

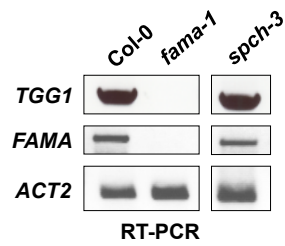


Supplemental Figure 11. Plant Morphology of *FAMA-sGFP* Overexpression Lines.

The 8-day-old *ProEstro:FAMA-sGFP* plants were transplanted onto inductive medium containing no estrogen (-Estrogen) or 10 μ M estrogen (+Estrogen) and incubated for two weeks.

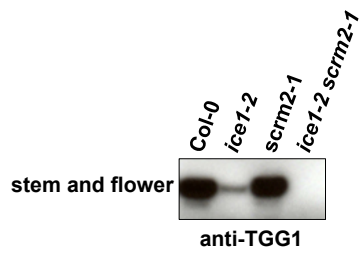


Supplemental Figure 12. *FAMA* Expression in Myrosin Cells Is Independent of *MUTE*. GUS staining of rosette leaves of *mute-2* expressing *ProFAMA:GUS*. Representative two examples are shown.



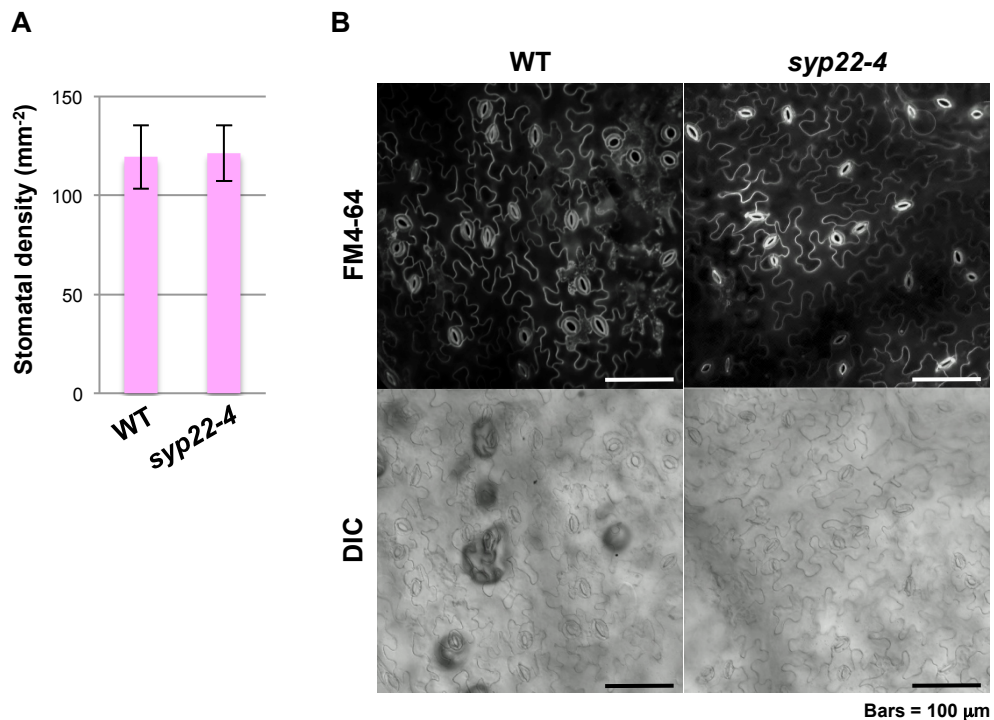
Supplemental Figure 13. *TGG1* and *FAMA* Transcript Levels in *spch*.

TGG1 and *FAMA* mRNA levels in rosette leaves of Col-0, *fama-1*, and *spch-3* were assessed by RT-PCR. *ACTIN2* (*ACT2*) was used as a control.



Supplemental Figure 14. Accumulation Levels of TGG1 in ICE1 and SCRM2 Mutants.

Stems and flowers of Col-0 and indicated mutants were subjected to immunoblotting with anti-TGG1 antibody.



Supplemental Figure 15. Distribution of Stomata in Wild-Type and *syp22-4*.
(A) Stomatal density of a first pair of true leaves of wild-type and *syp22-4*. Images of abaxial epidermis of matured true leaves stained by FM4-64 were obtained. Error bars indicate standard deviation ($n = 8$).
(B) Representative images of (A) in wild-type and *syp22-4*.

```

At_bHLH090      MMMMRGGERVKEFLRPFVDSRTWDLCVIWKLGDDPSRFIEWVGCCSCGYIDKNIKLENS 60
Al_bHLH090      MMMMRGGERVKEFLRPFVDSRTWDLCVIWKHGDDPSRFIEWVGCCSCGYIDKNIKLENS 60
Cr_bHLH090      -MMMRAGERVKEFLRPFVDSKTWDLCVIWKLGDDPSRFIEWVGCCSCGSYVDKNIKLENS 59
Es_bHLH090      --MMKSGERVKEFLRPFVDSRDWDLCVIWKLGDDPSRFIEWVGCCSCSHIDKNIKHEKV 58
                * _ . * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :
                * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :

At_bHLH090      EEGGTGRKKKASFCRDDHNKHRIRTLACEALSRFPFLMPLYPGIHGEVVMSPKPKWLNS 120
Al_bHLH090      EEE--TERRKKASFCRDEHNKHRIRTLACEALSHFPLFMPLYPGIHGEVVMSPKPKWLNS 119
Cr_bHLH090      EGT--AREKKGSFCRDEHNKHMRTLACEALSHFPLFMPLYPGIHGEVVMSPKPKWLNS 117
Es_bHLH090      EEG--IERKQTGSI CRDEHNKHYIRSLACEALTHFPLFMPLYPGIHGEVVMSPKPKWLNS 117
                *      * _ . * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :
                * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :

At_bHLH090      GS--KMFMFSTRVLVPVSDGLVELFAFDMRPFDESMVHLIMSRCTTFEPFPEQRLQFRI 178
Al_bHLH090      GS--KMDMFSTRVLVPVSDGLVELFSFDMKPFDESMVHLIMSRCTTFEPFPEQRLQFRI 177
Cr_bHLH090      GPGLKKDMFNTRVLVPVSDGLIELFSFKMKPFDPMPVDMIISRCNAFFEPFPEKLIQIRI 177
Es_bHLH090      GPGSKKIDFSTRVLIPVRDGLVELFSFTMKPVDESMVDMIIRRCNACFEPFPEQKLQFRI 177
                * . * : * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :
                * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :

At_bHLH090      IPRAEESMSGVNLVSEGGGSSSVSNPSEETQNLFGNYPNASCVEILREEQTPCLIMNKE 238
Al_bHLH090      IPRAEESMSGVNLVSEGGGSSSVSNPSEETQNLFGSYSNARCVIEILREEQAPCMVMNKE 237
Cr_bHLH090      IPRAEESISSGVNLVSEGGGSSSVSNHSSSETQNLFGNQPNARCVIEIFREEQAPCLVMNKE 237
Es_bHLH090      ISKAEESSMSGVNLVSEGGGSSSVSNPLSENQTLFGNQ--NARCGEHL-----PCLVFNKE 231
                * _ : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :
                * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :

At_bHLH090      KDVVVQNANDSKANKKLLPTENFKSKNLHSEKRRRERINQAMYGLRAVVPKITKLNKIGI 298
Al_bHLH090      KDGLVQNANDSKANKR--LPAENFKSKNLHSEKRRDRINQAMYGLRAVVPKITKLNKIGI 296
Cr_bHLH090      -DPVVQKAVDFKANKR--LPKENFKSKNLLSEKRRDRINQAMYALRAVVPKITKMNKIGI 295
Es_bHLH090      EDVVMQDTIDLKDNKK--PPKENFKSKNLHSEKRRDRINQMYALRAVVPKITKMNKIGI 290
                * _ : * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :
                * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :

At_bHLH090      FSDAVDYINELLVEKQKLEDELKGINEMECKEIAAEEQSAIADPEAEKVSSKSNKRVKKN 358
Al_bHLH090      FSDAVDYINELLAEKQKLEDELKGIEMECKEIAAEEQSAIADPGAQEKVSSKINKKRVKKN 356
Cr_bHLH090      FTDAVDYINELLVEKQKLEDELKGINEKECKEIAAEEESAIADPEAEKRASKLNKKMKKN 355
Es_bHLH090      FSDAVDYINELLVEKQKLEDELSGINEIECREIAAEEESAIANPEAEKVSSKVNKKVN-D 349
                * _ : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :
                * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :

At_bHLH090      EVKIEVHETGERDFLIRVVQEHKQDGFKRLIEAVDLCELEIIDVNFTRLDLTVMTVLNVK 418
Al_bHLH090      EVNLEVHEIGERDFLIRVVQEHKQDGFKRLIEAVDLCELEIIDVNFTRLDLTVLTILNVK 416
Cr_bHLH090      EVNLEVHEIGERDFLIRVVQEHKRDGFKRLIEAVDSCGLEIIDVNFTRLDLTVKTVLNVK 415
Es_bHLH090      EVNFEVHEIGERDFLIRVAQEHKRDGFKRLIEAVDSCGLEIIDVNFTRLDLTVMTVLNVK 409
                * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :
                * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :

At_bHLH090      ANKDGIAAGILRDLKMMITSI----- 441
Al_bHLH090      ANKDGITSGILRDLKMMITSI----- 439
Cr_bHLH090      ADKDGIASGDLRDSLKIMINQIDMKSP----- 444
Es_bHLH090      ANKDGISAGNLRDLKRMIAANNPNAESVKQSS 444
                * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :
                * : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * :

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Supplemental Figure 16. The bHLH Domain and Alignment of bHLH090 Homologues. ClustalW alignment of four bHLH090 homologues. Identical residues among all three marked with *, conservative substitutions with :, and semi-conservative changes with . . The bHLH domain is underlined. At=*Arabidopsis thaliana*, Al=*Arabidopsis lyrata*, Cr=*Capsella rubella*, Es=*Eutrema salsugineum*.

Supplemental Table 1. Primer Sets Used in This Study.

ID	purpose	name	sequence
1	genotyping of SALK T-DNA tagline	LBa1	5'-TGGTTCACGTAGTGGGCCATCG-3'
2	genotyping of SAIL T-DNA tagline	LB1	5'-GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC-3'
3	genotyping of FLAG_FST T-DNA tagline	LB4	5'-CGTGTGCCAGGTGCCACGGAATAGT-3'
4	genotyping of fama-1, -3	FAMA LP	5'-TTTTCGTAACATTCTTGTCTCCCTATC-3'
5	genotyping of fama-1, -3	FAMA RP	5'-GTCTTCTTCTACTATCTTGCATGTCTTG-3'
6	genotyping of spch-3	SPCH LP	5'-ATCTAAAACATAAATGAGACACGAAAAAC-3'
7	genotyping of spch-3	SPCH RP	5'-AGAACTTGTTGTAACCTCGCTTATGTACTC-3'
8	genotyping of mute-2	MUTE LP	5'-TGAAAACCTGTAAAACATCTCAATACAAAC-3'
9	genotyping of mute-2	MUTE RP	5'-TATGCATAACATATACAAACAAGGAAGTC-3'
10	genotyping of ice1-2	ICE1 LP	5'-GTTTTTCTTCACTCTTACATCATCAAAG-3'
11	genotyping of ice1-2	ICE1 RP	5'-AGCTTGTTTACTTGTTGCTGTTATAGAG-3'
12	genotyping of ice2-1	ICE2 LP	5'-TGAAATGTTTATTCAATATACTTTGTTGC-3'
13	genotyping of ice2-1	ICE2 RP	5'-GAAGAGAAACTATACAAGCTTTCGTAGC-3'
14	RT-PCR of FAMA, cloning of FAMA CDS	FAMA-F	5'-CACCATGGATAAAGATTACTCGGCACCAAA-3'
15	RT-PCR of FAMA, cloning of FAMA CDS	FAMA-R1	5'-TCAAGTAAACACAATATTTCCCAGGTTAGA-3'
16	cloning of FAMA CDS (not containing stop codon)	FAMA-R2	5'-AGTAAACACAATATTTCCCAGGTTAGAGCT-3'
17	cloning of FAMA-SRDX	FAMA-SRDX-R	5'-TTAAGCGAAACCCAAACGGAGTTCTAGATCCAGATCCAGAGTAAACACAATATTTCC-3'

ID	purpose	name	sequence
18	cloning of FAMA promoter	FAMApr-F	5'-CACCCCAAACCTTCATGTATGATTCCAAACT-3'
19	cloning of FAMA promoter	FAMApr-R	5'-TGCTATTCGTGGTAGTTGATTATAAACTGC-3'
20	cloning of tagRFP-FAMA genomic	tRFP-FAMAg-1	5'-CAAAGGGTGGGCGCGATGGTGTCTAAGGGCGAA-3'
21	cloning of tagRFP-FAMA genomic	tRFP-FAMAg-2	5'-AGCTGGGTCGGCGCGGTGTAAAAGCGTCACTTT-3'
22	cloning of tagRFP-FAMA genomic	FAMAg-F	5'-CACCATGGATAAAGATTACTCGGTACGTAC-3'
23	cloning of tagRFP-FAMA genomic	FAMAg-R	5'-GTGTAAAAGCGTCACTTTGTTTAACCGAATGGTCAA-3'
24	cloning of ICE1 promoter	ICE1pro-F	5'-CACCAAGACAACCGGACCACCGTCAATAAC-3'
25	cloning of ICE1 promoter	ICE1pro-R	5'-CGCCAAAGTTGACACCTTTACCCCAAAGTC-3'
26	cloning of amiRNA	amiRNA-F	5'-CACCTGCAAGGCGATTAAGTTGGGTAAC-3'
27	cloning of amiRNA	amiRNA-R	5'-GCGGATAACAATTTACACAGGAAACAG-3'
28	cloning of ICE1/ICE2 amiRNA	ICE1/2_amiRNA_1	5'-GATTAAGCCTATCATTAGGCTTTCTCTCTTTTGTATTCC-3'
29	cloning of ICE1/ICE2 amiRNA	ICE1/2_amiRNA_2	5'-GAAAGCCTAATGATAGGCTTTAATCAAAGAGAATCAATGA-3'
30	cloning of ICE1/ICE2 amiRNA	ICE1/2_amiRNA_3	5'-GAAAACCTAATGATACGCTTTATTACAGGTCGTGATATG-3'
31	cloning of ICE1/ICE2 amiRNA	ICE1/2_amiRNA_4	5'-GAATAAAGCGTATCATTAGGTTTTCTACATATATATTCCT-3'
32	RT-PCR of TGG1	TGG1-F	5'-CACCATGAAGCTTCTTATGCTCGCCTTTGT-3'
33	RT-PCR of TGG1	TGG1-R	5'-TCATGCATCTGCAAGACTCTTCCGATCACG-3'
34	RT-PCR of ACT2	ACT2-F	5'-GGCGATGAAGCTCAATCCAAACG-3'
35	RT-PCR of ACT2	ACT2-R	5'-GGTCACGACCAGCAAGATCAAGACG-3'
36	cloning of bHLH090 promoter	bHLH090pro-F	5'-CACCTAAGCAAGAATCAACTTCTAATTCT-3'
37	cloning of bHLH090 promoter	bHLH090pro-R	5'-CTCACTCTCTCTCTCTCTCTCTCACTCT-3'

ID	purpose	name	sequence
38	Real-Time PCR of bHLH090	bHLH090_RealTime_F	5'-TGGTCTCGTTGAGCTGTTTCG-3'
39	Real-Time PCR of bHLH090	bHLH090_RealTime_R	5'-ACTGCAGCCTTTGTTTCAGGG-3'
40	Real-Time PCR of ACT2	ACT2_RealTime_F	5'-TATGTCGCCATCCAAGCTGT-3'
41	Real-Time PCR of ACT2	ACT2_RealTime_R	5'-AAGGTCACGTCCAGCAAGGT-3'