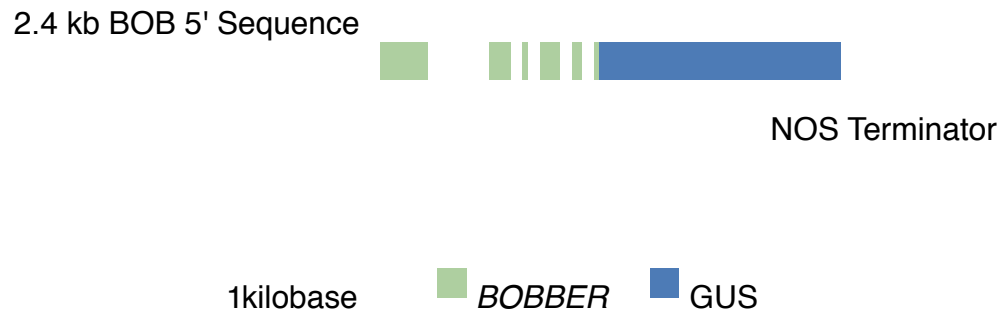


**Supplemental Figure 1. Map based cloning strategy for the *BOBBER1* locus.** **A.** Region of chromosome 5 to which the *bob1-1* mutation maps. **B.** Number of recombinants isolated between *bob1-1* and markers located on cosmids within a 600 bp region of chromosome 5. **C.** Annotated genes within the 53 kb region to which *bob1* was narrowed down. **D.** Intron-exon structure of MYN8-1 (At5g53400) showing position of stop codon in *bob1-1* mutation (asterisk) and the *bob1-2* T-DNA insertion (double asterisk).

**A. pREJ14 *BOBBER* rescue plasmid**



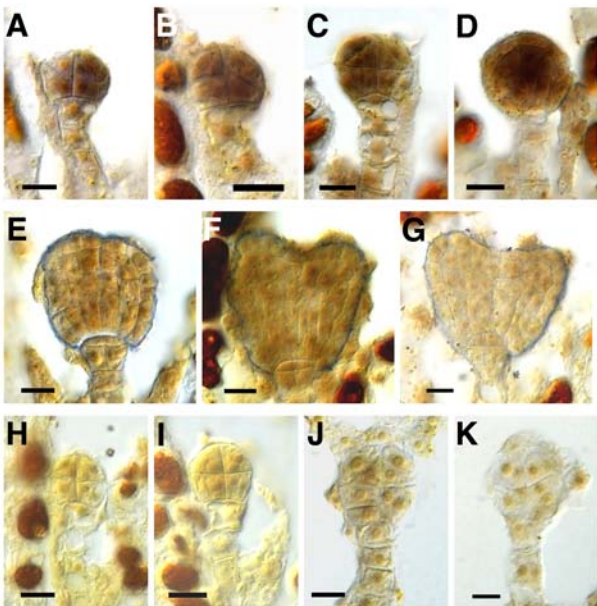
**B. pREJ 19 *BOBBER*-GUS reporter construct**



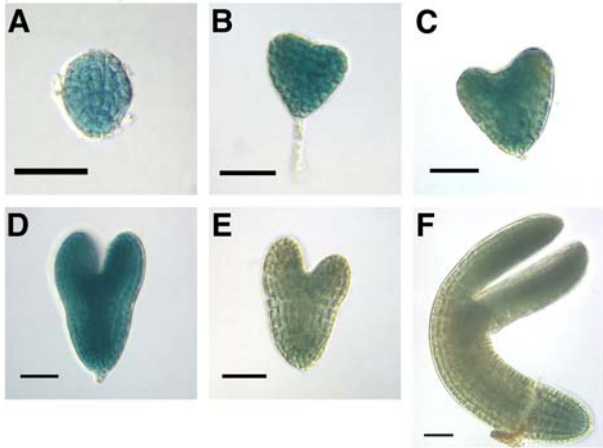
Supplemental Figure 2. Composition of constructs used to rescue *bob1* mutant phenotype (A) and to test localization of *BOBBER1* promoter activity (B).



Supplemental Figure 3. Homozygous bobber1-2 mutant embryo showing ectopic expression of STM reporter.



Supplemental Figure 4. *BOBBER* mRNA expression in wild-type and *bobber* mutant *Arabidopsis* embryos. *BOBBER* is expressed throughout the early embryo. A-B. Wild-type 4-8 celled embryos. C. Wild-type 16 celled embryo, just after protoderm division. D. Wild-type globular embryo. E. Wild-type transition-stage embryo. *BOB* expression does not appear to be as strong at this stage. F-G. Wild-type early heart-stage embryos. *BOB* expression is weaker and more variable at heart stage than at earlier stages in embryogenesis, and becomes undetectable after heart stage. H-K. There is no detectable *BOB* transcript accumulation in *bobber* mutant embryos. H-I. *bobber* embryos whose wild-type siblings are globular-stage embryos, similar to embryo in panel D. J. *bobber* embryo, sibling to wild-type transition-stage embryo in panel E. K. *bobber* embryo, sibling to wild-type early heart-stage embryo in panel G. Scale bars = 10  $\mu$ m.



Supplemental Figure 5. Expression of pREJ19, a BOBBER-GUS fusion protein, in wild-type embryos. A-F. Embryos from one individual in line pREJ19-1. Expression of BOB-GUS is ubiquitous throughout the early embryo (A-C), but becomes variable at about the heart stage (C-D) and mostly or completely ceases by the end of embryogenesis (F). Scale bars = 50  $\mu$ m.

**Supplemental Table 1: Segregation of *bobber1* mutant embryos in *bob1-1/+* and *bob1-1/+ stm-11/+* families.**

<b>Cross</b>	<b>F1 Progeny</b>	<b><i>STM</i> genotype</b>	<b><i>bob1</i> embryos</b>	<b>Wt embryos</b>	<b>% bobber1</b>
<i>bob1-1/+ x stm/+ individual 1</i>					
	<i>bob1-1/+ ind. 1</i>	<i>stm-11/+</i>	99	340	22.6%
	<i>bob1-1/+ ind. 2</i>	+/+	82	281	22.6%
	<i>bob1-1/+ ind. 3</i>	<i>stm-11/+</i>	65	180	26.5%
	<i>bob1-1/+ ind. 4</i>	+/+	71	216	24.7%
<i>bob1-1/+ x stm/+ individual 4</i>					
	<i>bob1-1/+ ind. 1</i>	<i>stm-11/+</i>	77	272	22.1%
<i>bob1-1/+ x stm/+ individual 5</i>					
	<i>bob1-1/+ ind. 1</i>	+/+	67	205	24.6%
	<i>bob1-1/+ ind. 2</i>	+/+	112	346	24.5%
	<i>bob1-1/+ ind. 3</i>	<i>stm-11/+</i>	61	204	23.0%
	<i>bob1-1/+ ind. 4</i>	+/+	83	262	24.1%
	<i>bob1-1/+ ind. 5</i>	+/+	62	224	21.7%
<i>bob1-1/+ x stm/+ individual 6</i>					
	<i>bob1-1/+ ind. 1</i>	+/+	96	310	23.6%
	<i>bob1-1/+ ind. 2</i>	+/+	65	212	23.5%
	<i>bob1-1/+ ind. 3</i>	<i>stm-11/+</i>	81	272	22.9%
	<i>bob1-1/+ ind. 4</i>	<i>stm-11/+</i>	61	179	25.4%
	<i>bob1-1/+ ind. 5</i>	+/+	85	225	27.4%
	<i>bob1-1/+ ind. 6</i>	+/+	64	166	27.8%
	Total for <i>stm/+</i> individuals		444	1447	23.5%
	Total for <i>+/+</i> individuals		787	2447	24.3%

Chi-squared (25%) =	2.3	0.25 < p < 0.1	H <sub>0</sub> is not rejected
Chi-squared (18.75%) =	27.8	p < 0.001	H <sub>0</sub> is rejected

**Supplemental Table 2: CAPS Markers Developed for Mapping the *bobber1* mutation.**

Marker	Primer sequences	Restriction Cleavage	
		enzyme	products (kb)
ILL3	F: 5'-GCGTTGGGTGGGAAGAAGAGA-3'	Nde I	Ler: 0.95, 0.25
	R: 5'-GCCAACACCGGATCAACACAA-3'		Col: 1.2
K19E1-17	F: 5'-ATGGCAGATGATGACTTGAG-3'	Rsa I	Ler: 0.9, 0.35
	R: 5'-ATTACGCTTTTCCATTACACA-3'		Col: 1.2
K19E1-53	F: 5'-CTCCGCCGGTAAGATTTTGTATGT-3'	Dpn II	Ler: 0.45, 0.25
	R: 5'-ATCTCCCGTATCGCTGTGAACC-3'		Col: 0.45, 0.2
MFH8-43	F: 5'-GGCTTCCCCGTTTGTTCATCA-3'	Ava I	Ler: 1.2, 0.4
	R: 5'-CATCAAGGTCCGGGTGGTCAT-3'		Col: 0.5, 0.7, 0.4
MGN6	F: 5'-GTGGCAGAAGTGTGGGTTGTT-3'	Dde I	Ler: top band at 1.1*
	R: 5'-TGAGCCGGTAAGCATCTGAA-3'		Col: top band at 0.9*
MNB8-26	F: 5'-GTGTCGGGTTTGGCTTCTTCTTG-3'	Xba I	Ler: 1.1, 0.4*
	R: 5'-TTATGTTGCGGCGACTTTTGTGTA-3'		Col: 1.5*
MXC20	F: 5'-AGCTCGCTCCCATGTTGTATC-3'	Mse I	Ler: doublet at 0.3*
	R: 5'-ACGGGGAAGACGGAGACC-3'		Col: 0.35, 0.2*
MYN8-33	F: 5'-TCTAGGGGACAGGCTTCTTTCAT-3'	Dde I	Ler: 1.0
	R: 5'-TGCGGCGTAATCGTAATCTGTAT-3'		Col: 0.7, 0.3

\*Other bands present but of equal size in two ecotypes.

**Supplemental Table 3. Complementation of the *bobber1* Phenotype by the Wild-type *BOBBER1* transgene.**

Cross	Progeny	<i>bob1</i> embryos	Wild-type embryos	Total embryos	% bobber1
pREJ14-9 x bob1/+ individual 1					
	Individual 1	9	73	82	11.0%
	Individual 2	3	62	65	4.6%
	Individual 3	3	46	49	6.1%
pREJ14-9 x bob1/+ individual 2					
	Individual 1	3	157	160	1.9%
	Individual 2	7	114	121	5.8%
	Individual 3	16	233	249	6.4%
	Total	41	685	726	5.6%

Chi-squared:            0.45            p = 0.5            for 1:15            H0 is not rejected  
                                  145.02            p << 0.001            for 1:3            H0 is rejected



**Supplemental Table 4. Complementation Data for *bob1-1* and *bob1-2*.**

<b>Cross</b>	<b>Numer of siliques scored</b>	<b>Aborted embryos</b>	<b>WT embryos</b>	<b>% aborted embryos</b>
<i>bob1-2/+</i> self-cross	10	86	252	25.4
<i>bob1-2/+</i> x <i>bob1-1/+</i>	8	82	210	28.1
Col-O x <i>bob1-2/+</i>	6	4	298	1.3