

Figure S1. KNOX gene expression in wild type and BOB mutant plants. RT-PCR was used to amplify *AS1* (At2g37630), *KNAT1/BP* (At4g08150), *KNAT2* (At1g70510), *STM* (At1g62360), and *ACTIN2* (At3g18780) transcripts from dissected young leaves and meristems of both wild type, *bob1-3*, and *bob1-3/bob1-1* plants. *AS1* is normally expressed only in leaves and not in meristems while the KNOX genes (*KNAT1/BP*, *KNAT2*, and *STM*) are normally expressed in meristems but not in leaves. *ACTIN2* is expressed in all plant cells and is used as a loading control. *AS1* expression can be detected in both WT and *bob1-3* leaf fractions as well as in meristem fractions indicating that the meristem fractions contain very young leaves that were too small to be dissected away from the meristem proper (lanes 1-4). Each of the KNOX genes was detected in the meristem but not in the leaves in all genotypes demonstrating that i) the leaf samples did not contain any meristematic tissue, and ii) that KNOX genes are not mis-expressed in the leaves in *bob1-3* mutants (lanes 6-9 *KNAT1/BP*, 11-14 *KNAT2*, and 15-18 *STM*). Primers were chosen to span introns where possible and amplified genomic DNA samples (lanes 5, 10, 19, and 24) demonstrate that the RNA samples did not contain detectable levels of genomic DNA (A). *KNAT1:GUS* and *KNAT2:GUS* reporter lines were crossed into *bob1-3* and *bob1-3/bob1-1* backgrounds. Expression of the reporters (blue) is restricted to the meristematic region in all genotypes (B).

Supplementary Figure 2.

Global analysis of *BOB1* co-expressed genes was performed using ATTED-II (Obayashi et al. 2007). Of the 300 most highly co-regulated genes, the genes listed below are known chaperones or genes involved in high temperature responses. Correlation was determined using 1388 array slides in 58 experiments (see http://atted.jp/top_help.shtml).

Correlation	Locus	Function
0.76	At3g44110	ATJ3 (Arabidopsis thaliana DnaJ homologue 3)
0.76	At5g09590	mtHSC70-2 (HEAT SHOCK PROTEIN 70)
0.72	At3g12050	Aha1 domain-containing protein
0.69	At5g22060	ATJ2 (Arabidopsis thaliana DnaJ homologue 2)
0.66	At2g25140	CLPB-M/CLPB4/HSP98.7 (HEAT SHOCK PROTEIN 98.7)
0.66	At3g23990	HSP60 (Heat shock protein 60)
0.64	At5g56030	HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8)
0.64	248043_s_at	At5g56010; At5g56000 - Hsp81-3 or Hsp81-4
0.61	At1g14980	CPN10 (CHAPERONIN 10)
0.56	At3g09440	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)
0.56	At3g12580	HSP70 (heat shock protein 70)
0.56	At3g08970	DNAJ heat shock N-terminal domain-containing protein
0.55	At5g02490	heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2)
0.55	At5g52640	HSP81-1 (HEAT SHOCK PROTEIN 81-1)
0.54	At4g28480	DNAJ heat shock family protein
0.54	At4g22670	ATHIP1 (ARABIDOPSIS THALIANA HSP70-INTERACTING PROTEIN 1)
0.53	At5g03160	DNAJ heat shock N-terminal domain-containing protein
0.53	At5g51440	23.5 kDa mitochondrial small heat shock protein (HSP23.5-M)
0.53	At3g13860	chaperonin, putative
0.51	At4g16660	heat shock protein 70, putative / HSP70, putative
0.49	At5g02500	HSC70-1 (heat shock cognate 70 kDa protein 1)
0.49	At1g74310	ATHSP101 (HEAT SHOCK PROTEIN 101)
0.48	At3g62600	DNAJ heat shock family protein
0.48	At5g56500	ATP binding / protein binding / unfolded protein binding
0.47	At2g20560	DNAJ heat shock family protein
0.47	At4g36990	HsfB1
0.45	At3g14200	DNAJ heat shock N-terminal domain-containing protein
0.42	At2g26150	ATHSFA2 (Arabidopsis thaliana heat shock transcription factor A2)
0.42	At4g11660	AT-HSFB2B (Arabidopsis thaliana heat shock transcription factor B2B)
0.42	At1g16030	HSP70B (heat shock protein 70B)
0.41	At2g32120	HSP70T-2
0.40	At2g29500	17.6 kDa class I small heat shock protein (HSP17.6B-CI)
0.40	At1g71000	DNAJ heat shock N-terminal domain-containing protein
0.39	At4g25200	ATHSP23.6-MITO (MITOCHONDRION-LOCALIZED SMALL HEAT SHOCK PROTEIN)
0.39	At5g37670	15.7 kDa class I-related small heat shock protein-like (HSP15.7-CI)
0.38	At5g12020	HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PROTEIN)
0.38	At5g12030	AT-HSP17.6A (Arabidopsis thaliana heat shock protein 17.6A)
0.32	At3g13310	DNAJ heat shock N-terminal domain-containing protein

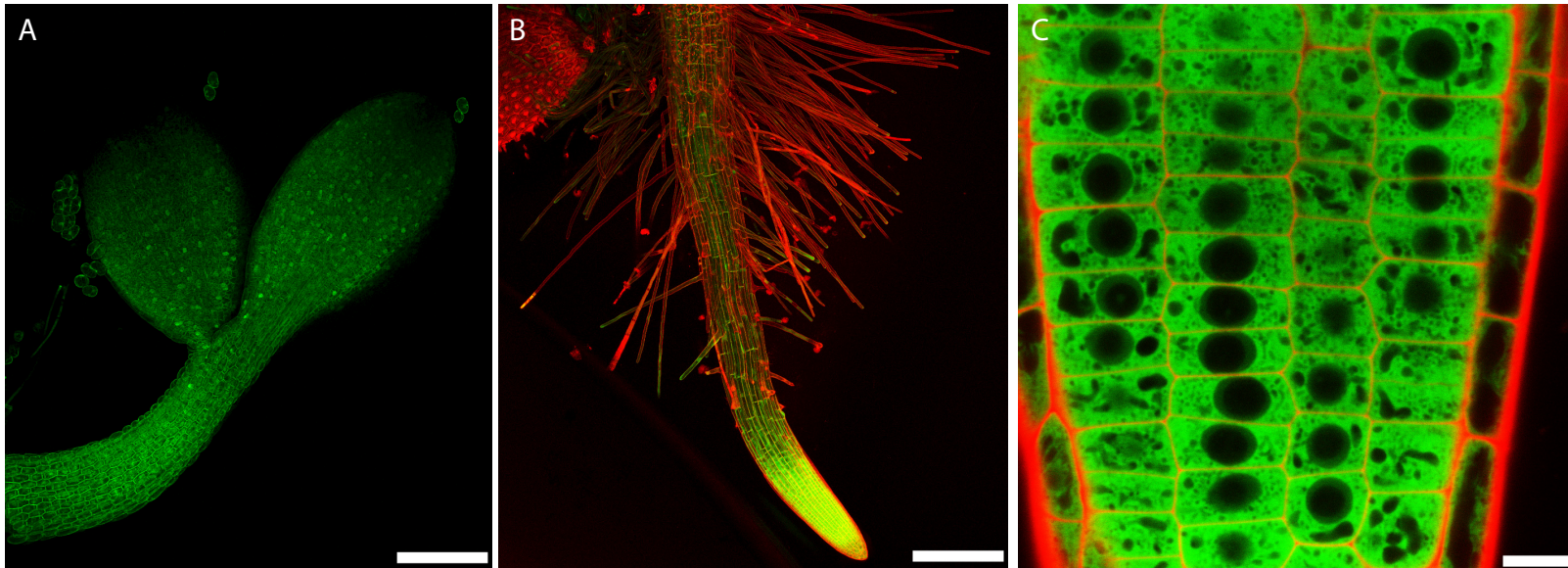


Fig.S3 BOB1:GFP is expressed in all cells of the shoot (A) and root (B) of seedlings with the highest expression levels found at the root tip. BOB1:GFP is localized to the cytoplasm with no obvious subcellular compartmentalization (C). Green signal is GFP, red signal is propidium iodide cell wall staining. Scale bars are 250 μ m (A and B), 10 μ m (C).