

Supplemental Figure 1. Sequence conservation and duplication in the BLH proteins.

(A) Protein sequence alignment of the 13 BLH proteins showing the conservation of amino acids in the SR/KY, BELL and homeodomain regions. The identical amino acids are shaded black and the similar amino acids are shaded grey.

(B) Graphical map of the homologous regions in the chromosomes 2 and 4 that include *SAW2* and *SAW1* genes respectively. The interspersed single copy genes have not been shown. Grey boxes highlight the locations of *SAW2* and *SAW1* in chromosomes 2 (top) and 4 (bottom) respectively. The graphical output was generated using the duplicated blocks finder at <http://wolfe.gen.tcd.ie/athal/index.html> (Blanc et al., 2003)

(C) Three conserved regions found in the 5' UTR of *SAW1* and *SAW2*. Identical residues are marked by *. Numerical values indicate distance upstream of the translational start site (0).

A

SR/KY Domain

BLH1	195	SKYLS	SPAQELL	EEFC	SSI
SAW1	316	SRYT	TAAQELL	EEFC	SV
SAW2	241	SKYL	KPAQELL	EEFC	SV
ATH1	205	SKYL	HSVQE	LLSH	EAA
BLH5	80	PTYL	KAAQELL	NEI	VNV
BLH1	193	SKYL	KAAQELL	DE	VNA
PNF	266	SR	LEPAQKML	EEFC	IS
BLR	174	SR	LEKPAQELL	DE	FCNV
BLH11	20	SR	YAKAVQ	LLVE	BEVIDI
BLH3	171	SR	YKFTQ	LLDE	VSV
BLH10	169	SR	YKPAQ	LLDE	VSV
BLH7	118	SKYL	KAAQELL	DE	VNV
BLH6	144	SKYL	KAAQ	LLDE	VNV

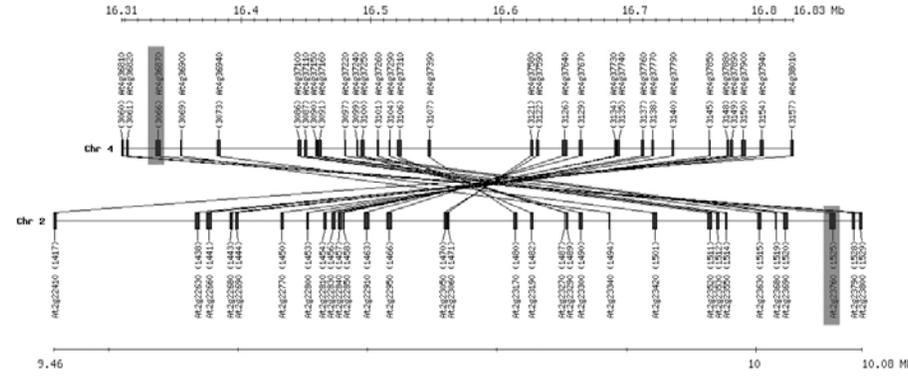
BELL Domain

BLH1	268	E	F	E	L	C	K	R	K	L	S	M	L	E	E	L	K	R	R	Y	G	H	R	E	O	M	R	V	A	A	A	F	E	A	V	G	L	G	G	A	E	I	Y	T	L	A	S	R	A	M	S	R	H	F	R	C	L	K	D	L	V	G	O	I			
SAW1	376	D	N	E	H	O	R	R	R	V	K	L	L	M	L	E	V	D	R	R	N	H	Y	C	O	M	O	V	N	S	F	D	I	V	M	G	H	G	A	A	P	T	L	A	O	K	A	M	S	R	H	F	R	C	L	K	D	A	V	A	O	I					
SAW2	302	D	N	E	H	O	R	R	R	V	K	L	L	M	L	E	V	D	R	R	N	H	Y	C	O	M	O	V	N	S	F	D	I	V	M	G	H	G	A	A	P	T	L	A	O	K	A	M	S	R	H	F	R	C	L	K	D	A	V	A	O	I					
ATH1	266	G	R	A	L	E	A	K	K	H	L	L	L	L	Q	M	V	D	R	Y	S	H	C	V	D	E	I	H	T	V	S	A	H	A	A	T	E	L	D	P	-	Q	L	H	T	R	F	A	L	O	T	V	S	F	L	Y	K	N	L	R	E	R	I	C	K	K	I
BLH5	128	G	V	A	L	O	M	K	R	K	L	S	M	L	E	V	E	O	R	Y	R	O	Y	H	D	O	M	T	L	S	S	F	E	O	A	G	L	G	S	A	N	S	Y	H	M	A	L	O	T	I	S	K	O	F	R	A	V	K	D	I	S	L	O	I			
BLH1	264	E	R	E	L	O	S	K	R	K	L	L	M	L	E	V	D	R	N	O	Y	H	O	M	E	A	L	A	S	S	F	E	D	I	V	M	G	H	G	A	A	P	T	L	A	O	K	A	M	S	R	H	F	R	C	L	K	D	A	I	K	E	O	I			
PNF	316	L	E	P	K	N	L	K	K	A	L	L	E	O	E	V	C	K	W	Y	K	L	N	H	O	L	O	T	V	S	S	E	N	T	V	A	G	L	N	T	A	P	T	I	S	L	A	K	R	T	S	R	S	F	K	A	L	R	H	A	I	E	H	V			
BLR	223	G	G	D	N	G	K	K	S	K	L	S	M	L	E	V	Y	R	R	Y	R	O	Y	E	O	L	C	A	V	M	S	S	F	E	O	V	A	G	L	G	H	A	P	P	N	L	A	K	A	L	S	H	F	R	C	L	K	N	A	I	T	D	L				
BLH11	81	E	N	H	E	H	I	R	I	T	K	L	L	S	L	L	E	V	E	R	E	O	Y	C	N	O	L	E	O	V	S	S	F	E	D	I	V	M	G	H	G	A	A	P	T	L	A	O	K	A	M	S	R	H	F	R	C	L	K	D	A	I	S	G	O	I	
BLH3	229	E	R	E	L	O	S	K	R	K	L	L	M	L	E	V	D	R	N	O	Y	H	O	M	E	A	L	A	S	S	F	E	D	I	V	M	G	H	G	A	A	P	T	L	A	O	K	A	M	S	R	H	F	R	C	L	K	D	A	I	K	E	O	I			
BLH10	231	E	R	E	L	O	S	K	R	K	L	L	M	L	E	V	D	R	N	O	Y	H	O	M	E	A	L	A	S	S	F	E	D	I	V	M	G	H	G	A	A	P	T	L	A	O	K	A	M	S	R	H	F	R	C	L	K	D	A	I	K	E	O	I			
BLH7	167	E	R	E	L	O	S	K	R	K	L	L	M	L	E	V	D	R	N	O	Y	H	O	M	E	A	L	A	S	S	F	E	D	I	V	M	G	H	G	A	A	P	T	L	A	O	K	A	M	S	R	H	F	R	C	L	K	D	A	I	S	G	O	I			
BLH6	200	E	R	E	M	O	S	K	R	K	L	L	M	L	E	V	D	R	R	Y	R	O	Y	O	M	O	V	N	S	S	F	E	D	I	V	M	G	H	G	A	A	P	T	L	A	O	K	A	M	S	R	H	F	R	C	L	K	D	A	I	S	G	O	I			

Homeodomain

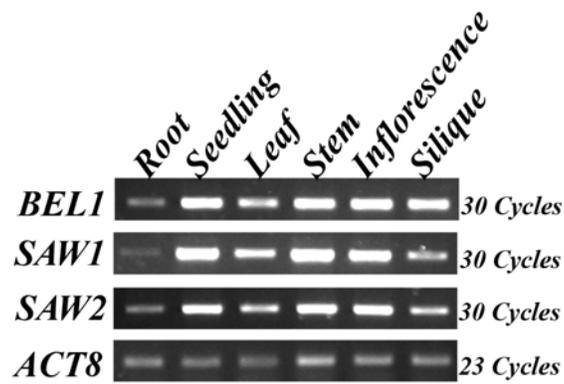
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SAW1	498	A	W	R	P	O	R	G	L	P	E	R	S	V	N	T	L	R	A	W	L	F	E	H	F	L	H	P	Y	P	S	D	R	K	H	L	A	R	O	T	G	L	S	R	N	O	V	S	N	W	F	I	N	A	R	V	R	L	W	K	P	M	V	E	E	M	Y	O	O	E
SAW2	424	A	W	R	P	O	R	G	L	P	E	R	S	V	N	T	L	R	A	W	L	F	E	H	F	L	H	P	Y	P	S	D	R	K	H	L	A	R	O	T	G	L	S	R	N	O	V	S	N	W	F	I	N	A	R	V	R	L	W	K	P	M	V	E	E	M	Y	O	O	E
ATH1	372	I	W	R	P	O	R	G	L	P	E	R	S	V	L	R	N	W	F	E	H	F	L	H	P	Y	P	K	D	S	E	K	H	L	A	I	R	S	G	L	R	S	O	V	S	N	W	F	I	N	A	R	V	R	L	W	K	P	M	E	E	M	Y	E	M					
BLH5	228	A	W	R	P	O	R	G	L	P	E	R	S	V	L	R	N	W	F	E	H	F	L	H	P	Y	P	S	D	R	K	H	L	A	R	O	T	G	L	S	R	O	V	S	N	W	F	I	N	A	R	V	R	L	W	K	P	M	V	E	E	M	Y	R	E	E				
BLH1	385	A	W	R	P	O	R	G	L	P	E	R	S	V	L	R	N	W	F	E	H	F	L	H	P	Y	P	K	D	S	D	R	K	H	L	A	R	O	T	G	L	S	R	O	V	S	N	W	F	I	N	A	R	V	R	L	W	K	P	M	V	E	E	M	Y	R	E	E		
PNF	424	I	W	R	P	O	R	G	L	P	E	R	S	V	L	R	N	W	F	E	H	F	L	H	P	Y	P	K	D	S	D	R	K	H	L	A	R	O	T	G	L	S	R	N	O	V	S	N	W	F	I	N	A	R	V	R	L	W	K	P	M	V	E	E	M	Y	R	E	E	
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BLH11	202	A	W	R	P	O	R	G	L	P	E	R	S	V	L	R	N	W	F	E	H	F	L	H	P	Y	P	K	D	S	D	R	K	H	L	A	R	O	T	G	L	S	R	N	O	V	S	N	W	F	I	N	A	R	V	R	L	W	K	P	M	V	E	E	M	Y	R	E	E	
BLH3	346	A	W	R	P	O	R	G	L	P	E	R	S	V	L	R	N	W	F	E	H	F	L	H	P	Y	P	K	D	S	E	K	H	L	A	I	R	S	G	L	R	S	O	V	S	N	W	F	I	N	A	R	V	R	L	W	K	P	M	V	E	E	M	Y	R	E	E			
BLH10	351	A	W	R	P	O	R	G	L	P	E	R	S	V	L	R	N	W	F	E	H	F	L	H	P	Y	P	K	D	S	E	K	H	L	A	I	R	S	G	L	R	S	N	O	V	S	N	W	F	I	N	A	R	V	R	L	W	K	P	M	V	E	E	M	Y	R	E	E		
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BLH6	314	A	W	R	P	O	R	G	L	P	E	R	S	V	L	R	N	W	F	E	H	F	L	H	P	Y	P	K	D	S	D	R	K	H	L	A	R	O	T	G	L	S	R	O	V	S	N	W	F	I	N	A	R	V	R	L	W	K	P	M	V	E	E	M	Y	R	E	E		

B



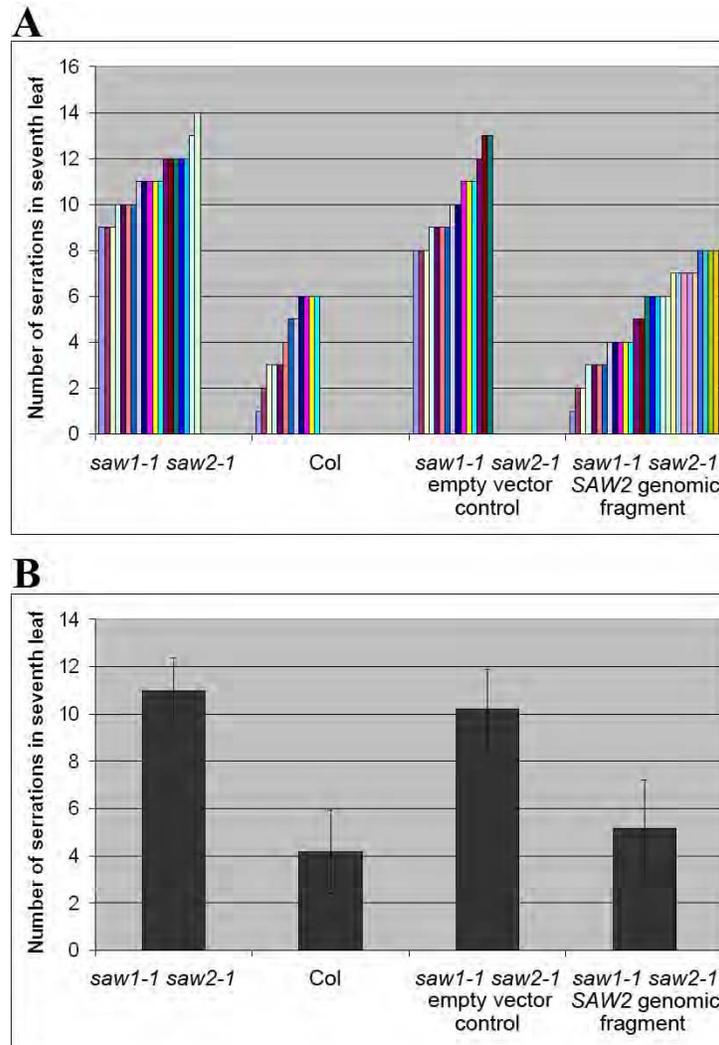
C

SAW1	AAAAAACAGCGTAAGACCTAGTT	-197 to -140
SAW2	AGAAAACTGTATAATACCTAGTT	
	* * * * * *	
SAW1	AAAAGGAGAGTCCAGAAAAAGAAAGCGGAGAAAGAGAG	-344 to -308
SAW2	AAAAGAGTACTCAAGAAAAAGAAAGCTAGAGAGAGAG	
	***** * * *	
SAW1	AACCACTAATAAAGAGATTGGTGGGCTAAAAAGGGTGACGAAGAAGAAGAGTACCTCT	-521 to -457
SAW2	AAAAAATATTAAGAAGATTGGTGGGTTAAAAAGGGAGCGATGAGAAAGAACAGCGACCTCT	
	** * * * *	



Supplemental Figure 2. RT-PCR analysis of *BEL1*, *SAW1* and *SAW2*.

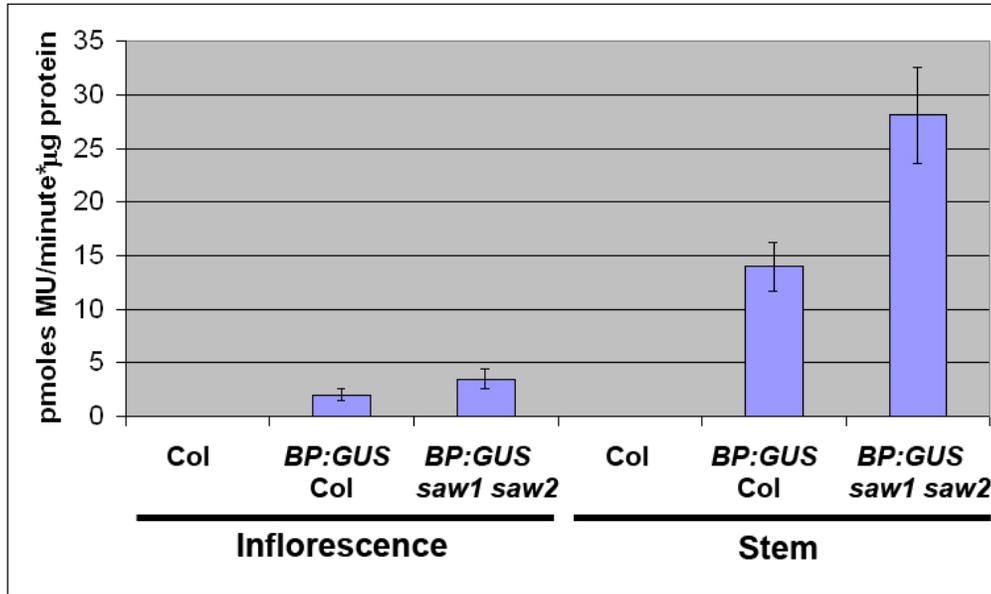
RNA was extracted from roots of 7 day old seedlings; whole 7 day old seedlings; rosette leaves (6,7 and 8) of 4-week-old plants; and stems, inflorescences and immature siliques of 5-week-old plants. *ACTIN8*, loading control.



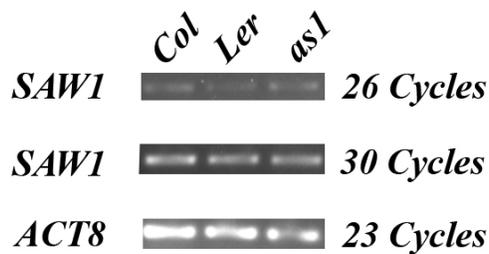
Supplemental Figure 3. Complementation of *saw1 saw2* double mutants by a *SAW2* genomic DNA fragment.

A. Number of serrations on the seventh leaf of *saw1 saw2* mutants, WT, and mutants transformed with the empty vector or with the *SAW2* genomic fragment. Each bar represents serrations found for an individual plant (independent transformant, for the transgenic plants).

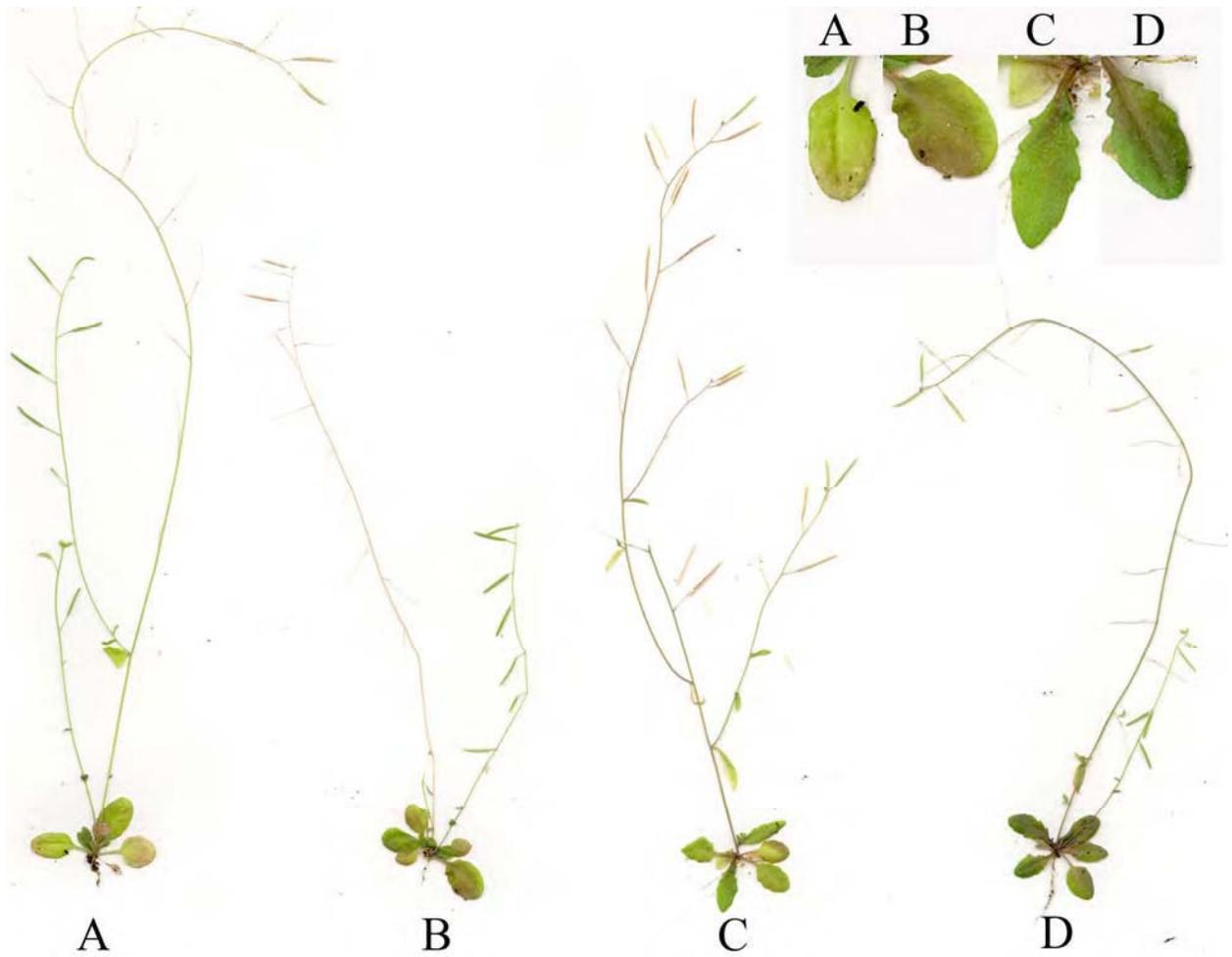
B. Average of number of serrations on the seventh leaves of controls and transformants. Error bars indicate SD.



Supplemental Figure 4. Increased *BP:GUS* activity in stems of *saw1 saw2* double mutants
 Protein was extracted from inflorescence apex and stem of WT (Col), *BP:GUS* in Col and *BP:GUS* in *saw1saw2*. Protein extract was used to assay *BP:GUS* activity by a MUG assay. The blue bars indicate the average amount of 4-MU produced. Error bars indicate SD (n = 6 from an experiment with two biological replicates, each having three technical replicates).

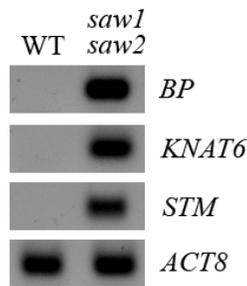


Supplemental Figure 5. RT PCR analysis of *SAW1*
 RNA was extracted from leaves of 4-week-old plants of Columbia (Col), Landsberg erecta (Ler), *asymmetric leaves 1 (as1)*. *ACTIN8* was used as a loading control.



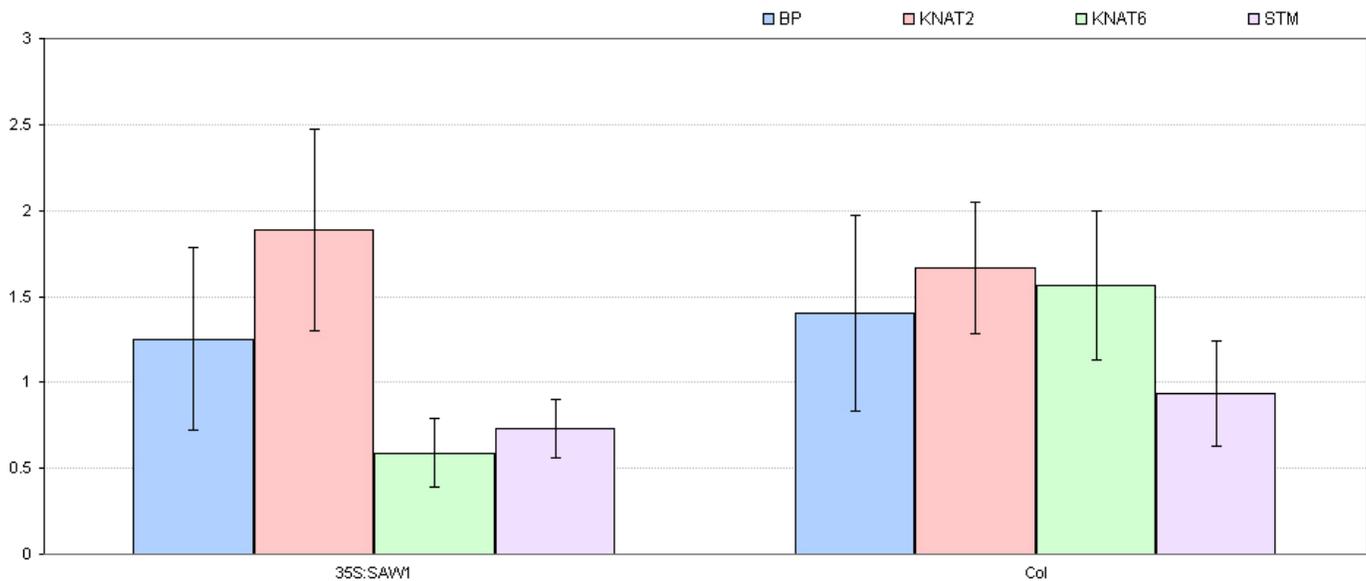
Supplemental Figure 6. *saw1 saw2 bp* triple mutant phenotype

Scanned images of 6-week-old plants of A. Col, B. *bp* X col, C. *saw1 saw2* and D. *saw1 saw2 bp*. Inset shows an enlarged view of the seventh rosette leaf from each genotype.



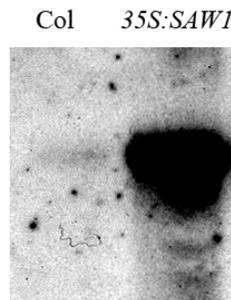
Supplemental Figure 7. RT PCR analysis of Class 1 *KNOX* gene expression

RNA was extracted from 7th, 8th and 9th leaves (pooled) of 6-week-old plants of Columbia (Col), and *saw1 saw2* and RT-PCR used to detect the presence of transcripts for *BP*, *STM* and *KNAT6*. *ACTIN8* was used as a loading control.



Supplemental Figure 8. Real-time PCR analysis of Class 1 *KNOX* genes.

RNA was extracted from the shoots of 4-day-old seedlings (cotyledons removed) of *35S:SAW1* and Columbia (Col) and Real time PCR used to quantify the relative amount of transcript for *BP*, *STM*, *KNAT2* and *KNAT6*. Bars represent SD. Numbers in the y-axis represent the gene expression relative to zero. *ACTIN8* was used as a reference.



Supplemental Figure 9. RNA blot comparing *SAW1* expression in WT and *35S:SAW1* plants.

RNA was extracted from the leaves of 3-week-old plants of *35S:SAW1* line 1 and Columbia (Col). Note that the faint band that is visible in Col is overshadowed by the dense band in *35S:SAW1*.