

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 | SKYLSPAQELLLEFFCSL |
| SAW1 | 316 | SRYTAAQELLLEFFCSV |
| SAW2 | 241 | SKYLKPAQELLLEFFCSV |
| ATH1 | 205 | SKYIHSVQELLSHBAAY |
| BLH5 | 80 | PTYLKAAQELLLEIVNV |
| BLH1 | 193 | SKYLKAAQELLLEVVNA |
| PNF | 266 | SRRLPAQKMLLEFFCIS |
| BLR | 174 | SRRLKPAQELLLEDFCNV |
| BLH11 | 20 | SRYLKAAQELLLEVEVDI |
| BLH3 | 171 | SRYLKPAQELLLEDEVSV |
| BLH10 | 169 | SRYLKPAQELLLEDEVSV |
| BLH7 | 118 | SKYLKAAQELLLEDEVNV |
| BLH6 | 144 | SKYLKAAQELLLEDEVNV |

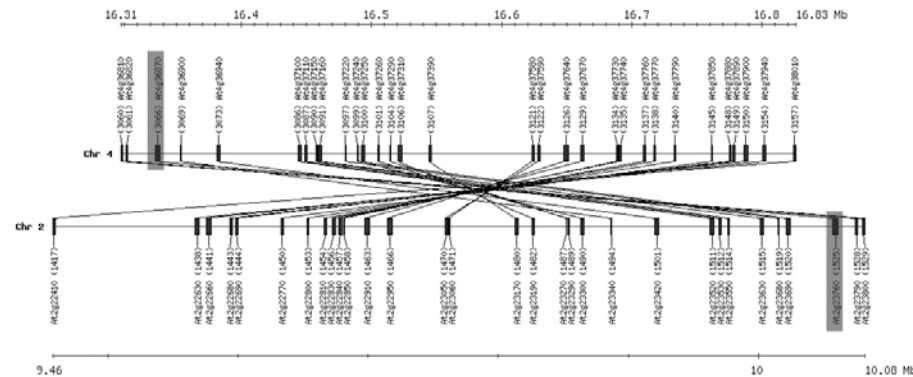
BELL Domain

| | | |
|-------|-----|--|
| BLH1 | 268 | EEMELCKRRKLLSMLLEFLKRYGHYREOMRVAAAPEAAVGLGGAIIYTLASRAMSRHFRLCKEGLVGOI |
| SAW1 | 376 | ENEFHRRRVKLLTMLBEVDRRYNHYCFOMQMVNSFDIWMGCGAIPYTLAOKAMSRHFRLCKDAVAACQ |
| SAW2 | 302 | DRTEHRRRVKLLSMLBEVDRRYNHYCFOMQMVNSFDQWVCGYGAIPYTLAOKAMSRHFRLCKDAVAVQL |
| ATH1 | 266 | GRRLBAKKTLLDLQWVDRYSHCVDEIHTVISAHAATEIDPQLHTRFALQTVSFLYKLRERICKKI |
| BLH5 | 128 | GVAALCKRRKLLSMLSEMVEORYKQYHDQMTLSSFEQAAGLGSANSYTHMALQTISSKQFRVAKDMISLQI |
| BLH1 | 264 | ERTEHCKRRKLLSMLBEVDRRYNHYCFOMQMVNSFDIWMGCGAIPYTLAOKAMSRHFRLCKDAIAGQI |
| PNF | 316 | LEPKNRLKRAKLLFLQEVCKWYKLYNHQIQVMSSENTVAGLNTAIPYISLAKRTRSRFKALRFAIAEHV |
| BLR | 223 | GGGDNCKRRKLLSMLBEVDRYKQYEQLEQAVMGSFEQVAGLGHAPPYANLALKALSIFRFLCKNAITDOL |
| BLH11 | 81 | ENHEFHRIKLLSMLQVEEREEQYCNLEQVSSFEQTAGESSRHYTGLALQAMTRHFGSLEPAITSQI |
| BLH3 | 229 | ERTELOSKRRKLLTMLBEVDRRYNHQYHHEMBAIASSFEMVITGLGSAKPYTSVALNRTSRHFRLCKDAIKEQI |
| BLH10 | 231 | ERTELOKRRKLLTMLBEVDRRYNHQYHHEMBAIASSFEMVITVAGLGSAPKPYTSVALNRTSRHFRLCKDAIKEQI |
| BLH7 | 167 | ERTELOSKRRKLLSMLBEVDRRYKQYEQLEQAVMGSFEQVAGLGHAPPYANLALKALSIFRFLCKDAISGOI |
| BLH6 | 200 | ERTELOSKRLLKLLSMLBEVDRRYKQYEQMCHVSSFEQVAGLGHAPPYANLALKALSIFRFLCKDAISGOI |

Homeodomain

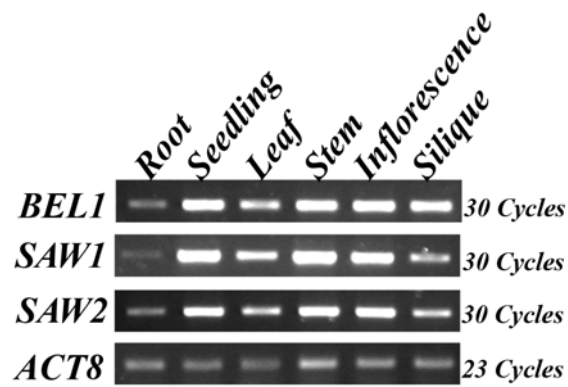
| | | |
|-------|-----|--|
| BLH1 | 390 | AWRPQRLPERVNTLRAWLFEHFLHPYPSVDKRLARQTLGSRGQVSNWFINARVRLWKPMTEEMYSDEE |
| SAW1 | 498 | AWRPQRLPERSVNTLRAWLFEHFLHPYPSDADKHLARQTLGSRNOVSNWFINARVRLWKPMVEEMYSDEE |
| SAW2 | 424 | AWRPQRLPERSVNTLRAWLFEHFLHPYPSDADKHLARQTLGSRNOVSNWFINARVRLWKPMVEEMYSDEE |
| ATH1 | 372 | IWRPQRLPEKRSVLRNWFQNLHHPYPKDSSEKHLAIRSGLRQVSNWFINARVRLWKPMTEEMYSDEM |
| BLH5 | 228 | AWRPQRLPEKRSVLRNWFQNLHHPYPKDSSEKHLAIRSGLRQVSNWFINARVRLWKPMVEELYSDEE |
| BLH1 | 385 | AWRPQRLPERVNTLRAWLFEHFLHPYPKDSKRMMLAKQTGLRQVSNWFINARVRLWKPMVEEMYSDEE |
| PNF | 424 | IWRPQRLPERVNTLRAWLFEHFLHPYPTDSDKMLAQTLGSRNOVSNWFINARVRLWKPMVEEHTHLE |
| BLR | 348 | VWRPQRLPERVNTLRAWLFEHFLHPYPTDSDKMLAKQTGLRQVSNWFINARVRLWKPMVEEHTHMLE |
| BLH11 | 202 | AWRPQRLPERVNTLRAWLFEHFLHPYPNEAKKMLASQTLGSRNOVSNWFINARVRLWKPMTEEMYSDEE |
| BLH3 | 346 | AWRPQRLPENSVTLRAWLFEHFLHPYPKDSSEKMLAKQTGLSKNOVSNWFINARVRLWKPMTEEMYSDEE |
| BLH10 | 351 | AWRPQRLPENSVTLRAWLFEHFLHPYPKDSSEKMLAKQTGLSKNOVSNWFINARVRLWKPMTEEMYSDEE |
| BLH7 | 285 | IWRPQRLPENSVTLRAWLFEHFLHPYPKDSKRMMLAKQTGLSRGQVSNWFINARVRLWKPMVEEMYSDEE |
| BLH6 | 314 | AWRPQRLPENSVTLRAWLFEHFLHPYPKDSKRMMLAKQTGLSRGQVSNWFINARVRLWKPMVEELYSDEE |

B



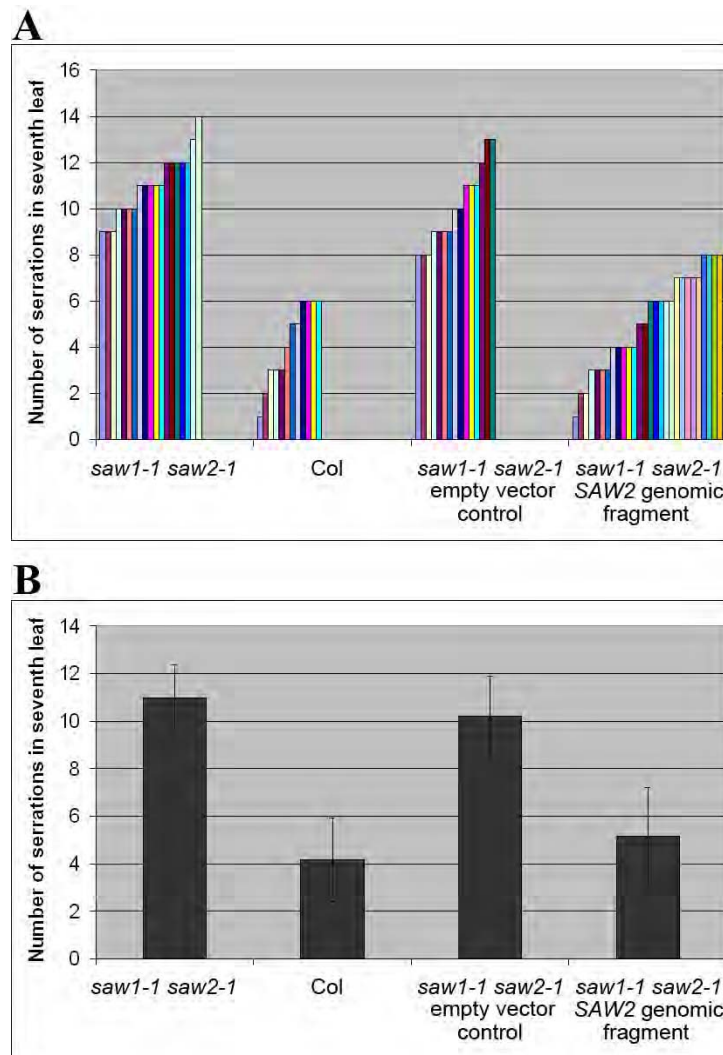
C

| | | |
|------|--|--------------|
| SAW1 | AAAAAACAGCGTAAGACCTAGTT | -197 to -140 |
| SAW2 | AGAAAACTGTATAATACCTAGTT | |
| | * * * * * * | |
| SAW1 | AAAAGGAGAGTCCAGAAAAAGAAAGCGGAGAAAGAGAG | -344 to -308 |
| SAW2 | AAAAGAGTACTCAAGAAAAAGAAAGCTAGAGAGAGAG | |
| | ***** * * * | |
| SAW1 | AACCACTAATAAAGAGATTGGTGGGCTAAAAAGGGTGACGAAGAAGAAGAGTGACCTCT | -521 to -457 |
| SAW2 | AAAAAATATTAAGAAGATTGGTGGGTAAAAAGGGAGCGATGAGAAAGAACAGCGACCTCT | |
| | ** * * * * | |



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

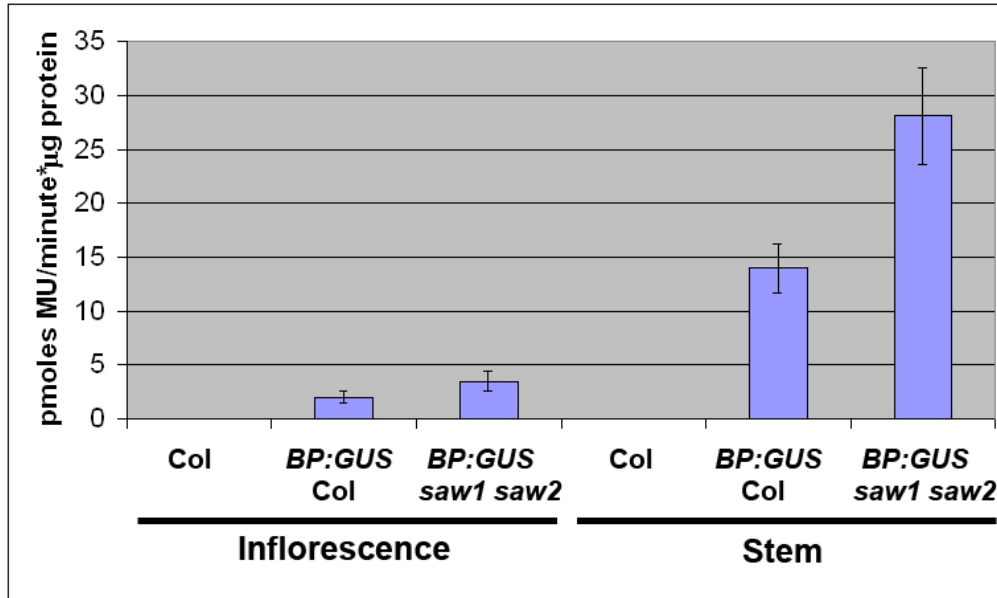
RNA was extracted from roots of 7 day old seedlings; whole 7 day old seedlings; rosette leaves (6,7 and 8) of 4-week-old plants; and stems, inflorescences and immature siliques of 5-week-old plants. *ACTIN8*, loading control.



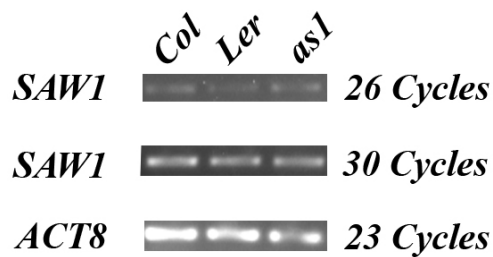
Supplemental Figure 3. Complementation of *saw1 saw2* double mutants by a *SAW2* genomic DNA fragment.

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).

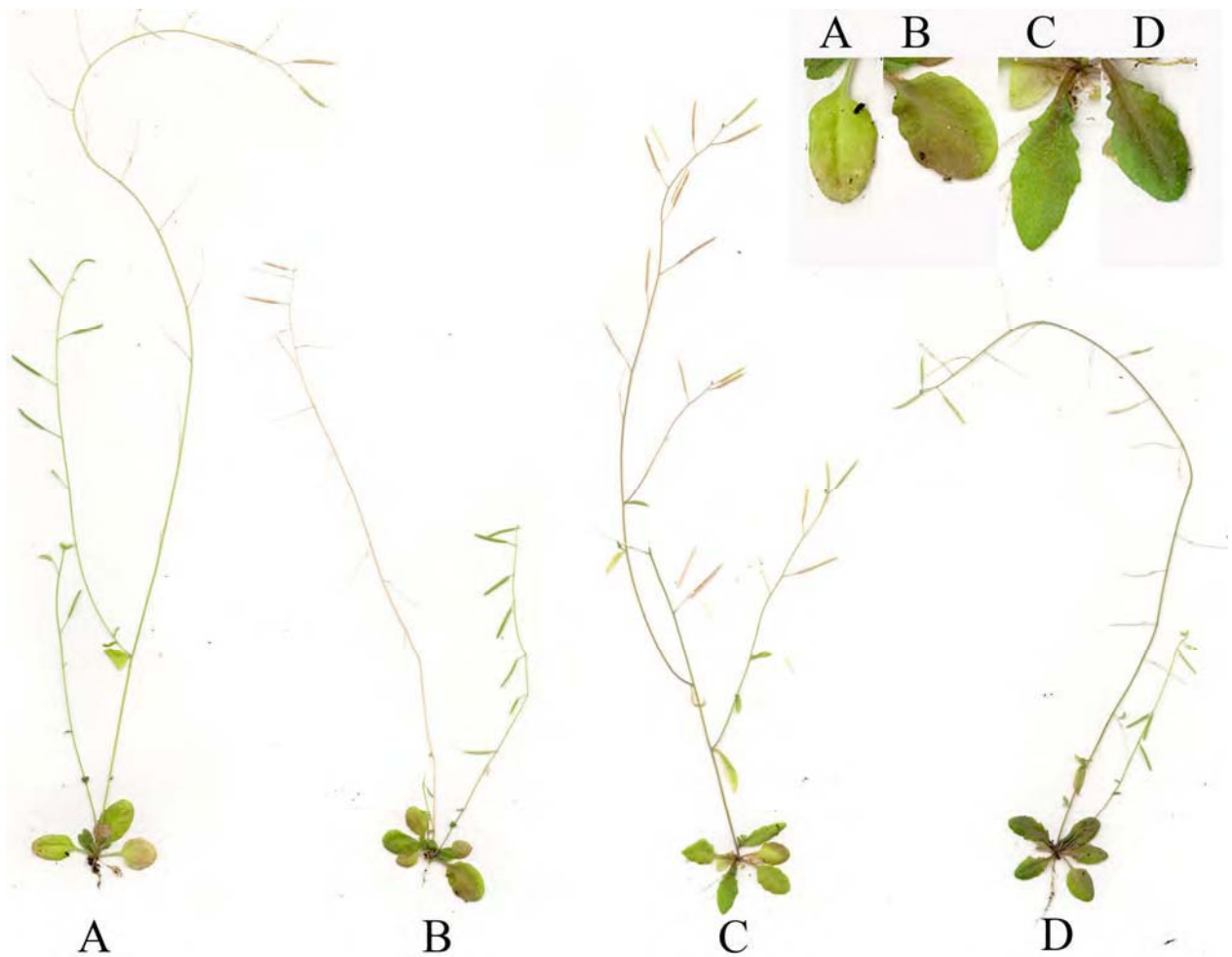
B. Average of number of serrations on the seventh leaves of controls and transformants. Error bars indicate SD.



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).

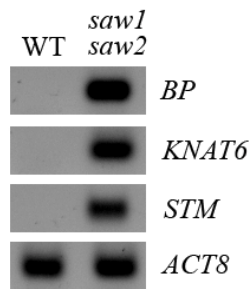


Supplemental Figure 5. RT PCR analysis of *SAW1*
 RNA was extracted from leaves of 4-week-old plants of Columbia (Col), Landsberg erecta (Ler), *asymmetric leaves 1 (as1)*. *ACTIN8* was used as a loading control.



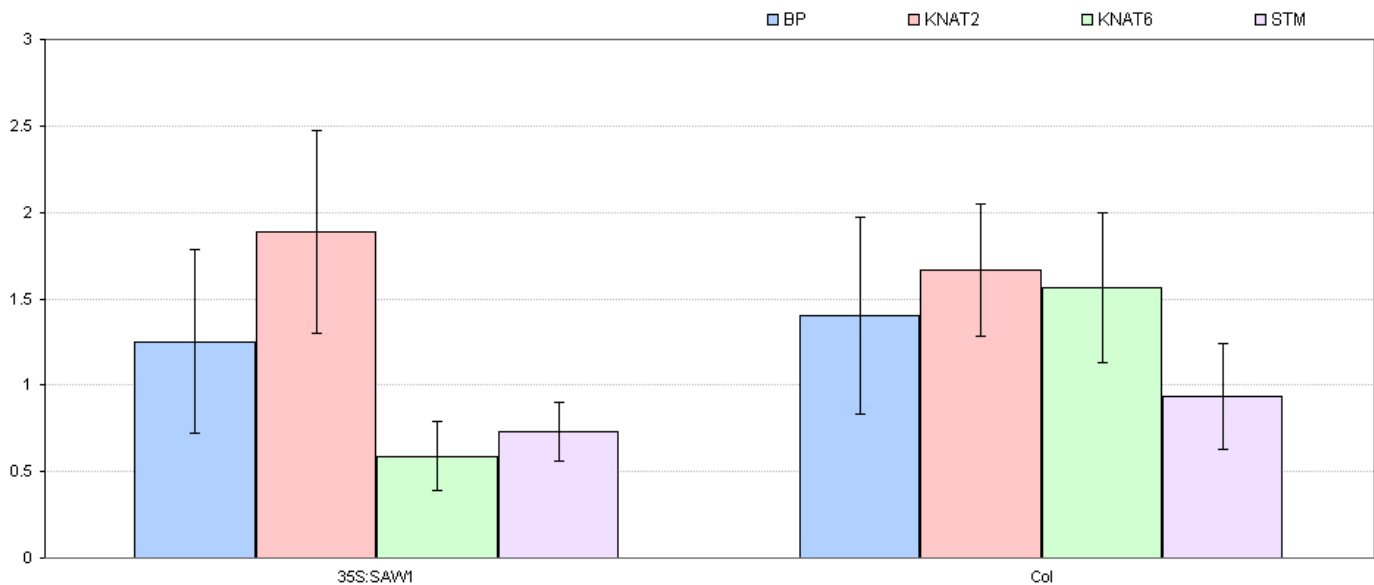
Supplemental Figure 6. *saw1 saw2 bp* triple mutant phenotype

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.



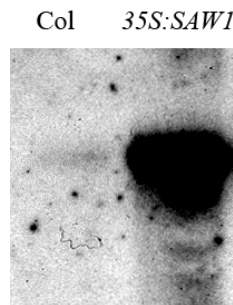
Supplemental Figure 7. RT PCR analysis of Class 1 *KNOX* gene expression

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*.