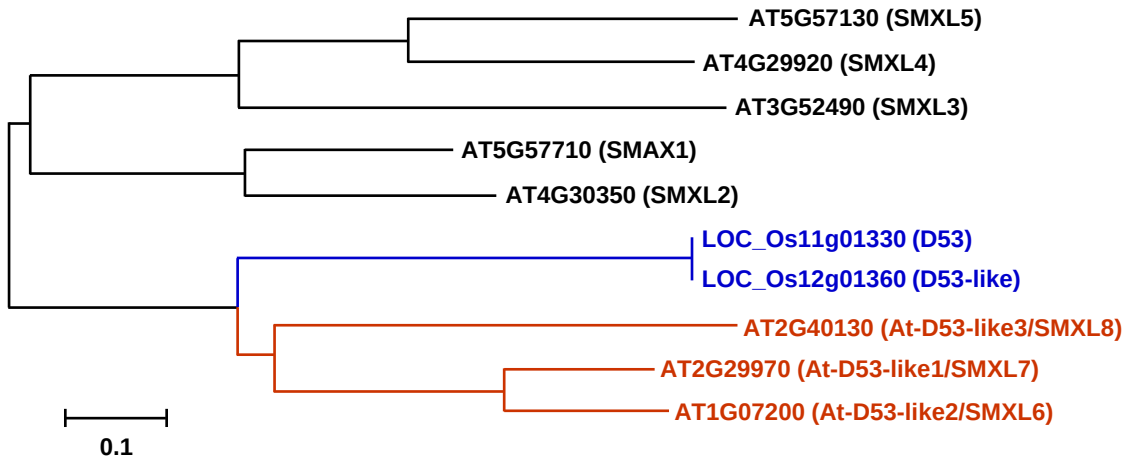
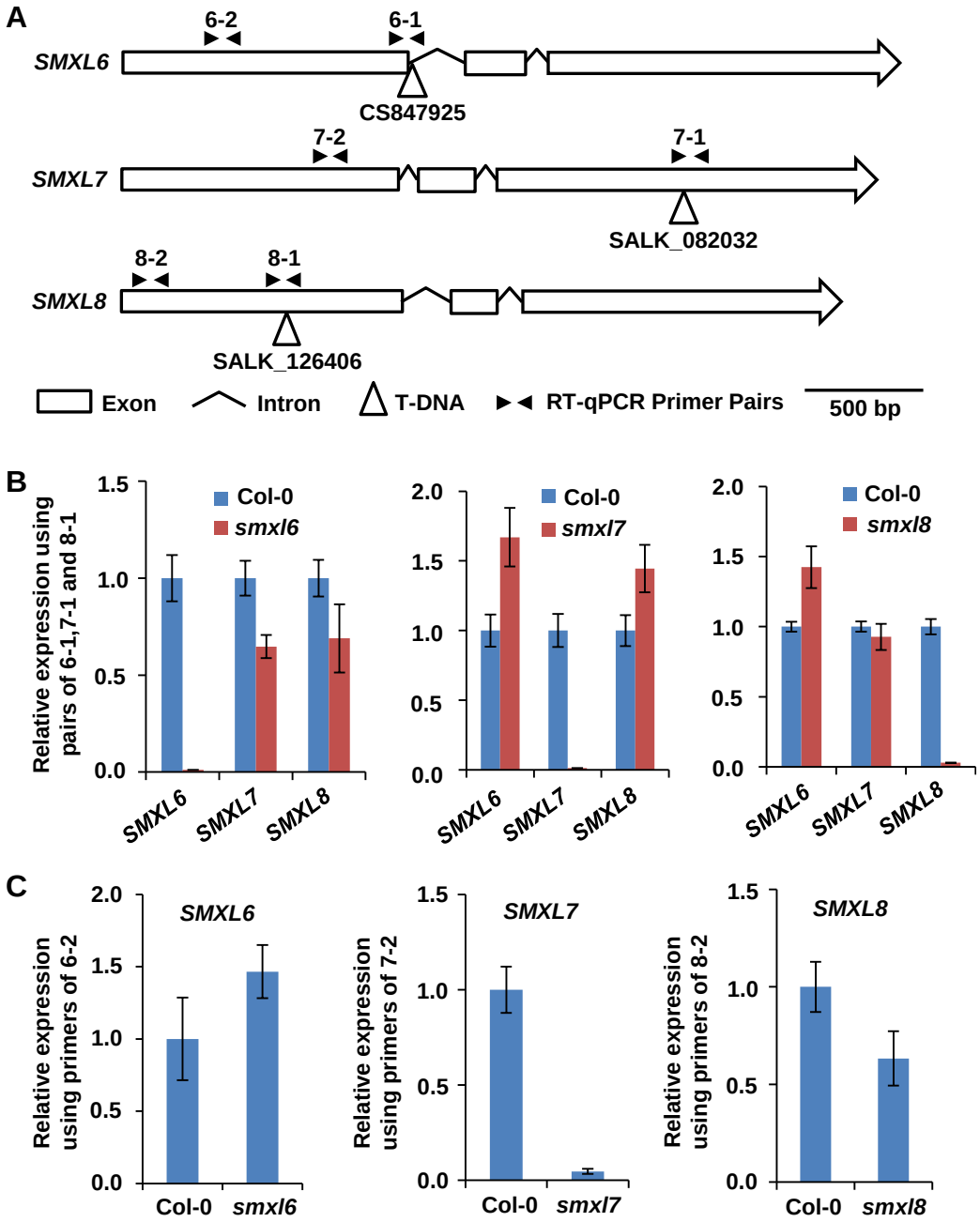


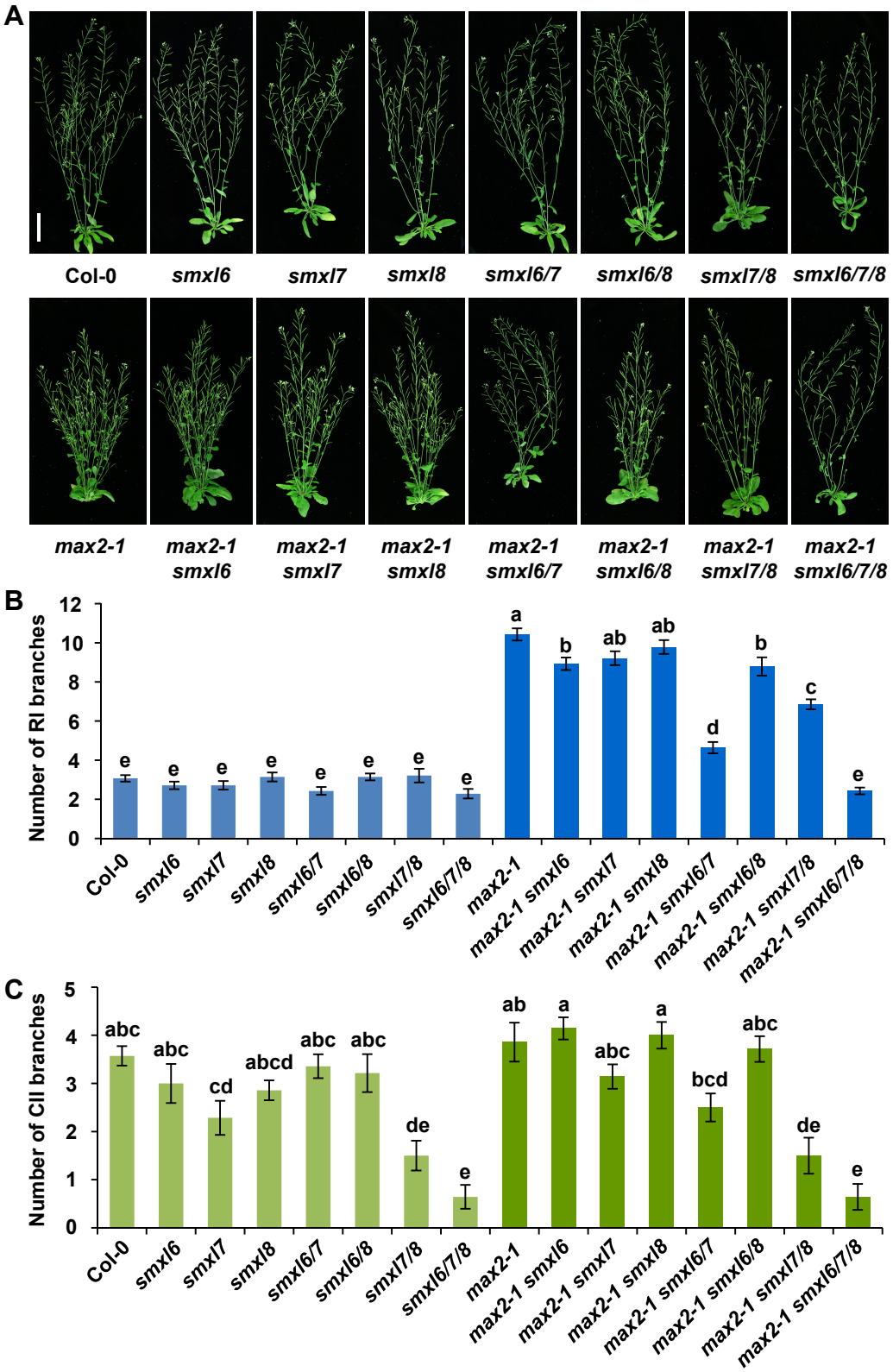
Supplemental Figure 1. Phylogenetic Tree of D53, D53-Like, and SMXL Family Proteins.

Multiple sequence alignment of D53, D53-like, and SMXL family proteins was carried out using Clustalw2. The phylogenetic tree was constructed using MEGA 5.1 software. The Arabidopsis D53-like1/SMXL7, D53-like2/SMXL6, and D53-like3/SMXL8 proteins (shown in red) are here classified as D53-like SMXLs. The rice orthologs are shown in blue.



Supplemental Figure 2. Identification of *smxl6*, *smxl7*, and *smxl8* Mutants in Arabidopsis.

(**A**) Schematic representation of T-DNA insertion mutants for the *SMXL6*, *SMXL7*, and *SMXL8* genes. The T-DNA insertion sites and positions of reverse transcription quantitative PCR (RT-qPCR) primers are indicated by triangles. The exact sites of T-DNA insertion from the ATG codon in the genomic sequence were as follows: *smxl6*, 1209 base pairs (bp); *smxl7*, 2375 bp; and *smxl8*, 692 bp.
(**B**) The expression of *SMXL6*, *SMXL7*, and *SMXL8* in 10-day-old seedlings of wild-type, *smxl6*, *smxl7*, and *smxl8* using primer pairs of 6-1, 7-1, and 8-1. Expression was detected by RT-qPCR using Arabidopsis *ACTIN2* (*ACT2*) as the internal control. Values are means ± SEM (n = 3).
(**C**) The expression of *SMXL6*, *SMXL7*, and *SMXL8* in 10-day-old seedlings of wild-type, *smxl6*, *smxl7*, and *smxl8* using primer pairs of 6-2, 7-2, and 8-2. Expression was detected by RT-qPCR using Arabidopsis *ACT2* as the internal control. Values are means ± SEM (n = 3).

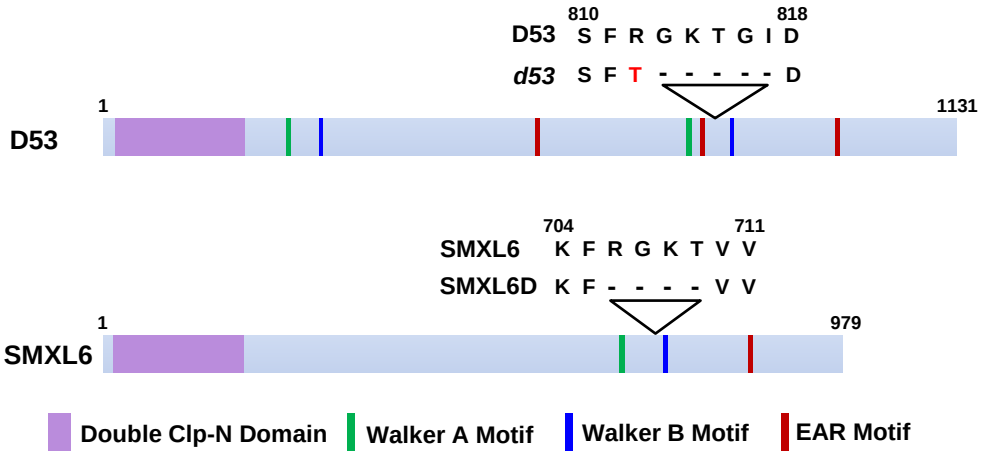


Supplemental Figure 3. The Shoot-Branching Phenotypes of *max2-1* Are Repressed by *smxl6/7/8*.

(A) Shoots of representative plants after 7-weeks growth in long-day photoperiod. All mutations are in the Col-0 background and genotypes of mutants are as indicated. Scale bar, 5 cm.

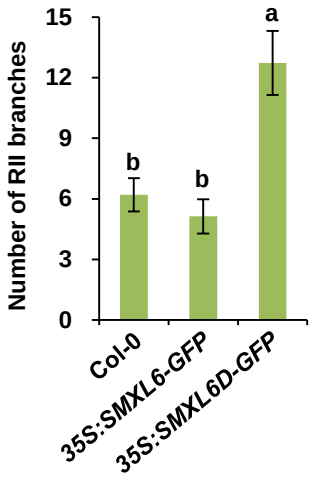
(**B**) Number of primary rosette (RI) branches of at least 0.5 cm recorded in plants shown in (**A**). Values are means ± SEM (n = 14); Significant differences revealed by Tukey's multiple comparison test are indicated by different letters above bars ($p < 0.05$).

(**C**) Number of secondary cauline (CII) branches of at least 0.5 cm recorded in plants shown in (**A**). Values are means ± SEM (n = 14); Significant differences revealed by Tukey's multiple comparison test are indicated by different letters above bars ($p < 0.05$).



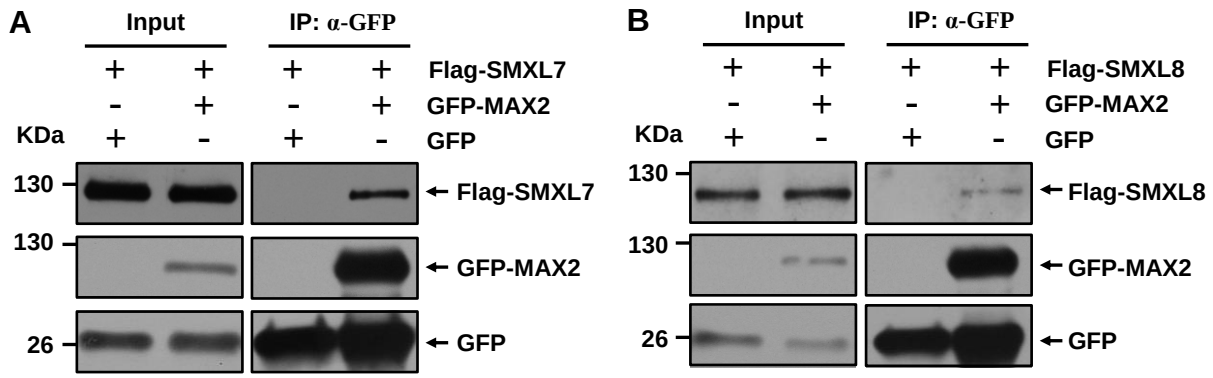
Supplemental Figure 4. Schematic Diagrams Showing the Amino Acid Changes of *d53* and SMXL6D Proteins.

The conserved double Clp-N domain (purple box), Walker A (green box) or B (blue box) motif, and EAR motif (red box) are indicated in D53 and SMXL6. The *d53* mutant protein exhibits an in-frame deletion of amino acids 813-817 (Gly-Lys-Thr-Gly-Ile) and an amino acid substitution at 812 (Arg to Thr). The SMXL6D protein carries a deletion of residues 706-709 (Arg-Gly-Lys-Thr), which is conserved in both D53 and SMXL6.



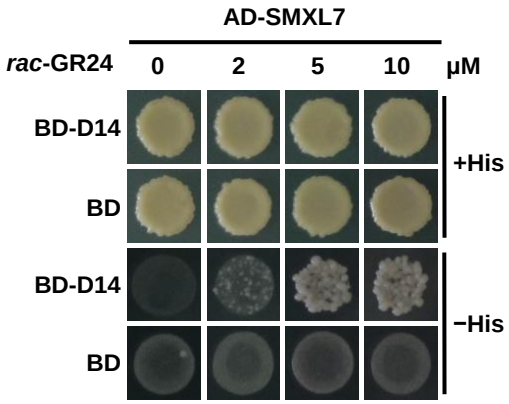
Supplemental Figure 5. The *35S:SMXL6D-GFP* Transgenic Plants Form More Branches Than the Wild Type.

Numbers of secondary rosette (RII) branches in adult wild-type (Col-0), *35S:SMXL6-GFP* and *35S:SMXL6D-GFP* plants after 7-weeks growth in long days. Values are represented as mean ± SEM (n = 15); Significant differences by Tukey's multiple comparison test are indicated by different letters above bars ($p < 0.05$).



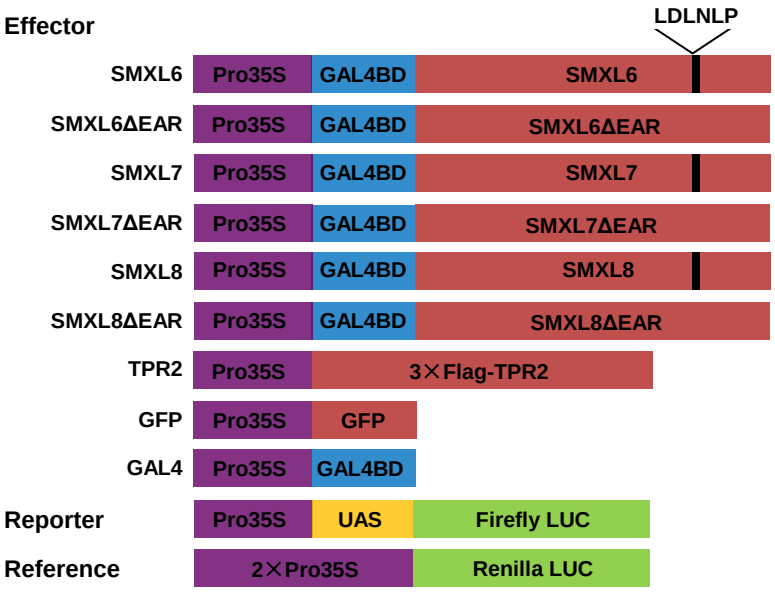
Supplemental Figure 6. SMXL7 and SMXL8 Interact with MAX2.

(**A**) Interaction *in vivo* between Flag-SMXL7 and GFP-MAX2 revealed by Co-IP assay in protoplasts prepared from wild-type (Col-0). After transformation and incubation for 12 h, cells were broken, then immunoprecipitation (IP) with agarose-conjugated anti-GFP monoclonal antibody was carried out, following which the Flag-SMXL7 recombinant protein was detected with an anti-Flag monoclonal antibody while GFP-MAX2 fusion protein and GFP were detected with an anti-GFP monoclonal antibody.
(**B**) Interaction *in vivo* between Flag-SMXL8 and GFP-MAX2 revealed by the same Co-IP assay in protoplasts prepared from wild-type (Col-0). The Flag-SMXL8, GFP-MAX2, and GFP proteins were expressed, isolated and detected as in (**A**).



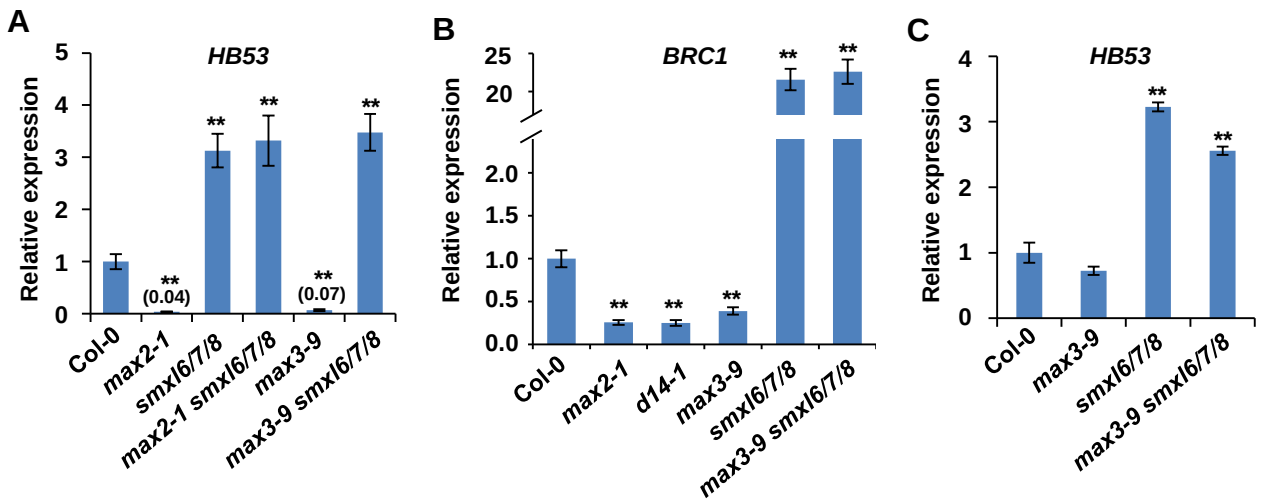
Supplemental Figure 7. Interaction between SMXL7 and D14 in Yeast Is Stimulated by Increasing GR24 Concentration.

Cells of yeast (AH109) were co-transformed with constructs encoding Binding Domain (BD) fused to D14 and Activation Domain (AD) fused to SMXL7. Cells were plated on selective media in the presence of increasing amounts of *rac*-GR24.



Supplemental Figure 8. Schematic Diagrams Showing the Constructs Used in the Transient Expression Assays in Protoplasts.

The small black rectangles represent the EAR motif in SMXL6, 7, and 8. GAL4BD, Binding Domain of the GAL4 transcriptional activator; UAS, Upstream Activator Sequence to which GAL4 binds; Firefly LUC, Firefly luciferase reporter gene; Renilla LUC, Renilla luciferase reporter gene. Firefly LUC activity was normalized against that of Renilla LUC.



Supplemental Figure 9. Expression of *HB53* and *BRC1* Is Reduced in *max2* and *max3* but Enhanced in *smxl6/7/8*.

(**A**) Expression of *HB53* in axillary buds of secondary cauline (CII) branches of Col-0 and the mutants indicated, determined by RT-qPCR using Arabidopsis *ACTIN2* (*ACT2*) as the internal control. Values are means ± SEM (n = 3); **p < 0.01 determined by Student's *t*-test.
(B) and **(C)** Expression of *BRC1* and *HB53* in 10-day-old seedlings of Col-0 and the mutants indicated, determined by RT-qPCR using Arabidopsis *ACT2* as the internal control. Values are means ± SEM (n = 3); **p < 0.01 determined by Student's *t*-test.

Supplemental Table 1. Primers Used in This Study.

Primer Name	Sequence
Primers for plasmid construction:	
SMXL6-OE-F	5’-ggggtaccATGCCGACGCCGGTGACT-3’
SMXL6-OE-R	5’-gcgtcgacCCATATCACATCCACCTTCG-3’
D14-BK-F	5’-cccatatgATGAGTCAACACAACATCTTAG-3’
D14-BK-R	5’-cggaattcTCACCGAGGAAGAGCTCGC-3’
SMXL6-BK-F	5’-cccccgggGATGCCGACGCCGGTGACTACGG-3’
SMXL6-BK-R	5’-gcgtcgacTCACCATATCACATCCACCTTCGC-3’
SMXL6-AD-R	5’-ccctcgagTCACCATATCACATCCACCTTCGC-3’
SMXL7-BK-F	5’-cggaattcATGCCGACACCAGTAACCAC-3’
SMXL7-BK-R	5’-cgggatccTCAGATCACTTCGACTCTCG-3’
SMXL8-BK-F	5’-cccatatgATGCCAACGGCGGTGAATG-3’
SMXL8-BK-R	5’-cggaattcCTACTGAGATTTTACAAAGAACA-3’
TPR2-BK-F	5’-cccatatgATGTCGTCTTTGAGCAGAGAG-3’
TPR2-BK-R	5’-cggaattcTTACCTTTGAATCTGATCCGAA-3’
SMXL6-GW-F	5’-GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCCGACGCCGGTGACT-3’
SMXL6-GW-R	5’-GGGGACCACTTTGTACAAGAAAGCTGGGTATCACCATATCACATCCACCTT-3’
SMXL7-GW-F	5’-GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCCGACACCAGTAACCAC-3’
SMXL7-GW-R	5’-GGGGACCACTTTGTACAAGAAAGCTGGGTATCAGATCACTTCGACTCTCG-3’
SMXL8-GW-F	5’-GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCCAACGGCGGTGAATG-3’
SMXL8-GW-R	5’-GGGGACCACTTTGTACAAGAAAGCTGGGTACTACTGAGATTTTACAAAGAACA-3’
D14-GW-F	5’-GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGTCAACACAACATCTTAG-3’
D14-GW-R	5’-GGGGACCACTTTGTACAAGAAAGCTGGGTATCACCGAGGAAGAGCTCGC-3’
TPR2-GW-F	5’-GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTCGTCTTTGAGCAGAGAG-3’
TPR2-GW-R	5’-GGGGACCACTTTGTACAAGAAAGCTGGGTATTACCTTTGAATCTGATCCGAA-3’
SMXL6ΔEAR-F	5’-AAGGTGCAACGTTCATATGTGAATGAAACAGAATTT-3’
SMXL6ΔEAR-R	5’-AAATTCTGTTTCATTCACATATGAACGTTGCACCTT-3’
SMXL7ΔEAR-F	5’-AAGTCTCAGCGTTCGTTTGTGGATGAGATTGAAGCA-3’
SMXL7ΔEAR-R	5’-TGCTTCAATCTCATCCACAAACGAACGCTGAGACTT-3’
SMXL8ΔEAR-F	5’-AGAACAACTAATGGAGTTGCTCAAGAAACCGAAATC-3’
SMXL8ΔEAR-R	5’-GATTTCGGTTTCTTGAGCAACTCCATTAGTTGTTCT-3’
SMXL6DEL-F	5’-CGGTTACGTAATCCACCACGAATTTGTCATCAAGGGAAC-3’
SMXL6DEL-R	5’-GTTCCCTTGATGACAAATTCGTGGTGGATTACGTAACCG-3’
SMXL6-GAL4-F	5’-gcgtcgacATGCCGACGCCGGTGACT-3’
SMXL6-GAL4-R	5’-ggggtaccTCACCATATCACATCCACCTT-3’
SMXL7-GAL4-F	5’-gcgtcgacATGCCGACACCAGTAACCAC-3’
SMXL7-GAL4-R	5’-ggggtaccTCAGATCACTTCGACTCTCG-3’
SMXL8-GAL4-F	5’-gcgtcgacATGCCAACGGCGGTGAATG-3’

SMXL8-GAL4-R	5’-ggggtaccCTACTGAGATTTTACAAAGAACA-3’

Primers for genotyping:

***smxl6*LP**	5’-AGCCAGAGAAAGACTCGAACC-3’
***smxl6*RP**	5’-TCAGATCCGAATCGTGAGTTC-3’
***smxl7*LP**	5’-CGTATTAGCCTCTCGGATTCC-3’
***smxl7*RP**	5’-GATCAAGAAACGAACGCTGAG-3’
***smxl8*LP**	5’-TAGCGAAACAATGCTTAACGG-3’
***smxl8*RP**	5’-TGGTGAGTAACTGCAAATCCC-3’
***max3-9*-F**	5’-AGGTGTATTTAAGATGCCA-3’
***max3-9*-R**	5’-CACAAAATGTGAAGTTGCTT-3’
***max2-1*-F**	5’-TCGCTCTCTACCCAAAG-3’
***max2-1*-R**	5’-GGCTACACGAACCAACT-3’
***d14*LP**	5’-AAGAATATGGCAAGTGCAAC-3’
***d14*RP**	5’-GATGATTCCGATCATAGCG-3’
LBb1	5’-GCGTGGACCGCTTGCTGCAACT-3’
LB1	5’-GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC-3’
L4_WiscLoxHS	5’-TGATCCATGTAGATTTCCCGGACATGAAG-3’

Primers for RT-qPCR:

Q-ACT2-F	5’-GCACCACCTGAAAGGAAGTACA-3’
Q-ACT2-R	5’-CGATTCCTGGACCTGCCTCATC-3’
Q-SMXL6-1F	5’-CCAATCACAGCCTCTACTA-3’
Q-SMXL6-1R	5’-TGCTACTCAATGGAACTCT-3’
Q-SMXL6-2F	5’-CGGAGTCGTATCATCTTCA-3’
Q-SMXL6-2R	5’-CACAATCGGATCGTCAAG-3’
Q-SMXL7-1F	5’-CCAGTGATTGTCATGTTCTT-3’
Q-SMXL7-1R	5’-TCCTCCTGTCTTCTCTTATTG-3’
Q-SMXL7-2F	5’-TGGGTTAAGTGTAGTTAGTATAAAG-3’
Q-SMXL7-2R	5’-CCATCCCTGACTTCAATCT-3’
Q-SMXL8-1F	5’-CCGTACCAAGCCTGAATT-3’
Q-SMXL8-1R	5’-GATACACCAACAAGCAGAG-3’
Q-SMXL8-2F	5’-AGAAGCATCCTACGCATTA-3’
Q-SMXL8-2R	5’-TTACGAACACGAGCACAT-3’
Q-BRC1-F	5’-CCAGTGATTAACCACCATC-3’
Q-BRC1-R	5’-GCCGAAGGAGTAATGAAG-3’
Q-MAX4-F	5’-GTCTCAACAAAGATACCTTCATT-3’
Q-MAX4-R	5’-CACCACAATCCGTTCCTT-3’
Q-HB53-F	5’-ACCAACAGTTCAAGTTCATC-3’
Q-HB53-R	5’-ACATACAAACCATCCCAATAC-3’