Supplemental Information

Strigolactone- and Karrikin-Independent
SMXL Proteins Are Central Regulators
of Phloem Formation

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Figure S1. Related to Figure 1. Gene transcription in smxl3-1, smxl4-1 and smxl5-1 and SMXL3, SMXL4 and SMXL5 promoter activity as well as the stele cell number in smxl4;smxl5 roots.

A  RT-PCR analysis of SMXL3, SMXL4 and SMXL5 transcription in T-DNA insertion lines. Primers were designed to flank the T-DNA insertions as shown in B. ACT2 was used as ubiquitously expressed control gene.

B  Location of T-DNA insertions (white triangles) for smxl3-1 (SALK_024706, 140 bp after the ATG), smxl4-1 (SALK_037136, 3180 bp after the ATG) and smxl5-1 (SALK_018522, 2219 bp after the ATG) as defined by Sanger sequencing of genomic DNA. White boxes indicate exon regions. Small black arrows represent the primers used for RT-PCR shown in A.

C – N  Promoter activity is shown in 7 day-old seedlings. Bright field images (grey) were merged with fluorescent reporter activity (yellow). Scale bars represent 200 µm.

O – Q  Optical cross sections of 2 day-old mPS-PI stained wild type (O) and smxl4;smxl5 (P) roots 200 µm proximal to the QC. Pericycle cells are marked by yellow asterisks enclosing the stele. Scale bars represent 20 µm. Cell numbers were compared by a Student’s t-test (n = 6, p-value = 0.234 at 95% CI).
Figure S2. Related to Figure 3. Phloem-specific defects in smxl4;smxl5 roots lead to decreased source-to-sink transport and affect overall plant growth.

A – C  Xylem formation in 5 day-old cotyledons was visualized by monitoring auto fluorescence using a DAPI filter. Scale bars represent 100 µm.

D – F  After VISUAL-treatment [S1] for 6 days, xylem trans-differentiation was induced. Scale bars represent 100 µm.

G – H  2 weeks after grafting, smxl4;smxl5 root growth was not recovered by wild type shoots. 3 independent experiments (n = 15-32 for the first two experiments, n = 36-50 for the third experiment). Statistical groups indicated by letters were determined by one-way ANOVA with post-hoc Bonferroni (IC 95%). Scale bar represents 1 cm.

I  Leaves of grafted plants, propagated on soil for 3 weeks, are smaller and darker if sustained by a smxl4;smxl5 root independent from the genotype of the shoot (n = 20). Scale bar represents 1 cm.

J  Leaves accumulate more sucrose when supported by a smxl4;smxl5 root independently from the genotype of the shoot. Error bars: ± standard deviation (n = 5). Statistical groups indicated by letters were determined by one-way ANOVA with post-hoc Bonferroni (IC 95%).

K  Sugar export from fully developed smxl5 and smxl4;smxl5 leaves is not reduced. Glucose, fructose, sucrose and maltose concentrations were measured from phloem exudates (n = 5). Statistical groups indicated by letters were determined by one-way ANOVA with post-hoc Bonferroni (homogeneous variances for glucose...
and fructose) or with post-hoc Tamhane-T2 (inhomogeneous variances for sucrose and maltose) tests (IC 95%).

**L – M** 5 day-old wild type shoots carrying the SUC2:GFP transgene were grafted onto 5 day-old wild type (K) or smxl4;smxl5 (L) roots. Shown are bright field (grey) and GFP fluorescence (green) confocal overlays of root tips taken 12 days after grafting. The longest root of each seedling was imaged (n = 20 in two experiments). Scale bars represent 50 µm.

**N** Seedlings 12 days after grafting. Orange rectangles mark the root tip of the longest root which was imaged in K-L. Blue rectangles indicate the main root, which is redundant to the longest root in wild type, but shorter than the lateral roots is smxl4;smxl5. Scale bar represents 1 cm.

**O** The primary root (marked by a blue rectangle in H) of smxl4;smxl5 has lost the capacity to transport GFP to the root tip (n = 10). The absence of GFP activity is marked by a white arrow. Scale bar represents 100 µm.
Figure S3. Related to Figure 3. The SL/KAR signalling pathway does not influence protophloem formation in the RAM.

A Shown are 10 day-old seedlings. Scale bar represents 1 cm.
B Root length analysis of the lines shown in A. Error bars: ± standard deviation (4 independent experiments with n = 37-52 per replicate). One-way ANOVA with post-hoc Tamhane-T2 (CI 95%) was performed.
C Number of cortical cells in the meristematic zone (n = 17-25). Statistical groups indicated by letters were determined by one-way ANOVA with post-hoc Tamhane-T2 (CI 95%). Error bars: ± standard deviation.
D – G Confocal analyses of PI stained primary root meristems grown for 10 days. Yellow arrows indicate the end of the meristematic zone and the beginning of the elongation zone by pointing to the first rapidly elongating cortical cell [S2]. Yellow asterisks mark the QC. Scale bars represent 100 µm.
H Quantification of the distance from the QC to the first and second tangential cell division (n = 11-14). Statistical groups indicated by letters were determined by one-way ANOVA with post-hoc Tamhane-T2 on datasets of the 2nd division (inhomogeneous variances) or post-hoc Bonferroni on datasets of the 1st division (homogeneous variances) (CI 95%). Error bars: ± standard deviation.
I – L Tangential cell divisions in protophloem differentiation of 2 day-old roots. The first tangential division is marked by orange arrows, the second division by blue arrows. The QC is marked by yellow asterisks. Scale bars represent 20 µm.
M – P Differentiating protophloem strands of 2 day-old PI stained roots are shown. The second tangential cell division of the sieve element precursors are marked by blue arrows. Pink arrows indicate the beginning of the protophloem sieve element strands displaying enhanced PI staining. These were absent in smxl4;smxl5 and smxl4;smxl5;max2. Scale bar represents 20 µm.
SMXL3-YFP and SMXL4-YFP proteins are resistant to GR24-mediated degradation.

A – F 5 day-old smxl3 smxl5 (A-B) and smxl4;smxl5 (C-F) root tips of lines carrying SMXL3:SMXL3-YFP (A-B), SMXL4:SMXL4-YFP (C-D) or SMXL5:SMAX1-YFP (E-F) transgenes. Shown are overlaps of bright field (grey) and YFP-derived signals (yellow). GR24 was applied to B, D and F, whereas A, C and E show mock-treated controls. Scale bars represent 50 µm.
Supplemental Experimental Procedures

Plant material and growth conditions

*Arabidopsis thaliana* (L.) Heynh. *Col-0* plants were used as genetic background. *smxl3-1* (*SALK_024706*), *smxl4-1* (*SALK_037136*), *smxl5-1* (*SALK_018522*), *max2-1* [S3], *smxl1-2* (*SALK_128579*) [S4], *smxl2-1* (*SAIL_596_E08*) [S5], *smxl6-4* (*SALK_049115*), *smxl7-3* (*WiDsLox339_C04*) and *smxl8-1* (*SALK_025338*) [S6] mutant alleles were used for genetic analyses. Genotyping was performed by PCR using primers listed in the primer list. Genotyping of *max2-1* was done as described previously [S4]. Seeds were liquid sterilized by 70% ethanol supplemented with 0.2% Tween-20 for 15 min, washed twice with 100% ethanol and air dried under sterile conditions. Seeds were stratified in microcentrifuge tubes containing dH$_2$O at 4°C in the dark for 3 days and then sown in rows on ½ Murashige and Skoog (MS) medium-plates supplemented with 1% sucrose and grown vertically. Seedlings were either grown in long day (LD, 16 h light and 8 h dark) conditions at 21°C for 2-10 days or in short day short day (SD, 12 h light, 12 h dark) conditions at 21°C for 5 days. For measuring root lengths, seedlings were scanned by a commercial scanner and analysed using ImageJ 1.49d [S7]. When propagated on soil, SD or LD conditions were applied at 21°C and a humidity of 60%.

Serial block-face scanning electron microscopy (SBEM)

4 day-old plants were prepared, processed and imaged as described earlier [S8]. Protophloem SE strands were identified by their position in relation to the central xylem pole. Collected images were batch converted to TIFs in Digital Micrograph (Gatan Inc.). Assembly of 3D stacks, image normalization, alignment and analyses were done in Microscopy Image Browser [S9]. The longitudinal planes were visualized in Amira (FEI).

Grafting

Prior to grafting, seedlings were grown for 5 days on ½ MS-plates in short day (SD, 12 h light, 12 h dark) conditions at 21°C. The grafting procedure was performed as described before [S10].
**rac-GR24 treatments**

A stock solution of 10 mM rac-GR24 (Chiralix, Nijmegen, The Netherlands) dissolved in pure acetone was stored at -20°C. To grow seedlings directly on MS-agar supplied with the hormone, ½ MS-plates containing 2 µM rac-GR24 were prepared. Seedlings grown on ½ MS-plates containing an equivalent amount of the solvent without hormone served as reference (mock control). Seedlings were grown for 10 days prior to analysis. For protein stability assays, *smxl4;smxl5* plants carrying *SMXL5:SMXL5-YFP* or *SMXL5:SMAX1-YFP* transgenes were grown for 5 days in SD conditions on ½ MS-plates. For short-term-rac-GR24 treatments, the rac-GR24 stock (10 mM) was used 1:1000 in liquid MS-medium, resulting in a final concentration of 10 µM. In parallel, a mock-solution was prepared by using an equivalent amount of solvent (acetone). Both solutions were prepared freshly prior to the treatments. Seedlings were incubated in 60 µl solution on microscope slides. Pictures of the fluorescence signal and bright field were taken every four minutes over a time frame of 12 or 60 minutes.

**Generation of plasmids and transgenic lines**

All generated plasmids were based on the vector *pGreen0229* or *pGreen0179* and used primer sequences can be found in the primer list [S11]. *SMAX1:YFP-ER*, *SMXL3:YFP-ER*, *SMXL4:YFP-ER*, *SMXL5:YFP-ER*, *SMXL5:SMAX1-YFP*, *SMXL3:SMXL3-YFP*, *SMXL4:SMXL4-YFP* and *SMXL5:SMXL5-YFP* constructs were generated via a two- or three-step cloning procedure. In the first step *SMXL* promoter regions up- and downstream of the start and stop codons, respectively, were amplified from genomic DNA. For the *SMAX1* promoter the primer pairs *CEB5rev2/CEB5for6* and *CEB5rev3/CEB5for7* were used. Both fragments were cloned using Cfr9I/Xbal and ApaI/PstI restriction sites, respectively, resulting in the plasmid *pKG63*. For the promoter of *SMXL3* the primer pairs *p3SMXL3for/p3SMXL3rev* and *p5SMXL3for2/p5SMXL3rev* were used. Both fragments were cloned using HindIII/Xhol and SacII/Cfr9I restriction sites, respectively, resulting in plasmid *pEW17*. For the promoter of *SMXL5* the primer pairs *CEB1for2/CEB1rev2* and *CEB1for3/CEB1rev3* were used. Both fragments were cloned using Ndel/KpnI and NotI/PstI restriction sites, respectively, resulting in plasmid *pJA22*. In a second step, a fragment encoding the YFP-HDEL (yellow fluorescent protein with a signal peptide targeting the endoplasmic reticulum [S12]) was cloned in between both promoter fragments, resulting in plasmids *pKG64* (*SMAX1:YFP-ER*), *pEW18* (*SMXL3:YFP-ER*) and *pJA24* (*SMXL5:YFP-*)
To clone SMXL3:SMXL3-YFP, the SMXL3 promoter from pEW17 served as starting point to insert the SMXL3 open reading frame that was amplified from cDNA using the primers SMXL3for/SMXL3rev2 and restriction sites Cfr9/EcoRI. The YFP sequence was subsequently fused to the C-terminus of SMXL3 using primers YFPrev4/YFPrev5 and restriction sites EcoRI/EcoRV, resulting in plasmid pEW20. To clone SMXL4:SMXL4-YFP, the SMXL4 promoter regions were cloned into pGreen0229 using primer pair p5SMXL4for/p5SMXL4rev with the restriction sites BamHI/XbaI and primer pair p3SMXL4for/p3SMXL4rev with restriction sites ApaI/KpnI. The YFP sequence and the SMXL4 open reading frame were inserted using primer pairs EYFPfor/EYFPrev with restriction sites EcoRI/Cfr9I and SMXL4for/SMXL4rev with restriction sites BamHI/Cfr9I, respectively, resulting in plasmid pEW23. To clone SMXL5:SMXL5-YFP, the SMXL5 promoter of pJA22 served as starting point to insert the SMXL5 open reading frame that was amplified from cDNA using the primer pair CEB1for16/CEB1rev13 and the restriction sites NdeI/BamHI. Subsequently, the YFP sequence was fused C-terminally to the SMXL5 open reading frame by using the primer pair YFP-CEB1/ YFP/CFPrev13 and the restriction sites BamHI/NsiI, resulting in plasmid pKG52. To clone SMXL5:SMAX1-YFP, construct pKG52 served as starting point to replace the SMXL5 open reading frame by the SMAX1 open reading frame that was amplified from cDNA using the primer pair CEB5for1/CEB5rev1 and digested by Ndel/BglII. For the cloning of SMXL4:YFP-ER, a plasmid containing a YFP-HDEL fragment (pIL00) was used. Two promoter regions were amplified using the primer pairs 46F/46R and ClathF1/Clath-F2. Both promoter regions were inserted up- and downstream using the restriction sites Smal/EcoRV and SalI/Xhol, respectively, resulting in plasmid pIL46. Subsequently, wild type plants were transformed using an Agrobacterium tumefaciens-based method. The CALS7:H2B-YFP construct was introduced into smxl4;smxl5 by crossing and was described earlier in [S8].

Microscopy

For studying reporter activities, the Leica TCS SP5 II (Leica) was used. YFP (yellow fluorescent protein) was excited by an argon laser at 514 nm and the emission detected in a range of 520-540 nm. GFP (green fluorescent protein) was excited by an argon laser at 488 nm, collecting the emission between 500-575 nm. The cell membrane dye FM® 4-64 Dye (Thermo Fisher Scientific) was used to visualize cell borders in seedlings. The dye was diluted 1:1000 in sterile tap water and seedlings incubated for 2 min. mPS-PI stained roots
were excited with 561 nm (DPSS laser) and wavelengths $>660$ nm were detected. 3D images were generated out of Z-stacks using Fiji/ImageJ [S7] in combination with UCSF Chimera 1.10.2. (University of California, San Francisco, supported by NIGMS P41-GM103311) [S13].

**mPS-PI staining and aniline staining**
The mPS-PI staining of roots was carried out as described before [S14]. The aniline staining was performed as described before [S15].

**Vascular Cell Induction Culture System Using Arabidopsis Leaves (VISUAL)**
VISUAL was performed as described [S1]. RNA from cultured cotyledons was extracted using the RNeasy Mini Kit (Qiagen). Relative gene expression was calculated by quantitative PCR using AT1G64230 (UBC28) as reference gene. Three independent quantitative PCR experiments were used for the statistical analysis. Aniline staining was performed as described before [S15]. For visualizing xylem, auto fluorescence of cotyledons was used as described in [S16]. As phloem-associated genes for RT-PCR analysis, *SIEVE ELEMENT OCCLUSION-RELATED1 (SEOR1)* [S17], *ALTERED PHLOEM DEVELOPMENT (APL)* [S18], *NAC45/86-DEPENDENT EXONUCLEASE-DOMAIN PROTEIN 4 (NEN4)* [S8], *NAC DOMAIN CONTAINING PROTEIN 86 (NAC086)* [S8] and *CALS7* [S19] were used. *IRREGULAR XYLEM 3 (IRX3)*, *MYB DOMAIN PROTEIN 46 (MYB46)* and *XYLEM CYSTEINE PEPTIDASE1 (XCP1)* [S1] were used as xylem markers.

**Sugar measurements by Ion Chromatography**
For phloem exudate analysis, fully developed rosette leaves of 6.5 week old plants (grown for 3 weeks in SD followed by 3.5 weeks in LD) were harvested at the end of the light cycle. Phloem exudates were collected in 15 mM EDTA (pH 7.25) for 16 h in a water saturated atmosphere in the dark prior to analysis [S20]. As a control, phloem exudates were collected in 5 mM CaCl$_2$, which is known to block SE function. These controls yielded sugar concentrations below the detection limit and therefore ensured that all measured sugars originated from active phloem transport. For sugar measurements in leaf tissues, 19-day old grafted seedlings were grown on soil for 3 weeks to the rosette stage. For each sample, three fully developed leaves from individual plants were pooled into one sample. Five
samples (biological replicates) were collected per grafted combination. Tissue samples were immediately frozen in liquid nitrogen and ground using a porcelain mortar prior to analysis. Soluble sugars were extracted and determined as described before [S21].

**Statistical analysis**
Statistical analyses were performed using IBM SPSS Statistics for Windows, Version 22.0. Armonk, NY: IBM Corp. Means were calculated from measurements with sample sizes as indicated in the respective figure legends. In general, all displayed data represents at least three independent, technical repetitions, unlike otherwise indicated. Error bars represent ± standard deviation. All analysed datasets were prior tested for homogeneity of variances by the Levene statistic. Significant differences between two datasets were calculated by applying a Welch’s t-tests or Student’s t-test depending on the homogeneity of variances. The significance thresholds were set to p-value < 0.05 (indicated by one asterisk) or p-value < 0.001 (indicated by two asterisks). For multiple comparisons between three or more datasets, a One-way ANOVA was performed, using a confidence interval (CI) of 95% and a post-hoc Tukey HSD for comparisons of five or more data sets of homogenous variances, a post-hoc Bonferroni for comparisons of four or less data sets of homogenous variances or a post-hoc Tamhane-T2 in case variances were not homogenous.
| Use     | Name                  | Primer name                  | Primer sequence (5’ → 3’)                  |
|---------|-----------------------|------------------------------|--------------------------------------------|
| Genotyping | smax1-2              | SALK_128579-LP SALK_128579-RP | GTGCCAAGCTTTAGGCTGAG AAGCTAGCTTTTCAGTCTCCG |
|          | smax2-1              | SALK_956_E08-LP SALK_956_E08-RP | GCTCCAAAGCTTATCAAACAC CACTTCAGTGCAGCTTC |
|          | smxi3-1              | SALK_024706_LP SALK_024706_RP | CCCTACACAGCTTCTCAGAG ACAAAGAATAAAGTCGAG   |
|          | smxi4-1              | SALK_037136-LP SALK_037136-RP | TGAAGCCTGAGAGATCTGAG ACAAGAATTGACGTGAG    |
|          | smxi5-1              | SALK_018522-LP SALK_018522-RP | TGTCCTATTGAGGCAAAACCC AATGTGGAAGAATTCGAG   |
|          | smxi6-4              | SALK_050363-LP SALK_050363-RP | AGCCAGAGAAGACATCGACA TTCGAAATATTACGATGAG   |
|          | smxi7-3              | WiscDsLox339C04_LP WiscDsLox339C04_RP | GAATCAGAAATTTCTCTGATGCC GCTACTAGCTCTCGATTCC |
|          | smxi8-1              | SALK_025338_LP SALK_025338_RP | AATGCACAAATTTCTCTGATGCC GCTACTAGCTCTCGATTCC |
|          | WiscDsLox_insertion  | WiscDsLox-LB-p745            | AACGTCGGCAATGCTATTTAGTTAGTGTC              |
|          | SAIL_insertion       | SAIL_LB3                     | TAGCATCTGACTTTCTACAACTCATCGATACAC          |
|          | SALK_insertion       | SALK_LBa1                    | TGGTTCACGTCATGGGCAATTCC                   |
|          | max2-1               | max2-1 dCAPS F max2-1 dCAPS R | TGGTTCACGTCATGGGCAATTCC                    |
|          | IRX3                 | IRX3-228F                    | TCCGGGCTGGTAGACCTTCTTTA                   |
|          | MYB46                | MYB46_q_PCR_fwd MYB46_q_PCR_rvs | CTGAGACTCTTGACTGGTCAGG GACATCGAGCTCTCGACTTTCC |
|          | XCP1                 | XCP1_q_PCR_fwd XCP1_q_PCR_rvs | TCCAGTACATATTTCTGACCGCG TTTAGGCGCATCTCGAG |
|          | SEOR1                | SEOR1_qPCR_FWD SEOR1_qPCR_rvs | TGAAGACAAACACGCGCTC GCAATGTGACATTCGAGAG   |
|          | APL                  | APLqPCRfor APLqPCRrev        | CACATCTACGAGAATTCGAGCTT GCAACCTTCCTGACCTTC |
|          | NEN4                 | NEN4_FWD NEN_rds             | TGGAGACTCTGCTGCTTTTG TGAGATGGAAGATACCTCGAG |
|          | NAC086               | NAC086_fwd NAC086_rvs        | GAGTCGACAGATATCTCAGGAC GAGACTACATCCCAGGTCAG |
|          | CALS7                | CSL7_fwd CSL7_rds            | GTCTGGTGTTTCTCTCTTAC CTTCGCTACCATCCAGAG   |
|          | UBC28                | UBC28qf for UBC28qrev        | TCCGAGGAAGATGCTTACAACTTCTGACAGT ATGGTACGAGAAGACACCCACGCCGTCAGAATA |
| qPCR     | smxi3-1              | SMXLE3_p2 SMXLE3_cDNA        | CACCTCCCATATAGACGCGC GAACCTAGTGGAAAAAGGAG |
|          | smxi4-1              | SMXL4_p3 SMXL4_p1            | TGTTGGGTAGACAAAGTTCC GAAACCGGAATAGTGGAGT |
|          | smxi5-1              | SMXL5_p3 CEB1for20           | GCTGATGCGCTGCAACCTT TGTGGGACTTCATCTGAGTC |
|          | ACT2                 | qACT2f qACT2r                | GCCATCCAAAGCTTTCTCTCT ACCTGATTACGAGACAG   |
| RT-qPCR  | smxi3-1 (spanning SALK T-DNA) | SMXLE3_p2 SMXLE3_cDNA | CACCTCCCATATAGACGCGC GAACCTAGTGGAAAAAGGAG |
|          | smxi4-1 (spanning SALK T-DNA) | SMXL4_p3 SMXL4_p1 | TGTTGGGTAGACAAAGTTCC GAAACCGGAATAGTGGAGT |
|          | smxi5-1 (spanning SALK T-DNA) | SMXL5_p3 | GCTGATGCGCTGCAACCTT TGTGGGACTTCATCTGAGTC |
|          | ACT2                 | qACT2f qACT2r                | GCCATCCAAAGCTTTCTCTCTACCTGAGATTACGAGACAG |
| Molecular cloning                                      | \[\text{SMAX1:YFP-ER}\]               | \[\text{SMAX1-YFP}\]                     |
|------------------------------------------------------|---------------------------------------|------------------------------------------|
| CEB5rev2                                             | ACTACCCGGGATCATATGCGTTCTGTTATTCCATCCAC | ACTACATATGCGAACAGTGTTATACGATTCCAGT    |
| CEB5for6                                            | ACTAGGGGGCGCGTTACTTCTTTAGCTTCAAC      | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| CEB5for7                                            | ACTACTGCAAGGTTTGAACAGAGATTG          | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| CEB5rev3                                            | ACTAGGGGGCGCGTTACTTCTTTAGCTTCAAC      | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| p3SMXL3rev                                          | ACTAAAGCTTTCACTAAAGGATGCGATGATG      | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| p3SMXL3for                                          | ACTACTGCAAGGTTTGAACAGAGATTG          | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| p5SMXL3rev                                          | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| p5SMXL3for2                                         | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| p5SMXL4rev                                          | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| p5SMXL4for2                                         | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| p5SMXL4rev2                                         | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| p5SMXL4rev3                                         | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| CEB1for2                                             | ACTTAGTAACACTTTGCCACTTTAGCTGCGTCCAACT | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| CEB1rev2                                             | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| CEB1for3                                             | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| CEB1rev3                                             | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| SMXL3for                                            | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| SMXL3for2                                           | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| YFPrev4                                              | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| YFPrev5                                              | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| SMXL4rev                                             | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| SMXL4for2                                           | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| SMXL4for3                                           | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| SMXL5for                                            | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| SMXL5rev2                                           | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| YFP/CEB1                                             | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| YFP/CFPrev13                                         | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| SMXL5for                                            | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| SMXL5rev2                                           | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| YFP/CFPrev13                                         | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       | ACTAGATCTCTCATGCGTTATTAGCTGTTAT       |
| SMXL5:SMAX1-YFP                                      | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| CEB5for1                                            | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
| CEB5rev1                                             | ACTACCCGGGAGGAGACACCTAATTAACACACCTAAC | ACTACAGCCGCGCAAGTGGAGAGATTG          |
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