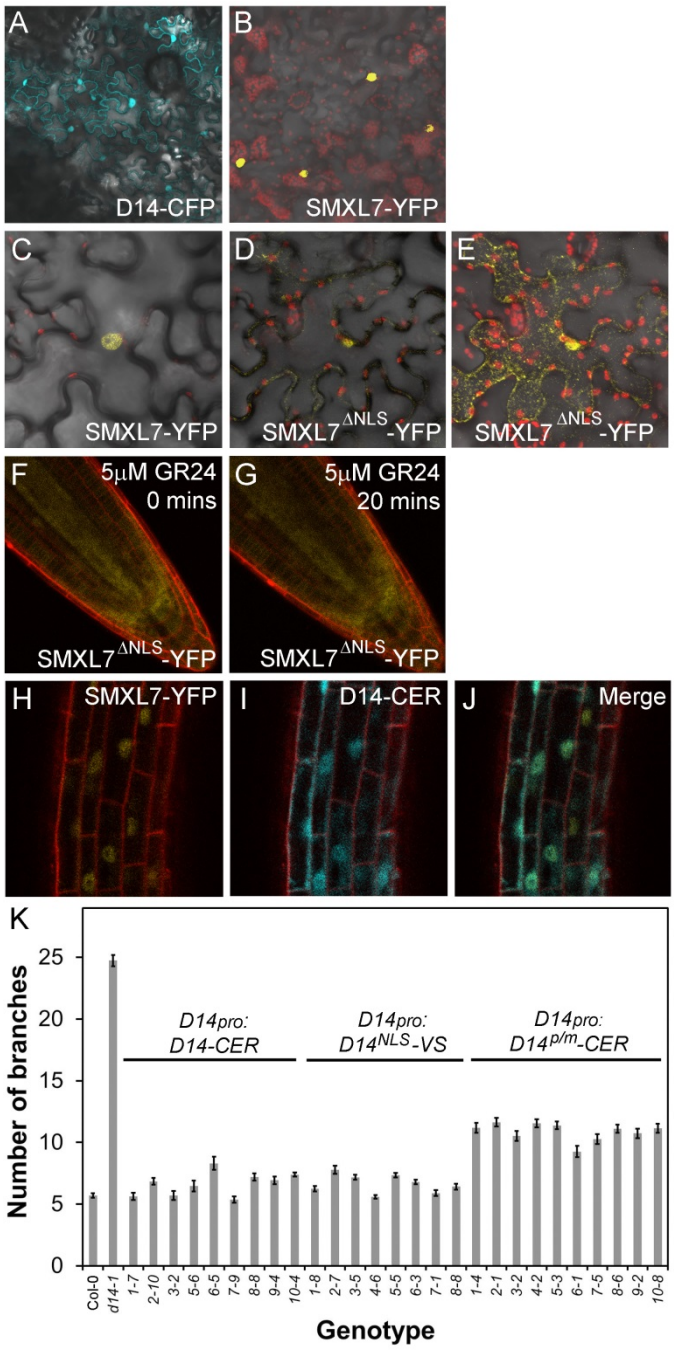


Supplemental Figure 1: SL signalling components function in the nucleus

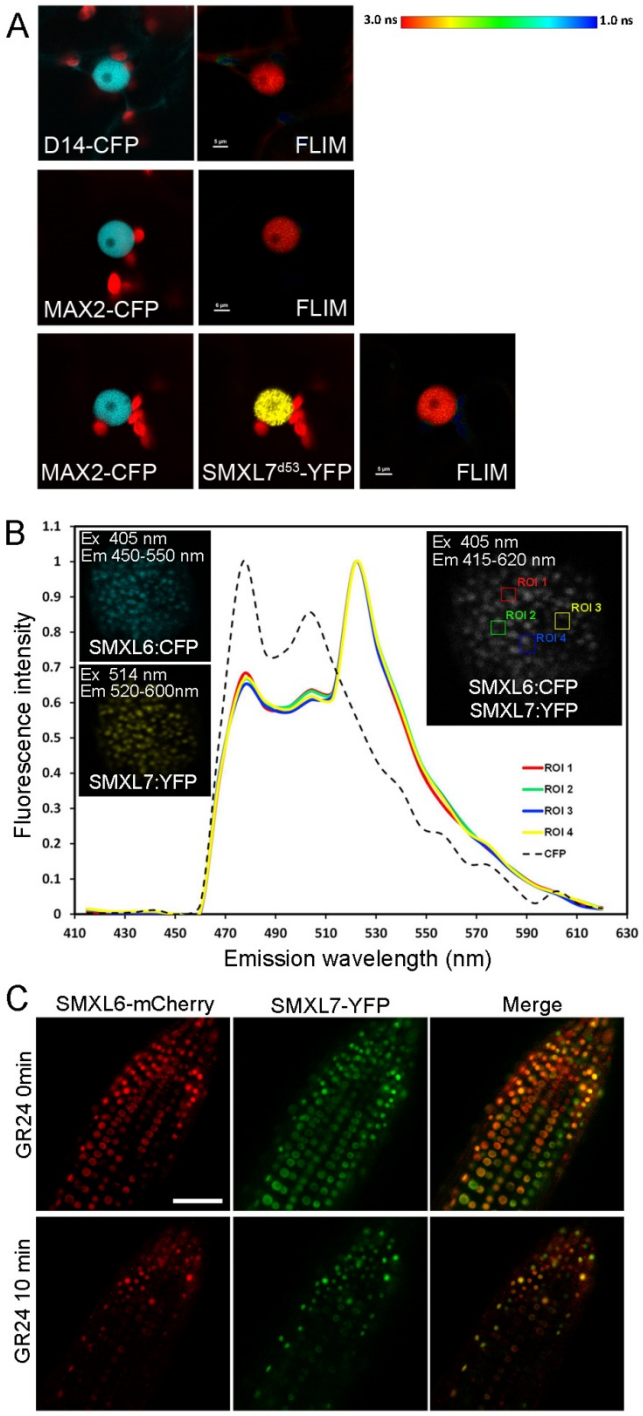
A-B): Maximum intensity confocal projections of fields of *N. benthamiana* epidermal cells expressing D14-CFP (A) and SMXL7-YFP (B) from the *35S* promoter.

C-E): Sub-cellular localization of SMXL7-YFP (C) and SMXL7DNLS-YFP (D-E) expressed in *N. benthamiana* epidermal cells from the *35S* promoter. C and D are single confocal slices, E is a maximum intensity projection of multiple slices through the same cell shown in D.

F-G) Localization of SMXL7$^{\Delta NLS}$-YFP in an Arabidopsis root meristem at 0 and 20 minutes after treatment with 5μM *rac*-GR24. Image F is also shown in Figure 2. Plants are from a homozygous transgenic line in which the fusion protein is expressed from the *35S* promoter.

H-J): Co-localization of SMXL7-YFP (H) and D14-CERULEAN (I) in an Arabidopsis root; merged image in (J). Plants are homozygous double transgenic lines in which the fusion proteins are expressed from the *35S* promoter.

K) Rosette branching levels in Col-0, *d14-1, d14-1 D14:D14-CERULEAN* (9 independent homozygous lines), *d14-1 D14:D14^{NLS}-VENUS* (9 independent homozygous lines) and *d14-1 D14:D14$^{palm/myr}$-CERULEAN* (10 independent homozygous lines). Plants were grown in short days for 4 weeks, then grown in long days until the inflorescence stem was 10cm long, and then decapitated. Primary rosette branches were counted 10 days later (Greb et al, 2003). Extracts of this complete dataset are shown in Figure 2. n=13-20 error bars indicate s.e.m.

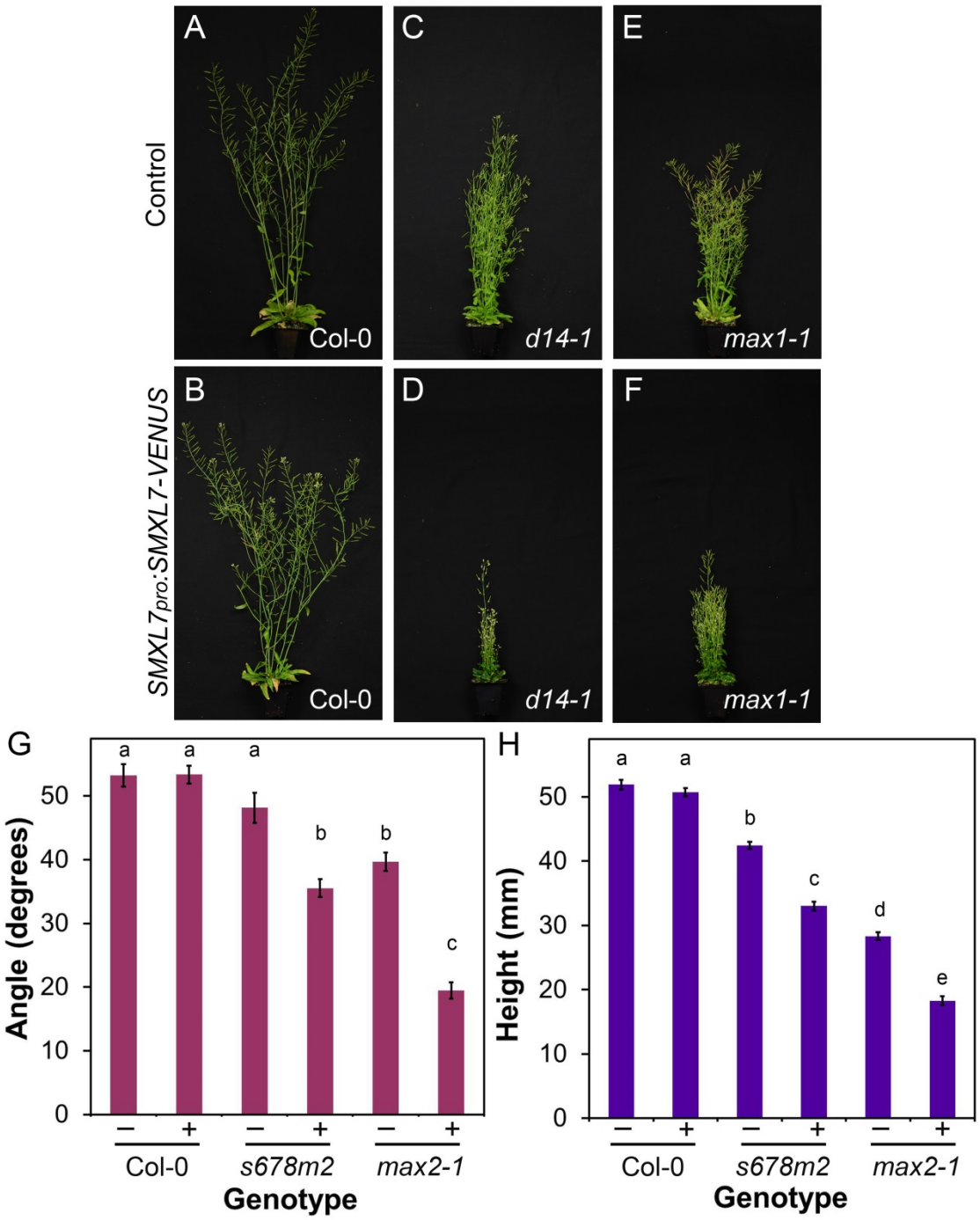


Supplemental Figure 2: SMXL7 physically interacts with D14 in a SL-dependent manner

A) Controls for Figure 3, showing lack of FRET in *N. benthamiana* epidermal cells singly-transfected with D14-CFP and MAX2-CFP as visualized by FLIM (top and middle row), and showing lack of FRET between MAX2-CFP and SMXL7^{d53}-YFP (bottom row). See Figure 3 for more detail. Scale bars indicate 5μM.

B) Detection of FRET between SMXL6-CFP and SMXL7-YFP using spectral analysis in doubly-transfected *N. benthamiana* epidermal cells, driven by the *35S* promoter. SMXL6 and SMXL7 co-localize in the nucleus. The SMXL6-CFP in four randomly selected regions of interest (ROI) was excited using a 405 nm laser line, and the resulting emission spectrum recorded. In addition to the expected CFP emission spectrum (dotted line) measured from a cell expressing only SMXL6-CFP, each region of interest showed an emission peak at 520-530 nm, consistent with emission of YFP-type spectra (coloured lines), implying FRET between SMXL6 and SMXL7.

C) Co-localization of SMXL6-mCherry and SMXL7-YFP in an Arabidopsis root meristem, and co-degradation in response to 10 minutes treatment with 5μM rac-GR24 (bottom row). Plants are doubly homozygous for transgenes driving expression of the fusion proteins from the *35S* promoter. Scale bar indicates 100μM.

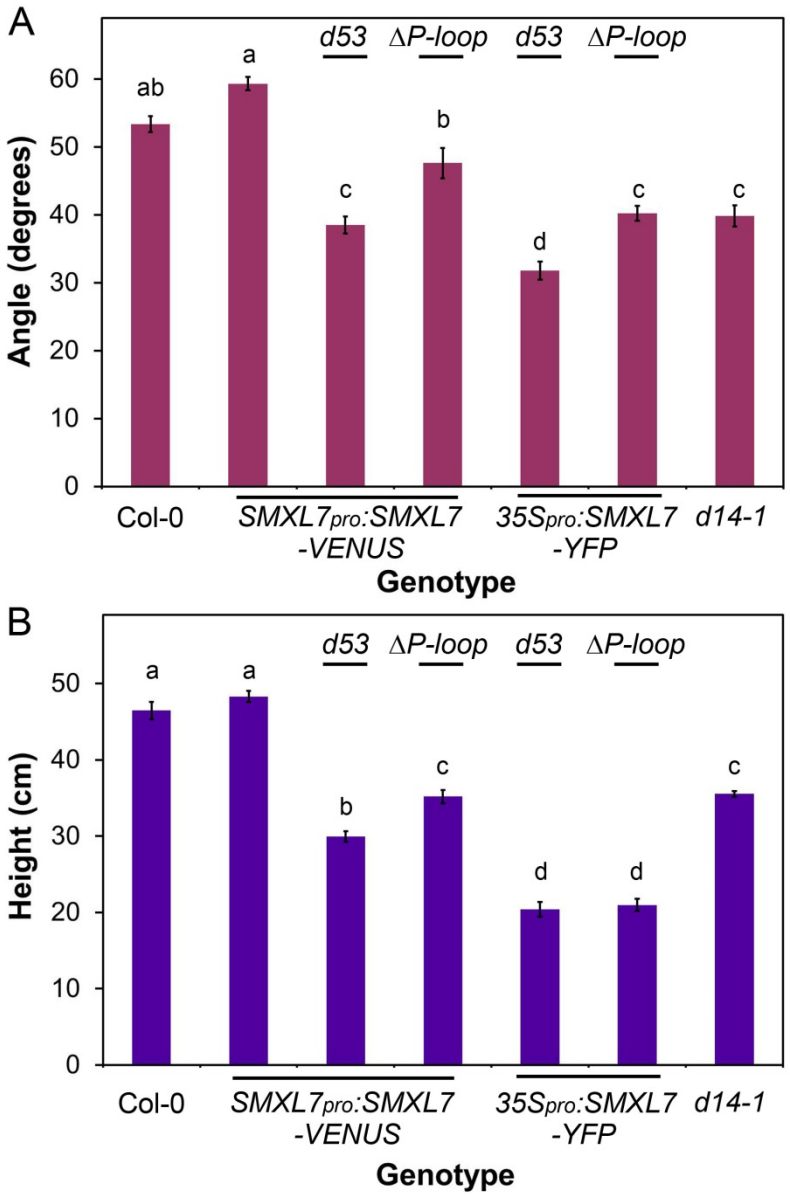


Supplemental Figure 3: Effect of SMXL7 dose on development.

A-F): Adult shoot morphology in Col-0 (A,B), *d14-1* (C,D) and *max1-1* (E,F) untransformed (A,C,E) or homozygous for *SMXL7$_{pro}$:SMXL7-VENUS* (B,D,F).

G): Branching angle in Col-0, *smxl6-4 smxl7-3 smxl8-1 max2-1* and *max2-1* untransformed ('-') or homozygous for *SMXL7$_{pro}$:SMXL7-VENUS* ('+'). n=18-39, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, $p<0.05$).

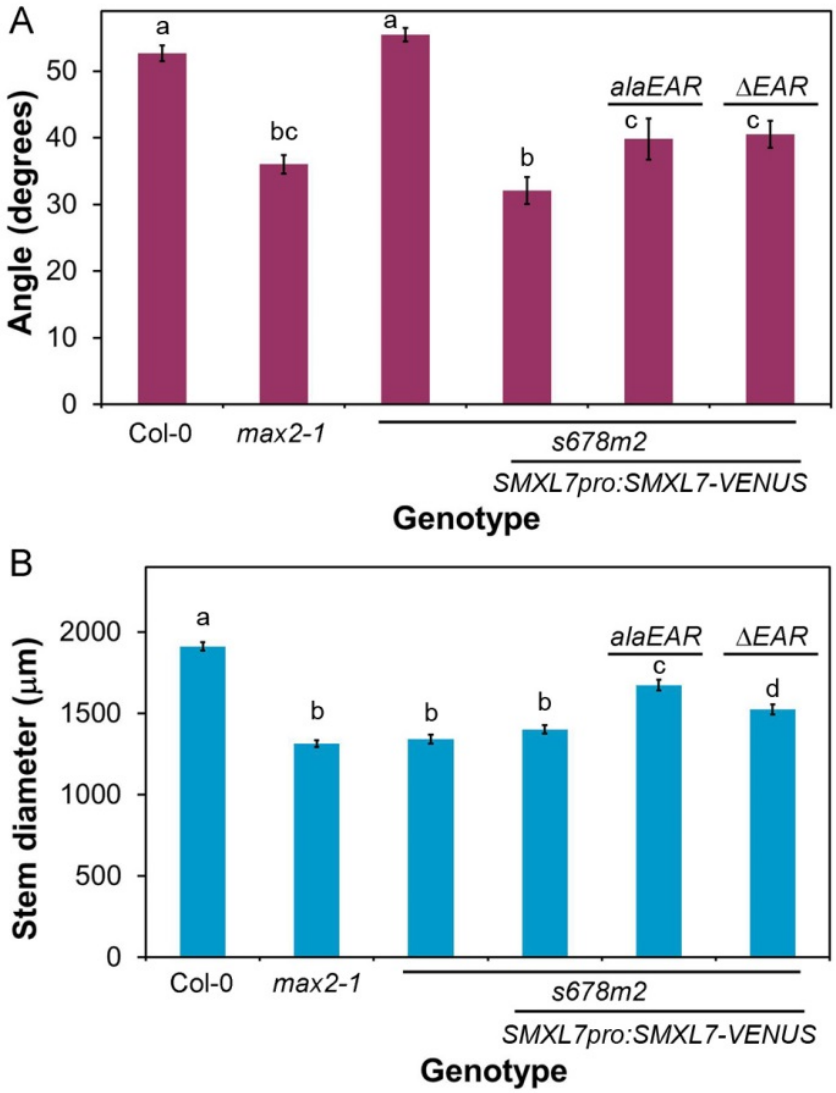
H): Height of the primary inflorescence stem in Col-0, *smxl6-4 smxl7-3 smxl8-1 max2-1* and *max2-1* untransformed ('-') or homozygous for *SMXL7$_{pro}$:SMXL7-VENUS* ('+'), measured at proliferative arrest. n=20-24, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, $p<0.05$).



Supplemental Figure 4: Effect of SMXL7 stabilization on development.

A): Branching angle in untransformed Col-0, Col-0 transformed with *SMXL7*$_{pro}$*:SMXL7-VENUS*, *SMXL7*$_{pro}$*:SMXL7*^{d53}*-VENUS*, *SMXL7*$_{pro}$*:SMXL7*$^{\Delta P\text{-}loop}$*-VENUS, 35S*$_{pro}$*:SMXL7*^{d53}*-YFP*, *35S*$_{pro}$*:SMXL7*$^{\Delta P\text{-}loop}$*-YFP (*hemizygous), and in *d14-1.* n=17-25, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, p<0.05).

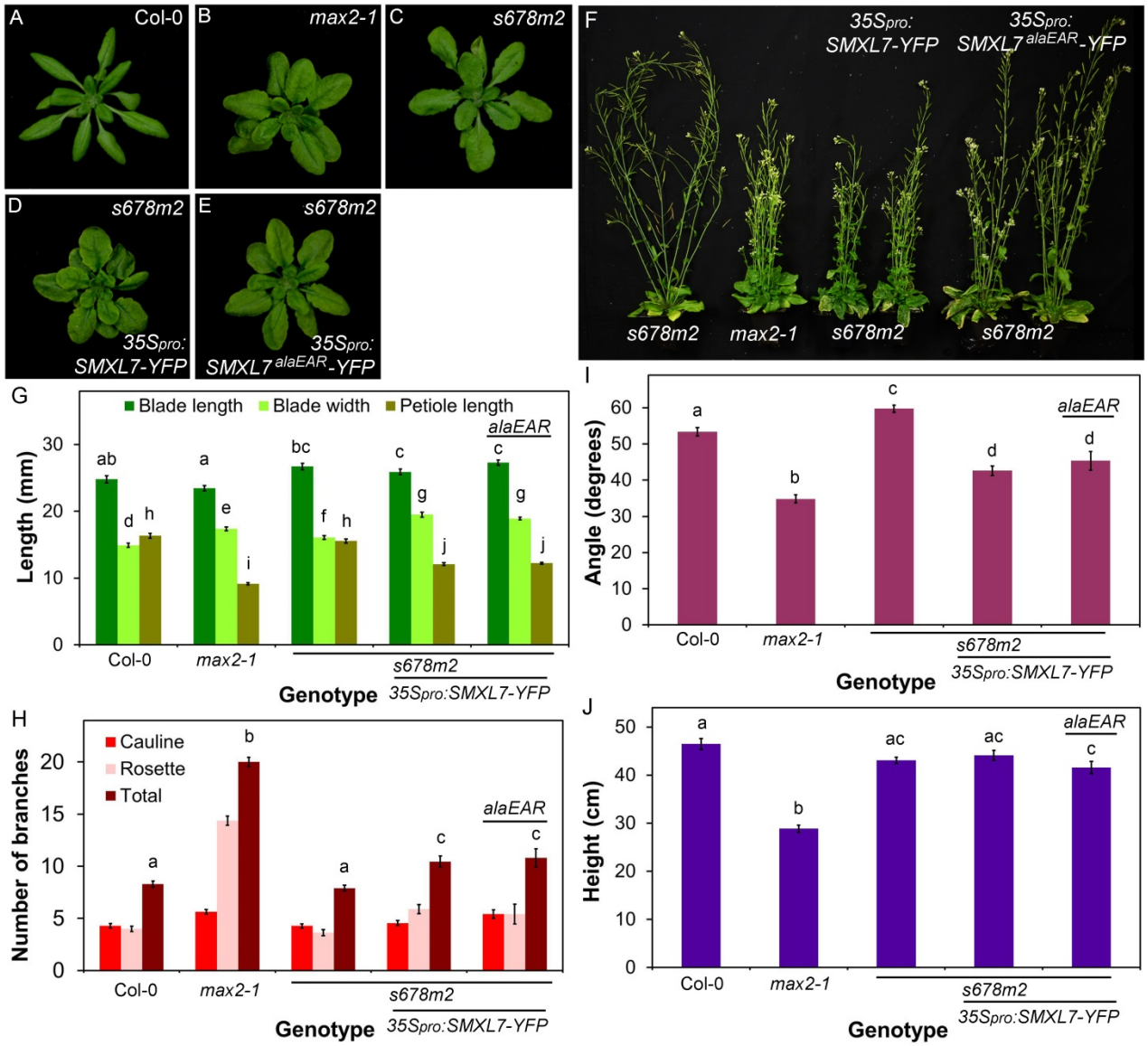
B): Height of the primary inflorescence stem in untransformed Col-0, Col-0 transformed with *SMXL7*$_{pro}$*:SMXL7-VENUS*, *SMXL7*$_{pro}$*:SMXL7*^{d53}*-VENUS*, *SMXL7*$_{pro}$*:SMXL7*$^{\Delta P\text{-}loop}$*-VENUS, 35S*$_{pro}$*:SMXL7*^{d53}*-YFP*, *35S*$_{pro}$*:SMXL7*$^{\Delta P\text{-}loop}$*-YFP (*hemizygous), and in *d14-1,* measured at proliferative arrest. n=10, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, p<0.05).



Supplemental Figure 5: Effects of SMXL7 are partially EAR-independent

A): Branching angle in Col-0, *max2-1*, untransformed *smxl6-4 smxl7-3 smxl8-1 max2-1* (*s678m2*) or *s678m2* homozygous for $SMXL7_{pro}$*:SMXL7-VENUS*, $SMXL7_{pro}$*:*$SMXL7^{alaEAR}$*-VENUS* and $SMXL7_{pro}$*:*$SMXL7^{\Delta EAR}$*-VENUS*. n=12-16, bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, $p<0.05$).

B): Diameter (μm) of the basal internode of the primary inflorescence stem in Col-0, *max2-1*, untransformed *smxl6-4 smxl7-3 smxl8-1 max2-1* (*s678m2*) or *s678m2* homozygous for *SMXL7:SMXL7-VENUS*, $SMXL7_{pro}$*:*$SMXL7^{alaEAR}$*-VENUS* and $SMXL7_{pro}$*:*$SMXL7^{\Delta EAR}$*-VENUS*, measured at proliferative arrest. n=12-16, bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, $p<0.05$).



Supplemental Figure 6: Effects of SMXL7 are partially EAR-independent

A-E): Rosette leaf morphology in Col-0 (A), *max2-1* (B), untransformed *smxl6-4 smxl7-3 smxl8-1 max2-1* (*s678m2*) (C) or *s678m2* homozygous for $35S_{pro}$*:SMXL7-YFP* (D) or $35S_{pro}$*:SMXL7*^{alaEAR}*-YFP* (E).

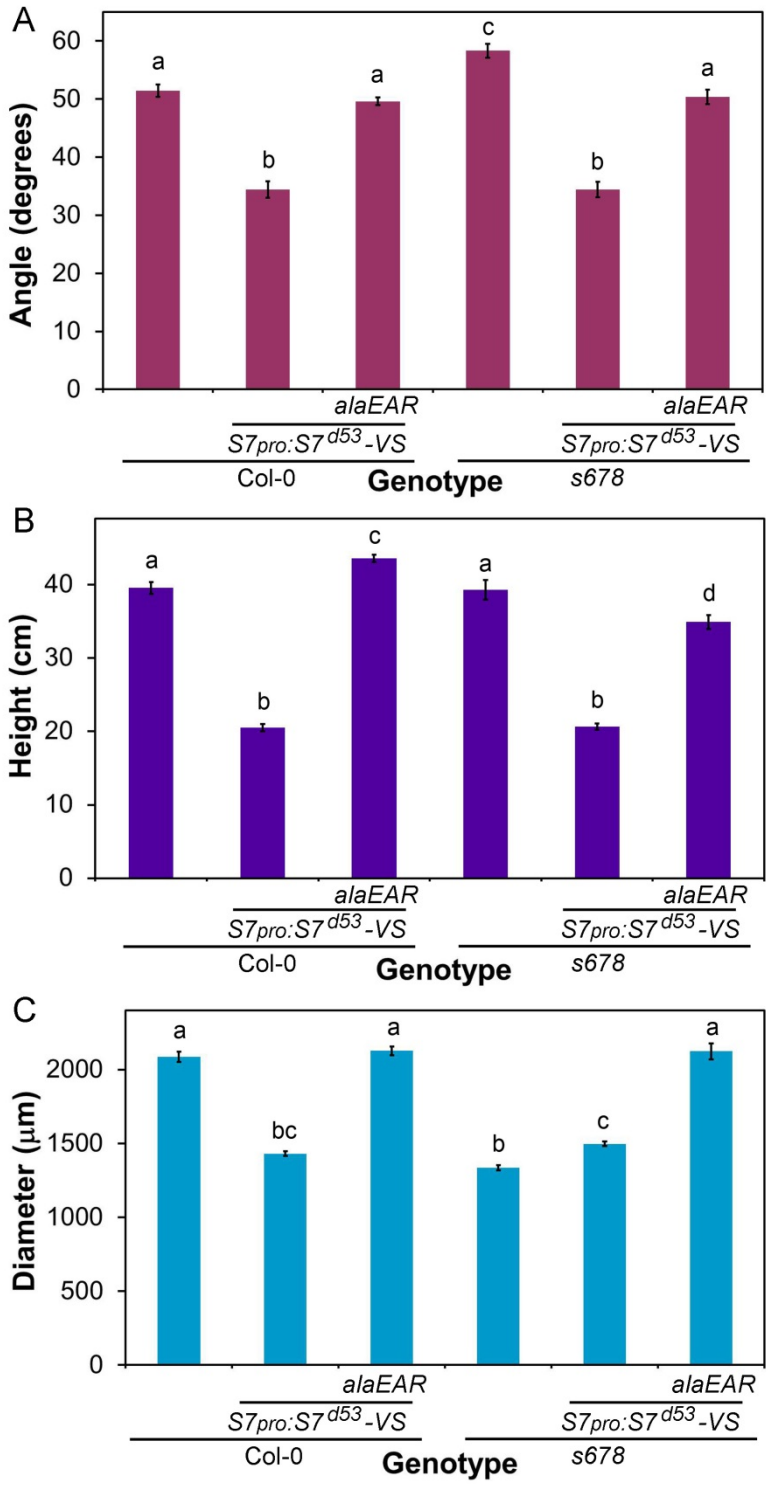
F): Adult shoot morphology in *max2-1*, untransformed *smxl6-4 smxl7-3 smxl8-1 max2-1* (*s678m2*) or *s678m2* homozygous for $35S_{pro}$*:SMXL7-YFP* or $35S_{pro}$*:SMXL7*^{alaEAR}*-YFP*.

G): Leaf blade length, blade width and petiole length in the 7th leaf of Col-0, *max2-1*, untransformed *smxl6-4 smxl7-3 smxl8-1 max2-1* (*s678m2*) or *s678m2* homozygous for $35S_{pro}$*:SMXL7-YFP* or $35S_{pro}$*:SMXL7*^{alaEAR}*-YFP.* n=10-11, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, p<0.05).

H): Number of cauline, rosette and total primary branches of Col-0, *max2-1*, untransformed *smxl6-4 smxl7-3 smxl8-1 max2-1* (*s678m2*) or *s678m2* homozygous for with $35S_{pro}$*:SMXL7-YFP* or $35S_{pro}$*:SMXL7*^{alaEAR}*-YFP.* n=9-11, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, p<0.05).

I): Branching angle in Col-0, *max2-1*, untransformed *smxl6-4 smxl7-3 smxl8-1 max2-1* (*s678m2*) or *s678m2* homozygous for $35S_{pro}$*:SMXL7-YFP* or $35S_{pro}$*:SMXL7*^{alaEAR}*-YFP.* n=17-20, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, p<0.05).

J): Height of the primary inflorescence stem in Col-0, *max2-1*, untransformed *smxl6-4 smxl7-3 smxl8-1 max2-1* (*s678m2*) or *s678m2* homozygous for $35S_{pro}$*:SMXL7-YFP* or $35S_{pro}$*:SMXL7*^{alaEAR}*-YFP*, measured at proliferative arrest. n=9-11, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, p<0.05).

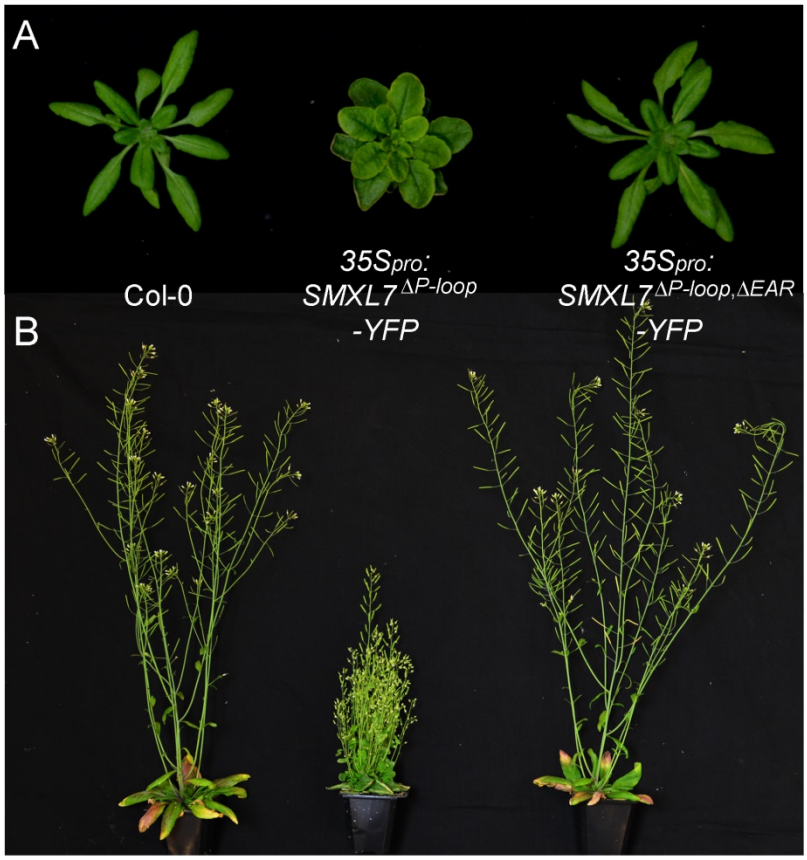


Supplemental Figure 7: Loss of the EAR motif counteracts SMXL7 stabilization

A): Branching angle in Col-0 and *smxl678*, either untransformed or homozygous for *SMXL7*$_{pro}$*:SMXL7*^{d53}*-VENUS* or *SMXL7*$_{pro}$*:SMXL7*^{d53,alaEAR}*-VENUS*. n=16-23, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, p<0.05).

B): Height of the primary inflorescence stem in Col-0 and *smxl678*, either untransformed or homozygous for *SMXL7*$_{pro}$*:SMXL7*^{d53}*-VENUS* or *SMXL7*$_{pro}$*:SMXL7*^{d53,alaEAR}*-VENUS*, measured at proliferative arrest. n=10, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, p<0.05).

C): Diameter of the basal internode of the primary inflorescence stem in Col-0 and *smxl678*, either untransformed or homozygous for *SMXL7*$_{pro}$*:SMXL7*^{d53}*-VENUS* or *SMXL7*$_{pro}$*:SMXL7*^{d53,alaEAR}*-VENUS*, measured at proliferative arrest. n=11-15, error bars indicate s.e.m, bars with the same letter are not significantly different from one another, (ANOVA + Tukey HSD, p<0.05).



Supplemental Figure 8: Loss of the EAR motif counteracts SMXL7 stabilization

A): Rosette leaf morphology in untransformed Col-0, or Col-0 homozygous for *35S$_{pro}$:SMXL7$^{\Delta P\text{-}loop}$-YFP* or *35S$_{pro}$:SMXL7$^{\Delta P\text{-}loop,\Delta EAR}$-YFP*.

B): Adult shoot morphology in Col-0, or Col-0 homozygous for *35S$_{pro}$:SMXL7$^{\Delta P\text{-}loop}$-YFP* or *35S$_{pro}$:SMXL7$^{\Delta P\text{-}loop,\Delta EAR}$-YFP*.

Variant	Position (aa)	Modification	Primers
SMXL7$^{\Delta NLS}$	85 to 117	deleted	F: CAACGACGTCATCCAGAG R: GTCTAGAGAAACGCCGAC
SMXL7$^{\Delta NTP1}$	624 to 796	deleted	F: GAACCAGTCAAATACTCCG R: TCTCGAAGCTGACAACAATTG
SMXL7$^{\Delta P\text{-}loop}$	718 to 725	deleted	F :TACATTGCTGGCGAAGTG R: TCTATCGTCAAGACTGTCTTG
SMXL7^{d53}	719 to 724	RGKTVV → T	F: AGATTACATTGCTGGCGAAGTG R: GTGAATCTATCGTCAAGACTGTCTTG
SMXL7$^{\Delta EAR}$	854 to 860	deleted	F: GATGAGATTGAAGCAAACG R: AAACGAACGCTGAGACTTAAG
SMXL7^{alaEAR}	854,856,858	LDLNLP → ADANAP	F: TGCTCCTGTGGATGAGATTGAAGCAAACG R: TTCGCATCTGCAAACGAACGCTGAGACTTAAG
SMXL7$^{\Delta P\text{-}loop,\Delta EAR}$	718 to 725 854 to 860	deleted	the same as SMXL7$^{\Delta P\text{-}loop}$ and S7$^{\Delta EAR}$
SMXL7$^{d53,\ alaEAR}$	719 to 724 854,856,858	RGKTVV → T, LDLNLP → ADANAP	the same as SMXL7^{alaEAR} and SMXL7^{d53}
SMXL7$^{\Delta NTP2}$	871 to 930	deleted	*F*: ATCCTTAAGATTCTTGCTGC *R*: CGCTTCGTCTTCGTTTGC
D14$^{palm/myr}$	after 1	added GGCFSKK	F: AGCAAGAAGAGTCAACACAACATCTT AGAAGCTCTAAATGTCC R: GAAACAGCCATTAAGCCATTAAGCCT GCTTTTTTGTACAAACTTTGG

Supplemental Table 1
Protein variants created in this study, indicating the position and type of modification, and the primers used for site-directed mutagenesis to create these variants.

Construct	Method	Binary vector	Species
$35S_{pro}$:SMXL7-YFP	Gateway	pEarleyGate101	Nb, At
$35S_{pro}$:SMXL7$^{\Delta NLS}$ -YFP	Gateway	pEarleyGate101	Nb, At
$35S_{pro}$:SMXL7$^{\Delta NTP1}$-YFP	Gateway	pEarleyGate101	Nb, At
$35S_{pro}$:SMXL7$^{\Delta P\text{-}loop}$ -YFP	Gateway	pEarleyGate101	Nb, At
$35S_{pro}$:SMXL7 ^{d53}-YFP	Gateway	pEarleyGate101	Nb, At
$35S_{pro}$:SMXL7$^{\Delta EAR}$ -YFP	Gateway	pEarleyGate101	Nb, At
$35S_{pro}$:SMXL7 ^{alaEAR} -YFP	Gateway	pEarleyGate101	Nb, At
$35S_{pro}$:SMXL7$^{\Delta P\text{-}loop,\Delta EAR}$ -YFP	Gateway	pEarleyGate101	Nb, At
$35S_{pro}$:SMXL7$^{\Delta NTP2}$-YFP	Gateway	pEarleyGate101	Nb, At
$35S_{pro}$:SMXL7-CFP	Gateway	pEarleyGate102	Nb
$SMXL7_{pro}$:SMXL7-VENUS	Gateway	pB7m34GW,0	At
$SMXL7_{pro}$:SMXL7$^{\Delta NLS}$ - VENUS	Gateway	pB7m34GW,0	At
$SMXL_{pro}$:SMXL7$^{\Delta P\text{-}loop}$ - VENUS	Gateway	pB7m34GW,0	At
$SMXL7_{pro}$:SMXL7 ^{d53}- VENUS	Gateway	pB7m34GW,0	At
$SMXL_{pro}$:SMXL7$^{\Delta EAR}$ - VENUS	Gateway	pB7m34GW,0	At
$SMXL7_{pro}$:SMXL7 ^{alaEAR} - VENUS	Gateway	pB7m34GW,0	At
$SMXL_{pro}$:SMXL7^{d53,alaEAR} -VENUS	Gateway	pB7m34GW,0	At
$SMXL7_{pro}$:GUS	Gateway	pH7m24GW,3	At
$35S_{pro}$:SMXL6-CFP	Gateway	pEarleyGate102	Nb
$35S_{pro}$:SMXL6-mCherry	Gateway	pK7m34GW,0	At
$35S_{pro}$:D14-CFP	Gateway	pEarleyGate102	Nb
$35S_{pro}$:D14-YFP	Gateway	pEarleyGate101	Nb
$35S_{pro}$:D14-CERULEAN	Gateway	pH7m34GW,0	Nb, At
$35S_{pro}$:D14^{NLS}-VENUS	Gateway	pH7m34GW,0	Nb, At
$35S_{pro}$:D14$^{palm/myr}$-GFP	Gateway	pH7m34GW,0	Nb, At
$D14_{pro}$:D14-CERULEAN	Gateway	pH7m34GW,0	At
$D14_{pro}$:D14^{NLS}-VENUS	Gateway	pH7m34GW,0	At
$D14_{pro}$:D14$^{palm/myr}$-CERULEAN	Gateway	pH7m34GW,0	At
$35S_{pro}$:MAX2-CFP	Gateway	pEarleyGate102	Nb
$35S_{pro}$:MAX2-CITRINE	Gateway	pB7m34GW,0	Nb
$MAX2_{pro}$:MAX2-GFP	Conventional	pBI101.3	At

Supplemental Table 2
List of constructs created in this study, with the method of construction and the binary vector used for agrobacterium mediated transformation indicated. The species the construct was transformed into are listed at the right; At = *Arabidopsis thaliana*, Nb = *Nicotiana benthamiana.*

Clone	Primers
$SMXL7_{pro}$	*F:* GGGGACAACTTTGTATAGAAAAGTTGTTTACAGTGTGCGATGTTGAGAC *R:* GGGGACTGCTTTTTTGTACAAACTTGTCGTCGCCGGTTTAGTTATAA
SMXL7	*F:* GGGGACAAGTTTGTACAAAAAAGCAGGCTTTATGCCGACACCAGTAACCAC *R:* GGGGACCACTTTGTACAAGAAAGCTGGGTTGATCACTTCGACTCTCGCCG
SMXL6	*F*: GGGGACAAGTTTGTACAAAAAAGCAGGCTTTATGCCGACGCCGGTGACTACG *R:* GGGGACCACTTTGTACAAGAAAGCTGGGTTCCATATCACATCCACCTTCGCCG
$D14_{pro}$	F: GGGGACAACTTTGTATAGAAAAGTTGCATTGTCCAGATACAATTC R: GGGGACTGCTTTTTTGTACAAACTTGATGTGTTTGGGTTTGAGGGA or XhoI-NotI-F: CTCGAGGCGGCCGCGTCCATTGTCCAGATACAATTCG KpnI-R: CCCGGGCCGAGGAAGAGCTCGCCGGAGAAC
D14	F: GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGAGTCAACACAACATCT R: GGGGACCACTTTGTACAAGAAAGCTGGGTTCCGAGGAAGAGCTCGCCGGA or KpnI-F: GGTACCATGAGTCAACACAACATCTTAG XmaI-R: CCCGGGCCGAGGAAGAGCTCGCCGGAGAAAC
$MAX2_{pro}$	F: GGGGACAACTTTGTATAGAAAAGTTGGATCCAGGACCATGAGACGT R: GGGGACTGCTTTTTTGTACAAACTTGGAGAAGCGGCAAATCTACAAG or SalI-F: GTCGACCTCATCATGCTTCAACGTGT BamHI-R: GGATCCGAGAAGCGGCAAATCTACAAG
MAX2	F: GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCTTCCACTACTCTCTCCGAC R: GGGGACCACTTTGTACAAGAAAGCTGCGTTGTCAATGATGTTGCGGCTGTTCAA or BamHI-F: CCGTTAGGATCCATGGCTTCCACTACTCTCTC XmaI-R: TAGGTACCCGGGGTCAATGATGTTGCGGCTG
CERULEAN	F: GGGGACAGCTTTCTTGTACAAAGTGGTAATGGTGAGCAAGGGCGAGGA R: GGGGACAACTTTGTATAATAAAGTTGTTTACTTGTACAGCTCGTCCA
CITRINE	F: GGGGACAGCTTTCTTGTACAAAGTGGTAATGGTGAGCAAGGGCGAGGA R: GGGGACAACTTTGTATAATAAAGTTGTCTTGTACAGCTCGTCCATGCC

Supplemental Table 3
Primers used for amplification of promoters, coding sequences and fluorescent protein tags used in this study.