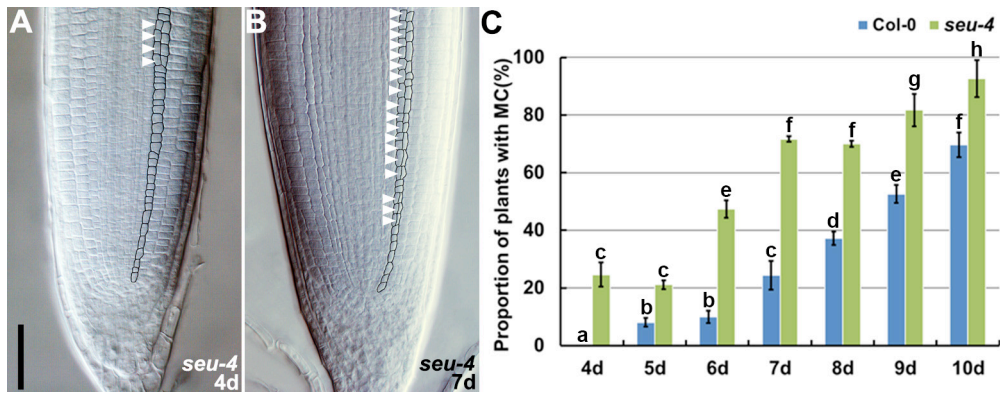


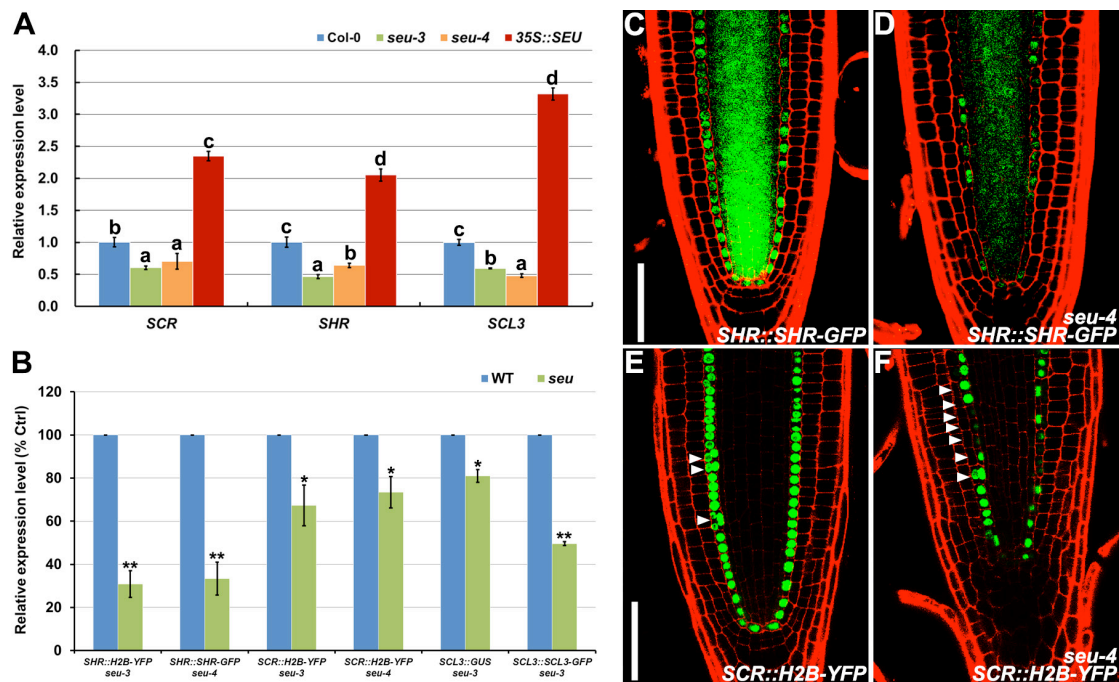
Supplemental Figure S1. Expression of *SEU* in different genetic backgrounds as indicated. (A) Schematic diagram of *SEU* protein (877 aa), which contains a LIM-domain-binding (LDB) motif and 2 Q-rich domains. Arrowheads point to the mutation sites in *seu-3* and *seu-4*. (B) qRT-PCR analysis of *SEU* transcript levels in roots of Col-0, *seu-3*, *seu-4* and 35S::*SEU* seedlings 7d after sowing. *GAPC* (AT3G04120) was chosen as the reference gene. The *SEU* mRNA level in Col-0 was arbitrarily set to 1. Error bars represent standard deviation (SD) of three independent experiments. Bars with different letters are significantly different at $P < 0.05$, ANOVA.



Supplemental Figure S2. MC formation in *seu-4*.

(A and B) Occurrence of MC formation in roots of *seu-4* at 4d (A) and 7d (B) after sowing. The black outlines and white arrowheads highlight the occurrence of MC formation in the root endodermis. Scale bar, 50 μ m.

(C) Time-course analysis of proportion of plants with MC formation in roots of Col-0 and *seu-4* seedlings. Error bars represent SD of three independent experiments ($n \geq 25$). Bars with different letters are significantly different at $P < 0.05$, ANOVA.

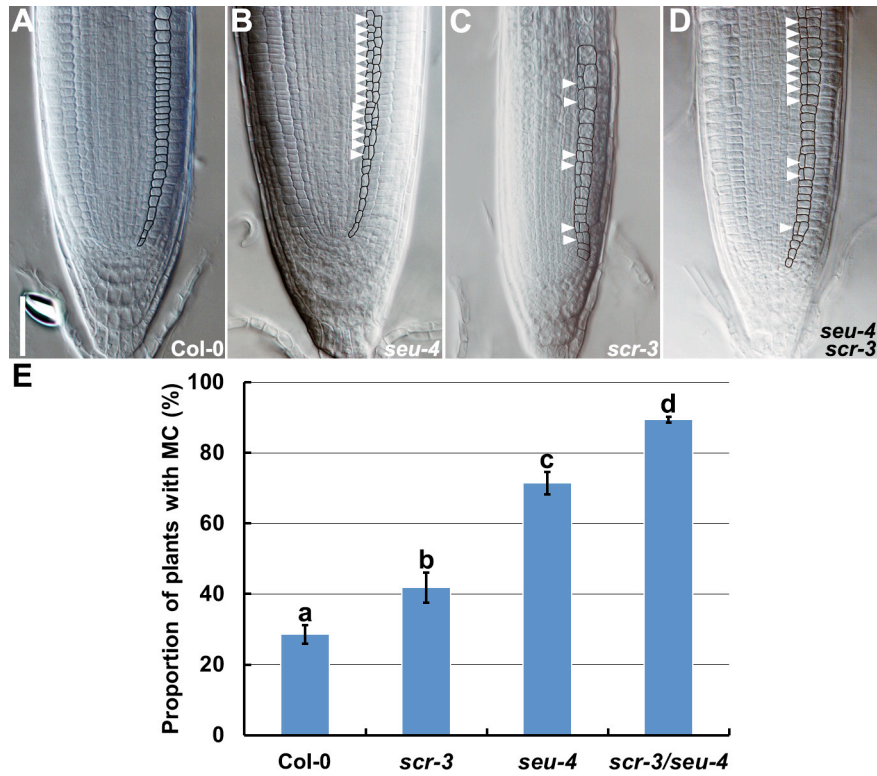


Supplemental Figure S3. Expression of *SCR*, *SHR* and *SCL3* in different genetic backgrounds as indicated.

(A) qRT-PCR analysis of *SCR*, *SHR* and *SCL3* transcript levels in roots of Col-0, *seu-3*, *seu-4* and *35S::SEU* seedlings 7d after sowing. *GAPC* (AT3G04120) was chosen as the reference gene. The mRNA level of each gene in Col-0 was arbitrarily set to 1. Error bars indicate SD of three independent experiments. Bars with different letters are significantly different at $P < 0.05$, ANOVA.

(B) The expression level of H2B-YFP, GFP or GUS in *seu* mutants relative to that of corresponding control transgene in Col-0, which was arbitrarily set to 100. Error bars indicate SD of three independent experiments. *, $P < 0.05$; **, $P < 0.01$, t-test.

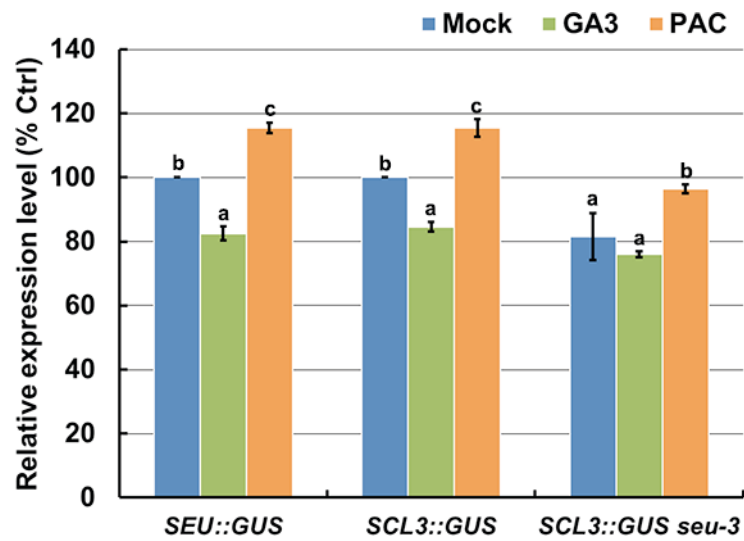
(C to F) Expression of *SHR::SHR-GFP* (C and D), *SCR::H2B-YFP* (E and F) in root tips of Col-0 (C and E), *seu-4* (D and F) seedlings. The white arrowheads indicate the occurrence of MC formation in the root endodermis. Scale bar, 50 μm .



Supplemental Figure S4. MC formation in different genetic backgrounds as indicated.

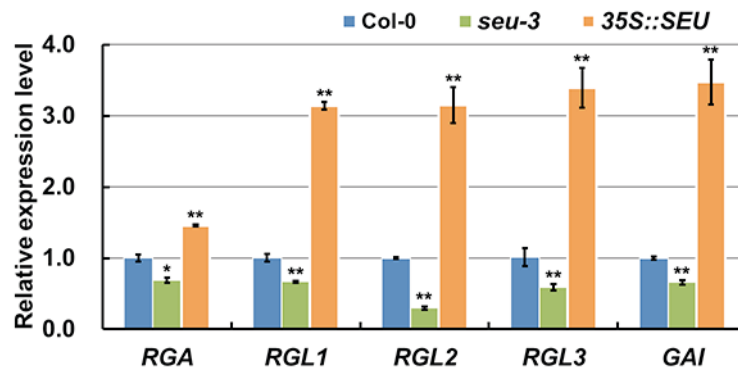
(A to D) Occurrence of MC formation in roots of Col-0 (A), *seu-4* (B), *scr-3* (C) and *seu-4 scr-3* (D) 7d after sowing. The black outlines and white arrowheads highlight the occurrence of MC formation in the root endodermis. Scale bar, 50 μ m.

(E) Time-course analysis of proportion of plants with MC formation in roots of Col-0 and *seu-4* seedlings. Error bars represent SD of three independent experiments ($n \geq 15$). Bars with different letters are significantly different at $P < 0.05$, ANOVA.



Supplemental Figure S5. SEU mediates the regulation of *SCL3* by GA signaling.

The relative expression level of *SEU::GUS* or *SCL3::GUS* in Col-0 or *seu-3* treated with mock, 10 μ M GA₃ or 10 μ M PAC. The expression level of *SEU::GUS* or *SCL3::GUS* in mock-treated Col-0 was arbitrarily to 100. Error bars indicate SD of three independent experiments. Bars with different letters are significantly different at $P < 0.05$, ANOVA.



Supplemental Figure S6. Expression of DELLA protein-encoding genes in different genetic backgrounds as indicated.

qRT-PCR analysis of *REPRESSOR OF GAI-3 (RGA)*, *RGA-LIKE1 (RGL1)*, *RGL2*, *RGL3* and *GIBBERELLIC ACID INSENSITIVE (GAI)* transcript levels in roots of Col-0, *seu-3* and *35S::SEU* seedlings 7d after sowing. *GAPC* (AT3G04120) was chosen as the reference gene. The mRNA level of each gene in Col-0 was arbitrarily set to 1. Error bars represent SD of three independent experiments. *, $P < 0.05$; **, $P < 0.01$, t-test.

Experiments / Primer names	Sequences (5' to 3')	Experiments / Primer names	Sequences (5' to 3')
Genotyping		CHIP-qPCR	
<i>seu-3</i>	L.P: GAAAATGTTCCGCCTTCGAT R.P: GAATTGCTGCGGTTCCAAC Digestion with <i>Bsl</i> I	SCR-CHIP-292-472-PF	CCGATCACCCACCTAATCTC
<i>scr-3</i>	L.P: ACTCAACTCGTGTCTCGGAAT R.P: TCTTCACTCTCTCGCCGTA Digestion with <i>Bsr</i> I	SCR-CHIP-292-472-PR	TGGCCGTATCTAAGTCGTC
<i>shr-2</i>	L.P: GCCACATCATCAACCCCTTCT R.P: GCCTAGCGAATTTCTCCATTC Wild type band: 679 bp; mutant band: 1100 bp	SCR-CHIP-798-856-PF	TGCTGACTCCATATGACCAT
<i>seu-4-LP</i>	TTCCGTGGTGTTCAGACTC	SCR-CHIP-798-856-PR	GAGCTACATGAGTTGGATT
<i>seu-4-RP</i>	TTTTGGCATTAGGAGCAAAG	SCR-CHIP-898-955-PF	CATCTTAGTAAGCACATCG
<i>gal-1-LP</i>	CAGACCCGAGACAGTAACCTGC	SCR-CHIP-898-955-PR	ATGGGATGAAGAAGTCTCTC
<i>gal-1-RP</i>	TCTACTCGAGGCAAGCTTG	SCR-CHIP-1208-1264-PF	TCAGATTTTATCGGGAAC
<i>scr3-LP</i>	TTCCTGTCTTTAACCCTC	SCR-CHIP-1208-1264-PR	GAGAGGCCATTACATACATAC
<i>scr3-RP</i>	AGCCGAGTCTTCTCATGAG	SCR-CHIP-1557-1614-PF	GACTTGGAGAAAGACATTCAG
lBb1.3	ATTTGGCCGATTCGGAAC	SCR-CHIP-1557-1614-PR	CACACGGCTCAATATGAAAG
		SCR-CHIP-2053-2131-PF	GCTGGTGTGAATGGATAAG
		SCR-CHIP-2053-2131-PR	ATAGGCCATTAAGGCCCA
Cloning			
promoter-SEU-PF-KpnI	TCCGGTACCACCATTAACCATTACAACCAACTC	SCL3-CHIP-88-191-PF	CTCTGAAAACCTAGTTCCTC
promoter-SEU-PR-BamHI	CGCGGATCCACTTTACTAATTCACAACCTCCAC	SCL3-CHIP-88-191-PR	CGAAGAACAACCAACCCAGAT
SEU-cds-PF-XhoI	TATCTCGAGATGGTACCATCAGAGCCGCC	SCL3-CHIP-169-278-PF	TAATTCAGCTCTCTGTTTGTG
SEU-cds-PR-SmaI	GTACCCGGG AGCGCGTTCCAATCAAAATTG	SCL3-CHIP-169-278-PR	CAGAGGAAGTGGGTTTGG
		SCL3-CHIP-418-498-PF	CATTTACACACACGCTATTAC
		SCL3-CHIP-418-498-PR	GTGAGAGGGTCTCTCAATCT
qRT-PCR			
GAPC-PF	GGAGCTGACTACGTTGTGAG	SCL3-CHIP-730-570-PF	GTAGTACTAGTACAATAATAG
GAPC-PR	TATTCGTGCTCGTTGACACC	SCL3-CHIP-730-570-PR	CGTACCAGACAATGCGTGATAG
SEU-PF	GCCACCTCTGAAACCAAGTGTATG	SCL3-CHIP-716-787-PF	CACCACCTTAAGGAGCCTC
SEU-PR	ACGCACCATCTCTTTTGG	SCL3-CHIP-716-787-PR	GTGTACTAGTACTACATGAATG
SCR-PF	TAGCGGTTGGAGACCATCG	SCL3-CHIP-1045-1141-PF	GTTGTATTCTGTATGTATCTA
SCR-PR	CGCTGTGTAGTGCATTTCC	SCL3-CHIP-1045-1141-PR	GCAACACTTAATTGAAGGAAG
SHR-PF	TGGTCGAGGAGGATGAGGAATAG	SCL3-CHIP-1191-1315-PF	CGTGTGGACGTTCTCTTCTC
SHR-PR	ACACTGTACCATCGACCAACACC	SCL3-CHIP-1191-1315-PR	CATGGCATGAGGTGGATTGG
SCL3-PF	TGGCTGTGTTGGGAATGTCC	SCL3-CHIP-1396-1410-PF	GTGAGCATTAAAGAAGAAAAGAC
SCL3-PR	ATTACTGCGCACCCGCTCTC	SCL3-CHIP-1396-1410-PR	GAGATGAGGCTGAGGCTGGGGT
RGA-PF	AGTTCGAATAGTCAAGAC	SCL3-CHIP-1543-1608-PF	CTGTAGAATCTCTGGTCAAT
RGA-PR	CATCCATTACTCTCCACAC	SCL3-CHIP-1543-1608-PR	CTGTGTGAGAGAGAACATTA
GAI-PF	CGTTGAGTCAGTGGAGGAA	SCL3-CHIP-1855-1915-PF	CGAGTAGCAGATCCAAAGTTG
GAI-PR	TGGCTATGAGCGGTCTGTGT	SCL3-CHIP-1855-1915-PR	CGAAGACCCTCAGAGAATA
RGL1-PF	ACCGGGTAGAGGCGATGAGACT	SHR-CHIP-133-208-PF	CTCACAATCCACCAAAACCA
RGL1-PR	CGATTGATCGCCACGCAGA	SHR-CHIP-133-208-PR	TCTTGTGTTCTCGGTGGGA
RGL2-PF	CGCTTACGCTACCCGAGATG	SHR-CHIP-690-761-PF	ACTTGGGTGGATCGATGTA
RGL2-PR	GAGTTCCACGCCGAGGTTG	SHR-CHIP-690-761-PR	AGGTCGATATCATGTAATGGCTT
RGL3-PF	GAAGCGCTTCACTATTACTCG	SHR-CHIP-956-1062-PF	GTCTGTTGATTAGGATGCGT
RGL3-PR	ACTGAGCCAGCTCTCGTGC	SHR-CHIP-956-1062-PR	ATATAGGCCAAATACATG
		SHR-CHIP-1337-1445-PF	TGGTGACCCTTAAGTATTTAT
		SHR-CHIP-1337-1445-PR	GCTAGCATCTACAATGAACAAG
YIH			
SCR-1-377-PF-EcoRI	GCGGAATTCGATGAATAGAGATAGAAAAGAGT	SHR-CHIP-1524-1602-PF	TGGAGAGAGGTTAGGAGGCA
SCR-1-377-PR-XhoI	TFACTCGAGGGAGATTGAAGGTTGTTGGT	SHR-CHIP-1524-1602-PR	CAGGCGTGAAGAAAAGCTGA
SCR-297-826-PF-EcoRI	GCGGAATTCGCGTTTATGAATCCAACCTCA	SHR-CHIP-1723-1859-PF	ATGGCATGACTTAGTGGAGAG
SCR-297-826-PR-XhoI	GCTCTCGAGTATCTAAGTCGTCTTCCACCT	SHR-CHIP-1723-1859-PR	ATGTGCATATTCTTACCT
SCR-836-2164-PF-EcoRI	GCGGAATTCAGATGTGATCCTCTGCAACA	SHR-CHIP-1978-2091-PF	AGACAAGATTAACTGTTGATCG
SCR-836-2164-PR-XhoI	TFACTCGAGATGGTATATGGAGTCAGCA	SHR-CHIP-1978-2091-PR	TCCATATGCTACTGTTTATGT
SCL3-1-715-PF-EcoRI	CAGGAATTCATAATAGTATAAGATAGAT	SHR-CHIP-2242-2383-PF	AGCCTAGGCTATAATGTAGAT
SCL3-1-715-PR-XhoI	CTGCTCGAGTGAAAGGCCAAAAGCTTGAT	SHR-CHIP-2242-2383-PR	CAAGCAAACCTACATTACATA
SCL3-651-1292-PF-EcoRI	CAGGAATTCAGAAATCAATATTTACCA	SHR-CHIP-3030-3191-PF	GGTGTCACTTATATGTAGT
SCL3-651-1292-PR-XhoI	CTGCTCGAGAAGAAATTTAAACAAAAGGTT	SHR-CHIP-3030-3191-PR	AGGTGACCAATTCGTACCAT
SHR-1-462-PF-EcoRI	GCGGAATTCGTCAAAATCTCAGTTAG		
SHR-1-462-PR-XhoI	GGCCTCGAGTTTTTTTTTAAATGAATAAGA		
SHR-444-1109-PF-EcoRI	GCGGAATTCGATTGGTTAGAAATGGTATTA		
SHR-444-1109-PR-XhoI	GGCCTCGAGTAACTGAGATTTTGGAC		
SEU-TRANS-PF-MfeI	ACTCAATTGATGGTACCATCAGAGCCGCT		
SEU-TRANS-PR-XhoI	TACCTCGAGTCACGCTTCCAATCAAAAAT		

Supplemental Table S1. Primers used in this study.