

Fig S1. *HDA19* gene structure and expression.

(a) Schematic representation of the *HDA19* gene and the SALK_139445 T-DNA insertion site.

(b - c) Relative expression level of *HDA19* in *hda19* mutant and in *HDA19* over-expressing line determined by qRT-PCR. The values over wild type (*Col*) are shown as means \pm SD, (**P < 0.01; Student's *t* test).

(d - e) Confocal microscopy images of 8 day-old root tip of (e) *HDA19pro:HDA19-EGFP/hda19* and (f) *HDA19pro:HDA19-EGFP/hda19/scr* seedlings. Scale bar = 100 μ m.

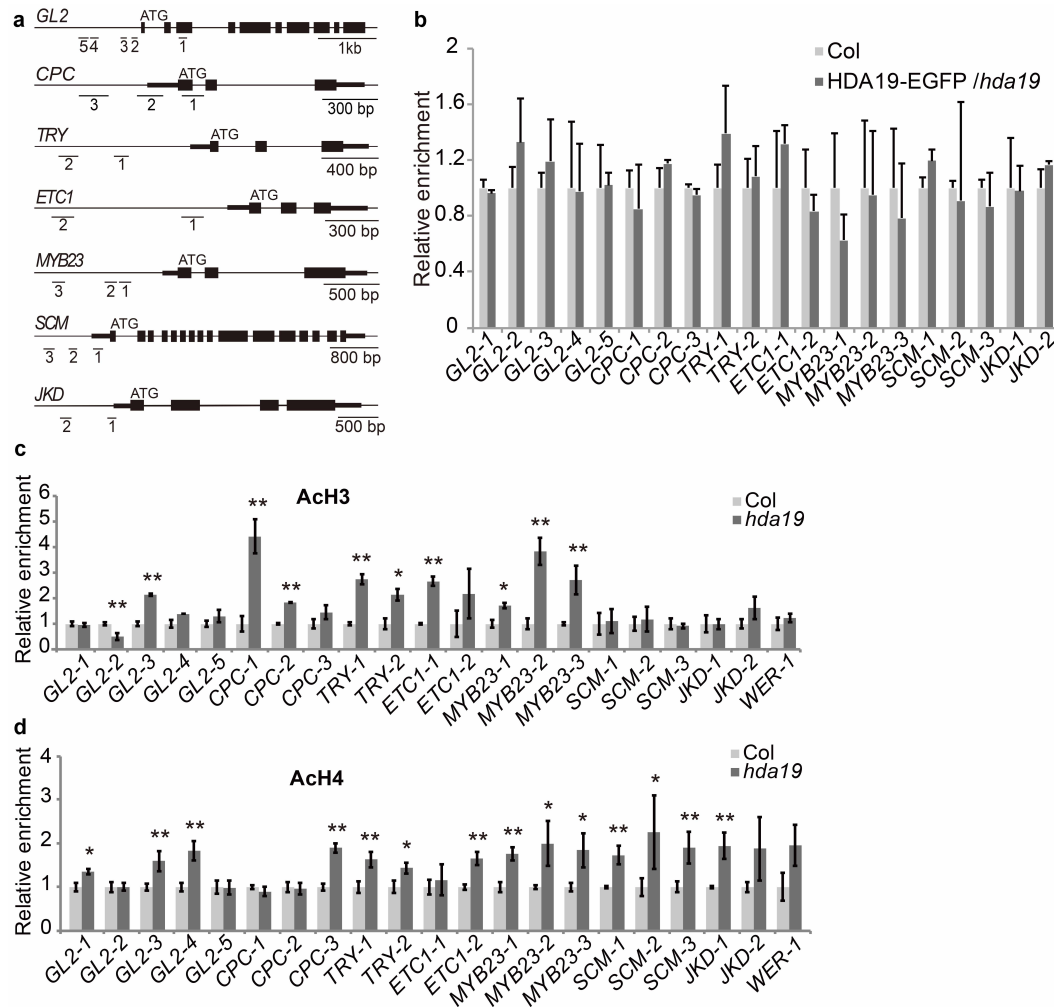


Fig S2. HDA19 affects histone acetylation levels of root epidermal patterning genes but does not directly bind to them.
 (a) Schematic representation of root epidermal patterning genes. Regions selected for ChIP analysis are underlined.
 (b) ChIP-qPCR analysis of HDA19 binding using GFP antibody in *HDA19pro:HDA19-EGFP/hda19*. Error bar represents SD value
 (c - d) ChIP-qPCR analysis of acetyl-histone H3 (c) and acetyl-H4 (d) level changes in *hda19* root tips compared to wild type (Col). Error bar represents SD value (*P < 0.05, **P < 0.01; Student's *t* test).

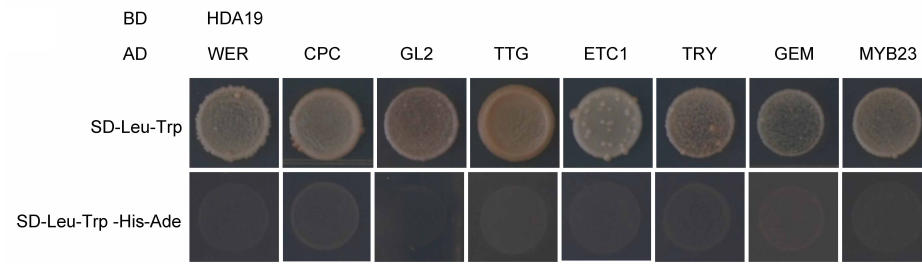


Fig S3. HDA19 does not interact with proteins of root epidermal patterning gene. Yeast-two-hybrid analysis did not detect any protein interaction between HDA19 and proteins of root epidermal patterning genes.

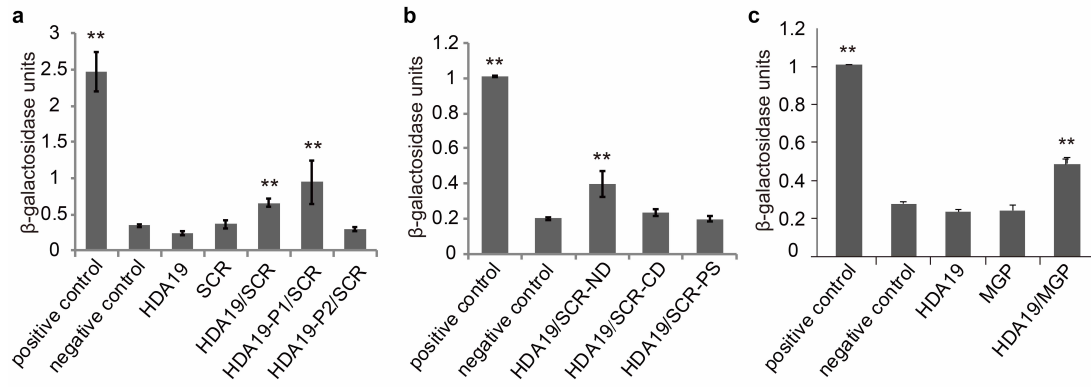


Fig S4. Quantification of the interaction between (a) HDA19 or fragments of HDA19 and SCR, (b) HDA19 and fragments of SCR described in Fig. 4b, and (c) HDA19 and MGP by β -galactosidase activity measurement. Error bar represents SD value (** $P < 0.01$; Student's t test).

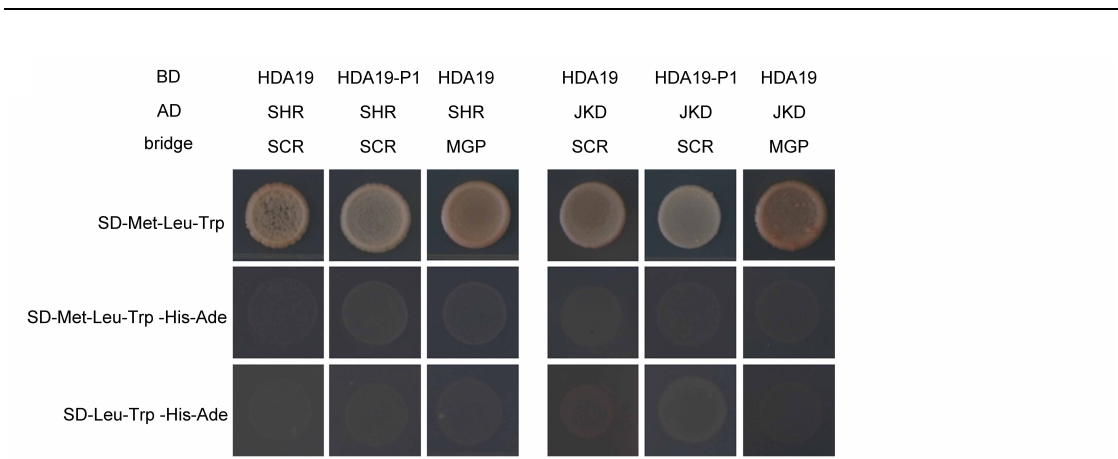


Fig S5. HDA19 does not interact with JKD or SHR indirectly. Yeast-three-hybrid analysis shows no indirect interaction between HDA19-JKD and HDA19-SHR via SCR or MGP as the bridge.

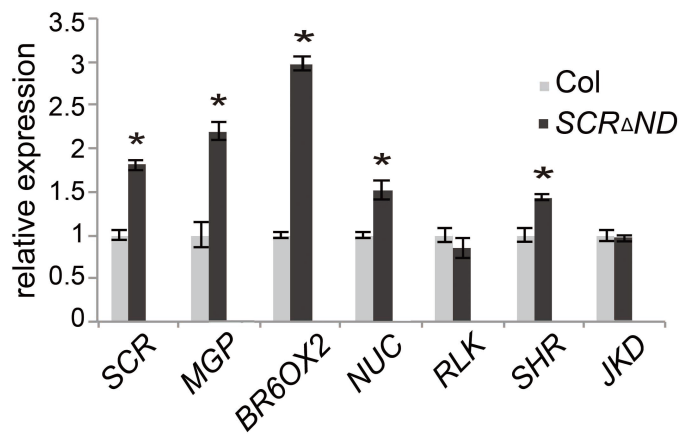


Fig S6. Expression of SCR target genes in *SCR ΔND* line. Expression determined by qRT-PCR in 8 day-old root tips. Error bar represents SD value (* $P < 0.01$; Student's *t* test).

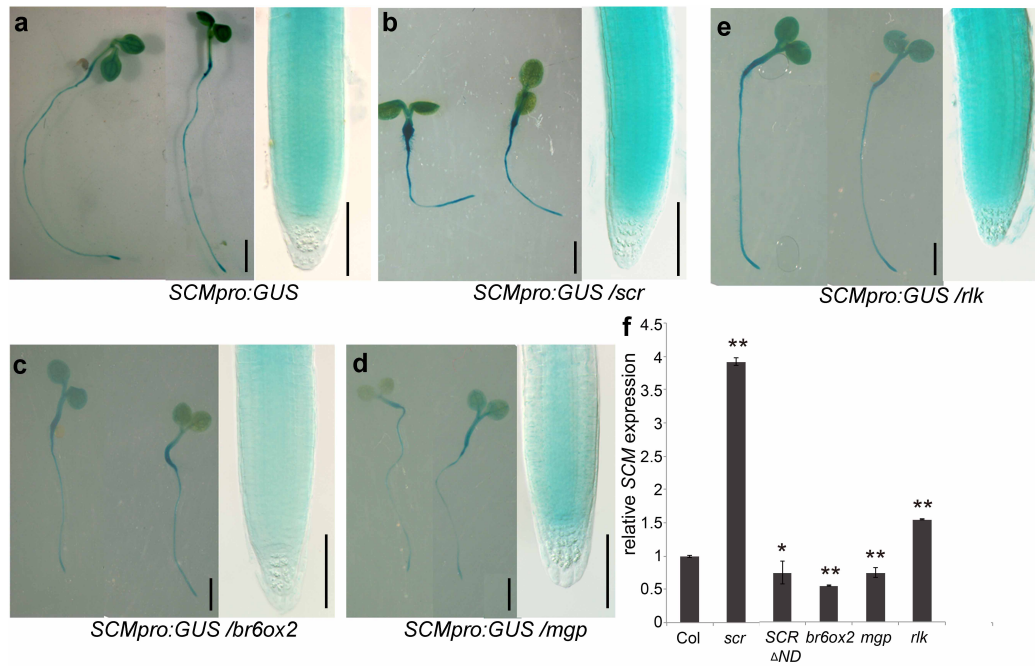


Fig S7. *SCM* expression in *scr* mutant alleles and mutants of SCR target genes. (a - e) *SCMpro:GUS* expression in 8 day-old seedling (left) and root tip (right). Scale bar left = 1mm, scale bar right = 100 μ m. (f) Expression level of *SCM* gene in 8 day-old root tips of *scr*, *SCR ΔND* and mutants of SCR target genes determined by qRT-PCR. Error bar represents SD value (**P < 0.01; *P < 0.05; Student's *t* test).

Table S1. Annotation of selected genes enriched in the root cortex.

Gene ID	Description	Go group
AT1G20010	Beta tubulin	Membrane; nucleotide-binding
AT1G20190	Alpha-expansin gene family	Membrane; signal
AT1G62580	Flavin monooxygenase that binds NO	Membrane
AT1G65060	COA Ligase 3	Nucleotide-binding
AT1G70580	Glyoxylate aminotransferase	
AT1G75780	beta tubulin gene	Nucleotide-binding
AT1G76100	One of two Arabidopsis plastocyanin genes	Membrane
AT2G02780	Leucine-rich repeat protein kinase family protein	Membrane; signal; nucleotide-binding; glycoprotein
AT2G39010	plasma membrane intrinsic protein 2E	Membrane
AT2G44740	cyclin p4;1 (CYCP4;1);	
AT2G48020	Major facilitator superfamily protein	Membrane
AT3G28040	Leucine-rich receptor-like protein kinase family protein	Membrane; signal; nucleotide-binding; glycoprotein
AT3G51240	flavanone 3-hydroxylase that is coordinately expressed with chalcone synthase and chalcone isomerases	Nucleotide-binding
AT4G00710	BR-signaling kinase 3 (BSK3)	Membrane; signal
AT4G04850	Member of putative potassium transporter family	Membrane
AT5G07190	unknown function	Membrane
AT5G07990	Required for flavonoid 3' hydroxylase activity	Membrane
AT5G10470	Kinesin that binds cyclin-dependent kinase CDKA	Membrane; nucleotide-binding
AT5G27450	Mevalonate Kinase	Nucleotide-binding
AT5G62210	Embryo-specific protein 3; lipase/lipoxygenase	Membrane
AT5G64330	Involved in blue light response signaling pathway; interacts with the blue light photoreceptor NPH1	Membrane; signal
AT5G64620	Plant cell wall and vacuolar invertases	Signal

Table S2. List of primers used in the experiments.

Real-time PCR primers to test gene expression level	
Gene	Sequence
<i>GAPDH</i>	CACCGAGGATGATGTTGTCT
	CCCATTCGTTGTCGTACCA
<i>WER</i>	TTCGGTAGGATTCGGGAGATT
	GGGTCGAACGGATAATCAAGTGA
<i>CPC</i>	CGACGACGGAGACAGAGCA
	TCGCCAACGAGTTTATACATCC
<i>GL2</i>	CTGGTGCTCGCGGGACAT
	CTTGGCTGTTTCTGTCGTCTTGT
<i>TTG</i>	ATTTGTTCTGGTGGTGATG
	GCCGAATAAACCGACAT
<i>GEM</i>	CATCAGCGAGCATAGTCAATCC
	GCGCCGTCGTAGTTTAAAAAA
<i>TRY</i>	TGTACAGACTTGTCGGTGATAGGTG
	TTATCAGCAAAGCCTTCACTGTTTC
<i>ETC1</i>	CTTAAGACCAATCCAACCATTGTTG
	CCTTTCACCGACAAGCTTATACATC
<i>MYB23</i>	GGGTATTGCCTTTGAATATCTTIG
	GCTACAAGCAAATATTCGGAAAA
<i>SCM</i>	CAATCGCTTCACTGGGAACATTC
	CCTGATAGAAGATTGCTTCCCAATG
<i>JKD</i>	GAGAGAATCATAATCGTGCTCCTC
	GATCGGTTGATTGAAAGGG
<i>MGP</i>	GTTGGTGTACAAACAATATG
	CAGCTTTGATAATTAAGTTC
<i>SCR</i>	ATTAGCGGTTGGAGG
	ACTAAGAACGAGGCGT
<i>BR6OX2</i>	TCTCAAGATCATAGAGGAGATGG
	TGGGTTACAAATTTACAAGATAAGAG
<i>RLK</i>	ACGGCTACGTCAAATGGTC
	CGGATTCCGATGTCTCAGAT
<i>NUC</i>	CCGCTTCAACCATTTGTACC
	GAGAGCGACGAAGAAGTTGG
Real-time PCR primers for ChIP assay	
Fragment	Sequence
<i>18S</i>	TACCGTCCTAGTCTCAACCA
	AACATCTAAGGGCATCACAG
<i>pSCR-1</i>	CGTCTTGTCCAATTCCTCTCAAG

	GCACAAAATTGCAAGTTGGTGC
<i>pSCR-2</i>	AGTTGGTGCCCCATCTTAGTAAGC
	TCATTATGTGAAATGAATGGGTTTC
<i>pSCR-3</i>	CGAAAGGTGGAAGACGACTTAG
	GTGAGAATTTGGAAGGATGTGG
<i>pSCR-4</i>	TTCCGATCACCCACCTAATCTC
	GTGAAGCCTGGCCGTATCTAAG
<i>pMGP-1</i>	TGAGACTTGAAGCCCAGAC
	TGAGTGCAAAGCGAGAAA
<i>pMGP-2</i>	AACGGAAAAGGTAAGGTGGTTG
	ATGGCCTTCTTGTTTTACTCGG
<i>pMGP-3</i>	ATATTCTTGTGCCGCCAAAGTTC
	TTGGAAGGAAGAGAAGTCGTCAG
<i>pMGP-4</i>	ATGACAATAGCTGCGACAGTTC
	CCTACACACTTAAGCCCCATATG
<i>pCYT-1</i>	CGAACTTTGTTATTTTCTTGGTACTGG
	GCAATTTTCAGCACGAAATTCAG
<i>pCYT-2</i>	AAATGCCTTCTCCTCTCATTAC
	GCAGCAGATTGCAAGATAACAATC
<i>pCYT3</i>	TGAGCGAAAATACTAACCAACC
	GGGTATCAGTAGCCCAAAAATC
<i>pCYT-4</i>	CCATGTGCCCATCCTCATC
	GTTTATGATTCGACAGTGTAGTAGGG
<i>pNUC-1</i>	TAAAGGGACCGATAAATAGT
	AATAAAGTTGTAAAAATGATAATA
<i>pNUC-2</i>	CTCAGGGATTATTAGTAGTT
	TAAGGAGGTATCAAGGTGTG

<i>pNUC-3</i>	CTCGCTTCGAATTTGCAAGGCTAT
	GCACCCTATGTTTGCAGTTTCACT
<i>pRLK-1</i>	AATCTTTATGCCCAACCAA
	TAGCAAATCACGTGTAAGAGAA
<i>pRLK-2</i>	GCGTAATCTCACGTCACAATTTCCG
	ACGTCGCTTTGTCGTTTTTCACG
<i>pWER</i>	ATCTCAGAAGTCCATTATTATTAC
	TCTTTTTGTTTCTTTGAATGATAGA
<i>pCPC</i>	GAAACAAGAACACATATAAGGGAC
	AAGAAGAACGACAGATACAACC
<i>pGL2</i>	CGTCTTCTAAACTTTCTCTATCCG
	CCCAATCGAATCTAATACTGA
<i>pETC1</i>	GAATAAAGGGTATATCCTCGACG
	TATGAAGTCCAATCTATTAC
<i>pTRY</i>	AAACATCGTTGAACTTGCATCTGCC
	GGCTAACTTTGTTCTCATTCGTAG
<i>pMYB23</i>	CACCGTTTTCAACTAATAGTTGAGG
	TGGAAGGGCTTGTTGACTCTC
<i>pSCM-1</i>	GCCACATTTGGTTTGAATAGCC
	AACATGCTTGGTGAGCTTATGTG
<i>pSCM-2</i>	AGAGCAAAAATGGACGTGGG
	GGGCAAGAAAACAGTTGAAG
<i>pSCM-3</i>	TTTGTAAGCCGCTCGTTCTTC
	GGGTGAAACAGGGATATTCCTG
<i>pSCM-4</i>	TTCAAGGGTTTTCTCATCTTCAGTG
	CAGCTGAGAAAGGCATTGTCAAG
<i>pJKD-1</i>	ATCCGTAAAAAGTGGAATCCG
	TGATGGGTTGAGTTGTAAATGG

<i>pJKD-2</i>	TCGTGCCTTGAAATTTTCTTCCTC
	TTTGGGTTTTAGGGCTTGAGAATG
<i>pJKD-3</i>	CCTGATCATCTTCTTGTTTTCTTGC
	GATCTCCTGGAATCATCTGCATATC
<i>pJKD-4</i>	GAAACACACCTTCATCATCTTCAGC
	CCTGGAGTGCCAGGTTGATTTC

Table S3. Detailed data in FCS analysis.

Filename	Line	Location	Pixel Size (μm)	% Monomer	% Dimer
Root2-6-young endo	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	endodermis	0.1	0.9402	0.0598
Root2-5-young endo	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	endodermis	0.1	0.9664	0.0336
Root2-4-young endo	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	endodermis	0.1	0.9864	0.0135
Root2-3-young endo	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	endodermis	0.1	0.9723	0.0277
Root2-1-QC	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	QC	0.1	0.9834	0.0166
Root 1-6 young endo	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	endodermis	0.1	0.9250	0.0749
Root 1-5 young endo	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	endodermis	0.1	0.9797	0.0203
Root 1-4 CEI/CEID	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	Stem cell	0.1	0.9858	0.0142
Root 1-3 QC	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	QC	0.1	0.9926	0.0073
Root 1-2 CEI	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	Stem cell	0.1	0.9930	0.0070
Root1-1 CEI	HDA19pro:HDA19-EGFP x SCRpro:SCR-mCherry	Stem cell	0.1	0.9892	0.0108
			average	0.9740	0.0260
			average endodermis	0.9617	0.0383
			average QC/SC	0.9888	0.0112
			stdev endodermis	0.0240	
			stdev QC/SC	0.0042	
Controls					
File name	line	monomeric value			
35S:GFP-root4-4	35Spro:GFP	1.143			
35S:GFP-root3-5	35Spro:GFP	1.536			
35S:GFP-root3-2	35Spro:GFP	1.59	average	1.42	

UBQ10:mCherry -root1-4	UBQ10pro:mCherry	1.3			
UBQ10:mCherry -root1-3	UBQ10pro:mCherry	1.37			
UBQ10:mCherry -root1-2	UBQ10pro:mCherry	1.27	average	1.31	