

FigS1. Mardaryev et al.

Figure S1. Dynamics of Rps27 and Gabpb2 gene expression during epidermal and dermal development. Changes in distances between Rps27 and Lor and between nuclear border and EDC or MMU3 in the developing epidermis.

(A) Microarray analysis of RNA from laser-captured epidermis and dermis of mice at distinct stages of expression. Means are shown for relative transcription activity normalized to the reference RNA levels for the indicated genes. Three samples were used for each stage. (B) Distances between Lor and Rps27 in basal epidermal keratinocytes normalized to the average nuclear radius at E11.5 and E16.5. Mean+S.E.M, n=60. Pair-wise comparisons – differences between the E11.5 versus E16.5 are significant ($p<0.01$, Newman-Keuls test after one way ANOVA test) (C) Distances between the EDC or centre of MMU3 and nuclear border in basal epidermal keratinocytes of WT mice (E11.5, E16.5). Mean+S.E.M, n=60, difference in the distances for EDC is significant ($p<0.001$, two- tailed t-test).

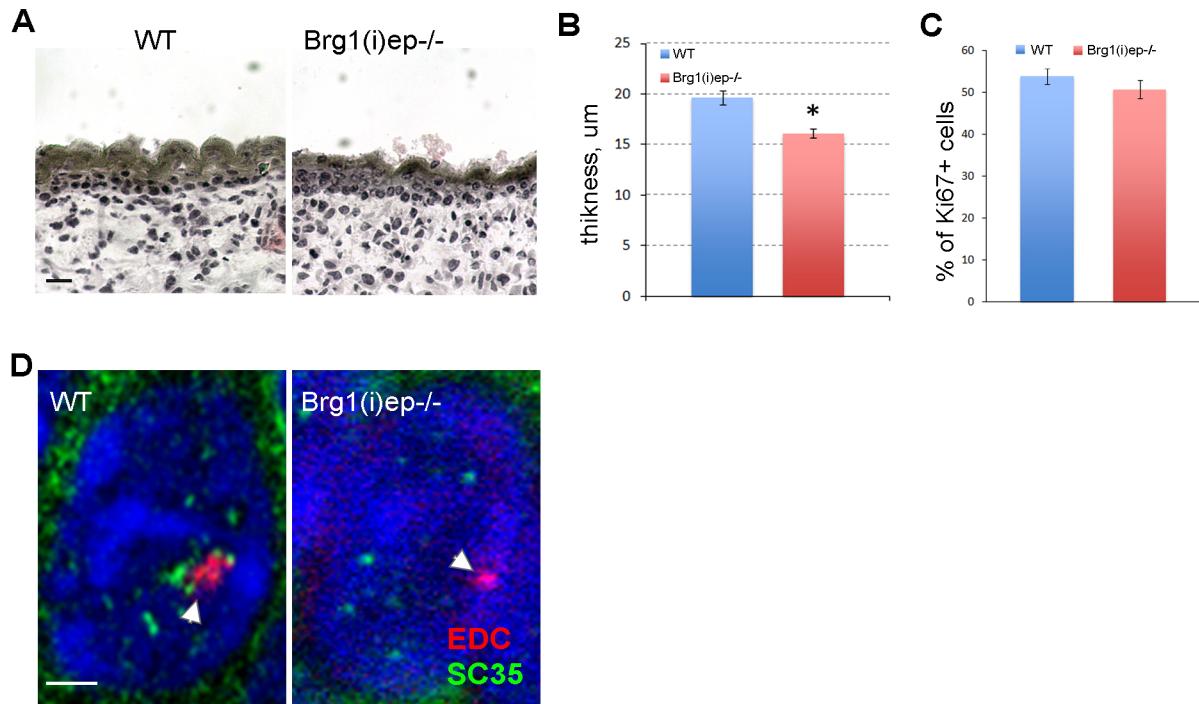
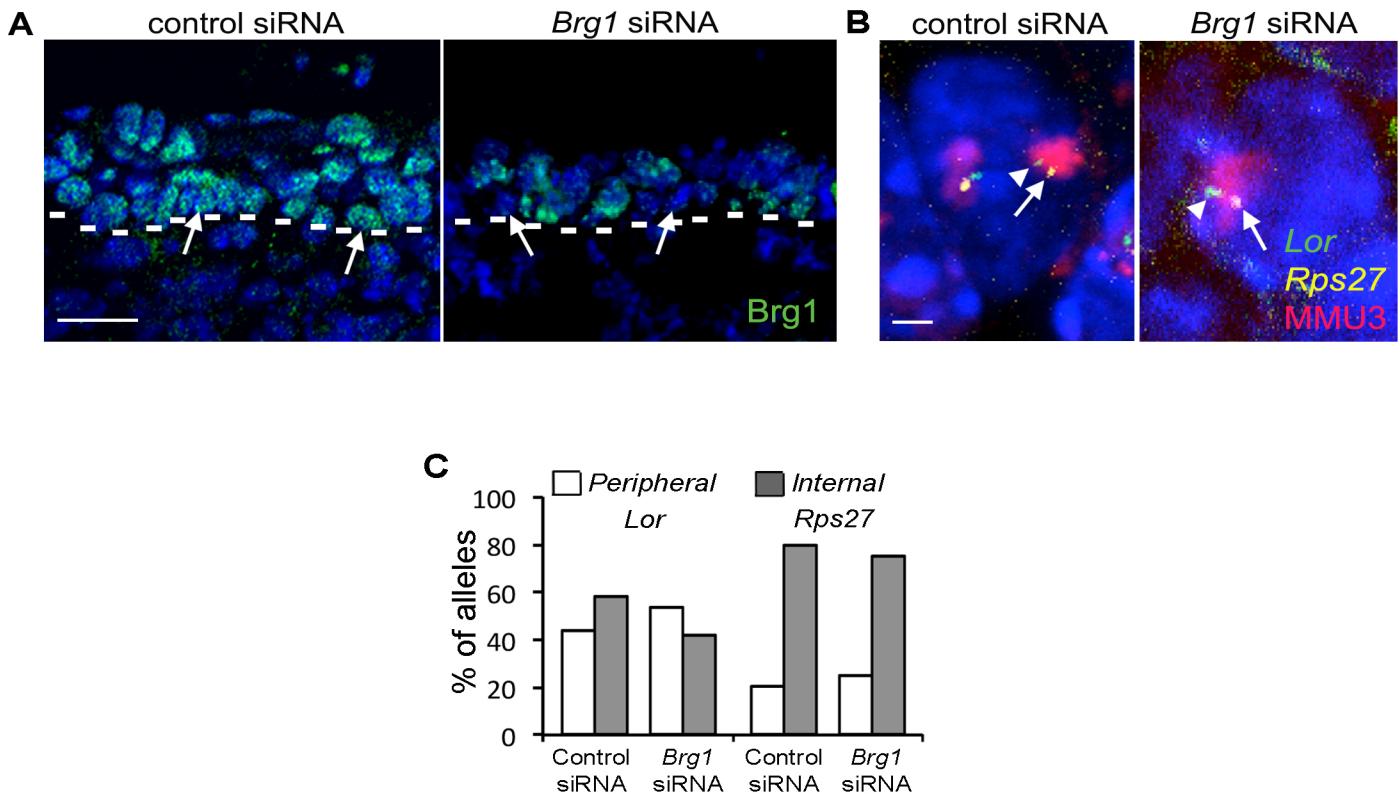


Fig S2. Mardaryev et al

Figure S2. Morphological analysis of the epidermis in Brg1(i)ep^{-/-} and control mice at E16.5.

(A) Hematoxylin staining of the Brg1(i)ep^{-/-} and control mouse skin at E16.5. (B) Epidermis of the Brg1(i)ep^{-/-} mice is significantly thinner than the controls at E16.5 Mean+S.E.M., $p<0.01$, two-tailed t-test. (C) No difference in the percentage of the Ki-67 positive cells between the epidermis of Brg1(i)ep^{-/-} and control mice at E16.5. (D) Multi-color 3D-FISH with BACs containing the EDC combined with immunostaining for SC-35 in the epidermis of control and Brg1(i)ep^{-/-} mice. Positions of the EDC in epidermal cell nuclei are shown by arrowheads in representative single Z-sections. Scale bar is 2 μm .



FigS3. Mardaryev et al.

Figure S3. Brg1 is involved in the relocation of Lor gene within MMU3 in developing epidermis.

(A) Reduction in the expression of Brg1 protein in the epidermis of E12.5 embryos treated with Brg1 siRNA for two days ex vivo in comparison with embryos treated with control siRNA. Notice the appearance of Brg1 negative cells in the epidermis of Brg1 siRNA treated embryos that are absent in the control epidermis (arrows) and reduction in protein expression level in the majority of the epidermal cells after Brg1 siRNA treatment. Scale bar is 25 um. (B) Multi-color 3D-FISH with BACs containing the Lor and Rps27 together with the whole mouse chromosome territory 3 (MMU3) paint in the epidermal cells of the E12.5 embryos treated ex vivo with Brg1 or control siRNA. Localization of Lor (shown by arrows) and localization of Rps27 (shown by arrowheads) in distinct regions within the MMU3 (p - peripheral versus i - internal) are shown in representative single Z-sections. Scale bar is 2 um. (C) Results of image analysis after Multi-color 3D-FISH with BACs containing the Lor and Rps27, and mouse chromosome territory 3 (MMU3). Frequencies of intra-MMU3 distribution (peripheral versus the internal parts of the MMU3) of Lor and Rps27 in basal epidermal cells in E12.5 embryos treated with Brg1 or control siRNA. For Brg1 siRNA n=88, for control siRNA n=110. P-values calculated for pair-wise comparison are: Lor ($p=0.035$), Rps27 ($p=0.45$), Chi-square test.

Table S1. Dynamics of gene expression in the EDC locus during skin development

		isoform								
90530874	90544432	Peptidoglycan recognition protein 4	Pglyrp4	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
90562587	90565233	apoptosis inhibitor 5 pseudogene	LOC329706	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
90579741	90581802	predicted gene, EG545541	EG545541	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
90682671	90692628	similar to Calgranulin B (Migration inhibitory factor-related protein 14)	LOC635737	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
90718795	90720856	predicted gene, EG668174	EG668174	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
90813317	90821107	similar to nischarin	LOC668179	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
90841248	90844152	similar to 60S acidic ribosomal protein P1	LOC635756	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
90875369	90880395	RIKEN cDNA 4930529C04Rik gene	4930529C04Rik	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
90892059	90894727	RIKEN cDNA 9130204L05 gene	9130204L05Rik	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
91542275	91544416	similar to S100 calcium-binding protein; S100RVP	LOC100042463	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
91818534	91835506	Peptidoglycan recognition protein 3	Pglyrp3	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
91828410	91828989	predicted gene, EG619750	EG619750	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
91884193	91887064	Loricrin	Lor	1.71	34.11	32.76	102.86	1.24	2.20	1.41
91926126	91927869	proline rich 9	Prr9	0.67	3.24	0.45	1.14	0.77	1.58	0.95
92019757	92026413	small proline-rich protein 2A1	Sprr2a1	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92054569	92061226	small proline-rich protein 2A2	Sprr2a2	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92120627	92122007	small proline-rich protein	Sprr2b	0.47	0.45	0.50	0.77	0.42	0.37	0.49

		2B								
92130521	92130751	small proline-rich protein 2C	Sprr2c	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92143080	92144793	small proline-rich protein 2D	Sprr2d	1.12	1.07	1.41	5.44	1.13	1.19	0.99
92156065	92157371	small proline-rich protein 2E	Sprr2e	0.64	0.44	0.62	0.63	0.59	0.43	0.61
92169109	92170364	small proline-rich protein 2F	Sprr2f	1.23	1.82	1.17	2.78	1.29	2.21	1.32
92177837	92179151	small proline-rich protein 2G	Sprr2g	0.95	1.25	0.94	1.36	0.95	1.16	1.02
92189607	92191246	small proline-rich protein 2H	Sprr2h	0.74	1.04	1.54	21.68	0.71	0.95	0.87
92211913	92213193	small proline-rich protein 2I	Sprr2i	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92222009	92223318	small proline-rich protein 2J	Sprr2j	0.64	0.79	0.62	0.78	0.60	0.64	0.61
92231960	92233348	similar to Adhesion regulating molecule 1	LOC100043022	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92236504	92237849	small proline-rich protein 2K	Sprr2k	0.54	0.70	0.63	0.76	0.40	0.32	0.53
92240731	92242701	small proline-rich protein 1B	Sprr1b	0.95	2.55	1.27	2.82	1.02	1.42	1.01
92260741	92261457	small proline-rich protein 3	Sprr3	0.82	0.90	0.80	1.57	0.81	1.19	0.94
92277107	92277467	similar to hCG1782414	LOC100042575	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92287876	92289803	small proline-rich protein 1A	Sprr1a	0.53	1.13	0.71	2.84	0.66	0.56	0.76
92304185	92304415	small proline-rich protein 4	Sprr4	1.06	1.81	0.88	2.81	1.03	1.77	1.14
92336432	92338490	similar to CG4877-PA	LOC100042581	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92374824	92377637	Involucrin	Ivl	1.08	2.48	1.77	27.33	1.03	2.45	1.47
92387788	92392946	sperm mitochondria-associated cysteine-rich	Smcp	1.34	2.44	0.91	3.44	1.11	2.23	1.55

		protein								
92424007	92425582	late cornified envelope 6A	Lce 6a	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92450454	92452229	late cornified envelope 1A1	Lce1a1	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92459572	92460848	late cornified envelope 1B	Lce1b	3.27	0.63	11.47	14.42	3.05	6.48	0.83
92468155	92468766	similar to 60S ribosomal protein L13 (A52)	LOC620325	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92472535	92474237	late cornified envelope 1A2	Lce1a2	1.41	0.78	12.83	209.28	1.30	1.88	1.30
92483169	92484840	late cornified envelope 1C	Lce1c	0.94	0.71	12.03	90.22	0.92	0.84	0.96
92489421	92491132	late cornified envelope 1D	Lce1d	1.22	0.47	8.84	111.73	1.16	3.31	1.29
92492476	92495109	similar to 14-3-3 zeta	LOC100043062	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92511322	92512996	late cornified envelope 1E	Lce1e	1.28	2.05	9.99	48.11	1.08	2.03	1.21
92522607	92524272	late cornified envelope 1F	Lce1f	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92541767	92542251	similar to small proline rich-like 9	LOC668264	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92554073	92556260	late cornified envelope 1G	Lce1g	0.96	0.97	0.89	1.58	1.03	1.00	1.00
92567137	92568987	late cornified envelope 1H	Lce1h	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92581132	92582821	late cornified envelope 1I	Lce1i	0.60	0.59	9.71	69.20	0.85	1.02	0.88
92593074	92594529	Hypothetical LOC545547	LOC545547	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92610213	92616300	Hypothetical protein LOC631101	LOC631101	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92626996	92631169	Keratinocyte expressed, proline-rich	Kprp	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92653871	92655208	late cornified envelope 1L	Lce1l	1.88	6.37	2.55	6.11	1.77	4.07	2.27

92672281	92673296	RIKEN cDNA 2310050C09 gene	2310050C09Rik	1.24	4.18	2.69	24.88	1.09	2.22	1.37
92729209	92730152	late cornified envelope 3A	Lce3a	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92736901	92738020	late cornified envelope 3B	Lce3b	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92748408	92749652	late cornified envelope 3C	Lce3c	1.08	1.02	1.12	2.37	1.18	2.95	1.65
92761249	92762495	similar to late cornified envelope protein	LOC630994	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92770705	92772203	RIKEN cDNA 2310001H18 gene	2310001H18Rik	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92796148	92797348	late cornified envelope 3F	Lce3f	1.23	1.97	0.89	2.97	1.03	0.95	1.30
92818129	92819608	cysteine-rich C-terminal 1	Crct1	1.36	11.23	13.65	195.88	1.38	2.19	1.11
92821729	92822982	late cornified envelope 1M	Lce1m	2.19	7.04	3.57	26.77	1.24	3.16	1.69
92872745	92879427	predicted gene, EG229571	EG229571	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
92948709	92953393	Cornulin	Crnn	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
93001195	93025299	filaggrin family member 2	Flg2	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
93081986	93083004	predicted gene, EG668300	EG668300	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
93086391	93097616	Filaggrin	Flg	0.92	0.56	41.84	137.00	0.88	2.23	1.03
93102884	93109394	Hypothetical protein LOC100042701	LOC100042701	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
93124477	93137494	Hornerin	Hrnr	0.65	1.19	1.60	2.68	0.84	0.84	0.96
93197621	93203364	Repetin	Rptn	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
93237137	93237688	predicted gene, EG383891	EG383891	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
93246252	93252999	Trichohyalin	Tchh	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
93272676	93275902	trichohyalin-like 1	Tchhl1	3.57	13.58	4.46	10.41	3.05	9.96	3.85
93324418	93330210	S100 calcium binding protein A11 (calgizzarin)	S100a11	0.27	0.32	0.35	0.30	0.22	0.27	0.17

93359039	93368567	S100 calcium binding protein A10 (calpastatin)	S100a10	0.30	0.52	0.61	0.37	0.22	0.58	0.15
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N.D. Not determined

Table S2. Dynamics of expression of *Rps27* and *Gabpb2* genes during skin development

Dynamics of expression of *Rps27* and *Gabpb2* genes in developing epidermis

Gene name	Gene symbol	E11.5 epidermis fluorescent signal	E11.5 epidermis signal vs reference RNA signal	E14.5 epidermis fluorescent signal	E14.5 epidermis signal vs reference RNA signal	E16.5 epidermis fluorescent signal	E16.5 epidermis signal vs reference RNA signal	Adult epidermis fluorescent signal
ribosomal protein S27	Rps27	183427.9	0.81	490939.00	1.88	184131.60	1.3	204156.10
GA repeat binding protein, beta 2	Gabpb2	259	1.25	462.22	2.78	292.59	0.52	669.10

Dynamics of expression of *Rps27* and *Gabpb2* genes in developing dermis

Gene name	Gene symbol	E11.5 dermis fluorescent signal	E11.5 dermis signal vs reference RNA signal	E16.5 dermis fluorescent signal	E16.5 dermis signal vs reference RNA signal	Adult dermis fluorescent signal	Adult dermis signal vs reference RNA signal
ribosomal protein S27	Rps27	155916.4	0.57	90937.4	0.62	167709.20	0.99
GA repeat binding protein, beta 2	Gabpb2	631.5	1.67	659.0	2.51	407.25	1.55

Table S3. 3D-FISH BAC probes generated to the distinct regions of mouse chromosome 3

Probe	BAC name	Featured Gene	BAC start	BAC end	gene start	gene end
Rps27	RP23-480F10	Rps27	89997746	90169775	90016591	90017569
EDC	RP24-318N12	S100a6	90284072	90451873	90416816	90418336
	RP24-61G19	Lor	91716002	91899804	91884193	91887064
	RP24-248L10	Ivl	92215201	92392463	91887064	92377637
	RP24-341I21	Lce3c	92634255	92806759	92748408	92749652
	RP23-425P7	S100a10	93215624	93411886	93359039	93368567
Gabpb2	RP24-363H12	Gabpb2	94926338	95086569	94985688	95021864

Table S4. Gene expression in the EDC locus in the Brg1(i)ep-/- epidermis in comparison to the control at E16.5

Gene start	Gene end	Gene name	Gene symbol	Control vs Brg1(i)ep-/-	Brg1(i)ep-/- vs Control
90314956	90318252	S100 calcium binding protein A1	S100a1	5	0.2
90318682	90328503	S100 calcium binding protein A13	S100a13	0.55	1.82
90330792	90332755	S100 calcium binding protein A14	S100a14	1.63	0.61
90345145	90347073	S100 calcium binding protein A16	S100a16	2.68	0.37
90394169	90395430	predicted gene, EG628324	EG628324	N.D.	N.D.
90404137	90406624	S100 calcium binding protein A3	S100a3	1.05	0.95
90407692	90409963	S100 calcium binding protein A4	S100a4	2.48	0.4
90412444	90415702	S100 calcium binding protein A5	S100a5	0.76	1.31
90416816	90418336	S100 calcium binding protein A6 (calcyclin)	S100a6	1.13	0.89
90458224	90462052	S100 calcium binding protein A7A	S100a7a	0.07	13.81

90472993	90473956	S100 calcium binding protein A8 (calgranulin A)	S100a8	0.07	13.81
90496555	90499613	S100 calcium binding protein A9 (calgranulin B)	S100a9	0.02	55.18
90512767	90514887	similar to 40S ribosomal protein S2	LOC668165	N.D.	N.D.
90526554	90527441	similar to Serine/threonine-protein phosphatase alpha-3 isoform	LOC383949	N.D.	N.D.
90530874	90544432	Peptidoglycan recognition protein 4	Pglyrp4	0.94	1.06
90562587	90565233	apoptosis inhibitor 5 pseudogene	LOC329706	N.D.	N.D.
90579741	90581802	predicted gene, EG545541	EG545541	N.D.	N.D.
90682671	90692628	similar to Calgranulin B (Migration inhibitory factor-related protein 14)	LOC635737	N.D.	N.D.
90718795	90720856	predicted gene, EG668174	EG668174	N.D.	N.D.
90813317	90821107	similar to nischarin	LOC668179	N.D.	N.D.
90841248	90844152	similar to 60S acidic ribosomal protein P1	LOC635756	N.D.	N.D.
90875369	90880395	RIKEN cDNA 4930529C04 gene	4930529C04Rik	N.D.	N.D.
90892059	90894727	RIKEN cDNA 9130204L05 gene	9130204L05Rik	N.D.	N.D.
91542275	91544416	similar to S100 calcium-binding protein; S100RVP	LOC100042463	N.D.	N.D.
91818534	91835506	Peptidoglycan recognition protein 3	Pglyrp3	1.02	0.98
91828410	91828989	predicted gene, EG619750	EG619750	N.D.	N.D.
91884193	91887064	Loricrin	Lor	61.63	0.02
91926126	91927869	proline rich 9	Prr9	0.81	1.24
92019757	92026413	small proline-rich protein 2A1	Sprr2a1	1.06	0.95
92054569	92061226	small proline-rich protein 2A2	Sprr2a2	23.57	0.04
92120627	92122007	small proline-rich protein 2B	Sprr2b	1.09	0.92
92130521	92130751	small proline-rich protein 2C	Sprr2c	N.D.	N.D.
92143080	92144793	small proline-rich protein 2D	Sprr2d	0.13	7.73
92156065	92157371	small proline-rich protein 2E	Sprr2e	1.06	0.95

92169109	92170364	small proline-rich protein 2F	Sprr2f	0.27	3.67
92177837	92179151	small proline-rich protein 2G	Sprr2g	0.09	10.83
92189607	92191246	small proline-rich protein 2H	Sprr2h	0.15	6.82
92211913	92213193	small proline-rich protein 2I	Sprr2i	0.48	2.09
92222009	92223318	small proline-rich protein 2J	Sprr2j	1.83	0.55
92231960	92233348	similar to Adhesion regulating molecule 1	LOC100043022	N.D.	N.D.
92236504	92237849	small proline-rich protein 2K	Sprr2k	3.25	0.31
92240731	92242701	small proline-rich protein 1B	Sprr1b	2.56	0.39
92260741	92261457	small proline-rich protein 3	Sprr3	1.06	0.94
92277107	92277467	similar to hCG1782414	LOC100042575	N.D.	N.D.
92287876	92289803	small proline-rich protein 1A	Sprr1a	2.24	0.45
92304185	92304415	small proline-rich protein 4	Sprr4	0.98	1.02
92336432	92338490	similar to CG4877-PA	LOC100042581	N.D.	N.D.
92374824	92377637	Involucrin	Ivl	1.84	0.54
92387788	92392946	sperm mitochondria-associated cysteine-rich protein	Smcp	1	1
92424007	92425582	late cornified envelope 6A	Lce 6a	N.D.	N.D.
92450454	92452229	late cornified envelope 1A1	Lce1a1	32.89	0.03
92459572	92460848	late cornified envelope 1B	Lce1b	8.66	0.12
92468155	92468766	similar to 60S ribosomal protein L13 (A52)	LOC620325	N.D.	N.D.
92472535	92474237	late cornified envelope 1A2	Lce1a2	32.59	0.03
92483169	92484840	late cornified envelope 1C	Lce1c	N.D.	N.D.
92489421	92491132	late cornified envelope 1D	Lce1d	10.44	0.1
92492476	92495109	similar to 14-3-3 zeta	LOC100043062	N.D.	N.D.
92511322	92512996	late cornified envelope 1E	Lce1e	4.09	0.24
92522607	92524272	late cornified envelope 1F	Lce1f	3.1	0.32
92541767	92542251	similar to small proline rich-like 9	LOC668264	N.D.	N.D.
92554073	92556260	late cornified envelope 1G	Lce1g	4.06	0.25
92567137	92568987	late cornified envelope 1H	Lce1h	2.72	0.37

92581132	92582821	late cornified envelope 1I	Lce1i	19.42	0.05
92593074	92594529	Hypothetical LOC545547	LOC545547	N.D.	N.D.
92610213	92616300	Hypothetical protein LOC631101	LOC631101	N.D.	N.D.
92626996	92631169	Keratinocyte expressed, proline-rich	Kprp	7.13	0.14
92653871	92655208	late cornified envelope 1L	Lce1l	8.76	0.11
92672281	92673296	RIKEN cDNA 2310050C09 gene	2310050C09Rik	3.29	0.3
92729209	92730152	late cornified envelope 3A	Lce3a	1.55	0.65
92736901	92738020	late cornified envelope 3B	Lce3b	6.98	0.14
92748408	92749652	late cornified envelope 3C	Lce3c	2.79	0.36
92761249	92762495	similar to late cornified envelope protein	LOC630994	N.D.	N.D.
92770705	92772203	RIKEN cDNA 2310001H18 gene	2310001H18Rik	N.D.	N.D.
92796148	92797348	late cornified envelope 3F	Lce3f	4.9	0.2
92818129	92819608	cysteine-rich C-terminal 1	Cret1	3.21	0.31
92821729	92822982	late cornified envelope 1M	Lce1m	16.23	0.06
92872745	92879427	predicted gene, EG229571	EG229571	1.51	0.66
92948709	92953393	Cornulin	Crnn	0.98	1.02
93001195	93025299	filaggrin family member 2	Flg2	1.6	0.63
93081986	93083004	predicted gene, EG668300	EG668300	N.D.	N.D.
93086391	93097616	Filaggrin	Flg	N.D.	N.D.
93102884	93109394	Hypothetical protein LOC100042701	LOC100042701	N.D.	N.D.
93124477	93137494	Hornerin	Hrnr	2.24	0.45
93197621	93203364	Repetin	Rptn	1.03	0.97
93237137	93237688	predicted gene, EG383891	EG383891	N.D.	N.D.
93246252	93252999	Trichohyalin	Tchh	0.63	1.59
93272676	93275902	trichohyalin-like 1	Tchhl1	1.09	0.91
93324418	93330210	S100 calcium binding protein A11 (calgizzarin)	S100a11	1.6	0.62
93359039	93368567	S100 calcium binding protein A10 (calpactin)	S100a10	2.27	0.44

N.D. Not determined

Table S5. Sites within the 5 Mb EDC containing region bound by Brg1

Peak start	Peak finish	Peak start	Peak finish	Peak start	Peak finish
89009600	89011000	90362400	90364000	94195000	94198400
89053600	89058400	90365800	90369800	94286200	94287800
89071600	89077600	90388200	90394600	94389000	94392400
89078600	89087600	90401000	90402800	94411800	94418400
89088400	89090600	90406400	90408600	94432200	94434600
89100800	89110400	90412400	90415800	94452400	94455200
89134000	89140400	90433200	90434800	94460600	94464000
89191200	89201000	90528000	90530800	94468000	94470200
89202000	89204000	90773000	90774000	94480800	94488800
89218000	89224000	91837000	91840800	94560200	94563800
89260000	89261800	91908200	91909400	94586600	94595600
89271600	89275000	91973800	91975000	94601800	94603400
89285200	89287400	91990400	91991800	94614400	94616400

89302200	89306200	92049600	92050800	94623000	94625200
89318600	89324400	92084600	92085600	94734200	94737800
89451200	89453000	92289800	92290800	94748400	94750200
89602200	89603600	92383000	92383800	94800000	94801800
89616400	89617800	92412800	92414000	94831000	94836600
89633600	89636400	92698000	92700000	94928400	94939000
89663800	89665400	92814600	92818800	95003800	95005400
89668800	89671000	92829400	92831400	95040400	95045000
89671800	89673600	92927000	92928600	95066000	95068000
89698000	89704000	92931600	92934000	95083600	95091200
89709000	89711400	93084000	93097200	95092800	95100400
89713600	89718000	93098000	93102000	95110000	95113000
89718800	89722200	93159200	93161600	95113800	95125200
89868600	89870800	93169400	93170200	95207800	95211000
89891200	89893000	93171000	93172000	95321400	95323200
90045200	90049200	93323800	93327200	95448600	95450600
90207000	90208800	93415600	93417800	95453400	95456600

90215000	90217000	93563800	93566000	95466200	95471600
90279200	90281200	94115600	94119200	95478800	95481600
90292600	90302200	94132600	94135600	95494600	95500600
90340200	90344000	94147600	94149400		

Table S6. List of PCR primers used for quantitative RT-PCR

Gene	Accession number	Forward/reverse primers
Smarca/Brg1	NM_009351	F:CGTAAGCGTAAGCGAGAC R:CATCTTCTGGTGAGGTTAGG
Flg2	NM_001013804	F:GGAACAGAAGGACAGGAG R:TATGTATATAGCGGAGTATTGC
Gabpb2	NM_026493	F:TTCCACTTAGTTCTGACATCTG R:GTACATAAAGCTGCCAGACAAC
Ivl	NM_008412	F:GCAGGAGAAGTAGATAGAG R:TTAAGGAAGTGTGGATGG
Lce1a1	NM_025984	F:TTCACCAGCAGAGATGTC R:CCAGACTACAGCAGGAAG
Lce1a2	NM_028625	F:TTCACCAGCAGAGATGTC R:TACAGCAGGAAGACACAG
Lce3	NM_033175	F:CCAGTTCTGCCGAGATG R:ACTTTGGAGAGGGACACTTG
Lor	NM_175656	F:TTCCAACCCTCACATTTAAG R:GGGAGGTAGTCATTAGAAC
Rps27	NM_033596	F:CTGCTCCACTGTCCTCTG R:GGTTCCCCTCATCTTCAATC

Table S7. List of PCR primers used for quantitative PCR after Chromatin Immuno-Precipitation

Genomic Region	Forwar/reverse primers
Brg1 893/1050	F: GCCCTTCCCAGTTTAAGATAG R:ACTCAAAGGCTGTCTGTCAGTTC
Brg1 1181/1440	F: GCAAATCGTTCCCTACATCATCA R:AAGGAGAAACGTCCCCATATT
Cld1 promoter	F: TGGAAGCATCCCTGTTTC R:TTGCTGTCCTCTGGGTCT

Table S8. List of primary antibodies

Antigen	Host	Dilution	Manufacturer
p63a	Rabbit	1:200	Santa Cruz Biotechnology, Santa Cruz, CA, USA
Satb1	Rabbit	1:100	Cell Signaling, Denvers, MA, USA
Loricrin	Rabbit	1:1000	Covance, Emeryville, CA
Ki-67	Rabbit	1:200	Abcam, Cambridge, UK
SC-35	Mouse	1:20	Sigma, St Louis, MO
Smarca4/Brg1	Rabbit	1:200	Santa Cruz Biotechnology, Santa Cruz, CA, USA