EMBO79677R

A unique role of Cohesin-SA1 in gene regulation and development

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Supplementary Figure Legends

Figure S1. SA2 expression remains unchanged in SA1-null embryos.

(A) Immunohistochemistry with SA1 and SA2 antibodies performed on tissue sections from wild-type and SA1-null E17.5 embryos. Scale bars, 5mm. I. Brain cortex. Scale bars, 100 μm. II. Interscapular adipose tissue. Scale bars, 50 μm. III. Skin. Scale bars, 50 μm. IV. Liver. Scale bars, 200 μm. V. Kidney. Scale bars, 50 μm. **(B)** Immunoblot analysis of brains from wild-type and SA1-null E17.5 embryos with the indicated antibodies. Tubulin was used as loading control. **(C)** mRNA levels of all cohesin complex subunits in brains from SA1-null E17.5 embryos relative to the wild-type littermates (3 embryos per genotype and 3 independent qPCR reactions per condition).

Figure S2. Chip-seq validation.

(A) Antibodies against SA1, SA2, SMC1 and SMC3 used for ChIP were previously tested for immunoprecipitation using a mouse cell extract enriched in chromatin-bound proteins. Immunoblot analysis with an antibody against Rad21, a subunit common to both cohesin-SA1 and cohesin-SA2, was used to assess the efficiency of the immunoprecipitation reactions. **(B)** Antibody validation for ChIP was done by ChIP-qPCR analysis of SA1 and SA2 binding to mouse IFNg locus (Hadjur et al., 2009), performed with chromatin from C2C12 mouse myoblasts treated with either mock, SA1 or SA2 siRNAs. **(C)** ChIP-qPCR validation of binding sites identified for SA1, SA2, SMC1 and SMC3 by ChIP-sequencing in wild-type and SA1-null MEFs . Regions with high cohesin occupancy (SA1 positive), low cohesin occupancy (SA1 negative), and negative for cohesin (negative) are shown. Dotted lines indicate the background level (cohesin binding in a negative region) for each antibody. Same analysis was performed for myc promoter and an adjacent negative region **(D)** and for Pcdh genes **(E).** Bars in (C-E) represent the average of two independent experiments performed with two different clones of MEFs per genotype.

Figure S3. Peak overlapping analysis.

(A) Venn diagrams showing the overlap between the binding sites identified for each cohesin subunit (SA1, SA2, SMC1 and SMC3) and CTCF (from Yale Dataset) in wild-type cells. **(B)** Additional Venn diagrams showing the overlap between the indicated groups of binding sites. **(C)** Representative image of the browser showing the redistribution of SMC1 and SMC3 in SA1-null cells with respect to wild-type cells.

Figure S4. Validation of microarray data.

Validation of microarray data from wild-type and SA1-null MEFs performed by RT-qPCR (2 different clones per genotype and 3 independent qPCR reactions). Values are represented as $\log_2$ of fold change (FC) versus wild-type. For statistical analysis, a two-tailed Student's t-test was done (***$p<0.001$, **$p<0.01$, *$p<0.05$).

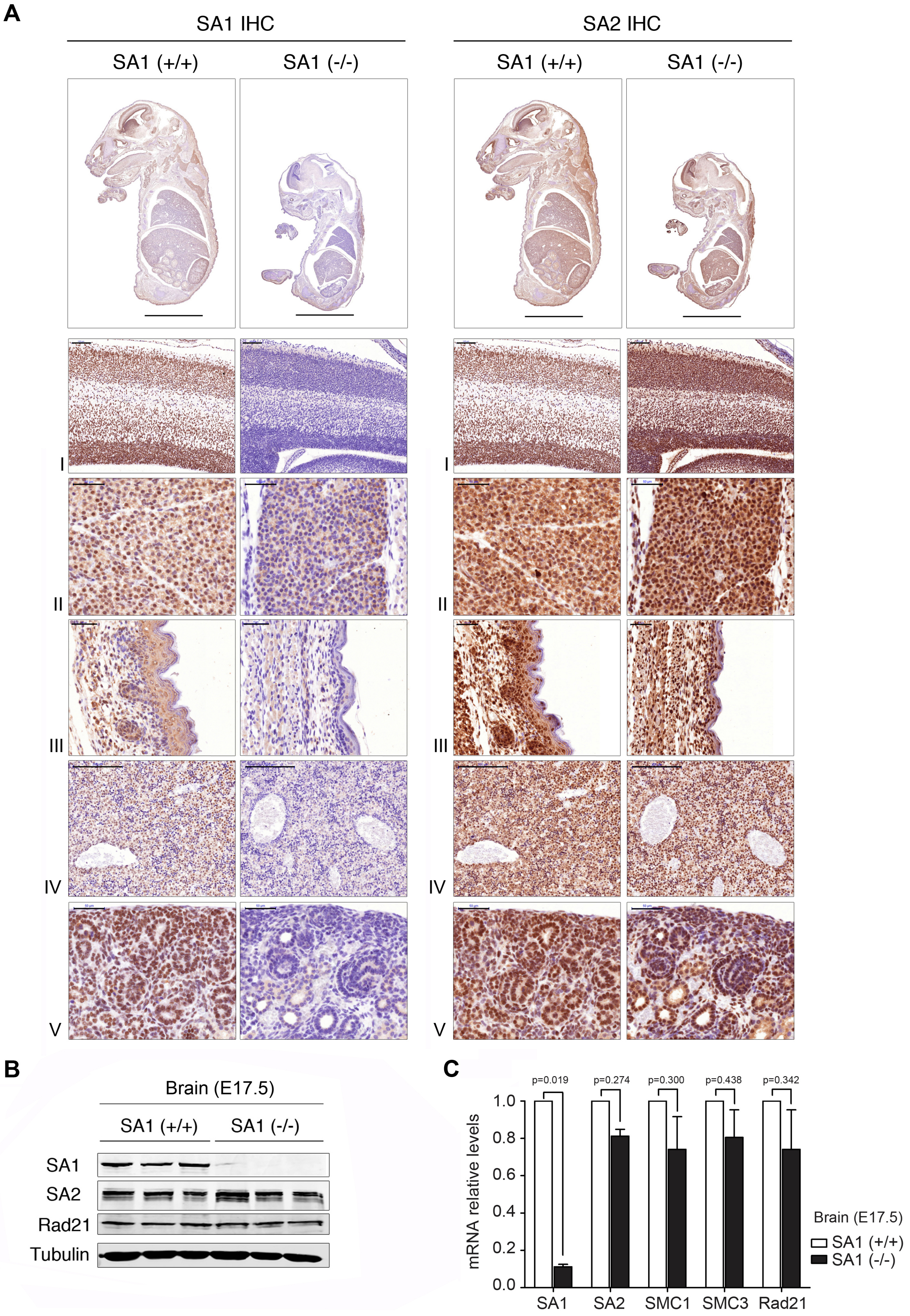
Figure S5. GSEA analysis of Myc target genes.

Gene set enrichment plot of the indicated Myc targets tested in microarrays from SA1-null and wild-type MEFs.

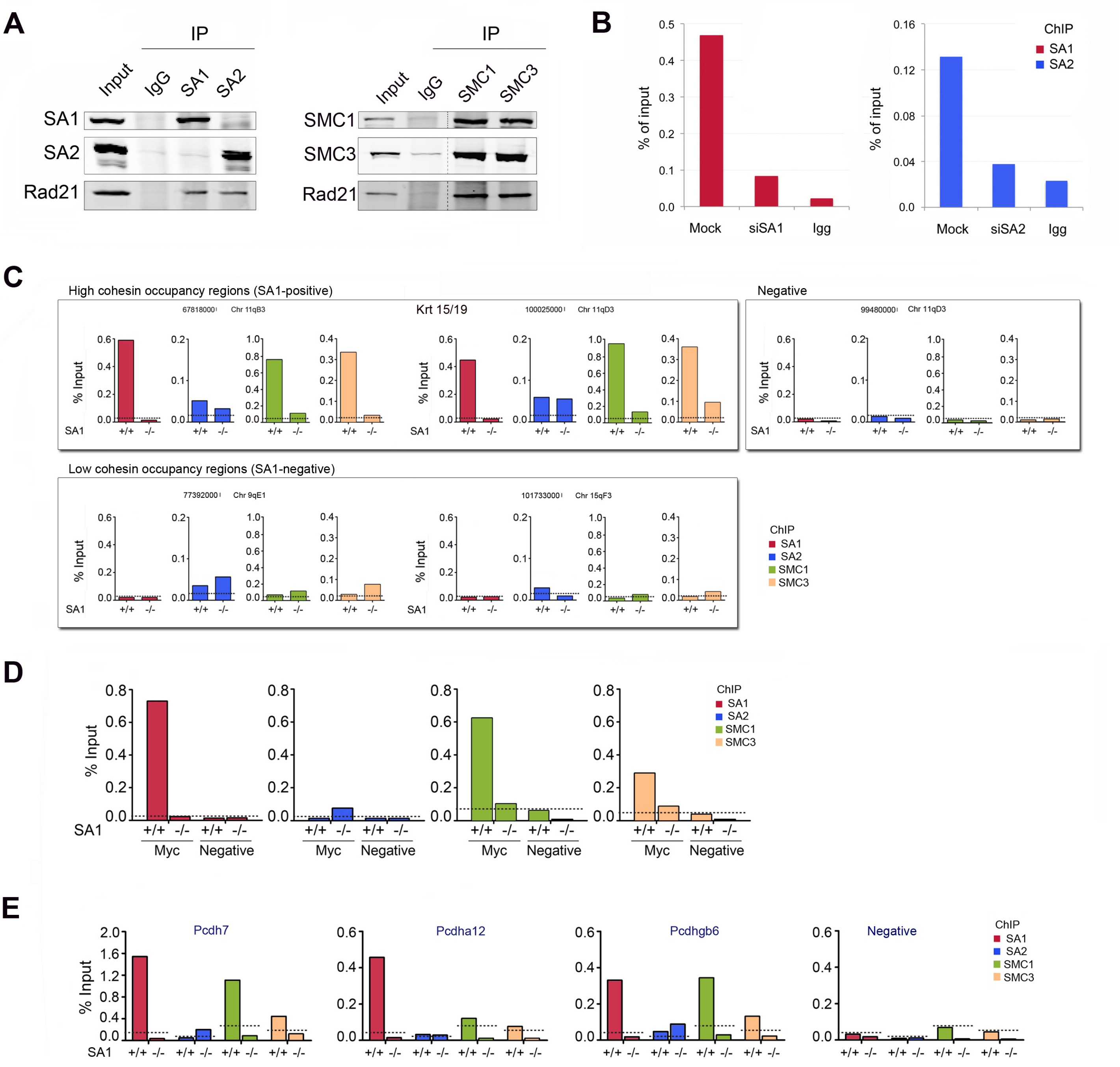
Figure S6. Cohesin-SA1 regulates skin-related genes.

(A) Gene set enrichment plot of the indicated skin-related genes tested in microarrays from SA1-null and wild-type MEFs. **(B)** Distribution of cohesin binding sites at the Cxcl cluster located on chromosome 5.

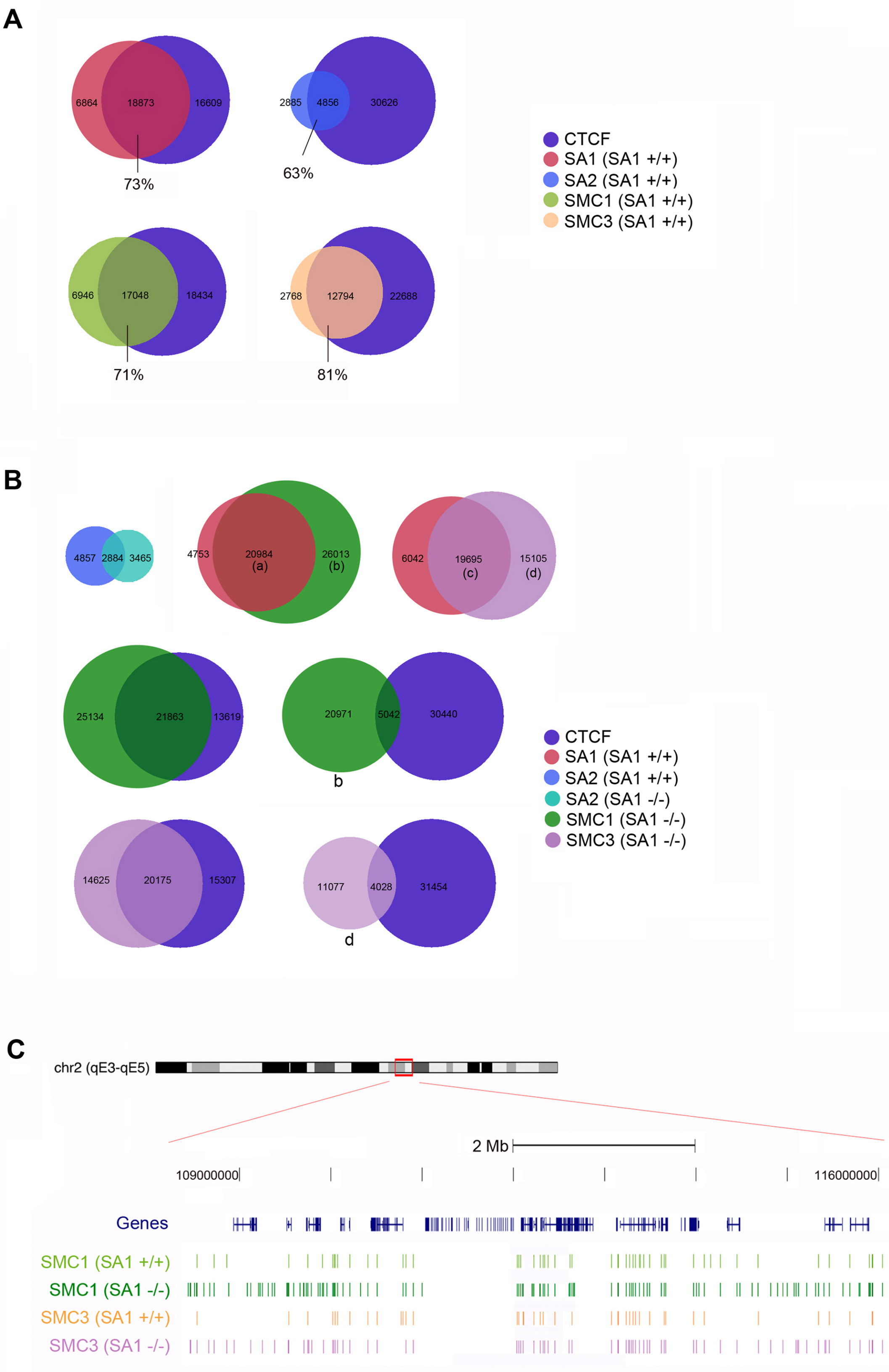
RemeseiroCuadrado_FigureS1



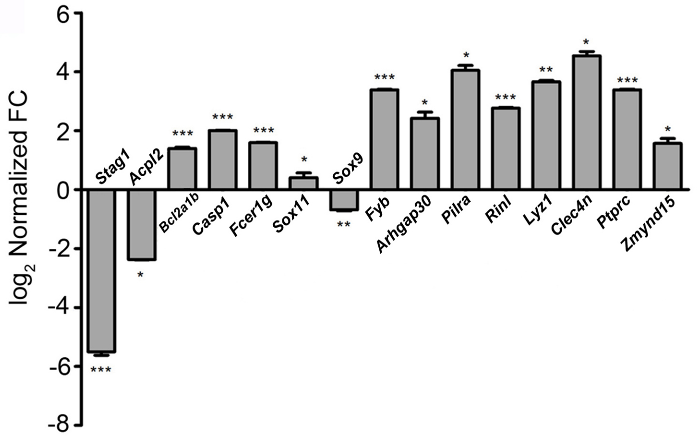
RemeseiroCuadrado_FigureS2



RemeseiroCuadrado_FigureS3

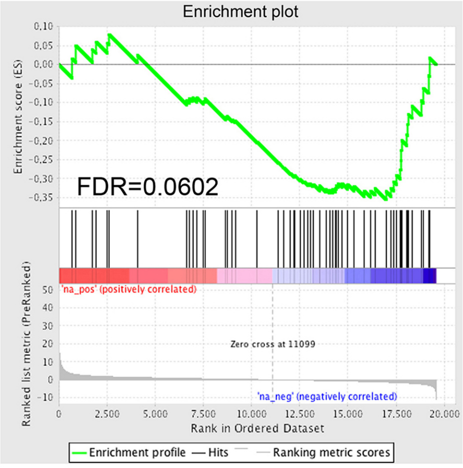


RemeseiroCuadrado_FigureS4



RemeseiroCuadrado_FigureS5

GSEA enrichment plot for MYC targets



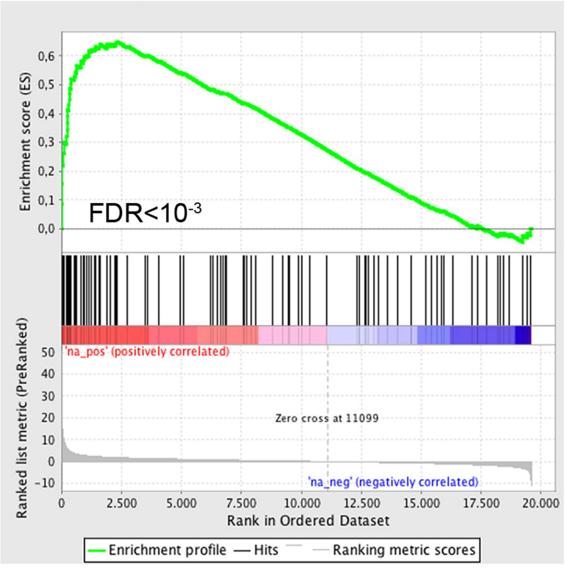
MYC targets gene set

Prdx1
Tardbp
Incenp
Rps27l
Atpif1
Rpl7
Sp1
Slc9a8
Laptm4a
Mrpl50
Zcchc7
Bre
Rps3
Slc3a2
Snrpa
St13
Hspd1
Nudcd2
Cstf1
Ebna1bp2
Pla2g6
Rplp1
Naca
Mcm5
Bc031781
Rps19
Uhrf1
Gars
Arv1
Sf3a1
Cct7
Kif20a
Rplp2
Ubap2
Atad3a
Xpo5
Eef1b2
Ranbp1
Cct4
Paics
Abce1
Mat2b
Tcfap4
Iars
Nolc1
Rsl1d1
Nvl
Mthfd1
Rps25
Nmd3
Ddb1
Luc7l
Nek8
Tcp1
Eef2
Ppan
Ddx39
Rpl32
Atf4

RemeseiroCuadrado_FigureS6

A

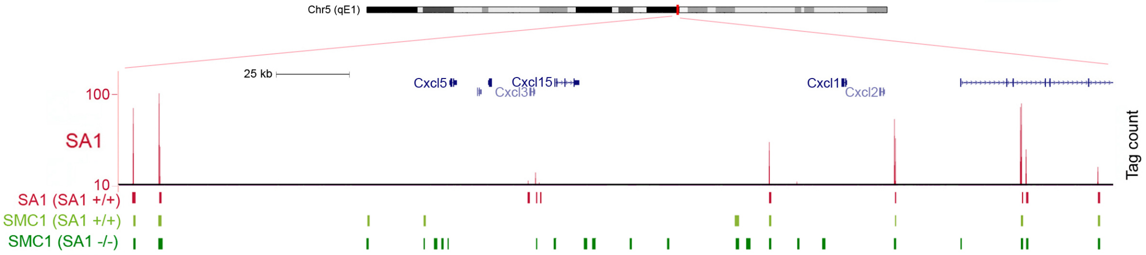
GSEA enrichment plots for skin gene set



Skin gene set

Areg
Btc
Ccl11
Ccl12
Ccl19
Ccl2
Ccl20
Ccl3
Ccl4
Ccl5
Ccl6
Ccl8
Ccl9
Ccr1
Ccr2
Cdh3
Cldn23
Cldnd1
Cts8
Ctsc
Ctss
Cx3cl1
Cx3cr1
Cxcl10
Cxcl11
Cxcl13
Cxcl14
Cxcl16
Cxcl2
Cxcl5
Cxcl9
Defb1
Defb3
Defb6
Epgn
Fil
Flg
Fos
FosL1
FosL2
Gjb2
Gjb3
Gjb4
Gjb5
Gjb6
Hbegf
Il133ra1
Il17a
Il17d
Il18
Il18rap
Il18rb
Il1a
Il1b
Il1f8
Il1r2
Il2ra
Il2rg
Il33
Il4ra
Il6
Itgal
Itgam
Itgb2
JunB
Krt10
Krt12
Krt13
Krt15
Krt16
Krt17
Krt18
Krt19
Krt2
Krt20
Krt25
Krt27
Krt28
Krt32
Krt6a
Krt6b
Krt7
Krt71
Krt75
Krt77
Krt79
Krt8
Krt80
Krt83
Krtap15
Krtap16-7
Krtap2-4
Krtap31-1
Krtap4-13
Krtap4-2
Krtap5-2
Krtap6-2
Krtdap
Lce1a1
Lce1a2
Lce1b
Lce1c
Lce1d
Lce1f
Lce1h
Lce1i
Lce3a
Lce3c
Lcn2
Lcn8
Lor
Lpo
Mmp10
Mmp12
Mmp13
Mmp15
Mmp1a
Mmp1b
Mmp3
Mmp7
Mmp8
Mmp9
Prss8
S100a1
S100a4
S100a5
S100a8
S100b
Scnn1a
Sprr1a
Sprr1b
Sprr2a
Sprr2d
Sprr2f
Sprr2i
Sprr2j
Sprr2k
Tchh
Tgfa
Tgfb1
Tgm1
Tgm3
Timb1
Tslp

B



Supplementary Table S1: ChIP-seq experiment summary. Overall reads obtained in Illumina ChIP-seq experiments. Alignments on NCBIm37 genome assembly were made with Illumina's Eland software (GAPileline 1.4.0), allowing no more than 2 mismatches within 36 base seed lenghts.

Sample	Sequenced reads (QC PASS)	Uniquely aligned reads	% uniquely aligned	Duplicate Filtered Tags (Redundant)
Input 1	30,837,796	21,931,673	71	21,298,545 (3%)
SA1 (SA1 +/+)	33,045,532	22,412,267	68	21,383,266 (5%)
SA2 (SA1 +/+)	34,511,610	21,521,101	62	19,456,228 (10%)
SA2 (SA1 -/-)	35,015,268	22,899,617	65	21,850,166 (5%)
Input 2	38,619369	26,929,896	70	26,239,283 (3%)
SA1 (SA1 -/-)	35,702,433	20,126,016	56	19,465,428 (3%)
SMC1 (SA1 +/+)	34,490,522	21,948,219	64	21,375,089 (3%)
SMC1 (SA1 -/-)	39,771,621	21,088,100	53	20,147,423 (4%)
SMC3 (SA1 +/+)	38,659,833	24,690,999	64	23,975,691 (3%)
SMC3 (SA1 -/-)	37,835,948	26,563,680	70	25,820,540 (3%)

Supplementary Table S2: ChIP-seq experiment, cleaning criteria. Peaks from chromosome Y and Mitochondrial DNA have been discarded. Inputs have been used as control condition in all experiments. Any region enriched in inputs has been eliminated. SA1 signals from SA1-/- have been removed from SA1+/+.

Sample	Regions/Peaks (FDR≤10%)	Input cleaned	SA1-/- cleaned	Double Enrichment
Input 1	436	0		
SA1 (SA1 +/+)	26,602	26,600	26,594	25,737
SA2 (SA1 +/+)	7,741	7,741		
SA2 (SA1 -/-)	6,352	6,349		
Input 2	417	0		
SA1 (SA1 -/-)	177	176		
SMC1 (SA1 +/+)	24,000	23,994		
SMC1 (SA1 -/-)	47,003	46,997		
SMC3 (SA1 +/+)	15,564	15,562		
SMC3 (SA1 -/-)	34,802	34,800		

Sample	Regions/Peaks (FDR≤10%)
CTCF_MEL_YALE	35,482

Supplementary Table S3: Dysregulated genes in SA1-null cells (p<0.01).
(Genes with FDR < 0.15 are shown in bold).

Gene Symbol	Accesion Number	log$_2$FC	p-value
Lyz1	NM_013590	3.63	2.13E-06
Marco	NM_010766	2.94	6.81E-06
Arhgap30	NM_001005508	2.19	1.38E-05
Lyz2	NM_017372	3.55	1.43E-05
Stag1	NM_009282	-3.56	1.59E-05
Msr1	NM_031195	2.75	1.81E-05
Tyrobp	NM_011662	3.13	1.92E-05
Igsf6	NM_030691	2.60	2.17E-05
Rapgef5	AK122234	1.99	2.61E-05
Ms4a7	NM_001025610	3.08	3.64E-05
Msr1	NM_031195	2.54	3.70E-05
Casp1	NM_009807	2.19	3.92E-05
AF251705	NM_134158	1.87	4.05E-05
Lyz2	NM_017372	2.72	4.43E-05
Mmp3	NM_010809	1.86	4.89E-05
Ms4a7	NM_001025610	2.85	5.41E-05
Hpgd	NM_008278	1.75	5.43E-05
Fyb	NM_011815	2.78	5.48E-05
Myo1f	NM_053214	2.12	5.64E-05
Pilra	NM_153510	2.43	5.69E-05
Lcp1	NM_008879	2.64	5.88E-05
BC013712	AK137465	2.83	6.21E-05
Ptprc	NM_011210	2.90	6.24E-05
Ebi3	NM_015766	2.03	6.42E-05
Cd14	NM_009841	1.91	6.87E-05
Alox5ap	NM_009663	2.67	7.05E-05
Lrrc25	NM_153074	2.45	7.05E-05
Clec4n	NM_020001	3.43	7.40E-05
Pilrb1	NM_133209	2.31	7.55E-05
Ptprc	NM_011210	2.95	8.24E-05
Ccl6	NM_009139	2.26	8.41E-05
Dock10	XM_891407	1.43	8.43E-05
Lair1	NM_178611	2.57	8.58E-05
Fcer1g	J05020	2.63	8.74E-05
Tcfec	NM_031198	1.33	9.14E-05
Itgal	AK156251	2.32	9.16E-05
Arhgap30	NM_001005508	2.11	9.62E-05
Stag1	NM_009282	-2.19	9.94E-05
Stag1	NM_009282	-3.53	1.01E-04
Ptprc	NM_011210	2.94	1.02E-04
Clec5a	NM_001038604	3.31	1.03E-04

Clec4a2	NM_011999	2.16	1.05E-04
Ptprc	NM_011210	2.81	1.07E-04
Ptprc	NM_011210	2.85	1.07E-04
Ptprc	NM_011210	2.95	1.10E-04
Ptprc	NM_011210	2.84	1.10E-04
Ncf4	NM_008677	3.15	1.11E-04
Tm6sf1	NM_145375	1.92	1.15E-04
Rinl	NM_177158	1.17	1.22E-04
Hk3	NM_001033245	1.32	1.24E-04
Rnd1	NM_172612	1.32	1.35E-04
Cxcl16	NM_023158	2.18	1.39E-04
Ptprc	NM_011210	2.89	1.43E-04
Tnf	NM_013693	1.20	1.45E-04
Hcls1	NM_008225	3.03	1.48E-04
Ms4a6d	AB026047	2.92	1.51E-04
Lrrc33	NM_146069	2.75	1.52E-04
Ptprc	NM_011210	2.91	1.52E-04
Acpl2	NM_153420	-2.14	1.55E-04
AF251705	NM_134158	2.82	1.56E-04
Bcl2a1b	NM_007534	2.98	1.58E-04
Ptprc	NM_011210	2.85	1.65E-04
Lrmp	NM_008511	1.76	1.81E-04
Lcp1	NM_008879	1.64	1.82E-04
Tnf	NM_013693	1.17	1.86E-04
Psmb9	NM_013585	1.34	1.86E-04
Rgs14	NM_016758	1.15	1.89E-04
Ptpn7	NM_177081	1.41	1.98E-04
Fcgr3	NM_010188	2.82	2.04E-04
Cd68	NM_009853	1.77	2.19E-04
Btk	NM_013482	1.48	2.23E-04
Lair1	NM_178611	1.69	2.25E-04
Oas1a	NM_145211	1.12	2.35E-04
Batf	NM_016767	1.03	2.36E-04
Zmynd15	NM_001029929	1.50	2.52E-04
Pycard	NM_023258	2.35	2.69E-04
Ptpro	NM_011216	1.78	2.90E-04
NA	TC1658525	2.09	3.06E-04
Msr1	NM_031195	2.58	3.10E-04
Cd84	NM_013489	1.81	3.11E-04
Cd200r1	NM_021325	0.96	3.13E-04
Plek	NM_019549	1.90	3.19E-04
Parvg	NM_022321	1.00	3.21E-04
Srgn	NM_011157	3.68	3.26E-04
Clec5a	NM_021364	1.35	3.26E-04
Neurl3	NM_153408	1.24	3.43E-04

Plek	NM_019549	2.16	3.50E-04
AI662270	AK028715	1.26	3.55E-04
P2ry6	NM_183168	2.50	3.63E-04
Bcl2a1c	NM_007535	1.81	3.88E-04
NA	XM_129176	2.62	3.96E-04
Samsn1	NM_023380	2.64	3.99E-04
Rapgef5	AK122234	1.68	4.00E-04
NA	A_51_P402908	2.28	4.04E-04
Cd86	NM_019388	0.88	4.05E-04
Btk	NM_013482	1.31	4.08E-04
Ncf2	NM_010877	2.50	4.18E-04
1810011H11Rik	AK007434	2.73	4.26E-04
Cd72	AK144191	2.09	4.36E-04
Lpxn	NM_134152	2.19	4.45E-04
Arhgap25	NM_001037727	2.75	4.59E-04
Bst1	NM_009763	1.38	4.62E-04
Coro1a	NM_009898	2.87	4.84E-04
Stab1	NM_138672	2.77	4.88E-04
Trem1	NM_021406	1.24	4.92E-04
Tnf	NM_013693	1.35	5.00E-04
Dlk1	L12721	-1.00	5.04E-04
Trem2	NM_031254	3.06	5.10E-04
Nckap1l	NM_153505	2.65	5.11E-04
Cd52	NM_013706	3.23	5.16E-04
Btk	NM_013482	1.39	5.34E-04
Cxcl16	NM_023158	1.88	5.40E-04
Trem2	NM_031254	2.24	5.58E-04
Oas1f	NM_145153	1.47	5.64E-04
Wdfy4	AK155186	2.66	5.66E-04
Psmb8	NM_010724	1.73	5.66E-04
Dennd1c	NM_153551	1.93	5.73E-04
Lpxn	NM_134152	2.09	5.79E-04
Snx20	NM_027840	2.37	5.82E-04
Tnf	NM_013693	1.35	5.84E-04
B3galt5	NM_033149	1.90	5.85E-04
Slc7a8	NM_016972	2.79	5.93E-04
Itgal	NM_008400	0.84	5.98E-04
Tnf	NM_013693	1.37	6.05E-04
Tm6sf1	NM_145375	2.18	6.08E-04
Adra2a	NM_007417	-0.95	6.09E-04
Pilra	AK041670	0.88	6.10E-04
Ap1s3	NM_183027	0.84	6.12E-04
Slc15a3	NM_023044	2.15	6.26E-04
Ptpn6	NM_001077705	2.66	6.29E-04
Pik3r5	NM_177320	1.19	6.30E-04

Rcsd1	NM_178593	1.67	6.34E-04
Tnf	NM_013693	1.26	6.40E-04
Slc5a7	NM_022025	-1.21	6.42E-04
Hhex	NM_008245	2.09	6.48E-04
Epsti1	NM_029495	0.78	6.51E-04
Lat2	NM_020044	2.12	6.51E-04
Egr3	AK141603	-1.15	6.54E-04
Fcgr3	NM_010188	3.03	6.61E-04
C5ar1	NM_007577	0.74	6.82E-04
Tnf	NM_013693	1.34	6.85E-04
Rac2	NM_009008	2.86	6.88E-04
Ms4a6d	NM_026835	2.93	6.98E-04
Tnf	NM_013693	1.19	7.03E-04
Hpgd	NM_008278	1.88	7.03E-04
Hpgds	NM_019455	1.32	7.08E-04
Sp110	NM_175397	2.68	7.09E-04
Eps8	NM_007945	-1.17	7.13E-04
Gm10345	AK005822	1.47	7.16E-04
Psmb8	NM_010724	1.50	7.20E-04
Slc39a4	NM_028064	1.31	7.29E-04
Btk	NM_013482	1.39	7.37E-04
Plscr2	NM_008880	1.24	7.63E-04
Cd72	NM_007654	1.96	7.65E-04
Btk	NM_013482	1.43	7.70E-04
Tnf	NM_013693	1.28	7.71E-04
Creg2	NM_170597	0.88	7.74E-04
Rab3il1	BC020147	1.13	7.80E-04
Fcgr2b	NM_001077189	3.89	7.94E-04
Spon2	NM_133903	-1.20	8.11E-04
Btk	NM_013482	1.29	8.22E-04
Fcgr2b	NM_001077189	3.72	8.28E-04
Vegfc	NM_009506	0.73	8.42E-04
Fcer1g	NM_010185	2.70	8.51E-04
Lst1	AF000427	1.74	8.58E-04
Arhgap9	NM_146011	1.15	8.60E-04
Tal1	NM_011527	1.73	8.82E-04
Ly6a	NM_010738	-1.75	8.84E-04
Mdk	NM_010784	-0.86	8.85E-04
Ctss	NM_021281	4.15	8.89E-04
Evi2a	NM_001033711	1.58	8.89E-04
Il6	NM_031168	0.96	9.13E-04
Fcgr2b	NM_001077189	3.77	9.19E-04
Pycard	NM_023258	1.81	9.24E-04
Trim30	NM_009099	1.33	9.37E-04
Ms4a6c	NM_028595	2.39	9.38E-04

Ptpn18	U52523	3.11	9.56E-04
Tnni2	NM_009405	0.91	9.62E-04
Pdgfra	NM_011058	-0.91	9.77E-04
C1qc	NM_007574	2.87	9.79E-04
Myo1g	NM_178440	2.41	9.90E-04
Slc11a1	NM_013612	2.32	1.01E-03
Csf2ra	NM_009970	1.42	1.05E-03
Plscr2	NM_008880	0.97	1.05E-03
Ifi27l2a	AK010014	1.19	1.05E-03
Fcgr2b	NM_001077189	3.59	1.05E-03
Fcgr2b	NM_001077189	3.89	1.07E-03
Tnf	NM_013693	1.32	1.07E-03
Hfe	NM_010424	0.64	1.07E-03
Cfp	NM_008823	2.62	1.08E-03
Btk	NM_013482	1.32	1.08E-03
Pdgfra	NM_011058	-0.92	1.09E-03
Traf3ip3	NM_153137	1.14	1.10E-03
Rhbdf2	NM_172572	1.21	1.12E-03
Btk	NM_013482	1.44	1.13E-03
Gpr65	NM_008152	2.82	1.13E-03
Sned1	NM_172463	-1.23	1.13E-03
Fermt3	NM_153795	1.89	1.14E-03
Zfp386	AK220544	-1.17	1.15E-03
Ccdc88b	BC038890	2.64	1.15E-03
Arap3	NM_139206	2.26	1.16E-03
Fcgr2b	NM_001077189	3.80	1.17E-03
Rgs17	NM_019958	-1.01	1.21E-03
C130050O18Rik	NM_177000	1.52	1.22E-03
Fyb	NM_011815	1.31	1.22E-03
Vav1	NM_011691	2.34	1.22E-03
Sox11	AK004158	1.11	1.22E-03
Nufip2	NM_001024205	-0.76	1.24E-03
Fam78a	NM_175511	1.32	1.25E-03
Parp14	NM_001039530	1.56	1.27E-03
Akap5	AK014386	1.18	1.29E-03
Fcgr2b	NM_001077189	3.79	1.29E-03
Vldlr	AK036010	-0.64	1.29E-03
Adam8	NM_007403	2.39	1.30E-03
Fcgr1	NM_010186	3.06	1.30E-03
Efs	NM_010112	-0.80	1.31E-03
Acot2	NM_134188	-0.80	1.32E-03
Eps8	NM_007945	-0.89	1.36E-03
Fcgr2b	NM_001077189	3.71	1.37E-03
Cyth1	NM_011180	0.66	1.37E-03
Amot	AK129277	0.71	1.38E-03

Trpv2	NM_011706	0.71	1.38E-03
Pkib	NM_001039050	1.15	1.39E-03
Aif1	NM_019467	2.98	1.39E-03
5430427O19Rik	AK155591	1.50	1.46E-03
D1Ertd622e	NM_133825	0.71	1.49E-03
St8sia4	NM_009183	1.50	1.50E-03
Sox11	AK004158	1.24	1.52E-03
Btk	NM_013482	1.28	1.52E-03
Fcgr2b	NM_001077189	3.71	1.52E-03
Pcdh21	NM_130878	-0.71	1.53E-03
Efemp1	NM_146015	-2.20	1.54E-03
Sh3tc1	NM_194344	1.33	1.56E-03
Cables1	NM_022021	0.75	1.57E-03
Pdgfra	NM_011058	-0.93	1.57E-03
Clec4d	NM_010819	2.97	1.59E-03
Nrn1	NM_153529	-1.64	1.59E-03
Trem1	NM_021406	0.97	1.59E-03
Gpbp1l1	AK139506	0.83	1.60E-03
Ces1	NM_021456	1.16	1.64E-03
Pilrb2	NM_001024932	1.15	1.65E-03
Emr1	NM_010130	0.61	1.66E-03
NA	TC1655572	-0.72	1.66E-03
Trpv4	NM_022017	-1.21	1.68E-03
Apobec1	NM_031159	1.86	1.68E-03
Sirpa	NM_007547	1.73	1.71E-03
Sirpb1	NM_178792	1.11	1.71E-03
Adarb1	NM_001024840	0.76	1.72E-03
Ecm1	NM_007899	-1.18	1.72E-03
Ifi27l2a	NM_029803	1.21	1.74E-03
Col4a4	NM_007735	-0.72	1.74E-03
Fcgr2b	NM_001077189	3.18	1.76E-03
Il6	NM_031168	1.02	1.76E-03
6430548M08Rik	AK133157	0.57	1.77E-03
Fcgr2b	NM_001077189	3.66	1.77E-03
Emr1	NM_010130	3.13	1.78E-03
Ambp	NM_007443	1.48	1.80E-03
Clec4a2	NM_011999	1.19	1.82E-03
Synpo	AK034012	-0.81	1.83E-03
Hdac9	NM_024124	0.69	1.83E-03
Arl15	NM_172595	-0.66	1.83E-03
Il6	NM_031168	0.97	1.84E-03
Il6	NM_031168	1.04	1.84E-03
Ms4a6b	NM_027209	3.81	1.85E-03
Mri1	NM_026423	-0.65	1.90E-03
Rhoh	BC094937	1.21	1.90E-03

H2afj	NM_177688	0.56	1.90E-03
Sp100	BC069183	0.57	1.94E-03
Rnd1	AK039992	0.64	1.98E-03
Clec4b1	NM_027218	1.67	1.98E-03
Was	NM_009515	1.94	1.98E-03
Kctd8	NM_175519	-0.76	2.00E-03
Idh3a	NM_029573	0.55	2.01E-03
Gpr84	NM_030720	3.06	2.02E-03
Glipr1	NM_028608	1.31	2.03E-03
Tcea3	NM_011542	-0.88	2.03E-03
Laptm5	NM_010686	1.45	2.04E-03
Acpl2	NM_153420	-0.60	2.04E-03
Vav1	NM_011691	2.13	2.05E-03
Tnfsf11	NM_011613	-0.63	2.05E-03
Plcg2	NM_172285	1.77	2.06E-03
Vcan	D28599	-0.79	2.07E-03
Ccl2	NM_011333	1.22	2.07E-03
NA	TC1717239	0.55	2.08E-03
6330442E10Rik	NM_178745	1.16	2.10E-03
Pdlim4	NM_019417	0.80	2.12E-03
Fcgr2b	NM_010187	3.06	2.12E-03
Pdgfra	NM_011058	-0.95	2.13E-03
Mgll	NM_011844	1.06	2.14E-03
Pdgfra	NM_011058	-0.93	2.15E-03
Fgl1	AK083397	0.63	2.15E-03
Ccl2	NM_011333	1.18	2.16E-03
Rnd1	BC048531	0.53	2.18E-03
Dcaf12l2	NM_175539	0.71	2.18E-03
NA	NM_001045537	0.53	2.21E-03
Tmem206	NM_025864	0.90	2.21E-03
Cobl	NM_172496	0.94	2.22E-03
NA	NAP037326-1	2.14	2.23E-03
Pdgfra	NM_011058	-0.91	2.24E-03
Ccl2	NM_011333	1.23	2.24E-03
Ccl2	NM_011333	1.16	2.27E-03
Trerf1	NM_172622	-0.74	2.28E-03
Mri1	NM_026423	-0.78	2.28E-03
Cd53	NM_007651	1.97	2.29E-03
Csf2rb	AK154286	2.66	2.29E-03
Mgat4a	NM_173870	0.68	2.31E-03
Chmp4b	NM_029362	-0.75	2.31E-03
Blnk	NM_008528	2.69	2.31E-03
Csf1r	NM_001037859	2.87	2.32E-03
Col15a1	NM_009928	-0.81	2.33E-03
Ccl2	NM_011333	1.21	2.34E-03

Lat2	NM_020044	0.86	2.34E-03
Lonrf3	NM_028894	1.44	2.34E-03
Cnn1	NM_009922	0.65	2.34E-03
NA	TC1709674	0.53	2.37E-03
C1qa	NM_007572	2.84	2.40E-03
Raet1e	NM_198193	-1.10	2.41E-03
Il6	NM_031168	0.86	2.43E-03
Il6	NM_031168	0.85	2.44E-03
Sncg	NM_011430	-0.95	2.45E-03
Il6	NM_031168	0.98	2.46E-03
Tnfaip8l2	NM_027206	1.81	2.47E-03
H1f0	NM_008197	-0.53	2.47E-03
Pdgfra	NM_011058	-0.83	2.50E-03
Cd48	NM_007649	1.38	2.50E-03
Ccl2	NM_011333	1.23	2.53E-03
Igf1	NM_010512	1.59	2.53E-03
Fam105a	NM_198301	1.45	2.55E-03
Clec4e	NM_019948	1.81	2.55E-03
NA	XM_203796	0.52	2.55E-03
Pdgfra	NM_011058	-0.88	2.57E-03
Ccl2	NM_011333	1.22	2.59E-03
Irf8	NM_008320	2.63	2.62E-03
Coro1a	NM_009898	2.36	2.62E-03
Arhgap4	NM_138630	2.12	2.64E-03
Sfpi1	NM_011355	0.94	2.65E-03
H2-DMb1	NM_010387	0.71	2.65E-03
Bmp2k	NM_080708	1.21	2.65E-03
Rab20	NM_011227	0.60	2.69E-03
Ly6c2	D86232	-1.81	2.70E-03
Ccl2	NM_011333	1.21	2.71E-03
Ifi27l2a	NM_029803	0.78	2.71E-03
Tlr1	NM_030682	0.96	2.74E-03
Crct1	NM_028798	0.72	2.74E-03
Plxnc1	AK011113	0.92	2.74E-03
Mafb	NM_010658	1.89	2.75E-03
Igf1	NM_010512	1.61	2.76E-03
Sirpb1	AK054545	2.15	2.76E-03
Cysltr1	NM_021476	1.09	2.76E-03
Inpp5d	NM_010566	2.97	2.77E-03
Ppap2b	NM_080555	-1.14	2.79E-03
Wisp2	NM_016873	-1.41	2.82E-03
Brwd2	NM_172255	-0.66	2.83E-03
Wnk4	NM_175638	-0.51	2.84E-03
Ebf2	NM_010095	-0.95	2.89E-03
Ncf1	NM_010876	1.38	2.90E-03

Epb4.1l1	NM_001003815	-0.54	2.92E-03
NA	A_52_P517668	0.63	2.94E-03
Tceal1	NM_146236	-0.52	2.95E-03
Ugdh	NM_009466	-0.95	2.96E-03
Tgm2	NM_009373	1.15	2.98E-03
Cyth4	NM_028195	1.93	2.99E-03
Rac2	NM_009008	2.14	3.03E-03
Klra7	NM_014194	0.70	3.06E-03
Pdgfra	NM_011058	-0.88	3.09E-03
Adra2a	NM_007417	-0.82	3.10E-03
Rcor3	AK135612	-0.63	3.13E-03
Mtap1a	AK018185	-0.66	3.13E-03
NA	NM_001033187	-0.63	3.14E-03
Cd83	NM_009856	1.29	3.14E-03
Plxna2	NM_008882	-0.66	3.18E-03
Cd55	AK030285	-0.63	3.18E-03
D630045M09Rik	AK131952	0.55	3.18E-03
Dnajc10	NM_024181	-0.52	3.18E-03
Treml1	NM_027763	0.88	3.21E-03
Ccl2	NM_011333	1.25	3.24E-03
NA	AK013239	0.64	3.26E-03
Luc7l2	NM_138680	0.48	3.29E-03
Unc93b1	NM_019449	1.69	3.33E-03
Lst1	NM_010734	0.51	3.34E-03
Cd300lf	AF251703	0.48	3.35E-03
Gmfg	NM_022024	2.65	3.35E-03
Ank3	NM_146005	-0.76	3.35E-03
Igf1	NM_010512	1.57	3.35E-03
Itgb2	NM_008404	1.81	3.36E-03
Icam1	BC008626	1.91	3.37E-03
Lilrb3	NM_011095	2.52	3.39E-03
Nfam1	NM_028728	1.25	3.39E-03
Lmo4	NM_010723	-0.70	3.40E-03
Dok3	NM_013739	1.55	3.40E-03
Ces1	NM_021456	0.60	3.41E-03
Cox6a2	NM_009943	-0.59	3.43E-03
Il6	NM_031168	0.91	3.45E-03
Cd200r1	NM_021325	0.56	3.45E-03
Rab3il1	BC020147	1.16	3.45E-03
Madd	NM_145527	1.09	3.46E-03
Ptma	NM_008972	0.51	3.47E-03
Siglec5	NM_145581	0.77	3.48E-03
Sox11	NM_009234	0.62	3.49E-03
Igf1	NM_010512	1.59	3.50E-03
Gpt2	NM_173866	-0.78	3.50E-03

NA	NAP071060-1	-0.64	3.50E-03
Rhbdf2	NM_172572	0.89	3.51E-03
Alox5	NM_009662	2.57	3.51E-03
Igf1	NM_010512	1.56	3.54E-03
Igf1	NM_184052	1.47	3.55E-03
Pdgfra	NM_011058	-0.88	3.57E-03
Igf1	NM_010512	1.59	3.58E-03
Nfatc4	NM_023699	-0.68	3.58E-03
C1qb	NM_009777	2.70	3.59E-03
Igfbp6	NM_008344	-0.72	3.59E-03
Atf5	NM_030693	-1.03	3.62E-03
LOC675366	XM_981337	0.52	3.63E-03
Icam1	BC008626	1.95	3.63E-03
Gm7120	NM_001039244	-0.79	3.64E-03
Ly6c1	NM_010741	-1.49	3.65E-03
Ptprj	NM_008982	0.51	3.69E-03
Tpbg	AK050794	-0.75	3.74E-03
Aatk	NM_007377	1.64	3.75E-03
Col16a1	NM_028266	-0.76	3.76E-03
NA	XM_884305	-0.53	3.77E-03
Tcta	NM_133986	-0.51	3.80E-03
Scrn3	NM_029022	-0.48	3.83E-03
Btk	NM_013482	1.18	3.84E-03
Icam1	BC008626	1.92	3.84E-03
Adamtsl5	AK154947	-0.52	3.85E-03
Hoxd8	NM_008276	-0.79	3.86E-03
Tnfaip2	NM_009396	-1.15	3.86E-03
Fgd3	NM_015759	0.59	3.90E-03
Icam1	BC008626	1.94	3.90E-03
Lrrcc1	NM_028915	-0.50	3.91E-03
Rtkn	NM_133641	-0.47	3.91E-03
9030409G11Rik	BC022941	0.61	3.93E-03
Fam20a	NM_153782	-0.72	4.00E-03
Pdgfrb	NM_008809	-0.86	4.02E-03
Dach2	NM_033605	-0.51	4.02E-03
Klhl9	NM_172871	-0.51	4.02E-03
Csf1r	NM_001037859	1.85	4.03E-03
Slc30a1	NM_009579	0.53	4.04E-03
Lmo2	NM_008505	1.17	4.12E-03
Mpped2	AK165186	-0.59	4.12E-03
Icam1	BC008626	1.93	4.13E-03
Sec23a	NM_009147	-0.64	4.13E-03
Icam1	BC008626	1.91	4.18E-03
Tubb3	NM_023279	-0.55	4.19E-03
Apobec3	AK049998	0.52	4.20E-03

Ripk4	NM_023663	0.51	4.23E-03
Bicd2	NM_001039179	0.50	4.24E-03
Snca	NM_001042451	0.93	4.24E-03
Naip2	NM_010872	1.75	4.25E-03
Icam1	BC008626	1.92	4.30E-03
Dip2c	BC089303	-0.45	4.40E-03
Stmn4	NM_019675	1.17	4.40E-03
Igf1	NM_010512	1.59	4.42E-03
Tmem171	NM_001025606	0.68	4.43E-03
Pf4	NM_019932	3.58	4.46E-03
Slc1a4	NM_018861	-0.80	4.46E-03
Tifa	NM_145133	0.66	4.48E-03
6720458D17Rik	AK032822	0.56	4.49E-03
Igf1	NM_010512	1.61	4.52E-03
Icam1	BC008626	2.02	4.52E-03
Ccl2	NM_011333	1.23	4.53E-03
Abhd14b	NM_029631	-0.59	4.53E-03
Ptprb	NM_029928	-0.59	4.54E-03
Hoxc6	X16511	-0.49	4.55E-03
Nfic	NM_008688	-0.49	4.63E-03
Klra15	NM_013793	1.17	4.64E-03
Cxcr7	NM_007722	-0.95	4.64E-03
Fhl1	NM_001077361	1.36	4.66E-03
Fam123a	NM_028113	0.79	4.69E-03
Gjb5	NM_010291	-0.95	4.70E-03
Lilrb3	NM_011095	2.45	4.72E-03
Igf1	NM_010512	1.54	4.72E-03
Shoc2	NM_019658	-0.51	4.73E-03
Icam1	BC008626	1.95	4.73E-03
Ncf1	NM_010876	1.82	4.74E-03
Il10ra	NM_008348	2.19	4.74E-03
Cnr2	NM_009924	1.09	4.74E-03
Pop4	NM_025390	0.61	4.76E-03
Cd86	NM_019388	0.91	4.79E-03
NA	XM_001002437	-0.63	4.81E-03
Rab3il1	NM_144538	0.72	4.82E-03
Lyl1	NM_008535	2.93	4.82E-03
B3gnt8	NM_146184	0.61	4.82E-03
Mpped2	AK165186	-0.50	4.83E-03
NA	TC1618787	-0.54	4.85E-03
Cd55	NM_010016	-0.81	4.86E-03
H2-K1	AK150790	0.68	4.92E-03
March1	NM_175188	2.11	4.96E-03
NA	NM_207269	1.45	4.97E-03
Il6	NM_031168	0.92	4.97E-03

Plxna2	NM_008882	-0.80	4.99E-03
NA	XM_131643	-0.45	4.99E-03
Zfp354c	NM_013922	-0.42	5.03E-03
Gmfg	NM_022024	2.16	5.05E-03
Cxcl10	NM_021274	1.51	5.05E-03
Trim23	NM_030731	-0.56	5.06E-03
NA	XM_983705	0.78	5.08E-03
Dock2	NM_033374	1.14	5.10E-03
Ceacam1	NM_001039185	0.91	5.11E-03
Zfp39	NM_011758	-0.47	5.12E-03
Icam1	BC008626	1.94	5.15E-03
Spon2	NM_133903	-1.54	5.18E-03
Snx2	NM_026386	0.42	5.19E-03
Il6	NM_031168	0.99	5.21E-03
Il1b	NM_008361	2.31	5.22E-03
Vps53	AK009586	0.72	5.25E-03
Eid1	NM_025613	-0.41	5.28E-03
Slamf9	NM_029612	2.58	5.29E-03
Ccrl2	NM_017466	0.60	5.31E-03
Junb	NM_008416	0.41	5.32E-03
Igf1	NM_010512	1.58	5.32E-03
Btg1	NM_007569	-0.69	5.34E-03
Stk10	NM_009288	0.46	5.34E-03
Rmnd1	NM_025343	-0.47	5.34E-03
Angptl4	NM_020581	1.14	5.39E-03
Wdr59	AK173301	-0.51	5.41E-03
Tspan33	NM_146173	1.41	5.43E-03
5730455P16Rik	NM_027472	-0.43	5.43E-03
H2-K1	AK150790	0.63	5.47E-03
Igfbp3	NM_008343	0.42	5.47E-03
Cd248	NM_054042	-1.28	5.53E-03
Col4a3bp	AK020301	0.54	5.55E-03
Gcnt1	NM_173442	1.86	5.64E-03
P2rx7	NM_011027	1.80	5.64E-03
Ldb2	NM_001077398	-0.86	5.66E-03
Exoc6	NM_175353	1.06	5.67E-03
NA	ENSMUST00000102563	2.25	5.69E-03
Rgs2	NM_009061	1.23	5.72E-03
Sirpa	NM_007547	0.61	5.78E-03
Prrx1	NM_175686	-1.21	5.79E-03
Tpd52l1	NM_009413	0.91	5.80E-03
Gpr183	NM_183031	1.53	5.81E-03
Csnk1g3	NM_152809	-0.50	5.82E-03
Tob1	NM_009427	-0.57	5.84E-03

Sirpa	NM_007547	0.45	5.86E-03
Fam38b	BC075677	-0.42	5.87E-03
Abcb1b	NM_011075	0.48	5.89E-03
Gm11428	BC089618	1.88	5.93E-03
Hist3h2a	NM_178218	0.77	5.93E-03
Arf5	NM_007480	-0.58	5.93E-03
Tnfsf11	NM_011613	-0.85	5.96E-03
Rgs1	NM_015811	1.40	5.97E-03
Cybb	NM_007807	1.87	5.97E-03
Irg1	L38281	1.76	5.97E-03
BC004728	NM_174992	1.66	6.01E-03
Il1b	NM_008361	2.25	6.04E-03
Cryl1	NM_030004	0.58	6.06E-03
NA	NAP055718-1	0.52	6.06E-03
C80913	NM_011274	-0.50	6.07E-03
Tubb3	NM_023279	-0.58	6.08E-03
Il1b	NM_008361	2.26	6.09E-03
Cfh	NM_009888	1.79	6.11E-03
Fgd2	NM_013710	1.78	6.14E-03
Unc13d	NM_001009573	0.42	6.14E-03
Gvin1	NM_029000	1.16	6.15E-03
NA	NM_019909	0.66	6.15E-03
Mrc1	NM_008625	2.42	6.15E-03
Laptm5	NM_010686	1.82	6.17E-03
Tmem180	NM_029186	0.63	6.20E-03
Mef2c	NM_025282	0.46	6.20E-03
1700029G01Rik	NM_025856	-0.44	6.21E-03
Slc9a3r2	NM_023449	-0.40	6.21E-03
Il1b	NM_008361	2.15	6.21E-03
Prkcb	NM_008855	1.98	6.22E-03
Tubb3	NM_023279	-0.54	6.25E-03
Gm9885	BC006942	-0.57	6.26E-03
Sppl3	NM_029012	-0.43	6.28E-03
Tubb3	NM_023279	-0.57	6.28E-03
Rnase6	NM_030098	0.49	6.29E-03
Sox9	NM_011448	-0.69	6.30E-03
Trem3	NM_021407	0.54	6.33E-03
Epha4	NM_007936	0.58	6.33E-03
A630001G21Rik	AK041324	0.70	6.33E-03
Il1b	NM_008361	2.33	6.36E-03
H2-K1	AK150790	0.63	6.37E-03
H2-K1	AK150790	0.61	6.40E-03
Pck2	NM_028994	-1.23	6.40E-03
H1f0	NM_008197	-0.56	6.41E-03
Klra22	NM_053152	0.64	6.46E-03

NA	NAP066348-1	0.91	6.48E-03
NA	NAP057003-1	0.54	6.52E-03
Tinagl1	NM_023476	-1.13	6.53E-03
Pgm2l1	NM_027629	0.41	6.55E-03
E2f2	NM_177733	0.94	6.56E-03
Cd244	NM_018729	2.92	6.57E-03
Fes	NM_010194	0.98	6.58E-03
Sec16b	NM_033354	-1.04	6.61E-03
Wnt10a	NM_009518	-0.98	6.64E-03
Rai14	NM_030690	-1.15	6.66E-03
Lcp2	NM_010696	2.29	6.67E-03
Fam20a	NM_153782	-0.71	6.69E-03
Dna2	AK129051	0.43	6.74E-03
Slc1a4	NM_018861	-0.85	6.77E-03
Dlk1	NM_010052	-1.12	6.78E-03
Nav1	NM_173437	-0.65	6.78E-03
Cds1	NM_173370	0.44	6.82E-03
Mboat2	NM_026037	0.48	6.84E-03
Irg1	AK152177	2.00	6.85E-03
Grap	NM_027817	0.68	6.86E-03
Tnfrsf13b	AK004668	0.97	6.86E-03
Acbd3	NM_133225	-0.79	6.87E-03
Tmod3	NM_016963	-1.07	6.88E-03
Fcgr4	NM_144559	1.21	6.88E-03
H2-K1	AK150790	0.64	6.92E-03
Tubb3	NM_023279	-0.58	6.92E-03
Hoxb9	NM_008270	-0.69	6.92E-03
Cd300ld	NM_145437	0.77	6.95E-03
Fam98b	NM_026620	0.44	6.95E-03
Abcb4	NM_008830	0.58	7.04E-03
NA	XM_994784	0.47	7.06E-03
Reg3a	NM_011259	0.48	7.08E-03
Hisppd1	AK087712	-0.43	7.09E-03
Ccr5	NM_009917	2.78	7.09E-03
Rapgef5	AK122234	0.39	7.10E-03
Atpbd4	NM_025675	-0.45	7.11E-03
Irgm2	NM_019440	0.64	7.11E-03
Rprm	NM_023396	1.04	7.14E-03
Coro2a	NM_178893	0.42	7.14E-03
Cyp2j6	NM_010008	-0.48	7.14E-03
Frmd4b	NM_145148	1.34	7.15E-03
Tubb3	NM_023279	-0.57	7.15E-03
Spopl	AK088955	-0.39	7.15E-03
Ahcyl1	NM_145542	-0.49	7.16E-03
Tmem106a	NM_144830	0.70	7.17E-03

Nat8l	NM_001001985	1.22	7.19E-03
Srf	NM_020493	0.39	7.21E-03
Acta2	NM_007392	0.74	7.22E-03
9330180L21Rik	AK029771	0.51	7.24E-03
Tlr2	NM_011905	2.09	7.28E-03
Kdelr1	NM_133950	-1.19	7.29E-03
Cse1l	NM_023565	-0.51	7.32E-03
Serpinb10	NM_198028	0.71	7.36E-03
Fbxl3	NM_015822	-0.49	7.39E-03
Bdnf	NM_007540	-0.40	7.40E-03
Abhd14a	NM_145919	-0.46	7.43E-03
Gstz1	NM_010363	-0.39	7.45E-03
Syngr1	NM_009303	1.47	7.47E-03
Cmbl	NM_181588	-0.66	7.48E-03
Prkg2	NM_008926	-0.57	7.54E-03
Scn1b	NM_011322	-0.57	7.54E-03
Rasgef1b	NM_181318	1.16	7.60E-03
Plcb2	NM_177568	0.51	7.61E-03
Arcn1	NM_145985	-0.70	7.64E-03
Rprm	NM_023396	1.03	7.65E-03
Rab32	NM_026405	0.81	7.66E-03
Rag1ap1	NM_009057	-0.49	7.68E-03
Stk17b	NM_133810	0.40	7.69E-03
Tubb3	NM_023279	-0.54	7.72E-03
Ano1	NM_178642	-0.99	7.73E-03
Nfx1	NM_023739	-0.62	7.73E-03
Il1b	NM_008361	2.23	7.73E-03
Tlr2	NM_011905	2.16	7.75E-03
Rpl13	NM_016738	-0.38	7.75E-03
Cdk5rap3	NM_030248	-0.43	7.75E-03
Lilrb4	NM_013532	1.98	7.77E-03
Pilrb2	NM_001024932	0.48	7.77E-03
Rhoq	NM_145491	-0.46	7.80E-03
Rcn1	NM_009037	-0.68	7.81E-03
Osbpl1a	NM_207530	-0.41	7.85E-03
Rpl5	NM_016980	0.44	7.85E-03
NA	ENSMUST00000100598	-0.49	7.88E-03
Lrrn3	NM_010733	-0.50	7.89E-03
Tubb3	NM_023279	-0.52	7.93E-03
Rai14	NM_030690	-0.84	7.93E-03
Bcat1	NM_001024468	-0.81	7.94E-03
Myl9	BC055439	0.50	7.96E-03
Tlr7	NM_133211	2.04	7.97E-03
Nqo1	NM_008706	-0.78	7.99E-03

Pir	NM_027153	-0.88	8.01E-03
Ccl12	NM_011331	4.03	8.03E-03
Plcl2	NM_013880	1.11	8.11E-03
Bri3bp	NM_029752	-0.59	8.14E-03
Farp2	NM_145519	-0.60	8.15E-03
Sdc4	NM_011521	0.41	8.16E-03
Nlrp6	BC031139	0.61	8.16E-03
Mrc2	NM_008626	-0.73	8.17E-03
Pop4	NM_025390	0.42	8.18E-03
Papola	NM_011112	-0.40	8.21E-03
Il1b	NM_008361	2.18	8.25E-03
Hmgcs1	NM_145942	-0.81	8.25E-03
Ppargc1b	AK042378	0.39	8.26E-03
Il1b	NM_008361	2.18	8.28E-03
Trpc6	NM_013838	-0.58	8.29E-03
Galnt9	NM_198306	-1.23	8.30E-03
5430435G22Rik	NM_145509	0.95	8.30E-03
Il2rg	NM_013563	0.79	8.30E-03
Bcl3	NM_033601	0.67	8.32E-03
Tlr2	NM_011905	2.08	8.40E-03
Rnf2	NM_011277	-0.56	8.40E-03
Hck	NM_010407	1.61	8.41E-03
Nacad	BC072589	-0.51	8.42E-03
Ctsc	NM_009982	2.39	8.47E-03
Sash3	NM_028773	1.74	8.47E-03
Icam1	NM_010493	0.61	8.48E-03
Cyth4	NM_028195	1.34	8.48E-03
Maf	AK132165	0.50	8.49E-03
Nptx2	NM_016789	0.51	8.49E-03
Sepp1	NM_001042614	2.39	8.50E-03
NA	XM_130987	-1.25	8.51E-03
Ssbp3	NM_023672	-0.68	8.52E-03
Ucp2	NM_011671	1.29	8.52E-03
Atp2c1	NM_175025	0.73	8.53E-03
Tlr2	NM_011905	2.14	8.55E-03
Ccdc45	AK089185	-0.36	8.56E-03
Nsbp1	NM_016710	0.84	8.58E-03
Dnase1l1	NM_027109	0.42	8.59E-03
Lmbr1	NM_020295	-0.55	8.60E-03
Ccrl2	NM_017466	0.42	8.60E-03
Abcg2	NM_011920	0.61	8.61E-03
H2-K1	AK150790	0.65	8.68E-03
Adcy3	NM_138305	-0.84	8.71E-03
Dhfr	NM_010049	0.53	8.72E-03
Gamt	NM_010255	-0.56	8.72E-03

Bst2	NM_198095	0.73	8.82E-03
Gng2	NM_010315	0.58	8.82E-03
Lrrc42	NM_029985	-0.47	8.82E-03
Tubb3	NM_023279	-0.58	8.82E-03
C330007P06Rik	BC021479	-0.41	8.84E-03
Cab39	NM_133781	0.40	8.89E-03
Caprin1	AK051363	0.36	8.90E-03
Rab19	NM_011226	0.77	8.93E-03
2810055F11Rik	NM_026038	-0.40	8.94E-03
Klf11	NM_178357	-0.36	8.96E-03
Ifitm6	NM_001033632	0.50	8.98E-03
Tlr2	NM_011905	2.11	9.04E-03
Tlr2	NM_011905	2.17	9.05E-03
1200016E24Rik	AK035396	1.28	9.05E-03
Adnp	NM_009628	-0.42	9.08E-03
Tcfl5	NM_178254	-0.68	9.08E-03
NA	BB345768	0.37	9.12E-03
Tlr2	NM_011905	2.13	9.15E-03
Spag4	NM_139151	-0.41	9.20E-03
Papola	NM_011112	-0.53	9.20E-03
Aif1	NM_019467	3.16	9.21E-03
Cox17	NM_001017429	0.53	9.38E-03
NA	NAP108462-1	-0.65	9.38E-03
Satb2	AK129270	-0.63	9.39E-03
Crabp1	NM_013496	-0.95	9.40E-03
Enpp1	NM_008813	0.69	9.42E-03
Trerf1	NM_172622	-0.51	9.42E-03
Pgap2	AK152420	-0.49	9.44E-03
Klf4	NM_010637	-1.78	9.44E-03
Tlr2	NM_011905	2.11	9.49E-03
Mboat2	NM_026037	1.02	9.49E-03
Cd34	NM_133654	1.61	9.50E-03
Pi4k2b	NM_028744	-0.43	9.54E-03
D430006K04	AK084893	0.41	9.54E-03
Zbtb1	NM_178744	-0.58	9.57E-03
Prss16	NM_019429	0.35	9.58E-03
Dlg5	AK147699	-0.71	9.58E-03
Syngr1	NM_009303	1.87	9.59E-03
Zfp788	NM_023363	-0.38	9.60E-03
Chpt1	NM_144807	-0.48	9.60E-03
Decr2	NM_011933	-0.35	9.60E-03
Serpinb8	NM_011459	-0.37	9.61E-03
Ftsjd1	NM_146215	-0.51	9.63E-03
Tubb3	NM_023279	-0.57	9.64E-03
Gamt	NM_010255	-0.61	9.70E-03

Slco4a1	NM_148933	1.97	9.70E-03
Selplg	NM_009151	2.52	9.72E-03
Acss1	NM_080575	2.12	9.76E-03
Arl11	NM_177337	0.72	9.77E-03
Rai14	NM_030690	-0.70	9.78E-03
Pisd-ps3	AK161130	0.69	9.80E-03
Kif7	BC034093	-0.43	9.81E-03
Bmpr1a	NM_009758	-0.46	9.82E-03
Ddr2	AK035414	-1.27	9.83E-03
NA	NAP057026-1	-0.41	9.84E-03
Cdk6	AK030810	0.79	9.84E-03
NA	TC1574886	0.37	9.85E-03
Tlr2	NM_011905	2.11	9.86E-03
Seh1l	BC027244	-0.47	9.86E-03
Frg1	NM_013522	-0.73	9.87E-03
Tmem143	NM_144801	-0.55	9.89E-03
Rem1	NM_009047	-0.40	9.92E-03
Alox5	NM_009662	2.10	9.93E-03
Ptn	NM_008973	-1.64	1.00E-02

Supplementary Table S4: Gene Ontology analysis according to biological process (FDR<0.05) in SA1-null cells: GO terms downregulated in SA1-null cells (blue table) and GO terms upregulated in SA1-null cells (red table) are listed.

GO term	Description	FDR
GO:0045947	negative regulation of translational initiation	4.00E-02
GO:0006613	cotranslational protein targeting to membrane	4.53E-02
GO:0016126	sterol biosynthetic process	2.30E-02
GO:0007224	smoothened signaling pathway	4.21E-02
GO:0045667	regulation of osteoblast differentiation	4.53E-02
GO:0007179	transforming growth factor beta receptor signaling pathway	1.11E-02
GO:0035108	limb morphogenesis	3.96E-03
GO:0030326	embryonic limb morphogenesis	7.83E-03
GO:0060173	limb development	3.85E-03
GO:0048754	branching morphogenesis of a tube	1.81E-02
GO:0001763	morphogenesis of a branching structure	1.11E-02
GO:0048706	embryonic skeletal system development	1.81E-02
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	3.00E-03
GO:0048705	skeletal system morphogenesis	2.13E-02
GO:0030324	lung development	4.19E-02
GO:0060541	respiratory system development	3.15E-02
GO:0016055	Wnt receptor signaling pathway	1.60E-02
GO:0035239	tube morphogenesis	1.76E-02
GO:0030323	respiratory tube development	4.53E-02
GO:0006520	cellular amino acid metabolic process	3.96E-03
GO:0001501	skeletal system development	5.92E-04
GO:0001503	ossification	1.60E-02
GO:0007507	heart development	1.11E-02
GO:0006396	RNA processing	9.45E-07
GO:0060348	bone development	3.15E-02
GO:0016568	chromatin modification	4.43E-03
GO:0007167	enzyme linked receptor protein signaling pathway	2.19E-03
GO:0048729	tissue morphogenesis	4.07E-02
GO:0006281	DNA repair	4.43E-03
GO:0048598	embryonic morphogenesis	1.11E-02
GO:0034984	response to DNA damage stimulus	4.93E-03
GO:0043009	chordate embryonic development	1.60E-02
GO:0044262	cellular carbohydrate metabolic process	4.00E-02
GO:0009792	embryo development ending in birth or egg hatching	1.81E-02
GO:0008610	lipid biosynthetic process	4.53E-02
GO:0006412	translation	3.11E-03

GO term	Description	FDR
GO:0051726	regulation of cell cycle	4.74E-02
GO:0043066	negative regulation of apoptosis	4.09E-02
GO:0060548	negative regulation of cell death	2.85E-02
GO:0043069	negative regulation of programmed cell death	2.83E-02
GO:0048514	blood vessel morphogenesis	4.10E-02
GO:0007265	Ras protein signal transduction	4.09E-02
GO:0045595	regulation of cell differentiation	1.02E-03
GO:0007243	intracellular protein kinase cascade	7.88E-04
GO:0000165	MAPKKK cascade	3.00E-02
GO:0046903	secretion	8.78E-04
GO:0001932	regulation of protein phosphorylation	4.12E-02
GO:0009967	positive regulation of signal transduction	5.90E-03
GO:0042060	wound healing	1.80E-02
GO:0051270	regulation of cellular component movement	1.84E-02
GO:0010942	positive regulation of cell death	4.66E-04
GO:0006916	anti-apoptosis	3.67E-02
GO:0043068	positive regulation of programmed cell death	4.35E-04
GO:0045597	positive regulation of cell differentiation	5.24E-03
GO:0043065	positive regulation of apoptosis	4.22E-04
GO:0051046	regulation of secretion	8.50E-03
GO:0032940	secretion by cell	3.15E-04
GO:0006887	exocytosis	4.09E-02
GO:0016477	cell migration	4.80E-05
GO:0051247	positive regulation of protein metabolic process	1.34E-02
GO:0008284	positive regulation of cell proliferation	3.42E-02
GO:0007599	hemostasis	3.03E-02
GO:0007596	blood coagulation	2.88E-02
GO:0043408	regulation of MAPKKK cascade	4.74E-02
GO:0030334	regulation of cell migration	6.52E-03
GO:0032270	positive regulation of cellular protein metabolic process	8.00E-03
GO:0006865	amino acid transport	4.09E-02
GO:0006917	induction of apoptosis	2.41E-04
GO:0006897	endocytosis	1.77E-04
GO:0030036	actin cytoskeleton organization	4.01E-02
GO:0018108	peptidyl-tyrosine phosphorylation	1.63E-02
GO:0002520	immune system development	4.12E-07
GO:0019216	regulation of lipid metabolic process	2.17E-02
GO:0032880	regulation of protein localization	2.44E-03
GO:0030217	T cell differentiation	5.09E-03
GO:0051054	positive regulation of DNA metabolic process	4.45E-02
GO:0034101	erythrocyte homeostasis	1.94E-02

GO:0050730	regulation of peptidyl-tyrosine phosphorylation	2.85E-02
GO:0032946	positive regulation of mononuclear cell proliferation	2.85E-02
GO:0034097	response to cytokine stimulus	7.25E-03
GO:0001894	tissue homeostasis	2.70E-02
GO:0030097	hemopoiesis	4.09E-08
GO:0048872	homeostasis of number of cells	4.22E-04
GO:0030099	myeloid cell differentiation	7.89E-05
GO:0009968	negative regulation of signal transduction	1.22E-02
GO:0002573	myeloid leukocyte differentiation	1.25E-02
GO:0032943	mononuclear cell proliferation	1.70E-04
GO:0042110	T cell activation	3.64E-06
GO:0042113	B cell activation	2.45E-04
GO:0070201	regulation of establishment of protein localization	4.66E-04
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB cascade	5.90E-03
GO:0042098	T cell proliferation	1.20E-03
GO:0043410	positive regulation of MAPKKK cascade	1.34E-02
GO:0030098	lymphocyte differentiation	1.29E-05
GO:0050727	regulation of inflammatory response	2.58E-03
GO:0051223	regulation of protein transport	3.10E-04
GO:0043122	regulation of I-kappaB kinase/NF-kappaB cascade	1.38E-03
GO:0007015	actin filament organization	3.41E-02
GO:0046649	lymphocyte activation	2.89E-10
GO:0019221	cytokine-mediated signaling pathway	9.91E-04
GO:0032496	response to lipopolysaccharide	5.20E-04
GO:0045767	regulation of anti-apoptosis	4.20E-02
GO:0045619	regulation of lymphocyte differentiation	2.46E-03
GO:0050776	regulation of immune response	5.40E-09
GO:0022904	respiratory electron transport chain	2.26E-02
GO:0002443	leukocyte mediated immunity	3.27E-07
GO:0050778	positive regulation of immune response	4.85E-07
GO:0007249	I-kappaB kinase/NF-kappaB cascade	2.97E-05
GO:0030183	B cell differentiation	3.08E-03
GO:0046631	alpha-beta T cell activation	3.08E-03
GO:0002237	response to molecule of bacterial origin	3.09E-05
GO:0001909	leukocyte mediated cytotoxicity	4.19E-03
GO:0051341	regulation of oxidoreductase activity	1.50E-02
GO:0042773	ATP synthesis coupled electron transport	4.87E-02
GO:0050863	regulation of T cell activation	7.14E-03
GO:0045087	innate immune response	2.57E-07
GO:0045639	positive regulation of myeloid cell differentiation	2.69E-02
GO:0002253	activation of immune response	5.92E-06
GO:0006954	inflammatory response	1.18E-15
GO:0006904	vesicle docking involved in exocytosis	4.45E-02

GO:0050714	positive regulation of protein secretion	5.90E-03
GO:0019724	B cell mediated immunity	7.45E-06
GO:0002821	positive regulation of adaptive immune response	3.00E-03
GO:0009306	protein secretion	1.22E-05
GO:0042129	regulation of T cell proliferation	3.99E-02
GO:0002367	cytokine production involved in immune response	4.10E-02
GO:0002286	T cell activation involved in immune response	4.10E-02
GO:0009617	response to bacterium	2.89E-10
GO:0051272	positive regulation of cellular component movement	9.94E-03
GO:0050729	positive regulation of inflammatory response	1.09E-02
GO:0006935	chemotaxis	2.44E-10
GO:0050708	regulation of protein secretion	3.33E-04
GO:0045637	regulation of myeloid cell differentiation	1.76E-04
GO:0045833	negative regulation of lipid metabolic process	3.71E-02
GO:0006898	receptor-mediated endocytosis	1.02E-03
GO:0050671	positive regulation of lymphocyte proliferation	3.40E-02
GO:0030155	regulation of cell adhesion	3.83E-02
GO:0030335	positive regulation of cell migration	7.23E-03
GO:0045061	thymic T cell selection	3.26E-02
GO:0051353	positive regulation of oxidoreductase activity	1.48E-02
GO:0002768	immune response-regulating cell surface receptor signaling pathway	7.89E-05
GO:0042742	defense response to bacterium	7.18E-07
GO:0050670	regulation of lymphocyte proliferation	2.48E-03
GO:0046651	lymphocyte proliferation	2.60E-04
GO:0043542	endothelial cell migration	2.48E-03
GO:0051251	positive regulation of lymphocyte activation	8.81E-04
GO:0030168	platelet activation	4.89E-03
GO:0050900	leukocyte migration	1.82E-06
GO:0014048	regulation of glutamate secretion	4.74E-02
GO:0045580	regulation of T cell differentiation	2.03E-02
GO:0050715	positive regulation of cytokine secretion	9.96E-03
GO:0016485	protein processing	2.60E-02
GO:0042107	cytokine metabolic process	1.36E-03
GO:0032760	positive regulation of tumor necrosis factor production	1.94E-02
GO:0042089	cytokine biosynthetic process	1.32E-03
GO:0001934	positive regulation of protein phosphorylation	4.53E-02
GO:0007229	integrin-mediated signaling pathway	4.44E-02
GO:0050867	positive regulation of cell activation	8.59E-05
GO:0030100	regulation of endocytosis	6.69E-03
GO:0002541	activation of plasma proteins involved in acute inflammatory response	3.47E-02
GO:0046632	alpha-beta T cell differentiation	3.47E-02

GO:0009615	response to virus	2.38E-03
GO:0001817	regulation of cytokine production	1.77E-06
GO:0051605	protein maturation by peptide bond cleavage	3.83E-02
GO:0033198	response to ATP	1.43E-02
GO:0002684	positive regulation of immune system process	1.78E-09
GO:0006956	complement activation	2.96E-02
GO:0060326	cell chemotaxis	5.04E-06
GO:0050870	positive regulation of T cell activation	7.93E-04
GO:0030595	leukocyte chemotaxis	1.06E-05
GO:0051604	protein maturation	6.89E-03
GO:0042035	regulation of cytokine biosynthetic process	6.51E-04
GO:0045577	regulation of B cell differentiation	1.23E-02
GO:0002920	regulation of humoral immune response	1.23E-02
GO:0050663	cytokine secretion	4.80E-05
GO:0002526	acute inflammatory response	1.24E-05
GO:0042102	positive regulation of T cell proliferation	9.67E-03
GO:0016064	immunoglobulin mediated immune response	6.97E-05
GO:0030593	neutrophil chemotaxis	2.27E-04
GO:0030218	erythrocyte differentiation	2.74E-02
GO:0043534	blood vessel endothelial cell migration	1.28E-03
GO:0050830	defense response to Gram-positive bacterium	1.28E-03
GO:0050701	interleukin- secretion	2.28E-02
GO:0050702	interleukin- beta secretion	2.28E-02
GO:0032770	positive regulation of monooxygenase activity	3.00E-03
GO:0045582	positive regulation of T cell differentiation	7.01E-03
GO:0045840	positive regulation of mitosis	1.69E-02
GO:0010595	positive regulation of endothelial cell migration	4.82E-02
GO:0032490	detection of molecule of bacterial origin	4.82E-02
GO:0046427	positive regulation of JAK-STAT cascade	4.43E-02
GO:0006910	phagocytosis, recognition	6.89E-03
GO:0050851	antigen receptor-mediated signaling pathway	4.64E-02
GO:0045123	cellular extravasation	2.05E-03
GO:0002455	humoral immune response mediated by circulating immunoglobulin	4.63E-03
GO:0007159	leukocyte cell-cell adhesion	7.89E-05
GO:0009408	response to heat	1.71E-02
GO:0006809	nitric oxide biosynthetic process	4.22E-03
GO:0045638	negative regulation of myeloid cell differentiation	1.19E-02
GO:0043536	positive regulation of blood vessel endothelial cell migration	4.10E-02
GO:0002925	positive regulation of humoral immune response mediated by circulating immunoglobulin	4.10E-02
GO:0045621	positive regulation of lymphocyte differentiation	1.26E-03
GO:0045055	regulated secretory pathway	1.10E-02

GO:0051971	positive regulation of transmission of nerve impulse	3.83E-02
GO:0001819	positive regulation of cytokine production	1.06E-05
GO:0002923	regulation of humoral immune response mediated by circulating immunoglobulin	1.26E-02
GO:0050718	positive regulation of interleukin- beta secretion	3.37E-02
GO:0019722	calcium-mediated signaling	1.20E-02
GO:0032731	positive regulation of interleukin- beta production	1.00E-02
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	2.36E-02
GO:0043367	CD-positive, alpha-beta T cell differentiation	7.13E-03
GO:0045428	regulation of nitric oxide biosynthetic process	1.90E-03
GO:0051607	defense response to virus	6.53E-03
GO:0051222	positive regulation of protein transport	9.71E-04
GO:0045576	mast cell activation	1.32E-03
GO:0006909	phagocytosis	1.77E-06
GO:0045807	positive regulation of endocytosis	3.35E-04
GO:0042226	interleukin- biosynthetic process	1.37E-02
GO:0045429	positive regulation of nitric oxide biosynthetic process	8.63E-04
GO:0045408	regulation of interleukin- biosynthetic process	1.19E-02
GO:0050853	B cell receptor signaling pathway	4.95E-02
GO:0002891	positive regulation of immunoglobulin mediated immune response	2.63E-03
GO:0002675	positive regulation of acute inflammatory response	1.08E-02
GO:0002863	positive regulation of inflammatory response to antigenic stimulus	4.30E-02
GO:0002437	inflammatory response to antigenic stimulus	1.32E-04
GO:0043303	mast cell degranulation	4.61E-02
GO:0032755	positive regulation of interleukin- production	4.79E-04
GO:0050710	negative regulation of cytokine secretion	4.07E-02
GO:0042534	regulation of tumor necrosis factor biosynthetic process	8.30E-03
GO:0050764	regulation of phagocytosis	8.20E-05
GO:0032651	regulation of interleukin- beta production	3.69E-02
GO:0006911	phagocytosis, engulfment	2.60E-04
GO:0050766	positive regulation of phagocytosis	3.24E-05
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	2.32E-02
GO:0048010	vascular endothelial growth factor receptor signaling pathway	5.75E-03
GO:0016068	type I hypersensitivity	2.62E-02
GO:0030851	granulocyte differentiation	2.62E-02
GO:0001805	positive regulation of type III hypersensitivity	1.54E-02
GO:0002548	monocyte chemotaxis	1.38E-03
GO:0030853	negative regulation of granulocyte differentiation	4.34E-02
GO:0048525	negative regulation of viral reproduction	3.69E-02
GO:0009311	oligosaccharide metabolic process	1.89E-02

GO:0009312	oligosaccharide biosynthetic process	1.38E-02
GO:0016998	cell wall macromolecule catabolic process	1.38E-02
GO:0050829	defense response to Gram-negative bacterium	1.30E-02
GO:0005989	lactose biosynthetic process	1.13E-02

Supplementary Table S5: Gene Ontology Comparative Analysis according to biological process (FDR<0.05) in SA1-null and *Nipbl*-heterozygous MEFs. GO terms common in both models are shown in bold.

SA1-null MEFs

GO TERM	Description	FDR
Skeletal and bone development		
GO:0001501	***skeletal system development***	5.92E-04
GO:0001503	ossification	1.60E-02
GO:0048706	**embryonic skeletal system development**	1.81E-02
GO:0048705	**skeletal system morphogenesis**	2.13E-02
GO:0060348	bone development	3.15E-02
GO:0045667	regulation of osteoblast differentiation	4.53E-02
GO:0060173	limb development	3.85E-03
GO:0035108	limb morphogenesis	3.96E-03
GO:0030326	embryonic limb morphogenesis	7.83E-03
Morphogenesis		
GO:0001763	**morphogenesis of a branching structure**	1.11E-02
GO:0048598	embryonic morphogenesis	1.11E-02
GO:0043009	chordate embryonic development	1.60E-02
GO:0035239	tube morphogenesis	1.76E-02
GO:0048754	branching morphogenesis of a tube	1.81E-02
GO:0009792	**embryo development ending in birth or egg hatching**	1.81E-02
GO:0048729	tissue morphogenesis	4.07E-02
Translation		
GO:0006412	**translation**	3.11E-03
GO:0045947	negative regulation of translational initiation	4.00E-02
Heart & Lung development		
GO:0007507	heart development	1.11E-02
GO:0060541	respiratory system development	3.15E-02
GO:0030324	lung development	4.19E-02
GO:0030323	respiratory tube development	4.53E-02
Lipid metabolism		
GO:0008610	lipid biosynthetic process	4.53E-02

***Nipbl*-heterozygous MEFs**

GO TERM	Description	FDR
Skeletal and bone development		
GO:0001501	**skeletal system development**	1.24E-02
GO:0048706	**embryonic skeletal system development**	4.43E-02
GO:0007519	skeletal muscle tissue development	4.58E-02
GO:0002051	osteoblast fate commitment	3.42E-02
GO:0048705	**skeletal system morphogenesis**	1.57E-02
Morphogenesis		
GO:0009792	**embryo development ending in birth or egg hatching**	4.87E-02
GO:0009880	embryonic pattern specification	4.91E-02
GO:0001763	**morphogenesis of a branching structure**	3.82E-02
GO:0031645	negative regulation of neurological system process	2.22E-02
GO:0007389	pattern specification process	2.80E-02
Translation		
GO:0006412	**translation**	1.07E-02
GO:0043039	tRNA aminoacylation	1.02E-02
Heart & Lung development		
GO:0002027	regulation of heart rate	2.20E-02
GO:0042310	vasoconstriction	3.51E-03
GO:0010460	positive regulation of heart rate	8.84E-03
GO:0045823	positive regulation of heart contraction	1.21E-02
GO:0045907	positive regulation of vasoconstriction	1.45E-02
GO:0045777	positive regulation of blood pressure	1.77E-02
Lipid metabolism		
GO:0050873	brown fat cell differentiation	1.32E-03
GO:0044255	cellular lipid metabolic process	2.24E-03
GO:0046889	positive regulation of lipid biosynthetic process	1.45E-02
GO:0050872	white fat cell differentiation	1.68E-02
GO:0019217	regulation of fatty acid metabolic process	3.31E-02
GO:0045834	positive regulation of lipid metabolic process	3.53E-02
GO:0045444	fat cell differentiation	3.74E-02

Supplementary Table S6: Differentially expressed genes in microarray analysis (FDR<0.15). Genes validated by RT-qPCR are highlighted in blue.

Gene Symbol	Accesion Number	FDR	log$_2$FC	SA1 (5kb up TSS)	Cluster
Lyz1	NM_013590	0.092	3.63		✓
AF251705	NM_134158	0.103	1.87		
Alox5ap	NM_009663	0.103	2.67		
Arhgap30	NM_001005508	0.103	2.19		
BC013712	AK137465	0.103	2.83		
Casp1	NM_009807	0.103	2.19		✓
Ccl6	NM_009139	0.103	2.26		✓
Cd14	NM_009841	0.103	1.91		
Clec4a2	NM_011999	0.103	2.16		✓
Clec4n	NM_020001	0.103	3.43		✓
Clec5a	NM_001038604	0.103	3.31		
Dock10	XM_891407	0.103	1.43		
Ebi3	NM_015766	0.103	2.03		
Fcer1g	J05020	0.103	2.63	✓	
Fyb	NM_011815	0.103	2.78		
Hpgd	NM_008278	0.103	1.75		
Igsf6	NM_030691	0.103	2.60	✓	
Itgal	AK156251	0.103	2.32		
Lair1	NM_178611	0.103	2.57		
Lcp1	NM_008879	0.103	2.64		
Lrrc25	NM_153074	0.103	2.45	✓	
Lyz2	NM_017372	0.103	3.55		✓
Marco	NM_010766	0.103	2.94		
Mmp3	NM_010809	0.103	1.86		
Ms4a7	NM_001025610	0.103	3.08		✓
Msr1	NM_031195	0.103	2.75		
Myo1f	NM_053214	0.103	2.12	✓	
Ncf4	NM_008677	0.103	3.15		
Pilra	NM_153510	0.103	2.43		✓
Pilrb1	NM_133209	0.103	2.31		✓
Ptprc	NM_011210	0.103	2.95		
Rapgef5	AK122234	0.103	1.99		
Tcfec	NM_031198	0.103	1.33		
Tyrobp	NM_011662	0.103	3.13		
Tm6sf1	NM_145375	0.104	1.92		
Hk3	NM_001033245	0.107	1.32		
Rinl	NM_177158	0.107	1.17		
Acpl2	NM_153420	0.112	-2.14	✓	
Bcl2a1b	NM_007534	0.112	2.98		
Cxcl16	NM_023158	0.112	2.18		
Hcls1	NM_008225	0.112	3.03		
Lrrc33	NM_146069	0.112	2.75		
Ms4a6d	AB026047	0.112	2.92	✓	✓
Rnd1	NM_172612	0.112	1.32		
Tnf	NM_013693	0.112	1.20		
Lrmp	NM_008511	0.123	1.76		
Psmb9	NM_013585	0.123	1.34		✓
Rgs14	NM_016758	0.123	1.15		
Ptpn7	NM_177081	0.126	1.41		
Fcgr3	NM_010188	0.128	2.82		✓
Btk	NM_013482	0.136	1.48		
Cd68	NM_009853	0.136	1.77		
Batf	NM_016767	0.138	1.03		

Oas1a	NM_145211	0.138	1.12		✓
Zmynd15	NM_001029929	0.146	1.50		

Supplementary Table S7: List of skin-related genes. The presence of SA1 and SA2 in the region 5kb upstream the TSS, as well as the clustered genes is shown.

				Presence up to 5kb upstream TSS			
Gene Symbol	**Chr**	**Start**	**End**	**SA1 (SA1 +/+)**	**SA2 (SA1 +/+)**	**SA2 (SA1 -/-)**	**Cluster**
Il1r2	chr1	40141613	40182064				✓
Ccl20	chr1	83113341	83115742				
Lcn2	chr2	32240153	32243317				
Il1a	chr2	129125346	129135708				✓
Il1b	chr2	129190306	129196875				✓
Mmp9	chr2	164766280	164781350				
Lce1f	chr3	92522607	92524272				✓
Lce3c	chr3	92748408	92749652				✓
Tchh	chr3	93246252	93252999				✓
Ctss	chr3	95330708	95360325				✓
Mmp16	chr4	17780040	18046292	✓			
Ccl27a	chr4	41716340	41721120				✓
Gjb3	chr4	127002479	127008088	✓			✓
Gjb5	chr4	127032053	127035425	✓			✓
Mmp23	chr4	155024764	155027493				
Il6	chr5	30339701	30346508	✓			
Cxcl5	chr5	91188325	91190651				✓
Cxcl15	chr5	91223560	91232093	✓			✓
Cxcl1	chr5	91320267	91322141				✓
Cxcl2	chr5	91332897	91334935				✓
Btc	chr5	91786287	91831939				
Cxcl10	chr5	92775664	92777915				✓
Cxcl13	chr5	96385945	96390086				
Ccl24	chr5	136045807	136048913				✓
Tgfa	chr6	86145420	86225151				
Cxcl12	chr6	117118553	117131385	✓		✓	
Scnn1a	chr6	125271358	125294958				
Cxcl17	chr7	26185072	26197905	✓			
Krtdap	chr7	31572924	31576102				
Ctsc	chr7	95426595	95459398	✓			
Itgam	chr7	135206154	135271674				✓
Krtap5-2	chr7	149360437	149361910				✓
Defb1	chr8	22887071	22905657				✓
Cx3cl1	chr8	97295909	97306323				✓
Ccl17	chr8	97334353	97335935				✓
Mmp15	chr8	97876168	97898193	✓			
Cdh3	chr8	109034791	109080808				✓
Mmp13	chr9	7272514	7283333				✓
Mmp12	chr9	7344381	7369499				✓
Mmp3	chr9	7445822	7455972				✓
Mmp10	chr9	7502352	7510238				✓
Mmp8	chr9	7558429	7568486	✓			✓
Mmp7	chr9	7692086	7699585				✓

Cx3cr1	chr9	119957811	119977400	✓	✓		
Ccr1	chr9	123876959	123883525				✓
Ccr2	chr9	124016689	124028296				✓
Itgb2	chr10	76992997	77028453				
Cxcl16	chr11	70267485	70273486				
Ccl2	chr11	81849073	81850955				✓
Ccl11	chr11	81871325	81876457				✓
Ccl12	chr11	81915347	81916902				✓
Ccl8	chr11	81928687	81930301				✓
Ccl5	chr11	83339280	83344020				✓
Ccl9	chr11	83386421	83392138				✓
Ccl6	chr11	83401384	83406589				✓
Ccl3	chr11	83461346	83462857				✓
Ccl4	chr11	83476086	83478185				✓
Krt28	chr11	99226186	99236217	✓		✓	✓
Krt10	chr11	99246568	99250678				✓
Krt12	chr11	99276980	99283573				✓
Krt20	chr11	99289717	99299464				✓
Krtap2-4	chr11	99475331	99476160				✓
Krtap4-2	chr11	99495428	99496398				✓
Krtap4-13	chr11	99670392	99671210				✓
Krtap31-1	chr11	99769234	99770204				✓
Krt13	chr11	99978641	99982880				✓
Krt15	chr11	99993072	99997263				✓
Krt19	chr11	100002124	100009979				✓
Mmp14	chr14	55050441	55060095	✓			
Tgm1	chr14	56318846	56332329				
Gjb2	chr14	57717437	57723539	✓	✓	✓	✓
Gjb6	chr14	57742140	57752448				✓
Krt80	chr15	101177875	101200556				✓
Krt7	chr15	101241474	101260744				✓
Krt83	chr15	101261921	101269235				✓
Krt75	chr15	101393776	101404335				✓
Krt2	chr15	101641120	101648600				✓
Krt79	chr15	101759763	101770755				✓
Krt8	chr15	101827142	101834773				✓
Krt18	chr15	101858647	101862457				✓
Krtap15	chr16	88820460	88829729	✓			✓
Krtap16-7	chr16	89403272	89404019				✓
Krtap6-2	chr16	89419855	89420322				✓
Hbegf	chr18	36664583	36675459				
Fosl1	chr19	5447703	5455945				
Il33	chr19	29999604	30035194				
Il13ra1	chrX	33652105	33711254				
Il2rg	chrX	98456744	98464362				

Table S8. Primers used for ChIP-seq validation (qPCR)

Genomic Region	Primers	Sequence (5'-3')
Chr 15: 61,814,801 - 61,815,300	***Myc***	Fw ACAAATCCGAGAGCCACAAC Rev TCGAGCTCATTGCACAATTC
Chr 15: 61,687,900 - 61,688,400	***Negative (Myc)***	Fw TGGGGTACTCTGGGTTCATC Rev TAGGGACTGGAAATGGCATC
Chr 11: 67,817,666 - 67,818,084	***11qB3***	Fw TAGCTGAATTTCCCCCACTG Rev CTGAATCAGCACCGACAGAA
Chr 14: 84,838,181 - 84,838,727	***Pcdh17***	Fw TTCCCGGTGTCAATCAATTT Rev TACATACTGG TCCCCCTTG
Chr 5: 58,105,123 - 58,105,623	***Pcdh7***	Fw TTTGTCCCTTGGTGGAGTTC Rev AGGGTCGGGAGTCTTTCATT
Chr 18: 37,179,478 - 37,179,961	***Pcdha12***	Fw CCTCATGATGTCGCTCTTCA Rev AGCATGGTACACACGCAGAA
Chr X: 117,401,147 - 117,401,603	***Pcdh11X***	Fw AGTCTGCTTTTGCCAGGTGT Rev ACCCTGAAAATCCTCCAAGG
Chr 18: 37,644,356 - 37,644,924	***Pcdhb17***	Fw GGCCAGTTTCTCACCACCTA Rev GCAGTCTCCATGGCTCTTTC
Chr 18: 37,300,013 - 37,300,550	***Negative (Pcdh)***	Fw GGGCGTTTTCTGAGATTGAG Rev CAGGGCATTGTGCTTGTTTA
Chr 18: 37,901,429 - 37,901,923	***Pcdhgb6***	Fw TCATAACCCCATGTTCAGAGC Rev GAGTTCCCCTTGGTGTGTGT
Chr 18: 37,672,967 - 37,673,448	***Pcdhb21***	Fw TGCAGGACAGGATGAGAGAA Rev GGCAGCTCAGAGAGTGGTTC
Chr 11: 100,030,172 - 100,030,721	***11qD3***	Fw TAGGCCAAACTGCACTTCCT Rev TCCTACTCTGGCTGGGAAGA
Chr 11: 99,482,356 - 99,482,857	***11qD3 (Negative)***	FW CTTGCGGCTGAAGTTTTAGG Rev CAGTTAGCAACCCTGCATGA
Chr 9: 77,391,786 - 77,392,244	***9qE1***	Fw CAAAATGAGGAGCTCCAAGC Rev GGAGAAACGTTCTGGTCCAC
Chr 15: 101,732,703 - 101,733,262	***15qF3***	Fw CCTTGCAAACCACAGCATTA Rev GGGCAAGCTAATCACCTGAA
Chr 10: 117,879,278 – 117,879,482	***IFNg***	Fw ATTTGTGGCCTTGCAGTTTC Rev TATTTCACCAATTGCCCTGA

Supplementary Table S9: Primers used for Real Time-qPCR

Primer	**Sequence (5’-3’)**
Gapdh Fw	TGCACCACCAACTGCTTAGC
Gapdh Rev	GAGGGGCCATCCACAGTCTTC
SA1 Fw	AGGCTTTCATGCTGCTCTGT
SA1 Rev	TCCATGCTTTGGTTTTCCTC
SA2 Fw	GGGGGAGGAACTGTCTTTCT
SA2 Rev	CCTTCAATGTCTTCAAAATCTGTG
Acpl2 Fw	AAGAATGGAGGAAGCAGCAA
Acpl2 Rev	ATGGCGAATGAACACATGAA
Bcl2a1b Fw	TCCCTGGCTGAGCACTATCT
Bcl2a1b Rev	TCCACGTGAAAGTCATCCAA
Casp1 Fw	ACCCTCAAGTTTTGCCCTTT
Casp1 Rev	GATCCTCCAGCAGCAACTTC
Cxcl16 Fw	GGGAAGAGTTTTCACCACCA
Cxcl16 Rev	GGTTGGGTGTGCTCTTTGTT
Fcer1g Fw	TGATCTCAGCCGTGATCTTG
Fcer1g Rev	CTGGCTATAGCTGCCTTTCG
Sox11 Fw	TCATGTTCGACCTGAGCTTG
Sox11 Rev	TAGTCGGGGAACTCGAAGTG
Sox9 Fw	AGGAAGCTGGCAGACCAGTA
Sox9 Rev	CGTTCTTCACCGACTTCCTC
Myc Fw	TCGCCTCACTCAGCTCCCCT
Myc Rev	ACCGTCCGCTCACTCCCTCT
Pcdh7 Fw	GACGGCTACTGCGCCTGGAT
Pcdh7 Rev	TGGGGGTGTCCACCAGGACA
Pcdh17 Fw	CCCAATAGGCTCTCGGCGCA
Pcdh17 Rev	AGCGGACTGCATCTCCGAGC
Pcdh11X Fw	CTGCGAGCTGTGGCGGTAGA
Pcdh11X Rev	TCTCCTGGGCGCCAGACTGA
Pcdhb16 Fw	AGGTCTCAGCCCTCGGAAAAGGA
Pcdhb16 Rev	GAATAGCGCCTCAGTTCCCCTGC
Pcdhb17 Fw	TGTGAAGCAAACGCCGAGGAAAGA
Pcdhb17 Rev	GGAAATGATCCGAGCCCTGCGAT
Pcdhb20 Fw	GGTATTACAGGAGCTTCACCGGCA
Pcdhb20 Rev	AGCACTCGCCTGAGACAATCCC
Pcdhb21 Fw	ACAAAGGTGGGGCACCCACAAG
Pcdhb21 Rev	TGGCAAGAACCGAGGACCCTTC
Pcdhb22 Fw	GGTCGACCACTGTCTGGATACCC
Pcdhb22 Rev	CGAGCAGCTAGCTCCGCAAC

Btk Fw	TGCTAAAGCAAGAGGGGAAA
Btk Rev	GGATGGTGCTGAAGAGGTGT
Ccl6 Fw	GGCATTGTCACCCACTTTCT
Ccl6 Rev	CCAGATGGCTCTAACCGTGT
Fyb Fw	CGATTTCCCAGACACACCTT
Fyb Rev	CTTGGTGCTCCATGGTCTTT
Zmynd15 Fw	GAGAAGGTGGAACCACAGGA
Zmynd15 Rev	GCCTCTGCATTCTTCTGTCC
Arhgap30 Fw	AGCAGTTCTCAGCCAAGCTC
Arhgap30 Rev	GATGTGGACACCAGCACAAC
Pilra Fw	TTGGGGTTTTGGGATTGATA
Pilra Rev	GGGTTTTCTTTGGGATCCAT
Rinl Fw	CTCAGAGCCCAGGAACTACG
Rinl Rev	CCCAGGGGCTCTTTATTCTC
Ctss Fw	TCCCTCAGTGCTCAGAACCT
Ctss Rev	CTTTTCATCCGTGGCTTTGT
Ccl12 Fw	GGGAAGCTGTGATCTTCAGG
Ccl12 Rev	GGGAACTTCAGGGGGAAATA
Gjb5 Fw	CCACGCATTCTATCCCAGAT
Gjb5 Rev	TAAGCAGGATGCAGATGACG
Lyz1 Fw	ATGGCGAACACAATGTCAAA
Lyz1 Rev	GCCCTGTTTCTGCTGAAGTC
Clec4n Fw	TGAGCCCTTTCTCCTTCTGA
Clec4n Rev	CCACCTGGACCCTCTTACAA
Ptprc Fw	CCTGCTCCTCAAACTTCGAC
Ptprc Rev	GACACCTCTGTCGCCTTAGC
Itgam Fw	TACGTAATTGGGGTGGGAAA
Itgam Rev	GTGCCCTCAATTGCAAAGAT
Mmp3 Fw	CAGACTTGTCCCGTTTCCAT
Mmp3 Rev	GGTGCTGACTGCATCAAAGA