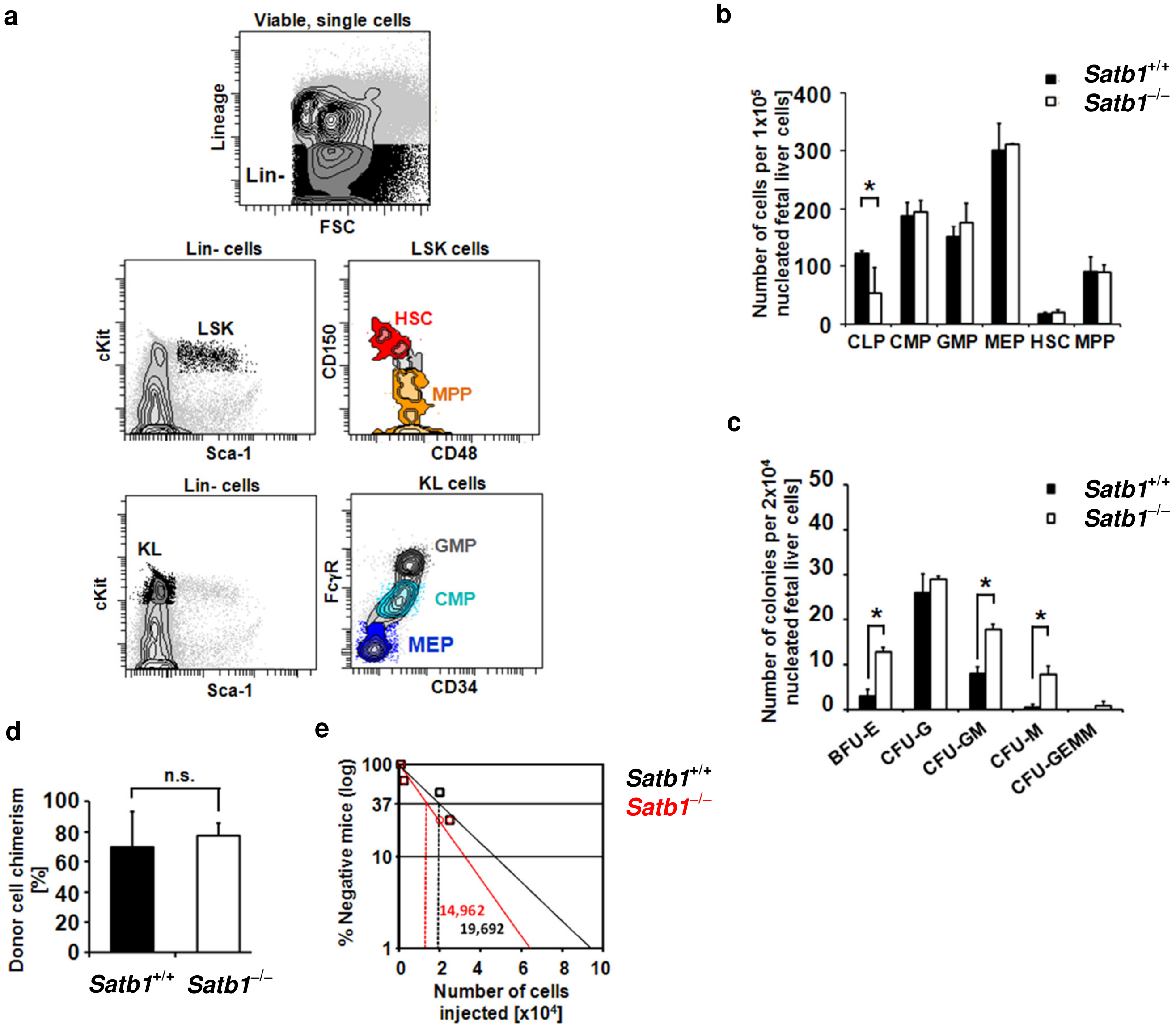
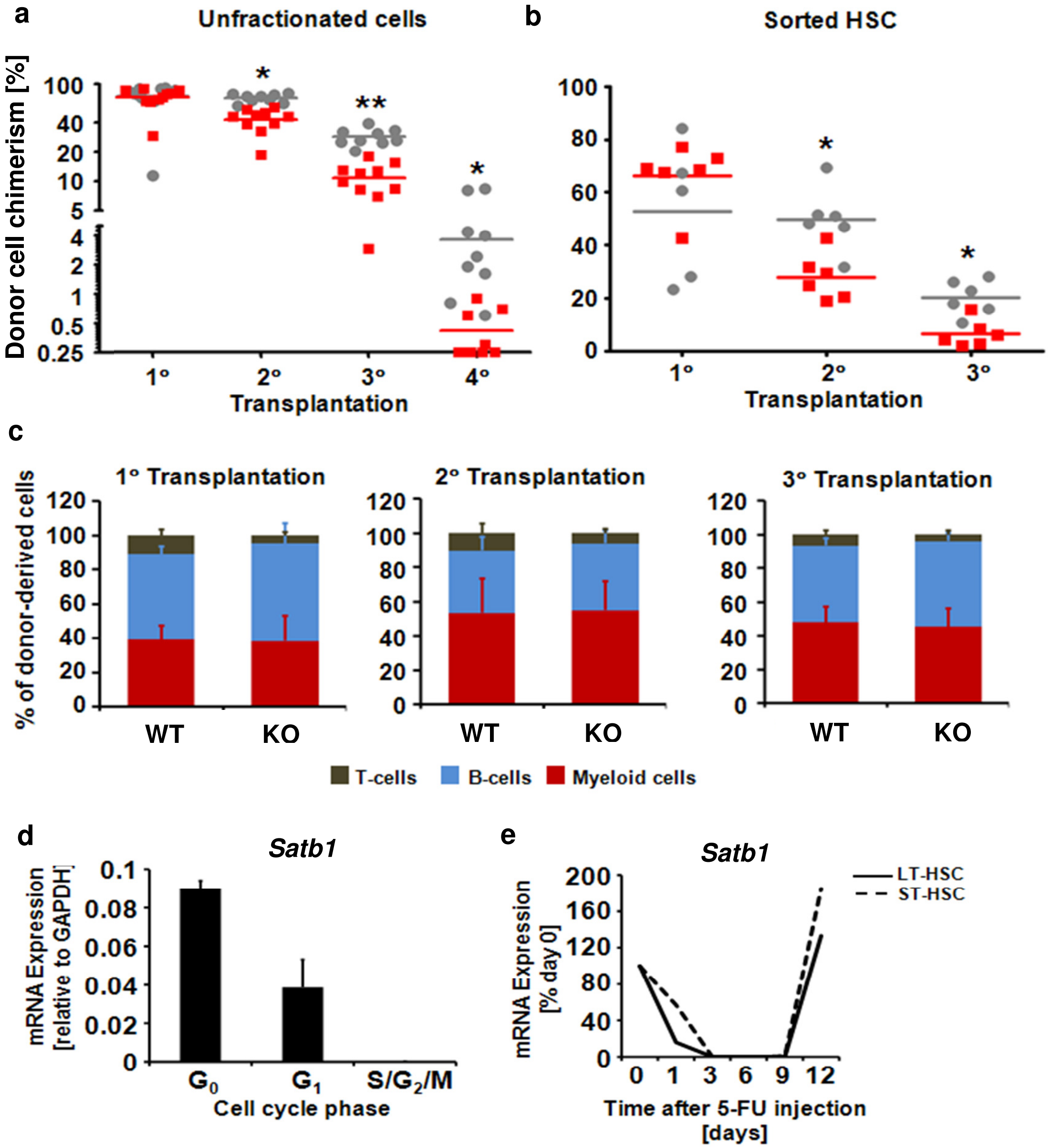
Supplementary Figure 1



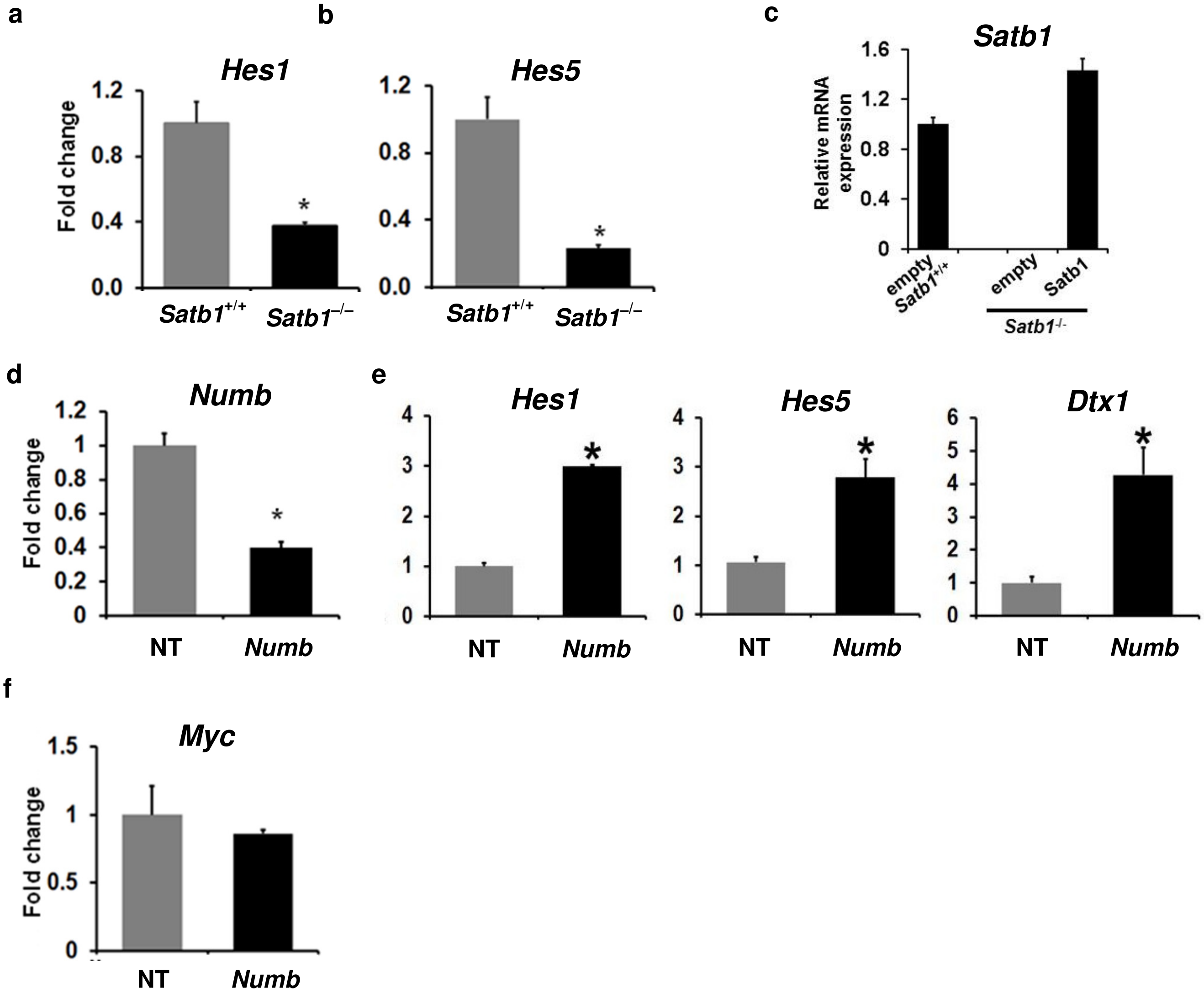
Sorting strategy for adult HSC, MPP, CMP, GMP, MEP, and analysis of hematopoiesis in absence of *Satb1* in the fetal liver. (**a**) CD150^{+} Lin^{-} Sca-1^{+}cKit^{+} (LSK) stem cells (HSC) CD150^{-} LSK multipotent progenitor cells (MPP), CD34^{-} FcγRII/III^{-} Sca-1^{-} cKit^{+} Lin^{-} megakaryocytic-erythroid progenitor cells (MEP), CD34^{+} FcγRII/III^{+-} Sca-1^{-} cKit^{+} Lin^{-} common myeloid progenitor cells (CMP) and CD34^{+} FcγRII/III^{+} Sca-1^{-} cKit^{+} Lin^{-} granulocytic-monocytic progenitor cells (GMP) were purified using FACS. (**b**) FACS analysis of phenotypical hematopoietic stem and progenitor fetal liver cells from Satb1 wild type (*Satb1*$^{+/+}$) and Satb1-deficient (*Satb*1$^{-/-}$) embryos at embryonic day 17-18.5 (n=2/genotype, *p<0.05). (**c**) Colony formation potential of fetal myeloid progenitor cells in methylcellulose assays (n=2/genotype, *p<0.05). (**d**) Analysis of repopulation capacity of *Satb1*$^{-/-}$ fetal liver cells by FACS analysis of donor-derived (CD45.2^{+}) cells in the peripheral blood of recipient animals 24 weeks after transplantation. Shown are averages and standard deviations (two independent experiments, n=20/genotype, *p<0.05). (**e**) Limiting dilution analysis of E17-18.5 *Satb1*$^{+/+}$ and *Satb*1$^{-/-}$ fetal liver cells 24 weeks after transplantation (n=3-4/cell dosage/group, two independent experiments).

Supplementary Figure 2



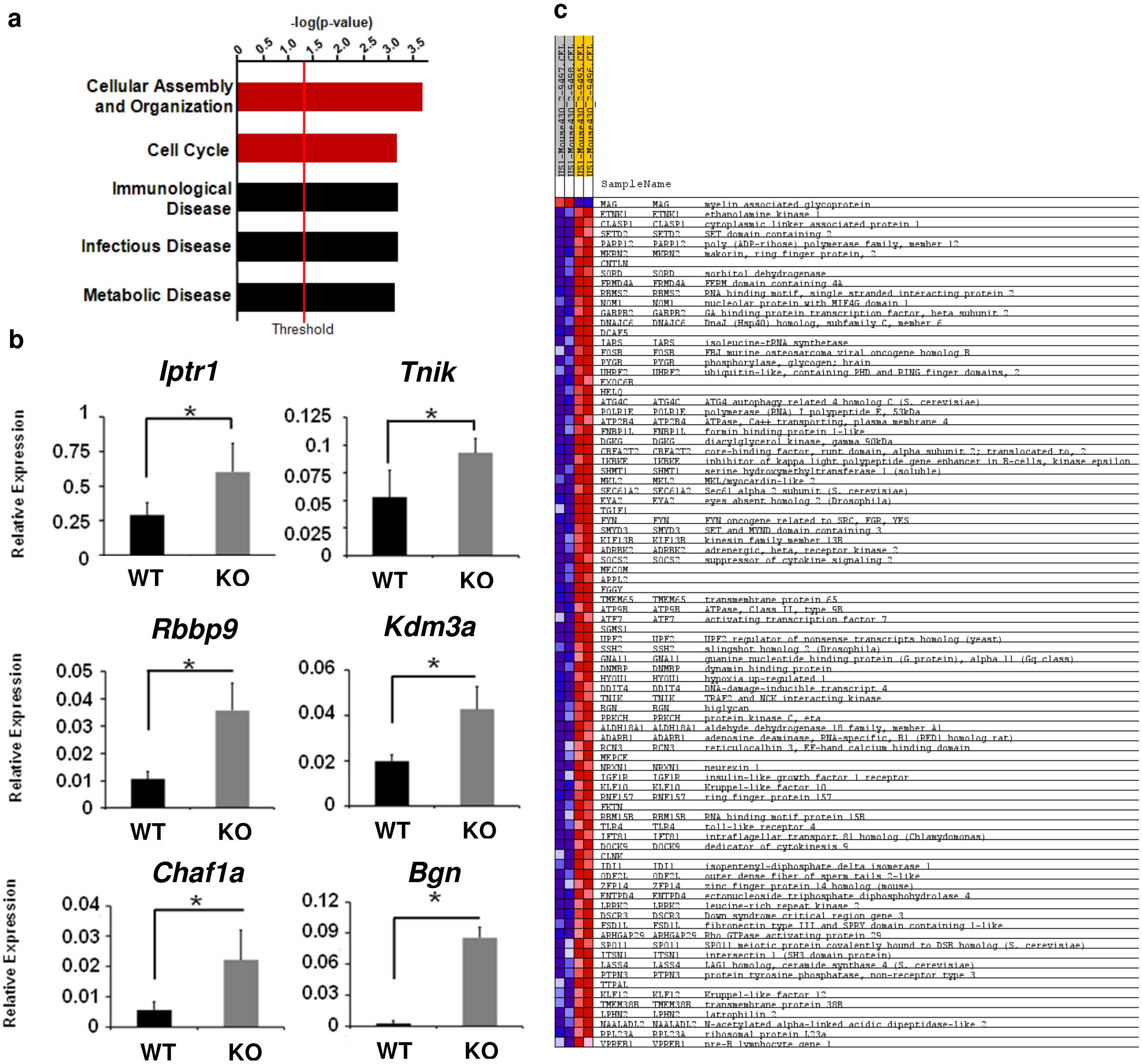
Characterization of multilineage reconstitution in serial transplantation assay, and cell cycle dependence of *Satb1* expression. (**a**) FACS analysis of total donor-cell chimerism in the peripheral blood of recipient animals 24 weeks after transplantation of *Satb1*$^{-/-}$ (red) or *Satb1*$^{+/+}$ (gray) unfractionated BM cells. Shown are averages and standard deviations (n=10/genotype; *p<0.05, two independent experiments). (**b**) Transplantation of sorted HSCs. Shown are percentages of CD45.2^{+} cells in individual recipients (n=5-6/genotype; *p<0.05). (**c**) FACS analysis of donor-derived myeloid cells (CD11b^{+} CD4^{-} B220^{-}), B-cells (B220^{+} CD4^{-} CD11b^{-}) and T-cells (CD4^{+} B220^{-} CD11b^{-}) after the first, second and third round of unfractionated CD45.2^{+} BM cell transplantation. Shown are percentages of CD45.2^{+} cells (n=10/genotype; *p<0.05, two independent experiments). (**d**) qRT-PCR of *Satb1* mRNA expression in wild-type LSK cells in G$_0$, G$_1$, S-G$_2$-M phase of the cell cycle (LSKs sorted based on Pyronin Y, Hoechst 3343 intercalation; see Fig. 2a). Shown are averages and standard deviations of *Gapdh*-normalized mRNA expression measured in technical triplicates (n=2, * p<0.05). (**e**) *Satb1* mRNA expression decreases significantly upon HSC activation with 5-fluorouracil (5-FU). Shown are averages and standard deviations of *Gapdh*-normalized mRNA expression of long-term HSCs (LT-HSC; CD150^{+} CD48^{-} LSK) and short-term HSCs (ST-HSC; CD150^{+} CD48^{+} LSK) from a pool of 3 animals/time point measured in technical triplicates.

Supplementary Figure 3



Transcript levels in *Satb1*$^{-/-}$ HSC, and upon Satb1 restoration, or Numb knockdown.
(**a**) *Hes1* and (**b**) *Hes5* mRNA expression detected by qRT-PCR in *Satb1*$^{+/+}$ (grey bars) and *Satb1*$^{-/-}$ (black bars) CD150^{+} CD48^{-} LSK cells. Shown are averages and standard deviations normalized to Gapdh (n=2/genotype, * $p<0.05$). (**c**) *Satb1* mRNA expression 48hrs after transduction and sorting of GFP+ *Satb1*$^{-/-}$ CD150^{+}CD48^{-}LSK cells transduced with either Satb1-IRES-GFP expressing vector or empty IRES-GFP expressing vector, or of GFP^{+} *Satb1*$^{+/+}$ CD150^{+} CD48^{-} LSK cells transduced with the empty IRES-GFP vector. Shown are averages of the fold change and standard deviations of *Gapdh*-normalized mRNA expression compared to *Satb1*$^{+/+}$ control transduced samples measured in technical triplicates. (**d**) Quantification of *Numb* mRNA expression by qRT-PCR in *Satb1*$^{-/-}$ CD150^{+} CD48^{-} LSK cells transduced with either a pool of shRNAs targeting murine *Numb* or non-targeting control (NT) shRNA-expressing lentivirus. (**e**) mRNA expression of Notch target genes *Hes1*, *Hes5* and *Dtx1* by qRT-PCR in *Satb1*$^{-/-}$ CD150^{+} CD48^{-} LSK cells transduced with either a pool of shRNAs targeting murine *Numb* or non-targeting control (NT) shRNA-expressing lentivirus. (**f**) *Myc* mRNA expression by qRT-PCR in *Satb1*$^{-/-}$ CD150^{+} CD48^{-} LSK cells transduced with either a pool of shRNAs targeting murine *Numb* or non-targeting (NT) control shRNA-expressing lentivirus. Shown are averages of the fold change and standard deviations of *Gapdh*-normalized mRNA expression compared to non-targeting control transduced samples from two independent experiments measured in technical triplicates.

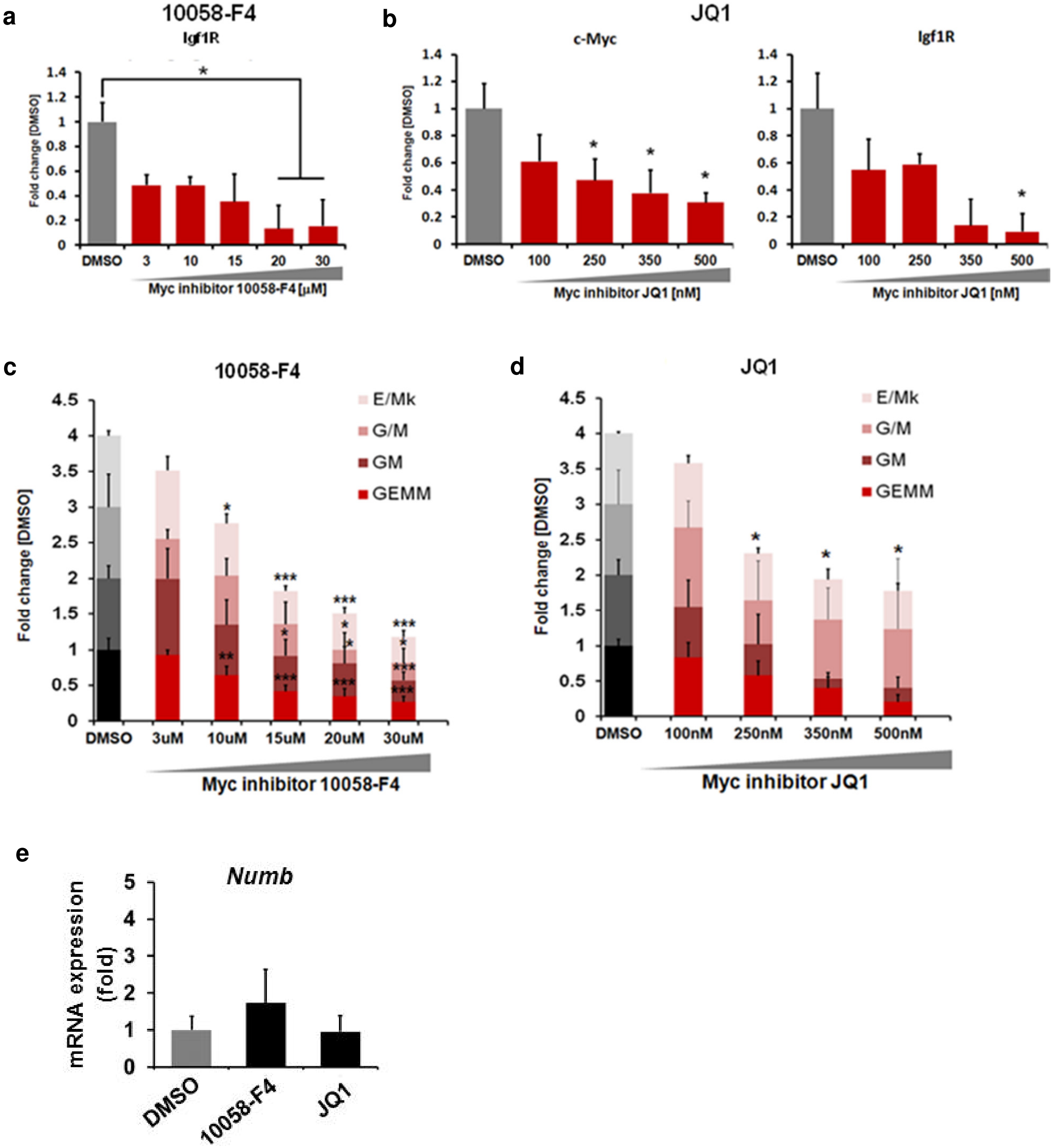
Supplementary Figure 4



MAG	MAG	myelin associated glycoprotein
ETNK1	ETNK1	ethanolamine kinase 1
CLASP1	CLASP1	cytoplasmic linker associated protein 1
SETD2	SETD2	SET domain containing 2
PARP12	PARP12	poly (ADP-ribose) polymerase family, member 12
MKRN2	MKRN2	makorin, ring finger protein, 2
CNTLN		
SORD	SORD	sorbitol dehydrogenase
FRMD4A	FRMD4A	FERM domain containing 4A
RBMS2	RBMS2	RNA binding motif, single stranded interacting protein 2
NOM1	NOM1	nucleolar protein with MIF4G domain 1
GABPB2	GABPB2	GA binding protein transcription factor, beta subunit 2
DNAJC6	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6
DCAF5		
IARS	IARS	isoleucine-tRNA synthetase
FOSB	FOSB	FBJ murine osteosarcoma viral oncogene homolog B
PYGB	PYGB	phosphorylase, glycogen; brain
UHRF2	UHRF2	ubiquitin-like, containing PHD and RING finger domains, 2
EXOC6B		
HELQ		
ATG4C	ATG4C	ATG4 autophagy related 4 homolog C (S. cerevisiae)
POLR1E	POLR1E	polymerase (RNA) I polypeptide E, 53kDa
ATP2B4	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4
FNBP1L	FNBP1L	formin binding protein 1-like
DGKG	DGKG	diacylglycerol kinase, gamma 90kDa
CBFA2T2	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2
IKBKE	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon
SHMT1	SHMT1	serine hydroxymethyltransferase 1 (soluble)
MKL2	MKL2	MKL/myocardin-like 2
SEC61A2	SEC61A2	Sec61 alpha 2 subunit (S. cerevisiae)
EYA2	EYA2	eyes absent homolog 2 (Drosophila)
TGIF1		
FYN	FYN	FYN oncogene related to SRC, FGR, YES
SMYD3	SMYD3	SET and MYND domain containing 3
KIF13B	KIF13B	kinesin family member 13B
ADRBK2	ADRBK2	adrenergic, beta, receptor kinase 2
SOCS2	SOCS2	suppressor of cytokine signaling 2
MECOM		
APPL2		
FGGY		
TMEM65	TMEM65	transmembrane protein 65
ATP9B	ATP9B	ATPase, Class II, type 9B
ATF7	ATF7	activating transcription factor 7
SGMS1		
UPF2	UPF2	UPF2 regulator of nonsense transcripts homolog (yeast)
SSH2	SSH2	slingshot homolog 2 (Drosophila)
GNA11	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
DNMBP	DNMBP	dynamin binding protein
HYOU1	HYOU1	hypoxia up-regulated 1
DDIT4	DDIT4	DNA-damage-inducible transcript 4
TNIK	TNIK	TRAF2 and NCK interacting kinase
BGN	BGN	biglycan
PRKCH	PRKCH	protein kinase C, eta
ALDH18A1	ALDH18A1	aldehyde dehydrogenase 18 family, member A1
ADARB1	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
RCN3	RCN3	reticulocalbin 3, EF-hand calcium binding domain
MEPCE		
NRXN1	NRXN1	neurexin 1
IGF1R	IGF1R	insulin-like growth factor 1 receptor
KLF10	KLF10	Kruppel-like factor 10
RNF157	RNF157	ring finger protein 157
FKTN		
RBM15B	RBM15B	RNA binding motif protein 15B
TLR4	TLR4	toll-like receptor 4
IFT81	IFT81	intraflagellar transport 81 homolog (Chlamydomonas)
DOCK9	DOCK9	dedicator of cytokinesis 9
CLNK		
IDI1	IDI1	isopentenyl-diphosphate delta isomerase 1
ODF2L	ODF2L	outer dense fiber of sperm tails 2-like
ZFP14	ZFP14	zinc finger protein 14 homolog (mouse)
ENTPD4	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4
LRRK2	LRRK2	leucine-rich repeat kinase 2
DSCR3	DSCR3	Down syndrome critical region gene 3
FSD1L	FSD1L	fibronectin type III and SPRY domain containing 1-like
ARHGAP29	ARHGAP29	Rho GTPase activating protein 29
SPO11	SPO11	SPO11 meiotic protein covalently bound to DSB homolog (S. cerevisiae)
ITSN1	ITSN1	intersectin 1 (SH3 domain protein)
LASS4	LASS4	LAG1 homolog, ceramide synthase 4 (S. cerevisiae)
PTPN3	PTPN3	protein tyrosine phosphatase, non-receptor type 3
TTPAL		
KLF12	KLF12	Kruppel-like factor 12
TMEM38B	TMEM38B	transmembrane protein 38B
LPHN2	LPHN2	latrophilin 2
NAALADL2	NAALADL2	N-acetylated alpha-linked acidic dipeptidase-like 2
RPL23A	RPL23A	ribosomal protein L23a
VPREB1	VPREB1	pre-B lymphocyte gene 1

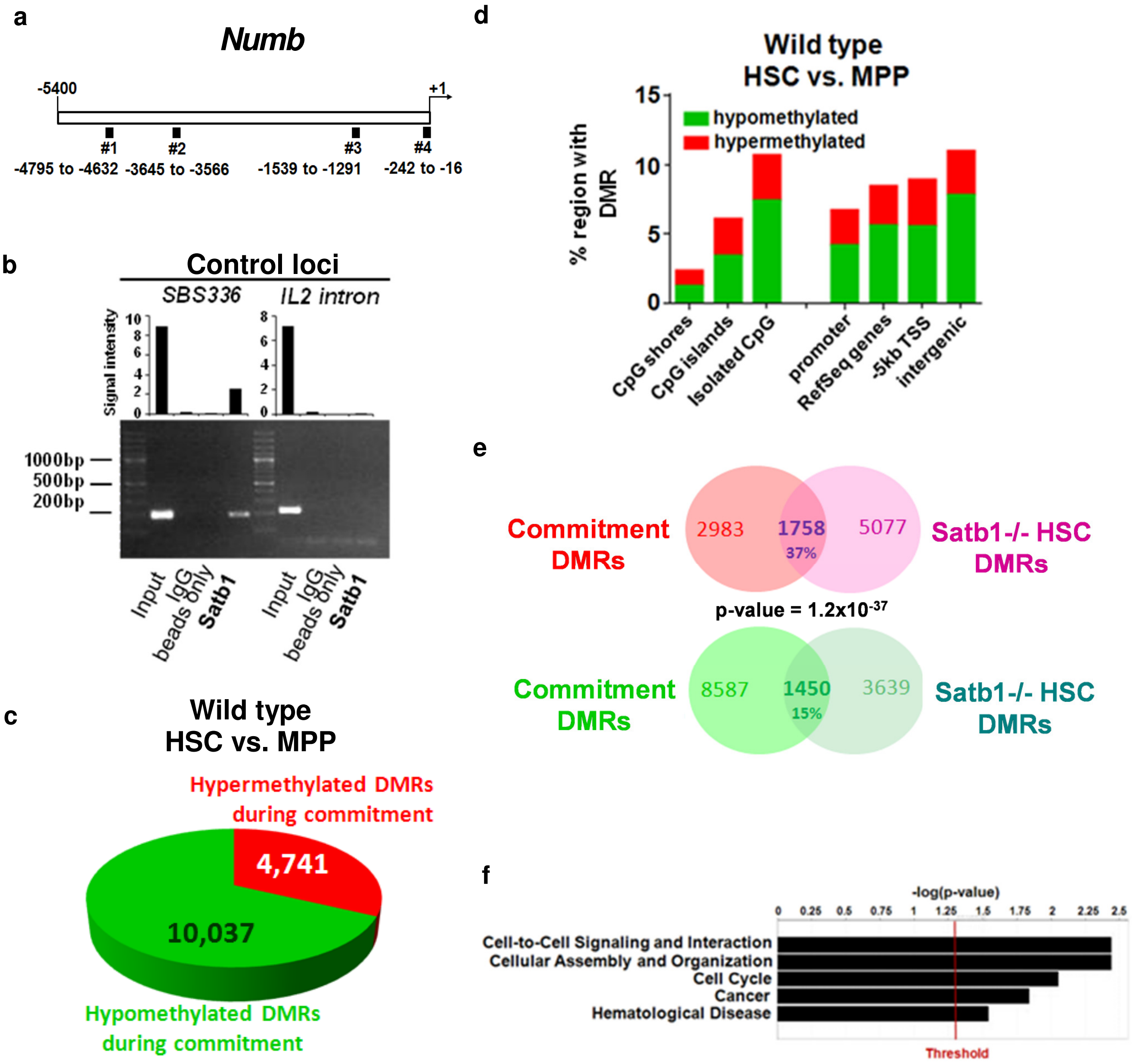
Microarray analysis and qRT-PCR validation of *Satb1*-/- compared to wild-type CD150+LSK HSCs, and differentially expressed genes within the MYC_CHIP_PET_2PLUS signature.
(**a**) Ingenuity Pathway Analysis (IPA) analysis of differentially expressed genes in donor-derived, *Satb1*$^{-/-}$ CD150^{+} LSKs. Shown are the top five networks of Satb1-dependent genes in HSCs. Threshold cut-off –log(p-value): 1.4. (**b**) Validation of differentially expressed genes in a second set of sorted donor-derived HSCs from *Satb1*$^{+/+}$ and *Satb1*$^{-/-}$ cell recipients by quantitative real-time PCR. Shown are averages and standard deviations of Gapdh-normalized mRNA expression; n=3-5/genotype, * p<0.05. (**c**) Differentially expressed genes within the MYC_CHIP_PET_2PLUS dataset in absence of *Satb1* in HSCs. Shown is a list of genes differentially expressed in absence of Satb1 which have been identified as directly bound by Myc. Shown is the GSEA list and expression values (blue = low expression, red = high expression) of individual *Satb1*$^{+/+}$ (gray) and *Satb1*$^{-/-}$ (yellow) CD150^{+} LSK cells as assessed by microarray analysis.

Supplementary Figure 5



Myc inhibition in *Satb1*$^{-/-}$ CD150^{+} CD48^{-} LSK HSCs using different concentrations of two small molecule inhibitors, 10058-F4 and JQ1. (**a,c,e**) Treatment of HSCs with10058-F4 (concentrations indicated in graph) (**b,d,f**) JQ1(concentrations indicated in graph) or 1% DMSO. Quantification of (**a**) *Igf1R*, and (**b**) *Myc* and *Igf1R* expression 48hrs after treatment by qRT-PCR. Shown are averages and standard deviations normalized to *Gapdh* as fold change compared to DMSO-treated controls (n=2/genotype, * $p<0.05$). (**c,d**) Colony formation assay of Myc inhibitor-treated HSCs in semisolid medium. Shown are averages and standard deviations of BFU-E, CFU-G/M, CFU-GM, and CFU-GEMM. CD150^{+} CD48^{-} KSL were plated in semisolid medium and colonies were scored (n=2/genotype; * $p<0.05$, ** $p<0.01$, *** $p<0.005$). (**e**) Quantification of *Numb* mRNA expression 48hrs after treatment by qRT-PCR. Shown are averages and standard deviations normalized to *Gapdh* as fold change compared to DMSO-treated controls (n=2/genotype).

Supplementary Figure 6



Epigenetic alterations in *Satb1*$^{-/-}$ HSCs. (**a**) Assessment of Satb1 binding to the candidate sites after ChIP in HPC7 cells by PCR. Shown is a schematic depicting primer locations in *Numb* locus interrogating Satb1 binding. (**b**) PCR of the Satb1 binding site SBS336 was used as a positive control, and an IL2 intron site was used as a negative control for Satb1 binding. Bar graphs show the quantification of signal intensities of the PCR products. (**c**) Representation of differentially hyper- and hypomethylated regions found during transition from wild type CD150^{+} LSK HSCs to wild-type CD150^{-} LSK MPPs ("commitment DMRs"). (**d**) Distribution of differentially methylated regions (DMR, 1kb tiles) within CpG shores, islands, and isolated CpGs as well as in the promoter (5kb upstream), RefSeq gene regions, 5kb downstream and in intergenic regions in wild-type HSCs compared to wild-type MPPs. (**e**) Intersection of "commitment DMRs" with *Satb1* knockout-associated HSC-specific DMRs ("*Satb1*$^{-/-}$ HSC DMRs") showing a high similarity between *Satb1*$^{-/-}$ HSC DMRs and methylation changes occurring in the transition from wild-type HSC to MPP, indicating a commitment-primed epigenetic stage of *Satb1*-deficient HSCs. Shown are Venn diagrams for hypermethylated (red) and hypomethylated (green) regions (overall p=1.2x10^{-37}; hypergeometrical testing). (**f**) Ingenuity Pathway analysis of the set of genes with altered expression and DNA cytosine methylation in *Satb1*$^{-/-}$ HSCs. Shown are the top five functional pathways with a significant enrichment with a threshold cut-off: -log(p-value) of 1.3.

Supplementary Table 1. **Differentially expressed genes in *Satb1*$^{-/-}$ HSCs.**

Probeset ID	Gene title	Gene Symbol	log2 FC
10538882	predicted gene, EG434025	EG434025	**3.28**
10494262	cathepsin K	Ctsk	**3.02**
10400072	scinderin	Scin	**2.84**
10438415	immunoglobulin lambda chain, variable 2 | immunoglobulin lambda chain, constant region 2	Igl-V2 | Igl-C2	**2.21**
10502770	similar to calcium-independent alpha-latrotoxin receptor homolog 2 | latrophilin 2	Lphn2 | LOC100048050	**2.20**
10438064	pre-B lymphocyte gene 1	Vpreb1	**1.88**
10504757	cDNA sequence BC005685	BC005685	**1.88**
10401935	cDNA sequence BC005685	BC005685	**1.79**
10538901	cDNA sequence BC005685	BC005685	**1.79**
10608107	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	Uty	**1.69**
10403060	immunoglobulin heavy variable V1-72 | similar to Ig heavy chain V-II region SESS precursor | immunoglobulin heavy chain Ia	Igh-VJ558 | AB069917 | Igh-Ia | V165-D-J-C mu | LOC546230 | LOC382693 | LOC631518 | Ighv1-72	**1.55**
10503176	chromodomain helicase DNA binding protein 7	Chd7	**1.53**
10608001	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	Eif2s3y	**1.52**
10590842	predicted gene, ENSMUSG00000074512	ENSMUSG00000074512	**1.44**
10504755	predicted gene, ENSMUSG00000056897	ENSMUSG00000056897	**1.32**
10428209	predicted gene, ENSMUSG00000072618	ENSMUSG00000072618	**1.28**
10515702	cDNA sequence BC059842	BC059842	**1.25**
10522666	RIKEN cDNA 2310040G07 gene	2310040G07Rik	**1.23**
10607738	carbonic anhydrase 5b, mitochondrial	Car5b	**1.23**
10513152	protein tyrosine phosphatase, non-receptor type 3	Ptpn3	**1.22**
10428594	sterile alpha motif domain containing 12	Samd12	**1.20**
10445373	RIKEN cDNA B230354K17 gene	B230354K17Rik	**1.18**
10513156	protein tyrosine phosphatase, non-receptor type 3	Ptpn3	**1.09**
10455112	protocadherin beta 17	Pcdhb17	**1.09**
10363455	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	Pcbd1	**1.08**
10368173	RIKEN cDNA 4933406P04 gene	4933406P04Rik	**1.08**
10386169	predicted gene, ENSMUSG00000053218	ENSMUSG00000053218	**1.07**
10352133	EF-hand calcium binding domain 2	Efcab2	**1.07**
10346678	calcium response factor	Carf	**1.07**
10511779	ATPase, H+ transporting, lysosomal V0 subunit D2	Atp6v0d2	**1.07**
10579012	chondroitin sulfate N-acetylgalactosaminyltransferase 1	Csgalnact1	**1.06**
10394674	predicted gene, ENSMUSG00000050974	ENSMUSG00000050974	**1.05**
10562963	DNA segment, Chr 7, Brigham & Women's Genetics 0826 expressed	D7Bwg0826e	**1.05**
10579958	interleukin 15	Il15	**1.04**
10560818	zinc finger protein 111	Zfp111	**1.02**
10558398	RIKEN cDNA 5430417C01 gene	5430417C01Rik	**1.01**
10502772	latrophilin 2	Lphn2	**1.00**
10569972	LAG1 homolog, ceramide synthase 4	Lass4	**1.00**
10415787	potassium channel regulator	Kcnrg	**0.98**
10413012	fucosyltransferase 11	Fut11	**0.98**
10388784	ribosomal protein L23a	Rpl23a	**0.98**
10593050	interleukin 10 receptor, alpha	Il10ra	**0.98**
10415413	cDNA sequence BC030046	BC030046	**0.98**
10528482	cDNA sequence BC050254	BC050254	**0.96**
10416199	ectonucleoside triphosphate diphosphohydrolase 4	Entpd4	**0.96**
10344952	retinol dehydrogenase 10 (all-trans)	Rdh10	**0.96**
10420846	frizzled homolog 3 (Drosophila)	Fzd3	**0.95**
10469571	OTU domain containing 1	Otud1	**0.95**

10441933	RIKEN cDNA 9030025P20 gene | hypothetical protein LOC100041621 | RIKEN cDNA 2210404J11 gene	2210404J11Rik | LOC100041621 | 9030025P20Rik	**0.94**
10513158	protein tyrosine phosphatase, non-receptor type 3	Ptpn3	**0.94**
10403018	immunoglobulin heavy chain Ia | immunoglobulin heavy chain (J558 family) | Ig mu chain V region AC38 205.12	Igh-VJ558 | Igh-Ia | IghmAC38.205.12	**0.94**
10566668	similar to suppressor of cytokine signaling 6	LOC675799	**0.94**
10495343	WD repeat domain 47	Wdr47	**0.93**
10514892	RIKEN cDNA 2210012G02 gene	2210012G02Rik	**0.93**
10422013	Kruppel-like factor 12	Klf12	**0.93**
10528038	a disintegrin and metallopeptidase domain 22	Adam22	**0.92**
10449687	radial spoke head 1 homolog (Chlamydomonas)	Rsph1	**0.91**
10601519	kelch-like 4 (Drosophila)	Klhl4	**0.91**
10442606	RIKEN cDNA 4930528F23 gene	4930528F23Rik	**0.90**
10383206	hypothetical LOC672511	LOC672511	**0.90**
10531201	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 3	Adamts3	**0.90**
10501235	glutathione S-transferase, mu 4	Gstm4	**0.90**
10440926	DnaJ (Hsp40) homolog, subfamily C, member 28	Dnajc28	**0.90**
10452613	Rho GTPase activating protein 28	Arhgap28	**0.90**
10403964	zinc finger protein 184 (Kruppel-like)	Zfp184	**0.89**
10478401	tocopherol (alpha) transfer protein-like	Ttpal	**0.88**
10445071	zinc finger protein 57	Zfp57	**0.87**
10600357	tafazzin	Taz	**0.87**
10508614	fatty acid binding protein 3, muscle and heart	Fabp3	**0.87**
10502776	similar to calcium-independent alpha-latrotoxin receptor homolog 2 | latrophilin 2	Lphn2 | LOC100048050	**0.87**
10543249	predicted gene, EG232599	EG232599	**0.87**
10505998	FGGY carbohydrate kinase domain containing	Fggy	**0.87**
10505994	FGGY carbohydrate kinase domain containing	Fggy	**0.86**
10454398	expressed sequence AW554918	AW554918	**0.86**
10577096	PCI domain containing 2	Pcid2	**0.85**
10579607	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	B3gnt3	**0.85**
10391454	vesicle amine transport protein 1 homolog (T californica)	Vat1	**0.85**
10538811	PR domain containing 5	Prdm5	**0.85**
10515086	RIKEN cDNA 9630013D21 gene	9630013D21Rik	**0.84**
10367982	G protein-coupled receptor 126	Gpr126	**0.84**
10497501	N-acetylated alpha-linked acidic dipeptidase-like 2	Naaladl2	**0.84**
10455901	solute carrier family 27 (fatty acid transporter), member 6	Slc27a6	**0.84**
10578623	WW, C2 and coiled-coil domain containing 2	Wwc2	**0.84**
10346810	par-3 partitioning defective 3 homolog B (C. elegans)	Pard3b	**0.84**
10585338	KDEL (Lys-Asp-Glu-Leu) containing 2	Kdelc2	**0.84**
10515698	cDNA sequence BC059842	BC059842	**0.84**
10352503	bisphosphate 3'-nucleotidase 1	Bpnt1	**0.83**
10444821	histocompatibility 2, Q region locus 8	H2-Q8	**0.83**
10467162	pantothenate kinase 1	Pank1	**0.83**
10408477	E2F transcription factor 3	E2f3	**0.83**
10436892	intersectin 1 (SH3 domain protein 1A)	Itsn1	**0.83**
10514510	cytochrome P450, family 2, subfamily j, polypeptide 6	Cyp2j6	**0.83**
10431935	adhesion molecule with Ig like domain 2	Amigo2	**0.82**
10576354	AFG3(ATPase family gene 3)-like 1 (yeast)	Afg3l1	**0.82**
10441064	Down syndrome critical region gene 3	Dscr3	**0.82**
10396606	synaptic nuclear envelope 2	Syne2	**0.81**
10382200	coiled-coil domain containing 46	Ccdc46	**0.81**
10546803	predicted gene, ENSMUSG00000072853	ENSMUSG00000072853	**0.81**
10383208	hypothetical LOC672511	LOC672511	**0.81**
10487392	Kv channel interacting protein 3, calsenilin	Kcnip3	**0.80**
10354979	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	Als2	**0.80**
10564507	arrestin domain containing 4	Arrdc4	**0.80**
10598107	TATA box binding protein (Tbp)-associated factor, RNA	Taf1a	**0.80**

	polymerase I, A		
10413574	Scm-like with four mbt domains 1	Sfmbt1	**0.79**
10443027	RIKEN cDNA A930001N09 gene	A930001N09Rik	**0.79**
10543120	islet cell autoantigen 1	Ica1	**0.79**
10401968	galactosylceramidase	Galc	**0.79**
10529711	cytokine-dependent hematopoietic cell linker	Clnk	**0.78**
10458247	leucine rich repeat transmembrane neuronal 2	Lrrtm2	**0.78**
10371502	fatty acid binding protein 3, muscle and heart	Fabp3	**0.78**
10443110	synaptic Ras GTPase activating protein 1 homolog (rat)	Syngap1	**0.78**
10411059	zinc finger, FYVE domain containing 16	Zfyve16	**0.78**
10534679	tripartite motif-containing 56	Trim56	**0.78**
10444824	histocompatibility 2, Q region locus 6	H2-Q6	**0.77**
10575578	RIKEN cDNA 4930402E16 gene	4930402E16Rik	**0.77**
10403081	WD repeat domain 60	Wdr60	**0.77**
10479981	GATA binding protein 3	Gata3	**0.76**
10512470	CD72 antigen	Cd72	**0.76**
10600825	zinc finger CCCH-type containing 12B	Zc3h12b	**0.76**
10515930	expressed sequence AA415398	AA415398	**0.76**
10416655	predicted gene, EG432879	EG432879	**0.76**
10368486	ring finger protein 146	Rnf146	**0.75**
10496638	outer dense fiber of sperm tails 2-like	Odf2l	**0.75**
10527918	mitochondrial transcription termination factor | predicted gene, ENSMUSG00000053178	Mterf | ENSMUSG00000053178	**0.75**
10523880	RNA polymerase II associated protein 2	Rpap2	**0.75**
10530013	gene model 447, (NCBI)	Gm447	**0.75**
10511975	solute carrier family 35 (CMP-sialic acid transporter), member 1	Slc35a1	**0.75**
10484402	catenin (cadherin associated protein), delta 1	Ctnnd1	**0.75**
10444591	heat shock protein 1-like	Hspa1l	**0.75**
10559644	cDNA sequence BC022651	BC022651	**0.74**
10532582	myosin XVIIIb	Myo18b	**0.74**
10504761	hypothetical protein LOC641050	LOC641050	**0.74**
10542040	poly (ADP-ribose) polymerase family, member 11	Parp11	**0.74**
10422436	dedicator of cytokinesis 9	Dock9	**0.74**
10380871	olfactory receptor 869 | START domain containing 3	Stard3 | Olfr869	**0.74**
10392983	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	Slc25a19	**0.74**
10553897	myotubularin related protein 10	Mtmr10	**0.74**
10440576	zinc finger protein 294	Zfp294	**0.74**
10575706	WW domain-containing oxidoreductase	Wwox	**0.74**
10554094	insulin-like growth factor I receptor	Igf1r	**0.73**
10605766	melanoma antigen, family D, 1	Maged1	**0.73**
10533504	intraflagellar transport 81 homolog (Chlamydomonas)	Ift81	**0.73**
10498357	RIKEN cDNA F630111L10 gene	F630111L10Rik	**0.73**
10407792	G protein-coupled receptor 137B | G protein-coupled receptor 137B, pseudogene	Gpr137b-ps | Gpr137b	**0.73**
10534921	methylphosphate capping enzyme	Mepce	**0.73**
10505071	transmembrane protein 38B	Tmem38b	**0.73**
10607302	guanine nucleotide binding protein-like 3 (nucleolar)-like	Gnl3l	**0.72**
10403413	isopentenyl-diphosphate delta isomerase	Idi1	**0.72**
10541191	RAD52 homolog (S. cerevisiae)	Rad52	**0.72**
10560832	zinc finger protein 61	Zfp61	**0.72**
10561799	zinc finger protein 74	Zfp74	**0.72**
10357239	transmembrane protein 37	Tmem37	**0.72**
10561810	zinc finger protein 14	Zfp14	**0.72**
10512682	zinc finger and BTB domain containing 5	Zbtb5	**0.71**
10551803	zinc finger protein 568	Zfp568	**0.71**
10389151	schlafen 8 | schlafen 10	Slfn8 | Slfn10	**0.71**
10541683	complement component C1rb | complement component 1, r subcomponent	C1r | C1rb	**0.71**
10356423	ubiquitin specific peptidase 40	Usp40	**0.70**

10563077	reticulocalbin 3, EF-hand calcium binding domain	Rcn3	**0.70**
10390505	ribosomal protein L23	Rpl23	**0.70**
10389134	schlafen 9	Slfn9	**0.70**
10392098	FtsJ homolog 3 (E. coli)	Ftsj3	**0.70**
10592471	GRAM domain containing 1B	Gramd1b	**0.70**
10505517	toll-like receptor 4	Tlr4	**0.70**
10428302	Kruppel-like factor 10	Klf10	**0.69**
10586384	programmed cell death 7	Pdcd7	**0.69**
10440077	RIKEN cDNA 2610528E23 gene	2610528E23Rik	**0.69**
10538892	hypothetical protein LOC641050	LOC641050	**0.69**
10396442	small nuclear RNA activating complex, polypeptide 1	Snapc1	**0.69**
10489266	chromodomain helicase DNA binding protein 6	Chd6	**0.68**
10421214	Rho-related BTB domain containing 2	Rhobtb2	**0.68**
10477717	protein C receptor, endothelial	Procr	**0.68**
10564520	ribosomal protein L23	Rpl23	**0.68**
10442691	chloride channel 7	Clcn7	**0.68**
10571312	dual specificity phosphatase 4	Dusp4	**0.68**
10469083	UPF2 regulator of nonsense transcripts homolog (yeast)	Upf2	**0.68**
10396402	protein kinase C, eta	Prkch	**0.67**
10491877	DNA segment, Chr 3, ERATO Doi 751, expressed	D3Ertd751e	**0.67**
10383198	hypothetical LOC672511	LOC672511	**0.67**
10605811	RIKEN cDNA 2810002O09 gene	2810002O09Rik	**0.67**
10596568	RNA binding motif protein 15B	Rbm15b	**0.67**
10584712	hypoxia up-regulated 1	Hyou1	**0.67**
10542875	RIKEN cDNA 3010003L21 gene	3010003L21Rik	**0.67**
10352178	saccharopine dehydrogenase (putative)	Sccpdh	**0.67**
10542896	bicaudal D homolog 1 (Drosophila)	Bicd1	**0.66**
10475946	zinc finger CCCH type containing 6	Zc3h6	**0.66**
10407481	phosphofructokinase, platelet	Pfkp	**0.66**
10453518	neurexin I	Nrxn1	**0.66**
10505030	fibronectin type III and SPRY domain containing 1-like	Fsd1l	**0.66**
10436451	syntaxin 19	Stx19	**0.66**
10501860	formin binding protein 1-like	Fnbp1l	**0.66**
10414433	RIKEN cDNA 6720456H20 gene	6720456H20Rik	**0.66**
10482301	RIKEN cDNA A930041I02 gene	A930041I02Rik	**0.66**
10495685	Rho GTPase activating protein 29	Arhgap29	**0.66**
10421517	cysteinyl leukotriene receptor 2	Cysltr2	**0.66**
10380252	coilin	Coil	**0.66**
10393272	ring finger protein 157	Rnf157	**0.66**
10439532	queuine tRNA-ribosyltransferase domain containing 1	Qtrtd1	**0.65**
10388734	Era (G-protein)-like 1 (E. coli)	Eral1	**0.65**
10449631	BTB (POZ) domain containing 9	Btbd9	**0.65**
10462613	interferon-induced protein with tetratricopeptide repeats 2	Ifit2	**0.64**
10557033	eukaryotic elongation factor-2 kinase	Eef2k	**0.64**
10372383	zinc finger, DHHC domain containing 17	Zdhhc17	**0.64**
10546710	SHQ1 homolog (S. cerevisiae)	Shq1	**0.64**
10454828	prenatal ethanol induced mRNA, pseudogene	Pnet-ps	**0.64**
10488944	ubiquinol-cytochrome c reductase complex chaperone, CBP3 homolog (yeast)	Uqcc	**0.64**
10383192	hypothetical LOC672511	LOC672511	**0.64**
10377982	kinesin family member 1C	Kif1c	**0.64**
10448459	TBC1 domain family, member 24	Tbc1d24	**0.64**
10467068	sphingomyelin synthase 1	Sgms1	**0.64**
10492997	ets variant gene 3	Etv3	**0.63**
10467470	aldehyde dehydrogenase 18 family, member A1	Aldh18a1	**0.63**
10433032	activating transcription factor 7	Atf7	**0.63**
10410366	RIKEN cDNA 3830402I07 gene	3830402I07Rik	**0.63**
10538142	GTPase, IMAP family member 5	Gimap5	**0.63**
10606619	synaptotagmin-like 4	Sytl4	**0.63**
10383196	hypothetical LOC672511	LOC672511	**0.63**
10352281	acyl-Coenzyme A binding domain containing 3	Acbd3	**0.63**

10468762	RIKEN cDNA 4930506M07 gene	4930506M07Rik	**0.63**
10560826	zinc finger protein 109	Zfp109	**0.63**
10485674	RIKEN cDNA 2700007P21 gene	2700007P21Rik	**0.63**
10437541	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	Nagpa	**0.62**
10479010	sporulation protein, meiosis-specific, SPO11 homolog (S. cerevisiae)	Spo11	**0.62**
10466903	RIKEN cDNA 4430402I18 gene	4430402I18Rik	**0.61**
10401937	cDNA sequence BC005685	BC005685	**0.61**
10450694	histocompatibility 2, T region locus 17 | histocompatibility 2, T region locus 22	H2-T9 | H2-T22 | H2-T10 | H2-T17	**0.61**
10483264	tetratricopeptide repeat domain 21B	Ttc21b	**0.61**
10442194	zinc finger protein 677	Zfp677	**0.61**
10453114	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	Dhx57	**0.61**
10349348	coiled-coil domain containing 93	Ccdc93	**0.61**
10443869	cytochrome P450, family 4, subfamily f, polypeptide 16	Cyp4f16	**0.61**
10599232	NFKB activating protein	Nkap	**0.61**
10367591	myc target 1	Myct1	**0.61**
10581625	RIKEN cDNA 2400003C14 gene	2400003C14Rik	**0.60**
10540408	inositol 1,4,5-triphosphate receptor 1	Itpr1	**0.60**
10384092	NudC domain containing 3	Nudcd3	**0.60**
10604076	small nucleolar RNA, H/ACA box 69	Snora69	**0.60**
10606770	zinc finger, matrin type 1	Zmat1	**0.60**
10491136	TRAF2 and NCK interacting kinase	Tnik	**0.60**
10464443	similar to ribosomal protein S25	LOC100045278	**0.60**
10377569	fragile X mental retardation, autosomal homolog 2	Fxr2	**0.60**
10515211	RIKEN cDNA 4930544O15 gene	4930544O15Rik	**0.60**
10357833	ATPase, Ca++ transporting, plasma membrane 4	Atp2b4	**0.59**
10494428	thioredoxin interacting protein	Txnip	**0.59**
10371356	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	Appl2	**0.59**
10535034	zinc finger protein 68	Zfp68	**0.59**
10428328	solute carrier family 25, member 32	Slc25a32	**0.59**
10486564	tau tubulin kinase 2 | congenital dyserythropoietic anemia, type I (human)	Ttbk2 | Cdan1	**0.59**
10473160	sperm specific antigen 2	Ssfa2	**0.59**
10497590	ecotropic viral integration site 1	Evi1	**0.59**
10557585	zinc finger protein 553	Zfp553	**0.59**
10424050	estrogen receptor-binding fragment-associated gene 9	Ebag9	**0.59**
10578189	similar to chromodomain helicase DNA binding protein 6	LOC676031	**0.58**
10346838	par-3 partitioning defective 3 homolog B (C. elegans)	Pard3b	**0.58**
10371230	guanine nucleotide binding protein, alpha 11	Gna11	**0.58**
10415021	abhydrolase domain containing 4	Abhd4	**0.58**
10538890	hypothetical protein LOC641050	LOC641050	**0.58**
10371676	UTP20, small subunit (SSU) processome component, homolog (yeast)	Utp20	**0.58**
10511416	thymocyte selection-associated high mobility group box	Tox	**0.58**
10381006	thyroid hormone receptor alpha	Thra	**0.58**
10364130	zinc finger protein 280b	Zfp280b	**0.58**
10393509	ubiquitin specific peptidase 36	Usp36	**0.58**
10459962	ATPase, class II, type 9B	Atp9b	**0.58**
10362596	Fyn proto-oncogene	Fyn	**0.58**
10476893	GDNF-inducible zinc finger protein 1	Gzf1	**0.57**
10436209	Casitas B-lineage lymphoma b	Cblb	**0.57**
10467871	dynamin binding protein	Dnmbp	**0.57**
10374706	pseudouridylate synthase 10	Pus10	**0.57**
10373036	amplified in osteosarcoma	Os9	**0.57**
10479672	transcription elongation factor A (SII), 2	Tcea2	**0.57**
10478219	phospholipase C, gamma 1	Plcg1	**0.57**
10383993	coiled-coil domain containing 117	Ccdc117	**0.57**
10453276	thyroid adenoma associated	Thada	**0.57**

10403558	ERO1-like beta (S. cerevisiae)	Ero1lb	**0.57**
10441919	RIKEN cDNA 1600012H06 gene	1600012H06Rik	**0.57**
10370303	adenosine deaminase, RNA-specific, B1	Adarb1	**0.57**
10377889	misshapen-like kinase 1 (zebrafish)	Mink1	**0.56**
10452633	TGFB-induced factor homeobox 1	Tgif1	**0.56**
10546855	SLIT-ROBO Rho GTPase activating protein 3	Srgap3	**0.56**
10433735	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Abcc1	**0.56**
10539220	expressed sequence AW146020	AW146020	**0.56**
10588642	tumor suppressor candidate 4	Tusc4	**0.56**
10462454	ubiquitin-like, containing PHD and RING finger domains 2	Uhrf2	**0.56**
10372385	zinc finger, DHHC domain containing 17	Zdhhc17	**0.56**
10560481	FBJ osteosarcoma oncogene B	Fosb	**0.56**
10432215	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	Ddx23	**0.56**
10381860	methyltransferase like 2	Mettl2	**0.56**
10593526	ataxia telangiectasia mutated homolog (human)	Atm	**0.56**
10396919	RIKEN cDNA 4933426M11 gene	4933426M11Rik	**0.56**
10383867	myotubularin related protein 3	Mtmr3	**0.56**
10516371	eukaryotic translation initiation factor 2C, 1	Eif2c1	**0.56**
10595979	muscle and microspikes RAS	Mras	**0.56**
10361620	required for meiotic nuclear division 1 homolog (S. cerevisiae) | predicted gene, EG433224	EG433224 | Rmnd1	**0.56**
10505109	cDNA sequence BC026590	BC026590	**0.56**
10584124	Rho GTPase-activating protein	Grit	**0.56**
10585988	myosin IXa	Myo9a	**0.55**
10360563	SET and MYND domain containing 3	Smyd3	**0.55**
10567702	Rho GTPase activating protein 17	Arhgap17	**0.55**
10581073	dynein, cytoplasmic 1 light intermediate chain 2	Dync1li2	**0.55**
10426368	leucine-rich repeat kinase 2	Lrrk2	**0.55**
10590962	RIKEN cDNA 1700012B09 gene	1700012B09Rik	**0.55**
10577824	leucine zipper-EF-hand containing transmembrane protein 2	Letm2	**0.55**
10504518	polymerase (RNA) I polypeptide E	Polr1e	**0.55**
10359303	RIKEN cDNA 4930562F07 gene	4930562F07Rik	**0.55**
10523974	predicted gene, ENSMUSG00000072769	ENSMUSG00000072769	**0.54**
10505044	fukutin	Fktn	**0.54**
10407392	cDNA sequence BC016423	BC016423	**0.54**
10479887	Sec61, alpha subunit 2 (S. cerevisiae)	Sec61a2	**0.54**
10541785	inhibitor of growth family, member 4 | proacrosin binding protein	Acrbp | Ing4	**0.54**
10496023	caspase 6	Casp6	**0.54**
10526133	RAB guanine nucleotide exchange factor (GEF) 1	Rabgef1	**0.54**
10518857	zinc finger and BTB domain containing 48	Zbtb48	**0.54**
10459837	RIKEN cDNA 8030462N17 gene	8030462N17Rik	**0.54**
10578521	sorting nexin 25	Snx25	**0.54**
10405918	regulator of sex limited protein 1	Rsl1	**0.54**
10471978	enhancer of polycomb homolog 2 (Drosophila)	Epc2	**0.54**
10478698	eyes absent 2 homolog (Drosophila)	Eya2	**0.54**
10496539	guanylate binding protein 5	Gbp5	**0.54**
10588283	RAB6B, member RAS oncogene family	Rab6b	**0.54**
10600372	RIKEN cDNA B230340J04 gene	B230340J04Rik	**0.54**
10353549	RIKEN cDNA 4921533L14 gene	4921533L14Rik	**0.54**
10498064	SET domain containing (lysine methyltransferase) 7	Setd7	**0.53**
10347232	X-ray repair complementing defective repair in Chinese hamster cells 5	Xrcc5	**0.53**
10389143	schlafen 8	Slfn8	**0.53**
10378855	slingshot homolog 2 (Drosophila)	Ssh2	**0.53**
10411156	secretory carrier membrane protein 1	Scamp1	**0.53**
10404941	amine oxidase, flavin containing 1	Aof1	**0.53**
10369290	DNA-damage-inducible transcript 4	Ddit4	**0.53**
10557575	myosin light chain, phosphorylatable, fast skeletal muscle	Mylpf	**0.53**

10519472	mitochondrial transcription termination factor | predicted gene, ENSMUSG00000053178	Mterf | ENSMUSG00000053178	**0.53**
10442199	zinc finger protein 54	Zfp54	**0.53**
10433639	MKL/myocardin-like 2	Mkl2	**0.53**
10475378	cancer susceptibility candidate 4	Casc4	**0.52**
10408475	E2F transcription factor 3	E2f3	**0.52**
10505996	FGGY carbohydrate kinase domain containing	Fggy	**0.52**
10485241	1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)	Accs	**0.52**
10494445	Lix1-like	Lix1l	**0.52**
10480064	F-box protein 18	Fbxo18	**0.52**
10386604	serine hydroxymethyltransferase 1 (soluble)	Shmt1	**0.52**
10405094	isoleucine-tRNA synthetase	Iars	**0.52**
10599200	progesterone receptor membrane component 1	Pgrmc1	**0.52**
10391732	G patch domain containing 8 | predicted gene, ENSMUSG00000075516	Gpatch8 | ENSMUSG00000075516	**0.52**
10549899	zinc finger protein 418	Zfp418	**0.52**
10477543	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human)	Cbfa2t2	**0.52**
10595529	RIKEN cDNA 4922501C03 gene	4922501C03Rik	**0.51**
10562439	G patch domain containing 1	Gpatch1	**0.51**
10514520	cytochrome P450, family 2, subfamily j, polypeptide 9	Cyp2j9	**0.51**
10489620	nuclear receptor coactivator 5	Ncoa5	**0.51**
10347741	monoacylglycerol O-acyltransferase 1	Mogat1	**0.51**
10461782	required for meiotic nuclear division 1 homolog (S. cerevisiae) | predicted gene, EG433224	Rmnd1 | EG433224	**0.51**
10516678	karyopherin (importin) alpha 6	Kpna6	**0.51**
10536061	RIKEN cDNA 2610021A01 gene	2610021A01Rik	**0.51**
10393177	acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	**0.51**
10515574	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	St3gal3	**0.50**
10415911	kinesin family member 13B	Kif13b	**0.50**
10596269	DnaJ (Hsp40) homolog, subfamily C, member 13	Dnajc13	**0.50**
10361200	expressed sequence AA408296	AA408296	**0.50**
10562897	zinc finger protein 473	Zfp473	**0.50**
10504106	interleukin 11 receptor, alpha chain 1 | interleukin 11 receptor, alpha chain 2	Il11ra1 | RP23-388P16.3 | Il11ra2 | LOC100038993	**0.50**
10449225	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Decr2	**0.50**
10545780	exocyst complex component 6B	Exoc6b	**0.50**
10349453	RAB3 GTPase activating protein subunit 1	Rab3gap1	**0.49**
10572989	solute carrier family 10 (sodium/bile acid cotransporter family), member 7	Slc10a7	**0.49**
10439895	activated leukocyte cell adhesion molecule	Alcam	**0.49**
10439960	centrosomal protein 97	Cep97	**0.49**
10417912	ubiquitin specific peptidase 54	Usp54	**0.49**
10554269	abhydrolase domain containing 2	Abhd2	**0.49**
10397866	golgi autoantigen, golgin subfamily a, 5	Golga5	**0.49**
10456439	centrosomal protein 192	Cep192	**0.49**
10442211	zinc finger protein 53	Zfp53	**0.49**
10418766	ankyrin repeat domain 28	Ankrd28	**0.49**
10495259	guanine nucleotide binding protein, alpha transducing 2	Gnat2	**0.49**
10551487	similar to EID-2-like inhibitor of differentiation-3	LOC434156	**0.49**
10562670	zinc finger protein 715	Zfp715	**0.49**
10599435	oculocerebrorenal syndrome of Lowe	Ocrl	**0.49**
10476969	brain glycogen phosphorylase	Pygb	**0.48**
10546402	zinc finger, FYVE domain containing 20	Zfyve20	**0.48**
10537834	Rho guanine nucleotide exchange factor (GEF) 5	Arhgef5	**0.48**
10542395	activating transcription factor 7 interacting protein	Atf7ip	**0.48**
10453026	protein kinase D3	Prkd3	**0.48**
10603431	suppressor of variegation 3-9 homolog 1 (Drosophila)	Suv39h1	**0.48**
10397666	zinc finger CCCH type containing 14	Zc3h14	**0.48**
10596119	centrosomal protein 63	Cep63	**0.48**

10600169	biglycan	Bgn	**0.48**
10428827	transmembrane protein 65	Tmem65	**0.48**
10402020	echinoderm microtubule associated protein like 5	Eml5	**0.48**
10532630	adrenergic receptor kinase, beta 2	Adrbk2	**0.48**
10590343	trafficking protein, kinesin binding 1	Trak1	**0.47**
10554419	vacuolar protein sorting 33B (yeast)	Vps33b	**0.47**
10544563	zinc finger protein 467	Zfp467	**0.47**
10381218	hydroxysteroid (17-beta) dehydrogenase 1	Hsd17b1	**0.47**
10510604	DnaJ (Hsp40) homolog, subfamily C, member 11	Dnajc11	**0.47**
10512949	ATP-binding cassette, sub-family A (ABC1), member 1	Abca1	**0.47**
10401852	RIKEN cDNA 4930534B04 gene	4930534B04Rik	**0.47**
10350977	RIKEN cDNA 4930523C07 gene	4930523C07Rik	**0.47**
10507484	prion protein interacting protein 1	Prnpip1	**0.47**
10430574	RIKEN cDNA 4933432B09 gene	4933432B09Rik	**0.47**
10506058	InaD-like (Drosophila)	Inadl	**0.47**
10487109	centrosomal protein 152	Cep152	**0.47**
10501762	sorting nexin 7	Snx7	**0.47**
10357604	inhibitor of kappaB kinase epsilon	Ikbke	**0.46**
10564839	adaptor-related protein complex 3, sigma 2 subunit	Ap3s2	**0.46**
10577838	DDHD domain containing 2	Ddhd2	**0.46**
10506274	DnaJ (Hsp40) homolog, subfamily C, member 6	Dnajc6	**0.46**
10357220	transmembrane protein 177	Tmem177	**0.46**
10589587	SET domain containing 2	Setd2	**0.46**
10360506	thymoma viral proto-oncogene 3	Akt3	**0.46**
10361956	microtubule-associated protein 7	Mtap7	**0.46**
10469720	acyl-Coenzyme A binding domain containing 5	Acbd5	**0.46**
10438639	diacylglycerol kinase, gamma	Dgkg	**0.46**
10452935	HEAT repeat containing 5B	Heatr5b	**0.46**
10500103	GA repeat binding protein, beta 2	Gabpb2	**0.45**
10554629	elongation factor Tu GTP binding domain containing 1	Eftud1	**0.45**
10479077	vesicle-associated membrane protein, associated protein B and C	Vapb	**0.45**
10432986	achalasia, adrenocortical insufficiency, alacrimia	Aaas	**0.45**
10534966	zinc finger protein 113	Zfp113	**0.45**
10457606	potassium channel tetramerisation domain containing 1	Kctd1	**0.45**
10598164	RIKEN cDNA 0610010K06 gene	0610010K06Rik	**0.45**
10491617	RIKEN cDNA 4932438A13 gene	4932438A13Rik	**0.45**
10531752	helicase, mus308-like (Drosophila)	Hel308	**0.45**
10435802	RIKEN cDNA 2610015P09 gene	2610015P09Rik	**0.44**
10416522	TSC22 domain family, member 1	Tsc22d1	**0.44**
10466682	structural maintenance of chromosomes 5	Smc5	**0.44**
10506134	autophagy-related 4C (yeast)	Atg4c	**0.44**
10481577	uridine-cytidine kinase 1	Uck1	**0.44**
10590004	golgi autoantigen, golgin subfamily a, 4	Golga4	**0.44**
10502042	alpha-kinase 1	Alpk1	**0.44**
10446027	chromatin assembly factor 1, subunit A (p150)	Chaf1a	**0.44**
10450372	heat shock protein 1-like	Hspa1l	**0.44**
10463751	programmed cell death 11	Pdcd11	**0.44**
10522627	centrosomal protein 135	Cep135	**0.44**
10401267	WD repeat domain 22	Wdr22	**0.44**
10416753	progesterone immunomodulatory binding factor 1	Pibf1	**0.44**
10475437	sorbitol dehydrogenase	Sord	**0.44**
10509930	F-box protein 42	Fbxo42	**0.43**
10357164	erythrocyte protein band 4.1-like 5	Epb4.1l5	**0.43**
10420694	integrator complex subunit 6	Ints6	**0.43**
10574789	RIKEN cDNA 2310066E14 gene	2310066E14Rik	**0.43**
10519857	hepatocyte growth factor	Hgf	**0.43**
10579079	RIKEN cDNA 1200003I07 gene	1200003I07Rik	**0.42**
10542677	ethanolamine kinase 1	Etnk1	**0.42**
10460221	choline kinase alpha	Chka	**0.42**
10558961	tetraspanin 4	Tspan4	**0.42**

10377984	zinc finger protein 3	Zfp3	0.42
10551061	zinc finger protein 574	Zfp574	0.42
10520405	gene model 1040, (NCBI)	Gm1040	0.42
10477649	myosin, heavy chain 7B, cardiac muscle, beta | acyl-CoA synthetase short-chain family member 2	Acss2 | Myh7b	0.42
10507334	RIKEN cDNA 0610037D15 gene	0610037D15Rik	0.41
10537410	thromboxane A synthase 1, platelet	Tbxas1	0.41
10488291	retinoblastoma binding protein 9	Rbbp9	0.41
10549655	EPS8-like 1	Eps8l1	0.41
10458424	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf7	0.41
10392910	RIKEN cDNA C630004H02 gene	C630004H02Rik	0.41
10483381	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	Stk39	0.41
10595452	ubiquitin-conjugating enzyme E2C binding protein	Ube2cbp	0.41
10466317	zinc finger protein 91, ciliary neurotrophic factor transcription unit | zinc finger protein 91 | ciliary neurotrophic factor	Zfp91-cntf | Cntf | Zfp91	0.41
10537227	transmembrane protein 140	Tmem140	0.40
10372069	suppressor of cytokine signaling 2	Socs2	0.40
10540923	makorin, ring finger protein, 2	Mkrn2	0.40
10505674	centlein, centrosomal protein	Cntln	0.40
10397377	tubulin tyrosine ligase-like family, member 5	Ttll5	0.40
10376021	septin 8	41160	0.40
10463404	RIKEN cDNA 6030443O07 gene	6030443O07Rik	0.40
10513061	catenin (cadherin associated protein), alpha-like 1	Ctnnal1	0.40
10544133	poly (ADP-ribose) polymerase family, member 12	Parp12	0.40
10441342	RIKEN cDNA 1810020G14 gene | synaptojanin 2 binding protein	1810020G14Rik | Synj2bp	0.40
10506397	mesoderm induction early response 1 homolog (Xenopus laevis	Mier1	0.40
10542522	pleckstrin homology domain containing, family A member 5	Plekha5	0.39
10508249	predicted gene, OTTMUSG00000009332 | zinc finger, MYM-type 6	Zmym6 | OTTMUSG00000009332	0.39
10394471	syndecan 1	Sdc1	0.39
10468992	FERM domain containing 4A	Frmd4a	0.39
10507299	GC-rich promoter binding protein 1-like 1	Gpbp1l1	0.38
10381419	neighbor of Brca1 gene 1	Nbr1	0.38
10416588	RIKEN cDNA 1300010F03 gene	1300010F03Rik	0.38
10454298	zinc finger protein 397	Zfp397	0.38
10499981	ornithine decarboxylase antizyme 3	Oaz3	0.38
10349249	CLIP associating protein 1	Clasp1	0.38
10373340	RNA binding motif, single stranded interacting protein 2	Rbms2	0.37
10595805	RAS p21 protein activator 2	Rasa2	0.37
10493394	secretory carrier membrane protein 3 | CDC-like kinase 2	Scamp3 | Clk2	0.37
10442986	Luc7 homolog (S. cerevisiae)-like	Luc7l	0.36
10344821	centrosome and spindle pole associated protein 1	Cspp1	0.36
10542241	taste receptor, type 2, member 120	Tas2r120	-0.53
10412211	granzyme A	Gzma	-0.56
10562093	RIKEN cDNA 4930479M11 gene	4930479M11Rik	-0.61
10562152	myelin-associated glycoprotein	Mag	-0.62
10605493	proline rich Gla (G-carboxyglutamic acid) 1	Prrg1	-0.65
10412911	farnesyl diphosphate farnesyl transferase 1	Fdft1	-0.65
10471761	olfactory receptor 352	Olfr352	-0.66
10537506	olfactory receptor 460	Olfr460	-0.67
10528615	predicted gene, ENSMUSG00000073129	ENSMUSG00000073129	-0.68
10580635	carboxylesterase 3	Ces3	-0.72
10428955	gasdermin C2	Gsdmc2	-0.72
10400607	MAM domain containing glycosylphosphatidylinositol anchor 2	Mdga2	-0.74

10500982	RIKEN cDNA I830077J02 gene	I830077J02Rik	-0.74
10606355	cysteinyl leukotriene receptor 1	Cysltr1	-0.74
10560791	predicted gene, EG628664 | predicted gene, EG545926	EG381936 | EG545926 | 100043625 | EG620736 |ENSMUSG00000074321 | EG628664 | EG545929	-0.75
10560764	predicted gene, EG628664 | predicted gene, ENSMUSG00000074321	EG381936 | EG620736 | ENSMUSG00000074321 | EG628664 | EG545929	-0.75
10560777	predicted gene, EG628664 | predicted gene, EG545926	EG381936 | EG545926 | 100043625 | EG620736 |ENSMUSG00000074321 | EG628664 | EG545929	-0.75
10477644	transformation related protein 53 inducible nuclear protein 2	Trp53inp2	-0.75
10550772	predicted gene, EG628475 | predicted gene, EG628664	EG381936 | EG628475 | EG545926 | 100043625 | EG620736 | ENSMUSG00000074321 | EG628664 | EG545929 |ENSMUSG00000074296	-0.75
10560807	predicted gene, EG628664 | predicted gene, EG545926	EG381936 | EG545926 | 100043625 | EG620736 |ENSMUSG00000074321 | EG628664 | EG545929	-0.75
10566696	olfactory receptor 509	Olfr509	-0.76
10423002	UDP glycosyltransferases 3 family, polypeptide A1	Ugt3a1	-0.76
10429100	leucine rich repeat containing 6 (testis)	Lrrc6	-0.76
10603533	synovial sarcoma, X member B, breakpoint 3	Ssxb3	-0.79
10394060	secreted and transmembrane 1B	Sectm1b	-0.82
10402347	interferon, alpha-inducible protein 27	Ifi27	-0.82
10564013	expressed sequence AF357427	AF357427	-0.82
10564017	expressed sequence AF357427	AF357427	-0.82
10406928	CD180 antigen	Cd180	-0.83
10489451	seminal vesicle secretory protein 2	Svs2	-0.85
10550762	predicted gene, EG628475 | predicted gene, EG628664	EG381936 | EG628475 | EG545926 | 100043625 | EG620736 | ENSMUSG00000074321 | EG628664 | EG545929 |ENSMUSG00000074296	-0.86
10542255	taste receptor, type 2, member 113	Tas2r113	-0.89
10400948	Six6 opposite strand transcript 1	Six6os1	-0.89
10360338	Fc receptor, IgE, high affinity I, alpha polypeptide	Fcer1a	-0.93
10552294	RIKEN cDNA 4930433I11 gene	4930433I11Rik	-0.95
10560760	predicted gene, EG628664 | predicted gene, EG545926	EG381936 | EG545926 | 100043625 | EG620736 | ENSMUSG00000074321 | EG628664 | EG545929	-0.96
10560773	predicted gene, EG628664 | predicted gene, EG545926	EG381936 | EG545926 | 100043625 | EG620736 |ENSMUSG00000074321 | EG628664 | EG545929	-0.96
10560803	predicted gene, EG545929	EG545929	-0.96
10598093	RIKEN cDNA 9930022N03 gene	9930022N03Rik	-0.99
10493820	S100 calcium binding protein A6 (calcyclin)	S100a6	-1.00
10597098	cathelicidin antimicrobial peptide	Camp	-1.02
10583100	matrix metallopeptidase 8	Mmp8	-1.04
10451646	RIKEN cDNA A530064D06 gene	A530064D06Rik	-1.05
10347925	component of Sp100-rs | predicted gene, EG665378	Csprs | EG665378	-1.06
10432774	keratin 6B	Krt6b	-1.07
10475517	expressed sequence AA467197	AA467197	-1.07
10550994	carcinoembryonic antigen-related cell adhesion molecule 10	Ceacam10	-1.08
10473089	deafness, autosomal recessive 59 (human)	Dfnb59	-1.09
10347915	component of Sp100-rs	Csprs	-1.09
10528191	spermatogenesis associated glutamate (E)-rich protein 4e | RIKEN cDNA 4930572O03 gene	ENSMUSG00000033219 | Speer4d | Speer4e | 4930572O03Rik	-1.11
10448124	formyl peptide receptor 1	Fpr1	-1.11
10386185	olfactory receptor 325 | olfactory receptor 330 | olfactory	Olfr325 | Olfr331 | Olfr329 | Olfr328 |	-1.12

	receptor 329 | olfactory receptor 331 | olfactory receptor 328	Olfr330	
10497356	signal-regulatory protein beta 1 | predicted gene, 668101	668101 | Sirpb1	**-1.13**
10563937	expressed sequence AF357427	AF357427	**-1.13**
10563947	expressed sequence AF357427	AF357427	**-1.13**
10563951	expressed sequence AF357427	AF357427	**-1.13**
10563953	expressed sequence AF357427	AF357427	**-1.13**
10563957	expressed sequence AF357427	AF357427	**-1.13**
10563995	expressed sequence AF357427	AF357427	**-1.13**
10563997	expressed sequence AF357427	AF357427	**-1.13**
10563999	expressed sequence AF357427	AF357427	**-1.13**
10564001	expressed sequence AF357427	AF357427	**-1.13**
10564003	expressed sequence AF357427	AF357427	**-1.13**
10564007	expressed sequence AF357427	AF357427	**-1.13**
10564029	expressed sequence AF357427	AF357427	**-1.13**
10564031	expressed sequence AF357427	AF357427	**-1.13**
10564065	predicted gene, 100040985	100040985	**-1.13**
10584458	olfactory receptor 920	Olfr920	**-1.16**
10528799	spermatogenesis associated glutamate (E)-rich protein 4a	Speer4a	**-1.16**
10363070	glycoprotein 49 A | leukocyte immunoglobulin-like receptor, subfamily B, member 4	Gp49a | Lilrb4	**-1.16**
10473604	olfactory receptor 46	Olfr46	**-1.18**
10528821	spermatogenesis associated glutamate (E)-rich protein 4b | spermatogenesis associated glutamate (E)-rich protein 4a	Speer4a | 5031410I06Rik | Speer4b	**-1.19**
10490244	predicted gene, 100039109	100039109	**-1.20**
10490271	predicted gene, 100039109	100039109	**-1.20**
10564011	expressed sequence AF357427	AF357427	**-1.21**
10498367	purinergic receptor P2Y, G-protein coupled 13	P2ry13	**-1.22**
10473483	olfactory receptor 1029	Olfr1029	**-1.25**
10509002	Rh blood group, D antigen	Rhd	**-1.26**
10440170	olfactory receptor 198	Olfr198	**-1.26**
10435748	RIKEN cDNA D930030D11 gene	D930030D11Rik	**-1.27**
10522573	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	E330014E10Rik | D5Ertd577e | 100041354 | AU018829	**-1.28**
10536021	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	E330014E10Rik | D5Ertd577e | 100041354 | AU018829	**-1.28**
10359419	RIKEN cDNA 4930469G21 gene	4930469G21Rik	**-1.29**
10420254	mast cell protease 8	Mcpt8	**-1.30**
10424683	lymphocyte antigen 6 complex, locus G	Ly6g	**-1.30**
10555781	olfactory receptor 603 | olfactory receptor 604 | predicted gene, OTTMUSG00000019046	Olfr604 | OTTMUSG00000019046 | Olfr603	**-1.30**
10569020	interferon induced transmembrane protein 6	Ifitm6	**-1.30**
10523341	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	LOC100040885 | 100041179 | E330014E10Rik | D5Ertd577e | 100041354 | AU018829 | EG665802 | 100041032	**-1.34**
10536037	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	E330014E10Rik | D5Ertd577e | 100041354 | AU018829	**-1.34**
10536048	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	E330014E10Rik | D5Ertd577e | 100041354 | AU018829	**-1.34**
10523312	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	E330014E10Rik | D5Ertd577e | 100041354 | AU018829	**-1.34**
10528815	spermatogenesis associated glutamate (E)-rich protein 4e	Speer4a | Speer4e | 4930572O03Rik | 5031410I06Rik | Speer4b	**-1.34**
10484510	olfactory receptor 988	Olfr988	**-1.34**
10522585	predicted gene, EG622744 | predicted gene, 624421	LOC624931 | 624698 | EG666209 | EG620551 | EG620639 | LOC625240 | 665551 | EG665031 | 624421 | EG622744	**-1.35**

10414250	RIKEN cDNA 1700049E17 gene, gene 1 | predicted gene 73415 | RIKEN cDNA 4930503E14 gene	1700049E17Rik1 | 73415 | 4930503E14Rik	-1.37
10542223	RIKEN cDNA 5430401F13 gene	5430401F13Rik	-1.37
10419446	olfactory receptor 731	Olfr731	-1.37
10523350	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	LOC100040885 | 100041179 | E330014E10Rik | D5Ertd577e | 100041354 | AU018829 | EG665802 | 100041032	-1.38
10528804	RIKEN cDNA 4930572O03 gene | spermatogenesis associated glutamate (E)-rich protein 4a	Speer4a | 4930572O03Rik | 5031410I06Rik	-1.38
10461820	olfactory receptor 1489	Olfr1489	-1.39
10349968	chitinase 3-like 1	Chi3l1	-1.39
10419111	predicted gene, ENSMUSG00000072602 | RIKEN cDNA 1700001F09 gene	1700001F09Rik | ENSMUSG00000072602	-1.39
10566249	olfactory receptor 68	Olfr68	-1.40
10522562	expressed sequence C87414 | RIKEN cDNA E330014E10 gene	AA792892 | C87414 | E330014E10Rik	-1.40
10451763	special AT-rich sequence binding protein 1	Satb1	-1.41
10530722	predicted gene, EG665020 | RIKEN cDNA A430089I19 gene	ENSMUSG00000072817 | EG545763 | EG666203 | A430089I19Rik | EG664941 | LOC665755 | EG665020 | 666187 | BC061212 | 100041115	-1.41
10523320	expressed sequence C87414 | RIKEN cDNA E330014E10 gene	AA792892 | C87414 | E330014E10Rik	-1.43
10566170	olfactory receptor 559	Olfr559	-1.43
10545096	RIKEN cDNA 2410003J06 gene | predicted gene, OTTMUSG00000018935	2410003J06Rik | OTTMUSG00000018935	-1.43
10573054	glycophorin A	Gypa	-1.44
10546233	vomeronasal 1 receptor, A5	V1ra5	-1.45
10407940	NLR family, apoptosis inhibitory protein 3 | T-cell receptor gamma, constant region	Naip3 | Tcrg-V1 | Tcrg-C | Tcrg-V2 | Tcrg-V3	-1.45
10466622	predicted gene, ENSMUSG00000074936	ENSMUSG00000074936	-1.46
10531497	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	E330014E10Rik | D5Ertd577e | 100041354 | AU018829	-1.47
10545217	similar to [Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds.], gene product	LOC100046973	-1.48
10445192	Rhesus blood group-associated A glycoprotein	Rhag	-1.48
10366446	tetraspanin 8	Tspan8	-1.51
10442292	vomeronasal 2, receptor 113	Vmn2r113	-1.52
10484735	olfactory receptor 1175	Olfr1175	-1.53
10555899	olfactory receptor 665	Olfr665	-1.54
10536147	expressed sequence AU018829	AU018829	-1.54
10522554	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	E330014E10Rik | D5Ertd577e | 100041354 | AU018829	-1.55
10522569	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	E330014E10Rik | D5Ertd577e | 100041354 | AU018829	-1.55
10367491	olfactory receptor 784	Olfr784	-1.55
10522577	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	LOC100040885 | 100041179 | E330014E10Rik | D5Ertd577e | 100041354 | AU018829 | EG665802 | 100041032	-1.56
10536159	expressed sequence AU018829	AU018829	-1.56
10427687	sperm flagellar 2	Spef2	-1.58
10450892	olfactory receptor 113	Olfr113	-1.59
10473537	olfactory receptor 1123	Olfr1123	-1.60
10549990	vomeronasal 1 receptor, G10-like | vomeronasal 1 receptor, G10	V1rg10 | LOC171266	-1.60
10522558	predicted gene, EG622744 | predicted gene, 624421	LOC624931 | 624698 | EG666209 | EG620551 | EG620639 | LOC625240 | LOC632173 | 665551 | EG665031 | 624421 | EG622744	-1.62

10546231	vomeronasal 1 receptor, A6	V1ra6	-1.65
10419162	RIKEN cDNA 1700024B05 gene | RIKEN cDNA 1700049E17 gene, gene 1	1700049E17Rik1 | 1700024B05Rik | EG434459 | 73415 | 4930503E14Rik	-1.68
10389654	eosinophil peroxidase	Epx	-1.70
10522581	predicted gene, 100041354 | RIKEN cDNA E330014E10 gene	LOC100040885 | 100041179 | E330014E10Rik | D5Ertd577e | 100041354 | AU018829 | EG665802 | 100041032	-1.72
10536155	expressed sequence AU018829	AU018829	-1.72
10560742	vomeronasal 1 receptor, D16 | vomeronasal 1 receptor, D14	V1rd16 | V1rd14	-1.73
10484636	olfactory receptor 1097	Olfr1097	-1.76
10439299	stefin A3 | stefin A1	Stfa1 | Stfa3	-1.76
10560795	vomeronasal 1 receptor, D16 | predicted gene, ENSMUSG00000074310	Gm1447 | V1rd16 | EG667240 | LOC100043067 | EG667292 | ENSMUSG00000074310	-1.77
10560789	vomeronasal 1 receptor, D16	V1rd16	-1.77
10397553	hypothetical protein LOC100039226	LOC100039226	-1.77
10414241	RIKEN cDNA 1700024B05 gene	1700024B05Rik	-1.78
10527878	vomeronasal 1 receptor, G10-like | vomeronasal 1 receptor, G10	V1rg10 | LOC171266	-1.78
10373660	olfactory receptor 818	Olfr818	-1.78
10591129	FAT tumor suppressor homolog 3 (Drosophila)	Fat3	-1.80
10414218	RIKEN cDNA 1700024B05 gene | RIKEN cDNA 1700049E17 gene, gene 1	1700049E17Rik1 | 1700024B05Rik | 73415 | 4930503E14Rik	-1.80
10545231	similar to monoclonal antibody kappa light chain	LOC100047053	-1.80
10403901	olfactory receptor 42	Olfr42	-1.81
10373634	olfactory receptor 803	Olfr803	-1.82
10358654	hemicentin 1	Hmcn1	-1.82
10373647	olfactory receptor 812	Olfr812	-1.83
10442762	protease, serine, 34	Prss34	-1.84
10373636	olfactory receptor 805	Olfr805	-1.84
10551758	RIKEN cDNA 6330444E15 gene	6330444E15Rik	-1.84
10608480	similar to spermiogenesis specific transcript on the Y 1	LOC100039910 | LOC100039147	-1.86
10445178	olfactory receptor 135 | olfactory receptor 134 | olfactory receptor 133	Olfr133 | Olfr134 | Olfr135	-1.86
10560797	vomeronasal 1 receptor, D16 | predicted gene, EG667464	V1rd16 | EG667464 | EG620574 | ENSMUSG00000074330 | V1rd21 | EG667240 | ENSMUSG00000074310	-1.88
10550778	predicted gene, EG667551 | predicted gene, EG667283 | predicted gene, 100043559	EG667283 | EG667551 | 100043559	-1.93
10472400	sodium channel, voltage-gated, type II, alpha 1	Scn2a1	-1.94
10560732	predicted gene, ENSMUSG00000074331 | predicted gene, ENSMUSG00000074310	Gm1447 | EG667472 | ENSMUSG00000074330 | V1rd21 | EG667240 | V1rd14 | ENSMUSG00000074331 | LOC100043067 | ENSMUSG00000074310 | EG667469	-1.96
10560744	vomeronasal 1 receptor, D16 | vomeronasal 1 receptor, D13 | vomeronasal 1 receptor, D15	V1rd13 | V1rd16 | V1rd15	-1.98
10560780	predicted gene, EG436135 | vomeronasal 1 receptor, D16	Gm1447 | V1rd16 | EG667599 | EG435947 | EG436135 | V1rd21 | EG667240 | LOC100043067 | EG435940	-2.01
10560728	predicted gene, EG436135 | vomeronasal 1 receptor, D16	Gm1447 | V1rd13 | V1rd16 | EG667599 | EG435947 | ENSMUSG00000074330 | EG436135 | V1rd21 | EG667240 | LOC100043067 | EG435940 | ENSMUSG00000074310	-2.03

10560740	predicted gene, ENSMUSG00000074310 | predicted gene, 670764 | vomeronasal 1 receptor, D21	ENSMUSG00000074330 | V1rd21 | EG667240 | 670764 | ENSMUSG00000074310	-2.05
10560787	predicted gene, EG667551 | predicted gene, ENSMUSG00000074310	EG667283 | EG667273 | ENSMUSG00000074330 | V1rd21 | EG667240 | EG667551 | 100043559 | ENSMUSG00000074310	-2.05
10416689	olfactomedin 4	Olfm4	-2.05
10560730	predicted gene, 620758 | predicted gene, EG667586	EG667504 | EG667586 | ENSMUSG00000074330 | 620758 | V1rd21 | EG667240 | V1rd15 | EG667404 | ENSMUSG00000074310	-2.08
10560783	predicted gene, 100043667 | predicted gene, ENSMUSG00000074331	EG667215 | EG667283 | EG667504 | EG667273 | EG667464 | EG667586 | ENSMUSG00000074330 | V1rd21 | EG667240 | V1rd15 | EG667404 | ENSMUSG00000074331 | V1rd14 | EG667551 | 100043559 | 100043667 | ENSMUSG00000074310 | EG667135 | EG667469	-2.08
10550782	vomeronasal 1 receptor, D16 | predicted gene, ENSMUSG00000074298	EG667186 | EG667485 | EG667215 | EG435949 | EG667283 | 621561 | V1rd13 | V1rd16 | 100042976 | EG667464 | EG435947 | EG435953 | V1rd21 | 670764 | Gm1446 | ENSMUSG00000074331 | V1rd14 | EG667551 | 100043559 | EG667135 | EG667469 | 100043061 | ENSMUSG00000074298	-2.10
10550786	predicted gene, EG667551 | predicted gene, EG667283	EG667283 | EG667551 | 100043559	-2.12
10358615	hemicentin 1	Hmcn1	-2.13
10560785	predicted gene, EG667551 | predicted gene, ENSMUSG00000074310	EG667215 | EG667283 | ENSMUSG00000074330 | V1rd21 | EG667240 | V1rd15 | EG667551 | 100043559 | ENSMUSG00000074310 | EG667469	-2.13
10576944	predicted gene, ENSMUSG00000059543	ENSMUSG00000059543	-2.14
10505237	predicted gene, OTTMUSG00000025544	620982 | OTTMUSG00000025544 | OTTMUSG00000007425 | OTTMUSG00000008510	-2.14
10560754	predicted gene, EG667551 | predicted gene, EG667283	EG667283 | EG667551 | 100043559	-2.14
10556145	olfactory receptor 498	Olfr498	-2.18
10461806	olfactory receptor 1471	Olfr1471	-2.18
10505240	predicted gene, OTTMUSG00000025544	620982 | OTTMUSG00000025544 | OTTMUSG00000007425 | OTTMUSG00000008510	-2.21
10373622	olfactory receptor 772 | olfactory receptor 773	Olfr773 | Olfr772	-2.26
10466351	olfactory receptor 1459	Olfr1459	-2.34
10550760	predicted gene, 620758 | vomeronasal 1 receptor, D16	EG667186 | EG667485 | EG667215 | EG435949 | EG667283 | 673902 | EG667504 | 621561 | EG667273 | V1rd13 | V1rd16 | EG667472 | EG667599 | 100042976 | EG667464 | EG667586 | EG435947 | EG435953 | ENSMUSG00000074330 | 620758 | V1rd21 | EG667240 | 670764 | Gm1446 | EG667404 | ENSMUSG00000074331 | V1rd14 | EG667551 | 100043559 |	-2.37

		EG435940 | EG667135 | EG667469 | 100043061 | ENSMUSG00000074298	
10450731	MHC class Ib T9	H2-t9	**-2.37**
10414262	eosinophil-associated, ribonuclease A family, member 2	Ear2	**-2.39**
10524068	vomeronasal 2, receptor 17	Vmn2r17	**-2.41**
10598175	eosinophil-associated, ribonuclease A family, member 3 | eosinophil-associated, ribonuclease A family, member 1	Ear10 | Ear12 | Ear3 | Ear1 | Ear2	**-2.48**
10397551	predicted gene, 100042776 | expressed sequence BB287469 | predicted gene, 100039100	100042776 | BB287469 | 100039100	**-2.49**
10473399	proteoglycan 2, bone marrow	Prg2	**-2.50**
10550193	predicted gene, 100042762 | predicted gene, 100042677	LOC100039390 | 100042677 | ENSMUSG00000074371 | 100042728 | LOC100039371 | Obox4 | 100042762 | LOC100039416	**-2.53**
10473406	proteoglycan 3	Prg3	**-2.55**
10550189	oocyte specific homeobox 4	Obox4	**-2.55**
10373630	olfactory receptor 801	Olfr801	**-2.73**
10505254	predicted gene, OTTMUSG00000025544	620982 | OTTMUSG00000025544 | OTTMUSG00000007425 | OTTMUSG00000008510	**-2.74**
10473469	olfactory receptor 1020	Olfr1020	**-2.75**
10419156	eosinophil-associated, ribonuclease A family, member 3 | eosinophil-associated, ribonuclease A family, member 1	Ear10 | Ear12 | Ear3 | Ear1 | Ear2	**-2.75**
10556141	olfactory receptor 495	Olfr495	**-2.84**
10566194	olfactory receptor 578	Olfr578	**-2.95**
10505249	predicted gene, OTTMUSG00000025544	620982 | OTTMUSG00000025544 |OTTMUSG00000007425 |OTTMUSG00000008510	**-3.05**
10559890	vomeronasal 2, receptor 35 | vomeronasal 2, receptor 43 | vomeronasal 2, receptor 50 | vomeronasal 2, receptor 39	Vmn2r39 | Vmn2r50 | Vmn2r35 | Vmn2r43	**-3.09**
10538871	immunoglobulin kappa chain variable 28 (V28)	Igk-V28	**-3.21**
10505246	predicted gene, OTTMUSG00000025544	620982 | OTTMUSG00000025544 | OTTMUSG00000007425 | OTTMUSG00000008510	**-3.22**
10505258	predicted gene, OTTMUSG00000025544	620982 | OTTMUSG00000025544 | OTTMUSG00000007425 | OTTMUSG00000008510	**-3.22**
10419154	eosinophil-associated, ribonuclease A family, member 3 | eosinophil-associated, ribonuclease A family, member 1	Ear10 | Ear12 | Ear3 | Ear2 | Ear1	**-3.30**
10419151	eosinophil-associated, ribonuclease A family, member 1	Ear1	**-3.35**
10414590	eosinophil-associated, ribonuclease A family, member 7 | eosinophil-associated, ribonuclease A family, member 6	Ear7 | Ear6	**-3.54**

Supplementary Table 2. **Primers used for real-time PCR.**

Gene	Accession #	Sequence	Purpose
Satb1	NM_001163630.1	FW 5’- CTC CAT TGA ATA TGA TTG CAA-3’ RV 5’- TCC AAC CTG GAT TAG CCC TTT-3’	mRNA quantification
Gapdh	NM_008084.2	FW 5’- CCA GCC TCG TCC CGT AGA C-3’ RV 5’- GCC TTG ACT GTG CCG TTG-3’	mRNA quantification
Numb	NM_001136075.1	FW 5’- ATG AGT TGC CTT CCA CTA TGC AG-3’ RV 5’- TGC TGA AGG CAG TGG TGA TCT GG-3’	mRNA quantification
Clasp1	NM_001081276.1	FW 5’- GTG CTG GCA GCC GGT CAA GT-3’ RV 5’- CGG CTG CTC CGT GCT AAT CC-3’	mRNA quantification
Rbbp9	NM_015754.2	FW 5’- GCG CGA GAG AGC ATC TGG CT-3’ RV 5’- GGG GCG GCT GAA GTA CCC ACT-3’	mRNA quantification
Kdm3a	NM_001038695.2	FW 5’- TGG GCG GCT GGG CTC TGT TG-3’ RV 5’- AGG GCT CCT CCC TTT CAA AGC TGG-3’	mRNA quantification
Chaf1a	NM_013733.3	FW 5’- CCA TCA TCC GCC CCC GGA AC-3’ RV 5’- TGC ACA CTC CTC AGT CAC GCC T-3’	mRNA quantification
Bgn	NM_007542.4	FW 5’- GTT GGC CCT GACGGA CAG AC-3’ RV 5’- GCC AGC AGC AAG GTG AGT AG-3’	mRNA quantification
c-Myc	NM_010849.4	FW 5’- ACA GGA CTC CCC AGG CTC CG-3’ RV 5’- CGT GGC TGT CTG CGG GGT TT-3’	mRNA quantification
Tlr4	NM_021297.2	FW 5’- GCT TTC ACC TCT GCC TTC AC-3’ RV 5’- AGG CGA TAC AAT TCC ACC TG-3’	mRNA quantification
Uhrf2	NM_144873.2	FW 5’- CGA GCG CAG GGC CAG ACA AA-3’ RV 5’- TTT CCA ACT GCT TGC CCC GGT-3’	mRNA quantification
Irf1R	NM_010513.2	FW 5’- GCT TCG TTA TCC ACG ACG ATG-3’ RV 5’- GAA TGG CGG ATC TTC ACG TAG-3’	mRNA quantification
Iptr1	NM_010585.5	FW 5’- GCG TTT CCT CAA GCC TGC CG-3’ RV 5’- ATC AGC TCC TTG GTG ACC GGG-3’	mRNA quantification
Tnik	NM_026910.1	FW 5’- GCA GCG GAC AAG CAG TGG CA-3’ RV 5’- GCT TTC TTA TAG CTA GCT GGC CGA C-3’	mRNA quantification
Hes1	NM_008235.2	FW 5’-AAA GCC TAT CAT GGA GAA GAG GCG -3’ RV 5’-GGA ATG CCG GGA GCT ATC TTT CTT-3’	mRNA quantification
Hes5	NM_010419.4	FW 5’-GCG TCG GGA CCG CAT CAA CA -3’	mRNA quantification

		RV 5’-GCG GCG AAG GCT TTG CTG TG -3’	
Dtx1	NM_008052.3	FW 5’-CTC CGG GTG CGC TCG TTG TG -3’ RV 5’-CCG GAA CCC CAG GCG GGA TA -3’	mRNA quantification
Hey1	NM_010423.2	FW 5’-CCA CGC TCC GCC ACC ATG AA -3’ RV 5’-CGG CGC TTC TCG ATG ATG CCT -3’	mRNA quantification

Supplementary Table 3. **Primers used for chromatin immunoprecipitation.**

Gene	Accession #	Sequence	Purpose
Numb #1	NC_000078.5	FW 5’-AGG CTC CAT GTG GCT GGG GT-3’ RV 5’-CAG CAG GGA GTG GGC CAA GC-3’	ChIP
Numb #2	NC_000078.5	FW 5’-GCT GGC TCA GCG CTC TCC TG-3’ RV 5’-GCC AGA GTT ACC TGC CGC CC-3’	ChIP
Numb #3	NC_000078.5	FW 5’- TGC CGC TAG CAT ACC TGC CA-3’ RV 5’-CCC TTG CTT CGC CTC CCT GC-3’	ChIP
Numb #4	NC_000078.5	FW 5’-TCC GGG ATC CAC CGG AAG GC-3’ RV 5’-CCC CAG CGC TTT TCC TGC TCC-3’	ChIP

Supplementary Table 4. **Quality control of ERRBS analysis.**

Sample name (experiment#)	CpG covered	Mean CpG coverage	BS conversion rate (%)	Total read count	Uniquely aligned read count	Alignment (%)
Satb1_KO_MPP (#1)	1770041	78.45	99.89	121762313	61182793	50.2
Satb1_KO_HSC (#1)	2178665	93.7	99.9	149398475	89566756	60
Satb1_WT_MPP (#1)	1474867	54.8	99.87	120128863	34717628	28.9
Satb1_WT_HSC (#1)	2177247	112.43	99.82	163263636	101048765	61.9
Satb1_KO_MPP (#2)	1642986	75.55	99.92	105655411	50057713	47.4
Satb1_KO_ HSC (#2)	1645776	98.52	99.93	105975760	64009297	60.4
Satb1_WT_MPP (#2)	1636549	58.31	99.92	101152392	36830336	36.4
Satb1_WT_ HSC (#2)	1681312	50.65	99.91	96316881	36771933	38.2

Supplementary Table 5. **Genes with altered expression and cytosine methylation in *Satb1*$^{-/-}$ HSCs.**

Gene Symbol	**Accession Number (RNA)**	**Accession Number (Genomic DNA)**	**Genomic Range**
1700113H08Rik	NM_029685.1	NC_000076.6	87058046..87230599
2900041M22Rik	NR_015489.2	NC_000077.6	117611247..117613417
4922501C03Rik	NM_199316.2	NC_000075.6	87191963..87255532
6720456H20Rik	NM_172600.3	NC_000080.6	48446352..48515159
Adrbk2	NM_001035531.1	NC_000071.6	112910478..113015514
Aig1	NM_025446.3	NC_000076.6	13652709..13868830
Arhgap17	NM_001122640.1	NC_000073.6	123279149..123369915
Atg4c	NM_001145967.1	NC_000070.6	99193934..99259787
Atp10a	NM_009728.2	NC_000073.6	58658202..58829426
Atpbd4	NM_025675.4	NC_000068.7	114516418..114654928
Brms1	NM_134155.1	NC_000085.6	5041404..5049917
Cblb	NM_001033238.1	NC_000082.6	52031549..52208047
Ccdc46	NM_029586.2	NC_000077.6	108425266..108860615
Cd180	NM_008533.2	NC_000079.6	102693558..102706631
Cep135	NM_199032.2	NC_000071.6	76591714..76646466
Chd9	NM_177224.2	NC_000074.6	90828835..91054508
Cyp4f16	NM_024442.1	NC_000083.6	32536629..32551797
Ddit4	NM_029083.2	NC_000076.6	59949675..59951770
Dnahc10	NM_019536.1	NC_000071.6	124725085..124834308
Dnajc11	NM_172704.3	NC_000070.6	151933720..151981959
Dpp4	NM_001159543.1	NC_000068.7	62330073..62412231
Drd5	NM_013503.2	NC_000071.6	38319509..38322310
Dync1li2	NM_001013380.2	NC_000074.6	104417674..104443047
Dync2h1	NM_029851.2	NC_000075.6	6928503..7177046
Eya2	NM_001271962.1	NC_000068.7	165655298..165771631
Frmd4a	NM_001177843.1	NC_000068.7	4152863..4614043
Fyn	NM_001122892.1	NC_000076.6	39369799..39565381
Ift81	NM_009879.3	NC_000071.6	122550204..122614518
Ints6	NM_008715.2	NC_000080.6	62676325..62761112
Itga8	NM_001001309.2	NC_000068.7	12106660..12301920
Itpr1	NM_010585.5	NC_000072.6	108213096..108551116
Lrrn3	NM_001271708.1	NC_000078.6	41451668..41485751
Lrrtm2	NM_178005.4	NC_000084.6	35209003..35215024
Maged1	NM_019791.2	NC_000086.7	94535474..94542074
Mtap7	NM_001198635.1	NC_000076.6	20148920..20281590
Myst3	NM_001081149.1	NC_000074.6	22859539..22943262
Naglu	NM_013792.2	NC_000077.6	101070094..101077672
Napg	NM_028017.1	NC_000084.6	62977916..62999450
Nrxn1	NM_020252.3	NC_000083.6	90033644..91092802
Parp11	NM_181402.3	NC_000072.6	127453723..127494239
Pcdh1	NM_029357.3	NC_000084.6	38196694..38209762
Pcmtd1	NM_183028.3	NC_000067.6	7088920..7173628
Plekha5	NM_144920.3	NC_000072.6	140424099..140594906

Gene Symbol	Accession Number (RNA)	Accession Number (Genomic DNA)	Genomic Range
Procr	NM_011171.2	NC_000068.7	155751217..155755478
Prrg1	NM_001164275.1	NC_000086.7	78449613..78583896
Rab6b	NM_173781.4	NC_000075.6	103112074..103185270
Rasa2	NM_053268.2	NC_000075.6	96539300..96631503
Sectm1b	NM_026907.3	NC_000077.6	121053423..121063569
Sesn3	NM_030261.4	NC_000075.6	14276301..14326134
Smyd3	NM_027188.3	NC_000067.6	178955031..179518003
Snora69	NR_002900.1	NC_000086.7	37082912..37083033
Snx25	NM_207213.2	NC_000074.6	46033261..46124146
Socs2	NM_001168655.1	NC_000076.6	95411490..95416857
Tdrd3	NM_001253755.1	NC_000080.6	87416583..87545508
Tnik	NM_001163007.1	NC_000069.6	28263214..28670585
Trim33	NM_001079830.1	NC_000069.6	103279293..103358768
Tsc22d1	NM_001177751.1	NC_000080.6	76415821..76507766
Tspan4	NM_001252588.1	NC_000073.6	141475236..141493427
Tspan5	NM_019571.4	NC_000069.6	138742195..138904424
Ttll5	NM_001081423.2	NC_000078.6	85824950..86053760
Txndc2	NM_001146002.1	NC_000083.6	65637505..65642204
Usp36	NM_001033528.1	NC_000077.6	118259653..118290244
Wdr5	NM_080848.2	NC_000068.7	27515147..27536535
Whsc1	NM_001081102.2	NC_000071.6	33843112..33897966
Xirp2	NM_001024618.2	NC_000068.7	67446002..67526606
Zfp661	NM_001111029.1	NC_000068.7	127575533..127584677
Zfp84	NM_023750.2	NC_000073.6	29768552..29781419

Supplementary Table 6. **Network analysis of gene set with altered expression and cytosine methylation in *Satb1*$^{-/-}$ HSCs by Ingenuity Pathway Analysis.**

Molecules in Network	Score	Focus Molecules	Top Functions
ADRBK2,APH1B,ARHGEF2,CASP3,CD180,CTNNB1, DDIT4,DPP4,DRD5,ERK1/2,HRAS,IPO7,ITPR1,MAP7, miR-17-3p (and other miRNAs w/seed CUGCAGU),MYC, NAP1L1,PERP,PLD1,PLEKHA5,PPT1,PROCR,PTPN14, RABEP1,RAD23A,SEMA3C,SESN1,SESN3,SH3BP4,SMYD3, TMSB10/TMSB4X,TNIK,TP53,TSC22D1,YWHAG	24	13	Cell-To-Cell Signaling and Interaction, Cellular Assembly and Organization, Tissue Development
ARHGAP17,ATAD2,BRCA2,CBLB,CCND1,CD28,CDCA4, CDCA7,CDCA7L,CDK5RAP2,CHD9,DLEU1,DLEU2,E2F1, ERG,EYA2,FLNA,FYN,LRRN3,LRRTM2,MAGED1,MAX, MGEA5,MTHFD1,PTK2B,PTPN4,RASA2,SKAP1,SOCS2, STARD4,TAF5L,TSPAN4,TSPAN5,UTRN,WDR5	24	13	Cancer, Hematological Disease, Reproductive System Disease