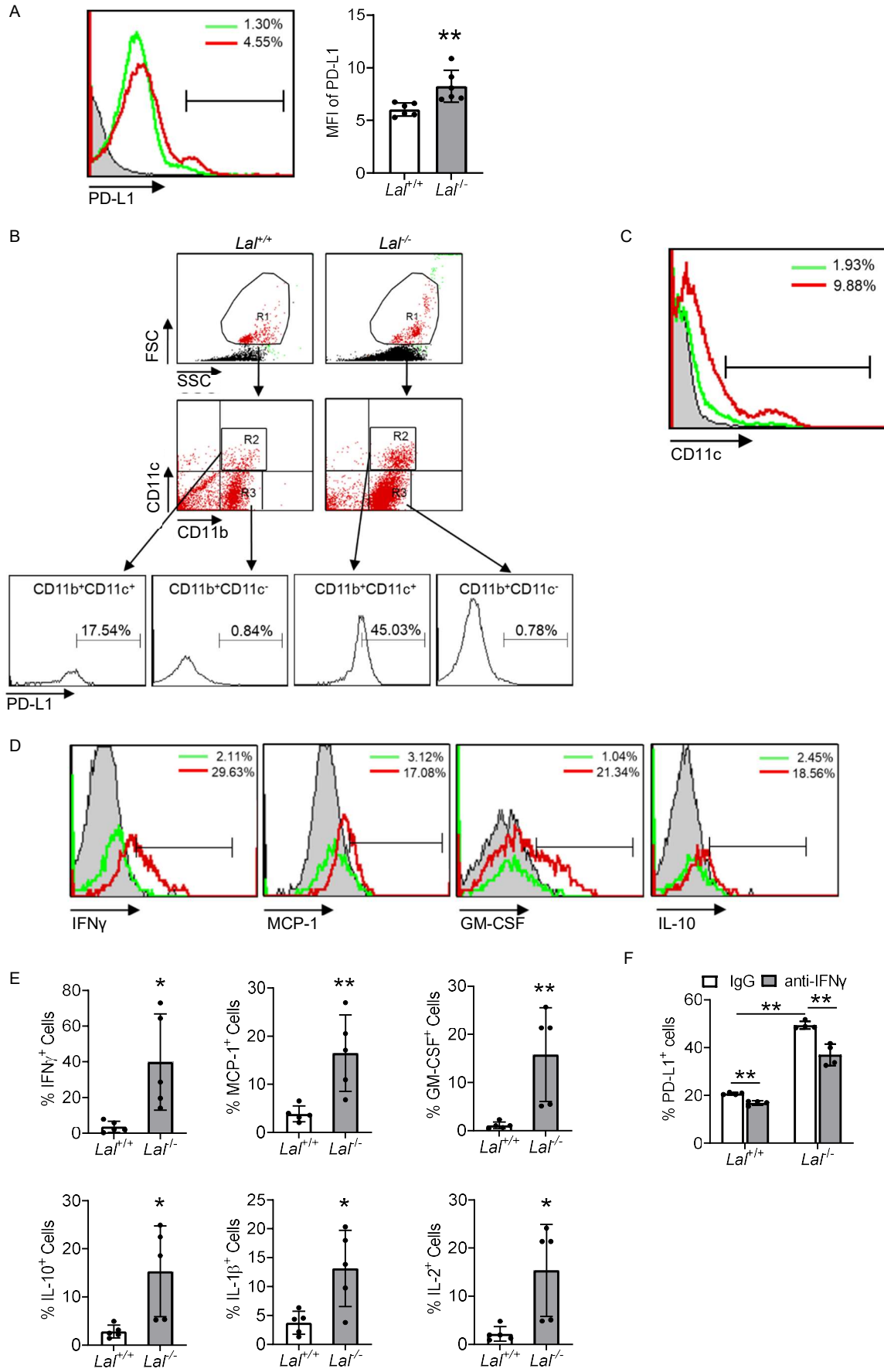
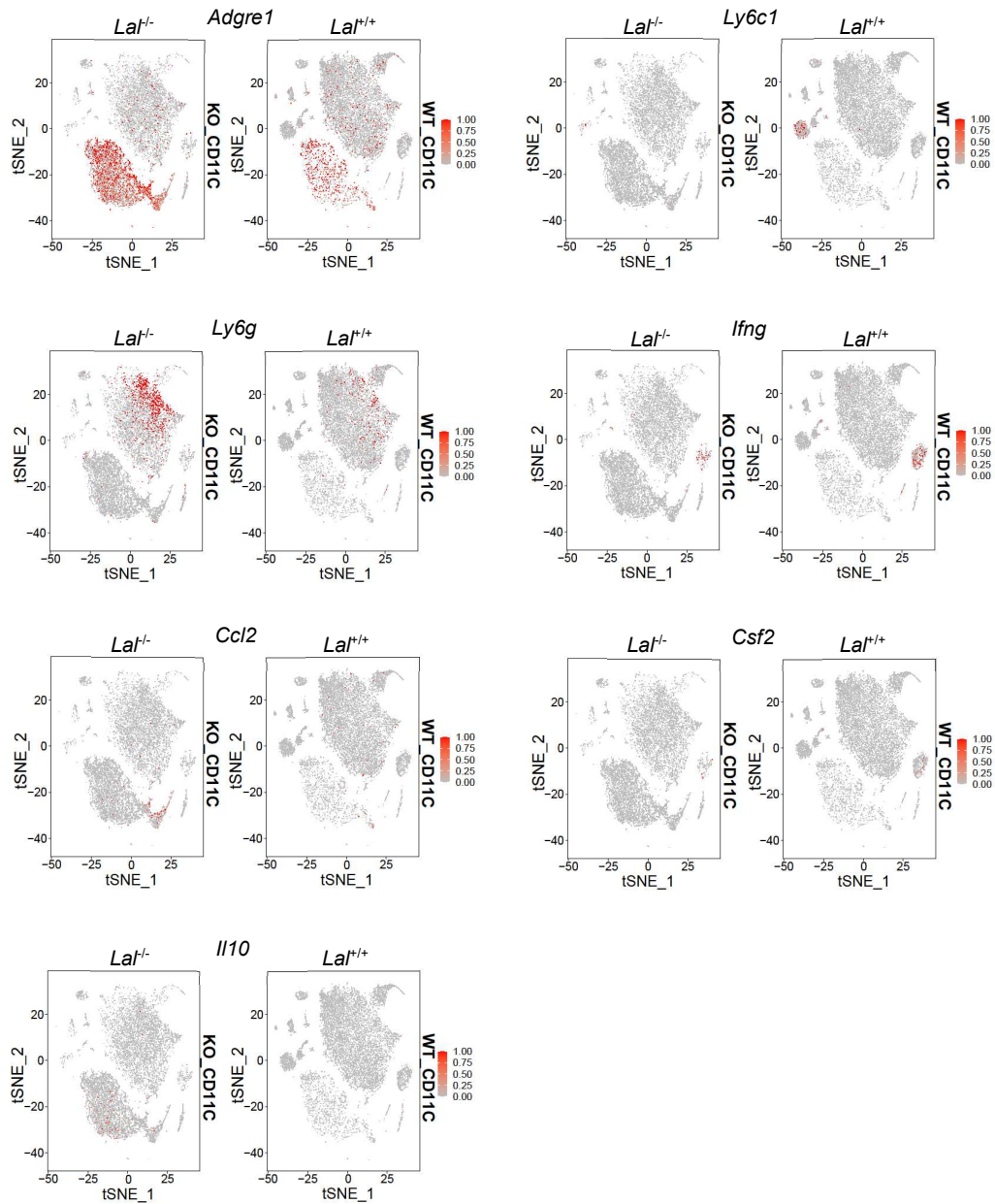
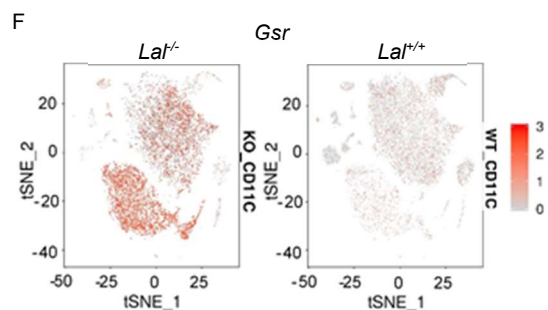




Supplemental Figure 1. Gating strategies of PD-L1⁺ and CD11c⁺ cells and percentages of cytokine-expressing cells in CD11c⁺ cells. **A)** White blood cells harvested from *Lal^{+/+}* and *Lal^{-/-}* mice were stained with fluorescence-conjugated antibodies against PD-L1, CD11c, MHCII, F4/80, CD11b, Ly6C, and Ly6G, and analyzed by flow cytometry. Left: A representative gating strategy of PD-L1⁺ cells in the blood. Right: MFI of PD-L1 expression in the blood of *Lal^{-/-}* vs. *Lal^{+/+}* mice by flow cytometry analysis. **B)** A representative gating strategy of PD-L1⁺ cells in CD11b⁺CD11c⁻ and CD11b⁺CD11c⁺ cells. **C)** A representative gating strategy of CD11c⁺ cells in the blood. **D)** Expression levels of cytokines in *Lal^{-/-}* vs. *Lal^{+/+}* CD11c⁺ cells were analyzed by flow cytometry. Gating strategies of IFN γ , MCP-1, GM-CSF, and IL-10 in CD11c⁺ cells. **E)** The percentages of IFN γ ⁺, MCP-1⁺, GM-CSF⁺, IL-10⁺, IL-1 β ⁺, and IL-2⁺ cells in *Lal^{-/-}* vs. *Lal^{+/+}* CD11c⁺ cells. **F)** The percentage of PD-L1⁺ cells in blood CD11c⁺ cells after treated with 5 μ g/mL IFN γ neutralizing antibody for 2 days. For (A), (C) and (D), the gray-shaded area is isotype control. The green and red lines represent the signals of *Lal^{+/+}* and *Lal^{-/-}* cells, respectively. The bracket shows the gating of “positives”. Data are expressed as mean $\pm$ SD; Experiments were independently repeated, n=6 for A-C, n=5 for D-E, n=4 for F. *p<0.05, **p<0.01, unpaired Student's *t* test for A and E, 2-way ANOVA for F.

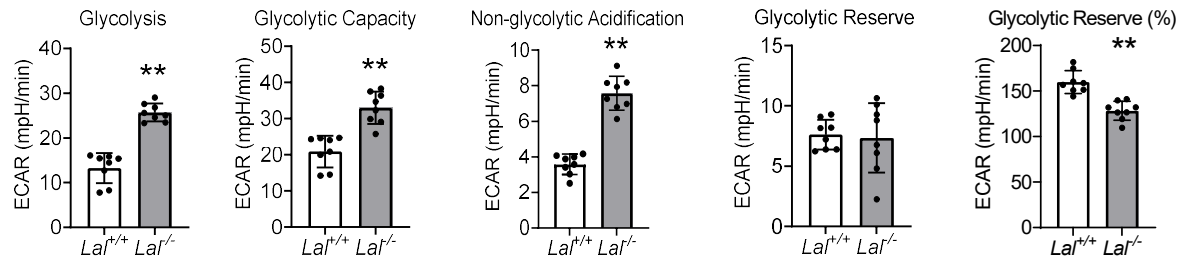


Supplemental Figure 2. Gene expressions across cell clusters in tSNE plots of CD11c⁺ cells. Gene expressions of F4/80 (*Adgre1*), Ly6C (*Ly6c1*), Ly6G (*Ly6g*), IFN γ (*Ifng*), MCP-1 (*Ccl2*), GM-CSF (*Csf2*), and IL-10 (*Il10*) across cell clusters in tSNE plots of CD11c⁺ cells from *LaI*^{-/-} vs. *LaI*^{+/+} mice.

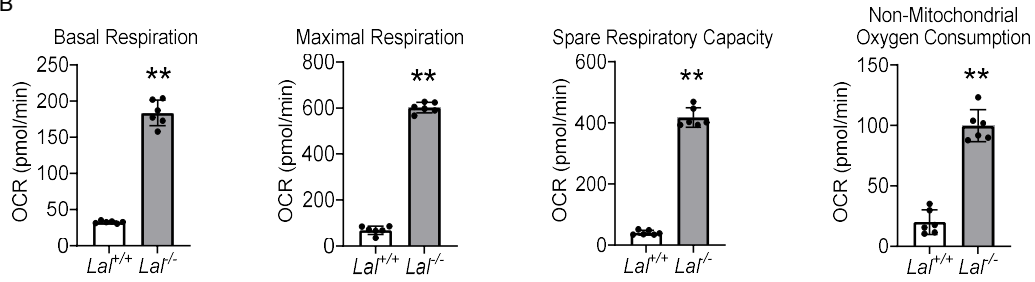


Supplemental Figure 3. Expression of metabolic enzymes and ROS in *LaI*^{-/-} CD11c⁺ cells. White blood cells were isolated from *LaI*^{+/+} and *LaI*^{-/-} mice for flow cytometry and scRNA sequencing. **A)** Differential expression of genes involved in glycolysis/gluconeogenesis in *LaI*^{-/-} vs. *LaI*^{+/+} CD11c⁺ cells (red boxes represent increased expression of enzymes). **B)** Differential expression of genes involved in citrate cycle in *LaI*^{-/-} vs. *LaI*^{+/+} CD11c⁺ cells (red boxes represent increased expression of enzymes). **C)** Expression of glycolysis-related gene *Aldoa*, *Gapdh*, *Gpil* and *Ldha* across cluster 158 in violin plots of CD11c⁺ cells from *LaI*^{-/-} vs. *LaI*^{+/+} mice. **D)** Left: Gating strategies of ROS-producing cells in CD11c⁺ cells. The gray-shaded area is isotype control. The green and red lines represent the signals of *LaI*^{+/+} and *LaI*^{-/-} CD11c⁺ cells, respectively. The bracket shows the gating of “positives”. Right: The percentage of ROS-producing cells in *LaI*^{-/-} vs. *LaI*^{+/+} CD11c⁺ cells by flow cytometry analysis. **E)** Group distribution in a two-dimensional independent component space generated by Monocle's pseudotime ordering of the cells. Solid black line indicates the main diameter path of the Minimum Spanning Tree (MST) and acts as the backbone of the trajectory. **F)** *Gsr* expression across cell clusters in tSNE plots of CD11c⁺ cells from *LaI*^{-/-} vs. *LaI*^{+/+} mice by scRNA sequencing. Data are expressed as mean ± SD; Experiments were independently repeated, n=4 for D. **p<0.01, unpaired Student's *t* test.

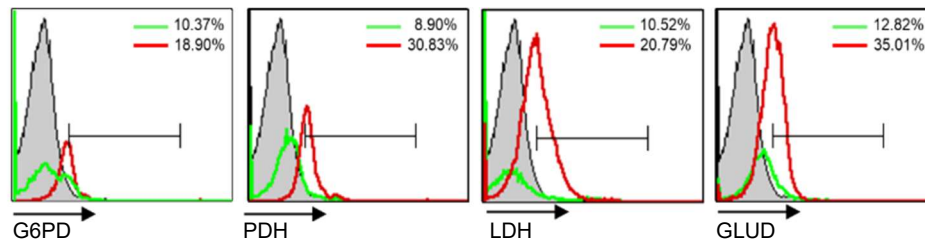
A



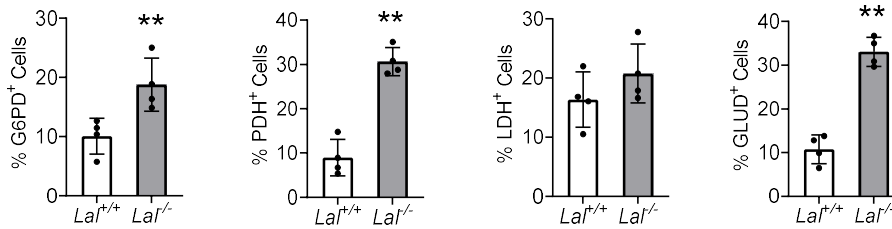
B



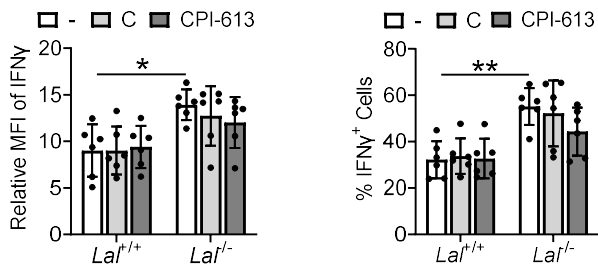
C



D

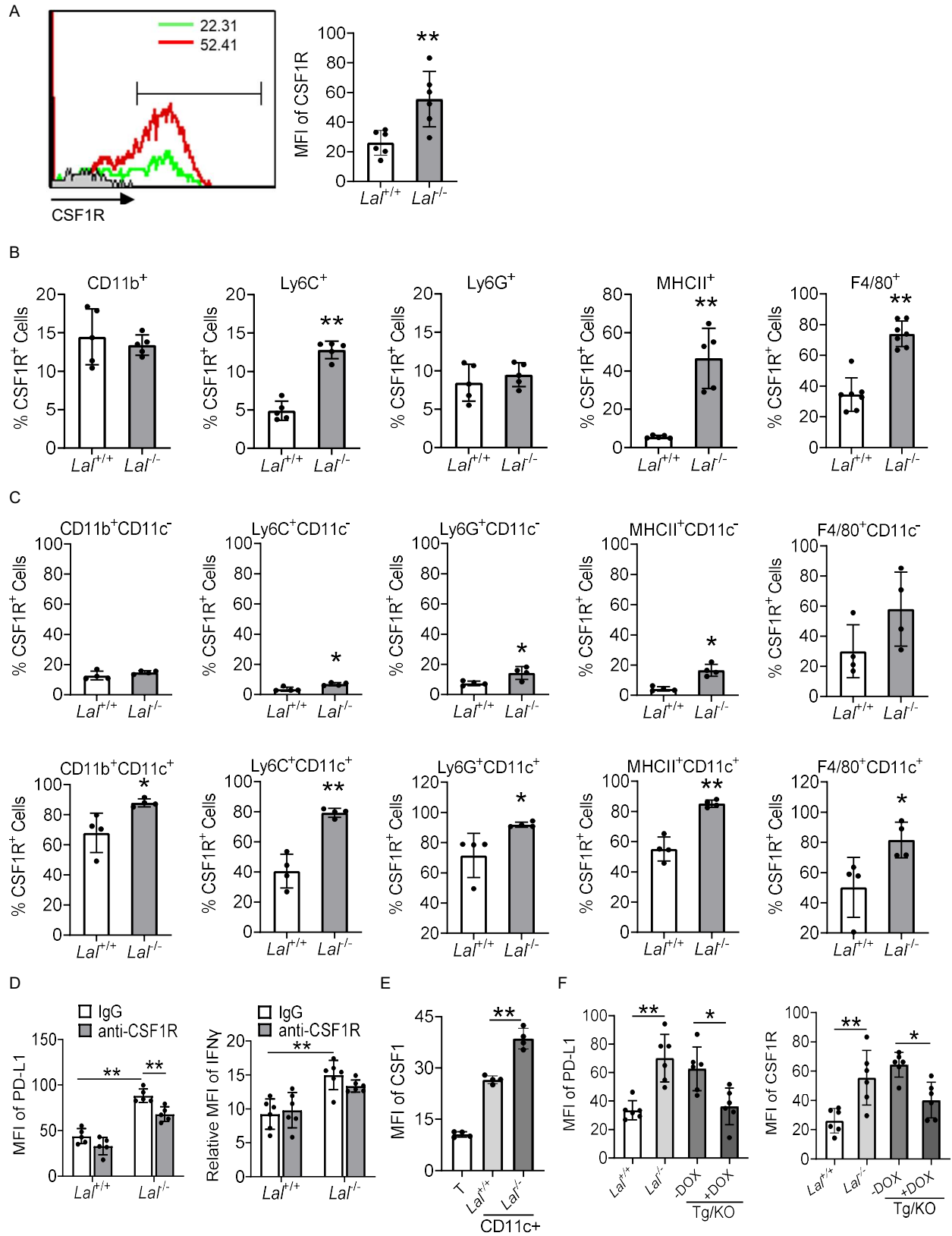


E



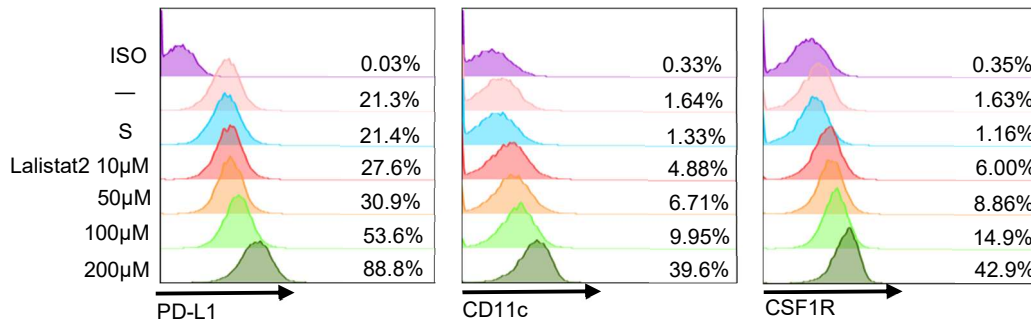
Supplemental Figure 4. Expression of metabolic enzymes in *LaI*^{-/-} CD11c⁺ cells. A)

Glycolysis, glycolytic capacity, non-glycolytic acidification, glycolytic reserve and glycolytic reserve (%) measured from Seahorse XF96. **B)** Basal and maximal respiration, spare respiratory capacity, and non-mitochondrial oxygen consumption measured from Seahorse XF96. **C)** Gating strategies of G6PD, PDH, LDH, and GLUD in CD11c⁺ cells by flow cytometry. The gray-shaded areas are isotype controls. The green and red lines represent the signals of *LaI*^{+/+} and *LaI*^{-/-} CD11c⁺ cells, respectively. The bracket shows the gating of “positives”. **D)** The percentages of G6PD⁺, PDH⁺, LDH⁺ and GLUD⁺ cells in *LaI*^{-/-} vs. *LaI*^{+/+} CD11c⁺ cells by flow cytometry analysis. **E)** Relative MFI of IFN γ and percentages of IFN γ ⁺ cells in CD11c⁺ cells after CPI-613 treatment by flow cytometry analysis. Data are expressed as mean $\pm$ SD; Experiments were independently repeated, n=8 for A, n=6 for B and E, n=4 for D. **p<0.01, unpaired Student's *t* test for A, B and D, 2-way ANOVA for E.

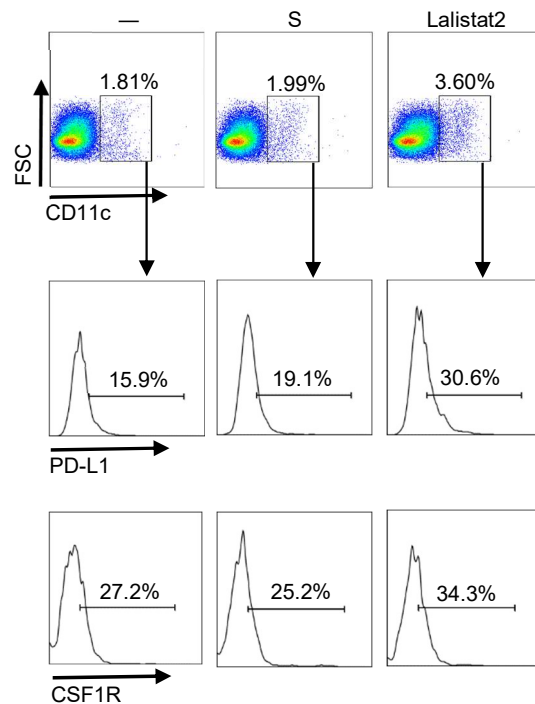


Supplemental Figure 5. CSF1R expression in *Lal*^{-/-} CD11c⁺ cells. **A)** MFI of CSF1R in blood CD11c⁺ cells of *Lal*^{-/-} vs. *Lal*^{+/+} mice by flow cytometry analysis. Left: Gating strategies of CSF1R in CD11c⁺ cells. The gray-shaded area is isotype control. The green and red lines represent the signals of *Lal*^{+/+} and *Lal*^{-/-} CD11c⁺ cells, respectively. The bracket shows the gating of “positives”. **B)** CSF1R expression in blood CD11b⁺, Ly6C⁺, Ly6G⁺, CD11b⁺, MHCII⁺, F4/80⁺ cells of *Lal*^{-/-} vs. *Lal*^{+/+} mice by flow cytometry analysis. **C)** CSF1R expression in CD11c⁻ and CD11c⁺ double-gated myeloid cells by flow cytometry analysis. **D)** MFI of PD-L1 and IFN γ expression in blood CD11c⁺ cells after anti-CSF1R antibody treatment (5 μ g/mL) by flow cytometry analysis. **E)** MFI of CSF1 expression in spleen CD4⁺ T cells and blood CD11c⁺ cells of *Lal*^{+/+} and *Lal*^{-/-} mice by flow cytometry analysis. **F)** MFI of CSF1R and PD-L1 expression in blood CD11c⁺ cells of *Lal*^{+/+}, *Lal*^{-/-}, untreated (-DOX), and DOX-treated (+DOX) Tg/KO mice by flow cytometry analysis. Data are expressed as mean $\pm$ SD; Experiments were independently repeated, n=6 for A and F, n=5 for B, n=5-6 for D, and n=4 for C and E. *p<0.05, **p<0.01, unpaired Student's *t* test for A-C, 2-way ANOVA for D, 1-way ANOVA for E and F.

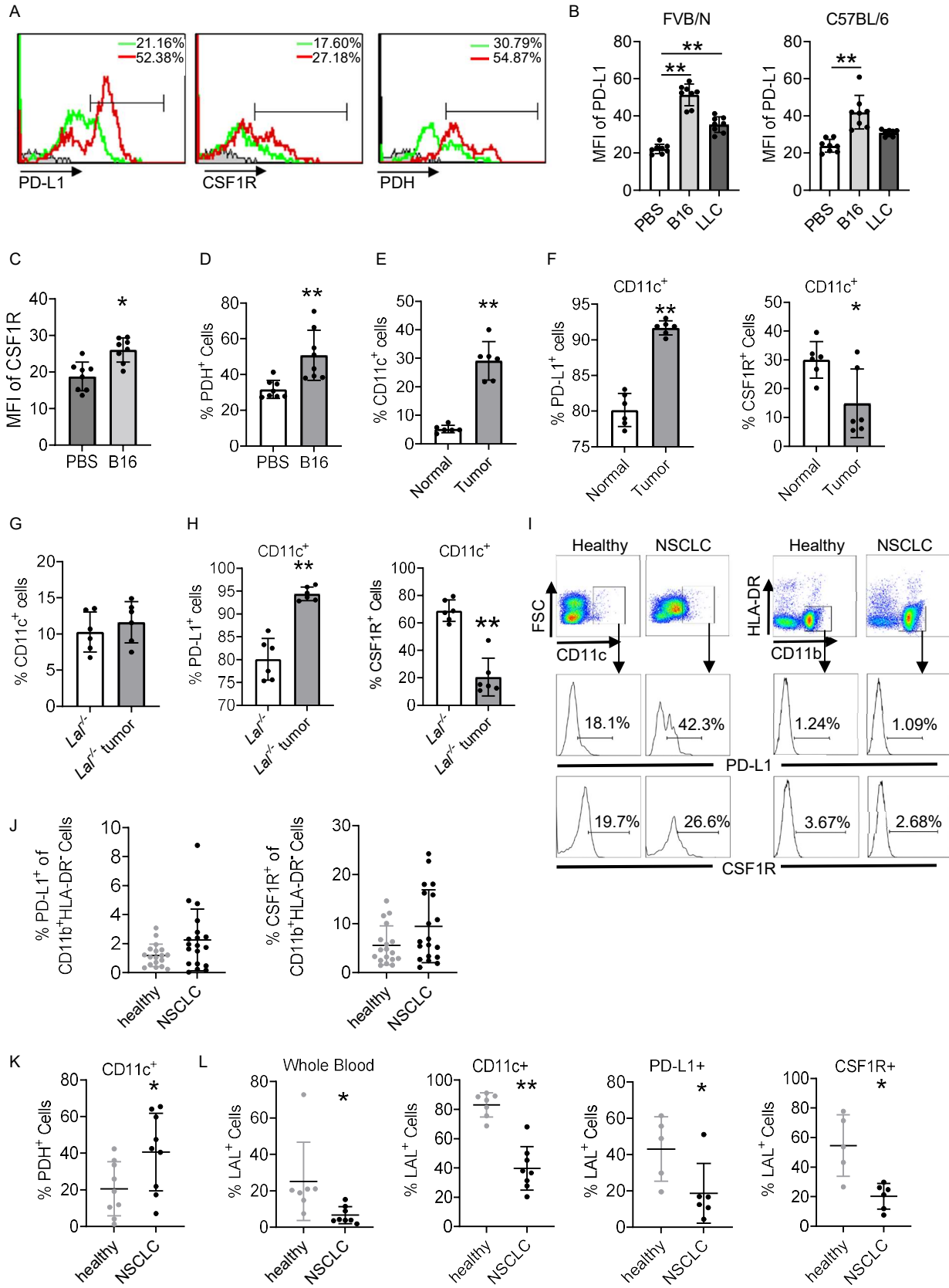
A



B



Supplemental Figure 6. Expression of PD-L1 and CSF1R in mouse myeloid cells and human blood CD11c⁺ cells after Lalistat2 treatment. A) A representative gating strategy of PD-L1⁺, CD11c⁺ and CSF1R⁺ cells in HD1A myeloid cells treated with Lalistat2 or DMSO. **B)** A representative gating strategy of PD-L1⁺ and CSF1R⁺ cells in CD11c⁺ cells of human blood cells treated with Lalistat2 at 10 µM or DMSO (S).



Supplemental Figure 7. Expressions of PD-L1 and CSF1R in CD11c⁺ cells of tumor bearing mice and NSCLC patients. **A)** Representative gating strategies of PD-L1, CSF1R, and PDH in CD11c⁺ cells. The gray-shaded areas are isotype controls. The green and red lines represent the signals of CD11c⁺ cells from PBS-injected and B16 melanoma cell-injected FVB/N *La^{+/+}* mice, respectively. The bracket shows the gating of “positives”. **B)** MFI of PD-L1 in blood CD11c⁺ cells of B16 melanoma or LLC cell-injected vs. PBS-injected FVB/N or C57BL/6 *La^{+/+}* mice by flow cytometry. **C)** MFI of CSF1R in blood CD11c⁺ of B16 melanoma cell-injected vs. PBS-injected FVB/N *La^{+/+}* mice. **D)** The percentage of PDH⁺ cells in blood CD11c⁺ cells of B16 melanoma cell-injected vs. PBS-injected FVB/N *La^{+/+}* mice. **E)** The percentage of CD11c⁺ cells in tumor tissues and **F)** the percentages of PD-L1⁺ and CSF1R⁺ cells in CD11c⁺ cells of tumors tissues from B16 melanoma cell-injected FVB/N *La^{+/+}* mice. **G)** The percentage of CD11c⁺ cells in tumor tissues and **H)** the percentages of PD-L1⁺ and CSF1R⁺ cells in CD11c⁺ cells of tumors tissues from B16 melanoma cell-injected FVB/N *La^{-/-}* mice. **I)** A representative gating strategy of PD-L1⁺ and CSF1R⁺ cells in CD11c⁺ cells and CD11b⁺HLA-DR⁻ cells of NSCLC patients vs. healthy individuals. **J)** Statistical analysis of percentages of PD-L1⁺ and CSF1R⁺ cells in blood CD11b⁺HLA-DR⁻ of NSCLC patients vs. healthy individuals. **K)** The percentage of PDH⁺ cells in blood CD11c⁺ cells of NSCLC patients vs. healthy individuals. **L)** The percentages of LAL⁺ cells in whole blood, CD11c⁺, PD-L1⁺, and CSF1R⁺ cells of NSCLC patients vs. healthy individuals. Data are expressed as mean ± SD; Experiments were independently repeated, n=8 for B-D, n=6 for E-H, n=17-19 for J, n=5-9 for K and L. *p<0.05, **p<0.01, 1-way ANOVA for B, unpaired Student's *t* test for C-H, J-L.

Supplemental Table 1. Identification and gene expression of *Lal*^{-/-} vs. *Lal*^{+/+} CD11c⁺ cell clusters by scRNA-seq.

Cluster	Labels	Ratios of CD11c ⁺ Cells		# of CD11c ⁺ Cells	
		<i>Lal</i> ^{+/+}	<i>Lal</i> ^{-/-}	<i>Lal</i> ^{+/+}	<i>Lal</i> ^{-/-}
0	Neutrophils (GN)	27.88	17.9	3009	1827
1	Monocytes (MO.6C-IIIINT)	8.77	38.1	946	3888
2	Neutrophils (GN)	15.81	18.76	1706	1914
3	Neutrophils (GN)	15.39	2.75	1661	281
4	T cells (T.CD4TESTCJ)	7.28	0.44	786	45
5	Monocytes (MO.6C-IIIINT)	0.86	6.7	93	684
6	Neutrophils (GN)	6.41	0.64	692	65
7	NK cells (NK.DAP10-)	5.23	1.39	564	142
8	Monocytes (MO.6C-II-)	0.32	3.97	35	405
9	Neutrophils (GN)	2.21	1.89	239	193
10	DC (DC.PDC.8-)	1.78	1.57	192	160
11	B cells (B.T3)	2.09	0.56	226	57
12	Neutrophils (GN)	0.92	1.73	99	177
13	Monocytes (MO.6C-II+)	0.97	0.86	105	88
14	T cells (T.CD4TESTCJ)	1.34	0.44	145	45
15	T cells (T.8EFF.OT1.48HR.LISOVA)	0.48	0.98	52	100
16	Monocytes (MO.6C-IIIINT)	0.73	0.56	79	57
17	Neutrophils (GN)	0.57	0.24	61	24
18	Basophils (BA)	0.68	0.02	73	2
19	Monocytes (MO.6C-IIIINT)	0.06	0.27	7	28
20	Macrophages (MF.II-480HI)	0.04	0.21	4	21
21	B cells (B1A)	0.17	0.02	18	2

Supplemental Table 2. Up-regulated genes in *Lal*^{-/-} CD11c⁺ cells (top 50)

Genes	Symbol	LogFC	# of cells		Expression	
			<i>Lal</i> ^{+/+}	<i>Lal</i> ^{-/-}	<i>Lal</i> ^{+/+}	<i>Lal</i> ^{-/-}
lectin, galactose binding, soluble 3	Lgals3	1.85	4759	9697	2.03	3.24
glutathione reductase	Gsr	1.84	2156	9397	1.48	2.33
chitinase-like 3	Chil3	1.76	249	4290	1.54	2.04
WAP four-disulfide core domain 17	Wfdc17	1.68	3036	6554	2.39	2.76
interferon induced transmembrane protein 1	Ifitm1	1.68	5727	6260	2.31	3.23
hypoxanthine guanine phosphoribosyl transferase	Hprt	1.45	6	6473	0.9	1.68
placenta-specific 8	Plac8	1.39	3067	7706	2.28	2.81
cytochrome b-245, beta polypeptide	Cybb	1.32	2439	6277	2.26	2.80
neutrophilic granule protein	Ngp	1.27	142	1031	1.73	2.30
membrane-spanning 4-domains, subfamily A, member 6C	Ms4a6c	1.24	1466	5439	1.66	2.18
lipocalin 2	Lcn2	1.18	2023	3508	2.23	2.55
peroxiredoxin 1	Prdx1	1.17	3011	6202	1.58	2.14
cathepsin B	Ctsb	1.17	4382	7619	2.00	2.64
serum amyloid A 3	Saa3	1.16	41	1054	1.45	1.94
transmembrane protein 14C	Tmem14c	1.16	1124	7349	1.21	1.56
interferon induced transmembrane protein 6	Ifitm6	1.10	1874	6571	1.85	1.90
predicted pseudogene 10320	Gm10320	1.08	28	5990	1.05	1.35
WAP four-disulfide core domain 21	Wfdc21	1.06	3740	4615	2.37	2.92
lysozyme 2	Lyz2	1.05	6580	9304	3.07	3.96
cathepsin S	Ctss	1.03	2896	6761	2.08	2.52
interferon induced transmembrane protein 3	Ifitm3	0.99	4598	8862	2.38	2.93
S100 calcium binding protein A4	S100a4	0.99	1619	5455	2.29	2.36
guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	Gngt2	0.98	4665	7237	2.14	2.67
coagulation factor X	F10	0.95	305	4593	1.11	1.42
superoxide dismutase 2, mitochondrial	Sod2	0.93	1867	5651	1.23	1.58
cathepsin C	Ctsc	0.93	1723	5174	1.22	1.63
adhesion G protein-coupled receptor E4	Adgre4	0.89	1140	4911	1.80	1.83
insulin-like growth factor binding protein 6	Igfbp6	0.89	663	3017	1.81	1.80
sphingomyelin phosphodiesterase, acid-like 3A	Smpdl3a	0.86	3011	6862	1.75	2.03
histocompatibility 2, class II antigen E beta	H2-Eb1	0.85	313	1262	1.02	1.95
CD302 antigen	Cd302	0.83	577	4922	1.16	1.37
colony stimulating factor 1 receptor	Csf1r	0.83	3292	6659	1.92	2.16
annexin A5	Anxa5	0.83	1223	5196	1.15	1.46
sphingomyelin phosphodiesterase, acid-like 3B	Smpdl3b	0.81	670	4328	1.25	1.45
uridine phosphorylase 1	Upp1	0.80	304	3749	1.68	1.42
Fc receptor, IgE, high affinity I, gamma polypeptide	Fcer1g	0.79	8849	9915	2.80	3.47
cathepsin Z	Ctsz	0.79	3911	7110	1.77	2.08
peroxiredoxin 5	Prdx5	0.78	7448	9201	2.06	2.56
mitochondrial ribosomal protein L52	Mrpl52	0.77	1825	5555	1.17	1.47
angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	Ace	0.75	1157	4615	2.03	1.85
apolipoprotein E	Apoe	0.75	2574	5906	2.72	2.64
ubiquinol-cytochrome c reductase binding protein	Uqcrb	0.73	2406	5907	1.23	1.53
chemokine (C-X3-C motif) receptor 1	Cx3cr1	0.73	1219	4537	1.55	1.61
POU domain, class 2, transcription factor 2	Pou2f2	0.73	2046	5528	2.24	2.23
enolase 3, beta muscle	Eno3	0.73	1004	4068	1.58	1.61
ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide	Atp1a1	0.72	3165	6202	1.61	1.90
cystatin C	Cst3	0.72	8352	9821	2.71	3.51
translocator protein	Tspo	0.71	5997	8820	1.80	2.02
coiled-coil domain containing 50	Ccdc50	0.71	1306	4751	1.13	1.37
triggering receptor expressed on myeloid cells-like 4	Trem14	0.70	2013	5459	1.81	1.82

Supplemental Table 3. Down-regulated genes in *La^{-/-}* CD11c⁺ cells (top 50)

Genes	Symbol	LogFC	# of cells		Expression	
			<i>La^{+/+}</i>	<i>La^{-/-}</i>	<i>La^{+/+}</i>	<i>La^{-/-}</i>
FBJ osteosarcoma oncogene	Fos	-2.17	8595	3549	3.09	1.55
dual specificity phosphatase 1	Dusp1	-1.58	8798	6456	3.20	1.75
ribosomal protein S18, pseudogene 6	Gm10260	-1.52	3736	70	2.23	0.47
early growth response 1	Egr1	-1.38	3368	321	2.21	1.26
predicted gene, 34084	Gm34084	-1.32	4162	30	1.95	1.04
immunoglobulin kappa constant	Igkc	-1.27	1145	223	2.17	2.03
myeloid-associated differentiation marker	Myadm	-1.21	7061	4385	2.27	1.28
zinc finger protein 36	Zfp36	-1.19	9144	7735	2.68	1.59
	Gm26532	-1.19	5443	1784	1.98	1.18
chemokine (C-C motif) ligand 5	Ccl5	-1.18	1406	436	3.14	2.53
FBJ osteosarcoma oncogene B	Fosb	-1.13	2941	173	1.96	0.77
colony stimulating factor 3 receptor (granulocyte)	Csf3r	-1.12	8487	7112	3.52	2.19
DENN/MADD domain containing 4A	Dennd4a	-1.08	7357	4275	2.27	1.47
Kruppel-like factor 6	Klf6	-1.05	9321	7725	2.52	1.58
immediate early response 2	Ier2	-1.03	8658	7038	2.31	1.46
jun B proto-oncogene	Junb	-1.00	10148	9097	3.14	2.13
neutrophil cytosolic factor 2	Ncf2	-0.98	8803	8521	2.74	1.80
TSC22 domain family, member 3	Tsc22d3	-0.98	9465	7495	2.56	1.63
chemokine (C-X-C motif) receptor 4	Cxcr4	-0.97	6777	4258	2.08	1.31
regulator of G-protein signaling	Rgs2	-0.97	8895	8317	2.81	1.85
jun D proto-oncogene	Jund	-0.97	10262	8732	2.84	1.85
nuclear paraspeckle assembly transcript 1 (non-protein coding)	Neat1	-0.96	9772	9346	3.04	2.16
elongator complex protein 1	Ikbkap	-0.96	4350	1597	1.93	1.20
prostaglandin-endoperoxide synthase 2	Ptgs2	-0.95	1199	118	2.46	1.84
BTG anti-proliferation factor 2	Btg2	-0.94	9020	7496	2.32	1.49
fibrinogen-like protein 2	Fgl2	-0.94	7965	4908	2.83	2.10
RAB11 family interacting protein 1 (class I)	Rab11fip1	-0.94	6216	3322	2.09	1.42
thioredoxin interacting protein	Txnip	-0.94	9419	6860	2.45	1.62
ATPase, class VI, type 11B	Atp11b	-0.93	7620	5414	2.13	1.37
insulin-like growth factor I receptor	Igf1r	-0.90	6580	3760	2.37	1.76
interleukin 1 beta	Il1b	-0.89	8688	6920	3.66	2.59
arginase type II	Arg2	-0.87	5248	2412	2.14	1.65
cytotoxic T lymphocyte-associated protein 2 alpha	Ctla2a	-0.87	2287	524	2.11	1.84
arrestin domain containing 3	Arrdc3	-0.85	5007	2627	1.97	1.33
immediate early response 5	Ier5	-0.85	9120	8059	2.40	1.59
chemokine (C-C motif) ligand 6	Ccl6	-0.80	7579	7024	2.68	1.79
junction adhesion molecule like	Jaml	-0.80	6351	4334	2.40	1.71
myelin basic protein	Mbp	-0.80	6823	5382	1.99	1.28
transmembrane and coiled coil domains 1	Tmcc1	-0.79	7641	6923	2.30	1.55
selectin, lymphocyte	Sell	-0.78	7555	4215	2.25	1.85
nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	Nfkbiz	-0.77	4985	4145	1.93	1.15
expressed sequence AI467606	AI467606	-0.77	6523	4063	1.87	1.29
matrix metalloproteinase 9	Mmp9	-0.77	7119	3988	2.83	2.47
nischarin	Nisch	-0.77	5804	4644	1.88	1.15
zinc finger protein 36, C3H type-like 2	Zfp36l2	-0.77	9364	8093	2.40	1.71
Kruppel-like factor 3 (basic)	Klf3	-0.76	8164	6950	2.15	1.45
CDC-like kinase 1	Clk1	-0.76	7611	6131	1.94	1.27
colony stimulating factor 1 (macrophage)	Csf1	-0.73	3845	1533	2.16	1.87
membrane-spanning 4-domains, subfamily A, member 4B	Ms4a4b	-0.73	1724	906	2.44	1.23
transient receptor potential cation channel, subfamily M, member 2	Trpm2	-0.73	3854	2491	1.93	1.17

Supplemental Table 4. Up-regulated genes in Cluster 158 of *Lal*^{-/-} CD11c⁺ cells (top 50)

Genes	Symbol	LogFC	# of cells		Expression	
			<i>Lal</i> ^{+/+}	<i>Lal</i> ^{-/-}	<i>Lal</i> ^{+/+}	<i>Lal</i> ^{-/-}
chitinase-like 3	Chil3	1.76	181	3551	1.48	2.09
hypoxanthine guanine phosphoribosyl transferase	Hprt	1.74	2	4717	0.93	1.66
haptoglobin	Hp	1.63	492	4748	1.34	2.39
glutathione reductase	Gsr	1.51	536	4903	1.04	2.11
lectin, galactose binding, soluble 3	Lgals3	1.25	1010	4964	2.06	3.29
predicted pseudogene 10320	Gm10320	1.18	2	4065	0.52	1.24
ferritin heavy polypeptide 1	Fth1	1.09	1072	4975	3.14	4.06
coagulation factor X	F10	1.09	235	4097	0.95	1.40
thioredoxin 1	Txn1	1.08	905	4941	1.51	2.48
transmembrane protein 14C	Tmem14c	1.07	358	4607	0.91	1.48
peroxiredoxin 5	Prdx5	1.07	927	4887	1.83	2.72
serum amyloid A 3	Saa3	1.04	5	744	0.84	1.65
superoxide dismutase 2, mitochondrial	Sod2	1.02	500	4431	1.02	1.57
WAP four-disulfide core domain 17	Wfdc17	1.02	105	2350	1.08	1.26
secretory leukocyte peptidase inhibitor	Slpi	0.96	229	3485	1.03	1.34
formyl peptide receptor 2	Fpr2	0.92	388	4391	1.24	1.58
CD302 antigen	Cd302	0.85	387	4358	0.97	1.36
chitinase-like 1	Chil1	0.84	201	3155	1.11	1.35
heme binding protein 1	Hebp1	0.84	176	3596	0.93	1.21
mitochondrial ribosomal protein L52	Mrpl52	0.84	493	4531	1.04	1.46
histocompatibility 2, class II antigen E beta	H2-Eb1	0.84	95	861	0.96	1.73
transforming growth factor, beta induced	Tgfb1	0.82	455	4000	1.30	1.66
formyl peptide receptor 1	Fpr1	0.82	72	2942	0.96	1.16
expressed sequence AW112010	AW112010	0.81	334	3594	1.09	1.39
cathepsin C	Ctsc	0.80	569	4410	1.28	1.66
C-type lectin domain family 4, member e	Clec4e	0.75	494	4389	1.24	1.51
interferon activated gene 207	Ifi207	0.75	62	3092	0.80	1.02
cathepsin B	Cstb	0.74	339	3418	0.98	1.30
cathepsin D	Ctsd	0.74	766	4546	1.34	1.72
inhibitor of kappaB kinase epsilon	Ikbke	0.73	39	3228	0.84	0.96
CD14 antigen	Cd14	0.69	424	4169	1.19	1.38
phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	Pla2g7	0.69	914	4900	1.74	2.32
inhibitor of DNA binding 2	Id2	0.69	365	3552	1.23	1.42
integrin alpha 4	Itga4	0.69	977	4887	1.67	2.24
placenta-specific 8	Plac8	0.68	1001	4893	2.45	3.08
protein tyrosine phosphatase, non-receptor type 1	Ptpn1	0.68	969	4934	1.76	2.37
guanylate binding protein 2	Gbp2	0.67	111	2198	0.97	1.17
allograft inflammatory factor 1	Aif1	0.67	325	3361	1.21	1.39
ribosomal protein S18	Rps18	0.67	1056	4964	2.33	3.01
ninjurin 1	Ninj1	0.67	297	3366	0.98	1.19
fatty acid binding protein 5, epidermal	Fabp5	0.67	134	2187	0.94	1.10
ubiquitin C	Ubc	0.66	928	4923	1.59	2.15
peroxiredoxin 1	Prdx1	0.66	998	4909	1.78	2.25
selection and upkeep of intraepithelial T cells 3	Skint3	0.66	0	2459	0	0.97
complement component 3	C3	0.66	348	3913	1.09	1.27
lectin, galactose binding, soluble 1	Lgals1	0.66	550	3674	1.21	1.50
C-type lectin domain family 4, member n	Clec4n	0.65	133	2502	0.90	1.11
uridine phosphorylase 1	Upp1	0.65	36	2069	0.91	1.10
interferon activated gene 204	Ifi204	0.63	102	2958	0.87	0.99
ubiquinol-cytochrome c reductase binding protein	Uqcrb	0.61	730	4667	1.15	1.54

Supplemental Table 5. Down-regulated genes in Cluster 158 of *Lal*^{-/-} CD11c⁺ cells (top 50)

Genes	Symbol	LogFC	# of cells		Expression	
			<i>Lal</i> ^{+/+}	<i>Lal</i> ^{-/-}	<i>Lal</i> ^{+/+}	<i>Lal</i> ^{-/-}
heat shock protein 1B	Hspa1b	-1.90	828	1523	2.30	1.01
heat shock protein 1A	Hspa1a	-1.89	780	1128	2.22	0.96
transferrin	Trf	-1.88	1036	1856	2.22	0.91
ribosomal protein S18, pseudogene 6	Gm10260	-1.86	985	54	1.83	0.47
B cell leukemia/lymphoma 2 related protein A1d	Bcl2a1d	-1.51	961	1627	1.82	0.80
eosinophil-associated, ribonuclease A family, member 1	Ear1	-1.50	796	6	1.58	0.67
CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Cd74	-1.43	938	2806	3.19	2.01
immunoglobulin heavy constant mu	Ighm	-1.23	816	652	1.48	0.79
phospholipid transfer protein	Pltp	-1.10	830	1616	1.66	1.04
TSC22 domain family, member 3	Tsc22d3	-1.08	1018	3572	1.93	1.08
FBJ osteosarcoma oncogene	Fos	-1.06	677	1383	1.65	0.98
jun D proto-oncogene	Jund	-1.05	1042	4212	2.25	1.31
histocompatibility 2, class II antigen A, beta 1	H2-Ab1	-1.00	402	1229	2.41	1.76
dual specificity phosphatase 1	Dusp1	-0.95	849	2816	1.74	1.04
histocompatibility 2, class II antigen A, alpha	H2-Aa	-0.91	387	1122	2.40	1.85
inactive X specific transcripts	Xist	-0.91	342	905	2.45	1.75
ATPase, class VI, type 11B	Atp11b	-0.85	919	3213	1.77	1.11
chemokine (C-C motif) ligand 9	Ccl9	-0.84	815	2233	1.74	1.20
	AC160336.1	-0.84	934	3590	1.78	1.12
polymerase (RNA) II (DNA directed) polypeptide L	Polr2l	-0.81	828	2899	1.61	0.99
chemokine (C-X-C motif) receptor 4	Cxcr4	-0.80	870	2479	1.50	0.96
BTG anti-proliferation factor 2	Btg2	-0.78	999	4172	1.87	1.20
CD83 antigen	Cd83	-0.78	551	624	1.29	0.87
thioredoxin interacting protein	Txnip	-0.77	862	2952	1.55	0.95
lysosomal acid lipase A	Lipa	-0.75	727	1659	1.27	0.74
zinc finger protein 36, C3H type-like 2	Zfp36l2	-0.75	1057	4441	2.15	1.48
Kruppel-like factor 6	Klf6	-0.74	980	3989	1.79	1.16
	Gm47283	-0.73	614	914	1.17	0.68
hes family bHLH transcription factor 1	Hes1	-0.72	744	2311	1.52	1.02
serine/threonine kinase 24	Stk24	-0.70	1014	4270	1.80	1.17
myelin basic protein	Mbp	-0.68	965	3639	1.65	1.11
DENN/MADD domain containing 4A	Dennd4a	-0.67	643	1625	1.30	0.82
terminal nucleotidyltransferase 5A	Fam46a	-0.67	981	4046	1.86	1.30
zinc finger protein 36	Zfp36	-0.67	981	4116	1.80	1.21
RAB11 family interacting protein 1 (class I)	Rab11fip1	-0.67	594	1131	1.20	0.74
CD36 molecule	Cd36	-0.66	736	1800	1.56	1.23
FXRD domain-containing ion transport regulator 5	Fxyd5	-0.65	1069	4848	2.63	1.95
transmembrane and coiled coil domains 1	Tmcc1	-0.65	995	4167	1.91	1.33
	Gm26532	-0.64	539	810	1.16	0.71
apolipoprotein E	Apoe	-0.62	1008	4440	3.72	2.89
ribosomal protein S18, pseudogene 5	Gm11361	-0.62	495	85	1.02	0.56
salt inducible kinase 1	Sik1	-0.61	655	1500	1.19	0.78
leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	Lilra5	-0.61	848	3094	1.71	1.24
myeloid-associated differentiation marker	Myadm	-0.61	716	2232	1.28	0.82
jun B proto-oncogene	Junb	-0.61	1014	4459	2.08	1.54
adhesion G protein-coupled receptor E5	Adgre5	-0.60	1068	4870	2.57	1.95
cysteine-rich protein 1 (intestinal)	Crip1	-0.58	1007	4160	2.52	1.97
complement component factor h	Cfh	-0.58	689	1569	1.27	0.97
AHNAK nucleoprotein (desmoyokin)	Ahnak	-0.58	926	3720	1.89	1.44
cDNA sequence AY036118	AY036118	-0.58	1054	4832	2.36	1.80

Supplemental Table 6. Up-regulated genes in Cluster 0236 of *Lal*^{-/-} CD11c⁺ cells (top 50)

Genes	Symbol	LogFC	# of cells		Expression	
			<i>Lal</i> ^{+/+}	<i>Lal</i> ^{-/-}	<i>Lal</i> ^{+/+}	<i>Lal</i> ^{-/-}
interferon induced transmembrane protein 1	Ifitm1	2.24	4747	3935	2.46	4.29
WAP four-disulfide core domain 17	Wfdc17	2.17	2626	3694	2.53	3.77
glutathione reductase	Gsr	2.14	1192	3864	1.81	2.70
lectin, galactose binding, soluble 3	Lgals3	1.99	2745	3902	2.12	3.32
neutrophilic granule protein	Ngp	1.99	121	823	1.78	2.58
lipocalin 2	Lcn2	1.69	1819	2440	2.31	3.04
WAP four-disulfide core domain 21	Wfdc21	1.55	3384	3366	2.44	3.41
interferon induced transmembrane protein 6	Ifitm6	1.51	711	1561	1.81	2.37
insulin-like growth factor binding protein 6	Igfbp6	1.41	581	2052	1.91	2.22
prokineticin 2	Prok2	1.15	42	852	1.88	2.16
transmembrane protein 14C	Tmem14c	1.14	444	2092	1.72	1.81
interferon induced transmembrane protein 3	Ifitm3	1.13	2983	3304	2.04	2.58
translocator protein	Tspo	1.12	3176	3335	2.02	2.59
resistin like gamma	Retnlg	1.12	4842	3110	3.18	3.89
uridine phosphorylase 1	Upp1	1.03	226	1477	1.88	1.86
placenta-specific 8	Plac8	1.03	1295	2105	2.18	2.26
hypoxanthine guanine phosphoribosyl transferase	Hprt	1.02	1	1079	1.28	1.89
RIKEN cDNA 1600014C10 gene	1600014C10Rik	1.01	759	1593	1.80	2.01
interferon induced transmembrane protein 2	Ifitm2	0.98	6033	4042	2.92	3.82
STEAP family member 4	Steap4	0.95	900	2043	2.12	2.09
leucine-rich alpha-2-glycoprotein 1	Lrg1	0.93	4264	3732	2.51	3.08
predicted pseudogene 10320	Gm10320	0.89	8	1258	1.62	1.64
cytochrome c oxidase I, mitochondrial	mt-Co1	0.86	4405	3699	2.43	2.97
predicted gene, 35082	Gm35082	0.84	287	1439	1.88	1.74
S100 calcium binding protein A9 (calgranulin B)	S100a9	0.83	6689	4014	5.36	6.17
destrin	Dstn	0.81	729	1699	1.79	1.84
catenin (cadherin associated protein), beta 1	Ctnnb1	0.81	1960	2685	1.90	2.02
stefin A2 like 1	Stfa2l1	0.81	1978	1993	2.66	2.91
chitinase-like 1	Chil1	0.80	2924	3087	2.03	2.28
sorcin	Sri	0.76	1482	2263	1.91	2.00
lymphocyte antigen 6 complex, locus G	Ly6g	0.73	245	880	1.82	1.91
ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit D	Atp5h	0.72	975	1902	1.77	1.75
S100 calcium binding protein A8 (calgranulin A)	S100a8	0.71	6680	3953	5.18	5.62
glyceraldehyde-3-phosphate dehydrogenase	Gapdh	0.69	4140	3422	2.18	2.55
ferritin heavy polypeptide 1	Fth1	0.66	6825	4073	3.74	4.26
fatty acid binding protein 5, epidermal	Fabp5	0.66	731	1406	1.82	1.81
Fc receptor, IgE, high affinity I, gamma polypeptide	Fcgr1g	0.64	6291	4042	2.81	3.37
neutrophil cytosolic factor 4	Ncf4	0.63	4763	3749	2.23	2.58
ribonuclease, RNase A family, 6	Rnase6	0.60	112	692	1.87	1.80
cytochrome c oxidase subunit 6C	Cox6c	0.60	1594	2134	1.86	1.84
cystatin C	Cst3	0.59	5504	3914	2.51	2.86
ectonucleoside triphosphate diphosphohydrolase 3	Entpd3	0.58	247	736	1.82	1.86
CD52 antigen	Cd52	0.57	6268	3995	2.87	3.36
BRD8 domain containing	4933408B17Rik	0.56	21	773	1.84	1.54
refilin B	Rflnb	0.56	694	1304	1.80	1.72
guanine nucleotide binding protein (G protein), gamma 12	Gng12	0.55	1643	2113	1.82	1.80
X-box binding protein 1	Xbp1	0.55	1012	1428	1.86	1.85
chitinase-like 3	Chil3	0.55	52	513	1.82	1.75
H3.3 histone A	H3f3a	0.53	6594	4060	3.08	3.59
cyclin dependent kinase inhibitor 2D	Cdkn2d	0.53	1631	2036	1.91	1.88

Supplemental Table 7. Down-regulated genes in Cluster 0236 of *LaI*^{-/-} CD11c⁺ cells (top 50)

Genes	Symbol	LogFC	# of cells		Expression	
			<i>LaI</i> ^{+/+}	<i>LaI</i> ^{-/-}	<i>LaI</i> ^{+/+}	<i>LaI</i> ^{-/-}
FBJ osteosarcoma oncogene	Fos	-2.03	6777	1869	3.43	2.01
early growth response 1	Egr1	-1.61	2856	110	2.35	1.92
predicted gene, 34084	Gm34084	-1.58	3536	12	2.07	1.82
FBJ osteosarcoma oncogene B	Fosb	-1.36	2309	28	2.15	1.77
dual specificity phosphatase 1	Dusp1	-1.28	6922	3280	3.55	2.38
	Gm26532	-1.17	4128	808	2.20	1.71
immediate early response 2	Ier2	-1.13	5900	2172	2.62	1.88
prostaglandin-endoperoxide synthase 2	Ptgs2	-1.11	1083	98	2.54	2.03
myeloid-associated differentiation marker	Myadm	-1.08	5442	1834	2.52	1.87
zinc finger protein 36	Zfp36	-1.07	6725	3046	3.02	2.13
nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	Nfkbiz	-0.99	3543	902	2.19	1.69
neutrophil cytosolic factor 2	Ncf2	-0.99	6723	3234	2.99	2.16
elongator complex protein 1	Ikbkap	-0.94	3750	941	2.05	1.57
regulator of G-protein signaling	Rgs2	-0.93	6707	3229	3.10	2.28
cytotoxic T lymphocyte-associated protein 2 alpha	Ctla2a	-0.91	1232	131	2.34	2.04
ATPase, class VI, type 11B	Atp11b	-0.90	5191	1701	2.40	1.91
myelin basic protein	Mbp	-0.90	4635	1396	2.25	1.81
chemokine (C-X-C motif) receptor 4	Cxcr4	-0.88	4674	1501	2.36	1.92
BTG anti-proliferation factor 2	Btg2	-0.85	5914	2625	2.60	1.98
Kruppel-like factor 6	Klf6	-0.85	6420	3079	2.87	2.17
nuclear paraspeckle assembly transcript 1 (non-protein coding)	Neat1	-0.84	6935	3761	3.48	2.66
DENN/MADD domain containing 4A	Dennd4a	-0.83	5494	2281	2.54	1.98
tribbles pseudokinase 1	Trib1	-0.82	2558	647	2.10	1.69
transmembrane and coiled coil domains 1	Tmcc1	-0.81	5561	2360	2.53	1.98
	AC160336.1	-0.79	3673	1261	2.21	1.78
Dr1 associated protein 1 (negative cofactor 2 alpha)	Drap1	-0.75	2168	390	1.95	1.63
arrestin domain containing 3	Arrdc3	-0.74	3958	1274	2.15	1.81
activating transcription factor 3	Atf3	-0.74	1988	290	1.98	1.84
RAB11 family interacting protein 1 (class I)	Rab11fip1	-0.73	5051	1987	2.27	1.82
nischarin	Nisch	-0.73	4073	1571	2.17	1.74
colony stimulating factor 3 receptor (granulocyte)	Csf3r	-0.72	7048	3997	3.85	3.03
jun B proto-oncogene	Junb	-0.71	7002	3889	3.63	2.86
transient receptor potential cation channel, subfamily M, member 2	Trpm2	-0.69	3266	1101	2.06	1.66
CDC-like kinase 1	Clk1	-0.68	4826	1954	2.24	1.82
TSC22 domain family, member 3	Tsc22d3	-0.68	6445	3304	2.90	2.28
immediate early response 5	Ier5	-0.68	6328	3164	2.73	2.15
Kruppel-like factor 3 (basic)	Klf3	-0.67	5356	2366	2.42	1.96
zinc finger protein 36, C3H type-like 2	Zfp36l2	-0.67	6131	2903	2.66	2.13
chemokine (C-C motif) ligand 6	Ccl6	-0.67	5973	2573	2.89	2.45
RIKEN cDNA 1700020D05 gene	1700020D05	-0.66	1188	2	1.82	1.64
	Rik					
guanine nucleotide binding protein (G protein), gamma 11	Gng11	-0.66	834	67	2.13	1.87
jun D proto-oncogene	Jund	-0.66	6773	3642	3.16	2.51
platelet factor 4	Pf4	-0.65	915	92	2.21	2.19
arginase type II	Arg2	-0.65	4702	1976	2.22	1.80
nucleosome assembly protein 1-like 1	Nap1l1	-0.63	2902	1011	2.16	1.83
ST3 beta-galactoside alpha-2,3-sialyltransferase 6	St3gal6	-0.62	2106	522	1.93	1.63
Hist1h1cR1 erythroid cis-regulatory module	Hist1h1c	-0.61	2700	991	2.20	1.86
activating transcription factor 4	Atf4	-0.61	2120	568	1.97	1.68
mitogen-activated protein kinase kinase kinase 5	Map3k5	-0.60	2449	697	1.96	1.69
thioredoxin interacting protein	Txnip	-0.59	6356	3232	2.79	2.27