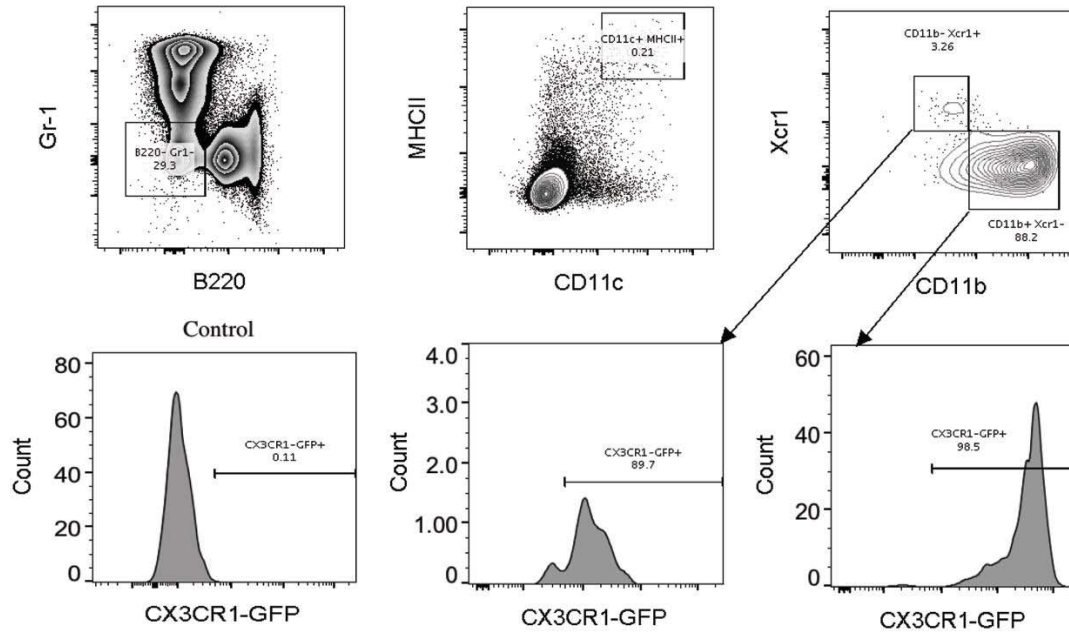
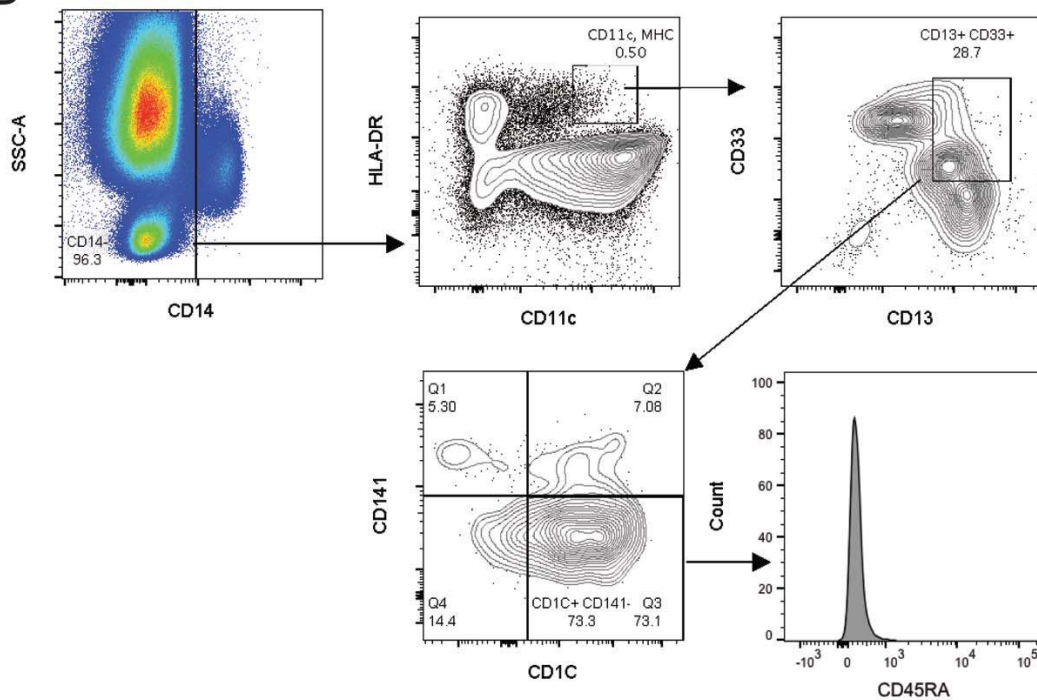


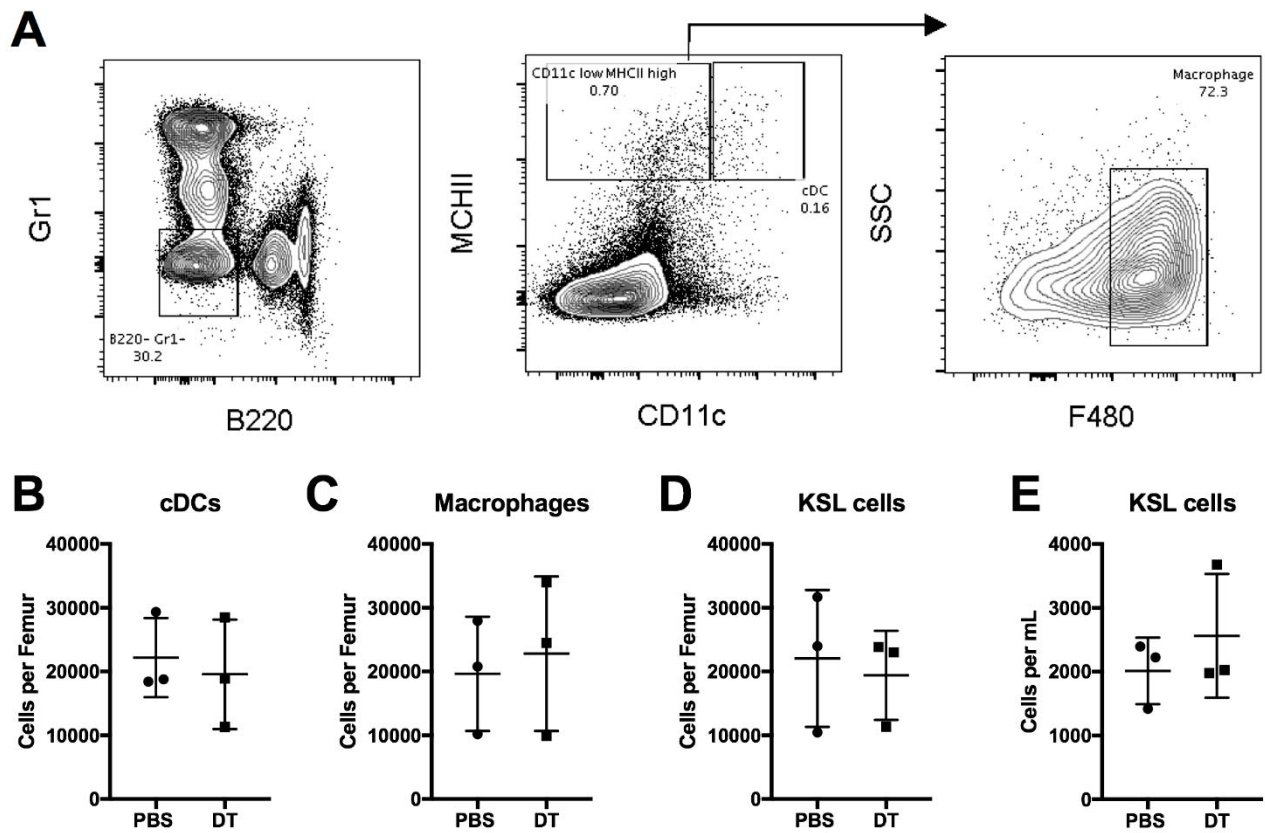
A



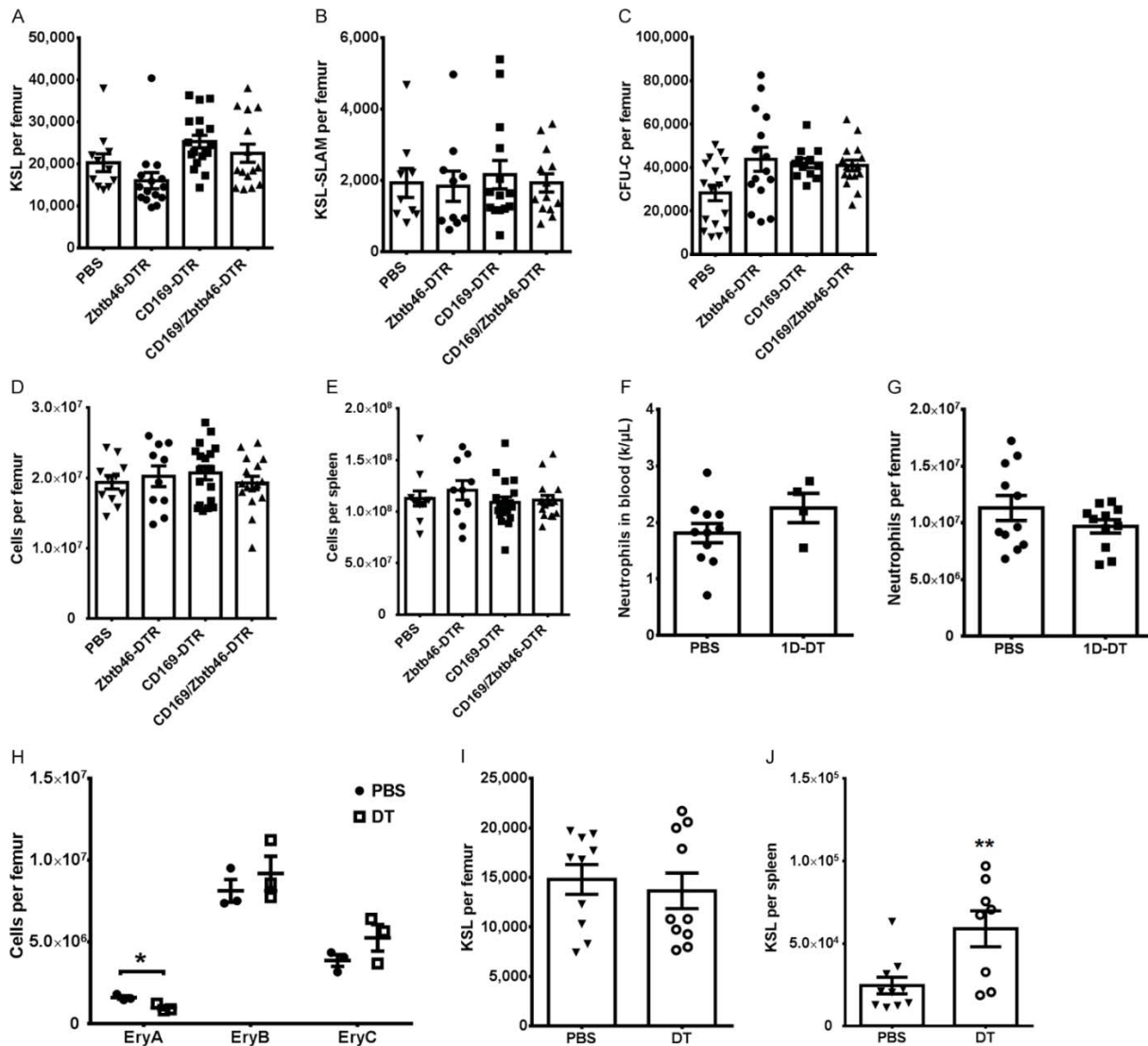
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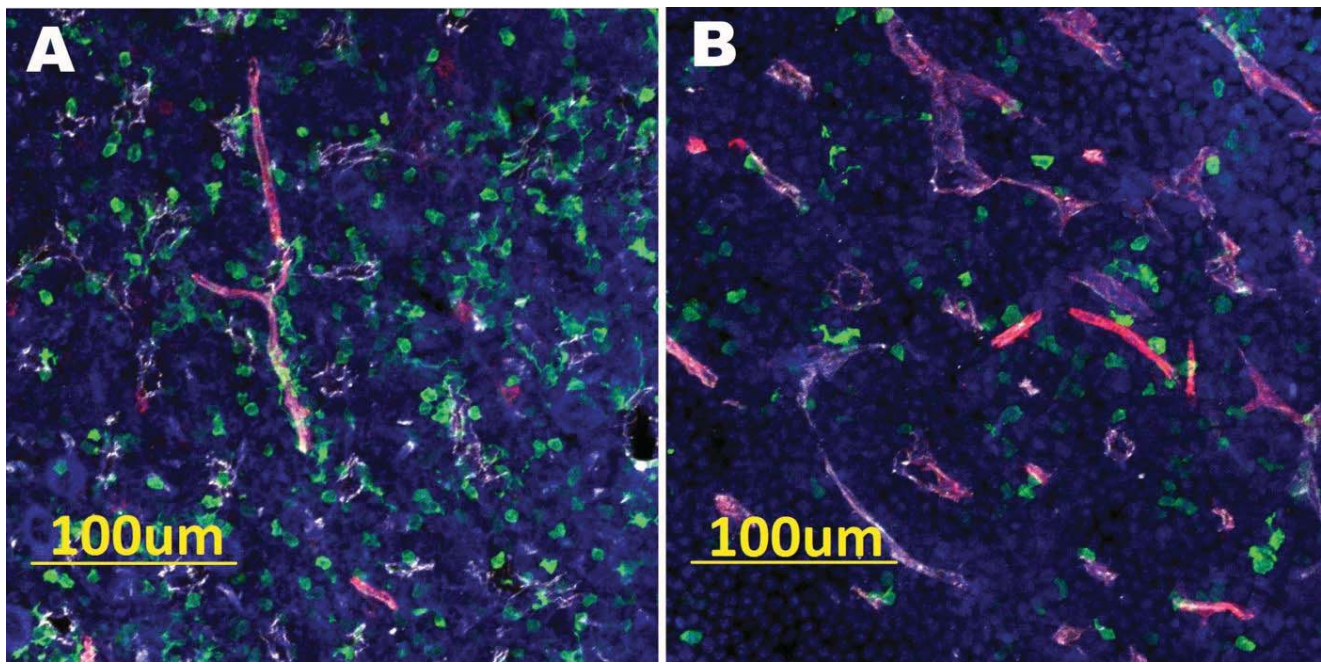
Supplemental Figure 1. Characterization of bone marrow dendritic cells. (A) Bone marrow from CX3CR1-GFP mice was analyzed to assess CX3CR1 expression in bone marrow cDC1 (lineage⁻ MHCII^{high} CD11c^{high} Xcr1⁺ CD11b⁻ cells) and cDC2 cells (lineage⁻ MHCII^{high} CD11c^{high} Xcr1⁻ CD11b⁺ cells). CX3CR1-GFP was expressed in both cDC1 and cDC2 cells, albeit at a higher level in cDC2 cells. Control represents cDC2 cells from wild-type mice gated in a similar fashion. (B) Representative flow plots showing gating strategy used to identify dendritic cells in human bone marrow. The majority of dendritic cells are mature CD1C⁺ CD141⁻ CD45RA⁻ cDC2s.



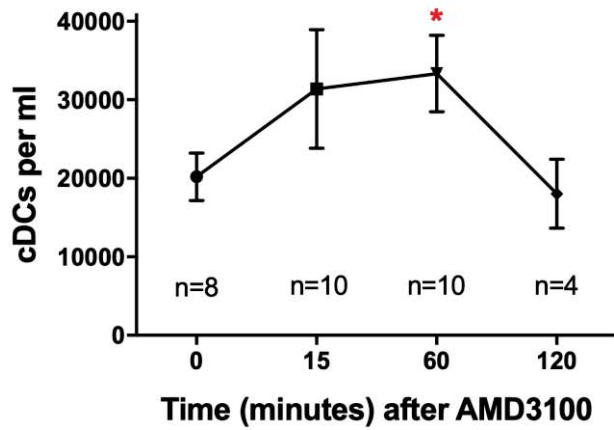
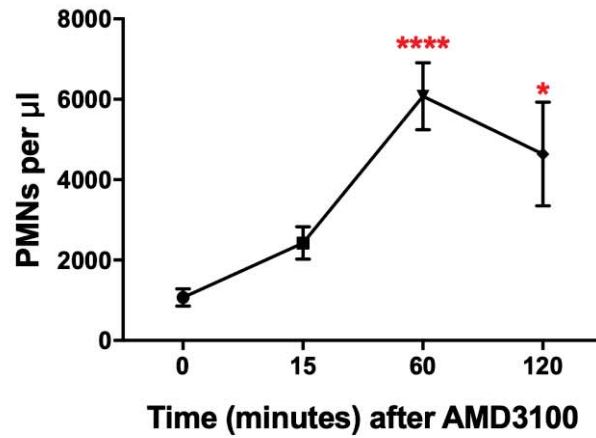
Supplemental Figure 2. Treatment of wildtype mice with diphtheria toxin (DT) does not induce changes in bone marrow cDCs or macrophages or HSPC mobilization. (A) Gating strategy used to identify conventional dendritic cells (cDCs) and macrophages in the bone marrow. (B-E) Wildtype mice were treated with DT or saline alone (PBS) for 6 days, and the number of cDCs (B), macrophages (C), or kit⁺ sca⁺ lineage⁻ (KSL) cells in the bone marrow (D) or KSL cells in the blood (E) were quantified. Data represent the mean \pm S.E.M. of 3 mice per cohort.



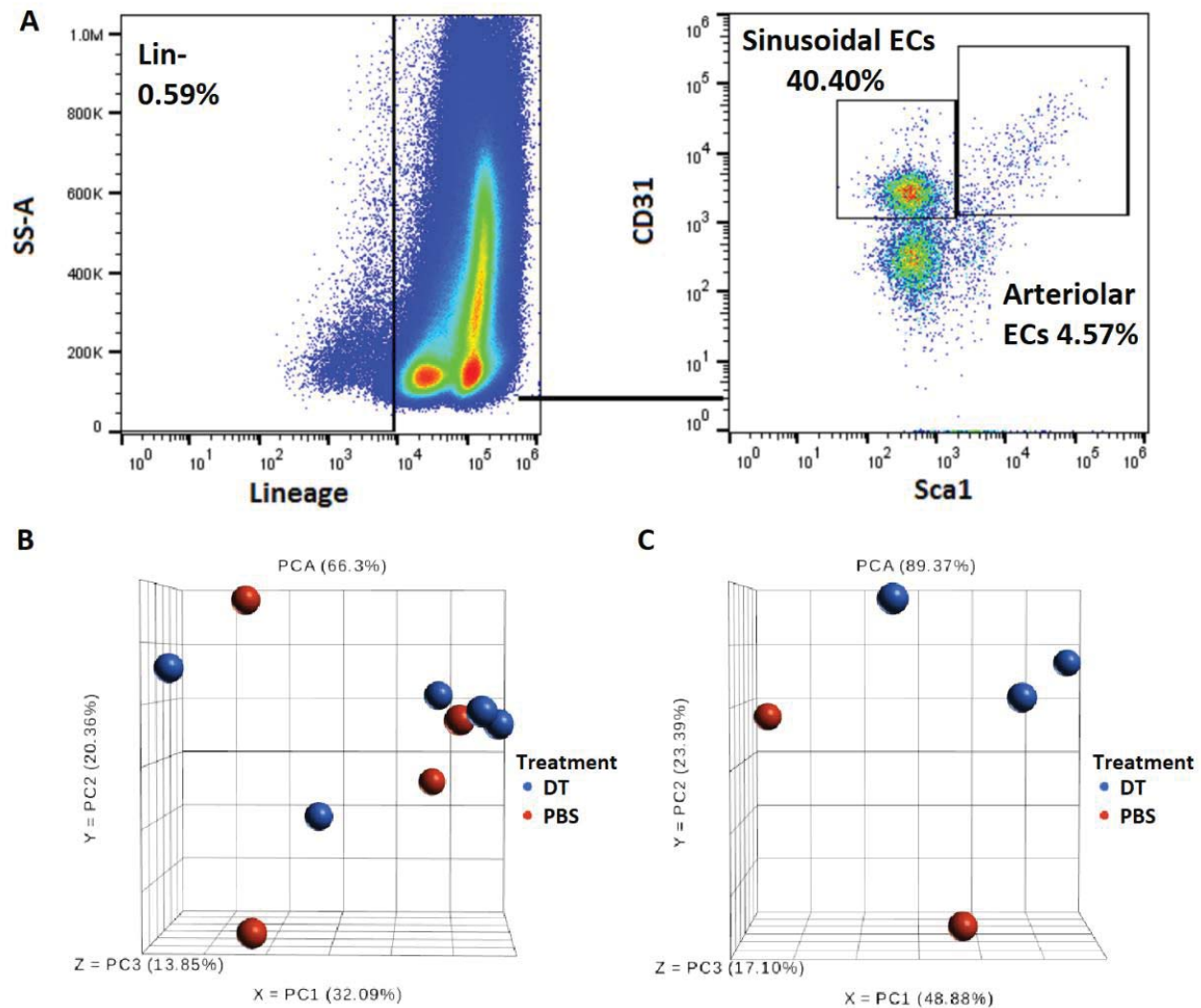
Supplemental Figure 3. Bone marrow DC ablation induces a loss of macrophage and HSPC mobilization. (A-E) *Zbtb46^{dtr}* (Zbtb46-DTR), *CD169^{dtr}* (CD169-DTR) and *CD169^{dtr}:Zbtb46^{dtr}* (CD169/Zbtb46-DTR) bone marrow were transplanted into wild-type recipients. Eight weeks after transplantation, mice were treated with PBS or DT for 6 days. KSL cells (A) (n = 11-18 mice), KSL-SLAM cells (B) (n = 9-14 mice) and CFU-C (C) (n = 12-17 mice) in the bone marrow, and total cellularity in bone marrow (D) and spleen (E) (n = 10-18 mice), were quantified. (F-G) *Zbtb46^{dtr}* bone marrow chimeras were treated with PBS or DT for 1 day, neutrophils were quantified in the blood (F) (n = 11 or 4 mice), and in the bone marrow (G) (n = 11 mice per cohort) by flow cytometry, gated as Gr-1^{high} cells. (H) *Zbtb46^{dtr}* bone marrow chimeras were treated with PBS or DT for 6 days, the number of Lin⁺(Gr1, B220,CD3e) Ter119⁺ CD71⁺ FSC-A^{high} basophilic erythroblasts (EryA), Lin⁺ Ter119⁺ CD71⁺ FSC-A^{low} late basophilic and polychromatic erythroblasts (EryB), and Lin⁺ Ter119⁺ CD71⁺ FSC-A^{low} orthochromatic erythroblasts or reticulocytes (EryC), were quantified (n = 3 mice per cohort). (I,J) Bone marrow from *CD11c^{dtr}* mice were transplanted into irradiated wild-type recipients and after eight weeks, the resulting chimeras were treated with PBS or DT for 6 days. KSL cells were quantified in bone marrow (I) and spleen (J) (n = 8-10 mice per cohort). **P < 0.01 compared to saline treated mice. Data represent the mean \pm S.E.M. Significance was determined using an unpaired student t-test or one-way Anova.



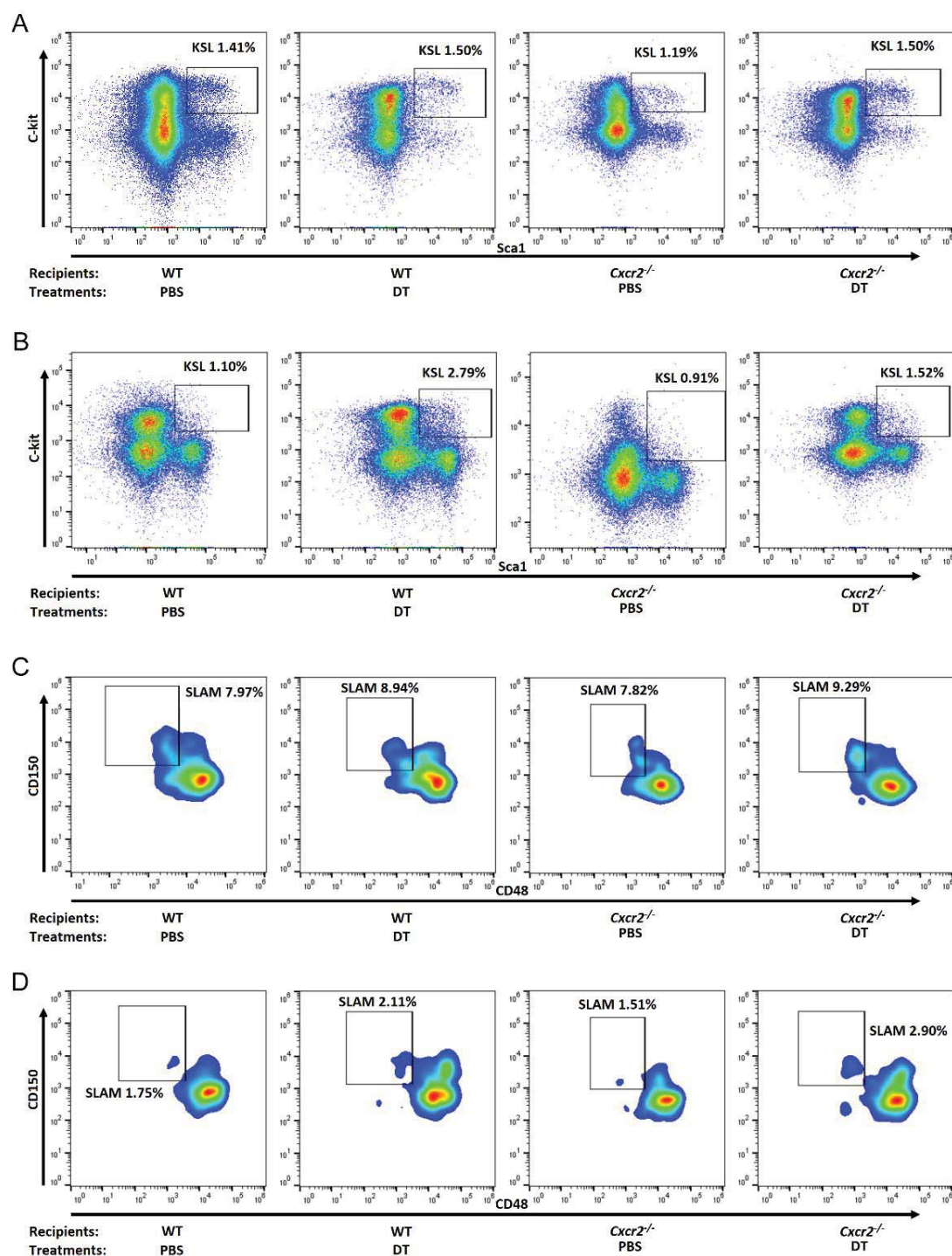
Supplemental Figure 4. G-CSF treatment is associated with a loss of bone marrow dendritic cells. Cx3Cr1^{gfp/+} mice were treated with saline alone or G-CSF (250 µg/kg SQ daily for 5 days). Shown are representative images of bone sections from saline treated (**A**) or G-CSF treated (**B**) mice. Merged images show CX3CR1-GFP (green), Sca1⁺ arterioles (red), and VE-Cadherin/CD31⁺ venous sinusoids, arterioles (white), and DAPI (blue). A decrease in stellate shaped perivascular GFP⁺ cDCs and oval GFP⁺ monocytes is evident. Data are representative of 4 independent experiments.

A**B**

Supplemental Figure 5. AMD3100 treatment mobilizes cDCs into the blood. Wild-type mice were treated with saline alone or a single subcutaneous dose of AMD3100 (5 mg/kg) (n = 8, 10, 10, 4 mice for each time point). Shown are the number of cDCs (**A**) and neutrophils (PMNs) (**B**) in the peripheral blood. *P < 0.05; ****P < 0.0001 compared to baseline (time = 0). Data represent the mean ± S.E.M. Significance was determined using an unpaired student t-test.



Supplemental Figure 6. Ablation of bone marrow DCs activates sinusoidal endothelial cells. Arteriolar and sinusoidal endothelial cells (ECs) were sorted from *Zbtb46^{dtr}* bone marrow chimeras 24 hours after treatment with a single dose of diphtheria toxin (DT) or saline alone (PBS). RNA expression profiling was performed on sorted ECs. **(A)** Representative flow plots showing the gating strategy used to isolate arteriolar and sinusoidal endothelial cells; the lineage panel included the following antibodies: CD45, Ter119, Gr1, CD11b. **(B, C)** Shown are principal component analysis (PCA) plots for arteriolar ECs **(B)** and sinusoidal ECs **(C)**.



Supplemental Figure 7. CXCR2 signaling contributes to HSPC mobilization following conventional dendritic cell ablation. Bone marrow cells from *Zbtb46*^{dtr} mice were transplanted into irradiated wild-type or *Cxcr2*^{-/-} recipients. Eight weeks after transplantation, mice were treated with saline alone (PBS) or diphtheria toxin (DT) for 6 days. For each cohort, representative flow plots used to quantify KSL cells (**A**) and KSL-SLAM cells (**C**) in bone marrow or KSL cells (**B**) and KSL-SLAM cells (**D**) in the spleen are shown.

Supplemental Table 1. Expression of selected cDC genes in bone marrow dendritic cells

Gene Symbol	Spl 1	Spl 2	BM 1	BM 2	BM 3	BM 4	Avg Spl	Avg BM	Ratio BM/Spl	pvalue
Shared cDC genes										
<i>Itgax</i>	5,834	5,993	6,533	6,433	6,003	6,686	5,913	6,414	1.08	0.090
<i>Flt3</i>	2,056	1,943	2,154	1,788	1,615	2,407	1,999	1,991	1.00	0.977
<i>Zbtb46</i>	326	279	238	221	182	218	303	215	0.71	0.018
<i>Btla</i>	377	395	349	406	295	460	386	377	0.98	0.884
<i>Dpp4</i>	1,613	1,625	1,823	1,814	1,961	2,012	386	377	0.98	0.019
<i>Csf3r</i>	222	235	2,325	2,394	2,459	2,225	228	2,351	10.30	0.000
cDC2 genes										
<i>Irf4</i>	1,242	1,235	533	644	375	682	1,239	559	0.45	0.003
<i>Zeb2</i>	491	459	2,194	2,228	2,165	1,995	475	2,145	4.52	0.000
<i>Cx3cr1</i>	398	417	2,989	3,391	2,956	3,340	407	3,169	7.78	0.000
<i>Itgam</i>	740	879	3,067	3,328	2,978	3,057	809	3,107	3.84	0.000
<i>Sirpa</i>	3,076	3,116	5,916	6,312	6,089	6,188	3,096	6,126	1.98	0.000
<i>Fcgr1</i>	53	51	969	1,418	1,379	1,421	52	1,297	25.1	0.002
cDC1 genes										
<i>Irf8</i>	336	277	2,151	2,510	2,321	2,775	307	2,439	7.95	0.000
<i>Id2</i>	654	676	313	500	319	371	665	376	0.56	0.012
<i>Batf3</i>	730	730	1,575	1,633	1,769	1,733	730	1,677	2.30	0.000
<i>Cd24a</i>	792	810	1,281	1,392	1,186	1,493	801	1,338	1.67	0.006
<i>Clec9a</i>	188	181	1,239	1,033	1,041	1,216	184	1,132	6.15	0.000

Shown are normalized expression values for spleen cDC2 cells (Spl) or bone marrow dendritic cells (BM). Avg: average; cDC: conventional dendritic cells. p values based on student t test.

Supplemental Table 2. Differentially expressed genes in bone marrow sinusoidal endothelial cells following dendritic cell ablation.

Gene ID	PBS 1	PBS 2	PBS 3	PBS 4	DT 1	DT 2	DT 3	PBS Avg	DT Avg	Fold change (DT vs. PBS)	FDR
Ifitm6	19.31	19.24	20.14	21.63	654.22	569.72	610.63	20.08	611.53	30.46	1.10E-07
Mmp9	19.37	20.60	23.06	23.57	687.83	648.60	613.33	21.65	649.92	30.02	1.10E-07
Mcomp1	10.66	9.76	11.41	10.27	276.60	273.35	251.65	10.53	267.20	25.38	2.66E-07
Itgb2l	8.80	6.03	7.62	8.02	250.24	244.94	233.34	7.62	242.84	31.88	6.95E-07
Hp	72.81	42.04	71.06	59.71	1520.24	1494.45	1669.85	61.41	1561.51	25.43	1.39E-06
Slfn4	21.31	13.29	15.64	15.69	351.05	360.40	476.32	16.48	395.92	24.02	1.39E-06
Plaur	17.38	12.63	17.98	14.00	323.11	324.57	421.78	15.49	356.49	23.01	1.39E-06
Pglyrp1	47.36	29.11	42.81	35.41	832.16	782.48	767.31	38.67	793.98	20.53	1.39E-06
Wfdc21	20.00	13.14	17.53	14.36	323.11	322.19	281.14	16.26	308.81	19.00	1.39E-06
Retnlg	105.41	80.50	84.32	118.32	2013.53	1471.05	1753.30	97.14	1745.96	17.97	1.39E-06
Mmp8	53.32	30.62	37.51	47.47	987.99	819.28	934.46	42.23	913.91	21.64	1.72E-06
Hdc	12.44	8.61	9.81	6.78	309.67	252.21	254.48	9.41	272.12	28.92	1.89E-06
I830127L07R ik	25.98	16.18	19.24	23.45	323.87	338.73	365.57	21.21	342.72	16.16	1.89E-06
Fxyd5	43.95	36.24	37.67	40.59	311.83	270.35	330.94	39.61	304.37	7.68	2.60E-06
Anxa1	186.62	111.15	190.99	189.78	3464.08	3068.95	3064.05	169.63	3199.03	18.86	2.76E-06
Nfam1	14.67	13.39	21.72	20.85	295.93	287.56	324.58	17.66	302.69	17.14	3.04E-06
Camp	204.12	115.49	219.43	138.73	3618.47	3526.98	3601.19	169.45	3582.21	21.14	3.68E-06
S100a8	660.72	364.88	588.29	535.78	10490.6	9990.20	8974.27	537.42	9818.36	18.27	3.68E-06
Lcn2	166.98	86.18	172.64	147.19	3116.86	3494.92	3286.40	143.25	3299.39	23.03	3.81E-06
Tgfb1	5.54	6.87	8.46	11.46	204.38	210.81	236.27	8.08	217.15	26.86	4.05E-06
Csf3r	15.60	6.91	10.78	10.48	318.43	263.10	296.66	10.94	292.73	26.75	4.40E-06
S100a9	548.13	279.17	488.44	398.47	7866.26	7878.36	7526.12	428.55	7756.91	18.10	4.40E-06
Lyz2	487.19	254.25	364.14	358.37	5577.32	5376.55	6715.10	365.98	5889.66	16.09	4.40E-06
Ckap4	12.11	9.56	11.70	9.47	115.22	119.35	99.99	10.71	111.52	10.41	4.40E-06
Dhrs7	21.57	16.84	21.46	24.27	196.14	167.86	181.30	21.03	181.77	8.64	4.40E-06
Gm12854	48.62	32.90	39.09	41.03	359.33	316.60	300.21	40.41	325.38	8.05	4.40E-06
Dgat1	15.66	14.77	14.68	16.58	109.53	127.96	147.10	15.43	128.19	8.31	4.43E-06
Prdx5	109.74	90.42	112.28	114.36	780.51	599.07	703.94	106.70	694.51	6.51	4.43E-06
Ighg1	0.84	0.49	0.95	0.67	206.11	392.16	105.24	0.74	234.50	317.87	4.46E-06
Ltf	335.41	152.19	316.51	325.70	8631.55	7848.16	8778.69	282.45	8419.47	29.81	4.46E-06
Ngp	928.77	469.68	949.62	758.21	19391.9	17453.6	18649.9	776.57	18498.5	23.82	4.46E-06
Padi4	10.51	6.93	13.26	8.28	168.16	164.96	176.48	9.74	169.87	17.43	4.46E-06
Itgb2	59.72	37.60	63.41	65.20	705.25	608.76	723.41	56.48	679.14	12.02	4.46E-06
Sfxn5	8.80	12.14	10.89	8.41	111.43	103.23	109.84	10.06	108.17	10.76	4.46E-06
Fes	12.98	10.79	16.67	13.06	135.58	129.46	145.07	13.38	136.70	10.22	4.46E-06
Cd9	34.87	43.68	27.56	32.72	301.48	287.20	294.71	34.71	294.46	8.48	4.46E-06
Cnn2	91.10	58.68	70.72	72.51	551.30	507.97	524.85	73.25	528.04	7.21	4.46E-06
Dstn	122.21	87.99	91.86	92.66	659.76	652.13	583.02	98.68	631.63	6.40	4.46E-06
Pgd	80.85	93.02	102.22	101.79	514.03	486.54	459.81	94.47	486.79	5.15	4.46E-06

Alox5	8.10	7.18	7.30	14.62	245.90	205.98	206.32	9.30	219.40	23.59	4.69E-06
Rps6ka1	36.55	33.73	41.24	35.06	228.28	188.29	203.99	36.65	206.85	5.64	4.69E-06
S100a11	82.02	53.43	66.76	70.15	576.10	494.42	465.16	68.09	511.89	7.52	4.88E-06
Cd177	59.13	25.25	57.12	29.26	1469.36	1370.99	1606.14	42.69	1482.16	34.72	5.10E-06
Actn1	10.42	8.57	10.75	7.92	136.68	105.19	95.82	9.42	112.56	11.96	5.10E-06
Glipr2	25.12	16.69	22.59	27.03	214.90	212.56	196.36	22.86	207.94	9.10	5.10E-06
Adgrg3	18.56	19.99	14.50	17.23	131.30	119.95	128.17	17.57	126.47	7.20	5.10E-06
Wfdc17	2.83	1.97	3.29	2.61	131.79	82.30	72.86	2.68	95.65	35.73	5.24E-06
Cxcr2	12.92	6.85	5.40	10.84	297.31	258.22	261.70	9.00	272.41	30.25	5.24E-06
Chil1	14.07	8.84	12.42	20.98	291.59	298.55	369.31	14.08	319.82	22.72	5.24E-06
Ly6g	7.10	5.02	5.14	5.62	73.92	69.65	68.38	5.72	70.65	12.36	5.52E-06
S100a6	33.14	17.07	23.54	21.39	334.45	297.38	269.45	23.79	300.43	12.63	5.67E-06
Pira2	4.93	3.60	3.18	5.35	112.46	78.90	130.12	4.27	107.16	25.12	5.90E-06
Pygl	15.63	19.07	29.73	19.79	299.27	255.04	233.66	21.06	262.66	12.47	5.90E-06
Slc2a3	18.04	30.00	23.56	33.97	346.73	289.27	318.47	26.39	318.16	12.05	5.90E-06
Fcer1g	52.27	27.29	31.10	40.25	433.95	428.34	418.44	37.73	426.91	11.32	6.14E-06
Adpgk	18.72	22.11	18.08	21.27	111.60	124.79	110.60	20.05	115.66	5.77	6.64E-06
Fcgr3	28.11	16.36	16.79	23.76	293.29	216.83	267.82	21.26	259.31	12.20	6.90E-06
Alox5ap	79.12	38.02	46.20	50.73	700.25	615.72	660.81	53.52	658.93	12.31	6.92E-06
Tyrobp	71.33	38.08	50.95	41.65	544.84	463.90	521.95	50.50	510.23	10.10	7.81E-06
Pirb	14.81	7.08	14.92	19.09	344.13	346.02	403.83	13.97	364.66	26.10	7.85E-06
Sema4a	11.60	8.92	11.70	6.26	132.88	133.21	127.41	9.62	131.17	13.63	7.85E-06
Grina	39.64	44.67	53.93	56.29	257.60	285.85	308.36	48.63	283.94	5.84	7.85E-06
Mmp25	0.66	1.12	1.61	0.54	86.74	78.62	80.20	0.98	81.85	83.13	8.16E-06
Plbd1	11.51	7.10	8.14	16.25	215.33	188.87	207.80	10.75	204.00	18.98	8.16E-06
Chil3	132.97	70.03	148.92	87.48	1694.19	2847.10	2670.28	109.85	2403.86	21.88	8.41E-06
Xdh	7.65	4.01	7.41	5.35	127.32	92.41	129.34	6.11	116.35	19.05	8.56E-06
Capg	38.24	38.75	46.59	51.93	229.66	221.07	267.11	43.88	239.28	5.45	8.92E-06
Pilrb2	3.86	1.98	4.92	3.52	97.18	95.87	98.03	3.57	97.03	27.19	9.12E-06
Crispld2	3.68	2.68	2.27	4.86	87.38	72.12	97.22	3.37	85.58	25.38	9.12E-06
Itgam	34.94	16.02	25.00	27.16	308.35	289.24	315.00	25.78	304.20	11.80	1.02E-05
Pfkfb4	3.34	5.98	6.27	6.49	101.96	87.53	88.69	5.52	92.73	16.79	1.04E-05
Clec4a2	9.73	5.46	12.80	8.59	155.66	147.96	142.68	9.15	148.77	16.27	1.05E-05
Evi2b	57.60	38.75	46.53	55.29	284.44	263.69	263.03	49.54	270.39	5.46	1.05E-05
Ncf4	48.50	29.82	54.67	35.47	376.97	345.92	391.35	42.11	371.41	8.82	1.06E-05
Gsr	30.64	47.13	34.32	33.11	331.50	257.15	226.24	36.30	271.63	7.48	1.13E-05
Csf2rb	25.12	21.07	32.29	37.39	252.15	229.04	218.29	28.97	233.16	8.05	1.17E-05
Clec12a	42.39	22.21	25.67	20.15	351.76	292.05	323.90	27.60	322.57	11.69	1.19E-05
Csf1r	12.87	14.13	10.28	12.71	85.19	75.45	97.92	12.50	86.19	6.90	1.19E-05
Cfp	33.23	14.64	25.70	25.33	327.90	294.53	402.10	24.72	341.51	13.81	1.20E-05
Pilra	3.75	10.82	6.22	8.89	187.49	204.22	210.48	7.42	200.73	27.06	1.20E-05
Serpinb1a	162.37	90.93	141.08	135.69	1021.92	868.93	926.76	132.52	939.21	7.09	1.21E-05
Ifitm1	4.95	5.78	9.12	7.05	83.23	78.47	71.97	6.73	77.89	11.58	1.36E-05
Anxa2	55.43	20.88	35.32	24.78	682.88	547.52	639.44	34.10	623.28	18.28	1.41E-05

Pram1	2.78	0.90	0.73	1.26	109.33	104.49	90.31	1.42	101.38	71.57	1.48E-05
Lrg1	11.36	3.22	8.72	8.87	282.04	342.05	307.91	8.04	310.67	38.62	1.52E-05
C3	14.67	5.62	6.67	11.33	199.14	191.09	212.92	9.57	201.05	21.00	1.52E-05
Hacd4	5.82	6.38	4.94	5.41	44.10	48.78	46.60	5.64	46.49	8.25	1.54E-05
Clec5a	9.52	13.65	8.88	4.89	167.34	185.20	170.67	9.23	174.40	18.89	1.55E-05
Il18rap	1.72	2.10	4.06	1.81	65.83	59.64	68.81	2.42	64.76	26.75	1.57E-05
Fn1	11.48	8.02	7.35	12.88	144.27	92.86	138.53	9.93	125.22	12.60	1.59E-05
Slpi	55.25	23.08	31.58	33.71	460.16	391.31	402.94	35.90	418.14	11.65	1.59E-05
Pstpip1	8.19	10.02	9.12	10.92	62.87	76.88	58.97	9.56	66.24	6.93	1.67E-05
Slc11a1	2.20	4.57	3.27	3.85	51.31	68.98	69.86	3.47	63.39	18.24	1.73E-05
Vsir	20.91	12.34	22.69	27.14	224.37	211.90	276.57	20.77	237.61	11.44	1.73E-05
Cd33	8.22	3.19	5.35	8.15	176.86	137.89	127.60	6.23	147.45	23.67	1.75E-05
Lilrb4a	19.78	7.94	31.11	26.38	831.35	807.90	949.89	21.30	863.05	40.52	1.80E-05
Fpr2	8.60	5.55	4.43	3.31	108.02	103.99	92.25	5.47	101.42	18.53	1.81E-05
Lilra6	1.20	1.38	2.20	2.81	46.06	55.63	66.60	1.90	56.09	29.58	2.00E-05
B430306N03 Rik	12.02	3.65	4.91	4.28	193.16	168.12	180.25	6.22	180.51	29.03	2.05E-05
Ppm1h	12.68	9.58	14.71	10.49	81.10	75.26	74.52	11.87	76.96	6.49	2.05E-05
Cd300lf	4.27	2.21	8.56	6.01	210.60	163.21	222.10	5.26	198.64	37.77	2.22E-05
Lilr4b	22.48	8.50	30.67	25.44	677.82	596.43	808.45	21.77	694.23	31.88	2.22E-05
Fcnb	25.43	8.92	27.39	11.30	590.31	473.13	558.33	18.26	540.59	29.61	2.22E-05
Il1rn	2.65	3.78	3.00	1.45	66.92	63.61	56.12	2.72	62.22	22.86	2.22E-05
Mrgpra2b	8.54	4.91	10.27	15.70	184.57	199.83	217.79	9.85	200.73	20.37	2.22E-05
Ms4a4c	6.93	5.70	4.40	3.65	75.86	53.39	74.33	5.17	67.86	13.13	2.22E-05
Tmem154	12.59	9.23	12.65	19.04	143.57	107.72	140.95	13.38	130.75	9.77	2.22E-05
Paqr7	6.54	5.39	7.70	4.55	64.20	61.59	50.48	6.04	58.76	9.72	2.22E-05
Rab3d	12.11	11.94	13.86	23.33	145.24	146.81	127.95	15.31	140.00	9.14	2.22E-05
Sirpa	10.69	8.38	6.85	11.72	78.65	73.67	101.67	9.41	84.66	8.99	2.22E-05
Cd63-ps	20.48	12.19	26.32	18.32	219.27	162.77	182.09	19.33	188.04	9.73	2.25E-05
Cd300a	7.79	5.63	6.77	10.65	75.03	66.77	90.18	7.71	77.32	10.03	2.27E-05
Ncam1	8.90	4.70	2.93	4.49	156.38	114.39	101.59	5.25	124.12	23.62	2.34E-05
Siglece	4.73	2.35	4.98	6.65	96.81	85.25	99.38	4.68	93.81	20.06	2.34E-05
Tnfrsf1a	13.16	5.88	7.17	8.38	93.07	101.73	97.20	8.65	97.33	11.25	2.34E-05
Lgals3	31.09	9.99	16.76	22.35	354.32	324.06	400.32	20.05	359.57	17.93	2.44E-05
Myo1f	21.12	6.52	16.32	10.99	337.67	253.24	331.03	13.74	307.31	22.37	2.48E-05
Hsd11b1	5.60	3.65	9.99	7.81	128.23	103.01	124.17	6.77	118.47	17.51	2.48E-05
Il1b	1.27	1.41	0.98	3.57	69.40	80.92	115.07	1.80	88.46	49.04	2.53E-05
Gm6560	57.33	29.08	45.45	60.41	445.28	362.86	402.50	48.07	403.55	8.40	2.60E-05
Cd300lb	11.66	3.76	8.22	10.37	205.45	166.22	188.99	8.50	186.89	21.98	2.62E-05
Pkm	261.99	135.49	205.17	263.45	1814.21	1471.37	1634.32	216.53	1639.97	7.57	2.62E-05
Cebpe	5.06	2.33	6.09	3.80	74.20	80.83	74.60	4.32	76.54	17.72	2.63E-05
Gca	7.11	2.35	7.20	6.29	144.21	142.10	148.86	5.74	145.06	25.29	2.81E-05
Ralb	12.11	12.37	8.72	12.62	61.48	68.72	82.44	11.46	70.88	6.19	3.12E-05
Orm1	1.54	0.66	0.94	1.24	27.43	29.53	28.14	1.09	28.37	25.93	3.18E-05
Ly6c2	178.15	81.70	96.65	96.85	845.68	855.49	899.40	113.34	866.86	7.65	3.18E-05

Slnf2	124.01	81.01	128.49	86.44	482.45	553.55	557.09	104.99	531.03	5.06	3.18E-05
A530064D06 Rik	2.99	1.59	5.33	2.63	79.05	73.18	71.84	3.14	74.69	23.82	3.29E-05
C5ar1	22.29	7.21	13.42	25.71	382.99	390.08	384.67	17.16	385.91	22.49	3.77E-05
Rab27a	27.08	15.41	12.70	21.91	173.01	145.59	162.29	19.28	160.30	8.32	3.79E-05
Trem3	18.98	6.93	19.77	8.38	303.81	236.01	271.36	13.51	270.40	20.01	4.20E-05
Ccl6	35.19	17.53	29.36	48.45	472.69	318.76	431.75	32.63	407.73	12.49	4.20E-05
Cybb	108.21	40.61	82.63	43.20	1020.84	820.69	894.47	68.66	912.00	13.28	4.90E-05
Tarm1	1.84	1.61	2.27	1.35	22.24	27.30	23.20	1.77	24.25	13.74	4.92E-05
Flot2	13.59	26.68	23.83	18.68	130.43	131.50	133.69	20.69	131.87	6.37	4.92E-05
Mxd1	32.29	12.70	27.04	23.70	275.09	230.66	217.85	23.93	241.20	10.08	4.96E-05
C1rl	2.86	4.55	5.51	4.45	40.08	46.30	40.37	4.34	42.25	9.73	4.97E-05
Slc16a3	2.23	3.58	3.56	5.02	40.82	41.00	49.86	3.60	43.89	12.21	5.26E-05
Ifitm3	28.77	65.46	31.64	44.94	344.56	311.93	377.61	42.70	344.70	8.07	5.26E-05
Csf2ra	14.49	9.58	12.49	14.80	62.77	80.66	68.77	12.84	70.73	5.51	5.26E-05
Anxa3	26.90	11.19	13.21	13.63	140.43	145.70	148.38	16.23	144.84	8.92	5.39E-05
Arrb2	11.96	10.48	12.55	7.58	61.08	89.89	67.54	10.64	72.84	6.84	5.48E-05
Ptafr	7.89	2.58	4.67	8.67	134.69	107.84	125.86	5.95	122.80	20.63	5.93E-05
Adam8	9.37	4.86	2.32	5.12	123.11	105.03	121.32	5.42	116.49	21.51	6.05E-05
Pik3r6	3.34	3.88	2.93	3.23	25.14	29.25	40.75	3.35	31.71	9.47	6.12E-05
Lcp1	269.31	116.44	181.41	269.20	1866.43	1592.85	1809.06	209.09	1756.11	8.40	6.16E-05
Igsf6	45.22	11.96	30.08	21.42	450.57	419.88	482.97	27.17	451.14	16.61	6.37E-05
Evi2a	16.68	7.56	14.23	14.37	105.74	96.27	118.79	13.21	106.93	8.10	6.37E-05
Prss57	9.42	7.23	14.14	6.95	84.11	68.36	74.28	9.43	75.58	8.01	6.37E-05
Sorl1	13.62	9.17	25.25	14.45	160.86	146.92	142.15	15.62	149.97	9.60	6.41E-05
Ctsh	29.00	11.50	18.87	15.64	170.94	141.79	194.20	18.75	168.98	9.01	6.52E-05
Rflnb	11.15	5.70	5.72	11.46	107.23	78.23	85.76	8.51	90.41	10.63	6.60E-05
Cd9-ps	2.70	3.11	2.35	2.15	23.07	23.56	23.66	2.58	23.43	9.09	6.74E-05
Ccr1	7.17	3.83	19.58	7.48	245.13	229.92	272.02	9.52	249.03	26.17	7.16E-05
Fgr	6.27	3.40	11.55	14.46	213.69	200.63	216.74	8.92	210.35	23.59	7.69E-05
Ncf1	38.51	12.85	37.32	23.45	367.06	360.62	326.73	28.03	351.47	12.54	7.76E-05
Oas3	3.74	3.76	2.64	5.69	39.73	36.43	56.63	3.95	44.26	11.19	7.76E-05
Lcp2	23.74	27.50	15.31	27.65	140.57	115.29	166.59	23.55	140.82	5.98	7.76E-05
Mtus1	15.68	5.11	7.06	11.08	122.99	117.19	127.65	9.73	122.61	12.60	7.91E-05
Alas1	76.65	39.77	43.68	40.41	250.68	293.42	336.67	50.12	293.59	5.86	8.15E-05
Mpeg1	9.43	6.18	8.38	7.27	48.07	47.23	38.01	7.82	44.44	5.69	8.20E-05
Ceacam10	2.86	1.13	3.67	2.33	46.93	48.22	45.36	2.50	46.83	18.77	8.29E-05
Nadk	34.52	47.77	65.16	62.86	276.03	246.93	272.87	52.58	265.28	5.05	8.29E-05
Fos	11.78	17.38	8.65	22.92	199.87	160.85	371.08	15.18	243.93	16.07	8.54E-05
Plek	35.37	48.86	23.74	38.01	176.74	197.10	197.15	36.50	190.33	5.22	8.54E-05
Ugt1a7c	12.86	7.82	4.57	8.35	103.63	74.68	91.48	8.40	89.93	10.70	8.55E-05
Gimap3	4.79	5.56	3.67	6.34	32.43	55.41	46.84	5.09	44.89	8.82	8.55E-05
Tmem64	25.58	29.72	32.00	35.62	4.48	5.07	6.40	30.73	5.31	0.17	8.80E-05
Gda	8.95	6.75	6.06	20.10	150.75	137.99	148.90	10.46	145.88	13.94	8.86E-05
Rab32	15.06	7.44	16.29	11.69	86.94	87.25	96.30	12.62	90.16	7.14	8.88E-05

Gcnt2	1.60	1.28	2.72	4.17	44.77	44.88	55.78	2.44	48.48	19.88	9.18E-05
Emb	52.72	21.44	21.38	25.83	247.60	230.33	260.17	30.34	246.04	8.11	9.62E-05
Nhsl2	10.36	7.39	8.43	4.42	64.52	55.93	68.06	7.65	62.84	8.21	1.01E-04
Cd300c2	1.25	1.21	0.97	2.03	21.28	16.58	26.26	1.37	21.37	15.64	1.01E-04
F10	5.51	4.45	4.43	2.22	43.52	41.78	47.13	4.15	44.14	10.63	1.01E-04
Oasl2	8.16	3.83	4.38	3.73	40.20	55.72	61.24	5.02	52.38	10.43	1.01E-04
Aldh3b1	13.10	10.55	16.07	27.52	171.03	118.18	159.06	16.81	149.43	8.89	1.01E-04
Mctp1	14.43	9.79	15.82	18.57	77.78	80.11	70.68	14.65	76.19	5.20	1.04E-04
Clec4d	3.92	2.20	2.93	2.17	27.49	25.97	24.49	2.80	25.98	9.27	1.08E-04
Nkg7	48.38	15.59	27.91	20.28	294.19	259.79	256.69	28.04	270.22	9.64	1.14E-04
Vcam1	13.53	12.14	7.51	9.18	147.33	95.76	334.39	10.59	192.49	18.18	1.16E-04
Lbp	8.62	4.45	2.72	5.12	67.91	65.08	55.13	5.22	62.71	12.00	1.17E-04
Clec7a	12.02	11.14	7.35	6.21	89.41	53.29	84.92	9.18	75.88	8.26	1.17E-04
Gm14005	2.32	2.38	1.13	1.09	26.55	25.61	26.27	1.73	26.14	15.12	1.20E-04
Dennd2d	4.47	3.16	3.46	4.72	24.36	35.28	27.51	3.95	29.05	7.35	1.21E-04
Hmox1	15.85	9.69	13.31	16.58	129.69	121.58	349.91	13.86	200.40	14.46	1.24E-04
Cd63	17.39	6.52	18.97	13.78	168.40	129.22	139.05	14.16	145.56	10.28	1.24E-04
Mapk13	5.39	2.15	3.00	1.27	52.57	67.82	59.65	2.95	60.02	20.32	1.25E-04
Slc2a6	1.54	1.76	4.30	0.80	59.95	50.67	74.41	2.10	61.68	29.37	1.27E-04
Hcst	2.86	2.35	2.40	4.04	23.31	26.30	22.71	2.91	24.11	8.28	1.29E-04
Tubb6	1.05	0.79	2.06	0.98	27.04	17.20	21.41	1.22	21.88	17.91	1.30E-04
Hk3	26.15	6.18	17.45	10.35	263.93	212.35	240.67	15.03	238.98	15.90	1.32E-04
B4galt6	1.93	0.97	1.69	2.56	28.06	25.18	22.03	1.79	25.09	14.03	1.32E-04
Gm19719	1.19	1.08	0.77	0.75	14.18	11.33	14.27	0.95	13.26	13.99	1.32E-04
Gapt	15.85	5.55	13.52	12.44	120.29	99.02	110.21	11.84	109.84	9.28	1.42E-04
Nupr1	1.51	3.12	1.90	2.04	23.43	18.81	28.45	2.14	23.56	11.00	1.42E-04
Naaa	8.37	5.32	7.41	5.10	33.72	39.97	40.86	6.55	38.19	5.83	1.43E-04
Ahnak	12.86	7.59	14.21	12.83	63.43	58.93	60.82	11.87	61.06	5.14	1.45E-04
Sort1	5.66	8.64	5.22	6.91	42.06	34.15	34.19	6.61	36.80	5.57	1.53E-04
Arg2	2.36	1.58	0.89	3.21	37.68	30.89	39.74	2.01	36.11	17.99	1.59E-04
Gm7823	9.74	3.69	6.82	10.45	77.35	67.28	79.86	7.67	74.83	9.75	1.61E-04
Adam15	2.44	2.01	1.27	1.76	18.09	24.72	17.00	1.87	19.94	10.66	1.61E-04
Pilrb1	1.58	0.64	5.19	1.60	88.77	79.75	98.12	2.25	88.88	39.50	1.62E-04
Rab44	17.41	10.76	8.49	6.44	74.34	106.58	84.59	10.78	88.51	8.21	1.62E-04
Itgal	21.69	8.10	10.17	12.62	88.67	104.20	95.27	13.15	96.05	7.31	1.64E-04
Gm5483	1.72	0.89	0.74	0.72	15.55	15.28	17.46	1.02	16.10	15.81	1.65E-04
Lst1	3.19	2.33	2.08	2.56	18.58	17.64	19.73	2.54	18.65	7.34	1.68E-04
Lin28a	0.75	1.41	1.34	1.32	29.09	17.83	13.29	1.21	20.07	16.65	1.71E-04
Cxcl2	1.17	0.41	0.21	1.44	53.24	51.44	172.24	0.81	92.31	114.03	1.72E-04
Id2	31.75	10.48	17.95	19.56	160.36	136.40	160.55	19.93	152.44	7.65	1.74E-04
Soat1	26.09	8.51	11.76	13.40	122.44	113.24	127.27	14.94	120.98	8.10	1.77E-04
Id1	0.87	1.61	1.85	1.50	14.08	19.95	19.53	1.46	17.85	12.25	1.85E-04
Gm7676	1.27	2.84	2.23	2.47	21.14	22.10	22.09	2.20	21.78	9.89	1.86E-04
Tagap	4.42	2.03	3.11	2.76	21.32	37.95	38.03	3.08	32.44	10.54	1.94E-04

Hpcal1	11.93	6.47	8.54	16.55	71.15	72.05	82.76	10.87	75.32	6.93	1.94E-04
Slnf1	12.21	2.52	9.92	13.45	237.14	199.66	237.49	9.53	224.76	23.59	1.96E-04
Sirpb1b	0.81	1.34	3.34	2.16	46.46	29.01	46.42	1.91	40.63	21.26	1.96E-04
App	9.04	3.53	9.30	9.24	71.77	73.22	65.64	7.78	70.21	9.03	1.96E-04
Rbm47	8.28	9.81	4.90	11.59	66.72	52.24	56.24	8.65	58.40	6.75	1.96E-04
Cyth4	28.98	10.73	32.42	21.39	174.45	197.37	199.57	23.38	190.46	8.15	2.08E-04
Icosl	0.63	1.74	2.14	1.86	27.61	24.02	31.51	1.59	27.71	17.41	2.11E-04
Agpat2	3.62	5.52	6.06	10.22	47.03	49.84	55.05	6.35	50.64	7.97	2.14E-04
Fpr1	4.86	1.43	8.80	9.70	192.85	198.18	189.23	6.20	193.42	31.21	2.18E-04
Tnfrsf1b	7.95	7.49	7.85	10.50	31.15	53.72	46.52	8.45	43.80	5.18	2.21E-04
Klf6	43.41	27.78	31.23	52.88	174.12	170.36	283.85	38.83	209.44	5.39	2.21E-04
Pla2g7	0.93	4.52	4.80	1.96	98.78	64.81	78.91	3.05	80.84	26.48	2.25E-04
Rasgrp4	2.91	0.78	4.19	2.55	55.57	62.90	55.35	2.61	57.94	22.20	2.25E-04
Apobr	3.44	1.68	4.28	0.86	63.69	53.99	53.52	2.57	57.07	22.24	2.26E-04
Zyx	28.47	38.03	18.50	45.32	178.82	194.04	160.21	32.58	177.69	5.45	2.41E-04
Stfa2l1	0.84	1.69	1.76	0.88	17.34	15.62	14.95	1.29	15.97	12.36	2.43E-04
Ffar2	3.83	1.05	3.19	1.91	38.69	39.76	31.89	2.49	36.78	14.74	2.49E-04
Mpo	874.82	264.36	390.41	324.49	3927.09	3550.09	3571.30	463.52	3682.83	7.95	2.50E-04
G0s2	0.96	0.43	2.82	1.73	40.10	48.08	43.01	1.49	43.73	29.39	2.55E-04
Bhlhe40	3.22	1.30	2.53	1.42	20.96	23.02	33.29	2.12	25.75	12.15	2.55E-04
Ebi3	9.73	2.58	6.00	4.20	55.69	64.52	66.57	5.63	62.26	11.06	2.57E-04
Scnn1a	1.21	1.35	1.53	0.60	13.36	15.77	17.11	1.17	15.41	13.16	2.74E-04
Cd68	15.76	9.58	4.27	9.57	97.63	84.23	158.67	9.80	113.51	11.59	2.77E-04
Ctsg	46.66	14.47	18.77	15.50	217.40	201.96	177.23	23.85	198.86	8.34	2.77E-04
Sgms2	12.83	2.89	5.17	4.71	79.19	71.12	78.76	6.40	76.36	11.93	2.88E-04
Csf2rb2	3.95	2.90	2.53	5.89	31.62	28.80	25.86	3.82	28.76	7.54	2.88E-04
Nod1	1.57	1.94	2.40	5.72	44.14	34.67	33.23	2.91	37.35	12.85	2.88E-04
Inhba	0.12	1.41	0.76	0.78	55.20	54.19	43.61	0.77	51.00	66.52	2.88E-04
Ltb4r1	2.11	1.64	7.62	6.67	98.49	82.13	96.79	4.51	92.47	20.51	2.88E-04
Tuba8	6.52	2.92	3.64	4.72	33.72	25.76	33.65	4.45	31.04	6.97	2.88E-04
Cd300ld	3.84	0.58	3.23	1.42	78.20	53.90	81.04	2.26	71.04	31.37	2.90E-04
Abcd2	4.61	1.53	3.66	2.74	60.44	25.11	50.37	3.14	45.31	14.44	3.13E-04
Sowahc	0.90	1.12	0.90	0.70	8.86	8.75	15.51	0.91	11.04	12.19	3.16E-04
Osm	9.94	3.58	6.14	9.18	49.48	64.28	98.70	7.21	70.82	9.82	3.17E-04
Lpl	3.65	5.26	4.85	3.75	34.96	23.38	64.57	4.38	40.97	9.36	3.17E-04
Ccr2	40.28	10.73	20.16	23.77	248.51	160.39	231.35	23.74	213.42	8.99	3.17E-04
F630028O10 Rik	20.97	7.67	16.40	8.43	118.43	90.08	188.65	13.37	132.39	9.91	3.18E-04
Fosl2	6.30	4.65	3.14	5.51	26.10	27.70	35.46	4.90	29.75	6.07	3.19E-04
Ms4a4a	0.78	0.97	0.92	0.62	10.79	7.02	12.72	0.82	10.18	12.34	3.21E-04
Ear2	2.10	4.46	2.74	1.29	23.97	33.80	40.51	2.65	32.76	12.37	3.24E-04
Cst7	10.60	4.50	11.55	6.03	63.46	55.45	52.86	8.17	57.26	7.01	3.31E-04
Ly6c1	2.70	1.16	2.10	1.57	15.64	16.29	18.70	1.88	16.88	8.97	3.39E-04
5830432E09 Rik	1.88	3.44	2.00	1.95	15.18	19.65	16.73	2.31	17.18	7.43	3.42E-04

Caprin2	9.64	12.22	11.26	5.04	0.62	0.78	0.80	9.54	0.73	0.08	3.59E-04
Ptgs1	5.60	6.87	6.48	1.66	72.32	65.64	68.77	5.15	68.91	13.38	3.63E-04
Gm14548	7.97	2.35	1.27	3.96	67.77	67.78	76.43	3.89	70.66	18.17	3.65E-04
Prtn3	147.49	41.79	71.07	47.55	557.86	622.36	592.24	76.97	590.82	7.68	3.74E-04
Slc31a2	4.25	5.72	13.13	7.68	59.30	49.13	65.47	7.70	57.97	7.53	3.74E-04
Pak1	7.35	11.14	4.80	7.17	35.97	53.93	42.09	7.61	44.00	5.78	3.80E-04
Galnt6	1.45	2.86	1.45	1.32	14.07	16.43	15.55	1.77	15.35	8.68	3.86E-04
Fmo5	5.99	3.48	7.96	3.36	37.26	41.16	31.57	5.20	36.66	7.05	3.92E-04
Syne1	4.10	5.88	15.08	6.39	67.22	63.49	66.41	7.86	65.71	8.36	4.00E-04
Fcgr4	2.56	0.56	1.03	2.02	31.96	20.95	33.93	1.54	28.95	18.77	4.19E-04
Il1f9	3.28	0.36	4.48	1.35	108.24	122.85	112.95	2.37	114.68	48.45	4.19E-04
RP24-427L24.1	2.42	1.30	1.85	2.80	18.28	14.72	16.09	2.09	16.36	7.83	4.19E-04
Pstpip2	1.87	1.30	1.05	0.44	16.94	18.81	19.22	1.17	18.32	15.72	4.27E-04
Sqrdl	7.86	17.40	14.73	19.27	108.64	67.80	83.85	14.82	86.76	5.85	4.33E-04
Pi16	1.21	0.31	1.16	3.21	42.11	55.24	48.32	1.47	48.55	33.03	4.37E-04
Gm11505	41.26	9.30	17.27	13.73	197.38	178.35	176.02	20.39	183.92	9.02	4.48E-04
C5ar2	3.25	6.18	4.71	5.32	24.43	26.99	22.92	4.87	24.78	5.09	4.50E-04
Ms4a3	48.95	10.84	33.24	12.96	345.44	333.76	277.38	26.50	318.86	12.03	4.58E-04
Mir22hg	1.78	1.69	0.71	3.07	22.74	22.12	26.52	1.81	23.79	13.13	4.64E-04
Gm15922	1.29	3.26	2.36	5.47	49.57	30.08	35.79	3.10	38.48	12.43	4.70E-04
G6pd2	2.43	3.41	2.71	1.98	15.21	14.45	16.27	2.63	15.31	5.82	4.80E-04
Clec4e	1.51	0.89	0.47	5.46	64.77	62.04	79.62	2.08	68.81	33.03	4.82E-04
6430548M08Rik	5.21	2.81	0.84	3.18	57.35	50.82	45.49	3.01	51.22	17.00	4.88E-04
Gpx3	2.92	2.15	3.61	7.04	28.92	34.41	34.25	3.93	32.53	8.28	4.88E-04
Elane	540.25	140.92	275.92	158.78	2401.09	2093.00	2279.65	278.97	2257.91	8.09	4.88E-04
Ms4a4b	3.13	1.84	5.85	4.75	28.74	33.91	38.01	3.89	33.55	8.62	4.96E-04
Lpcat2	3.65	3.02	6.74	10.45	58.97	46.85	51.28	5.96	52.37	8.78	5.00E-04
F13a1	120.41	31.36	49.87	70.91	472.42	436.99	616.40	68.14	508.61	7.46	5.01E-04
Ggt5	1.87	2.15	1.45	2.41	11.68	12.67	13.31	1.97	12.55	6.38	5.01E-04
Prok2	0.60	0.13	0.16	1.47	35.63	26.99	35.57	0.59	32.73	55.40	5.02E-04
Epx	0.33	0.10	0.16	1.63	30.70	36.50	31.16	0.56	32.79	59.03	5.13E-04
Sirpb1c	0.77	3.32	2.45	2.04	43.71	20.73	46.39	2.15	36.94	17.21	5.13E-04
Dram1	5.15	1.33	0.71	2.20	43.86	44.59	44.84	2.35	44.43	18.92	5.26E-04
AA467197	1.08	0.37	1.37	1.66	17.54	20.62	16.82	1.12	18.33	16.35	5.26E-04
Cldn15	6.09	1.10	1.32	0.83	56.43	39.71	55.67	2.33	50.61	21.70	5.34E-04
Ms4a6c	45.17	19.24	15.10	19.36	132.15	127.43	153.11	24.72	137.56	5.57	5.43E-04
Ifit1bl2	1.24	0.41	1.69	1.64	16.93	23.65	18.43	1.25	19.67	15.78	5.59E-04
9830107B12Rik	0.79	0.10	0.62	1.91	55.01	46.05	50.62	0.86	50.56	59.06	5.66E-04
Atp1a3	7.95	3.04	3.37	2.15	32.71	41.12	34.42	4.13	36.08	8.74	5.66E-04
Gm45836	52.17	21.13	39.62	30.68	4.40	7.02	5.89	35.90	5.77	0.16	5.66E-04
C1qb	5.21	1.84	3.56	5.64	33.62	41.45	100.89	4.06	58.65	14.44	5.77E-04
Al839979	3.86	1.30	3.61	2.66	25.68	23.19	22.58	2.86	23.81	8.33	6.00E-04
Il1r2	3.83	0.36	4.88	3.10	148.40	129.20	149.58	3.04	142.39	46.82	6.01E-04

Trim30b	4.96	1.89	2.52	10.13	79.20	50.62	71.54	4.87	67.12	13.77	6.01E-04
Trem1	0.33	2.04	0.82	4.11	68.65	50.15	113.61	1.83	77.47	42.41	6.06E-04
Prg2	16.99	18.09	2.66	5.54	172.24	244.10	218.79	10.82	211.71	19.57	6.06E-04
Atp8b4	20.91	4.45	14.29	9.78	118.95	116.04	106.53	12.35	113.84	9.21	6.07E-04
Pxylp1	16.72	3.96	7.88	6.98	73.88	62.18	76.44	8.89	70.83	7.97	6.28E-04
Scrg1	1.48	0.56	1.53	0.78	10.47	14.03	12.16	1.09	12.22	11.25	6.34E-04
Trpm2	2.11	0.43	3.03	0.93	38.00	26.92	44.55	1.63	36.49	22.43	6.37E-04
Cep19	5.81	8.61	9.07	15.11	45.25	62.04	43.69	9.65	50.33	5.22	6.44E-04
Ikbke	4.49	2.02	2.53	4.20	18.73	23.47	37.53	3.31	26.58	8.03	6.45E-04
Serpinb10	2.16	2.88	1.82	4.34	17.01	23.78	17.38	2.80	19.39	6.93	6.60E-04
4930438A08 Rik	5.63	0.49	2.64	0.72	78.03	84.15	77.37	2.37	79.85	33.70	6.66E-04
Nbeal2	4.16	4.32	5.32	5.85	19.17	35.31	21.11	4.91	25.20	5.13	6.66E-04
Cd302	3.80	2.25	3.93	4.40	22.19	15.98	23.96	3.59	20.71	5.77	6.69E-04
Blvrb	148.36	434.60	321.92	246.74	53.19	51.70	54.72	287.90	53.20	0.18	6.69E-04
Trim2	22.65	25.02	14.00	15.94	2.15	3.52	4.04	19.40	3.24	0.17	6.84E-04
BC100530	0.44	0.20	0.32	0.63	5.56	5.92	7.46	0.39	6.31	16.01	6.95E-04
1700047M1 1Rik	0.78	0.66	3.27	0.60	28.43	17.69	26.21	1.33	24.11	18.16	7.00E-04
Gm13810	1.84	1.00	1.38	1.88	12.75	9.38	11.20	1.52	11.11	7.29	7.06E-04
Gm13812	1.84	1.00	1.38	1.88	12.75	9.38	11.20	1.52	11.11	7.29	7.06E-04
Lyst	10.54	10.63	10.49	4.71	40.50	55.81	44.18	9.09	46.83	5.15	7.19E-04
Tlr4	4.94	4.09	2.08	4.11	39.81	27.58	18.52	3.81	28.64	7.52	7.56E-04
Dse	0.99	0.69	0.92	0.34	8.19	7.99	10.24	0.74	8.81	11.97	7.75E-04
Trbc1	0.57	0.71	0.87	0.17	8.17	13.34	15.10	0.58	12.20	21.03	8.29E-04
Lrp4	2.80	3.04	2.95	4.45	19.50	12.60	19.94	3.31	17.35	5.24	8.29E-04
Dusp1	2.77	5.80	4.09	4.94	23.40	19.78	40.14	4.40	27.78	6.31	8.42E-04
Gpr65	5.57	2.50	1.58	0.85	34.96	34.72	35.26	2.63	34.98	13.31	8.54E-04
Arl11	3.95	4.91	8.28	9.18	43.00	29.25	34.05	6.58	35.43	5.39	8.54E-04
Gm16194	0.69	0.59	0.18	0.23	7.00	7.56	7.67	0.42	7.41	17.45	8.66E-04
Igha	1.57	1.99	39.59	1.66	1017.02	460.16	516.40	11.20	664.53	59.32	8.67E-04
Fam129a	2.62	8.71	10.20	9.83	80.13	51.96	81.63	7.84	71.24	9.08	9.23E-04
Ica1	6.21	2.48	5.56	6.44	41.07	25.78	30.64	5.17	32.49	6.28	9.36E-04
Slc7a11	0.22	0.13	0.90	1.30	16.61	22.62	30.65	0.64	23.30	36.59	9.45E-04
Mefv	0.39	2.02	2.21	0.78	21.70	20.09	24.33	1.35	22.04	16.32	9.45E-04
Naip6	1.34	1.31	0.71	1.42	11.53	7.41	9.27	1.19	9.40	7.87	9.45E-04
RP23- 269O24.7	0.66	0.31	0.74	0.98	8.51	8.63	6.38	0.67	7.84	11.66	9.58E-04
Clec4a1	2.95	0.33	0.69	0.91	25.33	17.81	30.19	1.22	24.44	20.05	9.69E-04
Gm20406	0.36	0.23	0.51	0.33	4.18	4.81	3.94	0.36	4.31	12.03	1.02E-03
Ppp1r3b	2.71	0.95	0.74	3.49	21.65	24.45	32.49	1.97	26.19	13.28	1.04E-03
Ccl5	0.84	4.68	4.32	2.74	30.78	55.41	43.96	3.15	43.38	13.79	1.05E-03
F730016J06 Rik	0.48	0.18	0.98	0.88	9.67	10.99	12.25	0.63	10.97	17.44	1.07E-03
Tnnt1	1.42	1.79	2.40	2.33	17.12	10.63	9.80	1.98	12.52	6.31	1.08E-03
Asprv1	0.24	0.43	3.95	1.14	35.35	47.92	56.67	1.44	46.65	32.35	1.09E-03

Abhd5	5.96	15.00	7.62	13.68	66.43	54.03	42.34	10.57	54.27	5.14	1.09E-03
I830077J02R ik	5.63	4.78	2.00	0.85	45.94	40.78	55.32	3.32	47.35	14.27	1.11E-03
Ifi204	1.05	0.48	0.30	2.75	22.76	18.85	47.62	1.15	29.74	25.97	1.12E-03
Kcnj2	0.84	2.33	1.40	1.55	16.08	10.34	9.93	1.53	12.12	7.92	1.15E-03
Gpc1	5.28	4.26	1.56	3.09	19.72	39.12	27.80	3.55	28.88	8.14	1.17E-03
Dgkg	4.76	3.22	1.77	5.25	25.11	19.52	32.43	3.75	25.69	6.85	1.19E-03
Mrgpra2a	2.82	0.48	3.91	3.31	40.30	50.76	53.71	2.63	48.25	18.34	1.20E-03
Cd3e	0.81	1.43	0.29	0.67	10.54	12.46	8.22	0.80	10.41	12.98	1.23E-03
Tlr2	3.89	10.09	7.41	7.66	28.48	52.43	35.40	7.26	38.77	5.34	1.25E-03
Ldhb	2.29	1.97	6.07	3.11	18.20	21.90	34.14	3.36	24.75	7.36	1.25E-03
Dgat2	2.23	0.13	0.98	0.28	32.61	29.63	31.42	0.90	31.22	34.52	1.26E-03
Ptgir	2.29	0.26	0.21	1.79	36.32	37.07	37.97	1.14	37.12	32.70	1.26E-03
Prom1	0.33	2.15	4.16	1.68	47.05	40.19	45.88	2.08	44.37	21.32	1.33E-03
Card9	2.26	1.30	3.06	3.10	15.18	17.06	12.09	2.43	14.78	6.08	1.34E-03
Grk3	2.05	1.33	3.37	2.74	11.31	18.19	15.81	2.37	15.10	6.36	1.36E-03
Cdh23	0.42	1.51	0.50	0.70	8.19	6.90	9.11	0.78	8.07	10.31	1.38E-03
Reck	1.05	4.52	3.48	2.10	21.80	21.90	25.93	2.79	23.21	8.32	1.38E-03
Cr2	0.93	1.43	1.05	0.72	6.11	7.23	7.36	1.04	6.90	6.66	1.39E-03
Gm14699	0.62	0.43	0.70	0.82	5.14	4.40	5.62	0.64	5.05	7.87	1.48E-03
Gpr141	3.58	2.22	0.63	6.36	61.13	38.48	55.48	3.20	51.70	16.15	1.53E-03
Tlr13	1.42	1.20	1.74	0.10	45.60	33.86	49.10	1.12	42.85	38.43	1.55E-03
Gm16459	0.76	0.33	0.48	0.78	5.44	4.90	5.37	0.59	5.24	8.91	1.57E-03
Lrp1	3.28	1.71	1.16	0.96	16.72	10.34	15.90	1.78	14.32	8.06	1.59E-03
Cd209a	3.13	2.48	1.16	1.66	12.52	13.20	12.12	2.11	12.61	5.99	1.61E-03
Nphp1	4.88	6.36	2.79	6.26	0.49	0.69	0.27	5.07	0.49	0.10	1.63E-03
5730416F02 Rik	0.74	0.86	0.72	1.02	5.37	4.60	6.16	0.84	5.38	6.42	1.65E-03
Ly6a	2.20	1.88	4.33	4.43	13.51	23.04	29.91	3.21	22.15	6.90	1.66E-03
Trem14	0.24	0.54	1.66	1.06	10.64	11.34	24.22	0.87	15.40	17.60	1.70E-03
Dhrs9	0.15	0.10	1.32	0.98	25.95	25.21	15.01	0.64	22.06	34.54	1.71E-03
Rhd	20.48	299.87	172.15	157.08	3.36	4.54	3.98	162.39	3.96	0.02	1.72E-03
C1qa	0.87	1.20	0.76	0.52	6.98	5.97	21.95	0.84	11.63	13.86	1.74E-03
Fgd4	8.95	1.84	3.77	1.73	33.75	39.57	32.24	4.07	35.18	8.64	1.75E-03
Bmx	3.52	0.38	1.34	1.37	19.42	19.88	30.44	1.66	23.25	14.04	1.83E-03
Fas	2.50	1.12	4.27	3.49	30.70	14.22	28.82	2.85	24.58	8.63	1.83E-03
Slco4c1	1.69	0.23	2.95	2.28	40.57	46.06	33.25	1.79	39.96	22.37	1.84E-03
Gm5398	0.58	0.33	0.51	0.40	3.73	3.31	4.02	0.45	3.69	8.12	1.89E-03
Cask	2.59	2.12	4.09	6.18	27.76	17.00	19.36	3.75	21.37	5.71	1.90E-03
Pla2g12a	27.56	87.30	52.93	52.88	7.47	14.51	7.84	55.17	9.94	0.18	1.91E-03
P2ry13	1.57	0.15	2.64	1.06	29.52	39.88	34.97	1.35	34.79	25.69	1.92E-03
Fcer2a	2.50	2.27	9.01	1.09	28.72	42.35	60.61	3.72	43.89	11.80	1.93E-03
P2rx7	0.78	1.81	1.05	1.60	6.58	10.11	8.82	1.31	8.50	6.47	1.94E-03
Nt5e	0.09	0.05	0.13	1.45	13.09	13.74	17.64	0.43	14.82	34.43	1.95E-03
Tbxas1	3.68	3.81	5.03	2.64	16.38	14.03	34.31	3.79	21.57	5.69	1.95E-03

Dock5	2.71	4.75	9.23	5.77	36.67	36.38	21.80	5.61	31.62	5.63	1.98E-03
Il13ra1	0.72	0.13	1.05	0.05	15.46	19.71	20.88	0.49	18.69	38.19	1.99E-03
Ankrd22	1.93	2.68	0.47	2.48	18.18	24.52	18.48	1.89	20.39	10.78	2.02E-03
Stk39	1.17	0.15	0.66	0.47	11.23	7.82	8.16	0.61	9.07	14.79	2.03E-03
Acvr2a	2.70	6.34	5.17	4.98	0.71	0.31	0.61	4.80	0.54	0.11	2.05E-03
Olfrml2b	5.75	1.00	2.98	0.47	42.01	45.85	37.88	2.55	41.91	16.44	2.06E-03
Ifnlr1	0.63	0.20	0.87	0.80	6.04	7.66	6.99	0.63	6.89	10.99	2.06E-03
B230208H11 Rik	3.07	4.70	4.06	1.11	26.20	23.09	20.02	3.24	23.10	7.14	2.07E-03
RP24- 531B21.3	0.30	1.28	0.85	0.85	7.57	6.71	8.89	0.82	7.72	9.42	2.07E-03
Lpcat4	3.28	0.74	2.14	0.98	14.70	13.82	15.55	1.79	14.69	8.23	2.08E-03
Ldlr	3.19	7.26	9.12	2.10	45.62	38.88	30.36	5.42	38.29	7.07	2.13E-03
Ccl3	0.33	0.36	0.45	2.59	9.03	15.24	26.52	0.93	16.93	18.18	2.16E-03
2210406H18 Rik	1.05	1.38	2.87	0.67	9.70	11.99	12.55	1.50	11.41	7.63	2.17E-03
Klrk1	2.41	1.53	0.63	1.97	8.44	18.33	21.93	1.64	16.23	9.93	2.19E-03
Mocos	0.60	0.61	0.24	0.03	16.60	17.93	15.24	0.37	16.59	44.86	2.21E-03
Tnfsf13b	0.96	1.23	1.87	0.13	24.62	18.69	26.95	1.05	23.42	22.35	2.24E-03
Gfi1b	29.82	257.18	128.47	130.36	10.22	6.02	9.56	136.46	8.60	0.06	2.24E-03
Dtx4	1.39	0.26	0.53	1.09	9.15	7.18	11.86	0.81	9.40	11.55	2.32E-03
Stxbp1	10.36	24.48	17.45	10.45	2.52	3.78	2.77	15.69	3.03	0.19	2.37E-03
Jaml	6.81	1.28	5.14	4.29	31.95	28.73	37.61	4.38	32.77	7.48	2.39E-03
Ms4a2	2.26	1.92	1.08	4.22	23.24	16.21	11.36	2.37	16.94	7.15	2.39E-03
Cep170b	4.22	6.13	4.48	9.21	1.14	0.88	0.51	6.01	0.84	0.14	2.47E-03
Cd3d	1.24	0.82	1.58	0.44	5.99	9.63	8.96	1.02	8.19	8.04	2.48E-03
Rin2	1.72	3.19	2.08	4.06	11.13	19.02	12.41	2.76	14.19	5.13	2.51E-03
Jchain	0.78	3.63	38.72	1.66	337.04	353.21	232.76	11.20	307.67	27.48	2.56E-03
Tmem38b	5.96	0.87	3.51	4.40	42.65	31.41	29.56	3.68	34.54	9.38	2.59E-03
Rara	1.99	1.46	2.08	4.40	12.87	11.11	14.85	2.48	12.94	5.21	2.61E-03
Eps8l1	9.04	3.63	4.98	4.99	0.94	0.83	0.94	5.66	0.90	0.16	2.61E-03
AY036118	3550.15	5472.15	2590.06	2751.42	293.81	1151.94	625.84	3590.9 5	690.53	0.19	2.64E-03
NlrX1	1.14	6.64	2.92	3.90	29.85	23.55	25.86	3.65	26.42	7.23	2.66E-03
Fgl2	7.02	1.23	2.66	2.12	24.86	18.57	28.24	3.26	23.89	7.33	2.66E-03
Tnfsf14	1.66	0.92	1.03	0.10	16.90	18.71	27.07	0.93	20.89	22.53	2.72E-03
Elovl7	0.12	1.51	0.16	0.18	6.43	9.82	10.21	0.49	8.82	17.93	2.83E-03
Aldh1a7	2.29	33.20	18.55	21.88	0.82	0.13	0.19	18.98	0.38	0.02	2.89E-03
Inpp4b	1.24	1.18	2.69	1.01	12.96	7.09	8.12	1.53	9.39	6.15	2.91E-03
Tmem38a	1.54	0.18	0.87	0.70	7.92	9.63	22.32	0.82	13.29	16.19	3.04E-03
Il18bp	1.57	4.06	4.47	3.59	12.79	18.22	21.23	3.42	17.41	5.09	3.07E-03
Gpr27	0.18	0.54	0.84	0.23	4.43	5.02	4.66	0.45	4.70	10.49	3.09E-03
Trem2	2.05	0.69	1.90	1.29	6.75	9.99	10.83	1.48	9.19	6.20	3.18E-03
Haao	11.06	2.43	6.70	7.19	32.26	33.67	48.22	6.84	38.05	5.56	3.19E-03
Aif1	3.92	1.81	2.21	2.04	8.49	12.48	21.62	2.50	14.20	5.69	3.19E-03
Hcar2	2.89	0.26	3.93	0.67	21.90	45.25	111.83	1.94	59.66	30.80	3.22E-03

Rap1gap2	0.81	0.08	0.08	1.94	20.53	24.87	22.46	0.73	22.62	31.10	3.39E-03
Ly75	3.01	0.79	5.98	2.27	24.19	29.55	20.20	3.01	24.65	8.18	3.40E-03
Gpr35	0.09	2.30	0.11	0.10	15.10	13.89	13.35	0.65	14.11	21.71	3.42E-03
Gm13431	0.33	0.59	0.34	1.09	4.38	3.92	5.93	0.59	4.75	8.08	3.44E-03
Fgd2	23.11	4.24	10.07	6.83	48.47	62.47	75.64	11.06	62.19	5.62	3.48E-03
Sirpb1a	0.50	0.33	0.30	2.86	16.21	7.40	18.76	1.00	14.13	14.17	3.57E-03
Zfpm1	4.55	7.90	4.59	4.19	1.21	1.02	0.57	5.31	0.93	0.18	3.60E-03
Upp1	0.75	0.77	0.05	0.08	8.34	12.37	11.14	0.41	10.62	25.73	3.67E-03
Abcb4	11.82	60.45	61.41	55.77	2.86	5.58	5.44	47.36	4.63	0.10	3.69E-03
Itpripl2	1.05	0.87	2.66	0.23	13.76	24.68	10.24	1.20	16.23	13.47	3.76E-03
Aifm2	0.87	1.84	1.69	3.60	14.15	9.34	11.45	2.00	11.65	5.82	3.76E-03
L1cam	1.64	0.33	1.46	1.11	9.35	8.88	8.75	1.13	8.99	7.93	3.77E-03
Cib2	2.08	1.05	1.45	2.02	5.29	10.75	11.71	1.65	9.25	5.61	3.77E-03
Smox	1.11	6.01	2.14	2.10	15.24	15.50	24.22	2.84	18.32	6.46	3.79E-03
Gm43857	7.17	13.28	10.77	4.90	1.05	2.16	1.44	9.03	1.55	0.17	3.80E-03
Cpox	15.06	130.57	60.44	61.05	6.80	5.42	3.04	66.78	5.09	0.08	3.82E-03
1600010M07Rik	0.81	0.03	0.42	0.18	8.93	13.48	9.64	0.36	10.68	29.72	3.86E-03
Nfia	52.45	430.71	291.13	230.92	25.28	19.62	19.03	251.30	21.31	0.08	3.91E-03
Cpa3	4.61	1.84	3.87	0.85	53.32	31.77	12.78	2.79	32.62	11.67	3.92E-03
Spic	0.12	1.76	1.50	0.28	11.41	15.93	36.00	0.92	21.11	23.00	4.02E-03
Fcna	1.48	4.50	3.66	1.66	16.01	16.74	80.98	2.82	37.91	13.43	4.02E-03
Ccl4	1.45	1.94	0.90	4.09	10.81	11.79	31.71	2.09	18.11	8.65	4.05E-03
Minpp1	18.66	125.59	91.48	78.39	4.95	8.87	9.08	78.53	7.64	0.10	4.07E-03
Cd5l	2.41	0.18	0.82	2.59	23.01	17.05	71.95	1.50	37.34	24.92	4.13E-03
Stfa1	1.07	0.06	0.50	0.58	8.48	10.85	11.82	0.55	10.38	18.79	4.24E-03
Ccr5	0.18	0.92	0.66	0.47	4.31	8.33	4.05	0.56	5.56	9.99	4.24E-03
Chd7	1.72	4.47	8.36	5.56	20.98	30.65	30.15	5.03	27.26	5.42	4.26E-03
Acvrl1	2.29	0.15	0.98	1.58	20.73	13.58	22.48	1.25	18.93	15.16	4.30E-03
Jag1	0.21	0.49	0.92	0.49	4.48	3.69	4.06	0.53	4.07	7.72	4.31E-03
Car1	229.89	3651.04	2420.16	2338.38	79.89	102.72	45.06	2159.87	75.89	0.04	4.32E-03
Slco3a1	2.77	2.27	0.34	1.45	18.13	16.15	13.64	1.71	15.97	9.34	4.34E-03
Nlrp12	0.18	0.08	3.08	0.91	21.57	23.09	30.71	1.06	25.13	23.66	4.37E-03
Cldn13	7.02	164.64	79.71	65.73	1.51	3.07	1.00	79.27	1.86	0.02	4.38E-03
S100a4	4.94	1.07	1.58	1.01	13.09	13.25	12.81	2.15	13.05	6.07	4.47E-03
Lrrc25	2.59	0.15	2.24	0.13	28.01	28.20	34.33	1.28	30.18	23.60	4.52E-03
Fcgrt	6.18	2.10	1.27	1.71	15.14	14.10	44.78	2.81	24.68	8.78	4.52E-03
Gm5150	0.48	2.07	0.16	2.51	19.45	18.29	21.84	1.30	19.86	15.22	4.52E-03
Clstn1	5.42	35.78	31.00	27.63	0.69	2.38	2.30	24.96	1.79	0.07	4.72E-03
Arsg	0.72	2.30	3.51	1.68	15.66	8.54	16.37	2.05	13.52	6.59	4.75E-03
Mmp14	3.46	21.03	14.66	13.61	1.41	1.57	0.80	13.19	1.26	0.10	4.75E-03
Hnmt	1.57	1.81	0.37	4.71	19.74	19.36	20.86	2.11	19.99	9.45	4.86E-03
Atp7b	5.54	115.29	68.80	51.38	1.26	2.76	0.70	60.25	1.57	0.03	4.89E-03
Atp1b2	16.90	208.56	152.04	144.14	4.13	8.68	6.48	130.41	6.43	0.05	4.92E-03

Olfm4	1.57	0.18	1.40	0.03	30.13	21.62	46.15	0.79	32.63	41.20	5.01E-03
Marveld1	1.02	1.41	0.32	0.34	7.05	7.73	4.43	0.77	6.40	8.31	5.03E-03
Ccdc180	1.08	0.20	1.05	0.52	6.21	5.78	5.46	0.72	5.82	8.13	5.03E-03
Klrb1f	4.88	2.96	3.27	0.52	23.36	25.09	26.56	2.91	25.00	8.60	5.06E-03
Tbc1d2	1.11	1.69	3.22	1.84	12.07	6.11	11.34	1.96	9.84	5.01	5.20E-03
Alcam	1.87	0.56	1.29	2.30	12.99	6.85	8.45	1.51	9.43	6.26	5.21E-03
Mllt3	14.04	57.29	41.86	46.56	8.92	7.37	4.00	39.94	6.76	0.17	5.33E-03
Cd86	4.04	0.18	1.11	0.85	17.27	16.12	29.35	1.54	20.91	13.54	5.34E-03
Fam114a1	1.78	0.36	0.82	2.17	9.72	8.35	9.95	1.28	9.34	7.29	5.39E-03
Sox12	3.16	17.10	11.55	9.24	1.44	1.21	1.05	10.26	1.23	0.12	5.39E-03
Klrd1	0.39	2.27	1.32	0.72	6.58	7.99	10.36	1.18	8.31	7.06	5.42E-03
Igsf3	8.83	73.54	47.18	66.07	1.86	5.49	3.14	48.91	3.50	0.07	5.45E-03
Msantd3	1.75	0.18	1.92	0.31	15.81	10.06	12.90	1.04	12.92	12.42	5.48E-03
Rhag	10.87	198.70	107.19	135.34	1.51	4.61	4.85	113.03	3.66	0.03	5.61E-03
Cenpv	3.65	10.50	4.64	3.00	0.82	0.45	0.96	5.45	0.74	0.14	5.62E-03
Slc35d2	0.30	3.50	2.66	1.79	22.37	20.64	18.66	2.06	20.55	9.97	5.67E-03
Sept5	2.24	0.16	3.14	1.91	27.56	32.34	25.71	1.86	28.54	15.33	5.72E-03
Mgl2	0.11	0.13	2.24	1.48	14.91	22.11	18.62	0.99	18.54	18.71	5.76E-03
Vill	0.60	3.71	4.56	9.65	47.21	37.02	57.20	4.63	47.14	10.18	5.80E-03
Car2	418.09	5499.94	3314.26	3405.02	176.89	230.43	134.18	3159.3 3	180.50	0.06	5.88E-03
Slc7a8	0.06	1.66	0.55	0.16	9.67	7.09	16.92	0.61	11.23	18.48	5.88E-03
Cd101	0.21	0.05	0.98	1.81	19.37	9.89	22.89	0.76	17.38	22.81	5.88E-03
Fabp4	1.24	3.19	1.98	1.60	8.59	6.33	15.40	2.00	10.10	5.04	5.94E-03
Prr5l	0.15	0.95	0.34	1.37	6.11	5.64	10.95	0.70	7.56	10.77	5.95E-03
Ubac1	13.22	69.03	32.73	39.66	4.30	6.28	7.96	38.66	6.18	0.16	5.96E-03
Gm26625	8.79	4.00	8.64	2.76	0.88	0.96	0.97	6.05	0.94	0.15	6.04E-03
Siglech	5.99	1.35	6.85	0.54	39.81	55.36	27.44	3.69	40.87	11.09	6.07E-03
C130050018 Rik	1.55	0.10	1.65	1.53	17.13	15.78	25.96	1.21	19.62	16.25	6.09E-03
Acpp	0.15	2.94	0.13	1.47	29.29	17.57	16.72	1.17	21.20	18.05	6.12E-03
Ier3	1.69	0.08	3.03	2.20	30.41	44.80	59.99	1.75	45.06	25.77	6.24E-03
RP23- 320D23.6	2.23	0.60	1.46	3.30	13.52	9.83	9.82	1.90	11.06	5.83	6.31E-03
Rnd3	4.52	0.43	3.43	4.97	38.20	29.11	31.03	3.34	32.78	9.82	6.32E-03
Atp11a	1.56	1.66	5.46	0.49	15.57	24.39	14.12	2.29	18.03	7.86	6.37E-03
Cd200r1	0.78	0.79	6.88	2.28	18.78	20.08	19.63	2.68	19.50	7.27	6.49E-03
Nod2	0.66	0.79	0.63	1.71	4.87	3.59	7.86	0.95	5.44	5.74	6.53E-03
Dmkn	3.04	0.10	1.24	0.78	20.88	17.41	18.58	1.29	18.96	14.69	6.58E-03
Adap2	0.84	1.07	0.76	0.93	5.35	2.59	6.56	0.90	4.83	5.35	6.59E-03
Gm9733	0.30	0.03	1.98	0.18	13.41	10.04	17.37	0.62	13.60	21.90	6.61E-03
Aoah	2.50	0.08	2.48	0.31	20.24	31.08	31.73	1.34	27.68	20.64	6.63E-03
Tspan33	2.86	22.72	12.39	10.30	0.37	1.05	1.42	12.07	0.95	0.08	6.72E-03
Ifi207	0.94	1.35	2.09	0.08	18.51	14.36	21.58	1.12	18.15	16.27	6.78E-03
Mgam	2.62	0.28	1.19	1.99	18.80	12.27	9.56	1.52	13.55	8.91	6.83E-03
Rgs3	0.21	0.53	2.10	1.83	7.93	13.72	12.44	1.17	11.36	9.74	6.94E-03

Ermap	15.48	377.15	257.12	191.74	4.23	6.61	7.57	210.37	6.14	0.03	7.00E-03
Map3k8	7.62	0.92	1.95	1.81	13.36	19.19	27.24	3.08	19.93	6.48	7.04E-03
Aven	2.86	5.37	4.93	3.65	0.72	1.07	0.23	4.20	0.67	0.16	7.04E-03
Ap5b1	4.88	4.14	3.87	1.14	16.35	24.09	13.04	3.51	17.83	5.08	7.17E-03
Slc40a1	10.36	64.25	56.22	49.85	255.96	169.07	406.33	45.17	277.12	6.13	7.19E-03
Vegfb	3.83	13.11	10.25	5.56	1.61	1.69	1.09	8.19	1.46	0.18	7.22E-03
Olfm1	1.30	0.66	0.82	0.54	4.58	2.81	5.58	0.83	4.32	5.21	7.28E-03
Gm16712	2.19	0.34	1.44	1.70	8.75	9.25	9.79	1.42	9.27	6.53	7.29E-03
Ces2g	22.20	294.04	200.92	177.66	12.00	11.48	8.88	173.71	10.79	0.06	7.32E-03
Gm17122	2.87	5.65	2.59	3.21	0.21	0.45	0.98	3.58	0.55	0.15	7.41E-03
Cox6b2	11.27	81.37	58.17	49.59	7.25	5.07	5.74	50.10	6.02	0.12	7.42E-03
Rnf144b	0.21	2.17	0.37	0.96	9.23	9.46	5.56	0.93	8.08	8.72	7.52E-03
Chil5	0.07	1.92	0.13	0.39	8.18	6.36	9.33	0.63	7.96	12.69	7.68E-03
Tmem56	3.16	31.66	24.12	17.57	0.10	1.00	1.33	19.13	0.81	0.04	7.68E-03
Crip2	11.69	58.58	40.88	32.91	4.55	2.73	9.27	36.01	5.52	0.15	7.75E-03
Pla2g4c	6.63	14.49	5.11	9.86	2.13	0.21	0.94	9.02	1.09	0.12	7.83E-03
Ppp1r42	1.39	0.10	2.03	0.80	13.36	14.10	11.83	1.08	13.10	12.13	7.94E-03
Anxa11os	0.31	0.60	0.16	0.87	3.75	3.02	3.49	0.48	3.42	7.07	7.94E-03
Timp2	0.21	2.45	1.13	1.29	9.06	9.37	14.03	1.27	10.82	8.50	8.08E-03
Sept8	3.98	88.04	32.32	35.03	1.86	1.85	0.98	39.84	1.56	0.04	8.14E-03
Osgin1	1.02	1.33	0.03	2.20	33.18	29.20	47.11	1.14	36.50	31.88	8.22E-03
Gypa	8.47	88.99	47.55	47.70	2.40	5.56	4.37	48.18	4.11	0.09	8.39E-03
Msr1	0.90	0.08	0.03	1.89	17.47	13.86	19.63	0.72	16.99	23.47	8.41E-03
Mogat2	2.11	0.13	3.51	2.33	32.14	20.26	45.66	2.02	32.69	16.20	8.41E-03
Myh10	5.84	47.81	36.36	29.89	1.86	4.00	2.97	29.97	2.94	0.10	8.41E-03
Bex4	2.31	21.61	18.66	29.04	0.08	1.28	0.61	17.91	0.66	0.04	8.44E-03
Gm15915	3.13	48.66	33.08	37.28	1.48	1.90	0.43	30.54	1.27	0.04	8.55E-03
Cldn1	0.06	2.20	0.26	1.63	25.48	12.63	16.76	1.04	18.29	17.62	8.56E-03
Cacna2d1	23.50	18.76	14.08	16.87	0.67	3.69	5.44	18.30	3.27	0.18	8.56E-03
Epdr1	2.89	53.16	40.86	20.07	0.27	1.43	1.33	29.24	1.01	0.03	8.57E-03
Tgfbr3	3.80	13.44	9.86	8.38	1.14	2.62	1.34	8.87	1.70	0.19	8.58E-03
Gm37052	2.89	3.32	4.14	3.39	0.49	0.48	0.04	3.44	0.34	0.10	8.61E-03
Icam4	5.35	26.49	15.12	16.63	2.23	3.94	1.74	15.89	2.63	0.17	8.82E-03
Zfhx3	8.16	0.92	3.90	3.16	30.70	17.91	22.05	4.04	23.55	5.84	8.96E-03
Arhgef12	4.69	25.57	11.00	8.65	1.63	1.93	2.29	12.48	1.95	0.16	8.97E-03
Oas2	7.95	0.56	1.71	3.13	18.65	21.24	39.54	3.34	26.48	7.93	8.98E-03
Zg16	1.24	5.55	5.77	4.66	0.49	0.69	0.33	4.30	0.51	0.12	8.98E-03
Gm26762	3.77	0.66	2.24	1.37	7.90	11.64	11.18	2.01	10.24	5.09	9.06E-03
Cyth3	11.78	55.02	37.88	35.31	9.97	3.85	5.66	35.00	6.49	0.19	9.07E-03
Gm37335	1.46	4.85	3.55	3.32	0.28	0.47	0.78	3.29	0.51	0.15	9.08E-03
Eng	8.62	34.54	18.91	25.26	1.98	4.12	6.28	21.83	4.12	0.19	9.17E-03
Cystm1	1.72	0.72	0.32	0.85	4.87	3.95	6.77	0.90	5.20	5.77	9.20E-03
Mboat1	0.81	0.05	1.00	0.54	10.59	5.02	10.75	0.60	8.79	14.58	9.22E-03
Prelid2	4.79	35.06	20.61	25.69	1.48	3.64	2.19	21.54	2.44	0.11	9.25E-03

Creb3l1	1.39	0.28	0.63	0.31	4.21	5.09	2.99	0.65	4.09	6.27	9.36E-03
Abca13	0.33	0.05	1.58	3.34	23.65	25.92	20.20	1.33	23.26	17.55	9.50E-03
Camsap2	9.00	33.06	18.84	9.55	2.08	2.40	5.27	17.61	3.25	0.18	9.52E-03
Abcg4	3.28	29.80	10.46	16.30	0.07	1.69	0.62	14.96	0.80	0.05	9.53E-03
Ccr3	3.28	0.66	0.08	0.10	8.71	12.48	32.61	1.03	17.93	17.36	9.64E-03
Nrp1	6.09	3.25	0.55	2.01	23.70	13.60	22.79	2.98	20.03	6.73	9.72E-03
Trbc2	1.51	0.15	2.24	1.59	8.16	20.40	16.63	1.37	15.06	10.96	9.79E-03
Gm43051	3.71	1.28	3.03	1.86	0.27	0.57	0.35	2.47	0.40	0.16	9.82E-03
Olr1	1.78	0.05	1.66	0.18	16.87	16.74	10.30	0.92	14.64	15.95	1.01E-02
Skap1	0.36	0.71	1.37	1.40	3.31	5.54	10.09	0.96	6.31	6.57	1.01E-02
Gm14287	4.38	4.57	3.05	5.97	1.25	1.09	0.30	4.49	0.88	0.20	1.03E-02
Kel	3.71	57.94	47.31	41.83	2.40	2.31	0.98	37.70	1.89	0.05	1.05E-02
Klhdc8b	7.77	10.53	3.88	8.85	1.44	0.19	1.54	7.76	1.06	0.14	1.05E-02
Phf11d	1.20	0.18	0.48	0.61	4.48	2.50	7.08	0.62	4.69	7.58	1.06E-02
Rab20	0.09	1.58	1.13	1.29	10.57	8.26	15.52	1.02	11.45	11.18	1.11E-02
Gata1	14.82	183.50	128.55	102.96	8.14	10.61	8.14	107.46	8.96	0.08	1.11E-02
Klf1	5.15	115.08	73.12	61.23	1.36	5.26	1.46	63.65	2.69	0.04	1.12E-02
Rpl13-ps3	3.20	3.58	1.64	4.79	1.05	0.41	0.42	3.30	0.63	0.19	1.17E-02
Slc8b1	9.28	1.25	14.73	7.86	49.68	43.56	53.41	8.28	48.88	5.90	1.17E-02
Tfec	1.36	0.03	1.40	1.16	25.73	17.10	22.50	0.99	21.78	22.09	1.18E-02
Sept4	2.35	12.65	7.17	5.82	1.01	0.74	1.58	7.00	1.11	0.16	1.24E-02
Cd3g	0.72	0.10	1.16	0.65	2.75	10.18	7.88	0.66	6.94	10.54	1.24E-02
March1	0.60	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.00	16.90	1.25E-02
Rab4a	2.89	28.09	28.31	30.86	0.40	1.95	2.05	22.54	1.47	0.07	1.27E-02
Trim10	1.24	9.97	8.25	11.05	0.02	0.74	0.33	7.62	0.36	0.05	1.27E-02
Tiam2	0.37	2.53	4.81	1.68	18.48	9.78	20.98	2.35	16.41	6.99	1.29E-02
Hfe	3.23	2.82	2.85	0.68	6.64	16.34	15.32	2.39	12.76	5.33	1.32E-02
Aqp1	5.72	89.98	56.88	80.58	2.35	5.59	2.58	58.29	3.50	0.06	1.33E-02
Adgre1	3.80	0.18	7.30	2.38	38.17	27.97	55.44	3.41	40.53	11.87	1.33E-02
Gm21967	2.50	2.74	3.85	2.84	0.15	0.17	1.30	2.98	0.54	0.18	1.34E-02
Chdh	1.75	1.72	1.56	0.25	5.69	13.68	7.53	1.32	8.96	6.80	1.35E-02
Dmxl2	0.18	3.20	1.32	2.75	14.93	13.55	17.36	1.86	15.28	8.20	1.36E-02
Smim1	5.42	62.55	33.99	37.07	0.27	7.00	0.14	34.76	2.47	0.07	1.37E-02
Tspo2	3.65	102.71	59.81	52.67	1.26	4.19	0.82	54.71	2.09	0.04	1.37E-02
Thbs1	4.64	29.43	2.77	7.99	38.39	46.49	84.94	11.21	56.61	5.05	1.38E-02
Ryr1	0.12	0.38	1.21	0.54	2.03	5.03	12.33	0.56	6.46	11.44	1.39E-02
Klra2	2.71	0.03	0.05	1.86	35.03	14.39	28.14	1.16	25.85	22.23	1.39E-02
Dpep2	0.54	1.05	0.03	0.67	8.01	8.86	6.99	0.57	7.95	13.92	1.40E-02
Gm45819	1.42	3.42	2.27	2.04	0.79	0.21	0.31	2.29	0.44	0.19	1.40E-02
Ctsw	2.05	0.84	2.45	1.09	5.99	14.53	4.35	1.61	8.29	5.16	1.43E-02
Fut7	4.28	1.02	5.59	0.85	9.55	16.81	24.90	2.94	17.09	5.82	1.43E-02
Slc38a5	3.49	157.83	102.30	100.32	0.79	5.14	0.18	90.99	2.03	0.02	1.43E-02
Mt2	1.86	54.32	37.23	34.97	0.48	1.93	0.84	32.09	1.08	0.03	1.44E-02
RP24-395P13.1	2.80	0.54	0.03	0.60	19.30	12.44	12.76	0.99	14.83	14.98	1.44E-02

Gm37534	4.10	2.45	5.77	1.79	0.47	0.21	1.09	3.53	0.59	0.17	1.47E-02
Ttl	3.10	3.81	1.61	3.70	0.37	0.10	0.96	3.05	0.47	0.16	1.49E-02
Cd14	1.17	2.43	0.92	0.03	14.15	16.76	42.46	1.14	24.46	21.50	1.53E-02
Nckap1	2.17	11.30	14.37	11.36	0.05	2.26	0.23	9.80	0.85	0.09	1.53E-02
Cd300lg	0.30	0.59	2.45	0.05	8.09	7.56	7.65	0.85	7.77	9.16	1.56E-02
Ugt1a6a	1.78	0.36	2.30	1.48	8.61	4.89	9.63	1.48	7.71	5.21	1.56E-02
Gpd1	0.64	0.97	0.08	0.62	5.90	2.24	14.66	0.58	7.60	13.14	1.59E-02
Gm37124	10.06	2.53	8.96	4.71	2.10	0.81	0.76	6.57	1.22	0.19	1.59E-02
Tspan8	2.23	50.40	15.60	33.11	0.69	2.35	0.76	25.34	1.27	0.05	1.61E-02
Sphk1	3.80	125.25	86.66	73.70	0.10	6.04	0.66	72.35	2.27	0.03	1.61E-02
Ly6g5b	2.08	2.79	0.55	0.75	10.56	4.09	10.13	1.54	8.26	5.36	1.61E-02
Tlr7	0.45	0.05	2.79	0.21	6.14	10.30	6.95	0.88	7.79	8.90	1.62E-02
Al427809	1.72	19.83	3.43	9.13	0.42	0.02	0.76	8.53	0.40	0.05	1.64E-02
Mex3b	8.43	4.52	3.27	4.58	1.81	0.26	1.00	5.20	1.02	0.20	1.64E-02
Sulf2	0.95	0.65	0.03	1.31	8.93	5.95	18.30	0.73	11.06	15.09	1.69E-02
Glr5	5.42	32.35	17.95	17.69	4.75	3.50	2.40	18.36	3.55	0.19	1.71E-02
Slc25a21	3.86	36.70	23.51	23.33	0.77	3.59	0.06	21.85	1.47	0.07	1.71E-02
4933431E20 Rik	1.78	13.80	11.57	11.34	0.13	2.59	0.16	9.62	0.96	0.10	1.72E-02
Add2	4.67	106.47	79.08	75.94	3.29	5.26	0.70	66.54	3.08	0.05	1.76E-02
Plod1	2.80	0.72	0.69	0.03	10.71	12.25	24.16	1.06	15.71	14.86	1.78E-02
Nqo1	3.07	23.79	10.62	12.52	1.98	2.54	1.00	12.50	1.84	0.15	1.80E-02
Stard10	3.25	40.84	21.77	19.71	2.62	1.05	2.67	21.39	2.11	0.10	1.81E-02
Chst13	0.90	0.03	1.11	0.98	13.58	10.68	7.38	0.75	10.55	13.97	1.83E-02
Mcpt8	22.56	7.49	28.63	1.19	167.27	98.64	70.99	14.97	112.30	7.50	1.87E-02
Pklr	0.66	64.81	30.04	52.12	0.10	1.24	0.17	36.91	0.50	0.01	1.87E-02
Itk	0.21	0.03	0.87	1.45	5.20	6.71	10.03	0.64	7.31	11.44	1.95E-02
Acta2	0.88	0.08	0.11	2.63	6.69	6.07	10.14	0.92	7.63	8.28	1.96E-02
Gstm5	5.78	94.31	75.60	63.21	4.65	4.42	4.58	59.73	4.55	0.08	1.96E-02
Axl	1.05	0.10	2.08	2.54	10.54	7.42	37.58	1.44	18.51	12.82	1.96E-02
Gm37297	1.11	2.22	11.94	7.37	0.72	0.05	0.35	5.66	0.37	0.07	1.97E-02
Dock1	1.75	0.05	1.77	0.85	11.23	11.39	10.54	1.10	11.05	10.01	1.98E-02
Fam132a	12.95	220.03	133.32	112.68	9.28	13.60	7.55	119.75	10.14	0.08	1.98E-02
Nefh	2.71	30.80	22.40	13.84	0.25	2.47	1.72	17.44	1.48	0.08	1.99E-02

Zbtb46^{dtf} bone marrow chimeras were treated with a single dose of diphtheria toxin (DT) or PBS. Sinusoidal endothelial cells were sorted one day after treatment and RNA-sequencing was performed. Shown are normalized RNA expression values (FPKM) for the indicated genes. The average expression level of each gene for both conditions are calculated and shown as PBS Avg or DT Avg. Fold change is calculated as DT Avg / PBS Avg. FDR, false discovery rate.