

Table S1. List of 305 differentially expressed genes identified by RNA-Seq ($P < 0.05$), sorted byLog₂ fold change

Gene	Locus	Mean FPKM WT	Mean FPKM KO	Log ₂ fold change	P-value	q-value	Phag. ¹	SNPs ²
Spint1	chr2:119237359-119249513	55.71	0.56	-6.63	0.00E+00	0.00E+00	-	-
Jmjd7	chr2:120027482-120032604	1.15	0.03	-5.31	4.13E-06	4.37E-04	-	-
Bub1b	chr2:118598210-118641592	2.15	0.1	-4.47	0.00E+00	0.00E+00	-	-
Gpr176	chr2:118277097-118373419	0.9	0.05	-4.31	2.55E-13	1.35E-10	-	-
Prnp	chr2:131909927-131938431	7.96	0.42	-4.24	0.00E+00	0.00E+00	+	-
Slc15a2	chr16:36750163-36784962	1.11	0.22	-2.33	6.35E-07	8.25E-05	-	-
Hpgds	chr6:65117292-65144730	0.78	0.18	-2.13	1.17E-06	1.39E-04	-	-
Mamdc2	chr19:23302608-23448322	0.7	0.17	-2.06	5.10E-06	5.25E-04	-	-
Cdo1	chr18:46713204-46728342	4.44	1.2	-1.89	1.34E-08	3.01E-06	-	-
Rhov	chr2:119269200-119271226	11.06	3.01	-1.88	3.11E-15	2.78E-12	-	-
Hpgd	chr8:56294551-56321046	4.1	1.27	-1.69	7.18E-08	1.19E-05	-	-
AA467197,Mir147	chr2:122637886-122641076	7.7	2.4	-1.68	8.17E-06	7.66E-04	-	-
Gcnt1	chr19:17326140-17372844	10.23	3.57	-1.52	1.78E-15	1.72E-12	-	-
Arhgap22	chr14:33216822-33369936	1.81	0.64	-1.5	1.25E-05	1.11E-03	-	-
8430406107Rik	chr2:144271034-144281229	6.07	2.23	-1.45	1.95E-10	6.29E-08	-	+
Arhgap19	chr19:41766587-41802084	4.69	1.75	-1.42	1.02E-11	3.85E-09	-	-
Dkk2	chr3:132085291-132180304	3.76	1.44	-1.38	4.51E-09	1.12E-06	-	-
C1qc	chr4:136889801-136892914	286.23	114.96	-1.32	0.00E+00	0.00E+00	+	-
LOC100038947	chr3:15795146-15848487	8.92	3.65	-1.29	1.19E-07	1.89E-05	-	+
Gas6	chr8:13465373-13494535	2.37	0.98	-1.27	3.01E-05	2.27E-03	+	-
E2f2	chr4:136172393-136196056	0.74	0.31	-1.26	5.50E-04	2.61E-02	-	-
Rab3il1	chr19:10018227-10035586	4.85	2.05	-1.25	5.25E-07	7.11E-05	-	-
Cadm1	chr9:47530351-47853385	6.32	2.67	-1.24	2.05E-10	6.43E-08	-	-
Sirpb1b	chr3:15495753-15575065	3.26	1.4	-1.22	2.37E-04	1.29E-02	-	-
Ophn1	chrX:98557514-98890985	3.2	1.37	-1.22	2.14E-07	3.23E-05	-	-
Slc46a3	chr5:147878440-147894802	7.81	3.46	-1.17	3.12E-08	6.38E-06	-	-
Slc27a6	chr18:58556239-58612869	1.62	0.72	-1.17	5.82E-04	2.74E-02	-	-
C1qb	chr4:136880144-136886177	405.41	181.39	-1.16	1.53E-14	1.19E-11	+	-
Olfml3	chr3:103735393-103738001	14	6.3	-1.15	8.99E-09	2.14E-06	-	-
Apoc1	chr7:19689480-19692658	30.41	14.03	-1.12	4.29E-05	3.10E-03	-	-
Man2a2	chr7:80349096-80371375	14.1	6.5	-1.12	4.22E-14	3.07E-11	-	-

Spg11	chr2:122028582-122118386	8.82	4.1	-1.1	2.39E-08	4.97E-06	-	+
Stard13	chr5:151037514-151190193	1.52	0.71	-1.1	4.01E-04	1.99E-02	-	-
C1qa	chr4:136895915-136898844	324.73	152.9	-1.09	2.27E-13	1.26E-10	+	-
Gm11710	chr11:115020727-115027012	31.73	14.95	-1.09	6.85E-17	1.44E-15	-	-
Sepp1	chr15:3270766-3280508	139.37	66.18	-1.07	1.47E-12	6.60E-10	-	-
Aif1	chr17:35170991-35176001	20.99	10.02	-1.07	9.23E-07	1.13E-04	+	-
Enpp1	chr10:24641410-24712102	5.7	2.74	-1.06	3.17E-07	4.67E-05	-	-
Fcgr4	chr1:171018925-171029761	4.7	2.26	-1.05	8.21E-04	3.53E-02	+	-
Apcdd1	chr18:62922326-62953195	4.55	2.2	-1.05	7.79E-06	7.60E-04	-	-
Rnf150	chr8:82863355-83091271	2.58	1.27	-1.03	4.74E-08	8.36E-06	-	-
Tmem37	chr1:120067376-120073780	54.21	27.01	-1.01	1.04E-09	2.95E-07	-	-
Apoc2	chr7:19671578-19676864	76.59	38.56	-0.99	1.20E-08	2.73E-06	-	-
Cd300lh	chr11:115042130-115048295	24.25	12.33	-0.98	7.95E-06	7.64E-04	-	-
Ms4a7	chr19:11321405-11336116	60.5	30.74	-0.98	5.87E-08	9.91E-06	-	-
Siglec1	chr2:131069219-131086765	7.72	3.95	-0.97	2.03E-09	5.24E-07	-	-
Ccr5	chr9:124121542-124127183	31.57	16.11	-0.97	5.44E-11	1.86E-08	+	-
Arhgap15	chr2:43748823-44387623	4.98	2.57	-0.95	2.39E-05	1.92E-03	+	-
Lgals1	chr15:78926724-78930465	52.22	27.08	-0.95	3.51E-08	6.81E-06	+	-
Zfyve19	chr2:119172499-119217050	10.5	5.47	-0.94	8.84E-06	8.04E-04	-	+
Lgmn	chr12:102394097-102439697	325.24	170.66	-0.93	8.13E-09	1.97E-06	-	-
Egr1	chr18:34861206-34864956	3.5	1.83	-0.93	1.28E-04	7.78E-03	+	-
Fos	chr12:85473900-85477270	9.36	4.99	-0.91	6.93E-06	7.02E-04	+	-
Eif2ak4	chr2:118388616-118475234	7.03	3.86	-0.86	6.65E-07	8.50E-05	-	+
BC055004	chr5:138225903-138251875	5.34	2.96	-0.85	2.13E-04	1.19E-02	-	-
C530028O21Rik	chr6:124996719-125003097	9.76	5.46	-0.84	1.45E-04	8.60E-03	-	-
Sorl1	chr9:41968488-42124289	2.01	1.13	-0.83	1.24E-04	7.65E-03	-	-
Enc1	chr13:97241104-97253040	10.23	5.76	-0.83	1.82E-07	2.82E-05	-	-
Thbd	chr2:148404470-148408188	12.48	7.05	-0.82	3.16E-07	4.67E-05	-	-
Fam125b	chr2:33729955-33887946	10.54	6.07	-0.79	3.56E-07	5.05E-05	-	-
Igfbp4	chr11:99041259-99052643	9.82	5.7	-0.79	7.61E-05	4.97E-03	-	-
Fam105a	chr15:27655070-27681542	11.69	6.77	-0.79	1.32E-05	1.14E-03	-	-
Fabp4	chr3:10204342-10208576	380.32	221.92	-0.78	4.69E-08	8.36E-06	-	-
Dock4	chr12:40446052-40846488	5.59	3.25	-0.78	9.36E-07	1.13E-04	-	-
Stab1	chr14:31134852-31168641	25.8	15.06	-0.78	1.10E-07	1.77E-05	+	-
Fcgr1	chr3:96282908-	17.19	10.12	-0.76	2.15E-06	2.48E-04	+	-

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Klra2	chr6:131219234-131247362	15.11	8.9	-0.76	3.31E-05	2.46E-03	-	-
Daglb	chr5:143464492-143504442	23.16	13.85	-0.74	5.73E-07	7.66E-05	-	-
Rasgrp3	chr17:75435904-75529053	10.9	6.51	-0.74	2.65E-05	2.07E-03	+	-
Pld4	chr12:112760654-112768986	51.58	31.02	-0.73	3.41E-07	4.89E-05	+	-
D14Ert449e	chr14:25923297-25927672	6.2	3.72	-0.73	4.61E-10	4.84E-09	-	-
Ms4a6c	chr19:11469367-11482196	80.23	49.42	-0.7	2.63E-05	2.07E-03	-	-
Sh3bgrl2	chr9:83548337-83600291	9.41	5.81	-0.69	4.81E-05	3.40E-03	-	-
Malat1	chr19:5795689-5802671	124.79	77.55	-0.69	9.25E-04	3.85E-02	-	-
Zfp395	chr14:65358675-65398930	6.12	3.82	-0.68	1.69E-04	9.85E-03	-	-
Mafb	chr2:160363676-160367065	107.2	67.27	-0.67	6.93E-06	7.02E-04	+	-
Hgf	chr5:16553549-16619439	7.8	4.88	-0.67	3.83E-04	1.92E-02	+	-
Mtus1	chr8:40990911-41133726	36.97	23.21	-0.67	3.81E-06	4.14E-04	-	-
Abcc3	chr11:94343294-94392976	13.59	8.55	-0.67	7.05E-06	7.08E-04	-	-
Gpcpd1	chr2:132529082-132578248	20.04	12.71	-0.66	3.63E-05	2.67E-03	-	-
Fabp5	chr3:10012605-10016610	329.2	207.78	-0.66	4.30E-06	4.47E-04	-	-
Engase	chr11:118476959-118489198	23.36	14.74	-0.66	3.66E-06	4.01E-04	-	-
Arg1	chr10:24915206-24927470	321.13	204.41	-0.65	1.17E-04	7.34E-03	+	-
Zdhhc14	chr17:5492599-5753891	6.52	4.16	-0.65	8.07E-04	3.50E-02	-	-
Zranb3	chr1:127954185-128102408	5.04	3.24	-0.63	6.94E-04	3.13E-02	-	-
Fry	chr5:150259929-150497753	4.46	2.88	-0.63	5.10E-05	3.57E-03	-	-
Iqgap2	chr13:95627176-95891922	28.48	18.37	-0.63	1.35E-05	1.16E-03	-	-
Cd244	chr1:171559192-171585316	5.69	3.7	-0.62	1.04E-03	4.17E-02	-	-
Frm4b	chr6:97286866-97617657	12.44	8.11	-0.62	3.18E-05	2.39E-03	-	-
Lair1	chr7:4007072-4063204	9.79	6.37	-0.62	3.00E-04	1.57E-02	-	-
Maf	chr8:115703252-115706894	6.89	4.48	-0.62	6.60E-04	3.02E-02	+	-
Sgsh	chr11:119314786-119355510	7.99	5.2	-0.62	2.03E-04	1.14E-02	-	-
Rassf2	chr2:131992849-132029988	38.85	25.54	-0.61	1.84E-05	1.53E-03	-	-
Clec12a	chr6:129350243-129365303	16.78	10.96	-0.61	2.03E-04	1.14E-02	-	-
Mr1	chr1:155127877-155146780	9.38	6.18	-0.6	1.04E-03	4.17E-02	-	-
Usp35	chr7:97309379-97325964	6.56	4.31	-0.6	7.55E-04	3.35E-02	-	-
Ssh2	chr11:77216424-77460219	20.58	13.61	-0.6	2.51E-05	2.00E-03	-	-
Epas1	chr17:86753863-86833410	10.55	6.95	-0.6	6.78E-05	4.49E-03	-	-
Kif13b	chr14:64652530-64806296	11.4	7.58	-0.59	6.46E-05	4.32E-03	-	-
Dhrs3	chr4:144892826-144927645	90.01	60.34	-0.58	5.25E-05	3.66E-03	-	-

Per3	chr4:151003654-151044622	5.15	3.47	-0.57	8.23E-04	3.53E-02	-	-
Tmem176b	chr6:48833811-48841374	104.29	70.41	-0.57	2.63E-04	1.40E-02	-	-
Ccl6	chr11:83582060-83623693	193.94	130.83	-0.57	1.15E-04	7.27E-03	-	-
Bcl6	chr16:23965051-23988612	9.79	6.6	-0.57	8.01E-04	3.49E-02	-	-
Dock10	chr1:80501072-80758553	10.38	7.08	-0.55	1.22E-04	7.63E-03	-	-
C3ar1	chr6:122847139-122856157	134.63	91.83	-0.55	6.86E-04	3.11E-02	-	-
Abca9	chr11:110100821-110168153	22.04	15.03	-0.55	8.29E-05	5.39E-03	-	-
Gpr65	chr12:98268656-98276632	24.49	16.72	-0.55	3.98E-04	1.99E-02	-	-
Abhd12	chr2:150832514-150904731	146.07	100.78	-0.54	2.21E-04	1.22E-02	-	-
Plxnc1	chr10:94790865-94944578	10.01	6.86	-0.54	1.84E-04	1.05E-02	-	-
Nav1	chr1:135434579-135585355	8.4	5.82	-0.53	1.72E-04	9.87E-03	+	-
Adam8	chr7:139978940-139992488	88.42	61.22	-0.53	2.67E-04	1.42E-02	-	-
Sesn1	chr10:41810573-41908436	30.62	21.26	-0.53	6.15E-04	2.86E-02	-	-
Mctp1	chr13:76384960-77031810	9.16	6.35	-0.53	1.04E-03	4.17E-02	-	-
Ldlrad3	chr2:101950200-102186377	15.15	10.6	-0.52	6.08E-04	2.85E-02	-	-
Ptplad2	chr4:88412929-88438926	23.24	16.17	-0.52	7.98E-04	3.49E-02	-	-
Tef	chr15:81802672-81826863	32.45	22.67	-0.52	2.90E-04	1.53E-02	-	-
Slc37a2	chr9:37229148-37255738	16.55	11.59	-0.51	4.45E-04	2.18E-02	-	-
Fasn	chr11:120805957-120824547	14.35	10.05	-0.51	2.59E-04	1.39E-02	-	-
Itgb5	chr16:33829664-33949338	76.42	53.67	-0.51	4.20E-04	2.06E-02	+	-
Nceh1	chr3:27183003-27244911	36.08	25.44	-0.5	3.35E-04	1.72E-02	-	-
Atp8a1	chr5:67618140-67847431	7.14	5.03	-0.5	8.69E-04	3.68E-02	-	-
Trpm2	chr10:77907721-77969872	6.93	4.9	-0.5	1.08E-03	4.27E-02	-	-
Chd3	chr11:69344350-69369391	15.37	10.84	-0.5	3.65E-04	1.85E-02	-	-
Vps13c	chr9:67840395-67995634	18.84	13.42	-0.49	6.47E-04	3.00E-02	-	-
Nuak1	chr10:84371318-84440471	11.18	7.97	-0.49	1.14E-03	4.45E-02	-	-
Ttyh3	chr5:140620577-140649031	37.81	27.35	-0.47	9.03E-04	3.78E-02	-	-
Slc36a1	chr11:55204339-55236330	25.92	18.69	-0.47	7.67E-04	3.38E-02	-	-
Abcd2	chr15:91145870-91191807	21.2	15.26	-0.47	7.23E-04	3.22E-02	-	-
Rftn1	chr17:49993306-50190497	44.91	32.69	-0.46	1.09E-03	4.30E-02	-	-
Entpd4	chr14:69337150-69366742	20.21	15.51	-0.38	4.79E-06	3.36E-05	-	-
Zdhhc18	chr4:133606991-133633429	23.83	32.75	0.46	1.16E-03	4.52E-02	-	-
Zyx	chr6:42349827-42358395	63.95	88.08	0.46	1.12E-03	4.41E-02	-	-
Met	chr6:17463956-17573980	8.41	11.62	0.47	1.29E-03	4.96E-02	-	-
Sifn4	chr11:83175185-	14.27	19.84	0.47	9.49E-04	3.91E-02	-	-

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Gpr84	chr15:103308234-103310438	58.68	81.13	0.47	8.53E-04	3.64E-02	-	-	
B430306N03Rik	chr17:48316161-48326511	22.73	31.38	0.47	8.85E-04	3.72E-02	-	-	
Slc2a6	chr2:27021364-27027998	32.1	44.68	0.48	8.51E-04	3.64E-02	-	-	
Golim4	chr3:75876383-75956831	16.1	22.38	0.48	7.01E-04	3.15E-02	-	-	
Oasl2	chr5:114896933-114912245	14.23	19.91	0.48	1.04E-03	4.17E-02	-	-	
H2-Aa	chr17:34282750-34287771	59.85	83.2	0.48	9.30E-04	3.85E-02	+	-	
Filip1l	chr16:57301999-57606867	13.4	18.78	0.49	1.05E-03	4.17E-02	-	-	
Nfkb2	chr19:46304736-46327156	41.11	57.81	0.49	1.02E-03	4.14E-02	-	-	
Sod2	chr17:13007838-13018119	100.16	143.55	0.52	8.78E-04	3.70E-02	+	-	
Cd274	chr19:29367437-29388094	53.76	76.83	0.52	3.16E-04	1.64E-02	-	-	
Vsig4	chrX:96247202-96293438	41.88	59.95	0.52	3.55E-04	1.80E-02	-	-	
Smpd13b	chr4:132732965-132757171	33.27	48.05	0.53	1.88E-04	1.06E-02	-	-	
Ampd3	chr7:110772603-110812395	66.32	95.89	0.53	3.54E-04	1.80E-02	-	-	
Panx1	chr9:15005784-15045478	12.36	17.82	0.53	1.28E-03	4.95E-02	-	-	
Prkar2b	chr12:31958478-32061279	25.5	36.91	0.53	1.33E-04	7.98E-03	-	-	
Ephx1	chr1:180989555-181017495	106.75	155.25	0.54	1.68E-04	9.83E-03	-	-	
Spp1	chr5:104435110-104441053	154.37	224.33	0.54	6.76E-04	3.07E-02	+	-	
Rpl23	chr11:97777525-97782439	36.59	53.03	0.54	5.67E-04	2.68E-02	-	-	
Id2	chr12:25093798-25096092	61.57	89.63	0.54	1.11E-04	7.03E-03	-	-	
H2-Q4	chr17:35379616-35384674	65.04	94.87	0.54	9.06E-05	5.82E-03	+	-	
Fpr1	chr17:17876470-17883939	38.8	56.46	0.54	2.23E-04	1.22E-02	+	-	
Ptgr1	chr4:58965589-58987078	51.38	75.38	0.55	8.56E-05	5.54E-03	-	-	
Ppfibp2	chr7:107595050-107758032	16.67	24.39	0.55	5.15E-04	2.46E-02	-	-	
Egr2	chr10:67537868-67542188	62.34	91.31	0.55	1.27E-04	7.77E-03	+	-	
Gbp6	chr5:105270701-105293699	6.33	9.31	0.56	4.73E-04	2.28E-02	+	-	
Tln2	chr9:67217084-67559703	2.63	3.88	0.56	2.60E-04	1.39E-02	-	-	
Rai14	chr15:10568977-10714631	23.72	35.28	0.57	3.95E-05	2.89E-03	-	-	
Rpl7a	chr2:26910806-26913311	50.23	74.88	0.58	2.39E-04	1.29E-02	-	-	
Dnajc10	chr2:80315465-80354055	74.19	110.68	0.58	1.42E-04	8.45E-03	-	-	
Efnb2	chr8:8617438-8660773	15.15	22.58	0.58	4.48E-05	3.22E-03	-	-	
Phldb1	chr9:44686307-44735198	9.39	14.03	0.58	5.46E-05	3.76E-03	-	-	
Serpib9	chr13:33004540-33017955	16.73	25.02	0.58	4.66E-05	3.33E-03	-	-	
Pfkip	chr13:6548156-6648724	22.54	33.61	0.58	6.59E-04	3.02E-02	-	-	
Slc23a2	chr2:132052495-132145108	23.19	34.9	0.59	2.71E-05	2.10E-03	-	-	

5730494N06Rik	chr2:132239491-132247788	19.39	29.1	0.59	9.23E-04	3.85E-02	-	-
Icam1	chr9:21015959-21028796	38.47	57.88	0.59	2.29E-05	1.87E-03	+	-
Procr	chr2:155751216-155755478	127.52	192.71	0.6	2.99E-05	2.27E-03	-	-
Bcam	chr7:19756137-19770532	6.68	10.15	0.6	1.01E-03	4.11E-02	-	-
Src	chr2:157424292-157471838	6.92	10.58	0.61	1.23E-04	7.63E-03	+	-
Tnfaip3	chr10:19000909-19015410	21.69	33.39	0.62	1.68E-05	1.41E-03	-	-
Tpm4	chr8:72135291-72153129	171.12	264.81	0.63	5.57E-05	3.79E-03	-	-
Abcc4	chr14:118482691-118706219	14.28	22.09	0.63	7.83E-06	7.60E-04	-	-
Pcx	chr19:4510471-4621752	7.35	11.37	0.63	6.41E-05	4.31E-03	-	-
Rpl36a	chrX:134585653-134588062	43.1	66.61	0.63	1.08E-03	4.27E-02	-	-
Gpr35	chr1:92973118-92986391	17	26.56	0.64	4.82E-05	3.40E-03	-	-
1500003O03Rik	chr2:119547706-119587022	51.69	80.75	0.64	4.05E-06	4.36E-04	-	-
Gss	chr2:155563182-155592706	21.04	32.89	0.64	1.63E-05	1.38E-03	-	-
Car6	chr4:150187015-150201135	16.12	25.05	0.64	1.80E-04	1.03E-02	-	-
Rps12	chr10:23785182-23787209	60.69	94.26	0.64	2.42E-04	1.31E-02	-	-
Angptl2	chr2:33136972-33371478	11.27	17.67	0.65	2.63E-05	2.07E-03	-	-
Niacr1	chr5:123863569-123865516	6.17	9.7	0.65	1.02E-03	4.14E-02	-	-
Bcl2a1d	chr9:88723287-88731850	23.6	37.06	0.65	3.32E-04	1.71E-02	-	-
Dcbld2	chr16:58408534-58469745	3.71	5.82	0.65	6.08E-05	4.12E-03	-	-
Vmn2r26	chr6:124024757-124062035	9.25	14.57	0.66	6.90E-05	4.54E-03	-	-
Adora2a	chr10:75316942-75334788	9.36	14.79	0.66	6.65E-05	4.42E-03	+	-
Fpr2	chr17:17887823-17893952	31.46	49.64	0.66	1.24E-05	1.11E-03	+	-
Psma5	chr3:108256925-108279952	8.56	13.75	0.68	1.30E-03	4.96E-02	-	-
Rn4.5s	chr6:47654920-47655094	10.43	16.85	0.69	2.71E-03	1.42E-02	-	-
Rassf4	chr6:116633007-116673836	83.89	134.06	0.68	1.23E-04	7.63E-03	-	-
Dusp16	chr6:134715472-134792628	5.56	8.89	0.68	5.47E-05	3.76E-03	-	-
Chn2	chr6:54039931-54430221	7.18	11.69	0.7	4.97E-04	2.38E-02	-	-
Olr1	chr6:129485246-129507165	85.3	138.84	0.7	4.10E-06	4.37E-04	+	-
Slc7a2	chr8:40862366-40922070	86.04	140.17	0.7	1.46E-04	8.61E-03	-	-
Ahrr	chr13:74211117-74292309	5.68	9.2	0.7	1.31E-05	1.14E-03	+	-
Alas1	chr9:106233454-106247954	194.52	317.73	0.71	4.12E-05	3.00E-03	-	-
Dnmt3l	chr10:78030030-78063615	5.47	8.97	0.71	8.59E-04	3.65E-02	-	-
Slc22a23	chr13:34179157-34345182	1.53	2.49	0.71	6.62E-04	3.02E-02	-	-
Ets2	chr16:95702406-95721049	15.25	24.99	0.71	6.11E-07	8.08E-05	-	-
H2-Ab1	chr17:34263226-	69.92	114.49	0.71	4.33E-07	6.07E-05	+	-

	34269418								
Gstm2	chr3:107981701-107986436	10.48	17.3	0.72	4.56E-04	2.21E-02	-	-	
Slc28a2	chr2:122426476-122461130	2.33	3.88	0.73	4.63E-04	2.24E-02	-	+	
Srxn1	chr2:152105729-152111353	226.13	374.61	0.73	2.93E-05	2.24E-03	-	-	
Akr1b8	chr6:34354163-34368454	18.03	29.95	0.73	8.60E-06	7.94E-04	-	-	
Ppip5k1	chr2:121289601-121351013	3.88	6.49	0.74	2.35E-05	1.90E-03	-	+	
F3	chr3:121723536-121735052	6.42	10.69	0.74	1.71E-04	9.86E-03	-	-	
A530064D06Rik	chr17:48151895-48167257	18.11	30.27	0.74	3.23E-06	3.58E-04	-	-	
Cyp1b1	chr17:79706952-79715041	10.5	17.5	0.74	6.38E-07	8.25E-05	+	-	
Nfkbie	chr17:45555715-45563168	17.82	29.92	0.75	3.28E-07	4.77E-05	-	-	
Ralgds	chr2:28513166-28553082	8.69	14.72	0.76	8.47E-06	7.88E-04	+	-	
Cxcl14	chr13:56288642-56296551	63.47	107.74	0.76	5.62E-08	9.62E-06	-	-	
Rpl12	chr2:32961711-32964045	16.87	28.82	0.77	3.67E-04	1.85E-02	-	-	
Ppap2b	chr4:105157346-105232767	5.04	8.58	0.77	1.85E-05	1.53E-03	-	-	
Ripk3	chr14:55784994-55788857	9.73	16.68	0.78	1.24E-05	1.11E-03	-	-	
Rpl24	chr16:55966274-55971437	36.44	62.4	0.78	7.56E-06	7.46E-04	-	-	
Plcb2	chr2:118707516-118728438	4.17	7.21	0.79	1.48E-06	1.74E-04	-	+	
Cd53	chr3:106758860-106790149	233.15	402.03	0.79	1.48E-05	1.26E-03	-	-	
Nqo1	chr8:107388224-107403205	71.95	124.92	0.8	1.48E-08	3.25E-06	-	-	
Epha4	chr1:77367184-77515088	2.91	5.1	0.81	2.38E-06	2.69E-04	-	-	
Dnm1	chr2:32308470-32353304	1.52	2.67	0.81	9.55E-04	3.93E-02	-	-	
Vcan	chr13:89655309-89742512	2.54	4.45	0.81	5.55E-05	3.79E-03	-	-	
Slc6a9	chr4:117835257-117872470	13.95	24.71	0.82	1.51E-08	3.25E-06	-	-	
Socs2	chr10:95411489-95416857	6.58	11.66	0.82	1.26E-05	1.11E-03	-	-	
Ltc4s	chr11:50236471-50238471	19.16	33.78	0.82	2.25E-04	1.23E-02	-	-	
Pdgfb	chr15:79995875-80014808	14.97	26.5	0.82	2.08E-08	4.40E-06	-	-	
Rcan1	chr16:92391952-92466146	28.14	49.59	0.82	4.14E-08	7.77E-06	-	-	
Ifi205	chr1:174011997-174031755	3.27	5.82	0.83	8.10E-04	3.51E-02	-	-	
Ly6i	chr15:74979811-74983430	11.27	20.06	0.83	1.30E-04	7.86E-03	-	-	
Ass1	chr2:31470269-31520670	33.97	60.68	0.84	5.05E-07	6.91E-05	-	-	
Rps27	chr3:90212666-90213648	54.11	96.93	0.84	2.19E-04	1.21E-02	-	-	
1810029B16Rik	chr8:66476345-66486507	33.27	59.54	0.84	3.21E-08	6.44E-06	-	-	
H2-Q8	chr17:35394098-35395632	8.01	14.31	0.84	1.05E-04	6.68E-03	+	-	
Ptges	chr2:30889470-30903297	34.17	61.47	0.85	1.79E-09	4.74E-07	-	-	
Bcl2a1a	chr9:88956919-88962416	25.95	46.93	0.85	9.16E-07	1.13E-04	-	-	

Chst11	chr10:82985496-83195891	6.36	11.52	0.86	1.02E-08	2.36E-06	-	-
Gpr132	chr12:112850875-112860916	5.05	9.19	0.86	7.23E-06	7.19E-04	-	-
Susd2	chr10:75636618-75644008	1.43	2.61	0.87	1.15E-03	4.49E-02	-	-
Unc5b	chr10:60762594-60831581	4.08	7.52	0.88	3.42E-08	6.75E-06	-	-
Maff	chr15:79347677-79359076	2.77	5.11	0.88	7.08E-04	3.17E-02	-	-
Tmem119	chr5:113793728-113800352	6.4	11.84	0.89	2.34E-06	2.67E-04	-	-
Trem14	chr17:48264294-48275358	4.28	7.91	0.89	6.55E-04	3.02E-02	-	-
Malt1	chr18:65430996-65478792	13.06	24.17	0.89	5.32E-10	1.59E-07	+	-
Cxcl2	chr5:90903898-90905938	23.05	42.88	0.9	4.65E-08	8.36E-06	+	-
Igf2bp1,Mir3063	chr11:95957163-96005944	0.76	1.41	0.9	1.28E-04	7.78E-03	-	-
Tnfsf4	chr1:161395437-161418206	11.53	21.78	0.92	1.24E-07	1.94E-05	-	-
Cish	chr9:107296688-107301961	4.15	7.87	0.92	1.30E-05	1.14E-03	-	-
Nckap1	chr2:80501294-80580965	1.31	2.49	0.93	4.03E-04	2.00E-02	-	-
Clec5a	chr6:40529090-40910666	31.79	60.8	0.94	3.82E-11	1.35E-08	-	-
Hspa1a	chr17:34969358-34972156	1.93	3.69	0.94	1.67E-04	9.81E-03	-	-
Pf4	chr5:90772434-90773383	600.2	1159.14	0.95	1.55E-09	4.18E-07	+	-
Gbp2	chr3:142620662-142638008	22.24	43.92	0.98	4.25E-12	1.70E-09	-	-
Dcstamp	chr15:39745931-39760934	4.93	9.74	0.98	2.00E-06	2.33E-04	-	-
Chac1	chr2:119351241-119354327	4.96	9.88	0.99	8.08E-06	7.66E-04	-	+
H2-Q7	chr17:35439154-35443773	58.39	116.36	0.99	7.50E-10	2.18E-07	+	-
Gpr68	chr12:100876681-100908198	7.64	15.24	1	4.35E-08	8.03E-06	-	-
Il1a	chr2:129297369-129309972	19.27	39.18	1.02	6.01E-12	2.33E-09	+	-
Layn	chr9:51056779-51077094	10.93	22.12	1.02	1.37E-09	3.79E-07	-	-
Rasgrp1	chr2:117279992-117342877	0.46	0.94	1.04	1.23E-03	4.76E-02	-	-
Irg1	chr14:103047011-103056573	43.81	92.61	1.08	1.24E-14	1.03E-11	-	-
Il1b	chr2:129364579-129375733	25.65	54.76	1.09	5.89E-13	2.86E-10	+	-
Nnt	chr13:119334316-119409138	8.59	18.32	1.09	6.66E-13	3.10E-10	+	-
H2-Q6	chr17:35424876-35428361	32.54	69.21	1.09	2.29E-12	9.86E-10	+	-
A130040M12Rik	chr13:68233964-68450346	0.85	1.82	1.1	3.28E-04	1.69E-02	-	-
Heph	chrX:96455435-96574484	6.08	13.13	1.11	3.44E-11	1.25E-08	-	-
Csf1	chr3:107741047-107760469	21.98	48.32	1.14	1.75E-13	1.07E-10	+	-
Il20rb	chr9:100457718-100486473	4.52	9.97	1.14	3.12E-09	7.89E-07	-	-
Clec4e	chr6:123281788-123289871	224.77	506.54	1.17	9.20E-11	3.06E-08	-	-
Hspa1b	chr17:34956428-34959238	1.85	4.15	1.17	2.55E-06	2.85E-04	-	-
Adora2b	chr11:62248983-	1.99	4.53	1.18	2.82E-05	2.17E-03	-	-

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Serpinb1a	chr13:32842091-32851185	10.6	24.52	1.21	3.18E-13	1.61E-10	-	-	
Plcb1	chr2:134786163-135475258	0.92	2.15	1.22	9.88E-08	1.62E-05	-	-	
Traf1	chr2:34943257-34961772	2.41	5.65	1.23	1.99E-07	3.05E-05	-	+	
Il1rn	chr2:24336859-24351491	23.96	56.97	1.25	0.00E+00	0.00E+00	+	-	
Amotl1	chr9:14541966-14615000	0.49	1.17	1.26	8.58E-07	1.07E-04	-	-	
Cdc42ep2	chr19:5917555-5924816	2.45	5.86	1.26	8.14E-06	7.66E-04	-	-	
Flrt3	chr2:140395429-142390050	4.36	10.49	1.27	2.38E-12	9.89E-10	-	-	
Abcb4	chr5:8893720-8959226	0.84	2.05	1.28	4.30E-06	4.47E-04	-	-	
Dynlt1a	chr17:6310544-6317474	2.49	6.06	1.29	4.49E-04	2.19E-02	-	-	
Nfatc4	chr14:55824794-55833943	0.91	2.31	1.34	3.31E-05	2.46E-03	-	-	
Cxcl3	chr5:90786102-90788090	66.88	174.46	1.38	0.00E+00	0.00E+00	-	-	
Mtap1a	chr2:121289601-121351013	0.32	0.88	1.44	1.70E-04	9.86E-03	-	+	
Six1	chr12:73041826-73046712	1.2	3.47	1.53	3.81E-08	7.27E-06	-	-	
Col18a1	chr10:77052178-77166530	8.82	26.31	1.58	0.00E+00	0.00E+00	-	-	
Gatm	chr2:122594472-122611277	27.46	85.13	1.63	0.00E+00	0.00E+00	-	-	
Ccl24	chr5:135569936-135573043	100.51	318.64	1.66	0.00E+00	0.00E+00	-	-	
Tmc3	chr7:83584930-83623709	0.23	0.74	1.67	2.30E-05	1.87E-03	-	-	
Osmr	chr15:6813576-6874313	0.08	0.24	1.69	1.22E-03	4.72E-02	-	-	
Artn	chr4:117926161-117929763	1.51	5.18	1.78	2.28E-10	6.99E-08	-	-	
Six4	chr12:73100258-73113245	0.08	0.28	1.78	3.07E-04	1.60E-02	-	-	
Ccl22	chr8:94745683-94751388	0.57	2.17	1.94	1.10E-06	1.32E-04	+	-	
Thy1	chr9:44043383-44048579	0.14	0.58	2.06	7.58E-04	3.35E-02	-	-	
Atp8b1	chr18:64528978-64661000	0.09	0.41	2.27	4.60E-07	6.38E-05	-	-	
Dynlt1b	chr17:6430111-6436295	2.89	14.91	2.36	2.08E-13	1.21E-10	-	-	
Clu	chr14:65968482-65981545	0.05	0.42	3.14	4.10E-04	2.02E-02	-	-	
Exd1	chr2:119519403-119547627	0.06	0.57	3.25	4.83E-08	8.38E-06	-	+	
Gchfr	chr2:119167787-119172389	0.13	1.33	3.37	7.97E-04	3.49E-02	-	-	
Cd163l1	chr7:140218266-140231145	0.03	0.34	3.58	8.76E-06	8.03E-04	-	-	
Tmem181b-ps	chr17:6439001-6450994	0.39	5.6	3.84	0.00E+00	0.00E+00	-	-	
Gm14085	chr2:122484940-122528040	0.05	1.04	4.48	1.63E-13	1.06E-10	-	-	
Sfrp2	chr3:83766320-83774314	0	1.11	7.79	9.95E-04	4.08E-02	-	-	
Rpl31-ps12	chr16:16753015-16829363	0.37	146.86	8.64	0.00E+00	0.00E+00	-	-	

FPKM, fragments per kilobase of exon per million fragments mapped. In yellow are genes located on chromosome 2. Note that chromosome 2 contains significantly more differentially expressed genes (P

based on Z score [$Z > 44$] = 0.0011, corrected for chromosome size). This clustering is even more pronounced when considering the highly differentially expressed genes (absolute Log_2 fold change > 1) and correcting for chromosome size (P based on Z score [$Z > 29$] = 0.00039).

¹Involved in phagocytosis, if retrievable records on pubmed.gov using the search terms “gene xy phagocytosis”, and/or associated terms on geneontology.org, using unfiltered search parameters and considering all recorded species.

²Containing nonsynonymous SNPs between B6.129-Prnp^{wt/wt} and B6.129-Prnp^{Zrch1/Zrch1} pMΦs.