

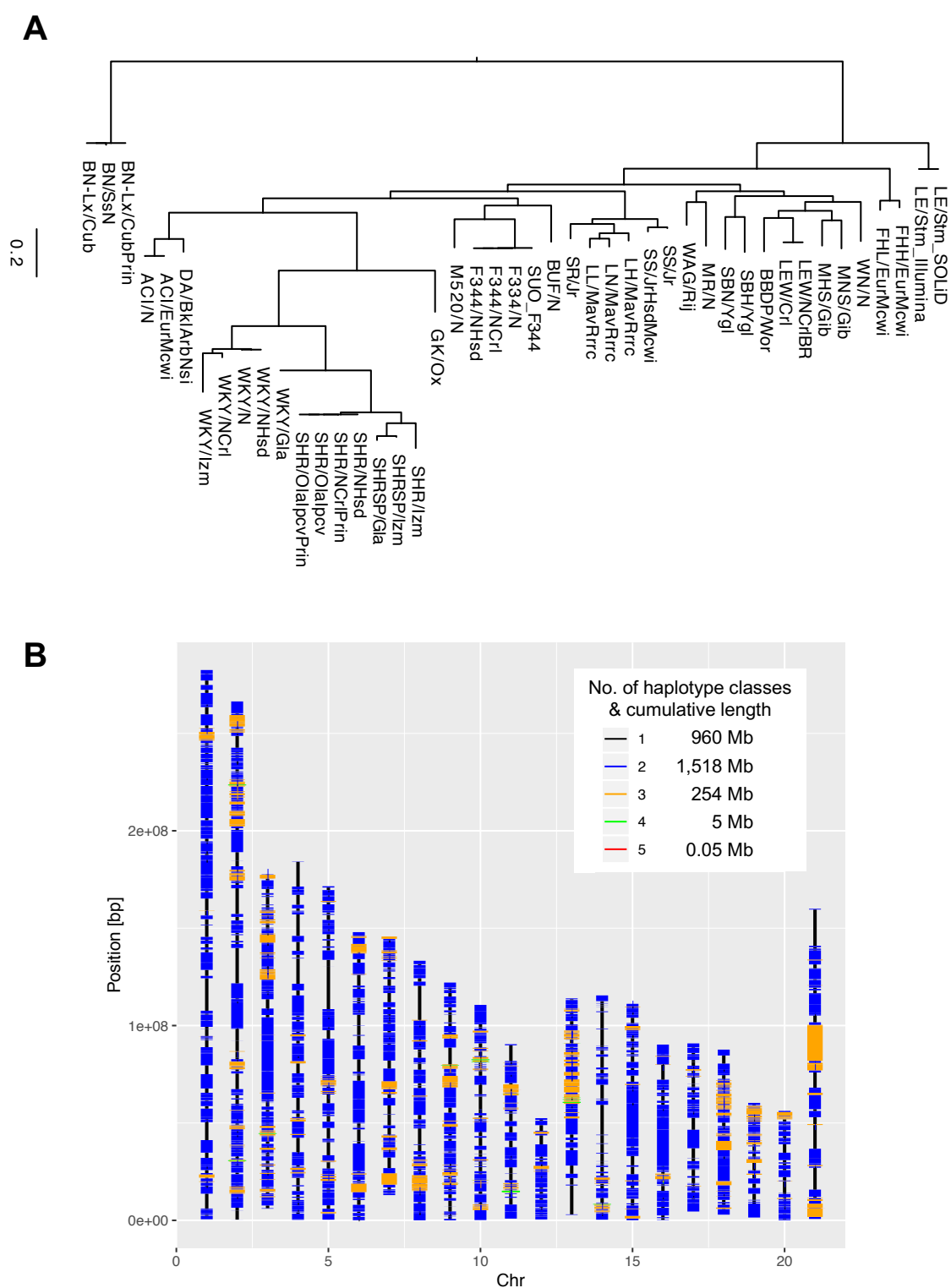


Fig. S1: Phylogenetic tree and ancestral haplotype map. (A) Whole genome sequencing (WGS) data for 12 Wistar Kyoto colony-derived strains and 33 other inbred rat strains are used for the construction of phylogenetic tree. To avoid bias in maximum likelihood estimation, the congenic strain 1pW9 is excluded from phylogenetic inference. **(B)** A map of ancestral haplotype is reconstructed for the Wistar Kyoto colony, based on WGS data for the present inbred strains. A cumulative length of chromosomal regions is shown for each number of ancestral haplotype classes (1 to 5) in the inset.

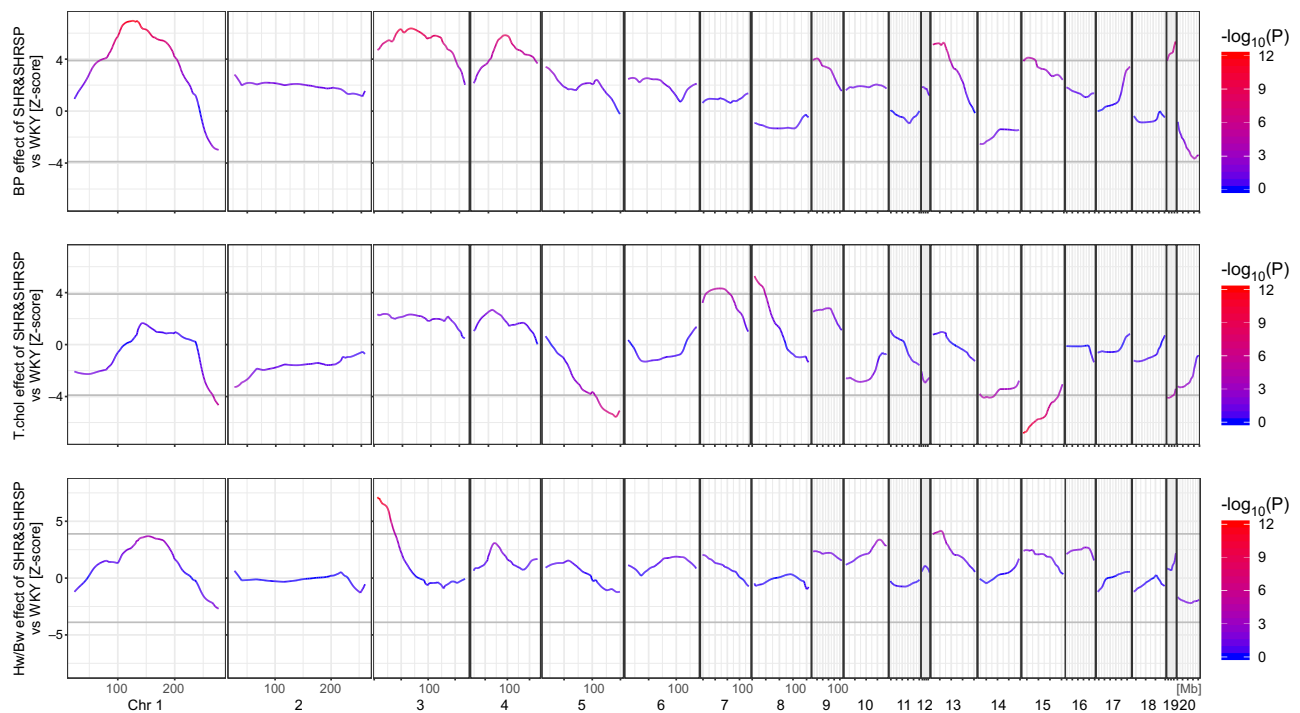


Fig. S2: Meta-analysis of genome-wide linkage scans. Genome-wide quantitative trait locus (QTL) mapping is performed on systolic blood pressure (BP) (in the top panel), plasma total cholesterol (in the middle panel) and heart weight divided by body weight (Hw/Bw) (in the bottom panel) in experimental crosses between WKY/lzm and SHR/lzm and between WKY/lzm and SHRSP/lzm. The underlying genotype is estimated at each locus on the genome, the genotype-phenotype association is examined under the additive model, and the strength of linkage is expressed in Z-score, where $|Z\text{-score}| > 3.89$, corresponding to $P < 1 \times 10^{-4}$, is defined to be genome-wide significant.

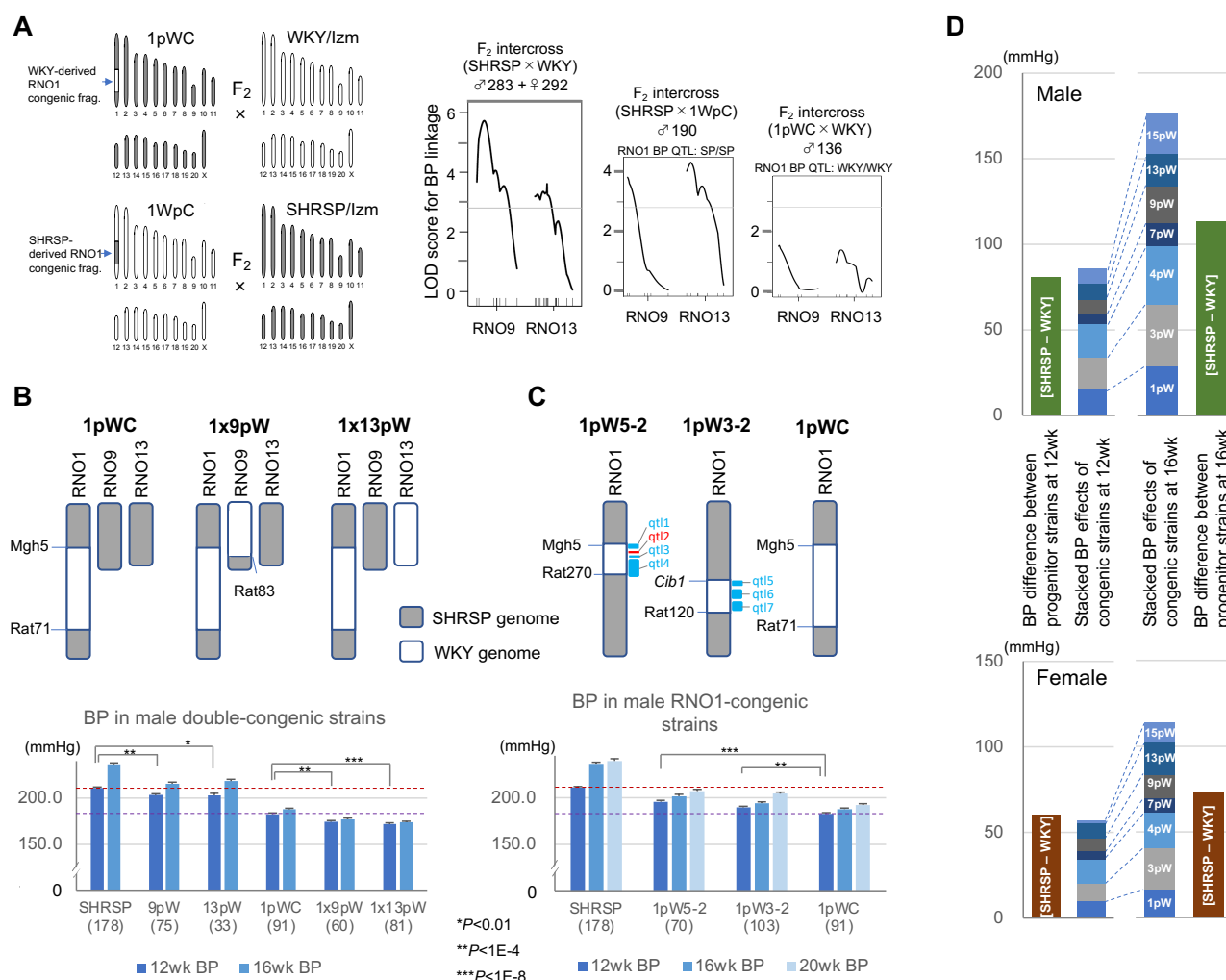


Fig. S3: Evaluation of potential epistatic interactions of BP QTLs. (A) Schematic explanation for the development of reciprocal F₂ intercrosses, which are produced between 1pWC and WKY and between SHRSP and 1WpC (see Methods). LOD score plots show potential epistatic interactions of BP QTLs between RNO1 and RNO9 and between RNO1 and RNO13. Comparison of BP measurements in two double congenic strains (1x9pW and 1x13pW) (**B**) and three RNO1-congenic strains (1pW5-2, 1pW3-2 and 1pWC) (**C**) with those in SHRSP/Izm indicates a diversity of composite effects of BP QTLs. See **Fig. S4A** about a panel of RNO1-congenic strains. (**D**) An aggregate of BP changes in 7 SHRSP-derived consomic strains is shown for males (in the upper panel) and females (in the lower panel).



Fig. S4: Panels of congenic strains developed for three rat chromosomes. (A) For RNO1, a consomic (1pW) and 15 congenic strains (1pW*; the asterisk indicates a further description of congenic strains) are

constructed from SHRSP/Izm and WKY/Izm, while consomic (1SW) and congenic (1SWC) strains are constructed from SHR/Izm and WKY/Izm. BP differences from the recipient (ie, hypertensive in this case) progenitor strains are shown in the left part; the location of congenic fragments and the likely interval of BP QTLs are shown together with a map of inter-strain genetic diversity (refer to **Fig. 3A**) in the right part. Here, the direction of BP changes at each QTL is colored in blue (decrease) or red (increase), compared with the recipient progenitor strains. **(B)** For RNO3, a consomic (3pW) and 5 congenic (3pW*) strains are constructed from SHRSP/Izm and WKY/Izm, while a consomic (3SW) and 6 congenic (3SW*) strains are constructed from SHR/Izm and WKY/Izm. **(C)** For RNO15, a consomic (15pW) and 2 congenic (15pW1 and 15pW2) strains are constructed from SHRSP/Izm and WKY/Izm, while a consomic (15SW) and 6 congenic (15SW1 and 15SW2) strains are constructed from SHR/Izm and WKY/Izm.

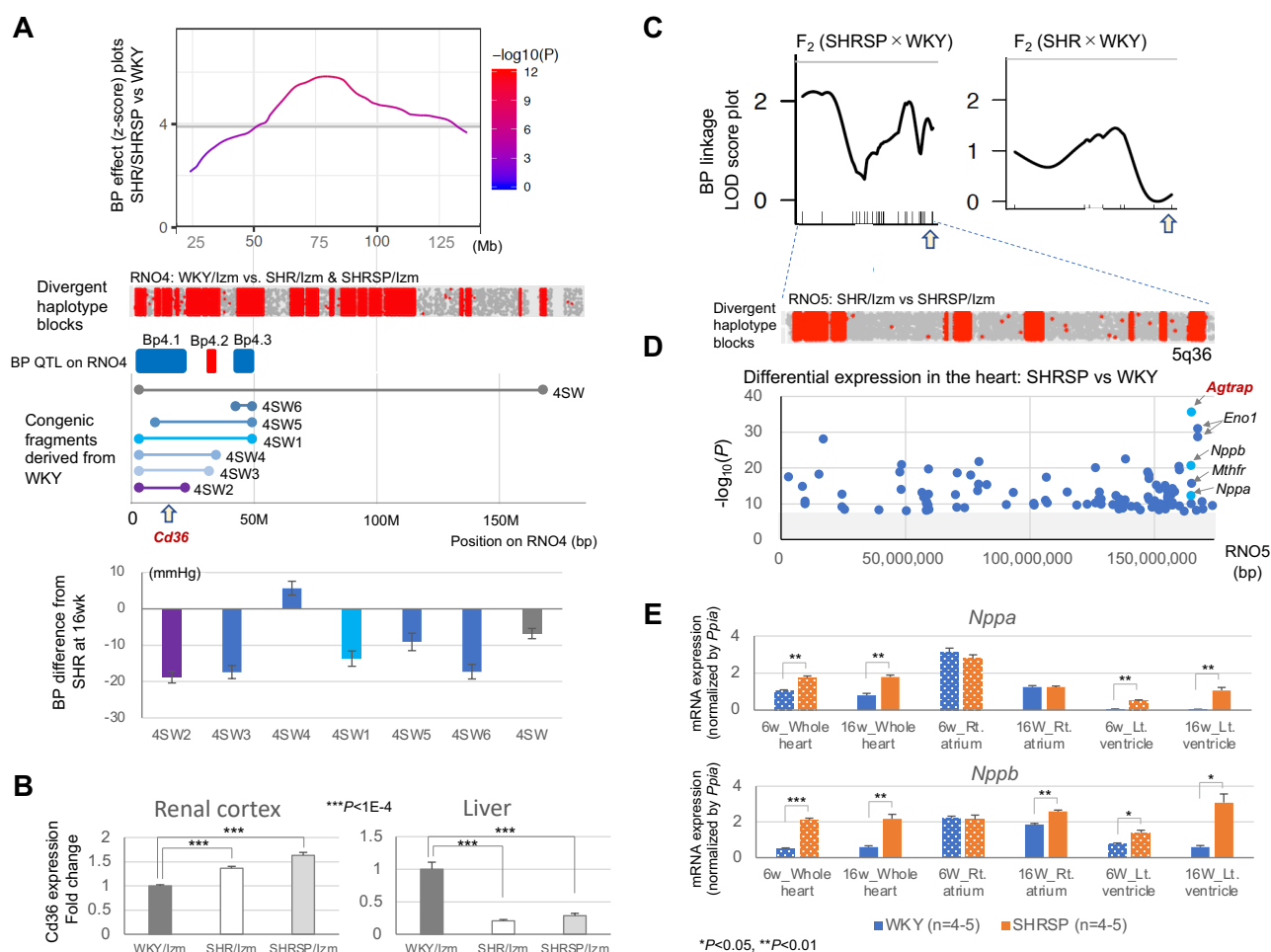


Fig. S5: BP QTLs with a complex genetic architecture on RNO4 and RNO5. (A) BP QTLs are detected in a region (3–49 Mb), at a distance from the linkage peak (81–87 Mb), in the upper panel: the location of congenic fragments and the likely interval of BP QTLs (Bp4.1 to 4.3) are shown together with a map of inter-strain genetic diversity (refer to Fig. 3A) in the middle panel; and BP differences from the recipient progenitor strain, SHR/Izm, are shown in the lower part. (B) Inter-strain differential mRNA expression of *Cd36*, located at Bp4.1, is significant ($P<1\times10^{-4}$) in the kidney and liver ($n=4$ per strain), shown by fold change (SHR/Izm versus WKY/Izm). (C) A tendency of BP linkage is detectable in F₂ (SHRSP/Izm×WKY/Izm) but not in F₂ (SHR/Izm×WKY/Izm) by linkage plots, where the position of 5q36 is indicated by arrows. (D) Regional plots of differential gene expression on RNO5 in the heart between SHRSP/Izm and WKY/Izm. The dots indicate significant ($P<1\times10^{-8}$) transcripts, with the names provided for some highly significant genes on 5q36. (E) Inter-strain differential gene expression of *Nppa* and *Nppb*, with each evaluated by qPCR for the whole heart, right atrium and left ventricle, longitudinally at 6 weeks and 16 weeks of age. * $P<0.05$, ** $P<0.01$ by unpaired *t* test.

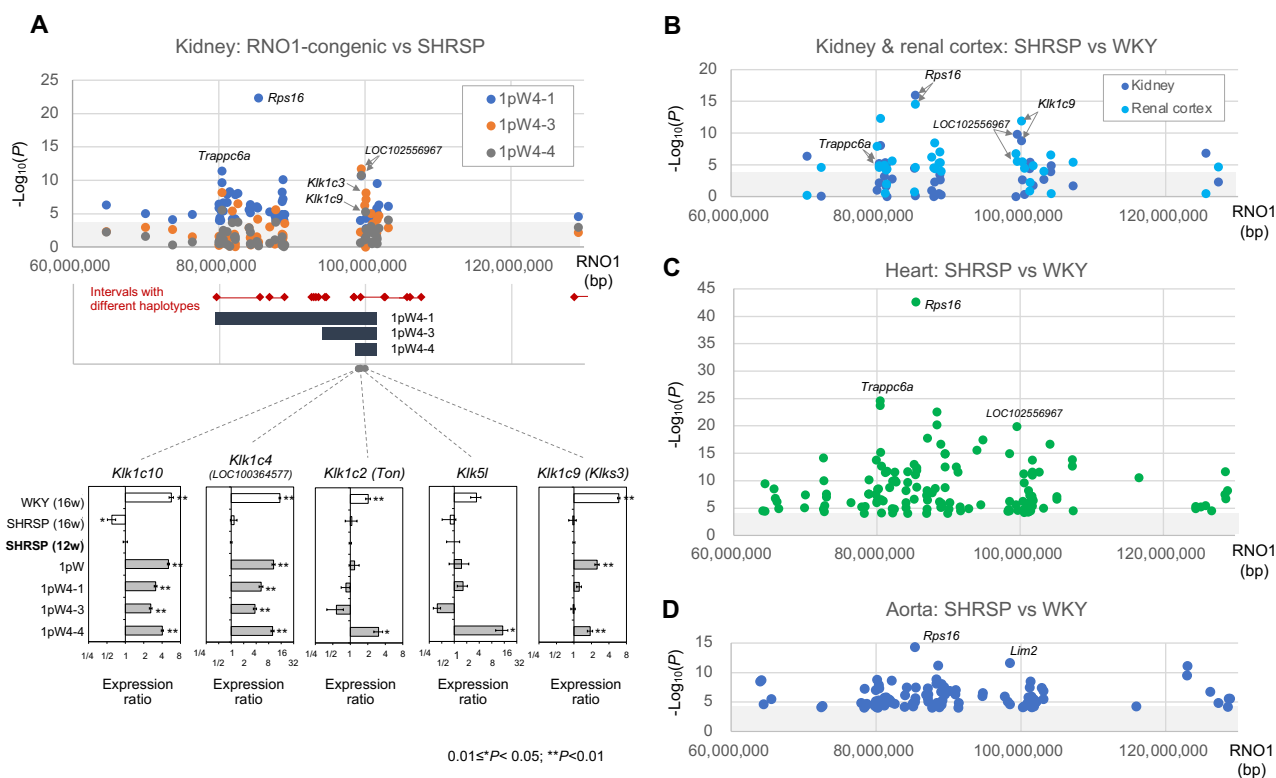


Fig. S6: Fine congenic mapping and gene expression profiling in the target region on RNO1. (A) Regional plots of differential gene expression in the kidney between SHRSP/Izm and each of three RNO1-congenic strains (1pW4-1, 1pW4-3 and 1pW4-4), in combination with fine congenic mapping and mRNA expression analysis of the *Kik1* paralogues. $*P < 0.05$, $**P < 0.01$. Regional plots of differential gene expression between SHRSP/Izm and WKY/Izm are also shown for the kidney and renal cortex (B), heart (C) and aorta (D). The dots indicate modestly significant ($P < 1 \times 10^{-4}$) transcripts, with the names provided for some highly significant genes. In panels, A and B, when a given transcript attains $P < 1 \times 10^{-4}$ in comparison with any of 3 congenic strains (in A) or either of 2 tissues (in B), $-\log_{10}(P)$ values of that transcript are displayed for all strains or tissues (which may show $P \geq 1 \times 10^{-4}$).

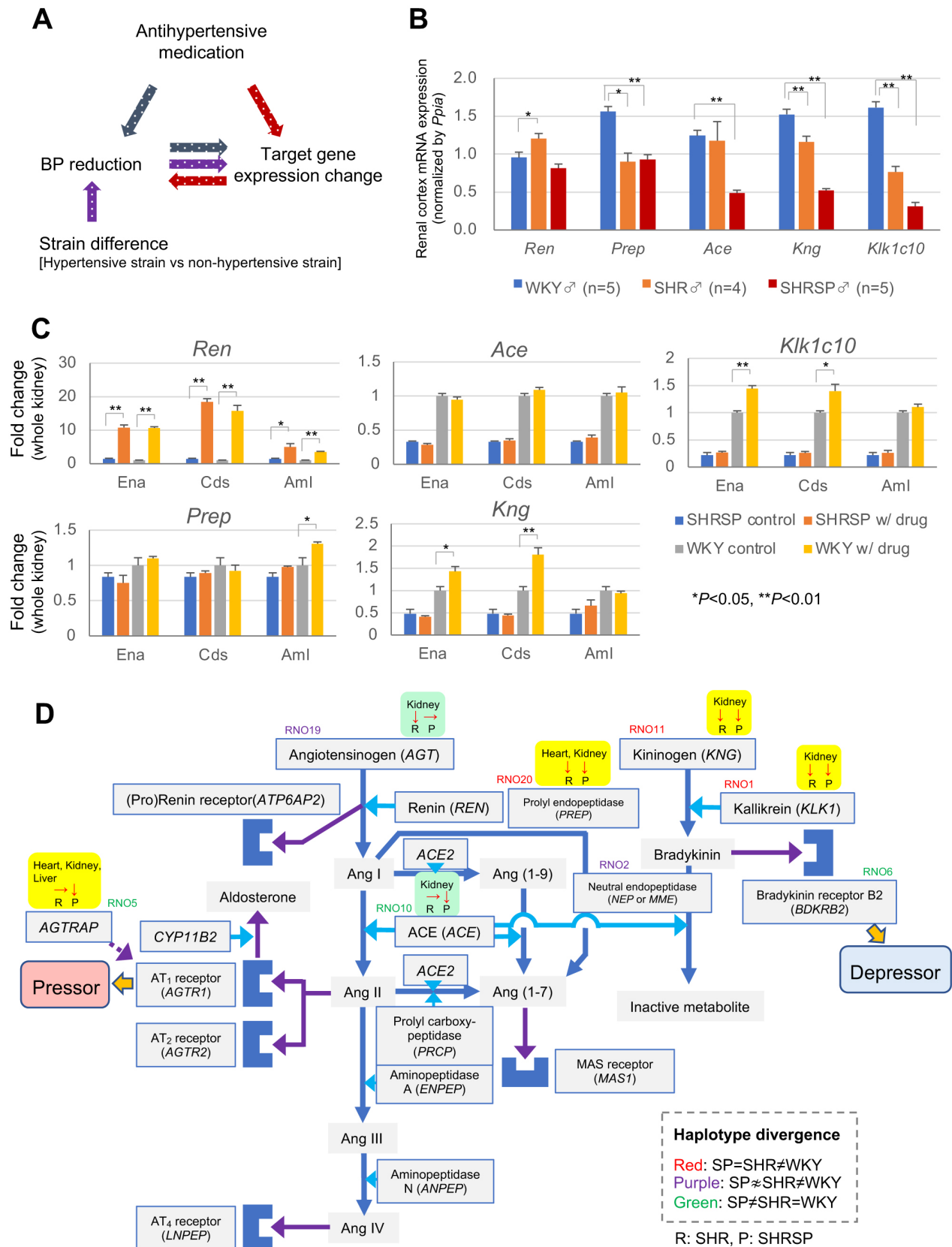


Fig. S7: Gene expression changes in target tissues of progenitor strains, induced by pharmacological intervention. (A) Cause and effect relationship of BP reduction. BP reduction can result from strain differences and antihypertensive medication, either of which will lead to gene expression changes in a BP-

dependent manner. On the other hand, some antihypertensive drugs may influence the expression of particular genes without changing systemic BP, ie, in a BP-independent manner via pharmacological activity, then causing BP reduction. **(B)** Inter-strain differential expression of 5 genes, which are components of the kallikrein-kinin and renin-angiotensin systems (KKS/RAS), in the renal cortex, evaluated by qPCR. **(C)** mRNA expression changes evaluated by qPCR for 5 KKS/RAS genes in the kidney of progenitor strains with and without a 4-week administration of enalapril (Ena), candesartan (Cds) and amlodipine (Aml), where mRNA expression level in WKY/Izm without drug administration is set to be 1. * $P < 0.05$, ** $P < 0.01$. **(D)** A diagram of the KKS/RAS and the relationship of KKS/RAS gene expression changes identified in SHR and SHRSP; in the diagram, enalapril prevents an enzyme, angiotensin converting enzyme (ACE), from producing angiotensin II (Ang II) and inactivating bradykinin, while candesartan blocks the action of Ang II by binding to and inhibiting the AT₁ receptor.

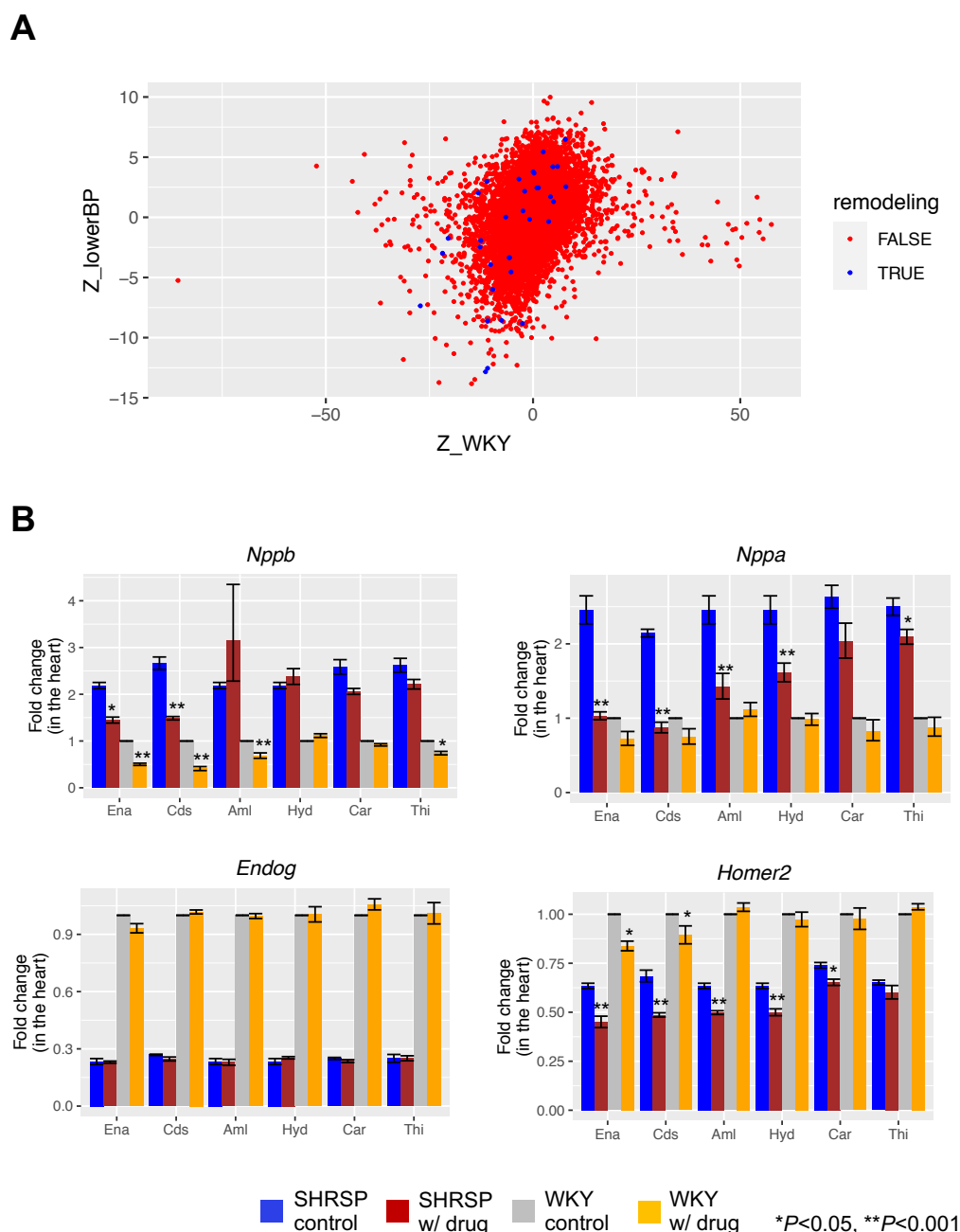


Fig. S8: Differential gene expression in the heart and drug specificity. (A) An overall fair correlation ($r=0.325$, $P<2.2\times 10^{-16}$) of differential gene expression between strain differences (non-hypertensive WKY/Izm versus hypertensive SHRSP/Izm, Z-score in x-axis) and antihypertensive medication (a group of rats treated with any of the four BP-decreasing drugs versus their control group, Z-score in y-axis) (refer to **Fig. 6**). WKY allele-associated effects tend to be positively correlated with BP lowering effects on mRNA expression differences; the correlation is pronounced for a group of genes (blue dots; the gene list is drawn from a study by Saucerman *et al.*, 2019, PMID: 30683889) that are involved in cardiac remodeling in response to alteration of mechanical cues ($r=0.590$). **(B)** mRNA expression changes of 4 candidate genes in the heart of progenitor strains with and without a 4-week administration of 6 antihypertensive drugs, where mRNA expression level in WKY/Izm without drug administration is set to be 1.

Table S1. Genome-wide haplotype structure of Wistar Kyoto colony-derived strains

No. of region	Chr	Start (Rnor_6.0)	End (Rnor_6.0)	No. of haplotype classes	LD clusters count	Ancestral haplotype segments [haplotype number for individual strain]	Wistar Kyoto colony-derived strains												
							SHRSP/ Glia	1pW9 (SHRSP- derived congenic)	SHRSP/ lzm	SHR/ Olapcv	SHR/ NCrlPrin	SHR/ NHsd	SHR/Ola lpcvPrin	SHR/lzm	WKY/Gla	WKY/ lzm	WKY/N	WKY/ NCrl	WKY/ NHsd
							[2]	[10]	[12]	[1]	[3]	[4]	[5]	[11]	[7]	[13]	[6]	[8]	[9]
1	1	558,853	2,371,874	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0_1.793	1	1	1	1	1	1	1	1	1	2	1	1	1
2	1	2,371,875	2,782,592	1	0														
3	1	2,782,593	3,385,165	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0_1.701	1	1	1	1	1	1	1	1	2	1	1	1	
4	1	3,385,166	3,537,217	1	0														
5	1	3,537,218	5,492,362	2	1	0_0_0_0_0_1_0_0_1_0_0_0_0_1.212	1	1	1	1	1	1	1	1	1	2	2	1	2
6	1	5,492,363	5,737,252	1	0														
7	1	5,737,253	6,088,449	2	1	0_0_0_0_0_1_0_0_1_0_0_0_0_1.500	1	1	1	1	1	1	1	1	1	2	2	1	2
8	1	6,088,450	13,700,488	1	0														
9	1	13,700,489	15,158,018	2	1	1_1_1_1_1_1_0_1_1_1_1_1.150	2	2	2	2	2	2	2	2	2	2	1	2	
10	1	15,158,019	15,160,758	1	0														
11	1	15,160,759	17,422,542	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0.334	2	2	2	2	2	2	2	2	2	1	1	1	
12	1	17,422,543	17,423,064	1	0														
13	1	17,423,065	17,473,223	2	1	1_1_1_1_1_1_0_1_1_1_1_1.1.86	2	2	2	2	2	2	2	2	2	2	1	2	
14	1	17,473,224	17,794,944	1	0														
15	1	17,794,945	19,128,873	2	1	0_0_0_0_0_0_0_1_0_0_0_0_0_1.631	1	1	1	1	1	1	1	1	1	2	1	2	
16	1	19,128,874	19,332,898	1	0														
17	1	19,332,899	19,779,021	2	1	0_1_0_0_0_1_0_0_1_1_0_1_0_1.0.530	2	2	2	1	1	1	1	1	1	1	2	1	
18	1	19,779,022	19,779,141	3	2	0_1_0_0_0_1_0_0_1_1_0_1_0_1.0.530	3	3	3	2	2	2	2	2	2	1	3	1	
19	1	19,779,142	20,001,852	3	3	0_0_0_0_0_0_0_1_0_0_0_0_0_1.940	2	2	2	1	1	1	1	1	1	3	2	3	
20	1	20,001,853	20,008,191	4	4	0_0_0_0_0_0_0_1_0_0_0_0_0_1.940	2	2	2	1	1	1	1	1	1	4	2	3	
21	1	20,008,192	20,013,655	4	3	0_1_0_0_0_1_0_0_1_1_0_1_0_1.0.530	4	4	4	3	3	3	3	3	3	2	4	1	
22	1	20,013,656	20,020,072	3	2	1_0_1_1_1_0_1_0_0_0_1_0_0.224	2	2	2	3	3	3	3	3	3	2	2	1	
23	1	20,020,073	20,041,244	2	1	1_1_1_1_1_1_0_1_0_1_1_1_1.1.77	2	2	2	2	2	2	2	2	2	2	2	1	
24	1	20,041,245	20,043,042	1	0														
25	1	20,043,043	21,529,918	2	1	0_1_0_0_0_1_0_0_1_1_0_1_0_1.0.131	2	2	2	1	1	1	1	1	1	2	1	2	
26	1	21,529,919	21,917,575	1	0														
27	1	21,917,576	21,921,040	2	1	0_0_0_0_0_0_0_1_0_0_0_0_0_1.512	1	1	1	1	1	1	1	1	1	2	1	2	
28	1	21,921,041	23,567,341	3	2	0_0_0_0_0_0_0_1_0_0_0_0_0_1.512	2	2	2	2	2	2	2	2	2	3	1	3	
29	1	23,567,342	24,270,697	2	1	0_0_0_0_0_0_0_1_0_0_0_0_0_1.512	1	1	1	1	1	1	1	1	1	2	1	2	
30	1	24,270,698	25,813,594	1	0														
31	1	25,813,595	27,430,847	2	1	1_1_1_1_1_0_1_1_0_1_1_1_1.1.419	2	2	2	2	2	2	2	2	2	2	1	2	
32	1	27,430,848	27,432,118	1	0														
33	1	27,432,119	28,365,567	2	1	1_1_1_1_1_0_1_0_0_1_1_1_1.1.904	2	2	2	2	2	2	2	2	2	2	1	1	
34	1	28,365,568	28,370,790	1	0														
35	1	28,370,791	32,065,780	2	1	1_1_1_1_1_0_1_1_0_1_1_1_1.1.275	2	2	2	2	2	2	2	2	2	2	1	2	
36	1	32,065,781	34,752,986	1	0														
37	1	34,752,987	41,194,064	2	1	0_1_0_0_0_0_0_0_0_1_0_1_0_1.0.282	2	2	2	1	1	1	1	1	1	1	1	1	
38	1	41,194,065	50,364,378	1	0														
39	1	50,364,379	51,093,314	2	1	1_0_1_1_1_1_1_0_1_1_1_1_1.1.104	1	2	2	2	2	2	2	2	2	2	1	2	
40	1	51,093,315	51,096,766	1	0														
41	1	51,096,767	51,856,782	2	1	1_0_1_1_1_1_1_0_1_1_1_1_1.0.803	1	2	2	2	2	2	2	2	2	1	2	2	
42	1	51,856,783	52,028,646	1	0														
43	1	52,028,647	52,889,397	2	1	1_0_1_1_1_1_1_0_1_1_1_1_1.0.115	1	2	2	2	2	2	2	2	2	1	2	2	
44	1	52,889,398	52,919,964	1	0														
45	1	52,919,965	53,268,709	2	1	1_0_1_1_1_1_1_1_1_1_1_1_1.0.244	1	2	2	2	2	2	2	2	2	1	2		
46	1	53,268,710	53,282,158	1	0														
47	1	53,282,159	57,362,320	2	1	1_0_1_1_1_1_1_1_1_1_1_1_1.1.111	1	2	2	2	2	2	2	2	2	2	2		
48	1	57,362,321	58,653,132	1	0														
49	1	58,653,133	61,220,168	2	1	1_0_1_1_1_1_1_1_1_1_1_1_1.1.976	1	2	2	2	2	2	2	2	2	2	2		
50	1	61,220,169	61,344,766	1	0														
51	1	61,344,767	61,465,598	2	1	1_0_1_1_1_1_1_1_1_1_1_1_1.1.36	1	2	2	2	2	2	2	2	2	2	2		
52	1	61,465,599	61,670,453	1	0														
53	1	61,670,454	63,132,940	2	1	1_0_1_1_1_1_1_1_1_1_1_1_1.1.960	1	2	2	2	2	2	2	2	2	2	2		
54	1	63,132,941	63,166,736	1	0														
55	1	63,166,737	64,648,925	2	1	0_0_0_0_0_1_1_1_1_1_0_1_1.1.784	1	2	2	1	1	1	1	1	2	2	2	2	
56	1	64,648,926	64,705,694	1	0														
57	1	64,705,695	65,498,384	2	1	1_0_1_1_1_1_1_1_1_1_1_1_1.1.185	1	2	2	2	2	2	2	2	2	2	2		
58	1	65,498,385	67,709,543	1	0														
59	1	67,709,544	75,061,343	2	1	0_0_0_0_0_1_1_1_1_1_0_1_1.1.314	1	2	2	1	1	1	1	1	2	2	2	2	
60	1	75,061,344	79,608,513	1	0														
61	1	79,608,514	85,545,574	2	1	0_1_0_0_0_0_0_0_0_1_0_1_0_1.0.437	2	2	2	1	1	1	1	1	1	1	1	1	
62	1	85,545,575	85,588,908	1	0														
63	1	85,588,909	85,976,721	2	1	1_1_1_1_1_0_1_1_0_1_1_1_1.1.695	2	2	2	2	2	2	2	2	2	2	1	2	
64	1	85,976,722	85,984,892	1	0														
65	1	85,984,893	86,825,798	2	1	1_0_1_1_1_1_1_1_1_1_1_1_1.1.505	1	2	2	2	2	2	2	2	2	2	2		
66	1	86,825,799	86,835,763	1	0														
67	1	86,835,764	88,914,994	2	1	0_1_0_0_0_0_0_0_0_1_0_1_0_1.0.104	2	2	2	1	1	1	1	1	1	1	1	1	
68	1	88,914,995	92,615,962	1	0														
69	1	92,615,963	92,917,237	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0_1.318	1	1	1	1	1	1	1	1	2	1	1		
70	1	92,917,238	93,229,460	1	0														
71	1	93,229,461	93,573,019	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0_1.290	1	1	1	1	1	1	1	1	2	1	1		
72	1	93,573,020	93,856,420	1	0														
73	1	93,856,421	94,462,831	2	1	1_1_1_1_1_0_0_0_0_0_1_1_1.1.1452	2	2	2	2	2	2	2	2	1	2	1		
74	1	94,462,832	94,508,155	3	2	1_1_1_1_1_0_0_0_0_0_1_1_1.0.171	3	3	3	3	3	3	3	3	1	2	1		
75	1	94,508,156	94,636,774	2	1	1_1_1_1_1_0_0_0_0_0_1_1_1.0.171	2	2	2	2	2	2	2	2	1	1	1	1	
76	1	94,636,775	98,360,380	1	0														
77	1	98,360,381	98,426,698	2	1	1_1_1_1_1_0_1_0_0_1_1_1_0.87	2	2	2	2	2	2	2	2	2	1	1	1	
78	1	98,426,699	99,315,979	1	0														

79	1	99,315,980	102,566,923	2	1	1_1_1_1_1_0_1_0_0_1_1_1_0.512	2	2	2	2	2	2	2	2	2	2	1	1	1	1
80	1	102,566,924	102,690,159	1	0															
81	1	102,690,160	105,670,912	2	1	0_1_0_0_0_0_0_0_0_1_1_0.221	2	2	2	2	1	1	1	1	2	1	1	1	1	
82	1	105,670,913	106,087,660	1	0															
83	1	106,087,661	107,612,574	2	1	0_1_0_0_0_0_0_0_0_1_1_0.138	2	2	2	2	1	1	1	1	2	1	1	1	1	
84	1	107,612,575	124,287,025	1	0															
85	1	124,287,026	125,499,215	2	1	1_1_1_1_1_0_1_0_0_1_1_1.648	2	2	2	2	2	2	2	2	2	2	1	1	1	
86	1	125,499,216	128,601,412	1	0															
87	1	128,601,413	132,276,744	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0307	2	2	2	2	2	2	2	2	2	2	1	1	1	
88	1	132,276,745	132,369,454	1	0															
89	1	132,369,455	137,606,926	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0498	2	2	2	2	2	2	2	2	2	2	1	1	1	
90	1	137,606,927	138,765,018	1	0															
91	1	138,765,019	139,067,793	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0382	2	2	2	2	2	2	2	2	2	2	1	1	1	
92	1	139,067,794	139,262,851	1	0															
93	1	139,262,852	140,123,614	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0911	2	2	2	2	2	2	2	2	2	2	1	1	1	
94	1	140,123,615	141,966,315	1	0															
95	1	141,966,316	143,583,679	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0127	2	2	2	2	2	2	2	2	2	2	1	1	1	
96	1	143,583,680	143,950,813	1	0															
97	1	143,950,814	145,513,870	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0103	2	2	2	2	2	2	2	2	2	2	1	1	1	
98	1	145,513,871	151,472,952	1	0															
99	1	151,472,953	151,779,500	2	1	1_0_1_1_1_0_1_0_0_1_1_1.1205	1	2	2	2	2	2	2	2	2	2	2	1	1	
100	1	151,779,501	154,682,506	1	0															
101	1	154,682,507	155,738,749	2	1	1_0_1_1_1_0_1_0_0_1_1_1.1738	1	2	2	2	2	2	2	2	2	2	2	1	1	
102	1	155,738,750	155,763,512	3	2	1_0_1_1_1_0_1_0_0_1_1_1.1738	2	3	3	3	3	3	3	3	3	3	3	1	1	
103	1	155,763,513	156,443,285	2	1	1_0_1_1_1_0_1_0_0_1_1_1.1738	1	2	2	2	2	2	2	2	2	2	2	1	1	
104	1	156,443,286	156,509,733	1	0															
105	1	156,509,734	156,638,901	2	1	1_1_1_1_1_0_1_0_0_1_1_1.174	2	2	2	2	2	2	2	2	2	2	2	1	1	
106	1	156,638,902	159,028,968	1	0															
107	1	159,028,969	159,029,403	2	1	1_0_1_1_1_0_0_0_0_0_0_0.123	1	1	1	2	2	2	2	2	1	1	2	1	1	
108	1	159,029,404	159,157,006	3	2	0_0_0_0_0_0_0_0_0_0_0_0.127	1	1	1	2	2	2	2	2	1	1	3	1	1	
109	1	159,157,007	159,157,695	2	1	1_0_1_1_1_0_0_0_0_0_0_0.123	1	1	1	2	2	2	2	2	1	1	2	1	1	
110	1	159,157,696	165,214,655	1	0															
111	1	165,214,655	168,469,070	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0301	2	2	2	2	2	2	2	2	2	2	1	1	1	
112	1	168,469,071	169,078,850	1	0															
113	1	169,078,851	170,041,068	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0797	2	2	2	2	2	2	2	2	2	2	1	1	1	
114	1	170,041,069	170,194,497	1	0															
115	1	170,194,498	176,044,710	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0394	2	2	2	2	2	2	2	2	2	2	1	1	1	
116	1	176,044,711	176,063,475	1	0															
117	1	176,063,476	177,038,679	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0107	2	2	2	2	2	2	2	2	2	2	1	1	1	
118	1	177,038,680	177,105,368	1	0															
119	1	177,105,369	177,395,264	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0298	2	2	2	2	2	2	2	2	2	2	1	1	1	
120	1	177,395,265	177,511,936	1	0															
121	1	177,511,937	184,474,684	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0193	2	2	2	2	2	2	2	2	2	2	1	1	1	
122	1	184,474,685	184,475,528	1	0															
123	1	184,475,529	184,993,034	2	1	1_1_1_1_1_0_1_0_0_1_1_1.1404	2	2	2	2	2	2	2	2	2	2	1	2	1	
124	1	184,993,035	184,993,652	1	0															
125	1	184,993,653	187,584,314	2	1	0_0_0_0_0_0_0_0_0_0_0_0.1267	1	1	1	1	1	1	1	1	1	1	2	1	2	
126	1	187,584,315	188,176,103	1	0															
127	1	188,176,104	189,081,346	2	1	0_0_0_0_0_0_0_0_0_0_0_0.1738	1	1	1	1	1	1	1	1	1	1	2	1	2	
128	1	189,081,347	189,082,713	1	0															
129	1	189,082,714	189,296,104	2	1	0_0_0_0_0_0_0_0_0_0_0_0.1360	1	1	1	1	1	1	1	1	1	1	2	1	1	
130	1	189,296,105	189,297,690	1	0															
131	1	189,297,691	189,388,700	2	1	1_1_1_1_1_0_1_0_0_1_1_1.125	2	2	2	2	2	2	2	2	2	2	2	1	1	
132	1	189,388,701	189,445,639	1	0															
133	1	189,445,640	193,635,180	2	1	1_1_1_1_1_0_1_0_0_1_1_1.1208	2	2	2	2	2	2	2	2	2	2	2	1	1	
134	1	193,635,181	193,699,572	1	0															
135	1	193,699,573	194,075,168	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0448	2	2	2	2	2	2	2	2	2	2	1	1	1	
136	1	194,075,169	194,076,882	1	0															
137	1	194,076,883	194,580,835	2	1	1_1_1_1_1_0_1_0_0_1_1_1.1362	2	2	2	2	2	2	2	2	2	2	2	1	1	
138	1	194,580,836	195,970,719	1	0															
139	1	195,970,720	197,993,994	2	1	1_1_1_1_1_0_1_0_0_1_1_1.0224	2	2	2	2	2	2	2	2	2	2	1	1	1	
140	1	197,993,995	197,999,055	1	0															
141	1	197,999,056	200,356,425	2	1	0_1_0_0_0_0_0_0_0_1_1_1.0148	2	2	2	2	1	1	1	1	2	1	1	1	1	
142	1	200,356,426	200,377,883	1	0															
143	1	200,377,884	201,929,971	2	1	0_0_0_0_0_0_0_0_0_0_0_0.0102	1	1	1	1	1	1	1	1	2	1	1	1	1	
144	1	201,929,972	202,033,374	1	0															
145	1	202,033,375	202,455,616	2	1	0_1_0_0_0_0_0_0_0_1_1_1.0233	2	2	2	2	1	1	1	1	2	1	1	1	1	
146	1	202,455,617	202,508,332	1	0															
147	1	202,508,333	205,418,671	2	1	0_0_0_0_0_0_0_0_0_0_0_0.0130	1	1	1	1	1	1	1	1	2	1	1	1	1	
148	1	205,418,672	206,474,727	1	0															
149	1	206,474,728	214,640,486	2	1	0_0_0_0_0_0_0_0_0_0_0_0.0704	1	1	1	1	1	1	1	1	2	1	1	1	1	
150	1	214,640,487	214,712,569	1	0															
151	1	214,712,570	218,155,530	2	1	0_0_0_0_0_0_0_0_0_0_0_0.0288	1	1	1	1	1	1	1	1	2	1	1	1	1	
152	1	218,155,531	218,390,296	1	0															
153	1	218,390,297	223,016,428	2	1	0_0_0_0_0_0_0_0_0_0_0_0.0330	1	1	1	1	1	1	1	1	2	1	1	1	1	
154	1	223,016,429	223,488,703	1	0															
155	1	223,488,704	226,821,144	2	1	0_0_0_0_0_0_0_0_0_0_0_0.0196	1	1	1	1	1	1	1	1	2	1	1	1	1	
156	1	226,821,145	226,822,470	1	0															
157	1	226,822,471	231,420,049	2	1	1_1_1_1_1_0_1_0_0_1_0_0.0368	2	2	2	2	2	2	2	2	2	1	2	1	1	
158	1	231,420,050	231,671,705	1	0															
159	1	231,671,706	232,127,607	2	1	0_0_0_0_0_0_1_0_1_1_1_0.1198	1	2	1	1	1	1	1	1	2	1	2	2	2	
160	1	232,127,608	232,299,761	1	0															
161	1	232,299,762	233,668,478	2	1	0_0_0_0_0_0_1_0_1_1_1_0.1108	1	2	1	1	1									

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504	2	203,212,047	203,688,491	3	3	0_0_0_0_0_0_0_0_0_0_1_0_0.225	2	2	2	2	2	2	2	3	1	1	1	1	1
505	2	203,688,492	203,725,561	3	2	0_0_0_0_0_0_0_0_0_0_1_0_0.225	2	2	2	2	2	2	2	3	1	1	1	1	1
506	2	203,725,562	206,020,275	3	3	0_0_0_0_0_0_0_0_0_0_1_0_0.225	2	2	2	2	2	2	2	3	1	1	1	1	1
507	2	206,020,276	206,025,814	3	2	0_0_0_0_0_0_0_0_0_0_1_0_0.225	2	2	2	2	2	2	2	3	1	1	1	1	1
508	2	206,025,815	207,253,169	2	1	1_1_1_1_1_0_0_0_0_0_1_1_1_0.192	2	2	2	2	2	2	2	2	1	1	1	1	1
509	2	207,253,170	207,298,915	3	2	1_1_1_1_1_0_0_0_0_0_1_0_1_0.118	3	3	3	3	3	3	3	2	1	1	1	1	1
510	2	207,298,916	207,713,827	2	1	1_1_1_1_1_0_0_0_0_0_1_0_1_0.118	2	2	2	2	2	2	2	1	1	1	1	1	1
511	2	207,713,828	208,867,193	3	2	0_0_0_0_0_0_0_0_0_0_1_0_1.578	2	2	2	2	2	2	2	3	1	3	1	1	1
512	2	208,867,194	208,913,444	2	1	1_1_1_1_1_0_0_0_0_0_1_0_1_0.118	2	2	2	2	2	2	2	1	1	1	1	1	1
513	2	208,913,445	209,565,206	3	2	0_0_0_0_0_0_0_0_0_0_1_0_1.727	2	2	2	2	2	2	2	3	1	3	1	1	1
514	2	209,565,207	209,794,898	3	3	0_0_0_0_0_0_0_0_0_0_1_0_1.727	2	2	2	2	2	2	2	3	1	3	1	1	1
515	2	209,794,899	209,922,119	3	2	0_0_0_0_0_0_0_0_0_0_1_0_1.727	2	2	2	2	2	2	2	3	1	3	1	1	1
516	2	209,922,120	210,014,948	2	1	0_0_0_0_0_0_0_0_0_0_1_0_1.727	1	1	1	1	1	1	1	2	1	2	1	1	1
517	2	210,014,949	210,017,247	1	0														
518	2	210,017,248	210,217,725	2	1	1_1_1_1_1_0_0_0_0_0_1_0_1_0.235	2	2	2	2	2	2	2	1	1	1	1	1	1
519	2	210,217,726	210,448,939	3	2	0_0_0_0_0_0_0_0_0_0_1_0_1.119	2	2	2	2	2	2	2	3	1	3	1	1	1
520	2	210,448,940	210,478,159	2	1	0_0_0_0_0_0_0_0_0_0_1_0_1.119	1	1	1	1	1	1	1	2	1	2	1	1	1
521	2	210,478,160	210,526,684	1	0														
522	2	210,526,685	211,034,632	2	1	1_1_1_1_1_0_0_0_0_0_1_1_1_1.334	2	2	2	2	2	2	2	2	1	2	1	1	1
523	2	211,034,633	211,040,401	1	0														
524	2	211,040,402	211,327,186	2	1	1_1_1_1_1_0_0_0_0_0_1_1_1_0.217	2	2	2	2	2	2	2	2	1	1	1	1	1
525	2	211,327,187	211,340,169	1	0														
526	2	211,340,170	212,232,015	2	1	0_0_0_0_0_0_0_0_0_0_1_0_0.702	1	1	1	1	1	1	1	2	1	1	1	1	1
527	2	212,232,016	212,330,382	1	0														
528	2	212,330,383	213,506,787	2	1	0_0_0_0_0_0_0_0_0_0_1_0_0.512	1	1	1	1	1	1	1	2	1	1	1	1	1
529	2	213,506,788	213,507,391	3	2	0_0_0_0_0_0_0_0_0_0_1_0_0.512	2	2	2	2	2	2	2	3	1	1	1	1	1
530	2	213,507,392	213,578,514	3	3	0_0_0_0_0_0_0_0_0_0_1_0_0.512	2	2	2	2	2	2	2	3	1	1	1	1	1
531	2	213,578,515	213,580,315	3	2	0_0_0_0_0_0_0_0_0_0_1_0_0.512	2	2	2	2	2	2	2	3	1	1	1	1	1
532	2	213,580,316	213,580,978	2	1	1_1_1_1_1_0_0_0_0_0_1_0_1_0.616	2	2	2	2	2	2	2	1	1	1	1	1	1
533	2	213,580,979	213,584,490	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.195	2	2	2	2	2	2	2	1	1	3	1	1	1
534	2	213,584,491	214,434,355	3	3	0_0_0_0_0_0_0_0_0_0_0_0_1.195	1	1	1	1	1	1	1	2	2	3	2	2	2
535	2	214,434,356	214,473,749	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.195	1	1	1	1	1	1	1	2	2	3	2	2	2
536	2	214,473,750	215,019,087	3	3	0_0_0_0_0_0_0_0_0_0_0_0_1.195	1	1	1	1	1	1	1	2	2	3	2	2	2
537	2	215,019,088	215,020,148	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.195	1	1	1	1	1	1	1	2	2	3	2	2	2
538	2	215,020,149	215,569,266	2	1	0_0_0_0_0_0_0_0_0_0_0_0_1.195	1	1	1	1	1	1	1	1	1	2	1	1	1
539	2	215,569,267	215,572,707	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.195	2	2	2	2	2	2	2	1	1	3	1	1	1
540	2	215,572,708	215,709,549	3	3	0_0_0_0_0_0_0_0_0_0_0_0_1.195	1	1	1	1	1	1	1	2	2	3	2	2	2
541	2	215,709,550	215,709,926	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.195	2	2	2	2	2	2	2	1	1	3	1	1	1
542	2	215,709,927	216,277,720	2	1	0_0_0_0_0_0_0_0_0_0_0_0_1.195	1	1	1	1	1	1	1	1	1	2	1	1	1
543	2	216,277,721	216,310,891	1	0														
544	2	216,310,892	217,141,195	2	1	0_0_0_0_0_0_0_0_0_0_0_0_1.268	1	1	1	1	1	1	1	1	1	2	1	1	1
545	2	217,141,196	217,143,761	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.268	1	1	1	1	1	1	1	2	2	3	2	2	2
546	2	217,143,762	217,522,235	3	3	0_0_0_0_0_0_0_0_0_0_0_0_1.268	1	1	1	1	1	1	1	2	2	3	2	2	2
547	2	217,522,236	217,538,310	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.268	1	1	1	1	1	1	1	2	2	3	2	2	2
548	2	217,538,311	218,255,268	2	1	0_0_0_0_0_0_0_0_0_0_0_0_1.268	1	1	1	1	1	1	1	1	1	2	1	1	1
549	2	218,255,269	218,255,396	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.268	1	1	1	1	1	1	1	2	2	3	2	2	2
550	2	218,255,397	219,341,826	3	3	0_0_0_0_0_0_0_0_0_0_0_0_1.223	1	1	1	1	1	1	1	2	2	3	2	2	2
551	2	219,341,827	219,341,965	3	2	0_0_0_0_0_1_1_1_1_0_1_0_0.636	2	2	2	2	2	2	2	3	3	1	3	3	3
552	2	219,341,966	219,869,904	2	1	1_1_1_1_1_0_0_0_0_0_1_0_1_0.154	2	2	2	2	2	2	2	1	1	1	1	1	1
553	2	219,869,905	219,874,659	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.223	2	2	2	2	2	2	2	1	1	3	1	1	1
554	2	219,874,660	219,946,542	2	1	0_0_0_0_0_0_0_0_0_0_0_0_1.223	1	1	1	1	1	1	1	1	1	2	1	1	1
555	2	219,946,543	219,946,823	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.223	2	2	2	2	2	2	2	1	1	3	1	1	1
556	2	219,946,824	220,292,851	3	3	0_0_0_0_0_0_0_0_0_0_0_0_1.223	1	1	1	1	1	1	1	2	2	3	2	2	2
557	2	220,292,852	220,294,975	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.223	2	2	2	2	2	2	2	1	1	3	1	1	1
558	2	220,294,976	220,902,465	2	1	1_1_1_1_1_0_0_0_0_0_1_0_1_0.131	2	2	2	2	2	2	2	1	1	1	1	1	1
559	2	220,902,466	220,911,834	1	0														
560	2	220,911,835	222,701,103	2	1	0_0_0_0_0_0_0_0_0_0_0_0_1.146	1	1	1	1	1	1	1	1	1	2	1	1	1
561	2	222,701,104	222,704,195	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.146	1	1	1	1	1	1	1	2	2	3	2	2	2
562	2	222,704,196	222,802,228	3	3	0_0_0_0_0_0_0_0_0_0_0_0_1.146	1	1	1	1	1	1	1	2	2	3	2	2	2
563	2	222,802,229	222,822,152	3	2	0_0_0_0_0_1_1_1_1_0_1_0_0.44	2	2	2	2	2	2	2	3	3	1	3	3	3
564	2	222,822,153	223,803,803	2	1	1_1_1_1_1_0_0_0_0_0_1_0_1_0.163	2	2	2	2	2	2	2	1	1	1	1	1	1
565	2	222,830,804	222,836,089	3	2	1_1_1_1_1_0_0_0_0_0_1_0_1_0.163	3	3	3	3	3	3	3	2	1	1	1	1	1
566	2	222,836,090	222,895,570	3	3	0_0_0_0_0_0_0_0_0_0_0_0_1_0.79	2	2	2	2	2	2	2	3	1	1	1	1	1
567	2	222,895,571	223,047,160	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1_0.79	2	2	2	2	2	2	2	3	1	1	1	1	1
568	2	223,047,161	223,130,500	4	3	0_0_0_0_0_0_0_0_0_0_0_0_1_0.79	3	3	3	3	3	3	3	4	2	1	1	1	1
569	2	223,130,501	223,160,800	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1_0.79	2	2	2	2	2	2	2	3	1	1	1	1	1
570	2	223,160,801	223,346,186	3	3	0_0_0_0_0_0_0_0_0_0_0_0_1_0.79	2	2	2	2	2	2	2	3	1	1	1	1	1
571	2	223,346,187	223,346,500	3	2	1_1_1_1_1_0_0_0_0_0_1_0_1_0.62	3	3	3	3	3	3	3	2	1	1	1	1	1
572	2	223,346,501	223,349,533	2	1	1_1_1_1_1_0_0_0_0_0_1_1_1_0.251	2	2	2	2	2	2	2	2	1	1	1	1	1
573	2	223,349,534	223,400,739	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.121	2	2	2	2	2	2	2	2	1	3	1	1	1
574	2	223,400,740	223,401,144	4	3	0_0_0_0_0_0_0_0_0_0_0_0_0_1.121	2	2	2	2	2	2	2	3	1	4	1	1	1
575	2	223,401,145	223,414,645	4	4	0_0_0_0_0_0_0_0_0_0_0_0_0_1.121	2	2	2	2	2	2	2	3	1	4	1	1	1
576	2	223,414,646	223,669,096	4	5	0_0_0_0_0_0_0_0_0_0_0_0_0_1.121	2	2	2	2	2								

589	2	224,957,141	224,958,244	4	4	0_0_0_0_0_1_1_1_0_1_0_0.0485	2	2	2	1	1	1	1	4	3	1	3	3	3
590	2	224,958,245	225,179,385	3	3	0_1_0_0_0_0_0_0_0_1_1_1.0.325	3	3	3	2	2	2	2	3	1	2	1	1	1
591	2	225,179,386	225,216,559	3	2	0_1_0_0_0_0_0_0_0_1_1_1.0.325	3	3	3	2	2	2	2	3	1	2	1	1	1
592	2	225,216,560	225,274,124	3	3	0_1_0_0_0_0_0_0_0_1_1_1.0.325	3	3	3	2	2	2	2	3	1	2	1	1	1
593	2	225,274,125	225,296,671	3	2	0_1_0_0_0_0_0_0_0_1_1_1.0.325	3	3	3	2	2	2	2	3	1	2	1	1	1
594	2	225,296,672	225,944,207	2	1	1_0_1_1_1_0_0_0_0_0_0_0.1.102	1	1	1	2	2	2	2	1	1	2	1	1	1
595	2	225,944,208	225,961,606	3	2	1_0_1_1_1_0_0_0_0_0_0_0.1.102	2	2	2	3	3	3	3	2	1	3	1	1	1
596	2	225,961,607	225,997,371	2	1	1_0_1_1_1_0_0_0_0_0_0_0.1.102	1	1	1	2	2	2	2	1	1	2	1	1	1
597	2	225,997,372	226,006,629	1	0														
598	2	226,006,630	226,007,077	2	1	0_0_0_0_0_1_1_1_0_1_0_0.0.230	1	1	1	1	1	1	1	2	2	1	2	2	2
599	2	226,007,078	226,010,214	3	2	0_0_0_0_0_0_0_0_0_0_0_0.1.482	2	0	0	1	1	1	1	2	2	3	2	2	2
600	2	226,010,215	226,311,641	3	3	0_0_0_0_0_0_0_0_0_0_0_0.1.482	1	1	1	1	1	1	1	2	2	3	2	2	2
601	2	226,311,642	226,313,974	3	2	0_0_0_0_0_0_0_0_0_0_0_0.1.482	1	1	1	1	1	1	1	2	2	3	2	2	2
602	2	226,313,975	226,486,938	2	1	0_0_0_0_0_0_0_0_0_0_0_0.1.482	1	1	1	1	1	1	1	1	1	2	1	1	1
603	2	226,486,939	226,555,064	1	0														
604	2	226,555,065	226,887,930	2	1	0_1_0_0_0_0_0_0_0_1_1_1.0.270	2	2	2	1	1	1	1	2	1	1	1	1	1
605	2	226,887,931	227,012,740	1	0														
606	2	227,012,741	227,049,765	2	1	0_1_0_0_0_0_0_0_0_1_1_1.0.105	2	2	2	1	1	1	1	2	1	1	1	1	1
607	2	227,049,766	227,097,283	3	2	0_1_0_0_0_0_0_0_0_1_1_1.0.105	3	3	3	2	2	2	2	3	1	2	1	1	1
608	2	227,097,284	228,673,321	2	1	1_0_1_1_1_0_0_0_0_0_0_0.1.228	1	1	1	2	2	2	2	1	1	2	1	1	1
609	2	228,673,322	228,783,689	1	0														
610	2	228,783,690	229,119,007	2	1	1_0_1_1_1_0_0_0_0_0_0_0.1.575	1	1	1	2	2	2	2	1	1	2	1	1	1
611	2	229,119,008	229,225,533	1	0														
612	2	229,225,534	229,852,405	2	1	1_0_1_1_1_0_0_0_0_0_0_0.1.658	1	1	1	2	2	2	2	1	1	2	1	1	1
613	2	229,852,406	230,216,797	1	0														
614	2	230,216,798	230,575,831	2	1	0_1_0_0_0_1_1_1_1_1													

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759	3	24,474,601	24,742,179	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.318	2	2	2	2	2	2	2	2	1	1	1	1	1
760	3	24,742,180	24,902,177	1	0														
761	3	24,902,178	25,913,973	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.131	2	2	2	2	2	2	2	2	1	1	1	1	1
762	3	25,913,974	27,567,189	1	0														
763	3	27,567,190	28,130,277	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.934	2	2	2	2	2	2	2	2	1	1	1	1	1
764	3	28,130,278	28,576,687	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.1541	2	2	2	2	2	2	2	2	1	3	1	1	1
765	3	28,576,688	28,629,879	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0.1541	1	1	1	1	1	1	1	1	1	2	1	1	1
766	3	28,629,880	28,707,164	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.1541	2	2	2	2	2	2	2	2	1	3	1	1	1
767	3	28,707,165	29,208,503	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.526	2	2	2	2	2	2	2	2	1	1	1	1	1
768	3	29,208,504	30,630,945	1	0														
769	3	30,630,946	32,878,546	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.198	2	2	2	2	2	2	2	2	1	1	1	1	1
770	3	32,878,547	33,563,875	1	0														
771	3	33,563,876	33,790,248	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.130	2	2	2	2	2	2	2	2	1	1	1	1	1
772	3	33,790,249	34,395,985	1	0														
773	3	34,395,986	34,996,202	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0.1767	1	1	1	1	1	1	1	1	1	2	1	2	1
774	3	34,996,203	35,030,702	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.1767	2	2	2	2	2	2	2	2	1	3	1	3	1
775	3	35,030,703	35,109,888	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0.1767	1	1	1	1	1	1	1	1	1	2	1	2	1
776	3	35,109,889	35,111,575	1	0														
777	3	35,111,576	36,275,005	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.280	2	2	2	2	2	2	2	2	1	1	1	1	1
778	3	36,275,005	36,275,810	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.257	2	2	2	2	2	2	2	2	3	1	1	1	1
779	3	36,275,811	36,839,848	3	3	0_0_0_0_0_0_0_0_0_0_0_0_0.257	2	2	2	2	2	2	2	2	3	1	1	1	1
780	3	36,839,849	36,865,664	3	2	1_1_1_1_1_0_0_0_0_1_0_1_0.392	3	3	3	3	3	3	3	3	2	1	1	1	1
781	3	36,865,665	36,916,385	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.280	2	2	2	2	2	2	2	2	1	1	1	1	1
782	3	36,916,386	36,930,982	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.80	2	2	2	2	2	2	2	2	3	1	1	1	1
783	3	36,930,983	37,208,623	3	3	0_0_0_0_0_0_0_0_0_0_0_0_0.80	2	2	2	2	2	2	2	2	3	1	1	1	1
784	3	37,208,624	37,253,308	3	2	1_1_1_1_1_0_0_0_0_1_0_1_0.137	3	3	3	3	3	3	3	3	2	1	1	1	1
785	3	37,253,309	37,288,189	3	3	0_0_0_0_0_0_0_0_0_0_0_0_0.407	2	2	2	2	2	2	2	2	3	1	1	1	1
786	3	37,288,190	37,293,299	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.407	2	2	2	2	2	2	2	2	3	1	1	1	1
787	3	37,293,300	37,691,544	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0.407	1	1	1	1	1	1	1	2	1	1	1	1	
788	3	37,691,545	37,712,848	1	0														
789	3	37,712,849	38,055,385	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.424	2	2	2	2	2	2	2	2	1	1	1	1	1
790	3	38,055,386	38,057,020	1	0														
791	3	38,057,021	39,056,799	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0.908	1	1	1	1	1	1	1	2	1	1	1	1	
792	3	39,056,800	39,204,796	1	0														
793	3	39,204,797	39,427,586	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0.150	1	1	1	1	1	1	1	2	1	1	1	1	
794	3	39,427,587	40,439,565	1	0														
795	3	40,439,566	42,545,008	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0.136	1	1	1	1	1	1	1	2	1	1	1	1	
796	3	42,545,009	42,619,021	1	0														
797	3	42,619,022	43,076,543	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0.076	1	1	1	1	1	1	1	2	1	1	1	1	
798	3	43,076,544	43,077,390	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.076	1	1	1	1	1	1	1	3	1	2	1	2	1
799	3	43,077,391	43,114,298	3	3	0_0_0_0_0_0_0_0_0_0_0_0_0.076	1	1	1	1	1	1	1	3	1	2	1	2	1
800	3	43,114,299	43,148,661	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.1143	2	2	2	2	2	2	2	1	2	3	2	3	2
801	3	43,148,662	43,279,208	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0.1143	1	1	1	1	1	1	1	1	1	2	1	2	1
802	3	43,279,209	43,279,292	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.1143	2	2	2	2	2	2	2	1	2	3	2	3	2
803	3	43,279,293	43,448,322	2	1	1_1_1_1_1_1_0_0_0_0_1_0_0.564	2	2	2	2	2	2	2	1	2	1	2	1	2
804	3	43,448,323	43,521,171	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.141	2	2	2	2	2	2	2	1	2	3	2	3	2
805	3	43,521,172	43,622,639	2	1	1_1_1_1_1_1_0_0_0_0_1_0_0.564	2	2	2	2	2	2	2	1	2	1	2	1	2
806	3	43,622,640	43,622,691	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.358	2	2	2	2	2	2	2	3	2	1	2	1	2
807	3	43,622,692	44,412,565	3	3	0_0_0_0_0_0_0_0_0_0_0_0_0.358	1	1	1	1	1	1	1	3	1	2	1	2	1
808	3	44,412,566	44,412,845	4	4	0_0_0_0_0_0_0_0_0_0_0_0_0.358	2	2	2	2	2	2	2	4	1	3	1	3	1
809	3	44,412,846	44,413,424	4	5	0_0_0_0_0_0_0_0_0_0_0_0_0.358	1	1	1	1	1	1	1	4	2	3	2	3	2
810	3	44,413,425	44,463,818	4	6	0_0_0_0_0_0_0_0_0_0_0_0_0.358	1	1	1	1	1	1	1	4	2	3	2	3	2
811	3	44,463,819	44,515,888	4	5	0_0_0_0_0_0_0_0_0_0_0_0_0.358	2	2	2	2	2	2	2	4	1	3	1	3	1
812	3	44,515,889	44,738,614	4	4	0_0_0_0_0_0_0_0_0_0_0_0_0.1417	3	3	3	3	3	3	3	2	1	4	1	4	1
813	3	44,738,615	44,738,718	4	3	0_0_0_0_0_0_0_0_0_0_0_0_0.1417	3	3	3	3	3	3	3	2	1	4	1	4	1
814	3	44,738,719	44,739,804	3	2	1_1_1_1_1_0_0_0_0_1_0_1_0.64	3	3	3	3	3	3	3	2	1	1	1	1	1
815	3	44,739,805	44,806,205	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.210	2	2	2	2	2	2	2	2	1	1	1	1	1
816	3	44,806,206	44,957,606	3	2	1_1_1_1_1_0_0_0_0_1_0_1_0.48	3	3	3	3	3	3	3	2	1	1	1	1	1
817	3	44,957,607	45,065,204	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.210	2	2	2	2	2	2	2	2	1	1	1	1	1
818	3	45,065,205	45,065,600	3	2	1_1_1_1_1_0_0_0_0_1_0_1_0.422	3	3	3	3	3	3	3	2	1	1	1	1	1
819	3	45,065,601	45,733,372	3	3	0_0_0_0_0_0_0_0_0_0_0_0_0.244	2	2	2	2	2	2	2	3	1	1	1	1	1
820	3	45,733,373	45,734,102	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.244	2	2	2	2	2	2	2	3	1	1	1	1	1
821	3	45,734,103	46,215,377	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.210	2	2	2	2	2	2	2	2	1	1	1	1	1
822	3	46,215,378	46,440,513	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.160	2	2	2	2	2	2	2	2	1	3	1	3	1
823	3	46,440,514	47,288,932	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.210	2	2	2	2	2	2	2	2	1	1	1	1	1
824	3	47,288,933	47,413,601	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.1420	2	2	2	2	2	2	2	2	1	3	1	3	1
825	3	47,413,602	47,554,126	2	1	0_0_0_0_0_0_0_0_0_0_0_0_0.1420	1	1	1	1	1	1	1	1	1	2	1	2	1
826	3	47,554,127	48,324,863	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.1420	2	2	2	2	2	2	2	2	1	3	1	3	1
827	3	48,324,864	48,484,065	3	3	0_0_0_0_0_0_0_0_0_0_0_0_0.1420	2	2	2	2	2	2	2	2	1	3	1	3	1
828	3	48,484,066	48,503,080	3	2	0_0_0_0_0_0_0_0_0_0_0_0_0.1420	2	2	2	2	2	2	2	2	1	3	1	3	1
829	3	48,503,081	49,321,629	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.144	2	2	2	2	2	2	2	2	1	1	1	1	1
830	3	49,321,630	49,535,372	1	0														
831	3	49,535,373	50,208,980	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.557	2	2	2	2	2	2	2	2	1	1	1	1	1
832	3	50,208,981	50,305,760	1	0														
833	3	50,305,761	51,895,694	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.171	2	2	2	2	2	2	2	2	1	1	1	1	1
834	3	51,895,695	51,967,342	1	0														

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3819	21	80,145,790	80,148,279	2	1	0_1_0_0_0_0_0_0_0_1_0_1_0.159	2	2	2	1	1	1	1	1	1	1	1	1	1
3820	21	80,148,280	80,886,206	3	2	0_1_0_0_0_0_0_0_0_1_0_1_0.159	3	3	3	2	2	2	2	2	1	1	1	1	1
3821	21	80,886,207	81,875,334	2	1	0_1_0_0_0_0_0_0_0_1_0_1_0.159	2	2	2	1	1	1	1	1	1	1	1	1	1
3822	21	81,875,335	82,190,617	3	2	0_1_0_0_0_0_0_0_0_1_0_1_0.159	3	3	3	2	2	2	2	2	1	1	1	1	1
3823	21	82,190,618	99,873,453	3	3	0_1_0_0_0_0_0_0_0_1_0_1_0.159	3	3	3	2	2	2	2	2	1	1	1	1	1
3824	21	99,873,454	99,882,483	3	2	0_1_0_0_0_0_0_0_0_1_0_1_0.159	3	3	3	2	2	2	2	2	1	1	1	1	1
3825	21	99,882,484	99,889,494	2	1	0_1_0_0_0_0_0_0_0_1_0_1_0.159	2	2	2	1	1	1	1	1	1	1	1	1	1
3826	21	99,889,495	99,890,537	3	2	0_1_0_0_0_0_0_0_0_1_0_1_0.159	3	3	3	1	1	1	1	2	1	1	1	1	1
3827	21	99,890,538	100,331,734	3	3	0_0_0_0_0_0_0_0_0_0_1_0_0.272	2	2	2	1	1	1	1	3	1	1	1	1	1
3828	21	100,331,735	100,361,947	3	2	0_0_0_0_0_0_0_0_0_0_1_0_0.272	2	2	2	1	1	1	1	3	1	1	1	1	1
3829	21	100,361,948	101,660,381	2	1	0_0_0_0_0_0_0_0_0_0_1_0_0.272	1	1	1	1	1	1	1	2	1	1	1	1	1
3830	21	101,660,382	105,151,536	1	0														
3831	21	105,151,537	105,739,048	2	1	0_1_0_0_0_0_0_0_0_1_1_1_0.236	2	2	2	1	1	1	1	2	1	1	1	1	1
3832	21	105,739,049	105,743,748	1	0														
3833	21	105,743,749	106,653,372	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.229	2	2	2	2	2	2	2	2	1	1	1	1	1
3834	21	106,653,373	106,664,867	1	0														
3835	21	106,664,868	110,662,271	2	1	0_0_0_0_0_0_0_0_0_0_1_0_0.332	1	1	1	1	1	1	1	2	1	1	1	1	1
3836	21	110,662,272	110,700,060	1	0														
3837	21	110,700,061	116,208,966	2	1	1_1_1_1_1_0_0_0_0_1_0_1_0.111	2	2	2	2	2	2	2	2	1	1	1	1	1
3838	21	116,208,967	116,215,635	1	0														
3839	21	116,215,636	116,596,329	2	1	0_0_0_0_0_0_0_0_0_0_1_0_0.79	1	1	1	1	1	1	1	2	1	1	1	1	1
3840	21	116,596,330	118,096,282	1	0														
3841	21	118,096,283	118,856,091	2	1	1_1_1_1_1_0_0_0_0_1_0_1_0.166	2	2	2	2	2	2	2	1	1	1	1	1	1
3842	21	118,856,092	119,297,417	1	0														
3843	21	119,297,418	119,517,235	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.42	2	2	2	2	2	2	2	2	1	1	1	1	1
3844	21	119,517,236	119,618,059	1	0														
3845	21	119,618,060	120,547,024	2	1	0_0_0_0_0_0_0_0_0_0_1_0_0.667	1	1	1	1	1	1	1	2	1	1	1	1	1
3846	21	120,547,025	120,698,171	3	2	0_0_0_0_0_0_0_0_0_0_1_0_0.667	2	2	2	2	2	2	2	2	3	1	1	1	1
3847	21	120,698,172	123,370,159	2	1	0_0_0_0_0_0_0_0_0_0_1_0_0.667	1	1	1	1	1	1	1	2	1	1	1	1	1
3848	21	123,370,160	123,555,755	1	0														
3849	21	123,555,756	123,749,281	2	1	1_1_1_1_1_0_0_0_0_1_0_1_0.54	2	2	2	2	2	2	2	2	1	1	1	1	1
3850	21	123,749,282	123,900,993	1	0														
3851	21	123,900,994	129,066,425	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.532	2	2	2	2	2	2	2	2	1	1	1	1	1
3852	21	129,066,426	129,115,315	1	0														
3853	21	129,115,316	129,401,977	2	1	0_0_0_0_0_0_0_0_0_0_0_0_1.44	1	1	1	1	1	1	1	1	1	2	1	1	1
3854	21	129,401,978	131,385,589	1	0														
3855	21	131,385,590	133,487,932	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.787	2	2	2	2	2	2	2	2	1	1	1	1	1
3856	21	133,487,933	133,865,381	3	2	0_0_0_0_0_0_0_0_0_0_0_0_1.51	2	2	2	2	2	2	2	2	1	3	1	1	1
3857	21	133,865,382	138,654,445	2	1	1_1_1_1_1_0_0_0_0_1_1_1_0.787	2	2	2	2	2	2	2	2	1	1	1	1	1
3858	21	138,654,446	138,898,783	1	0														
3859	21	138,898,784	139,537,737	2	1	1_1_1_1_1_0_0_0_0_1_1_1_1.124	2	2	2	2	2	2	2	2	1	2	1	1	1
3860	21	139,537,738	140,225,502	1	0														
3861	21	140,225,503	140,950,116	2	1	1_0_1_1_1_0_0_0_0_0_1_0_0.110	1	1	1	2	2	2	2	2	1	1	1	1	1
3862	21	140,950,117	159,553,583	1	0														
3863	21	159,553,584	159,949,745	2	1	1_0_1_1_1_0_0_0_0_0_1_0_0.41	1	1	1	2	2	2	2	2	1	1	1	1	1

Table S2. Progenitor strain samples used for microarray analysis of target tissues

	Heart	Whole kidney	Renal cortex	Aorta	Liver
SHR/lzm	4	8	4	4	4
SHRSP/lzm	16	4	5	5	4
WKY/lzm	20 (4 vs SHR, 16 vs SHRSP)	12 (8 vs SHR, 4 vs SHRSP)	5	9 (4 vs SHR, 5 vs SHRSP)	6

Eight (4 SHR/lzm and 4 WKY/lzm) samples are overlapped between whole kidney and renal cortex.

Two pairs of inter-strain comparisons (WKY/lzm vs SHR/lzm and WKY/lzm vs SHRSP/lzm) are made separately for the heart, whole kidney and aorta, and all the data are combined by regression.

Table S3A. A list of significant transcripts for shared differential expression in the heart.

no	ProbeName	SHR/lzm (vs WKY/lzm)			SHRSP/lzm (vs WKY/lzm)			GeneName	Ensembl_rat	Chr	Transcription_ start_site (Rnor_6.0)
		Fold change (log2-scale)	SE (log2-scale)	P-value	Fold change (log2-scale)	SE (log2-scale)	P-value				
13786	A_44_P101700	0.602	0.106	1.9E-06	0.374	0.053	2.7E-08	Stx11	ENSRNOG00000014902	1	7,064,870
814	A_44_P445359	0.649	0.088	1.2E-08	0.471	0.044	1.1E-12	Pex7	ENSRNOG00000012322	1	15,374,850
8464	A_64_P129293	1.418	0.171	1.1E-09	1.474	0.070	3.6E-21	RGD1306565	ENSRNOG000000031700	1	15,412,603
8390	A_43_P23129	-0.327	0.065	1.3E-05	-0.453	0.032	4.0E-16	Ptprk	ENSRNOG000000047605	1	18,058,055
1771	A_43_P12841	0.502	0.110	5.3E-05	0.254	0.055	4.6E-05	Enpp1	ENSRNOG000000013994	1	21,748,261
3394	A_42_P484738	1.000	0.123	1.1E-09	1.278	0.062	1.1E-21	Ctgf	ENSRNOG00000015036	1	21,854,773
6563	A_64_P119169	-0.329	0.054	4.8E-07	-0.342	0.027	6.5E-15	LOC684270	ENSRNOG000000050348	1	72,509,431
6169	A_64_P058871	0.525	0.119	8.6E-05	0.420	0.059	2.6E-08	Tnnt1	ENSRNOG000000028041	1	72,889,278
18278	A_44_P156211	0.505	0.113	7.8E-05	0.331	0.057	1.1E-06	Itpkc	ENSRNOG000000013945	1	84,040,433
28121	A_64_P027503	0.879	0.137	1.9E-07	0.469	0.068	5.1E-08	Fbxo17	ENSRNOG000000019942	1	86,914,137
603	A_44_P1018090	0.445	0.076	1.1E-06	0.423	0.038	3.2E-13	Lgi4	ENSRNOG000000021087	1	89,491,654
10829	A_44_P449994	0.983	0.098	6.1E-12	0.800	0.049	3.4E-18	LOC365238	ENSRNOG000000015168	1	94,784,451
11981	A_64_P148550	0.600	0.108	2.9E-06	0.731	0.054	1.1E-15	Lim2	ENSRNOG000000017681	1	98,501,249
13915	A_64_P080941	-1.547	0.164	3.9E-11	-1.656	0.084	1.2E-20	LOC102556967	ENSRNOG000000033729	1	99,505,677
19170	A_64_P049828	-1.609	0.169	2.1E-11	-0.868	0.084	2.8E-12	Dbp	ENSRNOG000000021027	1	101,687,855
3773	A_64_P049827	-1.515	0.176	2.9E-10	-0.865	0.088	9.8E-12	Dbp	ENSRNOG000000021027	1	101,687,855
24946	A_64_P017188	-1.481	0.155	2.0E-11	-0.955	0.078	1.7E-14	Dbp	ENSRNOG000000021027	1	101,687,855
13613	A_44_P466271	0.423	0.079	4.9E-06	0.213	0.039	4.3E-06	Sphk2	ENSRNOG000000021032	1	101,697,277
1350	A_42_P506076	1.275	0.263	2.4E-05	0.670	0.132	1.1E-05	Ptpn5	ENSRNOG000000013981	1	103,256,823
16073	A_44_P997843	0.611	0.081	6.6E-09	0.624	0.041	2.0E-17	Csrp3	ENSRNOG000000014327	1	104,157,855
259	A_44_P536125	0.836	0.121	4.3E-08	0.406	0.061	7.6E-08	Prmt3	ENSRNOG000000014829	1	105,113,595
7527	A_64_P151448	-0.712	0.095	7.7E-09	-0.589	0.048	1.5E-14	Fancf	ENSRNOG000000023968	1	107,232,305
225	A_42_P602570	2.254	0.188	3.5E-14	0.884	0.094	2.8E-11	Bex1	ENSRNOG000000033844	1	116,567,189
19183	A_64_P133177	-0.680	0.126	4.3E-06	-1.146	0.063	8.4E-20	Sema4b	ENSRNOG000000025167	1	141,986,145
26335	A_64_P157285	2.049	0.150	7.8E-16	2.170	0.075	1.4E-26		ENSRNOG000000025003	1	142,027,250
16081	A_43_P10751	0.467	0.089	7.5E-06	0.287	0.045	1.8E-07	Ngrn	ENSRNOG000000013553	1	142,050,458
5536	A_42_P528580	-0.338	0.055	4.7E-07	-0.301	0.028	5.6E-13	Hddc3	ENSRNOG000000012236	1	142,136,452
3363	A_64_P016059	-1.154	0.076	2.5E-17	-0.576	0.038	2.6E-17	Homer2	ENSRNOG000000061450	1	143,535,583
16902	A_64_P045536	-0.369	0.084	8.6E-05	-0.338	0.042	1.2E-09	Eftud1	ENSRNOG000000032723	1	144,601,410

70 A_42_P628981	0.543	0.105	8.4E-06	0.810	0.052	1.6E-17 Prss23	ENSRNOG000000017307	1	153,752,541
29997 A_42_P733209	-0.656	0.129	1.1E-05	-0.382	0.064	8.4E-07 Dgat2	ENSRNOG000000016573	1	164,143,818
10025 A_44_P301608	0.717	0.139	9.1E-06	1.128	0.069	3.4E-18 Ucp2	ENSRNOG000000017854	1	165,506,361
24566 A_43_P14847	-0.544	0.065	5.4E-10	-0.352	0.032	6.3E-13 Mrpl48	ENSRNOG000000018042	1	165,606,375
28025 A_44_P520159	-0.512	0.116	8.5E-05	-0.385	0.058	9.2E-08 P2ry2	ENSRNOG000000019283	1	166,037,424
29337 A_43_P22401	0.495	0.089	2.8E-06	0.451	0.045	4.5E-12 Lrrc51	ENSRNOG000000020124	1	167,005,839
599 A_64_P162476	-0.926	0.196	3.4E-05	-1.276	0.098	3.2E-15 Art1	ENSRNOG000000020251	1	167,197,549
18258 A_64_P042586	-0.950	0.136	3.6E-08	-1.005	0.068	7.4E-17 Art5	ENSRNOG000000020242	1	167,202,767
23520 A_64_P072633	-0.545	0.123	8.1E-05	-1.245	0.061	2.3E-21 Olr59	ENSRNOG000000018606	1	167,911,961
22874 A_64_P112431	1.082	0.205	6.2E-06	0.682	0.102	8.8E-08 Olr200	ENSRNOG000000048852	1	170,147,300
4890 A_42_P797965	1.687	0.107	7.9E-18	1.355	0.053	1.2E-24 RGD1306959	ENSRNOG000000013744	1	174,330,695
29915 A_64_P086565	0.619	0.064	1.5E-11	0.637	0.032	4.8E-21 Rras2	ENSRNOG000000012258	1	179,010,257
7347 A_42_P793598	0.472	0.094	1.3E-05	0.247	0.047	6.6E-06 LOC378467	ENSRNOG000000048250	1	189,870,622
9145 A_43_P12996	1.131	0.117	1.3E-11	0.650	0.058	2.9E-13 Crym	ENSRNOG000000061215	1	189,960,073
9654 A_64_P019021	2.218	0.267	3.5E-09	1.193	0.161	3.7E-08 LOC691551	ENSRNOG000000028473	1	190,914,946
3234 A_64_P084966	0.377	0.084	7.1E-05	-0.246	0.042	1.1E-06 Tnrc6a	ENSRNOG000000024737	1	193,076,430
8445 A_42_P791460	-0.342	0.066	8.0E-06	-0.379	0.033	1.1E-13 Jmjd5	ENSRNOG000000015180	1	196,839,321
16693 A_64_P089531	0.673	0.120	2.3E-06	0.612	0.060	3.5E-12 Il4ra	ENSRNOG000000015441	1	196,942,364
10614 A_44_P395538	-0.829	0.077	7.5E-13	-0.523	0.038	8.6E-16 Rabep2	ENSRNOG000000018462	1	197,839,430
12122 A_44_P321110	-0.320	0.067	3.2E-05	-0.289	0.034	2.9E-10 Eif3c	ENSRNOG000000018761	1	197,982,601
15860 A_44_P562972	0.521	0.103	1.3E-05	0.837	0.052	3.5E-18 Apob48r	ENSRNOG000000017403	1	197,999,037
5221 A_42_P812008	-0.963	0.097	7.0E-12	-0.338	0.048	3.4E-08 Nupr1	ENSRNOG000000050922	1	198,045,154
18482 A_44_P1002996	-0.788	0.105	7.4E-09	-0.866	0.053	2.2E-18 Ino80e	ENSRNOG000000019960	1	198,298,076
19479 A_44_P275029	-0.375	0.079	3.5E-05	-0.218	0.040	3.4E-06 Mvp	ENSRNOG000000020182	1	198,450,047
29205 A_44_P1029472	-0.906	0.069	2.3E-15	-0.430	0.034	1.1E-14 RGD1305592	ENSRNOG000000020217	1	198,450,688
6295 A_44_P473234	0.768	0.107	1.8E-08	0.886	0.053	1.7E-18 Znf688	ENSRNOG000000018379	1	198,869,009
14224 A_64_P045578	1.669	0.149	2.5E-13	1.304	0.074	3.0E-19 Rnf40	ENSRNOG000000018840	1	199,037,544
23664 A_64_P019325	0.930	0.066	3.1E-16	0.785	0.033	1.2E-23 Orai3	ENSRNOG000000039730	1	199,217,016
24684 A_64_P080856	0.334	0.075	8.3E-05	0.469	0.038	1.2E-14 RGD1310127	ENSRNOG000000020144	1	199,716,205
29778 A_44_P252921	-0.340	0.076	7.6E-05	-0.376	0.038	8.4E-12 Sec23ip	ENSRNOG000000020411	1	200,167,169
2815 A_42_P740370	0.688	0.106	1.4E-07	0.431	0.053	1.0E-09 Cpxm2	ENSRNOG000000015902	1	204,087,001
13842 A_64_P116485	0.571	0.088	1.6E-07	-0.320	0.044	1.5E-08 Pnpla2	ENSRNOG000000018736	1	214,434,626
5484 A_64_P153870	0.754	0.083	7.1E-11	0.465	0.041	2.5E-13 Chid1	ENSRNOG000000050181	1	214,511,529

22350 A_64_P097784	0.793	0.162	2.2E-05	0.559	0.084	1.3E-07 Fadd	ENSRNOG000000047035	1	217,748,628
5014 A_42_P614175	4.251	0.359	2.9E-13	1.344	0.153	4.8E-10 Gal	ENSRNOG000000015156	1	218,657,925
21228 A_64_P091940	4.413	0.351	8.0E-12	1.115	0.222	4.4E-05 Gal	ENSRNOG000000015156	1	218,657,925
4555 A_44_P367971	-0.441	0.094	3.8E-05	-0.289	0.047	4.2E-07 Ccdc85b	ENSRNOG000000046560	1	220,836,504
21831 A_64_P029622	-0.424	0.081	7.0E-06	-0.396	0.040	1.0E-11	ENSRNOG000000017884	1	223,549,904
21375 A_64_P024861	-0.420	0.090	4.4E-05	-0.278	0.045	4.3E-07	ENSRNOG000000017884	1	223,549,904
4232 A_64_P082401	0.545	0.099	3.0E-06	-0.245	0.049	1.6E-05 Ahnak	ENSRNOG000000057569	1	225,184,939
14221 A_64_P155741	-0.564	0.075	6.2E-09	-0.193	0.037	8.7E-06 Sdhaf2	ENSRNOG000000020646	1	226,572,349
30101 A_44_P896040	-0.916	0.081	2.0E-13	0.178	0.041	9.3E-05 Cybasc3	ENSRNOG000000020702	1	226,634,009
7124 A_64_P062545	-0.454	0.088	8.8E-06	0.626	0.044	2.0E-16 Tmem132a	ENSRNOG000000021338	1	226,924,244
11594 A_64_P146165	1.253	0.222	2.9E-06	1.543	0.125	9.7E-14 RGD1560242	ENSRNOG000000036615	1	241,460,868
5424 A_44_P315626	0.449	0.067	7.5E-08	0.257	0.033	3.9E-09 Kank1	ENSRNOG000000016023	1	243,276,403
16557 A_44_P310596	-0.713	0.133	4.8E-06	-0.515	0.066	3.2E-09 Il33	ENSRNOG000000016456	1	248,132,090
11396 A_44_P284753	1.043	0.073	2.1E-16	0.611	0.037	1.5E-18 Ankrd1	ENSRNOG000000018598	1	254,735,548
27529 A_43_P12437	-0.597	0.112	5.4E-06	-0.309	0.056	3.1E-06 Hhex	ENSRNOG000000016595	1	256,101,903
393 A_64_P082037	0.475	0.096	1.7E-05	0.278	0.048	1.2E-06 LOC679127	ENSRNOG000000048495	1	261,140,389
9329 A_44_P262593	2.500	0.306	9.9E-10	1.906	0.153	1.2E-14 Ankrd2	ENSRNOG000000013840	1	261,281,543
7394 A_42_P644278	-0.883	0.094	2.9E-11	-0.804	0.047	5.9E-19 Bloc1s2	ENSRNOG000000012684	1	263,920,962
25205 A_44_P325439	0.486	0.086	2.0E-06	0.369	0.043	3.1E-10 Fbxw4	ENSRNOG000000046211	1	265,420,503
1478 A_42_P759043	1.033	0.071	1.1E-16	1.050	0.035	6.1E-27 RGD1311783	ENSRNOG000000020076	1	266,451,021
27106 A_44_P995874	0.365	0.070	7.7E-06	0.488	0.035	4.2E-16 LOC100364597	ENSRNOG000000020179	1	266,782,910
2102 A_44_P990043	0.585	0.095	4.4E-07	0.396	0.048	6.4E-10 Pdcd11	ENSRNOG000000020304	1	266,866,931
2336 A_42_P462015	-0.579	0.093	3.3E-07	-0.237	0.046	1.0E-05 Obfc1	ENSRNOG000000020376	1	267,315,729
2768 A_42_P739860	0.662	0.141	3.9E-05	1.420	0.071	3.3E-21 Dusp5	ENSRNOG000000014061	1	274,245,184
22292 A_64_P026191	0.581	0.114	1.0E-05	0.289	0.057	1.1E-05 Nrap	ENSRNOG000000016714	1	277,181,414
20097 A_44_P183488	-0.483	0.067	1.5E-08	-0.164	0.033	1.9E-05 Casp7	ENSRNOG000000056216	1	277,190,964
15734 A_44_P403005	-0.769	0.100	3.8E-09	-0.599	0.050	3.6E-14 Trub1	ENSRNOG000000017321	1	278,311,244
17131 A_64_P088836	0.464	0.101	4.8E-05	-0.957	0.050	2.0E-20 Gpr98	ENSRNOG000000016306	2	8,939,686
528 A_42_P523612	-0.480	0.102	3.9E-05	-0.331	0.051	1.6E-07 Mef2c	ENSRNOG000000033134	2	11,658,568
14818 A_44_P337311	1.452	0.198	1.2E-08	2.251	0.099	5.5E-23 Thbs4	ENSRNOG000000012471	2	22,385,855
19077 A_44_P131470	0.471	0.065	1.7E-08	0.526	0.033	4.2E-18 Hexb	ENSRNOG000000025274	2	28,003,186
15807 A_64_P068038	0.508	0.101	1.4E-05	0.632	0.051	1.1E-14 Hexb	ENSRNOG000000025274	2	28,003,186
9172 A_43_P10887	0.969	0.151	2.0E-07	1.014	0.076	1.4E-15 Map1b	ENSRNOG000000017428	2	29,768,750

28802 A_42_P705481	0.584	0.097	6.3E-07	0.467	0.048	1.6E-11 Il6st	ENSRNOG00000013963	2	44,289,393
2831 A_42_P663871	-1.598	0.177	8.0E-11	-0.396	0.088	7.0E-05 Gzma	ENSRNOG00000010603	2	44,981,458
18451 A_43_P12257	1.200	0.223	4.7E-06	1.350	0.112	2.8E-14 Esm1	ENSRNOG00000010797	2	45,104,305
24749 A_43_P16449	0.568	0.070	9.7E-10	0.479	0.035	6.0E-16 Pelo	ENSRNOG000000061128	2	47,268,625
5239 A_42_P463754	0.704	0.087	1.2E-09	0.414	0.044	2.1E-11 Itga1	ENSRNOG000000053550	2	47,281,421
16351 A_43_P14915	-0.731	0.108	6.7E-08	-0.445	0.054	8.4E-10 C6	ENSRNOG000000024115	2	54,466,280
11752 A_64_P087930	-0.537	0.108	1.6E-05	-0.486	0.054	9.2E-11 C7	ENSRNOG000000061379	2	54,777,729
8100 A_44_P168265	0.721	0.137	7.0E-06	0.633	0.069	5.1E-11 Prkaa1	ENSRNOG000000012799	2	54,857,688
10271 A_44_P421887	0.606	0.134	6.4E-05	0.523	0.067	3.0E-09 Ankrd33b	ENSRNOG000000010888	2	84,436,912
2038 A_43_P10785	-0.431	0.096	7.4E-05	-0.650	0.048	1.1E-15 Cmb1	ENSRNOG000000011260	2	84,645,084
8628 A_64_P048755	-1.291	0.127	3.5E-12	-0.723	0.063	1.5E-13 LOC679974	ENSRNOG000000046390	2	102,370,757
10154 A_64_P092201	0.429	0.097	8.5E-05	0.416	0.048	3.1E-10 Cp	ENSRNOG000000011913	2	104,744,461
14034 A_44_P468304	-1.255	0.276	6.4E-05	-0.801	0.143	2.8E-06 Terc	ENSRNOG000000051777	2	116,432,691
17597 A_43_P23319	0.657	0.123	4.9E-06	0.286	0.061	4.1E-05 Usp13	ENSRNOG000000030639	2	119,197,239
10605 A_42_P462239	0.405	0.060	5.9E-08	0.347	0.030	8.6E-14 Acad9	ENSRNOG000000014178	2	122,782,060
29381 A_44_P472994	0.585	0.075	3.1E-09	0.600	0.038	5.8E-18 Anxa5	ENSRNOG000000014453	2	123,193,130
27496 A_44_P424218	-0.841	0.087	1.3E-11	-0.523	0.043	3.0E-14 Mif1	ENSRNOG000000012827	2	164,549,455
26163 A_43_P12345	-0.489	0.101	2.6E-05	-0.608	0.051	3.7E-14 Bche	ENSRNOG000000009826	2	171,196,395
25283 A_64_P050994	1.004	0.172	1.2E-06	1.161	0.087	2.9E-15 Sema4a	ENSRNOG000000019737	2	187,817,578
29294 A_44_P191285	0.932	0.160	1.2E-06	0.708	0.080	1.5E-10 RGD1564171	ENSRNOG000000037406	2	189,413,966
24202 A_64_P053307	1.255	0.160	1.5E-08	0.990	0.103	2.3E-10 Nup210l	ENSRNOG000000055790	2	189,454,340
299 A_42_P524308	-0.416	0.065	1.8E-07	-0.198	0.032	4.6E-07 Jtb	ENSRNOG000000016379	2	189,591,780
6842 A_42_P516658	-0.715	0.100	2.2E-08	-0.284	0.050	1.9E-06 Gatad2b	ENSRNOG000000015553	2	189,655,702
14525 A_64_P038452	0.358	0.068	6.4E-06	0.453	0.034	1.6E-15 Cdc42se1	ENSRNOG000000060538	2	196,402,837
10680 A_64_P140977	-0.978	0.100	9.9E-12	-0.962	0.050	1.3E-20 Prune	ENSRNOG000000021120	2	196,456,481
27712 A_64_P041307	-0.589	0.084	3.0E-08	-0.791	0.042	2.7E-20 Tars2	ENSRNOG000000057194	2	197,878,142
28265 A_44_P1033661	0.303	0.065	4.2E-05	0.249	0.032	4.3E-09 Prpf3	ENSRNOG000000025629	2	197,971,456
28118 A_64_P152753	-2.711	0.267	1.0E-11	-1.279	0.145	3.1E-10 RGD1566380	ENSRNOG000000042717	2	197,991,198
4465 A_44_P520475	0.735	0.152	2.4E-05	0.983	0.076	3.7E-15 Anp32e	ENSRNOG000000021168	2	198,040,536
8030 A_44_P393822	0.695	0.093	8.4E-09	0.804	0.047	5.1E-19 Plekho1	ENSRNOG000000021170	2	198,120,120
4450 A_42_P649672	0.929	0.195	3.1E-05	0.525	0.098	4.7E-06 Sv2a	ENSRNOG000000021182	2	198,321,142
25399 A_64_P102889	0.757	0.086	1.6E-10	0.213	0.043	1.7E-05 Polr3gl	ENSRNOG000000021209	2	198,706,428
20625 A_44_P548426	0.776	0.160	2.6E-05	0.493	0.065	8.6E-09 Ankrd35	ENSRNOG000000025108	2	198,797,159

20853 A_64_P076891	-1.724	0.133	3.6E-15	-1.778	0.066	2.0E-25 RGD1565469	ENSRNOG000000037217	2	198,834,925
21010 A_44_P513428	0.626	0.139	6.7E-05	0.627	0.069	8.6E-11 Polr3c	ENSRNOG000000033560	2	198,852,161
7498 A_44_P386936	0.395	0.063	2.7E-07	0.463	0.031	7.2E-17 Gpr89	ENSRNOG000000000095	2	199,038,702
20777 A_44_P544023	-0.367	0.081	6.5E-05	0.203	0.041	1.6E-05 Tuba1c	ENSRNOG000000015544	2	199,199,845
12118 A_64_P040804	0.329	0.054	4.7E-07	0.357	0.027	1.8E-15 Rpl38	ENSRNOG000000030747	2	199,479,309
18650 A_44_P1059229	-0.667	0.096	3.4E-08	-0.525	0.048	4.6E-13 Slc22a15	ENSRNOG000000033051	2	204,341,676
8432 A_64_P074102	-1.121	0.175	2.3E-07	-0.472	0.081	1.3E-06 Wnt2b	ENSRNOG000000014385	2	207,455,258
23813 A_43_P15024	0.734	0.162	6.3E-05	1.695	0.081	8.8E-22 Sypl2	ENSRNOG000000019780	2	211,017,778
19556 A_44_P822283	-1.341	0.081	1.9E-18	-0.299	0.041	1.1E-08 Sort1	ENSRNOG000000031814	2	211,078,334
20758 A_43_P11683	0.864	0.120	1.8E-08	0.429	0.060	2.1E-08 F3	ENSRNOG000000011800	2	225,310,624
2551 A_43_P11570	0.901	0.116	3.2E-09	0.570	0.058	9.5E-12 Abcd3	ENSRNOG000000011929	2	225,389,120
2707 A_64_P164926	0.410	0.069	7.2E-07	0.313	0.034	6.2E-11 LOC691931	ENSRNOG000000010875	2	232,245,319
8355 A_64_P151756	1.201	0.220	4.2E-06	1.295	0.090	4.1E-16 LOC679958	ENSRNOG000000023404	2	240,495,371
12459 A_64_P161185	0.615	0.090	5.6E-08	0.369	0.045	9.7E-10 Odf2l	ENSRNOG000000014059	2	250,995,517
8693 A_44_P1020608	-0.556	0.102	3.9E-06	-0.486	0.051	2.3E-11 Ifi44	ENSRNOG000000022218	2	256,915,569
6564 A_43_P11426	0.354	0.078	5.8E-05	0.538	0.039	5.0E-16 Pigk	ENSRNOG000000042359	2	257,911,126
20957 A_43_P23049	-1.359	0.101	1.3E-15	-1.223	0.051	6.3E-24 Cryz	ENSRNOG000000028319	2	260,884,337
1123 A_42_P558445	-0.288	0.066	9.6E-05	-0.193	0.033	1.0E-06 Surf1	ENSRNOG000000060005	3	5,483,239
26230 A_44_P213133	-2.126	0.078	1.3E-25	-2.025	0.039	1.8E-35 Endog	ENSRNOG000000016033	3	8,741,766
17007 A_64_P129901	-1.051	0.110	2.1E-11	-1.058	0.055	1.5E-20 Ccbl1	ENSRNOG000000016097	3	8,766,433
12417 A_64_P050722	0.304	0.068	7.4E-05	0.310	0.034	6.2E-11	ENSRNOG000000031434	3	8,955,538
22393 A_43_P18366	1.926	0.108	1.6E-19	2.056	0.054	8.3E-31 Tor1b	ENSRNOG000000006435	3	9,792,899
16409 A_44_P447373	1.253	0.280	7.9E-05	1.054	0.143	1.2E-08 Ass1	ENSRNOG000000008837	3	10,375,826
3868 A_64_P101908	0.719	0.129	2.6E-06	0.564	0.065	2.0E-10 LOC688582	ENSRNOG000000062252	3	10,408,115
16058 A_44_P1012226	-0.666	0.086	3.7E-09	-0.328	0.043	5.1E-09 Pomt1	ENSRNOG000000010477	3	11,254,026
2282 A_42_P553960	-0.404	0.060	7.4E-08	-0.366	0.030	2.3E-14 Uck1	ENSRNOG000000011467	3	11,277,757
29474 A_44_P532754	-0.506	0.094	4.8E-06	-0.333	0.047	2.7E-08 Pbx3	ENSRNOG000000022162	3	13,435,979
28010 A_64_P038074	0.888	0.154	1.4E-06	0.427	0.077	2.7E-06 Lypd6b	ENSRNOG000000004614	3	35,271,786
23123 A_64_P045400	-1.027	0.120	3.1E-10	-0.824	0.060	6.1E-16 Gca	ENSRNOG000000007359	3	48,626,038
16975 A_44_P960805	-0.584	0.094	3.7E-07	-0.848	0.047	1.2E-19 Gca	ENSRNOG000000007359	3	48,626,038
658 A_44_P231223	0.651	0.112	1.1E-06	0.748	0.056	1.3E-15 Xirp2	ENSRNOG000000034258	3	53,563,194
14170 A_64_P141349	1.294	0.207	2.7E-06	1.248	0.134	4.0E-09 B3galt1	ENSRNOG000000007625	3	54,253,949
19663 A_64_P084088	0.463	0.083	2.5E-06	0.318	0.041	4.5E-09 Cybrd1	ENSRNOG000000009620	3	57,718,364

14032 A_64_P134564	0.300	0.052	1.6E-06	0.326	0.026	1.2E-14 Dync1i2	ENSRNOG000000009781	3	57,817,693
1340 A_44_P653272	0.645	0.092	2.9E-08	0.587	0.046	5.2E-15 Gpr155	ENSRNOG000000018485	3	60,105,212
15603 A_44_P464145	0.782	0.140	2.6E-06	0.855	0.070	2.4E-14 Gpr155	ENSRNOG000000018485	3	60,105,212
24139 A_44_P992697	-1.507	0.098	1.8E-17	-1.179	0.049	7.0E-24 Dusp19	ENSRNOG000000008868	3	67,849,966
30134 A_64_P048824	0.364	0.079	4.9E-05	0.207	0.040	7.3E-06 Zc3h15	ENSRNOG000000005256	3	71,020,534
4545 A_44_P1011687	1.427	0.115	1.3E-14	1.194	0.057	1.1E-21 Tfpi	ENSRNOG000000005039	3	71,893,600
25328 A_64_P080025	0.504	0.091	3.1E-06	0.374	0.046	9.4E-10 Serping1	ENSRNOG000000007457	3	72,171,078
1516 A_42_P561644	-0.494	0.071	4.0E-08	-0.425	0.036	4.5E-14 Timm10	ENSRNOG000000007883	3	72,226,613
8277 A_64_P022076	0.910	0.163	2.5E-06	0.405	0.082	1.7E-05 Slc43a3	ENSRNOG0000000061768	3	72,329,967
17375 A_43_P15275	-1.626	0.089	8.4E-20	-1.083	0.045	5.8E-24 Ptprij	ENSRNOG0000000034025	3	79,390,956
18771 A_44_P107766	-0.740	0.074	6.2E-12	-0.445	0.037	3.6E-14 RGD1309540	ENSRNOG000000014798	3	80,349,145
10251 A_64_P045671	1.113	0.164	5.8E-08	0.520	0.082	2.3E-07 Mdk	ENSRNOG000000017560	3	80,842,916
18605 A_64_P126818	-0.534	0.111	2.7E-05	-0.652	0.056	7.0E-14 Tspan18	ENSRNOG000000008758	3	82,236,664
25223 A_64_P115142	-0.673	0.095	2.4E-08	-0.776	0.047	2.7E-18 Accs	ENSRNOG000000009199	3	82,756,953
15888 A_64_P164232	-0.589	0.098	7.3E-07	-0.366	0.049	8.6E-09 RGD1306717	ENSRNOG000000008663	3	93,698,121
2959 A_64_P135773	1.850	0.177	1.8E-12	2.045	0.089	3.0E-23 Prrg4	ENSRNOG000000022710	3	94,808,861
29107 A_64_P033322	0.483	0.087	2.8E-06	0.386	0.044	1.4E-10 Lin7c	ENSRNOG000000045698	3	101,010,899
18122 A_44_P852315	0.596	0.095	2.9E-07	0.658	0.047	4.8E-16 Fibin	ENSRNOG000000004699	3	101,547,478
10565 A_64_P078914	0.831	0.176	3.4E-05	0.975	0.088	3.5E-13 Phgr1	ENSRNOG0000000060434	3	110,508,403
16898 A_42_P527070	-0.356	0.080	8.0E-05	-0.185	0.040	4.8E-05 Gchfr	ENSRNOG000000012290	3	110,975,923
3204 A_42_P618145	0.829	0.081	3.6E-12	0.724	0.041	1.8E-19 Hisppd2a	ENSRNOG000000014436	3	113,312,127
20811 A_64_P156094	0.812	0.153	6.0E-06	0.943	0.077	1.7E-14 Hisppd2a	ENSRNOG000000014436	3	113,312,127
25901 A_44_P714860	0.325	0.070	4.4E-05	0.447	0.035	5.8E-15 Serf2	ENSRNOG000000015277	3	113,415,774
15624 A_43_P19265	0.346	0.076	6.2E-05	0.200	0.038	7.3E-06 Shf	ENSRNOG000000028685	3	114,307,250
17734 A_44_P122372	0.762	0.103	8.6E-09	0.717	0.051	3.6E-16 Pldn	ENSRNOG000000037160	3	114,869,459
5981 A_64_P111786	-0.678	0.084	1.2E-09	-0.673	0.042	4.6E-18 Sqrdl	ENSRNOG000000000172	3	114,900,343
26669 A_64_P100963	-0.941	0.155	5.5E-07	-0.392	0.077	1.3E-05 Ncaph	ENSRNOG000000012051	3	119,611,136
834 A_42_P561329	-0.668	0.096	3.4E-08	-0.494	0.048	2.5E-12 Anapc1	ENSRNOG000000016965	3	121,226,125
19676 A_64_P098527	-0.415	0.077	4.9E-06	-0.275	0.039	2.3E-08 Chchd5	ENSRNOG000000018491	3	121,660,110
29825 A_64_P000678	0.453	0.103	9.5E-05	0.247	0.052	2.9E-05 Sirpa	ENSRNOG000000004763	3	122,114,754
18410 A_64_P143459	-0.740	0.112	1.0E-07	-0.843	0.056	3.5E-17 Snrpb	ENSRNOG000000006961	3	122,703,705
5717 A_64_P024798	-0.904	0.084	7.8E-13	-0.258	0.042	4.2E-07 Ubox5	ENSRNOG000000021230	3	123,171,875
1564 A_42_P501233	-1.515	0.210	1.6E-08	-2.744	0.105	4.2E-25 Adra1d	ENSRNOG000000021256	3	124,145,566

27875 A_64_P015227	0.536	0.113	3.4E-05	0.428	0.057	6.0E-09 Trmt6	ENSRNOG000000021270	3	125,470,413
25424 A_44_P378742	-1.021	0.153	8.2E-08	-0.677	0.076	1.3E-10 Flrt3	ENSRNOG000000004874	3	134,696,654
13519 A_44_P370537	0.692	0.135	1.0E-05	0.653	0.067	1.4E-11 Polr3f	ENSRNOG000000007548	3	138,684,685
28840 A_44_P243599	-0.787	0.126	3.3E-07	-0.569	0.063	8.6E-11 RGD1566320	ENSRNOG000000036971	3	138,765,027
1909 A_43_P12825	-0.477	0.096	1.7E-05	-0.608	0.048	7.8E-15 Entpd6	ENSRNOG000000007427	3	146,546,387
8320 A_64_P144278	0.489	0.107	5.5E-05	0.499	0.053	3.6E-11 Snph	ENSRNOG000000009588	3	147,143,576
12668 A_44_P363204	-0.643	0.109	9.9E-07	-0.609	0.055	3.1E-13 Csnk2a1	ENSRNOG000000005276	3	147,713,821
24270 A_64_P117901	1.828	0.237	4.8E-09	1.823	0.110	3.4E-18 Trib3	ENSRNOG000000007319	3	147,819,571
18709 A_44_P305135	0.295	0.059	1.6E-05	0.464	0.030	1.2E-17 Epb41l1	ENSRNOG000000057817	3	152,552,822
2734 A_42_P777935	0.454	0.097	3.8E-05	0.506	0.048	1.9E-12 RGD1311066	ENSRNOG000000020086	3	152,626,757
19643 A_44_P761309	0.720	0.083	2.5E-10	0.479	0.042	1.2E-13 Lpin3	ENSRNOG000000016636	3	156,886,454
5599 A_43_P18817	-0.921	0.123	8.0E-09	-1.006	0.062	3.0E-18 Ifit52	ENSRNOG000000007692	3	159,392,193
608 A_42_P629321	0.853	0.191	7.5E-05	0.721	0.095	6.0E-09 Wisp2	ENSRNOG000000010666	3	160,207,913
18760 A_64_P037510	0.324	0.058	2.7E-06	0.299	0.029	3.0E-12 Rpl38	ENSRNOG000000048701	3	164,002,482
20958 A_64_P002904	0.566	0.094	6.5E-07	0.689	0.047	8.9E-17 Pmepa1	ENSRNOG000000050404	3	171,342,646
16812 A_64_P058749	0.909	0.080	1.6E-13	0.580	0.040	1.1E-16	ENSRNOG000000043150	3	176,479,335
15543 A_44_P307964	-0.653	0.079	6.8E-10	-0.585	0.039	5.6E-17 Polr3k	ENSRNOG000000017843	3	177,374,812
24680 A_43_P12222	-0.349	0.068	9.2E-06	-0.287	0.034	4.1E-10 Pmpcb	ENSRNOG000000012693	4	9,921,610
4023 A_64_P148535	0.580	0.113	1.0E-05	0.386	0.057	5.7E-08 Napepld	ENSRNOG000000011363	4	9,966,891
18208 A_64_P166489	0.471	0.108	9.9E-05	0.383	0.054	2.2E-08 Napepld	ENSRNOG000000011363	4	9,981,958
21357 A_64_P016751	-0.826	0.090	5.2E-11	-1.041	0.045	2.7E-23 Tmem243 (RGD1	ENSRNOG000000042758	4	21,920,651
9693 A_64_P039888	2.025	0.157	6.3E-15	1.703	0.080	1.0E-21 Abcb1b	ENSRNOG000000008012	4	22,307,453
17357 A_64_P095855	1.345	0.255	6.6E-06	0.715	0.128	2.3E-06 Rundc3b	ENSRNOG000000008463	4	22,445,414
5089 A_64_P113443	0.642	0.102	2.6E-07	0.295	0.051	1.3E-06 Cdk6	ENSRNOG000000009258	4	27,966,398
5850 A_44_P139763	0.441	0.068	1.3E-07	0.275	0.034	1.1E-09 Bet1	ENSRNOG000000011008	4	29,092,753
10442 A_44_P899239	-0.434	0.090	2.6E-05	-0.229	0.045	1.2E-05 Samd9l	ENSRNOG000000051922	4	31,229,913
10121 A_44_P338381	-0.904	0.156	1.7E-06	-1.084	0.083	1.3E-14 Cadps2	ENSRNOG000000007636	4	50,860,756
12560 A_44_P494632	0.608	0.118	9.9E-06	0.641	0.059	6.8E-13 Flnc	ENSRNOG000000007281	4	56,711,049
30022 A_44_P260072	0.642	0.133	2.5E-05	0.763	0.066	1.3E-13 Tbxas1	ENSRNOG000000007918	4	66,670,618
29522 A_44_P489995	-0.574	0.063	7.8E-11	-0.287	0.032	7.7E-11 Mrps33	ENSRNOG000000026528	4	67,610,710
2447 A_64_P002506	1.093	0.176	5.3E-07	1.590	0.098	2.3E-17	ENSRNOG000000005506	4	72,718,458
448 A_44_P930917	2.148	0.175	4.4E-14	1.997	0.071	3.9E-25 Arhgef5	ENSRNOG000000005506	4	72,718,458
13843 A_44_P990376	1.171	0.193	5.4E-07	0.740	0.096	4.2E-09 Gpnmb	ENSRNOG000000008816	4	78,694,447

4571 A_64_P044087	1.240	0.201	4.3E-07	0.922	0.101	6.1E-11 Nap1l5	ENSRNOG00000007808	4	89,151,184
21325 A_64_P152919	-0.565	0.096	8.9E-07	-0.295	0.048	4.0E-07	ENSRNOG000000023657	4	89,695,928
17936 A_64_P159902	-0.584	0.106	2.9E-06	-0.385	0.053	1.4E-08 Mmrn1	ENSRNOG000000024986	4	90,990,088
24747 A_64_P157405	-0.598	0.086	3.6E-08	-0.722	0.043	1.1E-18 Reep1	ENSRNOG000000008481	4	99,618,622
19570 A_64_P027404	-0.522	0.118	8.5E-05	-0.625	0.059	1.2E-12 Mat2a	ENSRNOG000000013520	4	100,303,080
20592 A_44_P402507	-1.909	0.082	2.4E-23	-2.219	0.041	3.4E-36 Retsat	ENSRNOG000000014090	4	100,465,170
8298 A_42_P693964	1.689	0.189	1.1E-10	0.598	0.095	2.6E-07 Cyp26b1	ENSRNOG000000015076	4	116,278,615
27845 A_44_P200846	-0.454	0.103	9.0E-05	-0.421	0.052	9.6E-10 Sfxn5	ENSRNOG000000037871	4	117,111,653
25583 A_64_P128971	0.684	0.132	8.2E-06	0.381	0.066	1.3E-06 Chst13	ENSRNOG000000025930	4	122,237,754
18655 A_64_P011674	2.176	0.225	1.5E-11	2.275	0.113	2.8E-21 Shq1	ENSRNOG000000005433	4	133,131,953
1140 A_64_P156263	0.491	0.087	2.2E-06	0.714	0.044	2.8E-18 Lmcd1	ENSRNOG000000005690	4	144,192,989
13196 A_44_P622992	-0.794	0.093	3.0E-10	-0.635	0.046	6.5E-16 Tuba8	ENSRNOG000000048169	4	153,774,486
14600 A_64_P157059	-0.796	0.159	1.4E-05	-0.403	0.079	1.1E-05 Usp18	ENSRNOG000000037198	4	153,805,993
16017 A_64_P038107	0.637	0.129	1.8E-05	0.450	0.064	3.4E-08 Apobec1	ENSRNOG000000015411	4	155,401,480
19984 A_64_P166460	1.400	0.210	1.1E-07	0.810	0.109	1.2E-08 C3ar1	ENSRNOG000000009211	4	155,690,869
6653 A_64_P101301	0.684	0.142	2.5E-05	0.574	0.071	1.2E-09 Clec4a3	ENSRNOG000000010018	4	155,923,079
12718 A_43_P17428	-0.443	0.074	6.3E-07	-0.260	0.037	2.7E-08 Lpcat3	ENSRNOG000000012269	4	157,181,795
5930 A_64_P026222	1.538	0.250	6.2E-07	1.751	0.104	8.3E-18 LOC689757	ENSRNOG000000037076	4	162,230,859
10286 A_64_P012119	1.184	0.207	2.4E-06	1.309	0.104	5.7E-14 Gprc5d	ENSRNOG000000008439	4	168,884,886
19079 A_64_P023431	0.784	0.120	1.2E-07	0.842	0.060	3.0E-16 Hebp1	ENSRNOG000000000024	4	168,933,079
19656 A_64_P113645	1.679	0.229	3.4E-08	2.197	0.134	1.6E-16 RGD1561551	ENSRNOG000000036959	4	177,039,677
26918 A_44_P372998	1.994	0.145	6.4E-16	0.980	0.073	1.1E-15 Cpa6	ENSRNOG000000005655	5	8,459,660
826 A_43_P20387	0.617	0.136	5.9E-05	0.305	0.068	7.0E-05 Arfgef1	ENSRNOG000000005703	5	8,666,200
15292 A_43_P14372	-1.136	0.075	3.0E-17	-1.266	0.037	5.7E-29	ENSRNOG000000031769	5	16,845,631
27282 A_64_P000859	0.413	0.094	8.9E-05	0.391	0.047	6.0E-10 Plekhf2	ENSRNOG000000026662	5	24,255,606
10504 A_44_P532297	-0.597	0.067	1.1E-10	-0.378	0.033	1.9E-13 RGD1309085 (N	ENSRNOG000000040040	5	24,320,786
4766 A_44_P775787	-0.808	0.106	5.3E-09	-0.316	0.053	8.2E-07 LOC500420	ENSRNOG000000028185	5	35,902,262
17136 A_64_P067968	-0.703	0.116	6.1E-07	-1.053	0.058	1.0E-19 RGD1562865	ENSRNOG000000006170	5	47,546,014
15347 A_64_P104850	-0.334	0.068	2.0E-05	-0.429	0.034	8.8E-15 Lym2	ENSRNOG000000043105	5	48,047,913
9389 A_44_P1041460	-1.359	0.149	6.4E-11	-1.549	0.074	1.0E-21 Rragd	ENSRNOG000000007331	5	48,224,994
9581 A_44_P715035	0.348	0.071	1.9E-05	0.260	0.035	1.1E-08 RGD1359108	ENSRNOG000000009478	5	50,684,409
23043 A_43_P18183	0.559	0.125	7.3E-05	0.429	0.063	7.5E-08 RGD1359108	ENSRNOG000000009478	5	50,684,409
20705 A_44_P576954	-0.757	0.112	6.7E-08	-0.662	0.056	5.5E-14 Ddx58	ENSRNOG000000006384	5	56,536,772

10900 A_42_P672071	0.734	0.121	5.7E-07	0.553	0.061	6.3E-11 Ccl19	ENSRNOG000000015668	5	58,183,017
29008 A_64_P144482	1.761	0.144	2.3E-14	1.380	0.072	1.8E-20	ENSRNOG000000016731	5	59,025,631
321 A_42_P698240	-0.854	0.153	2.6E-06	-1.305	0.077	7.7E-19 Ptgr1	ENSRNOG000000015072	5	76,129,441
13215 A_43_P15212	-0.373	0.079	3.5E-05	-0.178	0.040	6.5E-05 Pole3	ENSRNOG000000055277	5	78,384,047
9363 A_44_P146845	1.255	0.257	2.1E-05	1.818	0.128	2.5E-16 Orm1	ENSRNOG000000007886	5	79,179,417
13242 A_44_P1040796	1.265	0.116	6.1E-13	1.286	0.058	1.4E-22 Atp6v1g1	ENSRNOG000000008163	5	79,367,663
2972 A_42_P832422	0.677	0.130	8.4E-06	0.643	0.065	8.7E-12 Milt3	ENSRNOG000000011280	5	106,207,126
3813 A_44_P1008463	0.508	0.067	5.3E-09	0.544	0.033	3.1E-18 RGD1311849	ENSRNOG000000024402	5	106,409,456
946 A_44_P777439	-0.377	0.077	2.0E-05	-0.460	0.038	4.1E-14 Hook1	ENSRNOG000000026226	5	114,940,053
18791 A_64_P000171	0.526	0.069	4.3E-09	0.671	0.034	7.8E-21	ENSRNOG000000006787	5	126,164,674
28037 A_43_P10410	0.376	0.079	3.1E-05	0.400	0.040	4.3E-12 Txndc12	ENSRNOG000000008090	5	128,450,680
15449 A_64_P071918	-0.652	0.090	1.5E-08	-0.497	0.045	3.7E-13 Nsun4	ENSRNOG000000012020	5	134,382,794
12837 A_44_P558028	0.763	0.142	4.8E-06	0.606	0.071	3.5E-10 Ccdc17	ENSRNOG000000023216	5	135,442,031
9670 A_44_P117119	-0.720	0.108	8.1E-08	-0.422	0.054	2.5E-09 Hpdl	ENSRNOG000000018143	5	135,677,432
20248 A_64_P138415	2.267	0.139	3.3E-16	2.602	0.087	2.3E-23 Cldn19	ENSRNOG000000007922	5	138,300,107
955 A_64_P032604	-0.881	0.082	9.7E-13	-0.746	0.041	1.0E-19 Ak2	ENSRNOG000000000122	5	147,185,474
3334 A_64_P097842	-0.582	0.088	1.2E-07	-0.445	0.044	5.2E-12 Marcksl1	ENSRNOG000000009113	5	147,714,163
10388 A_64_P035962	-0.906	0.126	1.8E-08	-1.000	0.063	7.2E-18 LOC682360	ENSRNOG000000049425	5	147,784,311
22059 A_43_P17437	0.327	0.065	1.4E-05	0.302	0.033	4.5E-11 Taf12	ENSRNOG000000048288	5	150,459,713
23745 A_44_P175875	0.799	0.086	4.2E-11	0.548	0.043	6.2E-15 Pigv	ENSRNOG000000000121	5	151,895,016
5655 A_43_P11466	0.518	0.064	1.3E-09	0.439	0.032	6.9E-16 Fuca1	ENSRNOG000000009325	5	154,269,118
982 A_42_P636963	-0.481	0.083	1.4E-06	-0.375	0.042	9.5E-11 Zfp46	ENSRNOG000000049975	5	154,650,632
3505 A_42_P703647	-0.515	0.112	4.9E-05	-0.625	0.056	2.7E-13 Cda	ENSRNOG000000015677	5	156,734,541
15453 A_64_P048668	-0.745	0.108	3.9E-07	-1.037	0.091	3.6E-11 Pla2g2c	ENSRNOG000000016647	5	157,165,341
15824 A_44_P549075	-0.505	0.059	3.1E-10	-0.365	0.029	1.4E-14 Pla2g5	ENSRNOG000000016838	5	157,268,903
3322 A_42_P569711	0.641	0.100	2.1E-07	1.015	0.050	2.7E-21 Epha2	ENSRNOG000000009222	5	159,845,774
1445 A_64_P029878	-0.856	0.073	6.5E-14	-0.686	0.036	2.7E-20 Clcnkb	ENSRNOG000000009897	5	159,962,676
1979 A_42_P638494	1.146	0.131	1.9E-10	1.343	0.066	1.7E-21 Nppb	ENSRNOG000000008141	5	164,796,185
1363 A_44_P317600	2.413	0.233	2.3E-12	1.277	0.116	4.7E-13 Nppa	ENSRNOG000000008176	5	164,808,323
23292 A_64_P075910	1.060	0.142	7.9E-09	0.324	0.071	5.7E-05 Ajap1	ENSRNOG000000050137	5	170,679,315
21962 A_44_P100870	-0.379	0.077	2.0E-05	-0.186	0.039	2.5E-05 RGD1308251	ENSRNOG000000013468	5	172,307,431
28765 A_64_P038692	-0.323	0.067	2.4E-05	-0.371	0.033	3.1E-13 Cox7a2l	ENSRNOG000000004526	6	6,709,783
14904 A_44_P328717	-0.912	0.123	8.6E-09	-0.810	0.061	2.1E-15 Mtm1	ENSRNOG000000002516	6	18,821,815

26647 A_43_P11724	1.432	0.120	4.4E-14	0.658	0.060	4.9E-13 Gckr	ENSRNOG000000048874	6	26,385,761
18372 A_64_P017363	0.596	0.103	1.3E-06	0.635	0.051	1.6E-14 Slc30a3	ENSRNOG000000006204	6	26,642,783
24275 A_44_P413979	0.650	0.075	2.8E-10	0.797	0.038	6.1E-22 Rab10	ENSRNOG000000047088	6	27,721,120
4161 A_64_P076450	0.483	0.088	3.6E-06	0.475	0.044	8.3E-13 Pomc	ENSRNOG000000012686	6	28,382,962
28085 A_64_P108486	0.731	0.137	5.0E-06	0.729	0.068	1.0E-12 Dnajc27	ENSRNOG000000003988	6	28,515,025
7900 A_64_P155756	1.212	0.221	3.3E-06	0.673	0.110	5.2E-07 Tpo	ENSRNOG000000004646	6	49,089,855
16459 A_44_P222786	-0.442	0.054	9.6E-10	-0.513	0.027	2.2E-20 RGD1563296	ENSRNOG000000056610	6	50,954,631
12252 A_64_P145433	0.747	0.108	3.9E-08	0.404	0.054	7.0E-09	ENSRNOG000000004342	6	55,001,464
19783 A_64_P127402	-0.414	0.075	3.2E-06	-0.566	0.038	3.8E-17 Bzw2	ENSRNOG000000005096	6	55,647,665
1431 A_42_P600642	-0.606	0.106	1.7E-06	-0.534	0.053	5.3E-12 lspd	ENSRNOG000000006199	6	55,881,484
3423 A_44_P545553	-0.981	0.120	9.2E-10	-1.400	0.060	2.0E-23 Dgkb	ENSRNOG000000030771	6	57,516,713
4107 A_44_P211061	1.163	0.135	2.9E-10	1.179	0.068	3.6E-19 Etv1	ENSRNOG000000006867	6	58,467,254
6710 A_64_P008628	-0.386	0.082	3.5E-05	-0.336	0.041	8.3E-10 Ndufa10l1	ENSRNOG000000062245	6	62,798,384
1845 A_64_P013182	0.696	0.111	3.2E-07	0.640	0.056	1.3E-13 Stxbp6	ENSRNOG000000004198	6	65,319,527
17692 A_64_P124599	-0.685	0.092	8.9E-09	-0.508	0.046	4.1E-13	ENSRNOG000000004165	6	71,199,110
23405 A_64_P045378	-0.609	0.120	1.2E-05	-0.959	0.060	5.7E-18	ENSRNOG000000056721	6	86,852,323
1503 A_42_P789482	0.765	0.104	1.2E-08	0.451	0.052	2.5E-10 Daam1	ENSRNOG000000004345	6	94,636,222
30010 A_43_P19862	-1.264	0.202	3.1E-07	-1.115	0.101	3.9E-13 Lrrc9	ENSRNOG000000005409	6	95,205,153
28307 A_44_P285390	0.422	0.082	8.9E-06	0.282	0.041	4.3E-08 Atp6v1d	ENSRNOG000000009080	6	102,047,758
7901 A_64_P136751	-0.645	0.099	1.5E-07	-0.578	0.050	8.3E-14	ENSRNOG000000008082	6	106,496,992
8745 A_44_P260589	-1.755	0.187	7.4E-11	-1.871	0.100	3.1E-19	ENSRNOG000000009448	6	107,245,820
5759 A_64_P065368	1.384	0.204	6.2E-08	1.120	0.102	4.7E-13 Acot4	ENSRNOG000000046864	6	107,517,668
16745 A_64_P067447	2.065	0.312	1.8E-07	2.020	0.100	8.6E-20 Acot4	ENSRNOG000000046864	6	107,517,668
18088 A_44_P337991	0.724	0.107	6.6E-08	0.529	0.054	8.1E-12 Acot3	ENSRNOG000000053460	6	107,531,528
20123 A_64_P074370	-1.168	0.109	9.7E-13	-1.231	0.055	7.3E-23 Dnal1	ENSRNOG000000042333	6	107,596,785
29970 A_64_P064381	-0.387	0.072	4.8E-06	-0.609	0.036	9.3E-19 Ptgr2	ENSRNOG000000038166	6	107,999,846
28805 A_64_P028095	-0.315	0.071	8.0E-05	-0.673	0.035	2.0E-20 Abcd4	ENSRNOG000000011964	6	108,329,464
14620 A_64_P124473	1.208	0.187	1.7E-07	1.388	0.094	6.1E-17 Ltbp2	ENSRNOG000000012094	6	108,596,569
28988 A_64_P068847	1.017	0.226	7.3E-05	1.475	0.105	5.2E-16 Ltbp2	ENSRNOG000000012094	6	108,596,569
25368 A_64_P031035	-0.833	0.108	3.9E-09	-0.919	0.054	7.9E-19 Gatz1	ENSRNOG000000047708	6	111,176,798
4908 A_42_P720155	0.669	0.085	2.2E-09	0.245	0.042	1.3E-06 LOC500700	ENSRNOG000000003908	6	114,966,751
804 A_42_P701779	-0.456	0.077	8.3E-07	-0.287	0.038	7.6E-09 Rps6ka5	ENSRNOG000000004362	6	124,735,741
5142 A_43_P12172	0.279	0.059	3.8E-05	0.295	0.030	7.2E-12 Lgmn	ENSRNOG000000007089	6	126,320,726

29887 A_64_P148433	-0.688	0.109	2.7E-07	-0.439	0.055	1.4E-09	Ifi27	ENSRNOG000000009263	6	127,327,959
22152 A_44_P382464	0.488	0.079	4.3E-07	0.544	0.040	6.9E-16	RGD1308470	ENSRNOG000000042427	6	129,519,709
20830 A_44_P185355	-1.231	0.173	2.2E-08	-1.579	0.086	7.7E-20	Bcl11b	ENSRNOG000000005776	6	131,926,272
8534 A_64_P006368	-0.518	0.104	1.5E-05	-0.451	0.052	2.2E-10	RGD1565168	ENSRNOG000000033736	6	135,939,534
5921 A_64_P004007	0.689	0.130	5.8E-06	0.420	0.065	1.6E-07	RGD1305627	ENSRNOG000000043031	6	136,550,371
13859 A_64_P068378	-0.517	0.079	1.3E-07	-0.542	0.039	6.4E-16		ENSRNOG000000028650	6	137,164,535
16943 A_64_P079523	0.696	0.159	9.4E-05	0.860	0.079	6.4E-13	Ahnak2	ENSRNOG000000028545	6	137,353,249
1529 A_42_P742797	-0.581	0.059	7.6E-12	-0.521	0.029	1.9E-19	Brf1	ENSRNOG000000014595	6	137,808,303
15597 A_64_P103580	-1.015	0.151	8.2E-08	-0.695	0.077	1.0E-10	LOC690422	ENSRNOG000000005153	6	137,967,401
11175 A_64_P002455	-0.909	0.110	7.6E-10	-0.868	0.055	8.5E-18	LOC690422	ENSRNOG000000005153	6	137,967,401
13502 A_44_P852545	-0.523	0.116	6.8E-05	-0.451	0.058	3.2E-09	Tmem196	ENSRNOG000000037435	6	147,876,237
12833 A_44_P1015388	-0.396	0.080	1.7E-05	-0.415	0.040	2.1E-12	Ankrd24	ENSRNOG000000006759	7	10,936,415
974 A_42_P842823	0.701	0.097	1.6E-08	0.619	0.049	6.0E-15	Reep6	ENSRNOG000000033262	7	12,246,729
10600 A_64_P099017	-2.230	0.186	3.9E-14	-1.769	0.093	2.1E-20	Cyp4f17	ENSRNOG000000062306	7	14,529,483
2475 A_64_P079666	0.497	0.070	2.5E-08	0.311	0.035	1.4E-10	Cyp4f5	ENSRNOG000000042496	7	14,559,878
15805 A_64_P255450	-0.876	0.095	5.1E-11	-0.915	0.048	1.4E-20	Zfp799	ENSRNOG000000032552	7	15,072,703
22219 A_64_P108737	0.328	0.073	6.6E-05	0.285	0.036	2.8E-09		ENSRNOG000000046020	7	15,386,329
12870 A_64_P146682	-0.796	0.147	4.1E-06	-0.520	0.073	2.5E-08	Pctk2	ENSRNOG000000004148	7	34,001,506
13077 A_44_P1008751	0.510	0.115	8.6E-05	0.663	0.058	1.3E-13	Fgd6	ENSRNOG000000054515	7	34,952,011
27527 A_64_P108742	0.508	0.063	1.5E-09	0.312	0.032	8.4E-12	Ndufa12	ENSRNOG000000007407	7	35,125,424
1345 A_42_P543004	-0.721	0.094	4.3E-09	-0.585	0.047	1.2E-14	Socs2	ENSRNOG000000008965	7	36,499,784
17690 A_44_P216654	0.509	0.092	3.0E-06	0.480	0.046	2.1E-12	Nap1l1	ENSRNOG000000003890	7	54,213,319
29539 A_43_P11911	0.391	0.068	1.4E-06	0.435	0.034	4.9E-15	Rab3ip	ENSRNOG000000005362	7	59,957,232
9888 A_64_P025286	0.742	0.168	8.8E-05	0.832	0.084	7.8E-12	Lyz2	ENSRNOG000000005825	7	60,341,264
1448 A_42_P669907	0.879	0.153	1.5E-06	0.344	0.077	6.9E-05	Slc16a7	ENSRNOG000000007839	7	68,512,397
9948 A_44_P194803	-0.649	0.121	4.9E-06	-0.804	0.060	1.7E-15	Baalc	ENSRNOG000000004697	7	77,763,512
5860 A_64_P047206	0.864	0.187	4.6E-05	0.524	0.093	2.3E-06	Depdc6	ENSRNOG000000004328	7	94,795,214
4282 A_44_P686854	-0.547	0.105	8.4E-06	-0.456	0.053	2.5E-10	RGD1563224	ENSRNOG000000008934	7	98,709,344
18442 A_64_P044345	0.546	0.108	1.3E-05	0.686	0.054	6.9E-15	Plec	ENSRNOG000000023781	7	117,267,803
30277 A_64_P142942	-0.836	0.116	1.7E-08	-0.495	0.058	3.4E-10	Scx	ENSRNOG000000021812	7	117,519,075
12545 A_64_P039737	-0.893	0.081	4.3E-13	-0.800	0.041	6.2E-21	Scx	ENSRNOG000000021812	7	117,519,075
12381 A_64_P110838	0.429	0.093	4.9E-05	0.260	0.047	2.5E-06	Apol3	ENSRNOG000000042771	7	118,685,022
24480 A_44_P286788	0.911	0.187	2.1E-05	0.852	0.093	6.4E-11	Ncf4	ENSRNOG000000006940	7	119,482,272

22505 A_42_P809869	0.614	0.127	2.6E-05	0.852	0.064	1.5E-15 Tst	ENSRNOG00000000186	7	119,623,072
28193 A_44_P265709	1.441	0.108	1.8E-15	1.607	0.054	5.8E-27 Il2rb	ENSRNOG000000048636	7	119,712,888
19289 A_44_P975458	-0.745	0.119	3.1E-07	-0.449	0.060	6.2E-09 C1qtnf6	ENSRNOG000000007300	7	119,753,290
25974 A_43_P12557	0.834	0.066	7.9E-15	0.906	0.033	8.3E-26 Polr2f	ENSRNOG000000011214	7	120,380,544
13289 A_42_P620762	0.411	0.085	2.5E-05	0.219	0.043	9.4E-06 Atf4	ENSRNOG000000017801	7	121,480,723
3854 A_42_P633840	-0.815	0.160	1.1E-05	0.406	0.080	1.1E-05 Tll1	ENSRNOG000000010141	7	124,367,630
8829 A_64_P267897	-2.395	0.133	1.1E-19	0.386	0.066	1.2E-06	ENSRNOG000000011094	7	124,929,025
23584 A_64_P039342	0.470	0.091	9.0E-06	0.333	0.046	1.2E-08 Arhgap8	ENSRNOG000000033570	7	125,795,980
26976 A_64_P065313	0.527	0.089	9.5E-07	0.279	0.045	3.3E-07 RGD1304694	ENSRNOG000000031269	7	125,893,168
16279 A_44_P1034541	-0.571	0.103	2.9E-06	-0.640	0.052	1.3E-14 Pim3	ENSRNOG000000029698	7	129,860,114
2045 A_44_P179787	-1.366	0.113	2.9E-14	-0.857	0.057	3.0E-17 Panx2	ENSRNOG000000055530	7	130,042,947
27247 A_64_P005309	-0.658	0.094	3.3E-08	-0.410	0.047	2.0E-10 Mapk12	ENSRNOG000000031233	7	130,120,579
3165 A_42_P524610	0.539	0.063	2.9E-10	0.573	0.031	7.4E-20 Pph1n1	ENSRNOG000000022778	7	134,603,121
25471 A_44_P653647	0.534	0.099	4.6E-06	0.527	0.050	1.2E-12 Tmem117	ENSRNOG000000006068	7	136,182,224
14589 A_44_P152395	1.805	0.142	7.0E-15	1.278	0.071	1.3E-19 Rnd1	ENSRNOG000000059857	7	140,356,209
3857 A_64_P073129	-2.105	0.161	3.1E-15	-1.961	0.081	5.5E-24 Map3k12	ENSRNOG000000015134	7	144,109,116
3769 A_43_P12287	-0.508	0.060	3.4E-10	-0.413	0.030	4.6E-16 Ppp1r1a	ENSRNOG000000036827	7	145,154,131
11171 A_44_P436859	0.667	0.132	1.3E-05	0.751	0.066	1.8E-13 Mre11a	ENSRNOG000000009506	8	13,305,152
17711 A_44_P119527	-1.511	0.156	1.4E-11	-1.991	0.078	1.0E-24 Med17	ENSRNOG000000051989	8	13,526,025
8626 A_44_P100886	0.929	0.178	3.0E-05	1.426	0.115	1.8E-11	ENSRNOG000000010999	8	13,909,188
30089 A_42_P809733	-0.338	0.059	1.7E-06	-0.208	0.030	3.1E-08 RGD1309410	ENSRNOG000000011162	8	14,060,394
11775 A_44_P518434	-0.812	0.094	2.7E-10	-0.834	0.047	2.1E-19 Mrpl4	ENSRNOG000000020659	8	22,021,213
1575 A_44_P238246	0.718	0.134	4.9E-06	0.621	0.067	4.2E-11 Ilf3	ENSRNOG000000022741	8	22,402,890
25445 A_43_P11901	0.572	0.096	7.5E-07	-0.250	0.048	7.7E-06 Kcnj5	ENSRNOG000000033796	8	33,463,467
12442 A_42_P779282	1.385	0.110	9.0E-15	1.637	0.055	5.2E-27 Scn3b	ENSRNOG000000057221	8	44,136,496
12147 A_64_P118392	-0.326	0.070	4.0E-05	-0.286	0.035	9.0E-10 Nlr1	ENSRNOG000000052386	8	48,597,867
1405 A_42_P598602	-1.028	0.217	3.4E-05	-0.501	0.109	4.8E-05 Cd3g	ENSRNOG000000015945	8	49,280,901
12744 A_43_P11865	0.415	0.094	9.0E-05	0.301	0.047	2.2E-07 Pts	ENSRNOG000000009250	8	54,961,265
13478 A_64_P093452	-0.437	0.086	1.1E-05	-0.202	0.043	3.5E-05 RGD1305464	ENSRNOG000000018689	8	61,917,125
3353 A_44_P1030943	-0.341	0.061	2.4E-06	0.179	0.030	9.9E-07 Mpi	ENSRNOG000000018898	8	62,332,115
7313 A_64_P032579	-0.472	0.085	2.6E-06	-0.285	0.042	7.8E-08 Rab27a	ENSRNOG000000052499	8	79,722,334
26700 A_64_P151869	0.747	0.157	3.0E-05	0.830	0.078	1.2E-12 Myo5a	ENSRNOG000000058866	8	82,037,977
13551 A_64_P081939	2.769	0.310	8.3E-09	3.152	0.200	1.6E-13	ENSRNOG000000025957	8	85,720,790

26870 A_64_P001219	0.362	0.072	1.2E-05	0.167	0.036	4.3E-05 Mthfs	ENSRNOG000000013229	8	96,564,877
26117 A_44_P289125	0.557	0.105	5.8E-06	0.360	0.052	4.8E-08 Spsb4	ENSRNOG000000012862	8	104,912,959
18938 A_64_P048004	0.819	0.119	4.5E-08	0.406	0.059	5.4E-08	ENSRNOG000000010899	8	111,965,889
3885 A_43_P16086	-0.669	0.143	3.9E-05	-0.368	0.071	9.1E-06 Cish	ENSRNOG000000029543	8	116,054,465
2461 A_64_P025903	-0.496	0.089	2.4E-06	-0.361	0.044	1.1E-09 Slc26a6	ENSRNOG000000020450	8	117,648,745
27455 A_42_P834104	0.330	0.058	2.1E-06	0.278	0.029	2.3E-11 Cdc25a	ENSRNOG000000020737	8	117,953,444
21735 A_64_P149924	1.180	0.143	7.5E-10	0.498	0.071	3.4E-08 Fbxl2	ENSRNOG000000027099	8	122,311,431
13157 A_64_P020581	0.292	0.056	8.0E-06	0.195	0.028	3.7E-08 Crtap	ENSRNOG000000048343	8	122,421,384
5815 A_43_P11432	-0.608	0.085	2.1E-08	-0.837	0.043	6.7E-21 Acaa1a	ENSRNOG000000032908	8	128,027,958
360 A_64_P120679	-2.033	0.160	1.1E-14	-2.150	0.081	9.2E-25 Cck	ENSRNOG000000019321	8	130,127,392
588 A_44_P388755	0.843	0.167	6.9E-05	0.781	0.147	3.9E-05 Kif15	ENSRNOG000000060356	8	132,032,944
11481 A_44_P113974	1.170	0.169	3.9E-08	0.965	0.084	1.4E-13 Ccr5	ENSRNOG000000049115	8	133,210,473
11479 A_64_P153159	0.540	0.116	4.3E-05	1.240	0.058	4.3E-22 Ebi3	ENSRNOG000000050509	9	11,114,843
28637 A_64_P006077	-0.837	0.183	5.3E-05	-0.490	0.091	4.9E-06 LOC682829	ENSRNOG000000050521	9	14,513,037
6284 A_42_P512838	0.469	0.105	7.6E-05	0.856	0.053	3.1E-18 Trem2	ENSRNOG000000013578	9	14,618,013
22777 A_64_P146497	1.959	0.173	1.8E-13	1.148	0.086	1.7E-15 Cnpy3	ENSRNOG000000016315	9	16,543,688
26431 A_43_P15195	0.382	0.066	1.4E-06	0.169	0.033	1.1E-05 Polr1c	ENSRNOG000000019079	9	17,120,759
5468 A_43_P22042	0.698	0.115	5.6E-07	0.478	0.058	6.7E-10 Pla2g7	ENSRNOG000000025691	9	19,978,013
14908 A_64_P078852	0.919	0.178	8.9E-06	0.960	0.089	7.3E-13 RGD1560151	ENSRNOG000000046426	9	20,004,280
1988 A_42_P459212	0.687	0.120	1.6E-06	0.799	0.060	1.7E-15 Tnfrsf21	ENSRNOG000000011517	9	20,621,051
8885 A_44_P217919	1.747	0.169	2.4E-12	1.313	0.085	1.4E-17 Myot	ENSRNOG000000050004	9	37,728,008
8527 A_64_P069739	1.353	0.124	5.7E-13	1.196	0.062	1.4E-20 Ankrd23	ENSRNOG000000016151	9	43,116,521
20812 A_44_P166524	-0.721	0.136	5.7E-06	-0.467	0.068	4.5E-08 Lonrf2	ENSRNOG000000023312	9	45,505,767
3969 A_42_P825912	0.421	0.083	1.2E-05	-0.270	0.042	1.5E-07	ENSRNOG000000011677	9	60,039,297
5552 A_42_P667782	-0.501	0.073	5.6E-08	-0.342	0.037	4.0E-11 Fastkd2	ENSRNOG000000023923	9	70,450,444
29481 A_64_P024826	-0.718	0.148	8.5E-05	-0.642	0.125	4.4E-05 Crygd	ENSRNOG000000032219	9	71,778,323
4543 A_43_P14184	0.304	0.059	9.4E-06	0.139	0.029	3.5E-05 Acadl	ENSRNOG000000012966	9	73,871,888
13713 A_44_P531653	1.801	0.155	8.9E-14	1.849	0.077	9.8E-24 Myl1	ENSRNOG000000013262	9	73,958,480
25119 A_64_P102930	0.505	0.063	1.6E-09	0.446	0.032	2.6E-16 Atic	ENSRNOG000000015511	9	78,862,013
11375 A_64_P055930	0.605	0.130	4.0E-05	0.501	0.065	3.5E-09 Tmbim1	ENSRNOG000000014797	9	81,586,469
14961 A_64_P059491	-0.988	0.186	5.6E-06	-0.673	0.093	1.5E-08 Plcd4	ENSRNOG000000016361	9	81,816,872
8548 A_64_P139485	-1.192	0.169	2.6E-08	-0.566	0.084	7.5E-08 Plcd4	ENSRNOG000000016361	9	81,816,872
20938 A_42_P674200	0.367	0.076	2.8E-05	0.206	0.039	6.6E-06 Rnf25	ENSRNOG000000016886	9	81,879,211

16469 A_43_P11476	-1.206	0.202	7.4E-07	-0.589	0.101	1.1E-06 Inha	ENSRNOG000000020097	9	82,700,468
9798 A_44_P438863	0.501	0.091	3.0E-06	1.071	0.045	1.5E-23 Serpine2	ENSRNOG000000015461	9	85,626,094
29140 A_43_P18275	0.445	0.091	2.2E-05	0.482	0.046	1.4E-12 Agfg1	ENSRNOG000000015619	9	88,607,508
8283 A_43_P11985	1.607	0.296	4.3E-06	1.065	0.151	3.0E-08 Ccl20	ENSRNOG000000015992	9	88,918,433
25683 A_64_P157743	1.635	0.344	3.1E-05	1.070	0.172	3.4E-07 Ccl20	ENSRNOG000000015992	9	88,918,433
29722 A_64_P045191	2.635	0.379	7.0E-07	1.837	0.214	2.4E-08 Dner	ENSRNOG000000016640	9	92,291,220
18250 A_64_P091464	0.674	0.074	6.2E-11	0.659	0.037	1.5E-19 Sp100	ENSRNOG000000022769	9	92,681,078
18795 A_43_P10901	1.513	0.084	1.2E-19	1.406	0.042	8.1E-29 Itm2c	ENSRNOG000000017359	9	92,916,469
17490 A_64_P064234	-0.695	0.133	7.3E-06	-0.371	0.066	2.5E-06 B3gnt7	ENSRNOG000000018267	9	93,326,283
5606 A_44_P467591	-2.049	0.193	1.2E-12	-1.702	0.097	2.5E-19 Neu2	ENSRNOG000000016962	9	94,702,129
30046 A_64_P087940	1.313	0.171	4.1E-09	1.182	0.085	5.0E-16 Rbm44	ENSRNOG000000024878	9	98,279,022
16420 A_64_P110873	-0.458	0.084	4.0E-06	-0.466	0.042	3.8E-13 Ndufa10	ENSRNOG000000016470	9	99,651,813
1205 A_42_P739929	1.550	0.112	4.9E-16	1.218	0.056	2.2E-22	ENSRNOG000000051528	9	114,111,580
357 A_42_P744999	-0.368	0.061	5.6E-07	-0.350	0.030	1.1E-13 Rab12	ENSRNOG000000019295	9	114,709,546
20373 A_64_P034114	-0.802	0.139	1.5E-06	-1.019	0.070	9.5E-17 Epb41l3	ENSRNOG000000016724	9	117,538,009
11494 A_44_P123492	-0.842	0.119	2.5E-08	-1.414	0.059	1.1E-23 Epb41l3	ENSRNOG000000016724	9	117,538,009
300 A_42_P826853	0.785	0.166	3.3E-05	1.086	0.083	2.6E-15 Tnfrsf17	ENSRNOG000000021987	10	4,257,868
983 A_44_P1038028	1.108	0.160	4.2E-08	0.959	0.080	4.0E-14 Tnfrsf12a	ENSRNOG000000003546	10	12,997,930
16980 A_64_P159959	1.433	0.121	4.8E-14	1.524	0.060	1.4E-24 Tpsab1	ENSRNOG000000024181	10	14,703,668
7078 A_64_P060003	-0.807	0.144	2.4E-06	-0.454	0.072	2.8E-07 Wwc1	ENSRNOG000000008065	10	20,818,128
9066 A_64_P027288	1.047	0.183	1.6E-06	0.822	0.091	9.4E-11 RGD1564516	ENSRNOG000000038894	10	31,880,918
17349 A_44_P367550	0.768	0.123	3.4E-07	0.299	0.062	2.4E-05 Sqstm1	ENSRNOG000000003147	10	35,716,294
7761 A_44_P273989	0.355	0.066	4.8E-06	0.377	0.033	1.6E-13 Ppp2ca	ENSRNOG000000005389	10	37,554,664
9604 A_64_P067654	1.169	0.126	4.0E-11	0.619	0.063	8.9E-12 Aldh3a1	ENSRNOG000000002331	10	47,490,153
27222 A_64_P048486	0.876	0.166	8.4E-06	0.723	0.096	1.2E-08 Hs3st3a1	ENSRNOG000000024591	10	50,928,309
24608 A_64_P025618	-0.443	0.070	2.7E-07	-0.500	0.035	2.2E-16 Slc25a35	ENSRNOG000000004668	10	55,555,089
18624 A_64_P101792	-0.616	0.125	1.9E-05	-0.277	0.063	8.5E-05 Efnb3	ENSRNOG000000010320	10	56,167,426
1240 A_44_P477406	-0.575	0.115	1.6E-05	-0.401	0.058	3.5E-08 Slc2a4	ENSRNOG000000017226	10	56,558,487
14716 A_64_P104481	-0.395	0.088	7.5E-05	-0.213	0.044	2.7E-05 Spag7	ENSRNOG000000004246	10	57,291,146
11003 A_44_P853916	0.829	0.096	2.3E-10	0.436	0.048	6.7E-11 Slc43a2	ENSRNOG000000003835	10	63,677,396
23809 A_44_P1018622	0.889	0.139	2.2E-07	0.699	0.070	5.6E-12 Fam101b	ENSRNOG000000006674	10	64,202,380
17068 A_43_P17012	0.336	0.072	4.2E-05	0.264	0.036	1.3E-08 Glod4	ENSRNOG000000007788	10	64,398,294
12673 A_64_P066699	-0.540	0.108	1.5E-05	-0.383	0.054	2.5E-08 Timm22	ENSRNOG000000007988	10	64,556,064

6452 A_44_P839975	-0.654	0.127	9.8E-06	-0.378	0.064	8.1E-07 Tmem132e	ENSRNOG000000007455	10	69,737,422
7469 A_64_P039447	-0.408	0.090	6.3E-05	-0.500	0.045	3.5E-13 Heatr6	ENSRNOG000000002542	10	71,054,344
21499 A_44_P960156	-0.465	0.086	3.9E-06	-0.522	0.043	2.3E-14 Usp32	ENSRNOG0000000027711	10	72,417,070
20323 A_64_P091857	1.227	0.189	1.5E-07	1.150	0.095	2.4E-14 RGD1311564	ENSRNOG000000005447	10	74,298,599
4760 A_44_P762828	0.484	0.087	2.7E-06	-0.210	0.044	2.7E-05 LOC497978	ENSRNOG000000002338	10	76,407,989
1958 A_64_P075938	-0.580	0.108	4.6E-06	-0.554	0.054	2.8E-12 Cox11	ENSRNOG0000000052096	10	78,111,050
7956 A_64_P004584	0.744	0.148	1.4E-05	0.590	0.074	1.8E-09 Cacna1g	ENSRNOG0000000060528	10	82,197,848
5476 A_64_P150256	0.784	0.141	2.7E-06	-0.431	0.071	4.9E-07 Epn3	ENSRNOG000000003284	10	82,229,140
14953 A_64_P021606	-0.894	0.080	3.2E-13	-1.387	0.040	2.8E-29 Mycbpap	ENSRNOG0000000042912	10	82,252,963
9226 A_42_P458494	-1.327	0.164	1.3E-09	-1.296	0.082	8.7E-18 Acsf2	ENSRNOG000000003330	10	82,326,771
3031 A_43_P16949	-0.894	0.170	6.6E-06	-2.230	0.085	3.8E-25 Sgca	ENSRNOG000000003998	10	82,785,142
143 A_64_P070448	-0.487	0.074	1.2E-07	-0.760	0.037	1.7E-21 Nxph3	ENSRNOG000000005185	10	83,332,851
19934 A_64_P142229	1.421	0.090	8.7E-18	1.392	0.045	1.3E-27 Gngt2	ENSRNOG000000006108	10	83,655,460
112 A_42_P778587	1.383	0.076	1.1E-19	1.357	0.038	1.0E-29 Gngt2	ENSRNOG000000006108	10	83,655,460
27361 A_64_P049761	0.670	0.073	5.7E-11	0.319	0.037	2.0E-10 Nfe2l1	ENSRNOG000000008830	10	84,698,886
29794 A_43_P12209	-0.676	0.088	3.9E-09	-0.495	0.044	2.1E-13 Stat5b	ENSRNOG000000019075	10	88,754,829
14026 A_42_P829031	-0.300	0.056	4.4E-06	-0.216	0.028	3.3E-09 Coasy	ENSRNOG000000019918	10	88,992,487
17829 A_64_P147164	-0.376	0.070	5.1E-06	-0.200	0.035	1.8E-06 Tubg1	ENSRNOG0000000020213	10	89,030,865
6804 A_64_P150509	-0.824	0.169	2.3E-05	-1.007	0.086	1.1E-13 Ccr10	ENSRNOG0000000020275	10	89,088,993
24388 A_44_P377156	-1.018	0.209	2.2E-05	-0.561	0.104	4.6E-06 Cntnap1	ENSRNOG0000000020277	10	89,089,646
4593 A_42_P517554	-0.518	0.078	9.3E-08	-0.550	0.039	2.8E-16 Polg2	ENSRNOG000000013728	10	94,979,259
8186 A_44_P398864	0.494	0.088	2.0E-06	0.436	0.044	6.5E-12 Cog1	ENSRNOG000000002795	10	102,167,771
15465 A_64_P149794	0.588	0.077	5.2E-09	0.330	0.039	3.5E-10 Fam104a	ENSRNOG000000002851	10	102,200,400
2179 A_64_P100240	0.468	0.102	5.4E-05	0.249	0.051	2.2E-05 Llgl2	ENSRNOG000000004834	10	104,368,247
22560 A_64_P157691	-1.324	0.201	1.1E-07	-1.714	0.101	7.3E-19 RGD1559482	ENSRNOG0000000048771	10	104,952,237
29929 A_44_P497302	-0.638	0.109	1.1E-06	-0.566	0.055	2.3E-12 St6galnac2	ENSRNOG000000012083	10	105,668,593
10737 A_64_P001424	1.212	0.071	6.5E-19	1.304	0.035	2.9E-30 Mxra7	ENSRNOG0000000042915	10	105,771,972
12301 A_44_P520929	-0.930	0.106	1.9E-10	-0.786	0.053	6.7E-17 C1qtnf1	ENSRNOG000000003259	10	107,455,845
24209 A_44_P227616	-0.405	0.082	1.6E-05	-0.427	0.041	1.7E-12 Engase	ENSRNOG0000000027498	10	107,502,695
22363 A_64_P117233	-0.707	0.120	1.0E-06	-0.391	0.060	1.5E-07	ENSRNOG000000003699	10	108,630,823
27031 A_44_P506741	1.364	0.137	6.9E-12	0.970	0.069	2.6E-16 Azi1	ENSRNOG0000000047814	10	109,244,701
12448 A_64_P153134	-0.391	0.079	1.8E-05	-0.178	0.040	7.1E-05 LOC688310	ENSRNOG0000000047517	10	109,630,005
22449 A_42_P539095	-0.483	0.073	9.6E-08	-0.204	0.036	2.4E-06 LOC688311	ENSRNOG0000000049235	10	109,639,054

8870 A_42_P621872	-1.278	0.137	3.4E-11	-0.679	0.068	6.9E-12 Gcgr	ENSRNOG000000036692	10	109,707,962
9588 A_64_P032052	0.758	0.155	2.2E-05	0.542	0.078	3.4E-08 LOC688319	ENSRNOG000000048172	10	109,904,259
6976 A_44_P352538	1.781	0.198	4.8E-10	1.626	0.105	6.2E-16 Sectm1a	ENSRNOG000000036672	10	110,274,768
23085 A_64_P048951	2.739	0.231	5.0E-14	3.421	0.115	5.8E-27 Tex19	ENSRNOG000000036671	10	110,308,514
14465 A_64_P138565	-0.557	0.085	1.3E-07	-0.469	0.043	4.2E-13 Narf	ENSRNOG000000036664	10	110,445,797
22819 A_44_P159569	0.954	0.118	1.3E-09	1.102	0.059	3.9E-20 Wdr45l	ENSRNOG000000036662	10	110,555,629
1712 A_42_P727022	-0.712	0.088	1.4E-09	-0.574	0.044	3.5E-15 Rab40b	ENSRNOG000000036661	10	110,585,376
13697 A_64_P013526	-0.763	0.173	8.6E-05	-0.803	0.086	3.9E-11 Cxadr	ENSRNOG000000001557	11	16,826,399
20993 A_64_P071362	0.676	0.096	3.0E-08	0.670	0.048	4.2E-16 Krtap16-5	ENSRNOG000000040064	11	28,900,376
5982 A_64_P071367	0.617	0.092	8.4E-08	0.659	0.046	1.9E-16 Krtap16-5	ENSRNOG000000040064	11	28,900,376
17844 A_64_P067708	-0.532	0.076	2.8E-08	-0.657	0.038	3.8E-19 Tmem50b	ENSRNOG000000002028	11	31,752,243
1270 A_42_P581567	0.492	0.079	3.6E-07	0.562	0.040	2.4E-16 Gart	ENSRNOG000000028292	11	31,805,728
15351 A_64_P072973	1.097	0.139	3.4E-09	1.473	0.073	1.3E-20 Kcne2	ENSRNOG000000029811	11	32,440,237
12330 A_44_P121280	4.027	0.279	1.4E-16	3.838	0.140	7.7E-26 Kcne1	ENSRNOG000000001984	11	32,508,420
23688 A_64_P116600	1.543	0.131	5.7E-14	1.004	0.065	1.9E-17 Rcan1	ENSRNOG000000001979	11	32,550,539
26800 A_64_P116606	1.458	0.177	8.6E-10	0.915	0.089	2.6E-12 Rcan1	ENSRNOG000000001979	11	32,550,539
2645 A_44_P1039678	-0.398	0.081	2.0E-05	-0.302	0.041	8.5E-09 Setd4	ENSRNOG000000001699	11	33,801,999
16374 A_64_P036352	-0.774	0.094	8.1E-10	-0.779	0.047	1.8E-18 Cbr1	ENSRNOG000000049911	11	33,863,500
3179 A_42_P554722	-0.746	0.078	1.7E-11	-0.682	0.039	2.7E-19 Pign	ENSRNOG000000039850	11	34,598,275
8239 A_64_P103808	0.365	0.079	5.0E-05	0.220	0.040	2.8E-06 Dscr3	ENSRNOG000000001681	11	34,791,993
8216 A_64_P322881	0.568	0.092	4.0E-07	0.613	0.046	1.7E-15 Erg	ENSRNOG000000001652	11	35,749,594
1366 A_64_P057975	0.346	0.067	9.2E-06	0.170	0.034	1.2E-05 Hmgn1	ENSRNOG000000050978	11	36,479,868
6884 A_42_P732251	-0.943	0.100	3.1E-11	-1.160	0.050	3.1E-23 Phldb2	ENSRNOG000000002171	11	57,404,196
6750 A_64_P013875	-0.950	0.135	3.0E-08	-0.825	0.068	2.3E-14	ENSRNOG000000002171	11	57,430,166
24679 A_64_P058744	-0.426	0.074	1.3E-06	-0.418	0.037	1.8E-13 Abhd10	ENSRNOG000000043107	11	57,486,365
1239 A_43_P12572	0.558	0.101	2.7E-06	0.553	0.050	4.4E-13 Cd200	ENSRNOG000000002141	11	60,371,729
19518 A_64_P127803	-3.334	0.243	6.6E-16	-3.795	0.122	9.3E-28 Btla	ENSRNOG000000030246	11	60,547,201
7489 A_64_P083933	0.742	0.108	5.0E-08	0.750	0.054	4.9E-16 Adcy5	ENSRNOG000000002229	11	68,842,320
27241 A_43_P11558	1.277	0.275	4.5E-05	0.935	0.138	6.1E-08 Apod	ENSRNOG000000048273	11	72,705,129
13604 A_44_P436604	0.792	0.138	1.5E-06	1.030	0.069	4.6E-17 Leprel1	ENSRNOG000000055751	11	78,029,038
25187 A_44_P179145	1.134	0.167	1.6E-07	1.030	0.098	1.3E-11 Dgkg	ENSRNOG000000001796	11	81,972,219
18133 A_64_P009857	-1.017	0.137	9.1E-09	-0.599	0.069	1.9E-10 Tbx1	ENSRNOG000000001892	11	86,552,022
349 A_64_P043259	-1.072	0.180	1.1E-06	-0.655	0.087	1.1E-08 P2rx6	ENSRNOG000000001873	11	87,435,185

7350 A_64_P048136	-0.673	0.141	2.9E-05	-0.337	0.070	2.9E-05 Brca2	ENSRNOG000000001111	12	504,007
26071 A_64_P030834	7.370	0.256	1.7E-26	6.700	0.128	1.2E-35	ENSRNOG000000000952	12	9,607,168
16025 A_64_P148325	1.383	0.218	2.7E-07	1.314	0.111	8.0E-14	ENSRNOG000000062055	12	11,083,897
3604 A_42_P746109	-0.766	0.085	9.1E-11	-0.618	0.043	1.1E-16 Asmtl	ENSRNOG000000028166	12	18,531,990
19145 A_64_P081501	1.142	0.097	5.5E-14	1.785	0.048	2.6E-30 Mcm7	ENSRNOG000000001349	12	19,314,016
1521 A_44_P534154	0.634	0.110	1.3E-06	0.820	0.055	4.6E-17 Cnpy4	ENSRNOG000000027175	12	19,328,957
23117 A_42_P540609	-1.064	0.122	1.9E-10	-1.150	0.061	2.5E-20 LOC680711	ENSRNOG000000031343	12	19,440,501
24237 A_64_P194847	-0.750	0.159	3.8E-05	-1.023	0.074	8.1E-16	ENSRNOG000000027061	12	19,512,591
25622 A_64_P119299	-1.267	0.190	8.9E-08	-1.190	0.095	1.0E-14	ENSRNOG000000027061	12	19,512,591
8198 A_64_P027108	-1.371	0.167	3.6E-09	-1.282	0.088	3.1E-15 RGD1562319	ENSRNOG000000039216	12	19,561,347
18384 A_64_P079080	0.729	0.165	8.6E-05	1.129	0.082	7.0E-16	ENSRNOG000000059625	12	20,667,601
1742 A_64_P144034	1.856	0.256	3.7E-07	2.770	0.181	6.4E-13 LOC363894	ENSRNOG000000045875	12	20,814,122
15839 A_64_P032265	1.212	0.193	2.8E-07	1.429	0.096	6.1E-17	ENSRNOG000000033017	12	21,678,580
29237 A_43_P17858	0.663	0.126	6.5E-06	0.600	0.063	2.1E-11 LOC685020	ENSRNOG000000033017	12	21,678,580
21128 A_43_P12143	0.459	0.089	9.1E-06	0.406	0.044	6.4E-11 Clip2	ENSRNOG000000021611	12	25,173,005
17101 A_64_P051322	-0.679	0.129	7.1E-06	-0.500	0.065	3.7E-09 Ncf1	ENSRNOG000000001480	12	25,497,104
4649 A_43_P12593	-0.696	0.157	8.0E-05	-0.911	0.078	8.6E-14 Phkg1	ENSRNOG000000000920	12	30,450,316
1906 A_64_P142962	1.811	0.276	3.4E-07	1.886	0.097	2.9E-18 Ccdc92	ENSRNOG000000021691	12	37,211,316
3175 A_44_P1030714	2.361	0.133	2.1E-19	2.524	0.067	1.1E-30 Ccdc92	ENSRNOG000000021691	12	37,211,316
16497 A_64_P032524	0.307	0.070	8.9E-05	0.367	0.035	1.4E-12 Atp6v0a2	ENSRNOG000000052704	12	37,398,329
9969 A_42_P747877	0.348	0.076	5.5E-05	0.250	0.038	1.2E-07 Eif2b1	ENSRNOG000000001039	12	37,444,103
13814 A_43_P10909	-0.430	0.092	4.0E-05	-0.344	0.046	7.6E-09 Gtf2h3	ENSRNOG000000001035	12	37,444,282
13761 A_64_P135202	-0.886	0.117	5.3E-09	-1.171	0.058	3.3E-21 Snmp35	ENSRNOG000000001060	12	37,538,403
11508 A_64_P043731	0.607	0.090	7.1E-08	0.216	0.045	2.7E-05 Vps37b	ENSRNOG000000001086	12	37,984,790
28906 A_64_P112312	0.696	0.126	3.1E-06	0.547	0.063	2.4E-10 Clip1	ENSRNOG000000001247	12	38,345,456
6196 A_44_P686406	0.422	0.095	7.8E-05	0.213	0.047	6.7E-05 RGD1562310	ENSRNOG000000001123	12	43,940,798
12127 A_44_P1056161	-0.357	0.073	1.9E-05	-0.518	0.036	2.0E-16 Prkab1	ENSRNOG000000001142	12	46,316,236
741 A_42_P548796	-1.021	0.083	1.5E-14	-0.387	0.041	3.4E-11 Tsn	ENSRNOG000000002319	13	34,251,650
4104 A_44_P346848	-0.759	0.103	1.1E-08	-0.338	0.052	1.3E-07 Tmem177	ENSRNOG000000025484	13	35,933,243
28389 A_44_P574134	0.524	0.112	4.1E-05	0.652	0.056	9.3E-14 Slc35f5	ENSRNOG000000003403	13	41,883,137
1167 A_64_P119588	1.248	0.255	2.4E-05	0.705	0.104	8.6E-08 Tmem163	ENSRNOG000000003769	13	44,345,735
5228 A_64_P081287	-2.041	0.200	3.7E-12	-1.322	0.100	2.2E-15 Klhdc8a	ENSRNOG000000000036	13	49,074,644
23346 A_64_P013147	0.626	0.124	1.3E-05	0.729	0.062	6.5E-14 Prelp	ENSRNOG000000003120	13	50,761,306

19228 A_44_P452176	1.940	0.253	4.2E-09	2.356	0.126	3.8E-20 Chi3l1	ENSRNOG000000053272	13	51,022,681
10145 A_64_P103707	0.403	0.063	2.1E-07	-0.179	0.032	1.8E-06 Ndufv3	ENSRNOG000000027593	13	51,297,621
28935 A_64_P141541	0.342	0.055	3.5E-07	-0.221	0.028	1.6E-09 Ndufv3	ENSRNOG000000027593	13	51,297,621
3383 A_42_P653257	0.534	0.117	5.7E-05	0.367	0.059	3.0E-07 Ptpn7	ENSRNOG000000005807	13	51,958,834
22664 A_42_P577677	0.850	0.135	2.8E-07	0.349	0.068	8.9E-06 Tnni1	ENSRNOG000000009073	13	52,624,878
16675 A_64_P055196	0.552	0.125	8.9E-05	0.514	0.063	8.9E-10 Camsap1l1	ENSRNOG000000008741	13	53,225,349
19291 A_44_P475444	1.543	0.106	1.2E-16	1.264	0.053	1.1E-23 RGD1564614	ENSRNOG000000042369	13	56,958,549
2005 A_42_P819656	1.928	0.097	5.3E-21	1.469	0.049	3.1E-27 Cfh	ENSRNOG000000030715	13	57,080,549
17693 A_64_P034344	1.398	0.088	6.7E-18	0.961	0.044	2.0E-22 Cfh	ENSRNOG000000030715	13	57,080,549
6797 A_64_P035709	0.685	0.123	2.5E-06	0.296	0.061	2.6E-05 B3galt2	ENSRNOG000000003251	13	60,435,946
5214 A_44_P109862	2.093	0.166	8.9E-15	1.275	0.083	2.1E-17 Ivns1abp	ENSRNOG000000002618	13	68,707,776
24164 A_44_P971500	1.898	0.112	1.0E-18	1.111	0.056	5.8E-21	ENSRNOG000000002618	13	68,707,776
17011 A_64_P097847	-0.390	0.089	9.5E-05	-0.454	0.044	3.4E-12 RGD1309104	ENSRNOG000000028236	13	69,385,074
9844 A_64_P113615	1.142	0.209	4.1E-06	0.973	0.109	1.9E-10	ENSRNOG000000057851	13	75,059,927
17702 A_64_P033270	1.080	0.073	6.5E-17	1.061	0.037	1.1E-26 LOC680254	ENSRNOG000000057851	13	75,059,927
4122 A_44_P358194	2.488	0.238	1.8E-12	2.534	0.119	4.9E-22 Fmo3	ENSRNOG000000003620	13	80,862,963
14514 A_44_P180259	0.804	0.092	2.2E-10	1.585	0.046	3.5E-29 Dpt	ENSRNOG000000002947	13	83,073,550
26528 A_64_P016901	1.309	0.118	3.7E-13	1.261	0.059	4.5E-22 Creg1	ENSRNOG000000003291	13	83,972,212
22348 A_44_P1018997	-0.373	0.075	1.7E-05	-0.411	0.038	5.1E-13 Tmco1	ENSRNOG000000003928	13	85,465,792
3268 A_64_P005029	0.823	0.101	1.1E-09	0.715	0.051	2.9E-16 Pcp4l1	ENSRNOG000000003209	13	89,565,813
314 A_42_P487031	-0.319	0.053	6.8E-07	-0.225	0.027	4.3E-10 B4galt3	ENSRNOG000000003551	13	89,643,881
13087 A_44_P282716	0.515	0.067	4.1E-09	0.538	0.034	5.1E-18 Nit1	ENSRNOG000000003881	13	89,725,806
12930 A_64_P014213	0.467	0.081	1.4E-06	0.226	0.041	2.5E-06 Pex19	ENSRNOG000000057116	13	90,514,336
6787 A_64_P067035	-0.660	0.099	8.4E-08	-0.266	0.049	4.5E-06 Casq1	ENSRNOG000000006930	13	90,602,365
6685 A_64_P126623	0.617	0.140	8.7E-05	0.658	0.070	2.8E-11 Fcgr2a	ENSRNOG000000046663	13	91,228,901
20982 A_64_P126851	0.656	0.131	1.4E-05	0.796	0.065	2.4E-14 LOC498276	ENSRNOG000000046663	13	91,228,935
1235 A_64_P069641	0.383	0.087	8.6E-05	0.285	0.043	1.1E-07 Psen2	ENSRNOG000000002879	13	98,529,040
23959 A_44_P177914	0.504	0.115	9.1E-05	0.323	0.057	2.1E-06 Nvl	ENSRNOG000000003629	13	99,468,778
4088 A_44_P217715	0.953	0.132	1.7E-08	0.932	0.066	2.9E-16 Enah	ENSRNOG000000031934	13	100,405,339
19118 A_43_P12532	1.235	0.170	1.5E-08	1.300	0.085	2.4E-17 Tgfb2	ENSRNOG000000002418	13	105,141,030
3795 A_43_P13418	-0.886	0.145	4.6E-07	-0.604	0.072	5.9E-10 Kcnk2	ENSRNOG000000002653	13	107,831,014
10054 A_64_P054568	1.261	0.233	6.0E-06	0.729	0.100	2.5E-08 Vash2	ENSRNOG000000003832	13	109,552,589
9059 A_42_P803590	-1.434	0.080	1.6E-19	-1.374	0.040	3.8E-29 LOC289378	ENSRNOG000000046460	13	109,663,364

10206 A_64_P052464	1.769	0.181	2.9E-11	1.270	0.087	5.6E-16	Ints7	ENSRNOG000000004263	13	110,257,571
3954 A_42_P661065	1.382	0.150	5.4E-11	1.345	0.075	1.5E-19	Ints7	ENSRNOG000000004263	13	110,257,571
4659 A_64_P155629	0.554	0.098	2.1E-06	0.697	0.049	2.3E-16	Csf2ra	ENSRNOG0000000049782	14	1,462,358
16112 A_64_P072873	1.459	0.176	6.8E-10	1.390	0.088	8.0E-18	Cplx1	ENSRNOG000000000060	14	2,194,933
3732 A_42_P522488	-0.498	0.098	1.2E-05	-0.476	0.049	1.4E-11	Znf644	ENSRNOG000000002112	14	4,125,380
12879 A_44_P552655	-0.881	0.118	7.8E-09	-0.450	0.059	4.8E-09	Abcg31l	ENSRNOG0000000030216	14	6,541,171
21816 A_64_P085715	0.702	0.086	9.8E-10	0.491	0.043	1.5E-13	Pkd2	ENSRNOG000000002146	14	6,645,257
3605 A_44_P491796	3.152	0.357	1.5E-10	1.735	0.178	1.2E-11	Spp1	ENSRNOG0000000043451	14	6,679,901
10617 A_44_P1043814	-0.397	0.079	1.4E-05	-0.335	0.040	4.2E-10	Hsd17b11	ENSRNOG000000002210	14	7,073,445
19510 A_64_P021440	0.781	0.157	1.6E-05	0.481	0.072	1.1E-07	Slc10a6	ENSRNOG000000002057	14	7,618,022
16277 A_64_P138543	0.435	0.080	4.2E-06	0.267	0.040	9.3E-08	Bmp2k	ENSRNOG000000002040	14	14,192,048
18694 A_44_P325508	0.473	0.069	5.7E-08	0.274	0.035	2.2E-09	Anxa3	ENSRNOG000000002045	14	14,426,437
23631 A_64_P013437	0.991	0.144	4.4E-08	0.399	0.072	2.7E-06	Cxcl13	ENSRNOG0000000024899	14	15,258,207
13827 A_44_P404591	0.933	0.127	1.2E-08	0.703	0.064	3.9E-13	Hopx	ENSRNOG0000000024689	14	33,354,807
1112 A_64_P041476	-0.524	0.094	2.5E-06	-0.481	0.047	3.1E-12	LOC498368	ENSRNOG000000002191	14	46,054,022
21733 A_44_P386824	0.435	0.092	3.5E-05	0.484	0.046	1.6E-12	Yipf7	ENSRNOG000000002224	14	62,595,854
22 A_44_P992306	-0.549	0.085	1.5E-07	-0.209	0.042	1.8E-05	Gnpda2	ENSRNOG000000002177	14	62,646,110
18510 A_64_P143400	1.275	0.156	9.9E-10	0.897	0.078	1.2E-13	Gba3	ENSRNOG0000000024634	14	64,535,170
21557 A_44_P177950	0.331	0.076	9.8E-05	0.260	0.038	4.7E-08	Med28	ENSRNOG000000003592	14	70,098,021
25255 A_64_P150071	-0.251	0.057	9.4E-05	-0.249	0.029	2.2E-10	Rab28	ENSRNOG000000017074	14	73,889,213
3647 A_42_P571433	-0.527	0.117	6.9E-05	-0.649	0.059	3.6E-13	Msx1	ENSRNOG000000006876	14	77,712,240
8159 A_44_P898195	0.802	0.155	8.8E-06	0.380	0.078	2.0E-05	Cytl1	ENSRNOG0000000028108	14	77,810,147
9903 A_64_P155691	-0.342	0.072	3.2E-05	-0.630	0.036	2.9E-19	Zfp278	ENSRNOG0000000018709	14	83,510,640
18032 A_44_P402445	1.076	0.161	4.3E-07	1.851	0.113	2.6E-15	Nefh	ENSRNOG000000008716	14	85,191,557
19355 A_64_P244845	0.726	0.084	2.9E-10	0.510	0.042	2.9E-14	Tns3	ENSRNOG0000000025695	14	88,886,198
21874 A_64_P089280	0.609	0.106	1.6E-06	0.584	0.053	4.7E-13	Tns3	ENSRNOG0000000025695	14	88,886,198
5272 A_64_P038050	1.268	0.083	2.6E-17	-0.209	0.042	1.4E-05	Acyp2	ENSRNOG0000000042419	14	115,052,450
10722 A_64_P108876	0.873	0.078	2.7E-13	0.256	0.039	1.2E-07	Dusp13	ENSRNOG0000000057795	15	2,526,368
30065 A_42_P829349	0.498	0.067	9.2E-09	0.176	0.034	7.0E-06	Comtd1	ENSRNOG000000013968	15	2,631,529
736 A_42_P653332	-0.342	0.063	3.7E-06	-0.163	0.031	8.4E-06	Mrps16	ENSRNOG000000006898	15	4,351,292
15076 A_44_P289862	0.437	0.093	3.8E-05	0.412	0.047	1.4E-10	Abhd6	ENSRNOG000000008167	15	18,675,431
18294 A_44_P234129	-0.817	0.108	5.9E-09	-0.678	0.054	9.7E-15	Dlgap5	ENSRNOG000000010721	15	24,199,341
12606 A_64_P098006	-0.457	0.070	1.4E-07	-0.356	0.035	3.9E-12	Fitm1	ENSRNOG000000019019	15	34,251,606

27632 A_64_P151264	-0.607	0.100	5.0E-07	-0.699	0.050	3.3E-16 Fam158a	ENSRNOG000000019162	15	34,263,224
12799 A_64_P153273	-1.241	0.172	2.0E-08	-0.430	0.080	4.8E-06 Mcpt10	ENSRNOG000000049991	15	34,694,180
510 A_64_P068192	-1.435	0.122	6.3E-14	-0.680	0.061	2.9E-13 Mcpt8	ENSRNOG000000049991	15	34,694,244
10995 A_64_P124294	-1.413	0.130	6.0E-13	-0.813	0.065	1.1E-14 Mcpt9	ENSRNOG000000031792	15	35,002,406
10858 A_64_P028371	-0.713	0.124	1.5E-06	-1.747	0.062	3.4E-26 Phf11	ENSRNOG000000053891	15	38,709,984
23836 A_64_P151851	-0.668	0.150	7.8E-05	-1.125	0.075	4.2E-17 Phf11	ENSRNOG000000053891	15	38,709,984
7039 A_64_P022452	0.670	0.144	4.6E-05	1.509	0.073	3.5E-21 Pebp4	ENSRNOG000000026247	15	51,535,864
16197 A_44_P654933	-0.653	0.144	6.2E-05	-0.380	0.072	6.5E-06 Piwil2	ENSRNOG000000009871	15	52,116,001
17860 A_64_P142046	-0.358	0.069	7.3E-06	0.253	0.034	1.0E-08 Nudt15	ENSRNOG000000025239	15	55,424,024
12137 A_43_P14977	0.617	0.085	1.6E-08	1.364	0.043	4.2E-28 Tsc22d1	ENSRNOG000000001030	15	58,554,374
6846 A_64_P005043	0.847	0.088	1.7E-11	0.773	0.044	2.9E-19 Nt5dc2	ENSRNOG000000018358	16	7,212,488
30347 A_64_P066923	0.810	0.115	3.0E-08	0.716	0.058	1.3E-14 Ncoa4	ENSRNOG000000019768	16	8,302,950
25712 A_64_P153759	1.297	0.132	9.0E-12	0.890	0.066	1.1E-15	ENSRNOG000000029662	16	9,430,743
23686 A_64_P131151	0.556	0.088	2.3E-07	0.688	0.044	9.4E-18 Opn4	ENSRNOG000000053893	16	10,952,549
5974 A_42_P596050	1.857	0.215	2.5E-10	0.941	0.107	1.8E-10 Pcdh21	ENSRNOG000000013330	16	14,348,046
1186 A_42_P467381	1.103	0.062	2.0E-19	0.870	0.031	4.3E-26 Fam32a	ENSRNOG000000039528	16	19,308,842
9044 A_64_P137784	-0.580	0.102	1.8E-06	-0.698	0.051	7.4E-16 Plvap	ENSRNOG000000017676	16	19,918,689
11317 A_44_P177414	-0.349	0.067	7.0E-06	-0.157	0.033	3.6E-05 Fam125a	ENSRNOG000000017949	16	19,973,636
10403 A_64_P011489	2.738	0.225	2.3E-14	2.453	0.112	2.1E-22 Gdf15	ENSRNOG000000019661	16	20,555,395
19569 A_44_P1024788	0.465	0.079	1.1E-06	0.547	0.040	5.9E-16 LOC498606	ENSRNOG000000019971	16	20,657,099
6546 A_64_P124701	0.940	0.139	6.3E-08	1.325	0.069	1.8E-20 Crlf1	ENSRNOG000000020030	16	20,686,317
9891 A_64_P056648	0.948	0.099	1.7E-11	1.544	0.049	8.8E-28 Crlf1	ENSRNOG000000020030	16	20,686,317
15836 A_44_P295789	1.122	0.235	2.9E-05	0.601	0.117	1.0E-05 Comp	ENSRNOG000000048472	16	20,807,070
23904 A_64_P100904	-1.239	0.163	5.4E-09	-1.289	0.082	8.2E-18 LOC688966	ENSRNOG000000020427	16	21,029,134
25971 A_64_P004531	-1.051	0.084	9.0E-15	-0.926	0.042	1.2E-22 LOC688966	ENSRNOG000000020427	16	21,029,134
4835 A_44_P1016480	0.723	0.091	1.8E-09	0.405	0.045	1.2E-10 Lpl	ENSRNOG000000012181	16	22,561,496
8763 A_64_P144978	0.704	0.099	2.4E-08	0.602	0.050	2.5E-14 Csgalnact1	ENSRNOG000000013024	16	22,979,444
8543 A_44_P265003	-1.024	0.113	8.5E-11	-1.128	0.057	4.7E-21 Anxa10	ENSRNOG000000014339	16	29,674,793
24363 A_64_P010393	0.461	0.093	1.8E-05	0.377	0.047	1.3E-09 Clcn3	ENSRNOG000000010682	16	32,449,116
15146 A_44_P1036068	-0.479	0.072	9.0E-08	-0.472	0.036	2.6E-15 RGD1311747	ENSRNOG000000011293	16	32,540,217
26255 A_64_P130050	1.081	0.197	3.3E-06	0.976	0.098	7.5E-12 Hand2	ENSRNOG000000060448	16	36,373,546
3982 A_64_P007462	0.653	0.111	1.0E-06	1.047	0.056	2.9E-20 Spcs3	ENSRNOG000000038933	16	40,050,734
26075 A_64_P041016	-1.311	0.125	1.7E-12	-1.202	0.063	1.5E-20 Wwc2	ENSRNOG000000013248	16	47,368,768

8059 A_42_P664913	-1.245	0.191	1.4E-07	-0.703	0.095	1.1E-08	Ankrd37	ENSRNOG000000031335	16	49,462,889
27848 A_44_P1021361	0.977	0.105	4.2E-11	0.744	0.053	2.6E-16	Tlr3	ENSRNOG000000021726	16	50,016,857
171 A_64_P040806	1.184	0.086	9.0E-16	1.126	0.044	1.9E-24	Tlr3	ENSRNOG000000021726	16	50,016,857
25609 A_64_P097598	0.408	0.079	8.3E-06	0.461	0.039	7.3E-14	Mtus1	ENSRNOG000000010748	16	54,332,660
9554 A_64_P048315	1.067	0.119	1.0E-10	1.308	0.059	1.6E-22		ENSRNOG000000055088	16	59,517,000
27771 A_44_P1000842	1.166	0.145	2.6E-08	0.723	0.091	3.7E-08	Tex15	ENSRNOG000000007748	16	62,373,253
28774 A_44_P438492	0.493	0.078	2.6E-07	0.986	0.039	1.4E-24	Mak16	ENSRNOG000000010783	16	64,729,221
11412 A_44_P1042163	0.906	0.089	4.0E-12	1.279	0.045	1.8E-26	RGD1310414	ENSRNOG000000023494	16	64,745,207
1931 A_43_P12961	0.470	0.089	6.4E-06	0.297	0.045	8.9E-08	Eif4ebp1	ENSRNOG000000012582	16	68,968,248
1443 A_42_P798776	-0.453	0.087	8.4E-06	-0.555	0.044	6.7E-15	LOC100364957	ENSRNOG000000059911	16	70,905,993
17467 A_64_P121981	-1.234	0.206	7.9E-07	-0.688	0.105	1.4E-07	Htra4	ENSRNOG000000061160	16	71,787,966
28259 A_64_P157693	-0.489	0.095	8.7E-06	-0.677	0.047	1.8E-16	Ank1	ENSRNOG000000018241	16	73,827,488
4278 A_43_P12782	0.536	0.071	5.5E-09	0.291	0.035	7.6E-10	Ikbkb	ENSRNOG000000019073	16	74,177,215
1616 A_43_P12689	2.315	0.426	5.1E-06	2.577	0.205	3.6E-14	Defb1	ENSRNOG000000013768	16	75,309,176
6310 A_44_P368065	0.713	0.118	6.2E-07	0.284	0.059	2.7E-05	Adprhl1	ENSRNOG000000062013	16	81,616,604
28399 A_44_P189837	-0.470	0.098	2.6E-05	-0.522	0.049	9.6E-13	Carkd	ENSRNOG000000015021	16	83,342,667
18894 A_64_P022751	1.110	0.104	9.6E-13	0.884	0.052	7.8E-19	Isca1	ENSRNOG000000018343	17	5,281,727
19764 A_44_P429781	0.361	0.065	2.8E-06	0.177	0.033	4.1E-06	Mak10	ENSRNOG000000018417	17	5,463,898
30268 A_44_P215479	0.725	0.081	1.2E-10	0.495	0.041	2.6E-14	Rmi1	ENSRNOG000000019108	17	6,660,536
20495 A_64_P300082	0.610	0.111	3.1E-06	0.581	0.055	1.6E-12	Spin1	ENSRNOG000000046068	17	14,091,766
8900 A_64_P059262	1.105	0.061	1.1E-19	1.070	0.031	1.7E-29	Riok1	ENSRNOG000000014049	17	27,451,832
21031 A_64_P067678	-0.671	0.088	4.7E-09	-0.565	0.044	4.6E-15	Aldh5a1	ENSRNOG000000023538	17	42,133,076
23925 A_64_P030919	-0.723	0.075	1.3E-11	-0.714	0.037	1.6E-20		ENSRNOG000000023538	17	42,133,076
24052 A_64_P017273	0.645	0.105	4.5E-07	0.388	0.053	1.0E-08	Lrrc16a	ENSRNOG000000016576	17	43,050,789
14569 A_64_P057801	0.478	0.087	3.2E-06	0.658	0.043	3.1E-17	Hist1h2bl	ENSRNOG000000047776	17	43,808,673
20825 A_64_P004639	0.508	0.093	3.4E-06	0.675	0.046	1.1E-16	Hist1h2bc	ENSRNOG000000059382	17	44,738,330
13074 A_64_P130572	0.464	0.096	2.5E-05	0.679	0.048	2.6E-16	Hist1h2bc	ENSRNOG000000059382	17	44,738,330
5615 A_44_P506017	0.483	0.109	8.6E-05	0.681	0.055	1.2E-14		ENSRNOG000000054296	17	44,793,927
25440 A_43_P12803	0.490	0.104	3.7E-05	0.363	0.052	3.5E-08	Arid4b	ENSRNOG000000049751	17	53,915,076
17147 A_44_P238897	0.832	0.141	9.1E-07	0.811	0.070	1.2E-13		ENSRNOG000000018110	17	55,346,279
17288 A_64_P165005	-0.506	0.090	2.3E-06	-0.545	0.045	2.9E-14	Fzd8	ENSRNOG000000061031	17	62,262,129
22265 A_64_P014867	0.579	0.113	9.8E-06	0.643	0.056	1.6E-13	Pfkf	ENSRNOG000000017163	17	68,559,471
25805 A_44_P220256	-0.633	0.092	4.8E-08	-0.669	0.046	1.2E-16	Prtfcd1	ENSRNOG000000024874	17	88,037,040

20226 A_64_P104454	-0.992	0.101	1.0E-11	-0.634	0.051	9.9E-15 Impad1	ENSRNOG000000046647	17	90,218,013
20714 A_64_P056712	0.963	0.144	9.9E-08	0.479	0.067	2.3E-08 Gpr137b	ENSRNOG000000002480	17	90,696,019
30354 A_64_P089742	-0.338	0.073	4.4E-05	-0.427	0.036	6.6E-14 Cdig2	ENSRNOG000000012016	18	3,662,683
14497 A_64_P174430	-0.324	0.072	6.5E-05	-0.351	0.036	1.0E-11 Cdig2	ENSRNOG000000012016	18	3,662,683
16785 A_44_P1028952	-0.393	0.079	1.7E-05	-0.297	0.040	7.0E-09	ENSRNOG000000016467	18	6,474,990
3764 A_44_P469584	0.902	0.204	8.6E-05	0.685	0.102	7.6E-08 Cd14	ENSRNOG000000017819	18	29,562,153
24116 A_64_P026818	0.662	0.101	1.2E-07	0.465	0.050	5.1E-11 Gramd3	ENSRNOG000000015225	18	51,492,196
2027 A_44_P1006931	-1.192	0.087	7.4E-16	-0.311	0.044	2.1E-08 LOC100174910	ENSRNOG000000013738	18	52,047,816
1555 A_64_P079379	-0.997	0.193	8.6E-06	-0.433	0.096	6.8E-05 Fbn2	ENSRNOG000000043219	18	53,181,503
25074 A_64_P045764	0.669	0.116	1.4E-06	0.563	0.058	1.3E-11 Adamts19	ENSRNOG000000019577	18	53,915,807
2039 A_64_P135224	2.710	0.116	2.3E-23	2.459	0.058	2.2E-32 RGD1309362	ENSRNOG000000038960	18	55,505,993
3030 A_44_P538334	-0.615	0.136	6.6E-05	-0.571	0.068	5.6E-10 Impa2	ENSRNOG000000018516	18	63,016,577
10937 A_43_P22556	-0.902	0.094	1.6E-11	-1.264	0.047	1.5E-25 Cidea	ENSRNOG000000018505	18	63,098,144
9291 A_64_P156333	-0.699	0.085	8.4E-10	-1.314	0.042	1.3E-27 Cidea	ENSRNOG000000018505	18	63,098,144
12179 A_64_P078837	-1.349	0.131	2.9E-12	-1.059	0.066	4.3E-18	ENSRNOG000000055190	18	63,839,026
18168 A_44_P213175	-1.357	0.129	1.5E-12	-0.534	0.065	7.3E-10 Ccdc68	ENSRNOG000000021381	18	68,408,890
17166 A_44_P419615	-1.078	0.138	2.9E-09	-0.842	0.069	2.3E-14 Stard6	ENSRNOG000000026324	18	68,983,545
24668 A_64_P128569	0.281	0.058	2.2E-05	0.322	0.029	3.0E-13 Rpl38	ENSRNOG000000033808	18	69,818,720
7335 A_42_P595630	-0.607	0.059	2.9E-12	-0.537	0.030	9.3E-20 Pqlc1	ENSRNOG000000059215	18	76,770,012
22519 A_64_P021320	-0.659	0.056	6.3E-14	-0.671	0.028	8.6E-24 Pqlc1	ENSRNOG000000059215	18	76,770,012
24850 A_64_P102870	0.350	0.076	4.6E-05	0.337	0.038	1.2E-10 Fam96b	ENSRNOG000000011865	19	551,708
18626 A_64_P097078	-0.735	0.115	1.9E-07	-0.632	0.057	4.0E-13 Pdp2	ENSRNOG000000012343	19	601,469
17810 A_64_P148413	-0.474	0.100	3.5E-05	-0.886	0.050	2.4E-19 Ces1d	ENSRNOG000000015519	19	15,033,108
6593 A_42_P721692	-0.771	0.105	1.0E-08	-0.751	0.052	1.6E-16 Inpp4b	ENSRNOG000000018382	19	29,951,493
7992 A_44_P1046713	0.367	0.082	6.8E-05	0.197	0.041	2.6E-05 Cog4	ENSRNOG000000017745	19	43,391,828
28178 A_64_P103254	-0.410	0.091	6.5E-05	-0.202	0.045	8.1E-05 Khl36	ENSRNOG000000016422	19	52,515,022
13312 A_64_P117413	0.819	0.147	2.6E-06	1.020	0.073	4.7E-16 RGD1304884	ENSRNOG000000017431	19	53,723,822
18126 A_44_P192288	0.527	0.121	9.9E-05	0.304	0.060	1.3E-05 RGD1561507	ENSRNOG000000038239	19	56,010,085
12200 A_64_P035694	1.361	0.158	2.6E-10	0.752	0.079	2.0E-11 LOC678766	ENSRNOG000000057601	19	56,443,632
1276 A_43_P18610	0.684	0.129	5.7E-06	0.506	0.064	2.4E-09 RGD1563235	ENSRNOG000000017690	19	56,633,633
26328 A_44_P255236	0.839	0.109	3.8E-09	1.479	0.054	1.1E-25 Acta1	ENSRNOG000000017786	19	56,677,084
8933 A_64_P121016	0.696	0.114	4.6E-07	0.675	0.057	4.8E-14 Exoc8	ENSRNOG000000019766	19	57,649,827
12642 A_64_P121262	-1.059	0.065	3.5E-18	-0.860	0.033	3.3E-25 Sipa1l2	ENSRNOG000000019791	19	58,399,816

28321 A_44_P299349	-0.737	0.126	1.0E-06	-1.198	0.063	1.9E-20 Prr3	ENSRNOG000000025806	20	3,300,247
4436 A_42_P627572	-0.979	0.116	4.7E-10	-0.812	0.058	3.8E-16 Mdc1	ENSRNOG000000032813	20	3,405,285
16747 A_64_P113970	-0.298	0.064	4.5E-05	-0.292	0.032	6.9E-11 Gtf2h4	ENSRNOG000000000831	20	3,582,742
18363 A_64_P134927	0.477	0.109	9.6E-05	0.433	0.054	1.8E-09 RT1-Db1	ENSRNOG000000033215	20	4,087,618
27475 A_44_P991532	0.492	0.109	7.0E-05	0.506	0.055	4.7E-11 RT1-Da	ENSRNOG000000032844	20	4,132,616
8347 A_44_P367438	0.449	0.081	2.8E-06	0.505	0.041	1.2E-14 Stk38	ENSRNOG000000000519	20	6,257,604
14913 A_44_P914438	1.506	0.134	2.3E-13	1.000	0.067	4.6E-17 Cdkn1a	ENSRNOG000000000521	20	6,356,423
20527 A_43_P15406	1.904	0.156	2.1E-13	0.606	0.085	5.3E-08 Grm4	ENSRNOG000000000487	20	6,772,903
10330 A_44_P1000115	0.511	0.091	2.2E-06	0.595	0.045	2.6E-15 RGD735065	ENSRNOG000000000524	20	6,869,767
12621 A_44_P532249	0.706	0.150	3.7E-05	0.445	0.075	8.6E-07 Fkbp5	ENSRNOG000000022523	20	8,019,020
21148 A_64_P145286	-1.591	0.183	2.2E-10	-1.198	0.092	2.8E-15 Dnah8	ENSRNOG000000000542	20	9,313,271
7522 A_64_P121031	-1.732	0.196	1.4E-10	-1.529	0.098	1.1E-17	ENSRNOG000000000542	20	9,313,271
17120 A_44_P305200	-0.284	0.063	6.9E-05	-0.176	0.032	2.4E-06 Cstb	ENSRNOG000000001201	20	10,968,432
3691 A_42_P781999	-0.689	0.096	1.9E-08	-0.558	0.048	9.0E-14 Agpat3	ENSRNOG000000001205	20	11,114,164
8306 A_64_P008361	0.635	0.108	1.1E-06	0.660	0.054	2.4E-14 Pwp2	ENSRNOG000000001210	20	11,228,844
25935 A_64_P146698	0.664	0.100	9.3E-08	0.691	0.050	5.1E-16 Pwp2	ENSRNOG000000001210	20	11,228,844
24999 A_44_P840891	-1.392	0.161	1.6E-09	-1.013	0.091	4.7E-12 Icoslg	ENSRNOG000000023109	20	11,340,296
9892 A_44_P992662	1.504	0.159	3.2E-11	1.100	0.081	1.4E-15 Ftcd	ENSRNOG000000001261	20	12,820,466
19033 A_44_P1015203	1.111	0.127	1.9E-10	0.753	0.064	5.2E-14 Gstt3	ENSRNOG000000001242	20	13,817,795
25463 A_43_P13290	3.615	0.189	1.6E-20	2.924	0.094	1.2E-27 Pbld	ENSRNOG000000000386	20	27,117,663
8781 A_44_P152177	4.190	0.339	5.7E-14	3.800	0.107	6.0E-28 Spock2	ENSRNOG000000061544	20	29,655,226
405 A_42_P559737	0.579	0.082	2.8E-08	0.566	0.041	5.7E-16 Srgn	ENSRNOG000000000394	20	32,133,431
987 A_42_P461003	-0.421	0.082	1.0E-05	-0.203	0.041	1.7E-05 Snx3	ENSRNOG000000046705	20	47,253,664
4080 A_64_P076865	-0.518	0.091	1.9E-06	-0.729	0.046	6.0E-18 LOC641520	ENSRNOG000000047102	20	50,394,650
110 A_64_P099457	-0.838	0.169	2.8E-05	-0.580	0.106	7.0E-06 Hoxa9	ENSRNOG000000060292	L567939	87,504
20987 A_64_P141038	0.837	0.120	3.4E-08	0.297	0.060	1.7E-05 Bex4	ENSRNOG000000060103	L568122	30,542
10171 A_64_P022135	0.571	0.129	8.3E-05	0.617	0.064	1.9E-11	ENSRNOG000000031780	MT	1
4493 A_64_P147403	2.008	0.103	1.1E-20	2.105	0.052	8.5E-32	ENSRNOG000000031780	MT	1
7214 A_44_P759995	1.477	0.135	5.5E-13	0.855	0.068	8.1E-15	ENSRNOG000000031780	MT	1
16708 A_44_P311620	-0.648	0.093	3.4E-08	-0.305	0.046	1.2E-07	ENSRNOG000000031780	MT	1
889 A_44_P403017	0.805	0.108	8.5E-09	0.553	0.054	3.3E-12	ENSRNOG000000031780	MT	1
5065 A_64_P146350	-0.516	0.101	1.1E-05	-0.327	0.051	1.7E-07	ENSRNOG000000031780	MT	1
23156 A_44_P914760	1.038	0.102	3.4E-12	0.289	0.051	1.8E-06	ENSRNOG000000031780	MT	1

26156 A_64_P068425	0.685	0.143	2.8E-05	0.770	0.071	7.7E-13	ENSRNOG000000031780	MT	1
24098 A_64_P042811	-1.527	0.218	3.2E-08	-2.384	0.109	2.0E-22	ENSRNOG000000031780	MT	1
24070 A_64_P085331	0.332	0.075	8.7E-05	0.328	0.038	2.0E-10	ENSRNOG000000031780	MT	1
22332 A_64_P040803	0.373	0.066	1.8E-06	0.360	0.033	4.9E-13	ENSRNOG000000031780	MT	1
29125 A_64_P084699	0.323	0.062	8.6E-06	0.365	0.031	7.6E-14	ENSRNOG000000031780	MT	1
9394 A_64_P119214	0.492	0.073	6.8E-08	0.715	0.036	7.1E-21	ENSRNOG000000031780	MT	1
24899 A_64_P063443	-0.720	0.141	3.0E-05	-0.489	0.084	5.5E-06	ENSRNOG000000031780	MT	1
9336 A_64_P063588	-0.745	0.085	1.9E-10	-0.819	0.043	1.4E-20	ENSRNOG000000031780	MT	1
24429 A_64_P086550	-1.074	0.159	6.6E-08	-0.792	0.079	6.5E-12	ENSRNOG000000031780	MT	1
15576 A_64_P073174	0.312	0.068	4.9E-05	0.175	0.034	8.7E-06	ENSRNOG000000031780	MT	1
21135 A_64_P118308	-1.194	0.206	1.2E-06	-1.017	0.103	8.1E-12	ENSRNOG000000031780	MT	1
27679 A_64_P143154	0.712	0.111	2.0E-07	0.744	0.056	1.5E-15	ENSRNOG000000031780	MT	1
211 A_42_P619996	-0.326	0.071	5.2E-05	-0.356	0.036	5.8E-12	ENSRNOG000000031780	MT	1
19166 A_64_P052972	-0.855	0.117	1.2E-08	-0.689	0.058	5.7E-14	ENSRNOG000000031780	MT	1
5482 A_64_P326359	1.678	0.101	1.6E-18	1.243	0.050	3.4E-24	ENSRNOG000000031780	MT	1
16475 A_64_P071381	0.657	0.096	4.7E-08	0.687	0.048	1.6E-16	ENSRNOG000000031780	MT	1
17573 A_64_P042099	0.562	0.094	7.3E-07	0.601	0.047	5.5E-15	ENSRNOG000000031780	MT	1
6958 A_64_P042096	0.604	0.111	3.6E-06	0.619	0.055	2.6E-13	ENSRNOG000000031780	MT	1
12287 A_64_P047720	-1.136	0.228	3.1E-05	-2.481	0.149	9.5E-16	ENSRNOG000000031780	MT	1
186 A_64_P148326	0.880	0.177	1.7E-05	0.778	0.089	1.8E-10	ENSRNOG000000031780	MT	1
28481 A_44_P392004	2.168	0.145	1.0E-15	2.790	0.081	2.1E-26	ENSRNOG000000031780	MT	1
29293 A_64_P029190	0.744	0.142	7.5E-06	1.109	0.071	1.3E-17	ENSRNOG000000031780	MT	1
23113 A_64_P145766	0.543	0.124	9.7E-05	0.440	0.062	2.3E-08	ENSRNOG000000031780	MT	1
2399 A_44_P793124	-0.376	0.061	3.7E-07	-0.281	0.030	4.3E-11	ENSRNOG000000031780	MT	1
10120 A_64_P135893	1.059	0.102	1.4E-11	1.440	0.059	7.8E-22	ENSRNOG000000031780	MT	1
22436 A_64_P045775	1.252	0.149	1.3E-09	1.902	0.074	4.3E-23	ENSRNOG000000031780	MT	1
25519 A_64_P129231	0.547	0.090	5.0E-07	0.440	0.045	9.3E-12	ENSRNOG000000031780	MT	1
11784 A_64_P085918	0.395	0.078	1.2E-05	0.415	0.039	1.1E-12	ENSRNOG000000031780	MT	1
7558 A_64_P119802	-0.551	0.086	1.9E-07	-0.200	0.043	4.0E-05	ENSRNOG000000031780	MT	1
1339 A_64_P042093	1.090	0.150	1.4E-08	1.563	0.075	9.0E-22	ENSRNOG000000031780	MT	1
26291 A_64_P142460	-0.628	0.127	1.8E-05	-0.807	0.064	7.2E-15	ENSRNOG000000031780	MT	1
13083 A_64_P077603	-0.673	0.103	1.2E-07	-0.844	0.051	2.3E-18	ENSRNOG000000031780	MT	1
4008 A_64_P098848	0.595	0.120	1.9E-05	0.485	0.062	4.9E-09	ENSRNOG000000031780	MT	1

18772 A_64_P090798	0.601	0.135	7.9E-05	0.388	0.068	1.5E-06	ENSRNOG000000031780	MT	1
4590 A_64_P033230	-0.820	0.169	2.4E-05	-0.611	0.085	1.7E-08	ENSRNOG000000031780	MT	1
28308 A_64_P028365	0.335	0.042	1.9E-09	0.315	0.021	5.0E-17	ENSRNOG000000031780	MT	1
21103 A_64_P039347	0.627	0.116	4.1E-06	0.262	0.058	6.2E-05	ENSRNOG000000031780	MT	1
6792 A_64_P157318	0.720	0.117	4.3E-07	0.334	0.059	1.7E-06	ENSRNOG000000031780	MT	1
2193 A_44_P535899	0.814	0.110	9.3E-09	0.331	0.055	6.4E-07	ENSRNOG000000029707	MT	10,160
28451 A_64_P123361	-2.154	0.296	1.4E-08	-1.032	0.148	3.4E-08	ENSRNOG000000029042	MT	14,061
1960 A_42_P508471	-0.659	0.123	7.0E-06	-0.335	0.068	2.5E-05 Rgn	ENSRNOG000000007949	X	1,848,904
8917 A_64_P145716	1.748	0.146	4.0E-14	1.053	0.073	1.5E-16 Maoa	ENSRNOG000000002848	X	6,620,722
8786 A_64_P062462	0.723	0.104	3.8E-08	0.300	0.052	1.4E-06 Pir	ENSRNOG000000003674	X	31,968,152
15094 A_64_P102468	1.020	0.193	6.0E-06	0.566	0.096	1.0E-06	ENSRNOG0000000024479	X	39,956,841
15483 A_64_P111300	-0.553	0.095	1.2E-06	-0.357	0.048	7.3E-09 LOC678880	ENSRNOG0000000045535	X	73,616,348
8565 A_64_P087409	0.527	0.110	2.9E-05	0.528	0.055	1.9E-11 RGD1561318	ENSRNOG0000000050970	X	99,389,351
8471 A_64_P288221	3.241	0.235	2.2E-11	2.837	0.182	2.5E-12 LOC679989	ENSRNOG0000000011034	X	106,116,886
17278 A_64_P140144	2.735	0.163	1.1E-18	1.871	0.081	3.4E-23 LOC679989	ENSRNOG0000000011034	X	106,116,886
3600 A_64_P102049	1.728	0.186	3.8E-11	1.125	0.093	2.7E-14 LOC680319	ENSRNOG0000000037645	X	106,774,980
27661 A_64_P102043	1.572	0.154	3.3E-12	1.054	0.077	7.0E-16 LOC680319	ENSRNOG0000000037645	X	106,774,980
1547 A_42_P803274	1.223	0.117	1.7E-12	0.583	0.058	6.4E-12 Wbp5	ENSRNOG0000000034198	X	106,791,333
1615 A_42_P741034	-0.381	0.084	5.8E-05	-0.653	0.042	1.3E-17	ENSRNOG0000000055721	X	110,818,716
265 A_64_P121643	-0.674	0.154	9.4E-05	-0.524	0.077	5.5E-08 Capn6	ENSRNOG000000004882	X	115,073,890
15663 A_64_P048852	-1.576	0.087	1.1E-19	-1.417	0.044	2.3E-28	ENSRNOG000000006459	X	120,313,696
187 A_64_P130668	-0.672	0.108	3.5E-07	-0.501	0.054	4.2E-11 Kihl13	ENSRNOG0000000014029	X	121,731,543
18535 A_64_P070155	2.245	0.251	1.1E-10	2.102	0.126	1.3E-18 Rhox5	ENSRNOG0000000046548	X	123,912,361
948 A_42_P637189	-1.043	0.176	8.5E-07	-1.044	0.088	4.9E-14 Apln	ENSRNOG000000003984	X	134,866,210
18231 A_64_P045426	1.170	0.153	4.7E-09	1.449	0.077	2.5E-20	ENSRNOG0000000048494	X	145,822,398
11811 A_43_P11812	0.669	0.102	1.1E-07	0.463	0.051	6.6E-11 Bgn	ENSRNOG0000000055962	X	157,331,204
3177 A_42_P476474	0.693	0.132	7.3E-06	0.845	0.066	5.8E-15 Fhl1	ENSRNOG000000000875	X	159,112,880
27064 A_64_P004348	0.344	0.071	2.4E-05	0.280	0.036	2.3E-09 Ftl			
12619 A_64_P060319	-0.743	0.118	2.9E-07	-0.857	0.059	1.2E-16 no transcript			
6725 A_64_P063194	-0.399	0.070	1.8E-06	-0.187	0.035	5.5E-06 no transcript			
17114 A_44_P877632	0.483	0.095	1.1E-05	0.348	0.047	1.2E-08 Otulin (LOC10031	ENSRNOG0000000012017	2	80,267,724
5960 A_44_P114491	0.535	0.092	1.2E-06	0.600	0.046	3.1E-15 no transcript			
25822 A_44_P314087	1.143	0.221	1.0E-05	0.770	0.115	1.1E-07 no transcript			

21575 A_64_P110744	-0.460	0.086	4.7E-06	-0.330	0.043	3.7E-09 Shld1 (LOC681292)_partial		
28819 A_64_P004279	-0.722	0.140	9.6E-06	-0.924	0.070	2.3E-15 RGD1561472		
17474 A_44_P201084	-0.856	0.162	6.3E-06	-0.704	0.081	2.2E-10 Fgfr1l		
7034 A_44_P534028	1.057	0.119	1.2E-10	0.971	0.059	2.7E-18 no transcript		
28213 A_44_P476598	1.208	0.155	3.2E-09	0.923	0.078	4.9E-14 Phf24 (RGD1559864)_no homolog		
21356 A_42_P588504	1.400	0.104	1.1E-15	0.858	0.052	1.8E-18 Phf24 (RGD1559864)_no homolog		
30162 A_44_P745269	-0.573	0.077	9.5E-09	-0.292	0.039	6.4E-09 no transcript		
8819 A_64_P132726	-1.060	0.125	4.4E-10	-0.711	0.063	1.8E-13 no transcript		
27091 A_64_P025432	5.071	0.215	1.4E-23	4.681	0.107	7.3E-33 no transcript		
9344 A_64_P029333	-0.610	0.094	1.6E-07	-0.814	0.047	4.9E-19 Acaa1b		
12460 A_64_P029335	-0.703	0.092	4.2E-09	-0.769	0.046	1.1E-18 Acaa1b		
19485 A_64_P161768	0.404	0.087	4.2E-05	0.408	0.043	2.9E-11 Synrg		
10999 A_64_P070586	0.639	0.092	3.6E-08	0.680	0.046	6.3E-17 Krtap21-2		
20392 A_64_P081063	2.195	0.157	8.9E-13	2.735	0.094	9.3E-20 no transcript		
15659 A_43_P18931	0.797	0.102	2.9E-09	0.537	0.051	1.5E-12 Tp53i3 (RGD130 ENSRNOG000000005177	13	75,101,759
15442 A_64_P155603	-1.444	0.143	4.3E-12	-0.725	0.071	3.8E-12 RGD1565970		
26191 A_44_P154298	-1.538	0.177	2.3E-10	-1.091	0.089	1.7E-14 RGD1565970		
17854 A_64_P116919	1.279	0.176	1.4E-08	0.579	0.088	1.1E-07 LOC681303		
8329 A_64_P124041	-1.598	0.202	2.1E-09	-0.788	0.101	2.9E-09 Ddx60		
6183 A_42_P546857	-0.353	0.062	1.7E-06	-0.201	0.031	1.4E-07 Coprs (RGD1565675)_no homolog		
16435 A_64_P078050	1.236	0.134	4.6E-11	0.933	0.067	3.9E-16 RGD1559908		
7429 A_64_P157171	1.307	0.169	3.7E-09	0.848	0.085	5.7E-12 no transcript		
25709 A_64_P011719	-0.909	0.077	5.9E-14	-0.885	0.039	3.8E-23 Chmp1b	N/A	18 62,923,620
24897 A_64_P150597	-1.990	0.214	6.9E-11	-0.714	0.101	3.4E-08 no transcript		
11195 A_64_P084698	0.317	0.070	6.2E-05	0.395	0.035	2.0E-13 LOC680353		

Genes are regarded as significant for “shared” differential expression when they show $P < 1 \times 10^{-4}$ reproducibly in two types of comparison, ie, SHR/lzm versus WKY/lzm and SHRSP/lzm versus WKY/lzm, with a concordant direction of differential expression.

Table S3B. A list of significant transcripts for shared differential expression in the aorta.

no	ProbeName	SHR/lzm (vs WKY/lzm)			SHRSP/lzm (vs WKY/lzm)			GeneName	Ensembl_rat	Chr	Transcription_ start_site (Rnor_6.0)
		Fold change (log2-scale)	SE (log2-scale)	P-value	Fold change (log2-scale)	SE (log2-scale)	P-value				
14405	A_44_P452186	1.467	0.196	1.3E-06	1.402	0.175	5.6E-07	Epm2a	ENSRNOG00000040242	1	5,448,958
8464	A_64_P129293	2.185	0.164	1.1E-09	1.706	0.156	1.5E-08	RGD1306565	ENSRNOG00000031700	1	15,412,603
8390	A_43_P23129	-0.685	0.125	5.0E-05	-0.834	0.112	1.4E-06	Ptpk	ENSRNOG00000047605	1	18,058,055
3394	A_42_P484738	1.439	0.261	4.8E-05	2.613	0.234	5.9E-09	Ctgf	ENSRNOG00000015036	1	21,854,773
11848	A_64_P121575	-1.029	0.111	7.8E-08	-0.574	0.099	2.8E-05	Slc12a7	ENSRNOG00000016372	1	32,140,137
22666	A_44_P866091	-0.964	0.122	6.6E-07	-0.631	0.109	2.8E-05	Slc12a7	ENSRNOG00000016372	1	32,140,137
24761	A_64_P139942	-1.439	0.237	3.0E-05	-1.328	0.220	3.1E-05	Slc6a19	ENSRNOG00000026501	1	32,199,810
5937	A_64_P110103	-0.414	0.076	5.3E-05	-0.578	0.068	2.5E-07	Sod2	ENSRNOG00000019048	1	47,921,587
16064	A_64_P107642	-0.406	0.073	4.4E-05	-0.621	0.065	5.7E-08	Tmem160	ENSRNOG00000015304	1	78,417,719
16383	A_64_P042455	-0.567	0.074	1.1E-06	-0.704	0.067	1.3E-08	Bloc1s3	ENSRNOG00000017463	1	80,416,273
1747	A_42_P641234	-0.628	0.077	4.3E-07	-0.540	0.069	7.2E-07	Snrpa	ENSRNOG00000001501	1	84,008,293
27603	A_64_P125676	-1.111	0.168	6.2E-06	-1.480	0.151	3.6E-08	Sptbn4	ENSRNOG00000055371	1	84,254,645
24147	A_64_P131903	-0.673	0.104	8.1E-06	-0.563	0.093	1.7E-05	Dyrk1b	ENSRNOG00000019254	1	85,112,247
6144	A_42_P554610	-0.736	0.127	2.8E-05	-1.116	0.114	3.7E-08	Eid2	ENSRNOG00000019310	1	85,517,360
4928	A_64_P079807	-0.435	0.078	4.5E-05	-0.499	0.070	2.5E-06	Yif1b	ENSRNOG00000020616	1	87,180,624
17505	A_64_P063428	-1.035	0.170	1.6E-05	-1.318	0.152	1.9E-07	Tmem149	ENSRNOG00000020957	1	89,020,341
17701	A_64_P078982	-0.656	0.123	6.6E-05	-1.191	0.110	9.0E-09	LOC688869	ENSRNOG00000024309	1	89,084,859
9877	A_64_P060305	-0.875	0.149	2.4E-05	-1.077	0.133	5.0E-07	Lsr	ENSRNOG00000021053	1	89,399,041
19858	A_64_P060303	-0.746	0.124	1.8E-05	-1.105	0.111	3.0E-08	Lsr	ENSRNOG00000021053	1	89,399,041
11122	A_44_P515321	-0.521	0.083	1.2E-05	-0.560	0.075	1.3E-06	LOC499136	ENSRNOG00000014455	1	97,785,490
11981	A_64_P148550	-1.309	0.134	3.8E-08	-2.256	0.120	2.6E-12	Lim2	ENSRNOG00000017681	1	98,501,249
25711	A_44_P215157	-1.314	0.174	1.7E-06	-2.120	0.174	3.6E-09	Lin7b	ENSRNOG00000020746	1	101,360,971
15212	A_64_P166076	1.472	0.198	1.4E-06	0.933	0.177	7.7E-05	Bcat2	ENSRNOG00000020956	1	101,554,642
456	A_64_P016403	-0.724	0.123	2.4E-05	-1.070	0.110	4.3E-08	Ldha	ENSRNOG00000013009	1	102,900,286
22429	A_44_P1046705	-0.587	0.087	4.7E-06	-0.841	0.078	9.4E-09	Mrps11	ENSRNOG00000018531	1	140,477,868
26335	A_64_P157285	1.157	0.209	4.6E-05	1.349	0.187	2.1E-06	AC114460.1 (par	ENSRNOG00000025003	1	142,027,250
3363	A_64_P016059	-1.620	0.120	3.8E-10	-1.541	0.107	1.5E-10	Homer2	ENSRNOG000000061450	1	143,535,583
6438	A_64_P084767	-0.564	0.088	9.5E-06	-0.446	0.079	3.8E-05	Aamdc (RGD156	ENSRNOG00000012584	1	162,533,893
4323	A_64_P028140	0.865	0.102	2.7E-07	0.597	0.091	7.0E-06	Plekhhb1	ENSRNOG00000018627	1	165,680,206

8799 A_64_P095313	-0.778	0.124	1.2E-05	-1.152	0.111	1.8E-08	ENSRNOG000000051149	1	166,727,805
28650 A_44_P177931	-0.673	0.071	6.5E-08	-0.616	0.064	4.7E-08 Anapc15 (RGD11	ENSRNOG000000019936	1	166,983,175
10242 A_64_P019125	-0.998	0.101	3.4E-08	-0.465	0.090	9.8E-05 AC098008.3	ENSRNOG000000051318	1	167,654,236
28504 A_64_P092754	1.270	0.204	2.3E-05	1.227	0.221	7.2E-05 Mrvi1	ENSRNOG000000017767	1	175,796,040
887 A_64_P152697	-1.237	0.144	2.2E-07	-0.728	0.128	3.6E-05 AABR07005563.	ENSRNOG000000062034	1	187,634,359
29269 A_64_P151353	1.131	0.116	4.2E-08	0.779	0.104	1.3E-06 Acsm5	ENSRNOG000000031211	1	189,241,593
9654 A_64_P019021	0.949	0.150	5.7E-05	1.108	0.102	3.5E-07 LOC691551	ENSRNOG000000028473	1	190,914,946
26011 A_64_P158793	-0.755	0.096	7.6E-07	-0.526	0.086	1.6E-05 AABR07005667.	ENSRNOG000000024217	1	193,537,137
21952 A_64_P024138	-6.085	0.184	4.2E-16	-6.806	0.165	1.2E-17 Sbk1	ENSRNOG000000057696	1	197,659,187
19479 A_44_P275029	-1.291	0.117	7.4E-09	-0.997	0.105	5.7E-08 Mvp	ENSRNOG000000020182	1	198,450,047
29205 A_44_P1029472	-1.901	0.115	1.9E-11	-1.366	0.103	4.9E-10 Pagr1 (RGD1305	ENSRNOG000000020217	1	198,450,688
6234 A_42_P505241	2.110	0.193	8.2E-09	1.298	0.173	1.3E-06 Qprt	ENSRNOG000000016980	1	198,559,568
13092 A_44_P285803	-0.659	0.091	2.0E-06	-0.667	0.082	4.3E-07 Dctpp1	ENSRNOG000000017850	1	198,706,852
14224 A_64_P045578	1.869	0.106	7.6E-12	2.035	0.095	3.7E-13 Rnf40	ENSRNOG000000018840	1	199,037,544
9878 A_42_P834903	-1.007	0.108	7.4E-08	-0.529	0.097	5.1E-05 Bckdk	ENSRNOG000000019485	1	199,351,628
3819 A_44_P409232	3.458	0.260	4.9E-10	1.563	0.233	5.0E-06 Cyp2e1	ENSRNOG000000012458	1	213,511,874
28576 A_64_P036285	-1.759	0.208	2.7E-07	-1.422	0.186	1.0E-06 Scgb1c1	ENSRNOG000000012847	1	213,595,240
1482 A_42_P495579	0.862	0.148	2.6E-05	1.407	0.132	1.2E-08 Ano1	ENSRNOG000000020865	1	217,844,957
5014 A_42_P614175	1.138	0.199	4.1E-05	1.962	0.189	3.2E-08 Gal	ENSRNOG000000015156	1	218,657,925
19340 A_44_P132522	-0.740	0.129	3.0E-05	-0.691	0.115	1.9E-05 Ndufs8	ENSRNOG000000017446	1	219,144,610
21218 A_64_P089356	-2.090	0.202	1.8E-08	-1.356	0.181	1.3E-06 Syt12	ENSRNOG000000019306	1	219,719,272
5718 A_64_P119314	-1.694	0.320	7.4E-05	-2.442	0.286	2.5E-07 LOC689065	ENSRNOG000000036641	1	219,745,654
9900 A_44_P635869	1.109	0.152	1.9E-06	0.808	0.136	2.1E-05 Bbs1	ENSRNOG000000019832	1	220,165,678
20841 A_64_P051802	-0.593	0.085	3.1E-06	-0.407	0.076	6.4E-05 Rab1b	ENSRNOG000000050510	1	220,491,469
27062 A_64_P150876	-0.924	0.146	1.4E-05	-1.979	0.146	8.5E-10 Cst6	ENSRNOG000000020455	1	220,729,000
18532 A_64_P053322	0.442	0.077	3.2E-05	0.465	0.069	5.0E-06 Sf1	ENSRNOG000000021085	1	221,735,517
200 A_42_P780882	-0.468	0.080	2.4E-05	-0.450	0.071	1.0E-05 Esrra	ENSRNOG000000021139	1	222,178,725
22791 A_64_P193845	-0.568	0.086	5.9E-06	-0.913	0.077	2.4E-09 Ppp1r14b	ENSRNOG000000021151	1	222,229,835
10859 A_64_P128124	-0.700	0.099	2.6E-06	-0.911	0.088	1.8E-08 Bsc12	ENSRNOG000000052393	1	225,037,737
9 A_44_P944998	-0.746	0.090	3.7E-07	-1.001	0.081	1.3E-09 LOC690344	ENSRNOG000000045561	1	225,077,079
20761 A_44_P532027	-0.749	0.127	2.4E-05	-0.681	0.114	2.0E-05 B3gat3	ENSRNOG000000019804	1	225,120,061
3243 A_42_P651632	0.675	0.097	3.3E-06	1.098	0.087	1.0E-09 Tut1	ENSRNOG000000020047	1	225,151,404
7775 A_64_P033447	-0.871	0.135	7.9E-06	-0.881	0.120	1.8E-06 Dagla	ENSRNOG000000027264	1	226,353,611

26689 A_44_P335974	1.537	0.129	2.4E-09	1.389	0.115	2.0E-09 Aldh1a7	ENSRNOG000000017878	1	240,601,744
9329 A_44_P262593	-1.610	0.180	1.3E-07	-1.746	0.161	9.3E-09 Ankrd2	ENSRNOG000000013840	1	261,281,543
7394 A_42_P644278	-1.146	0.086	4.8E-10	-0.995	0.077	7.4E-10 Bloc1s2	ENSRNOG000000012684	1	263,920,962
14196 A_64_P062643	-1.167	0.158	2.3E-06	-0.854	0.158	7.3E-05 Pkd2l1	ENSRNOG000000012591	1	263,959,318
22924 A_64_P062648	-0.992	0.175	3.6E-05	-2.154	0.157	2.9E-10 Pkd2l1	ENSRNOG000000012591	1	263,959,318
27137 A_64_P017268	-1.270	0.168	1.2E-06	-1.330	0.150	1.5E-07 Trim8	ENSRNOG000000019968	1	266,255,797
2102 A_44_P990043	0.712	0.131	5.5E-05	1.014	0.117	2.0E-07 Pdcd11	ENSRNOG000000020304	1	266,866,931
2768 A_42_P739860	2.756	0.371	1.5E-06	1.909	0.332	3.0E-05 Dusp5	ENSRNOG000000014061	1	274,245,184
28938 A_44_P240330	-0.721	0.126	3.3E-05	-1.131	0.113	2.8E-08 AABR07007032	ENSRNOG000000046333	1	277,867,630
9184 A_43_P21414	-0.923	0.103	1.2E-07	-1.010	0.092	7.4E-09 Atg10	ENSRNOG000000016342	2	20,152,884
26408 A_44_P306344	1.133	0.181	1.6E-05	1.381	0.181	1.6E-06 F2rl2	ENSRNOG000000018054	2	26,240,385
1004 A_42_P640277	0.985	0.176	4.1E-05	0.963	0.157	1.5E-05 Enc1	ENSRNOG000000016541	2	28,049,217
15719 A_44_P202659	-0.699	0.122	3.2E-05	-0.696	0.109	9.6E-06 Ndufs4	ENSRNOG000000011383	2	46,476,203
19499 A_44_P244851	1.383	0.203	4.2E-06	1.969	0.181	8.9E-09 Car3	ENSRNOG000000010079	2	88,135,410
21613 A_43_P10081	-1.230	0.199	1.8E-05	-1.350	0.199	6.5E-06 Aadacl1	ENSRNOG000000013313	2	112,868,707
3745 A_64_P093467	3.369	0.362	3.2E-06	3.499	0.362	2.3E-06 Trpc4	ENSRNOG000000011133	2	143,475,323
4422 A_44_P761041	-1.008	0.154	6.7E-06	-0.860	0.137	1.2E-05 Trim2	ENSRNOG000000010124	2	183,210,799
29014 A_64_P154297	-0.881	0.157	3.9E-05	0.767	0.140	5.2E-05 Iqgap3	ENSRNOG000000027894	2	187,447,501
10652 A_44_P508711	-0.871	0.105	3.3E-07	-0.526	0.093	3.8E-05 Flad1	ENSRNOG000000020642	2	188,736,462
21227 A_64_P159614	-0.592	0.077	9.6E-07	-0.629	0.069	1.0E-07 Lenep	ENSRNOG000000020642	2	188,736,462
6842 A_42_P516658	-0.704	0.093	1.2E-06	-0.870	0.083	1.5E-08 Gatad2b	ENSRNOG000000015553	2	189,655,702
998 A_43_P15245	0.701	0.099	2.7E-06	0.521	0.089	2.4E-05 Npr1	ENSRNOG000000014684	2	189,856,090
20304 A_44_P132960	-1.194	0.199	2.5E-05	-1.252	0.199	1.5E-05 S100a3	ENSRNOG000000012008	2	189,955,836
3660 A_44_P184817	1.513	0.185	4.3E-07	1.723	0.166	1.6E-08 Selenbp1	ENSRNOG000000047158	2	195,423,787
27712 A_64_P041307	-1.380	0.090	6.3E-11	-1.453	0.081	5.3E-12 Tars2	ENSRNOG000000057194	2	197,878,142
16742 A_64_P155201	-1.389	0.193	4.9E-06	-1.410	0.209	9.6E-06 LOC690126	ENSRNOG000000028975	2	198,380,836
9919 A_64_P004344	-0.862	0.089	4.6E-08	-0.958	0.080	2.2E-09	ENSRNOG000000052555	2	198,388,809
19415 A_64_P098081	-2.171	0.226	8.8E-08	-2.231	0.226	6.2E-08 RGD1563516	ENSRNOG000000052555	2	198,388,809
8080 A_64_P013900	-0.648	0.112	2.7E-05	-0.600	0.100	1.8E-05 Hist2h4	ENSRNOG000000032224	2	198,412,350
18785 A_44_P269697	-1.315	0.162	4.8E-07	-1.107	0.145	1.1E-06	ENSRNOG000000060366	2	198,417,619
28930 A_64_P043871	0.519	0.081	8.6E-06	0.483	0.072	5.4E-06 Polr3gl	ENSRNOG000000021209	2	198,706,428
13090 A_64_P061012	-1.255	0.178	4.1E-06	-1.334	0.178	2.0E-06 Itga10	ENSRNOG000000021217	2	198,772,937
20853 A_64_P076891	-1.809	0.140	1.6E-09	-1.903	0.140	7.8E-10 RGD1565469	ENSRNOG000000037217	2	198,834,925

14417 A_44_P220193	-0.538	0.083	8.1E-06	-0.396	0.075	7.1E-05	ENSRNOG000000000098	2	198,852,500
12118 A_64_P040804	0.386	0.064	1.9E-05	0.404	0.058	3.0E-06 Rpl38	ENSRNOG000000030747	2	199,479,309
1601 A_64_P078624	2.678	0.297	1.9E-07	2.814	0.282	5.3E-08 Vtn1	ENSRNOG000000015279	2	203,200,427
20012 A_42_P783572	-0.584	0.100	2.6E-05	-1.116	0.090	1.3E-09 Atp1a1	ENSRNOG000000030019	2	204,032,023
8411 A_42_P716352	1.713	0.219	7.5E-07	1.064	0.196	5.6E-05 Gstm7	ENSRNOG000000018937	2	210,782,856
2086 A_42_P488758	-0.769	0.066	3.4E-09	-0.528	0.059	1.3E-07 Alg14	ENSRNOG000000011528	2	224,851,383
1835 A_44_P1029956	0.930	0.162	3.2E-05	0.794	0.145	5.3E-05 Cnn3	ENSRNOG000000011559	2	225,005,019
16874 A_44_P323053	1.135	0.158	7.5E-06	1.393	0.194	7.4E-06 Usp53	ENSRNOG000000014660	2	227,160,379
745 A_42_P775635	-0.627	0.118	7.3E-05	-1.047	0.106	3.3E-08 Hs2st1	ENSRNOG000000012549	2	250,600,517
1173 A_64_P091053	-1.059	0.111	5.4E-08	-1.740	0.099	7.7E-12 Hs2st1	ENSRNOG000000012549	2	250,600,517
26425 A_43_P12207	1.565	0.201	8.0E-07	2.108	0.180	3.0E-09 Ddah1	ENSRNOG000000014613	2	251,634,431
20558 A_44_P114500	-1.557	0.248	1.5E-05	-2.209	0.248	2.3E-07 Gipc2	ENSRNOG000000042152	2	257,376,756
20957 A_43_P23049	-0.933	0.119	7.2E-07	-0.888	0.106	3.2E-07 Cryz	ENSRNOG000000028319	2	260,884,337
29729 A_44_P745585	-0.699	0.120	2.7E-05	-0.579	0.107	6.1E-05 LOC499749	ENSRNOG000000010896	3	2,480,232
12397 A_64_P007965	-1.936	0.169	4.1E-09	-1.424	0.151	6.3E-08 Gpsm1	ENSRNOG000000018666	3	3,767,394
24094 A_64_P064944	-0.420	0.080	8.0E-05	-0.695	0.071	4.2E-08 Trub2	ENSRNOG000000043189	3	8,348,746
29855 A_44_P945862	-0.637	0.099	8.1E-06	-0.960	0.088	8.7E-09 Trub2	ENSRNOG000000043189	3	8,348,746
19528 A_44_P1007333	0.610	0.117	8.6E-05	0.919	0.105	1.7E-07 Gle1	ENSRNOG000000015237	3	8,498,122
26230 A_44_P213133	-2.546	0.124	6.6E-13	-3.034	0.111	7.7E-15 Endog	ENSRNOG000000016033	3	8,741,766
12417 A_64_P050722	0.513	0.083	1.4E-05	0.476	0.074	9.0E-06	ENSRNOG000000031434	3	8,955,538
22393 A_43_P18366	1.570	0.142	7.1E-09	2.278	0.127	5.5E-12 Tor1b	ENSRNOG000000006435	3	9,792,899
25202 A_42_P472520	-0.774	0.074	1.6E-08	-0.638	0.066	4.8E-08 RGD1561113	ENSRNOG000000022681	3	11,410,732
1661 A_42_P705502	-1.467	0.171	2.2E-07	-1.205	0.153	6.8E-07	ENSRNOG000000050834	3	11,554,457
4674 A_42_P512417	-0.488	0.071	4.1E-06	-0.488	0.064	1.0E-06 Dpm2	ENSRNOG000000049110	3	11,587,941
13641 A_44_P466189	1.130	0.196	2.9E-05	1.017	0.175	2.7E-05 Angptl2	ENSRNOG000000016678	3	12,262,822
16648 A_64_P052670	0.478	0.087	5.1E-05	0.852	0.078	8.2E-09 Gsn	ENSRNOG000000018991	3	14,467,330
28766 A_44_P536749	-0.799	0.098	4.3E-07	-0.810	0.087	8.1E-08 Map1d	ENSRNOG000000061587	3	58,084,606
24139 A_44_P992697	-1.726	0.108	3.3E-11	-1.845	0.097	2.2E-12 Dusp19	ENSRNOG000000008868	3	67,849,966
7192 A_42_P811170	-0.576	0.095	1.6E-05	-0.801	0.085	6.1E-08 Med19	ENSRNOG000000006050	3	72,080,630
1516 A_42_P561644	-0.707	0.124	3.3E-05	-1.106	0.111	3.0E-08 Timm10	ENSRNOG000000007883	3	72,226,613
17375 A_43_P15275	-1.600	0.160	2.8E-08	-1.286	0.143	1.2E-07 Ptprij	ENSRNOG000000034025	3	79,390,956
11832 A_64_P130763	-0.639	0.083	9.6E-07	-0.474	0.074	9.4E-06 Ptpmt1	ENSRNOG000000009723	3	79,743,737
13379 A_44_P271769	-0.529	0.081	7.5E-06	-0.420	0.073	2.9E-05 Acp2	ENSRNOG000000013594	3	80,021,440

25223 A_64_P115142	-1.277	0.154	3.6E-07	-1.936	0.138	2.1E-10 Accs	ENSRNOG000000009199	3	82,756,953
9425 A_64_P110971	-0.447	0.077	2.7E-05	-0.602	0.069	1.8E-07 Rfk	ENSRNOG000000004381	3	89,745,705
14812 A_64_P143307	-0.521	0.085	1.4E-05	-1.142	0.076	7.5E-11 Rfk	ENSRNOG000000004381	3	89,745,705
4693 A_44_P340143	-0.602	0.078	9.0E-07	-0.630	0.070	1.1E-07 Commd9	ENSRNOG000000004755	3	91,463,660
6359 A_64_P097527	-0.938	0.087	1.0E-08	-0.548	0.078	2.9E-06	ENSRNOG000000006947	3	92,969,050
25469 A_64_P122489	-0.805	0.118	4.0E-06	-1.073	0.105	2.2E-08 Hdc	ENSRNOG000000010262	3	119,075,619
12846 A_44_P530547	-0.970	0.156	1.2E-05	-1.469	0.139	1.3E-08 Prom2	ENSRNOG000000014710	3	120,106,697
19676 A_64_P098527	-1.078	0.066	2.4E-11	-1.248	0.059	4.6E-13 Chchd5	ENSRNOG000000018491	3	121,660,110
29198 A_44_P1013851	1.454	0.209	3.4E-06	1.115	0.187	2.1E-05 Bmp2	ENSRNOG000000021276	3	126,335,863
18447 A_44_P336489	0.962	0.186	9.6E-05	0.991	0.167	2.1E-05 Tmx4	ENSRNOG000000024852	3	127,569,093
8484 A_64_P052705	1.975	0.136	1.3E-10	2.140	0.121	7.2E-12 Ankrd5	ENSRNOG000000005792	3	129,501,105
28951 A_64_P086580	-0.660	0.095	3.4E-06	-0.471	0.085	4.5E-05	ENSRNOG000000027574	3	132,052,612
6630 A_42_P471608	-0.544	0.102	6.6E-05	-0.670	0.091	1.6E-06 Kif16b	ENSRNOG000000004951	3	136,936,674
13519 A_44_P370537	0.912	0.145	1.4E-05	1.489	0.145	3.5E-08 Polr3f	ENSRNOG000000007548	3	138,684,685
9033 A_64_P122790	-1.195	0.149	5.6E-07	-1.074	0.133	5.3E-07 Acss1	ENSRNOG000000007102	3	146,470,293
18341 A_42_P842833	-0.725	0.123	2.2E-05	-1.384	0.110	1.0E-09 Srxn1	ENSRNOG000000031167	3	147,609,095
12668 A_44_P363204	-0.594	0.101	2.5E-05	-0.775	0.091	2.4E-07 Csnk2a1	ENSRNOG000000005276	3	147,713,821
3654 A_44_P529403	-0.755	0.131	2.9E-05	-0.866	0.117	1.5E-06 Tbc1d20	ENSRNOG000000005766	3	147,772,165
8852 A_64_P152189	-0.410	0.064	9.1E-06	-0.599	0.057	1.6E-08 Map1lc3a	ENSRNOG000000025443	3	150,801,289
15681 A_44_P389034	-1.168	0.212	4.8E-05	-1.176	0.190	1.3E-05 Tp53inp2	ENSRNOG000000018225	3	150,910,398
6036 A_44_P262407	-1.976	0.237	5.4E-07	-1.676	0.237	3.9E-06 Ggt7	ENSRNOG000000018441	3	151,032,302
2025 A_64_P073974	-0.843	0.113	1.3E-06	-0.980	0.101	4.1E-08 Myh7b	ENSRNOG000000018997	3	151,126,591
6299 A_64_P011194	-0.345	0.064	6.4E-05	-0.565	0.057	3.6E-08 Romo1	ENSRNOG000000019823	3	151,688,454
11686 A_64_P103956	-0.997	0.100	2.9E-08	-1.771	0.089	1.2E-12 Acot8	ENSRNOG000000015187	3	161,272,460
2951 A_42_P666951	-1.162	0.199	2.6E-05	-1.125	0.178	1.1E-05 Cd40	ENSRNOG000000018488	3	161,519,743
29765 A_64_P139173	-1.395	0.196	2.5E-06	-0.935	0.175	6.8E-05 Cd40	ENSRNOG000000018488	3	161,519,743
28578 A_64_P008473	0.373	0.070	7.0E-05	0.357	0.063	3.4E-05 Rpl38	ENSRNOG000000048701	3	164,002,482
13887 A_44_P317539	-0.508	0.076	5.3E-06	-0.422	0.068	1.2E-05 Psma7	ENSRNOG000000056853	3	175,426,395
16812 A_64_P058749	0.718	0.085	3.0E-07	0.691	0.076	1.1E-07	ENSRNOG000000043150	3	176,479,335
14217 A_64_P136394	1.446	0.161	2.3E-06	1.861	0.236	7.9E-06 Col20a1	ENSRNOG000000010326	3	176,494,768
29541 A_64_P059775	-2.182	0.171	1.9E-09	-3.425	0.171	3.3E-12 Stmn3	ENSRNOG000000013657	3	176,816,114
15543 A_44_P307964	-0.969	0.096	2.5E-08	-0.673	0.086	7.3E-07 Polr3k	ENSRNOG000000017843	3	177,374,812
7521 A_64_P158058	-0.511	0.086	2.0E-05	-0.680	0.077	1.5E-07 Slc4a2	ENSRNOG000000014347	4	7,281,223

24680 A_43_P12222	-0.426	0.074	3.0E-05	-0.494	0.066	1.4E-06 Pmpcb	ENSRNOG000000012693	4	9,921,610
21357 A_64_P016751	-0.982	0.104	6.1E-08	-1.208	0.093	6.6E-10 Tmem243 (RGD1	ENSRNOG000000042758	4	21,920,651
9693 A_64_P039888	0.923	0.171	9.3E-05	1.151	0.184	2.2E-05 Abcb1b	ENSRNOG000000008012	4	22,307,453
5850 A_44_P139763	0.636	0.097	6.3E-06	0.900	0.086	1.6E-08 Bet1	ENSRNOG000000011008	4	29,092,753
24172 A_64_P025464	-0.467	0.063	1.4E-06	-0.461	0.056	4.0E-07 Shfm1	ENSRNOG000000010420	4	32,087,600
29522 A_44_P489995	-0.795	0.072	6.8E-09	-1.019	0.064	3.5E-11 Mrps33	ENSRNOG000000026528	4	67,610,710
26495 A_64_P143875	0.950	0.165	3.0E-05	1.335	0.148	1.1E-07 Zyx	ENSRNOG000000017354	4	71,740,532
13479 A_64_P092534	1.255	0.168	1.4E-06	2.129	0.150	1.9E-10 Sspo	ENSRNOG000000025848	4	78,080,310
24482 A_64_P118256	-0.469	0.082	3.3E-05	-0.404	0.074	5.0E-05 Ccdc72	ENSRNOG000000043400	4	79,015,660
29493 A_44_P278387	-0.572	0.096	2.0E-05	-0.532	0.086	1.3E-05 Wipf3	ENSRNOG000000009571	4	84,597,323
19084 A_64_P078538	-0.412	0.066	1.2E-05	-0.523	0.059	1.5E-07	ENSRNOG000000011052	4	85,235,172
7404 A_43_P23115	1.650	0.122	4.0E-10	1.251	0.110	4.4E-09 Inmt	ENSRNOG000000011250	4	85,386,231
11506 A_44_P671449	-0.492	0.095	9.3E-05	-0.677	0.085	6.0E-07 Mrpl35	ENSRNOG000000008546	4	99,746,560
1827 A_64_P025633	0.707	0.110	8.4E-06	0.606	0.098	1.4E-05 Tmem150a	ENSRNOG000000061100	4	100,218,661
20592 A_44_P402507	-1.273	0.112	4.7E-09	-1.086	0.100	9.3E-09 Retsat	ENSRNOG000000014090	4	100,465,170
23887 A_44_P248947	-0.928	0.086	1.0E-08	-0.852	0.077	6.8E-09 Pole4	ENSRNOG000000006102	4	113,497,455
17379 A_44_P358440	2.744	0.385	5.3E-06	2.117	0.281	2.8E-06 Cml3	ENSRNOG000000015763	4	117,490,721
8677 A_64_P090548	-1.256	0.133	6.4E-08	-0.983	0.119	3.9E-07 Rassf4	ENSRNOG000000013526	4	148,803,988
13196 A_44_P622992	-1.353	0.245	4.7E-05	-2.276	0.219	1.7E-08 Tuba8	ENSRNOG000000048169	4	153,774,486
7183 A_64_P013456	-0.436	0.082	6.9E-05	-0.456	0.073	1.3E-05 Atn1	ENSRNOG000000060594	4	157,274,755
3106 A_64_P003046	-0.835	0.086	4.4E-08	-0.491	0.077	9.5E-06 Gapdh	ENSRNOG000000018630	4	157,679,962
19879 A_64_P052510	-0.978	0.105	7.8E-08	-0.519	0.094	4.8E-05 Gapdh	ENSRNOG000000018630	4	157,679,962
3747 A_64_P022586	-1.484	0.182	4.4E-07	-1.019	0.163	1.2E-05 Vamp1	ENSRNOG000000019219	4	157,726,941
7314 A_42_P560781	-1.162	0.189	1.4E-05	-1.002	0.169	2.1E-05 Vamp1	ENSRNOG000000019219	4	157,726,941
14671 A_64_P060628	-0.969	0.173	6.7E-05	-1.552	0.160	1.5E-07	ENSRNOG000000053804	4	160,334,910
13001 A_44_P409860	-0.839	0.147	3.2E-05	-0.773	0.131	2.3E-05	ENSRNOG000000048735	4	170,092,848
2691 A_42_P754654	-1.247	0.131	5.4E-08	-0.826	0.117	2.7E-06 RGD1562378	ENSRNOG000000045840	4	170,763,916
13669 A_64_P037993	0.913	0.177	9.6E-05	-0.846	0.158	6.7E-05 Rps4y2	ENSRNOG000000031041	4	182,745,448
11610 A_44_P271062	-0.522	0.099	7.8E-05	-0.665	0.089	1.3E-06 Tmem70	ENSRNOG000000006608	5	2,037,038
25630 A_64_P078937	0.435	0.081	7.6E-05	0.481	0.081	2.7E-05 Rpl7	ENSRNOG000000006992	5	2,632,712
17621 A_44_P412710	1.355	0.239	3.5E-05	1.705	0.214	5.8E-07 Adhfe1	ENSRNOG000000007069	5	9,429,859
2369 A_44_P415901	-0.470	0.079	2.0E-05	-0.380	0.070	6.0E-05 Mrpl15	ENSRNOG000000008566	5	14,609,674
15292 A_43_P14372	-0.590	0.083	2.6E-06	-0.853	0.074	4.2E-09	ENSRNOG000000031769	5	16,845,631

4766 A_44_P775787	-1.410	0.199	2.6E-06	-1.893	0.178	1.2E-08 LOC500420	ENSRNOG000000028185	5	35,902,262
9389 A_44_P1041460	-2.122	0.193	7.3E-09	-2.444	0.172	1.9E-10 Rragd	ENSRNOG000000007331	5	48,224,994
16552 A_44_P1060444	-0.573	0.096	2.1E-05	-0.640	0.086	1.5E-06 RGD1305158	ENSRNOG000000023035	5	50,239,458
28980 A_64_P101386	-0.640	0.079	4.9E-07	-0.565	0.071	5.9E-07 RGD1305158	ENSRNOG000000023035	5	50,239,458
21588 A_42_P680570	-0.942	0.148	9.2E-06	-0.687	0.132	8.7E-05 Nfx1	ENSRNOG000000009015	5	57,291,156
321 A_42_P698240	-1.571	0.113	2.6E-10	-1.652	0.101	2.3E-11 Ptgr1	ENSRNOG000000015072	5	76,129,441
13424 A_44_P175822	-0.907	0.097	6.8E-08	-0.618	0.086	2.3E-06 Hdhd3	ENSRNOG000000015195	5	78,361,647
29448 A_64_P090543	-0.647	0.066	3.5E-08	-0.657	0.059	5.9E-09 Hdhd3	ENSRNOG000000015195	5	78,361,647
13242 A_44_P1040796	1.850	0.073	2.6E-14	1.898	0.065	3.1E-15 Atp6v1g1	ENSRNOG000000008163	5	79,367,663
12871 A_44_P438675	0.865	0.135	8.5E-06	1.442	0.120	2.2E-09 Pappa	ENSRNOG000000033527	5	80,920,568
1289 A_42_P528537	1.364	0.263	9.0E-05	1.212	0.235	9.7E-05 Cdkn2b	ENSRNOG000000006735	5	107,857,320
19065 A_64_P138420	0.916	0.149	1.4E-05	1.664	0.133	1.2E-09 Cldn19	ENSRNOG000000007922	5	138,300,107
20248 A_64_P138415	2.383	0.271	2.8E-07	3.523	0.271	1.5E-09 Cldn19	ENSRNOG000000007922	5	138,300,107
7584 A_64_P055067	-0.849	0.113	1.3E-06	-1.106	0.101	8.6E-09 Ppcs	ENSRNOG000000008572	5	138,470,096
8503 A_44_P361357	0.699	0.115	1.7E-05	0.549	0.103	7.0E-05	ENSRNOG000000058461	5	145,079,803
29067 A_64_P092971	-0.808	0.097	3.3E-07	-1.364	0.087	3.9E-11 Fndc5	ENSRNOG000000030238	5	147,323,240
17989 A_44_P943514	0.484	0.080	1.7E-05	0.455	0.071	9.3E-06 Rbbp4	ENSRNOG000000021492	5	147,535,240
22186 A_64_P001401	0.820	0.126	7.7E-06	0.661	0.113	2.5E-05 Tinagl1	ENSRNOG000000013179	5	148,392,697
29934 A_64_P110798	-1.599	0.160	2.9E-08	-1.877	0.143	5.9E-10 Serinc2	ENSRNOG000000012989	5	148,492,232
12678 A_44_P262091	-2.094	0.324	8.0E-06	-2.120	0.290	1.8E-06 Fabp3	ENSRNOG000000012879	5	148,528,725
23071 A_64_P063696	-1.131	0.114	3.3E-08	-1.126	0.102	7.4E-09 Ptpru	ENSRNOG000000013515	5	149,987,910
4986 A_43_P13041	-2.783	0.220	1.0E-09	-4.205	0.197	3.8E-13 Nr0b2	ENSRNOG000000007229	5	151,776,004
23953 A_44_P279208	-0.709	0.133	6.7E-05	-0.699	0.119	2.3E-05 Eif4g3	ENSRNOG000000014368	5	156,396,695
28038 A_64_P052422	-1.513	0.192	6.9E-07	-2.480	0.172	1.4E-10 Otud3	ENSRNOG000000017037	5	157,368,450
22754 A_64_P051064	-0.444	0.079	3.8E-05	-0.599	0.071	2.6E-07 RGD1560286	ENSRNOG000000009183	5	159,662,754
27403 A_64_P052453	-0.678	0.116	2.5E-05	-0.823	0.104	6.4E-07 RGD1560286	ENSRNOG000000009183	5	159,662,754
3322 A_42_P569711	1.272	0.174	1.8E-06	1.236	0.156	6.4E-07 Epha2	ENSRNOG000000009222	5	159,845,774
11232 A_44_P731487	-0.636	0.099	8.7E-06	-0.708	0.089	5.7E-07 Fbxo44	ENSRNOG000000009298	5	164,971,903
28901 A_44_P429298	-2.217	0.259	2.4E-07	-2.894	0.232	1.2E-09 Tnfrsf9	ENSRNOG000000036942	5	168,009,393
11565 A_64_P127337	1.358	0.222	1.5E-05	1.069	0.199	6.3E-05 Per3	ENSRNOG000000018413	5	168,123,030
15177 A_64_P119405	1.274	0.208	1.5E-05	0.973	0.186	8.4E-05 Per3	ENSRNOG000000018413	5	168,123,030
8236 A_42_P586154	0.678	0.122	4.5E-05	0.698	0.109	9.3E-06 Vwa1	ENSRNOG000000018338	5	173,222,440
10772 A_64_P013112	-1.612	0.231	4.4E-06	-2.073	0.231	2.0E-07 Sult6b1	ENSRNOG000000049335	6	1,493,670

14831 A_44_P340316	-0.833	0.106	6.9E-07	-0.633	0.094	5.2E-06	RGD1311578	ENSRNOG000000005279	6	1,534,594
26699 A_64_P028551	-0.734	0.131	4.1E-05	-0.817	0.117	3.3E-06	RGD1311578	ENSRNOG000000005279	6	1,534,594
3693 A_44_P840715	1.000	0.129	8.9E-07	0.645	0.116	4.3E-05	Galm	ENSRNOG000000007023	6	2,808,841
17323 A_44_P119486	1.719	0.298	6.6E-05	2.161	0.365	5.1E-05	Plekhh2	ENSRNOG000000005124	6	7,793,735
18372 A_64_P017363	-0.766	0.088	1.8E-07	-0.759	0.078	4.5E-08	Slc30a3	ENSRNOG000000006204	6	26,642,783
6402 A_43_P17213	-1.644	0.205	5.7E-07	-2.291	0.184	1.2E-09	Abhd1	ENSRNOG0000000025689	6	26,792,808
2913 A_64_P036900	-0.739	0.081	1.1E-07	-0.482	0.073	6.0E-06	Kcnk3	ENSRNOG000000009790	6	27,190,132
24275 A_44_P413979	0.482	0.080	1.8E-05	0.828	0.071	3.6E-09	Rab10	ENSRNOG0000000047088	6	27,721,120
4161 A_64_P076450	-0.564	0.106	6.9E-05	-0.955	0.095	2.6E-08	Pomc	ENSRNOG0000000012686	6	28,382,962
3618 A_44_P377278	-1.883	0.225	3.1E-07	-1.491	0.201	1.5E-06	Adcy3	ENSRNOG000000003999	6	28,571,351
1796 A_42_P525962	-1.107	0.078	1.7E-10	-1.583	0.069	1.4E-13	RGD1561792	ENSRNOG000000004059	6	28,663,602
4792 A_42_P570241	-0.574	0.111	9.3E-05	-0.551	0.099	4.4E-05	Nampt	ENSRNOG000000009754	6	52,122,085
27573 A_44_P945846	1.077	0.164	1.3E-05	1.556	0.178	4.9E-07	Twistnb	ENSRNOG0000000010750	6	52,751,106
12252 A_64_P145433	0.547	0.098	4.2E-05	0.535	0.088	1.6E-05		ENSRNOG000000004342	6	55,001,464
18239 A_44_P504133	1.328	0.222	2.0E-05	2.585	0.199	6.7E-10	Tmem195	ENSRNOG0000000023116	6	56,846,789
4189 A_64_P098703	-0.521	0.063	3.8E-07	-0.605	0.057	1.1E-08	LOC288913	ENSRNOG0000000053727	6	69,619,295
6785 A_42_P483463	-0.420	0.074	3.4E-05	-0.575	0.066	1.8E-07	Ap4s1	ENSRNOG000000005765	6	72,461,977
24462 A_64_P071223	-0.386	0.075	1.0E-04	-0.502	0.067	1.4E-06	Psma3l	ENSRNOG000000007851	6	93,423,002
28435 A_64_P057261	-0.733	0.088	3.6E-07	-0.585	0.079	1.6E-06	Synj2bp	ENSRNOG000000006399	6	105,261,549
8745 A_44_P260589	-1.354	0.180	1.2E-06	-0.925	0.161	3.0E-05		ENSRNOG000000009448	6	107,245,820
12379 A_44_P417429	-0.450	0.074	1.6E-05	-0.652	0.066	3.6E-08	Coq6	ENSRNOG0000000011164	6	108,076,306
25368 A_64_P031035	1.510	0.139	9.1E-09	1.545	0.124	1.3E-09	Gstz1	ENSRNOG0000000047708	6	111,176,798
474 A_42_P799159	-0.481	0.078	1.4E-05	-0.884	0.070	9.7E-10	LOC688717	ENSRNOG0000000012314	6	111,476,768
3674 A_64_P164400	-0.501	0.088	3.6E-05	-0.822	0.079	1.7E-08	LOC688717	ENSRNOG0000000012314	6	111,476,768
13736 A_44_P455065	-0.891	0.079	5.1E-09	-0.983	0.071	2.4E-10	Ppp2r5c	ENSRNOG000000004973	6	134,804,141
22919 A_64_P056406	-0.888	0.087	2.3E-08	-0.945	0.078	1.9E-09	Ppp2r5c	ENSRNOG000000004973	6	134,804,141
13877 A_64_P124863	-0.569	0.089	8.8E-06	-0.669	0.079	2.9E-07	RGD1304719	ENSRNOG0000000011542	6	136,185,487
28369 A_64_P148906	-4.601	0.599	9.6E-07	-3.860	0.536	2.2E-06	Aspg	ENSRNOG0000000012843	6	136,682,126
1529 A_42_P742797	-0.599	0.089	5.1E-06	-0.435	0.080	5.4E-05	Brf1	ENSRNOG0000000014595	6	137,808,303
1701 A_64_P145857	-0.786	0.089	1.6E-07	-0.788	0.080	3.3E-08	LOC100359980	ENSRNOG0000000028837	7	2,912,491
9961 A_64_P030554	-0.589	0.076	8.7E-07	-0.383	0.068	3.8E-05	Mbd3	ENSRNOG0000000028956	7	12,179,203
7110 A_44_P236761	-1.497	0.124	2.0E-09	-1.749	0.111	3.9E-11	Rasal3	ENSRNOG000000006167	7	14,418,950
10600 A_64_P099017	-1.956	0.173	5.1E-09	-1.939	0.155	1.2E-09	Cyp4f17	ENSRNOG0000000062306	7	14,529,483

9077 A_64_P091460	0.652	0.124	8.0E-05	1.238	0.111	6.2E-09	ENSRNOG000000048170	7	20,075,974
24192 A_64_P043738	-0.745	0.086	1.9E-07	-0.589	0.077	9.7E-07 Mrpl42	ENSRNOG000000042740	7	36,597,462
24727 A_64_P158133	-0.623	0.088	2.6E-06	-0.523	0.079	5.7E-06 Rap1b	ENSRNOG000000007048	7	60,860,990
1448 A_42_P669907	0.739	0.136	5.8E-05	0.884	0.122	2.0E-06 Slc16a7	ENSRNOG000000007839	7	68,512,397
21486 A_64_P018497	-0.490	0.071	3.9E-06	-0.496	0.064	8.4E-07 Mterfd1	ENSRNOG000000004492	7	71,293,823
5860 A_64_P047206	-1.093	0.162	5.0E-06	-1.682	0.145	3.6E-09 Depdc6	ENSRNOG000000004328	7	94,795,214
12545 A_64_P039737	1.506	0.260	2.8E-05	2.089	0.233	1.3E-07 Scx	ENSRNOG000000021812	7	117,519,075
30277 A_64_P142942	0.913	0.145	1.1E-05	0.666	0.129	9.8E-05 Scx	ENSRNOG000000021812	7	117,519,075
12493 A_44_P537024	-0.476	0.083	3.2E-05	-0.697	0.074	7.0E-08 Gpr172a	ENSRNOG000000032561	7	117,605,050
13898 A_44_P445070	-0.484	0.077	1.2E-05	-0.545	0.069	7.1E-07 Lgals1	ENSRNOG000000009884	7	120,153,184
7934 A_44_P309650	-0.901	0.135	5.4E-06	-0.998	0.121	3.7E-07 Nol12	ENSRNOG000000010209	7	120,161,091
6095 A_64_P039165	0.761	0.096	6.3E-07	0.647	0.086	1.2E-06 Gcat	ENSRNOG000000055408	7	120,263,054
21107 A_44_P758203	-0.422	0.080	8.2E-05	-0.414	0.072	3.0E-05 Srek1ip1	ENSRNOG000000047506	7	122,160,171
10558 A_43_P12905	-0.798	0.141	4.5E-05	-0.894	0.141	1.3E-05 Bik	ENSRNOG000000010359	7	124,391,432
3165 A_42_P524610	0.451	0.085	7.0E-05	0.484	0.076	9.3E-06 Pphln1	ENSRNOG000000022778	7	134,603,121
22334 A_64_P113640	-0.810	0.111	1.8E-06	-0.775	0.099	7.7E-07 Nckap5l	ENSRNOG000000056678	7	141,093,924
1937 A_42_P751562	0.837	0.162	9.6E-05	0.915	0.145	1.1E-05 Mettl7a	ENSRNOG000000001376	7	141,973,553
28027 A_64_P110526	-1.146	0.211	5.8E-05	-1.550	0.189	4.2E-07 LOC683720	ENSRNOG000000058340	7	143,538,579
19949 A_64_P070736	0.782	0.136	3.0E-05	0.930	0.122	1.0E-06 Eif4b	ENSRNOG000000010103	7	143,679,617
6078 A_42_P589680	-0.682	0.079	2.1E-07	-0.591	0.071	3.2E-07 Tarbp2	ENSRNOG000000042355	7	144,121,744
3769 A_43_P12287	2.135	0.122	8.2E-12	2.029	0.109	3.3E-12 Ppp1r1a	ENSRNOG000000036827	7	145,154,131
25629 A_64_P145261	2.073	0.113	3.8E-12	2.070	0.101	7.0E-13 Ppp1r1a	ENSRNOG000000036827	7	145,154,131
2497 A_64_P064621	0.933	0.130	3.3E-06	0.740	0.124	2.5E-05 Trpc6	ENSRNOG000000006324	8	6,811,543
24267 A_64_P120759	-1.103	0.174	1.0E-05	-1.311	0.156	2.9E-07	ENSRNOG000000008990	8	13,109,487
17711 A_44_P119527	-1.588	0.176	1.2E-07	-1.471	0.158	7.5E-08 Med17	ENSRNOG000000051989	8	13,526,025
8626 A_44_P100886	1.676	0.142	1.4E-07	1.662	0.208	6.7E-06	ENSRNOG000000010999	8	13,909,188
11775 A_44_P518434	-1.274	0.140	1.0E-07	-1.217	0.125	4.2E-08 Mrpl4	ENSRNOG000000020659	8	22,021,213
19561 A_64_P051647	-1.079	0.098	7.5E-09	-0.838	0.088	5.4E-08 Pde4a	ENSRNOG000000020828	8	22,189,600
22156 A_64_P121123	-1.328	0.145	9.1E-08	-0.935	0.129	2.1E-06 Pde4a	ENSRNOG000000020828	8	22,189,600
20324 A_64_P114595	-0.813	0.138	2.3E-05	-1.007	0.123	4.3E-07 Atg4d	ENSRNOG000000047625	8	22,291,445
1575 A_44_P238246	0.650	0.095	4.1E-06	1.152	0.085	3.6E-10 Ilf3	ENSRNOG000000022741	8	22,402,890
28744 A_43_P11181	-0.391	0.075	8.6E-05	-0.548	0.067	4.4E-07 Elof1	ENSRNOG000000014284	8	23,130,877
1785 A_42_P553201	-1.233	0.117	1.3E-08	-0.704	0.105	4.9E-06 Acp5	ENSRNOG000000046261	8	23,148,396

13689 A_42_P820829	-0.715	0.111	7.8E-06	-0.527	0.099	6.9E-05 Oaf	ENSRNOG00000009243	8	47,529,689
3609 A_44_P122206	-0.890	0.144	1.3E-05	-1.510	0.129	2.9E-09 Timm8b	ENSRNOG00000009888	8	55,037,750
3560 A_42_P624403	-0.407	0.072	3.7E-05	-0.466	0.064	2.0E-06 Fdx1	ENSRNOG00000012123	8	56,393,233
21973 A_44_P272353	-0.757	0.092	3.8E-07	-0.716	0.082	1.8E-07 LOC367117	ENSRNOG000000031132	8	86,286,991
5042 A_64_P093234	-0.587	0.106	4.8E-05	-1.248	0.095	5.9E-10 Col12a1	ENSRNOG00000058470	8	87,158,368
3358 A_43_P10191	-0.493	0.089	4.6E-05	-0.716	0.080	1.2E-07 Rnf7	ENSRNOG00000011663	8	104,335,729
4841 A_44_P373483	-1.805	0.149	4.1E-09	-1.374	0.149	1.5E-07 Slco2a1	ENSRNOG00000009005	8	111,495,331
21381 A_43_P16567	-1.832	0.199	8.9E-08	-2.056	0.178	3.7E-09 Glytk	ENSRNOG00000046307	8	114,853,103
23112 A_42_P834090	-0.826	0.106	7.7E-07	-0.712	0.095	1.2E-06 LOC686298	ENSRNOG00000046535	8	114,892,910
18260 A_43_P16646	-0.525	0.085	1.3E-05	-0.921	0.076	1.7E-09 Tex264	ENSRNOG00000013201	8	115,388,266
29684 A_44_P1024703	-0.769	0.130	2.3E-05	-1.026	0.117	1.6E-07 Cyb561d2	ENSRNOG00000021887	8	116,297,850
20909 A_44_P509845	-0.643	0.087	1.5E-06	-0.620	0.077	5.6E-07 Dag1	ENSRNOG00000019400	8	116,993,193
23340 A_44_P550228	0.815	0.144	3.6E-05	1.030	0.129	5.7E-07 Lamb2	ENSRNOG00000047768	8	117,268,337
3435 A_42_P573412	0.871	0.142	1.5E-05	0.664	0.127	8.7E-05 Spink8	ENSRNOG000000037199	8	117,906,014
23743 A_44_P126027	-2.101	0.181	7.0E-09	-1.388	0.181	1.5E-06 Pfkfb4	ENSRNOG00000048130	8	118,392,773
18691 A_64_P057548	-0.697	0.081	2.3E-07	-0.841	0.073	3.6E-09 Cmc1	ENSRNOG00000010149	8	126,495,347
8158 A_42_P671285	0.940	0.131	2.2E-06	1.491	0.117	8.8E-10 Ctdspl	ENSRNOG00000046257	8	127,702,534
14049 A_44_P625333	0.816	0.125	6.8E-06	1.242	0.111	6.2E-09 Ctdspl	ENSRNOG00000046257	8	127,702,534
26317 A_44_P431661	1.438	0.218	6.4E-06	1.509	0.195	9.0E-07 Vill	ENSRNOG00000011446	8	127,735,258
1637 A_42_P586141	-1.117	0.125	1.3E-07	-1.131	0.112	2.5E-08 Plcd1	ENSRNOG00000032238	8	127,782,070
20183 A_44_P306507	-0.970	0.122	6.3E-07	-1.112	0.109	2.2E-08 Higd1a	ENSRNOG00000019428	8	130,491,998
24536 A_64_P118187	0.843	0.127	5.9E-06	1.253	0.114	7.2E-09 Hdgf2	ENSRNOG00000049142	9	10,991,820
13374 A_44_P405628	-0.665	0.100	5.4E-06	-0.715	0.089	5.4E-07 Ubxn6	ENSRNOG00000048509	9	10,995,198
8822 A_64_P160484	-0.989	0.137	2.0E-06	-1.253	0.122	2.0E-08 Trem3	ENSRNOG00000013748	9	14,724,093
16969 A_64_P045957	-0.597	0.068	1.6E-07	-0.928	0.061	6.1E-11 Mrpl14	ENSRNOG00000019734	9	17,698,569
4274 A_44_P428507	-1.261	0.119	1.3E-08	-1.599	0.106	7.8E-11 Nfkbie	ENSRNOG00000019907	9	17,835,240
2347 A_44_P111507	-1.756	0.177	5.6E-08	-2.377	0.177	9.3E-10 Tcte1	ENSRNOG00000019961	9	17,866,927
17848 A_64_P004231	1.356	0.171	6.2E-07	2.127	0.153	2.4E-10 Gsta5	ENSRNOG00000056847	9	27,402,381
3838 A_42_P624195	1.590	0.219	1.9E-06	1.895	0.195	4.4E-08 Gsta3	ENSRNOG00000013484	9	27,452,902
11587 A_64_P139113	-0.456	0.086	7.1E-05	-0.441	0.077	3.1E-05 Arpc5l	ENSRNOG00000016444	9	49,795,936
25117 A_64_P060967	0.995	0.087	4.4E-09	0.921	0.078	2.7E-09 Lancl1	ENSRNOG00000013557	9	74,048,244
8097 A_44_P1031737	0.761	0.134	3.5E-05	0.753	0.120	1.1E-05 Pocr	ENSRNOG00000055295	9	79,630,536
17524 A_44_P384090	0.890	0.170	8.1E-05	1.148	0.152	1.2E-06 Des	ENSRNOG00000019810	9	82,556,573

18795 A_43_P10901	1.889	0.189	2.9E-08	2.520	0.169	8.9E-11 Itm2c	ENSRNOG000000017359	9	92,916,469
3751 A_42_P471768	-0.641	0.074	2.1E-07	-0.657	0.066	3.3E-08 Eif4e2	ENSRNOG000000019634	9	94,310,921
5606 A_44_P467591	-1.808	0.243	1.4E-06	-3.265	0.217	7.8E-11 Neu2	ENSRNOG000000016962	9	94,702,129
7344 A_64_P010174	0.920	0.133	3.6E-06	0.821	0.119	3.7E-06 Man2a1	ENSRNOG000000015439	9	112,293,388
8020 A_64_P054942	0.450	0.073	1.4E-05	0.491	0.065	1.2E-06 Wash2	ENSRNOG000000053306	9	113,918,858
9804 A_64_P148368	1.173	0.149	6.9E-07	0.954	0.133	2.3E-06 RGD1308319	ENSRNOG000000025527	9	114,619,711
11494 A_44_P123492	-1.026	0.176	2.5E-05	-0.913	0.157	2.7E-05 Epb41l3	ENSRNOG000000016724	9	117,538,009
6655 A_64_P105228	0.718	0.129	4.5E-05	0.903	0.116	7.8E-07 RGD1309537	ENSRNOG000000015278	9	119,332,967
9876 A_64_P105231	0.678	0.122	4.2E-05	0.769	0.109	2.7E-06 RGD1309537	ENSRNOG000000015278	9	119,332,967
970 A_44_P163018	-0.551	0.070	7.2E-07	-0.484	0.063	9.1E-07 Nubp1	ENSRNOG000000002574	10	5,344,121
22702 A_64_P088038	-0.519	0.100	9.5E-05	-0.739	0.090	3.9E-07 Tmem186	ENSRNOG000000027087	10	7,077,488
22463 A_44_P142850	-0.826	0.113	1.7E-06	0.984	0.101	4.0E-08 Fam86a	ENSRNOG000000002876	10	10,530,365
29102 A_42_P475151	0.673	0.123	5.1E-05	1.031	0.110	6.9E-08 Rogdi	ENSRNOG000000003125	10	10,761,477
12289 A_43_P12438	-0.359	0.069	9.0E-05	-0.804	0.062	6.8E-10 Hmox2	ENSRNOG000000003773	10	11,035,484
24015 A_44_P331119	-0.466	0.085	4.8E-05	-0.622	0.076	4.0E-07 Spsb3	ENSRNOG000000015300	10	14,248,399
10341 A_64_P006373	-0.478	0.071	4.6E-06	-0.689	0.063	8.4E-09 Mrps34	ENSRNOG000000015479	10	14,257,001
21059 A_64_P066501	0.963	0.131	1.7E-06	1.243	0.117	1.3E-08 Gng13	ENSRNOG000000039350	10	15,088,935
23671 A_64_P062663	0.944	0.132	2.4E-06	1.301	0.118	7.5E-09 Gng13	ENSRNOG000000039350	10	15,088,935
4846 A_44_P114851	-0.766	0.106	2.1E-06	-1.220	0.095	7.8E-10 Tmem8a	ENSRNOG000000020374	10	15,485,905
7281 A_64_P062288	-1.072	0.166	7.9E-06	-0.812	0.148	5.2E-05 Ccdc99	ENSRNOG000000007292	10	19,652,898
14617 A_64_P028561	1.747	0.277	1.1E-05	1.769	0.248	2.4E-06	ENSRNOG000000058024	10	29,806,895
4451 A_44_P1001820	-1.079	0.136	6.1E-07	-1.053	0.121	1.9E-07 Slc22a5	ENSRNOG000000008432	10	39,323,816
11928 A_64_P043746	-0.427	0.065	6.7E-06	-0.604	0.058	1.7E-08 Mrpl22	ENSRNOG000000027039	10	43,601,689
5028 A_64_P015236	-0.683	0.108	1.1E-05	-1.102	0.097	4.7E-09 RGD1306000	ENSRNOG000000022725	10	45,514,878
22884 A_64_P058312	-0.534	0.103	9.4E-05	-0.654	0.092	2.6E-06 RGD1306000	ENSRNOG000000022725	10	45,514,878
27887 A_44_P258277	-0.682	0.106	8.4E-06	-0.608	0.095	8.8E-06 Dhrr7b	ENSRNOG000000005360	10	47,065,850
13618 A_64_P017053	-2.728	0.250	6.7E-08	-1.720	0.204	1.3E-06	ENSRNOG000000004171	10	52,710,862
4290 A_64_P011819	-0.586	0.088	5.4E-06	-0.421	0.078	6.4E-05 Sco1	ENSRNOG000000028699	10	53,595,854
22062 A_64_P112579	1.396	0.185	1.2E-06	1.031	0.165	1.2E-05 Slc16a11	ENSRNOG000000018748	10	56,822,756
2308 A_44_P993464	-0.318	0.061	9.0E-05	-0.441	0.055	5.3E-07 Med11	ENSRNOG000000019384	10	57,057,608
23056 A_64_P032833	-0.565	0.103	4.9E-05	-0.704	0.092	9.9E-07 Aspa	ENSRNOG000000019659	10	59,888,200
7399 A_44_P332734	-0.545	0.105	8.7E-05	-0.601	0.094	8.8E-06 LOC100365943	ENSRNOG000000022652	10	65,835,966
23384 A_64_P016978	1.185	0.163	2.0E-06	0.936	0.146	8.9E-06 Ccl11	ENSRNOG000000007335	10	69,434,941

3550 A_42_P785926	-0.549	0.069	5.7E-07	-0.538	0.061	1.7E-07 Mrps23	ENSRNOG000000010363	10	75,529,009
26348 A_64_P009540	-1.088	0.202	6.3E-05	-1.261	0.181	3.3E-06 Akap1	ENSRNOG000000002373	10	76,166,276
28956 A_43_P12890	-0.966	0.183	7.4E-05	-1.004	0.163	1.4E-05 Akap1	ENSRNOG000000002373	10	76,166,276
8482 A_44_P292487	-1.113	0.086	7.2E-10	-1.009	0.077	5.8E-10 Scsep1	ENSRNOG000000002358	10	76,263,866
1958 A_64_P075938	-0.828	0.157	7.4E-05	-1.387	0.140	3.3E-08 Cox11	ENSRNOG000000052096	10	78,111,050
23141 A_64_P068570	-0.877	0.144	1.6E-05	-1.119	0.128	1.9E-07 Cox11	ENSRNOG000000052096	10	78,168,715
15574 A_64_P057453	-1.108	0.101	7.6E-09	-0.467	0.090	9.2E-05 LOC303448	ENSRNOG000000054719	10	78,690,857
6815 A_44_P407138	-0.716	0.082	1.9E-07	-0.902	0.074	1.6E-09 Nme1	ENSRNOG000000002693	10	81,666,523
5476 A_64_P150256	-2.105	0.172	1.6E-09	-2.302	0.154	8.3E-11 Epn3	ENSRNOG000000003284	10	82,229,140
14953 A_64_P021606	-2.380	0.192	1.4E-09	-3.235	0.172	2.6E-12 Mycbpap	ENSRNOG000000042912	10	82,252,963
3474 A_64_P063871	-1.444	0.219	6.3E-06	-1.293	0.196	6.2E-06 Phospho1	ENSRNOG000000005569	10	83,636,518
27361 A_64_P049761	-0.923	0.109	2.8E-07	-0.739	0.098	1.2E-06 Nfe2l1	ENSRNOG000000008830	10	84,698,886
3940 A_42_P453894	-0.519	0.080	7.8E-06	-0.662	0.072	8.4E-08 RGD1306682	ENSRNOG000000050874	10	84,847,857
15673 A_64_P097994	-0.612	0.074	3.6E-07	-0.504	0.066	1.0E-06 Npepps	ENSRNOG000000023095	10	85,222,861
11808 A_64_P024482	-0.678	0.080	2.6E-07	-0.783	0.071	8.0E-09 Cisd3	ENSRNOG000000036894	10	85,628,491
28614 A_44_P1038655	-2.330	0.307	1.1E-06	-2.029	0.274	1.6E-06 Ttc25	ENSRNOG000000017473	10	88,459,490
29794 A_43_P12209	-0.862	0.159	5.6E-05	-0.879	0.142	1.3E-05 Stat5b	ENSRNOG000000019075	10	88,754,829
10835 A_42_P652586	-0.982	0.127	9.1E-07	-1.446	0.114	9.5E-10 Stat5a	ENSRNOG000000019496	10	88,764,732
6804 A_64_P150509	-1.360	0.215	1.1E-05	-2.176	0.193	5.2E-09 Ccr10	ENSRNOG000000020275	10	89,088,993
24388 A_44_P377156	-1.065	0.153	3.3E-06	-1.219	0.137	1.4E-07 Cntnap1	ENSRNOG000000020277	10	89,089,646
24058 A_64_P141424	-0.700	0.086	4.6E-07	-0.934	0.077	1.8E-09 Ccdc56	ENSRNOG000000020487	10	89,199,736
14741 A_64_P100516	0.668	0.101	5.9E-06	0.468	0.090	9.0E-05 Aoc3	ENSRNOG000000051307	10	89,251,370
12992 A_64_P051393	-1.926	0.166	3.6E-09	-1.547	0.149	1.7E-08 Pyy	ENSRNOG000000020877	10	90,049,112
25120 A_64_P051392	-1.342	0.157	2.4E-07	-1.158	0.140	3.9E-07 Pyy	ENSRNOG000000020877	10	90,049,112
21785 A_44_P130785	-0.468	0.077	1.7E-05	-0.490	0.069	2.6E-06 Slc25a39	ENSRNOG000000020994	10	90,356,242
12629 A_64_P073629	-0.578	0.094	1.5E-05	-0.644	0.084	1.1E-06 Magmas	ENSRNOG000000028427	10	91,752,934
7748 A_42_P612977	-1.157	0.142	4.6E-07	-0.782	0.127	1.4E-05 Cyb561	ENSRNOG000000007433	10	94,147,556
15636 A_64_P143770	-0.984	0.127	8.3E-07	-0.640	0.113	3.7E-05	ENSRNOG000000030224	10	102,289,837
8362 A_64_P055738	0.515	0.078	6.2E-06	0.923	0.070	5.3E-10 Itgb4	ENSRNOG000000005580	10	104,523,996
3531 A_64_P059385	0.634	0.105	1.7E-05	0.592	0.094	1.0E-05 Acox1	ENSRNOG000000008755	10	104,748,050
22560 A_64_P157691	-2.001	0.197	2.3E-08	-1.721	0.176	3.9E-08 RGD1559482	ENSRNOG000000048771	10	104,952,237
25707 A_44_P436597	-0.551	0.094	2.6E-05	-0.890	0.084	1.4E-08 RGD1306284	ENSRNOG000000000249	10	105,787,935
4081 A_64_P085405	-1.608	0.140	4.1E-09	-1.012	0.125	5.1E-07 9-Sep	ENSRNOG000000002807	10	106,264,434

22449 A_42_P539095	-0.895	0.066	3.8E-10	-0.876	0.059	1.0E-10 LOC688311	ENSRNOG000000049235	10	109,639,054
18404 A_43_P13256	1.550	0.183	2.8E-07	1.342	0.164	4.3E-07 Dcxr	ENSRNOG000000050315	10	109,909,646
17254 A_64_P138560	-1.015	0.148	4.1E-06	-0.992	0.133	1.4E-06 Narf	ENSRNOG000000061691	10	110,125,109
15351 A_64_P072973	1.950	0.156	1.2E-09	2.174	0.140	4.6E-11 Kcne2	ENSRNOG000000029811	11	32,440,237
23285 A_44_P884080	-0.478	0.089	6.1E-05	-0.435	0.079	5.0E-05 LOC100174909	ENSRNOG000000039877	11	32,450,587
26800 A_64_P116606	1.291	0.202	1.7E-05	1.588	0.218	4.2E-06 Rcan1	ENSRNOG000000001979	11	32,550,539
3179 A_42_P554722	-0.701	0.119	2.3E-05	-0.808	0.107	1.1E-06 Pignp	ENSRNOG000000039850	11	34,598,275
1366 A_64_P057975	0.876	0.109	5.4E-07	1.202	0.098	1.5E-09 Hmgn1	ENSRNOG000000050978	11	36,479,868
6802 A_42_P625419	0.940	0.172	5.2E-05	1.154	0.154	1.3E-06 RGD1565927	ENSRNOG000000001645	11	45,124,423
6884 A_42_P732251	-0.935	0.163	3.0E-05	-0.925	0.145	9.7E-06 Phldb2	ENSRNOG000000002171	11	57,404,196
22903 A_43_P12844	-0.355	0.068	8.7E-05	-1.050	0.061	1.0E-11 Cox17	ENSRNOG000000038951	11	64,968,437
29503 A_64_P124200	1.293	0.240	6.0E-05	1.126	0.214	7.9E-05 Gp1bb	ENSRNOG000000046981	11	86,520,992
2679 A_64_P160658	-0.714	0.093	9.3E-07	-0.438	0.083	7.6E-05 Txnrd2	ENSRNOG000000001890	11	86,716,063
16895 A_64_P038926	1.281	0.194	6.1E-06	1.345	0.173	8.3E-07 Prodh	ENSRNOG000000000281	11	87,058,616
24093 A_44_P244257	0.987	0.151	6.9E-06	0.780	0.135	2.9E-05 Fgd4	ENSRNOG000000059491	11	88,699,222
9868 A_64_P013239	-0.481	0.078	1.3E-05	-0.584	0.069	2.9E-07 Higd2a	ENSRNOG000000001071	12	4,546,287
12967 A_64_P047002	0.895	0.137	6.9E-06	0.813	0.122	5.8E-06 Fry	ENSRNOG000000000894	12	5,682,608
16115 A_44_P267068	-0.465	0.078	1.9E-05	-0.427	0.069	1.4E-05 Nudt1	ENSRNOG000000001260	12	16,395,029
3604 A_42_P746109	-0.846	0.071	2.4E-09	-0.638	0.063	2.6E-08 Asmtl	ENSRNOG000000028166	12	18,531,990
1594 A_64_P024429	0.583	0.107	5.6E-05	1.081	0.096	5.4E-09 Il3ra	ENSRNOG000000001325	12	18,540,166
19145 A_64_P081501	1.255	0.163	9.3E-07	1.561	0.146	1.1E-08 Mcm7	ENSRNOG000000001349	12	19,314,016
23117 A_42_P540609	-1.633	0.155	2.6E-08	-1.668	0.155	1.9E-08 LOC680711	ENSRNOG000000031343	12	19,440,501
24237 A_64_P194847	-1.462	0.187	1.2E-06	-1.797	0.187	9.0E-08	ENSRNOG000000027061	12	19,512,591
25622 A_64_P119299	-1.703	0.217	1.1E-06	-1.840	0.217	4.2E-07	ENSRNOG000000027061	12	19,512,591
21845 A_44_P1012866	-0.550	0.072	9.6E-07	-0.611	0.064	5.5E-08 RGD1309735	ENSRNOG000000027028	12	19,573,909
1742 A_64_P144034	1.243	0.167	4.0E-05	1.915	0.167	1.2E-06 LOC363894	ENSRNOG000000045875	12	20,814,122
19679 A_64_P045833	-1.142	0.176	7.4E-06	-1.517	0.157	4.6E-08	ENSRNOG000000050128	12	21,450,204
15839 A_64_P032265	0.707	0.120	2.3E-05	1.079	0.107	2.7E-08	ENSRNOG000000033017	12	21,678,580
21526 A_44_P579382	-1.327	0.188	2.7E-06	-2.279	0.168	3.6E-10 Zcwpw1	ENSRNOG000000024425	12	21,720,094
25316 A_64_P053855	-0.498	0.082	1.7E-05	-0.680	0.073	8.1E-08 Znhit1	ENSRNOG000000001418	12	22,726,643
25740 A_44_P1041034	-0.600	0.080	1.2E-06	-0.650	0.071	1.0E-07 Polr2j	ENSRNOG000000001430	12	23,592,774
18878 A_44_P992908	1.628	0.263	1.3E-05	1.294	0.235	4.9E-05 Hspb1	ENSRNOG000000023546	12	23,841,049
17894 A_64_P069394	0.947	0.144	6.7E-06	1.283	0.129	3.1E-08 Styxl1	ENSRNOG000000023366	12	23,954,574

6654 A_44_P1009552	0.974	0.182	6.5E-05	0.914	0.163	3.9E-05	Gtf2ird1	ENSRNOG000000001478	12	25,264,192
4941 A_42_P589190	1.553	0.266	2.5E-05	2.949	0.238	1.3E-09	Aacs	ENSRNOG000000000967	12	36,555,694
3175 A_44_P1030714	1.490	0.147	2.4E-08	2.102	0.132	3.2E-11	Ccdc92	ENSRNOG0000000021691	12	37,211,316
13761 A_64_P135202	-0.879	0.086	2.2E-08	-0.806	0.077	1.5E-08	Snmp35	ENSRNOG0000000001060	12	37,538,403
24243 A_44_P184650	-0.773	0.083	8.2E-08	-0.730	0.075	3.9E-08	Rilpl2	ENSRNOG0000000001061	12	37,544,918
2306 A_42_P630463	-1.026	0.197	8.7E-05	-2.218	0.176	1.1E-09	Abcb9	ENSRNOG0000000001082	12	37,923,528
6667 A_44_P187005	-1.246	0.195	9.1E-06	-1.851	0.174	1.2E-08	Abcb9	ENSRNOG0000000001082	12	37,923,528
2579 A_64_P024060	-0.437	0.073	1.9E-05	-0.489	0.065	1.3E-06		ENSRNOG0000000001106	12	38,116,919
29139 A_44_P838992	-2.382	0.189	1.1E-09	-1.494	0.169	1.5E-07	LOC687609	ENSRNOG0000000042607	12	38,880,377
2210 A_64_P023670	0.527	0.087	1.6E-05	0.897	0.077	3.6E-09	Aldh2	ENSRNOG0000000001344	12	40,466,495
19071 A_43_P17480	-0.897	0.169	7.1E-05	-0.971	0.151	8.6E-06	RGD1306772	ENSRNOG0000000037720	12	41,486,076
17976 A_64_P106176	0.479	0.082	2.6E-05	0.454	0.073	1.3E-05		ENSRNOG0000000001120	12	43,503,456
6196 A_44_P686406	1.149	0.165	3.4E-06	1.064	0.148	2.2E-06	RGD1562310	ENSRNOG0000000001123	12	43,940,798
741 A_42_P548796	-0.875	0.130	5.1E-06	-0.623	0.117	6.7E-05	Tsn	ENSRNOG0000000002319	13	34,251,650
20428 A_44_P272253	-0.496	0.088	3.6E-05	-0.952	0.078	1.8E-09	LOC288978	ENSRNOG0000000045570	13	36,156,182
23346 A_64_P013147	0.865	0.161	6.4E-05	1.032	0.144	2.3E-06	Preip	ENSRNOG0000000003120	13	50,761,306
10145 A_64_P103707	-0.708	0.098	2.2E-06	-0.830	0.088	6.4E-08	Ndufv3	ENSRNOG0000000027593	13	51,297,621
28935 A_64_P141541	-0.616	0.078	6.9E-07	-0.795	0.070	4.7E-09	Ndufv3	ENSRNOG0000000027593	13	51,297,621
16455 A_64_P145820	0.721	0.078	8.7E-08	0.940	0.070	4.1E-10	Gpr37l1	ENSRNOG0000000006237	13	51,992,693
19291 A_44_P475444	1.000	0.184	5.6E-05	1.036	0.165	1.1E-05	RGD1564614	ENSRNOG0000000042369	13	56,958,549
2005 A_42_P819656	1.339	0.223	1.8E-05	1.385	0.199	3.3E-06	Cfh	ENSRNOG0000000030715	13	57,080,549
4627 A_42_P553319	-0.734	0.137	6.6E-05	-0.885	0.123	2.1E-06		ENSRNOG0000000004736	13	74,520,634
4122 A_44_P358194	2.817	0.289	4.2E-08	3.061	0.259	2.7E-09	Fmo3	ENSRNOG0000000003620	13	80,862,963
19873 A_64_P055216	3.019	0.145	5.3E-13	1.876	0.129	1.3E-10	RGD1309708	ENSRNOG0000000002860	13	82,574,966
27423 A_64_P083364	-0.634	0.104	1.6E-05	-0.755	0.093	5.0E-07	Brp44	ENSRNOG0000000003150	13	83,681,322
26528 A_64_P016901	0.777	0.102	1.1E-06	1.198	0.091	6.0E-10	Creg1	ENSRNOG0000000003291	13	83,972,212
22348 A_44_P1018997	-0.964	0.077	1.3E-09	-0.478	0.069	3.6E-06	Tmco1	ENSRNOG0000000003928	13	85,465,792
20771 A_64_P001255	-0.863	0.123	3.0E-06	-0.957	0.110	1.9E-07	Ppox	ENSRNOG0000000003567	13	89,654,244
502 A_64_P051346	-1.316	0.135	4.2E-08	-1.195	0.121	3.4E-08	Pex19	ENSRNOG0000000057116	13	90,514,362
1369 A_42_P647505	0.555	0.092	1.9E-05	0.870	0.083	1.4E-08		ENSRNOG0000000023541	13	98,078,555
43 A_44_P174374	1.120	0.120	7.2E-08	1.310	0.107	1.6E-09	Ephx1	ENSRNOG0000000003515	13	99,300,579
2623 A_64_P057526	1.433	0.137	1.5E-08	1.095	0.123	1.3E-07		ENSRNOG0000000037928	13	99,335,020
23959 A_44_P177914	0.577	0.089	7.3E-06	0.786	0.079	3.2E-08	Nvl	ENSRNOG0000000003629	13	99,468,778

11923 A_44_P313786	-0.538	0.078	4.0E-06	-0.793	0.070	5.1E-09 Tmem14c	ENSRNOG000000022144	13	107,580,629
1758 A_64_P027298	-0.806	0.124	7.8E-06	-0.867	0.111	8.0E-07 Ptpn14	ENSRNOG000000003407	13	108,841,482
9059 A_42_P803590	-1.556	0.105	9.6E-11	-1.424	0.094	6.8E-11 LOC289378	ENSRNOG000000046460	13	109,663,364
3954 A_42_P661065	1.100	0.140	7.0E-07	1.219	0.125	4.1E-08 Ints7	ENSRNOG000000004263	13	110,257,571
10206 A_64_P052464	1.059	0.190	4.3E-05	1.320	0.170	8.5E-07 Ints7	ENSRNOG000000004263	13	110,257,571
18334 A_64_P124502	-0.567	0.108	8.3E-05	-0.597	0.097	1.4E-05 Rcor3	ENSRNOG000000046445	13	110,864,469
3766 A_42_P601802	0.679	0.085	5.7E-07	0.727	0.076	5.2E-08 Crlf2	ENSRNOG000000049828	14	1,461,543
3061 A_44_P454646	-0.612	0.093	6.0E-06	-0.665	0.083	5.4E-07 Fam69a	ENSRNOG000000023533	14	2,789,650
2950 A_42_P683634	1.158	0.157	1.6E-06	1.398	0.140	2.9E-08 Sparcl1	ENSRNOG000000015093	14	6,994,190
10617 A_44_P1043814	-0.670	0.104	8.1E-06	-0.701	0.093	1.2E-06 Hsd17b11	ENSRNOG000000002210	14	7,073,445
4776 A_43_P14648	0.837	0.154	5.4E-05	0.709	0.137	9.6E-05 Art3	ENSRNOG000000002256	14	17,225,389
8045 A_64_P151226	0.855	0.150	3.3E-05	0.952	0.134	2.6E-06 Art3	ENSRNOG000000002256	14	17,225,389
6146 A_64_P144670	-0.841	0.163	9.8E-05	-1.273	0.146	1.9E-07 Usp46	ENSRNOG000000002106	14	36,687,134
11340 A_64_P150662	2.078	0.170	1.7E-09	2.024	0.152	4.9E-10 Corin	ENSRNOG000000002302	14	38,247,791
14100 A_44_P376940	-0.926	0.150	1.3E-05	-0.699	0.134	8.4E-05 Otop1	ENSRNOG000000028423	14	77,263,729
6252 A_64_P074260	-0.908	0.102	1.3E-07	-1.145	0.091	1.1E-09 Letm1	ENSRNOG000000016427	14	82,227,708
2976 A_43_P19289	-0.765	0.101	1.1E-06	-0.750	0.090	3.5E-07 Mtp18	ENSRNOG000000004640	14	84,334,066
10255 A_64_P115903	-0.603	0.092	6.4E-06	-0.481	0.082	2.4E-05 Zmat5	ENSRNOG000000007849	14	84,953,786
16167 A_64_P046754	0.781	0.079	3.6E-08	0.730	0.071	1.9E-08 Igfbp3	ENSRNOG000000061910	14	87,465,374
13521 A_64_P007498	-2.087	0.228	9.7E-08	-3.682	0.204	5.0E-12 Fam161a	ENSRNOG000000009881	14	107,785,029
5167 A_64_P049628	-1.080	0.108	2.7E-08	-1.102	0.096	4.2E-09 Acyp2	ENSRNOG000000042419	14	115,052,450
8650 A_42_P607939	-0.742	0.069	1.0E-08	-0.561	0.062	1.0E-07 Chchd1	ENSRNOG000000009297	15	4,026,637
30150 A_64_P031606	-0.520	0.078	5.5E-06	-0.807	0.070	3.6E-09 Mrps16	ENSRNOG000000006898	15	4,351,292
14168 A_43_P12698	-1.089	0.167	7.1E-06	0.779	0.149	8.5E-05 Lgals3	ENSRNOG000000010645	15	24,141,651
22906 A_44_P465868	-0.830	0.098	2.8E-07	-0.810	0.088	8.7E-08 Dhrrs4	ENSRNOG000000018239	15	34,155,504
25572 A_64_P157611	0.899	0.170	7.5E-05	1.445	0.152	5.8E-08 Cpne6	ENSRNOG000000018399	15	34,187,223
4177 A_42_P597308	-0.515	0.083	1.3E-05	-0.680	0.074	9.5E-08 N6amt2	ENSRNOG000000009849	15	37,830,131
21303 A_44_P206091	-0.374	0.072	9.4E-05	-0.447	0.065	3.5E-06 Mrp63	ENSRNOG000000010855	15	38,095,803
9768 A_64_P102498	-1.773	0.266	5.5E-06	-3.282	0.238	2.8E-10 LOC683415	ENSRNOG000000047258	15	47,442,664
24711 A_44_P321176	-1.647	0.209	7.0E-07	-1.080	0.187	2.9E-05 Hr	ENSRNOG000000011427	15	52,241,801
5602 A_64_P153447	-1.551	0.285	6.8E-05	-2.380	0.285	5.1E-07 Dct	ENSRNOG000000008671	15	103,244,494
25871 A_44_P308369	1.223	0.232	7.7E-05	2.139	0.207	1.9E-08	ENSRNOG000000058057	15	104,349,745
15927 A_44_P250594	1.232	0.132	2.4E-07	0.951	0.143	1.1E-05	ENSRNOG000000058057	15	104,393,682

12187 A_43_P16710	0.532	0.087	1.5E-05	0.743	0.078	5.4E-08	Ipo5	ENSRNOG00000010989	15	106,257,650
18365 A_43_P14210	-0.730	0.128	3.3E-05	-0.731	0.114	9.2E-06	Ppif	ENSRNOG00000010558	16	1,979,191
20187 A_44_P481160	-0.786	0.137	3.2E-05	-1.855	0.123	7.4E-11	Wnt5a	ENSRNOG00000015618	16	4,469,468
6846 A_64_P005043	1.370	0.123	6.0E-09	1.068	0.110	4.0E-08	Nt5dc2	ENSRNOG00000018358	16	7,212,488
11411 A_64_P158738	-1.310	0.153	6.3E-07	-1.748	0.165	4.8E-08	Dnah1	ENSRNOG00000026914	16	7,406,951
30347 A_64_P066923	0.728	0.132	4.8E-05	1.000	0.118	2.8E-07	Ncoa4	ENSRNOG00000019768	16	8,302,950
16759 A_43_P14157	0.484	0.091	7.4E-05	0.456	0.082	4.3E-05	Glud1	ENSRNOG000000057367	16	10,662,021
18286 A_44_P384017	1.193	0.112	1.1E-08	0.964	0.100	4.6E-08	Sncg	ENSRNOG000000058006	16	10,726,707
5974 A_42_P596050	-1.734	0.281	2.5E-05	-2.034	0.260	1.9E-06	Pcdh21	ENSRNOG00000013330	16	14,348,046
1186 A_42_P467381	0.497	0.073	4.5E-06	0.796	0.065	1.8E-09	Fam32a	ENSRNOG000000039528	16	19,308,842
9955 A_64_P063014	-0.538	0.093	2.9E-05	-0.437	0.083	8.2E-05	Ocel1	ENSRNOG000000032575	16	19,767,264
14171 A_64_P077627	-0.518	0.064	5.2E-07	-0.466	0.058	4.8E-07	MGC94542	ENSRNOG00000017071	16	19,792,838
22813 A_64_P028088	-0.896	0.092	4.2E-08	-0.838	0.082	2.3E-08	Lsm4	ENSRNOG00000019572	16	20,511,818
15836 A_44_P295789	1.832	0.296	1.3E-05	2.057	0.265	8.4E-07	Comp	ENSRNOG000000048472	16	20,807,070
23904 A_64_P100904	-1.012	0.147	3.7E-06	-1.478	0.131	5.4E-09	LOC688966	ENSRNOG00000020427	16	21,029,134
25971 A_64_P004531	-1.129	0.069	2.1E-11	-1.338	0.061	2.8E-13	LOC688966	ENSRNOG00000020427	16	21,029,134
231 A_64_P154034	-1.260	0.125	2.6E-08	-1.129	0.112	2.5E-08	Hapln4	ENSRNOG000000049949	16	21,089,508
16603 A_44_P508691	-1.713	0.248	3.6E-06	-2.224	0.222	2.7E-08	Tm6sf2	ENSRNOG000000042237	16	21,099,878
21524 A_64_P148892	-1.410	0.157	1.3E-07	-1.586	0.141	5.2E-09	Tm6sf2	ENSRNOG000000042237	16	21,099,878
30226 A_64_P158345	-0.687	0.122	3.9E-05	-0.991	0.109	1.1E-07	Ddx60	ENSRNOG000000056947	16	31,301,880
15146 A_44_P1036068	-0.719	0.086	3.1E-07	-0.636	0.077	3.5E-07	RGD1311747	ENSRNOG000000011293	16	32,540,217
26075 A_64_P041016	-0.738	0.124	2.2E-05	-1.432	0.111	7.8E-10	Wwc2	ENSRNOG00000013248	16	47,368,768
9194 A_44_P297252	-1.033	0.145	2.4E-06	-0.989	0.129	1.0E-06	Cyp4v3	ENSRNOG000000042426	16	50,111,306
9554 A_64_P048315	-1.056	0.139	1.1E-06	-0.696	0.124	4.1E-05		ENSRNOG000000055088	16	59,517,000
1443 A_42_P798776	-0.582	0.084	3.7E-06	-0.779	0.076	1.9E-08	LOC100364957	ENSRNOG000000059911	16	70,905,993
7832 A_44_P289173	-0.897	0.127	2.7E-06	-1.377	0.114	1.8E-09	Grtp1	ENSRNOG00000019504	16	81,616,642
3375 A_44_P309325	1.169	0.135	2.1E-07	1.018	0.121	2.9E-07	Lig4	ENSRNOG00000014605	16	85,331,866
5624 A_64_P096459	-1.239	0.202	1.4E-05	-1.330	0.180	1.6E-06	Fbp2	ENSRNOG00000017637	17	389,967
18894 A_64_P022751	0.440	0.077	3.1E-05	0.418	0.069	1.6E-05	Isca1	ENSRNOG00000018343	17	5,281,727
23510 A_44_P1039249	-0.990	0.133	1.4E-06	0.847	0.119	2.4E-06	Dok3	ENSRNOG00000013564	17	9,639,330
20732 A_42_P712949	-0.751	0.137	5.0E-05	-1.430	0.122	3.2E-09		ENSRNOG00000018122	17	10,364,503
3376 A_64_P025459	0.662	0.104	9.5E-06	0.582	0.093	1.2E-05	Bicd2	ENSRNOG00000016031	17	15,718,035
18820 A_64_P109392	0.660	0.117	3.9E-05	0.580	0.105	4.7E-05	Bicd2	ENSRNOG00000016031	17	15,718,035

22979 A_64_P133632	-0.455	0.073	1.2E-05	-0.497	0.065	1.0E-06	RGD1306058	ENSRNOG00000016560	17	15,845,931
9723 A_64_P062368	-0.483	0.091	7.2E-05	-0.616	0.081	1.2E-06	Tpmt	ENSRNOG00000016468	17	18,031,228
9873 A_44_P768945	-0.512	0.092	4.2E-05	-0.496	0.082	1.7E-05	Dtnbp1	ENSRNOG00000048719	17	20,090,246
8900 A_64_P059262	1.018	0.126	5.3E-07	1.510	0.113	4.6E-10	Riok1	ENSRNOG00000014049	17	27,451,832
21031 A_64_P067678	-1.054	0.176	1.9E-05	-1.429	0.158	1.1E-07	Aldh5a1	ENSRNOG00000023538	17	42,133,076
23925 A_64_P030919	-0.953	0.146	7.3E-06	-1.252	0.131	5.3E-08		ENSRNOG00000023538	17	42,133,076
3516 A_64_P091282	-1.807	0.203	2.3E-07	-1.261	0.203	1.7E-05	Hist1h2bb	ENSRNOG00000059949	17	43,627,930
18292 A_64_P057562	-0.680	0.111	1.5E-05	-0.525	0.099	7.5E-05		ENSRNOG00000046636	17	43,673,294
9685 A_64_P020269	-1.395	0.224	1.2E-05	-1.138	0.200	3.4E-05	Hist1h2bh	ENSRNOG00000021198	17	43,689,311
10957 A_64_P162197	-1.831	0.204	1.2E-07	-1.562	0.182	2.3E-07	Hist1h2bh	ENSRNOG00000021198	17	43,689,311
16404 A_64_P068622	-0.649	0.110	2.2E-05	-0.885	0.098	1.2E-07	Hist1h2ail	ENSRNOG00000061185	17	43,776,460
4753 A_64_P150321	-0.909	0.163	4.3E-05	-1.438	0.146	3.5E-08		ENSRNOG00000049198	17	43,791,657
14569 A_64_P057801	-1.769	0.172	1.9E-08	-1.350	0.154	1.7E-07	Hist1h2bl	ENSRNOG00000047776	17	43,808,673
12452 A_64_P063035	-1.392	0.148	1.2E-07	-1.077	0.148	2.8E-06	LOC680097	ENSRNOG00000050933	17	43,821,536
24323 A_64_P063038	-0.833	0.125	5.7E-06	-0.637	0.112	3.4E-05		ENSRNOG00000050933	17	43,821,536
13074 A_64_P130572	-1.779	0.135	5.4E-10	-1.315	0.121	8.4E-09	Hist1h2bc	ENSRNOG00000059382	17	44,738,330
20825 A_64_P004639	-1.794	0.133	3.9E-10	-1.300	0.119	8.3E-09	Hist1h2bc	ENSRNOG00000059382	17	44,738,330
5615 A_44_P506017	-1.724	0.139	1.3E-09	-1.226	0.124	3.5E-08		ENSRNOG00000054296	17	44,793,927
13053 A_64_P112008	-0.600	0.108	4.3E-05	-0.577	0.096	2.0E-05	Hist1h4b	ENSRNOG00000057690	17	44,815,995
8233 A_64_P014508	-1.598	0.157	2.3E-08	-1.358	0.141	4.6E-08	Hist1h2bm	ENSRNOG00000054966	17	44,841,000
11231 A_44_P665075	1.290	0.196	6.5E-06	1.432	0.176	4.4E-07	Dhtkd1	ENSRNOG00000023587	17	76,306,585
22322 A_64_P066267	-1.347	0.186	2.0E-06	-1.724	0.166	1.7E-08	Ccdc3	ENSRNOG00000017933	17	77,093,308
1172 A_42_P509365	0.884	0.145	1.6E-05	1.438	0.130	6.9E-09	Vim	ENSRNOG00000018087	17	80,882,666
515 A_42_P499282	0.692	0.093	1.4E-06	0.642	0.083	9.0E-07	Msr2	ENSRNOG00000016873	17	86,066,833
13071 A_43_P17392	0.571	0.095	1.8E-05	0.819	0.085	4.6E-08	Arhgap21	ENSRNOG00000008659	17	87,826,421
16586 A_64_P071639	-0.864	0.121	2.4E-06	-1.094	0.108	2.5E-08	Thnsl1	ENSRNOG00000033076	17	88,095,830
20226 A_64_P104454	-0.967	0.165	2.5E-05	-1.015	0.148	3.8E-06	Impad1	ENSRNOG00000046647	17	90,218,013
4237 A_64_P071695	-0.522	0.101	9.4E-05	-0.753	0.090	3.3E-07	Mtcp1	ENSRNOG00000056435	18	410,098
24027 A_64_P056485	-0.558	0.081	3.8E-06	-0.672	0.073	8.1E-08	Mtcp1	ENSRNOG00000056435	18	410,098
7739 A_43_P16725	-0.673	0.093	2.0E-06	-0.573	0.083	3.7E-06	RGD1311805	ENSRNOG00000012597	18	3,597,240
17665 A_64_P113692	-2.118	0.107	4.8E-11	-4.714	0.131	2.4E-14	Myo7b	ENSRNOG00000015035	18	24,823,858
12527 A_44_P165870	0.685	0.133	9.8E-05	0.733	0.119	1.4E-05	Cdo1	ENSRNOG00000000158	18	40,716,686
2039 A_64_P135224	3.385	0.164	6.6E-13	3.763	0.147	2.3E-14	RGD1309362	ENSRNOG00000038960	18	55,505,993

6991 A_64_P050921	-0.978	0.112	1.9E-07	-1.167	0.100	3.4E-09	Ablim3	ENSRNOG000000019365	18	57,201,740
16799 A_64_P022357	2.303	0.184	2.6E-09	2.953	0.175	4.0E-11	Mc2r	ENSRNOG000000016681	18	64,177,729
17166 A_44_P419615	-1.480	0.147	2.7E-08	-1.193	0.132	1.1E-07	Stard6	ENSRNOG000000026324	18	68,983,545
24668 A_64_P128569	0.369	0.069	6.2E-05	0.355	0.061	2.8E-05	Rpl38	ENSRNOG000000033808	18	69,818,720
8500 A_64_P027255	-1.366	0.134	1.5E-07	-1.764	0.134	7.2E-09	Katnal2	ENSRNOG000000017788	18	73,360,373
4027 A_64_P158234	-0.585	0.080	1.8E-06	-0.387	0.072	6.1E-05		ENSRNOG000000023805	19	8,943,956
301 A_42_P491486	-1.920	0.242	6.5E-07	-1.489	0.217	3.8E-06	Plip	ENSRNOG000000016558	19	10,731,855
1045 A_42_P540711	1.899	0.264	2.2E-06	1.416	0.236	1.9E-05	Rasd2	ENSRNOG000000014761	19	14,653,198
2495 A_44_P555689	1.615	0.273	2.8E-05	2.611	0.259	4.7E-08	LOC291863	ENSRNOG000000015519	19	15,033,108
17810 A_64_P148413	1.586	0.184	2.2E-07	1.962	0.165	2.4E-09	Ces1d	ENSRNOG000000015519	19	15,033,108
6652 A_64_P141469	1.255	0.150	1.5E-06	1.678	0.184	5.5E-07	Ces1a	ENSRNOG000000039725	19	15,339,152
17218 A_64_P068930	1.888	0.139	2.0E-09	3.134	0.150	6.7E-12	Ces1a	ENSRNOG000000039725	19	15,339,152
12326 A_64_P016398	-0.748	0.132	3.6E-05	-1.102	0.118	7.3E-08		ENSRNOG000000030864	19	17,967,827
27160 A_44_P482605	-0.554	0.071	7.2E-07	-0.393	0.063	1.2E-05	Gipc1	ENSRNOG000000003864	19	24,786,628
22335 A_44_P464196	-0.726	0.089	4.8E-07	-0.639	0.080	5.8E-07	Cd97	ENSRNOG000000004489	19	24,875,137
24628 A_44_P539047	-0.628	0.096	6.6E-06	-0.885	0.086	1.8E-08	Tmem208	ENSRNOG000000015974	19	37,282,018
4796 A_64_P094515	0.641	0.103	1.3E-05	-0.999	0.092	9.4E-09		ENSRNOG000000053623	19	38,643,108
7237 A_64_P052690	-0.527	0.078	4.4E-06	-0.456	0.069	6.5E-06	Pdf	ENSRNOG000000022303	19	39,246,545
21761 A_64_P127678	-0.581	0.107	5.5E-05	-1.250	0.095	6.0E-10	Dhodh	ENSRNOG000000015063	19	42,066,351
26931 A_64_P335246	0.523	0.090	2.6E-05	0.412	0.080	9.8E-05	Fuk	ENSRNOG000000059453	19	43,338,171
18704 A_43_P18171	0.572	0.106	6.1E-05	1.171	0.095	1.5E-09	Ldhd	ENSRNOG000000019036	19	43,848,937
364 A_64_P111604	-0.636	0.099	8.7E-06	-0.756	0.089	2.5E-07	Gabarapl2	ENSRNOG000000019425	19	44,164,935
12878 A_64_P138281	-1.310	0.134	3.9E-08	-1.042	0.120	1.9E-07	Cenpn	ENSRNOG000000011296	19	49,340,184
21514 A_43_P10505	1.691	0.249	4.3E-06	1.498	0.222	4.9E-06	Jph3	ENSRNOG000000018784	19	54,553,419
12200 A_64_P035694	1.262	0.155	4.5E-07	1.099	0.138	6.3E-07	LOC678766	ENSRNOG000000057601	19	56,443,632
13304 A_64_P067878	-1.194	0.227	8.0E-05	-1.452	0.203	2.4E-06	Trim67	ENSRNOG000000019024	19	57,556,694
21048 A_64_P084234	-0.741	0.135	5.2E-05	-0.950	0.121	7.4E-07	Egln1	ENSRNOG000000019773	19	57,699,113
4436 A_42_P627572	-1.452	0.134	9.3E-09	-1.104	0.120	8.8E-08	Mdc1	ENSRNOG000000032813	20	3,405,285
13335 A_43_P14382	0.727	0.113	8.2E-06	0.647	0.101	8.7E-06		ENSRNOG000000054031	20	4,873,982
10076 A_64_P056247	-1.369	0.231	2.1E-05	-1.970	0.206	5.4E-08	Msh5	ENSRNOG000000000857	20	5,037,088
21960 A_64_P139202	0.609	0.099	1.4E-05	0.903	0.089	2.1E-08	RT1-A1	ENSRNOG000000038999	20	5,414,448
20712 A_64_P094812	-0.516	0.097	7.1E-05	-0.659	0.087	1.1E-06	RGD1306917	ENSRNOG000000025909	20	5,723,737
10233 A_44_P258008	-1.828	0.163	5.8E-09	-1.028	0.146	2.8E-06	Fgd2	ENSRNOG000000000528	20	6,973,398

12621 A_44_P532249	1.435	0.254	3.7E-05	2.158	0.227	5.9E-08 Fkbp5	ENSRNOG000000022523	20	8,019,020
3691 A_42_P781999	-1.571	0.224	3.0E-06	-1.234	0.201	1.4E-05 Agpat3	ENSRNOG000000001205	20	11,114,164
8306 A_64_P008361	0.903	0.120	1.2E-06	1.209	0.107	5.1E-09 Pwp2	ENSRNOG000000001210	20	11,228,844
25935 A_64_P146698	1.112	0.127	1.8E-07	1.249	0.114	7.8E-09 Pwp2	ENSRNOG000000001210	20	11,228,844
9503 A_44_P447650	0.815	0.154	7.3E-05	0.789	0.137	3.1E-05 Adarb1	ENSRNOG000000001227	20	11,972,381
26210 A_42_P701582	1.238	0.095	6.4E-10	1.935	0.085	1.4E-13 Gstt1	ENSRNOG000000049771	20	13,799,102
14331 A_64_P152447	2.057	0.159	2.2E-08	2.960	0.180	1.5E-09 Gstt3	ENSRNOG000000001242	20	13,817,795
19033 A_44_P1015203	2.262	0.134	1.4E-11	2.584	0.120	3.4E-13 Gstt3	ENSRNOG000000001242	20	13,817,795
4293 A_64_P159078	1.959	0.269	1.9E-06	1.802	0.241	1.3E-06 RGD1306739	ENSRNOG000000000634	20	21,316,826
16577 A_64_P055843	-0.618	0.081	1.1E-06	-0.475	0.073	7.2E-06 Ascc1	ENSRNOG000000056647	20	29,558,689
8781 A_44_P152177	3.507	0.171	2.5E-12	4.400	0.163	4.3E-14 Spock2	ENSRNOG000000061544	20	29,655,226
20647 A_64_P039414	-0.687	0.105	7.1E-06	-0.858	0.094	1.0E-07 Pcbd1	ENSRNOG000000000566	20	30,690,810
14899 A_44_P1042436	-0.539	0.094	3.3E-05	-0.656	0.084	8.3E-07 Lace1	ENSRNOG000000043033	20	47,044,786
6389 A_64_P117488	-0.705	0.109	7.9E-06	-0.513	0.097	7.8E-05 Sobpl	ENSRNOG000000000316	20	47,910,375
20987 A_64_P141038	1.441	0.134	2.0E-08	0.947	0.134	3.9E-06 Bex4	ENSRNOG000000060103	568122	30,542
141 A_64_P114320	-0.916	0.117	7.3E-07	-0.547	0.104	8.3E-05	ENSRNOG000000031780	MT	1
518 A_64_P151924	-0.968	0.110	1.6E-07	-0.517	0.098	7.8E-05	ENSRNOG000000031780	MT	1
1164 A_44_P173370	-0.911	0.096	5.5E-08	-0.445	0.085	8.8E-05	ENSRNOG000000031780	MT	1
1339 A_64_P042093	1.029	0.180	3.2E-05	1.425	0.161	1.5E-07	ENSRNOG000000031780	MT	1
1784 A_64_P108963	-0.720	0.087	3.5E-07	-0.433	0.078	4.2E-05	ENSRNOG000000031780	MT	1
1962 A_64_P011664	-1.163	0.111	1.4E-08	-0.681	0.099	3.8E-06	ENSRNOG000000031780	MT	1
3749 A_64_P046398	-1.288	0.124	1.6E-08	-0.716	0.111	7.9E-06	ENSRNOG000000031780	MT	1
3901 A_64_P067650	-0.713	0.105	4.6E-06	-0.708	0.094	1.3E-06	ENSRNOG000000031780	MT	1
3942 A_64_P023336	-0.638	0.107	2.0E-05	-0.997	0.095	1.6E-08	ENSRNOG000000031780	MT	1
4044 A_64_P072545	-1.242	0.184	4.7E-06	-0.930	0.164	3.6E-05	ENSRNOG000000031780	MT	1
4493 A_64_P147403	1.797	0.188	5.4E-08	2.134	0.168	9.7E-10	ENSRNOG000000031780	MT	1
4577 A_64_P016393	-0.692	0.094	1.6E-06	-1.154	0.084	2.9E-10	ENSRNOG000000031780	MT	1
4711 A_44_P414984	-0.931	0.162	3.0E-05	-1.247	0.145	2.2E-07	ENSRNOG000000031780	MT	1
5065 A_64_P146350	-0.861	0.161	6.5E-05	-1.453	0.144	2.4E-08	ENSRNOG000000031780	MT	1
5091 A_44_P342334	-0.551	0.070	7.4E-07	-0.391	0.063	1.3E-05	ENSRNOG000000031780	MT	1
5100 A_64_P128335	-0.668	0.106	1.0E-05	-0.495	0.094	8.2E-05	ENSRNOG000000031780	MT	1
5223 A_64_P049606	-1.160	0.155	1.3E-06	-0.719	0.138	8.9E-05	ENSRNOG000000031780	MT	1
5273 A_64_P005669	-1.081	0.099	8.7E-09	-0.662	0.089	1.4E-06	ENSRNOG000000031780	MT	1

5295 A_64_P159095	-0.971	0.107	1.1E-07	-0.528	0.096	4.9E-05	ENSRNOG000000031780	MT	1
5482 A_64_P326359	0.840	0.088	5.5E-08	1.272	0.079	2.7E-11	ENSRNOG000000031780	MT	1
5765 A_64_P069541	-1.266	0.112	4.9E-09	-0.695	0.100	3.3E-06	ENSRNOG000000031780	MT	1
5941 A_64_P136655	-0.573	0.106	6.0E-05	-0.679	0.095	2.4E-06	ENSRNOG000000031780	MT	1
5979 A_64_P127664	-0.625	0.091	3.7E-06	-0.690	0.081	2.6E-07	ENSRNOG000000031780	MT	1
6008 A_64_P013827	-1.043	0.104	2.8E-08	-0.593	0.093	9.5E-06	ENSRNOG000000031780	MT	1
6077 A_44_P854356	1.401	0.170	6.1E-07	1.049	0.162	1.0E-05	ENSRNOG000000031780	MT	1
6153 A_64_P068832	-0.877	0.103	2.6E-07	-0.522	0.092	3.6E-05	ENSRNOG000000031780	MT	1
6998 A_64_P115122	0.652	0.094	3.3E-06	0.447	0.084	6.8E-05	ENSRNOG000000031780	MT	1
7558 A_64_P119802	-1.208	0.156	8.6E-07	-0.749	0.140	6.3E-05	ENSRNOG000000031780	MT	1
7605 A_64_P048712	-1.558	0.204	3.8E-06	-1.759	0.166	9.9E-08	ENSRNOG000000031780	MT	1
7864 A_64_P060396	-1.342	0.114	2.8E-09	-0.819	0.102	5.3E-07	ENSRNOG000000031780	MT	1
8064 A_64_P004327	-1.159	0.165	3.0E-06	-0.814	0.148	4.8E-05	ENSRNOG000000031780	MT	1
8089 A_64_P030000	-1.010	0.104	4.3E-08	-0.614	0.093	6.2E-06	ENSRNOG000000031780	MT	1
8258 A_64_P028824	-0.997	0.156	9.2E-06	-0.809	0.140	2.8E-05	ENSRNOG000000031780	MT	1
8379 A_64_P005704	-1.029	0.108	5.6E-08	-0.648	0.097	5.2E-06	ENSRNOG000000031780	MT	1
8814 A_64_P134032	-1.611	0.174	8.1E-08	-0.909	0.155	2.5E-05	ENSRNOG000000031780	MT	1
9679 A_64_P061971	-1.082	0.106	2.2E-08	-0.614	0.095	7.9E-06	ENSRNOG000000031780	MT	1
9737 A_64_P152543	-0.928	0.110	2.8E-07	-0.506	0.098	9.7E-05	ENSRNOG000000031780	MT	1
9965 A_64_P022180	-1.046	0.106	3.2E-08	-0.701	0.094	1.5E-06	ENSRNOG000000031780	MT	1
10100 A_64_P138684	-0.842	0.098	2.4E-07	-0.628	0.088	2.4E-06	ENSRNOG000000031780	MT	1
10707 A_44_P295548	-0.968	0.096	2.6E-08	-0.594	0.086	3.6E-06	ENSRNOG000000031780	MT	1
10749 A_44_P410318	-0.773	0.113	4.0E-06	0.616	0.101	1.6E-05	ENSRNOG000000031780	MT	1
10987 A_64_P147669	-1.182	0.150	7.1E-07	-0.694	0.134	9.7E-05	ENSRNOG000000031780	MT	1
11073 A_64_P053888	-1.372	0.141	4.1E-08	-0.759	0.126	1.8E-05	ENSRNOG000000031780	MT	1
11217 A_64_P161448	-1.476	0.120	1.6E-09	-0.850	0.108	6.8E-07	ENSRNOG000000031780	MT	1
11571 A_64_P070896	-1.044	0.092	4.7E-09	-0.570	0.082	3.4E-06	ENSRNOG000000031780	MT	1
11646 A_64_P049816	-0.952	0.091	1.5E-08	-0.458	0.081	3.7E-05	ENSRNOG000000031780	MT	1
11648 A_64_P003045	-1.011	0.097	1.5E-08	-0.561	0.086	7.6E-06	ENSRNOG000000031780	MT	1
12489 A_64_P121623	-0.720	0.104	3.6E-06	-0.564	0.093	1.7E-05	ENSRNOG000000031780	MT	1
13083 A_64_P077603	-0.700	0.128	5.2E-05	-1.061	0.115	8.2E-08	ENSRNOG000000031780	MT	1
13321 A_44_P335415	-1.235	0.106	3.3E-09	-0.731	0.095	9.1E-07	ENSRNOG000000031780	MT	1
13469 A_64_P232363	-0.877	0.108	4.8E-07	-0.497	0.097	1.0E-04	ENSRNOG000000031780	MT	1

13844 A_64_P054907	-0.386	0.067	2.8E-05	-0.570	0.060	5.3E-08	ENSRNOG000000031780	MT	1
13857 A_64_P155584	-1.049	0.114	9.2E-08	-0.540	0.102	7.5E-05	ENSRNOG000000031780	MT	1
14000 A_64_P069824	-1.155	0.102	4.6E-09	-0.693	0.091	1.0E-06	ENSRNOG000000031780	MT	1
14216 A_64_P079438	-1.298	0.147	1.5E-07	-0.789	0.131	1.8E-05	ENSRNOG000000031780	MT	1
14499 A_64_P074731	-0.620	0.103	1.8E-05	-0.653	0.092	2.5E-06	ENSRNOG000000031780	MT	1
15006 A_64_P083725	-0.635	0.090	2.8E-06	-0.485	0.081	1.8E-05	ENSRNOG000000031780	MT	1
15317 A_64_P086459	-0.819	0.125	6.9E-06	-0.631	0.112	3.8E-05	ENSRNOG000000031780	MT	1
15462 A_64_P057452	-0.852	0.100	2.5E-07	-0.492	0.089	4.9E-05	ENSRNOG000000031780	MT	1
15472 A_64_P103681	-0.920	0.092	3.0E-08	-0.474	0.083	3.1E-05	ENSRNOG000000031780	MT	1
15612 A_64_P010052	-1.732	0.218	2.4E-06	-1.523	0.267	7.3E-05	ENSRNOG000000031780	MT	1
15639 A_44_P468694	-0.979	0.114	2.2E-07	-0.561	0.102	4.7E-05	ENSRNOG000000031780	MT	1
15646 A_64_P258712	-1.070	0.108	3.1E-08	-0.504	0.096	8.3E-05	ENSRNOG000000031780	MT	1
15692 A_44_P147356	-0.987	0.107	8.1E-08	-0.554	0.095	2.7E-05	ENSRNOG000000031780	MT	1
16690 A_64_P005724	-1.057	0.104	2.4E-08	-0.625	0.093	5.2E-06	ENSRNOG000000031780	MT	1
16734 A_64_P046785	-0.777	0.098	6.8E-07	-0.574	0.088	7.2E-06	ENSRNOG000000031780	MT	1
16966 A_44_P138098	-0.640	0.081	7.2E-07	-0.769	0.073	1.3E-08	ENSRNOG000000031780	MT	1
17820 A_64_P106351	-0.940	0.098	4.9E-08	-0.632	0.087	2.1E-06	ENSRNOG000000031780	MT	1
18412 A_64_P059846	-0.618	0.096	8.6E-06	-0.520	0.086	1.8E-05	ENSRNOG000000031780	MT	1
18542 A_64_P134283	-1.021	0.133	9.5E-07	-0.679	0.119	3.2E-05	ENSRNOG000000031780	MT	1
18662 A_64_P105019	-0.915	0.084	8.2E-09	-0.537	0.075	2.3E-06	ENSRNOG000000031780	MT	1
19007 A_64_P115916	-0.668	0.093	2.4E-06	-0.735	0.084	1.7E-07	ENSRNOG000000031780	MT	1
19023 A_64_P066639	-1.189	0.124	5.3E-08	-0.742	0.111	5.5E-06	ENSRNOG000000031780	MT	1
19449 A_64_P098784	-0.805	0.133	2.3E-05	-0.870	0.133	9.9E-06	ENSRNOG000000031780	MT	1
19614 A_64_P005744	-0.976	0.099	3.4E-08	-0.566	0.088	8.9E-06	ENSRNOG000000031780	MT	1
19768 A_64_P064259	-1.041	0.097	9.9E-09	-0.646	0.086	1.4E-06	ENSRNOG000000031780	MT	1
20224 A_64_P066848	-1.022	0.097	1.4E-08	-0.640	0.087	1.6E-06	ENSRNOG000000031780	MT	1
20460 A_64_P029376	-1.219	0.161	1.1E-06	-0.767	0.144	6.8E-05	ENSRNOG000000031780	MT	1
20800 A_44_P545895	-1.063	0.113	6.8E-08	1.043	0.101	1.9E-08	ENSRNOG000000031780	MT	1
21135 A_64_P118308	-1.654	0.131	1.0E-09	-0.631	0.117	6.1E-05	ENSRNOG000000031780	MT	1
21251 A_64_P154655	-1.374	0.106	7.4E-10	-0.732	0.095	9.4E-07	ENSRNOG000000031780	MT	1
21285 A_64_P083179	-1.539	0.183	2.9E-07	-0.899	0.163	4.9E-05	ENSRNOG000000031780	MT	1
21806 A_64_P094555	-0.983	0.135	1.8E-06	-1.179	0.120	3.8E-08	ENSRNOG000000031780	MT	1
21864 A_44_P114892	-0.956	0.104	8.6E-08	-0.549	0.093	2.2E-05	ENSRNOG000000031780	MT	1

21883 A_64_P123207	-0.898	0.089	2.5E-08	-0.454	0.079	3.3E-05	ENSRNOG000000031780	MT	1
22460 A_44_P105441	-0.943	0.098	5.1E-08	-0.496	0.088	3.8E-05	ENSRNOG000000031780	MT	1
22492 A_64_P086469	-1.184	0.114	1.7E-08	-0.681	0.102	5.3E-06	ENSRNOG000000031780	MT	1
23014 A_64_P152542	-1.027	0.096	1.1E-08	-0.508	0.086	2.1E-05	ENSRNOG000000031780	MT	1
23075 A_64_P076495	-0.844	0.104	4.9E-07	-0.502	0.093	6.1E-05	ENSRNOG000000031780	MT	1
23570 A_64_P112534	-0.792	0.138	3.2E-05	-1.270	0.124	2.0E-08	ENSRNOG000000031780	MT	1
23622 A_64_P132427	-1.014	0.096	1.3E-08	-0.640	0.086	1.4E-06	ENSRNOG000000031780	MT	1
23877 A_64_P086353	-1.232	0.112	7.5E-09	-0.689	0.100	3.8E-06	ENSRNOG000000031780	MT	1
24034 A_64_P044613	-0.722	0.096	1.2E-06	-0.506	0.086	2.2E-05	ENSRNOG000000031780	MT	1
24098 A_64_P042811	-2.145	0.201	1.2E-08	-2.160	0.180	2.1E-09	ENSRNOG000000031780	MT	1
24790 A_64_P104314	-1.090	0.123	1.5E-07	-0.615	0.110	4.1E-05	ENSRNOG000000031780	MT	1
25275 A_64_P055502	-1.452	0.207	2.9E-06	-1.001	0.185	5.8E-05	ENSRNOG000000031780	MT	1
25367 A_64_P052280	0.459	0.089	9.9E-05	0.551	0.080	3.6E-06	ENSRNOG000000031780	MT	1
25459 A_64_P146637	-1.103	0.163	4.6E-06	-2.882	0.146	1.2E-12	ENSRNOG000000031780	MT	1
25465 A_64_P154826	0.702	0.110	8.9E-06	0.843	0.098	2.2E-07	ENSRNOG000000031780	MT	1
26291 A_64_P142460	-0.691	0.112	1.3E-05	-0.993	0.100	3.1E-08	ENSRNOG000000031780	MT	1
26385 A_64_P081630	-0.682	0.089	1.0E-06	-0.734	0.080	9.0E-08	ENSRNOG000000031780	MT	1
26390 A_64_P034947	-0.817	0.096	2.4E-07	-0.453	0.085	7.3E-05	ENSRNOG000000031780	MT	1
26402 A_64_P162272	-1.046	0.130	5.1E-07	-1.867	0.116	2.8E-11	ENSRNOG000000031780	MT	1
26659 A_64_P051019	-1.086	0.099	7.8E-09	-0.711	0.089	5.5E-07	ENSRNOG000000031780	MT	1
26716 A_64_P070288	-1.071	0.107	2.8E-08	-0.685	0.096	2.3E-06	ENSRNOG000000031780	MT	1
26724 A_64_P128336	-0.939	0.092	2.1E-08	-0.557	0.082	4.5E-06	ENSRNOG000000031780	MT	1
26751 A_64_P119395	-0.972	0.102	5.8E-08	-0.482	0.092	7.7E-05	ENSRNOG000000031780	MT	1
27129 A_64_P162408	-0.717	0.095	1.2E-06	-0.891	0.085	1.5E-08	ENSRNOG000000031780	MT	1
27262 A_64_P143003	-0.960	0.185	9.2E-05	-1.292	0.166	7.9E-07	ENSRNOG000000031780	MT	1
27283 A_64_P014787	-0.895	0.113	6.7E-07	-0.528	0.101	8.6E-05	ENSRNOG000000031780	MT	1
27679 A_64_P143154	0.526	0.099	7.1E-05	0.981	0.089	6.8E-09	ENSRNOG000000031780	MT	1
27740 A_64_P024476	-0.813	0.121	5.0E-06	-0.679	0.108	1.1E-05	ENSRNOG000000031780	MT	1
28018 A_64_P101600	-5.911	0.243	3.5E-10	-6.418	0.188	1.3E-11	ENSRNOG000000031780	MT	1
28168 A_64_P001399	-0.912	0.084	9.4E-09	-0.439	0.075	2.7E-05	ENSRNOG000000031780	MT	1
28308 A_64_P028365	0.359	0.064	4.3E-05	0.408	0.058	2.7E-06	ENSRNOG000000031780	MT	1
28481 A_44_P392004	2.345	0.212	1.3E-08	2.771	0.201	6.8E-10	ENSRNOG000000031780	MT	1
29033 A_64_P150064	-0.813	0.090	1.1E-07	-0.579	0.081	2.2E-06	ENSRNOG000000031780	MT	1

29125 A_64_P084699	0.366	0.068	5.9E-05	0.344	0.061	3.5E-05	ENSRNOG000000031780	MT	1
29480 A_64_P134485	-1.022	0.170	1.9E-05	-1.269	0.152	3.3E-07	ENSRNOG000000031780	MT	1
29528 A_64_P096684	-0.871	0.090	4.5E-08	-0.436	0.080	5.8E-05	ENSRNOG000000031780	MT	1
29633 A_64_P005745	-0.915	0.094	4.0E-08	-0.469	0.084	4.1E-05	ENSRNOG000000031780	MT	1
29738 A_44_P898566	-1.095	0.167	6.9E-06	-1.393	0.150	7.7E-08	ENSRNOG000000031780	MT	1
29810 A_64_P034311	-0.852	0.094	1.1E-07	-0.445	0.084	7.4E-05	ENSRNOG000000031780	MT	1
21771 A_44_P808769	-1.209	0.142	2.5E-07	-1.303	0.127	2.0E-08 Clcn4-2	ENSRNOG000000003533	X	25,016,401
5870 A_64_P018964	-1.516	0.220	5.4E-06	-1.298	0.220	3.0E-05 Hmga1	ENSRNOG000000026969	X	33,349,481
3164 A_44_P389448	-0.896	0.113	6.1E-07	-0.893	0.101	1.5E-07	ENSRNOG000000003860	X	43,831,892
4242 A_44_P356605	0.503	0.088	3.1E-05	0.800	0.078	2.1E-08 Las1l	ENSRNOG000000021748	X	65,083,911
29031 A_64_P067148	-1.082	0.098	6.7E-09	-0.647	0.087	1.5E-06	ENSRNOG0000000051290	X	70,234,622
29973 A_64_P098404	-0.493	0.094	8.3E-05	-0.581	0.084	3.7E-06	ENSRNOG000000018301	X	74,372,283
1020 A_42_P764985	1.026	0.156	6.4E-06	1.138	0.139	4.4E-07 Nap1l3	ENSRNOG000000029087	X	95,062,132
1864 A_44_P534557	1.385	0.232	2.0E-05	1.245	0.207	1.9E-05 Gprasp2	ENSRNOG000000037658	X	106,360,393
17032 A_42_P822638	1.124	0.125	1.2E-07	0.637	0.111	3.2E-05 Tsc22d3	ENSRNOG000000056135	X	111,887,906
15663 A_64_P048852	-1.668	0.118	1.9E-10	-1.512	0.105	1.5E-10	ENSRNOG000000006459	X	120,313,696
16887 A_64_P065957	-0.523	0.088	2.2E-05	-0.583	0.079	1.6E-06 Ube2a	ENSRNOG000000039985	X	123,486,989
25743 A_64_P076705	0.497	0.088	3.6E-05	0.462	0.079	2.4E-05 Gdi1	ENSRNOG000000056870	X	156,407,404
2375 A_43_P16542	-0.478	0.091	7.8E-05	-0.667	0.081	4.0E-07 no transcript			
3613 A_64_P154736	-0.566	0.087	7.4E-06	-0.662	0.078	2.5E-07 LOC690885			
6725 A_64_P063194	-0.779	0.089	1.8E-07	-1.105	0.080	2.7E-10 RGD1311186			
7034 A_44_P534028	1.150	0.176	7.1E-06	1.473	0.158	7.2E-08 Stau2			
7737 A_64_P123798	-0.523	0.078	5.0E-06	-0.389	0.070	4.0E-05 LOC681193			
7826 A_64_P024117	-2.112	0.208	1.5E-06	-2.002	0.269	2.3E-05 LOC497952			
8329 A_64_P124041	-0.847	0.120	4.0E-06	-1.056	0.120	2.7E-07 Ddx60			
9001 A_42_P483302	0.875	0.119	1.6E-06	1.044	0.106	3.7E-08 Znf23			
10788 A_43_P18376	-2.525	0.213	2.6E-09	-3.772	0.190	1.2E-12 Tex49 (RGD1305928)_partial			
11195 A_64_P084698	0.458	0.072	9.1E-06	0.394	0.064	1.4E-05 LOC680353			
15156 A_64_P133051	1.389	0.195	2.5E-06	0.950	0.174	5.5E-05 RGD1566102			
15289 A_44_P393282	-1.498	0.162	8.4E-08	-1.287	0.145	1.4E-07 44083			
15659 A_43_P18931	0.813	0.102	6.0E-07	0.852	0.091	7.3E-08 Tp53i3_RGD130	ENSRNOG000000005177	13	75,101,759
17474 A_44_P201084	-0.949	0.154	1.3E-05	-0.932	0.137	4.5E-06 Fgfr1l			
19713 A_44_P160189	-0.601	0.100	1.8E-05	-0.459	0.089	9.8E-05 Smim20_RGD15	N/A	14	60,057,493

20392 A_64_P081063	2.293	0.216	1.9E-07	2.765	0.341	3.4E-06 LOC363746			
20627 A_64_P091328	-1.011	0.128	6.9E-07	-1.124	0.115	3.8E-08 Rrm1-ps1			
20926 A_64_P106426	0.452	0.082	5.0E-05	0.400	0.074	5.5E-05 LOC688632			
21953 A_64_P005659	-1.217	0.212	3.1E-05	-1.070	0.190	3.8E-05 Gapdh-ps1			
23957 A_64_P139208	-0.551	0.105	8.4E-05	-0.500	0.094	7.2E-05 RT1-N1			
24017 A_64_P060938	-1.580	0.196	5.1E-07	-1.945	0.175	6.5E-09 LOC686120			
24789 A_44_P324482	0.719	0.133	5.7E-05	0.887	0.119	1.3E-06 Smyd3			
25709 A_64_P011719	-0.951	0.106	1.3E-07	-0.768	0.095	5.0E-07 Chmp1b	N/A	18	62,923,620
25822 A_44_P314087	-1.292	0.194	5.5E-06	-1.453	0.173	3.1E-07 LOC681186			

Genes are regarded as significant for “shared” differential expression when they show $P < 1 \times 10^{-4}$ reproducibly in two types of comparison, ie, SHR/lzm versus WKY/lzm and SHRSP/lzm versus WKY/lzm, with a concordant direction of differential expression.

Table S3C. A list of significant transcripts for shared differential expression in the whole kidney.

no	ProbeName	SHR/lzm (vs WKY/lzm)			SHRSP/lzm (vs WKY/lzm)			GeneName	Ensembl_rat	Chr	Transcription_ start_site (Rnor_6.0)
		Fold change (log2-scale)	SE (log2-scale)	P-value	Fold change (log2-scale)	SE (log2-scale)	P-value				
2382	A_64_P063358	1.040	0.166	2.3E-06	1.586	0.235	7.5E-07	Samd5	ENSRNOG000000023549	1	3,763,392
8464	A_64_P129293	1.425	0.178	4.4E-08	1.848	0.251	1.9E-07	RGD1306565	ENSRNOG000000031700	1	15,412,603
11055	A_44_P128306	0.448	0.065	4.7E-07	0.578	0.091	1.9E-06	Aldh8a1	ENSRNOG000000014907	1	16,910,069
21505	A_64_P117799	0.753	0.145	2.9E-05	-1.092	0.205	2.2E-05	Slc9a3	ENSRNOG000000015159	1	31,777,070
7941	A_42_P689905	1.273	0.130	1.3E-09	1.626	0.184	8.2E-09	Apoc2	ENSRNOG000000018402	1	80,594,136
15577	A_44_P370267	-0.377	0.069	1.4E-05	0.560	0.097	7.4E-06	Ethe1	ENSRNOG000000019982	1	81,456,984
13915	A_64_P080941	-1.273	0.095	5.7E-12	-1.456	0.130	1.6E-10	LOC102556967	ENSRNOG000000033729	1	99,505,677
22453	A_44_P163243	-1.604	0.153	3.6E-10	-2.088	0.217	1.7E-09	Klks3	ENSRNOG000000032857	1	100,059,967
19183	A_64_P133177	-0.914	0.092	9.1E-10	-1.135	0.130	9.8E-09	Sema4b	ENSRNOG000000025167	1	141,986,145
26335	A_64_P157285	0.978	0.134	2.0E-07	1.228	0.189	1.3E-06	RGD1560277 (in	ENSRNOG000000025003	1	142,027,250
25376	A_64_P109232	-2.130	0.082	2.3E-17	-2.703	0.120	4.5E-16	Nmb	ENSRNOG000000011011	1	142,724,511
14093	A_42_P788740	0.537	0.105	3.7E-05	0.986	0.149	9.7E-07	Folr2	ENSRNOG000000019890	1	166,919,302
20060	A_44_P384389	0.540	0.081	9.1E-07	-1.289	0.115	9.0E-11		ENSRNOG000000033924	1	178,367,828
21647	A_64_P150981	0.510	0.102	4.5E-05	-0.918	0.144	1.7E-06		ENSRNOG000000025122	1	183,630,695
29269	A_64_P151353	1.764	0.086	3.5E-16	2.146	0.122	8.7E-15	Acsm5	ENSRNOG000000031211	1	189,241,593
5216	A_43_P15937	0.425	0.077	1.3E-05	0.700	0.109	1.5E-06	Acsm3	ENSRNOG000000032246	1	189,514,553
15247	A_44_P1005462	1.210	0.144	1.9E-08	1.329	0.203	1.2E-06	Mylpf	ENSRNOG000000017645	1	198,655,742
4048	A_44_P452222	2.154	0.133	2.3E-10	1.491	0.211	6.0E-06	Itgal	ENSRNOG000000017980	1	198,744,050
14224	A_64_P045578	1.120	0.153	1.9E-07	1.128	0.216	2.8E-05	Rnf40	ENSRNOG000000018840	1	199,037,544
4254	A_42_P784614	0.545	0.083	1.0E-06	0.780	0.117	8.7E-07	Htra1	ENSRNOG000000020533	1	201,499,028
10007	A_44_P196717	3.476	0.212	1.9E-10	-2.705	0.501	9.9E-05	Stk32c	ENSRNOG000000006962	1	211,520,699
13890	A_64_P031501	-0.915	0.102	5.7E-09	-0.685	0.144	8.5E-05	Slc22a9	ENSRNOG000000056396	1	222,975,509
11870	A_64_P073303	-0.691	0.132	2.8E-05	-1.962	0.187	3.5E-10	Plac1l (OOSP2)	ENSRNOG000000036624	1	228,014,924
13	A_42_P751152	-0.382	0.050	1.1E-07	-0.380	0.071	2.1E-05	Ndufb8	ENSRNOG000000014078	1	264,303,762
26828	A_64_P043941	-1.461	0.150	1.4E-09	-1.512	0.212	3.2E-07	Sorcs1	ENSRNOG000000011313	1	270,472,866
3220	A_64_P066271	-0.754	0.083	5.1E-09	-0.772	0.118	1.1E-06	Mxi1	ENSRNOG000000034078	1	274,030,978
17839	A_64_P115991	-0.895	0.098	4.4E-09	-0.706	0.139	3.8E-05	Mxi1	ENSRNOG000000034078	1	274,030,978
22136	A_64_P066276	-1.000	0.101	1.1E-09	-0.724	0.143	4.3E-05	Mxi1	ENSRNOG000000034078	1	274,030,978
18506	A_64_P087184	0.704	0.113	2.3E-06	0.760	0.159	8.4E-05	Vwa2	ENSRNOG000000025581	1	277,689,729
22904	A_44_P535284	-0.634	0.098	1.3E-06	-1.027	0.138	1.5E-07	Bhmt	ENSRNOG000000011200	2	23,256,158

8784 A_44_P899264	-0.722	0.104	4.9E-07	-0.772	0.147	2.6E-05	Lhfp12	ENSRNOG000000011032	2	23,770,721
8031 A_64_P163219	-2.065	0.119	3.3E-14	-1.535	0.163	3.8E-09		ENSRNOG000000018615	2	30,780,121
18451 A_43_P12257	1.641	0.098	2.9E-14	1.742	0.139	1.1E-11	Esm1	ENSRNOG000000010797	2	45,104,305
912 A_42_P603536	0.420	0.087	7.2E-05	0.661	0.123	1.9E-05	Arl15	ENSRNOG000000011105	2	45,668,969
24926 A_64_P154605	-0.705	0.096	1.7E-07	-0.665	0.135	5.8E-05	Fst	ENSRNOG000000011631	2	46,544,457
5239 A_42_P463754	0.628	0.063	9.2E-10	0.529	0.089	5.1E-06	Itga1	ENSRNOG000000053550	2	47,281,421
1843 A_42_P469751	-0.901	0.068	3.5E-12	-1.026	0.096	2.5E-10	C7	ENSRNOG000000061379	2	54,777,729
11752 A_64_P087930	-1.108	0.106	3.4E-10	-1.046	0.149	4.1E-07	C7	ENSRNOG000000061379	2	54,777,729
5037 A_44_P187181	-0.849	0.088	1.6E-09	-0.841	0.124	7.1E-07	Prlr	ENSRNOG000000057557	2	60,131,776
27013 A_64_P111315	-0.781	0.133	6.0E-06	-1.028	0.189	1.6E-05	Ropn1l	ENSRNOG000000042781	2	84,531,192
15982 A_42_P778330	-1.703	0.153	1.9E-10	-1.890	0.209	7.6E-09	Sox2	ENSRNOG000000012199	2	121,165,137
30009 A_64_P144879	0.502	0.076	9.2E-07	0.779	0.107	2.2E-07	Rarres1	ENSRNOG000000037853	2	164,684,985
16967 A_44_P773166	-0.796	0.122	1.2E-06	-1.013	0.172	5.6E-06	Tmem144	ENSRNOG000000010081	2	178,612,470
11879 A_64_P020616	-0.480	0.081	5.0E-06	-0.778	0.115	6.6E-07	Clk2	ENSRNOG000000020500	2	188,476,820
21728 A_64_P009738	1.012	0.125	2.2E-06	1.704	0.204	1.6E-06	RGD1559714	ENSRNOG000000061251	2	195,279,218
10680 A_64_P140977	-0.900	0.169	2.1E-05	-1.452	0.238	3.4E-06	Prune	ENSRNOG000000021120	2	196,456,481
27712 A_64_P041307	-0.793	0.061	5.7E-12	-0.886	0.087	5.7E-10	Tars2	ENSRNOG000000057194	2	197,878,142
7908 A_64_P126230	-0.527	0.091	6.5E-06	-0.914	0.128	3.0E-07	Car14	ENSRNOG000000023162	2	198,016,898
4450 A_42_P649672	1.501	0.142	2.9E-10	2.169	0.201	1.9E-10	Sv2a	ENSRNOG000000021182	2	198,321,142
4369 A_64_P069023	0.412	0.068	1.4E-05	-0.754	0.109	2.8E-06	Cd160	ENSRNOG000000000097	2	198,942,732
4856 A_64_P139078	3.583	0.163	6.6E-16	3.520	0.282	3.9E-11	Hsd3b6	ENSRNOG000000019441	2	202,350,929
24143 A_44_P506299	1.322	0.185	2.9E-07	1.833	0.261	4.0E-07	RGD1562344	ENSRNOG000000037149	2	206,314,213
8954 A_64_P052833	0.434	0.074	5.5E-06	-0.751	0.104	2.6E-07		ENSRNOG000000053044	2	208,225,888
18048 A_44_P398167	-0.646	0.069	2.9E-09	-0.513	0.098	2.6E-05	Prdx1	ENSRNOG000000017695	2	208,738,132
18309 A_64_P071615	0.474	0.076	2.2E-06	-0.796	0.107	1.5E-07		ENSRNOG000000030491	2	226,825,635
1880 A_42_P770336	1.222	0.131	2.9E-09	1.380	0.185	1.4E-07	Mcoln2	ENSRNOG000000015089	2	252,018,597
6820 A_64_P116854	0.317	0.058	1.4E-05	-0.385	0.081	9.3E-05		ENSRNOG000000036451	3	1,260,569
28745 A_43_P15529	-0.726	0.130	1.1E-05	-1.188	0.183	1.3E-06	Ptgds	ENSRNOG000000015550	3	2,689,084
26230 A_44_P213133	-2.047	0.091	4.7E-17	-2.158	0.129	2.6E-14	Endog	ENSRNOG000000016033	3	8,741,766
6137 A_64_P119821	-0.868	0.132	1.1E-06	-1.059	0.187	9.2E-06	RGD1311084	ENSRNOG000000018486	3	9,636,058
22393 A_43_P18366	1.402	0.094	3.0E-13	1.682	0.133	8.7E-12	Tor1b	ENSRNOG000000006435	3	9,792,899
24771 A_43_P10292	-0.579	0.065	7.4E-09	-0.460	0.092	4.9E-05	siat7D	ENSRNOG000000048870	3	11,607,225
19913 A_44_P102477	-1.659	0.208	4.9E-08	-2.107	0.295	2.9E-07	Morn5	ENSRNOG000000026111	3	15,379,109

9295 A_64_P057740	-1.207	0.184	1.1E-06	-1.581	0.260	3.5E-06 Ccdc148	ENSRNOG000000057740	3	45,210,474
12780 A_64_P025310	-1.072	0.115	3.3E-09	-1.441	0.163	8.2E-09 Galnt3	ENSRNOG000000005727	3	52,212,412
8214 A_64_P077658	-0.990	0.120	2.6E-08	-1.737	0.169	5.0E-10	ENSRNOG000000005868	3	52,361,060
30302 A_64_P308666	-1.227	0.130	2.3E-09	-1.853	0.183	6.8E-10 Ttc21b	ENSRNOG000000005868	3	52,361,060
25593 A_44_P166206	0.876	0.105	2.2E-08	0.830	0.148	1.1E-05 Nostrin	ENSRNOG000000006611	3	55,369,214
16738 A_44_P344777	0.425	0.063	8.0E-07	-0.704	0.090	6.2E-08	ENSRNOG000000047948	3	57,770,948
24139 A_44_P992697	-1.777	0.169	3.2E-10	-1.411	0.239	5.2E-06 Dusp19	ENSRNOG000000008868	3	67,849,966
17375 A_43_P15275	-1.700	0.071	1.1E-17	-1.534	0.100	1.7E-13 Ptpnj	ENSRNOG000000034025	3	79,390,956
18771 A_44_P107766	-1.048	0.100	3.5E-10	-0.984	0.141	4.6E-07 RGD1309540	ENSRNOG000000014798	3	80,349,145
7851 A_64_P062618	0.609	0.109	1.1E-05	1.024	0.154	9.4E-07 Chst1	ENSRNOG000000007989	3	81,498,022
25223 A_64_P115142	-0.809	0.087	3.3E-09	-0.833	0.123	7.1E-07 Accs	ENSRNOG000000009199	3	82,756,953
30117 A_64_P058202	0.589	0.090	1.2E-06	-1.173	0.127	3.9E-09	ENSRNOG000000045620	3	85,544,827
3427 A_44_P1024721	1.005	0.116	1.1E-08	1.337	0.164	3.2E-08 Slc28a2	ENSRNOG000000028668	3	114,355,798
12403 A_44_P398033	0.443	0.085	2.8E-05	0.818	0.120	6.3E-07 Prnp	ENSRNOG000000021259	3	124,515,978
12542 A_64_P042611	-2.639	0.171	1.5E-13	-3.020	0.242	1.1E-11	ENSRNOG000000036900	3	147,992,754
26332 A_64_P088452	-1.796	0.197	4.4E-09	-2.854	0.278	5.1E-10 Defb29	ENSRNOG000000023195	3	148,010,176
5599 A_43_P18817	-1.356	0.150	5.4E-09	-1.237	0.212	6.3E-06 Ifit52	ENSRNOG000000007692	3	159,392,193
27964 A_44_P576289	-1.028	0.170	3.7E-06	-1.323	0.240	1.4E-05 Stk4	ENSRNOG000000013529	3	160,467,552
11686 A_64_P103956	-0.380	0.059	1.6E-06	-0.438	0.084	2.7E-05 Acot8	ENSRNOG000000015187	3	161,272,460
16812 A_64_P058749	0.569	0.074	8.2E-08	0.534	0.104	3.5E-05	ENSRNOG000000043150	3	176,479,335
21357 A_64_P016751	-1.150	0.101	7.5E-11	-1.207	0.143	1.9E-08 Tmem243 (RGD1	ENSRNOG000000042758	4	21,920,651
12659 A_64_P010925	0.846	0.082	4.5E-10	1.004	0.116	1.1E-08 Abcb1b	ENSRNOG000000008012	4	22,307,453
4219 A_64_P103537	0.944	0.143	1.1E-06	1.206	0.203	4.8E-06 Cfr	ENSRNOG000000055103	4	42,692,836
17535 A_64_P072314	0.747	0.056	2.6E-12	0.733	0.079	3.1E-09	ENSRNOG000000052702	4	43,915,333
15750 A_64_P077103	-0.397	0.083	9.0E-05	-0.899	0.113	6.8E-08 Kcp	ENSRNOG000000021855	4	56,786,754
12618 A_64_P009490	0.998	0.171	6.3E-06	1.285	0.242	2.2E-05 LOC679651	ENSRNOG000000047635	4	68,011,932
7316 A_43_P16967	-1.420	0.099	2.9E-12	-1.099	0.146	2.2E-07 Snx10	ENSRNOG000000011944	4	81,311,490
7404 A_43_P23115	1.592	0.144	1.2E-10	2.436	0.203	2.6E-11 Inmt	ENSRNOG000000011250	4	85,386,231
4571 A_64_P044087	0.505	0.097	3.3E-05	0.846	0.132	2.0E-06 Nap1l5	ENSRNOG000000007808	4	89,151,184
24747 A_64_P157405	-1.076	0.093	1.6E-10	-1.470	0.137	6.0E-10 Reep1	ENSRNOG000000008481	4	99,618,622
19570 A_64_P027404	-0.682	0.091	1.3E-07	-0.647	0.128	4.2E-05 Mat2a	ENSRNOG000000013520	4	100,303,080
6906 A_64_P130496	-0.596	0.093	2.3E-06	-0.685	0.136	5.9E-05	ENSRNOG000000013605	4	100,380,578
20592 A_44_P402507	-1.036	0.075	1.4E-12	-0.969	0.106	4.2E-09 Retsat	ENSRNOG000000014090	4	100,465,170

6125 A_44_P399999	0.424	0.055	9.6E-08	0.391	0.078	4.9E-05	Suc1g1	ENSRNOG000000005587	4	101,180,404
4924 A_42_P508921	1.020	0.100	5.6E-10	0.910	0.141	1.5E-06	Aqp3	ENSRNOG000000009797	5	57,429,245
321 A_42_P698240	-1.913	0.081	1.6E-17	-2.051	0.115	6.6E-15	Ptgr1	ENSRNOG000000015072	5	76,129,441
22698 A_43_P13226	0.622	0.124	4.7E-05	-1.241	0.176	3.5E-07	Slc31a1	ENSRNOG000000014475	5	78,222,504
29448 A_64_P090543	-0.752	0.072	3.7E-10	-0.649	0.102	1.7E-06	Hdhd3	ENSRNOG000000015195	5	78,361,647
29767 A_44_P454532	1.140	0.158	2.5E-07	1.139	0.223	3.7E-05	Ambp	ENSRNOG000000006889	5	78,985,990
13242 A_44_P1040796	0.831	0.066	1.0E-11	1.018	0.094	1.7E-10	Atp6v1g1	ENSRNOG000000008163	5	79,367,663
19537 A_44_P996124	0.557	0.091	3.6E-06	0.999	0.124	5.4E-08	Tlr4	ENSRNOG000000010522	5	82,587,420
12084 A_64_P061875	0.805	0.096	2.0E-08	-1.280	0.135	2.4E-09		ENSRNOG000000056007	5	110,978,644
15856 A_64_P065280	0.646	0.076	1.8E-08	0.593	0.108	1.4E-05	Fam151a	ENSRNOG000000007799	5	126,334,803
23037 A_43_P15784	-0.928	0.076	1.7E-11	-1.583	0.107	3.7E-13	Cyp4a3	ENSRNOG000000009741	5	134,484,839
3744 A_43_P10290	-2.605	0.107	8.3E-18	-2.319	0.152	1.8E-13	Tspan1	ENSRNOG000000023320	5	135,024,447
9670 A_44_P117119	1.177	0.079	3.3E-13	2.175	0.112	1.1E-15	Hpdl	ENSRNOG000000018143	5	135,677,432
10831 A_64_P362701	-1.326	0.163	3.3E-08	-1.575	0.230	5.8E-07	RGD1563714	ENSRNOG000000031494	5	136,112,344
16661 A_44_P511294	-0.494	0.070	3.7E-07	-0.686	0.099	4.9E-07	Tmem53	ENSRNOG000000019186	5	136,112,417
9897 A_44_P314295	-1.575	0.099	2.3E-12	-1.507	0.213	1.1E-06	Zmynd12	ENSRNOG000000022199	5	138,470,069
955 A_64_P032604	0.581	0.065	7.3E-09	0.766	0.092	2.5E-08	Ak2	ENSRNOG000000000122	5	147,185,474
1608 A_64_P032611	0.726	0.064	8.5E-11	0.734	0.091	4.1E-08	Ak2	ENSRNOG000000000122	5	147,185,474
22000 A_64_P007550	-1.576	0.119	1.3E-11	-0.895	0.175	4.7E-05	Matn1	ENSRNOG000000010932	5	149,077,412
23745 A_44_P175875	0.818	0.090	5.0E-09	1.174	0.128	3.8E-09	Pigv	ENSRNOG000000000121	5	151,895,016
8203 A_44_P1004790	1.334	0.097	1.5E-12	0.810	0.137	5.0E-06	Slc30a2	ENSRNOG000000054142	5	152,559,577
28901 A_44_P429298	-1.254	0.167	1.8E-07	-1.444	0.228	2.3E-06	Tnfrsf9	ENSRNOG000000036942	5	168,009,393
4895 A_64_P146507	0.607	0.101	3.9E-06	0.838	0.142	5.4E-06		ENSRNOG000000042062	5	173,139,628
23507 A_64_P160689	0.737	0.118	2.4E-06	-1.092	0.167	1.2E-06		ENSRNOG000000062235	6	11,580,965
26647 A_43_P11724	0.945	0.137	5.5E-06	1.163	0.202	4.0E-05	Gckr	ENSRNOG000000048874	6	26,385,761
24275 A_44_P413979	0.790	0.074	2.3E-10	0.562	0.104	1.9E-05	Rab10	ENSRNOG000000047088	6	27,721,120
3618 A_44_P377278	-0.759	0.114	1.2E-06	-0.806	0.156	3.6E-05	Adcy3	ENSRNOG000000003999	6	28,571,351
12750 A_64_P147334	-0.686	0.099	5.1E-07	-0.844	0.140	4.1E-06	Fkbp1b	ENSRNOG000000047143	6	29,977,797
27573 A_44_P945846	0.870	0.172	4.1E-05	1.163	0.243	8.2E-05	Twistnb	ENSRNOG000000010750	6	52,751,106
22866 A_64_P123690	0.582	0.099	6.0E-06	-1.127	0.141	4.4E-08	RGD1563613	ENSRNOG000000029737	6	57,396,220
18839 A_44_P363009	0.962	0.180	2.0E-05	1.422	0.254	1.1E-05	Scin	ENSRNOG000000004498	6	60,054,279
9915 A_64_P045102	0.704	0.114	2.7E-06	-1.259	0.161	6.6E-08		ENSRNOG000000032000	6	96,202,477
5759 A_64_P065368	0.610	0.077	5.8E-08	0.852	0.109	7.1E-08	Acot4	ENSRNOG000000046864	6	107,517,668

16745 A_64_P067447	0.718	0.075	2.0E-09	0.747	0.106	4.0E-07	Acot4	ENSRNOG000000046864	6	107,517,668
18088 A_44_P337991	0.592	0.086	5.5E-07	0.962	0.122	5.6E-08	Acot3	ENSRNOG000000053460	6	107,531,528
28805 A_64_P028095	-0.544	0.109	5.0E-05	-0.839	0.155	1.7E-05	Abcd4	ENSRNOG000000011964	6	108,329,464
4675 A_44_P539231	0.481	0.068	3.1E-07	-0.825	0.095	1.2E-08		ENSRNOG000000042542	6	115,769,793
7028 A_43_P13410	0.885	0.122	2.5E-07	1.297	0.173	1.4E-07	Serpina4	ENSRNOG000000009788	6	127,743,971
11175 A_64_P002455	-1.025	0.100	5.3E-10	-0.793	0.141	1.1E-05	LOC690422	ENSRNOG000000005153	6	137,967,401
17240 A_44_P147572	-2.227	0.145	1.7E-13	-1.495	0.205	2.2E-07		ENSRNOG000000034190	6	138,508,753
10291 A_64_P095554	-2.609	0.353	1.7E-07	-3.259	0.499	1.2E-06		ENSRNOG000000034190	6	138,632,203
10600 A_64_P099017	-2.008	0.064	1.2E-17	-1.944	0.139	2.1E-11	Cyp4f17	ENSRNOG000000062306	7	14,529,483
23692 A_64_P044648	0.604	0.098	3.0E-06	-0.735	0.139	2.4E-05		ENSRNOG000000048170	7	20,075,974
29455 A_64_P130573	0.604	0.093	1.3E-06	-0.980	0.132	1.5E-07		ENSRNOG000000032424	7	29,909,120
9888 A_64_P025286	0.921	0.067	1.4E-12	1.177	0.094	1.1E-11	Lyz2	ENSRNOG000000005825	7	60,341,264
18940 A_64_P072442	0.903	0.118	1.0E-07	1.160	0.167	4.9E-07	Tsfm	ENSRNOG000000048843	7	70,319,346
23558 A_64_P144913	0.437	0.091	7.4E-05	0.859	0.128	8.1E-07	Nab2	ENSRNOG000000008415	7	70,969,905
19834 A_64_P036553	1.809	0.112	6.1E-14	2.053	0.159	5.7E-12	Rdh2	ENSRNOG000000029651	7	70,980,422
7840 A_44_P318662	-1.097	0.165	9.2E-07	-1.329	0.233	8.7E-06	Tac2	ENSRNOG000000004229	7	71,023,976
27443 A_64_P036548	1.168	0.145	4.0E-08	1.277	0.205	2.4E-06	Rdh2	ENSRNOG000000029651	7	71,057,911
14630 A_64_P134465	-0.465	0.086	1.9E-05	-0.638	0.122	2.8E-05	Fam91a1	ENSRNOG000000008271	7	98,302,953
16387 A_64_P012232	-1.133	0.100	8.4E-11	-1.352	0.142	2.1E-09	Sqle	ENSRNOG000000009550	7	99,609,191
2500 A_64_P065611	1.029	0.099	3.8E-10	1.310	0.140	2.7E-09	Khdrbs3	ENSRNOG000000009539	7	110,031,696
26593 A_44_P1049252	0.456	0.059	7.5E-08	0.410	0.083	5.5E-05	Naprt1	ENSRNOG000000007939	7	116,926,555
18442 A_64_P044345	0.698	0.091	8.5E-08	0.784	0.128	3.1E-06	Plec	ENSRNOG000000023781	7	117,267,803
7795 A_64_P044137	-0.499	0.102	6.1E-05	-0.738	0.144	3.5E-05	Lrrc24	ENSRNOG000000016204	7	117,784,638
28509 A_44_P267706	0.869	0.101	1.4E-08	1.119	0.143	6.9E-08	Apol11a	ENSRNOG000000023122	7	118,840,634
19289 A_44_P975458	-0.966	0.105	3.7E-09	-0.766	0.148	3.1E-05	C1qtnf6	ENSRNOG000000007300	7	119,753,290
25974 A_43_P12557	0.442	0.090	5.9E-05	0.708	0.127	1.2E-05	Polr2f	ENSRNOG000000011214	7	120,380,544
30340 A_44_P930152	1.029	0.145	3.2E-07	1.815	0.205	7.6E-09	Mpped1	ENSRNOG000000010834	7	124,680,294
13547 A_44_P204758	0.747	0.096	6.9E-08	0.759	0.135	1.1E-05	Sult4a1	ENSRNOG000000046975	7	124,982,566
4907 A_64_P138430	-0.941	0.123	1.4E-07	-0.908	0.168	2.1E-05	Odf3b	ENSRNOG000000037060	7	130,350,570
26026 A_64_P060569	-0.530	0.072	1.7E-07	-0.638	0.102	2.1E-06	Arsa	ENSRNOG000000012953	7	130,451,283
25452 A_64_P012962	-1.813	0.089	3.2E-15	-1.931	0.131	1.8E-12		ENSRNOG000000054046	7	143,239,617
15494 A_44_P138838	-3.657	0.169	1.0E-16	-3.757	0.239	9.9E-14	Krt76	ENSRNOG000000031785	7	143,497,108
17711 A_44_P119527	-1.418	0.128	1.2E-10	-1.651	0.181	4.5E-09	Med17	ENSRNOG000000051989	8	13,526,025

8626 A_44_P100886	1.773	0.196	4.6E-08	1.504	0.266	2.4E-05	ENSRNOG00000010999	8	13,909,188
11775 A_44_P518434	-1.043	0.090	5.3E-11	-1.125	0.128	8.5E-09 Mrpl4	ENSRNOG00000020659	8	22,021,213
29723 A_64_P148966	0.394	0.067	5.2E-06	0.443	0.094	9.9E-05	ENSRNOG00000009373	8	33,075,211
15342 A_44_P161233	0.460	0.097	8.5E-05	0.674	0.137	5.6E-05 Il18	ENSRNOG00000009848	8	54,993,859
8832 A_42_P794120	-0.520	0.103	4.3E-05	-1.071	0.146	2.0E-07 Stra6	ENSRNOG00000008312	8	62,925,357
26700 A_64_P151869	0.713	0.097	1.8E-07	0.773	0.137	9.8E-06 Myo5a	ENSRNOG000000058866	8	82,037,977
8558 A_64_P080566	0.281	0.049	7.0E-06	0.360	0.069	2.6E-05 LOC494499	ENSRNOG00000000201	8	85,553,734
21497 A_44_P604824	-1.261	0.237	2.1E-05	-1.617	0.335	7.3E-05 Prss35	ENSRNOG000000025184	8	94,423,808
12498 A_44_P162115	1.860	0.108	1.4E-14	1.283	0.152	1.9E-08 Slc9a9	ENSRNOG00000008554	8	102,304,095
20855 A_64_P026828	-0.398	0.081	5.7E-05	-0.551	0.114	7.2E-05 Abhd14a	ENSRNOG000000011936	8	115,149,527
5815 A_43_P11432	-0.388	0.053	1.9E-07	-0.400	0.075	1.9E-05 Acaa1a	ENSRNOG000000032908	8	128,027,958
25489 A_44_P387780	4.859	0.122	2.2E-20	3.389	0.161	5.2E-15 Cyp8b1	ENSRNOG000000019481	8	130,550,388
588 A_44_P388755	1.634	0.112	5.5E-11	1.417	0.150	3.9E-08 Kif15	ENSRNOG000000060356	8	132,032,944
22889 A_44_P342756	0.532	0.084	2.1E-06	-0.981	0.119	2.9E-08	ENSRNOG000000042034	9	25,203,534
17867 A_44_P1029892	1.788	0.080	5.8E-17	2.189	0.114	1.3E-15 Tmem14a	ENSRNOG000000046593	9	27,343,853
17848 A_64_P004231	0.398	0.083	7.8E-05	0.643	0.117	1.5E-05 Gsta5	ENSRNOG000000056847	9	27,402,381
3838 A_42_P624195	0.471	0.076	2.5E-06	0.643	0.107	4.2E-06 Gsta3	ENSRNOG000000013484	9	27,452,902
2478 A_42_P623733	0.568	0.091	2.3E-06	0.701	0.129	1.6E-05 LOC501110	ENSRNOG000000033402	9	27,511,176
19994 A_64_P097257	-0.994	0.188	3.7E-05	-1.845	0.249	3.9E-07	ENSRNOG000000058900	9	29,356,963
6671 A_64_P159044	0.477	0.091	2.6E-05	-1.160	0.129	5.5E-09 LOC685674	ENSRNOG000000055155	9	56,454,959
10938 A_44_P998060	0.470	0.092	4.4E-05	-0.868	0.126	6.6E-07 Mobkl3	ENSRNOG000000014980	9	61,720,583
9937 A_64_P024841	-2.098	0.131	7.0E-14	-1.666	0.186	6.1E-09 Cryga	ENSRNOG000000014790	9	71,830,730
27465 A_64_P055450	-0.426	0.075	8.5E-06	-0.497	0.106	9.8E-05 Idh1	ENSRNOG000000015020	9	71,900,044
8097 A_44_P1031737	-0.838	0.096	9.6E-09	-1.012	0.135	1.4E-07 Pecr	ENSRNOG000000055295	9	79,630,536
29277 A_64_P008502	-0.941	0.176	2.0E-05	-1.831	0.249	1.9E-07 Tmem169	ENSRNOG000000016091	9	79,630,604
21241 A_64_P123879	-0.474	0.078	3.5E-06	-0.545	0.110	5.6E-05 Xrcc5	ENSRNOG000000016105	9	79,659,251
11810 A_43_P12005	-0.809	0.063	7.3E-12	-0.475	0.090	2.3E-05 Resp18	ENSRNOG000000019704	9	82,477,181
18795 A_43_P10901	1.248	0.089	9.9E-13	1.153	0.125	3.9E-09 Itm2c	ENSRNOG000000017359	9	92,916,469
273 A_44_P143922	0.494	0.063	7.0E-08	0.562	0.090	2.2E-06 Hes6	ENSRNOG000000020194	9	98,551,410
11494 A_44_P123492	-0.585	0.085	5.6E-07	-0.644	0.120	2.0E-05 Epb41l3	ENSRNOG000000016724	9	117,538,009
21591 A_64_P058107	-0.515	0.062	2.5E-08	-0.491	0.088	1.1E-05 Enpp6	ENSRNOG000000053864	10	197,050
19341 A_44_P274762	0.447	0.092	6.3E-05	0.692	0.129	2.0E-05 Cpped1	ENSRNOG000000015118	10	3,655,038
21059 A_64_P066501	-0.509	0.068	1.4E-07	-1.746	0.096	4.8E-15 Gng13	ENSRNOG000000039350	10	15,088,935

23671 A_64_P062663	-0.527	0.067	5.4E-08	-1.596	0.094	2.1E-14 Gng13	ENSRNOG000000039350	10	15,088,935
6367 A_64_P133657	-2.225	0.134	3.2E-14	-2.614	0.190	1.5E-12 Timd2	ENSRNOG000000021345	10	31,790,263
9066 A_64_P027288	0.863	0.122	1.4E-05	1.485	0.234	3.9E-05 RGD1564516	ENSRNOG000000038894	10	31,880,918
24608 A_64_P025618	-0.504	0.077	1.0E-06	-0.620	0.108	7.9E-06 Slc25a35	ENSRNOG000000004668	10	55,555,089
92 A_42_P520349	0.810	0.122	9.5E-07	0.840	0.173	6.8E-05 Clec10a	ENSRNOG000000018715	10	56,764,927
25686 A_43_P23363	0.868	0.146	4.7E-06	1.180	0.206	8.2E-06 Spata22	ENSRNOG000000037307	10	59,893,067
23809 A_44_P1018622	0.594	0.089	9.2E-07	1.496	0.126	3.3E-11 Fam101b	ENSRNOG000000006674	10	64,202,380
5923 A_64_P006628	-1.536	0.228	7.4E-07	-1.522	0.322	9.5E-05 Tac4	ENSRNOG000000004404	10	83,081,168
26032 A_44_P384066	0.603	0.098	2.8E-06	0.731	0.138	2.3E-05 G6pc	ENSRNOG000000053448	10	89,236,258
29333 A_64_P066261	-0.731	0.103	4.2E-07	-0.745	0.140	2.6E-05 Cacng5	ENSRNOG000000003288	10	96,131,880
9292 A_44_P555201	-4.289	0.175	1.3E-14	0.842	0.142	1.8E-05 Apoh	ENSRNOG000000003566	10	96,639,924
9605 A_44_P1011244	-0.649	0.100	1.3E-06	-0.674	0.141	8.3E-05 MGC95210	ENSRNOG000000024780	10	102,199,837
14484 A_64_P050477	0.438	0.070	2.3E-06	0.579	0.099	6.0E-06 Hn1	ENSRNOG000000003661	10	104,075,777
3531 A_64_P059385	0.673	0.071	2.2E-09	0.534	0.100	2.2E-05 Acox1	ENSRNOG000000008755	10	104,748,050
28378 A_64_P059390	0.713	0.080	6.7E-09	0.835	0.113	1.7E-07 Acox1	ENSRNOG000000008755	10	104,748,050
19778 A_64_P131873	-1.814	0.091	4.2E-14	-1.383	0.196	1.1E-06 Galr2	ENSRNOG000000061733	10	105,156,632
10355 A_64_P100346	-0.867	0.116	1.4E-07	-1.143	0.164	4.4E-07 Qrich2	ENSRNOG000000025254	10	105,412,627
21260 A_44_P237153	-2.053	0.197	3.7E-10	-1.847	0.278	9.3E-07 Birc5	ENSRNOG000000050819	10	106,856,097
22449 A_42_P539095	-0.858	0.083	4.2E-10	-0.783	0.117	8.4E-07 LOC688311	ENSRNOG000000049235	10	109,639,054
18404 A_43_P13256	0.278	0.054	3.2E-05	0.454	0.076	4.7E-06 Dcxr	ENSRNOG000000050315	10	109,909,646
5982 A_64_P071367	0.687	0.104	1.0E-06	1.014	0.147	5.3E-07 Krtap16-5	ENSRNOG000000040064	11	28,900,376
20993 A_64_P071362	0.684	0.094	2.3E-07	0.919	0.133	5.2E-07 Krtap16-5	ENSRNOG000000040064	11	28,900,376
12330 A_44_P121280	-1.652	0.153	2.0E-10	-1.682	0.217	7.6E-08 Kcne1	ENSRNOG000000001984	11	32,508,420
16374 A_64_P036352	-1.257	0.098	6.3E-12	-1.096	0.138	5.4E-08 Cbr1	ENSRNOG000000049911	11	33,863,500
3179 A_42_P554722	-0.581	0.072	3.7E-08	-0.517	0.101	3.8E-05 Piggp	ENSRNOG000000039850	11	34,598,275
16198 A_43_P18730	0.976	0.087	9.3E-11	1.199	0.123	1.3E-09 LOC304000	ENSRNOG000000028216	11	36,736,586
6884 A_42_P732251	-1.283	0.097	3.5E-12	-1.429	0.137	3.9E-10 Phldb2	ENSRNOG000000002171	11	57,404,196
6750 A_64_P013875	-1.193	0.096	1.1E-11	-1.107	0.135	3.1E-08	ENSRNOG000000002171	11	57,430,166
1239 A_43_P12572	0.704	0.095	1.6E-07	0.788	0.134	5.7E-06 Cd200	ENSRNOG000000002141	11	60,371,729
10972 A_64_P118532	-0.525	0.077	6.5E-07	-0.623	0.109	8.4E-06 Casr	ENSRNOG000000002265	11	67,188,630
8585 A_64_P101978	-1.128	0.120	2.7E-09	-1.425	0.170	2.0E-08 Cldn16	ENSRNOG000000055138	11	77,703,255
22617 A_44_P635089	-0.514	0.089	6.9E-06	-0.815	0.126	1.3E-06 Etf5	ENSRNOG000000001785	11	82,194,657
26833 A_43_P13230	0.421	0.088	8.0E-05	0.668	0.124	1.9E-05 Ehhadh	ENSRNOG000000001770	11	82,945,104

24638 A_64_P005893	-0.809	0.143	1.1E-05	-1.412	0.195	3.1E-07	ENSRNOG000000050898	11	85,532,526
10269 A_64_P126226	-0.606	0.116	2.8E-05	-0.832	0.165	4.2E-05 Car15	ENSRNOG000000037983	11	87,762,301
7350 A_64_P048136	-0.719	0.086	3.0E-08	-0.622	0.117	2.6E-05 Brca2	ENSRNOG000000001111	12	504,007
1534 A_42_P762213	-0.752	0.087	1.1E-08	-0.639	0.123	2.9E-05 Lrrc8e	ENSRNOG000000028460	12	2,568,382
3604 A_42_P746109	-0.715	0.072	9.9E-10	-0.604	0.102	5.1E-06 Asmtl	ENSRNOG000000028166	12	18,531,990
19145 A_64_P081501	1.197	0.095	8.6E-12	1.895	0.134	8.7E-13 Mcm7	ENSRNOG000000001349	12	19,314,016
1742 A_64_P144034	1.964	0.146	4.2E-11	1.266	0.195	3.4E-06 LOC363894	ENSRNOG000000045875	12	20,814,122
17119 A_44_P654973	0.950	0.110	1.3E-08	1.050	0.156	7.7E-07 Rimb2	ENSRNOG000000022893	12	31,530,699
28008 A_43_P15918	0.845	0.131	1.4E-06	1.004	0.185	1.6E-05 Rimb2	ENSRNOG000000022893	12	31,530,699
3175 A_44_P1030714	1.054	0.120	8.4E-09	1.807	0.169	2.4E-10 Ccdc92	ENSRNOG000000021691	12	37,211,316
13761 A_64_P135202	-0.873	0.092	2.4E-09	-0.666	0.131	3.8E-05 Snmp35	ENSRNOG000000001060	12	37,538,403
5287 A_64_P115222	0.758	0.089	1.5E-08	0.727	0.126	6.9E-06 Pitpm2	ENSRNOG000000029260	12	37,805,332
29139 A_44_P838992	-0.989	0.145	6.1E-07	-1.085	0.205	2.3E-05 LOC687609	ENSRNOG000000042607	12	38,880,377
2789 A_42_P612939	-0.781	0.134	8.8E-06	-1.053	0.197	2.7E-05 Tmem119	ENSRNOG000000000700	12	48,598,647
14258 A_43_P13249	1.131	0.066	1.7E-14	0.962	0.094	4.9E-10 Acmsd	ENSRNOG000000003884	13	44,424,689
4010 A_64_P083623	0.779	0.085	4.4E-09	-1.247	0.121	4.4E-10	ENSRNOG000000022174	13	56,262,190
12995 A_44_P349273	1.791	0.124	6.1E-13	1.467	0.176	2.2E-08 F13b	ENSRNOG000000012613	13	56,598,957
19291 A_44_P475444	0.393	0.080	6.4E-05	0.613	0.114	1.8E-05 RGD1564614	ENSRNOG000000042369	13	56,958,549
2005 A_42_P819656	0.652	0.081	3.8E-08	0.593	0.114	2.9E-05 Cfh	ENSRNOG000000030715	13	57,080,549
11876 A_64_P068222	0.662	0.093	9.2E-07	2.042	0.200	4.1E-09 Fam129a	ENSRNOG000000002403	13	68,949,665
20329 A_44_P538789	0.350	0.071	6.2E-05	-0.579	0.101	8.0E-06	ENSRNOG000000051105	13	79,493,365
1416 A_64_P091088	0.857	0.105	3.3E-08	1.112	0.149	1.4E-07 Fmo2	ENSRNOG000000003510	13	80,775,264
20699 A_44_P486312	1.127	0.100	7.8E-11	1.193	0.141	1.7E-08 Fmo2	ENSRNOG000000003510	13	80,775,264
14514 A_44_P180259	1.452	0.084	1.5E-14	1.835	0.119	1.6E-13 Dpt	ENSRNOG000000002947	13	83,073,550
16004 A_64_P086314	0.397	0.070	9.0E-06	-0.684	0.099	4.9E-07	ENSRNOG000000054035	13	84,272,663
22348 A_44_P1018997	-0.559	0.082	5.7E-07	-0.571	0.115	5.4E-05 Tmco1	ENSRNOG000000003928	13	85,465,792
12064 A_64_P027625	-4.487	0.123	2.5E-20	-0.888	0.159	1.6E-05 Rxrg	ENSRNOG000000004537	13	85,818,427
21779 A_44_P306439	0.806	0.113	3.2E-07	1.284	0.160	4.5E-08 Fcgr3a	ENSRNOG000000024382	13	89,385,859
25592 A_44_P575255	1.966	0.113	1.2E-14	2.153	0.160	2.6E-12 RGD1562658	ENSRNOG000000034221	13	89,480,058
20771 A_64_P001255	-0.533	0.075	3.1E-07	-0.749	0.106	3.4E-07 Ppox	ENSRNOG000000003567	13	89,654,244
22158 A_64_P003491	-1.903	0.193	1.7E-09	-2.045	0.263	1.0E-07 LOC689766	ENSRNOG000000021411	13	95,887,708
9059 A_42_P803590	-1.682	0.159	2.9E-10	-1.715	0.225	1.0E-07 LOC289378	ENSRNOG000000046460	13	109,663,364
3954 A_42_P661065	0.694	0.138	4.4E-05	1.168	0.195	4.3E-06 Ints7	ENSRNOG000000004263	13	110,257,571

10206 A_64_P052464	1.019	0.162	2.2E-06	1.358	0.230	5.2E-06	Ints7	ENSRNOG000000004263	13	110,257,571
29630 A_64_P015335	1.814	0.128	8.7E-13	2.207	0.181	1.8E-11	Mfsd7	ENSRNOG000000023937	14	2,311,122
783 A_64_P071159	-3.773	0.096	1.7E-22	-4.096	0.135	6.3E-20	LOC360919	ENSRNOG000000039504	14	19,072,677
17181 A_64_P071158	-3.726	0.098	4.2E-22	-4.197	0.139	6.9E-20	LOC360919	ENSRNOG000000039504	14	19,072,677
16082 A_44_P353446	-2.403	0.169	8.0E-13	-2.285	0.239	1.9E-09	Afm	ENSRNOG00000002878	14	19,132,208
7897 A_43_P13995	1.707	0.127	2.4E-12	1.974	0.179	1.3E-10	Gc	ENSRNOG000000003119	14	20,266,891
8034 A_43_P12233	0.460	0.077	4.2E-06	0.843	0.108	7.4E-08	Sult1b1	ENSRNOG000000001967	14	22,142,364
27643 A_64_P053257	0.449	0.070	1.6E-06	0.721	0.099	2.2E-07	Sult1b1	ENSRNOG000000001967	14	22,142,364
16339 A_43_P11686	0.508	0.071	2.6E-07	0.478	0.100	8.2E-05	Kdr	ENSRNOG000000046829	14	34,727,623
28582 A_43_P11601	-1.099	0.092	2.5E-11	-1.016	0.130	6.4E-08	Sod3	ENSRNOG000000003869	14	60,964,324
28877 A_64_P043150	-0.425	0.071	1.1E-05	0.974	0.157	7.9E-06	Ccdc157	ENSRNOG000000005147	14	84,393,421
18032 A_44_P402445	1.950	0.085	1.1E-14	1.630	0.177	3.5E-08	Nefn	ENSRNOG000000008716	14	85,191,557
11690 A_44_P330188	2.958	0.094	2.8E-20	2.380	0.133	6.5E-15	Acox2	ENSRNOG000000007378	15	18,451,144
17115 A_64_P031249	0.834	0.080	4.2E-10	1.240	0.114	1.6E-10	Gnpnat1	ENSRNOG000000008641	15	19,733,967
1315 A_64_P134160	-2.289	0.183	2.0E-11	-2.448	0.279	1.3E-08	Defb42	ENSRNOG000000038762	15	46,166,335
22837 A_44_P428988	0.516	0.071	2.5E-07	-1.035	0.101	5.3E-10		ENSRNOG000000038122	15	66,165,529
1825 A_42_P787239	0.644	0.079	3.3E-08	0.729	0.112	1.2E-06	Farp1	ENSRNOG000000011203	15	106,434,177
7588 A_64_P029008	-0.400	0.069	6.2E-06	-0.604	0.097	2.4E-06	Chdh	ENSRNOG000000015859	16	6,078,122
30347 A_64_P066923	0.800	0.113	3.7E-07	1.173	0.160	2.0E-07	Ncoa4	ENSRNOG000000019768	16	8,302,950
1186 A_42_P467381	0.539	0.073	1.9E-07	0.712	0.104	5.7E-07	Fam32a	ENSRNOG000000039528	16	19,308,842
8703 A_64_P085936	-2.522	0.149	2.2E-14	-2.728	0.211	5.8E-12	Mef2b	ENSRNOG000000020400	16	21,017,163
25971 A_64_P004531	-0.970	0.089	1.7E-10	-0.776	0.126	3.0E-06	LOC688966	ENSRNOG000000020427	16	21,029,134
10778 A_44_P204704	0.593	0.114	2.9E-05	1.005	0.161	2.4E-06	Cpe	ENSRNOG000000043387	16	26,906,716
8243 A_44_P652899	-0.545	0.112	6.7E-05	-0.754	0.158	8.7E-05	Gpm6a	ENSRNOG000000010731	16	39,719,187
26075 A_64_P041016	-0.813	0.084	1.4E-09	-0.912	0.118	8.5E-08	Wwc2	ENSRNOG000000013248	16	47,368,768
171 A_64_P040806	0.816	0.092	7.6E-09	0.812	0.130	2.4E-06	Tlr3	ENSRNOG000000021726	16	50,016,857
11412 A_44_P1042163	0.640	0.089	2.9E-07	1.154	0.126	4.4E-09	RGD1310414	ENSRNOG000000023494	16	64,745,207
7494 A_42_P633958	0.552	0.101	1.6E-05	0.927	0.143	1.4E-06	Col4a2	ENSRNOG000000023972	16	83,438,561
11386 A_64_P014278	-1.416	0.074	1.6E-15	-1.255	0.105	2.6E-11	LOC680692	ENSRNOG000000018400	17	5,382,034
4329 A_44_P620106	0.596	0.076	7.1E-08	0.962	0.108	7.1E-09	Tgfb1	ENSRNOG000000012216	17	8,429,338
24746 A_64_P163822	-1.348	0.181	1.5E-07	-1.291	0.256	4.3E-05	Cks2	ENSRNOG000000014130	17	13,593,423
4180 A_64_P165035	5.867	0.143	6.5E-23	6.191	0.202	4.6E-20	RGD1305679	ENSRNOG000000014481	17	22,619,891
8900 A_64_P059262	0.837	0.136	2.8E-06	1.295	0.192	7.3E-07	Riok1	ENSRNOG000000014049	17	27,451,832

28972 A_64_P060715	-0.873	0.164	2.2E-05	-1.401	0.232	3.8E-06	ENSRNOG000000022505	17	43,458,553
7060 A_42_P555365	0.641	0.067	1.8E-09	0.564	0.094	4.5E-06 Slc17a3	ENSRNOG000000032745	17	43,537,293
14149 A_64_P080667	-1.245	0.135	3.8E-09	-1.270	0.191	9.2E-07 LOC684841	ENSRNOG000000045644	17	43,807,540
18077 A_64_P127848	-1.336	0.108	2.7E-11	-1.486	0.148	1.2E-09 Aoah	ENSRNOG000000054964	17	46,115,004
17105 A_64_P040038	2.659	0.091	1.4E-19	2.441	0.129	1.8E-15 RGD1563564	ENSRNOG000000016217	17	63,145,577
13903 A_44_P515798	1.895	0.162	4.1E-11	2.855	0.229	1.2E-11 Ucma	ENSRNOG000000017987	17	77,261,731
23649 A_44_P191021	0.389	0.073	2.1E-05	0.771	0.103	1.4E-07 Phyh	ENSRNOG000000018044	17	77,304,530
26649 A_64_P059949	0.759	0.110	6.9E-07	0.987	0.150	1.4E-06 C1ql3	ENSRNOG000000017459	17	80,320,681
20714 A_64_P056712	0.621	0.096	1.3E-06	0.819	0.135	3.7E-06 Gpr137b	ENSRNOG000000002480	17	90,696,019
14941 A_64_P041481	-0.573	0.072	4.9E-08	-0.868	0.102	1.5E-08 Mep1b	ENSRNOG000000049345	18	15,089,988
23099 A_44_P173289	-0.846	0.154	1.4E-05	-1.244	0.218	8.5E-06 Pkd2l2	ENSRNOG000000025489	18	27,190,974
2039 A_64_P135224	2.504	0.113	6.5E-17	2.592	0.160	5.2E-14 RGD1309362	ENSRNOG000000038960	18	55,505,993
4992 A_44_P549494	0.841	0.062	2.3E-12	1.046	0.088	3.0E-11 Cd74	ENSRNOG000000018735	18	56,071,478
17166 A_44_P419615	-1.462	0.122	1.5E-10	-1.038	0.203	5.4E-05 Stard6	ENSRNOG000000026324	18	68,983,545
25215 A_64_P118728	-0.597	0.109	1.7E-05	-1.071	0.148	3.2E-07 LOC100192205	ENSRNOG000000059055	18	76,753,902
7335 A_42_P595630	-0.865	0.084	4.4E-10	-0.997	0.118	1.9E-08 Pqlc1	ENSRNOG000000059215	18	76,770,012
22519 A_64_P021320	-0.914	0.074	1.3E-11	-1.069	0.104	5.0E-10 Pqlc1	ENSRNOG000000059215	18	76,770,012
30080 A_64_P110941	-2.256	0.173	4.4E-12	-1.736	0.244	3.2E-07 Cndp1	ENSRNOG000000027739	18	81,499,051
15276 A_44_P1039606	-0.699	0.116	1.9E-05	-2.190	0.317	3.8E-06 Cenpt	ENSRNOG000000024178	19	37,819,789
5405 A_64_P121061	-1.053	0.111	2.3E-09	-1.256	0.157	4.8E-08 Tmed6	ENSRNOG000000020406	19	39,267,928
19705 A_44_P220325	-1.578	0.181	1.4E-08	-1.333	0.246	2.0E-05 Dynlrb2	ENSRNOG000000012450	19	49,016,891
10809 A_44_P374638	-0.899	0.173	2.9E-05	-1.167	0.245	8.4E-05 Hsd17b2	ENSRNOG000000013982	19	50,246,402
4436 A_42_P627572	-1.466	0.120	1.8E-11	-1.367	0.170	4.2E-08 Mdc1	ENSRNOG000000032813	20	3,405,285
7136 A_64_P062110	0.466	0.063	1.5E-07	0.685	0.088	7.9E-08 RT1-DMb	ENSRNOG000000049491	20	3,945,601
1417 A_64_P043911	0.673	0.092	2.1E-07	0.915	0.131	4.0E-07 RT1-Bb	ENSRNOG000000032708	20	4,039,413
27475 A_44_P991532	0.491	0.079	2.5E-06	0.578	0.112	3.1E-05 RT1-Da	ENSRNOG000000032844	20	4,132,616
12415 A_64_P128478	0.831	0.071	3.6E-11	0.854	0.100	1.4E-08 RT1-DMa	ENSRNOG000000047864	20	5,241,496
15230 A_64_P048033	0.727	0.082	6.9E-09	0.778	0.115	7.5E-07 Agpat3	ENSRNOG000000001205	20	11,114,164
25935 A_64_P146698	0.590	0.095	2.4E-06	0.803	0.134	4.2E-06 Pwp2	ENSRNOG000000001210	20	11,228,844
7074 A_64_P001461	-1.188	0.152	8.8E-08	-1.039	0.207	5.0E-05 Dnmt3l	ENSRNOG000000001212	20	11,359,090
19033 A_44_P1015203	0.690	0.059	4.8E-11	0.515	0.084	3.1E-06 Gstt3	ENSRNOG000000001242	20	13,817,795
1320 A_42_P604331	1.412	0.119	3.2E-11	1.564	0.169	3.4E-09 Spock2	ENSRNOG000000061544	20	29,655,226
405 A_42_P559737	0.763	0.080	1.8E-09	0.962	0.113	1.4E-08 Srgn	ENSRNOG000000000394	20	32,133,431

220 A_42_P796980	-2.546	0.211	2.2E-11	-3.337	0.298	9.6E-11 Ros1	ENSRNOG00000000406	20	33,323,367
24586 A_43_P14875	-0.678	0.069	1.2E-09	-0.462	0.098	9.4E-05 Prep	ENSRNOG000000051061	20	50,172,618
18623 A_64_P042519	-1.027	0.107	4.1E-09	-0.787	0.157	6.0E-05 Grik2	ENSRNOG000000000368	20	54,517,709
11936 A_44_P547801	-0.878	0.092	2.2E-09	-0.777	0.131	4.9E-06 Gstt2	ENSRNOG000000052360	568423	501
1141 A_64_P097927	0.570	0.115	5.5E-05	-0.779	0.163	8.2E-05	ENSRNOG000000031780	MT	1
1339 A_64_P042093	0.940	0.124	1.2E-07	1.710	0.176	1.4E-09	ENSRNOG000000031780	MT	1
1670 A_64_P110465	0.607	0.113	1.9E-05	-1.150	0.160	2.6E-07	ENSRNOG000000031780	MT	1
2034 A_64_P012268	0.617	0.112	1.4E-05	-0.820	0.159	3.2E-05	ENSRNOG000000031780	MT	1
2130 A_64_P030494	0.820	0.100	2.9E-08	-1.525	0.141	2.0E-10	ENSRNOG000000031780	MT	1
3172 A_64_P122755	0.407	0.056	2.3E-07	-0.831	0.079	3.3E-10	ENSRNOG000000031780	MT	1
3666 A_64_P108841	0.682	0.076	5.6E-09	-0.738	0.107	5.1E-07	ENSRNOG000000031780	MT	1
4385 A_42_P471835	0.566	0.085	8.7E-07	0.734	0.120	3.2E-06	ENSRNOG000000031780	MT	1
5091 A_44_P342334	-0.743	0.077	1.8E-09	-0.541	0.109	5.5E-05	ENSRNOG000000031780	MT	1
5336 A_64_P112262	0.660	0.118	1.2E-05	-1.207	0.167	2.5E-07	ENSRNOG000000031780	MT	1
5482 A_64_P326359	1.084	0.087	1.3E-11	0.987	0.124	4.7E-08	ENSRNOG000000031780	MT	1
5682 A_64_P035685	0.726	0.131	1.3E-05	-1.272	0.185	5.5E-07	ENSRNOG000000031780	MT	1
6703 A_64_P005742	0.413	0.083	4.8E-05	-0.661	0.117	9.5E-06	ENSRNOG000000031780	MT	1
6958 A_64_P042096	0.911	0.131	4.5E-07	0.949	0.185	3.5E-05	ENSRNOG000000031780	MT	1
8758 A_64_P147268	0.385	0.063	3.5E-06	-0.844	0.090	2.5E-09	ENSRNOG000000031780	MT	1
9083 A_64_P130249	0.591	0.091	1.4E-06	-0.821	0.129	1.8E-06	ENSRNOG000000031780	MT	1
9336 A_64_P063588	0.655	0.080	3.2E-08	0.717	0.113	2.0E-06	ENSRNOG000000031780	MT	1
9394 A_64_P119214	0.808	0.062	5.5E-12	1.163	0.088	3.8E-12	ENSRNOG000000031780	MT	1
9586 A_64_P007528	0.460	0.073	2.1E-06	-0.725	0.103	4.0E-07	ENSRNOG000000031780	MT	1
10091 A_64_P150008	-0.951	0.124	8.8E-08	-1.025	0.175	5.7E-06	ENSRNOG000000031780	MT	1
10168 A_64_P014010	2.213	0.078	2.5E-19	2.340	0.110	1.5E-16	ENSRNOG000000031780	MT	1
10544 A_64_P085915	-1.055	0.147	2.8E-07	-1.659	0.208	4.8E-08	ENSRNOG000000031780	MT	1
11098 A_44_P156705	0.410	0.071	6.9E-06	-0.648	0.100	1.4E-06	ENSRNOG000000031780	MT	1
11823 A_64_P143271	0.381	0.079	7.6E-05	-0.558	0.112	5.0E-05	ENSRNOG000000031780	MT	1
12614 A_64_P098021	0.688	0.104	9.8E-07	-1.101	0.147	1.4E-07	ENSRNOG000000031780	MT	1
13135 A_64_P131326	0.538	0.110	6.1E-05	-1.217	0.155	6.5E-08	ENSRNOG000000031780	MT	1
13275 A_64_P016797	0.566	0.082	5.0E-07	-1.053	0.116	4.8E-09	ENSRNOG000000031780	MT	1
13523 A_64_P118493	0.530	0.079	7.8E-07	-0.877	0.112	6.3E-08	ENSRNOG000000031780	MT	1
14338 A_64_P031397	0.814	0.083	1.2E-09	-1.157	0.118	1.1E-09	ENSRNOG000000031780	MT	1

14637 A_64_P068112	0.333	0.068	6.1E-05	-0.572	0.096	4.7E-06	ENSRNOG000000031780	MT	1
15278 A_64_P013704	-1.317	0.144	1.0E-08	-1.202	0.212	1.3E-05	ENSRNOG000000031780	MT	1
15949 A_64_P024000	0.514	0.089	6.7E-06	-0.812	0.125	1.4E-06	ENSRNOG000000031780	MT	1
16302 A_64_P079528	-0.764	0.155	5.7E-05	-1.161	0.219	2.3E-05	ENSRNOG000000031780	MT	1
16858 A_64_P146089	-1.602	0.188	1.5E-08	-1.613	0.265	3.5E-06	ENSRNOG000000031780	MT	1
17319 A_64_P109342	0.556	0.115	7.7E-05	-0.752	0.156	8.4E-05	ENSRNOG000000031780	MT	1
17552 A_64_P127173	0.542	0.089	3.7E-06	0.663	0.127	2.6E-05	ENSRNOG000000031780	MT	1
17573 A_64_P042099	0.955	0.117	3.0E-08	0.823	0.165	4.9E-05	ENSRNOG000000031780	MT	1
17634 A_64_P011339	0.578	0.071	3.1E-08	-0.988	0.100	1.0E-09	ENSRNOG000000031780	MT	1
19318 A_44_P393985	0.712	0.095	1.3E-07	-0.857	0.134	1.6E-06	ENSRNOG000000031780	MT	1
19343 A_64_P070068	0.762	0.107	3.3E-07	-1.201	0.152	5.5E-08	ENSRNOG000000031780	MT	1
19358 A_64_P114888	0.750	0.103	2.0E-07	-1.181	0.145	3.4E-08	ENSRNOG000000031780	MT	1
21099 A_64_P143316	0.659	0.102	1.3E-06	-1.123	0.144	6.8E-08	ENSRNOG000000031780	MT	1
21135 A_64_P118308	-1.481	0.108	3.6E-12	-1.374	0.148	4.9E-09	ENSRNOG000000031780	MT	1
21748 A_64_P071088	0.827	0.065	6.7E-12	1.108	0.091	2.0E-11	ENSRNOG000000031780	MT	1
22005 A_64_P114908	0.548	0.097	9.2E-06	-1.103	0.137	3.9E-08	ENSRNOG000000031780	MT	1
22436 A_64_P045775	1.023	0.130	5.7E-08	1.071	0.183	6.1E-06	ENSRNOG000000031780	MT	1
22567 A_64_P073048	0.723	0.097	1.6E-07	-1.097	0.138	4.7E-08	ENSRNOG000000031780	MT	1
22908 A_64_P130311	0.332	0.067	5.2E-05	-0.570	0.095	4.0E-06	ENSRNOG000000031780	MT	1
23212 A_44_P189674	0.660	0.105	2.2E-06	-0.952	0.149	1.7E-06	ENSRNOG000000031780	MT	1
23791 A_64_P067858	0.668	0.129	2.9E-05	-1.209	0.182	9.2E-07	ENSRNOG000000031780	MT	1
23878 A_64_P127998	0.496	0.087	9.1E-06	-1.072	0.124	1.1E-08	ENSRNOG000000031780	MT	1
23968 A_64_P039666	0.632	0.122	3.1E-05	-1.239	0.173	2.8E-07	ENSRNOG000000031780	MT	1
24098 A_64_P042811	-1.839	0.077	1.1E-17	-2.237	0.109	3.0E-16	ENSRNOG000000031780	MT	1
24725 A_64_P134912	0.820	0.110	1.4E-07	-1.534	0.155	1.0E-09	ENSRNOG000000031780	MT	1
25303 A_44_P450278	0.478	0.096	4.9E-05	-0.893	0.135	1.0E-06	ENSRNOG000000031780	MT	1
25670 A_64_P084678	0.384	0.078	5.5E-05	-0.587	0.110	2.0E-05	ENSRNOG000000031780	MT	1
28639 A_64_P068703	0.619	0.105	5.2E-06	-0.873	0.148	5.3E-06	ENSRNOG000000031780	MT	1
28808 A_64_P086859	0.612	0.077	4.9E-08	-0.805	0.109	1.6E-07	ENSRNOG000000031780	MT	1
28920 A_64_P087796	0.369	0.061	3.7E-06	-0.705	0.086	3.1E-08	ENSRNOG000000031780	MT	1
29106 A_64_P178321	-2.202	0.188	4.5E-10	-2.067	0.406	6.6E-05	ENSRNOG000000031780	MT	1
30061 A_64_P086167	2.938	0.101	1.7E-19	2.543	0.144	7.9E-15	ENSRNOG000000031780	MT	1
18904 A_64_P115786	2.713	0.096	3.0E-19	2.305	0.136	2.0E-14	ENSRNOG000000009609	X	1,615,920

28256 A_64_P003219	-1.225	0.143	2.0E-08	-1.004	0.195	3.7E-05 Asb11	ENSRNOG000000003452	X	31,780,425
11061 A_64_P095116	0.552	0.088	2.4E-06	-0.924	0.125	1.7E-07	ENSRNOG000000061492	X	50,184,697
14632 A_64_P136780	0.558	0.075	1.5E-07	-1.111	0.106	3.4E-10	ENSRNOG000000038181	X	63,440,163
15663 A_64_P048852	-1.237	0.079	9.6E-14	-1.005	0.111	5.2E-09	ENSRNOG00000006459	X	120,313,696
245 A_64_P024665	0.688	0.085	3.5E-08	0.874	0.120	2.1E-07 LOC688090			
415 A_42_P803752	-1.184	0.184	1.5E-06	-1.491	0.260	8.1E-06 RGD1562146			
6789 A_64_P046733	3.745	0.185	3.5E-12	2.781	0.235	5.9E-09 Idi2l			
7899 A_64_P006498	-1.466	0.142	4.6E-10	-1.852	0.201	3.8E-09 Ces1e			
10999 A_64_P070586	0.621	0.098	2.0E-06	0.804	0.139	7.1E-06 Krtap21-2			
11437 A_64_P154992	-0.595	0.088	8.3E-07	-0.671	0.119	1.2E-05 Trim30			
12669 A_64_P115157	-0.606	0.087	4.5E-07	-1.682	0.123	1.8E-12 Ces1e			
12941 A_64_P141251	0.656	0.125	2.6E-05	-0.997	0.177	1.0E-05 LOC681152			
15275 A_44_P760998	0.660	0.115	9.1E-06	1.019	0.156	1.5E-06 Fam185a			
18349 A_64_P157474	-0.453	0.080	9.4E-06	-0.623	0.113	1.4E-05 LOC500956			
19748 A_44_P142179	0.737	0.091	3.5E-08	0.697	0.128	1.6E-05 LOC679547			
19910 A_44_P138800	-0.699	0.135	3.2E-05	-1.036	0.192	1.7E-05 Gcap14			
22943 A_64_P037000	2.684	0.168	3.7E-13	3.498	0.291	7.9E-11 Fam155a			
23957 A_64_P139208	-1.455	0.140	4.3E-10	-1.841	0.199	3.4E-09 RT1-N1			
24636 A_42_P835445	-2.452	0.142	1.3E-14	-2.696	0.200	2.4E-12 LOC688893			
25709 A_64_P011719	-1.117	0.110	6.2E-10	-1.053	0.155	6.9E-07 Chmp1b			

Genes are regarded as significant for “shared” differential expression when they show $P < 1 \times 10^{-4}$ reproducibly in two types of comparison, ie, SHR/lzm versus WKY/lzm and SHRSP/lzm versus WKY/lzm, with a concordant direction of differential expression.

Table S3D. A list of significant transcripts for shared differential expression in the renal cortex.

no	ProbeName	SHR/lzm (vs WKY/lzm)			SHRSP/lzm (vs WKY/lzm)			GeneName	Ensembl_rat	Chr	Transcription_ start_site (Rnor_6.0)
		Fold change (log2-scale)	SE (log2-scale)	P-value	Fold change (log2-scale)	SE (log2-scale)	P-value				
2382	A_64_P063358	1.033	0.182	5.7E-05	1.519	0.171	4.1E-07	Samd5	ENSRNOG000000023549	1	3,763,392
20438	A_64_P063363	0.972	0.177	7.9E-05	1.412	0.167	7.1E-07	Samd5	ENSRNOG000000023549	1	3,763,392
30230	A_44_P1025861	0.693	0.082	7.4E-07	0.720	0.077	2.3E-07	Shprh	ENSRNOG00000014450	1	5,240,180
7233	A_64_P165046	-0.563	0.101	6.9E-05	-0.517	0.095	9.0E-05	RGD1309903	ENSRNOG00000011460	1	13,915,594
8464	A_64_P129293	1.273	0.221	5.0E-05	1.249	0.208	3.4E-05	RGD1306565	ENSRNOG000000031700	1	15,412,603
11055	A_44_P128306	0.372	0.068	8.1E-05	0.532	0.064	8.8E-07	Aldh8a1	ENSRNOG00000014907	1	16,910,069
914	A_44_P353836	-0.809	0.111	6.0E-06	-0.635	0.096	1.7E-05	RGD1306962	ENSRNOG00000016371	1	22,748,422
23955	A_64_P162940	-1.796	0.089	9.5E-12	-1.377	0.084	1.5E-10		ENSRNOG000000038251	1	77,782,825
7941	A_42_P689905	1.581	0.090	6.7E-11	2.157	0.085	4.5E-13	Apoc2	ENSRNOG00000018402	1	80,594,136
13915	A_64_P080941	-1.202	0.134	3.7E-07	-0.957	0.127	2.7E-06	LOC102556967	ENSRNOG000000033729	1	99,505,677
19968	A_44_P280954	-1.026	0.124	4.7E-06	-1.442	0.124	1.6E-07	Klk1c10	ENSRNOG000000046297	1	99,894,353
22453	A_44_P163243	-1.414	0.122	1.5E-08	-2.715	0.115	1.1E-12	Klks3	ENSRNOG000000032857	1	100,059,967
21264	A_44_P989658	1.262	0.151	1.4E-06	1.117	0.143	3.0E-06	(Klk4)	ENSRNOG000000032170	1	100,205,147
456	A_64_P016403	0.678	0.058	1.2E-08	0.321	0.054	3.8E-05	Ldha	ENSRNOG00000013009	1	102,900,286
9360	A_43_P11305	-1.940	0.104	2.8E-11	-0.941	0.098	1.5E-07	Tmem86a	ENSRNOG00000013663	1	103,172,987
26600	A_64_P131806	-1.831	0.145	5.2E-09	-0.739	0.137	9.6E-05	Tmem86a	ENSRNOG00000013663	1	103,172,987
14268	A_44_P250476	-0.928	0.082	2.0E-08	-0.714	0.077	2.5E-07	Zdhhc13	ENSRNOG00000014277	1	104,106,245
7527	A_64_P151448	-0.972	0.108	3.3E-07	-0.739	0.101	4.1E-06	Fancf	ENSRNOG000000023968	1	107,232,305
27710	A_44_P273783	-0.765	0.135	7.9E-05	-0.879	0.135	2.0E-05	Aldh1a3	ENSRNOG000000052070	1	127,337,882
4552	A_44_P496255	0.582	0.087	1.1E-05	0.507	0.082	2.5E-05	Slco3a1	ENSRNOG000000032798	1	136,073,540
30158	A_64_P035162	1.078	0.166	1.5E-05	1.223	0.157	1.8E-06	Ntrk3	ENSRNOG00000018674	1	140,262,503
19183	A_64_P133177	-0.799	0.069	1.5E-08	-0.677	0.065	5.7E-08	Sema4b	ENSRNOG000000025167	1	141,986,145
26335	A_64_P157285	0.964	0.081	1.1E-08	1.061	0.076	1.4E-09	RGD1560277 (in	ENSRNOG000000025003	1	142,027,250
25376	A_64_P109232	-2.306	0.137	1.1E-10	-2.115	0.129	1.6E-10	Nmb	ENSRNOG00000011011	1	142,724,511
3363	A_64_P016059	-1.183	0.085	1.3E-09	-1.085	0.080	1.9E-09	Homer2	ENSRNOG000000061450	1	143,535,583
4323	A_64_P028140	-0.661	0.082	1.4E-06	-0.733	0.078	2.0E-07	Plekhb1	ENSRNOG00000018627	1	165,680,206
28025	A_44_P520159	-0.684	0.108	1.8E-05	-0.669	0.101	1.2E-05	P2ry2	ENSRNOG00000019283	1	166,037,424
8799	A_64_P095313	0.751	0.068	2.7E-08	0.417	0.064	1.4E-05		ENSRNOG000000051149	1	166,727,805
14093	A_42_P788740	0.989	0.124	1.4E-06	0.754	0.117	1.5E-05	Folr2	ENSRNOG00000019890	1	166,919,302
11154	A_44_P398300	0.499	0.061	1.1E-06	0.421	0.057	3.8E-06	Fam160a2	ENSRNOG00000017408	1	170,238,890

13671 A_44_P212813	0.759	0.088	5.6E-07	0.977	0.083	1.2E-08	Acsm5	ENSRNOG000000031211	1	189,233,141
29269 A_64_P151353	1.895	0.058	1.4E-14	2.031	0.055	2.3E-15	Acsm5	ENSRNOG000000031211	1	189,241,593
10614 A_44_P395538	-0.402	0.053	2.8E-06	-0.294	0.050	4.4E-05	Rabep2	ENSRNOG000000018462	1	197,839,430
24957 A_64_P011779	0.696	0.105	1.2E-05	0.657	0.099	1.1E-05	Sult1a1	ENSRNOG000000019342	1	198,104,109
18482 A_44_P1002996	-0.516	0.067	2.3E-06	-0.535	0.063	7.6E-07	Ino80e	ENSRNOG000000019960	1	198,298,076
29205 A_44_P1029472	-0.533	0.064	9.4E-07	-0.357	0.061	4.1E-05	RGD1305592	ENSRNOG000000020217	1	198,450,688
15247 A_44_P1005462	1.462	0.141	5.9E-08	1.087	0.133	1.0E-06	Mylpf	ENSRNOG000000017645	1	198,655,742
14224 A_64_P045578	1.842	0.295	2.2E-05	1.944	0.278	6.5E-06	Rnf40	ENSRNOG000000018840	1	199,037,544
29778 A_44_P252921	-0.539	0.074	4.3E-06	-0.499	0.070	5.3E-06	Sec23ip	ENSRNOG000000020411	1	200,167,169
4254 A_42_P784614	0.518	0.093	7.1E-05	0.575	0.088	1.3E-05	Htra1	ENSRNOG000000020533	1	201,499,028
26900 A_44_P1039994	-0.915	0.157	4.3E-05	0.854	0.148	4.7E-05	Irf7	ENSRNOG000000017414	1	214,252,456
21515 A_44_P107596	-1.188	0.205	8.6E-05	-1.271	0.188	2.1E-05	Ctsw (interrupted	ENSRNOG000000027096	1	220,848,153
25349 A_44_P478066	-1.719	0.127	2.0E-09	0.643	0.119	9.7E-05	Incenp	ENSRNOG000000032929	1	225,948,626
20969 A_64_P081982	-1.214	0.121	9.5E-08	-0.949	0.114	9.0E-07	Pgm5	ENSRNOG000000015406	1	242,765,807
19312 A_44_P480433	-1.532	0.113	2.0E-09	-0.979	0.106	2.6E-07	Kazald1	ENSRNOG000000016058	1	264,827,739
25963 A_64_P129182	-1.130	0.136	9.0E-07	-0.805	0.128	2.1E-05	Npm3	ENSRNOG000000017622	1	265,506,046
2901 A_64_P157239	-0.575	0.081	5.8E-06	-0.660	0.077	5.9E-07	Sfxn2	ENSRNOG000000049308	1	266,333,440
26828 A_64_P043941	-1.751	0.131	2.4E-09	-1.335	0.124	3.7E-08	Sorcs1	ENSRNOG000000011313	1	270,472,866
3220 A_64_P066271	-0.742	0.090	9.3E-07	-0.561	0.084	1.1E-05	Mxi1	ENSRNOG000000034078	1	274,030,978
17839 A_64_P115991	-0.851	0.091	2.1E-07	-0.636	0.086	3.3E-06	Mxi1	ENSRNOG000000034078	1	274,030,978
22136 A_64_P066276	-0.974	0.075	3.7E-09	-0.751	0.071	4.9E-08	Mxi1	ENSRNOG000000034078	1	274,030,978
20097 A_44_P183488	0.493	0.078	1.9E-05	0.630	0.074	6.2E-07	Casp7	ENSRNOG000000056216	1	277,190,964
15734 A_44_P403005	-0.743	0.096	2.0E-06	-0.733	0.090	1.2E-06	Trub1	ENSRNOG000000017321	1	278,311,244
9184 A_43_P21414	-0.946	0.102	2.4E-07	-0.629	0.096	1.3E-05	Atg10	ENSRNOG000000016342	2	20,152,884
13620 A_43_P17958	0.535	0.074	4.6E-06	0.598	0.070	6.4E-07	Atg10	ENSRNOG000000016342	2	20,152,884
6596 A_43_P13126	0.671	0.095	5.9E-06	0.999	0.090	2.5E-08	Acot12	ENSRNOG000000061414	2	20,857,202
8784 A_44_P899264	-0.936	0.081	1.6E-08	-1.235	0.076	2.0E-10	Lhfp12	ENSRNOG000000011032	2	23,770,721
8031 A_64_P163219	-2.408	0.146	1.3E-09	-1.997	0.110	4.6E-10		ENSRNOG000000018615	2	30,780,121
18451 A_43_P12257	2.413	0.076	2.1E-14	1.563	0.072	3.6E-12	Esm1	ENSRNOG000000010797	2	45,104,305
13783 A_44_P252220	0.524	0.080	1.3E-05	0.488	0.075	1.5E-05	Mocs2	ENSRNOG000000056325	2	46,980,976
5239 A_42_P463754	0.445	0.079	6.5E-05	0.496	0.075	1.1E-05	Itga1	ENSRNOG000000053550	2	47,281,421
27193 A_64_P112889	-1.166	0.155	2.8E-06	-0.985	0.146	9.4E-06	Ccdc152	ENSRNOG000000039473	2	53,140,637
14909 A_64_P092509	-0.593	0.072	9.4E-07	-0.466	0.068	7.3E-06	Fbxo4	ENSRNOG000000015622	2	53,811,134

1843 A_42_P469751	-1.304	0.190	7.8E-06	-1.656	0.179	2.4E-07 C7	ENSRNOG000000061379	2	54,777,729
11752 A_64_P087930	-1.070	0.110	1.4E-07	-1.533	0.104	6.8E-10 C7	ENSRNOG000000061379	2	54,777,729
8100 A_44_P168265	0.704	0.109	1.6E-05	0.865	0.103	7.9E-07 Prkaa1	ENSRNOG000000012799	2	54,857,688
13068 A_44_P226928	-0.827	0.129	1.6E-05	-0.688	0.121	5.9E-05 Pdzd2	ENSRNOG000000013140	2	62,634,785
15982 A_42_P778330	-2.434	0.118	2.7E-11	-2.180	0.102	1.7E-11 Sox2	ENSRNOG000000012199	2	121,165,137
16967 A_44_P773166	-0.672	0.122	7.6E-05	-1.119	0.115	1.3E-07 Tmem144	ENSRNOG000000010081	2	178,612,470
22744 A_64_P055364	-0.670	0.103	1.4E-05	-0.891	0.097	2.8E-07 Tmem144	ENSRNOG000000010081	2	178,612,470
17924 A_64_P151602	-1.397	0.145	1.5E-07	-1.093	0.137	1.4E-06 Trim46	ENSRNOG000000055433	2	188,553,289
6842 A_42_P516658	-1.052	0.101	5.7E-08	-0.996	0.095	5.4E-08 Gatad2b	ENSRNOG000000015553	2	189,655,702
14643 A_43_P12519	-0.561	0.087	1.6E-05	-0.482	0.082	4.3E-05 S100a10	ENSRNOG000000023226	2	193,892,589
17352 A_44_P116875	0.988	0.118	8.5E-07	0.836	0.112	3.0E-06	ENSRNOG000000020836	2	195,617,021
10680 A_64_P140977	-1.175	0.103	1.9E-08	-0.959	0.097	1.2E-07 Prune	ENSRNOG000000021120	2	196,456,481
27712 A_64_P041307	-0.856	0.086	1.0E-07	-0.773	0.081	1.8E-07 Tars2	ENSRNOG000000057194	2	197,878,142
8030 A_44_P393822	0.479	0.086	6.8E-05	0.463	0.081	5.2E-05 Plekho1	ENSRNOG000000021170	2	198,120,120
4450 A_42_P649672	1.667	0.107	3.1E-10	1.759	0.101	7.0E-11 Sv2a	ENSRNOG000000021182	2	198,321,142
29644 A_44_P428326	3.907	0.154	4.6E-13	1.806	0.146	6.3E-09 Hmgcs2	ENSRNOG000000019120	2	200,452,624
24143 A_44_P506299	1.677	0.126	2.6E-09	1.671	0.119	1.3E-09 RGD1562344	ENSRNOG000000037149	2	206,314,213
30118 A_64_P039308	-0.570	0.068	7.5E-07	-0.466	0.064	3.9E-06 Phf1f1	ENSRNOG000000019785	2	206,454,208
18048 A_44_P398167	-0.826	0.062	2.5E-09	-0.761	0.058	3.4E-09 Prdx1	ENSRNOG000000017695	2	208,738,132
12324 A_43_P11776	0.952	0.072	3.0E-09	0.417	0.068	2.8E-05 Gstm1	ENSRNOG000000029726	2	210,809,306
25176 A_64_P083399	-0.838	0.127	1.2E-05	-0.879	0.119	3.6E-06	ENSRNOG000000023148	2	216,863,428
27544 A_44_P385704	-1.003	0.115	5.0E-07	-0.971	0.108	3.6E-07	ENSRNOG000000023148	2	216,863,428
8271 A_64_P080876	-0.756	0.105	4.7E-06	-0.671	0.099	9.2E-06 Clca4	ENSRNOG000000029889	2	250,862,419
4532 A_44_P264102	-0.673	0.062	3.6E-08	-0.510	0.059	5.3E-07 Bcl10	ENSRNOG000000042389	2	251,805,392
17603 A_64_P061658	-1.244	0.089	3.4E-09	-0.725	0.077	3.7E-07 Entpd2	ENSRNOG000000013102	3	2,617,805
24094 A_64_P064944	-0.444	0.059	3.0E-06	-0.395	0.056	5.8E-06 Trub2	ENSRNOG000000043189	3	8,348,746
24380 A_64_P151046	-0.610	0.064	1.8E-07	-0.486	0.060	1.3E-06 Trub2	ENSRNOG000000043189	3	8,348,746
29855 A_44_P945862	-0.795	0.076	5.8E-08	-0.595	0.072	9.7E-07 Trub2	ENSRNOG000000043189	3	8,348,746
26230 A_44_P213133	-1.738	0.070	6.2E-13	-1.840	0.066	1.3E-13 Endog	ENSRNOG000000016033	3	8,741,766
21696 A_64_P096782	-0.868	0.101	6.3E-07	-0.633	0.096	1.2E-05 Ier5l	ENSRNOG000000024846	3	9,037,942
6137 A_64_P119821	-1.265	0.083	4.6E-10	-0.906	0.079	1.6E-08 RGD1311084	ENSRNOG000000018486	3	9,636,058
22393 A_43_P18366	1.644	0.084	1.5E-11	1.627	0.079	7.8E-12 Tor1b	ENSRNOG000000006435	3	9,792,899
24771 A_43_P10292	-0.459	0.079	4.8E-05	-0.414	0.075	7.3E-05 siat7D (St6galna	ENSRNOG000000048870	3	11,607,225

29474 A_44_P532754	-0.576	0.092	2.2E-05	-0.590	0.087	8.9E-06 Pbx3	ENSRNOG000000022162	3	13,435,979
19913 A_44_P102477	-1.700	0.152	2.3E-08	-1.118	0.143	1.8E-06 Morn5	ENSRNOG000000026111	3	15,379,109
9295 A_64_P057740	-0.890	0.127	6.2E-06	-0.862	0.120	4.6E-06 Ccdc148	ENSRNOG000000057740	3	45,210,474
19516 A_64_P074918	0.574	0.093	2.5E-05	0.501	0.088	5.5E-05 Grb14	ENSRNOG000000052498	3	51,054,378
12780 A_64_P025310	-1.558	0.094	1.4E-10	-1.284	0.089	8.6E-10 Galnt3	ENSRNOG00000005727	3	52,212,412
8214 A_64_P077658	-1.615	0.180	3.5E-07	-1.055	0.169	2.2E-05	ENSRNOG000000005868	3	52,361,060
30302 A_64_P308666	-1.744	0.200	5.1E-07	-1.180	0.189	2.2E-05 Ttc21b	ENSRNOG000000005868	3	52,361,060
25593 A_44_P166206	1.049	0.104	8.5E-08	0.644	0.098	1.3E-05 Nostrin	ENSRNOG000000006611	3	55,369,214
17479 A_64_P154292	-0.305	0.053	5.2E-05	-0.406	0.050	1.2E-06 Hnrnpa3	ENSRNOG000000052968	3	62,481,323
26189 A_43_P23211	-0.624	0.104	3.4E-05	-0.562	0.099	5.5E-05 Ssfa2	ENSRNOG000000005865	3	66,593,934
24139 A_44_P992697	-1.587	0.088	4.9E-11	-1.272	0.083	4.2E-10 Dusp19	ENSRNOG000000008868	3	67,849,966
8277 A_64_P022076	1.121	0.070	2.3E-10	0.494	0.066	3.1E-06 Slc43a3	ENSRNOG000000061768	3	72,329,967
17375 A_43_P15275	-1.960	0.075	3.1E-13	-2.078	0.071	6.2E-14 Ptpnj	ENSRNOG000000034025	3	79,390,956
13379 A_44_P271769	-0.589	0.076	1.9E-06	-0.551	0.071	2.1E-06 Acp2	ENSRNOG000000013594	3	80,021,440
18771 A_44_P107766	-1.021	0.073	1.3E-09	-0.858	0.069	5.9E-09 RGD1309540	ENSRNOG000000014798	3	80,349,145
25223 A_64_P115142	-0.559	0.090	2.4E-05	-0.636	0.085	3.1E-06 Accs	ENSRNOG000000009199	3	82,756,953
21496 A_44_P808666	0.802	0.085	1.9E-07	0.795	0.080	1.0E-07 Wt1	ENSRNOG000000013074	3	95,133,713
11265 A_43_P14888	-0.662	0.083	1.4E-06	-0.465	0.078	3.4E-05 Scg5	ENSRNOG000000007542	3	105,279,462
15624 A_43_P19265	0.642	0.065	1.2E-07	0.621	0.061	8.3E-08 Shf	ENSRNOG000000028685	3	114,307,250
3427 A_44_P1024721	1.039	0.111	2.1E-07	1.168	0.104	2.3E-08 Slc28a2	ENSRNOG000000028668	3	114,355,798
5981 A_64_P111786	-1.068	0.049	3.7E-12	-0.446	0.046	1.5E-07 Sqrdl	ENSRNOG000000000172	3	114,900,343
16711 A_64_P081944	-0.425	0.068	2.0E-05	-0.384	0.064	3.1E-05 Eid1	ENSRNOG000000008452	3	117,938,500
834 A_42_P561329	-0.897	0.095	1.9E-07	-0.812	0.089	3.1E-07 Anapc1	ENSRNOG000000016965	3	121,226,125
19676 A_64_P098527	-0.708	0.066	4.4E-08	-0.562	0.063	3.6E-07 Chchd5	ENSRNOG000000018491	3	121,660,110
29825 A_64_P000678	0.582	0.082	5.3E-06	0.501	0.077	1.4E-05 Sirpa	ENSRNOG000000004763	3	122,114,754
14641 A_64_P000596	-0.412	0.074	6.9E-05	-0.455	0.070	1.4E-05 Nop56	ENSRNOG000000056237	3	122,807,236
12403 A_44_P398033	0.668	0.074	3.5E-07	1.165	0.070	1.4E-10 Prnp	ENSRNOG000000021259	3	124,515,978
18620 A_64_P125275	0.397	0.073	8.8E-05	0.506	0.069	3.7E-06 Snrpb2	ENSRNOG000000004967	3	137,137,980
18341 A_42_P842833	-0.696	0.081	6.5E-07	-0.790	0.077	6.8E-08 Srxn1	ENSRNOG000000031167	3	147,609,095
12668 A_44_P363204	-0.496	0.080	2.4E-05	-0.424	0.076	6.5E-05 Csnk2a1	ENSRNOG000000005276	3	147,713,821
12542 A_64_P042611	-2.250	0.295	2.5E-06	-1.973	0.279	5.6E-06	ENSRNOG000000036900	3	147,992,754
2111 A_64_P009255	1.315	0.128	7.1E-08	1.174	0.121	1.4E-07 Foxs1	ENSRNOG000000008529	3	148,407,778
2734 A_42_P777935	0.567	0.096	3.9E-05	0.742	0.091	1.1E-06 RGD1311066	ENSRNOG000000020086	3	152,626,757

18249 A_64_P011809	-2.363	0.159	6.2E-10	-1.940	0.150	3.8E-09 RGD1563354	ENSRNOG000000014424	3	154,716,239
5599 A_43_P18817	-1.405	0.144	1.3E-07	-1.291	0.136	1.8E-07 Ifi52	ENSRNOG000000007692	3	159,392,193
27964 A_44_P576289	-1.363	0.169	1.3E-06	-1.007	0.159	1.9E-05 Stk4	ENSRNOG000000013529	3	160,467,552
3790 A_42_P589025	-0.848	0.140	3.0E-05	-0.713	0.132	9.6E-05 Slc12a5	ENSRNOG000000018111	3	161,425,988
20958 A_64_P002904	-0.594	0.103	4.7E-05	-0.587	0.097	2.9E-05 Pmepa1	ENSRNOG000000050404	3	171,342,646
16812 A_64_P058749	0.530	0.073	4.4E-06	0.465	0.069	9.7E-06	ENSRNOG000000043150	3	176,479,335
13444 A_42_P623913	0.707	0.107	1.2E-05	0.634	0.101	2.1E-05 Sox18	ENSRNOG000000016248	3	177,179,127
15543 A_44_P307964	-0.743	0.067	2.5E-08	-0.645	0.063	7.2E-08 Polr3k	ENSRNOG000000017843	3	177,374,812
9300 A_64_P054808	0.490	0.069	5.3E-06	0.598	0.065	2.6E-07 Cd36	ENSRNOG000000040108	4	14,001,761
15617 A_64_P113793	0.448	0.071	1.8E-05	0.703	0.066	4.8E-08 Cd36	ENSRNOG000000040108	4	14,151,374
11416 A_64_P113795	0.633	0.106	3.3E-05	0.871	0.100	4.9E-07 LOC685953	ENSRNOG000000062188	4	16,825,767
21357 A_64_P016751	-0.875	0.069	4.6E-09	-0.870	0.065	2.3E-09 Tmem243 (RGD1	ENSRNOG000000042758	4	21,920,651
12659 A_64_P010925	1.207	0.099	7.9E-09	1.442	0.093	3.6E-10 Abcb1b	ENSRNOG000000008012	4	22,307,453
1809 A_43_P12783	-0.615	0.075	1.1E-06	-0.627	0.071	4.5E-07 Col1a2	ENSRNOG000000011292	4	31,534,225
15433 A_44_P959463	1.181	0.132	3.8E-07	1.223	0.124	1.2E-07 AABR07059877.	ENSRNOG000000039626	4	39,727,953
17535 A_64_P072314	0.726	0.067	3.5E-08	0.721	0.063	1.8E-08 AABR07059925.	ENSRNOG000000052702	4	43,915,333
7925 A_64_P015312	-0.542	0.077	6.3E-06	-0.422	0.073	4.8E-05 Fam3c	ENSRNOG000000060349	4	49,439,867
15750 A_64_P077103	-0.580	0.097	3.4E-05	-0.587	0.091	1.6E-05 Kcp	ENSRNOG000000021855	4	56,786,754
29522 A_44_P489995	-0.627	0.050	6.3E-09	-0.600	0.048	5.1E-09 Mrps33	ENSRNOG000000026528	4	67,610,710
12618 A_64_P009490	0.766	0.122	2.1E-05	1.019	0.115	4.3E-07 LOC679651	ENSRNOG000000047635	4	68,011,932
29383 A_44_P228928	0.916	0.131	6.2E-06	1.284	0.123	5.7E-08 Trpv5	ENSRNOG000000015394	4	70,974,006
7316 A_43_P16967	-1.396	0.148	6.9E-07	-1.453	0.136	1.8E-07 Snx10	ENSRNOG000000011944	4	81,311,490
7404 A_43_P23115	1.842	0.119	3.5E-10	2.550	0.112	2.0E-12 Inmt	ENSRNOG000000011250	4	85,386,231
7853 A_44_P758470	-1.096	0.072	4.6E-10	-1.100	0.068	2.0E-10 Ecop	ENSRNOG00000006646	4	88,441,067
13336 A_64_P097974	0.490	0.072	9.1E-06	0.372	0.068	8.5E-05 St3gal5	ENSRNOG000000010284	4	99,937,558
6906 A_64_P130496	-1.252	0.158	1.6E-06	-1.377	0.149	2.5E-07	ENSRNOG000000013605	4	100,380,578
20592 A_44_P402507	-0.772	0.072	3.8E-08	-1.029	0.068	4.4E-10 Retsat	ENSRNOG000000014090	4	100,465,170
6125 A_44_P399999	0.407	0.052	2.0E-06	0.429	0.049	5.4E-07 Suc1g1	ENSRNOG000000005587	4	101,180,404
9251 A_64_P019687	-1.130	0.129	4.7E-07	-0.658	0.121	9.0E-05 LOC500227	ENSRNOG000000009917	4	114,854,458
14517 A_44_P1010867	-0.358	0.065	7.4E-05	-0.405	0.061	1.1E-05 Mobkl1b	ENSRNOG000000059474	4	115,024,927
21301 A_44_P268864	0.692	0.081	6.3E-07	0.446	0.076	4.2E-05 Mgl1	ENSRNOG000000014508	4	120,671,489
25583 A_64_P128971	1.199	0.153	3.0E-06	1.050	0.146	6.9E-06 Chst13	ENSRNOG000000025930	4	122,237,754
11102 A_44_P917327	1.199	0.183	1.3E-05	1.872	0.172	3.4E-08 Lrtm2	ENSRNOG000000007508	4	151,390,263

9034 A_64_P114913	-1.000	0.134	3.1E-06	-1.189	0.126	2.0E-07 Vwf	ENSRNOG00000019689	4	158,088,505
12161 A_64_P136501	-0.804	0.111	4.2E-06	-1.020	0.104	1.3E-07 Vwf	ENSRNOG00000019689	4	158,088,505
9918 A_64_P033872	-0.964	0.091	4.4E-08	-0.460	0.085	9.6E-05 Etf6	ENSRNOG00000005984	4	167,754,525
11993 A_43_P21564	0.667	0.105	2.7E-05	0.817	0.105	3.2E-06 Tp53inp1	ENSRNOG00000007964	5	24,410,863
5840 A_42_P526030	0.798	0.073	3.0E-08	0.382	0.068	6.8E-05 Decr1	ENSRNOG00000008236	5	29,601,748
17136 A_64_P067968	-0.789	0.109	4.4E-06	-0.850	0.103	9.5E-07 RGD1562865	ENSRNOG00000006170	5	47,546,014
21588 A_42_P680570	-0.682	0.079	5.8E-07	-0.548	0.075	3.7E-06 Nfx1	ENSRNOG00000009015	5	57,291,156
4924 A_42_P508921	1.397	0.114	7.6E-09	1.195	0.108	2.6E-08 Aqp3	ENSRNOG00000009797	5	57,429,245
321 A_42_P698240	-1.872	0.102	3.7E-11	-1.899	0.096	1.4E-11 Ptgr1	ENSRNOG00000015072	5	76,129,441
13424 A_44_P175822	-0.813	0.116	6.1E-06	-0.693	0.109	1.8E-05 Hdhd3	ENSRNOG00000015195	5	78,361,647
29767 A_44_P454532	1.034	0.162	1.7E-05	0.943	0.153	2.5E-05 Ambp	ENSRNOG00000006889	5	78,985,990
13242 A_44_P1040796	0.926	0.054	9.8E-11	1.064	0.051	6.9E-12 Atp6v1g1	ENSRNOG00000008163	5	79,367,663
12834 A_44_P189461	1.108	0.135	1.0E-06	0.829	0.127	1.4E-05 C8b	ENSRNOG00000007639	5	124,300,477
23037 A_43_P15784	-1.177	0.114	6.2E-08	-1.423	0.107	2.6E-09 Cyp4a3	ENSRNOG00000009741	5	134,484,839
16873 A_64_P040870	1.716	0.119	9.2E-10	0.658	0.112	4.3E-05 Cyp4a1	ENSRNOG00000009597	5	134,492,756
3744 A_43_P10290	-3.319	0.093	3.9E-15	-3.022	0.087	6.3E-15 Tspan1	ENSRNOG00000023320	5	135,024,447
9670 A_44_P117119	1.443	0.145	1.0E-07	2.621	0.137	2.1E-11 Hpdl	ENSRNOG00000018143	5	135,677,432
20248 A_64_P138415	0.595	0.107	7.2E-05	0.671	0.101	1.1E-05 Cldn19	ENSRNOG00000007922	5	138,300,107
9897 A_44_P314295	-1.334	0.125	9.1E-07	-0.845	0.109	1.6E-05 Zmynd12	ENSRNOG00000022199	5	138,470,069
7584 A_64_P055067	0.352	0.055	1.7E-05	0.603	0.052	1.4E-08 Ppcs	ENSRNOG00000008572	5	138,470,096
24137 A_64_P114308	-0.677	0.098	7.3E-06	-0.592	0.092	1.7E-05 Heyl	ENSRNOG00000015318	5	140,923,914
13799 A_64_P157944	0.615	0.075	1.0E-06	0.415	0.071	4.0E-05	ENSRNOG00000043364	5	146,973,932
955 A_64_P032604	0.789	0.073	3.8E-08	0.669	0.069	1.4E-07 Ak2	ENSRNOG00000000122	5	147,185,474
1608 A_64_P032611	0.641	0.066	1.4E-07	0.720	0.062	1.6E-08 Ak2	ENSRNOG00000000122	5	147,185,474
4477 A_42_P766913	-0.395	0.064	2.4E-05	-0.378	0.060	2.0E-05 Ccdc28b	ENSRNOG00000047578	5	147,828,449
4551 A_43_P16491	-0.497	0.089	6.6E-05	-0.511	0.084	2.7E-05 Col16a1	ENSRNOG000000031475	5	148,257,642
22186 A_64_P001401	0.613	0.089	7.7E-06	0.584	0.084	7.0E-06 Tinagl1	ENSRNOG00000013179	5	148,392,697
29934 A_64_P110798	-0.646	0.108	3.3E-05	-0.708	0.102	6.6E-06 Serinc2	ENSRNOG00000012989	5	148,492,232
2829 A_43_P15141	-0.538	0.067	1.3E-06	-0.471	0.063	3.0E-06 LOC682988	ENSRNOG00000047303	5	150,653,172
23745 A_44_P175875	0.884	0.101	5.1E-07	0.966	0.096	8.5E-08 Pigv	ENSRNOG00000000121	5	151,895,016
8203 A_44_P1004790	1.129	0.136	9.4E-07	0.691	0.129	1.0E-04 Slc30a2	ENSRNOG000000054142	5	152,559,577
28501 A_64_P036381	1.102	0.128	6.0E-07	0.690	0.121	5.4E-05 Paqr7	ENSRNOG00000022054	5	152,708,775
9445 A_44_P398691	-0.598	0.083	4.8E-06	-0.525	0.078	1.0E-05 Atp13a2	ENSRNOG00000008052	5	159,512,285

7805 A_44_P291028	-0.739	0.100	3.4E-06	-0.939	0.094	1.0E-07	Arhgef19	ENSRNOG000000047967	5	159,755,535
24005 A_64_P001225	-0.916	0.144	1.7E-05	-2.365	0.135	7.0E-11	Mthfr	ENSRNOG000000008553	5	164,845,925
24306 A_44_P999125	1.583	0.101	2.9E-10	0.901	0.095	1.9E-07	Masp2	ENSRNOG000000011258	5	165,415,278
28901 A_44_P429298	-1.738	0.129	2.3E-09	-2.512	0.122	7.7E-12	Tnfrsf9	ENSRNOG000000036942	5	168,009,393
14557 A_44_P272301	-0.587	0.091	1.5E-05	-0.657	0.085	2.2E-06	Mxra8	ENSRNOG000000019244	5	173,288,447
2366 A_42_P538617	-0.451	0.067	9.5E-06	-0.349	0.063	7.3E-05	Ift172	ENSRNOG000000057813	6	26,474,071
3481 A_43_P19743	0.491	0.061	1.2E-06	0.488	0.057	6.6E-07	Krtcap3	ENSRNOG000000047941	6	26,486,695
12750 A_64_P147334	-0.832	0.118	5.7E-06	-0.663	0.111	3.4E-05	Fkbp1b	ENSRNOG000000047143	6	29,977,797
27284 A_43_P14872	0.740	0.119	2.3E-05	0.634	0.112	6.1E-05	Sdc1	ENSRNOG000000059947	6	33,885,495
3351 A_64_P061830	-1.168	0.136	5.9E-07	-0.786	0.128	2.6E-05	Fam84a	ENSRNOG000000004084	6	39,363,458
25705 A_64_P061835	-1.255	0.150	8.0E-07	-0.820	0.141	4.6E-05	Fam84a	ENSRNOG000000004084	6	39,363,458
1766 A_42_P622681	1.705	0.187	3.1E-07	1.732	0.177	1.2E-07	Prkar2b	ENSRNOG000000009079	6	51,356,383
27573 A_44_P945846	0.648	0.103	2.0E-05	1.049	0.097	3.6E-08	Twistnb	ENSRNOG000000010750	6	52,751,106
1431 A_42_P600642	-0.706	0.103	7.9E-06	-0.652	0.097	1.0E-05	Ispd	ENSRNOG000000006199	6	55,881,484
6710 A_64_P008628	-0.528	0.058	3.0E-07	-0.323	0.055	3.9E-05	Ndufa10l1	ENSRNOG000000062245	6	62,798,384
6674 A_64_P080871	-0.611	0.103	3.6E-05	-0.552	0.097	5.6E-05	RGD1307621	ENSRNOG000000023230	6	86,651,196
23405 A_64_P045378	-0.603	0.069	5.2E-07	-0.656	0.065	9.1E-08		ENSRNOG000000056721	6	86,852,323
9006 A_64_P003859	-0.928	0.140	1.2E-05	-0.912	0.132	7.3E-06	Rtn1	ENSRNOG000000004794	6	94,980,004
5759 A_64_P065368	0.836	0.081	6.7E-08	0.789	0.076	6.6E-08	Acot4	ENSRNOG000000046864	6	107,517,668
16745 A_64_P067447	0.827	0.066	6.0E-09	0.703	0.063	2.3E-08	Acot4	ENSRNOG000000046864	6	107,517,668
18088 A_44_P337991	0.638	0.075	7.1E-07	0.737	0.071	6.0E-08	Acot3	ENSRNOG000000053460	6	107,531,528
15326 A_64_P103936	-2.982	0.227	1.8E-08	-1.924	0.171	1.1E-07	Acot5	ENSRNOG000000032508	6	107,550,904
14620 A_64_P124473	-1.305	0.128	7.5E-08	-1.615	0.121	2.3E-09	Ltbp2	ENSRNOG000000012094	6	108,596,569
20332 A_64_P067000	-1.738	0.171	7.7E-08	-0.966	0.161	3.3E-05	Prima1	ENSRNOG000000008915	6	127,127,413
7028 A_43_P13410	1.888	0.157	9.6E-09	2.046	0.148	1.6E-09	Serpina4	ENSRNOG000000009788	6	127,743,971
1711 A_44_P530131	-0.702	0.118	3.6E-05	-0.779	0.111	6.3E-06	Asb2	ENSRNOG000000057803	6	128,989,812
3416 A_64_P019200	-0.756	0.124	7.8E-05	-1.015	0.124	5.3E-06	RGD1560608	ENSRNOG000000043137	6	135,856,218
9408 A_64_P051786	-0.541	0.076	5.1E-06	-0.574	0.071	1.3E-06	Klc1	ENSRNOG000000011572	6	136,330,383
17421 A_64_P018891	-0.724	0.122	3.9E-05	-0.643	0.115	7.0E-05		ENSRNOG000000013661	6	136,720,266
11175 A_64_P002455	-1.007	0.066	4.2E-10	-1.005	0.062	2.0E-10	LOC690422	ENSRNOG000000005153	6	137,967,401
15597 A_64_P103580	-1.172	0.083	1.2E-09	-1.081	0.078	1.6E-09	LOC690422	ENSRNOG000000005153	6	137,967,401
17240 A_44_P147572	-2.190	0.272	1.3E-06	-2.776	0.257	3.6E-08		ENSRNOG000000034190	6	138,508,753
21885 A_44_P643807	-0.374	0.063	3.4E-05	-0.382	0.059	1.5E-05	Arl13b	ENSRNOG000000047194	7	1,188,165

15222 A_64_P040620	-0.551	0.052	4.4E-08	-0.365	0.049	3.0E-06	Sarnp	ENSRNOG000000030520	7	3,246,220
5393 A_64_P017836	2.047	0.258	1.5E-06	1.684	0.243	7.0E-06	Creb3l3	ENSRNOG000000032202	7	11,490,852
12776 A_64_P142988	-0.755	0.079	1.6E-07	-0.733	0.074	1.1E-07	Tmprss9	ENSRNOG000000032429	7	11,699,436
28290 A_64_P139250	-0.853	0.094	3.3E-07	-0.737	0.089	9.4E-07	Tmprss9	ENSRNOG000000032429	7	11,699,436
13366 A_64_P085595	-0.371	0.059	2.1E-05	-0.372	0.056	1.1E-05	Ilvbl	ENSRNOG000000028512	7	14,054,639
10600 A_64_P099017	-1.919	0.193	1.0E-07	-1.716	0.182	1.9E-07	Cyp4f17	ENSRNOG000000062306	7	14,529,483
15805 A_64_P255450	-0.860	0.081	4.5E-08	-0.575	0.076	2.7E-06	Zfp799	ENSRNOG000000032552	7	15,072,703
5343 A_64_P088382	2.179	0.212	6.8E-08	1.866	0.200	2.2E-07	Angptl4	ENSRNOG000000007545	7	18,634,079
11774 A_42_P827204	-1.013	0.099	7.2E-08	-0.792	0.093	6.9E-07	Ckap4	ENSRNOG000000008016	7	24,939,498
19762 A_64_P076900	-0.586	0.082	5.0E-06	-0.493	0.077	1.7E-05	Nedd1	ENSRNOG000000004011	7	33,584,564
12870 A_64_P146682	-1.052	0.107	1.2E-07	-1.050	0.101	6.0E-08	Pctk2	ENSRNOG000000004148	7	34,001,506
9888 A_64_P025286	0.983	0.088	2.3E-08	1.231	0.083	5.7E-10	Lyz2	ENSRNOG000000005825	7	60,341,264
18940 A_64_P072442	1.288	0.135	1.7E-07	1.466	0.127	1.7E-08	Tsfm	ENSRNOG000000048843	7	70,319,346
19834 A_64_P036553	1.719	0.105	1.6E-10	1.915	0.099	1.7E-11	Rdh2	ENSRNOG000000029651	7	70,980,422
7840 A_44_P318662	-1.140	0.177	1.5E-05	-1.376	0.167	9.6E-07	Tac2	ENSRNOG000000004229	7	71,023,976
27443 A_64_P036548	0.926	0.121	2.4E-06	1.193	0.114	5.8E-08	Rdh2	ENSRNOG000000029651	7	71,057,911
27543 A_44_P366303	-1.447	0.137	5.0E-08	-1.284	0.129	1.1E-07	Matn2	ENSRNOG000000006060	7	72,985,495
6053 A_44_P417489	-0.731	0.061	1.0E-08	-0.615	0.058	4.4E-08	Utp23	ENSRNOG000000004387	7	91,384,187
27530 A_44_P341075	0.648	0.080	1.2E-06	0.719	0.075	1.7E-07	Enpp2	ENSRNOG000000004089	7	94,563,001
13819 A_44_P324066	-0.782	0.129	3.0E-05	-0.739	0.122	2.9E-05	Fam91a1	ENSRNOG000000008271	7	98,302,953
14630 A_64_P134465	-0.713	0.057	5.9E-09	-0.629	0.054	1.4E-08	Fam91a1	ENSRNOG000000008271	7	98,302,953
16387 A_64_P012232	-1.294	0.123	5.0E-08	-1.247	0.116	3.8E-08	Sqle	ENSRNOG000000009550	7	99,609,191
2500 A_64_P065611	1.405	0.085	1.4E-10	1.336	0.080	1.2E-10	Khdrbs3	ENSRNOG000000009539	7	110,031,696
26593 A_44_P1049252	0.446	0.055	1.2E-06	0.321	0.052	2.4E-05	Naprt1	ENSRNOG000000007939	7	116,926,555
18442 A_64_P044345	0.984	0.089	2.6E-08	0.886	0.083	4.5E-08	Plec	ENSRNOG000000023781	7	117,267,803
21070 A_42_P692476	0.946	0.142	1.1E-05	0.761	0.134	5.8E-05	Slc39a4	ENSRNOG000000014314	7	117,680,004
28100 A_44_P450471	-0.527	0.084	2.0E-05	-0.466	0.079	3.9E-05	Ppp1r16a	ENSRNOG000000015450	7	117,734,002
7795 A_64_P044137	-0.579	0.088	1.3E-05	-0.555	0.083	1.0E-05	Lrrc24	ENSRNOG000000016204	7	117,784,638
28509 A_44_P267706	0.933	0.105	4.2E-07	0.897	0.099	3.3E-07	Apol11a	ENSRNOG000000023122	7	118,840,634
24480 A_44_P286788	0.826	0.116	5.0E-06	0.659	0.109	3.0E-05	Ncf4	ENSRNOG000000006940	7	119,482,272
19289 A_44_P975458	-0.747	0.091	1.1E-06	-0.711	0.086	9.5E-07	C1qtnf6	ENSRNOG000000007300	7	119,753,290
13898 A_44_P445070	-0.906	0.093	1.3E-07	-0.928	0.087	4.6E-08	Lgals1	ENSRNOG000000009884	7	120,153,184
25974 A_43_P12557	0.696	0.058	9.6E-09	0.693	0.055	4.8E-09	Polr2f	ENSRNOG000000011214	7	120,380,544

30340 A_44_P930152	1.587	0.106	5.5E-10	1.738	0.100	7.5E-11 Mpped1	ENSRNOG00000010834	7	124,680,294
4907 A_64_P138430	-1.169	0.114	1.4E-07	-1.053	0.099	8.6E-08 Odf3b	ENSRNOG00000037060	7	130,350,570
16698 A_64_P000650	-0.664	0.085	1.7E-06	-0.626	0.080	1.8E-06 Arsa	ENSRNOG00000012953	7	130,451,283
26026 A_64_P060569	-0.566	0.061	2.6E-07	-0.482	0.058	8.9E-07 Arsa	ENSRNOG00000012953	7	130,451,283
25452 A_64_P012962	-2.088	0.106	6.6E-10	-1.872	0.085	2.0E-10	ENSRNOG00000054046	7	143,239,617
15494 A_44_P138838	-3.557	0.138	3.7E-13	-3.767	0.130	7.5E-14 Krt76	ENSRNOG00000031785	7	143,497,108
8405 A_42_P660129	-0.995	0.122	1.1E-06	-0.771	0.115	1.0E-05 Casp12	ENSRNOG00000033434	8	2,659,865
17711 A_44_P119527	-1.887	0.105	4.6E-11	-1.778	0.099	4.6E-11 Med17	ENSRNOG00000051989	8	13,526,025
8626 A_44_P100886	1.345	0.128	2.2E-07	1.368	0.123	1.1E-07	ENSRNOG00000010999	8	13,909,188
11775 A_44_P518434	-0.901	0.080	2.2E-08	-0.763	0.076	8.6E-08 Mrpl4	ENSRNOG00000020659	8	22,021,213
16694 A_64_P153442	-0.454	0.061	3.4E-06	-0.318	0.058	8.0E-05	ENSRNOG00000014331	8	23,282,989
28883 A_44_P177678	-0.770	0.120	1.6E-05	-0.660	0.113	4.4E-05 LOC503192	ENSRNOG00000014331	8	23,282,989
18590 A_64_P025538	-1.055	0.143	3.5E-06	-0.905	0.135	1.0E-05 UBASH3B*	ENSRNOG00000008187	8	45,375,435
20866 A_44_P1030225	1.209	0.135	3.7E-07	1.526	0.127	9.7E-09 Apoa4	ENSRNOG00000055909	8	50,537,009
15342 A_44_P161233	0.456	0.067	8.1E-06	0.401	0.063	1.7E-05 Il18	ENSRNOG00000009848	8	54,993,859
12430 A_43_P14436	-0.908	0.124	3.8E-06	-0.723	0.117	2.4E-05 Pou2af1	ENSRNOG00000011500	8	55,603,968
8832 A_42_P794120	-0.930	0.156	3.6E-05	-1.432	0.147	1.4E-07 Stra6	ENSRNOG00000008312	8	62,925,357
10264 A_64_P149824	0.540	0.077	6.2E-06	0.476	0.073	1.3E-05 Ostbeta	ENSRNOG00000028889	8	70,932,986
26700 A_64_P151869	0.679	0.082	9.9E-07	0.749	0.078	1.5E-07 Myo5a	ENSRNOG00000058866	8	82,037,977
14777 A_64_P156682	-0.946	0.083	1.8E-08	-0.569	0.078	4.0E-06 Hmgn3	ENSRNOG00000031032	8	90,664,554
16214 A_64_P006794	-0.884	0.094	2.0E-07	-0.890	0.088	8.8E-08 Plod2	ENSRNOG00000030183	8	99,977,334
12498 A_44_P162115	2.037	0.086	1.1E-12	2.045	0.081	4.7E-13 Slc9a9	ENSRNOG00000008554	8	102,304,095
1145 A_42_P466706	-1.610	0.122	2.8E-09	-0.903	0.115	1.7E-06 PCOLCE2	ENSRNOG00000046848	8	103,459,161
9017 A_44_P189262	-1.007	0.141	1.2E-05	1.019	0.107	6.0E-07 Camkv	ENSRNOG00000058938	8	116,715,755
11142 A_44_P396460	-0.445	0.063	5.6E-06	-0.319	0.059	9.8E-05 Scap	ENSRNOG00000020853	8	118,570,503
5560 A_64_P047233	0.869	0.109	1.5E-06	0.591	0.103	5.1E-05 Dlec1	ENSRNOG00000032085	8	127,789,048
5404 A_44_P335703	-0.896	0.099	3.2E-07	-0.532	0.093	5.4E-05 Toag1	ENSRNOG00000004085	8	131,845,696
5468 A_43_P22042	0.778	0.086	3.3E-07	1.439	0.081	5.8E-11 Pla2g7	ENSRNOG00000025691	9	19,978,013
17867 A_44_P1029892	2.016	0.077	2.9E-13	2.257	0.073	2.8E-14 Tmem14a	ENSRNOG00000046593	9	27,343,853
13592 A_64_P147029	-0.753	0.085	4.2E-07	-0.681	0.080	6.9E-07 Gulp1	ENSRNOG00000003242	9	51,263,622
22746 A_44_P146518	-0.954	0.088	3.7E-08	-0.895	0.083	3.9E-08 Col3a1	ENSRNOG00000003357	9	52,023,295
10412 A_64_P092419	-0.416	0.070	3.4E-05	-0.484	0.066	3.5E-06 Col5a2	ENSRNOG00000003736	9	52,238,564
22021 A_64_P101204	-0.447	0.063	5.7E-06	-0.331	0.060	7.2E-05 Slc40a1	ENSRNOG00000049995	9	52,830,457

4692 A_42_P501877	-0.551	0.072	2.5E-06	-0.473	0.068	7.0E-06	Gls	ENSRNOG000000056246	9	54,212,767
3969 A_42_P825912	-0.627	0.095	1.2E-05	-0.503	0.089	6.2E-05		ENSRNOG000000011677	9	60,039,297
9937 A_64_P024841	-2.160	0.105	7.6E-12	-2.094	0.099	5.2E-12	Cryga	ENSRNOG000000014790	9	71,830,730
25119 A_64_P102930	0.439	0.049	4.1E-07	0.439	0.047	2.0E-07	Atic	ENSRNOG000000015511	9	78,862,013
21094 A_64_P105432	1.038	0.179	4.5E-05	1.271	0.168	2.7E-06		ENSRNOG000000059494	9	79,450,320
29277 A_64_P008502	-1.020	0.072	1.1E-09	-0.912	0.068	2.3E-09	Tmem169	ENSRNOG000000016091	9	79,630,604
21241 A_64_P123879	-0.432	0.057	2.8E-06	-0.475	0.054	4.6E-07	Xrcc5	ENSRNOG000000016105	9	79,659,251
18795 A_43_P10901	1.274	0.100	4.7E-09	1.289	0.095	1.9E-09	Itm2c	ENSRNOG000000017359	9	92,916,469
16972 A_64_P022090	-0.755	0.097	1.8E-06	-0.732	0.091	1.3E-06	Ramp1	ENSRNOG000000019926	9	98,313,632
26373 A_64_P085053	-0.476	0.083	5.4E-05	-0.508	0.078	1.5E-05	Scly	ENSRNOG000000020083	9	98,438,439
26397 A_64_P021433	-0.357	0.065	7.8E-05	-0.381	0.061	2.2E-05	Scly	ENSRNOG000000020083	9	98,438,439
7344 A_64_P010174	0.441	0.074	3.4E-05	0.501	0.069	4.6E-06	Man2a1	ENSRNOG000000015439	9	112,293,388
10864 A_64_P048013	0.657	0.112	4.0E-05	0.681	0.105	1.5E-05	Arhgap28	ENSRNOG000000017065	9	116,222,440
11494 A_44_P123492	-0.746	0.105	5.5E-06	-0.913	0.099	2.6E-07	Epb41l3	ENSRNOG000000016724	9	117,538,009
20373 A_64_P034114	-0.789	0.103	2.3E-06	-0.893	0.097	2.7E-07	Epb41l3	ENSRNOG000000016724	9	117,538,009
21591 A_64_P058107	-0.429	0.080	9.4E-05	-0.556	0.075	3.3E-06	Enpp6	ENSRNOG000000053864	10	197,050
29536 A_44_P288794	-0.458	0.084	8.6E-05	0.701	0.079	4.3E-07	Bfar	ENSRNOG000000003151	10	1,464,765
3252 A_64_P080524	0.680	0.062	2.8E-08	0.648	0.058	2.5E-08	Snn	ENSRNOG000000058739	10	4,644,570
21658 A_64_P010569	0.949	0.084	2.2E-08	0.790	0.079	1.0E-07	Ciita	ENSRNOG000000002659	10	5,260,608
10584 A_44_P337294	1.415	0.089	2.6E-10	0.686	0.084	1.1E-06	Eci1	ENSRNOG000000008843	10	13,797,562
19247 A_64_P077648	0.479	0.084	5.9E-05	0.532	0.080	1.1E-05	Hs3st6	ENSRNOG000000014672	10	14,122,878
1430 A_64_P028788	0.494	0.082	3.1E-05	0.502	0.077	1.4E-05	RGD1311273	ENSRNOG000000020029	10	15,235,740
29411 A_64_P054881	0.428	0.069	2.5E-05	0.503	0.065	2.2E-06	RGD1311273	ENSRNOG000000020029	10	15,235,740
7281 A_64_P062288	0.667	0.093	5.0E-06	0.542	0.088	2.5E-05	Ccdc99	ENSRNOG000000007292	10	19,652,898
24792 A_64_P127609	-1.097	0.110	9.5E-08	-1.107	0.103	4.1E-08	Slit3	ENSRNOG000000007377	10	20,320,878
14617 A_64_P028561	1.457	0.240	3.0E-05	1.496	0.226	1.2E-05		ENSRNOG000000058024	10	29,806,895
6367 A_64_P133657	-2.595	0.109	1.1E-12	-2.529	0.103	7.2E-13	Timd2	ENSRNOG000000021345	10	31,790,263
10135 A_43_P10530	-1.259	0.145	5.2E-07	-1.126	0.137	9.8E-07	Mfap4	ENSRNOG000000002382	10	47,765,432
92 A_42_P520349	1.410	0.115	7.0E-09	0.853	0.108	1.6E-06	Clec10a	ENSRNOG000000018715	10	56,764,927
25686 A_43_P23363	1.348	0.148	3.0E-07	1.606	0.139	1.6E-08	Spata22	ENSRNOG000000037307	10	59,893,067
23809 A_44_P1018622	0.481	0.070	8.2E-06	0.597	0.066	3.4E-07	Fam101b	ENSRNOG000000006674	10	64,202,380
7702 A_42_P695401	-1.290	0.227	5.8E-05	-1.997	0.214	2.3E-07	Ccl2	ENSRNOG000000007159	10	69,412,017
6462 A_64_P099573	-0.902	0.140	1.6E-05	-0.850	0.132	1.6E-05	Rad51l3	ENSRNOG000000021780	10	70,241,254

28401 A_44_P373236	0.705	0.115	2.6E-05	1.137	0.108	5.2E-08 Slfn8	ENSRNOG000000021412	10	70,339,578
7469 A_64_P039447	-0.641	0.081	1.5E-06	-0.561	0.076	3.5E-06 Heatr6	ENSRNOG000000002542	10	71,054,344
27034 A_64_P006943	0.987	0.110	3.6E-07	0.931	0.104	3.6E-07 Wfikkn2	ENSRNOG000000002831	10	81,942,188
17149 A_64_P040278	-1.750	0.157	2.5E-08	-1.261	0.148	6.6E-07 Col1a1	ENSRNOG000000003897	10	82,745,801
20882 A_44_P350521	-0.996	0.087	1.9E-08	-0.688	0.082	8.6E-07 Col1a1	ENSRNOG000000003897	10	82,745,801
5923 A_64_P006628	-1.530	0.209	3.9E-06	-1.204	0.197	2.7E-05 Tac4	ENSRNOG000000004404	10	83,081,168
8853 A_44_P401161	-0.783	0.063	6.6E-09	-0.391	0.060	1.3E-05	ENSRNOG000000022375	10	83,147,888
16864 A_43_P16767	0.491	0.090	8.5E-05	0.977	0.085	1.6E-08 Igfbp4	ENSRNOG000000010635	10	86,950,557
27721 A_44_P100207	-1.017	0.078	8.5E-09	-0.979	0.068	2.4E-09 Cnp	ENSRNOG000000017496	10	88,490,798
9605 A_44_P1011244	-0.568	0.079	4.7E-06	-0.635	0.075	6.7E-07 MGC95210	ENSRNOG000000024780	10	102,199,837
14484 A_64_P050477	0.570	0.050	1.9E-08	0.559	0.047	1.1E-08 Hn1	ENSRNOG000000003661	10	104,075,777
3531 A_64_P059385	0.727	0.050	8.4E-10	0.393	0.047	8.9E-07 Acox1	ENSRNOG000000008755	10	104,748,050
28378 A_64_P059390	0.834	0.059	1.1E-09	0.462	0.056	8.8E-07 Acox1	ENSRNOG000000008755	10	104,748,050
10355 A_64_P100346	-1.134	0.120	1.8E-07	-1.061	0.113	2.0E-07 Qrich2	ENSRNOG000000025254	10	105,412,627
1106 A_42_P607183	0.654	0.099	1.1E-05	0.546	0.093	4.1E-05 Ube2o	ENSRNOG000000011007	10	105,552,986
29929 A_44_P497302	-0.731	0.098	3.2E-06	-0.645	0.092	6.6E-06 St6galnac2	ENSRNOG000000012083	10	105,668,593
21260 A_44_P237153	-2.045	0.138	6.3E-10	-1.460	0.130	2.3E-08 Birc5	ENSRNOG000000050819	10	106,856,097
22121 A_44_P147726	-0.632	0.066	1.6E-07	-0.511	0.062	9.8E-07 Pgs1	ENSRNOG000000002949	10	106,991,935
19470 A_44_P1017481	-0.506	0.070	4.5E-06	-0.569	0.066	5.9E-07 Timp2	ENSRNOG000000003148	10	107,386,072
26357 A_64_P094249	-1.120	0.143	1.7E-06	-1.028	0.134	2.4E-06	ENSRNOG000000047367	10	108,440,950
22449 A_42_P539095	-0.719	0.063	1.8E-08	-0.733	0.059	6.4E-09 LOC688311	ENSRNOG000000049235	10	109,639,054
3389 A_64_P009335	-0.503	0.067	3.1E-06	-0.473	0.064	3.2E-06 LOC688318	ENSRNOG000000045926	10	109,893,700
22819 A_44_P159569	0.557	0.081	8.0E-06	0.609	0.077	1.5E-06 Wdr45l	ENSRNOG000000036662	10	110,555,629
5982 A_64_P071367	1.111	0.128	5.3E-07	1.123	0.121	2.3E-07 Krtap16-5	ENSRNOG000000040064	11	28,900,376
20993 A_64_P071362	0.985	0.094	5.1E-08	0.966	0.088	3.1E-08 Krtap16-5	ENSRNOG000000040064	11	28,900,376
6903 A_43_P16731	-0.471	0.081	4.3E-05	-0.439	0.076	4.9E-05 Ifngr2	ENSRNOG000000002032	11	31,694,339
9149 A_64_P162743	-0.884	0.119	3.3E-06	-0.856	0.112	2.4E-06 Dnajc28	ENSRNOG000000002026	11	31,772,984
12330 A_44_P121280	-1.648	0.102	1.9E-10	-0.854	0.096	3.9E-07 Kcne1	ENSRNOG000000001984	11	32,508,420
2645 A_44_P1039678	-0.670	0.064	5.9E-08	-0.543	0.061	3.7E-07 Setd4	ENSRNOG000000001699	11	33,801,999
14097 A_64_P064949	-0.612	0.066	2.5E-07	-0.445	0.062	5.1E-06	ENSRNOG000000051106	11	33,840,530
16374 A_64_P036352	-1.102	0.091	8.6E-09	-0.979	0.086	1.8E-08 Cbr1	ENSRNOG000000049911	11	33,863,500
4611 A_64_P043033	-1.259	0.136	2.5E-07	-1.016	0.128	1.6E-06 Cbr3	ENSRNOG000000001701	11	33,909,439
6829 A_43_P17424	-0.904	0.118	2.3E-06	-0.599	0.111	9.8E-05 Chaf1b	ENSRNOG000000001692	11	34,101,197

23291 A_44_P380384	-1.120	0.133	7.6E-07	-1.280	0.125	7.5E-08 Dscr6	ENSRNOG000000001684	11	34,557,679
29585 A_64_P104237	-0.360	0.063	5.8E-05	-0.474	0.060	1.6E-06 Ttc3	ENSRNOG000000001682	11	34,598,492
28300 A_44_P100023	0.323	0.054	3.1E-05	0.313	0.050	2.4E-05 Wrb	ENSRNOG000000001629	11	36,497,509
16198 A_43_P18730	1.147	0.092	6.3E-09	1.238	0.087	1.1E-09 LOC304000	ENSRNOG0000000028216	11	36,736,586
15995 A_44_P215917	-1.036	0.152	8.4E-06	-0.888	0.143	2.3E-05 Plcxd2	ENSRNOG0000000042289	11	57,207,656
6884 A_42_P732251	-1.590	0.105	4.5E-10	-1.661	0.099	1.1E-10 Phldb2	ENSRNOG0000000002171	11	57,404,196
6750 A_64_P013875	-1.566	0.083	2.6E-11	-1.530	0.078	1.6E-11	ENSRNOG0000000002171	11	57,430,166
3428 A_42_P840460	-0.679	0.086	1.6E-06	-0.668	0.081	9.6E-07 Ccdc52	ENSRNOG0000000039024	11	61,287,914
10972 A_64_P118532	-0.802	0.103	1.9E-06	-0.529	0.097	8.5E-05 Casr	ENSRNOG0000000002265	11	67,188,630
7015 A_64_P140781	0.788	0.135	4.2E-05	0.861	0.127	8.9E-06 Ostalpha	ENSRNOG000000001765	11	71,533,078
13604 A_44_P436604	0.504	0.070	4.6E-06	0.475	0.066	4.6E-06 Leprel1	ENSRNOG0000000055751	11	78,029,038
5488 A_44_P379377	-0.723	0.113	1.7E-05	0.772	0.107	4.5E-06 Fetub	ENSRNOG000000001806	11	81,660,395
26833 A_43_P13230	0.679	0.077	4.2E-07	0.463	0.072	1.7E-05 Ehhadh	ENSRNOG000000001770	11	82,945,104
2087 A_64_P015758	-2.556	0.366	6.6E-06	-2.187	0.345	1.9E-05	ENSRNOG0000000050000	11	86,092,468
16311 A_44_P139291	0.898	0.124	4.3E-06	0.990	0.117	7.1E-07 Prodh	ENSRNOG0000000000281	11	87,058,616
16895 A_64_P038926	1.071	0.141	2.6E-06	0.943	0.133	5.6E-06 Prodh	ENSRNOG0000000000281	11	87,058,616
7350 A_64_P048136	-1.131	0.102	2.6E-08	-0.724	0.096	2.8E-06 Brca2	ENSRNOG000000001111	12	504,007
2456 A_64_P245720	0.665	0.098	8.8E-06	0.531	0.092	5.1E-05 Zinki	ENSRNOG0000000030410	12	5,490,935
3604 A_42_P746109	-0.613	0.069	3.8E-07	-0.564	0.065	5.1E-07 Asmtl	ENSRNOG0000000028166	12	18,531,990
19145 A_64_P081501	1.197	0.068	6.9E-11	1.220	0.065	2.4E-11 Mcm7	ENSRNOG0000000001349	12	19,314,016
7888 A_64_P156448	-0.660	0.092	5.0E-06	-0.800	0.087	2.7E-07 LOC685157	ENSRNOG0000000050981	12	21,362,205
25485 A_64_P057626	-1.977	0.156	1.1E-08	-1.392	0.135	1.3E-07	ENSRNOG0000000057201	12	22,380,027
28649 A_44_P975437	0.444	0.069	1.7E-05	0.739	0.065	2.1E-08 Cldn4	ENSRNOG0000000001476	12	24,761,210
3110 A_64_P129805	0.493	0.069	5.1E-06	0.538	0.065	9.5E-07 Rfc2	ENSRNOG000000001457	12	25,143,480
7243 A_64_P113867	-0.688	0.117	4.0E-05	-0.706	0.110	1.7E-05 Caln1	ENSRNOG0000000000886	12	29,743,705
17119 A_44_P654973	0.559	0.098	5.3E-05	0.596	0.092	1.5E-05 Rimbp2	ENSRNOG0000000022893	12	31,530,699
9922 A_42_P818240	-0.474	0.063	2.8E-06	-0.328	0.059	7.5E-05 Ncor2	ENSRNOG000000001004	12	36,871,999
1906 A_64_P142962	1.063	0.136	1.8E-06	1.184	0.128	2.6E-07 Ccdc92	ENSRNOG0000000021691	12	37,211,316
3175 A_44_P1030714	1.135	0.072	2.7E-10	1.341	0.068	1.3E-11 Ccdc92	ENSRNOG0000000021691	12	37,211,316
13761 A_64_P135202	-0.779	0.105	3.2E-06	-0.657	0.099	1.1E-05 Snrnp35	ENSRNOG0000000001060	12	37,538,403
5287 A_64_P115222	0.587	0.065	3.2E-07	0.487	0.061	1.4E-06 Pitpm2	ENSRNOG0000000029260	12	37,805,332
29139 A_44_P838992	-0.681	0.105	1.4E-05	-0.840	0.099	6.9E-07 LOC687609	ENSRNOG0000000042607	12	38,880,377
16776 A_44_P226999	-1.002	0.180	9.2E-05	1.000	0.156	2.3E-05 Oas1i	ENSRNOG0000000047076	12	41,155,497

22173 A_64_P025839	-1.043	0.155	1.0E-05	0.816	0.146	6.9E-05 Oas1k	ENSRNOG000000033220	12	41,307,352
2789 A_42_P612939	-1.178	0.152	2.1E-06	-1.155	0.144	1.3E-06 Tmem119	ENSRNOG000000000700	12	48,598,647
15771 A_64_P038532	-0.578	0.089	1.4E-05	-0.479	0.084	5.4E-05 Hps4	ENSRNOG000000000661	12	50,314,406
28389 A_44_P574134	-0.584	0.060	1.3E-07	-0.340	0.057	3.2E-05 Slc35f5	ENSRNOG000000003403	13	41,883,137
11088 A_42_P763058	1.498	0.123	8.1E-09	1.119	0.116	1.5E-07 Lypd1	ENSRNOG000000003453	13	42,263,024
14258 A_43_P13249	1.127	0.089	4.8E-09	1.025	0.084	7.7E-09 Acmsd	ENSRNOG000000003884	13	44,424,689
7157 A_64_P007633	0.712	0.109	1.3E-05	0.861	0.102	7.8E-07 C4bpb	ENSRNOG000000004125	13	47,397,890
22069 A_44_P764174	1.377	0.122	2.1E-08	0.881	0.115	2.3E-06 Faim3	ENSRNOG000000004441	13	47,602,692
585 A_42_P707818	-0.675	0.094	4.6E-06	-1.152	0.088	3.3E-09 Tmcc2	ENSRNOG000000000033	13	49,169,918
5286 A_44_P434271	1.155	0.192	3.3E-05	1.271	0.181	6.2E-06 Cntn2	ENSRNOG000000009033	13	49,313,940
19857 A_43_P15590	-0.432	0.071	2.9E-05	-0.396	0.067	3.8E-05 Fmod	ENSRNOG000000003183	13	50,873,605
16675 A_64_P055196	0.795	0.127	2.2E-05	0.731	0.120	2.8E-05 Camsap111	ENSRNOG000000008741	13	53,225,349
12995 A_44_P349273	1.732	0.129	2.2E-09	1.959	0.121	2.0E-10 F13b	ENSRNOG000000012613	13	56,598,957
2005 A_42_P819656	0.594	0.094	2.0E-05	0.501	0.089	6.3E-05 Cfh	ENSRNOG000000030715	13	57,080,549
7372 A_64_P001066	1.135	0.211	9.9E-05	1.107	0.199	7.1E-05 RGD1561738	ENSRNOG000000042995	13	73,661,131
1416 A_64_P091088	1.064	0.096	2.7E-08	1.322	0.091	7.5E-10 Fmo2	ENSRNOG000000003510	13	80,775,264
20699 A_44_P486312	0.955	0.102	2.2E-07	1.021	0.096	4.7E-08 Fmo2	ENSRNOG000000003510	13	80,775,264
14514 A_44_P180259	1.853	0.115	2.1E-10	1.680	0.108	3.5E-10 Dpt	ENSRNOG000000002947	13	83,073,550
22348 A_44_P1018997	-0.425	0.064	1.2E-05	-0.527	0.061	5.3E-07 Tmco1	ENSRNOG000000003928	13	85,465,792
12064 A_64_P027625	-4.908	0.087	7.6E-18	-0.575	0.082	6.6E-06 Rxrg	ENSRNOG000000004537	13	85,818,427
21779 A_44_P306439	0.950	0.104	2.9E-07	1.759	0.098	4.9E-11 Fcgr3a	ENSRNOG000000024382	13	89,385,859
3217 A_42_P735417	1.129	0.189	3.5E-05	0.974	0.178	8.4E-05 Fcgr2b	ENSRNOG000000046452	13	89,433,815
25592 A_44_P575255	2.333	0.113	7.0E-12	2.309	0.106	3.6E-12 RGD1562658	ENSRNOG000000034221	13	89,480,058
3268 A_64_P005029	-0.915	0.087	4.9E-08	-0.742	0.082	3.1E-07 Pcp4l1	ENSRNOG000000003209	13	89,565,813
23319 A_64_P072455	-1.892	0.112	1.2E-08	-2.076	0.128	1.8E-08 LOC689766	ENSRNOG000000021411	13	95,887,708
9059 A_42_P803590	-1.853	0.112	1.5E-10	-1.660	0.106	2.9E-10 LOC289378	ENSRNOG000000046460	13	109,663,364
3954 A_42_P661065	0.953	0.094	8.0E-08	1.120	0.089	5.0E-09 Ints7	ENSRNOG000000004263	13	110,257,571
10206 A_64_P052464	1.761	0.117	5.3E-10	1.897	0.111	9.1E-11 Ints7	ENSRNOG000000004263	13	110,257,571
4910 A_43_P12200	0.424	0.068	2.3E-05	0.448	0.064	7.0E-06 Slc26a1	ENSRNOG000000000041	14	2,050,483
23982 A_64_P015340	1.414	0.180	7.9E-06	1.565	0.174	2.2E-06 Mfsd7	ENSRNOG000000023937	14	2,311,122
29630 A_64_P015335	2.104	0.127	1.4E-10	2.094	0.120	6.9E-11 Mfsd7	ENSRNOG000000023937	14	2,311,122
3061 A_44_P454646	0.641	0.108	3.6E-05	0.621	0.102	2.7E-05 Fam69a	ENSRNOG000000023533	14	2,789,650
27220 A_64_P165953	-1.355	0.180	2.9E-06	-1.292	0.170	2.5E-06 Znf644	ENSRNOG000000002112	14	4,125,380

5642 A_42_P715210	1.079	0.092	1.3E-08	0.933	0.087	4.0E-08 Abcg3l3	ENSRNOG000000039890	14	6,058,544
21816 A_64_P085715	0.539	0.071	2.6E-06	0.551	0.067	1.0E-06 Pkd2	ENSRNOG000000002146	14	6,645,257
10617 A_44_P1043814	-0.495	0.061	1.2E-06	-0.463	0.058	1.3E-06 Hsd17b11	ENSRNOG000000002210	14	7,073,445
15964 A_64_P041270	0.906	0.146	2.3E-05	0.980	0.137	5.1E-06 Fras1	ENSRNOG000000002053	14	14,689,554
23631 A_64_P013437	1.886	0.246	2.3E-06	2.144	0.232	2.5E-07 Cxcl13	ENSRNOG000000024899	14	15,258,207
783 A_64_P071159	-4.520	0.278	1.8E-10	-3.917	0.262	5.6E-10 LOC360919	ENSRNOG000000039504	14	19,072,677
17181 A_64_P071158	-4.519	0.278	1.8E-10	-3.829	0.262	7.4E-10 LOC360919	ENSRNOG000000039504	14	19,072,677
16082 A_44_P353446	-3.330	0.357	2.2E-07	-2.572	0.336	2.3E-06 Afn	ENSRNOG000000002878	14	19,132,208
7897 A_43_P13995	1.851	0.236	1.7E-06	1.899	0.222	6.5E-07 Gc	ENSRNOG000000003119	14	20,266,891
8034 A_43_P12233	0.748	0.068	2.7E-08	0.837	0.064	3.1E-09 Sult1b1	ENSRNOG000000001967	14	22,142,364
27643 A_64_P053257	0.811	0.073	2.4E-08	0.926	0.069	2.1E-09 Sult1b1	ENSRNOG000000001967	14	22,142,364
4292 A_64_P119836	-1.059	0.176	3.3E-05	-1.102	0.166	1.2E-05 Shisa3	ENSRNOG000000025670	14	42,221,225
29204 A_44_P123033	-0.428	0.076	6.3E-05	-0.487	0.072	8.8E-06 Khl5	ENSRNOG000000008421	14	44,845,218
28582 A_43_P11601	-1.251	0.081	3.6E-10	-1.060	0.076	1.5E-09 Sod3	ENSRNOG000000003869	14	60,964,324
22 A_44_P992306	-1.037	0.092	2.0E-08	-1.038	0.086	9.4E-09 Gnpda2	ENSRNOG000000002177	14	62,646,110
5318 A_42_P674050	-1.136	0.132	6.0E-07	-0.940	0.125	2.7E-06 Sorcs2	ENSRNOG000000007033	14	79,538,911
11690 A_44_P330188	2.796	0.173	1.9E-10	2.826	0.163	7.6E-11 Acox2	ENSRNOG000000007378	15	18,451,144
17115 A_64_P031249	0.909	0.081	2.2E-08	0.911	0.076	1.0E-08 Gnpnat1	ENSRNOG000000008641	15	19,733,967
12606 A_64_P098006	1.071	0.135	1.5E-06	0.807	0.127	1.8E-05 Fitm1	ENSRNOG000000019019	15	34,251,606
510 A_64_P068192	-0.834	0.120	6.7E-06	-0.923	0.113	1.1E-06 Mcpt8_rat	ENSRNOG000000049991	15	34,694,244
10995 A_64_P124294	-1.372	0.171	1.3E-06	-1.167	0.161	4.4E-06 Mcpt9_rat	ENSRNOG000000031792	15	35,002,406
23836 A_64_P151851	-0.742	0.122	3.0E-05	-0.642	0.115	7.1E-05 Phf11	ENSRNOG000000053891	15	38,709,984
22768 A_64_P001612	-0.373	0.062	3.2E-05	-0.411	0.059	6.2E-06 Trim35	ENSRNOG000000009449	15	42,960,307
1315 A_64_P134160	-2.430	0.197	6.7E-09	-2.272	0.185	7.5E-09 Defb42	ENSRNOG000000038762	15	46,166,335
3047 A_44_P105225	-0.765	0.138	7.3E-05	-0.792	0.130	2.9E-05 Loxl2	ENSRNOG000000051538	15	51,364,261
29985 A_44_P520441	-2.843	0.121	7.0E-08	-2.499	0.121	1.7E-07 Pcdh9	ENSRNOG000000038068	15	77,736,892
27981 A_64_P150884	-0.773	0.118	1.9E-05	-0.838	0.118	8.3E-06 Scel	ENSRNOG000000024237	15	87,704,340
1825 A_42_P787239	0.673	0.064	5.6E-08	0.619	0.061	7.6E-08 Farp1	ENSRNOG000000011203	15	106,434,177
6846 A_64_P005043	0.449	0.081	6.9E-05	0.693	0.076	2.9E-07 Nt5dc2	ENSRNOG000000018358	16	7,212,488
30347 A_64_P066923	0.975	0.117	8.5E-07	1.230	0.110	2.4E-08 Ncoa4	ENSRNOG000000019768	16	8,302,950
25096 A_64_P142026	1.136	0.138	1.0E-06	1.105	0.130	7.0E-07 Ppyr1	ENSRNOG000000061026	16	10,490,706
27813 A_44_P228059	0.628	0.100	2.0E-05	0.676	0.094	4.8E-06 Mbl1	ENSRNOG000000011706	16	18,736,154
1186 A_42_P467381	0.660	0.076	5.2E-07	0.565	0.072	1.6E-06 Fam32a	ENSRNOG000000039528	16	19,308,842

6443 A_44_P196779	-0.604	0.085	5.1E-06	-0.465	0.080	4.4E-05 Haus8	ENSRNOG000000052038	16	19,669,196
21276 A_64_P051636	-0.958	0.107	3.5E-07	-1.253	0.100	5.9E-09 Pde4c	ENSRNOG000000019518	16	20,460,959
19242 A_64_P119675	-0.572	0.079	4.5E-06	-0.481	0.075	1.6E-05 Jund	ENSRNOG000000019568	16	20,486,707
6546 A_64_P124701	-1.558	0.176	4.2E-07	-1.921	0.166	1.5E-08 Crllf1	ENSRNOG000000020030	16	20,686,317
17539 A_44_P463822	-0.735	0.082	3.7E-07	-0.727	0.078	2.1E-07 Homer3	ENSRNOG000000020229	16	20,888,907
8703 A_64_P085936	-2.563	0.121	5.3E-12	-2.769	0.114	8.2E-13 Mef2b	ENSRNOG000000020400	16	21,017,163
23904 A_64_P100904	-0.920	0.126	4.0E-06	-0.717	0.119	3.1E-05 LOC688966	ENSRNOG000000020427	16	21,029,134
25971 A_64_P004531	-0.950	0.075	4.5E-09	-0.741	0.070	5.1E-08 LOC688966	ENSRNOG000000020427	16	21,029,134
9569 A_64_P087014	1.039	0.128	1.2E-06	0.711	0.121	4.0E-05 Slc18a1	ENSRNOG000000011992	16	22,361,998
4835 A_44_P1016480	2.037	0.163	5.8E-09	1.746	0.154	2.0E-08 Lpl	ENSRNOG000000012181	16	22,561,496
8763 A_64_P144978	0.703	0.082	6.3E-07	0.505	0.077	1.4E-05 Csgalnact1	ENSRNOG000000013024	16	22,979,444
15146 A_44_P1036068	-0.509	0.060	7.5E-07	-0.494	0.057	5.3E-07 RGD1311747	ENSRNOG000000011293	16	32,540,217
3982 A_64_P007462	0.863	0.098	4.5E-07	1.068	0.092	1.5E-08 Spcs3	ENSRNOG000000038933	16	40,050,734
26075 A_64_P041016	-0.997	0.081	6.8E-09	-1.073	0.076	1.2E-09 Wwc2	ENSRNOG000000013248	16	47,368,768
9554 A_64_P048315	0.916	0.085	3.7E-08	0.893	0.080	2.4E-08	ENSRNOG000000055088	16	59,517,000
28774 A_44_P438492	0.426	0.067	1.8E-05	0.540	0.063	6.3E-07 Mak16	ENSRNOG000000010783	16	64,729,221
11412 A_44_P1042163	0.796	0.061	3.1E-09	0.983	0.057	9.0E-11 RGD1310414	ENSRNOG000000023494	16	64,745,207
18101 A_44_P941895	0.442	0.078	5.6E-05	0.403	0.073	7.8E-05 Prosc	ENSRNOG000000013751	16	69,176,036
7165 A_64_P087109	-0.398	0.073	8.8E-05	-0.440	0.069	1.7E-05 Ankrd10	ENSRNOG000000013618	16	83,206,004
6176 A_64_P150047	-0.457	0.060	2.3E-06	-0.369	0.056	1.3E-05 Rab20	ENSRNOG000000023991	16	83,358,116
3375 A_44_P309325	0.793	0.123	1.5E-05	0.650	0.116	6.5E-05 Lig4	ENSRNOG000000014605	16	85,331,866
18894 A_64_P022751	0.441	0.061	4.0E-06	0.484	0.057	7.1E-07 Isca1	ENSRNOG000000018343	17	5,281,727
11386 A_64_P014278	-1.584	0.057	1.4E-13	-1.410	0.054	3.2E-13 LOC680692	ENSRNOG000000018400	17	5,382,034
30268 A_44_P215479	0.523	0.071	3.9E-06	0.382	0.067	5.8E-05 Rmi1	ENSRNOG000000019108	17	6,660,536
24746 A_64_P163822	-1.220	0.083	6.9E-10	-1.123	0.078	9.5E-10 Cks2	ENSRNOG000000014130	17	13,593,423
16526 A_44_P260348	0.851	0.118	4.5E-06	0.674	0.111	2.9E-05 LOC689316	ENSRNOG000000058611	17	15,108,456
4180 A_64_P165035	6.620	0.112	3.9E-18	5.843	0.106	9.7E-18 RGD1305679	ENSRNOG000000014481	17	22,619,891
8900 A_64_P059262	0.995	0.087	1.8E-08	1.029	0.082	5.5E-09 Riok1	ENSRNOG000000014049	17	27,451,832
5827 A_64_P055102	0.450	0.052	5.9E-07	0.340	0.049	7.5E-06 Eci3	ENSRNOG000000029549	17	30,617,382
21031 A_64_P067678	-0.615	0.111	7.4E-05	-0.624	0.105	3.6E-05 Aldh5a1	ENSRNOG000000023538	17	42,133,076
23925 A_64_P030919	-0.805	0.112	4.6E-06	-0.784	0.105	3.2E-06	ENSRNOG000000023538	17	42,133,076
4429 A_64_P127026	-0.506	0.085	3.6E-05	-0.551	0.080	7.9E-06 Cmah	ENSRNOG000000003094	17	42,640,221
7060 A_42_P555365	0.751	0.083	3.1E-07	0.672	0.078	5.8E-07 Slc17a3	ENSRNOG000000032745	17	43,537,293

14149 A_64_P080667	-0.766	0.125	2.6E-05	-0.743	0.117	1.9E-05 LOC684841	ENSRNOG000000045644	17	43,807,540
18077 A_64_P127848	-1.330	0.151	8.1E-07	-1.420	0.131	7.3E-08 Aoah	ENSRNOG000000054964	17	46,115,004
1977 A_64_P100530	-0.420	0.078	9.7E-05	-0.435	0.074	3.8E-05 Arhgap12	ENSRNOG000000017791	17	54,280,851
17105 A_64_P040038	2.256	0.209	3.6E-08	2.471	0.197	5.3E-09 RGD1563564	ENSRNOG000000016217	17	63,145,577
13903 A_44_P515798	2.632	0.099	2.4E-13	2.608	0.093	1.2E-13 Ucma	ENSRNOG000000017987	17	77,261,731
14129 A_44_P491929	-0.477	0.084	5.9E-05	-0.438	0.079	7.7E-05 Prpf18	ENSRNOG000000018396	17	77,601,914
20226 A_64_P104454	-0.723	0.099	4.1E-06	-0.541	0.094	4.9E-05 Impad1	ENSRNOG000000046647	17	90,218,013
25656 A_44_P245616	-1.011	0.098	6.3E-08	-0.531	0.092	5.0E-05 Nid1	ENSRNOG000000002461	17	90,627,101
20714 A_64_P056712	0.852	0.067	4.8E-09	0.767	0.063	8.6E-09 Gpr137b	ENSRNOG000000002480	17	90,696,019
14497 A_64_P174430	-0.477	0.085	6.4E-05	-0.596	0.080	3.2E-06 Cdig2	ENSRNOG000000012016	18	3,662,683
30354 A_64_P089742	-0.486	0.068	4.7E-06	-0.545	0.064	6.3E-07 Cdig2	ENSRNOG000000012016	18	3,662,683
25080 A_64_P029377	1.155	0.157	3.7E-06	1.179	0.148	1.5E-06 Hrh4	ENSRNOG000000016887	18	4,365,429
16785 A_44_P1028952	-0.596	0.079	2.6E-06	-0.488	0.074	1.2E-05	ENSRNOG000000016467	18	6,474,990
13848 A_43_P19054	1.007	0.130	9.4E-06	1.438	0.126	2.0E-07 Dsc2	ENSRNOG000000039969	18	11,858,744
7111 A_44_P241308	-0.755	0.116	1.4E-05	-0.861	0.109	1.7E-06 LOC100360334	ENSRNOG000000027230	18	16,650,806
28984 A_64_P034128	-1.109	0.156	5.3E-06	-0.797	0.147	9.1E-05 Nrep	ENSRNOG000000020467	18	26,211,445
2039 A_64_P135224	2.166	0.146	6.0E-10	3.101	0.137	2.2E-12 RGD1309362	ENSRNOG000000038960	18	55,505,993
4992 A_44_P549494	0.833	0.086	1.4E-07	1.090	0.081	2.1E-09 Cd74	ENSRNOG000000018735	18	56,071,478
14590 A_64_P160393	-0.454	0.080	6.1E-05	-0.498	0.076	1.3E-05 Tcf4	ENSRNOG000000012405	18	65,285,318
17166 A_44_P419615	-1.487	0.139	1.8E-07	-1.251	0.105	5.4E-08 Stard6	ENSRNOG000000026324	18	68,983,545
7335 A_42_P595630	-1.153	0.070	1.6E-10	-1.060	0.066	2.3E-10 Pqlc1	ENSRNOG000000059215	18	76,770,012
22519 A_64_P021320	-1.114	0.065	9.3E-11	-1.077	0.061	6.7E-11 Pqlc1	ENSRNOG000000059215	18	76,770,012
30080 A_64_P110941	-2.155	0.153	1.2E-09	-1.316	0.144	3.0E-07 Cndp1	ENSRNOG000000027739	18	81,499,051
17183 A_44_P116591	-0.433	0.075	4.8E-05	-0.397	0.071	6.4E-05 Cx3cl1	ENSRNOG000000016326	19	10,653,800
5572 A_64_P123603	0.672	0.111	3.1E-05	0.866	0.105	9.6E-07 Mt1a	ENSRNOG000000025764	19	11,302,938
14056 A_64_P162764	0.828	0.148	6.6E-05	1.117	0.139	1.4E-06 Mt1a_partial	ENSRNOG000000025764	19	11,302,938
2726 A_44_P996729	-0.888	0.104	6.9E-07	-0.887	0.099	3.5E-07 Mmp2	ENSRNOG000000016695	19	15,570,611
6691 A_44_P100716	-1.037	0.126	9.9E-07	-0.763	0.119	1.6E-05 Mylk3	ENSRNOG000000017546	19	27,404,712
13133 A_44_P133335	-1.169	0.150	4.9E-06	-0.856	0.113	6.8E-06 NA	ENSRNOG000000049468	19	28,645,488
3248 A_64_P000604	-0.633	0.088	4.6E-06	-0.461	0.083	7.0E-05 Tradd	ENSRNOG000000015179	19	37,216,572
7827 A_64_P017565	-0.787	0.084	2.3E-07	-0.614	0.080	2.1E-06 Cdh3	ENSRNOG000000020129	19	38,669,230
7237 A_64_P052690	-0.401	0.055	4.2E-06	-0.452	0.052	5.4E-07 PDF*	ENSRNOG000000022303	19	39,246,545
18072 A_44_P184497	0.462	0.085	8.5E-05	0.460	0.080	5.0E-05 Cyb5b	ENSRNOG000000011142	19	39,357,814

19705 A_44_P220325	-1.242	0.142	1.5E-06	-1.237	0.107	7.6E-08 Dynlrb2	ENSRNOG000000012450	19	49,016,891
10809 A_44_P374638	-0.905	0.163	7.3E-05	-1.022	0.154	1.1E-05 Hsd17b2	ENSRNOG000000013982	19	50,246,402
18230 A_44_P340193	-0.568	0.085	1.0E-05	-0.469	0.080	4.0E-05 Hsd11	ENSRNOG000000015576	19	52,217,728
6490 A_42_P620006	-1.374	0.164	7.9E-07	-0.862	0.154	6.8E-05 Wfdc1	ENSRNOG000000015904	19	52,313,795
28178 A_64_P103254	-0.560	0.074	2.8E-06	-0.437	0.070	2.2E-05 Khlh36	ENSRNOG000000016422	19	52,515,022
4436 A_42_P627572	-1.457	0.066	2.9E-12	-1.519	0.062	7.3E-13 Mdc1	ENSRNOG000000032813	20	3,405,285
7136 A_64_P062110	0.673	0.110	2.8E-05	0.664	0.104	1.7E-05 RT1-DMb	ENSRNOG000000049491	20	3,945,601
1417 A_64_P043911	0.741	0.135	8.1E-05	1.099	0.127	5.8E-07 RT1-Bb	ENSRNOG000000032708	20	4,039,413
18363 A_64_P134927	0.523	0.089	3.8E-05	0.873	0.083	5.5E-08 RT1-Db1	ENSRNOG000000033215	20	4,087,618
12415 A_64_P128478	1.163	0.115	8.0E-08	1.031	0.108	1.7E-07 RT1-DMa	ENSRNOG000000047864	20	5,241,496
8347 A_44_P367438	0.462	0.059	1.8E-06	0.415	0.056	3.1E-06 Stk38	ENSRNOG000000000519	20	6,257,604
18720 A_64_P150618	-0.846	0.127	1.1E-05	-0.675	0.120	6.4E-05 LOC689755	ENSRNOG000000000531	20	8,384,088
15230 A_64_P048033	0.861	0.098	4.5E-07	0.784	0.092	6.8E-07 Agpat3	ENSRNOG000000001205	20	11,114,164
25935 A_64_P146698	0.750	0.061	7.5E-09	0.797	0.058	1.6E-09 Pwp2	ENSRNOG000000001210	20	11,228,844
24999 A_44_P840891	-2.028	0.107	2.3E-11	-1.846	0.101	3.6E-11 Icoslg	ENSRNOG000000023109	20	11,340,296
7074 A_64_P001461	-1.312	0.144	5.5E-07	-0.803	0.125	2.3E-05 Dnmt3l	ENSRNOG000000001212	20	11,359,090
19033 A_44_P1015203	0.554	0.086	1.6E-05	0.811	0.081	1.0E-07 Gstt3	ENSRNOG000000001242	20	13,817,795
23216 A_64_P042607	-1.418	0.178	1.5E-06	-1.135	0.168	9.5E-06 Ctnna3	ENSRNOG000000000378	20	26,589,209
405 A_42_P559737	1.012	0.105	1.5E-07	0.944	0.099	1.7E-07 Srgn	ENSRNOG000000000394	20	32,133,431
220 A_42_P796980	-2.674	0.252	4.7E-08	-2.596	0.238	3.2E-08 Ros1	ENSRNOG000000000406	20	33,323,367
27233 A_44_P942367	-1.581	0.165	1.6E-07	-1.596	0.155	6.8E-08 Tspyl4	ENSRNOG000000000547	20	41,100,071
26015 A_64_P147443	-2.080	0.216	1.5E-07	-1.631	0.204	1.4E-06 LOC679824	ENSRNOG000000051272	20	44,606,610
29075 A_64_P020516	-0.342	0.053	1.7E-05	-0.319	0.050	1.9E-05 Rev3l	ENSRNOG000000000593	20	44,803,666
16018 A_44_P1035656	-0.592	0.086	7.4E-06	-0.552	0.081	8.4E-06 Cd24	ENSRNOG000000000321	20	48,335,540
18623 A_64_P042519	-1.154	0.132	4.8E-07	-1.124	0.124	3.2E-07 Grik2	ENSRNOG000000000368	20	54,517,709
11936 A_44_P547801	-0.872	0.058	5.8E-10	-0.626	0.055	2.0E-08 Gstt2	ENSRNOG000000052360	L568423	501
3314 A_64_P149779	0.763	0.113	1.3E-05	0.742	0.107	1.0E-05	ENSRNOG000000031780	MT	1
4051 A_64_P011635	-0.685	0.086	1.5E-06	-0.487	0.081	3.3E-05	ENSRNOG000000031780	MT	1
5091 A_44_P342334	-0.759	0.071	4.3E-08	-0.768	0.067	1.8E-08	ENSRNOG000000031780	MT	1
5482 A_64_P326359	1.069	0.063	1.1E-10	1.286	0.060	4.0E-12	ENSRNOG000000031780	MT	1
6741 A_64_P123502	-0.933	0.111	8.0E-07	-0.586	0.105	6.8E-05	ENSRNOG000000031780	MT	1
7686 A_64_P011389	0.836	0.145	5.1E-05	1.009	0.137	3.6E-06	ENSRNOG000000031780	MT	1
7793 A_64_P052878	-0.647	0.107	2.9E-05	-0.693	0.101	7.6E-06	ENSRNOG000000031780	MT	1

8774 A_64_P164751	1.238	0.160	3.3E-06	1.123	0.152	5.3E-06	ENSRNOG000000031780	MT	1
9302 A_64_P010221	1.467	0.173	6.9E-07	1.061	0.163	1.4E-05	ENSRNOG000000031780	MT	1
9336 A_64_P063588	0.760	0.072	4.9E-08	0.765	0.068	2.2E-08	ENSRNOG000000031780	MT	1
9394 A_64_P119214	1.075	0.063	1.0E-10	0.639	0.060	4.0E-08	ENSRNOG000000031780	MT	1
9500 A_64_P159175	-0.847	0.119	5.3E-06	-0.730	0.112	1.4E-05	ENSRNOG000000031780	MT	1
10091 A_64_P150008	-1.022	0.119	5.9E-07	-1.172	0.112	5.4E-08	ENSRNOG000000031780	MT	1
10168 A_64_P014010	2.047	0.181	2.0E-08	2.186	0.170	4.1E-09	ENSRNOG000000031780	MT	1
10192 A_64_P060434	1.086	0.108	8.6E-08	0.643	0.101	1.9E-05	ENSRNOG000000031780	MT	1
10320 A_64_P096929	-1.188	0.092	3.6E-09	-0.956	0.086	2.7E-08	ENSRNOG000000031780	MT	1
10544 A_64_P085915	-1.074	0.129	8.7E-07	-0.926	0.121	2.4E-06	ENSRNOG000000031780	MT	1
11592 A_64_P152094	0.930	0.149	2.3E-05	0.801	0.141	5.7E-05	ENSRNOG000000031780	MT	1
11641 A_44_P899149	0.889	0.117	2.4E-06	0.760	0.110	7.3E-06	ENSRNOG000000031780	MT	1
11809 A_64_P024675	-2.523	0.167	1.3E-09	-2.405	0.145	4.0E-10	ENSRNOG000000031780	MT	1
12260 A_64_P147014	0.544	0.076	4.7E-06	0.406	0.071	5.6E-05	ENSRNOG000000031780	MT	1
12390 A_64_P143186	-1.046	0.167	2.1E-05	-0.917	0.158	4.5E-05	ENSRNOG000000031780	MT	1
14345 A_64_P020880	-0.644	0.089	4.3E-06	-0.752	0.084	3.5E-07	ENSRNOG000000031780	MT	1
14912 A_64_P097468	1.233	0.099	5.6E-09	0.806	0.093	5.4E-07	ENSRNOG000000031780	MT	1
15455 A_64_P039840	0.695	0.125	7.3E-05	0.642	0.118	8.9E-05	ENSRNOG000000031780	MT	1
15612 A_64_P010052	-1.703	0.121	8.4E-09	-1.859	0.111	1.2E-09	ENSRNOG000000031780	MT	1
16475 A_64_P071381	1.018	0.129	1.7E-06	1.002	0.122	1.0E-06	ENSRNOG000000031780	MT	1
16858 A_64_P146089	-1.963	0.099	1.3E-11	-1.388	0.094	6.2E-10	ENSRNOG000000031780	MT	1
19343 A_64_P070068	1.661	0.277	3.3E-05	1.465	0.261	6.5E-05	ENSRNOG000000031780	MT	1
19961 A_64_P117198	-0.698	0.119	4.2E-05	-0.622	0.112	7.5E-05	ENSRNOG000000031780	MT	1
20674 A_64_P078577	0.682	0.108	2.0E-05	0.633	0.102	2.3E-05	ENSRNOG000000031780	MT	1
21135 A_64_P118308	-1.437	0.086	1.3E-10	-1.512	0.081	3.0E-11	ENSRNOG000000031780	MT	1
21748 A_64_P071088	0.834	0.100	8.9E-07	1.043	0.094	2.8E-08	ENSRNOG000000031780	MT	1
21806 A_64_P094555	0.993	0.114	5.0E-07	0.608	0.107	5.9E-05	ENSRNOG000000031780	MT	1
22371 A_64_P039036	-0.557	0.061	2.8E-07	-0.522	0.057	3.0E-07	ENSRNOG000000031780	MT	1
22436 A_64_P045775	1.063	0.083	4.2E-09	1.033	0.078	2.9E-09	ENSRNOG000000031780	MT	1
22975 A_64_P162760	1.002	0.164	2.8E-05	1.266	0.155	1.1E-06	ENSRNOG000000031780	MT	1
24098 A_64_P042811	-2.176	0.100	3.8E-12	-2.155	0.095	1.9E-12	ENSRNOG000000031780	MT	1
24429 A_64_P086550	-1.365	0.143	1.7E-07	-1.330	0.135	1.1E-07	ENSRNOG000000031780	MT	1
27262 A_64_P143003	1.008	0.110	2.9E-07	0.664	0.104	1.7E-05	ENSRNOG000000031780	MT	1

27514 A_64_P037848	0.797	0.145	7.8E-05	0.779	0.136	5.4E-05	ENSRNOG000000031780	MT	1
27679 A_64_P143154	0.541	0.085	1.8E-05	0.767	0.080	1.6E-07	ENSRNOG000000031780	MT	1
29480 A_64_P134485	1.107	0.124	3.7E-07	0.667	0.117	5.3E-05	ENSRNOG000000031780	MT	1
30061 A_64_P086167	2.970	0.298	1.0E-07	3.074	0.281	3.2E-08	ENSRNOG000000031780	MT	1
30345 A_64_P139614	-0.818	0.122	1.1E-05	-0.827	0.115	4.9E-06	ENSRNOG000000031780	MT	1
18904 A_64_P115786	2.417	0.200	9.0E-09	2.588	0.189	1.7E-09	ENSRNOG000000009609	X	1,615,920
28608 A_43_P11444	0.529	0.091	4.4E-05	0.595	0.085	6.8E-06 S100g	ENSRNOG000000004222	X	33,443,186
10435 A_64_P010338	0.718	0.072	1.0E-07	0.494	0.068	4.2E-06	ENSRNOG000000051268	X	62,977,719
28414 A_64_P085732	0.726	0.095	2.3E-06	0.640	0.089	4.8E-06 Arhgef9	ENSRNOG000000007733	X	64,428,444
11028 A_64_P072533	1.103	0.100	2.7E-08	1.047	0.094	2.5E-08	ENSRNOG000000011100	X	115,426,083
15663 A_64_P048852	-1.660	0.080	7.2E-12	-1.766	0.076	1.4E-12	ENSRNOG000000006459	X	120,313,696
20264 A_44_P478319	0.836	0.127	1.2E-05	0.750	0.120	2.1E-05 Lonrf3	ENSRNOG000000013092	X	122,938,009
3602 A_64_P060874	-0.979	0.085	1.8E-08	-0.781	0.081	1.4E-07 Gpc3	ENSRNOG000000060179	X	139,916,883
245 A_64_P024665	0.895	0.162	7.4E-05	1.304	0.152	6.3E-07 LOC688090			
415 A_42_P803752	-1.044	0.176	3.7E-05	-1.157	0.166	6.6E-06 RGD1562146			
4900 A_44_P668185	-0.471	0.068	7.3E-06	-0.421	0.064	1.3E-05 RGD1310444			
5530 A_42_P538334	0.433	0.061	5.5E-06	0.392	0.058	8.7E-06 Snhg8			
7682 A_64_P077935	0.936	0.147	1.7E-05	1.212	0.138	4.7E-07 LOC690776			
7826 A_64_P024117	-1.376	0.119	8.5E-06	-1.034	0.119	5.5E-05 LOC497952			
7899 A_64_P006498	-1.666	0.166	9.4E-08	-1.449	0.157	2.5E-07 Ces1e_rat			
8819 A_64_P132726	-1.552	0.130	1.0E-08	-1.405	0.122	1.7E-08 no transcript			
10176 A_43_P15246	1.156	0.150	2.2E-06	0.891	0.142	2.0E-05 Pthlh	N/A	4	181,663,425
10999 A_64_P070586	0.874	0.105	8.8E-07	0.907	0.099	2.8E-07 Krtap21-2			
12619 A_64_P060319	-0.658	0.102	1.5E-05	-0.582	0.096	2.9E-05 Gsg1l			
12669 A_64_P115157	-1.112	0.116	1.7E-07	-1.076	0.110	1.2E-07 Ces1e_rat			
15289 A_44_P393282	-0.406	0.056	4.0E-06	-0.300	0.052	5.3E-05 no transcript			
15442 A_64_P155603	-1.327	0.148	3.7E-07	-1.007	0.140	4.6E-06 Mcpt8_RGD1565970			
16545 A_44_P369612	-0.537	0.095	5.7E-05	-0.617	0.089	7.2E-06 LOC305633			
16795 A_64_P009823	0.924	0.132	6.4E-06	0.674	0.125	9.3E-05 Slc39a4l			
17474 A_44_P201084	-1.297	0.156	9.0E-07	-1.286	0.147	4.9E-07 Fgfr1l			
18051 A_43_P11739	-0.779	0.055	1.3E-09	-0.546	0.052	5.7E-08 Ctsl1	ENSRNOG000000018566	17	1,873,105
18349 A_64_P157474	-0.544	0.077	6.0E-06	-0.701	0.073	1.6E-07 LOC500956			
22943 A_64_P037000	3.271	0.152	6.1E-11	3.475	0.145	1.8E-11 no transcript			

23854 A_64_P021149	-1.449	0.114	2.6E-08	-1.684	0.105	1.8E-09	LOC686141			
23957 A_64_P139208	-1.817	0.118	3.8E-10	-1.585	0.111	1.1E-09	RT1-N1 (part)			
24636 A_42_P835445	-2.341	0.228	7.0E-08	-2.094	0.215	1.3E-07	no transcript			
25709 A_64_P011719	-1.134	0.082	1.5E-09	-0.816	0.077	4.7E-08	Chmp1b	N/A	18	62,923,620
26309 A_44_P960266	-0.831	0.085	1.2E-07	-0.706	0.080	4.2E-07	RGD1307493			
30047 A_64_P096096	-0.736	0.111	1.1E-05	-0.572	0.104	8.2E-05	RGD1562551			

Genes are regarded as significant for “shared” differential expression when they show $P < 1 \times 10^{-4}$ reproducibly in two types of comparison, ie, SHR/lzm versus WKY/lzm and SHRSP/lzm versus WKY/lzm, with a concordant direction of differential expression.

Table S3E. A list of significant transcripts for shared differential expression in the liver.

no	ProbeName	SHR/lzm (vs WKY/lzm)			SHRSP/lzm (vs WKY/lzm)			GeneName	Ensembl_rat	Chr	Transcription_ start_site (Rnor_6.0)
		Fold change (log2-scale)	SE (log2-scale)	P-value	Fold change (log2-scale)	SE (log2-scale)	P-value				
12215	A_44_P973511	-1.097	0.129	1.4E-06	-1.368	0.129	1.2E-07	Lrp11	ENSRNOG00000014303	1	1,702,696
24903	A_64_P062353	-0.677	0.109	3.5E-05	-0.930	0.109	1.3E-06	Lrp11	ENSRNOG00000014303	1	1,702,696
11055	A_44_P128306	0.816	0.144	8.5E-05	0.890	0.144	3.7E-05	Aldh8a1	ENSRNOG00000014907	1	16,910,069
26496	A_44_P182431	-2.251	0.260	1.1E-06	-2.882	0.260	6.9E-08	Srd5a1	ENSRNOG00000017601	1	36,320,461
27411	A_44_P519871	-2.153	0.271	2.9E-06	-2.567	0.271	4.2E-07	Srd5a1	ENSRNOG00000017601	1	36,320,461
14176	A_64_P164736	1.403	0.240	6.4E-05	1.921	0.240	2.7E-06	LOC100359930	ENSRNOG00000028852	1	82,653,633
22179	A_64_P129593	-1.566	0.228	1.3E-05	-1.594	0.228	1.1E-05	Atp4a	ENSRNOG00000020985	1	89,162,639
7527	A_64_P151448	-0.957	0.151	2.9E-05	-0.908	0.151	4.9E-05	Fancf	ENSRNOG00000023968	1	107,232,305
19183	A_64_P133177	-0.724	0.123	5.9E-05	-1.006	0.123	2.1E-06	Sema4b	ENSRNOG00000025167	1	141,986,145
27674	A_64_P000452	-0.741	0.110	1.6E-05	-0.657	0.110	5.4E-05	Cyp2c7	ENSRNOG00000059330	1	147,435,897
6483	A_44_P154040	2.085	0.146	3.4E-09	1.545	0.146	1.1E-07	Nox4	ENSRNOG00000013925	1	150,797,084
21821	A_44_P975945	1.135	0.191	5.4E-05	1.238	0.191	2.3E-05	Fam168a	ENSRNOG00000018873	1	165,724,451
15042	A_64_P043101	-0.832	0.146	8.1E-05	-0.982	0.146	1.6E-05	Dnhd1	ENSRNOG00000051291	1	170,471,272
18186	A_64_P016077	-0.951	0.154	3.8E-05	-0.952	0.154	3.7E-05	Dnhd1	ENSRNOG00000051291	1	170,471,272
4890	A_42_P797965	0.539	0.079	1.4E-05	0.497	0.079	3.2E-05	RGD1306959	ENSRNOG00000013744	1	174,330,695
13671	A_44_P212813	2.113	0.169	1.7E-08	2.699	0.169	9.0E-10	Acsm5	ENSRNOG00000031211	1	189,233,141
29269	A_64_P151353	3.026	0.130	9.1E-12	3.700	0.130	7.4E-13	Acsm5	ENSRNOG00000031211	1	189,241,593
21952	A_64_P024138	-1.464	0.163	7.3E-07	-0.923	0.163	8.4E-05	Sbk1	ENSRNOG00000057696	1	197,659,187
14224	A_64_P045578	1.176	0.119	2.7E-07	1.251	0.119	1.3E-07	Rnf40	ENSRNOG00000018840	1	199,037,544
22149	A_64_P056569	-0.771	0.114	1.5E-05	-0.778	0.114	1.4E-05	Fus	ENSRNOG00000023360	1	199,412,834
7351	A_42_P718022	1.317	0.233	8.8E-05	1.319	0.233	8.6E-05	Tnni2	ENSRNOG00000020276	1	215,609,036
5718	A_64_P119314	-3.232	0.499	2.4E-05	-3.573	0.499	8.5E-06	LOC689065	ENSRNOG00000036641	1	219,745,654
13480	A_44_P228859	0.932	0.095	2.7E-07	0.841	0.095	8.4E-07	Ust5r	ENSRNOG00000061890	1	224,533,219
2047	A_44_P1012567	2.491	0.159	1.2E-09	1.820	0.159	4.8E-08	Fads3	ENSRNOG00000020385	1	226,091,774
18981	A_64_P013243	-1.712	0.257	1.8E-05	-1.846	0.257	8.3E-06		ENSRNOG00000021811	1	239,319,737
26560	A_64_P071983	1.437	0.218	2.0E-05	1.532	0.218	1.0E-05	Ppp1r3c	ENSRNOG00000018494	1	255,376,833
15747	A_44_P139673	-1.538	0.177	1.1E-06	-2.912	0.177	6.1E-10	Cyp2c12	ENSRNOG00000047945	1	258,766,881
26738	A_64_P143725	0.547	0.097	8.7E-05	0.695	0.097	8.1E-06	Poll	ENSRNOG00000016748	1	265,298,797
25627	A_44_P107308	2.135	0.147	2.8E-09	2.094	0.147	3.6E-09	Gfra1	ENSRNOG00000017438	1	279,277,339
19125	A_64_P001710	1.391	0.187	5.7E-06	1.437	0.187	4.0E-06	Mblac2	ENSRNOG00000016252	2	9,578,345

528 A_42_P523612	-0.753	0.094	2.7E-06	-0.840	0.094	8.1E-07 Mef2c	ENSRNOG000000033134	2	11,658,568
6596 A_43_P13126	1.201	0.157	4.4E-06	1.054	0.157	1.7E-05 Acot12	ENSRNOG000000061414	2	20,857,202
655 A_42_P744291	-1.316	0.138	3.8E-07	-1.234	0.138	7.8E-07 Zbed3	ENSRNOG000000028941	2	25,041,185
15807 A_64_P068038	0.590	0.088	1.7E-05	0.551	0.088	3.3E-05 Hexb	ENSRNOG000000025274	2	28,003,186
19077 A_44_P131470	0.536	0.084	2.7E-05	0.483	0.084	7.3E-05 Hexb	ENSRNOG000000025274	2	28,003,186
28124 A_44_P468239	-1.011	0.123	1.9E-06	-1.116	0.123	6.5E-07 Sgtb	ENSRNOG000000011937	2	34,186,091
2831 A_42_P663871	0.646	0.114	8.7E-05	0.744	0.114	2.3E-05 Gzma	ENSRNOG000000010603	2	44,981,458
27193 A_64_P112889	-1.092	0.154	9.2E-06	-1.436	0.154	4.8E-07 Ccdc152	ENSRNOG000000039473	2	53,140,637
9724 A_43_P11817	1.126	0.180	3.2E-05	1.524	0.180	1.4E-06 Ghr	ENSRNOG000000015654	2	53,313,884
13369 A_44_P320858	0.787	0.086	5.9E-07	0.685	0.086	2.7E-06 Ghr	ENSRNOG000000015654	2	53,313,884
29351 A_64_P041812	1.050	0.128	2.0E-06	1.451	0.128	5.2E-08 Ghr	ENSRNOG000000015654	2	53,313,884
5037 A_44_P187181	-4.170	0.358	2.1E-07	-3.879	0.270	2.6E-08 Prlr	ENSRNOG000000057557	2	60,131,776
465 A_42_P524633	3.946	0.216	1.8E-10	3.908	0.216	2.0E-10 Fam134b	ENSRNOG000000057522	2	78,391,921
19499 A_44_P244851	1.990	0.247	2.4E-06	1.839	0.247	5.6E-06 Car3	ENSRNOG000000010079	2	88,135,410
22736 A_44_P1029241	1.756	0.291	4.7E-05	2.098	0.291	7.9E-06 Car1	ENSRNOG000000010698	2	88,217,188
7069 A_44_P575424	-1.469	0.178	1.9E-06	-1.026	0.178	7.2E-05 Chmp4c	ENSRNOG000000010238	2	93,641,497
5175 A_44_P362981	-1.673	0.233	8.4E-06	-1.667	0.233	8.7E-06 Fabp5	ENSRNOG000000049075	2	93,985,378
29777 A_44_P487504	1.219	0.124	2.8E-07	1.349	0.124	8.9E-08	ENSRNOG000000032715	2	148,262,110
16967 A_44_P773166	-1.044	0.120	1.1E-06	-0.966	0.120	2.4E-06 Tmem144	ENSRNOG000000010081	2	178,612,470
27712 A_64_P041307	-0.986	0.095	1.4E-07	-0.895	0.095	4.3E-07 Tars2	ENSRNOG000000057194	2	197,878,142
29595 A_64_P060667	-4.329	0.146	5.2E-10	-4.105	0.146	8.2E-10 Reg4	ENSRNOG000000019046	2	200,397,967
13762 A_64_P055472	0.879	0.121	7.4E-06	0.727	0.121	4.9E-05 Vangl1	ENSRNOG000000016477	2	204,625,743
10760 A_44_P109455	0.932	0.102	6.1E-07	0.875	0.102	1.2E-06 Gstm2	ENSRNOG000000018937	2	210,782,746
6775 A_64_P027971	3.463	0.193	2.2E-10	3.010	0.193	1.2E-09 Dnase2b	ENSRNOG000000016262	2	252,451,999
3199 A_44_P281352	1.261	0.106	3.2E-08	0.935	0.106	9.4E-07 Dnajb4	ENSRNOG000000013011	2	257,418,425
26230 A_44_P213133	-2.350	0.104	1.3E-11	-2.466	0.104	6.9E-12 Endog	ENSRNOG000000016033	3	8,741,766
22393 A_43_P18366	1.368	0.118	4.0E-08	1.218	0.118	1.5E-07 Tor1b	ENSRNOG000000006435	3	9,792,899
17373 A_42_P638620	1.086	0.110	2.7E-07	1.007	0.110	6.3E-07 Lcn2	ENSRNOG000000013973	3	11,417,546
24771 A_43_P10292	1.628	0.110	2.3E-09	1.237	0.110	5.8E-08 siat7D	ENSRNOG000000048870	3	11,607,225
13463 A_42_P835462	-1.062	0.132	2.5E-06	-1.421	0.132	9.6E-08 Ak1	ENSRNOG000000049056	3	11,653,529
14170 A_64_P141349	2.530	0.225	5.7E-08	2.565	0.225	4.9E-08 B3galt1	ENSRNOG000000007625	3	54,253,949
12228 A_64_P152790	1.510	0.141	1.0E-07	1.102	0.141	3.4E-06 Frzb	ENSRNOG000000007765	3	67,668,772
24139 A_44_P992697	-1.126	0.122	5.5E-07	-1.415	0.122	4.1E-08 Dusp19	ENSRNOG000000008868	3	67,849,966

1902 A_64_P018681	0.712	0.119	5.2E-05	0.728	0.119	4.3E-05 P2rx3	ENSRNOG00000008552	3	72,445,775
17375 A_43_P15275	-2.102	0.099	2.9E-11	-1.961	0.099	6.7E-11 Ptprij	ENSRNOG000000034025	3	79,390,956
18771 A_44_P107766	-1.335	0.138	3.2E-07	-1.319	0.138	3.7E-07 RGD1309540	ENSRNOG000000014798	3	80,349,145
3735 A_42_P665509	0.896	0.094	4.1E-07	1.000	0.094	1.2E-07 Mapk8ip1	ENSRNOG000000058478	3	81,304,181
23303 A_44_P362954	1.152	0.185	3.5E-05	1.075	0.185	6.8E-05 Cat	ENSRNOG00000008364	3	93,412,058
3427 A_44_P1024721	0.764	0.120	2.7E-05	0.956	0.120	2.7E-06 Slc28a2	ENSRNOG000000028668	3	114,355,798
27910 A_64_P158384	-1.350	0.159	1.4E-06	-1.106	0.159	1.1E-05 RGD1359452	ENSRNOG000000037124	3	118,427,851
16566 A_44_P1011953	-1.283	0.133	3.3E-07	-0.762	0.133	7.4E-05 Gpcpd1	ENSRNOG000000053201	3	125,213,607
28840 A_44_P243599	-0.830	0.126	4.6E-05	-0.770	0.095	7.3E-06 RGD1566320	ENSRNOG000000036971	3	138,765,027
5599 A_43_P18817	-0.955	0.156	6.0E-05	-1.225	0.170	1.3E-05 Ifit52	ENSRNOG000000007692	3	159,392,193
20958 A_64_P002904	0.849	0.126	1.5E-05	0.726	0.126	7.1E-05 Pmepa1	ENSRNOG000000050404	3	171,342,646
14169 A_64_P124090	-0.749	0.111	1.6E-05	-0.656	0.111	5.9E-05 Ntsr1	ENSRNOG000000028708	3	175,885,894
15543 A_44_P307964	-0.725	0.089	2.1E-06	-0.639	0.089	8.2E-06 Polr3k	ENSRNOG000000017843	3	177,374,812
9300 A_64_P054808	-2.114	0.188	5.8E-08	-1.655	0.188	9.2E-07 Cd36	ENSRNOG000000040108	4	14,001,761
15617 A_64_P113793	-1.749	0.160	8.0E-08	-1.101	0.160	1.3E-05 Cd36	ENSRNOG000000040108	4	14,151,374
16630 A_44_P1003728	2.170	0.141	4.0E-09	1.736	0.141	4.7E-08 Lmod2	ENSRNOG000000049639	4	51,661,654
30022 A_44_P260072	0.698	0.094	5.8E-06	0.754	0.094	2.6E-06 Tbxas1	ENSRNOG000000007918	4	66,670,618
7276 A_64_P135813	0.716	0.123	6.5E-05	0.821	0.123	1.7E-05 Mkkn1	ENSRNOG000000009280	4	67,206,426
7404 A_43_P23115	4.828	0.192	3.4E-12	3.929	0.192	4.4E-11 Inmt	ENSRNOG000000011250	4	85,386,231
841 A_44_P299247	-2.158	0.100	2.3E-11	-1.772	0.100	2.6E-10 Aqp1	ENSRNOG000000011648	4	85,551,503
13336 A_64_P097974	1.289	0.091	4.0E-09	1.248	0.091	5.9E-09 St3gal5	ENSRNOG000000010284	4	99,937,558
859 A_64_P145166	0.574	0.102	9.5E-05	0.692	0.102	1.6E-05 Ggcn	ENSRNOG000000012975	4	100,277,391
930 A_44_P512828	-0.607	0.107	8.7E-05	-0.641	0.107	5.2E-05 Nup210	ENSRNOG000000005390	4	122,741,110
10944 A_44_P337351	-0.767	0.118	2.2E-05	-0.661	0.118	9.2E-05 Cxcl12	ENSRNOG000000013589	4	149,261,044
11102 A_44_P917327	1.053	0.164	2.6E-05	0.938	0.164	7.9E-05 Lrtm2	ENSRNOG000000007508	4	151,390,263
17411 A_64_P095378	1.407	0.188	2.6E-05	1.279	0.188	5.7E-05 Lrtm2	ENSRNOG000000007508	4	151,390,263
22190 A_64_P038872	1.530	0.238	2.6E-05	1.395	0.238	6.2E-05 A2m	ENSRNOG000000028896	4	154,309,426
2217 A_64_P091148	2.651	0.255	1.4E-07	2.270	0.255	8.1E-07 Tuba3a	ENSRNOG000000031707	4	157,798,868
25815 A_43_P13004	-4.095	0.331	1.9E-08	-4.757	0.331	3.2E-09 Cdh17	ENSRNOG000000015562	5	25,391,115
1894 A_64_P118499	0.947	0.164	7.0E-05	0.914	0.164	9.7E-05 RGD1561916	ENSRNOG000000013320	5	57,896,475
21610 A_64_P013398	-2.611	0.154	4.4E-10	-2.275	0.154	2.3E-09 Gne	ENSRNOG000000014365	5	59,543,101
696 A_64_P091926	1.306	0.122	1.1E-07	1.354	0.122	7.0E-08 Acnat2	ENSRNOG000000051912	5	64,674,250
19017 A_64_P078573	1.459	0.113	1.1E-08	1.446	0.113	1.3E-08	ENSRNOG000000056688	5	64,718,131

6106 A_44_P283971	1.122	0.159	1.0E-05	0.911	0.159	7.9E-05 Zfp189	ENSRNOG000000006972	5	64,789,456
321 A_42_P698240	-0.809	0.113	8.4E-06	-0.784	0.113	1.2E-05 Ptgr1	ENSRNOG000000015072	5	76,129,441
20157 A_64_P137461	-1.506	0.204	6.2E-06	-1.296	0.204	2.8E-05 Bspry	ENSRNOG000000015105	5	78,334,284
13424 A_44_P175822	-1.006	0.129	3.5E-06	-0.772	0.129	5.1E-05 Hdhd3	ENSRNOG000000015195	5	78,361,647
29448 A_64_P090543	-1.135	0.122	5.0E-07	-0.868	0.122	8.9E-06 Hdhd3	ENSRNOG000000015195	5	78,361,647
29932 A_64_P082212	-1.717	0.110	1.3E-09	-1.426	0.110	1.2E-08 Kif12	ENSRNOG000000007080	5	79,008,363
13242 A_44_P1040796	1.527	0.091	4.7E-10	1.553	0.091	3.8E-10 Atp6v1g1	ENSRNOG000000008163	5	79,367,663
22473 A_64_P040989	2.030	0.199	1.8E-07	2.868	0.199	3.1E-09 Cyp4a8	ENSRNOG000000008842	5	134,008,255
23745 A_44_P175875	0.930	0.125	5.7E-06	0.896	0.125	8.5E-06 Pigv	ENSRNOG000000000121	5	151,895,016
4895 A_64_P146507	1.747	0.211	1.8E-06	1.447	0.211	1.3E-05	ENSRNOG000000042062	5	173,139,628
6351 A_44_P163242	-0.979	0.153	2.6E-05	-1.120	0.153	6.7E-06 Epcam	ENSRNOG000000015667	6	11,298,216
24965 A_64_P122457	0.510	0.082	3.7E-05	0.543	0.082	2.0E-05 Rbks	ENSRNOG000000004710	6	26,051,396
3481 A_43_P19743	-2.642	0.142	1.5E-10	-2.664	0.142	1.3E-10 Krtcap3	ENSRNOG000000047941	6	26,486,695
18372 A_64_P017363	3.713	0.140	1.7E-12	2.448	0.140	2.9E-10 Slc30a3	ENSRNOG000000006204	6	26,642,783
6427 A_64_P037020	0.657	0.093	1.0E-05	0.550	0.093	5.9E-05 Seli	ENSRNOG000000059295	6	27,487,284
24275 A_44_P413979	0.691	0.095	7.2E-06	0.970	0.095	1.8E-07 Rab10	ENSRNOG000000047088	6	27,721,120
2367 A_42_P816740	0.956	0.105	6.7E-07	0.844	0.105	2.6E-06 Sh3yl1	ENSRNOG000000005522	6	49,852,130
12825 A_44_P267628	1.597	0.127	1.5E-08	1.286	0.127	1.9E-07 LOC690226	ENSRNOG000000025648	6	95,502,775
4312 A_44_P684199	2.574	0.182	4.0E-09	2.059	0.182	5.5E-08 Dhrr7	ENSRNOG000000025648	6	95,502,845
3166 A_44_P353157	-2.621	0.205	8.4E-08	-3.148	0.155	7.3E-10 Tmem30b	ENSRNOG000000008046	6	96,442,682
8745 A_44_P260589	-1.001	0.125	7.6E-06	-1.084	0.125	3.6E-06	ENSRNOG000000009448	6	107,245,820
15326 A_64_P103936	-4.755	0.217	3.2E-10	-4.713	0.217	3.5E-10 Acot5	ENSRNOG000000032508	6	107,550,904
1038 A_44_P470661	-2.094	0.121	3.4E-10	-2.767	0.121	1.1E-11 Serpina3m	ENSRNOG000000009921	6	127,816,055
29681 A_44_P412140	-4.335	0.123	4.8E-14	-4.868	0.123	1.1E-14 LOC299282	ENSRNOG000000010478	6	128,046,780
2823 A_42_P581060	0.864	0.097	8.7E-07	1.062	0.097	8.5E-08 Glrx5	ENSRNOG000000004206	6	128,750,795
12961 A_44_P974862	1.161	0.157	6.0E-06	1.191	0.157	4.6E-06 Plid4	ENSRNOG000000028566	6	137,323,713
17240 A_44_P147572	-0.836	0.134	3.4E-05	-0.900	0.134	1.7E-05	ENSRNOG000000034190	6	138,508,753
29256 A_44_P321532	1.125	0.083	6.5E-09	0.819	0.083	2.6E-07 Apon	ENSRNOG000000033466	7	2,677,199
1509 A_42_P744495	1.074	0.133	2.4E-06	0.789	0.133	5.5E-05 Cd63	ENSRNOG000000007650	7	3,320,103
23314 A_44_P462040	1.116	0.116	3.6E-07	1.293	0.116	6.6E-08 Mettl7b	ENSRNOG000000007927	7	3,386,522
14192 A_64_P161250	0.810	0.088	5.8E-07	1.039	0.088	3.4E-08 Mier2	ENSRNOG000000000175	7	13,039,781
10600 A_64_P099017	-2.291	0.213	1.0E-07	-2.073	0.213	3.1E-07 Cyp4f17	ENSRNOG000000062306	7	14,529,483
2475 A_64_P079666	1.775	0.135	9.7E-09	1.648	0.135	2.3E-08 Cyp4f5	ENSRNOG000000042496	7	14,559,878

15805 A_64_P255450	-1.071	0.174	3.8E-05	-0.979	0.174	8.9E-05 Zfp799	ENSRNOG000000032552	7	15,072,703
17688 A_64_P012739	-1.126	0.155	7.4E-06	-1.162	0.155	5.3E-06 LOC314600	ENSRNOG000000048577	7	15,785,410
21207 A_44_P607542	1.163	0.146	2.8E-06	1.454	0.146	2.4E-07	ENSRNOG000000005758	7	24,313,885
24430 A_44_P1038341	0.733	0.101	7.6E-06	0.921	0.101	6.5E-07 Hal	ENSRNOG000000004502	7	34,326,087
1344 A_42_P647599	0.962	0.100	3.6E-07	1.095	0.100	8.2E-08 Dcn	ENSRNOG000000004554	7	38,742,051
17690 A_44_P216654	0.693	0.111	3.3E-05	0.703	0.111	2.9E-05 Nap1l1	ENSRNOG000000003890	7	54,213,319
23558 A_64_P144913	2.073	0.151	5.7E-09	1.607	0.151	1.1E-07 Nab2	ENSRNOG000000008415	7	70,969,905
19834 A_64_P036553	4.049	0.135	3.7E-13	3.295	0.135	4.8E-12 Rdh2	ENSRNOG000000029651	7	70,980,422
27443 A_64_P036548	3.547	0.194	1.7E-10	3.225	0.194	5.4E-10 Rdh2	ENSRNOG000000029651	7	71,057,911
4653 A_44_P516093	1.009	0.106	4.0E-07	1.321	0.106	1.8E-08 Colec10	ENSRNOG000000008591	7	93,975,451
14838 A_64_P006590	2.181	0.287	4.6E-06	3.816	0.287	8.2E-09 Cyp2b2	ENSRNOG000000033680	7	99,142,450
1609 A_64_P143947	-0.729	0.102	8.6E-06	-0.691	0.102	1.5E-05	ENSRNOG000000055178	7	101,138,860
2438 A_42_P797218	1.591	0.117	6.5E-09	1.484	0.117	1.5E-08 Gpt	ENSRNOG000000033915	7	117,759,083
24492 A_43_P16804	0.636	0.112	8.5E-05	0.812	0.112	7.7E-06 Pole3	ENSRNOG000000004843	7	118,816,655
28509 A_44_P267706	-1.472	0.167	9.2E-07	-1.091	0.167	2.1E-05 Apol11a	ENSRNOG000000023122	7	118,840,634
15205 A_64_P111893	-2.002	0.182	7.5E-08	-1.372	0.182	4.9E-06 Apol9a	ENSRNOG000000023410	7	118,933,812
25974 A_43_P12557	0.820	0.097	1.5E-06	0.707	0.097	7.4E-06 Polr2f	ENSRNOG000000011214	7	120,380,544
3278 A_64_P001211	0.460	0.078	6.1E-05	0.483	0.078	3.8E-05 Cyp2d5	ENSRNOG000000029128	7	123,621,102
13515 A_64_P019790	0.448	0.078	7.3E-05	0.464	0.078	5.2E-05 Cyp2d1	ENSRNOG000000029179	7	123,638,765
21368 A_44_P914022	1.607	0.160	2.0E-06	1.094	0.160	5.3E-05 LOC689933	ENSRNOG000000042056	7	130,368,819
1918 A_64_P019051	-0.804	0.104	3.9E-06	-0.850	0.104	2.2E-06 Smug1	ENSRNOG000000036842	7	144,778,339
8405 A_42_P660129	1.782	0.164	8.9E-08	2.808	0.164	4.0E-10 Casp12	ENSRNOG000000033434	8	2,659,865
17711 A_44_P119527	-1.698	0.183	5.1E-07	-1.704	0.183	4.9E-07 Med17	ENSRNOG000000051989	8	13,526,025
11775 A_44_P518434	-1.027	0.122	1.6E-06	-0.988	0.122	2.4E-06 Mrpl4	ENSRNOG000000020659	8	22,021,213
582 A_42_P577421	1.567	0.261	5.0E-05	1.900	0.261	7.2E-06 Nnmt	ENSRNOG000000005930	8	52,937,972
9382 A_44_P531758	1.556	0.178	1.0E-06	1.254	0.178	1.0E-05 Cryab	ENSRNOG000000010524	8	55,178,289
27101 A_64_P118047	1.003	0.151	1.9E-05	1.127	0.151	5.7E-06 Prtg	ENSRNOG000000055251	8	79,489,790
11738 A_43_P13967	0.645	0.116	9.9E-05	0.688	0.116	5.3E-05 Gsta2	ENSRNOG000000000201	8	85,553,734
29727 A_44_P119575	0.912	0.128	1.4E-05	1.228	0.128	7.2E-07	ENSRNOG000000009613	8	91,099,491
22148 A_44_P283339	1.939	0.133	2.8E-09	1.383	0.133	1.5E-07 Tmed3	ENSRNOG000000013889	8	97,083,120
5815 A_43_P11432	-0.674	0.081	1.6E-06	-0.629	0.081	3.4E-06 Acaa1a	ENSRNOG000000032908	8	128,027,958
11481 A_44_P113974	0.899	0.121	6.0E-06	0.831	0.121	1.4E-05 Ccr5	ENSRNOG000000049115	8	133,210,473
1203 A_44_P974940	2.290	0.145	1.1E-09	2.514	0.145	3.4E-10 RGD1562392	ENSRNOG000000047369	9	4,072,901

7083 A_64_P001334	2.745	0.147	1.3E-10	3.038	0.147	3.8E-11 Sult1c2	ENSRNOG000000047369	9	4,094,995
257 A_42_P501679	-0.795	0.119	1.7E-05	-0.803	0.119	1.5E-05 M6prbp1	ENSRNOG000000048834	9	10,773,901
5143 A_43_P18744	-1.127	0.126	5.6E-06	-1.285	0.112	6.2E-07 Enpp5	ENSRNOG000000010232	9	19,476,646
17867 A_44_P1029892	4.273	0.156	1.2E-12	4.225	0.156	1.4E-12 Tmem14a	ENSRNOG000000046593	9	27,343,853
23432 A_64_P039432	-0.655	0.097	1.6E-05	-0.673	0.097	1.2E-05 Clk1	ENSRNOG000000025768	9	65,307,995
25117 A_64_P060967	0.777	0.102	4.4E-06	0.900	0.102	9.1E-07 Lancl1	ENSRNOG000000013557	9	74,048,244
20772 A_43_P15154	-1.760	0.257	1.4E-05	-1.509	0.257	6.1E-05 lhh	ENSRNOG000000018059	9	82,214,440
18795 A_43_P10901	1.372	0.094	2.6E-09	1.021	0.094	8.5E-08 ltm2c	ENSRNOG000000017359	9	92,916,469
11494 A_44_P123492	-1.195	0.095	1.5E-08	-1.054	0.095	6.7E-08 Epb41l3	ENSRNOG000000016724	9	117,538,009
9066 A_64_P027288	2.191	0.160	5.6E-09	2.559	0.160	8.7E-10 RGD1564516	ENSRNOG000000038894	10	31,880,918
19797 A_64_P017631	-0.714	0.117	4.2E-05	-0.763	0.117	2.2E-05 RGD1563669	ENSRNOG000000053961	10	46,314,375
21936 A_44_P493911	3.290	0.262	1.6E-08	2.812	0.262	1.0E-07 Slc13a5	ENSRNOG000000014870	10	58,834,538
8183 A_64_P033710	1.137	0.172	2.9E-05	1.114	0.172	3.5E-05 Hlf	ENSRNOG000000002456	10	77,918,191
22560 A_64_P157691	-1.460	0.114	1.3E-08	-1.785	0.114	1.2E-09 RGD1559482	ENSRNOG000000048771	10	104,952,237
25284 A_44_P356866	-1.493	0.175	1.4E-06	-1.753	0.175	2.3E-07 RGD1311078	ENSRNOG000000060307	10	105,073,077
22449 A_42_P539095	-0.646	0.096	1.5E-05	-0.781	0.096	2.1E-06 LOC688311	ENSRNOG000000049235	10	109,639,054
21718 A_44_P239300	1.331	0.121	7.9E-08	1.111	0.121	6.1E-07 RGD1307119	ENSRNOG000000036680	10	109,840,047
18404 A_43_P13256	0.669	0.102	2.1E-05	0.764	0.102	5.3E-06 Dcxr	ENSRNOG000000050315	10	109,909,646
6976 A_44_P352538	0.721	0.095	4.6E-06	0.550	0.095	6.9E-05 Sectm1a	ENSRNOG000000036672	10	110,274,768
22819 A_44_P159569	1.289	0.103	1.7E-08	1.140	0.103	7.2E-08 Wdr45l	ENSRNOG000000036662	10	110,555,629
28640 A_44_P228942	-0.762	0.137	9.8E-05	-0.809	0.137	5.6E-05 Runx1	ENSRNOG000000001704	11	32,858,830
6823 A_44_P761087	-0.861	0.122	1.0E-05	-1.099	0.122	7.5E-07 Ets2	ENSRNOG000000001647	11	36,075,709
6166 A_64_P024394	0.526	0.092	7.6E-05	0.906	0.092	2.6E-07 Hrg	ENSRNOG000000001809	11	81,639,952
2087 A_64_P015758	-1.105	0.195	8.3E-05	-1.223	0.195	3.2E-05	ENSRNOG000000050000	11	86,092,468
9870 A_64_P012902	0.761	0.096	3.1E-06	0.606	0.096	3.2E-05 Sdf2l1	ENSRNOG000000001859	11	88,122,271
14260 A_64_P019401	0.787	0.129	4.1E-05	0.742	0.129	7.2E-05 Sdf2l1	ENSRNOG000000001859	11	88,122,271
1534 A_42_P762213	-2.406	0.185	2.7E-08	-2.319	0.170	1.6E-08 Lrrc8e	ENSRNOG000000028460	12	2,568,382
29020 A_44_P116660	-0.671	0.105	2.6E-05	-0.955	0.105	6.3E-07 Cd209b	ENSRNOG000000029881	12	2,826,378
3552 A_42_P679814	1.385	0.156	8.5E-07	1.690	0.156	9.0E-08 Cyp3a18	ENSRNOG000000000969	12	10,636,275
578 A_44_P1009594	1.804	0.147	2.0E-08	1.754	0.147	2.8E-08 Cyp3a62	ENSRNOG000000001379	12	18,678,594
17338 A_44_P1037342	-2.575	0.141	1.8E-10	-2.375	0.141	5.0E-10 Cyp3a9	ENSRNOG000000046643	12	19,114,399
19145 A_64_P081501	0.750	0.119	3.2E-05	1.291	0.119	9.2E-08 Mcm7	ENSRNOG000000001349	12	19,314,016
23117 A_42_P540609	-0.646	0.112	7.0E-05	-0.641	0.112	7.4E-05 LOC680711	ENSRNOG000000031343	12	19,440,501

25622 A_64_P119299	-0.773	0.094	2.0E-06	-0.775	0.094	1.9E-06	ENSRNOG000000027061	12	19,512,591
8198 A_64_P027108	-0.802	0.116	1.2E-05	-0.811	0.116	1.1E-05 RGD1562319	ENSRNOG000000039216	12	19,561,347
551 A_64_P164498	1.342	0.095	4.2E-09	1.408	0.095	2.3E-09 LOC685438	ENSRNOG000000047079	12	20,276,121
18384 A_64_P079080	1.158	0.096	2.5E-08	1.219	0.096	1.4E-08	ENSRNOG000000059625	12	20,667,601
7888 A_64_P156448	1.063	0.101	1.2E-07	1.103	0.101	8.0E-08 LOC685157	ENSRNOG000000050981	12	21,362,205
15839 A_64_P032265	1.708	0.099	3.8E-10	1.817	0.099	1.8E-10	ENSRNOG000000033017	12	21,678,580
28441 A_64_P022248	-0.719	0.127	8.6E-05	-0.979	0.127	4.0E-06 Ccdc62	ENSRNOG000000038002	12	38,093,050
29139 A_44_P838992	-2.255	0.197	1.1E-07	-2.984	0.214	1.3E-08 LOC687609	ENSRNOG000000042607	12	38,880,377
6196 A_44_P686406	1.339	0.131	1.7E-07	0.806	0.131	3.8E-05 RGD1562310	ENSRNOG000000001123	12	43,940,798
15981 A_44_P224631	0.837	0.120	1.1E-05	0.912	0.120	4.5E-06 Dao	ENSRNOG000000054962	12	48,365,784
14258 A_43_P13249	2.207	0.209	1.2E-07	2.917	0.209	4.7E-09 Acmsd	ENSRNOG000000003884	13	44,424,689
13363 A_42_P667960	0.747	0.115	2.2E-05	0.939	0.115	2.1E-06 Ikbke	ENSRNOG000000025100	13	48,056,394
824 A_44_P137633	-2.198	0.291	4.9E-06	-1.828	0.291	3.2E-05 Adora1	ENSRNOG000000003442	13	51,076,165
16686 A_44_P283508	1.575	0.137	4.5E-08	1.458	0.137	1.1E-07 Fmo1	ENSRNOG000000034191	13	80,745,347
4122 A_44_P358194	0.969	0.114	1.4E-06	1.095	0.114	3.6E-07 Fmo3	ENSRNOG000000003620	13	80,862,963
14514 A_44_P180259	0.663	0.109	4.3E-05	0.816	0.109	5.2E-06 Dpt	ENSRNOG000000002947	13	83,073,550
12064 A_64_P027625	-1.761	0.184	3.7E-07	-1.025	0.184	9.9E-05 Rxrg	ENSRNOG000000004537	13	85,818,427
339 A_42_P743580	1.704	0.146	5.3E-07	-2.229	0.243	4.4E-06 Rgs4	ENSRNOG000000002773	13	88,061,108
21779 A_44_P306439	0.687	0.115	5.3E-05	0.809	0.115	1.1E-05 Fcgr3a	ENSRNOG000000024382	13	89,385,859
25592 A_44_P575255	3.161	0.133	6.7E-12	2.966	0.133	1.5E-11 RGD1562658	ENSRNOG000000034221	13	89,480,058
3268 A_64_P005029	3.908	0.264	2.3E-09	3.025	0.264	4.8E-08 Pcp4l1	ENSRNOG000000003209	13	89,565,813
24112 A_64_P109496	3.085	0.215	3.4E-09	2.726	0.215	1.5E-08 Nr1i3	ENSRNOG000000003260	13	89,586,283
29177 A_64_P109497	2.684	0.168	9.2E-10	2.315	0.168	5.5E-09 Nr1i3	ENSRNOG000000003260	13	89,586,283
5407 A_42_P565621	0.561	0.084	1.7E-05	0.818	0.084	3.1E-07 Slamf9	ENSRNOG000000008045	13	90,839,411
1758 A_64_P027298	1.003	0.135	5.8E-06	0.968	0.135	8.3E-06 Ptpn14	ENSRNOG000000003407	13	108,841,482
9059 A_42_P803590	-2.145	0.153	4.5E-09	-2.213	0.153	3.1E-09 LOC289378	ENSRNOG000000046460	13	109,663,364
2950 A_42_P683634	0.614	0.086	9.3E-06	0.619	0.086	8.5E-06 Sparcl1	ENSRNOG000000015093	14	6,994,190
783 A_64_P071159	-1.822	0.096	1.1E-10	-1.723	0.096	2.1E-10 LOC360919	ENSRNOG000000039504	14	19,072,677
17181 A_64_P071158	-1.872	0.101	1.5E-10	-1.746	0.101	3.4E-10 LOC360919	ENSRNOG000000039504	14	19,072,677
5419 A_64_P045325	2.210	0.093	6.7E-12	2.616	0.093	8.1E-13	ENSRNOG000000001973	14	22,192,970
11942 A_64_P062143	1.330	0.112	3.1E-08	1.740	0.112	1.3E-09 Ugt2a3	ENSRNOG000000001973	14	22,192,970
11973 A_44_P236068	0.685	0.103	1.8E-05	0.795	0.103	3.8E-06 Ugt2b36	ENSRNOG000000001980	14	22,553,662
27421 A_44_P447623	0.694	0.110	3.1E-05	0.824	0.110	5.4E-06 Ugdh	ENSRNOG000000002643	14	44,479,614

22 A_44_P992306	-1.110	0.192	7.0E-05	-1.297	0.192	1.5E-05 Gnpda2	ENSRNOG000000002177	14	62,646,110
22164 A_64_P132516	-1.651	0.175	4.3E-07	-1.943	0.175	6.8E-08 Rtn4	ENSRNOG000000004621	14	114,126,943
29558 A_44_P477322	-1.417	0.174	2.2E-06	-1.999	0.174	4.7E-08 Rtn4	ENSRNOG000000004621	14	114,126,943
11690 A_44_P330188	1.889	0.117	8.1E-10	1.893	0.117	7.9E-10 Acox2	ENSRNOG000000007378	15	18,451,144
3800 A_64_P100123	-0.910	0.102	8.2E-07	-0.938	0.102	5.9E-07 Pxx	ENSRNOG000000008024	15	18,616,589
8986 A_44_P1057690	0.638	0.090	9.2E-06	0.637	0.090	9.4E-06 Dnase1l3	ENSRNOG000000009291	15	18,710,492
5685 A_42_P775609	-1.005	0.145	1.2E-05	-0.951	0.145	2.0E-05 Jub	ENSRNOG000000012791	15	33,218,456
2966 A_64_P106162	0.522	0.092	8.7E-05	0.569	0.092	3.8E-05 Pck2	ENSRNOG000000018536	15	34,216,833
6846 A_64_P005043	1.219	0.093	9.8E-09	1.045	0.093	6.0E-08 Nt5dc2	ENSRNOG000000018358	16	7,212,488
18552 A_64_P142248	-1.152	0.171	1.5E-05	-1.255	0.171	6.4E-06 Colq	ENSRNOG000000019615	16	7,681,576
19242 A_64_P119675	-0.963	0.165	6.4E-05	-0.920	0.165	9.8E-05 Jund	ENSRNOG000000019568	16	20,486,707
25971 A_64_P004531	-0.623	0.092	1.4E-05	-0.778	0.092	1.4E-06 LOC688966	ENSRNOG000000020427	16	21,029,134
28374 A_64_P315172	0.996	0.135	1.7E-05	1.420	0.135	5.8E-07 Nat2	ENSRNOG000000049498	16	23,991,570
3982 A_64_P007462	1.283	0.127	2.0E-07	1.149	0.127	6.8E-07 Spcs3	ENSRNOG000000038933	16	40,050,734
26075 A_64_P041016	-1.211	0.113	1.0E-07	-0.880	0.113	3.5E-06 Wwc2	ENSRNOG000000013248	16	47,368,768
18238 A_43_P11534	-0.577	0.100	7.3E-05	-0.640	0.100	2.7E-05 Klb1	ENSRNOG000000014118	16	50,152,008
9554 A_64_P048315	1.548	0.109	3.6E-09	1.378	0.109	1.4E-08	ENSRNOG000000055088	16	59,517,000
11412 A_44_P1042163	0.821	0.096	1.2E-06	0.634	0.096	1.9E-05 RGD1310414	ENSRNOG000000023494	16	64,745,207
26021 A_64_P085286	1.218	0.138	8.9E-07	1.335	0.138	3.2E-07 Rnf170	ENSRNOG000000045943	16	70,705,128
28250 A_64_P017645	-0.617	0.100	3.9E-05	-0.721	0.100	8.1E-06 Atp7b	ENSRNOG000000012878	16	74,865,516
712 A_42_P558354	-0.721	0.090	2.5E-06	-0.814	0.090	6.6E-07 Cln8	ENSRNOG000000012565	16	79,838,212
26198 A_64_P064008	2.060	0.315	2.2E-05	2.015	0.315	2.7E-05	ENSRNOG000000061436	17	445,236
11386 A_64_P014278	-0.961	0.117	1.9E-06	-0.728	0.117	3.4E-05 LOC680692	ENSRNOG000000018400	17	5,382,034
23308 A_64_P136894	1.159	0.160	7.7E-06	0.918	0.160	7.7E-05 Omd	ENSRNOG000000039560	17	15,484,269
4180 A_64_P165035	6.544	0.115	1.2E-16	6.715	0.115	8.6E-17 RGD1305679	ENSRNOG000000014481	17	22,619,891
8900 A_64_P059262	0.742	0.125	5.5E-05	0.851	0.125	1.4E-05 Riok1	ENSRNOG000000014049	17	27,451,832
23925 A_64_P030919	-0.911	0.140	2.2E-05	-0.832	0.140	5.4E-05	ENSRNOG000000023538	17	42,133,076
28972 A_64_P060715	-1.519	0.170	8.0E-07	-1.376	0.170	2.3E-06	ENSRNOG000000022505	17	43,458,553
29478 A_64_P100482	-1.604	0.153	1.3E-07	-1.367	0.153	7.8E-07 LOC684568	ENSRNOG000000022505	17	43,458,553
7060 A_42_P555365	1.104	0.159	1.1E-05	1.542	0.159	3.1E-07 Slc17a3	ENSRNOG000000032745	17	43,537,293
14149 A_64_P080667	-1.461	0.153	3.8E-07	-1.383	0.153	7.0E-07 LOC684841	ENSRNOG000000045644	17	43,807,540
13074 A_64_P130572	0.736	0.100	6.3E-06	0.576	0.100	7.2E-05 Hist1h2bc	ENSRNOG000000059382	17	44,738,330
13903 A_44_P515798	4.879	0.168	3.1E-12	4.529	0.168	7.2E-12 Ucma	ENSRNOG000000017987	17	77,261,731

25656 A_44_P245616	1.340	0.193	1.2E-05	1.618	0.193	1.6E-06	Nid1	ENSRNOG000000002461	17	90,627,101
7301 A_64_P024440	-1.203	0.124	3.2E-07	-0.871	0.124	1.0E-05	Rbbp8	ENSRNOG000000012899	18	3,163,214
10422 A_64_P024439	-1.141	0.096	2.9E-08	-0.874	0.096	6.2E-07	Rbbp8	ENSRNOG000000012899	18	3,163,214
26378 A_64_P026928	0.914	0.136	1.7E-05	1.384	0.136	1.9E-07	Prr16	ENSRNOG000000019744	18	46,148,849
2039 A_64_P135224	6.025	0.228	1.9E-12	6.883	0.228	3.6E-13	RGD1309362	ENSRNOG000000038960	18	55,505,993
6991 A_64_P050921	-2.248	0.337	1.8E-05	-2.289	0.337	1.5E-05	Ablim3	ENSRNOG000000019365	18	57,201,740
22519 A_64_P021320	-0.506	0.088	7.3E-05	-0.534	0.088	4.4E-05	Pqlc1	ENSRNOG000000059215	18	76,770,012
18626 A_64_P097078	-1.813	0.185	2.9E-07	-1.166	0.185	3.1E-05	Pdp2	ENSRNOG000000012343	19	601,469
2495 A_44_P555689	2.477	0.276	7.5E-07	2.184	0.276	2.9E-06	LOC291863	ENSRNOG000000015519	19	15,033,108
17810 A_64_P148413	1.773	0.133	7.6E-09	1.774	0.133	7.5E-09	Ces1d	ENSRNOG000000015519	19	15,033,108
9089 A_64_P005208	-2.387	0.204	3.7E-08	-1.679	0.204	1.9E-06	Nqo1	ENSRNOG000000012772	19	38,422,164
1018 A_44_P222122	2.564	0.147	3.1E-10	2.605	0.147	2.6E-10	Bcmo1	ENSRNOG000000012027	19	49,637,016
6248 A_64_P157604	-0.824	0.122	1.6E-05	-0.848	0.122	1.2E-05	Cpne7	ENSRNOG000000015397	19	55,929,609
26400 A_64_P064371	-1.330	0.158	1.5E-06	-1.406	0.158	8.2E-07	Spat2L	ENSRNOG000000016167	19	56,037,077
17609 A_64_P058266	-2.143	0.293	6.8E-06	-2.158	0.293	6.3E-06	Cox6c1	ENSRNOG000000032602	19	56,983,807
4436 A_42_P627572	-1.481	0.122	2.4E-08	-1.078	0.122	9.1E-07	Mdc1	ENSRNOG000000032813	20	3,405,285
14913 A_44_P914438	2.115	0.229	5.4E-07	2.099	0.229	5.9E-07	Cdkn1a	ENSRNOG000000000521	20	6,356,423
1872 A_64_P117171	0.774	0.103	5.0E-06	0.653	0.103	2.8E-05	LOC689755	ENSRNOG000000000531	20	8,384,088
15230 A_64_P048033	1.525	0.177	1.2E-06	1.371	0.177	3.7E-06	Agpat3	ENSRNOG000000001205	20	11,114,164
14331 A_64_P152447	2.310	0.146	1.0E-09	3.070	0.146	3.2E-11	Gstt3	ENSRNOG000000001242	20	13,817,795
19033 A_44_P1015203	2.407	0.141	4.0E-10	3.197	0.141	1.2E-11	Gstt3	ENSRNOG000000001242	20	13,817,795
8444 A_44_P1005649	1.422	0.129	7.5E-08	1.341	0.129	1.5E-07	Dnajc12	ENSRNOG000000051960	20	26,893,016
21326 A_44_P496643	-1.641	0.268	4.1E-05	-1.742	0.268	2.3E-05		ENSRNOG000000048535	20	29,280,386
23912 A_64_P126135	-1.877	0.163	4.5E-08	-1.508	0.163	5.5E-07		ENSRNOG000000055765	568414	23,534
711 A_64_P157099	5.460	0.179	3.0E-13	5.061	0.179	7.8E-13		ENSRNOG000000031780	MT	1
889 A_44_P403017	0.638	0.106	4.9E-05	0.638	0.106	4.9E-05		ENSRNOG000000031780	MT	1
5482 A_64_P326359	1.780	0.171	1.4E-07	1.579	0.171	5.3E-07		ENSRNOG000000031780	MT	1
7877 A_64_P156662	2.486	0.191	1.1E-08	2.116	0.191	7.0E-08		ENSRNOG000000031780	MT	1
8649 A_64_P164474	0.935	0.145	2.5E-05	1.360	0.145	4.7E-07		ENSRNOG000000031780	MT	1
10091 A_64_P150008	-1.370	0.180	4.4E-06	-1.554	0.180	1.1E-06		ENSRNOG000000031780	MT	1
10171 A_64_P022135	1.523	0.137	6.4E-08	1.313	0.137	3.5E-07		ENSRNOG000000031780	MT	1
10544 A_64_P085915	-1.260	0.137	5.6E-07	-1.076	0.137	3.1E-06		ENSRNOG000000031780	MT	1
10820 A_64_P143542	1.650	0.188	9.7E-07	1.907	0.188	1.9E-07		ENSRNOG000000031780	MT	1

11809 A_64_P024675	-1.786	0.143	1.7E-08	-1.953	0.143	5.7E-09	ENSRNOG000000031780	MT	1
12812 A_64_P038099	-0.697	0.117	5.3E-05	-0.828	0.117	9.6E-06	ENSRNOG000000031780	MT	1
12900 A_64_P054953	2.614	0.119	1.8E-11	2.940	0.119	4.2E-12	ENSRNOG000000031780	MT	1
12960 A_64_P158343	0.850	0.146	6.8E-05	0.901	0.146	3.9E-05	ENSRNOG000000031780	MT	1
16302 A_64_P079528	-1.095	0.125	3.3E-06	-0.972	0.102	1.5E-06	ENSRNOG000000031780	MT	1
17252 A_44_P900209	-0.797	0.133	4.9E-05	-0.904	0.133	1.4E-05	ENSRNOG000000031780	MT	1
21135 A_64_P118308	-1.630	0.138	7.8E-08	-1.514	0.127	6.9E-08	ENSRNOG000000031780	MT	1
22371 A_64_P039036	-0.674	0.098	1.3E-05	-0.635	0.098	2.4E-05	ENSRNOG000000031780	MT	1
22836 A_64_P123792	0.877	0.126	1.1E-05	1.654	0.126	9.4E-09	ENSRNOG000000031780	MT	1
24098 A_64_P042811	-2.322	0.134	3.2E-10	-2.463	0.134	1.6E-10	ENSRNOG000000031780	MT	1
24283 A_64_P138744	1.607	0.159	2.0E-07	1.501	0.159	4.3E-07	ENSRNOG000000031780	MT	1
24791 A_64_P142146	1.003	0.124	2.4E-06	1.858	0.124	2.0E-09	ENSRNOG000000031780	MT	1
25880 A_64_P006473	-1.765	0.177	2.3E-07	-1.094	0.177	3.7E-05	ENSRNOG000000031780	MT	1
26581 A_64_P135939	2.288	0.273	1.6E-06	2.001	0.273	6.6E-06	ENSRNOG000000031780	MT	1
28018 A_64_P101600	-1.533	0.182	1.5E-06	-1.022	0.182	9.4E-05	ENSRNOG000000031780	MT	1
29293 A_64_P029190	1.132	0.084	7.4E-09	1.222	0.084	3.0E-09	ENSRNOG000000031780	MT	1
8786 A_64_P062462	0.841	0.105	2.7E-06	1.375	0.105	1.0E-08 Pir	ENSRNOG000000003674	X	31,968,152
19288 A_64_P128433	-1.097	0.104	1.2E-07	-1.107	0.104	1.1E-07 Ctps2	ENSRNOG000000004257	X	33,522,836
20840 A_64_P037631	2.887	0.197	2.5E-09	2.709	0.197	5.4E-09 Ar	ENSRNOG000000005639	X	67,656,253
15663 A_64_P048852	-1.298	0.115	5.4E-08	-1.176	0.115	1.7E-07	ENSRNOG000000006459	X	120,313,696
25430 A_64_P008527	-1.469	0.189	6.8E-05	-1.430	0.189	8.2E-05 Wdr44	ENSRNOG000000029068	X	120,860,178
3086 A_42_P768355	2.866	0.179	2.9E-08	2.715	0.179	4.7E-08 no transcript			
4576 A_64_P011301	1.171	0.081	3.0E-09	1.314	0.081	7.4E-10 Ugt2b17 (Ugt2b5)			
5530 A_42_P538334	0.639	0.102	3.2E-05	0.662	0.102	2.3E-05 Snhg8			
6876 A_64_P102739	-1.997	0.124	8.5E-10	-0.990	0.124	2.8E-06 LOC690340			
9344 A_64_P029333	-0.764	0.097	3.0E-06	-0.669	0.097	1.2E-05 Acaa1b			
12669 A_64_P115157	-0.854	0.089	3.7E-07	-0.853	0.089	3.7E-07 Ces1e			
14531 A_64_P098926	1.664	0.126	9.1E-09	1.052	0.126	1.7E-06 no transcript			
15451 A_64_P004422	-0.864	0.124	1.1E-05	-0.878	0.124	9.2E-06 LOC687708			
23957 A_64_P139208	-1.808	0.168	9.9E-08	-1.525	0.168	6.8E-07 RT1-N1 (part)			
25709 A_64_P011719	-1.519	0.153	2.5E-07	-1.198	0.153	3.3E-06 Chmp1b	N/A	18	62,923,620
26531 A_64_P063641	-1.526	0.199	1.2E-05	-1.597	0.263	9.3E-05 LOC501251			
27091 A_64_P025432	1.945	0.274	9.4E-06	3.546	0.274	1.1E-08 LOC498829			

28226_A_64_P029191	0.770	0.095	2.4E-06	1.021	0.095	1.0E-07	no transcript
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Genes are regarded as significant for “shared” differential expression when they show $P < 1 \times 10^{-4}$ reproducibly in two types of comparison, ie, SHR/lzm versus WKY/lzm and SHRSP/lzm versus WKY/lzm, with a concordant direction of differential expression.

Table S3F. A list of significant transcripts for non-shared differential expression in the heart.

no	ProbeName	SHR/lzm (vs WKY/lzm)			SHRSP/lzm (vs WKY/lzm)			GeneName	Ensembl_rat	Chr	Transcription_ start_site (Rnor_6.0)
		Fold change (log2-scale)	SE (log2-scale)	P-value	Fold change (log2-scale)	SE (log2-scale)	P-value				
23135	A_64_P147549	-0.114	0.095	2.4E-01	-0.389	0.047	8.1E-10	Ust	ENSRNOG00000016381	1	2,627,747
4209	A_42_P547213	0.125	0.080	1.2E-01	0.415	0.040	1.9E-12	Fbxo30	ENSRNOG00000014852	1	5,366,379
14654	A_44_P255294	0.064	0.067	3.5E-01	0.261	0.034	3.6E-09	Hbs1l	ENSRNOG00000014531	1	16,819,170
14291	A_44_P191715	-0.183	0.115	1.2E-01	-0.684	0.057	4.6E-14	Trdn	ENSRNOG00000012609	1	25,839,198
27952	A_64_P086235	0.281	0.105	1.1E-02	-0.669	0.053	6.6E-15	lrx1	ENSRNOG00000033609	1	33,910,912
17452	A_64_P042302	-0.094	0.126	4.6E-01	-0.523	0.063	7.1E-10	Ube2ql1	ENSRNOG00000034075	1	36,185,916
24774	A_44_P794669	0.091	0.086	3.0E-01	-0.334	0.043	3.5E-09	Afdn (Mlt4)	ENSRNOG00000023753	1	53,802,658
26771	A_64_P032991	0.024	0.066	7.2E-01	-0.255	0.033	3.3E-09	none	ENSRNOG00000019623	1	65,597,899
21540	A_64_P001475	-0.067	0.060	2.7E-01	-0.369	0.030	1.8E-14	lrf2bp1	ENSRNOG00000014132	1	79,899,155
9254	A_42_P769597	-0.038	0.085	6.6E-01	-0.330	0.043	3.5E-09	Qpctl	ENSRNOG00000015413	1	80,056,574
1817	A_42_P773606	-0.003	0.185	9.9E-01	0.718	0.093	3.3E-09	Ppm1n (RGD156	ENSRNOG00000059266	1	80,191,618
9837	A_42_P496411	-0.146	0.077	6.4E-02	0.957	0.038	2.0E-24	Trappc6a	ENSRNOG00000017468	1	80,417,310
17625	A_64_P047432	-0.130	0.085	1.3E-01	1.126	0.042	2.7E-25	Trappc6a	ENSRNOG00000017468	1	80,417,310
17009	A_64_P010196	0.085	0.102	4.1E-01	0.697	0.051	6.6E-16	Gemin7	ENSRNOG00000049772	1	80,483,487
13331	A_44_P575055	0.049	0.121	6.9E-01	0.622	0.061	3.0E-12	Zfp61	ENSRNOG00000019416	1	81,144,024
28240	A_44_P897008	0.008	0.073	9.1E-01	-0.379	0.036	2.1E-12	lrgq	ENSRNOG00000046500	1	81,395,841
13176	A_64_P003994	0.126	0.081	1.3E-01	0.321	0.040	1.9E-09	Rps19	ENSRNOG00000037897	1	81,750,928
28172	A_44_P318448	0.171	0.103	1.1E-01	0.458	0.052	1.3E-10	Megf8	ENSRNOG00000052687	1	82,185,034
24505	A_43_P15665	0.038	0.133	7.8E-01	-0.601	0.067	8.2E-11	Bckdha	ENSRNOG00000020607	1	82,452,281
8860	A_44_P520943	-0.096	0.095	3.2E-01	-0.490	0.048	2.6E-12	Exosc5	ENSRNOG00000020635	1	82,452,469
11718	A_64_P034456	0.131	0.131	3.3E-01	0.496	0.066	6.1E-09	Adck4	ENSRNOG00000020848	1	84,044,551
10912	A_64_P086519	-0.069	0.053	2.0E-01	0.274	0.026	2.2E-12	Blvrb	ENSRNOG00000024410	1	84,256,159
24874	A_64_P071840	-0.066	0.110	5.5E-01	0.478	0.055	2.1E-10	Blvrb	ENSRNOG00000024410	1	84,256,159
23715	A_64_P024297	-0.017	0.098	8.6E-01	0.486	0.049	8.2E-12	Gmfg	ENSRNOG00000019838	1	85,317,968
16474	A_64_P068858	0.108	0.067	1.2E-01	2.881	0.034	2.3E-43	Rps16	ENSRNOG00000019578	1	85,408,444
25138	A_64_P133421	0.257	0.147	9.0E-02	-0.777	0.074	1.4E-12	Eid2b	ENSRNOG00000045545	1	85,510,114
17605	A_44_P186860	0.073	0.131	5.8E-01	0.495	0.065	6.1E-09	Nfkbib	ENSRNOG00000020063	1	86,948,845
22916	A_44_P997962	0.170	0.135	2.1E-01	-0.528	0.067	2.6E-09	Fam98c (RGD13	ENSRNOG00000024036	1	88,098,785

6002 A_64_P139457	-0.078	0.090	3.9E-01	-1.039	0.045	2.7E-23	LOC499124	ENSRNOG00000030932	1	88,361,712
8683 A_42_P644209	-0.237	0.142	1.1E-01	1.334	0.066	5.9E-21	LOC499124	ENSRNOG00000030932	1	88,361,712
15811 A_64_P110309	0.154	0.091	1.0E-01	-2.533	0.046	1.3E-36	none_LOC68750	ENSRNOG00000047364	1	88,620,317
22281 A_64_P126065	-0.041	0.093	6.6E-01	-0.713	0.047	2.2E-17	Hcst	ENSRNOG00000020849	1	88,881,460
26746 A_64_P083600	0.182	0.134	1.9E-01	0.535	0.067	1.8E-09	Fxyd5	ENSRNOG00000021062	1	89,474,252
16896 A_64_P025098	0.087	0.076	2.6E-01	0.390	0.038	2.8E-12	Cebpg	ENSRNOG00000021144	1	91,296,656
18861 A_64_P006072	0.137	0.098	1.7E-01	-0.694	0.049	2.7E-16	Znf536	ENSRNOG00000014163	1	93,949,187
3330 A_44_P474037	0.250	0.158	1.2E-01	0.594	0.079	6.8E-09	Igf1r	ENSRNOG00000014187	1	128,924,966
1418 A_42_P497225	0.137	0.111	2.2E-01	0.433	0.055	2.6E-09	Mfge8	ENSRNOG00000017510	1	140,860,882
29968 A_64_P131086	0.224	0.126	8.4E-02	0.614	0.063	1.1E-11	Rab30	ENSRNOG00000010224	1	157,573,324
26276 A_44_P344181	0.177	0.114	1.3E-01	0.765	0.057	1.5E-15	Map6	ENSRNOG00000027204	1	164,225,934
14093 A_42_P788740	0.133	0.107	2.2E-01	0.621	0.054	1.0E-13	Folr2	ENSRNOG00000019890	1	166,919,302
28650 A_44_P177931	0.127	0.080	1.2E-01	0.401	0.040	5.9E-12	Anapc15 (RGD13	ENSRNOG00000019936	1	166,983,175
821 A_64_P117345	0.368	0.190	6.1E-02	1.105	0.090	3.9E-14	Arntl	ENSRNOG00000014448	1	178,039,063
22652 A_64_P001922	0.109	0.074	1.5E-01	0.298	0.037	1.5E-09	Vps35l (LOC3616	ENSRNOG00000016063	1	188,448,478
30295 A_44_P337300	0.033	0.109	7.6E-01	0.431	0.054	1.9E-09	Il4ra	ENSRNOG00000015441	1	196,942,364
7398 A_42_P495691	0.079	0.091	3.9E-01	0.345	0.045	5.0E-09	Bcl7c	ENSRNOG00000018916	1	199,159,125
22149 A_64_P056569	-0.106	0.080	1.9E-01	-0.444	0.040	2.9E-13	Fus	ENSRNOG00000023360	1	199,412,834
10630 A_64_P088990	-0.078	0.072	2.8E-01	-0.321	0.036	1.0E-10	Ctbp2	ENSRNOG00000017326	1	205,030,567
18089 A_44_P271720	0.046	0.083	5.8E-01	0.346	0.042	6.4E-10	Cd151	ENSRNOG00000046094	1	214,446,659
28707 A_64_P066601	0.057	0.099	5.6E-01	-0.391	0.049	2.0E-09	Rhod	ENSRNOG00000019220	1	219,682,287
21794 A_42_P837214	-0.268	0.085	3.4E-03	0.416	0.043	1.2E-11	Mgmt	ENSRNOG00000016038	1	209,237,233
5502 A_64_P087105	0.080	0.097	4.2E-01	0.425	0.048	1.7E-10	Gpr137	ENSRNOG00000021145	1	222,197,252
27738 A_64_P159519	0.294	0.076	4.0E-04	-0.288	0.038	4.8E-09	Pla2g16	ENSRNOG00000021206	1	222,844,144
30101 A_44_P896040	-0.916	0.081	2.0E-13	0.178	0.041	9.3E-05	Cybas3	ENSRNOG00000020702	1	226,634,009
7124 A_64_P062545	-0.454	0.088	8.8E-06	0.626	0.044	2.0E-16	Tmem132a	ENSRNOG00000021338	1	226,924,244
2519 A_64_P065422	0.012	0.185	9.5E-01	-1.519	0.103	6.5E-16	none	ENSRNOG00000047349	1	227,670,159
1377 A_42_P711568	-0.064	0.060	2.9E-01	-0.222	0.030	8.6E-09	Ranbp6	ENSRNOG00000053859	1	247,985,497
13746 A_44_P536613	0.543	0.288	6.7E-02	1.157	0.144	1.4E-09	Ch25h	ENSRNOG00000019141	1	252,808,380
11472 A_44_P198112	0.096	0.087	2.8E-01	0.340	0.043	2.6E-09	Marchf5	ENSRNOG00000017396	1	255,842,783
20886 A_64_P088575	0.308	0.172	8.2E-02	1.901	0.095	5.1E-20	Dhdpsl	ENSRNOG00000029501	1	261,291,870

25963 A_64_P129182	-0.023	0.196	9.1E-01	-0.755	0.098	3.7E-09 Npm3	ENSRNOG00000017622	1	265,506,046
17232 A_43_P12332	-0.150	0.076	5.5E-02	-0.300	0.038	2.2E-09 Nlcl1	ENSRNOG00000018704	1	265,829,108
23837 A_42_P658264	0.122	0.069	8.5E-02	0.433	0.035	9.9E-15 Nfkb2	ENSRNOG00000019311	1	266,053,002
23188 A_44_P1002173	-0.057	0.082	4.9E-01	0.480	0.041	8.2E-14 Cuedc2	ENSRNOG00000019574	1	266,086,299
688 A_42_P473812	0.003	0.110	9.8E-01	0.491	0.055	1.0E-10 Rbm20	ENSRNOG00000014705	1	274,391,932
17131 A_64_P088836	0.464	0.101	4.8E-05	-0.957	0.050	2.0E-20 Gpr98	ENSRNOG00000016306	2	8,939,686
19833 A_64_P158035	0.474	0.123	4.5E-04	-0.887	0.061	1.4E-16 RGD1562101	ENSRNOG00000016306	2	8,939,686
22758 A_44_P377432	0.382	0.098	4.0E-04	-0.880	0.049	1.3E-19 Gpr98	ENSRNOG00000016306	2	8,939,686
752 A_44_P158798	0.226	0.175	2.1E-01	0.749	0.088	3.3E-10 Vcan	ENSRNOG00000029212	2	18,565,842
16284 A_44_P236418	0.230	0.120	6.3E-02	0.465	0.060	3.1E-09 Gfm2	ENSRNOG00000025285	2	27,949,208
3372 A_43_P10200	0.202	0.110	7.5E-02	-0.445	0.055	1.3E-09 Slc30a5	ENSRNOG00000018746	2	30,846,149
23871 A_64_P104820	0.351	0.192	7.5E-02	0.719	0.096	6.9E-09 Plpp1	ENSRNOG00000009980	2	44,664,124
24142 A_44_P122386	0.121	0.073	1.1E-01	0.511	0.037	3.9E-16 Hspb3	ENSRNOG00000010992	2	45,518,502
3710 A_44_P175584	0.355	0.183	6.1E-02	0.680	0.092	9.0E-09 RGD1561520	ENSRNOG00000026899	2	52,171,016
8809 A_44_P256677	0.421	0.138	4.3E-03	-0.561	0.069	1.1E-09 RGD1308448	ENSRNOG00000014550	2	54,191,538
26171 A_64_P099923	0.129	0.079	1.1E-01	0.453	0.040	1.5E-13 Dap	ENSRNOG00000010747	2	84,275,884
3010 A_42_P581863	0.064	0.071	3.7E-01	0.371	0.036	2.0E-12 Pfn2	ENSRNOG00000017427	2	147,959,567
23875 A_43_P12315	-0.240	0.097	1.8E-02	0.366	0.048	5.6E-09 P2ry12	ENSRNOG00000013902	2	149,444,548
9313 A_43_P11484	0.480	0.154	3.5E-03	-0.586	0.077	4.9E-09 Mme	ENSRNOG00000009514	2	153,803,349
14592 A_64_P104688	0.004	0.065	9.5E-01	0.254	0.033	2.7E-09 Cks1b	ENSRNOG00000042561	2	188,745,144
62 A_42_P548763	0.143	0.105	1.8E-01	0.461	0.052	1.6E-10 Slc39a1	ENSRNOG00000059463	2	189,609,800
998 A_43_P15245	-0.142	0.088	1.2E-01	-0.437	0.044	8.1E-12 Npr1	ENSRNOG00000014684	2	189,856,090
27575 A_44_P355928	0.117	0.112	3.0E-01	0.435	0.056	3.0E-09 Ctss	ENSRNOG00000021157	2	197,655,786
29124 A_44_P836445	-0.071	0.071	3.2E-01	-0.310	0.036	2.0E-10 Aph1a	ENSRNOG00000023816	2	198,006,322
21603 A_44_P354806	-0.085	0.105	4.2E-01	0.389	0.053	9.6E-09 Vps45	ENSRNOG00000021173	2	198,184,739
28930 A_64_P043871	0.669	0.075	1.3E-10	0.041	0.038	2.8E-01 Polr3gl	ENSRNOG00000021209	2	198,706,428
5164 A_64_P078592	-0.108	0.101	2.9E-01	0.467	0.051	5.1E-11 Man1a2	ENSRNOG00000015226	2	203,043,847
3071 A_64_P005243	-0.047	0.098	6.4E-01	-0.503	0.049	2.5E-12 Tspan2	ENSRNOG00000023338	2	205,160,405
5675 A_44_P838096	-0.147	0.088	1.0E-01	-0.665	0.044	3.8E-17 Rsbn1	ENSRNOG00000019671	2	206,392,200
15672 A_44_P328008	-0.124	0.142	3.9E-01	-0.703	0.071	7.4E-12 Alx3	ENSRNOG00000018290	2	210,381,829
12171 A_44_P771864	0.103	0.102	3.2E-01	-0.406	0.051	1.7E-09 Cdc14a	ENSRNOG00000014515	2	219,458,271

28932 A_44_P478176	-0.104	0.086	2.4E-01	-0.324	0.043	6.6E-09 Lrrc39	ENSRNOG000000015117	2	219,598,162
24834 A_64_P086083	0.048	0.089	5.9E-01	-0.330	0.044	9.3E-09 Slc35a3	ENSRNOG000000061832	2	219,741,886
23100 A_44_P1011780	0.205	0.085	2.1E-02	-0.369	0.043	2.3E-10 Pla2g12a	ENSRNOG000000057470	2	235,311,719
3199 A_44_P281352	0.249	0.130	6.4E-02	0.533	0.065	9.1E-10 Dnajb4	ENSRNOG000000013011	2	257,418,425
28745 A_43_P15529	0.054	0.116	6.5E-01	0.559	0.058	1.5E-11 Ptgds	ENSRNOG000000015550	3	2,689,084
22299 A_64_P083610	0.245	0.165	1.5E-01	0.679	0.082	7.9E-10 Dbh	ENSRNOG000000006641	3	5,709,236
25202 A_42_P472520	0.088	0.111	4.3E-01	0.598	0.055	7.4E-13 RGD1561113	ENSRNOG000000022681	3	11,410,732
12233 A_44_P474559	0.214	0.108	5.5E-02	0.569	0.054	1.5E-12 Eng	ENSRNOG000000050190	3	11,679,530
19913 A_44_P102477	-0.368	0.190	6.1E-02	-0.947	0.097	1.5E-11 Morn5	ENSRNOG000000026111	3	15,379,109
11083 A_64_P099011	-0.021	0.091	8.2E-01	-0.686	0.046	3.9E-17 Scn1a	ENSRNOG000000053122	3	52,447,622
9452 A_64_P032018	-0.052	0.348	8.8E-01	1.113	0.102	5.6E-12 none	ENSRNOG000000009382	3	57,270,036
25648 A_64_P101921	0.154	0.092	1.0E-01	0.410	0.046	1.3E-10 Dync1i2	ENSRNOG000000009781	3	57,817,693
23651 A_64_P039081	0.110	0.058	6.5E-02	-1.663	0.029	3.7E-37 Eno1	ENSRNOG000000028543	3	59,408,546
14850 A_64_P101032	0.099	0.076	2.0E-01	0.337	0.038	1.5E-10 none	ENSRNOG000000001510	3	59,587,569
21396 A_64_P071585	0.138	0.080	9.3E-02	0.336	0.040	5.2E-10 Fkbp7	ENSRNOG000000011758	3	63,535,991
20525 A_64_P038827	0.117	0.073	1.2E-01	0.303	0.037	7.5E-10 Jmjd7	ENSRNOG000000050072	3	111,818,150
27910 A_64_P158384	-0.076	0.119	5.3E-01	-0.526	0.059	1.3E-10 Fam227b (RGD1	ENSRNOG000000037124	3	118,427,851
30000 A_64_P144492	-0.195	0.110	8.4E-02	-0.547	0.055	6.1E-12 Mall	ENSRNOG000000015599	3	120,306,551
2596 A_64_P004292	0.115	0.098	2.5E-01	0.369	0.049	6.3E-09 Ttl	ENSRNOG000000018205	3	121,596,791
10669 A_44_P792628	0.033	0.097	7.4E-01	0.368	0.048	5.0E-09 Spef1 (RGD1311	ENSRNOG000000021247	3	123,718,432
12403 A_44_P398033	0.719	0.081	1.4E-10	0.080	0.041	5.7E-02 Prnp	ENSRNOG000000021259	3	124,515,978
6630 A_42_P471608	-0.174	0.087	5.4E-02	-0.341	0.044	2.9E-09 Kif16b	ENSRNOG000000004951	3	136,936,674
8939 A_64_P021980	-0.186	0.182	3.1E-01	-0.694	0.091	5.0E-09 Sstr4	ENSRNOG000000004641	3	142,739,781
12022 A_64_P132971	-0.189	0.221	4.0E-01	1.076	0.123	3.7E-10 Dusp15	ENSRNOG000000008534	3	148,428,494
4481 A_64_P164610	0.051	0.065	4.4E-01	-0.807	0.033	2.7E-24 Tti1 (RGD156258	ENSRNOG000000012880	3	154,490,851
17021 A_64_P023008	-0.022	0.212	9.2E-01	1.048	0.106	8.4E-12 none_SNORA71	ENSRNOG000000056385	3	154,846,116
927 A_64_P091016	0.197	0.173	2.6E-01	0.689	0.091	7.3E-09 Ppp1r16b	ENSRNOG000000015614	3	155,160,481
17071 A_64_P134303	-0.141	0.108	2.0E-01	-0.542	0.054	5.6E-12 Zhx3	ENSRNOG000000027988	3	156,777,999
3911 A_42_P597242	-0.017	0.067	8.0E-01	0.254	0.033	5.7E-09 RGD1303142	ENSRNOG000000008297	3	159,802,952
17113 A_64_P139590	-0.208	0.107	5.9E-02	1.393	0.053	4.5E-25 Slc35c2	ENSRNOG000000018649	3	161,812,291
15238 A_64_P033979	-0.173	0.153	2.6E-01	1.136	0.076	5.5E-17 Cdh22	ENSRNOG000000018557	3	161,917,285

861 A_42_P485932	0.056	0.088	5.3E-01	0.379	0.044	2.8E-10	Sulf2	ENSRNOG00000006052	3	162,872,831
4982 A_64_P155186	-0.112	0.094	2.4E-01	0.402	0.047	3.0E-10	Aurka	ENSRNOG00000004479	3	170,378,210
20646 A_64_P101847	0.012	0.049	8.1E-01	-0.193	0.025	3.1E-09	Ythdf1	ENSRNOG000000027015	3	176,431,423
6319 A_64_P028431	-0.102	0.136	4.6E-01	-0.519	0.068	4.5E-09	Znf512b	ENSRNOG000000015558	3	177,089,199
24460 A_44_P143886	0.103	0.138	4.6E-01	0.627	0.069	7.4E-11	Insig1	ENSRNOG000000006859	4	342,302
23936 A_44_P294359	-0.083	0.100	4.1E-01	-0.405	0.050	1.2E-09	none	ENSRNOG000000040214	4	8,256,611
3918 A_42_P604399	0.149	0.077	6.1E-02	0.346	0.039	9.8E-11	Cyp51	ENSRNOG000000007234	4	27,175,243
26944 A_43_P15431	-0.898	0.074	2.9E-14	-0.050	0.037	1.9E-01	Mterf	ENSRNOG000000007899	4	27,365,376
24172 A_64_P025464	0.107	0.071	1.4E-01	0.280	0.036	2.5E-09	Shfm1	ENSRNOG000000010420	4	32,087,600
15563 A_64_P106533	0.018	0.129	8.9E-01	-0.673	0.067	8.8E-12	Thsd7a	ENSRNOG000000030151	4	39,102,807
19396 A_64_P058923	-0.931	0.114	1.1E-09	-0.091	0.057	1.2E-01	Tes	ENSRNOG000000051952	4	44,321,883
762 A_64_P151146	0.233	0.169	1.8E-01	-1.483	0.085	3.1E-19	lqub	ENSRNOG000000021729	4	51,586,881
4359 A_44_P326727	-0.077	0.111	4.9E-01	0.510	0.055	5.1E-11	Snd1	ENSRNOG000000031173	4	55,772,377
7030 A_44_P426107	0.123	0.108	2.6E-01	0.466	0.054	2.8E-10	Akr1b8	ENSRNOG000000009734	4	61,772,064
10688 A_44_P492808	-0.008	0.098	9.3E-01	0.476	0.049	1.4E-11	Agk	ENSRNOG000000011509	4	68,483,320
28386 A_64_P153338	-0.005	0.104	9.6E-01	0.460	0.052	1.3E-10	Agk	ENSRNOG000000011509	4	68,483,320
14746 A_44_P638290	-0.156	0.078	5.3E-02	-0.316	0.039	1.1E-09	Znf467	ENSRNOG000000007707	4	78,074,906
5573 A_42_P640700	0.156	0.101	1.3E-01	0.393	0.051	3.3E-09	Tmem176a	ENSRNOG000000023708	4	78,458,625
1042 A_64_P079478	0.053	0.100	6.0E-01	0.713	0.050	1.8E-16	Jazf1	ENSRNOG000000027026	4	83,137,527
20794 A_64_P160437	0.076	0.091	4.1E-01	0.705	0.045	1.5E-17	Jazf1	ENSRNOG000000027026	4	83,137,527
740 A_44_P242614	0.166	0.124	1.9E-01	0.559	0.062	8.4E-11	Znrf2	ENSRNOG000000049057	4	85,009,350
6838 A_42_P507035	0.048	0.079	5.5E-01	-0.397	0.039	5.1E-12	Nod1	ENSRNOG000000010629	4	85,174,951
27937 A_64_P084188	-0.166	0.116	1.6E-01	-0.906	0.058	1.1E-17	Nod1	ENSRNOG000000010629	4	85,174,951
23985 A_44_P216395	-0.156	0.093	1.0E-01	-0.439	0.047	2.9E-11	Gadd45a	ENSRNOG000000005615	4	97,784,842
859 A_64_P145166	0.114	0.066	9.4E-02	0.489	0.033	6.5E-17	Ggcx	ENSRNOG000000012975	4	100,277,391
6104 A_44_P1032296	0.057	0.104	5.9E-01	0.476	0.052	6.0E-11	Capg	ENSRNOG000000013668	4	100,407,658
4378 A_64_P029142	0.208	0.150	1.7E-01	0.718	0.075	1.8E-11	Loxl3	ENSRNOG000000061373	4	113,866,804
26314 A_44_P465660	0.138	0.093	1.5E-01	0.385	0.047	7.4E-10	Anxa4	ENSRNOG000000018159	4	118,595,580
5621 A_64_P110654	0.087	0.108	4.3E-01	0.567	0.054	1.7E-12	Slc25a26	ENSRNOG000000012831	4	126,522,326
22626 A_43_P12768	-0.871	0.090	1.4E-11	-0.002	0.045	9.7E-01	Bhlhe40	ENSRNOG000000007152	4	140,703,619
20302 A_64_P114369	0.117	0.075	1.3E-01	0.289	0.037	3.4E-09	Thumpd3	ENSRNOG000000006941	4	144,985,880

3107 A_44_P541456	-0.273	0.103	1.2E-02	0.622	0.052	3.3E-14 Arpc4	ENSRNOG00000008994	4	145,330,457
9721 A_64_P133343	0.031	0.089	7.3E-01	0.397	0.045	1.2E-10 LOC679934	ENSRNOG00000010184	4	145,559,206
21876 A_64_P037666	0.025	0.167	8.8E-01	-0.726	0.084	2.3E-10 Iqsec3	ENSRNOG00000014083	4	154,044,493
11748 A_64_P039482	0.007	0.176	9.7E-01	0.668	0.088	5.6E-09 Cd4	ENSRNOG00000016294	4	157,408,176
10235 A_64_P034244	0.631	0.434	1.5E-01	2.017	0.177	3.5E-13 Olr1	ENSRNOG000000056219	4	163,261,958
26036 A_44_P807058	0.148	0.122	2.3E-01	0.478	0.061	2.4E-09 Emp1	ENSRNOG00000008676	4	169,147,243
13001 A_44_P409860	0.169	0.111	1.4E-01	0.963	0.055	3.6E-19 none	ENSRNOG000000048735	4	170,092,848
15950 A_64_P039911	0.168	0.100	1.0E-01	1.064	0.050	5.2E-22 none	ENSRNOG000000045840	4	170,763,916
25290 A_64_P048941	-0.418	0.207	5.2E-02	-1.203	0.104	9.8E-14 Art4	ENSRNOG000000005670	4	170,841,187
29087 A_44_P283941	0.094	0.083	2.7E-01	0.526	0.042	7.0E-15 Arhgdib	ENSRNOG000000005809	4	170,932,618
13310 A_44_P884766	0.214	0.212	3.2E-01	-1.020	0.106	1.7E-11 Vxn (RGD156184	ENSRNOG000000021663	5	9,381,214
17621 A_44_P412710	-0.099	0.108	3.7E-01	-0.487	0.054	8.3E-11 Adhfe1	ENSRNOG000000007069	5	9,429,859
11193 A_64_P136641	0.216	0.173	2.2E-01	-1.496	0.086	4.4E-19 Rp1	ENSRNOG000000008807	5	15,043,955
17422 A_44_P159305	-0.155	0.104	1.5E-01	-0.402	0.052	3.9E-09 Kihl32	ENSRNOG000000007441	5	39,215,102
11969 A_44_P195291	0.077	0.091	4.0E-01	-0.396	0.046	2.1E-10 Ccdc107	ENSRNOG000000017253	5	58,995,249
20055 A_44_P323106	0.118	0.126	3.5E-01	-0.706	0.063	2.4E-13 Abca1	ENSRNOG000000018126	5	69,983,015
4055 A_42_P504549	-0.020	0.083	8.1E-01	0.736	0.041	1.7E-19 Tmem38b	ENSRNOG000000028063	5	70,639,156
19775 A_44_P963812	0.314	0.119	1.2E-02	-0.481	0.059	1.2E-09 Ctnna1	ENSRNOG000000010593	5	73,621,070
3541 A_64_P130627	0.243	0.152	1.2E-01	0.672	0.076	1.4E-10 LOC298139	ENSRNOG000000045733	5	90,338,795
7988 A_42_P623839	-0.003	0.138	9.8E-01	0.627	0.069	7.0E-11 Ttc39b	ENSRNOG000000042603	5	101,405,656
5062 A_44_P134672	0.078	0.076	3.1E-01	0.330	0.038	2.3E-10 Snapc3	ENSRNOG000000010825	5	101,526,551
7815 A_42_P498273	0.153	0.109	1.7E-01	0.472	0.054	2.2E-10 Pgm1	ENSRNOG000000009889	5	118,743,632
4744 A_44_P1015839	0.107	0.140	4.5E-01	-0.651	0.070	4.3E-11 Mrh7 (RGD1563	ENSRNOG000000058870	5	126,323,799
7726 A_64_P112295	-0.066	0.118	5.8E-01	-0.605	0.059	3.1E-12 Slc1a7	ENSRNOG000000011644	5	127,571,114
20004 A_44_P217189	-0.125	0.082	1.4E-01	-0.488	0.041	4.7E-14 Echdc2	ENSRNOG000000029333	5	127,770,570
16154 A_64_P100684	0.015	0.073	8.3E-01	-0.320	0.036	1.7E-10 Trabd2b	ENSRNOG000000029141	5	133,221,139
1850 A_42_P570919	0.033	0.062	6.0E-01	0.276	0.031	1.2E-10 Akr1a1	ENSRNOG000000016727	5	135,498,822
11409 A_64_P044221	-0.108	0.067	1.1E-01	-0.270	0.033	1.4E-09 Hyi (RGD156141	ENSRNOG000000037518	5	137,189,473
30286 A_64_P148183	-0.016	0.094	8.7E-01	0.409	0.047	2.1E-10 LOC679583	ENSRNOG000000062077	5	137,350,525
18178 A_64_P161655	0.136	0.072	6.6E-02	0.303	0.036	4.3E-10 Ppt1	ENSRNOG000000012616	5	140,538,260
25379 A_44_P501752	0.044	0.076	5.7E-01	0.320	0.038	4.2E-10 RGD1559909	ENSRNOG000000042421	5	142,845,116

24535 A_64_P137198	-0.077	0.057	1.9E-01	-0.221	0.029	3.9E-09	Trappc3	ENSRNOG00000010550	5	144,281,614
17496 A_43_P11236	0.169	0.088	6.2E-02	0.364	0.044	7.1E-10	Laptn5	ENSRNOG00000011054	5	149,047,681
27859 A_64_P080248	0.038	0.086	6.6E-01	0.387	0.043	9.0E-11	Dhdds	ENSRNOG00000014665	5	152,227,677
24569 A_42_P534172	-0.465	0.223	4.4E-02	0.981	0.111	1.6E-10	Cd52	ENSRNOG00000015403	5	152,324,469
22414 A_44_P466209	0.121	0.080	1.4E-01	0.317	0.040	2.2E-09	Tceb3	ENSRNOG00000010902	5	154,363,329
27126 A_44_P359032	-0.046	0.093	6.3E-01	-0.411	0.046	1.3E-10	Pink1	ENSRNOG00000015385	5	156,689,258
26599 A_64_P157371	0.116	0.192	5.5E-01	0.710	0.096	9.2E-09	Pdpm	ENSRNOG00000014961	5	161,981,441
11847 A_44_P306355	-0.023	0.080	7.7E-01	0.360	0.040	8.2E-11	Plod1	ENSRNOG00000007763	5	164,747,083
272 A_44_P318661	0.085	0.124	5.0E-01	-0.886	0.062	1.7E-16	Mthfr	ENSRNOG00000008553	5	164,845,925
8266 A_64_P114713	-0.142	0.134	3.0E-01	-3.658	0.067	2.2E-36	Agtrap	ENSRNOG00000008619	5	164,898,420
892 A_44_P321510	0.064	0.152	6.8E-01	0.573	0.076	6.3E-09	Slc25a33	ENSRNOG00000016949	5	166,726,794
21282 A_64_P093037	0.029	0.090	7.5E-01	-1.846	0.045	7.5E-32	Eno1	ENSRNOG00000017895	5	167,288,223
25873 A_64_P067525	-0.167	0.088	6.5E-02	-1.533	0.044	1.8E-29	Eno1	ENSRNOG00000017895	5	167,288,223
24228 A_64_P068252	0.183	0.129	1.6E-01	0.840	0.064	2.9E-15	Fam179a	ENSRNOG00000026344	6	23,404,368
6402 A_43_P17213	0.121	0.132	3.7E-01	-0.505	0.066	4.6E-09	Abhd1	ENSRNOG00000025689	6	26,792,808
6427 A_64_P037020	-0.070	0.065	2.9E-01	-0.274	0.033	5.1E-10	Seli	ENSRNOG00000059295	6	27,487,284
1354 A_42_P575104	-0.220	0.138	1.2E-01	-0.515	0.069	7.9E-09	Sostdc1	ENSRNOG00000005770	6	55,812,747
14875 A_44_P147560	0.121	0.080	1.4E-01	0.326	0.040	1.1E-09	Cfl2	ENSRNOG00000045892	6	75,763,185
8871 A_64_P019638	-0.131	0.087	1.4E-01	-0.340	0.043	2.7E-09	Prkch	ENSRNOG00000004873	6	96,479,430
29048 A_44_P139742	0.135	0.073	7.3E-02	0.361	0.036	7.7E-12	Npc2	ENSRNOG00000012062	6	108,488,330
6398 A_64_P120640	-0.385	0.229	1.0E-01	-0.926	0.117	2.3E-09	Pgf	ENSRNOG00000005650	6	109,004,598
5025 A_43_P14012	-0.047	0.052	3.7E-01	-0.197	0.026	6.8E-09	Mlh3	ENSRNOG00000006699	6	109,095,557
7582 A_42_P759524	0.013	0.202	9.5E-01	-0.762	0.101	6.0E-09	Serpina5	ENSRNOG00000009855	6	127,766,470
7786 A_44_P111337	0.192	0.113	9.8E-02	0.494	0.056	1.8E-10	Traf3	ENSRNOG00000008145	6	135,610,743
12539 A_64_P015739	-0.007	0.100	9.5E-01	0.399	0.050	1.8E-09	Mta1	ENSRNOG00000004711	6	137,924,293
5400 A_64_P082217	-0.379	0.239	1.2E-01	-0.902	0.119	6.0E-09	Dnah11	ENSRNOG00000005451	6	146,099,053
2313 A_64_P049027	-0.125	0.073	9.6E-02	-0.295	0.037	1.3E-09	Sppl2b	ENSRNOG000000057881	7	11,724,843
6397 A_64_P052740	-0.146	0.148	3.3E-01	-0.570	0.074	3.6E-09	Igf1	ENSRNOG00000004517	7	28,412,198
14916 A_44_P366723	-0.252	0.128	5.6E-02	-0.608	0.064	2.0E-11	Igf1	ENSRNOG00000004517	7	28,412,198
19762 A_64_P076900	-0.002	0.078	9.8E-01	0.331	0.039	4.1E-10	Nedd1	ENSRNOG00000004011	7	33,584,564
9651 A_44_P993671	-0.058	0.209	7.8E-01	-0.943	0.104	8.4E-11	Epyc	ENSRNOG00000004717	7	38,897,278

15370 A_44_P874636	0.020	0.077	8.0E-01	-0.338	0.038	1.7E-10 Cpsf6	ENSRNOG00000005927	7	60,416,925
5063 A_44_P375553	0.243	0.122	5.4E-02	0.460	0.061	6.3E-09 Lrp1	ENSRNOG000000025053	7	70,926,903
22629 A_44_P108003	-0.208	0.103	5.2E-02	-0.429	0.052	6.3E-10 Nipal2	ENSRNOG000000005190	7	73,450,262
21449 A_64_P104488	0.010	0.155	9.5E-01	-0.868	0.078	2.8E-13 Spag1	ENSRNOG000000010078	7	74,994,605
8600 A_44_P144591	0.524	0.354	1.5E-01	1.545	0.154	2.9E-11 Cthrc1	ENSRNOG000000004578	7	77,966,722
19370 A_64_P062869	-0.076	0.170	6.6E-01	-0.586	0.066	2.5E-10 Pkhd11	ENSRNOG000000004398	7	83,373,022
24750 A_44_P1016829	0.269	0.233	2.6E-01	0.933	0.116	1.5E-09 Trib1	ENSRNOG000000004100	7	99,954,492
14240 A_64_P123307	0.096	0.139	5.0E-01	0.533	0.070	4.3E-09 Zfat	ENSRNOG000000025140	7	109,205,354
22083 A_64_P107623	0.087	0.078	2.7E-01	0.305	0.039	3.0E-09 Rps19	ENSRNOG000000031474	7	111,722,964
10974 A_44_P1003602	-0.049	0.097	6.2E-01	0.602	0.049	1.5E-14 LOC300024	ENSRNOG000000048850	7	116,376,897
9125 A_64_P162437	-0.278	0.145	6.2E-02	-1.029	0.072	2.1E-16 Ly6h	ENSRNOG000000007334	7	116,607,473
21302 A_44_P291102	-0.254	0.149	9.7E-02	-0.635	0.075	3.8E-10 Smpd5	ENSRNOG000000037299	7	117,351,648
2438 A_42_P797218	0.073	0.111	5.2E-01	-0.436	0.056	2.6E-09 Gpt	ENSRNOG000000033915	7	117,759,083
10586 A_64_P025496	-0.218	0.158	1.8E-01	0.710	0.079	9.7E-11 Maff	ENSRNOG000000012886	7	120,580,743
24866 A_44_P123677	0.086	0.093	3.6E-01	0.442	0.046	2.1E-11 Syngr1	ENSRNOG000000017108	7	121,311,024
8729 A_64_P152878	-0.255	0.194	2.0E-01	-0.879	0.100	3.0E-10 Shisa8 (RGD156	ENSRNOG000000049407	7	123,445,613
12113 A_64_P133261	-0.209	0.191	2.8E-01	-0.729	0.095	4.8E-09 A4galt	ENSRNOG000000009736	7	124,089,385
8829 A_64_P267897	-2.395	0.133	1.1E-19	0.386	0.066	1.2E-06 Efcab6	ENSRNOG000000011094	7	124,929,025
4907 A_64_P138430	-0.094	0.131	4.8E-01	-0.579	0.065	1.3E-10 Odf3b	ENSRNOG000000037060	7	130,350,570
27123 A_64_P133967	-0.203	0.179	2.6E-01	-0.728	0.093	4.0E-09 Abcd2	ENSRNOG000000015538	7	132,343,169
27271 A_64_P061865	0.015	0.070	8.3E-01	-0.261	0.035	8.1E-09 Tcfcp2	ENSRNOG000000032395	7	142,180,794
18693 A_64_P030474	-0.003	0.075	9.7E-01	-0.362	0.038	1.7E-11 Tns2	ENSRNOG000000010588	7	143,707,237
27165 A_44_P378799	0.144	0.128	2.7E-01	0.548	0.064	3.3E-10 Igfbp6	ENSRNOG000000010977	7	143,749,221
27356 A_43_P12384	0.106	0.119	3.8E-01	0.453	0.059	4.6E-09 Birc3	ENSRNOG000000005731	8	6,076,598
16694 A_64_P153442	0.031	0.084	7.1E-01	-0.335	0.042	1.6E-09 Zfp810	ENSRNOG000000014331	8	23,282,989
8883 A_64_P151774	-0.153	0.100	1.3E-01	-0.648	0.050	3.3E-15 Bmper	ENSRNOG000000015357	8	24,369,916
26835 A_64_P145023	0.165	0.084	5.6E-02	-0.340	0.042	1.2E-09 Snx19	ENSRNOG000000014719	8	31,497,639
418 A_42_P558703	-0.277	0.177	1.3E-01	-1.087	0.088	1.8E-14 Adamts15	ENSRNOG000000009892	8	32,000,378
20835 A_44_P607412	0.134	0.083	1.1E-01	-0.338	0.041	1.0E-09 Nfrkb	ENSRNOG000000008278	8	32,530,412
14190 A_44_P107097	0.072	0.085	4.0E-01	0.350	0.042	7.6E-10 Dcps	ENSRNOG000000009993	8	36,374,673
8990 A_42_P506685	0.197	0.173	2.6E-01	0.805	0.086	3.9E-11 Fxyd2	ENSRNOG000000016469	8	49,710,477

22171 A_64_P126756	0.173	0.159	2.8E-01	0.702	0.079	1.4E-10 Fxyd2	ENSRNOG00000016469	8	49,713,190
24881 A_43_P19907	-0.012	0.144	9.3E-01	0.786	0.072	4.8E-13 Loxl1	ENSRNOG00000008680	8	63,092,009
12017 A_64_P019130	-0.063	0.076	4.1E-01	-0.322	0.038	3.6E-10 Ccpg1	ENSRNOG000000053428	8	79,660,657
14777 A_64_P156682	-0.105	0.080	2.0E-01	-0.361	0.040	9.3E-11 Hmgn3	ENSRNOG000000031032	8	90,664,554
12686 A_64_P136153	-0.023	0.087	7.9E-01	0.321	0.043	9.7E-09 Me1	ENSRNOG000000009715	8	94,352,246
22148 A_44_P283339	0.175	0.105	1.0E-01	0.577	0.052	4.4E-13 Tmed3	ENSRNOG000000013889	8	97,083,120
1145 A_42_P466706	0.022	0.083	8.0E-01	0.383	0.041	4.2E-11 PCOLCE2	ENSRNOG000000046848	8	103,459,161
3780 A_44_P242924	0.013	0.079	8.7E-01	-0.309	0.040	2.9E-09 Trpc1	ENSRNOG000000054902	8	103,554,399
51 A_64_P049401	0.002	0.097	9.9E-01	-0.383	0.048	2.0E-09 RGD1310507	ENSRNOG000000009434	8	111,777,677
6747 A_44_P1024981	-0.725	0.094	4.1E-09	-0.038	0.047	4.2E-01 Alas1	ENSRNOG000000056596	8	114,940,163
18110 A_64_P042591	0.193	0.111	8.9E-02	-0.601	0.055	6.1E-13 RGD1307461	ENSRNOG000000015718	8	116,094,851
21487 A_64_P099055	0.176	0.098	7.9E-02	0.475	0.049	1.2E-11 Lsmem2 (LOC68	ENSRNOG000000052634	8	116,349,896
9855 A_44_P382831	-0.172	0.108	1.2E-01	-0.411	0.054	5.6E-09 Epm2aip1	ENSRNOG000000043006	8	119,524,039
9908 A_42_P689873	-0.032	0.106	7.6E-01	-0.437	0.053	7.3E-10 Cmtm8	ENSRNOG000000011201	8	122,904,913
25973 A_44_P284129	0.121	0.119	3.2E-01	0.483	0.059	1.1E-09 Csrnp1	ENSRNOG000000033433	8	128,672,284
5839 A_64_P173102	-0.016	0.098	8.7E-01	0.399	0.049	1.1E-09 Rpsa	ENSRNOG000000018645	8	128,806,129
14280 A_44_P699398	0.052	0.083	5.4E-01	-0.365	0.042	1.8E-10 Zfp445	ENSRNOG000000025554	8	131,899,023
3570 A_64_P084445	0.047	0.120	7.0E-01	-0.605	0.060	4.5E-12 Prr22	ENSRNOG000000047295	9	10,290,035
257 A_42_P501679	-0.093	0.067	1.8E-01	-0.248	0.034	9.3E-09 M6prbp1	ENSRNOG000000048834	9	10,773,901
18255 A_64_P126165	-0.005	0.075	9.5E-01	-1.350	0.037	6.0E-30 LOC681367	ENSRNOG000000046871	9	16,519,144
9309 A_64_P011739	0.087	0.062	1.7E-01	-0.271	0.031	1.9E-10 Xpo5	ENSRNOG000000019085	9	17,163,170
26450 A_44_P258417	0.100	0.149	5.1E-01	0.716	0.078	8.7E-11 Mad2l1bp	ENSRNOG000000019463	9	17,216,495
16969 A_64_P045957	-0.088	0.073	2.4E-01	-0.429	0.036	5.9E-14 Mrpl14	ENSRNOG000000019734	9	17,698,569
20361 A_44_P241616	-0.039	0.081	6.4E-01	-0.571	0.040	2.7E-16 Ogfrl1	ENSRNOG000000014142	9	29,647,903
15120 A_64_P115204	-0.106	0.110	3.4E-01	0.533	0.055	1.4E-11 Sdhaf4	ENSRNOG000000028087	9	30,251,388
27130 A_44_P451120	0.200	0.118	9.9E-02	0.492	0.059	6.6E-10 Lmbrd1	ENSRNOG000000012178	9	30,939,555
5786 A_44_P975235	0.112	0.076	1.5E-01	-0.291	0.038	4.7E-09 RGD1309220	ENSRNOG000000015417	9	42,943,198
29640 A_44_P822041	0.118	0.139	4.0E-01	0.554	0.070	1.9E-09 none	ENSRNOG000000055728	9	52,937,765
18668 A_64_P142330	-0.057	0.099	5.7E-01	0.479	0.050	1.6E-11 Tmem258b	ENSRNOG000000032740	9	61,552,374
5919 A_42_P664544	0.188	0.168	2.7E-01	0.619	0.084	9.9E-09 Rftn2	ENSRNOG000000015594	9	61,810,417
9726 A_44_P277068	-0.009	0.064	8.9E-01	0.236	0.032	9.3E-09 RGD1562399	ENSRNOG000000032289	9	66,045,962

6093 A_64_P151012	0.042	0.120	7.3E-01	0.448	0.060	7.9E-09	Pard3b	ENSRNOG000000024345	9	68,414,339
20354 A_64_P077570	0.013	0.176	9.4E-01	0.655	0.083	3.3E-09	Fn1	ENSRNOG000000014288	9	78,969,078
21414 A_43_P11879	0.406	0.255	1.2E-01	0.832	0.081	6.8E-12	Htr2b	ENSRNOG000000017625	9	93,125,014
273 A_44_P143922	0.163	0.107	1.4E-01	0.483	0.053	8.5E-11	Hes6	ENSRNOG000000020194	9	98,551,410
27882 A_44_P381270	0.273	0.172	1.2E-01	0.705	0.088	1.8E-09	Macir (RGD1562	ENSRNOG000000032398	9	111,327,402
9804 A_64_P148368	-0.120	0.085	1.7E-01	-0.388	0.043	7.4E-11	Mtcl1 (RGD1308	ENSRNOG000000025527	9	114,619,711
20174 A_64_P044435	0.252	0.159	1.2E-01	0.680	0.080	3.3E-10	Tgif1	ENSRNOG000000015906	9	119,190,698
22463 A_44_P142850	-0.399	0.109	8.2E-04	1.351	0.055	3.0E-24	Fam86a	ENSRNOG00000002876	10	10,530,365
7939 A_64_P031975	-0.106	0.092	2.6E-01	0.490	0.046	1.2E-12	Alg1	ENSRNOG00000002883	10	10,550,138
20155 A_44_P298013	-0.143	0.078	7.4E-02	-0.318	0.039	9.6E-10	Nudt16l1	ENSRNOG00000003224	10	10,831,782
12289 A_43_P12438	-0.100	0.062	1.2E-01	-0.712	0.031	4.3E-23	Hmox2	ENSRNOG00000003773	10	11,035,484
12372 A_64_P071193	-0.369	0.119	3.8E-03	0.663	0.060	3.1E-13	Nmral1	ENSRNOG00000003794	10	11,046,024
26992 A_42_P826202	0.217	0.191	2.7E-01	2.546	0.081	2.7E-19	Znf597	ENSRNOG00000007576	10	11,912,543
17837 A_64_P050084	0.327	0.189	9.2E-02	0.954	0.094	4.3E-12	Npw	ENSRNOG000000012390	10	14,022,452
17979 A_43_P12626	-4.067	0.231	5.3E-19	-0.202	0.107	6.8E-02	Msln	ENSRNOG000000019445	10	15,125,408
14401 A_44_P419922	0.166	0.193	3.9E-01	-2.750	0.098	1.2E-25	Haghl	ENSRNOG000000019612	10	15,155,412
24121 A_43_P18716	-0.098	0.136	4.8E-01	-3.029	0.089	2.1E-24	RGD1560244	ENSRNOG000000022331	10	15,156,207
21202 A_64_P055748	0.167	0.098	9.7E-02	-0.706	0.049	1.3E-16	Rhbdf1	ENSRNOG000000020594	10	15,672,382
14109 A_44_P556319	0.039	0.137	7.8E-01	-1.444	0.068	6.1E-22	Fgf18	ENSRNOG000000048389	10	18,063,391
3403 A_64_P045750	0.252	0.351	4.8E-01	0.951	0.097	3.2E-10	Kcnmb1	ENSRNOG00000005465	10	18,906,010
21683 A_64_P070801	-0.156	0.238	5.2E-01	-1.029	0.119	2.5E-10	LOC684480	ENSRNOG000000046377	10	34,439,470
21210 A_64_P025690	0.029	0.063	6.5E-01	-1.469	0.031	6.1E-34	none	ENSRNOG000000001512	10	44,659,707
11237 A_64_P023975	0.113	0.082	1.8E-01	-0.338	0.041	9.1E-10	Zbtb4	ENSRNOG000000014689	10	56,381,813
18295 A_64_P009032	-0.123	0.089	1.7E-01	-0.378	0.044	3.5E-10	Camta2	ENSRNOG000000004283	10	57,309,298
6320 A_64_P119134	-0.009	0.095	9.3E-01	-0.362	0.047	4.8E-09	Smtnl2	ENSRNOG000000015157	10	58,973,020
7671 A_44_P135082	0.284	0.238	2.4E-01	0.659	0.079	3.2E-09	P2rx1	ENSRNOG000000017606	10	59,566,223
864 A_44_P144202	-0.026	0.086	7.7E-01	0.466	0.043	6.9E-13	Serpinf1	ENSRNOG000000003172	10	62,254,287
25258 A_44_P961164	0.004	0.117	9.7E-01	-0.622	0.059	1.2E-12	Rhbdl3	ENSRNOG000000005515	10	67,677,071
5896 A_64_P019759	0.124	0.084	1.5E-01	0.351	0.042	5.6E-10	none	ENSRNOG000000037114	10	70,366,725
20882 A_44_P350521	-0.464	0.187	1.8E-02	0.711	0.094	5.3E-09	Col1a1	ENSRNOG000000003897	10	82,745,801
4178 A_64_P008216	0.033	0.096	7.3E-01	0.539	0.048	2.5E-13	Ppp1r9b	ENSRNOG000000052113	10	82,800,704

17635 A_42_P528374	-0.028	0.140	8.4E-01	0.616	0.070	1.7E-10 Pnmt	ENSRNOG000000046057	10	86,340,940
10623 A_44_P491759	-0.185	0.158	2.5E-01	0.660	0.079	6.0E-10 Krt24	ENSRNOG000000010970	10	87,195,075
23747 A_64_P096046	0.051	0.092	5.9E-01	-1.545	0.046	8.5E-29 none	ENSRNOG000000051172	10	87,936,692
6755 A_64_P065032	-0.005	0.088	9.6E-01	0.343	0.044	2.9E-09 Sc65	ENSRNOG000000015787	10	88,325,326
30281 A_42_P834852	0.300	0.072	1.7E-04	-0.265	0.036	9.0E-09 Higd1b	ENSRNOG000000002814	10	90,929,423
23038 A_64_P083384	0.060	0.073	4.2E-01	0.418	0.036	1.2E-13 Nmt1	ENSRNOG000000002989	10	91,126,689
28777 A_64_P028270	0.105	0.111	3.5E-01	2.018	0.055	4.0E-30 Mettl2	ENSRNOG000000006131	10	93,354,003
28992 A_44_P680749	0.088	0.091	3.4E-01	-0.412	0.045	7.4E-11 RGD1565033	ENSRNOG000000043295	10	95,242,986
6640 A_64_P064488	0.103	0.063	1.1E-01	0.300	0.032	2.4E-11 RGD1359290	ENSRNOG000000027271	10	95,642,640
76 A_43_P19450	0.193	0.164	2.5E-01	0.644	0.082	2.3E-09 Prkca	ENSRNOG000000003491	10	96,584,947
25564 A_64_P019608	-0.076	0.108	4.9E-01	0.631	0.054	7.8E-14 Prkca	ENSRNOG000000003491	10	96,584,947
25996 A_64_P121995	-0.142	0.093	1.4E-01	-0.397	0.047	3.6E-10 Sap30bp	ENSRNOG000000005482	10	104,483,042
18881 A_64_P134245	0.154	0.088	8.7E-02	0.369	0.044	4.7E-10 Fbf1	ENSRNOG000000008577	10	104,718,621
11007 A_44_P381917	-0.155	0.168	3.6E-01	0.727	0.095	9.0E-09 Sphk1	ENSRNOG000000010626	10	105,498,728
14738 A_44_P380392	0.003	0.059	9.6E-01	0.241	0.030	1.1E-09 Slc38a10	ENSRNOG000000004604	10	109,333,899
13966 A_64_P094267	0.039	0.156	8.0E-01	-0.607	0.078	3.0E-09 Pde6g (LOC6882	ENSRNOG000000046962	10	109,622,745
23270 A_64_P055509	0.180	0.121	1.5E-01	0.507	0.060	5.3E-10 none	ENSRNOG000000050286	11	2,813,912
28311 A_42_P830311	-0.067	0.102	5.1E-01	-0.508	0.051	6.8E-12 Mrap	ENSRNOG000000021524	11	30,904,733
9149 A_64_P162743	-0.027	0.114	8.1E-01	-0.656	0.057	1.3E-13 Dnajc28	ENSRNOG000000002026	11	31,772,984
29585 A_64_P104237	-0.137	0.072	6.5E-02	-0.312	0.036	2.4E-10 Ttc3	ENSRNOG000000001682	11	34,598,492
8596 A_64_P136279	-0.003	0.067	9.6E-01	-0.255	0.034	6.2E-09 Senp7	ENSRNOG000000001616	11	47,027,667
13054 A_43_P11086	-3.201	0.249	4.8E-15	-0.145	0.125	2.5E-01 Upk1b	ENSRNOG000000027380	11	64,522,130
917 A_42_P576953	0.149	0.089	1.0E-01	0.390	0.044	1.7E-10 Pla1a	ENSRNOG000000057153	11	64,882,288
24062 A_64_P087768	-0.031	0.114	7.9E-01	-0.605	0.057	1.1E-12 Nr1i2	ENSRNOG000000002906	11	65,022,100
24064 A_64_P023222	0.167	0.084	5.5E-02	0.468	0.042	3.5E-13 Gtf2e1	ENSRNOG000000026008	11	66,078,820
1641 A_42_P571235	-0.175	0.092	6.7E-02	-0.457	0.046	7.7E-12 lqcb1	ENSRNOG000000038868	11	66,878,551
27889 A_43_P14782	0.070	0.079	3.8E-01	-0.524	0.040	1.9E-15 Tnk2	ENSRNOG000000001769	11	71,368,456
13359 A_44_P214811	-1.709	0.181	2.6E-11	0.077	0.090	4.0E-01 Tfrc	ENSRNOG000000001766	11	71,419,223
20227 A_64_P047537	-0.048	0.137	7.3E-01	0.675	0.069	9.0E-12 Tmem44	ENSRNOG000000001726	11	73,738,433
7118 A_64_P054708	-0.157	0.211	4.6E-01	1.606	0.106	2.8E-17 Hes1	ENSRNOG000000001720	11	74,315,248
19826 A_64_P129273	-0.149	0.097	1.3E-01	-0.435	0.048	9.4E-11 Hrasls	ENSRNOG000000001711	11	75,144,903

6841 A_42_P554157	-0.016	0.110	8.9E-01	0.491	0.055	1.1E-10 Dnajb11	ENSRNOG000000001803	11	81,757,813
16895 A_64_P038926	-0.279	0.144	6.1E-02	-0.773	0.072	8.6E-13 Prodh	ENSRNOG000000000281	11	87,058,616
24450 A_42_P762829	0.263	0.183	1.6E-01	0.683	0.092	7.8E-09 Cebp	ENSRNOG000000050869	11	89,008,008
27850 A_44_P406805	-0.114	0.069	1.1E-01	0.294	0.034	3.0E-10 Rfc3	ENSRNOG000000001088	12	1,460,538
22669 A_44_P164824	0.053	0.091	5.7E-01	-0.363	0.046	1.8E-09 Ttyh3	ENSRNOG000000055583	12	16,084,266
2131 A_44_P852017	0.038	0.102	7.1E-01	0.448	0.051	1.5E-10 Gpr146	ENSRNOG000000001288	12	17,358,617
4574 A_64_P038729	0.312	0.167	6.9E-02	0.993	0.083	4.3E-14 none_LOC68134	ENSRNOG000000047077	12	20,882,344
25539 A_64_P094434	-0.015	0.083	8.6E-01	0.445	0.042	1.0E-12 Pcolce	ENSRNOG000000025001	12	22,153,983
29597 A_42_P833212	-0.088	0.056	1.2E-01	-0.235	0.028	4.8E-10 Eif4h	ENSRNOG000000001454	12	25,093,149
3110 A_64_P129805	-0.007	0.105	9.5E-01	0.460	0.052	1.6E-10 Rfc2	ENSRNOG000000001457	12	25,143,480
23298 A_64_P110474	0.034	0.061	5.8E-01	-0.234	0.030	4.0E-09 Gtf2i	ENSRNOG000000001479	12	25,411,292
932 A_64_P073004	0.179	0.120	1.4E-01	0.463	0.060	3.7E-09 Gusb	ENSRNOG000000000913	12	30,198,822
1282 A_44_P249902	0.054	0.066	4.1E-01	0.261	0.033	1.8E-09 Vps29	ENSRNOG000000001274	12	39,699,113
12850 A_64_P143507	-0.129	0.100	2.1E-01	-0.388	0.050	3.6E-09 Alkbh2	ENSRNOG000000028584	12	48,257,609
7231 A_44_P776918	0.117	0.147	4.3E-01	-0.737	0.074	5.8E-12 Rnf152	ENSRNOG000000014859	13	25,262,469
25890 A_64_P084578	0.237	0.135	8.7E-02	-0.500	0.067	9.4E-09 Rnf152	ENSRNOG000000014859	13	25,262,469
2841 A_42_P507072	-0.092	0.084	2.8E-01	-0.357	0.042	3.7E-10 none	ENSRNOG000000053210	13	50,196,042
28935 A_64_P141541	0.342	0.055	3.5E-07	-0.221	0.028	1.6E-09 Ndufv3	ENSRNOG000000027593	13	51,297,621
9518 A_44_P560973	-0.049	0.093	6.0E-01	-0.745	0.046	5.1E-18 Lamc2	ENSRNOG000000002667	13	70,626,252
26569 A_44_P480361	-0.024	0.086	7.8E-01	0.320	0.043	8.2E-09 Cenpl	ENSRNOG000000038789	13	78,886,163
13738 A_64_P050502	-0.308	0.186	1.1E-01	-0.998	0.095	2.0E-12 Ankrd45	ENSRNOG000000051303	13	78,976,154
6395 A_42_P547246	-0.221	0.155	1.6E-01	-0.710	0.078	6.0E-11 Myoc	ENSRNOG000000003221	13	80,517,536
6836 A_43_P10161	0.114	0.085	1.9E-01	-0.335	0.042	2.1E-09 Kifap3	ENSRNOG000000002544	13	82,072,497
29150 A_44_P435604	0.056	0.072	4.5E-01	-0.350	0.036	1.3E-11 Atp1b1	ENSRNOG000000002934	13	82,758,004
5634 A_64_P018081	-0.078	0.085	3.6E-01	-0.454	0.043	1.1E-12 Ddr2	ENSRNOG000000002881	13	88,436,789
21779 A_44_P306439	0.300	0.162	7.3E-02	1.147	0.083	7.9E-16 Fcgr3a	ENSRNOG000000024382	13	89,385,859
5407 A_42_P565621	0.141	0.149	3.5E-01	0.692	0.074	3.9E-11 Slamf9	ENSRNOG000000008045	13	90,839,411
27586 A_64_P236342	-0.527	0.167	3.6E-03	1.185	0.086	8.2E-15 Tgfb2	ENSRNOG000000002418	13	105,141,030
6518 A_43_P11044	0.839	0.197	1.4E-04	-0.789	0.099	1.6E-09 G0s2	ENSRNOG000000006019	13	112,005,052
29630 A_64_P015335	0.143	0.105	1.8E-01	0.415	0.053	2.3E-09 Mfsd7	ENSRNOG000000023937	14	2,311,122
27087 A_64_P103517	0.243	0.227	2.9E-01	-0.910	0.113	1.5E-09 Ephx4	ENSRNOG000000023389	14	3,389,943

25065 A_64_P247541	-0.140	0.076	7.5E-02	-0.355	0.038	3.9E-11	Pcdh7	ENSRNOG000000012367	14	55,081,551
3786 A_43_P21699	0.090	0.116	4.4E-01	0.490	0.058	4.7E-10	Pi4k2b	ENSRNOG000000003924	14	60,594,844
4984 A_64_P020244	0.152	0.136	2.7E-01	-0.675	0.068	7.9E-12	Prom1	ENSRNOG000000003098	14	71,533,063
19807 A_64_P073904	0.076	0.117	5.2E-01	-0.692	0.058	5.2E-14	Prom1	ENSRNOG000000003098	14	71,533,063
22474 A_64_P079751	0.081	0.112	4.7E-01	0.437	0.056	2.9E-09	Bst1	ENSRNOG000000003064	14	71,814,523
27240 A_44_P248172	-0.052	0.074	4.8E-01	0.489	0.037	2.1E-15	C1qtnf7	ENSRNOG000000005094	14	72,122,158
3073 A_64_P031329	-0.276	0.232	2.4E-01	-1.050	0.116	8.0E-11	Stk32b	ENSRNOG0000000031397	14	77,829,400
2419 A_42_P833264	-0.172	0.133	2.0E-01	-0.494	0.066	8.8E-09	Zfp278	ENSRNOG000000018709	14	83,510,640
15680 A_64_P063896	-0.145	0.082	8.3E-02	0.320	0.041	2.5E-09	Selm	ENSRNOG0000000061231	14	83,752,393
18458 A_64_P138889	-0.116	0.060	6.0E-02	-0.292	0.030	1.1E-11	Pold2	ENSRNOG000000014098	14	86,116,363
2451 A_42_P491505	-0.099	0.061	1.2E-01	-0.390	0.031	6.9E-15	Purb	ENSRNOG0000000056150	14	86,739,335
7796 A_42_P466997	0.024	0.085	7.8E-01	0.357	0.043	5.5E-10	Ccm2	ENSRNOG0000000060825	14	86,813,082
12854 A_64_P129855	-0.050	0.102	6.3E-01	-0.466	0.051	6.4E-11	Meis1	ENSRNOG000000004606	14	103,321,270
5272 A_64_P038050	1.268	0.083	2.6E-17	-0.209	0.042	1.4E-05	Acyp2	ENSRNOG0000000042419	14	115,052,450
17821 A_64_P100148	1.767	0.152	9.1E-14	-0.264	0.076	1.4E-03	Lrmda (LOC6813N/A		15	1,269,869
8650 A_42_P607939	-0.676	0.074	5.6E-11	-0.072	0.037	5.8E-02	Chchd1	ENSRNOG000000009297	15	4,026,637
1991 A_42_P723584	-0.023	0.058	7.0E-01	-0.225	0.029	3.7E-09	Nat12	ENSRNOG0000000014192	15	26,033,791
5685 A_42_P775609	0.161	0.091	8.5E-02	-0.408	0.046	9.9E-11	Jub	ENSRNOG000000012791	15	33,218,456
25995 A_42_P641517	0.432	0.217	5.4E-02	0.916	0.109	4.6E-10	Mcpt111 (intrupte	ENSRNOG0000000053494	15	34,612,432
10880 A_44_P238556	0.380	0.193	5.9E-02	0.941	0.101	2.4E-10	Mcpt2	ENSRNOG0000000020625	15	34,862,281
1636 A_42_P684885	-0.244	0.182	1.9E-01	-1.120	0.091	1.6E-14	Atp12a	ENSRNOG0000000020685	15	36,565,495
15751 A_44_P531870	-0.072	0.155	6.4E-01	-2.707	0.077	1.8E-29	Ephx2	ENSRNOG0000000017286	15	42,794,279
22768 A_64_P001612	-0.101	0.077	2.0E-01	-0.569	0.039	7.1E-17	Trim35	ENSRNOG000000009449	15	42,960,307
10988 A_44_P304057	0.093	0.061	1.4E-01	0.260	0.031	3.4E-10	Ppp2r2a	ENSRNOG000000011158	15	43,733,182
7867 A_44_P498522	0.122	0.076	1.2E-01	0.292	0.038	3.7E-09	Kctd9	ENSRNOG000000012951	15	44,411,865
19433 A_44_P432388	-0.096	0.176	5.9E-01	-1.194	0.131	1.3E-09	Tdh	ENSRNOG000000011342	15	46,681,467
4844 A_64_P010902	0.040	0.128	7.5E-01	0.963	0.064	3.6E-17	Msra	ENSRNOG000000012440	15	47,800,024
21894 A_64_P069071	0.320	0.216	1.5E-01	-1.344	0.108	1.3E-14	Lpar6	ENSRNOG000000015577	15	55,126,953
18762 A_44_P135531	0.185	0.108	1.0E-01	-2.319	0.108	3.3E-17	RGD1304929	ENSRNOG0000000022760	15	57,065,428
23905 A_64_P163718	0.168	0.086	5.9E-02	-0.346	0.043	1.5E-09	Slc25a30	ENSRNOG000000001052	15	57,834,173
1297 A_44_P276220	0.094	0.102	3.6E-01	0.446	0.051	1.7E-10	Gtf2f2	ENSRNOG0000000029316	15	58,068,892

8579 A_64_P057340	-0.025	0.074	7.3E-01	-0.421	0.037	1.7E-13 Abcc4	ENSRNOG00000010064	15	103,927,592
4173 A_64_P117248	-0.076	0.100	4.5E-01	0.427	0.050	3.0E-10 Ppif	ENSRNOG00000010558	16	1,979,191
14428 A_44_P1000888	0.029	0.125	8.2E-01	0.755	0.062	2.7E-14 Plac9	ENSRNOG00000011263	16	3,851,270
20576 A_64_P122190	0.194	0.152	2.1E-01	0.787	0.076	2.2E-12 Plac9	ENSRNOG00000011263	16	3,851,270
23502 A_64_P070756	-0.039	0.065	5.5E-01	-0.266	0.032	8.9E-10 Anxa11	ENSRNOG00000010984	16	3,912,148
11180 A_64_P068548	0.242	0.139	9.0E-02	0.710	0.069	3.2E-12 Arhgap22	ENSRNOG00000024728	16	9,486,832
18286 A_44_P384017	0.096	0.172	5.8E-01	0.739	0.086	3.0E-10 Sncg	ENSRNOG00000058006	16	10,726,707
24518 A_64_P046248	0.512	0.206	1.8E-02	-0.774	0.103	7.1E-09 Mat1a	ENSRNOG00000011351	16	18,690,246
24366 A_44_P290394	-0.324	0.162	5.3E-02	-0.823	0.081	4.1E-12 Slc27a1	ENSRNOG00000018170	16	19,999,112
22352 A_44_P215131	0.025	0.098	8.0E-01	0.418	0.049	3.1E-10 Mk1	ENSRNOG00000019657	16	20,534,209
2924 A_43_P14632	-0.119	0.095	2.2E-01	-0.377	0.048	1.9E-09 Acs1	ENSRNOG00000010633	16	48,981,980
11713 A_64_P014366	0.018	0.146	9.0E-01	0.633	0.073	2.3E-10 Sorbs2	ENSRNOG00000013391	16	49,820,235
15277 A_64_P054561	0.030	0.125	8.1E-01	0.563	0.062	8.7E-11 LOC498662	ENSRNOG00000027245	16	80,729,400
7494 A_42_P633958	0.262	0.152	9.4E-02	1.051	0.076	5.6E-16 Col4a2	ENSRNOG00000023972	16	83,438,561
17237 A_42_P679295	0.188	0.105	8.3E-02	0.438	0.053	6.4E-10 RGD1311345	ENSRNOG00000019232	17	6,683,152
4329 A_44_P620106	-0.026	0.084	7.5E-01	0.312	0.042	8.2E-09 Tgfb1	ENSRNOG00000012216	17	8,429,338
12435 A_64_P054743	-0.001	0.086	9.9E-01	-0.346	0.043	1.5E-09 Pcbd2	ENSRNOG00000047796	17	8,980,571
23510 A_44_P1039249	0.248	0.153	1.1E-01	0.579	0.077	6.0E-09 Dok3	ENSRNOG00000013564	17	9,639,330
24240 A_64_P156438	0.094	0.094	3.3E-01	0.809	0.047	6.1E-19 Zfp346	ENSRNOG00000016867	17	10,061,772
19380 A_64_P155920	-0.104	0.123	4.0E-01	-0.512	0.061	5.9E-10 Cplx2	ENSRNOG00000000105	17	10,818,835
9101 A_44_P201028	-0.103	0.151	5.0E-01	0.568	0.076	6.8E-09 Nfil3	ENSRNOG00000011668	17	12,261,102
20867 A_64_P059032	-0.230	0.163	1.7E-01	0.666	0.077	4.1E-10 Susd3	ENSRNOG00000016525	17	15,814,132
1813 A_42_P783550	-0.050	0.087	5.7E-01	-0.325	0.043	7.5E-09 Rreb1	ENSRNOG00000015701	17	27,602,934
6034 A_64_P023472	0.229	0.164	1.7E-01	0.633	0.082	3.5E-09 Serpinb1a	ENSRNOG00000016581	17	32,904,119
3910 A_64_P045057	-0.004	0.102	9.7E-01	-0.405	0.051	2.1E-09 Gpld1	ENSRNOG00000017702	17	42,127,678
9068 A_44_P548468	-0.037	0.090	6.8E-01	0.394	0.045	1.8E-10 Kif5b	ENSRNOG00000017466	17	54,181,419
16401 A_64_P149491	-0.153	0.135	2.7E-01	-0.640	0.068	2.5E-11 Mpp7	ENSRNOG00000018760	17	60,059,949
23495 A_64_P036509	1.277	0.153	5.6E-10	-0.014	0.076	8.6E-01 Chrm3	ENSRNOG00000049410	17	63,994,169
23649 A_44_P191021	0.004	0.105	9.7E-01	0.468	0.053	1.2E-10 Phyh	ENSRNOG00000018044	17	77,304,530
1142 A_44_P823025	-0.180	0.093	6.2E-02	-0.438	0.047	3.2E-11 Sephs1	ENSRNOG00000018125	17	77,340,934
6327 A_64_P148776	-0.106	0.067	1.2E-01	-0.375	0.033	2.5E-13 Sephs1	ENSRNOG00000018125	17	77,340,934

3451 A_64_P126750	0.020	0.108	8.5E-01	0.611	0.054	2.1E-13 Cdnf	ENSRNOG00000026493	17	78,735,324
1172 A_42_P509365	0.086	0.085	3.2E-01	0.348	0.042	8.3E-10 Vim	ENSRNOG00000018087	17	80,882,666
13848 A_43_P19054	-0.131	0.138	3.5E-01	-0.626	0.069	7.1E-11 Dsc2	ENSRNOG00000039969	18	11,858,744
28750 A_44_P382255	0.164	0.115	1.6E-01	-0.513	0.058	1.2E-10 none_Dtna	ENSRNOG00000016671	18	14,471,213
10876 A_64_P049411	-0.012	0.113	9.2E-01	-0.419	0.057	9.4E-09 LOC679229	ENSRNOG00000048101	18	15,856,801
13454 A_64_P109506	0.209	0.140	1.5E-01	0.612	0.070	2.0E-10 Moccos	ENSRNOG00000015113	18	16,590,408
24597 A_64_P083905	0.107	0.068	1.2E-01	0.465	0.034	5.7E-16 Pik3c3	ENSRNOG00000017840	18	22,964,210
18807 A_64_P158068	0.010	0.090	9.1E-01	0.624	0.045	4.5E-16 Wdr36	ENSRNOG00000027355	18	25,637,588
27518 A_44_P1033758	0.141	0.175	4.2E-01	-1.241	0.088	2.4E-16 Wdr36	ENSRNOG00000027355	18	25,637,588
479 A_42_P776018	-0.109	0.084	2.0E-01	-0.554	0.042	2.3E-15 Stard4	ENSRNOG00000020468	18	25,997,555
2083 A_42_P625263	-0.081	0.099	4.2E-01	-0.662	0.049	1.4E-15 Epb41l4a	ENSRNOG00000026050	18	26,658,892
5557 A_43_P15754	-0.100	0.080	2.2E-01	0.352	0.040	1.7E-10 none	ENSRNOG00000019525	18	27,749,235
950 A_64_P124641	-0.100	0.103	3.4E-01	0.414	0.051	1.3E-09 none	ENSRNOG00000060829	18	29,535,280
20756 A_64_P036233	-0.065	0.103	5.3E-01	0.480	0.051	3.4E-11 none	ENSRNOG00000060829	18	29,535,280
9887 A_64_P038414	0.328	0.182	8.0E-02	0.776	0.091	3.6E-10 Lox	ENSRNOG00000014426	18	47,513,065
26924 A_64_P155509	-0.125	0.067	6.9E-02	-0.342	0.033	3.1E-12 Snx2	ENSRNOG00000017832	18	48,132,414
5554 A_44_P897023	-0.187	0.220	4.0E-01	-0.894	0.112	2.0E-09 Snx24	ENSRNOG00000017488	18	48,201,728
8407 A_64_P058564	-0.719	0.057	8.1E-15	0.054	0.028	6.7E-02 Prrc1	ENSRNOG00000016433	18	52,423,883
7776 A_44_P203859	-0.201	0.202	3.3E-01	-0.819	0.101	1.2E-09 none_Piezo2	ENSRNOG00000038784	18	58,499,836
1853 A_64_P039601	0.097	0.065	1.4E-01	0.485	0.032	4.6E-17 Sec11c	ENSRNOG00000017036	18	61,490,031
8960 A_64_P029646	0.055	0.070	4.4E-01	0.319	0.035	6.3E-11 Rpl17	ENSRNOG00000018680	18	70,970,596
19064 A_64_P052765	0.415	0.212	5.8E-02	0.924	0.106	2.1E-10 Cdh16	ENSRNOG00000012222	19	568,287
14056 A_64_P162764	-0.127	0.175	4.7E-01	0.751	0.087	2.9E-10 none	ENSRNOG00000025764	19	11,302,938
12160 A_43_P11151	-0.053	0.083	5.3E-01	-0.338	0.041	1.0E-09 Nfatc3	ENSRNOG00000054264	19	38,039,729
4796 A_64_P094515	0.305	0.092	2.1E-03	-1.317	0.046	1.8E-26 LOC100360619	ENSRNOG00000053623	19	38,643,108
14458 A_44_P480636	0.143	0.113	2.1E-01	0.446	0.056	2.1E-09 Ddx19a	ENSRNOG00000018033	19	43,217,161
27532 A_44_P252441	0.056	0.110	6.1E-01	0.428	0.055	2.9E-09 St3gal2	ENSRNOG00000017932	19	43,290,363
1581 A_42_P712297	1.754	0.196	1.1E-10	-0.068	0.098	4.9E-01 Fa2h	ENSRNOG00000018950	19	43,596,801
21295 A_43_P11451	0.345	0.170	5.0E-02	1.119	0.085	2.3E-15 Ctrb1	ENSRNOG00000019068	19	43,911,057
25128 A_44_P491393	0.300	0.095	3.1E-03	-0.523	0.047	3.9E-13 Nudt7	ENSRNOG00000011976	19	46,455,761
6940 A_64_P052791	-0.016	0.122	9.0E-01	-0.561	0.061	5.1E-11 Cdh13	ENSRNOG00000014371	19	50,848,736

10658 A_44_P561084	-0.018	0.090	8.4E-01	-0.338	0.045	7.1E-09	Cdh13	ENSRNOG000000014371	19	50,848,736
24895 A_44_P529581	0.348	0.175	5.4E-02	0.710	0.087	1.2E-09	Osgin1	ENSRNOG000000014948	19	52,077,109
3616 A_64_P102518	0.091	0.108	4.1E-01	0.735	0.054	9.3E-16	Zc3h18	ENSRNOG000000028501	19	55,197,704
20497 A_44_P311821	0.139	0.077	7.8E-02	0.782	0.038	2.0E-21	Afg3l1	ENSRNOG000000026994	19	56,272,162
14753 A_64_P023365	-0.590	0.070	5.5E-10	-0.017	0.035	6.2E-01	Abcb10	ENSRNOG000000017993	19	56,772,904
27136 A_64_P108001	0.127	0.067	6.6E-02	-0.333	0.033	6.6E-12	Galnt2	ENSRNOG000000019143	19	57,047,830
25296 A_64_P108692	-0.081	0.070	2.5E-01	-0.613	0.035	2.5E-19	Ttc13	ENSRNOG000000018884	19	57,484,566
2423 A_42_P567268	0.496	0.268	7.3E-02	1.001	0.134	7.8E-09	Mt2A	ENSRNOG000000028841	20	3,677,474
21444 A_64_P158939	0.271	0.211	2.1E-01	0.885	0.105	5.1E-10	Mt2A	ENSRNOG000000028841	20	3,677,474
13348 A_64_P130578	0.198	0.127	1.3E-01	0.535	0.063	4.5E-10	RT1-Db1	ENSRNOG000000033215	20	4,087,618
11988 A_64_P026316	-1.203	0.162	8.7E-09	0.000	0.081	1.0E+00	none_C4b	ENSRNOG000000030729	20	4,316,715
15626 A_44_P332606	-0.089	0.081	2.8E-01	0.306	0.040	6.1E-09	C2	ENSRNOG000000000419	20	4,542,947
2785 A_64_P140658	-0.231	0.117	5.7E-02	-0.444	0.059	5.8E-09	Anks1a	ENSRNOG000000000498	20	7,484,550
1548 A_42_P535085	0.769	0.094	9.6E-10	-0.141	0.047	4.8E-03	Ndufv3	ENSRNOG000000001182	20	10,265,806
6923 A_64_P048765	0.421	0.134	3.4E-03	-0.614	0.067	5.8E-11	Cbs	ENSRNOG000000029528	20	10,386,663
21940 A_64_P228661	-0.137	0.070	5.9E-02	0.291	0.035	7.6E-10	Pcbp3	ENSRNOG000000001245	20	12,429,315
23949 A_64_P164581	-0.084	0.115	4.7E-01	0.543	0.058	2.8E-11	Pcbp3	ENSRNOG000000001245	20	12,429,315
13884 A_44_P1047108	-0.065	0.068	3.4E-01	-0.287	0.034	4.3E-10	Ddt	ENSRNOG000000001239	20	13,827,132
6478 A_44_P303982	0.006	0.113	9.6E-01	0.468	0.057	7.7E-10	Susd2	ENSRNOG000000033389	20	13,965,121
25896 A_64_P037095	-0.079	0.125	5.3E-01	-0.479	0.063	4.4E-09	Pald	ENSRNOG000000000561	20	30,975,472
3760 A_44_P393551	0.085	0.084	3.2E-01	-0.334	0.042	2.0E-09	Gja1	ENSRNOG000000000805	20	37,876,650
26775 A_44_P384677	0.102	0.113	3.8E-01	0.447	0.057	2.3E-09	Rtn4ip1	ENSRNOG000000000279	20	48,881,194
18300 A_44_P124772	0.099	0.085	2.5E-01	0.357	0.042	5.1E-10	Ascc3	ENSRNOG000000037604	20	55,253,686
23473 A_43_P12070	-0.046	0.105	6.6E-01	0.637	0.052	2.2E-14	Ly6c	ENSRNOG000000061813	chr7_KL	23,908
558 A_64_P073899	0.125	0.121	3.1E-01	-0.542	0.060	9.3E-11		ENSRNOG000000031780	MT	1
822 A_64_P044731	0.100	0.081	2.3E-01	0.334	0.041	8.8E-10		ENSRNOG000000031780	MT	1
1765 A_42_P661992	-0.315	0.163	6.1E-02	-0.670	0.081	8.3E-10		ENSRNOG000000031780	MT	1
2055 A_44_P232030	-0.092	0.064	1.6E-01	-1.543	0.032	2.1E-34		ENSRNOG000000031780	MT	1
2356 A_64_P153314	-0.067	0.078	4.0E-01	0.305	0.039	3.0E-09		ENSRNOG000000031780	MT	1
3189 A_64_P058192	-0.275	0.159	9.3E-02	-0.677	0.080	3.9E-10		ENSRNOG000000031780	MT	1
3581 A_64_P148683	-0.081	0.069	2.5E-01	-0.364	0.035	1.6E-12		ENSRNOG000000031780	MT	1

3842 A_44_P405704	0.072	0.148	6.3E-01	0.586	0.074	2.2E-09	ENSRNOG00000031780	MT	1
4783 A_44_P306863	0.014	0.079	8.6E-01	0.310	0.040	2.8E-09	ENSRNOG00000031780	MT	1
4915 A_64_P024630	0.164	0.090	7.5E-02	0.418	0.045	3.7E-11	ENSRNOG00000031780	MT	1
5961 A_44_P960035	0.096	0.078	2.3E-01	-0.307	0.039	2.6E-09	ENSRNOG00000031780	MT	1
6646 A_44_P713970	-0.094	0.077	2.3E-01	-1.609	0.039	3.9E-32	ENSRNOG00000031780	MT	1
7968 A_64_P110003	0.165	0.095	9.3E-02	0.455	0.048	2.0E-11	ENSRNOG00000031780	MT	1
8465 A_64_P147586	-0.142	0.097	1.5E-01	-2.394	0.049	1.0E-34	ENSRNOG00000031780	MT	1
8573 A_43_P11131	-0.044	0.090	6.3E-01	-0.396	0.045	1.5E-10	ENSRNOG00000031780	MT	1
9438 A_44_P394150	-0.056	0.100	5.8E-01	-1.588	0.050	5.1E-28	ENSRNOG00000031780	MT	1
10234 A_64_P058928	0.027	0.076	7.2E-01	0.293	0.038	3.4E-09	ENSRNOG00000031780	MT	1
10366 A_64_P118117	0.081	0.079	3.2E-01	0.412	0.040	2.1E-12	ENSRNOG00000031780	MT	1
11796 A_44_P398462	-0.114	0.100	2.6E-01	-1.715	0.050	3.3E-29	ENSRNOG00000031780	MT	1
12392 A_44_P318891	-0.159	0.111	1.6E-01	-2.378	0.055	1.3E-32	ENSRNOG00000031780	MT	1
12488 A_64_P078924	0.119	0.088	1.9E-01	0.326	0.044	9.8E-09	ENSRNOG00000031780	MT	1
13255 A_64_P077069	0.216	0.170	2.1E-01	-0.688	0.085	1.3E-09	ENSRNOG00000031780	MT	1
13682 A_64_P027242	0.075	0.087	4.0E-01	0.395	0.044	8.1E-11	ENSRNOG00000031780	MT	1
13826 A_64_P054363	-0.123	0.133	3.6E-01	-0.554	0.067	6.2E-10	ENSRNOG00000031780	MT	1
13880 A_44_P713734	0.123	0.069	8.1E-02	0.318	0.034	4.7E-11	ENSRNOG00000031780	MT	1
14301 A_43_P16020	0.203	0.355	5.7E-01	3.101	0.185	4.9E-18	ENSRNOG00000031780	MT	1
14314 A_44_P496853	-0.033	0.053	5.4E-01	-1.454	0.027	2.4E-36	ENSRNOG00000031780	MT	1
14990 A_64_P131111	-0.164	0.122	1.9E-01	-0.468	0.061	4.4E-09	ENSRNOG00000031780	MT	1
15048 A_64_P017103	0.055	0.111	6.2E-01	-1.601	0.056	1.7E-26	ENSRNOG00000031780	MT	1
18226 A_44_P836900	0.091	0.069	2.0E-01	0.388	0.034	2.2E-13	ENSRNOG00000031780	MT	1
18386 A_64_P155290	-0.105	0.079	1.9E-01	-0.329	0.040	6.4E-10	ENSRNOG00000031780	MT	1
18880 A_64_P057622	0.030	0.087	7.3E-01	-1.461	0.043	6.1E-29	ENSRNOG00000031780	MT	1
18983 A_64_P047391	0.106	0.072	1.5E-01	0.366	0.036	3.5E-12	ENSRNOG00000031780	MT	1
19493 A_64_P025507	-0.025	0.097	7.9E-01	0.451	0.048	3.7E-11	ENSRNOG00000031780	MT	1
19765 A_64_P155950	0.566	0.309	7.6E-02	0.815	0.098	1.2E-09	ENSRNOG00000031780	MT	1
20422 A_64_P128815	0.020	0.215	9.2E-01	-1.760	0.108	2.7E-18	ENSRNOG00000031780	MT	1
20790 A_64_P033001	0.200	0.113	8.6E-02	0.673	0.057	5.1E-14	ENSRNOG00000031780	MT	1
20800 A_44_P545895	-0.056	0.075	4.6E-01	-0.406	0.038	8.1E-13	ENSRNOG00000031780	MT	1

20804 A_44_P468573	-0.046	0.084	5.9E-01	-1.376	0.042	1.4E-28	ENSRNOG000000031780	MT	1
21008 A_43_P22501	0.011	0.082	9.0E-01	-0.402	0.041	1.2E-11	ENSRNOG000000031780	MT	1
22321 A_42_P603213	-0.028	0.158	8.6E-01	-0.595	0.079	6.1E-09	ENSRNOG000000031780	MT	1
22975 A_64_P162760	-0.093	0.153	5.5E-01	0.687	0.076	9.4E-11	ENSRNOG000000031780	MT	1
23524 A_64_P031108	-0.041	0.158	8.0E-01	-1.120	0.079	2.6E-16	ENSRNOG000000031780	MT	1
23698 A_64_P028379	0.415	0.224	7.3E-02	0.825	0.071	3.1E-13	ENSRNOG000000031780	MT	1
24076 A_44_P945336	-0.076	0.080	3.5E-01	-0.475	0.040	5.0E-14	ENSRNOG000000031780	MT	1
24540 A_64_P050969	0.236	0.140	1.0E-01	-0.532	0.070	5.4E-09	ENSRNOG000000031780	MT	1
24634 A_64_P069294	0.000	0.063	1.0E+00	-1.484	0.032	4.7E-34	ENSRNOG000000031780	MT	1
26704 A_64_P066586	-0.179	0.091	5.6E-02	0.435	0.045	1.7E-11	ENSRNOG000000031780	MT	1
27068 A_64_P143415	0.023	0.087	7.9E-01	-0.631	0.043	1.1E-16	ENSRNOG000000031780	MT	1
27129 A_64_P162408	0.069	0.076	3.7E-01	-1.910	0.038	4.2E-35	ENSRNOG000000031780	MT	1
27926 A_64_P122775	-0.013	0.127	9.2E-01	-1.564	0.064	3.8E-24	ENSRNOG000000031780	MT	1
28053 A_64_P127136	0.078	0.069	2.7E-01	0.369	0.035	9.8E-13	ENSRNOG000000031780	MT	1
28354 A_64_P025510	-0.081	0.112	4.7E-01	0.476	0.056	4.0E-10	ENSRNOG000000031780	MT	1
29141 A_64_P017493	-0.088	0.096	3.7E-01	-2.018	0.048	2.4E-32	ENSRNOG000000031780	MT	1
29296 A_44_P152335	0.090	0.095	3.5E-01	0.357	0.048	7.8E-09	ENSRNOG000000031780	MT	1
29449 A_64_P132109	-0.111	0.086	2.1E-01	-0.447	0.043	2.4E-12	ENSRNOG000000031780	MT	1
11763 A_64_P031741	0.404	0.099	2.3E-04	-0.412	0.049	6.0E-10	ENSRNOG000000031780	MT	1
2074 A_44_P238204	-0.042	0.116	7.2E-01	-0.664	0.058	1.4E-13	Mid1ip1	X	13,116,743
11421 A_44_P180060	0.226	0.120	6.9E-02	0.583	0.060	1.4E-11	Hdac6	X	15,396,895
17831 A_43_P13307	0.305	0.154	5.6E-02	0.950	0.077	1.6E-14	Gpm6b	X	29,648,403
6662 A_44_P1005051	-0.230	0.211	2.8E-01	-0.883	0.112	4.6E-09	Car5b	X	32,232,142
2763 A_42_P685330	-0.047	0.062	4.5E-01	-0.375	0.031	3.2E-14	Ap1s2	X	32,355,296
25456 A_44_P480696	-0.138	0.081	9.8E-02	-0.379	0.041	3.7E-11	Ap1s2	X	32,355,296
19304 A_64_P123949	-0.079	0.117	5.0E-01	-0.443	0.058	5.5E-09	Gk	X	54,303,825
28798 A_44_P473510	0.177	0.301	5.6E-01	2.265	0.206	3.2E-10	Vsig4	X	65,400,298
709 A_44_P260502	-0.034	0.100	7.3E-01	-2.485	0.050	6.5E-35	none	X	67,980,381
8429 A_44_P488594	0.009	0.086	9.1E-01	0.325	0.043	5.8E-09	Tspan6	X	104,726,816
37 A_64_P019719	-0.104	0.140	4.6E-01	0.670	0.070	1.8E-11	SrpX2	X	104,734,082
24862 A_64_P132324	0.009	0.063	8.9E-01	0.300	0.031	1.9E-11	none	X	106,607,352

9321 A_44_P263635	-0.086	0.056	1.3E-01	-0.233	0.028	6.4E-10 Prps1	ENSRNOG00000060262	X	111,798,233
28862 A_64_P012725	-0.047	0.203	8.2E-01	-0.874	0.101	2.6E-10 Atp2b3	ENSRNOG00000061304	X	157,312,028
958 A_42_P552341	0.138	0.100	1.8E-01	-0.529	0.050	1.4E-12 Sorl1	N/A	8	46,228,077
2550 A_44_P671340	-0.009	0.113	9.4E-01	0.431	0.056	4.6E-09 none_LOC498601		16	
2624 A_64_P023587	0.080	0.103	4.4E-01	0.419	0.052	1.1E-09 none_Ly96			
7696 A_64_P147838	0.050	0.077	5.2E-01	0.487	0.039	7.7E-15 LOC679199			
10852 A_44_P313230	-0.091	0.096	3.5E-01	0.421	0.048	1.6E-10 LOC685888			
15274 A_64_P095948	-0.058	0.109	6.0E-01	0.517	0.055	2.5E-11 LOC690138			
16008 A_44_P538165	0.053	0.130	6.9E-01	0.936	0.065	1.4E-16 Tspan17 (Fbxo23)	ENSRNOG00000018122	17	10,356,980
16163 A_64_P143161	0.112	0.074	1.4E-01	-0.415	0.037	2.5E-13 RGD1309747			
19575 A_44_P986792	-0.104	0.159	5.2E-01	-0.708	0.083	4.9E-10 Sorl1	N/A	8	46,228,077
20759 A_64_P020968	0.314	0.169	7.3E-02	0.915	0.088	1.5E-11 Raet1l			
18371 A_43_P17271	0.784	0.102	4.3E-09	0.098	0.051	6.3E-02 none_RGD1307569		11	

Genes are regarded as significant for “non-shared” differential expression when they show $P < 1 \times 10^{-8}$ in one comparison but not in the other ($P \geq 0.05$ with a concordant direction or all P -values in the opposite direction).

Table S3G. A list of significant transcripts for non-shared differential expression in the aorta.

no	ProbeName	SHR/lzm (vs WKY/lzm)			SHRSP/lzm (vs WKY/lzm)			GeneName	Ensembl_rat	Chr	Transcription_ start_site (Rnor_6.0)
		Fold change (log2-scale)	SE (log2-scale)	P-value	Fold change (log2-scale)	SE (log2-scale)	P-value				
30079	A_64_P153441	-0.206	0.109	7.6E-02	1.186	0.097	1.7E-09	no transcript	ENSRNOG00000018935	1	47,588,122
26822	A_64_P150067	-0.057	0.071	4.3E-01	-0.764	0.064	2.2E-09	Ndufa3	ENSRNOG000000060293	1	64,175,099
28760	A_64_P060497	6.097	0.273	3.8E-09	-0.336	0.170	8.0E-02	Apoc4	ENSRNOG00000018405	1	80,599,572
16474	A_64_P068858	0.011	0.099	9.1E-01	2.496	0.089	5.0E-15	Rps16	ENSRNOG00000019578	1	85,408,444
8683	A_42_P644209	-0.028	0.156	8.6E-01	1.722	0.139	1.4E-09	no transcript	ENSRNOG00000030932	1	88,361,712
5564	A_42_P696282	0.002	0.115	9.8E-01	-1.138	0.103	6.6E-09	Fuom (RGD1311	ENSRNOG00000018476	1	212,568,224
24939	A_64_P036440	-0.091	0.093	3.4E-01	-0.989	0.083	2.4E-09	Cox8b	ENSRNOG00000014656	1	213,650,247
10669	A_44_P792628	-1.011	0.093	9.0E-09	0.101	0.083	2.4E-01	Spef1 (RGD1311	ENSRNOG00000021247	3	123,718,432
13942	A_44_P271405	-1.633	0.109	8.2E-11	0.058	0.097	5.6E-01	Pxmp4	ENSRNOG00000016975	3	150,108,898
17113	A_64_P139590	-0.016	0.108	8.9E-01	1.168	0.096	1.9E-09	Slc35c2	ENSRNOG00000018649	3	161,812,291
9281	A_44_P885189	0.042	0.137	7.6E-01	1.950	0.131	2.2E-10	Lrrc4	ENSRNOG00000008098	4	56,114,254
8266	A_64_P114713	-0.095	0.164	5.7E-01	-3.665	0.164	6.6E-13	Agtrap	ENSRNOG00000008619	5	164,898,420
19445	A_44_P250988	-3.804	0.176	3.2E-13	0.117	0.158	4.7E-01	Serhl2	ENSRNOG00000022932	7	123,963,381
13264	A_44_P145970	0.217	0.115	7.8E-02	1.326	0.103	7.6E-10	Hs6st1	ENSRNOG00000014516	9	42,620,006
11810	A_43_P12005	-0.190	0.095	6.3E-02	-1.520	0.085	5.7E-12	Resp18	ENSRNOG00000019704	9	82,477,181
21443	A_44_P748640	0.077	0.102	4.6E-01	1.480	0.091	2.6E-11	Parn	ENSRNOG00000002912	10	1,461,269
17678	A_64_P038142	0.193	0.107	9.1E-02	1.037	0.096	9.7E-09	Tubd1	ENSRNOG00000053309	10	73,868,943
28777	A_64_P028270	0.004	0.179	9.8E-01	1.921	0.160	2.1E-09	Mettl2	ENSRNOG00000006131	10	93,354,003
16173	A_64_P050025	0.028	0.099	7.8E-01	-1.064	0.088	2.0E-09	Cyyr1	ENSRNOG00000001544	11	25,078,740
20991	A_64_P004477	-0.015	0.146	9.2E-01	1.696	0.131	6.9E-10	Adora1	ENSRNOG00000003442	13	51,076,165
5214	A_44_P109862	0.214	0.152	1.8E-01	1.942	0.136	1.6E-10	lns1abp	ENSRNOG00000002618	13	68,707,776
10858	A_64_P028371	-0.111	0.120	3.7E-01	-1.487	0.107	2.5E-10	Phf11	ENSRNOG00000053891	15	38,709,984
15751	A_44_P531870	-0.052	0.149	7.3E-01	-3.518	0.134	1.5E-14	Ephx2	ENSRNOG00000017286	15	42,794,279
14880	A_64_P009576	0.128	0.124	3.2E-01	1.290	0.111	3.4E-09	AABR07018792.	ENSRNOG00000038078	15	73,180,671
2879	A_43_P13409	-0.205	0.104	6.6E-02	-1.013	0.093	8.7E-09	Zdhhc2	ENSRNOG00000022686	16	55,002,322
27518	A_44_P1033758	0.146	0.138	3.1E-01	-1.591	0.123	7.7E-10	Wdr36	ENSRNOG00000027355	18	25,637,588
27532	A_44_P252441	0.191	0.161	2.5E-01	1.827	0.144	9.4E-10	St3gal2	ENSRNOG00000017932	19	43,290,363
22427	A_64_P154849	-2.880	0.165	8.0E-12	0.094	0.147	5.3E-01	Agt	ENSRNOG00000018445	19	57,333,433

4094 A_64_P132069	0.132	0.104	2.2E-01	1.112	0.093	2.4E-09 RT1-CE15	ENSRNOG000000048951	20	2,707,108
5268 A_44_P852241	0.093	0.082	2.8E-01	1.056	0.074	1.6E-10 none	ENSRNOG000000031780	MT	1
1388 A_43_P11495	0.010	0.137	9.4E-01	2.093	0.123	1.2E-11 Prps2	ENSRNOG000000004160	X	28,435,507
22516 A_64_P072813	0.128	0.155	4.3E-01	3.547	0.155	3.0E-09 no transcript			

Genes are regarded as significant for “non-shared” differential expression when they show $P < 1 \times 10^{-8}$ in one comparison but not in the other ($P \geq 0.05$ with a concordant direction or all P-values in the opposite direction).

Table S3H. A list of significant transcripts for non-shared differential expression in the whole kidney.

no	ProbeName	SHR/lzm (vs WKY/lzm)			SHRSP/lzm (vs WKY/lzm)			GeneName	Ensembl_rat	Chr	Transcription_ start_site (Rnor_6.0)
		Fold change (log2-scale)	SE (log2-scale)	P-value	Fold change (log2-scale)	SE (log2-scale)	P-value				
25	A_42_P520891	-0.873	0.083	9.5E-10	-0.245	0.123	6.0E-02	Prc1	ENSRNOG00000013057	1	142,087,208
5874	A_42_P495598	-1.383	0.114	2.0E-11	-0.277	0.161	9.9E-02	Clrn3	ENSRNOG00000028288	1	207,766,250
5564	A_42_P696282	0.786	0.081	1.4E-09	-0.119	0.114	3.1E-01	Fuom (RGD1311	ENSRNOG00000018476	1	212,568,224
17305	A_64_P002924	-0.954	0.065	4.4E-13	-0.035	0.092	7.1E-01	Asrgl1	ENSRNOG00000020202	1	225,329,770
30101	A_44_P896040	-1.063	0.099	2.2E-10	0.061	0.140	6.7E-01	Cybasc3	ENSRNOG00000020702	1	226,634,009
5085	A_44_P534089	-1.281	0.123	6.0E-10	-0.319	0.167	7.0E-02	Ccnb1	ENSRNOG00000058539	2	30,791,221
20681	A_44_P747071	0.729	0.070	3.8E-10	-0.195	0.099	6.1E-02	Vav3	ENSRNOG00000020485	2	212,247,451
10958	A_44_P480573	-1.006	0.112	5.7E-09	-0.211	0.158	2.0E-01	Cytip	ENSRNOG00000004772	3	44,177,689
23902	A_44_P192224	0.198	0.119	1.1E-01	1.584	0.162	1.9E-09	Upp2	ENSRNOG00000005341	3	44,806,106
16485	A_44_P208138	-1.345	0.100	2.4E-12	0.078	0.141	5.9E-01	F2	ENSRNOG00000016325	3	80,543,031
13942	A_44_P271405	-1.754	0.085	3.0E-16	0.085	0.120	4.9E-01	Pxmp4	ENSRNOG00000016975	3	150,108,898
5160	A_44_P1019604	-1.000	0.100	1.3E-09	-0.205	0.136	1.5E-01	Ube2c	ENSRNOG00000015131	3	161,236,971
17113	A_64_P139590	-0.088	0.065	1.9E-01	1.390	0.092	2.5E-13	Slc35c2	ENSRNOG00000018649	3	161,812,291
26944	A_43_P15431	-1.058	0.083	6.8E-12	-0.001	0.117	9.9E-01	Mterf	ENSRNOG00000007899	4	27,365,376
2691	A_42_P754654	-0.122	0.126	3.4E-01	1.638	0.178	3.8E-09	RGD1562378	ENSRNOG00000045840	4	170,763,916
15950	A_64_P039911	-0.219	0.122	8.5E-02	1.536	0.172	6.8E-09	none	ENSRNOG00000045840	4	170,763,916
8266	A_64_P114713	0.053	0.074	4.8E-01	-3.505	0.104	6.5E-21	Agtrap	ENSRNOG00000008619	5	164,898,420
22457	A_44_P128186	0.207	0.104	5.8E-02	2.236	0.147	1.9E-13	Tas1r1	ENSRNOG00000009708	5	169,212,170
16904	A_64_P134445	-1.544	0.113	1.5E-10	-0.143	0.266	6.0E-01	Tmem179 (RGD1	ENSRNOG00000013128	6	137,084,739
19445	A_44_P250988	-2.969	0.125	1.3E-17	-0.126	0.176	4.8E-01	Serhl2	ENSRNOG00000022932	7	123,963,381
2132	A_64_P136083	-0.132	0.075	9.3E-02	-1.122	0.107	3.2E-10	Itga11	ENSRNOG00000006723	8	67,615,635
22463	A_44_P142850	-0.208	0.109	7.0E-02	1.350	0.155	9.9E-09	Fam86a	ENSRNOG00000002876	10	10,530,365
26992	A_42_P826202	0.065	0.073	3.8E-01	1.734	0.094	1.6E-13	Znf597	ENSRNOG00000007576	10	11,912,543
21202	A_64_P055748	-0.025	0.077	7.5E-01	-1.213	0.109	1.0E-10	Rhbdf1	ENSRNOG00000020594	10	15,672,382
25156	A_64_P064516	-0.014	0.078	8.6E-01	2.798	0.183	2.7E-11	Kcnp1	ENSRNOG00000005365	10	18,579,632
14617	A_64_P028561	1.289	0.100	6.2E-12	0.198	0.142	1.8E-01	none	ENSRNOG00000058024	10	29,806,895
14158	A_44_P1011918	3.148	0.134	1.1E-13	-0.142	0.287	6.3E-01	none	ENSRNOG00000042833	10	91,661,558
28777	A_64_P028270	-0.100	0.145	5.0E-01	2.252	0.205	1.4E-10	Mettl2	ENSRNOG00000006131	10	93,354,003

24814 A_64_P010531	0.244	0.134	8.1E-02	-1.955	0.189	4.5E-10 Ace	ENSRNOG000000062101	10	94,170,766
24567 A_43_P17925	0.153	0.085	8.5E-02	-1.136	0.120	2.3E-09 Abca8	ENSRNOG000000004040	10	98,294,522
7468 A_64_P024395	0.205	0.144	1.7E-01	2.789	0.204	1.8E-12 LOC681544	ENSRNOG000000001809	11	81,639,952
8935 A_64_P049423	-1.186	0.100	3.3E-11	0.231	0.142	1.2E-01 Sds	ENSRNOG000000001388	12	41,627,741
28125 A_64_P106543	2.126	0.224	8.1E-09	0.444	0.296	1.5E-01 none	ENSRNOG000000052604	13	56,763,981
20637 A_64_P003621	0.036	0.099	7.2E-01	3.006	0.261	8.6E-09 LOC498308	ENSRNOG000000032812	13	108,460,362
23631 A_64_P013437	1.346	0.152	7.4E-09	0.055	0.214	8.0E-01 Cxcl13	ENSRNOG000000024899	14	15,258,207
5038 A_42_P843692	-2.149	0.094	1.0E-16	-0.177	0.128	1.8E-01 Cadps	ENSRNOG000000060863	15	12,756,403
15751 A_44_P531870	0.137	0.095	1.6E-01	-4.041	0.135	7.9E-20 Ephx2	ENSRNOG000000017286	15	42,794,279
29819 A_64_P101346	-0.124	0.073	1.0E-01	0.991	0.103	1.8E-09 Ppic	ENSRNOG000000017416	18	48,384,645
24729 A_64_P014774	-0.038	0.099	7.0E-01	-1.706	0.158	5.8E-09 Mcm5	ENSRNOG000000014336	19	14,523,554
13133 A_44_P133335	-1.141	0.112	1.0E-09	-0.081	0.153	6.0E-01 none	ENSRNOG000000049468	19	28,645,488
14753 A_64_P023365	-1.511	0.100	2.2E-13	-0.032	0.141	8.2E-01 Abcb10	ENSRNOG000000017993	19	56,772,904
6103 A_64_P174934	-0.704	0.067	3.3E-10	0.131	0.095	1.8E-01 Cog2	ENSRNOG000000018228	19	57,286,985
22427 A_64_P154849	-0.915	0.093	1.2E-09	0.000	0.132	1.0E+00 Agt	ENSRNOG000000018445	19	57,333,433
21684 A_44_P421672	0.071	0.090	4.4E-01	-1.637	0.144	2.5E-09 Ager	ENSRNOG000000000439	20	4,363,152
27477 A_44_P335079	-0.682	0.068	7.6E-10	-0.179	0.096	7.6E-02 Tff3	ENSRNOG000000001159	20	9,855,481
20800 A_44_P545895	-0.068	0.085	4.3E-01	1.192	0.120	9.4E-10	ENSRNOG000000031780	MT	1
24540 A_64_P050969	0.123	0.113	2.9E-01	-1.990	0.160	1.1E-11	ENSRNOG000000031780	MT	1
15913 A_64_P148027	1.081	0.085	5.0E-10	-0.098	0.201	6.3E-01	ENSRNOG000000031780	MT	1
20235 A_44_P472776	0.071	0.101	4.9E-01	-3.018	0.238	5.0E-10 Nr0b1	ENSRNOG000000003765	X	54,734,385
27742 A_64_P085946	-1.149	0.125	6.0E-09	0.353	0.171	5.0E-02 Rtl4	ENSRNOG000000031638	X	116,399,611
22516 A_64_P072813	0.060	0.104	5.7E-01	4.295	0.147	3.4E-15 none_LOC680802			
22795 A_64_P164240	-0.205	0.117	9.2E-02	-1.454	0.165	8.4E-09 LOC301193			
9010 A_64_P012759	-0.913	0.094	1.5E-09	-0.098	0.133	4.7E-01 Fhit	N/A	15	15,697,292

Genes are regarded as significant for “non-shared” differential expression when they show $P < 1 \times 10^{-8}$ in one comparison but not in the other ($P \geq 0.05$ with a concordant direction or all P -values in the opposite direction).

Table S3I. A list of significant transcripts for non-shared differential expression in the renal cortex.

no	ProbeName	SHR/lzm (vs WKY/lzm)			SHRSP/lzm (vs WKY/lzm)			GeneName	Ensembl_rat	Chr	Transcription_ start_site (Rnor_6.0)
		Fold change (log2-scale)	SE (log2-scale)	P-value	Fold change (log2-scale)	SE (log2-scale)	P-value				
16474	A_64_P068858	-0.067	0.072	3.7E-01	2.501	0.068	2.7E-15	Rps16	ENSRNOG000000019578	1	85,408,444
6002	A_64_P139457	0.009	0.077	9.1E-01	-1.286	0.073	5.9E-11	LOC499124	ENSRNOG000000030932	1	88,361,712
30101	A_44_P896040	-1.204	0.072	1.2E-10	-0.028	0.068	6.9E-01	Cybas3	ENSRNOG000000020702	1	226,634,009
22220	A_64_P005320	0.062	0.072	4.0E-01	1.066	0.068	3.0E-10	no transcript	ENSRNOG000000005112	1	231,365,651
13942	A_44_P271405	-1.713	0.122	1.3E-09	0.168	0.115	1.7E-01	Pxmp4	ENSRNOG000000016975	3	150,108,898
4481	A_64_P164610	-0.015	0.051	7.8E-01	-0.731	0.048	4.3E-10	Tti1 (RGD156258	ENSRNOG000000012880	3	154,490,851
17113	A_64_P139590	-0.075	0.065	2.7E-01	1.151	0.062	2.8E-11	Slc35c2	ENSRNOG000000018649	3	161,812,291
26944	A_43_P15431	-0.959	0.068	1.1E-09	-0.056	0.064	4.0E-01	Mterf	ENSRNOG000000007899	4	27,365,376
2691	A_42_P754654	-0.071	0.117	5.5E-01	1.338	0.110	8.6E-09	no transcript	ENSRNOG000000045840	4	170,763,916
8266	A_64_P114713	-0.072	0.069	3.1E-01	-4.091	0.065	1.4E-18	Agtrap	ENSRNOG000000008619	5	164,898,420
17155	A_64_P051430	1.355	0.105	4.0E-09	-0.034	0.099	7.4E-01	Gpx2	ENSRNOG000000055672	6	99,843,245
19445	A_44_P250988	-2.841	0.080	4.5E-15	-0.010	0.076	8.9E-01	Serhl2	ENSRNOG000000022932	7	123,963,381
18255	A_64_P126165	-0.019	0.072	8.0E-01	-1.077	0.068	2.3E-10	no transcript	ENSRNOG000000046871	9	16,519,144
2629	A_64_P166218	-0.126	0.068	8.6E-02	0.865	0.064	2.2E-09	no transcript	ENSRNOG000000045696	10	1,464,780
26992	A_42_P826202	-0.103	0.138	4.6E-01	2.462	0.130	2.3E-11	Znf597	ENSRNOG000000007576	10	11,912,543
21202	A_64_P055748	-0.067	0.053	2.2E-01	-0.766	0.050	3.8E-10	Rhbdf1	ENSRNOG000000020594	10	15,672,382
14158	A_44_P1011918	2.707	0.084	5.4E-13	0.114	0.091	2.4E-01	no transcript	ENSRNOG000000042833	10	91,661,558
28777	A_64_P028270	0.046	0.081	5.8E-01	1.932	0.076	4.5E-13	Mettl2	ENSRNOG000000006131	10	93,354,003
7468	A_64_P024395	0.179	0.117	1.5E-01	2.841	0.110	3.7E-13	LOC681544	ENSRNOG000000001809	11	81,639,952
5272	A_64_P038050	1.060	0.079	2.4E-09	-0.055	0.075	4.8E-01	Acyp2	ENSRNOG000000042419	14	115,052,450
7829	A_44_P107634	-0.147	0.086	1.1E-01	-1.263	0.081	3.0E-10	Haus4	ENSRNOG000000039284	15	33,193,537
11203	A_64_P139544	-0.273	0.129	5.2E-02	-1.888	0.121	3.2E-10	Scara3	ENSRNOG000000016177	15	42,638,392
15751	A_44_P531870	0.256	0.122	5.5E-02	-3.952	0.115	7.2E-15	Ephx2	ENSRNOG000000017286	15	42,794,279
26808	A_64_P110009	-0.035	0.055	5.4E-01	-0.639	0.052	6.9E-09	Hsd17b4	ENSRNOG000000015840	18	44,810,388
18168	A_44_P213175	0.029	0.088	7.5E-01	-0.998	0.083	9.4E-09	Ccdc68	ENSRNOG000000021381	18	68,408,890
14753	A_64_P023365	-1.415	0.087	1.9E-10	-0.083	0.082	3.3E-01	Abcb10	ENSRNOG000000017993	19	56,772,904
14301	A_43_P16020	0.118	0.231	6.2E-01	3.684	0.212	8.8E-09		ENSRNOG000000031780	MT	1
20800	A_44_P545895	-0.132	0.096	1.9E-01	1.675	0.091	3.4E-11		ENSRNOG000000031780	MT	1
10896	A_44_P140429	-0.085	0.101	4.2E-01	-1.243	0.095	3.3E-09	Asb9	ENSRNOG000000003452	X	31,759,161
9010	A_64_P012759	-0.888	0.066	2.2E-09	-0.062	0.062	3.4E-01	Fhit	N/A	15	15,697,292

Genes are regarded as significant for "non-shared" differential expression when they show $P < 1 \times 10^{-8}$ in one comparison but not in the other ($P \geq 0.05$ with a concordant direction or all P -values in the opposite direction).

Table S3J. A list of significant transcripts for non-shared differential expression in the liver.

no	ProbeName	SHR/lzm (vs WKY/lzm)			SHRSP/lzm (vs WKY/lzm)			GeneName	Ensembl_rat	Chr	Transcription_ start_site (Rnor_6.0)
		Fold change (log2-scale)	SE (log2-scale)	P-value	Fold change (log2-scale)	SE (log2-scale)	P-value				
28738	A_64_P053124	-2.258	0.122	1.6E-10	-0.175	0.122	1.8E-01	LOC690948	ENSRNOG000000058538	1	63,964,155
16474	A_64_P068858	0.193	0.101	7.9E-02	2.459	0.101	5.0E-12	Rps16	ENSRNOG000000019578	1	85,408,444
17305	A_64_P002924	-1.299	0.086	1.7E-09	0.173	0.086	6.5E-02	Asrgl1	ENSRNOG000000020202	1	225,329,770
12403	A_44_P398033	0.131	0.083	1.4E-01	2.949	0.083	4.9E-14	Prnp	ENSRNOG000000021259	3	124,515,978
17113	A_64_P139590	0.151	0.085	9.9E-02	4.147	0.085	8.3E-16	Slc35c2	ENSRNOG000000018649	3	161,812,291
21898	A_64_P153502	0.152	0.110	1.9E-01	1.593	0.110	2.9E-09	Armc9	ENSRNOG000000025418	9	93,172,673
26992	A_42_P826202	0.152	0.110	2.0E-01	2.439	0.110	3.0E-10	Znf597	ENSRNOG000000007576	10	11,912,543
28777	A_64_P028270	-0.206	0.156	2.1E-01	2.826	0.156	1.9E-10	Mettl2	ENSRNOG000000006131	10	93,354,003
24567	A_43_P17925	0.017	0.122	8.9E-01	-1.651	0.122	6.4E-09	Abca8	ENSRNOG000000004040	10	98,294,522
20334	A_44_P368461	0.109	0.127	4.1E-01	-2.465	0.127	8.8E-11	Cpn2	ENSRNOG000000024384	11	74,057,361
11763	A_64_P031741	0.116	0.097	2.5E-01	-1.287	0.097	8.7E-09		ENSRNOG000000031780	MT	1
24540	A_64_P050969	-0.036	0.119	7.7E-01	-2.152	0.119	2.0E-10		ENSRNOG000000031780	MT	1

Genes are regarded as significant for “non-shared” differential expression when they show $P < 1 \times 10^{-8}$ in one comparison but not in the other ($P \geq 0.05$ with a concordant direction or all P-values in the opposite direction).

Table S4A. A list of significant genes for shared differential expression in any of target tissues on RNO1.

Gene	Agilent probe	Pos. on RNO1 (Rnor_6.0)	D/E	Heart		D/E	Aorta		D/E	Renal cortex		D/E	Kidney		D/E	Liver	
				SHR log2(FC)	SHRSP log2(FC)		SHR log2(FC)	SHRSP log2(FC)		SHR log2(FC)	SHRSP log2(FC)		SHR log2(FC)	SHRSP log2(FC)		SHR log2(FC)	SHRSP log2(FC)
Lrp11	A_44_P973511	1,702,696	●	<u>-1.10</u>	<u>-1.37</u>		-0.22	0.03		-0.26	-0.18		-0.09	-0.19	●	<u>-1.10</u>	<u>-1.37</u>
Samd5	A_64_P063358	3,763,392		N/A	N/A		N/A	N/A	●	<u>1.03</u>	<u>1.52</u>		<u>1.04</u>	<u>1.59</u>		N/A	N/A
Shprh	A_44_P1025861	5,240,180		0.24	0.03	○	0.53	0.72	●	<u>0.69</u>	<u>0.72</u>		<u>0.63</u>	0.41		0.01	0.20
Epm2a	A_44_P452186	5,448,958		0.27	0.12	●	<u>1.47</u>	<u>1.40</u>		-0.33	0.21		-0.06	-0.17		0.02	-0.26
Stx11	A_44_P101700	7,064,870	●	<u>0.60</u>	<u>0.37</u>		0.57	0.99		N/A	N/A		N/A	N/A		N/A	N/A
Arfgef3 (RGD1309903)	A_64_P165046	13,915,594		N/A	N/A		0.30	0.56	●	<u>-0.56</u>	<u>-0.52</u>		-0.02	-0.07		0.10	0.15
Pex7	A_44_P445359	15,374,850	●	<u>0.65</u>	<u>0.47</u>	●	0.24	<u>0.59</u>		0.11	0.15		0.09	0.34	○	0.45	0.53
Map3k5 (RGD1306565)	A_64_P129293	15,412,603	●	<u>1.42</u>	<u>1.47</u>	●	<u>2.18</u>	<u>1.71</u>	●	<u>1.27</u>	<u>1.25</u>		<u>1.42</u>	<u>1.85</u>	○	1.79	1.74
Aldh8a1	A_44_P128306	16,910,069		N/A	N/A		N/A	N/A	●	<u>0.37</u>	<u>0.53</u>		<u>0.45</u>	<u>0.58</u>	●	<u>0.82</u>	<u>0.89</u>
Ptpkr	A_43_P23129	18,058,055	●	<u>-0.33</u>	<u>-0.45</u>	●	<u>-0.68</u>	<u>-0.83</u>	○	-0.29	-0.31		-0.16	-0.23		-0.23	0.01
Enpp1	A_43_P12841	21,748,261	●	<u>0.50</u>	<u>0.25</u>	●	0.40	<u>0.71</u>		-0.09	0.09		0.02	0.17	○	0.32	0.56
Ctgf (Ccn2)	A_42_P484738	21,854,773	●	<u>1.00</u>	<u>1.28</u>	●	<u>1.44</u>	<u>2.61</u>	●	0.67	0.57		0.45	<u>1.09</u>		-0.71	0.37
Slc18b1 (RGD1306962)	A_44_P353836	22,748,422		-0.71	<u>-0.95</u>		-0.67	-0.03	●	<u>-0.81</u>	<u>-0.64</u>		<u>-0.85</u>	-0.73		-0.24	-0.05
Slc12a7	A_64_P121575	32,140,137		-0.01	0.27	●	<u>-1.03</u>	<u>-0.57</u>		-0.10	-0.15		-0.06	0.12		-0.06	-0.11
Slc6a19	A_64_P139942	32,199,810		N/A	N/A	●	<u>-1.44</u>	<u>-1.33</u>		0.15	-0.02		0.14	0.01		N/A	N/A
Srd5a1	A_44_P182431	36,320,461		-0.36	0.12	●	-0.42	<u>-1.33</u>		<u>0.81</u>	0.01		-0.03	-0.14	●	<u>-2.25</u>	<u>-2.88</u>
Sod2	A_64_P110103	47,921,587		0.05	-0.06	●	<u>-0.41</u>	<u>-0.58</u>		0.04	0.11		0.09	0.16		0.08	0.27
LOC684270	A_64_P119169	72,509,431	●	<u>-0.33</u>	<u>-0.34</u>		0.48	0.00		0.01	0.03		-0.05	-0.02		0.11	0.12
Tnnt1	A_64_P058871	72,889,278	●	<u>0.52</u>	<u>0.42</u>		-1.70	0.34		-0.53	0.25		-0.59	0.69		-0.46	0.17
AABR07002623.1	A_64_P162940	77,782,825		N/A	N/A		N/A	N/A	●	<u>-1.80</u>	<u>-1.38</u>		<u>-1.83</u>	-0.77		0.29	-0.34
Tmem160	A_64_P107642	78,417,719		0.20	0.14	●	<u>-0.41</u>	<u>-0.62</u>	○	-0.22	-0.15		-0.29	-0.06		0.20	0.22
Bloc1s3	A_64_P042455	80,416,273		0.18	0.09	●	<u>-0.57</u>	<u>-0.70</u>		-0.02	-0.04		-0.27	0.12		0.06	0.08
Apoc2	A_42_P689905	80,594,136		-0.03	-0.20		3.14	-0.17	●	<u>1.58</u>	<u>2.16</u>		<u>1.27</u>	<u>1.63</u>		-0.11	-0.33
LOC100359930	A_64_P164736	82,653,633		N/A	N/A		N/A	N/A		N/A	N/A		N/A	N/A	●	<u>1.40</u>	<u>1.92</u>
Snrpa	A_42_P641234	84,008,293		-0.30	0.26	●	<u>-0.63</u>	<u>-0.54</u>		-0.07	-0.23		-0.32	-0.17		-0.10	-0.08
Itpkc	A_44_P156211	84,040,433	●	<u>0.50</u>	<u>0.33</u>		-0.03	0.44		0.01	-0.01		-0.11	0.29	○	0.49	0.38
Sptbn4	A_64_P125676	84,254,645		0.35	0.01	●	<u>-1.11</u>	<u>-1.48</u>		0.68	-0.53		0.29	0.14		N/A	N/A
Dyrk1b	A_64_P131903	85,112,247		-0.31	0.01	●	<u>-0.67</u>	<u>-0.56</u>		-0.33	-0.26		-0.24	0.02		-0.24	-0.01
Eid2	A_42_P554610	85,517,360	○	-0.26	<u>-0.38</u>	●	<u>-0.74</u>	<u>-1.12</u>		-0.16	0.06		-0.20	0.07		-0.23	-0.31
Fbxo17	A_64_P027503	86,914,137	●	<u>0.88</u>	<u>0.47</u>		0.09	0.01		0.16	0.25		0.06	-0.25		0.41	0.09
Yif1b	A_64_P079807	87,180,624		-0.36	0.01	●	<u>-0.43</u>	<u>-0.50</u>		-0.22	0.00		-0.27	-0.12		0.32	-0.02
Tmem149	A_64_P063428	89,020,341		0.27	-0.18	●	<u>-1.03</u>	<u>-1.32</u>		-0.23	0.10		-0.27	0.32		-0.04	-0.34
LOC688869	A_64_P078982	89,084,859		0.04	0.03	●	<u>-0.66</u>	<u>-1.19</u>		0.003	0.09		-0.25	-0.22		0.16	-0.03

Atp4a	A_64_P129593	89,162,639		0.02	0.10		-0.16	0.26		-0.06	-0.10	0.09	-0.09	●	<u>-1.57</u>	<u>-1.59</u>
Lsr	A_64_P060303	89,399,041		<u>-0.59</u>	0.04	●	<u>-0.75</u>	<u>-1.10</u>	○	-0.15	-0.20	-0.28	0.16	○	-0.36	-0.24
Lgi4	A_44_P1018090	89,491,654	●	<u>0.44</u>	<u>0.42</u>	●	0.31	<u>0.83</u>		N/A	N/A	N/A	N/A		N/A	N/A
LOC365238	A_44_P449994	94,784,451	●	<u>0.98</u>	<u>0.80</u>	●	0.26	<u>0.74</u>	○	0.54	0.72	-0.02	0.51		0.35	0.13
LOC499136	A_44_P515321	97,785,490		-0.22	0.11	●	<u>-0.52</u>	<u>-0.56</u>		-0.14	-0.09	-0.35	0.05		0.25	-0.09
Lim2	A_64_P148550	98,501,249	●	<u>0.60</u>	<u>0.73</u>	●	<u>-1.31</u>	<u>-2.26</u>		N/A	N/A	N/A	N/A		N/A	N/A
LOC102556967	A_64_P080941	99,505,677	●	<u>-1.55</u>	<u>-1.66</u>		-1.07	-0.24	●	<u>-1.20</u>	<u>-0.96</u>	<u>-1.27</u>	<u>-1.46</u>	●	-0.90	<u>-1.19</u>
Klk1c10	A_44_P280954	99,894,353		N/A	N/A		N/A	N/A	●	<u>-1.03</u>	<u>-1.44</u>	<u>-1.18</u>	N/A		N/A	N/A
Klks3	A_44_P163243	100,059,967		N/A	N/A		N/A	N/A	●	<u>-1.41</u>	<u>-2.71</u>	<u>-1.60</u>	<u>-2.09</u>		N/A	N/A
(Klk4_low expression)	A_44_P989658	100,205,147		0.42	-0.04		-0.04	0.26	●	<u>1.26</u>	<u>1.12</u>	<u>0.76</u>	0.96	●	<u>2.85</u>	<u>2.00</u>
Lin7b	A_44_P215157	101,360,971		-0.24	-0.01	●	<u>-1.31</u>	<u>-2.12</u>		N/A	N/A	<u>-0.60</u>	N/A		N/A	N/A
Bcat2	A_64_P166076	101,554,642		-0.19	-0.18	●	<u>1.47</u>	<u>0.93</u>		0.05	0.26	-0.08	0.31		0.26	0.65
Dbp	A_64_P017188	101,687,855	●	<u>-1.48</u>	<u>-0.95</u>		1.65	0.65		<u>-1.16</u>	0.13	-0.39	-0.45		-0.54	-0.32
Sphk2	A_44_P466271	101,697,277	●	<u>0.42</u>	<u>0.21</u>		-0.41	0.04		0.12	-0.14	-0.09	0.04		-0.24	-0.07
Ldha	A_64_P016403	102,900,286		0.005	<u>-0.001</u>	●	<u>-0.72</u>	<u>-1.07</u>	●	<u>0.68</u>	<u>0.32</u>	<u>0.30</u>	0.28		-0.33	-0.59
Tmem86a	A_43_P11305	103,172,987	○	-0.53	-0.26		0.41	<u>-1.25</u>	●	<u>-1.94</u>	<u>-0.94</u>	<u>-0.88</u>	-0.62		0.11	0.15
Ptpn5	A_42_P506076	103,256,823	●	<u>1.28</u>	<u>0.67</u>		N/A	N/A	●	0.50	N/A	<u>1.33</u>	1.42		N/A	N/A
Zdhhc13	A_44_P250476	104,106,245		0.21	0.30		-0.14	0.14	●	<u>-0.93</u>	<u>-0.71</u>	<u>-1.05</u>	-1.02		-0.05	0.04
Csrp3	A_44_P997843	104,157,855	●	<u>0.61</u>	<u>0.62</u>		0.71	0.05		N/A	N/A	N/A	N/A		N/A	N/A
Prmt3	A_44_P536125	105,113,595	●	<u>0.84</u>	<u>0.41</u>		0.01	0.51		0.09	0.15	-0.06	0.24		N/A	N/A
Fancf	A_64_P151448	107,232,305	●	<u>-0.71</u>	<u>-0.59</u>		<u>-0.98</u>	-0.06	●	<u>-0.97</u>	<u>-0.74</u>	<u>-1.08</u>	-0.60	●	<u>-0.96</u>	<u>-0.91</u>
Bex1	A_42_P602570	116,567,189	●	<u>2.25</u>	<u>0.88</u>		0.89	0.99	●	<u>0.61</u>	0.27	0.37	0.40		-0.28	-0.20
Aldh1a3	A_44_P273783	127,337,882		N/A	N/A		0.07	0.71	●	<u>-0.77</u>	<u>-0.88</u>	<u>-0.60</u>	-0.54		N/A	N/A
Slco3a1	A_44_P496255	136,073,540		0.22	<u>0.31</u>		0.30	<u>1.13</u>	●	<u>0.58</u>	<u>0.51</u>	0.52	0.51		N/A	N/A
Ntrk3	A_64_P035162	140,262,503		0.48	0.37		0.62	-0.01	●	<u>1.08</u>	<u>1.22</u>	0.90	<u>1.90</u>		N/A	N/A
Mrps11	A_44_P1046705	140,477,868		-0.18	0.14	●	<u>-0.59</u>	<u>-0.84</u>		-0.01	0.09	-0.30	0.01		0.03	-0.05
Sema4b	A_64_P133177	141,986,145	●	<u>-0.68</u>	<u>-1.15</u>	●	<u>-0.88</u>	-0.46	●	<u>-0.80</u>	<u>-0.68</u>	<u>-0.91</u>	<u>-1.13</u>	●	<u>-0.72</u>	<u>-1.01</u>
Ngrn	A_43_P10751	142,050,458	●	<u>0.47</u>	<u>0.29</u>		-0.17	0.53		-0.19	-0.04	-0.27	0.09	○	-0.38	-0.39
Hddc3	A_42_P528580	142,136,452	●	<u>-0.34</u>	<u>-0.30</u>	●	-0.22	<u>-0.78</u>	○	0.05	-0.02	-0.15	-0.21		-0.30	-0.43
Nmb	A_64_P109232	142,724,511	●	-0.47	<u>-0.75</u>		<u>1.25</u>	0.89	●	<u>-2.31</u>	<u>-2.12</u>	<u>-2.13</u>	<u>-2.70</u>		0.41	0.34
Homer2	A_64_P016059	143,535,583	●	<u>-1.15</u>	<u>-0.58</u>	●	<u>-1.62</u>	<u>-1.54</u>	●	<u>-1.18</u>	<u>-1.09</u>	<u>-0.78</u>	-0.59		-0.22	-0.13
Eftud1	A_64_P045536	144,601,410	●	<u>-0.37</u>	<u>-0.34</u>		-0.08	-0.06	○	-0.32	-0.18	-0.19	-0.36		-0.05	0.15
Cyp2c7	A_64_P000452	147,435,897		N/A	N/A		N/A	N/A		N/A	N/A	N/A	N/A	●	<u>-0.74</u>	<u>-0.66</u>
Nox4	A_44_P154040	150,797,084		N/A	N/A	○	1.33	1.01		-0.37	-0.10	-0.15	-0.20	●	<u>2.09</u>	<u>1.55</u>
Prss23	A_42_P628981	153,752,541	●	<u>0.54</u>	<u>0.81</u>		0.43	<u>1.56</u>		-0.02	-0.01	-0.09	-0.08		0.02	0.16
Aamdc (RGD1561459)	A_64_P084767	162,533,893	○	-0.26	-0.13	●	<u>-0.56</u>	<u>-0.45</u>		-0.06	0.04	-0.27	-0.09		0.27	0.10
Dgat2	A_42_P733209	164,143,818	●	<u>-0.66</u>	<u>-0.38</u>		0.48	0.58		0.22	0.14	-0.08	0.30		-0.02	0.09
Ucp2	A_44_P301608	165,506,361	●	<u>0.72</u>	<u>1.13</u>	○	0.77	0.77		0.08	0.31	-0.14	0.28		0.24	0.58

Mrpl48	A_43_P14847	165,606,375	●	<u>-0.54</u>	<u>-0.35</u>		0.01	-0.30	○	-0.12	-0.12	-0.19	0.05	-0.03	0.03	
Plekhh1	A_64_P028140	165,680,206		0.08	<u>0.22</u>	●	<u>0.86</u>	<u>0.60</u>	●	<u>-0.66</u>	<u>-0.73</u>	<u>-0.68</u>	-0.57	0.23	-0.30	
Fam168a (RGD1308929)	A_44_P975945	165,724,451	●	0.56	<u>0.58</u>	○	0.42	0.70	●	0.34	<u>0.56</u>	0.39	0.71	●	<u>1.13</u>	<u>1.24</u>
P2ry2	A_44_P520159	166,037,424	●	<u>-0.51</u>	<u>-0.38</u>	○	0.46	0.63	●	<u>-0.68</u>	<u>-0.67</u>	-0.76	-0.12	●	-1.09	<u>-1.29</u>
Folr2	A_42_P788740	166,919,302		0.13	<u>0.62</u>		-0.29	0.61	●	<u>0.99</u>	<u>0.75</u>	<u>0.54</u>	<u>0.99</u>	○	0.42	0.55
Anapc15 (RGD1311634)	A_44_P177931	166,983,175		0.13	<u>0.40</u>	●	<u>-0.67</u>	<u>-0.62</u>		-0.07	0.10	-0.26	0.08		0.05	0.09
Lrrc51	A_43_P22401	167,005,839	●	<u>0.50</u>	<u>0.45</u>		0.18	0.27		0.02	0.26	-0.19	0.30	○	0.65	0.83
Art1	A_64_P162476	167,197,549	●	<u>-0.93</u>	<u>-1.28</u>		0.05	-0.21		N/A	N/A	N/A	N/A		N/A	N/A
Art5	A_64_P042586	167,202,767	●	<u>-0.95</u>	<u>-1.01</u>		-0.34	0.62		N/A	N/A	N/A	N/A		N/A	N/A
Olr59	A_64_P072633	167,911,961	●	<u>-0.54</u>	<u>-1.25</u>		-0.80	-0.59	○	-0.42	-0.34	0.25	-0.42		0.03	0.00
Olr200	A_64_P112431	170,147,300	●	<u>1.08</u>	<u>0.68</u>		1.02	0.28	○	0.57	0.77	0.29	0.66		N/A	N/A
Fam160a2	A_44_P398300	170,238,890	○	0.45	0.16		0.22	0.26	●	<u>0.50</u>	<u>0.42</u>	0.35	0.16		-0.25	-0.06
Dnhd1	A_64_P043101	170,471,272		-0.17	-0.39		0.47	<u>0.96</u>	○	-0.36	-0.49	-0.06	-0.18	●	<u>-0.83</u>	<u>-0.98</u>
Akip1 (RGD1306959)	A_42_P797965	174,330,695	●	<u>1.69</u>	<u>1.36</u>	●	0.55	<u>0.93</u>	○	0.23	0.24	0.13	0.35	●	<u>0.54</u>	<u>0.50</u>
Mrv1	A_64_P092754	175,796,040		N/A	N/A	●	<u>1.27</u>	<u>1.23</u>		N/A	N/A	N/A	N/A		N/A	N/A
Rras2	A_64_P086565	179,010,257	●	<u>0.62</u>	<u>0.64</u>	●	0.42	<u>0.71</u>	●	<u>0.37</u>	0.30	0.18	0.13		0.10	0.02
AcsM5	A_64_P151353	189,241,593		N/A	N/A	●	<u>1.13</u>	<u>0.78</u>	●	<u>1.89</u>	<u>2.03</u>	<u>1.76</u>	<u>2.15</u>	●	<u>3.03</u>	<u>3.70</u>
AcsM3	A_43_P15937	189,514,553		N/A	N/A		-0.05	0.60	●	0.31	<u>0.55</u>	<u>0.43</u>	<u>0.70</u>		0.25	0.31
LOC378467	A_42_P793598	189,870,622	●	<u>0.47</u>	<u>0.25</u>		-0.03	0.11		-0.09	-0.15	-0.20	0.03		-0.24	-0.52
Crym	A_43_P12996	189,960,073	●	<u>1.13</u>	<u>0.65</u>		-0.04	-0.11		0.22	0.10	0.14	-0.10	●	<u>0.82</u>	0.51
LOC691551	A_64_P019021	190,914,946	●	<u>2.22</u>	<u>1.19</u>	●	<u>0.95</u>	<u>1.11</u>		-0.30	0.32	-0.10	0.21		N/A	N/A
Jmjd5	A_42_P791460	196,839,321	●	<u>-0.34</u>	<u>-0.38</u>		-0.06	-0.17		0.09	0.08	-0.03	-0.03		-0.25	-0.09
Il4ra	A_64_P089531	196,942,364	●	<u>0.67</u>	<u>0.61</u>		0.27	-0.02		-0.49	-0.09	-0.50	0.25	○	0.66	0.55
Sbk1	A_64_P024138	197,659,187		-0.04	-0.03	●	<u>-6.08</u>	<u>-6.81</u>	●	<u>-0.58</u>	-0.30	-0.54	-0.17	●	<u>-1.46</u>	<u>-0.92</u>
Rabep2	A_44_P395538	197,839,430	●	<u>-0.83</u>	<u>-0.52</u>		-0.11	0.02	●	<u>-0.40</u>	<u>-0.29</u>	<u>-0.39</u>	-0.04		-0.20	-0.03
Eif3c	A_44_P321110	197,982,601	●	<u>-0.32</u>	<u>-0.29</u>	○	-0.24	-0.22		-0.12	-0.07	-0.13	-0.14		-0.27	0.05
Apob48r	A_44_P562972	197,999,037	●	<u>0.52</u>	<u>0.84</u>	○	0.38	0.42	○	0.61	0.57	0.55	0.98		0.31	0.49
Nupr1	A_42_P812008	198,045,154	●	<u>-0.96</u>	<u>-0.34</u>		-0.16	0.80	○	-0.89	-0.58	-0.38	0.29		-0.25	<u>-1.15</u>
Sult1a1	A_64_P011779	198,104,109		0.07	<u>-0.45</u>	●	0.79	<u>1.10</u>	●	<u>0.70</u>	<u>0.66</u>	0.41	0.59		0.15	0.13
Ino80e (Ccdc95)	A_44_P1002996	198,298,076	●	<u>-0.79</u>	<u>-0.87</u>	●	<u>-0.77</u>	-0.55	●	<u>-0.52</u>	<u>-0.53</u>	<u>-0.53</u>	-0.46	○	-0.30	-0.36
Mvp	A_44_P275029	198,450,047	●	<u>-0.37</u>	<u>-0.22</u>	●	<u>-1.29</u>	<u>-1.00</u>		0.13	-0.06	0.02	-0.24		-0.12	0.09
Pagr1 (RGD1305592)	A_44_P1029472	198,450,688	●	<u>-0.91</u>	<u>-0.43</u>	●	<u>-1.90</u>	<u>-1.37</u>	●	<u>-0.53</u>	<u>-0.36</u>	<u>-0.49</u>	-0.20		-0.05	0.05
Qprt	A_42_P505241	198,559,568	●	0.72	<u>0.79</u>	●	<u>2.11</u>	<u>1.30</u>		-0.07	0.05	-0.08	-0.20		0.01	-0.33
Mylpf	A_44_P1005462	198,655,742		-0.28	0.15		-1.01	-2.56	●	<u>1.46</u>	<u>1.09</u>	<u>1.21</u>	<u>1.33</u>		0.12	0.37
Dctpp1 (Xtp3tpa)	A_44_P285803	198,706,852		-0.16	0.02	●	<u>-0.66</u>	<u>-0.67</u>	●	-0.37	-0.14	<u>-0.50</u>	-0.37		-0.03	-0.23
Itgal	A_44_P452222	198,744,050		-0.02	<u>0.87</u>		0.47	0.88	●	0.80	0.53	<u>2.15</u>	<u>1.49</u>		-0.10	N/A

Znf688	A_44_P473234	198,869,009	●	<u>0.77</u>	<u>0.89</u>		-0.14	0.14		0.08	0.26	-0.12	0.18		0.14	0.26
Rnf40	A_64_P045578	199,037,544	●	<u>1.67</u>	<u>1.30</u>	●	<u>1.87</u>	<u>2.03</u>	●	<u>1.84</u>	<u>1.94</u>	<u>1.12</u>	<u>1.13</u>	●	<u>1.18</u>	<u>1.25</u>
Orai3	A_64_P019325	199,217,016	●	<u>0.93</u>	<u>0.79</u>		0.02	0.05		-0.19	-0.14	-0.22	-0.06		-0.08	-0.23
Bckdk	A_42_P834903	199,351,628		-0.11	0.13	●	<u>-1.01</u>	<u>-0.53</u>		-0.44	-0.05	-0.32	0.06		-0.62	-0.31
Fus	A_64_P056569	199,412,834		-0.11	<u>-0.44</u>		<u>0.41</u>	0.28		-0.07	-0.20	-0.02	-0.46	●	<u>-0.77</u>	<u>-0.78</u>
RGD1310127	A_64_P080856	199,716,205	●	<u>0.33</u>	<u>0.47</u>	●	0.30	<u>0.52</u>		0.07	0.13	0.19	0.19		0.16	0.05
Sec23ip	A_44_P252921	200,167,169	●	<u>-0.34</u>	<u>-0.38</u>		-0.31	-0.06	●	<u>-0.54</u>	<u>-0.50</u>	<u>-0.59</u>	-0.52	○	-0.53	-0.39
Htra1	A_42_P784614	201,499,028		-0.22	0.00		-0.07	<u>1.02</u>	●	<u>0.52</u>	<u>0.58</u>	<u>0.54</u>	<u>0.78</u>		0.20	-0.04
Cpxm2	A_42_P740370	204,087,001	●	<u>0.69</u>	<u>0.43</u>	○	0.83	0.85	●	-0.91	-0.70	-0.46	-0.26		N/A	N/A
Cyp2e1	A_44_P409232	213,511,874		0.60	-0.65	●	<u>3.46</u>	<u>1.56</u>	●	<u>1.35</u>	0.53	<u>0.98</u>	0.43		0.45	0.34
Scgb1c1	A_64_P036285	213,595,240		0.69	0.04	●	<u>-1.76</u>	<u>-1.42</u>		-0.32	-0.01	-0.44	-0.46		N/A	N/A
Chid1	A_64_P153870	214,511,529	●	<u>0.75</u>	<u>0.46</u>		-0.23	<u>-0.46</u>		0.41	0.09	0.22	0.20		<u>0.82</u>	0.16
Tnni2	A_42_P718022	215,609,036		1.15	0.43		0.79	-1.13		0.44	-0.03	-0.03	0.36	●	<u>1.32</u>	<u>1.32</u>
Fadd	A_64_P097784	217,748,628	●	<u>0.79</u>	<u>0.56</u>		-0.28	-0.04		<u>0.77</u>	0.22	0.34	0.41		N/A	N/A
Ano1 (Tmem16a)	A_42_P495579	217,844,957		0.27	-0.08	●	<u>0.86</u>	<u>1.41</u>		-0.30	-0.03	-0.50	0.02		-0.09	-0.02
Gal	A_42_P614175	218,657,925	●	<u>4.25</u>	<u>1.34</u>	●	<u>1.14</u>	<u>1.96</u>		-0.05	0.14	0.03	-0.03		N/A	N/A
Ndufs8	A_44_P132522	219,144,610		0.06	-0.07	●	<u>-0.74</u>	<u>-0.69</u>		-0.32	-0.12	-0.18	0.01		0.07	-0.15
LOC689065	A_64_P119314	219,745,654		-0.51	-0.04	●	<u>-1.69</u>	<u>-2.44</u>		-0.50	0.53	-0.51	0.98	●	<u>-3.23</u>	<u>-3.57</u>
Bbs1	A_44_P635869	220,165,678		0.37	0.01	●	<u>1.11</u>	<u>0.81</u>		0.40	-0.24	0.50	0.09		0.33	-0.08
Rab1b	A_64_P051802	220,491,469		-0.03	0.06	●	<u>-0.59</u>	<u>-0.41</u>		-0.19	-0.16	-0.14	0.09		-0.16	0.22
Cst6	A_64_P150876	220,729,000		<u>-0.89</u>	0.23	●	<u>-0.92</u>	<u>-1.98</u>		-0.38	0.12	-0.64	0.26		0.08	0.15
Ccdc85b	A_44_P367971	220,836,504	●	<u>-0.44</u>	<u>-0.29</u>		0.31	<u>0.48</u>		<u>-0.47</u>	-0.04	-0.38	0.19		-0.26	-0.17
Ctsw	A_44_P107596	220,848,153		N/A	-0.24		-0.60	-0.88	●	<u>-1.19</u>	<u>-1.27</u>	<u>-1.35</u>	-0.17		N/A	N/A
Sf1	A_64_P053322	221,735,517		0.25	0.01	●	<u>0.44</u>	<u>0.46</u>		-0.04	0.11	0.01	0.03		-0.02	-0.05
Esrra	A_42_P780882	222,178,725	●	-0.11	<u>-0.17</u>	●	<u>-0.47</u>	<u>-0.45</u>		0.15	0.03	0.14	0.03		-0.11	0.05
Ppp1r14b	A_64_P193845	222,229,835		0.13	<u>0.33</u>	●	<u>-0.57</u>	<u>-0.91</u>		0.09	0.02	-0.05	0.03		0.04	0.34
Slc22a9	A_64_P031501	222,975,509		N/A	N/A		N/A	N/A	●	-1.47	-0.65	<u>-0.91</u>	<u>-0.68</u>		N/A	N/A
AABR07006160.1	A_64_P029622	223,549,904	●	<u>-0.42</u>	<u>-0.40</u>		0.13	0.11	○	-0.14	-0.10	-0.20	-0.26		-0.34	-0.13
Ust5r	A_44_P228859	224,533,219		N/A	N/A		N/A	N/A		0.10	0.07	0.05	0.00	●	<u>0.93</u>	<u>0.84</u>
Bscl2	A_64_P128124	225,037,737	●	<u>-0.32</u>	-0.10	●	<u>-0.70</u>	<u>-0.91</u>	○	-0.07	0.02	-0.15	-0.29		-0.07	0.18
LOC690344	A_44_P944998	225,077,079		<u>-0.49</u>	0.04	●	<u>-0.75</u>	<u>-1.00</u>		0.01	0.04	-0.34	-0.07		0.28	0.20
B3gat3	A_44_P532027	225,120,061		-0.08	<u>0.21</u>	●	<u>-0.75</u>	<u>-0.68</u>		0.00	0.05	-0.18	0.06		0.06	0.12
Tut1	A_42_P651632	225,151,404		-0.06	-0.19	●	<u>0.68</u>	<u>1.10</u>		-0.15	-0.04	-0.07	0.02		0.00	0.02
Fads3	A_44_P1012567	226,091,774		0.00	0.20	●	0.73	<u>0.87</u>		0.17	-0.08	0.07	0.05	●	<u>2.49</u>	<u>1.82</u>
Dagla	A_64_P033447	226,353,611		-0.09	-0.33	●	<u>-0.87</u>	<u>-0.88</u>		0.18	<u>0.45</u>	0.01	0.11		N/A	N/A
Sdhaf2 (RGD1309216)	A_64_P155741	226,572,349	●	<u>-0.56</u>	<u>-0.19</u>		-0.40	-0.25		-0.12	0.05	<u>-0.33</u>	-0.11		-0.27	-0.01
Plac11 (Oosp2)	A_64_P073303	228,014,924		N/A	N/A		N/A	N/A	●	-1.02	<u>-1.68</u>	<u>-0.69</u>	<u>-1.96</u>		N/A	N/A
AABR07006542.1	A_64_P013243	239,319,737	○	-0.31	-0.17	○	-0.29	-0.49		-0.10	-0.02	0.00	-0.17	●	<u>-1.71</u>	<u>-1.85</u>

Aldh1a7	A_44_P335974	240,601,744		N/A	N/A	●	<u>1.54</u>	<u>1.39</u>		0.12	<u>1.04</u>	0.21	0.26		<u>-2.26</u>	-1.25
RGD1560242	A_64_P146165	241,460,868	●	<u>1.25</u>	<u>1.54</u>		N/A	N/A		N/A	N/A	N/A	N/A		N/A	N/A
Pgm5	A_64_P081982	242,765,807		-0.29	0.01		0.53	<u>1.84</u>	●	<u>-1.21</u>	<u>-0.95</u>	<u>-1.02</u>	-0.64		-0.61	-0.12
Kank1 (Ankrd15)	A_44_P315626	243,276,403	●	<u>0.45</u>	<u>0.26</u>	●	0.61	<u>1.21</u>		0.13	-0.07	0.12	0.21		-0.15	-0.11
Il33	A_44_P310596	248,132,090	●	<u>-0.71</u>	<u>-0.52</u>		-0.10	0.35	○	-0.43	-0.30	-0.37	-0.55	●	<u>-1.31</u>	-1.10
Ankrd1	A_44_P284753	254,735,548	●	<u>1.04</u>	<u>0.61</u>		-0.38	2.28		-0.11	-0.10	-0.14	0.33		N/A	N/A
Ppp1r3c	A_64_P071983	255,376,833	●	<u>0.66</u>	0.21		-0.19	<u>-1.33</u>	○	0.29	0.27	-0.25	-0.16	●	<u>1.44</u>	<u>1.53</u>
Hhex	A_43_P12437	256,101,903	●	<u>-0.60</u>	<u>-0.31</u>		0.24	-0.53		-0.15	0.23	-0.19	0.00		0.19	0.94
Cyp2c12	A_44_P139673	258,766,881		N/A	N/A		N/A	N/A		N/A	N/A	N/A	N/A	●	<u>-1.54</u>	<u>-2.91</u>
Rrp12 (LOC679127)	A_64_P082037	261,140,389	●	<u>0.47</u>	<u>0.28</u>		0.13	0.40		0.16	0.04	0.03	0.13		-0.10	0.24
Ankrd2	A_44_P262593	261,281,543	●	<u>2.50</u>	<u>1.91</u>	●	<u>-1.61</u>	<u>-1.75</u>		N/A	N/A	0.12	-0.20		N/A	N/A
Bloc1s2	A_42_P644278	263,920,962	●	<u>-0.88</u>	<u>-0.80</u>	●	<u>-1.15</u>	<u>-1.00</u>	●	-0.32	-0.32	<u>-0.49</u>	-0.50	○	-0.68	-0.75
Pkd2l1	A_64_P062648	263,959,318	●	N/A	N/A	●	<u>-1.17</u>	<u>-0.85</u>		N/A	N/A	-1.49	0.38		N/A	N/A
Ndufb8	A_42_P751152	264,303,762		-0.07	-0.09		0.03	-0.13	●	<u>-0.49</u>	-0.37	<u>-0.38</u>	<u>-0.38</u>		-0.20	-0.13
Kazald1	A_44_P480433	264,827,739	●	<u>-0.61</u>	-0.20		-0.78	0.22	●	<u>-1.53</u>	<u>-0.98</u>	<u>-1.34</u>	-0.61	○	-0.60	-0.76
Poll	A_64_P143725	265,298,797	●	0.23	<u>0.47</u>		0.06	0.03	●	0.22	<u>0.37</u>	0.12	0.59	●	<u>0.55</u>	<u>0.70</u>
Fbxw4	A_44_P325439	265,420,503	●	<u>0.49</u>	<u>0.37</u>		-0.36	0.21		-0.29	-0.34	-0.13	-0.10		-0.17	-0.09
Npm3	A_64_P129182	265,506,046		-0.02	<u>-0.75</u>	○	-1.17	-0.97	●	<u>-1.13</u>	<u>-0.80</u>	<u>-1.13</u>	-0.69		-0.24	0.18
Trim8	A_64_P017268	266,255,797		-0.24	-0.05	●	<u>-1.27</u>	<u>-1.33</u>	○	-0.66	-0.32	-0.58	-0.37		-0.20	-0.24
RGD1311783	A_42_P759043	266,451,021	●	<u>1.03</u>	<u>1.03</u>	○	-0.23	-0.37	○	-0.39	-0.31	-0.49	-0.34		-0.22	-0.34
LOC100364597	A_44_P995874	266,782,910	●	<u>0.37</u>	<u>0.37</u>		0.24	<u>0.67</u>		0.19	0.07	0.12	0.30		-0.15	0.11
Pdcd11	A_44_P990043	266,866,931	●	<u>0.58</u>	<u>0.40</u>	●	<u>0.71</u>	<u>1.01</u>	○	0.23	0.13	0.30	0.38		0.05	0.41
Obfc1	A_42_P462015	267,315,729	●	<u>-0.58</u>	<u>-0.24</u>		0.10	0.07	●	-0.25	-0.25	<u>-0.54</u>	-0.42		-0.11	-0.36
Sorcs1	A_64_P043941	270,472,866		-0.25	0.07		-0.17	0.07	●	<u>-1.75</u>	<u>-1.34</u>	<u>-1.46</u>	-1.51		N/A	N/A
Mxi1	A_64_P066276	274,030,978		0.17	-0.08		0.38	0.12	●	<u>-0.97</u>	<u>-0.75</u>	<u>-1.00</u>	-0.72		0.72	0.60
Dusp5	A_42_P739860	274,245,184	●	<u>0.66</u>	<u>1.42</u>	●	<u>2.76</u>	<u>1.91</u>	●	0.27	0.71	<u>0.92</u>	1.02		0.07	-0.24
Nrap	A_64_P026191	277,181,414	●	<u>0.58</u>	<u>0.29</u>		0.18	1.29		N/A	N/A	N/A	N/A		N/A	N/A
Casp7	A_44_P183488	277,190,964	●	<u>-0.48</u>	<u>-0.16</u>		0.09	0.28	●	<u>0.49</u>	<u>0.63</u>	0.39	0.54		0.08	0.13
Vwa2	A_64_P087184	277,689,729		0.34	0.08		0.11	-0.24	●	0.55	<u>0.99</u>	<u>0.70</u>	<u>0.76</u>		0.97	0.52
AABR07007032.1	A_44_P240330	277,867,630		-0.04	-0.13	●	<u>-0.72</u>	<u>-1.13</u>		0.08	0.08	0.03	-0.02		N/A	N/A
Trub1	A_44_P403005	278,311,244	●	<u>-0.77</u>	<u>-0.60</u>		-0.26	-0.08	●	<u>-0.74</u>	<u>-0.73</u>	<u>-0.88</u>	-0.88	○	-0.97	-0.81
Gfra1	A_44_P107308	279,277,339		-0.24	<u>-0.40</u>		-0.83	-0.35		-0.13	0.16	-0.28	-0.30	●	<u>2.14</u>	<u>2.09</u>

Fold changes (hypertensive strain vs WKY; log₂-transformed values) are shown in each cell. Significant values are underlined ($P < 1 \times 10^{-4}$) or in bold letter ($1 \times 10^{-4} \leq P < 0.05$).

Significant genes are initially selected for "shared" differential expression (D/E) when they show $P < 10^{-4}$ reproducibly in two types of inter-strain comparison, ie, SHRSP/lzm versus WKY/lzm and SHR/lzm versus WKY/lzm, with a concordant direction of D/E in a primary target tissue. Then, to validate D/E of the corresponding genes in tissues other than the primary one, we set suggestive and significant evidence for shared D/E. We consider it as suggestive (open circle in the column D/E) when both types of comparison show $P < 0.05$; we claim it to be significant (closed circle in the column D/E) when $P < 10^{-4}$ is further attained for at least one type of comparison (ie, $P < 0.05$ for the other type).

In some genes, the direction of differential expression is opposite to that in the primary tissue. Some genes are not included in the list when there is no appropriate transcript for the microarray probes annotated.

Table S4B. A list of significant genes for non-shared differential expression in any of target tissues on RNO1.

Gene	Agilent probe	Pos. on RNO1 (Rnor_6.0)	Heart			Renal cortex			Kidney		Liver			Aorta		
			D/E	SHR log2(FC)	SHRSP log2(FC)	D/E	SHR log2(FC)	SHRSP log2(FC)	SHR log2(FC)	SHRSP log2(FC)	D/E	SHR log2(FC)	SHRSP log2(FC)	D/E	SHR log2(FC)	SHRSP log2(FC)
Ust	A_64_P147549	2,627,747	●	-0.11	<u>-0.39</u>		0.18	0.17	-0.03	-0.01		0.17	-0.08		0.16	0.37
Fbxo30	A_42_P547213	5,366,379	●	0.13	<u>0.41</u>		0.10	0.10	0.00	0.04		0.15	0.30		0.64	0.30
Hbs1l	A_44_P255294	16,819,170	●	0.06	<u>0.26</u>		-0.21	-0.30	-0.28	-0.27		-0.04	-0.14		-0.19	0.34
Trdn	A_44_P191715	25,839,198	●	-0.18	<u>-0.68</u>		N/A	N/A	N/A	N/A		N/A	N/A		0.02	0.49
Irx1	A_64_P086235	33,910,912	●	0.28	<u>-0.67</u>		-0.20	-0.02	0.09	-0.14		-0.91	-0.73		-0.29	-0.46
Ube2ql1	A_64_P042302	36,185,916	●	-0.09	<u>-0.52</u>		0.12	0.59	0.09	-0.24		N/A	N/A		0.42	0.63
Afdn (Milt4)	A_44_P794669	53,802,658	●	0.09	<u>-0.33</u>		0.18	0.00	0.26	0.06		-0.08	0.01		0.02	-0.18
LOC690948	A_64_P053124	63,964,155		0.26	0.26		0.55	-0.06	0.20	0.08	●	<u>-2.26</u>	-0.18		-0.10	-0.30
Ndufa3	A_64_P150067	64,175,099		0.21	0.11		0.10	-0.09	0.08	0.00		0.39	0.18	●	-0.06	<u>-0.76</u>
Irf2bp1	A_64_P001475	79,899,155	●	-0.07	<u>-0.37</u>		-0.07	0.13	-0.19	0.18		0.13	0.22		0.04	0.07
Qpctl	A_42_P769597	80,056,574	●	-0.04	<u>-0.33</u>		-0.20	-0.22	-0.24	-0.09		0.11	-0.09		-0.07	0.00
Ppm1n (RGD1562091)	A_42_P773606	80,191,618	●	0.00	<u>0.72</u>		-0.03	0.12	-0.35	-0.02		-0.17	0.27		0.05	0.48
Trappc6a	A_64_P047432	80,417,310	●	-0.13	<u>1.13</u>	○	-0.20	0.50	-0.29	0.60		0.17	0.34	○	0.03	0.60
Gemin7	A_64_P010196	80,483,487	●	0.09	<u>0.70</u>	○	0.17	1.68	-0.02	1.66	○	-0.38	1.78	○	-0.09	1.23
Apoc4	A_64_P060497	80,599,572		N/A	0.10		N/A	N/A	0.24	N/A		0.05	-0.30	●	<u>6.10</u>	-0.34
Zfp61	A_44_P575055	81,144,024	●	0.05	<u>0.62</u>	○	-0.19	0.54	-0.20	0.75		0.10	0.49	○	0.05	1.31
Irgq	A_44_P897008	81,395,841	●	0.01	<u>-0.38</u>	○	-0.08	-0.33	0.06	-0.35	○	-0.14	-0.50		0.03	-0.12
Rps19	A_64_P003994	81,750,928	●	0.13	<u>0.32</u>		-0.02	-0.05	-0.12	0.20		0.05	-0.07		0.04	0.12
Megf8	A_44_P318448	82,185,034	●	0.17	<u>0.46</u>	○	-0.26	0.67	0.00	0.76		N/A	N/A	○	-0.10	0.82
Bckdha	A_43_P15665	82,452,281	●	0.04	<u>-0.60</u>		-0.22	0.13	-0.26	0.19		-0.18	0.04		0.22	0.02
Exosc5	A_44_P520943	82,452,469	●	-0.10	<u>-0.49</u>	○	-0.13	-0.15	-0.23	-0.16	○	0.08	-0.42	○	-0.17	-0.29
Coq8b (Adck4)	A_64_P034456	84,044,551	●	0.13	<u>0.50</u>		-0.25	-0.12	-0.20	0.07		-0.03	0.17		0.14	0.17
Blvrb	A_64_P086519	84,256,159	●	-0.07	<u>0.27</u>		-0.04	0.18	-0.20	-0.07		-0.05	0.19		-0.27	-0.61
Gmfg	A_64_P024297	85,317,968	●	-0.02	<u>0.49</u>		0.08	0.10	0.03	0.35		0.11	0.21		-0.02	0.29
Rps16	A_64_P068858	85,408,444	●	0.11	<u>2.88</u>	●	-0.07	<u>2.50</u>	-0.24	2.68	●	0.19	<u>2.46</u>	●	0.01	<u>2.50</u>
Eid2b	A_64_P133421	85,510,114	●	0.26	<u>-0.78</u>		-0.28	-0.36	-0.42	0.05		-0.12	-0.49		-0.44	-0.30
Nfkbib	A_44_P186860	86,948,845	●	0.07	<u>0.49</u>		-0.09	0.02	-0.19	0.23		0.02	0.28		-0.42	0.29
Fam98c (RGD1303117)	A_44_P997962	88,098,785	●	0.17	<u>-0.53</u>		-0.26	-0.74	-0.25	-0.43	○	-0.25	-0.72		-0.23	-0.18
Hcst	A_64_P126065	88,881,460	●	-0.04	<u>-0.71</u>		-0.21	-0.75	-0.55	-0.54	○	-0.21	-0.74	○	-0.11	-0.96

Fxyd5	A_64_P083600	89,474,252	●	0.18	<u>0.53</u>		-0.18	-0.07	-0.27	0.36	-0.17	-0.09	0.19	-0.26
Cebpg	A_64_P025098	91,296,656	●	0.09	<u>0.39</u>		-0.02	0.10	-0.12	-0.05	-0.52	-0.36	-0.05	0.15
Znf536	A_64_P006072	93,949,187	●	0.14	<u>-0.69</u>		0.09	-0.34	0.03	-0.69	N/A	N/A	0.47	0.58
Igf1r	A_44_P474037	128,924,966	●	0.25	<u>0.59</u>		0.02	0.10	0.21	0.44	N/A	N/A	○ 0.35	1.06
Mfge8	A_42_P497225	140,860,882	●	0.14	<u>0.43</u>		0.31	0.37	0.17	0.48	0.15	-0.03	○ 0.45	1.80
Prc1	A_42_P520891	142,087,208		-0.48	0.40	●	-1.05	-0.37	<u>-0.87</u>	-0.24	N/A	N/A	-1.06	1.05
Rab30	A_64_P131086	157,573,324	●	0.22	<u>0.61</u>		0.08	-0.04	-0.07	0.57	-0.70	-1.52	-0.20	0.20
Map6	A_44_P344181	164,225,934	●	0.18	<u>0.76</u>		0.23	0.33	-0.10	0.16	N/A	N/A	-0.04	0.47
Arntl	A_64_P117345	178,039,063	●	0.37	<u>1.10</u>		0.49	-0.17	-0.10	0.52	N/A	N/A	-1.29	-0.28
Vps35l (LOC361635)	A_64_P001922	188,448,478	●	0.11	<u>0.30</u>		-0.04	0.03	0.04	0.38	-0.07	-0.11	0.30	0.14
Il4ra	A_44_P337300	196,942,364	●	0.03	<u>0.43</u>		-0.47	-0.25	-0.52	-0.02	-0.31	-0.35	-0.21	0.18
Bcl7c	A_42_P495691	199,159,125	●	0.08	<u>0.35</u>		-0.16	-0.14	-0.17	0.01	0.16	0.15	-0.12	0.08
Ctbp2	A_64_P088990	205,030,567	●	-0.08	<u>-0.32</u>		-0.02	-0.09	0.05	0.04	-0.01	0.13	0.07	0.21
Clrn3	A_42_P495598	207,766,250		N/A	N/A	●	-1.41	-0.02	<u>-1.38</u>	-0.28	N/A	N/A	N/A	N/A
Mgmt	A_42_P837214	209,237,233	●	-0.27	<u>0.42</u>		0.04	0.70	-0.15	0.14	○ -0.24	0.57	-0.23	-0.12
Fuom (RGD1311186)	A_42_P696282	212,568,224		0.19	-0.23	●	0.76	0.03	<u>0.79</u>	-0.12	0.13	-0.68	● 0.00	<u>-1.14</u>
Cox8b	A_64_P036440	213,650,247		-0.06	-0.03		0.72	0.38	-1.67	-2.06	0.43	0.17	● -0.09	<u>-0.99</u>
Cd151	A_44_P271720	214,446,659	●	0.05	<u>0.35</u>		-0.26	-0.14	-0.32	-0.09	-0.39	-0.02	○ 0.00	0.74
Rhod	A_64_P066601	219,682,287	●	0.06	<u>-0.39</u>		-0.26	-0.04	-0.31	0.18	-0.54	-0.23	0.26	0.61
Gpr137	A_64_P087105	222,197,252	●	0.08	<u>0.42</u>		-0.23	-0.13	-0.30	-0.16	0.08	0.14	0.03	0.34
Plaat3 (Pla2g16)	A_64_P159519	222,844,144	●	0.29	<u>-0.29</u>	●	-0.62	-0.25	<u>-0.58</u>	-0.22	-0.77	-0.48	-0.01	-0.02
Asrgl1	A_64_P002924	225,329,770		-0.24	-0.01	●	-1.34	0.14	<u>-0.95</u>	-0.03	● <u>-1.30</u>	0.17	-0.71	0.54
Cybasc3	A_44_P896040	226,634,009	●	<u>-0.92</u>	0.18	●	<u>-1.20</u>	-0.03	<u>-1.06</u>	0.06	-0.74	0.10	○ -0.97	0.12
Tmem132a	A_64_P062545	226,924,244	●	-0.45	<u>0.63</u>		-0.15	-0.03	-0.06	0.39	0.44	0.47	○ 0.31	0.59
Ranbp6	A_42_P711568	247,985,497	●	-0.06	<u>-0.22</u>		0.04	0.11	-0.08	-0.02	-0.26	-0.18	0.07	0.26
Ch25h	A_44_P536613	252,808,380	●	0.54	<u>1.16</u>		-0.10	-0.21	0.20	0.81	-0.25	-0.10	1.46	0.04
Marchf5	A_44_P198112	255,842,783	●	0.10	<u>0.34</u>		-0.10	0.00	-0.19	0.18	0.15	0.25	-0.50	-0.81
Hoga1 (Dhdpsl)	A_64_P088575	261,291,870	●	0.31	<u>1.90</u>		-0.24	-0.11	-0.21	-0.20	-0.25	-0.14	-0.03	-0.40
Nolc1	A_43_P12332	265,829,108	●	-0.15	<u>-0.30</u>		-0.05	0.05	-0.01	0.02	-0.36	0.02	0.01	0.18
Nfkb2	A_42_P658264	266,053,002	●	0.12	<u>0.43</u>		0.01	-0.08	-0.05	0.13	0.31	0.21	0.00	0.37
Cuedc2	A_44_P1002173	266,086,299	●	-0.06	<u>0.48</u>		0.11	0.18	0.05	0.39	0.36	0.42	0.19	0.33
Rbm20	A_42_P473812	274,391,932	●	0.00	<u>0.49</u>		N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Fold changes (hypertensive strain vs WKY; log₂-transformed values) are shown in each cell. Significant values are underlined ($P < 1 \times 10^{-8}$) or in bold letter ($1 \times 10^{-8} \leq P < 1 \times 10^{-4}$).

Significant genes are initially selected for “non-shared” differential expression (D/E) when they show $P < 1 \times 10^{-8}$ in one type of inter-strain comparison but not in the other ($P \geq 0.05$ with a concordant direction or all P-values in the opposite direction). Then, to validate D/E of the corresponding genes in tissues other than the primary one, we set suggestive and significant evidence for non-shared D/E. We consider it as suggestive (open circle in the column D/E) when D/E show $P < 10^{-4}$, in the direction concordant with the primary tissue; we claim it to be significant (closed circle in the column D/E) when criteria for the primary tissue is satisfied in another tissue.

In some genes, the direction of differential expression is opposite to that in the primary tissue. Some genes are not included in the list when there is no appropriate transcript for the microarray probes annotated.

Table S5. A list of genes that are likely to be under cis-acting influences

Gene	Agilent probe	Chr	Pos. (Rnor_6.0)	Heart		Aorta		Whole kidney		Renal cortex		Liver	
				SHR	SHRSP	SHR	SHRSP	SHR	SHRSP	SHR	SHRSP	SHR	SHRSP
Map3k5	A_64_P129293	1	15,412,603	1E-09	4E-21	1E-09	2E-08	4E-08	2E-07	5E-05	3E-05	9E-04	0.001
Sema4b	A_64_P133177	1	141,986,145	4E-06	8E-20	4E-07	2E-04	9E-10	1E-08	2E-08	6E-08	6E-05	2E-06
Homer2	A_64_P016059	1	143,535,583	2E-17	3E-17	4E-10	2E-10	3E-08	3E-04	1E-09	2E-09	0.202	0.456
Acsn5	A_64_P151353	1	189,241,593	N/A	N/A	4E-08	1E-06	3E-16	9E-15	1E-14	2E-15	9E-12	7E-13
Pagr1	A_44_P1029472	1	198,450,688	2E-15	1E-14	2E-11	5E-10	6E-06	0.103	9E-07	4E-05	0.582	0.62
Rnf40	A_64_P045578	1	199,037,544	3E-13	3E-19	8E-12	4E-13	2E-07	3E-05	2E-05	6E-06	3E-07	1E-07
Gatad2b	A_42_P516658	2	189,655,702	2E-08	2E-06	1E-06	2E-08	7E-06	0.001	6E-08	5E-08	0.040	0.014
Tars2	A_64_P041307	2	197,878,142	3E-08	3E-20	6E-11	5E-12	6E-12	6E-10	1E-07	2E-07	1E-07	4E-07
Endog	A_44_P213133	3	8,741,766	1E-25	2E-35	7E-13	8E-15	5E-17	3E-14	6E-13	1E-13	1E-11	7E-12
Tor1b	A_43_P18366	3	9,792,899	2E-19	8E-31	7E-09	6E-12	3E-13	9E-12	2E-11	8E-12	4E-08	2E-07
Dusp19	A_44_P992697	3	67,849,966	2E-17	7E-24	3E-11	2E-12	3E-10	5E-06	5E-11	4E-10	6E-07	4E-08
Ptprj	A_43_P15275	3	79,390,956	8E-20	6E-24	3E-08	1E-07	1E-17	2E-13	3E-13	6E-14	3E-11	7E-11
RGD1309540	A_44_P107766	3	80,349,145	6E-12	4E-14	2E-04	1E-04	3E-10	5E-07	1E-09	6E-09	3E-07	4E-07
Accs	A_64_P115142	3	82,756,953	2E-08	3E-18	4E-07	2E-10	3E-09	7E-07	2E-05	3E-06	2E-04	0.002
Chchd5	A_64_P098527	3	121,660,110	5E-06	2E-08	2E-11	5E-13	9E-10	2E-04	4E-08	4E-07	0.397	0.113
Irf52	A_43_P18817	3	159,392,193	8E-09	3E-18	5E-08	3E-04	5E-09	6E-06	1E-07	2E-07	6E-05	1E-05
Pmepa1	A_64_P002904	3	171,342,646	6E-07	9E-17	0.392	0.001	2E-05	0.021	5E-05	3E-05	2E-05	7E-05
Polr3k	A_44_P307964	3	177,374,812	7E-10	6E-17	2E-08	7E-07	9E-09	5E-04	3E-08	7E-08	2E-06	8E-06
Tmem243	A_64_P016751	4	21,920,651	5E-11	3E-23	6E-08	7E-10	8E-11	2E-08	5E-09	2E-09	0.003	0.006
Mrps33	A_44_P489995	4	67,610,710	8E-11	8E-11	7E-09	3E-11	4E-06	0.001	6E-09	5E-09	0.001	9E-04
Inmt	A_43_P23115	4	85,386,231	N/A	N/A	4E-10	4E-09	1E-10	3E-11	3E-10	2E-12	3E-12	4E-11
Retsat	A_44_P402507	4	100,465,170	2E-23	3E-36	5E-09	9E-09	1E-12	4E-09	4E-08	4E-10	0.294	0.956
Ptgr1	A_42_P698240	5	76,129,441	3E-06	8E-19	3E-10	2E-11	2E-17	7E-15	4E-11	1E-11	8E-06	1E-05

Hdhd3	A_44_P175822	5	78,361,647	8E-04	0.103	7E-08	2E-06	5E-08	0.002	6E-06	2E-05	3E-06	5E-05
Hdhd3	A_64_P090543	5	78,361,647	0.012	0.024	3E-08	6E-09	4E-10	2E-06	2E-04	5E-04	5E-07	9E-06
Atp6v1g1	A_44_P1040796	5	79,367,663	6E-13	1E-22	3E-14	3E-15	1E-11	2E-10	1E-10	7E-12	5E-10	4E-10
Hpd1	A_44_P117119	5	135,677,432	8E-08	3E-09	0.114	0.479	3E-13	1E-15	1E-07	2E-11	NA	NA
Cldn19	A_64_P138415	5	138,300,107	3E-16	2E-23	3E-07	2E-09	2E-05	0.539	7E-05	1E-05	NA	NA
Pigv	A_44_P175875	5	151,895,016	4E-11	6E-15	0.001	5E-07	5E-09	4E-09	5E-07	9E-08	6E-06	8E-06
Slc30a3	A_64_P017363	6	26,642,783	1E-06	2E-14	2E-07	4E-08	0.954	0.453	0.098	0.839	2E-12	3E-10
Rab10	A_44_P413979	6	27,721,120	3E-10	6E-22	2E-05	4E-09	2E-10	2E-05	0.002	0.014	7E-06	2E-07
Cyp4f17	A_64_P099017	7	14,529,483	4E-14	2E-20	5E-09	1E-09	1E-17	2E-11	1E-07	2E-07	1E-07	3E-07
Zfp799	A_64_P255450	7	15,072,703	5E-11	1E-20	0.809	0.994	6E-07	0.005	4E-08	3E-06	4E-05	9E-05
Polr2f	A_43_P12557	7	120,380,544	8E-15	8E-26	4E-04	1E-06	6E-05	1E-05	1E-08	5E-09	2E-06	7E-06
Med17	A_44_P119527	8	13,526,025	1E-11	1E-24	1E-07	7E-08	1E-10	5E-09	5E-11	5E-11	5E-07	5E-07
Cep295	A_44_P100886	8	13,909,188	3E-05	2E-11	1E-07	7E-06	5E-08	2E-05	2E-07	1E-07	0.371	0.334
Mrpl4	A_44_P518434	8	22,021,213	3E-10	2E-19	1E-07	4E-08	5E-11	9E-09	2E-08	9E-08	2E-06	2E-06
Acaa1a	A_43_P11432	8	128,027,958	2E-08	7E-21	0.577	0.532	2E-07	2E-05	9E-04	3E-04	2E-06	3E-06
Itm2c	A_43_P10901	9	92,916,469	1E-19	8E-29	3E-08	9E-11	1E-12	4E-09	5E-09	2E-09	3E-09	8E-08
Epb41l3	A_44_P123492	9	117,538,009	2E-08	1E-23	3E-05	3E-05	6E-07	2E-05	5E-06	3E-07	2E-08	7E-08
Timd4	A_64_P027288	10	31,880,918	2E-06	9E-11	7E-04	0.001	1E-05	4E-05	N/A	N/A	6E-09	9E-10
RGD1559482	A_64_P157691	10	104,952,237	1E-07	7E-19	2E-08	4E-08	2E-06	0.497	0.232	N/A	1E-08	1E-09
Arl16	A_42_P539095	10	109,639,054	1E-07	2E-06	4E-10	1E-10	4E-10	8E-07	2E-08	6E-09	2E-05	2E-06
Dcxr	A_43_P13256	10	109,909,646	0.025	2E-08	3E-07	4E-07	3E-05	5E-06	0.003	2E-05	2E-05	5E-06
Wdr45l	A_44_P159569	10	110,555,629	1E-09	4E-20	0.006	8E-04	0.005	3E-05	8E-06	2E-06	2E-08	7E-08
Pigp	A_42_P554722	11	34,598,275	2E-11	3E-19	2E-05	1E-06	4E-08	4E-05	2E-05	4E-04	0.004	4E-05
Phldb2	A_42_P732251	11	57,404,196	3E-11	3E-23	3E-05	1E-05	4E-12	4E-10	4E-10	1E-10	6E-06	4E-04
Asmtl	A_42_P746109	12	18,531,990	9E-11	1E-16	2E-09	3E-08	1E-09	5E-06	4E-07	5E-07	0.004	0.009
Mcm7	A_64_P081501	12	19,314,016	5E-14	3E-30	9E-07	1E-08	9E-12	9E-13	7E-11	2E-11	3E-05	9E-08

Nxpe5	A_42_P540609	12	19,440,501	2E-10	3E-20	3E-08	2E-08	0.029	0.014	0.002	0.001	7E-05	7E-05
Ccdc92	A_44_P1030714	12	37,211,316	2E-19	1E-30	2E-08	3E-11	8E-09	2E-10	3E-10	1E-11	0.004	0.002
Snrnp35	A_64_P135202	12	37,538,403	5E-09	3E-21	2E-08	2E-08	2E-09	4E-05	3E-06	1E-05	0.001	2E-04
Rhof	A_44_P838992	12	38,880,377	0.003	6E-13	1E-09	2E-07	6E-07	2E-05	1E-05	7E-07	1E-07	1E-08
RGD1562310	A_44_P686406	12	43,940,798	8E-05	7E-05	3E-06	2E-06	0.039	4E-04	5E-04	1E-04	2E-07	4E-05
RGD1564614	A_44_P475444	13	56,958,549	1E-16	1E-23	6E-05	1E-05	6E-05	2E-05	5E-04	0.013	0.049	0.001
Cfh	A_42_P819656	13	57,080,549	5E-21	3E-27	2E-05	3E-06	4E-08	3E-05	2E-05	6E-05	0.575	0.013
Fmo3	A_44_P358194	13	80,862,963	2E-12	5E-22	4E-08	3E-09	5E-05	8E-04	0.498	0.003	1E-06	4E-07
Dpt	A_44_P180259	13	83,073,550	2E-10	3E-29	5E-04	4E-09	2E-14	2E-13	2E-10	3E-10	4E-05	5E-06
Tmco1	A_44_P1018997	13	85,465,792	2E-05	5E-13	1E-09	4E-06	6E-07	5E-05	1E-05	5E-07	0.033	2E-04
Pcp4l1	A_64_P005029	13	89,565,813	1E-09	3E-16	2E-05	1E-04	2E-05	0.182	5E-08	3E-07	2E-09	5E-08
Tatdn3	A_42_P803590	13	109,663,364	2E-19	4E-29	1E-10	7E-11	3E-10	1E-07	1E-10	3E-10	4E-09	3E-09
Ints7	A_42_P661065	13	110,257,571	5E-11	2E-19	7E-07	4E-08	4E-05	4E-06	8E-08	5E-09	0.004	5E-04
Ints7	A_64_P052464	13	110,257,571	3E-11	6E-16	4E-05	9E-07	2E-06	5E-06	5E-10	9E-11	NA	NA
Hsd17b11	A_44_P1043814	14	7,073,445	1E-05	4E-10	8E-06	1E-06	5E-08	5E-04	1E-06	1E-06	0.392	0.378
Gnpda2	A_44_P992306	14	62,646,110	2E-07	2E-05	0.002	1E-06	9E-04	0.544	2E-08	9E-09	7E-05	2E-05
Nt5dc2	A_64_P005043	16	7,212,488	2E-11	3E-19	6E-09	4E-08	0.045	5E-04	7E-05	3E-07	1E-08	6E-08
Ncoa4	A_64_P066923	16	8,302,950	3E-08	1E-14	5E-05	3E-07	4E-07	2E-07	8E-07	2E-08	2E-05	3E-04
Fam32a	A_42_P467381	16	19,308,842	2E-19	4E-26	4E-06	2E-09	2E-07	6E-07	5E-07	2E-06	5E-04	2E-04
Borcs8	A_64_P100904	16	21,029,134	5E-09	8E-18	4E-06	5E-09	2E-06	2E-04	4E-06	3E-05	1E-04	1E-05
Borcs8	A_64_P004531	16	21,029,134	9E-15	1E-22	2E-11	3E-13	2E-10	3E-06	5E-09	5E-08	1E-05	1E-06
Hpfl	A_44_P1036068	16	32,540,217	9E-08	3E-15	3E-07	4E-07	7E-07	0.007	7E-07	5E-07	0.011	0.102
Spcs3	A_64_P007462	16	40,050,734	1E-06	3E-20	0.012	0.011	8E-04	1E-04	4E-07	2E-08	2E-07	7E-07
Wwc2	A_64_P041016	16	47,368,768	2E-12	2E-20	2E-05	8E-10	1E-09	9E-08	7E-09	1E-09	1E-07	3E-06
Tti2	A_44_P1042163	16	64,745,207	4E-12	2E-26	0.005	1E-06	3E-07	4E-09	3E-09	9E-11	1E-06	2E-05
Isca1	A_64_P022751	17	5,281,727	1E-12	8E-19	3E-05	2E-05	5E-08	4E-04	4E-06	7E-07	9E-04	0.003

Riok1	A_64_P059262	17	27,451,832	1E-19	2E-29	5E-07	5E-10	3E-06	7E-07	2E-08	5E-09	5E-05	1E-05
Aldh5a1	A_64_P030919	17	42,133,076	1E-11	2E-20	7E-06	5E-08	5E-07	4E-04	5E-06	3E-06	2E-05	5E-05
Aldh5a1	A_64_P067678	17	42,133,076	5E-09	5E-15	2E-05	1E-07	3E-06	3E-04	7E-05	4E-05	4E-05	1E-04
Hist1h2bc	A_64_P130572	17	44,738,330	2E-05	3E-16	5E-10	8E-09	0.108	0.002	0.842	0.695	6E-06	7E-05
Impad1	A_64_P104454	17	90,218,013	1E-11	1E-14	2E-05	4E-06	2E-05	0.075	4E-06	5E-05	8E-06	1E-04
Chmp1b	A_64_P011719	18	62,923,620	6E-14	4E-23	1E-07	5E-07	6E-10	7E-07	1E-09	5E-08	2E-07	3E-06
Stard6	A_44_P419615	18	68,983,545	3E-09	2E-14	3E-08	1E-07	1E-10	5E-05	2E-07	5E-08	NA	NA
Pqlc1	A_64_P021320	18	76,770,012	6E-14	9E-24	0.083	0.006	1E-11	5E-10	9E-11	7E-11	7E-05	4E-05
Ces1d	A_64_P148413	19	15,033,108	3E-05	2E-19	2E-07	2E-09	5E-06	0.735	9E-04	7E-06	8E-09	8E-09
Mdc1	A_42_P627572	20	3,405,285	5E-10	4E-16	9E-09	9E-08	2E-11	4E-08	3E-12	7E-13	2E-08	9E-07
Pwp2	A_64_P146698	20	11,228,844	9E-08	5E-16	2E-07	8E-09	2E-06	4E-06	8E-09	2E-09	0.038	0.007
Gstt3	A_44_P1015203	20	13,817,795	2E-10	5E-14	1E-11	3E-13	5E-11	3E-06	2E-05	1E-07	4E-10	1E-11
	A_64_P326359	MT		2E-18	3E-24	5E-08	3E-11	1E-11	5E-08	1E-10	4E-12	1E-07	5E-07
	A_64_P042093	MT		1E-08	9E-22	3E-05	1E-07	1E-07	1E-09	0.324	0.013	0.002	4E-06
	A_64_P042811	MT		3E-08	2E-22	1E-08	2E-09	1E-17	3E-16	4E-12	2E-12	3E-10	2E-10
	A_64_P118308	MT		1E-06	8E-12	1E-09	6E-05	4E-12	5E-09	1E-10	3E-11	8E-08	7E-08
	A_64_P143154	MT		2E-07	1E-15	7E-05	7E-09	0.003	5E-04	2E-05	2E-07	7E-04	0.033
AABR07041140.1	A_64_P048852	X	120,313,696	1E-19	2E-28	2E-10	2E-10	1E-13	5E-09	7E-12	1E-12	5E-08	2E-07

Genes that demonstrate shared differential expression in ≥ 3 tissues are listed in the table.

For each cell, P -values are shown for the analysis of differential expression in each inter-strain comparison.

Fold change (FC; hypertensive strain vs WKY) is largely grouped into 3 classes: $|FC| \geq 4$ (dark blue or red), $4 > |FC| \geq 2$ (medium blue or red), and $2 > |FC|$ (light blue or red).

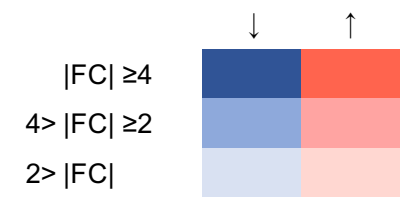


Table S6. A list of SSLP markers originally developed

Marker	Gene Symbol	Chr	Position (Rnor_6.0)		PCR product size (bp)			Forward primer (5'-to-3')	Reverse primer (5'-to-3')
			start	end	SHRSP	SHR	WKY		
D1Tkyo24	Igf1r	1	129,086,255	129,086,495	241	243	227	CTCTTGACTGTGGGTTGCTA	CGGAACCAGAAATCTGATCT
D1Tkyo26	Ntrk3_RFLP	1	139,943,456	139,943,630	135+40	135+40	96+79	AGAAGGTTGGCTCCAAC TAG	CAGATGCGATGATCCTTGTG
D1Tkyo27	Cib1	1	142,016,448	142,016,558	84	84	109	ACAGAAGGCATTCTTATGTAGGCC	CAGGAGGTCCAGGAAGTCCT
D1Tkyo32	Ctsc	1	151,919,661	151,919,851	175	180	171	GGAGAGACAGGGTTGGCATT	GCAGCTTCCCAATAAACCTGA
D1Tkyo44	Ctsd	1	215,558,920	215,559,126	192	210	192	CCAGCTCCCTATTTC	TGGTGCTCTGTGGGTCAAG
D1Tkyo49	Insl6	1	247,468,493	247,468,684	183	176	183	CTGGAGGGGTTGCGTTACCACT	TAGGGCAGGAGACTTTGTGCTCAG
D1Tkyo56	Scd (Scd1)	1	264,157,471	264,157,740	268	266	266	ACTGGTGCAGCTGGAAGGTCTCAT	GCAGACTTGTACCGCAGTT
D1Tkyo58	Add3	1	273,957,142	273,957,325	171	171	163	CATCGTCTTCAAACCGCATGG	CACAAACAAATGAGCGGGTAA
D2Tkyo1	Hmgcr	2	27,480,425	27,480,570	151	151	148	GCGGACGTCTGTGTAGAAGA	GAGGCGCAACTGAAACT
D2Tkyo2	Hmgcs1	2	52,424,108	52,424,275	172	172	157	TATAGCCAATTTTGTAGTGACTGAG	GGCAAGCATTAAATTACGTGAGAC
D2Tkyo6	Selenof (Sep15)	2	250,631,666	250,631,848	194	194	188	CCTCCAGGACAGCCAAGACTACC	TTCACCTCAGTCGCCAGA
D2Tkyo7	Bcl10	2	251,827,434	251,827,641	178	178	206	AACTCCAGGGAGGTGAGA ACTA	TGGAGTTTCTGTTGGTAGTAAGAA
D2Tkyo10	Uox	2	252,491,774	252,492,002	215	211	207	TCATACCCAGCACCGAACTC	ACATATCAATACATACACGGAGA
D2Tkyo12	Adgrl4 (Etl)	2	256,616,152	256,616,295	158	158	154	ACAAATGCTGCTGACCACTTA	ATAAAAGAGAGGGAAGTGAATAT
D2Tkyo13	St6galnac3 (Siat7c)	2	259,430,257	259,430,397	159	159	146	GGGACCTAGGCACAATCGAGTG	CGCTTCCATAGCTTGCTCAGTT
D3Tkyo4	Kynu	3	28,448,867	28,449,010	158	152	144	TATGCTCTTTTTTCTCACAGAAAC	TCCACCCTCATAATATGTTCTC
D3Tkyo9	Bfsp1	3	137,952,204	137,952,438	225	225	227	AAGACTATAGAGAGGCCATTAG	GTCAAGGGCTTCATCTAGG
D3Tkyo11	Tgm2	3	154,604,389	154,604,514	131	135	127	TGATAATGGTGATTGTACCTGAA	GGCCAAATGTTCTTTCTTAGTAT
D4Tkyo1	Tpra1 (Tpra40)	4	120,858,124	120,858,241	119	119	123	TAAGTACAGGGAGGGCTGCGTTGT	CCGCAGCAGCCTTCAAAGGTGTG
D4Tkyo2	Fmd4b (Grsp1)	4	129,769,006	129,769,143	135	135	131	GTGCTTACATCTGCGAACA	GGCATATGGTTACAATGAGTTATC
D4Tkyo8	Slc6a13	4	153,903,676	153,903,876	200	208	200	TGTAGCCCACTATATATCCAATA	GCCAACCTGGACTACATGAGTT
D8Tkyo1	Cnn1_Ecsit	8	23,095,882	23,096,123	212	212	216	TGCTGCTAGTCTGACAACC	ACTGTGTCTGGCTCAACTAGAG
D8Tkyo5	Gldn (Crgl2)	8	58,902,089	58,902,286	191	191	187	ATCTGTCTCAAATTTTCTCAGTA	TTGATTTTTAGAGCAGATATT
D8Tkyo9	Plod2	8	100,011,322	100,011,577	239	239	243	ACACTGTGGCACGGACCTA	GACCCAGTCAGCTGTCAGTACC
D8Tkyo10	Acaa1a (Acaa1)	8	128,032,912	128,033,050	131	131	137	GGTATGAGATCAATGCTGCC	GGTGCATTGGACATTGTAG
D9Tkyo4	Kcnq5	9	27,587,386	27,587,578	208	208	216	AGAAAGATATTTCCCGATTATCCTC	AACGTTCTTATGTACTAAGCCGCTC
D9Tkyo5	Rims1 (Rim1)	9	28,466,437	28,466,705	273	279	276	GAAACCTTGCCTCGAAA	CAGATGCCTCCTTCTCATACTG
D9Tkyo11	LOC102554599	9	79,270,504	79,270,660	158	158	174	CCTCCAAGAACATCAAAATGA	CGGGCTCATAGGAGTACACAG
D13Tkyo1	Bcl2	13	26,605,475	26,605,732	250	250	254	TCTCTGAAGACGCTGCTC	TTTGACCAATTTGCCTGAA
D15Tkyo3	Fhit	15	15,826,116	15,826,369	256	270	256	GGGCAGAAGGAGAGACTAACTA	GATGTCCACAAAACCTTAACCCTGAC
D15Tkyo6	Rabggta	15	34,385,010	34,385,188	178	178	176	CCATTTAATTCTCCCAACTACAC	GATATTGGCAAGGAAGTACC
D15Tkyo8	Clu	15	42,655,149	42,655,254	87	107	107	TCTGGGCAGGGTTAGAGATG	GAAGCTGGATTGGTTGCAT
D15Tkyo18	Ednrb	15	88,011,655	88,011,915	254	254	256	GCTTCTGACTCCCAATGAT	GATGCCCTACTCTGAACC

Table S7. A list of SSLP markers used for a speed-congenic approach to the development of consomic/congenic lines

Marker	Chr	Position (v6.0)	SHRSP-derived consomic/congenic lines								Marker	Chr	Position (v6.0)	SHR-derived consomic/congenic lines					
			RNO1	RNO3	RNO4	RNO7	RNO8	RNO9	RNO13	RNO15				RNO1	RNO2	RNO3	RNO4	RNO15	RNO19
D1Mgh2	1	23,406,428	W	P	P	P	P	P	P	P	D1Mgh2	1	23,406,428	W	S	S	S	S	S
D1Rat13	1	40,881,280	W	P	P	P	P	P	P	P	D1Rat125	1	51,412,813	W	S	S	S	S	S
D1Rat125	1	51,412,813	W	P	P	P	P	P	P	P	D1Rat316	1	72,887,924	W	S	S	S	S	S
D1Rat196	1	58,354,072	W								D1Rat27	1	94,201,400	W		S			
D1Mgh5	1	79,689,548	W	P	P	P	P	P	P	P	D1Wox18	1	100,133,276	W	S	S	S	S	S
D1Wox17	1	83,103,580	W								D1Tkyo24	1	129,086,255	W	S	S	S	S	S
D1Rat27	1	94,201,400	W								D1Rat200	1	133,076,978	W	S	S	S	S	S
D1Wox18	1	100,133,276	W	P	P	P	P	P	P	P	D1Rat36	1	135,022,396	W					
D1Wox29	1	130,779,148	W								D1Rat40	1	135,428,373	W	S	S	S	S	S
D1Rat269	1	132,448,117	W	P	P	P	P	P	P	P	D1Rat43	1	144,634,295	W	S	S	S	S	S
D1Rat43	1	144,634,295	W	P	P	P	P	P	P	P	D1Rat106	1	145,140,412	W					
D1Rat44	1	161,493,758	W	P	P	P	P	P	P	P	D1Tkyo32	1	151,919,661	W	S	S	S	S	S
D1Rat193	1	193,968,438	W								D1Rat44	1	161,493,758	W					
D1Wox19	1	197,963,658	W			P					D1Rat236	1	162,891,429	W					
D1Arb21	1	199,254,518	W	P	P	P	P	P	P	P	D1Wox33	1	168,126,089	W	S	S	S	S	S
D1Rat112	1	219,238,476	W	P	P	P	P	P	P	P	D1Rat132	1	172,789,146	W	S	S	S	S	S
D1Rat295	1	227,107,736	W								D1Rat164	1	177,235,071	W					
D1Rat71	1	230,420,627	W	P	P	P	P	P	P	P	D1Wox19	1	197,963,658	W	S	S	S	S	S
D1Wox10	1	236,763,415	W	P	P	P	P	P	P	P	D1Tkyo44	1	215,558,920	W	S	S	S	S	S
D1Tkyo49	1	247,468,493	W	P	P	P	P	P	P	P	D1Rat112	1	219,238,476	W	S	S	S	S	S
D1Tkyo56	1	264,157,471	W	P							D1Wox10	1	236,763,415	W	S	S	S	S	S
D1Mgh13	1	266,793,821	W	P	P	P	P	P	P	P	D1Tkyo49	1	247,468,493	W	S	S	S	S	S
D1Rat376	1	270,122,137	W								D1Mgh13	1	266,793,821	W	S	S	S	S	S
D1Rat122	1	278,048,619	W	P	P	P	P	P	P	P	D1Rat376	1	270,122,137	W					
D1Rat156	1	278,806,691	W	P	P	P	P	P	P	P	D1Rat122	1	278,048,619	W	S	S	S	S	S
D1Mit14	1	280,632,517	W	P	P	P	P	P	P	P	D1Rat156	1	278,806,691	W					
D1Rat90	1	281,795,624	W	P	P	P	P	P	P	P	D1Mit14	1	280,632,517	W	S	S	S	S	S
											D1Rat90	1	281,795,624	W	S	S	S	S	S
D2Rat3	2	8,579,280	P	P	P	P	P	P	P	P	D2Rat3	2	8,579,280	S	W	S	S	S	S
D2Tkyo1	2	27,480,425	P	P	P	P	P	P	P	P	D2Rat189	2	14,564,017		W				
D2Mgh2	2	40,171,834	P	P	P	P	P	P	P	P	D2Rat191	2	20,321,436		W				
D2Mit5	2	66,828,049	P	P	P	P	P	P	P	P	D2Rat124	2	26,186,097		W				
D2Wox6	2	115,783,552	P	P	P	P	P	P	P	P	D2Tkyo1	2	27,480,425	S	W	S	S	S	S
D2Mgh24	2	140,565,889	P	P	P	P	P	P	P	P	D2Mgh2	2	40,171,834	S	W	S	S	S	S

D2Rat97	2	174,210,477	P	P	P	P	P	P	P	P
D2Wox24	2	189,854,122	P	P	P	P	P	P	P	P
D2Mgh12	2	217,498,545	P	P	P	P	P	P	P	P
D2Tkyo6	2	250,631,666	P	P	P	P	P	P	P	P
D2Tkyo7	2	251,827,434	P	P	P	P	P	P	P	P
D2Mgh13	2	252,466,425	P	P	P	P	P	P	P	P
D2Tkyo10	2	252,491,774	P	P	P	P	P	P	P	P
D2Mit16	2	260,543,076	P	P	P	P	P	P	P	P

D3Mgh16	3	6,000,748	P	W	P	P	P	P	P	P
D3Mgh19	3	15,203,122	P	W	P	P	P	P	P	P
D3Mit9	3	34,394,121	P	W	P	P	P	P	P	P
D3Wox3	3	30,846,101	P	W	P	P	P	P	P	P
D3Rat80	3	36,599,933		W						
D3Rat186	3	45,228,240		W						
D3Rat227	3	45,406,058		W						
D3Rat110	3	47,155,167	P	W	P	P	P	P	P	P
D3Mgh6	3	54,630,948	P	W	P	P	P	P	P	P
D3Rat108	3	63,849,481		W						
D3Rat74	3	66,480,395		W						
D3Rat93	3	79,874,819		W						
D3Rat127	3	92,851,616		W						
D3Wox16	3	94,028,502	P	W	P	P	P	P	P	P

D2Tkyo2	2	52,424,108		W						
D2Mit5	2	66,828,049	S	W	S	S	S	S		
D2Rat21	2	75,687,495	S	W	S	S	S	S		
D2Rat122	2	98,545,920	S	W	S	S	S	S		
D2Rat160	2	113,358,300		W						
D2Wox6	2	115,783,552	S	W	S	S	S	S		
D2Rat171	2	116,075,644	S	W	S	S	S	S		
D2Mgh24	2	140,565,889	S	W	S	S	S	S		
D2Rat283	2	174,171,668	S	W	S	S	S	S		
D2Rat97	2	174,210,477		W			S			
D2Wox24	2	189,854,122	S	W	S	S	S	S		
D2Rat231	2	196,644,924		W						
D2Rat239	2	213,923,459	S	W	S	S	S	S		
D2Mgh12	2	217,498,545		W						
D2Rat241	2	224,954,385	S	W	S	S	S	S		
D2Rat59	2	228,582,621		W						
D2Rat88	2	228,984,526		W						
D2Tkyo6	2	250,631,666		W						
D2Tkyo7	2	251,827,434	S	W	S	S	S	S		
D2Tkyo10	2	252,491,774		W						
D2Tkyo12	2	256,616,152		W						
D2Rat106	2	257,446,379	S	W	S	S	S	S		
D2Tkyo13	2	259,430,257		W						
D2Mit16	2	260,543,076	S	W	S	S	S	S		
D3Mgh16	3	6,000,748	S	S	W	S	S	S		
D3Mgh19	3	15,203,122	S	S	W	S	S	S		
D3Tkyo4	3	28,448,867		S	W					
D3Mit9	3	34,394,121			W					
D3Wox3	3	30,846,101	S	S	W	S	S	S		
D3Rat80	3	36,599,933	S	S	W	S	S	S		
D3Rat110	3	47,155,167			W					
D3Mgh6	3	54,630,948	S	S	W	S	S	S		
D3Rat108	3	63,849,481			W					
D3Rat74	3	66,480,395		S	W					
D3Rat93	3	79,874,819	S	S	W	S	S	S		
D3Rat127	3	92,851,616	S	S	W	S	S	S		
D3Wox16	3	94,028,502			W					
D3Rat166	3	106,900,427			W					

D3Rat166	3	106,900,427		W						
D3Mit14	3	120,917,788	P	W	P	P	P	P	P	P
D3Mit13	3	120,917,851	P	W						
D3Mgh15	3	123,599,592		W						
D3Rat157	3	128,716,357		W						
D3Kyo3	3	129,787,213	P	W	P	P	P	P	P	P
D3Tkyo9	3	137,952,204	P	W	P	P	P	P	P	P
D3Rat148	3	146,426,801		W						
D3Mit2	3	148,348,517	P	W	P	P	P	P	P	P
D3Rat61	3	153,381,237		W						
D3Rat5	3	154,416,635		W						
D3Wox7	3	160,632,397	P	W	P	P	P	P	P	P
D3Rat1	3	176,417,943		W						
D4Wox27	4	3,044,017			W					
D4Rat4	4	4,364,715	P	P	W	P	P	P	P	P
D4Rat10	4	26,753,655	P	P	W	P	P	P	P	P
D4Rat11	4	34,379,764	P	P	W	P	P	P	P	P
D4Rat101	4	47,638,322			W					
D4Rat15	4	46,898,276			W					
D4Mit9	4	55,324,857	P	P	W	P	P	P	P	P
D4Wox24	4	70,773,499	P	P	W	P	P	P	P	P
D4Rat34	4	86,438,317	P	P	W	P	P	P	P	P
D4Rat41	4	97,758,884	P	P	W	P	P	P	P	P
D4Mgh17	4	113,100,978	P	P	W	P	P	P	P	P
D4Tkyo1	4	120,858,124			W					
D4Tkyo2	4	129,769,006			W					
D4Mgh7	4	136,351,734	P	P	W	P	P	P	P	P
D4Mgh8	4	145,254,666	P	P	W	P	P	P	P	P
D4Mgh11	4	168,046,938	P	P	W	P	P	P	P	P

D5Rat116	5	1,525,098	P	P	P	P	P	P	P	P
D5Mgh1	5	4,644,684	P	P	P	P	P	P	P	P
D5Mgh17	5	14,408,903	P	P	P	P	P	P	P	P
D5Rat190	5	24,382,492	P	P	P	P	P	P	P	P
D5Rat4	5	48,722,038	P	P	P	P	P	P	P	P
D5Mit10	5	56,902,367	P	P	P	P	P	P	P	P

F	D3Mit14	3	120,917,788	S	S	W	S	S	S
	D3Rat157	3	128,716,357	S	S	W	S	S	S
	D3Kyo3	3	129,787,213			W			
	D3Rat63	3	146,076,361			W			
	D3Rat148	3	146,426,801			W			
	D3Mit2	3	148,348,517	S	S	W	S	S	S
	D3Rat61	3	153,381,237			W			
	D3Rat6	3	153,412,455			W			
	D3Rat5	3	154,416,635	S	S	W	S	S	S
	D3Tkyo11	3	154,604,389		S	W			
	D3Wox7	3	160,632,397	S	S	W	S	S	S
	D3Rat1	3	176,417,943	S	S	W	S	S	S

D4Wox27	4	3,044,017	S	S	S	W	S	S
D4Rat4	4	4,364,715	S	S	S	W	S	S
D4Rat10	4	26,753,655	S	S	S	W	S	S
D4Rat11	4	34,379,764	S	S	S	W	S	S
D4Rat101	4	47,638,322				W		
D4Rat15	4	46,898,276	S	S	S	W	S	S
D4Rat122	4	64,915,651				W		
D4Wox24	4	70,773,499	S	S	S	W	S	S
D4Rat163	4	74,293,997				W		
D4Rat34	4	86,438,317	S	S	S	W	S	S
D4Rat41	4	97,758,884	S	S	S	W	S	S
D4Rat176	4	112,807,675				W		
D4Mgh17	4	113,100,978	S	S	S	W	S	S
D4Tkyo1	4	120,858,124				W		
D4Tkyo2	4	129,769,006				W		
D4Mgh7	4	136,351,734	S	S	S	W	S	S
D4Tkyo8	4	153,903,676	S	S	S	W	S	S
D4Mgh11	4	168,046,938	S	S	S	W	S	S

D5Rat116	5	1,525,098	\$	\$	\$	\$	\$	\$
D5Rat126	5	24,197,001	\$	\$	\$	\$	\$	\$
D5Rat4	5	48,722,038	\$	\$	\$	\$	\$	\$
D5Mit10	5	56,902,367	\$	\$	\$	\$	\$	\$
D5Mit1	5	57,148,431	\$	\$	\$	\$	\$	\$
D5Rat8	5	59,908,789	\$	\$	\$	\$	\$	\$

D5Mit1	5	57,148,431	P	P	P	P	P	P	P	P	D5Rat179	5	70,452,899	S	S	S	S	S	S
D5Rat179	5	70,452,899	P	P	P	P	P	P	P	P	D5Mgh11	5	76,608,035	S	S	S	S	S	S
D5Mit11	5	86,205,719	P	P	P	P	P	P	P	P	D5Mit11	5	86,205,719	S	S	S	S	S	S
D5Wox4	5	102,331,548	P	P	P	P	P	P	P	P	D5Rat24	5	105,106,199	S	S	S	S	S	S
D5Rat24	5	105,106,199	P	P	P	P	P	P	P	P	D5Mit13	5	136,640,731	S	S	S	S	S	S
D5Mit13	5	136,640,731	P	P	P	P	P	P	P	P	D5Mgh8	5	149,029,982	S	S	S	S	S	S
D5Mgh8	5	149,029,982	P	P	P	P	P	P	P	P									
D5Wox10	5	164,807,242	P	P	P	P	P	P	P	P									
D5Rat48	5	166,237,695	P	P	P	P	P	P	P	P									
D6Mit5	6	12,856,626	P	P	P	P	P	P	P	P	D6Rat62	6	5,000,456	S	S	S	S	S	S
D6Rat147	6	24,862,818	P	P	P	P	P	P	P	P	D6Mit5	6	12,856,626	S	S	S	S	S	S
D6Mit9	6	36,260,131	P	P	P	P	P	P	P	P	D6Mit9	6	36,260,131	S	S	S	S	S	S
D6Mit4	6	60,606,186	P	P	P	P	P	P	P	P	D6Mit4	6	60,606,186	S	S	S	S	S	S
D6Rat129	6	76,902,074	P	P	P	P	P	P	P	P	D6Rat129	6	76,902,074	S	S	S	S	S	S
D6Mit2	6	84,763,275	P	P	P	P	P	P	P	P	D6Mit2	6	84,763,275	S	S	S	S	S	S
D6Rat124	6	95,059,735	P	P	P	P	P	P	P	P	D6Rat121	6	100,120,078	S	S	S	S	S	S
D6Mgh4	6	108,154,445	P	P	P	P	P	P	P	P	D6Mgh4	6	108,154,445	S	S	S	S	S	S
D6Rat75	6	127,363,380	P	P	P	P	P	P	P	P	D6Rat9	6	126,394,515					S	S
D6Mit10	6	134,727,413	P	P	P	P	P	P	P	P	D6Rat75	6	127,363,380	S	S	S	S	S	S
D6Mgh1	6	135,956,771	P	P	P	P	P	P	P	P	D6Mit10	6	134,727,413	S	S	S	S	S	S
											D6Mgh1	6	135,956,771	S	S	S	S	S	S
											D6Rat2	6	138,031,220	S	S	S	S	S	S
D7Rat35	7	24,175,337	P	P	P	W	P	P	P	P	D7Rat35	7	24,175,337	S	S	S	S	S	S
D7Rat92	7	36,695,145	P	P	P	W	P	P	P	P	D7Rat92	7	36,695,145	S	S	S	S	S	S
D7Arb16	7	51,251,919	P	P	P	W	P	P	P	P	D7Wox27	7	66,701,808	S	S	S	S	S	S
D7Wox27	7	66,701,808	P	P	P	W	P	P	P	P	D7Rat69	7	67,801,457	S	S	S	S	S	S
D7Rat69	7	67,801,457	P	P	P	W	P	P	P	P	D7Rat141	7	91,832,949	S	S	S	S	S	S
D7Rat141	7	91,832,949				W					D7Rat20	7	98,200,188	S	S	S	S	S	S
D7Rat20	7	98,200,188	P	P	P	W	P	P	P	P	D7Mgh5	7	119,130,825	S	S	S	S	S	S
D7Mgh5	7	119,130,825	P	P	P	W	P	P	P	P	D7Rat77	7	134,876,951	S	S	S	S	S	S
D7Rat9	7	128,085,642	P	P	P	W	P	P	P	P	D7Rat94	7	145,692,398	S	S	S	S	S	S
D7Rat77	7	134,876,951	P	P	P	W	P	P	P	P									
D7Rat94	7	145,692,398	P	P	P	W	P	P	P	P									
D8Rat77	8	2,108,128	P	P	P	P	W	P	P	P	D8Rat56	8	9,531,047	S	S	S	S	S	S
D8Rat55	8	8,578,850	P	P	P	P	W	P	P	P	D8Rat53	8	21,813,070	S	S	S	S	S	S
D8Rat56	8	9,531,047	P	P	P	P	W	P	P	P	D8Rat51	8	30,918,112	S	S	S	S	S	S
D8Rat53	8	21,813,070	P	P	P	P	W	P	P	P	D8Rat146	8	74,920,991	S	S	S	S	S	S

D8Tkyo1	8	23,095,882	P		P		W		
D8Rat51	8	30,918,112	P	P	P	P	W	P	P
D8Tkyo5	8	58,902,089					W		
D8Rat146	8	74,920,991	P	P	P	P	W	P	P
D8Mgh4	8	89,058,229	P	P	P	P	W	P	P
D8Rat75	8	91,990,411	P	P	P	P	W	P	P
D8Tkyo9	8	100,011,322					W		P
D8Rat16	8	101,304,999	P	P	P	P	W	P	P
D8Mgh1*	8	120,496,008	P	P	P	P	P	P	P
D8Tkyo10	8	128,032,912	P	P	P	P	W	P	P
D9Rat135	9	13,713,787					W		
D9Wox18	9	25,692,373	P	P	P	P	W	P	P
D9Tkyo4	9	27,587,386					W		
D9Tkyo5	9	28,466,437					W		
D9Rat70	9	29,075,079	P	P	P	P	W	P	P
D9Rat128	9	29,354,313					W		
D9Rat29	9	29,466,970					W		
D9Rat122	9	62,132,598	P	P	P	P	W	P	P
D9Wox4	9	71,268,192	P	P	P	P	W	P	P
D9Rat113	9	78,984,875					W		
D9Rat9	9	89,606,579					W		
D9Rat5	9	93,442,819	P	P	P	P	W	P	P
D9Rat67	9	94,845,971					W		
D9Rat4	9	98,606,676					W		
D9Rat83	9	99,498,209		P			W		
D9Mit1	9	113,343,366	P	P	P	P	W	P	P
D10Rat47	10	16,094,246	P	P	P	P	P	P	P
D10Rat182	10	17,555,386	P	P	P	P	P	P	P
D10Rat42	10	21,707,766	P	P	P	P	P	P	P
D10Rat72	10	23,941,190	P	P	P	P	P	P	P
D10Mgh10	10	36,185,929	P	P	P	P	P	P	P
D10Mgh6	10	64,648,175	P	P	P	P	P	P	P
D10Rat21	10	82,675,233	P	P	P	P	P	P	P
D10Rat99	10	88,250,522	P	P	P	P	P	P	P
D10Mgh4	10	95,638,234	P	P	P	P	P	P	P
D10Rat13	10	95,967,019	P	P	P	P	P	P	P
D10Rat7	10	104,329,177	P	P	P	P	P	P	P

D8Mgh4	8	89,058,229	S	S	S	S	S	S
D8Rat75	8	91,990,411	S	S	S	S	S	S
D8Rat16	8	101,304,999	S	S	S	S	S	S
D8Mgh1	8	120,496,008	S	S	S	S	S	S
D8Tkyo10	8	128,032,912	S	S	S	S	S	S

D9Rat135	9	13,713,787	S	S	S	S	S	S
D9Tkyo4	9	27,587,386	S	S	S	S	S	S
D9Rat122	9	62,132,598	S	S	S	S	S	S
D9Wox4	9	71,268,192	S	S	S	S	S	S
D9Tkyo11	9	79,270,504	S	S	S	S	S	S
D9Rat5	9	93,442,819	S	S	S	S	S	S
D9Rat83	9	99,498,209	S	S	S	S	S	S
D9Mit1	9	113,343,366	S	S	S	S	S	S

D10Rat182	10	17,555,386				S	S	
D10Rat42	10	21,707,766	S	S	S	S	S	S
D10Mgh10	10	36,185,929	S	S	S	S	S	S
D10Mgh6	10	64,648,175	S	S	S	S	S	S
D10Rat21	10	82,675,233	S	S	S	S	S	S
D10Rat99	10	88,250,522	S	S	S	S	S	S
D10Rat13	10	95,967,019	S	S	S	S	S	S
D10Rat16	10	96,406,074	S	S	S	S	S	S
D10Mgh1	10	[107,490,444]*	S	S	S	S	S	S

D10Mgh1	10	[107,490,444]*	P	P	P	P	P	P	P	P	
D11Rat31	11	6,673,351	P	P	P	P	P	P	P	P	
D11Rat76	11	27,344,036	P	P	P	P	P	P	P	P	
D11Mgh5	11	44,444,112	P	P	P	P	P	P	P	P	
D11Mgh4	11	62,653,194	P	P	P	P	P	P	P	P	
D11Mgh2	11	79,885,154	P	P	P	P	P	P	P	P	
D12Rat63	12	11,986,905	P	P	P	P	P	P	P	P	
D12Mit2	12	22,650,702	P	P	P	P	P	P	P	P	
D12Mgh5	12	31,723,565	P	P	P	P	P	P	P	P	
D12Rat36	12	37,521,884	P	P	P	P	P	P	P	P	
D12Mit4	12	43,798,958	P	P	P	P	P	P	P	P	
D13Tkyo1	13	26,605,475	P	P	P	P	P	P	W	P	
D13Mgh4	13	42,310,744	P	P	P	P	P	P	W	P	
D13Rat122	13	45,955,609							W		
D13Rat123	13	48,776,655							W		
D13Rat41	13	49,058,507							W		
D13Wox5	13	50,507,819	P	P	P	P	P	P	W	P	
D13Wox6	13	51,576,838	P	P	P	P	P	P	W	P	
D13Mgh7	13	67,206,802	P	P	P	P	P	P	W	P	
D13Rat85	13	74,568,378							W		
D13Rat56	13	87,815,427	P	P	P	P	P	P	W	P	
D13Mgh6	13	103,613,626	P	P	P	P	P	P	W	P	
D13Rat51	13	108,770,533							W		
D14Rat2	14	2,813,534	P	P	P	P	P	P	P	P	
D14Mgh3	14	20,266,223	P	P	P	P	P	P	P	P	
D14Rat24	14	44,088,622	P	P	P	P	P	P	P	P	
D14Rat45	14	69,672,685	P	P	P	P	P	P	P	P	
D14Mgh2	14	78,270,281	P	P	P	P	P	P	P	P	
D14Got87	14	88,876,924	P	P	P	P	P	P	P	P	
D14Rat110	14	110,419,380	P	P	P	P	P	P	P	P	
D15Rat2	15	11,605,245	P	P	P	P	P	P	P	W	
D15Mgh7	15	18,513,913	P	P	P	P	P	P	P	W	
D15Mit3	15	18,093,208	P	P	P	P	P	P	P	W	
D15Rat6	15	63,498,932	P	P	P	P	P	P	P	W	
D15Tkyo8	15	42,655,149	P	P	P	P	P	P	P	W	
D15Rat61	15	50,700,465	P	P	P	P	P	P	P	W	
D11Rat76	11	27,344,036	S	S	S	S	S	S	S	S	
D11Rat75	11	30,537,317		S				S			
D11Rat11	11	33,739,895	S	S	S	S	S	S	S	S	
D11Mgh5	11	44,444,112	S	S	S	S	S	S	S	S	
D11Mgh4	11	62,653,194	S	S	S	S	S	S	S	S	
D11Mgh2	11	79,885,154	S	S	S	S	S	S	S	S	
D12Rat63	12	11,986,905	S	S	S	S	S	S	S	S	
D12Mit2	12	22,650,702	S	S	S	S	S	S	S	S	
D12Mgh5	12	31,723,565	S	S	S	S	S	S	S	S	
D12Rat36	12	37,521,884	S	S	S	S	S	S	S	S	
D12Mit4	12	43,798,958	S	S	S	S	S	S	S	S	
D13Tkyo1	13	26,605,475	S	S	S	S	S	S	S	S	
D13Mgh4	13	42,310,744	S	S	S	S	S	S	S	S	
D13Rat41	13	49,058,507	S	S	S	S	S	S	S	S	
D13Wox5	13	50,507,819	S	S	S	S	S	S	S	S	
D13Wox6	13	51,576,838	S	S	S	S	S	S	S	S	
D13Mgh7	13	67,206,802	S	S	S	S	S	S	S	S	
D13Mgh9	13	86,272,806	S	S	S	S	S	S	S	S	
D13Rat49	13	106,676,710	S	S	S	S	S	S	S	S	
D13Rat51	13	108,770,533	S	S	S	S	S	S	S	S	
D14Rat2	14	2,813,534	S	S	S	S	S	S	S	S	
D14Mgh3	14	20,266,223	S	S	S	S	S	S	S	S	
D14Rat24	14	44,088,622	S	S	S	S	S	S	S	S	
D14Mgh2	14	78,270,281	S	S	S	S	S	S	S	S	
D14Got87	14	88,876,924	S	S	S	S	S	S	S	S	
D14Mco5	14	103,778,284	S	S	S	S	S	S	S	S	
D15Mgh7	15	18,513,913	S	S	S	S		W		S	
D15Mit3	15	18,093,208	S	S	S	S		W		S	
D15Tkyo6	15	34,385,010						W			
D15Rat68	15	63,498,932	S	S	S	S		W		S	
D15Rat95	15	70,559,420						W			
D15Rat94	15	77,072,146	S	S	S	S		W		S	

D15Rat92	15	54,656,296								W	D15Tkyo18	15	88,011,655	S	S	S	S	W	S
D15Rat20	15	59,616,275								W	D15Rat102	15	98,027,558					W	
D15Rat68	15	63,498,932	P	P	P	P	P	P	P	W	D15Mgh6	15	104,003,455	S	S	S	S	W	S
D15Arb2	15	68,366,508	P	P	P	P	P	P	P	W	D15Rat106	15	106,550,444					W	S
D15Rat94	15	77,072,146	P	P	P	P	P	P	P	W									
D15Tkyo18	15	88,011,655	P	P	P	P	P	P	P	W									
D15Mgh6	15	104,003,455	P	P	P	P	P	P	P	W									
D15Rat106	15	106,550,444								W									
D16Rat22	16	19,398,173	P	P	P	P	P	P	P	P	D16Rat22	16	19,398,173	S	S	S	S	S	S
D16Wox10	16	19,398,173	P	P	P	P	P	P	P	P	D16Wox10	16	19,398,173	S	S	S	S	S	S
D16Mit3	16	47,346,470	P	P	P	P	P	P	P	P	D16Mit3	16	47,346,470	S	S	S	S	S	S
D16Rat64	16	59,285,775	P	P	P	P	P	P	P	P	D16Rat58	16	69,058,102	S	S	S	S	S	S
D16Rat58	16	69,058,102	P	P	P	P	P	P	P	P	D16Rat93	16	85,005,570	S	S	S	S	S	S
D16Rat108	16	71,460,724	P	P	P	P	P	P	P	P	D16Rat15	16	80,316,290	S	S	S	S	S	S
D16Rat93	16	85,005,570	P	P	P	P	P	P	P	P									
D16Rat15	16	80,316,290	P	P	P	P	P	P	P	P									
D17Mgh1	17	396,662	P	P	P	P	P	P	P	P	D17Rat6	17	10,529,709	S	S	S	S	S	S
D17Rat6	17	10,529,709	P	P	P	P	P	P	P	P	D17Rat61	17	14,009,679	S	S	S	S	S	S
D17Rat143	17	15,134,275	P	P	P	P	P	P	P	P	D17Rat12	17	27,690,959	S	S	S	S	S	S
D17Rat12	17	27,690,959	P	P	P	P	P	P	P	P	D17Mgh4	17	46,867,215	S	S	S	S	S	S
D17Mgh4	17	46,867,215	P	P	P	P	P	P	P	P	D17Mit4	17	63,994,205	S	S	S	S	S	S
D17Mit4	17	63,994,205	P	P	P	P	P	P	P	P	D17Rat49	17	85,236,284	S	S	S	S	S	S
D17Rat99	17	81,334,009	P	P	P	P	P	P	P	P									
D17Rat49	17	85,236,284	P	P	P	P	P	P	P	P									
D18Rat48	18	5,950,917	P	P	P	P	P	P	P	P	D18Rat48	18	5,950,917	S	S	S	S	S	S
D18Wox7	18	15,539,551	P	P	P	P	P	P	P	P	D18Wox7	18	15,539,551	S	S	S	S	S	S
D18Rat105	18	17,807,783	P	P	P	P	P	P	P	P	D18Rat57	18	53,861,252	S	S	S	S	S	S
D18Mit4	18	27,728,134	P	P	P	P	P	P	P	P	D18Mit8	18	61,985,648	S	S	S	S	S	S
D18Rat57	18	53,861,252	P	P	P	P	P	P	P	P	D18Mgh4	18	79,948,616	S	S	S	S	S	S
D18Rat41	18	58,476,128	P	P	P	P	P	P	P	P									
D18Mit8	18	61,985,648	P	P	P	P	P	P	P	P									
D18Rat123	18	70,370,954	P	P	P	P	P	P	P	P									
D18Mgh4	18	79,948,616	P	P	P	P	P	P	P	P									
D19Mit3	19	15,702,328	P	P	P	P	P	P	P	P	D19Mit3	19	15,702,328	S	S	S	S	S	W
D19Rat101	19	15,939,528	P	P	P	P	P	P	P	P	D19Rat15	19	15,721,763	S	S	S	S	S	W
D19Wox3	19	31,194,301	P	P	P	P	P	P	P	P	D19Rat101	19	15,939,528	S	S	S	S	S	W
D19Wox4	19	41,685,949	P	P	P	P	P	P	P	P	D19Rat48	19	30,683,540	S	S	S	S	S	W

D19Mgh3	19	48,139,992	P	P	P	P	P	P	P	P	P	D19Wox3	19	31,194,301	S	S	S	S	S	W
D19Rat57	19	60,220,451	P	P	P	P	P	P	P	P	P	D19Rat35	19	41,471,460						W
												D19Wox4	19	41,685,949	S	S	S	S	S	W
												D19Rat7	19	49,873,186	S	S	S	S	S	W
												D19Rat58	19	56,723,500						W
												D19Rat5	19	57,094,703						W
												D19Rat104	19	58,308,034	S	S	S	S	S	W
												D19Rat57	19	60,220,451						W
D20Mgh5	20	9,655,642	P	P	P	P	P	P	P	P	P	D20Rat31	20	10,800,308	S	S	S	S	S	S
D20Rat4	20	12,482,277	P							P		D20Rat4	20	12,482,277				S	S	
D20Rat11	20	40,871,079	P	P	P	P	P	P	P	P	P	D20Rat11	20	40,871,079	S	S	S	S	S	S
D20Rat29	20	49,108,730	P	P	P	P	P	P	P	P	P	D20Rat29	20	49,108,730	S	S	S	S	S	S
D20Mgh1	20	51,892,390	P	P	P	P	P	P	P	P	P	D20Mgh1	20	51,892,390	S	S	S	S	S	S
DXMit1	X	12,150,263	P	P	P	P	P	P	P	P	P	DXMit1	X	12,150,263	S	S	S	S	S	S
DXMit4	X	61,397,905	P	P	P	P	P	P	P	P	P	DXMit4	X	61,397,905	S	S	S	S	S	S
DXRat17	X	95,021,031	P	P	P	P	P	P	P	P	P	DXRat17	X	95,021,031	S	S	S	S	S	S
DXRat18	X	106,240,541	P	P	P	P	P	P	P	P	P	DXRat18	X	106,240,541	S	S	S	S	S	S
DXRat19	X	114,961,056	P	P	P	P	P	P	P	P	P	DXMgh7	X	119,394,326	S	S	S	S	S	S
DXMgh7	X	119,394,326	P	P	P	P	P	P	P	P	P									

Allele designation: P, SHRSP/lzm; S, SHR/lzm; W, WKY/lzm.

The position of D10Mgh1 is arbitrarily mapped to the m6 reference genome (NCBI) using the information for its neighboring SSLP markers (D10Rat7 and D10Rat13) on the Celera map.

*In the RNO8 consomic strain, a chromosomal segment (<27 Mb) remains to exist, interrupting the congenic fragment.

Table S8A. Phenotype comparison in male rats between progenitor and consomic/congenic strains involving SHRSP or SHR and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*
SHRSP	38-173	1.07 ± 0.01	—	3.82 ± 0.03	—	211.0 ± 1.0	—	236.6 ± 1.5	—	283.9 ± 1.5	—	11.05 ± 0.22	—	8.22 ± 0.23	—	133.9 ± 3.3	—	52.2 ± 1.0	—	15.7 ± 0.8	—	1.12 ± 0.06	—
WKY	10-27	0.98 ± 0.01	—	2.61 ± 0.03	—	130.3 ± 2.0	—	123.4 ± 2.3	—	366.6 ± 4.6	—	13.25 ± 0.31	—	10.72 ± 0.34	—	108.3 ± 4.5	—	83.1 ± 3.1	—	12.5 ± 1.3	—	1.30 ± 0.06	—
1pW	58-132	1.02 ± 0.01	1.1E-04	3.51 ± 0.02	4.4E-12	195.7 ± 1.0	7.3E-24	207.6 ± 1.3	3.3E-34	305.5 ± 2.0	1.1E-15	8.00 ± 0.12	2.8E-17	7.25 ± 0.12	4.0E-04	112.2 ± 2.6	8.5E-07	46.4 ± 0.8	1.9E-05	8.4 ± 0.4	1.9E-11	0.97 ± 0.04	0.048
3pW	40-67	1.01 ± 0.01	4.3E-04	3.50 ± 0.02	6.0E-12	192.7 ± 1.6	1.3E-16	200.7 ± 1.7	1.7E-31	285.1 ± 2.4	0.510	9.45 ± 0.20	1.3E-06	9.42 ± 0.17	5.9E-05	127.1 ± 2.5	0.103	39.8 ± 0.6	6.8E-16	8.8 ± 0.5	2.5E-10	0.98 ± 0.04	0.066
4pW	32-80	0.99 ± 0.01	4.8E-08	3.47 ± 0.02	2.4E-13	191.2 ± 1.2	7.4E-29	202.4 ± 1.8	6.1E-32	287.4 ± 2.2	0.128	9.61 ± 0.21	1.3E-05	8.14 ± 0.18	0.773	138.2 ± 2.6	0.303	47.5 ± 0.6	2.1E-04	10.9 ± 0.5	2.6E-06	1.17 ± 0.05	0.511
7pW	24-49	1.00 ± 0.01	2.5E-05	3.53 ± 0.03	9.3E-09	204.8 ± 1.6	9.5E-04	222.9 ± 2.7	4.8E-05	291.5 ± 2.7	0.011	9.56 ± 0.22	1.3E-05	6.93 ± 0.17	2.9E-05	149.5 ± 3.1	7.2E-04	43.7 ± 0.7	1.2E-09	9.0 ± 0.4	2.3E-10	0.84 ± 0.04	2.4E-04
8pW	27-68	1.08 ± 0.01	0.646	3.78 ± 0.03	0.451	210.2 ± 1.6	0.638	232.4 ± 2.3	0.104	279.9 ± 3.2	0.364	11.22 ± 0.19	0.556	8.77 ± 0.14	0.043	142.7 ± 3.0	0.051	46.3 ± 0.6	5.9E-06	14.6 ± 0.8	0.337	1.02 ± 0.05	0.231
9pW	33-70	1.03 ± 0.01	0.025	3.47 ± 0.02	6.0E-13	202.7 ± 1.4	2.5E-06	215.3 ± 1.7	3.5E-17	302.1 ± 2.5	8.7E-09	9.19 ± 0.31	7.2E-06	8.65 ± 0.25	0.207	134.5 ± 2.6	0.886	51.0 ± 0.5	0.301	12.0 ± 0.5	2.5E-04	0.95 ± 0.05	0.029
13pW	26-47	1.01 ± 0.01	5.0E-06	3.50 ± 0.02	3.4E-12	201.8 ± 2.1	1.7E-04	218.0 ± 2.0	2.8E-10	294.7 ± 2.4	2.1E-04	9.59 ± 0.21	1.5E-05	7.83 ± 0.30	0.300	131.8 ± 3.0	0.642	57.7 ± 0.8	7.5E-05	10.1 ± 0.5	1.6E-07	0.94 ± 0.05	0.028
15pW	24-102	0.96 ± 0.01	1.8E-13	3.51 ± 0.03	4.3E-10	202.1 ± 2.0	7.3E-05	213.1 ± 1.7	2.0E-20	287.5 ± 1.9	0.094	9.65 ± 0.20	1.7E-04	8.36 ± 0.21	0.692	141.0 ± 3.5	0.096	64.7 ± 0.7	9.1E-16	13.1 ± 0.6	0.011	1.01 ± 0.04	0.132
1pWC	27-91	—	—	—	—	182.6 ± 1.3	1.5E-42	187.8 ± 1.1	4.6E-58	288.6 ± 2.6	0.122	—	—	—	—	116.8 ± 3.8	0.001	37.5 ± 0.8	7.6E-18	9.8 ± 0.5	2.4E-08	1.01 ± 0.08	0.262
1pWC×9pW	57-60	0.95 ± 0.06	—	3.19 ± 0.07	—	174.3 ± 1.3	1.4E-05	176.8 ± 1.4	6.5E-09	301.2 ± 4.0	0.003	9.93 ± 0.17	—	8.51 ± 0.22	—	137.4 ± 2.0	1.1E-05	—	—	—	—	—	—
1pWC×13pW	68-81	0.92 ± 0.05	—	3.21 ± 0.01	—	172.0 ± 1.2	6.6E-09	173.8 ± 1.1	2.5E-15	284.1 ± 1.5	0.136	9.93 ± 0.11	—	7.72 ± 0.12	—	137.6 ± 1.7	5.9E-06	—	—	—	—	—	—
SHR	23-74	1.11 ± 0.01	—	3.42 ± 0.04	—	186.1 ± 1.6	—	197.6 ± 2.0	—	322.1 ± 2.1	—	12.00 ± 0.33	—	9.74 ± 0.33	—	123.8 ± 3.5	—	59.9 ± 0.9	—	12.4 ± 0.5	—	0.98 ± 0.04	—
1SW	58-132	1.12 ± 0.01	0.512	3.31 ± 0.02	0.013	182.9 ± 1.3	0.116	191.8 ± 1.3	0.017	342.0 ± 2.3	2.2E-09	8.50 ± 0.16	5.4E-11	7.36 ± 0.18	3.4E-07	112.8 ± 2.3	0.010	60.4 ± 0.9	0.709	9.7 ± 0.4	7.2E-05	1.16 ± 0.06	0.030
2SW	27-91	1.12 ± 0.01	0.547	3.35 ± 0.02	0.106	170.2 ± 1.5	5.6E-11	180.7 ± 2.0	2.7E-08	330.8 ± 2.7	0.014	9.47 ± 0.20	9.7E-08	7.89 ± 0.20	2.8E-05	137.7 ± 2.3	0.001	63.3 ± 1.0	0.013	13.9 ± 0.6	0.063	1.20 ± 0.04	0.001
3SW	53-67	1.03 ± 0.01	3.0E-06	3.27 ± 0.02	0.002	176.3 ± 1.1	2.5E-06	183.5 ± 1.3	4.0E-08	316.7 ± 2.0	0.066	9.81 ± 0.18	1.2E-06	9.89 ± 0.18	0.702	115.1 ± 2.4	0.044	47.3 ± 1.1	6.4E-14	6.8 ± 0.2	2.0E-14	1.05 ± 0.05	0.312
4SW	26-103	0.99 ± 0.01	7.5E-11	3.28 ± 0.02	0.002	182.9 ± 1.7	0.172	190.8 ± 1.4	0.006	303.4 ± 2.3	3.7E-08	10.30 ± 0.24	1.5E-04	8.77 ± 0.24	0.022	118.0 ± 2.9	0.207	54.0 ± 0.8	1.6E-06	13.3 ± 0.8	0.295	1.16 ± 0.04	0.004
15SW	22-75	0.90 ± 0.02	9.3E-13	3.15 ± 0.02	1.7E-07	168.7 ± 2.1	8.9E-11	172.3 ± 1.9	1.8E-15	310.9 ± 3.0	0.003	11.14 ± 0.33	0.090	9.18 ± 0.36	0.289	137.8 ± 3.2	0.004	64.1 ± 1.2	0.006	13.3 ± 0.9	0.395	0.94 ± 0.03	0.380
19SW	28-103	1.09 ± 0.02	0.400	3.43 ± 0.10	0.932	178.6 ± 1.7	0.002	188.2 ± 1.6	4.2E-04	323.0 ± 2.8	0.799	10.68 ± 0.21	0.002	10.88 ± 0.26	0.010	133.2 ± 3.6	0.062	65.9 ± 1.0	1.8E-05	13.6 ± 0.9	0.230	0.87 ± 0.04	0.053
1SWC	50-126	1.12 ± 0.01	0.241	3.43 ± 0.02	0.773	168.8 ± 1.2	4.9E-14	167.8 ± 1.0	7.8E-22	328.9 ± 1.6	0.011	7.91 ± 0.12	2.9E-12	6.78 ± 0.16	3.5E-09	191.0 ± 3.5	3.2E-27	—	—	—	—	—	—
4SWC(1)	33-49	1.06 ± 0.01	0.011	3.33 ± 0.02	0.056	175.8 ± 1.8	4.6E-05	183.9 ± 2.1	8.4E-06	317.6 ± 3.2	0.241	10.71 ± 0.19	0.002	8.50 ± 0.17	0.002	136.5 ± 2.3	0.003	63.3 ± 0.9	0.010	11.3 ± 0.7	0.186	1.30 ± 0.04	9.3E-07

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

For double congenic rats (1pWC×9pW and 1pWC×13pW), t-test was performed in comparison with 1pWC, into which another chromosomal regions (RNO9 and RNO13) were introgressed.

Table S8B. Phenotype comparison in female rats between progenitor and consomic/congenic strains involving SHRSP or SHR and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP*	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP
SHRSP	35-195	0.72 ± 0.01	—	3.86 ± 0.02	—	176.3 ± 0.8	—	191.3 ± 1.1	—	189.4 ± 0.9	—	—	—	6.92 ± 0.26	—	129.5 ± 1.9	—	69.7 ± 1.0	—	15.7 ± 0.6	—	0.88 ± 0.03	—
WKY	10-15	0.62 ± 0.01	—	2.66 ± 0.03	—	116.0 ± 1.8	—	118.8 ± 2.3	—	227.2 ± 2.2	—	—	—	11.43 ± 0.40	—	108.9 ± 4.0	—	89.9 ± 3.1	—	15.3 ± 0.6	—	1.18 ± 0.08	—
1pW	30-123	0.72 ± 0.01	0.491	3.67 ± 0.02	6.9E-13	166.2 ± 1.0	9.6E-14	174.6 ± 1.0	1.0E-22	198.7 ± 1.0	5.0E-12	—	—	6.41 ± 0.14	0.084	117.8 ± 2.7	5.7E-04	78.0 ± 1.2	1.3E-06	11.2 ± 0.8	1.5E-05	1.25 ± 0.06	8.0E-07
3pW	31-64	0.73 ± 0.01	0.533	3.80 ± 0.03	0.120	166.3 ± 1.4	4.5E-09	167.5 ± 1.9	2.5E-17	187.3 ± 1.5	0.227	—	—	9.64 ± 0.17	2.6E-12	128.9 ± 2.5	0.841	63.3 ± 1.5	8.2E-04	12.3 ± 0.6	8.9E-05	0.91 ± 0.05	0.604
4pW	23-91	0.69 ± 0.01	0.024	3.56 ± 0.02	4.6E-15	162.3 ± 1.3	8.3E-17	170.7 ± 1.2	3.6E-26	194.6 ± 1.4	0.001	—	—	7.27 ± 0.22	0.307	142.8 ± 3.0	2.7E-04	61.9 ± 1.4	2.0E-05	10.9 ± 0.5	1.6E-08	0.91 ± 0.04	0.441
7pW	33-58	0.70 ± 0.01	0.026	3.72 ± 0.02	4.9E-08	171.5 ± 1.3	0.002	182.6 ± 1.3	5.9E-06	189.6 ± 1.2	0.850	—	—	5.31 ± 0.19	5.0E-06	141.0 ± 2.9	0.001	65.2 ± 1.1	0.002	11.6 ± 0.4	7.9E-08	0.96 ± 0.04	0.089
8pW	25-84	0.74 ± 0.01	0.093	3.90 ± 0.03	0.237	182.7 ± 1.4	0.002	193.6 ± 1.3	0.226	191.5 ± 1.4	0.782	—	—	6.69 ± 0.18	0.464	132.0 ± 2.6	0.030	65.1 ± 0.9	0.004	16.0 ± 0.7	0.670	1.05 ± 0.04	0.001
9pW	23-72	0.73 ± 0.01	0.684	3.68 ± 0.03	1.8E-06	168.7 ± 1.3	3.0E-06	178.1 ± 1.7	7.9E-09	197.5 ± 1.7	4.9E-05	—	—	8.21 ± 0.30	0.002	133.4 ± 3.0	0.272	63.3 ± 1.6	0.001	13.2 ± 0.5	0.002	0.92 ± 0.05	0.496
13pW	32-47	0.71 ± 0.01	0.178	3.65 ± 0.03	1.2E-08	167.5 ± 1.8	4.0E-05	172.3 ± 1.8	4.9E-12	195.3 ± 1.5	0.001	—	—	5.98 ± 0.16	0.003	136.1 ± 3.3	0.083	73.8 ± 1.3	0.015	13.5 ± 0.5	0.006	1.18 ± 0.03	2.6E-11
15pW	30-121	0.67 ± 0.01	1.3E-05	3.60 ± 0.02	6.5E-14	174.8 ± 1.7	0.424	179.6 ± 1.2	1.0E-10	186.3 ± 0.9	0.015	—	—	6.31 ± 0.28	0.083	141.0 ± 2.5	4.1E-04	90.1 ± 1.7	1.0E-14	16.7 ± 0.9	0.347	0.94 ± 0.04	0.157
1pWC	24-110	—	—	—	—	154.1 ± 0.9	9.4E-49	158.0 ± 1.2	2.6E-46	188.1 ± 1.3	0.411	—	—	—	—	127.2 ± 2.3	0.443	62.4 ± 1.6	3.3E-04	12.6 ± 0.7	0.001	1.09 ± 0.04	6.9E-05
1pWC×9pW	74-85	0.67 ± 0.01	—	3.46 ± 0.03	—	147.5 ± 1.0	1.6E-06	152.6 ± 1.1	0.002	194.7 ± 1.5	0.001	—	—	7.59 ± 0.14	—	141.7 ± 1.8	3.6E-06	—	—	—	—	—	—
1pWC×13pW	45-65	0.63 ± 0.01	—	3.51 ± 0.02	—	143.4 ± 1.2	1.3E-10	147.0 ± 1.5	1.1E-07	180.2 ± 1.2	1.6E-05	—	—	6.62 ± 0.20	—	147.1 ± 1.5	3.4E-10	—	—	—	—	—	—
SHR	26-85	0.74 ± 0.01	—	3.83 ± 0.05	—	161.9 ± 1.3	—	173.6 ± 1.6	—	190.9 ± 1.2	—	—	—	7.29 ± 0.19	—	120.5 ± 3.2	—	69.0 ± 1.1	—	10.8 ± 0.3	—	1.13 ± 0.04	—
1SW	32-125	0.73 ± 0.01	0.221	3.62 ± 0.02	0.001	163.2 ± 1.2	0.482	167.8 ± 1.5	0.010	207.5 ± 1.5	1.7E-14	—	—	6.67 ± 0.19	0.025	115.1 ± 2.5	0.180	76.3 ± 1.9	0.002	13.2 ± 0.5	2.0E-04	0.97 ± 0.04	0.007
2SW	24-110	0.76 ± 0.01	0.057	3.74 ± 0.03	0.129	153.0 ± 1.1	1.2E-06	159.0 ± 2.0	2.1E-07	198.4 ± 2.0	0.002	—	—	5.99 ± 0.17	5.8E-06	141.2 ± 1.8	2.3E-07	86.2 ± 1.7	2.2E-12	14.5 ± 0.6	8.1E-07	1.16 ± 0.04	0.600
3SW	53-78	0.68 ± 0.005	1.2E-07	3.58 ± 0.02	5.4E-05	154.2 ± 1.1	1.1E-05	155.7 ± 1.4	7.1E-14	189.9 ± 1.3	0.564	—	—	8.86 ± 0.18	8.9E-08	120.9 ± 2.9	0.937	65.7 ± 1.1	0.039	9.1 ± 0.2	9.6E-06	0.99 ± 0.04	0.010
4SW	30-122	0.70 ± 0.01	0.001	3.69 ± 0.02	0.015	158.9 ± 1.6	0.157	166.7 ± 1.5	0.002	189.8 ± 2.1	0.634	—	—	7.28 ± 0.21	0.969	118.7 ± 3.2	0.692	74.4 ± 1.6	0.008	11.3 ± 0.5	0.417	1.32 ± 0.06	0.009
15SW	28-106	0.64 ± 0.01	3.0E-12	3.58 ± 0.03	1.4E-04	146.2 ± 1.6	3.6E-12	144.0 ± 1.4	7.7E-28	191.7 ± 1.4	0.663	—	—	6.95 ± 0.25	0.282	140.3 ± 2.7	7.2E-06	86.0 ± 1.1	2.4E-17	12.4 ± 0.5	0.008	1.15 ± 0.03	0.618
19SW	26-79	0.72 ± 0.01	0.026	3.53 ± 0.04	1.8E-05	154.6 ± 1.5	3.9E-04	161.1 ± 1.7	6.5E-07	202.4 ± 2.4	5.6E-05	—	—	8.14 ± 0.25	0.009	136.3 ± 2.6	2.2E-04	70.8 ± 1.4	0.318	9.6 ± 0.4	0.024	1.09 ± 0.04	0.508
1SWC	28-64	0.76 ± 0.01	0.046	3.77 ± 0.02	0.319	148.3 ± 1.4	2.1E-10	152.9 ± 1.3	2.1E-17	203.7 ± 1.2	6.5E-13	—	—	5.72 ± 0.12	1.0E-08	153.7 ± 3.4	5.6E-11	—	—	—	—	—	—
4SWC(1)	32-38	0.70 ± 0.01	2.8E-04	3.72 ± 0.03	0.083	156.0 ± 1.8	0.011	163.2 ± 1.7	3.2E-05	188.2 ± 2.0	0.262	—	—	6.75 ± 0.18	0.045	131.9 ± 1.8	0.002	77.2 ± 1.4	3.4E-05	8.9 ± 0.4	9.6E-04	1.34 ± 0.04	5.4E-04

Table S9A. Phenotype comparison in male rats between progenitor and RNO1 congenic strains involving SHRSP and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		20wk BP (mmHg)		12wk Bw (g)		16wk Bw (g)		20wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP
SHRSP	38-173	1.07 ± 0.01	—	3.82 ± 0.03	—	211.0 ± 1.0	—	236.6 ± 1.5	—	239.5 ± 2.4	—	251.4 ± 1.4	—	283.9 ± 1.5	—	305.2 ± 3.0	—	11.05 ± 0.22	—	8.22 ± 0.23	—	133.9 ± 3.3	—	52.2 ± 1.0	—	15.7 ± 0.8	—	1.12 ± 0.06	—
WKY	10-27	0.98 ± 0.01	—	2.61 ± 0.03	—	130.3 ± 2.0	—	123.4 ± 2.3	—	129.1 ± 2.0	—	312.8 ± 2.3	—	366.6 ± 4.6	—	397.4 ± 8.4	—	13.25 ± 0.31	—	10.72 ± 0.34	—	108.3 ± 4.5	—	83.1 ± 3.1	—	12.5 ± 1.3	—	1.30 ± 0.06	—
1pW	58-132	1.02 ± 0.01	1.1E-04	3.51 ± 0.02	4.4E-12	195.7 ± 1.0	7.3E-24	207.6 ± 1.3	3.3E-34	202.8 ± 1.8	4.7E-23	269.4 ± 1.6	2.7E-16	305.5 ± 2.0	1.1E-15	344.4 ± 2.0	6.2E-20	8.00 ± 0.12	2.8E-17	7.25 ± 0.12	4.0E-04	112.2 ± 2.6	8.5E-07	46.4 ± 0.8	1.9E-05	8.4 ± 0.4	1.9E-11	0.97 ± 0.04	0.048
1pWC	27-91	—	—	—	—	182.6 ± 1.3	1.5E-42	187.8 ± 1.1	4.6E-58	192.2 ± 1.4	8.5E-33	247.9 ± 1.8	0.118	288.6 ± 2.6	0.122	311.1 ± 2.4	0.124	—	—	—	—	116.8 ± 3.8	0.001	37.5 ± 0.8	7.6E-18	9.8 ± 0.5	2.4E-08	1.01 ± 0.08	0.262
1pW2	26-103	—	—	—	—	192.1 ± 1.3	3.1E-25	199.4 ± 1.7	1.5E-32	206.0 ± 2.2	1.5E-18	248.2 ± 2.0	0.182	274.1 ± 3.0	0.005	296.8 ± 3.0	0.049	—	—	—	—	114.2 ± 2.6	9.3E-06	43.8 ± 1.0	1.4E-07	10.9 ± 0.5	5.8E-06	0.97 ± 0.08	0.149
1pW5-2	26-70	—	—	—	—	195.8 ± 1.4	2.6E-15	201.6 ± 2.1	1.7E-25	207.2 ± 1.8	2.9E-19	256.9 ± 2.6	0.062	285.9 ± 2.7	0.528	308.6 ± 3.2	0.432	—	—	—	—	147.2 ± 2.7	0.002	44.5 ± 1.4	5.1E-05	11.0 ± 1.0	5.1E-04	1.08 ± 0.05	0.680
1pW4-1	31-82	1.07 ± 0.02	0.989	3.69 ± 0.03	0.004	202.0 ± 1.4	3.6E-07	214.9 ± 1.7	2.2E-16	216.1 ± 2.2	7.6E-11	250.9 ± 2.2	0.823	281.9 ± 2.1	0.449	299.3 ± 3.0	0.161	11.07 ± 0.36	0.954	8.83 ± 0.30	0.112	134.8 ± 3.7	0.858	48.5 ± 1.0	0.012	10.3 ± 0.7	2.0E-06	1.09 ± 0.08	0.780
1pW4-2	27-70	—	—	—	—	201.2 ± 1.8	7.9E-06	209.8 ± 1.4	2.4E-26	219.3 ± 1.5	1.1E-10	253.2 ± 2.1	0.480	285.9 ± 2.4	0.470	308.5 ± 2.3	0.379	—	—	—	—	132.7 ± 2.5	0.778	43.1 ± 1.0	1.9E-08	8.3 ± 0.3	9.5E-12	1.00 ± 0.07	0.219
1pW4-3	62-100	1.09 ± 0.01	0.150	3.93 ± 0.03	0.011	202.9 ± 1.4	2.0E-06	219.9 ± 2.0	1.7E-10	222.1 ± 2.9	3.6E-06	256.4 ± 2.7	0.046	279.0 ± 1.7	0.038	286.1 ± 4.2	1.6E-05	10.11 ± 0.30	0.015	7.44 ± 0.21	0.013	150.7 ± 3.6	1.1E-04	—	—	—	—	—	—
1pW4-4	60-93	1.12 ± 0.02	0.015	4.01 ± 0.05	0.003	197.2 ± 1.6	3.2E-11	208.2 ± 3.0	2.7E-13	218.0 ± 3.0	2.0E-07	253.1 ± 2.2	0.491	278.5 ± 1.9	0.032	292.9 ± 3.8	0.004	9.86 ± 0.35	0.008	7.43 ± 0.23	0.019	141.9 ± 3.2	0.056	—	—	—	—	—	—
1pW6-2	25-62	—	—	—	—	197.0 ± 1.8	1.3E-09	207.7 ± 1.6	3.4E-26	216.0 ± 1.9	1.5E-12	245.1 ± 3.6	0.117	290.3 ± 3.5	0.098	306.8 ± 4.1	0.746	—	—	—	—	130.3 ± 3.1	0.432	42.8 ± 0.7	1.2E-10	11.6 ± 0.7	3.5E-04	1.11 ± 0.06	0.911
1pW6-1	26-60	0.99 ± 0.01	2.2E-05	3.54 ± 0.02	2.6E-09	200.2 ± 1.5	2.8E-08	212.1 ± 1.8	4.2E-18	219.8 ± 1.6	5.8E-10	256.7 ± 2.3	0.049	286.0 ± 2.2	0.441	305.7 ± 2.6	0.902	9.85 ± 0.29	0.092	7.18 ± 0.23	0.039	134.4 ± 3.6	0.918	41.3 ± 0.9	1.5E-11	9.2 ± 0.5	2.4E-09	1.09 ± 0.05	0.744
1pW3-2	28-103	—	—	—	—	189.7 ± 1.1	4.8E-34	194.2 ± 1.4	6.6E-50	204.4 ± 1.6	8.0E-23	252.4 ± 1.7	0.655	287.2 ± 2.0	0.192	295.5 ± 5.1	0.102	—	—	—	—	123.4 ± 4.0	0.046	38.5 ± 0.7	1.4E-16	12.7 ± 0.6	0.005	0.96 ± 0.05	0.049
1pW3-1	25-116	—	—	—	—	198.0 ± 1.2	1.2E-14	212.5 ± 1.6	4.3E-21	216.3 ± 2.4	4.4E-10	253.2 ± 2.3	0.516	284.0 ± 2.6	0.965	305.4 ± 3.4	0.962	—	—	—	—	127.0 ± 3.0	0.127	39.2 ± 0.7	8.3E-16	13.7 ± 0.6	0.059	0.91 ± 0.04	0.005
1pW8	28-64	—	—	—	—	208.8 ± 1.6	0.251	223.9 ± 3.1	4.3E-04	237.1 ± 3.0	0.525	245.9 ± 3.0	0.097	276.1 ± 3.3	0.038	287.5 ± 3.9	4.9E-04	—	—	—	—	124.4 ± 3.5	0.051	45.3 ± 1.0	1.0E-05	11.8 ± 0.8	0.001	1.16 ± 0.08	0.650
1pW10	12-28	—	—	—	—	220.3 ± 2.8	0.011	238.4 ± 4.3	0.830	—	—	227.8 ± 3.1	8.2E-09	235.3 ± 6.7	2.1E-04	—	—	—	—	—	—	—	—	64.3 ± 1.3	6.5E-09	—	—	—	—
1pW9	69-111	—	—	—	—	212.9 ± 1.5	0.781	228.2 ± 2.4	0.001	—	—	266.7 ± 1.7	1.1E-09	277.1 ± 3.6	0.132	—	—	—	—	—	—	—	—	59.9 ± 1.1	5.1E-06	—	—	—	—
1pW11	37-44	—	—	—	—	203.2 ± 2.1	2.0E-04	228.1 ± 3.2	0.012	239.6 ± 3.2	0.801	264.9 ± 1.9	1.1E-06	289.8 ± 3.7	0.127	303.1 ± 4.4	0.679	—	—	—	—	—	—	72.6 ± 1.5	1.7E-17	—	—	—	—

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S9B. Phenotype comparison in female rats between progenitor and RNO1 congenic strains involving SHRSP and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		20wk BP (mmHg)		12wk Bw (g)		16wk Bw (g)		20wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP
SHRSP	35-195	0.72 ± 0.01	—	3.86 ± 0.02	—	176.3 ± 0.8	—	191.3 ± 1.1	—	198.7 ± 1.2	—	170.7 ± 0.8	—	189.4 ± 0.9	—	200.3 ± 1.1	—	6.92 ± 0.26	—	129.5 ± 1.9	—	69.7 ± 1.0	—	15.7 ± 0.6	—	—	—	0.88 ± 0.03	—
WKY	10-15	0.62 ± 0.01	—	2.66 ± 0.03	—	116.0 ± 1.8	—	118.8 ± 2.3	—	124.9 ± 3.5	—	197.6 ± 1.4	—	227.2 ± 2.2	—	239.8 ± 1.8	—	11.43 ± 0.40	—	108.9 ± 4.0	—	89.9 ± 3.1	—	15.3 ± 0.6	—	—	—	1.18 ± 0.08	—
1pW	32-125	0.72 ± 0.01	0.491	3.66 ± 0.02	3.4E-13	167.1 ± 1.1	3.8E-11	174.9 ± 1.0	3.7E-23	173.6 ± 1.3	2.5E-30	179.3 ± 0.8	9.4E-13	198.7 ± 1.0	8.6E-12	211.5 ± 1.3	1.2E-09	6.41 ± 0.14	0.084	117.8 ± 2.7	5.7E-04	78.0 ± 1.2	1.3E-06	11.2 ± 0.8	1.5E-05	1.25 ± 0.06	8.0E-07	—	—
1pWC	24-110	—	—	—	—	154.1 ± 0.9	9.4E-49	158.0 ± 1.2	2.6E-46	161.4 ± 1.4	3.7E-40	168.6 ± 1.0	0.103	188.1 ± 1.3	0.411	202.9 ± 1.6	0.170	—	—	—	—	127.2 ± 2.3	0.443	62.4 ± 1.6	3.3E-04	12.6 ± 0.7	0.001	1.09 ± 0.04	6.9E-05
1pW2	30-122	—	—	—	—	164.0 ± 1.1	1.7E-16	174.4 ± 1.4	1.2E-16	179.3 ± 1.4	1.3E-19	167.2 ± 1.3	0.023	183.6 ± 1.6	0.002	196.7 ± 1.6	0.071	—	—	—	—	125.0 ± 2.5	0.157	60.7 ± 1.1	8.4E-08	12.6 ± 1.1	0.018	0.80 ± 0.05	0.248
1pW5-2	30-88	—	—	—	—	168.0 ± 1.2	1.9E-08	172.8 ± 1.8	5.4E-14	177.7 ± 1.7	3.0E-17	175.2 ± 1.1	8.9E-04	190.6 ± 1.4	0.503	200.0 ± 1.5	0.870	—	—	—	—	134.1 ± 2.4	0.134	66.2 ± 1.5	0.058	10.9 ± 0.6	2.8E-07	0.88 ± 0.06	0.9835
1pW4-1	29-98	0.74 ± 0.01	0.225	4.02 ± 0.04	2.9E-04	171.5 ± 1.3	0.002	183.0 ± 1.4	5.7E-06	185.3 ± 1.4	1.8E-11	171.0 ± 1.0	0.811	185.3 ± 1.0	0.002	195.0 ± 0.4	0.002	6.00 ± 0.26	0.015	120.8 ± 3.6	0.037	66.9 ± 2.7	0.342	11.2 ± 0.5	3.6E-08	0.87 ± 0.05	0.967	—	—
1pW4-2	27-72	—	—	—	—	172.9 ± 1.3	0.023	179.0 ± 1.3	9.2E-11	190.4 ± 1.5	4.6E-05	174.4 ± 6.5	0.011	191.0 ± 1.4	0.351	200.9 ± 1.4	0.719	—	—	—	—	128.0 ± 2.2	0.608	67.2 ± 2.2	0.303	13.3 ± 0.7	0.012	0.85 ± 0.03	0.624
1pW4-3	42-67	0.75 ± 0.01	0.038	4.19 ± 0.05	2.8E-06	172.9 ± 1.4	0.018	178.9 ± 0.5	2.1E-09	194.0 ± 2.5	0.0617	168.1 ± 1.7	0.071	182.1 ± 1.3	7.7E-06	192.6 ± 2.4	1.2E-04	5.18 ± 0.21	2.5E-06	155.8 ± 4.5	6.1E-11	—	—	—	—	—	—	—	—
1pW4-4	61-83	0.73 ± 0.01	0.567	4.13 ± 0.04	3.8E-06	171.2 ± 1.4	0.002	180.0 ± 1.7	2.2E-07	187.7 ± 1.8	1.9E-06	171.4 ± 1.2	0.634	184.1 ± 1.3	0.001	196.7 ± 1.4	0.034	5.38 ± 0.22	3.5E-05	147.2 ± 2.4	7.4E-09	—	—	—	—	—	—	—	—
1pW6-2	27-65	—	—	—	—	165.9 ± 1.6	1.5E-07	172.0 ± 1.5	2.0E-18	176.8 ± 1.8	6.6E-17	171.4 ± 1.6	0.726	187.4 ± 1.8	0.325	194.9 ± 2.1	0.025	—	—	—	—	130.6 ± 3.1	0.776	56.3 ± 1.2	3.5E-12	10.5 ± 0.9	6.3E-06	1.08 ± 0.05	7.0E-04
1pW6-1	27-85	0.68 ± 0.01	9.1E-04	3.88 ± 0.03	0.680	167.5 ± 1.4	3.3E-07	172.4 ± 1.2	5.1E-22	180.5 ± 1.5	1.8E-16	172.7 ± 1.0	0.113	185.1 ± 1.1	0.002	196.9 ± 1.5	0.073	4.87 ± 0.21	6.8E-07	133.7 ± 3.3	0.271	58.8 ± 1.5	1.5E-07	10.7 ± 0.4	1.2E-09	1.05 ± 0.05	0.0024	—	—
1pW3-2	26-79	—	—	—	—	157.5 ± 1.3	7.4E-25	157.6 ± 1.5	8.9E-35	165.9 ± 1.5	7.7E-33	168.0 ± 1.1	0.045	183.7 ± 1.3	2.7E-04	196.0 ± 1.4	0.016	—	—	—	—	132.4 ± 3.9	0.508	57.8 ± 1.7	2.4E-07	10.7 ± 0.5	1.2E-08	1.08 ± 0.05	7.8E-04
1pW3-1	24-116	—	—	—	—	170.7 ± 1.1	4.2E-05	176.5 ± 1.8	9.8E-09	184.2 ± 2.3	3.9E-07	174.4 ± 1.1	0.009	189.9 ± 1.4	0.804	203.3 ± 2.2	0.225	—	—	—	—	124.1 ± 2.3	0.074	55.4 ± 2.6	1.4E-05	14.1 ± 1.0	0.150	0.87 ± 0.05	0.968
1pW8	25-68	—	—	—	—	174.5 ± 1.2	0.199	180.6 ± 1.8	2.4E-06	188.2 ± 1.9	1.7E-05	167.8 ± 1.5	0.082	182.9 ± 1.8	0.002	196.0 ± 1.8	0.051	—	—	—	—	123.9 ± 4.2	0.220	60.3 ± 1.7	2.1E-05	12.0 ± 0.4	1.7E-06	0.86 ± 0.03	0.7409
1pW10	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
1pW9	61-90	—	—	—	—	179.9 ± 1.3	0.022	189.6 ± 1.4	0.479	—	—	180.1 ± 1.1	1.8E-08	196.7 ± 1.6	4.1E-04	—	—	—	—	—	—	—	88.1 ± 2.3	1.0E-07	—	—	—	—	—
1pW11	38-47	—	—	—	—	173.5 ± 1.4	0.093	183.7 ± 2.0	0.003	195.9 ± 2.1	0.363	170.5 ± 2.2	0.474	186.5 ± 3.2	0.323	192.3 ± 3.9	0.036	—	—	—	—	—	—	81.5 ± 2.6	3.0E-04	—	—	—	—

Table S10A. Phenotype comparison in male rats between progenitor and RNO3 congenic strains involving SHR and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR
SHR	23-74	1.11 ± 0.01	—	3.42 ± 0.04	—	166.1 ± 1.6	—	197.6 ± 2.0	—	322.1 ± 2.1	—	12.00 ± 0.33	—	9.74 ± 0.33	—	123.8 ± 3.5	—	59.9 ± 0.9	—	12.4 ± 0.5	—	0.98 ± 0.04	—
WKY	10-17	0.98 ± 0.01	—	2.61 ± 0.03	—	130.3 ± 2.0	—	123.4 ± 2.3	—	366.1 ± 4.6	—	13.25 ± 0.31	—	10.72 ± 0.34	—	108.3 ± 3.3	—	83.1 ± 3.1	—	12.5 ± 1.3	—	1.30 ± 0.06	—
3SW1	51-54	1.08 ± 0.01	0.039	3.19 ± 0.01	3.4E-06	179.2 ± 1.2	7.4E-04	187.6 ± 1.2	3.5E-05	337.5 ± 2.2	1.7E-06	8.92 ± 0.14	1.2E-09	8.02 ± 0.18	6.4E-05	120.4 ± 1.9	0.392	54.4 ± 0.9	2.1E-05	5.7 ± 0.3	1.5E-17	1.33 ± 0.06	9.3E-06
3SW4	85-120	1.10 ± 0.02	0.934	3.40 ± 0.05	0.744	170.3 ± 1.1	7.4E-13	176.5 ± 1.2	1.8E-14	327.3 ± 1.8	0.067	10.05 ± 0.12	5.9E-06	9.99 ± 0.18	0.526	124.6 ± 2.2	0.841	58.0 ± 0.1	0.149	9.3 ± 0.5	8.2E-05	1.35 ± 0.04	4.0E-08
3SW	53-67	1.03 ± 0.01	3.0E-06	3.27 ± 0.02	0.002	176.3 ± 1.1	2.5E-06	183.5 ± 1.3	4.0E-08	316.7 ± 2.0	0.066	9.81 ± 0.18	1.2E-06	8.99 ± 0.18	0.702	115.1 ± 2.4	0.044	47.3 ± 1.1	6.4E-14	6.8 ± 0.2	2.0E-14	1.05 ± 0.05	0.312
3SW5	36-39	1.01 ± 0.01	6.7E-07	3.42 ± 0.03	0.989	166.9 ± 2.5	9.9E-09	169.5 ± 2.2	3.4E-15	296.6 ± 3.0	9.5E-10	11.95 ± 0.18	0.896	10.54 ± 0.25	0.064	144.2 ± 2.6	8.7E-06	52.0 ± 0.8	2.7E-09	7.5 ± 0.5	8.2E-10	1.24 ± 0.05	1.0E-04
3SW3	30-33	1.08 ± 0.02	0.275	3.39 ± 0.05	0.642	175.2 ± 1.6	4.9E-06	177.4 ± 1.7	3.0E-11	322.0 ± 2.8	0.970	10.10 ± 0.18	1.4E-05	9.03 ± 0.22	0.083	143.5 ± 2.9	3.9E-05	56.4 ± 1.1	0.012	5.8 ± 0.3	1.2E-16	0.97 ± 0.04	0.756
3SW6	35-45	1.14 ± 0.01	0.038	3.54 ± 0.02	0.005	172.7 ± 1.9	6.2E-07	184.2 ± 1.9	4.0E-06	322.6 ± 3.3	0.911	11.17 ± 0.17	0.033	9.28 ± 0.28	0.294	134.6 ± 4.3	0.053	64.2 ± 1.0	0.002	12.5 ± 0.7	0.875	1.43 ± 0.04	2.3E-11
3SW2	29-30	1.07 ± 0.02	0.109	3.39 ± 0.05	0.701	175.9 ± 2.3	5.9E-04	183.2 ± 1.7	3.1E-07	315.5 ± 4.0	0.153	11.43 ± 0.23	0.161	8.97 ± 0.36	0.124	126.4 ± 3.4	0.589	54.7 ± 1.0	1.8E-04	8.7 ± 0.7	1.9E-04	1.33 ± 0.05	5.6E-07

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10B. Phenotype comparison in female rats between progenitor and RNO3 congenic strains involving SHR and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR
SHR	26-85	0.74 ± 0.01	—	3.83 ± 0.05	—	161.9 ± 1.3	—	173.6 ± 1.6	—	190.9 ± 1.2	—	7.29 ± 0.19	—	120.5 ± 3.2	—	69.0 ± 1.1	—	15.8 ± 0.3	—	1.13 ± 0.04	—	—	—
WKY	10-15	0.62 ± 0.01	—	2.66 ± 0.03	—	116.0 ± 1.8	—	118.8 ± 2.3	—	227.2 ± 2.2	—	11.43 ± 0.4	—	108.9 ± 4.0	—	89.9 ± 1.0	—	15.0 ± 0.6	—	1.18 ± 0.08	—	—	—
3SW1	39-45	0.74 ± 0.01	0.894	3.53 ± 0.02	3.1E-06	156.5 ± 1.0	0.001	161.5 ± 1.4	1.9E-07	210.2 ± 1.4	1.3E-17	7.20 ± 0.16	0.729	129.4 ± 2.5	0.038	84.7 ± 1.2	4.0E-15	10.2 ± 0.4	0.249	1.40 ± 0.04	1.5E-05	—	—
3SW4	79-125	0.73 ± 0.01	0.187	3.70 ± 0.03	0.036	153.1 ± 1.0	3.5E-07	160.7 ± 1.3	3.0E-09	202.5 ± 3.8	5.7E-05	8.20 ± 0.12	1.8E-04	124.2 ± 2.1	0.331	77.0 ± 0.9	3.8E-07	11.2 ± 0.6	0.508	1.24 ± 0.04	0.054	—	—
3SW	53-78	0.68 ± 0.005	1.2E-07	3.58 ± 0.02	5.4E-05	154.2 ± 1.1	1.1E-05	155.7 ± 1.4	7.1E-14	189.9 ± 1.3	0.564	8.86 ± 0.18	8.9E-08	120.9 ± 2.9	0.937	65.7 ± 1.1	0.039	9.1 ± 0.2	9.6E-06	0.99 ± 0.04	0.010	—	—
3SW5	33-37	0.71 ± 0.01	0.002	3.92 ± 0.03	0.119	146.1 ± 1.7	1.7E-10	150.4 ± 1.9	4.9E-14	180.2 ± 1.7	2.4E-08	7.88 ± 0.16	0.019	151.1 ± 2.2	6.2E-12	71.3 ± 1.1	0.156	7.7 ± 0.5	1.3E-06	1.19 ± 0.04	0.309	—	—
3SW3	45-51	0.74 ± 0.01	0.779	3.78 ± 0.03	0.484	156.0 ± 1.7	0.007	159.9 ± 1.2	3.7E-10	195.9 ± 1.4	0.008	7.23 ± 0.15	0.810	134.2 ± 2.0	4.2E-04	74.6 ± 0.8	1.1E-04	6.5 ± 0.4	2.0E-13	1.10 ± 0.03	0.566	—	—
3SW6	45-59	0.75 ± 0.01	0.759	3.98 ± 0.02	0.009	152.0 ± 1.6	3.7E-06	158.1 ± 1.6	4.4E-10	188.2 ± 1.5	0.148	7.38 ± 0.18	0.739	149.1 ± 2.5	1.6E-10	78.3 ± 1.7	2.0E-05	10.9 ± 0.6	0.876	1.52 ± 0.04	8.0E-10	—	—
3SW2	41-44	0.72 ± 0.01	0.025	3.82 ± 0.02	0.964	155.3 ± 1.4	9.6E-04	161.4 ± 1.3	6.0E-08	187.8 ± 1.5	0.106	7.31 ± 0.14	0.931	139.9 ± 2.4	4.5E-06	75.7 ± 1.0	2.7E-05	8.5 ± 0.6	0.001	1.17 ± 0.04	0.468	—	—

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10C. Pairwise phenotype comparison (in male and female rats) between RNO3 congenic strains involving SHR and WKY for sequential analysis

A pair of congenic strains	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P
3SW1_3SW4	0.125	0.150	9.8E-05	8.2E-06	1.5E-07	0.016	6.8E-10	0.518	5.2E-04	0.009	2.1E-08	N/A	4.5E-12	3.9E-06	0.146	0.137	0.007	1.7E-06	3.8E-07	0.151	0.736	0.007
3SW4_3SW	1.1E-04	5.5E-07	0.022	0.001	1.8E-04	0.472	7.9E-05	0.008	1.6E-04	1.8E-05	0.275	N/A	0.710	0.003	0.005	0.349	2.5E-10	5.6E-12	1.4E-04	9.3E-04	1.1E-05	1.6E-05
3SW_3SW5	0.174	0.009	4.2E-04	5.2E-12	1.0E-03	1.6E-04	4.6E-07	0.029	4.0E-07	2.3E-05	9.1E-13	N/A	0.042	9.0E-05	3.3E-12	1.2E-12	8.6E-04	5.8E-04	0.179	0.013	0.005	5.0E-04
3SW5_3SW3	0.001	7.3E-04	0.637	0.004	0.0056	8.1E-05	0.0056	7.8E-05	4.3E-08	9.8E-10	7.0E-10	N/A	3.0E-05	0.004	0.855	2.4E-07	0.002	0.016	0.004	0.054	1.8E-05	0.085
3SW4_3SW6	0.069	0.077	0.007	2.2E-10	0.272	0.716	0.0009	0.939	0.215	2.6E-06	1.5E-06	N/A	0.038	2.7E-04	0.041	7.3E-12	3.9E-05	0.475	4.7E-04	0.694	0.181	4.1E-06

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10D. Phenotype comparison in male rats between progenitor and RNO3 congenic strains involving SHRSP and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP
SHRSP	38-173	1.07 ± 0.01	—	3.82 ± 0.03	—	211.1 ± 1.0	—	236.9 ± 1.5	—	283.7 ± 1.7	—	11.05 ± 0.22	—	8.22 ± 0.23	—	133.9 ± 3.3	—	52.2 ± 1.0	—	15.7 ± 0.8	—	1.12 ± 0.06	—
WKY	10-27	0.88 ± 0.01	—	2.61 ± 0.03	—	130.3 ± 2.0	—	123.4 ± 2.3	—	366.1 ± 4.6	—	13.25 ± 0.31	—	10.72 ± 0.34	—	108.3 ± 3.3	—	83.1 ± 3.1	—	12.5 ± 1.3	—	1.30 ± 0.06	—
3PW1	35-36	1.02 ± 0.01	0.001	3.44 ± 0.02	2.5E-15	198.6 ± 2.1	2.1E-06	205.3 ± 2.0	3.1E-20	295.6 ± 4.2	0.009	9.26 ± 0.17	2.5E-08	7.53 ± 0.20	0.027	132.7 ± 2.7	0.787	49.2 ± 0.5	0.010	10.0 ± 0.5	6.0E-08	1.33 ± 0.05	0.011
3PW4	34-37	1.00 ± 0.01	1.2E-08	3.55 ± 0.03	6.5E-09	201.2 ± 1.8	1.0E-05	211.7 ± 2.1	1.2E-14	280.8 ± 1.6	0.296	9.22 ± 0.22	1.4E-07	7.88 ± 0.17	0.229	132.1 ± 2.4	0.656	40.5 ± 0.7	2.0E-13	8.8 ± 0.5	5.6E-10	1.05 ± 0.06	0.453
3PW	40-67	1.01 ± 0.01	4.3E-04	3.50 ± 0.02	6.0E-12	192.7 ± 1.6	1.3E-16	200.7 ± 1.7	1.7E-31	285.1 ± 2.4	0.510	9.45 ± 0.20	1.3E-06	9.42 ± 0.17	5.9E-05	127.1 ± 2.5	0.013	39.8 ± 0.6	6.8E-16	8.6 ± 1.2	1.4E-04	0.98 ± 0.04	0.066
3PW5	70-80	1.07 ± 0.01	0.966	3.72 ± 0.02	0.008	188.0 ± 1.7	3.9E-22	203.5 ± 1.7	5.0E-32	287.5 ± 2.0	0.103	11.08 ± 0.13	0.903	9.75 ± 0.19	1.7E-06	139.7 ± 1.8	0.121	48.6 ± 0.6	2.0E-13	7.6 ± 0.7	3.1E-11	1.10 ± 0.04	0.794
3PW3	33-39	0.97 ± 0.01	8.6E-08	3.45 ± 0.03	4.5E-12	191.0 ± 2.0	1.1E-12	197.9 ± 2.4	1.5E-20	282.3 ± 2.8	0.790	10.25 ± 0.17	0.006	9.27 ± 0.24	0.002	132.7 ± 2.0	0.763	49.0 ± 0.6	0.009	5.8 ± 0.4	2.5E-16	0.86 ± 0.03	3.0E-04
3PW2	83-89	1.06 ± 0.01	0.477	3.72 ± 0.02	0.011	201.0 ± 1.5	4.4E-08	215.5 ± 1.8	7.7E-17	285.9 ± 1.6	0.242	12.02 ± 0.17	8.3E-04	9.08 ± 0.16	0.003	131.7 ± 2.2	0.588	50.7 ± 0.5	0.190	11.1 ± 0.6	1.6E-05	1.27 ± 0.05	0.066

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10E. Phenotype comparison in female rats between progenitor and RNO3 congenic strains involving SHRSP and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP
SHRSP	35-195	0.72 ± 0.01	—	3.86 ± 0.02	—	176.3 ± 0.8	—	190.8 ± 1.1	—	189.4 ± 0.8	—	6.92 ± 0.26	—	129.5 ± 1.9	—	69.7 ± 1.0	—	15.7 ± 0.6	—	0.88 ± 0.03	—
WKY	10-15	0.62 ± 0.01	—	2.66 ± 0.03	—	118.0 ± 1.8	—	118.8 ± 2.3	—	227.2 ± 2.2	—	11.43 ± 0.4	—	109.9 ± 4.0	—	89.9 ± 3.1	—	15.3 ± 0.6	—	1.18 ± 0.08	—
3Pw1	39-41	0.73 ± 0.01	0.496	3.65 ± 0.01	3.2E-14	176.5 ± 2.1	0.941	178.5 ± 1.9	3.0E-07	199.8 ± 1.9	4.7E-06	6.81 ± 0.15	0.703	135.2 ± 1.7	0.027	70.5 ± 0.9	0.556	11.9 ± 0.5	2.3E-06	0.86 ± 0.04	0.762
3Pw4	43-54	0.67 ± 0.01	0.536	3.79 ± 0.03	0.003	179.3 ± 0.9	0.189	176.5 ± 0.4	0.068	178.5 ± 1.6	0.048	7.85 ± 0.16	0.048	139.1 ± 1.6	3.1E-04	51.2 ± 1.0	4.8E-10	10.4 ± 0.4	7.1E-11	0.97 ± 0.04	0.663
3Pw5	34-40	0.73 ± 0.01	0.536	3.80 ± 0.03	0.120	166.3 ± 1.4	5.9E-09	167.5 ± 1.9	2.5E-17	187.3 ± 1.2	0.227	9.64 ± 0.17	2.6E-12	128.9 ± 2.5	0.841	63.3 ± 0.6	0.001	12.3 ± 0.5	9.8E-05	0.91 ± 0.06	0.604
3Pw5	79	0.73 ± 0.00	0.625	3.93 ± 0.02	0.003	160.5 ± 1.6	1.1E-14	170.4 ± 1.1	3.9E-19	184.9 ± 1.0	7.2E-04	9.27 ± 0.16	1.1E-10	150.5 ± 2.2	1.2E-10	64.3 ± 1.3	0.008	9.5 ± 0.7	1.4E-09	0.94 ± 0.03	0.187
3Pw3	28-35	0.67 ± 0.01	1.4E-04	3.61 ± 0.03	5.1E-10	166.2 ± 1.6	8.6E-07	169.0 ± 2.0	4.9E-13	185.4 ± 2.1	0.086	8.38 ± 0.21	5.1E-05	145.0 ± 2.5	6.9E-06	64.3 ± 1.5	0.003	10.9 ± 0.9	5.6E-05	0.85 ± 0.04	0.640
3Pw2	69-72	0.74 ± 0.01	0.065	4.00 ± 0.02	4.4E-07	170.7 ± 1.7	0.003	179.4 ± 1.7	1.6E-07	185.6 ± 1.0	0.005	7.92 ± 0.13	0.001	142.9 ± 2.9	2.6E-04	64.3 ± 1.2	0.007	9.7 ± 0.4	7.9E-13	0.86 ± 0.03	0.764

Table S10G. Phenotype comparison in male rats between progenitor and RNO4 congenic strains involving SHR and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR
SHR	23-74	1.11 ± 0.01	—	3.42 ± 0.04	—	186.1 ± 1.6	—	197.6 ± 2.0	—	322.1 ± 2.1	—	12.00 ± 0.33	—	9.74 ± 0.33	—	123.8 ± 3.5	—	59.9 ± 0.9	—	12.4 ± 0.5	—	0.98 ± 0.04	—
WKY	10-27	0.98 ± 0.01	—	2.61 ± 0.03	—	130.3 ± 2.0	—	123.4 ± 2.3	—	366.6 ± 4.6	—	13.25 ± 0.31	—	10.72 ± 0.34	—	108.3 ± 3.3	—	83.1 ± 3.1	—	12.5 ± 1.3	—	1.30 ± 0.06	—
4SW2	32-39	1.10 ± 0.01	0.620	3.50 ± 0.03	0.081	173.9 ± 1.7	1.E-06	178.8 ± 1.6	6.E-11	312.6 ± 2.9	0.010	10.60 ± 0.16	0.001	8.70 ± 0.25	0.016	129.8 ± 2.0	0.132	62.7 ± 0.8	0.026	9.6 ± 0.4	3.E-05	1.11 ± 0.03	0.022
4SW3	33-43	1.07 ± 0.01	0.021	3.48 ± 0.02	0.151	175.1 ± 1.6	4.E-06	180.2 ± 1.8	4.E-09	307.4 ± 2.8	6.E-05	10.77 ± 0.22	0.003	8.16 ± 0.22	3.E-04	120.0 ± 2.7	0.068	66.1 ± 0.9	5.E-06	11.1 ± 0.5	0.075	1.27 ± 0.03	1.E-06
4SW4	33-40	1.12 ± 0.01	0.526	3.53 ± 0.03	0.032	187.8 ± 1.8	0.480	203.3 ± 1.9	0.040	315.2 ± 2.8	0.053	10.82 ± 0.22	0.004	8.55 ± 0.22	0.005	115.9 ± 3.0	0.089	66.2 ± 0.8	1.E-06	11.9 ± 0.5	0.523	1.41 ± 0.03	1.E-11
4SW1	33-49	1.06 ± 0.01	0.011	3.33 ± 0.02	0.056	175.8 ± 1.8	5.E-05	183.9 ± 2.1	8.E-06	317.6 ± 3.2	0.241	10.71 ± 0.19	0.002	8.50 ± 0.17	0.002	136.5 ± 2.3	0.003	63.3 ± 0.9	0.010	11.3 ± 0.7	0.186	1.30 ± 0.04	9.E-07
4SW5	38-51	1.10 ± 0.02	0.703	3.47 ± 0.03	0.279	175.9 ± 1.8	6.E-05	188.5 ± 2.4	0.005	316.1 ± 3.5	0.145	11.57 ± 0.32	0.349	9.96 ± 0.38	0.665	134.9 ± 3.2	0.021	68.6 ± 1.0	5.E-09	13.9 ± 1.4	0.288	1.41 ± 0.05	4.E-09
4SW6	37-50	1.14 ± 0.02	0.118	3.65 ± 0.04	1.E-04	173.7 ± 1.8	1.E-06	180.3 ± 2.0	2.E-08	313.2 ± 3.3	0.025	10.31 ± 0.21	1.E-04	7.61 ± 0.18	2.E-06	133.3 ± 2.2	0.022	62.5 ± 1.2	0.089	10.8 ± 0.4	0.016	1.30 ± 0.04	1.E-06
4SW	34-43	0.99 ± 0.01	7.E-11	3.28 ± 0.02	0.002	182.9 ± 1.7	0.172	190.8 ± 1.4	0.006	303.4 ± 2.3	4.E-08	10.30 ± 0.24	2.E-04	8.77 ± 0.24	0.022	118.0 ± 2.9	0.207	54.0 ± 0.8	2.E-06	13.3 ± 0.8	0.295	1.16 ± 0.04	0.004

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10H. Phenotype comparison in female rats between progenitor and RNO4 congenic strains involving SHR and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR
SHR	26-85	0.74 ± 0.01	—	3.83 ± 0.05	—	161.9 ± 1.3	—	173.6 ± 1.6	—	190.9 ± 1.2	—	7.29 ± 0.19	—	120.5 ± 3.2	—	69.0 ± 1.1	—	10.8 ± 0.3	—	1.13 ± 0.04	—
WKY	10-15	0.62 ± 0.01	—	2.66 ± 0.03	—	116.0 ± 1.8	—	118.8 ± 2.3	—	227.2 ± 2.2	—	11.43 ± 0.4	—	108.9 ± 4.0	—	89.9 ± 3.1	—	15.3 ± 0.6	—	1.18 ± 0.08	—
4SW2	32-38	0.76 ± 0.01	0.152	3.91 ± 0.03	0.163	152.8 ± 1.4	1.E-05	157.7 ± 1.2	4.E-12	194.5 ± 1.4	0.054	6.96 ± 0.15	0.004	122.9 ± 3.7	0.626	85.0 ± 1.2	1.E-14	9.2 ± 0.4	0.002	1.43 ± 0.04	3.E-07
4SW3	30-38	0.72 ± 0.01	0.054	3.92 ± 0.02	0.076	155.7 ± 1.6	0.004	152.2 ± 1.5	3.E-15	184.1 ± 1.5	9.E-04	6.50 ± 0.18	0.003	131.1 ± 2.9	0.017	78.8 ± 1.4	2.E-06	9.7 ± 0.5	0.074	1.45 ± 0.04	5.E-07
4SW4	32-38	0.73 ± 0.01	0.419	3.88 ± 0.02	0.341	155.4 ± 1.6	0.002	168.6 ± 1.8	0.041	189.1 ± 1.6	0.348	6.81 ± 0.21	0.090	117.2 ± 4.0	0.519	79.4 ± 1.3	3.E-08	9.8 ± 0.6	0.124	1.53 ± 0.05	5.E-09
4SW1	32-38	0.70 ± 0.01	3.E-04	3.72 ± 0.03	0.083	156.0 ± 1.8	0.011	163.2 ± 1.7	3.E-05	188.2 ± 2.0	0.262	6.75 ± 0.18	0.045	131.9 ± 1.8	0.002	77.2 ± 1.4	3.E-05	8.9 ± 0.4	0.001	1.34 ± 0.04	5.E-04
4SW5	37-57	0.76 ± 0.01	0.187	3.92 ± 0.04	0.141	154.4 ± 1.7	8.E-04	161.1 ± 1.8	1.E-06	192.7 ± 2.1	0.459	8.28 ± 0.45	0.045	135.4 ± 3.2	6.E-04	84.2 ± 1.3	8.E-14	13.0 ± 1.2	0.083	1.60 ± 0.04	3.E-13
4SW6	34-49	0.75 ± 0.01	0.460	4.03 ± 0.03	6.E-04	156.9 ± 1.2	0.005	159.1 ± 1.5	3.E-09	186.4 ± 1.4	0.018	6.69 ± 0.15	0.018	134.2 ± 2.6	0.001	85.4 ± 1.5	8.E-13	10.4 ± 0.5	0.487	1.33 ± 0.05	0.002
4SW	26-41	0.70 ± 0.01	0.001	3.69 ± 0.02	0.015	158.9 ± 1.6	0.157	166.7 ± 1.5	0.002	189.8 ± 2.1	0.634	7.28 ± 0.21	0.969	118.7 ± 3.2	0.692	74.4 ± 1.6	0.008	11.3 ± 0.5	0.417	1.32 ± 0.06	0.009

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10I. Pairwise phenotype comparison (in male and female rats) between RNO4 congenic strains involving SHR and WKY for sequential analysis

A pair of congenic strains	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P	Male, P	Female, P
4SW2_4SW3	0.091	3.E-04	0.508	0.616	0.617	0.188	0.560	0.005	0.202	6.E-06	0.532	0.111	0.778	0.549	0.088	0.007	0.002	0.011	0.452	0.002	0.636	
4SW3_4SW4	0.006	0.267	0.203	0.160	9.E-07	0.879	2.E-13	3.E-09	0.051	0.030	0.886	0.220	0.258	2.E-04	0.007	0.955	0.731	0.266	0.932	0.003	0.228	
4SW4_4SW1	0.003	0.002	8.E-06	3.E-04	9.E-06	0.794	1.E-09	0.037	0.573	0.745	0.731	0.866	0.840	5.E-07	0.002	0.019	0.242	0.446	0.256	0.041	0.003	
4SW1_4SW5	0.071	3.2E-07	5.E-04	2.E-04	0.966	0.535	0.159	0.393	0.745	0.133	0.025	0.001	0.003	0.681	0.297	2.E-04	6.E-04	0.083	0.003	0.102	3.E-05	
4SW5_4SW6	7.E-15	0.620	4.E-16	0.012	0.691	0.256	0.011	0.413	0.549	0.017	2.E-09	9.E-07	0.002	0.685	0.759	8.E-16	0.550	2.E-06	0.051	3.E-12	6.E-05	
4SW1_4SW	2.E-04	0.897	0.048	0.430	0.005	0.241	0.009	0.130	5.E-04	0.600	0.191	0.380	0.060	4.E-06	7.E-04	5.E-11	0.197	0.042	0.001	0.015	0.816	

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10J. Phenotype comparison in male rats between progenitor and RNO15 congenic strains involving SHR and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR
SHR	23-74	1.11 ± 0.01	—	3.42 ± 0.04	—	186.1 ± 1.6	—	197.6 ± 2.0	—	322.1 ± 2.1	—	12.00 ± 0.33	—	9.74 ± 0.33	—	123.8 ± 3.5	—	59.9 ± 0.9	—	12.4 ± 0.5	—	0.98 ± 0.04	—
WKY	10-27	0.98 ± 0.01	—	2.61 ± 0.03	—	130.3 ± 2.0	—	123.4 ± 2.3	—	366.6 ± 4.6	—	13.25 ± 0.31	—	10.72 ± 0.34	—	108.3 ± 3.3	—	83.1 ± 3.1	—	12.5 ± 1.3	—	1.30 ± 0.06	—
15SW2	34-74	1.06 ± 0.02	0.081	3.46 ± 0.04	0.404	172.0 ± 1.5	4.4E-09	179.3 ± 1.4	2.5E-11	315.5 ± 2.2	0.093	10.24 ± 0.21	3.5E-04	8.32 ± 0.25	0.010	129.1 ± 2.9	0.088	59.1 ± 0.8	0.334	11.6 ± 0.5	0.430	1.03 ± 0.05	0.5630
15SW	22-75	0.90 ± 0.02	9.3E-13	3.15 ± 0.02	1.7E-07	168.2 ± 1.9	8.9E-11	172.3 ± 1.9	1.8E-15	310.9 ± 3.0	0.003	11.14 ± 0.33	0.090	9.18 ± 0.36	0.289	137.8 ± 3.2	0.004	64.1 ± 1.2	0.006	13.3 ± 0.9	0.395	0.94 ± 0.03	0.3799
15SW1	34-67	1.05 ± 0.01	0.001	3.28 ± 0.04	0.009	170.3 ± 1.4	1.5E-11	177.2 ± 1.3	1.5E-13	323.7 ± 2.0	0.587	11.24 ± 0.19	0.053	8.72 ± 0.26	0.020	143.5 ± 3.3	8.8E-05	51.8 ± 0.8	2.2E-09	16.4 ± 0.9	2.8E-04	0.95 ± 0.05	0.6369

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10K. Phenotype comparison in female rats between progenitor and RNO15 congenic strains involving SHR and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR	mean ± SE	P, vs SHR
SHR	26-85	0.74 ± 0.01	—	3.83 ± 0.05	—	161.9 ± 1.3	—	173.6 ± 1.6	—	190.9 ± 1.2	—	7.29 ± 0.19	—	120.5 ± 3.2	—	69.0 ± 1.1	—	10.8 ± 0.3	—	1.13 ± 0.04	—
WKY	10-15	0.62 ± 0.01	—	2.66 ± 0.03	—	116.0 ± 1.8	—	118.8 ± 2.3	—	227.2 ± 2.2	—	11.43 ± 0.4	—	108.9 ± 4.0	—	89.9 ± 3.1	—	15.3 ± 0.6	—	1.18 ± 0.08	—
15SW2	33-58	0.72 ± 0.01	0.054	3.78 ± 0.03	0.405	156.7 ± 1.4	0.008	164.2 ± 1.6	5.9E-05	196.8 ± 1.5	0.003	7.84 ± 0.15	0.108	128.7 ± 3.2	0.071	82.4 ± 1.5	1.5E-09	11.9 ± 0.5	0.047	0.94 ± 0.04	0.001
15SW	28-106	0.64 ± 0.01	3.0E-12	3.58 ± 0.03	1.4E-04	146.2 ± 1.6	3.6E-12	144.0 ± 1.4	7.7E-28	191.7 ± 1.4	0.663	6.95 ± 0.25	0.282	140.3 ± 2.7	7.2E-06	86.0 ± 1.1	2.4E-17	12.4 ± 0.5	0.008	1.15 ± 0.03	0.618
15SW1	33-63	0.70 ± 0.01	0.001	3.71 ± 0.02	0.044	149.6 ± 1.4	3.7E-09	153.2 ± 1.2	8.1E-18	191.3 ± 1.3	0.845	5.99 ± 0.23	2.2E-06	144.1 ± 2.1	1.8E-08	72.0 ± 1.0	0.046	14.5 ± 0.4	1.2E-11	1.04 ± 0.04	0.107

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10L. Pairwise phenotype comparison (in male and female rats) between RNO15 congenic strains involving SHR and WKY for sequential analysis

A pair of congenic strains	Hw (g)			Hw/Bw (%)			12wk BP (mmHg)			16wk BP (mmHg)			16wk Bw (g)			T.adip./BW (%)			P.adip./BW (%)			FPG			T.chol			TG			NEFA		
	Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P	
15SW2-15SW	1.0E-08	4.9E-10		4.E-08	3.0E-05		0.170	2.2E-06		0.004	9.0E-17		0.221	0.017		0.040	N/A		0.078	0.020		0.047	0.007		9.3E-04	0.064		0.113	0.488		0.105	4.9E-05	
15SW-15SW1	1.7E-08	9.9E-07		0.003	0.002		0.484	0.125		0.034	1.6E-06		4.7E-04	0.813		0.823	N/A		0.345	0.002		0.223	0.266		8.E-12	4.8E-14		0.017	0.001		0.803	0.029	

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10M. Phenotype comparison in male rats between progenitor and RNO15 congenic strains involving SHRSP and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		T.adip./BW (%)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP
SHRSP	38-173	1.07 ± 0.01	—	3.82 ± 0.03	—	211.1 ± 1.0	—	236.9 ± 1.5	—	283.7 ± 1.7	—	11.05 ± 0.22	—	8.22 ± 0.23	—	133.9 ± 3.3	—	52.2 ± 1.0	—	15.7 ± 0.8	—	1.12 ± 0.06	—
WKY	10-27	0.98 ± 0.01	—	2.61 ± 0.03	—	130.3 ± 2.0	—	123.4 ± 2.3	—	366.6 ± 4.6	—	13.25 ± 0.31	—	10.72 ± 0.34	—	108.3 ± 3.3	—	83.1 ± 3.1	—	12.5 ± 1.3	—	1.30 ± 0.06	—
15pW2	27-63	1.05 ± 0.01	0.177	3.60 ± 0.02	9.3E-07	197.4 ± 1.2	2.4E-15	208.7 ± 1.6	3.2E-25	290.0 ± 1.7	0.005	10.86 ± 0.20	0.529	7.83 ± 0.26	0.263	145.2 ± 2.4	0.007	44.4 ± 1.2	4.5E-06	14.6 ± 0.8	0.340	0.89 ± 0.05	0.006
15pW	24-102	0.96 ± 0.01	1.8E-13	3.51 ± 0.03	4.3E-10	202.1 ± 2.0	7.3E-05	213.1 ± 1.7	2.0E-20	287.5 ± 1.9	0.094	9.65 ± 0.20	1.7E-04	8.36 ± 0.21	0.692	141.0 ± 3.5	0.096	64.7 ± 0.7	9.1E-16	13.1 ± 0.6	0.011	1.01 ± 0.04	0.132
15pW1	30-72	1.09 ± 0.01	0.225	3.52 ± 0.02	1.7E-11	197.4 ± 1.5	2.5E-12	211.2 ± 1.6	2.6E-23	311.6 ± 1.8	4.2E-24	10.67 ± 0.19	0.198	8.28 ± 0.18	0.825	132.7 ± 2.7	0.775	59.7 ± 2.7	0.013	14.7 ± 0.8	0.428	1.04 ± 0.04	0.319

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10N. Phenotype comparison in female rats between progenitor and RNO15 congenic strains involving SHRSP and WKY

Strain	n	Hw (g)		Hw/Bw (%)		12wk BP (mmHg)		16wk BP (mmHg)		16wk Bw (g)		P.adip./BW (%)		FPG		T.chol		TG		NEFA	
		mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP	mean ± SE	P, vs SHRSP
SHRSP	35-195	0.72 ± 0.01	—	3.86 ± 0.02	—	176.3 ± 0.8	—	190.8 ± 1.1	—	189.4 ± 0.8	—	6.92 ± 0.26	—	129.5 ± 1.9	—	69.7 ± 1.0	—	15.7 ± 0.6	—	0.88 ± 0.03	—
WKY	10-15	0.62 ± 0.01	—	2.66 ± 0.03	—	116.0 ± 1.8	—	118.8 ± 2.3	—	227.2 ± 2.2	—	11.43 ± 0.4	—	108.9 ± 4.0	—	89.9 ± 3.1	—	15.3 ± 0.6	—	1.18 ± 0.08	—
15pW2	31-74	0.71 ± 0.01	0.404	3.75 ± 0.02	0.001	170.5 ± 1.3	2.0E-04	177.8 ± 1.4	2.1E-11	188.5 ± 1.1	0.551	7.13 ± 0.19	0.503	145.4 ± 1.7	7.7E-09	53.2 ± 1.7	3.5E-11	14.1 ± 0.6	0.052	0.70 ± 0.03	1.0E-04
15pW	30-121	0.67 ± 0.01	1.3E-05	3.60 ± 0.02	6.5E-14	174.8 ± 1.7	0.424	179.6 ± 1.2	1.0E-10	186.3 ± 0.9	0.015	6.31 ± 0.28	0.083	141.0 ± 2.5	4.1E-04	90.1 ± 1.7	1.0E-14	16.7 ± 0.9	0.347	0.94 ± 0.04	0.157
15pW1	31-72	0.73 ± 0.01	0.305	3.71 ± 0.02	3.5E-08	171.9 ± 1.8	0.031	181.1 ± 1.7	4.1E-06	195.8 ± 1.4	1.2E-04	6.38 ± 0.21	0.098	137.3 ± 1.8	0.004	82.5 ± 3.2	0.001	14.6 ± 0.7	0.234	0.88 ± 0.04	0.928

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S10O. Pairwise phenotype comparison (in male and female rats) between RNO15 congenic strains involving SHRSP and WKY for sequential analysis

A pair of congenic strains	Hw (g)			Hw/Bw (%)			12wk BP (mmHg)			16wk BP (mmHg)			16wk Bw (g)			T.adip./BW (%)			P.adip./BW (%)			FPG			T.chol			TG			NEFA		
	Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P		Male, P	Female, P	
15pW2-15pW	5.7E-09	5.6E-06		0.015	1.9E-05		0.042	0.044		0.061	0.332		0.332	0.124		0.001	N/A		0.165	0.007		0.264	0.147		5.9E-19	5.7E-23		0.118	0.014		0.060	7.9E-06	
15pW-15pW1	7.0E-15	8.4E-08		0.851	0.001		0.057	0.244		0.413	0.482		8.E-17	6.0E-08		0.003	N/A		0.813	0.825		0.032	0.243		0.080	0.042		0.108	0.065		0.587	0.266	

Hw, heart weight; Hw/Bw, heart weight divided by body weight; BP, blood pressure; T.adip, peri-testis fat pad; P.adip, retroperitoneal fat pad; FPG, fasting plasma glucose; T.chol, total cholesterol; TG, triglycerides; NEFA, non-esterified fatty acid.

Table S11A. Chromosomal fragments introgressed into SHRSP/SHR-derived RNO1 congenic rat strains

Marker	Position: Rnor_6.0*	Allele			SHRSP-derived																SHR-derived	
		SHRSP	SHR	WKY	1pW	1pWC	1pW2	1pW5-2	1pW4-1	1pW4-2	1pW4-3	1pW4-4	1pW6-2	1pW6-1	1pW3-2	1pW3-1	1pW8	1pW10	1pW9	1pW11	1SW	1SWC
D1Mgh2	23,406,428	145	145	153	○																○	○
D1Rat196	58,354,072	192	192	190		*	*	*	*	*												
D1Mgh5	79,689,548	157	161	161		○	○	○	○	○												
D1Rat178	88,429,368	124	120	120						○	*											
D1Rat224	93,410,058	166	166	169						*	*											
D1Rat27	94,201,400	182	184	187							○											
intergenic	98,018,170	-	-	TATAT ATACA C					○		○	☆										
rs64143603	98,394,078	G/G	G/G	T/T					○		○	○										
<i>Klk1b3</i> (Ngfg_2)	100,198,334	T.T	T.T	del.A					○		○	○										
intergenic	102,082,430	C/C	del	del					○		○	○										
rs105531410	102,691,817	C/C	C/C	A/A					*		*	*										
D1Rat348	135,005,392	119	119	129									*									
D1Rat36	135,022,396	120	120	136									○									
D1Rat37	135,040,605	122	122	126										*								
D1Rat40	135,428,373	122	122	130																		
D1Rat270	135,611,773	215	215	238				○						○								
D1Tkyo26 (<i>Ntrk3</i>)	139,865,346	135	135	96				*							*							
D1Mit2	140,953,686	148	148	146											*							
D1Tkyo27 (<i>Cib1</i>)	142,014,962	84	84	109											○							
D1Rat106	145,140,412	139	139	133			○						○	○		*						
D1Tkyo32 (<i>Ctsc</i>)	151,918,514	175	180	171			*						○	*		*						
D1Rat44	161,493,758	120	158	130									*				○					
D1Rat164	177,235,071	221	221	240													*					
D1Smu11 (<i>Calca</i>)	184,185,140	186	186	184														○				
D1Rat109	199,953,026	153	153	157														○	○	○		
D1Rat120	202,111,380	211	211	199														○	○	○		
D1Wox22	215,830,072	144	144	135											*	*	*					
D1Rat71	230,420,627	143	148	148															*	*		
D1Rat116	232,297,062	165	175	175														○	○			
D1Rat117	233,490,105	132	125	125		○												○	○			
D1Wox10	236,763,415	120	116	114		*												○	○			○
intergenic	237,963,635	C/C	T/T	T/T														○	○			
<i>Tmc1</i> (intron)	238,523,462	A/A	A/A	G/G															*			
D1Tkyo49 (<i>InsI6</i>)	247,468,493	183	176	183																		*
intergenic	252,270,835	T/T	T/T	C/C															*			
intergenic	252,279,320	T/T	T/T	G/G															○			
D1Tkyo56 (<i>Scd</i>)	264,157,471	268	266	266														*				
rs198971711	269,979,231	T/T	T/T	C/C														*		*		
D1Rat376 (<i>Sorcs1</i>)	270,122,139	219	219	217																*		
D1Tkyo58 (<i>Add3</i>)	273,856,421	171	171	163															○			
D1Rat90	281,795,624	156	156	128	○													*	○	○		○

Symbols show variants characterized on the border of congenic fragments: open circle (○) for the WKY allele and asterisk (*) for the recipient (SHRSP or SHR) allele.

*For SSLP markers, the position of 5'-primer site is shown.

Table S11B. Chromosomal fragments introgressed into SHRSP/SHR-derived RNO3 congenic rat strains

Marker	Position: Rnor_6.0*	Allele			SHRSP-derived						SHR-derived						
		SHRSP	SHR	WKY	3pW1	3pW4	3pW	3pW5	3pW3	3pW2	3SW1	3SW4	3SW	3SW5	3SW3	3SW6	3SW2
D3Mgh16	6,000,748	135	135	121	○	○	○				○	○	○				
D3Tkyo4 (Kynu)	28,448,867	158	152	144													*
D3Mit9	34,394,121	248	248	250													○
D3Rat80	36,599,933	272	242	212				*		*							
D3Rat186	45,228,240	140	140	147				○		○							
D3Rat110	47,155,167	133	133	117							○			*			
D3Mgh6	54,630,948	109	109	106	*						*			○		*	
D3Rat108	63,849,481	248	248	228												○	
D7Rat130	94,187,793	155	155	171													○
D3Mit16	97,537,495	293	293	289											*		*
D3Mgh5	103,141,814	136	136	128					*						○		
D3Rat166	106,900,427	186	186	175					○	○		○				○	
D3Mit14	120,917,788	196	196	202						*		*				*	
D3Mgh15	123,599,592	123	123	109		○											
D3Rat157	128,716,357	178	178	200		*											
D3Rat1	176,417,943	138	138	148			○	○	○				○	○	○		

Symbols show variants characterized on the border of congenic fragments: open circle (○) for the WKY allele and asterisk (*) for the recipient (SHRSP or SHR) allele.
*For SSLP markers, the position of 5'-primer site is shown.

Table S11C. Chromosomal fragments introgressed into SHR-derived RNO4 congenic rat strain

Marker	Position: Rnor_6.0*	Allele			SHR-derived						
		SHRSP	SHR	WKY	4SW	4SW6	4SW5	4SW1	4SW4	4SW3	4SW2
D4Wox27	3,044,017	109	109	119	○			○	○	○	○
D4Rat4	4,364,715	186	186	180			*				
D4Rat136	9,657,095	153	153	159			○				
intergenic	21,827,813	T	T	C							○
D4Rat10	26,753,655	175	173	171							*
intergenic	31,561,535	T	T	A						○	
intergenic	31,782,622	T	T	C						*	
D4Rat89	34,418,190	175/180	182	180/184		*			○		
intergenic	42,486,449	T	T	C		○			*		
D4Rat15	48,656,252	149	149	165	○			○			
intergenic	49,200,013	C	C	T		○	○	○			
intergenic	49,492,085	A	A	C		*	*	*			
D4Mgh11	168,046,938	158	158	151	○						

Cd36(chr4:14,150,309)

Symbols show variants characterized on the border of congenic fragments: open circle (○) for the WKY allele and asterisk (*) for the recipient (SHRSP or SHR) allele.

*For SSLP markers, the position of 5'-primer site is shown.

Table S11D. Chromosomal fragments introgressed into SHR-derived RNO15 congenic rat strains

Marker	Position: Rnor_6.0*	Allele			SHRSP-derived			SHR-derived		
		SHRSP	SHR	WKY	15pW2	15pW	15pW1	15SW2	15SW	15SW1
D15Rat2	11,605,245	196	172	172		○	○			
D15Tkyo3 (<i>Fhit</i>)	14,053,354	256	270	256					○	○
D15Mgh7	18,513,913	142	142	144						
D15Rat20	59,616,275	156	148	148	*					
D15Rat39	62,315,021	240	244	240				*		
D15Rat68	63,498,932	132	134	150	○			○		○
D15Arb2	68,366,508	221	229	229						
D15Rat95	70,559,420	226	226	208						*
D15Rat94	77,072,146	185	185	173			○			
D15Tkyo18 (<i>Ednrb</i>)	88,060,793	254	254	256			*			
D15Rat106	106,550,444	220	220	182	○	○		○	○	

Symbols show variants characterized on the border of congenic fragments: open circle (○) for the WKY allele and asterisk (*) for the recipient (SHRSP or SHR) allele.

*For SSLP markers, the position of 5'-primer site is shown.

Table S12. Inter-strain comparison of quantitative PCR in the kidney for selected genes located in the 1q21-1q22 region

Gene ^a	Position on RNO1 (v6.0)	Normal rat chow									Enalapril administration						Forward primer seq. (5'-to-3')	Reverse primer seq. (5'-to-3')
		1pW/SHRSP		1pW4-1/SHRSP		1pW4-3/SHRSP		1pW4-4/SHRSP		Ave. quantity ^b	WKY			SHRSP				
		Fold change (congenic / SHRSP)	P value	Fold change (congenic / SHRSP)	P value	Fold change (congenic / SHRSP)	P value	Fold change (congenic / SHRSP)	P value		Fold change (Drug/ control)	P value	Ave. quantity ^b	Fold change (Drug/ control)	P value	Ave. quantity ^b		
<i>Uri1</i>	94,346,513 - 94,404,362 (-)	0.77	2E-06	0.95	0.222	0.84	0.009	1.00	0.937	0.012	-	-	-	-	-	-	AAGAGAACCACCCCAAGAAG	ATGAGCAATGGCTGAGTGTG
<i>Ccne1</i>	94,485,830 - 94,495,112 (-)	1.23	0.074	0.66	0.0002	0.68	0.0009	0.78	0.038	0.0004	-	-	-	-	-	-	TTCCAAGCTCAAGCACTTCC	ACTCGGAGGAGGAGAAATCC
<i>LOC690000</i>	94,572,714 - 94,587,842 (+)	0.82	0.051	0.76	0.010	0.79	0.016	1.20	0.223	0.004	-	-	-	-	-	-	TGCCCATCATGGTAGATGAC	GCCGCCTTCATTTTCTTCTC
<i>Plekhl1</i>	94,609,041 - 94,616,565 (-)	1.25	0.014	1.15	0.104	1.24	0.003	1.02	0.740	0.008	-	-	-	-	-	-	ATGACGATGACTCCGATGAG	TGACCAGGAGACACCAGAAG
<i>Zfp715*</i>	98,614,943 - 98,631,142 (+)	1.12	0.260	0.92	0.594	1.00	0.954	0.92	0.488	0.003	-	-	-	-	-	-	TATGTGTGTGCCGAATGTGG	GGATGTCACTTGTGAATTCCTGC
<i>Klk1c12</i>	99,298,965 - 99,303,048 (-)	0.95	0.383	1.29	0.063	0.86	0.081	1.03	0.592	0.001	-	-	-	-	-	-	TTTAAAGATGAACCCCTTTCAC	AGCATCAGGTCAATTGCTGTG
<i>Klk1c8 (Klk1b21)</i>	99,352,114 - 99,355,976 (+)	1.44	0.0007	1.11	0.455	0.73	0.007	1.19	0.135	0.001	-	-	-	-	-	-	AGATCACACCCCTCAAATG	TATCTTGGCCCCATCCATC
<i>Klk15</i>	99,393,283 - 99,401,339 (+)	0.88	0.553	0.36	0.003	0.69	0.059	1.90	0.025	6.9E-05	0.68	0.040	4.3E-05	1.03	0.850	3.2E-05	GTGACTCTGGAGGACCCTTG	ACTCCAGGCTTGGTGGTAGTATC
<i>Klk1c10</i>	99,890,294 - 99,894,353 (-)	5.07	6E-06	3.13	3E-05	2.60	3E-05	4.03	2E-06	0.0002	1.67	0.009	3E-05	1.19	0.570	0.0003	CACCAAACCCCTGAATTGG	GAGATCTGTACCTTCTGTTCGT
<i>Klk1c4 (LOC100364577)</i>	94,412,788 - 94,418,026	10.50	0.0004	5.26	0.001	3.74	0.001	9.92	0.0005	0.0002	1.49	0.049	3.8E-05	1.99	0.006	0.0006	TCATGCTGTGTGCAGGAAAG	TGTAGATGCCTGGGTTATGG
<i>Klk1c6 (Gk11)</i>	99,947,714 - 99,964,824 (-)	1.01	0.804	0.77	0.004	0.72	0.197	0.75	0.002	0.044	-	-	-	-	-	-	TGCTGTGTGCAGGAGATTTG	GGTAGATAGGCTGGCATATTG
<i>Klk1c2 (Ton)</i>	99,981,045 - 99,985,422 (-)	1.18	0.481	0.84	0.338	0.58	0.080	3.07	0.017	1.5E-05	1.25	0.027	4.9E-06	1.11	0.340	1E-05	GCTTCGACACCCCTGACTATATC	GTCATTGCTGTGGTCATGCAC
<i>Klk5l</i>	100,055,956 - 100,058,334 (+)	1.49	0.572	1.62	0.301	0.39	0.156	14.73	0.044	1.4E-06	1.99	0.026	1.2E-05	1.89	0.006	1.1E-05	AGGATCCATAGAGGCTGCAAG	CTGTGAGTGCTCATTGTGGTTG
<i>Klk1c9 (Klks3)</i>	100,086,520 - 100,090,406 (+)	2.50	0.002	1.23	0.122	0.97	0.736	1.90	0.009	0.006	1.63	0.007	0.003	1.68	0.002	0.016	GCAAGTGGCTGTCAATTGGTAC	CCAGCAAAACACGATAAATCTTCTG
<i>Klk1c7</i>	100,131,562 - 100,135,556 (+)	1.01	0.969	0.90	0.611	0.59	0.067	1.05	0.811	0.232	-	-	-	-	-	-	CAGTCAAAGCTTCCCTCACC	GATCATTGCTGTGGTCATCG
<i>Klk1c3</i>	100,141,205 - 100,163,945 (+)	0.70	0.453	0.63	0.403	1.14	0.735	0.91	0.857	3.3E-06	-	-	-	-	-	-	TGCTATAGTGATGCCCTCAGC	CATCAGGTCAATTGCTGTAGTCCT
<i>Klk1b3 (Klk1c1, Ngfg)</i>	100,199,057 - 100,203,260 (+)	0.93	0.616	0.75	0.087	0.67	0.032	0.85	0.271	0.337	-	-	-	-	-	-	CCCTGGGACGGAATGATG	GCCGAAGTAGTACACAGCCACTT
<i>Dbp</i>	101,687,896 - 101,692,845 (+)	1.28	0.061	0.48	0.005	0.94	0.624	0.92	0.576	0.053	-	-	-	-	-	-	GGTCCTGTGTGCACCTTTTAGC	TTCAGGATTGTGTTGATGGAG

1pW, an RNO1 consomic strain derived from SHRSP/lzm; 1pW4-1, 1pW4-3 and 1pW4-4, RNO1 congenic strains derived from SHRSP/lzm.

qPCR is performed on the kidney of progenitor and consomic/congenic strains (n=5 per strain) for genes listed in the table with the primers originally designed. For part of the *Klk1* paralogs (or *Klk* homologs), the effect of enalapril administration is examined in progenitor strains. Inter-strain comparison is done with unpaired *t*-test.

^a Genes with asterisks are annotated in Ensembl but not in Entrez database. In some cases, aliases are shown in the parenthesis.

^b The average quantity is arbitrarily defined for reference (or control) rats as a ratio of mRNA expression level of tested gene to *Ppia*.

Supplementary Table 13. Differential expression of candidate genes in the known BP regulatory pathways

Agilent probe	Gene name	Chr	Transcription _start_site (Rnor_6.0)	SHRSP/lzm (versus WKY/lzm)										SHR/lzm (versus WKY/lzm)											
				Heart		Aorta		Renal cortex		Whole kidney		Liver		Heart		Aorta		Renal cortex		Whole kidney		Liver			
				log ₂ FC (SHRSP /WKY)	P-value	log ₂ FC (SHRSP /WKY)	P-value	log ₂ FC (SHRSP /WKY)	P-value	log ₂ FC (SHRSP /WKY)	P-value	log ₂ FC (SHRSP /WKY)	P-value	log ₂ FC (SHRSP /WKY)	P-value	log ₂ FC (SHRSP /WKY)	P-value	log ₂ FC (SHRSP /WKY)	P-value	log ₂ FC (SHRSP /WKY)	P-value	log ₂ FC (SHRSP /WKY)	P-value		
Kallikrein-kinin & renin-angiotensin systems																									
A_44_P1029253	Mas1	1	48,077,033		N/A	0.458	0.148	-0.25	0.207		N/A		N/A		N/A		0.159	0.482	0.002	0.992	0.056	0.772		N/A	
A_64_P337849	Lnpep	1	68,436,593	-0.166	0.002	-0.253	0.017	-0.014	0.864	0.155	0.337	0.699	0.01	-0.117	0.247	0.39	0.002	-0.105	0.232	-0.043	0.703	0.389	0.116		
A_64_P108993	Klk11	1	99,712,108		N/A		N/A		N/A		N/A		N/A		N/A		N/A		N/A		-0.288	6E-04		N/A	
A_44_P280954	Klk1c10	1	99,894,353		N/A		N/A	-1.442	2E-07		N/A		N/A		N/A		N/A		-1.175	5E-06	-1.175	1E-08		N/A	
A_44_P163243	Klk1c9 (Klks3)	1	100,059,967		N/A		N/A	-2.715	1E-12	-2.088	2E-09		N/A		N/A		N/A		-1.414	1E-08	-1.604	4E-10		N/A	
A_44_P399414	Klk1c7 (Klk1)	1	100,059,967	0.17	0.213	-1.618	9E-04	-0.296	0.001	-0.204	0.031		N/A		0.542	0.046	-2.492	4E-05	-0.141	0.091	-0.237	0.001		N/A	
A_44_P374824	Klk1c3	1	100,161,872	0.029	0.847	-0.723	0.174	-0.285	0.001	0.048	0.599		N/A		0.236	0.436	-2.412	0.01	-0.183	0.031	-0.152	0.026		N/A	
A_44_P500013	Anpep	1	141,564,994	-0.118	0.051	0.527	0.001	-0.398	0.002	-0.199	0.064	0.188	0.164	0.009	0.939	-0.01	0.948	-0.305	0.018	-0.109	0.145	0.358	0.015		
A_64_P113184	Prnp	1	157,701,089	-0.101	0.346	-0.069	0.598	-0.113	0.209	-0.271	0.234		N/A		-0.411	0.034	-0.711	1E-04	-0.241	0.031	0.017	0.908		N/A	
A_64_P109894	Agtr1b	2	105,224,295	N/A		N/A	-0.085	0.75	0.072	0.527	0.142	0.438		N/A		N/A		0.392	0.177	0.029	0.809	-0.071	0.581		N/A
A_44_P209788	Enpep	2	233,743,866	-0.161	0.005	0.655	1E-04	-0.131	0.064	-0.118	0.257	-0.141	0.331	-0.234	0.037	0.094	0.528	-0.064	0.37	-5E-04	0.995	-0.329	0.036		
A_64_P114713	Agtr1a	5	164,898,420	-3.658	2E-36	-3.665	7E-13	-4.091	1E-18	-3.505	7E-21	-4.448	2E-10	-0.142	0.297	-0.095	0.571	-0.072	0.314	0.053	0.478	-0.236	0.043		
A_64_P036715	Bdkrb2	6	129,399,468	0.139	0.339	-0.046	0.816		N/A	0.645	0.036		N/A		0.446	0.041	0.085	0.643		N/A	0.216	0.282		N/A	
A_43_P10861	Dnpep	9	82,514,399	0.32	5E-06	0.14	0.131	-0.19	0.04	-0.1	0.417	-0.115	0.526	0.097	0.422	-0.333	0.004	-0.272	0.009	-0.331	8E-04	-0.307	0.106		
A_64_P010531	Ace	10	94,170,766	0.188	0.063	0.807	6E-06	-1.53	2E-04	-1.955	5E-10		N/A		0.871	8E-05	0.189	0.186	-0.088	0.785	0.244	0.081		N/A	
A_64_P098230	Ace	10	94,170,766	0.091	0.209	0.288	0.058	-1.398	1E-05	-1.372	6E-09	-0.291	0.106	0.873	4E-07	0.222	0.179	-0.139	0.551	0.334	0.005	-0.028	0.871		
A_44_P348781	Kng1	11	81,444,621		N/A		N/A	-1.82	6E-11	-1.09	2E-04	0.071	0.679		N/A		N/A		-0.469	7E-04	-0.87	4E-05	0.194	0.269	
A_64_P059056	Ren	13	50,514,151	-0.059	0.468	0.14	0.282	0.056	0.534	-0.09	0.421	-0.295	0.137	0.554	0.001	-0.026	0.857	0.556	4E-05	0.483	3E-06	-0.79	1E-03		
A_42_P486203	Agtr1a	17	35,958,077	-0.236	0.002	0.405	0.002	-0.281	0.003	0.016	0.893	-0.576	0.001	0.081	0.562	0.18	0.154	-0.193	0.039	-0.153	0.079	-0.478	0.005		
A_64_P154849	Agt	19	57,333,433	-0.883	2E-05	0.094	0.534	-0.073	0.701	3E-04	0.998	0.138	0.228	-0.13	0.717	-2.88	8E-12	-1.126	6E-05	-0.915	1E-09	-0.051	0.646		
A_43_P14875	Prep	20	50,172,618	-0.225	5E-10	-0.687	3E-08	-0.386	0.044	-0.462	9E-05	0.128	0.352	-0.22	2E-04	-0.254	0.005	-0.888	3E-04	-0.678	1E-09	-0.159	0.254		
A_44_P1011008	Atp6ap2	X	11,164,915	0.12	0.004	0.63	4E-04	-0.035	0.577	0.039	0.736	-0.156	0.167	0.129	0.107	0.063	0.694	-0.074	0.272	-0.03	0.713	0.066	0.544		
A_64_P132696	Ace2	X	32,096,016	-0.058	0.325	-0.583	0.001	-0.182	0.407	0.011	0.943		N/A		0.662	2E-06	-0.887	7E-05	-0.487	0.049	-0.429	4E-04	0.17	0.174	
Sympathetic nervous system																									
A_44_P491621	Adrbk1 (Grk2)	1	219,544,328	0.105	0.087	-0.175	0.015	-0.011	0.892	0.075	0.587	-7E-04	0.995	-0.145	0.231	-0.189	0.019	-0.08	0.379	-0.187	0.065	-0.136	0.274		
A_64_P130105	Adrb1	1	277,537,585	-0.443	2E-07	-0.363	0.049	0.012	0.933	-0.11	0.331	0.635	0.039	-0.372	0.011	0.089	0.648	0.084	0.578	-0.234	0.009	0.402	0.17		
A_64_P053785	Adra2a	1	274,766,283		N/A		N/A		N/A	0.087	0.61		N/A		N/A		N/A		N/A		0.435	0.002		N/A	
A_64_P138008	Adra2b	3	119,805,941	0.073	0.391	-0.537	0.009	0.461	4E-04	-0.035	0.807	-0.039	0.746	-0.043	0.802	-0.419	0.054	0.436	0.001	0.216	0.043	0.146	0.242		
A_42_P501233	Adra1d	3	124,145,566	-2.744	4E-25	-0.549	0.002	0.112	0.502	0.634	0.048		N/A		-1.515	2E-08	-0.325	0.071	-0.161	0.364	-0.77	0.002		N/A	
A_64_P138011	Adra1b	10	29,450,644	-0.33	8E-09	0.901	1E-03	0.172	0.087	0.204	0.148	0.325	0.002	-0.276	0.004	0.467	0.079	0.498	2E-04	0.468	7E-05	7E-04	0.994		
A_64_P053790	Adra1a	15	43,298,794	-0.641	4E-11	-1.073	3E-05	-0.134	0.148	-0.303	0.129		N/A		-0.388	0.008	-0.472	0.04	0.037	0.696	-0.104	0.455		N/A	
A_64_P150549	Adrb3	16	69,003,868	-0.985	0.004	0.743	0.002		N/A	-0.384	0.336	0.622	0.015		N/A	0.709	0.006		N/A	-0.867	0.039	0.681	0.029		
A_44_P188280	Adrb2	18	57,515,834	0.23	4E-04	1.239	1E-05	0.201	0.051	0.374	0.282	0.464	0.001	1.011	3E-04	-0.161	0.179	-0.177	0.099	-0.34	0.169	0.21	0.08		
Natriuretic peptide system																									
A_44_P317600	Nppa	5	164,808,323	1.277	5E-13		N/A	-0.102	0.409		N/A		N/A		2.413	2E-12		N/A	-0.218	0.115	-0.26	0.01		N/A	
A_42_P638494	Nppb	5	164,796,185	1.343	2E-21		N/A		N/A		N/A		N/A		1.146	2E-10		N/A		N/A		N/A		N/A	
A_44_P240696	Nppc	9	93,735,636		N/A		N/A		N/A		N/A		N/A		N/A		N/A		N/A		N/A		N/A		N/A
A_43_P15245	NPR1 (Gca)	2	189,856,090	-0.437	8E-12	0.521	2E-05	-0.151	0.076	0.043	0.709	-0.064	0.455	-0.142	0.116	0.701	3E-06	-0.035	0.68	0.057	0.487	0.005	0.952		
A_42_P726573	NPR2	5	59,128,315	-0.167	0.002	0.126	0.277	-0.49	2E-05	-0.185	0.269	0.182	0.262	-0.159	0.12	0.438	0.003	-0.33	0.002	-0.441	9E-04	0.293	0.082		
A_64_P036616	NPR3	2	61,949,926	0.068	0.456	-2.398	4E-07	0.576	8E-04	0.499	0.03		N/A		0.499	0.009	-0.25	0.451	0.466	0.006	0.273	0.087		N/A	
A_42_P641962	Pcsk6	1	126,749,508	-0.256	3E-05	0.12	0.317	-0.331	0.294	-0.521	3E-04	-0.634	6E-04	-0.14	0.198	0.051	0.698	-0.38	0.258	0.06	0.493	-0.626	7E-04		
A_64_P021014	Pcsk6	1	126,749,508	-0.083	0.328	-0.175	0.34		N/A	0.087	0.708	0.115	0.682	-0.175	0.299	-0.344	0.103		N/A	0.114	0.474	-0.112	0.713		
A_64_P160586	Furin	1	142,197,182	-8E-04	0.988	0.075	0.288	0.067	0.282	0.186	0.101	0.407	0.009	-0.075	0.464	-0.082	0.297	-0.05	0.446	0.169	0.038	0.349	0.021		
A_64_P150662	Corin	14	38,247,791	-0.198	0.014	2.024	5E-10		N/A		N/A		N/A		-0.066	0.672	2.078	2E-09		N/A		N/A		N/A	
A_43_P11484	Mme (Nep)	2	153,803,349	-0.586	5E-09	-1.281	7E-08	-0.294	0.055	-0.242	0.026	0.157	0.517	0.48	0.004	-0.372	0.027	-0.084	0.582	-0.09	0.222	-0.053	0.825		

Gene expression data in the table are produced by microarray analysis. Fold changes (hypertensive strain vs WKY; log₂-transformed values) are shown in each cell.

For Ace and Corin, the microarray includes two distinct probes, for each of which the expression data are shown in the table.

N/A, data not available because of low mRNA expression of the gene.

Table S14. A list of primers for quantitative RT-PCR

Gene Symbol	Forward primer (5'-to-3')	Reverse primer (5'-to-3')	Original design or drawn from literature
<i>Nppa</i>	CTCCCAGGCCATATTGGAG	TCCAGGTGGTCTAGCAGGTT	PMID: 27161004
<i>Nppb</i>	GCTCTCAAAGGACCAAGGC	CCTAAAACAACCTCAGCCCG	Original
<i>Ren</i>	CTCTGGGCACTCTTGTTGCTC	GCACTGATCCTGGTCATGTCTAC	Original
<i>Prep</i>	ATTTGCGACCCCTTATGCTTG	TTCTGTGCCTCCACGAAAG	Original
<i>Ace</i>	TTGTCTGTCACTGGAGCCTGAT	CACCCAAAGCAATTCTTCGTATT	Original
<i>Knq2</i>	TCACAGGTGGTTGCTGGAGT	CCGAGGTGTTTGGTCTCACAA	Original
<i>Klk1c10</i>	TGGTGTGCTTCAAGGCATCA	GACAGTGTGACACTCAGGGG	Original
<i>Homer2</i>	GGTCCGAGAAAAGGAAATGG	GAGACCGCACTTTGTCTTCC	Original
<i>Endog</i>	CCAATCACCGCTGGAGTCA	AGGCCCTGTGCAGACATAAAC	Original
<i>Sgk1</i>	AGATCACGCCCCCATTTAAC	TGTGACAAGGATGCTGTCAG	Original
<i>Cd36</i>	TCAAGGTGTGCTCAACAGCC	ACTCCATCTACAGTGTTATTG	PMID: 18587397