Supplemental Information

Primer information for chromatin immunoprecipitation (ChIP)

For data in **Fig. 6*A***, position of primers relative to the transcription start site of the gene and their sequences were listed as follow:

Plagl1, -2993 to -2873:	forward 5' TGGCCTTGAACTCCCTTGTAA
	reverse 5' TTTATCGGTCAGGCATGGTG
-2093 to -1960:	forward 5' TCCCAAACGGCATTCTTACAG
	reverse 5' TGACTGACTTCCAATGTGGCA
-974 to -872:	forward 5' CGAAGGCAATA TAAACAGCGG
	reverse 5' TTTCGCCATCTCCTGAGTGAG
254 to 380:	forward 5' CAGCC AGAGATGCAGCAAAAG
	reverse 5' TGTCGCCAGGTTGTAAAGACC
Mdk, -1973 to -1872:	forward 5' TCATGCACCGTGACCAGAA
	reverse 5' ACGCAGCTTACCATGATCCAG
141 to 29:	forward 5' AGCTCTTGTCAGCGACAAGATT
	reverse 5' CGAGAGCCTTTTTCTAGTGCAG
147 to 233:	forward 5' TGTGACACCAGGACATACTCCC
	reverse 5' TACTTTTCCCTCTCGCAGCCT
672 to 806:	forward 5' GCTGAGACATCGGTTCCAAGT
	reverse 5' TCGCCTAGTCTCTTCTCCGCTA
Peg3, -2921 to -2839:	forward 5' AAGACATTGAGAGGCACCACG
	reverse 5' TCTTTTCCCCCCTAGTCTGAGT
-875 to -749:	forward 5' TTCTACAAACTTCGGCAACGG
	reverse 5' TAACGGAGGTATCGCTGCCAT
-145 to -63:	forward 5' TGCCTTGACAACAGCAGTCTG
	reverse 5' ACCAATCCAAGACCCCATTCC
518 to 630:	forward 5' CGCAGATGATGCAGAAGTCCT
	reverse 5' GCCCTTAGACTTTGCTGAGCA

For data in **Fig. 6*B*,** the sequences of primers used were listed as follow:

Plagl1	forward 5' CAGCC AGAGATGCAGCAAAAG
	reverse 5' TGTCGCCAGGTTGTAAAGACC
Mdk	forward 5' GCTGAGACATCGGTTCCAAGT
	reverse 5' TCGCCTAGTCTCTTCTCCGCTA
Peg3	forward 5' GATTTTGTACGCCTGCCCGTT
	reverse 5' CAGTGGATAATGCCTTCCCCA
Mest	forward 5' GCAGCCTGTCCATGAATGTGT
	reverse 5' TCCTACGTGTGTTTTGAGCCC
Ezh2	forward 5' CTGTCCATGGCTTTCCTGAGA
	reverse 5' AACCCAATCGCCATCGCTT
Gpc3	forward 5' CTGCGAGGAAACTTTTGCG
	reverse 5' AGAGTGGCAATAAGAGCCGGA
Meis1	forward 5' CATCGATCGTGGCTCCTTTAA
	reverse 5' AAATGCACAAAGCCCTAGCG
Igf2	forward 5' CAGCTGACCTCATTTCCCGAT
	reverse 5' TATGCAAACCGAACAGCGG
Skp2	forward 5' AAACCTGCTCCCAGTCAATCG
	reverse 5' TTCCACTCTGATTTCGGACCA
Bub1	forward 5' CACGTTCGACATCACAAGTGC
	reverse 5' CCTGACCGACACTTACCGAAA

Mmp14	forward 5' GCCTGCACCACAGAAAAGACA reverse 5' TCTGCTTAGTCGGCGAACTGA
Fgf1	forward 5' CGAGCTGGATTTGGCTGTTT reverse 5' TGCTGCACCTCCTTTCAAAGT
Klf9	forward 5' GCTCCGAGCAGTTTCCCTTTT reverse 5' TCCCATCACGTCACAATCCAG
Pim3	forward 5' AAACGCCCACGAAGAACGA reverse 5' GGCCGCATAAGCCAATGAA
Gstm	forward 5' TGTGCAAAACAGAATCCCGG reverse 5' TCCCAATTAGGCACTCCCCTT
Inmt	forward 5' TGGCAATGTGTGCAGATCCAG reverse 5' TTGGTGCCCAGTCCTATGTCA
Col10a1	forward 5' CTTGCTAGCCCCAAGACACAA reverse 5' CCATGCATCATTCCGCTGTAC
Chromosome19: 23.12Mb	forward 5' TGGACTGCCAGAAAACAGAGC reverse 5' AGCCACGGTGGAAGACATTT
Gapdh	forward 5' CATCTTCTTGTGCAGTGCCAG reverse 5' AGCATCCCTAGACCCGTACAGT

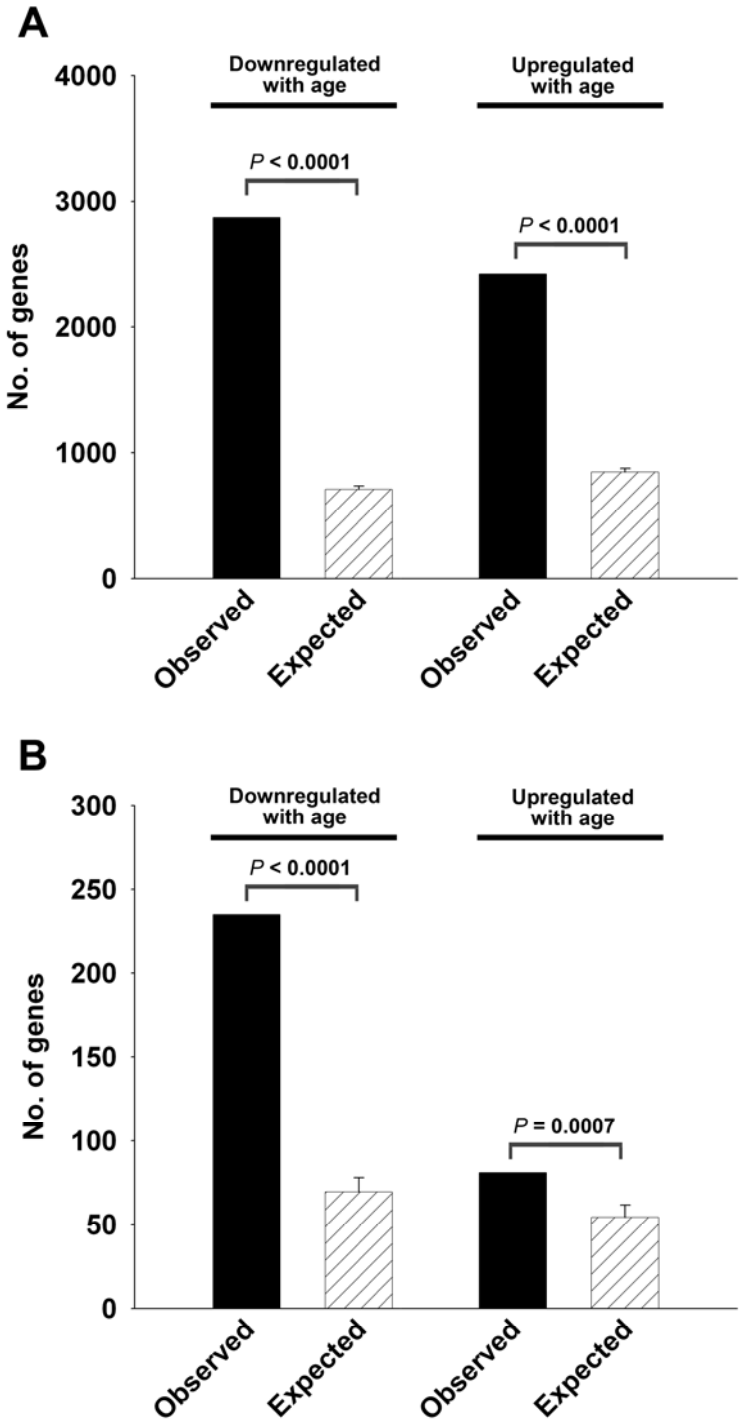

Fig. S1. The number of genes commonly regulated with age in multiple organs of rats and mice. (A) The number of genes up- or downregulated with age in both rat kidney and lung. The solid bars represent the observed number of genes commonly regulated (defined by P < 0.01) in both kidney and lung with age. The hatched bars represent the number of commonly regulated genes that would be expected by chance (mean ± SD). The observed overlap between organs was significantly greater than the overlap expected by chance (Pearson's Chi-square test). **(B)** The number of genes up- or downregulated with age in both rat and mouse, in all organs studied. Among genes that changed substantially in either the mouse (≥2.0-fold, $P < 0.05$, same direction in all 3 organs studied) or the rat (≥2.0-fold, $P < 0.05$, same direction in both organs studied), the observed overlap (defined by $P < 0.05$, same direction in all organs of both species, solid bars) was significantly greater than the overlap expected by chance (hatched bars, mean ± SD).

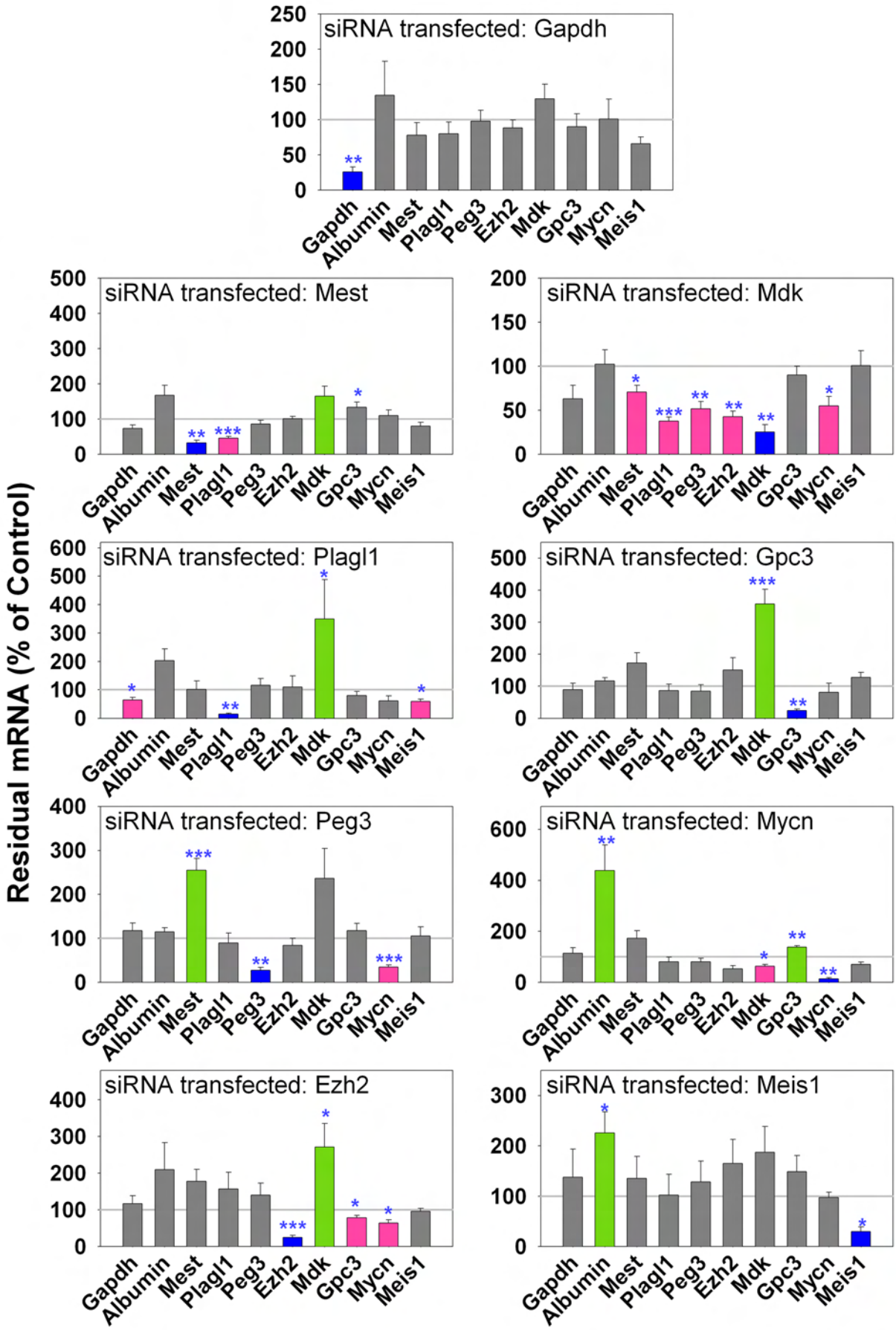

Fig. S2. Changes in mRNA expression (mean ± SEM) in primary hepatocytes transfected with siRNA. Cultured murine hepatocytes isolated from fetal liver (E15) were used to evaluate the effect of target gene knockdown on expression of other genes. siRNA against Gapdh, Mest, Plagl1, Peg3, Ezh2, Mdk, Gpc3, Mycn, and Meis1 was used as indicated. All expression values were compared to hepatocytes transfected with control siRNA. Blue bars represent the target gene of the transfected siRNA. Significant changes are color coded (pink, downregulation; green, upregulation). All data were collected from transfection in hepatocytes from five different isolations. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

Table S1. 316 genes that showed uniform up- or downregulation with age in all organs studied by microarray. Negative fold change indicates declining expression with age. A gene was included only if it was uniformly upregulated (81 genes) or downregulated (235 genes) with age (rat kidney and lung, 1 to 5 wk; mouse kidney and lung, 1 to 8 wk; mouse heart, 1 to 4 wk) at least 2.0 fold with $P < 0.05$ in all organs studied in both species. ID numbers are for Affymetrix Mouse Genome 430 2.0 Array GeneChip or the Affymetrix Rat Genome 230 2.0 Array GeneChip.

Gene Symbol in Mouse	Fold Change from 1 to 4 wk Mouse Heart	*P* value 1 vs 4 wk Mouse Heart	Fold Change from 1 to 4 wk Mouse Kidney	*P* value 1 vs 4 wk Mouse Kidney	Fold Change from 1 to 8 wk Mouse Kidney	*P* value 1 vs 8 wk Mouse Kidney	Fold Change from 1 to 4 wk Mouse Lung	*P* value 1 vs 4 wk Mouse Lung	Fold Change from 1 to 8 wk Mouse Lung	*P* value 1 vs 8 wk Mouse Lung	Fold Change from 1 to 5 wk Rat Lung	*P* value 1 vs 5 wk Rat Lung	Fold Change from 1 to 5 wk Rat Kidney	*P* value 1 vs 5 wk Rat Kidney
2810433K01Rik	-5.419	3.58E-02	-3.350	1.69E-02	-11.010	1.36E-04	-4.464	6.72E-05	-3.583	2.73E-04	-2.800	2.888E-10	-2.494	2.876E-09
Abcb1a	1.654	2.71E-03	3.793	4.69E-08	6.204	1.32E-09	1.922	1.46E-07	2.209	1.71E-08	2.186	1.503E-04	2.496	2.172E-05
Adamts19	-5.997	3.71E-02	-4.120	2.08E-02	-3.732	2.93E-02	-3.591	1.54E-02	-7.570	7.65E-04	-6.922	6.515E-19	-7.435	2.804E-19
Adhfe1	2.050	5.97E-05	2.350	2.68E-07	2.510	1.19E-07	2.338	3.17E-04	2.795	5.92E-05	1.176	1.021E-03	2.680	9.783E-18
Adra1a	4.347	7.53E-03	1.794	3.14E-01	4.132	2.54E-02	1.985	1.16E-01	4.241	3.86E-03	1.139	2.925E-02	1.301	9.139E-05
Afap1l2	-2.393	1.42E-04	-2.772	1.90E-05	-2.927	1.14E-05	-3.452	6.80E-10	-2.786	6.03E-09	-1.176	1.067E-02	-1.721	2.101E-09
Agtrl1	-2.176	1.07E-03	-4.653	3.71E-07	-5.617	1.05E-07	-2.035	2.54E-08	-2.032	2.59E-08	-1.405	3.551E-05	-2.223	1.521E-11
Aldh18a1	-2.130	3.99E-05	-4.035	6.10E-08	-4.436	2.92E-08	-2.082	1.09E-06	-2.150	6.88E-07	-1.448	1.190E-10	-1.967	2.731E-16
Anln	-3.224	5.09E-05	-3.321	1.32E-07	-5.707	1.98E-09	-3.241	2.24E-07	-3.141	3.01E-07	-2.419	9.876E-16	-1.951	4.567E-13
Ar	2.812	5.42E-05	5.918	3.48E-09	5.813	3.90E-09	2.280	7.79E-07	3.326	1.22E-08	1.574	9.880E-10	2.745	3.548E-17
Arhgap11a	-2.410	2.72E-03	-1.960	1.30E-03	-3.392	6.60E-06	-1.977	1.09E-03	-2.615	6.07E-05	-1.998	2.232E-08	-2.279	8.780E-10
Arhgap28	-2.277	1.03E-05	-2.595	1.24E-06	-2.657	9.59E-07	-2.902	9.84E-09	-2.308	1.47E-07	-1.899	4.074E-08	-2.300	3.060E-10
Armcx2	-3.804	1.57E-06	-4.227	2.67E-07	-5.110	6.88E-08	-2.753	1.65E-10	-2.582	3.53E-10	-2.437	2.612E-20	-5.587	4.535E-27
Armcx6	-3.349	1.70E-02	-3.647	2.27E-03	-3.435	3.15E-03	-4.953	1.75E-02	-3.909	3.71E-02	-1.512	2.882E-12	-1.635	7.075E-14
Aspm	-3.634	2.94E-03	-1.570	2.09E-01	-2.633	1.47E-02	-2.486	3.12E-02	-3.487	5.81E-03	-2.267	9.313E-12	-2.426	1.749E-12
Atp7a	-1.436	2.64E-02	-1.440	2.22E-05	-1.399	4.88E-05	-1.229	1.14E-04	-1.251	5.36E-05	-2.518	2.095E-02	-2.377	2.937E-02
Aurka	-3.795	7.82E-04	-1.541	1.56E-02	-2.358	1.19E-04	-1.997	1.67E-06	-2.332	1.92E-07	-1.489	2.840E-06	-1.474	4.144E-06
B2m	1.475	9.15E-04	1.146	5.75E-02	1.362	4.65E-04	1.708	6.76E-07	1.760	3.74E-07	2.802	9.377E-16	4.236	4.149E-19
B4galt2	-2.007	2.73E-03	-3.667	3.03E-04	-3.924	1.97E-04	-1.786	2.64E-04	-2.333	7.78E-06	-1.633	3.329E-13	-1.952	3.429E-16
Bcl6b	-1.578	1.26E-02	-3.266	1.05E-05	-4.011	2.07E-06	-2.581	2.12E-04	-2.257	7.44E-04	-2.061	4.924E-06	-2.205	1.290E-06
Birc5	-3.223	5.90E-04	-3.187	3.24E-06	-46.155	4.39E-12	-3.047	4.03E-08	-3.214	2.39E-08	-2.197	4.345E-12	-1.914	2.215E-10
Brca1	-2.111	4.21E-05	-3.057	3.03E-02	-16.399	4.99E-05	-2.486	2.72E-06	-3.523	8.44E-08	-1.947	8.211E-12	-2.077	1.175E-12
Bub1	-5.625	2.87E-02	-8.578	2.32E-04	-37.395	1.54E-06	-3.794	5.23E-06	-3.011	3.39E-05	-2.185	1.406E-08	-3.073	1.209E-11
Bub1b	-6.287	2.81E-04	-10.223	2.06E-08	-11.851	1.02E-08	-4.632	1.54E-03	-4.749	1.37E-03	-2.516	1.159E-09	-2.996	3.745E-11
C4b	1.547	9.72E-03	1.319	4.64E-02	1.458	1.05E-02	2.727	2.84E-10	3.674	1.35E-11	5.149	2.119E-13	5.092	2.459E-13
Cacna1g	-2.071	2.27E-03	-10.654	5.78E-08	-14.432	1.49E-08	-7.847	2.02E-05	-10.812	4.80E-06	-1.251	3.524E-04	-1.933	7.992E-12
Cacnb3	-3.003	1.69E-02	-1.989	2.25E-04	-2.480	1.77E-05	-2.398	6.44E-07	-2.664	1.89E-07	-2.190	1.142E-11	-3.608	2.454E-16
Capn6	-12.118	1.15E-05	-1.832	2.97E-04	-2.155	3.56E-05	-8.257	2.73E-05	-11.259	7.11E-06	-1.561	6.265E-05	-3.918	1.370E-13
Cbx7	2.409	2.93E-04	1.930	7.08E-06	2.152	1.47E-06	2.848	1.81E-08	3.811	1.10E-09	2.571	3.442E-17	2.057	1.487E-14
Ccdc99	-3.514	1.01E-02	-4.110	8.08E-04	-10.355	8.96E-06	-4.121	6.10E-03	-6.435	9.18E-04	-1.612	1.031E-05	-1.405	5.967E-04
Ccl5	4.770	1.62E-02	3.701	5.53E-03	5.525	8.54E-04	2.163	1.50E-03	2.331	7.45E-04	3.444	1.447E-09	2.073	9.778E-06
Ccl6	2.604	1.16E-04	2.146	3.19E-03	2.088	4.07E-03	2.600	2.67E-08	2.228	1.89E-07	2.595	4.099E-11	3.543	1.048E-13
Ccna2	-2.182	2.50E-03	-2.459	9.69E-09	-3.486	2.23E-10	-2.938	6.27E-07	-3.220	2.60E-07	-2.828	3.555E-12	-2.726	7.549E-12

Ccnb1	-4.180	2.99E-04	-5.028	7.60E-03	-19.666	7.18E-05	-7.274	2.02E-03	-8.369	1.23E-03	-2.194	1.004E-09	-1.720	7.074E-07
Ccnb2	-2.881	9.54E-06	-3.403	8.81E-04	-11.634	1.40E-06	-2.687	4.86E-07	-2.804	3.07E-07	-2.572	3.756E-10	-2.440	1.150E-09
Ccnd2	-2.112	3.11E-05	-4.639	4.15E-10	-4.948	2.58E-10	-1.612	3.68E-07	-1.539	1.10E-06	-2.522	9.632E-06	-2.472	1.303E-05
Ccnf	-2.832	5.47E-03	-3.404	2.63E-04	-4.961	2.31E-05	-2.877	3.87E-03	-2.487	9.61E-03	-1.230	1.165E-03	-1.237	9.148E-04
Cd276	-3.262	1.77E-03	-6.703	6.85E-03	-14.427	6.42E-04	-1.913	1.43E-03	-2.428	1.11E-04	-1.496	1.867E-10	-2.812	1.881E-19
Cd302	1.266	1.76E-02	2.581	2.83E-07	3.101	4.01E-08	1.485	1.85E-06	1.552	6.09E-07	2.432	2.982E-11	5.711	1.153E-17
Cd74	4.584	2.65E-07	3.510	3.86E-07	6.018	7.28E-09	2.172	1.06E-07	2.643	8.52E-09	2.201	3.013E-08	5.880	1.908E-15
Cdc20	-3.874	1.12E-04	-2.683	1.81E-05	-6.122	2.94E-08	-2.554	6.60E-06	-3.059	1.07E-06	-1.746	1.387E-08	-1.634	1.264E-07
Cdc2a	-3.434	5.45E-05	-2.682	2.04E-04	-8.523	8.50E-08	-3.145	3.30E-07	-4.468	1.72E-08	-2.424	1.316E-10	-2.637	2.084E-11
Cdca2	-3.622	1.27E-02	-2.041	5.91E-02	-5.907	2.25E-04	-2.917	4.12E-07	-2.915	4.14E-07	-1.921	3.482E-07	-1.739	4.469E-06
Cdca3	-3.553	9.69E-05	-1.963	5.16E-04	-3.543	1.38E-06	-2.545	1.26E-05	-3.008	2.37E-06	-2.456	4.245E-11	-1.887	3.226E-08
Cdca7	-4.984	9.92E-03	-20.648	2.27E-05	-29.685	7.44E-06	-3.997	9.00E-08	-3.382	3.66E-07	-2.186	5.075E-12	-3.195	9.157E-16
Cdca8	-3.884	1.55E-05	-2.550	3.74E-05	-5.174	1.12E-07	-3.049	1.44E-06	-2.911	2.25E-06	-2.092	5.835E-11	-1.884	1.204E-09
Cdh11	-3.375	1.32E-05	-13.658	4.93E-13	-11.160	1.28E-12	-3.779	2.17E-12	-4.308	7.11E-13	-4.027	3.257E-21	-5.760	1.482E-23
Cdk4	-2.044	2.15E-04	-2.539	2.82E-09	-2.684	1.45E-09	-2.364	2.88E-09	-2.315	3.81E-09	-1.597	1.596E-15	-2.217	7.770E-21
Cdk5rap2	-2.547	2.81E-02	-1.821	3.94E-02	-3.786	2.47E-04	-3.214	4.95E-04	-2.235	6.91E-03	-1.331	4.717E-09	-1.331	4.721E-09
Cdkn1c	-1.396	1.78E-02	-15.084	2.48E-13	-18.496	1.05E-13	-1.166	4.78E-03	-1.757	2.66E-08	-2.358	1.679E-12	-8.524	1.647E-21
Cdt1/Ris2	-2.039	1.10E-04	-2.138	3.95E-08	-2.888	8.86E-10	-2.339	1.71E-08	-2.442	9.73E-09	-2.016	5.468E-09	-3.015	5.899E-13
Cenpe	-4.012	9.59E-04	-1.623	6.19E-02	-2.473	2.32E-03	-2.629	4.10E-04	-4.179	1.16E-05	-2.413	2.451E-13	-1.940	9.481E-11
Cenpi	-2.807	1.42E-02	-4.111	4.67E-04	-4.766	2.03E-04	-6.039	3.60E-07	-7.483	1.05E-07	-2.092	1.090E-09	-1.620	1.754E-06
Cenpk	-2.921	2.46E-03	-1.986	5.60E-05	-2.886	7.20E-07	-2.899	5.60E-07	-3.527	8.88E-08	-2.438	5.660E-10	-2.203	5.645E-09
Cenpn	-2.667	2.15E-04	-1.547	6.00E-04	-2.002	9.04E-06	-1.927	2.35E-02	-2.569	2.85E-03	-1.845	1.017E-08	-1.378	1.640E-04
Centa2	2.223	1.06E-03	1.989	4.84E-03	2.125	2.64E-03	2.357	4.24E-06	2.139	1.41E-05	2.073	4.175E-10	3.837	9.244E-16
Chek1	-2.105	5.79E-03	-2.270	3.45E-02	-6.588	1.40E-04	-2.137	4.05E-05	-2.903	1.37E-06	-1.846	9.420E-11	-2.470	2.544E-14
Cirbp	-1.954	5.81E-04	-2.804	1.77E-05	-2.595	3.76E-05	-2.407	3.31E-06	-2.714	8.69E-07	-2.565	4.401E-09	-3.874	3.145E-12
Ckap4	-2.071	1.54E-08	-5.230	8.25E-09	-5.825	4.02E-09	-3.000	3.93E-11	-3.466	9.22E-12	-2.385	1.853E-11	-2.606	2.467E-12
Cks1b	-3.410	4.39E-07	-5.986	1.15E-07	-9.682	7.97E-09	-3.552	9.44E-09	-3.900	4.21E-09	-2.310	2.459E-13	-2.480	4.156E-14
Clec7a	1.956	3.70E-04	1.358	1.72E-03	1.551	9.14E-05	1.473	8.25E-05	1.642	7.80E-06	2.153	6.226E-12	2.187	4.061E-12
Clip3	-1.691	1.04E-02	-2.616	8.37E-07	-2.961	2.28E-07	-2.581	1.56E-06	-2.765	7.43E-07	-3.008	6.483E-18	-3.310	9.466E-19
Cmah	3.507	6.40E-03	1.626	7.65E-02	2.916	1.09E-03	2.182	6.80E-05	2.191	6.47E-05	2.057	3.263E-09	4.088	2.871E-15
Cmbl	1.464	3.06E-03	2.118	1.09E-07	2.429	1.67E-08	1.636	6.74E-05	1.755	1.90E-05	2.495	6.720E-11	2.500	6.440E-11
Col1a1	-3.453	4.62E-07	-5.475	8.25E-07	-12.505	1.05E-08	-2.517	8.20E-06	-3.566	2.89E-07	-1.271	8.927E-04	-3.680	9.023E-17
Col1a2	-2.277	3.91E-06	-4.490	7.58E-12	-6.358	6.43E-13	-1.472	1.18E-05	-2.130	8.78E-09	-1.257	3.744E-04	-3.489	1.071E-17
Col24a1	-5.296	3.96E-03	-4.773	9.13E-03	-5.403	5.78E-03	-7.626	3.47E-05	-12.257	4.39E-06	-2.041	9.156E-09	-9.716	1.368E-19
Col5a1	-2.270	8.33E-06	-4.038	2.89E-12	-4.854	6.67E-13	-2.766	5.32E-08	-3.585	4.09E-09	-2.255	2.083E-17	-2.358	6.102E-18
Col5a2	-2.699	7.48E-06	-2.699	2.77E-10	-3.027	7.75E-11	-1.986	2.17E-10	-2.555	5.52E-12	-1.405	2.123E-07	-4.683	2.322E-21
Cpeb1	2.320	2.08E-04	2.209	1.27E-04	2.838	9.48E-06	2.883	5.73E-05	2.352	3.72E-04	1.124	4.716E-02	1.928	2.025E-11
Cpxm1	-1.741	4.22E-03	-2.716	6.31E-06	-2.908	3.22E-06	-1.805	3.76E-06	-1.800	3.95E-06	-3.752	2.860E-16	-4.614	1.039E-17
Crebl2	2.941	1.29E-04	2.473	1.93E-09	2.472	1.94E-09	2.859	7.36E-09	3.159	2.61E-09	2.484	5.520E-16	2.464	6.769E-16
Crispld2	2.550	1.30E-04	2.478	3.65E-02	2.695	2.45E-02	7.338	9.09E-11	7.119	1.09E-10	2.450	2.915E-16	1.193	7.490E-04
Cry1	-1.242	2.02E-02	-1.491	1.80E-02	-4.363	3.19E-07	-1.332	1.75E-02	-1.806	1.03E-04	-2.033	5.598E-10	-2.411	7.271E-12
Cspg2	-2.133	5.17E-04	-4.586	4.08E-07	-5.284	1.55E-07	-12.577	5.58E-12	-16.561	1.65E-12	-5.883	3.217E-18	-6.782	5.399E-19
Csrp1	-2.290	5.74E-04	-4.251	1.17E-06	-4.138	1.42E-06	-1.986	1.78E-07	-2.061	1.00E-07	-1.116	1.492E-02	-1.965	2.027E-14

Cthrc1	-6.871	2.01E-08	-2.143	2.09E-03	-2.927	1.36E-04	-2.083	5.69E-06	-2.071	6.18E-06	-3.947	2.212E-16	-9.120	3.647E-21
Ctss	1.557	2.99E-04	1.093	4.93E-01	1.517	6.23E-03	1.386	4.09E-04	1.517	4.82E-05	2.197	1.351E-12	3.612	2.595E-17
Cxcl9	9.594	3.33E-04	4.162	1.23E-06	9.287	9.07E-09	1.395	4.88E-01	4.627	6.39E-03	2.004	1.073E-06	1.796	1.329E-05
Cybb	1.566	5.86E-04	1.255	7.19E-02	1.580	1.83E-03	1.258	1.94E-02	1.302	9.24E-03	2.510	1.302E-04	3.107	9.012E-06
Cyp1a1	2.239	3.04E-02	1.885	3.47E-04	2.025	1.39E-04	8.715	1.25E-08	10.217	5.57E-09	49.623	1.411E-15	4.397	3.692E-07
Cyp2e1	2.017	3.64E-03	8.206	6.09E-09	10.282	1.90E-09	2.237	3.56E-02	3.146	5.59E-03	4.385	3.013E-09	1.507	1.857E-02
Cyp4b1	2.010	1.61E-04	15.391	2.96E-11	13.787	4.79E-11	3.358	1.23E-12	3.848	3.48E-13	2.455	1.307E-11	1.248	6.960E-03
D10Ertd610e	-1.448	8.39E-04	-3.096	4.10E-09	-3.831	5.62E-10	-1.533	7.66E-07	-1.827	1.76E-08	-2.195	2.128E-16	-3.195	2.601E-20
Dact1	-1.957	1.23E-05	-2.846	9.12E-07	-2.803	1.07E-06	-1.323	3.11E-03	-1.645	2.73E-05	-2.156	6.361E-12	-3.180	8.575E-16
Dbn1	-2.236	2.00E-06	-2.651	5.50E-07	-2.860	2.45E-07	-3.967	1.21E-10	-4.272	6.54E-11	-3.615	1.973E-21	-5.284	4.398E-24
Dbp	4.293	6.49E-06	10.137	7.79E-09	8.272	2.20E-08	9.311	2.82E-09	4.356	2.97E-07	3.047	3.959E-13	2.926	8.756E-13
Dedd2	2.494	5.15E-03	2.142	6.04E-04	2.151	5.77E-04	2.881	7.02E-06	3.836	5.82E-07	1.411	7.005E-08	1.402	9.629E-08
Dennd2a	-2.757	4.93E-02	-5.570	8.50E-05	-8.332	1.15E-05	-2.993	1.02E-08	-3.281	4.10E-09	-1.720	1.988E-11	-2.092	2.738E-14
Depdc1a	-4.455	1.53E-05	-3.609	3.41E-04	-4.498	8.61E-05	-6.000	2.63E-06	-5.925	2.83E-06	-3.020	3.084E-13	-2.875	8.169E-13
Dlk1	-4.419	1.25E-05	-6.504	4.12E-05	-6.013	6.14E-05	-14.710	2.72E-08	-17.208	1.44E-08	-1.100	4.622E-03	-1.176	1.851E-05
Dscc1	-8.009	9.62E-03	-4.144	1.59E-04	-6.262	1.48E-05	-7.727	9.29E-05	-8.086	7.62E-05	-2.390	2.684E-11	-3.473	1.296E-14
Dzip1	-1.316	3.97E-02	-2.088	8.43E-06	-1.727	1.40E-04	-1.381	5.79E-04	-1.262	5.83E-03	-2.127	4.432E-15	-2.775	4.706E-18
E130203B14Rik	-1.559	2.33E-05	-2.371	2.29E-08	-2.248	4.69E-08	-1.174	6.91E-02	-1.431	7.81E-04	-2.078	2.282E-14	-3.271	3.965E-19
E2f8	-2.662	4.49E-02	-3.494	2.54E-03	-5.140	3.26E-04	-6.114	2.17E-03	-8.839	5.38E-04	-2.484	4.062E-13	-2.345	1.644E-12
Ect2	-2.487	2.38E-05	-1.984	1.03E-02	-4.384	2.70E-05	-2.148	6.75E-05	-2.943	2.29E-06	-2.113	2.949E-09	-1.940	2.725E-08
Eif5a2	-1.740	8.69E-03	-1.418	3.15E-02	-1.664	4.00E-03	-1.448	7.05E-04	-1.754	1.76E-05	-2.168	7.856E-13	-2.075	2.704E-12
Eln	-7.873	3.25E-07	-3.603	1.09E-09	-4.518	1.65E-10	-2.917	4.97E-07	-6.475	9.70E-10	-1.222	8.532E-03	-2.841	1.243E-13
Emilin1	-3.376	9.84E-03	-7.865	2.56E-04	-8.351	2.00E-04	-4.513	7.69E-04	-2.800	1.00E-02	-2.051	2.968E-14	-3.709	3.272E-20
Ephx1	2.177	5.06E-06	2.403	1.88E-09	1.852	1.00E-07	3.212	1.52E-09	3.668	4.38E-10	2.059	2.202E-17	3.245	2.517E-22
Esco2	-4.705	3.01E-02	-2.997	2.54E-02	-64.686	5.03E-07	-3.015	3.23E-06	-4.118	2.31E-07	-2.575	3.618E-11	-2.114	3.522E-09
Espl1	-1.517	1.58E-02	-2.012	4.63E-05	-3.138	3.11E-07	-1.816	7.84E-07	-1.911	3.24E-07	-2.673	2.616E-12	-3.215	6.469E-14
Evl	-2.232	2.65E-05	-3.894	6.08E-09	-5.778	3.23E-10	-2.024	3.50E-07	-2.202	1.02E-07	-1.450	1.321E-10	-1.665	1.754E-13
Ezh2	-2.647	8.29E-04	-2.737	4.44E-07	-3.622	2.98E-08	-2.734	3.01E-09	-3.139	6.83E-10	-2.195	2.013E-13	-2.848	3.531E-16
F630043A04Rik	-3.925	1.47E-02	-3.657	1.10E-02	-18.889	1.89E-05	-3.760	1.76E-06	-5.111	1.89E-07	-2.341	3.813E-11	-2.115	4.844E-10
Fam171a1	-1.899	8.73E-05	-1.917	4.96E-07	-1.759	2.21E-06	-1.697	1.42E-06	-1.941	1.24E-07	-2.220	9.049E-05	-2.612	8.073E-06
Fam83d	-3.743	4.63E-03	-1.539	1.73E-02	-2.210	2.75E-04	-1.826	2.38E-03	-2.400	1.21E-04	-1.465	4.477E-06	-2.056	6.000E-11
Fas	2.797	4.64E-04	2.048	1.83E-02	2.423	5.57E-03	3.026	2.16E-06	2.648	7.99E-06	1.409	5.132E-07	1.129	2.492E-02
Fat4	-2.658	1.38E-05	-6.746	1.12E-06	-7.842	4.99E-07	-2.654	3.67E-06	-2.545	5.74E-06	-1.982	1.846E-10	-5.237	7.213E-19
Fbln2	-1.755	1.13E-04	-2.202	1.89E-04	-2.331	1.03E-04	-2.208	5.02E-05	-2.900	2.73E-06	-2.954	4.606E-18	-3.042	2.482E-18
Fbn1	-2.238	6.69E-05	-3.898	2.64E-09	-6.281	8.09E-11	-2.340	5.88E-09	-2.810	6.25E-10	-1.926	2.272E-12	-3.294	3.789E-18
Fbn2	-9.365	6.98E-06	-9.223	5.48E-05	-8.119	9.41E-05	-9.921	2.55E-09	-14.197	4.77E-10	-32.264	2.613E-27	-22.707	3.311E-26
Fgd1	-2.451	3.04E-02	-2.736	3.96E-02	-6.917	8.14E-04	-1.992	7.43E-02	-2.541	2.14E-02	-1.640	4.523E-10	-1.569	2.715E-09
Fgf1	2.116	1.44E-05	1.781	4.09E-07	1.956	7.91E-08	1.706	2.90E-07	1.916	3.32E-08	2.475	7.359E-13	4.112	3.761E-17
Figf	-1.422	2.22E-02	-1.467	7.39E-05	-2.238	3.39E-08	-1.361	5.49E-04	-2.024	1.79E-07	-3.634	2.549E-16	-2.307	3.495E-12
Fkbp10	-2.385	2.10E-05	-3.188	5.53E-07	-4.273	4.70E-08	-2.711	6.77E-07	-4.288	1.04E-08	-2.057	7.289E-17	-3.586	1.224E-22
Fmo1	1.714	2.42E-05	2.304	4.23E-10	2.480	1.58E-10	2.547	1.40E-11	2.652	8.47E-12	8.250	1.579E-20	3.521	2.253E-15
Fmo2	2.687	7.84E-03	2.276	3.54E-08	2.136	8.69E-08	7.707	6.22E-12	5.003	1.02E-10	12.864	4.270E-19	3.011	4.904E-11
Fn1	-4.034	5.34E-08	-4.937	2.03E-10	-6.332	3.72E-11	-1.807	1.01E-09	-2.762	1.79E-12	-1.457	1.165E-10	-3.731	7.418E-23

Fndc1	-2.405	2.46E-05	-3.250	1.41E-05	-3.688	5.10E-06	-4.232	4.98E-10	-3.852	1.09E-09	-5.279	1.165E-16	-4.122	4.372E-15
Foxm1	-2.452	1.13E-02	-2.633	1.54E-02	-3.664	2.61E-03	-3.954	5.83E-03	-4.292	4.04E-03	-2.208	7.909E-14	-1.954	2.895E-12
Fras1	-4.259	6.86E-06	-2.714	3.73E-07	-3.288	5.43E-08	-2.402	5.77E-07	-3.664	7.38E-09	-1.236	7.686E-03	-1.451	3.111E-05
Fscn1	-2.116	3.31E-05	-4.931	1.49E-08	-6.533	2.34E-09	-4.043	1.30E-09	-3.704	2.74E-09	-2.048	7.697E-09	-2.508	6.245E-11
Fstl1	-2.216	1.52E-06	-9.118	7.29E-11	-12.766	1.38E-11	-2.905	1.38E-09	-4.502	2.50E-11	-1.645	6.983E-12	-3.377	1.356E-20
Gbp3	2.127	1.13E-05	2.272	1.03E-03	2.696	2.23E-04	2.738	9.48E-08	2.624	1.52E-07	2.333	4.886E-10	1.402	5.404E-04
Gda	3.875	2.57E-06	3.546	3.06E-09	3.151	9.32E-09	1.501	1.34E-03	1.349	9.97E-03	2.129	6.773E-08	4.274	1.630E-13
Gja7	-2.383	2.65E-04	-8.082	1.18E-03	-13.895	1.82E-04	-1.676	3.59E-02	-2.137	4.61E-03	-3.625	9.330E-21	-3.809	3.864E-21
Gli2	-3.926	4.41E-03	-15.054	3.30E-09	-21.042	8.65E-10	-3.167	5.15E-06	-4.849	1.86E-07	-1.693	2.277E-09	-2.455	3.718E-14
Glul	2.284	3.63E-04	4.823	1.78E-09	3.799	1.17E-08	2.146	2.56E-06	2.167	2.24E-06	1.221	2.851E-04	1.863	1.616E-12
Got1l1	2.832	2.85E-02	2.506	1.46E-02	2.447	1.67E-02	4.529	6.78E-04	2.811	9.08E-03	1.235	2.909E-04	1.124	2.762E-02
Gpc2	-1.587	8.86E-03	-2.444	9.56E-03	-4.346	2.79E-04	-2.347	1.30E-03	-3.360	6.96E-05	-2.267	8.224E-15	-3.462	6.202E-19
Gpc3	-2.829	1.89E-03	-7.146	2.02E-09	-11.240	1.83E-10	-1.757	1.49E-06	-2.352	1.56E-08	-2.498	2.137E-09	-8.827	1.960E-17
Gpr23	-3.000	1.24E-04	-8.300	1.46E-07	-7.617	2.29E-07	-2.749	2.66E-06	-5.445	9.51E-09	-2.287	6.974E-10	-2.856	5.710E-12
Gpsm2	-5.859	1.72E-02	-2.592	2.25E-03	-2.168	8.55E-03	-2.559	2.86E-07	-2.964	5.79E-08	-2.045	6.354E-10	-1.584	1.477E-06
Gpx7	-2.310	1.11E-06	-2.571	1.72E-07	-3.795	3.56E-09	-1.766	1.90E-07	-2.393	1.53E-09	-1.294	2.929E-05	-2.145	7.839E-14
Grb10	-2.443	7.13E-07	-4.316	1.23E-10	-4.654	6.81E-11	-3.029	5.05E-10	-3.533	1.11E-10	-2.593	5.281E-21	-2.313	1.040E-19
Gsta3	33.739	2.59E-05	4.024	1.28E-08	4.413	6.19E-09	7.358	1.33E-09	5.521	7.91E-09	4.269	6.208E-17	9.360	2.747E-21
Gstm1	3.171	2.36E-07	3.468	1.97E-11	3.850	7.61E-12	2.726	1.38E-11	3.354	1.49E-12	1.557	1.081E-02	1.419	3.884E-02
Gtse1	-3.010	1.12E-02	-4.662	4.95E-07	-5.044	2.89E-07	-3.648	7.15E-04	-2.903	2.96E-03	-1.186	5.171E-03	-1.268	2.534E-04
H1fx	-8.592	2.29E-04	-5.621	3.21E-05	-9.253	2.58E-06	-3.638	4.50E-03	-5.051	9.10E-04	-1.886	5.765E-10	-3.483	3.170E-16
H2afx	-2.351	5.36E-05	-2.140	1.05E-06	-2.648	7.20E-08	-2.322	4.51E-08	-2.191	9.97E-08	-2.107	9.957E-10	-2.282	1.343E-10
H2afy2	-3.168	1.52E-05	-1.955	8.07E-04	-2.458	6.68E-05	-2.744	2.02E-07	-3.398	2.41E-08	-2.215	5.406E-17	-2.223	4.872E-17
H2-D1	1.769	5.48E-04	1.367	1.18E-02	1.857	7.64E-05	2.523	4.58E-08	3.415	1.85E-09	7.150	6.714E-05	4.060	2.205E-03
H2-DMa	1.488	1.42E-02	1.054	5.12E-01	1.188	4.76E-02	1.991	1.97E-06	3.027	1.09E-08	2.035	1.410E-11	2.563	3.480E-14
H2-Eb1	2.645	1.37E-05	2.045	1.50E-04	3.187	1.38E-06	2.985	1.78E-08	5.030	2.01E-10	4.061	9.523E-10	8.355	1.838E-13
H2-T23	1.956	4.03E-05	2.607	4.52E-06	2.968	1.21E-06	2.551	8.40E-10	3.535	2.57E-11	2.825	1.747E-11	2.727	3.549E-11
H3f3b	-2.888	2.80E-02	-3.416	9.57E-03	-3.304	1.12E-02	-1.331	1.89E-01	-2.027	4.87E-03	-1.303	3.962E-12	-1.710	5.509E-19
Herpud1	2.487	1.76E-04	5.698	1.85E-08	5.295	3.01E-08	2.319	1.42E-08	2.904	9.43E-10	1.875	4.751E-12	2.077	1.878E-13
Hist1h2bc	1.161	5.79E-03	1.765	5.91E-05	2.105	4.27E-06	1.653	4.43E-07	2.126	4.84E-09	2.295	2.047E-12	4.253	9.020E-18
Hmcn1	-2.899	1.02E-04	-16.566	2.99E-09	-24.032	7.14E-10	-2.132	4.92E-07	-2.126	5.12E-07	-2.181	5.529E-13	-7.008	4.891E-22
Hmgb2	-2.572	5.01E-04	-5.018	3.59E-07	-6.522	6.90E-08	-2.640	6.59E-07	-3.283	7.25E-08	-1.854	5.608E-11	-3.442	1.443E-17
Hmgn2	-2.063	1.85E-05	-2.540	1.51E-06	-3.426	7.46E-08	-1.822	8.38E-05	-2.172	7.15E-06	-1.471	3.338E-13	-2.041	3.285E-19
Hsd11b1	2.716	6.52E-05	4.706	6.67E-10	5.369	2.58E-10	3.492	8.23E-11	2.671	1.36E-09	1.610	4.831E-10	10.993	7.443E-26
Hspa4	2.084	2.04E-04	2.206	2.50E-07	2.138	3.87E-07	3.162	2.69E-05	5.434	5.27E-07	1.359	1.323E-08	1.266	1.130E-06
Hspa4l	1.599	4.28E-06	1.528	6.30E-06	1.790	2.24E-07	2.420	1.29E-09	2.598	5.26E-10	2.009	4.803E-10	3.197	1.059E-14
Hspa8	2.144	1.77E-02	2.131	9.63E-04	3.847	5.34E-06	1.847	1.87E-02	4.336	2.95E-05	1.076	3.758E-04	1.096	2.628E-05
Ifi205	6.041	4.40E-06	2.064	7.07E-04	2.660	5.35E-05	3.230	2.35E-07	4.715	1.05E-08	1.677	2.469E-03	2.602	1.838E-06
Ifi27	3.973	2.25E-05	1.945	9.10E-03	1.848	1.42E-02	4.076	6.29E-08	6.597	2.25E-09	2.793	2.436E-07	3.351	1.442E-08
Ifit3	3.367	1.96E-06	1.752	1.36E-05	1.504	2.54E-04	5.930	1.20E-11	4.209	1.48E-10	3.682	2.187E-12	2.314	1.324E-08
Igf2	-7.117	7.41E-07	-4.712	5.94E-08	-4.905	4.47E-08	-4.367	1.90E-08	-5.181	5.49E-09	-5.113	4.048E-13	-10.390	1.354E-16
Igf2bp3	-7.982	4.44E-04	-4.099	4.35E-03	-4.915	1.91E-03	-5.283	7.90E-04	-5.418	7.02E-04	-4.420	9.587E-17	-5.259	7.629E-18
Igh-6	1.990	1.38E-03	1.380	2.31E-02	1.707	9.95E-04	1.875	1.72E-01	3.843	9.01E-03	2.172	5.057E-06	2.200	3.978E-06

Igsf3	-1.794	2.64E-04	-1.767	8.98E-05	-1.758	9.81E-05	-1.631	2.05E-05	-1.901	1.30E-06	-2.265	1.351E-09	-2.278	1.182E-09
Igtp	2.033	2.35E-05	1.547	4.48E-03	2.136	5.58E-05	1.569	1.37E-03	1.787	1.78E-04	2.971	4.079E-10	2.275	7.396E-08
Incenp	-2.503	9.53E-05	-2.471	2.06E-05	-3.427	8.91E-07	-2.829	9.10E-07	-2.775	1.11E-06	-1.606	1.569E-07	-1.215	6.163E-03
Inmt	3.638	1.04E-02	8.433	3.42E-12	12.595	4.44E-13	23.967	1.20E-10	23.488	1.29E-10	2.908	8.531E-06	3.628	4.971E-07
Iqgap3	-2.611	1.59E-04	-1.848	1.85E-03	-2.900	1.68E-05	-2.232	5.97E-07	-2.474	1.61E-07	-1.706	2.223E-06	-1.985	3.779E-08
Irf7	1.841	5.52E-04	1.470	6.53E-03	1.391	1.56E-02	1.746	1.06E-05	1.633	3.64E-05	3.124	7.251E-10	3.718	4.277E-11
Kcne1l	-5.867	1.07E-03	-2.507	3.97E-02	-9.365	1.13E-04	-3.284	7.08E-03	-5.363	6.36E-04	-2.371	1.789E-09	-6.541	1.217E-16
Kif20a	-3.367	3.66E-03	-2.050	1.00E-01	-6.427	5.98E-04	-3.210	2.19E-05	-3.634	8.11E-06	-2.346	3.320E-10	-1.652	3.327E-06
Kif22	-3.219	1.67E-05	-5.023	1.32E-05	-11.546	1.71E-07	-4.124	4.84E-07	-3.764	9.85E-07	-2.406	8.958E-11	-2.452	5.802E-11
Kif2c	-3.548	2.40E-03	-2.776	2.33E-04	-5.171	2.51E-06	-3.390	4.11E-06	-4.581	4.05E-07	-1.780	8.814E-13	-1.323	7.897E-07
Klf9	4.379	6.39E-07	3.312	1.05E-04	3.852	3.52E-05	6.621	4.13E-13	6.497	4.66E-13	2.832	9.232E-12	2.844	8.476E-12
Kntc1	-2.718	9.95E-03	-2.588	1.58E-02	-5.871	2.13E-04	-3.175	2.61E-06	-3.213	2.35E-06	-2.380	6.536E-12	-2.419	4.406E-12
Kntc2	-3.517	3.03E-04	-3.288	5.27E-03	-6.051	2.44E-04	-2.241	1.64E-06	-2.288	1.25E-06	-2.284	7.884E-10	-1.893	8.737E-08
Lamb1-1	-2.589	1.68E-04	-3.211	4.15E-06	-3.615	1.52E-06	-2.110	1.92E-05	-2.953	4.21E-07	-2.142	9.502E-19	-2.464	1.878E-20
Lhfpl2	-4.682	4.76E-05	-5.401	1.17E-09	-6.743	2.78E-10	-5.866	8.75E-10	-6.134	6.56E-10	-2.105	8.728E-10	-2.395	3.668E-11
Lims2	1.601	1.72E-04	2.152	6.38E-08	2.180	5.28E-08	3.308	6.23E-11	3.073	1.31E-10	2.940	6.736E-17	2.863	1.185E-16
Loxl2	-1.405	2.24E-03	-1.895	1.26E-07	-2.421	3.28E-09	-3.033	4.27E-10	-3.573	8.57E-11	-2.580	7.154E-13	-2.006	4.098E-10
Lrrc17	-2.343	4.13E-05	-12.252	9.87E-09	-12.443	9.20E-09	-2.531	6.02E-06	-3.735	1.49E-07	-2.471	1.365E-12	-5.711	5.723E-19
Mad2l1	-2.710	1.64E-04	-2.302	5.35E-05	-3.789	4.73E-07	-2.772	3.18E-06	-3.265	6.67E-07	-1.799	3.461E-09	-1.325	2.331E-04
Maged1	-2.030	2.21E-06	-2.418	2.32E-09	-2.327	3.87E-09	-2.301	9.95E-10	-2.472	3.83E-10	-1.751	8.528E-20	-1.899	3.623E-21
Maged2	-4.402	2.00E-06	-5.232	2.16E-09	-6.429	5.59E-10	-2.979	2.06E-08	-3.709	2.57E-09	-2.429	1.884E-18	-4.641	4.974E-24
Mapt	2.257	1.93E-02	3.071	6.62E-06	3.390	2.80E-06	1.999	1.09E-07	2.297	1.41E-08	1.838	2.853E-17	1.710	5.064E-16
Marcksl1	-5.744	2.38E-07	-7.652	2.82E-08	-9.962	7.11E-09	-6.267	1.54E-12	-7.246	6.24E-13	-2.194	2.615E-18	-4.453	7.397E-25
Mcm2	-2.437	3.45E-03	-2.754	1.07E-03	-5.188	1.53E-05	-2.454	3.62E-06	-2.726	1.14E-06	-1.747	1.470E-10	-2.073	5.754E-13
Mcm3	-2.018	4.45E-03	-6.154	8.34E-04	-20.746	8.53E-06	-4.187	4.86E-03	-3.709	8.34E-03	-1.735	1.371E-07	-2.721	1.319E-12
Mcm4	-2.280	2.31E-03	-2.269	9.20E-03	-2.564	3.91E-03	-2.495	1.19E-05	-3.157	1.14E-06	-2.434	3.578E-09	-3.273	1.216E-11
Mcm5	-2.765	4.58E-05	-2.526	5.20E-05	-6.464	3.61E-08	-3.145	1.83E-07	-3.730	3.96E-08	-2.021	7.934E-09	-2.253	5.161E-10
Mcm6	-2.887	3.48E-06	-2.852	1.52E-03	-7.125	5.94E-06	-2.388	7.14E-06	-2.918	8.39E-07	-2.408	1.267E-09	-3.815	2.222E-13
Mcm7	-2.400	5.75E-06	-2.140	6.19E-10	-3.120	5.55E-12	-2.016	5.00E-08	-2.106	2.54E-08	-1.584	9.052E-13	-2.163	9.042E-18
Mdk	-4.513	8.89E-08	-2.620	4.88E-09	-2.245	3.52E-08	-7.403	9.11E-13	-11.078	1.03E-13	-3.869	2.609E-17	-3.832	3.070E-17
Meis1	-1.455	4.55E-02	-8.784	4.27E-06	-6.090	2.65E-05	-1.354	5.22E-04	-1.406	1.95E-04	-2.219	5.332E-08	-4.257	4.088E-13
Mest	-8.066	1.81E-08	-13.935	4.46E-14	-13.360	5.41E-14	-10.946	1.98E-15	-18.063	2.04E-16	-3.944	1.369E-13	-14.533	3.547E-20
Mettl7a	2.045	4.85E-05	4.064	2.51E-11	4.166	2.04E-11	3.754	1.08E-08	3.690	1.26E-08	1.972	7.749E-10	1.935	1.346E-09
Mfap2	-3.543	4.48E-06	-6.644	1.00E-08	-8.331	2.76E-09	-1.627	2.15E-04	-2.197	2.17E-06	-4.415	8.804E-19	-8.315	2.175E-22
Mki67	-2.848	9.07E-03	-3.606	8.16E-05	-11.716	1.07E-07	-4.347	4.80E-08	-4.689	2.73E-08	-2.483	2.732E-11	-2.984	5.745E-13
Mmp14	-3.943	3.85E-07	-5.690	2.62E-09	-5.540	3.13E-09	-2.983	1.08E-12	-3.591	1.68E-13	-2.150	2.083E-07	-4.267	9.217E-13
Mmp23	-3.517	2.84E-02	-9.314	4.69E-06	-11.433	1.89E-06	-1.893	5.55E-04	-2.135	1.29E-04	-2.506	1.790E-15	-2.794	1.427E-16
Mphosph1	-2.105	6.18E-04	-1.943	2.58E-03	-2.631	1.32E-04	-2.060	3.77E-04	-2.184	1.96E-04	-2.541	6.602E-13	-1.695	4.856E-08
Mpzl1	-2.615	7.29E-08	-2.566	5.60E-08	-2.500	7.62E-08	-2.470	1.54E-10	-2.512	1.24E-10	-1.462	8.242E-11	-2.066	6.474E-17
Mthfd2l	-1.270	4.94E-02	-1.641	7.64E-05	-1.601	1.21E-04	-1.286	1.45E-03	-1.409	1.16E-04	-2.226	2.593E-11	-3.919	2.320E-16
Mxd3	-3.677	8.91E-04	-2.552	3.53E-03	-3.085	9.45E-04	-5.010	1.50E-06	-4.117	5.74E-06	-2.428	4.243E-13	-1.773	3.027E-09
Mycn	-1.398	1.14E-02	-1.831	1.55E-05	-2.011	3.66E-06	-5.835	2.54E-05	-8.430	3.87E-06	-2.002	1.287E-04	-2.433	1.802E-10
Myh10	-2.499	2.92E-05	-2.907	3.93E-10	-3.138	1.75E-10	-1.994	1.63E-09	-2.100	7.08E-10	-1.417	2.921E-10	-2.957	3.542E-21

Myl9	-2.573	2.66E-04	-4.050	6.48E-12	-4.379	3.41E-12	-2.213	8.10E-07	-2.717	6.64E-08	-1.715	4.054E-10	-3.811	1.015E-18
Nampt	4.342	4.44E-05	2.623	1.22E-03	2.578	1.39E-03	3.014	5.07E-07	2.099	2.91E-05	1.785	6.685E-14	1.853	1.676E-14
Ncapd2	-1.656	5.76E-03	-3.058	4.77E-06	-4.053	4.53E-07	-3.352	4.58E-06	-3.744	1.86E-06	-2.527	9.193E-12	-2.722	1.817E-12
Ncapg2	-2.102	1.85E-03	-2.419	3.50E-03	-4.413	5.42E-05	-2.873	6.46E-07	-4.182	2.28E-08	-1.348	3.085E-05	-1.286	2.398E-04
Ncaph	-2.035	1.74E-04	-2.219	2.02E-05	-2.680	2.39E-06	-2.524	1.55E-08	-2.550	1.37E-08	-2.423	2.401E-13	-1.987	4.997E-11
Ndn	-2.498	1.03E-07	-7.157	2.00E-11	-10.491	2.46E-12	-2.965	9.73E-10	-3.634	1.32E-10	-1.831	1.123E-09	-6.440	2.254E-20
Nnat	-4.148	2.37E-05	-7.716	1.44E-05	-14.056	1.04E-06	-3.409	1.51E-10	-3.058	4.45E-10	-1.792	1.290E-05	-4.240	9.910E-13
Nope	-1.775	6.41E-04	-6.068	2.11E-03	-6.062	2.11E-03	-2.422	6.30E-05	-3.736	1.20E-06	-4.627	1.097E-18	-6.265	1.641E-20
Npas3	-6.718	3.21E-02	-6.990	4.32E-03	-5.660	8.73E-03	-5.482	7.34E-03	-9.950	9.45E-04	-1.274	1.512E-05	-1.899	3.125E-13
Nr1d1	2.507	4.37E-04	4.260	4.32E-05	6.270	4.25E-06	11.694	1.68E-07	13.576	8.76E-08	5.892	3.037E-18	3.914	1.195E-15
Nr1d2	2.917	6.03E-05	3.376	9.94E-09	2.856	5.25E-08	4.277	1.65E-10	3.435	1.10E-09	1.928	1.111E-10	1.815	7.429E-10
Nrm	-2.116	3.99E-03	-1.983	3.08E-04	-2.088	1.65E-04	-1.773	6.43E-05	-2.185	3.09E-06	-2.041	3.144E-10	-2.516	1.628E-12
Nt5dc2	-2.386	1.65E-07	-2.083	2.46E-07	-3.236	1.24E-09	-1.371	9.09E-04	-1.808	2.91E-06	-2.120	7.375E-12	-4.505	1.467E-18
Nuf2	-4.173	4.42E-04	-3.216	2.50E-03	-17.548	7.47E-07	-4.830	3.34E-08	-5.220	1.94E-08	-2.392	9.247E-11	-2.297	2.378E-10
Nupr1	1.751	6.63E-03	1.200	8.05E-02	1.275	2.61E-02	2.234	4.46E-07	2.089	1.13E-06	2.083	1.532E-04	3.096	3.825E-07
Nusap1	-2.117	4.45E-05	-2.197	1.50E-05	-4.969	7.31E-09	-3.180	3.02E-08	-3.601	9.56E-09	-2.259	4.308E-11	-2.496	3.985E-12
Oas1a	2.463	1.78E-04	1.573	1.19E-02	1.408	4.54E-02	1.753	5.06E-04	2.290	1.53E-05	5.205	1.050E-13	2.453	2.159E-08
Omd	2.179	4.92E-04	4.398	3.07E-08	4.299	3.65E-08	6.110	2.15E-06	5.280	5.11E-06	3.314	2.940E-11	2.132	1.633E-07
Osgin1	3.526	2.91E-02	9.384	2.24E-08	9.118	2.59E-08	10.206	2.43E-07	10.155	2.49E-07	1.509	2.760E-08	11.272	3.087E-25
Parp14	2.028	1.42E-03	1.292	5.87E-02	1.525	4.93E-03	1.773	3.71E-05	2.009	5.39E-06	2.246	4.679E-12	1.996	1.189E-10
Pbk	-2.687	6.64E-06	-1.806	2.19E-03	-4.773	2.72E-07	-3.233	4.68E-07	-3.671	1.53E-07	-1.920	7.823E-08	-1.418	4.451E-04
Pcolce2	2.089	5.01E-05	4.441	6.41E-05	4.820	3.90E-05	3.407	4.96E-12	3.066	1.43E-11	7.631	6.012E-13	1.860	2.935E-04
Pdlim3	-2.326	1.30E-05	-3.183	9.38E-03	-4.101	2.69E-03	-6.250	2.35E-07	-4.674	1.49E-06	-2.070	4.201E-13	-2.314	1.872E-14
Pdlim7	-2.009	2.34E-05	-3.573	5.43E-08	-4.308	1.17E-08	-2.412	5.68E-10	-2.576	2.45E-10	-2.215	1.626E-12	-3.445	9.479E-17
Pdzrn3	-1.490	1.46E-03	-1.877	9.76E-06	-1.956	5.13E-06	-2.785	8.86E-09	-2.852	6.84E-09	-2.275	1.143E-17	-2.275	1.149E-17
Peg3	-3.101	5.07E-05	-6.290	3.43E-11	-6.519	2.73E-11	-5.410	1.76E-12	-8.545	1.02E-13	-2.064	9.322E-11	-2.186	1.972E-11
Pim3	2.716	3.67E-05	3.926	3.35E-08	4.459	1.23E-08	2.520	5.75E-07	4.202	4.31E-09	1.546	2.816E-06	3.044	5.143E-14
Plagl1	-5.515	6.69E-06	-3.281	1.97E-09	-3.461	1.19E-09	-1.816	4.77E-08	-2.118	3.55E-09	-4.667	4.640E-17	-5.580	3.734E-18
Plekhh2	-1.593	1.07E-02	-3.353	2.04E-05	-3.750	8.55E-06	-1.536	1.09E-04	-1.707	1.38E-05	-2.189	2.292E-06	-4.837	6.348E-12
Plk4	-2.035	1.85E-02	-1.626	3.78E-03	-2.402	3.15E-05	-1.895	5.70E-04	-2.479	2.59E-05	-2.434	1.324E-10	-3.190	5.309E-13
Plscr2	2.884	6.24E-04	2.402	3.34E-04	2.434	2.94E-04	3.908	2.24E-07	3.315	8.95E-07	6.081	8.696E-17	2.270	1.708E-09
Plxnd1	-1.628	7.84E-05	-2.791	1.24E-07	-3.269	2.51E-08	-1.940	4.01E-07	-1.821	1.18E-06	-2.179	5.742E-12	-2.170	6.448E-12
Podxl2	-3.818	5.02E-04	-26.686	3.88E-07	-33.244	1.92E-07	-2.908	9.94E-03	-3.670	2.91E-03	-2.294	1.728E-12	-4.235	7.950E-18
Pole	-3.088	2.35E-04	-10.072	1.17E-08	-19.137	7.02E-10	-22.157	7.79E-08	-23.879	5.98E-08	-2.241	2.933E-12	-2.641	5.453E-14
Prc1	-2.524	7.14E-04	-2.798	1.78E-04	-4.016	1.07E-05	-3.047	1.42E-08	-3.872	1.53E-09	-1.844	2.113E-08	-1.805	3.937E-08
Prelp	1.643	1.30E-03	2.448	2.57E-06	2.599	1.31E-06	5.784	4.63E-12	7.195	1.16E-12	3.224	1.517E-17	2.683	7.387E-16
Prkg1	-1.252	4.05E-02	-1.862	3.96E-05	-1.817	5.79E-05	-1.270	1.80E-05	-1.383	7.82E-07	-2.352	3.829E-10	-4.995	5.403E-16
Psmb8	2.215	3.27E-05	1.164	3.14E-01	1.563	9.35E-03	1.919	4.64E-07	2.594	6.79E-09	3.380	6.004E-11	3.267	1.063E-10
Psmb9	1.880	6.04E-03	1.345	3.29E-02	1.631	1.82E-03	1.905	4.96E-07	2.593	6.44E-09	2.884	3.725E-10	3.082	1.114E-10
Ptbp2	-1.321	1.74E-02	-1.494	3.49E-02	-1.627	1.37E-02	-1.450	2.97E-05	-1.580	3.79E-06	-2.746	7.249E-13	-5.063	1.927E-17
Ptk7	-2.421	3.07E-03	-12.125	5.07E-07	-19.441	7.66E-08	-2.223	1.19E-06	-3.297	1.47E-08	-1.706	1.889E-13	-3.764	1.782E-22
Ptn	-11.663	1.81E-07	-16.372	1.97E-08	-15.161	2.70E-08	-4.452	3.95E-06	-5.766	7.45E-07	-2.885	1.531E-11	-2.967	8.892E-12
Pycr1	-1.342	4.10E-02	-8.477	1.43E-05	-10.917	4.66E-06	-1.664	1.01E-03	-2.324	1.19E-05	-2.026	1.358E-15	-2.518	2.968E-18

Racgap1	-2.223	3.58E-03	-1.694	4.61E-04	-2.424	3.74E-06	-2.337	3.89E-06	-2.481	1.92E-06	-2.172	8.971E-11	-2.466	3.948E-12
Rad51	-4.707	1.52E-02	-9.011	3.89E-07	-18.675	1.64E-08	-2.840	1.09E-06	-3.379	2.08E-07	-2.293	1.551E-07	-3.270	2.209E-10
Rad51ap1	-11.552	4.48E-04	-8.021	2.12E-03	-9.124	1.38E-03	-6.033	3.24E-03	-15.067	1.30E-04	-1.762	2.826E-10	-1.850	5.400E-11
Rap2a	-1.538	4.46E-04	-1.919	1.65E-09	-1.905	1.87E-09	-2.093	3.33E-10	-2.128	2.57E-10	-2.009	7.946E-08	-2.433	9.402E-10
Rcor2	-2.506	4.49E-03	-3.209	7.90E-04	-2.254	9.14E-03	-2.929	4.01E-03	-2.556	9.21E-03	-1.229	1.192E-04	-1.352	6.139E-07
Rfc3	-3.201	1.39E-03	-3.832	7.73E-06	-6.239	3.03E-07	-2.546	7.72E-07	-2.988	1.39E-07	-1.877	3.817E-13	-2.237	1.713E-15
Rhobtb3	-2.458	3.90E-04	-2.817	1.69E-02	-3.127	1.00E-02	-3.041	7.51E-07	-3.603	1.62E-07	-1.659	5.642E-10	-1.286	4.989E-05
Rkhd3	-3.977	4.49E-05	-4.149	1.27E-06	-4.668	5.44E-07	-3.996	1.07E-07	-4.101	8.75E-08	-1.462	5.766E-05	-4.898	1.178E-16
Robo1	-3.316	2.73E-05	-7.260	1.82E-08	-8.914	5.95E-09	-2.617	7.72E-06	-3.989	1.69E-07	-2.149	1.887E-12	-2.020	1.114E-11
Rps4y2	-2.273	6.00E-04	-3.160	3.91E-05	-3.421	2.07E-05	-1.808	1.19E-04	-2.078	1.66E-05	-1.555	1.120E-02	-1.677	3.681E-03
Rrm1	-2.357	3.81E-05	-2.199	9.32E-06	-3.205	1.54E-07	-2.285	1.61E-07	-3.000	6.66E-09	-2.072	4.327E-09	-1.748	4.496E-07
Rrm2	-7.854	1.08E-05	-2.600	1.28E-05	-7.533	4.00E-09	-4.931	2.92E-10	-5.527	1.31E-10	-2.145	4.294E-08	-1.912	6.662E-07
Selenbp1	1.321	6.20E-03	2.550	1.73E-10	2.716	8.09E-11	2.966	2.07E-09	2.774	4.28E-09	1.997	1.615E-16	2.014	1.218E-16
Sema4a	4.030	4.19E-03	1.763	2.28E-06	2.015	2.41E-07	2.307	2.37E-05	2.737	3.72E-06	2.459	7.165E-18	1.988	3.275E-15
Sema5a	-3.609	1.47E-04	-3.338	6.58E-09	-3.666	2.80E-09	-1.586	1.57E-03	-2.306	8.69E-06	-2.197	4.407E-15	-2.316	1.026E-15
Serf1	-2.867	1.80E-04	-1.566	1.00E-02	-2.035	4.08E-04	-2.019	5.59E-04	-2.166	2.56E-04	-1.333	3.851E-05	-2.052	4.594E-12
Serpine2	-1.922	4.67E-05	-8.993	3.96E-13	-10.931	1.44E-13	-2.226	2.59E-10	-2.774	1.50E-11	-3.130	1.050E-11	-3.824	3.418E-13
Sertad4	-2.548	4.41E-05	-4.165	8.62E-09	-5.065	1.98E-09	-2.518	4.49E-06	-2.300	1.26E-05	-3.280	3.683E-15	-3.004	2.024E-14
Sgol1	-4.105	1.79E-03	-4.895	1.55E-06	-5.573	6.74E-07	-4.432	1.43E-03	-4.311	1.63E-03	-2.749	8.311E-13	-2.590	3.016E-12
Skp2	-2.001	1.14E-02	-3.160	4.51E-04	-4.610	3.69E-05	-3.115	8.58E-08	-3.159	7.47E-08	-2.063	1.862E-08	-3.432	4.605E-13
Slc25a33	5.848	2.62E-06	3.391	8.74E-11	2.470	2.84E-09	3.609	3.07E-11	2.802	3.99E-10	4.063	2.103E-14	2.303	1.043E-09
Slc38a4	-2.232	7.46E-04	-7.334	5.05E-03	-9.552	2.20E-03	-1.967	4.64E-05	-1.717	3.37E-04	-6.074	6.295E-14	-3.518	1.234E-10
Smarca1	-3.058	2.19E-05	-7.486	4.43E-07	-9.010	1.70E-07	-4.681	1.89E-08	-5.512	6.05E-09	-1.712	1.660E-10	-4.541	1.874E-20
Smarcb1	-2.580	2.22E-02	-2.564	3.81E-02	-3.416	1.03E-02	-1.638	4.68E-02	-2.177	4.42E-03	-1.349	2.411E-08	-1.460	2.901E-10
Smo	-1.722	1.67E-03	-1.516	5.36E-06	-1.597	1.60E-06	-1.945	1.56E-07	-2.183	2.62E-08	-2.312	1.880E-17	-2.461	3.611E-18
Smtnl2	-2.499	1.95E-04	-3.193	3.88E-07	-3.584	1.38E-07	-1.351	1.67E-03	-2.288	1.16E-07	-1.476	1.192E-07	-1.629	2.058E-09
Sox11	-5.492	1.90E-02	-3.783	7.68E-06	-3.870	6.48E-06	-1.944	2.16E-05	-2.242	3.11E-06	-2.722	2.671E-12	-2.570	9.255E-12
Sox4	-5.976	2.10E-08	-8.088	1.04E-05	-6.125	4.14E-05	-3.323	1.03E-09	-4.049	1.75E-10	-2.081	1.151E-08	-5.639	1.832E-16
Spn	1.461	4.75E-02	1.402	7.21E-02	1.789	5.31E-03	1.544	4.17E-03	1.599	2.47E-03	2.022	7.515E-09	2.345	1.940E-10
Srgap1	-2.647	1.41E-02	-3.088	1.16E-02	-4.429	2.00E-03	-4.818	4.30E-04	-4.619	5.36E-04	-1.570	2.276E-07	-2.992	4.591E-15
Stat1	1.452	5.96E-03	1.011	9.18E-01	1.393	6.96E-03	1.356	7.61E-03	1.547	6.21E-04	2.147	9.772E-13	2.097	1.891E-12
Stfa3	-43.731	8.01E-05	-11.358	4.50E-05	-22.827	3.77E-06	-19.370	2.25E-07	-38.027	2.32E-08	-9.950	3.808E-14	-1.394	3.225E-02
Stox2	-2.710	1.72E-02	-8.496	3.18E-05	-12.149	7.02E-06	-2.323	9.54E-05	-2.080	3.23E-04	-1.265	1.287E-02	-1.524	6.597E-05
Sult1a1	2.482	3.51E-04	2.392	1.89E-07	2.034	1.71E-06	4.798	4.57E-09	4.115	1.47E-08	2.574	5.758E-09	4.720	2.546E-13
Tacc3	-2.886	6.13E-03	-2.451	2.91E-04	-3.435	1.58E-05	-2.343	9.33E-05	-2.435	6.24E-05	-2.119	7.872E-09	-2.573	9.366E-11
Tcf21	-2.634	5.24E-07	-6.964	1.62E-12	-8.552	4.92E-13	-1.443	1.38E-05	-2.125	5.91E-09	-1.218	1.612E-02	-5.146	3.350E-17
Tcfe2a	-2.299	5.76E-03	-4.087	6.75E-03	-3.690	1.05E-02	-4.378	4.91E-03	-3.401	1.46E-02	-1.773	1.002E-08	-2.212	1.725E-11
Tdg	-2.112	3.42E-06	-1.721	1.66E-05	-2.149	4.91E-07	-1.945	5.91E-08	-2.127	1.44E-08	-1.295	7.206E-08	-1.599	5.970E-13
Tead2	-3.621	1.59E-06	-8.598	1.13E-05	-7.865	1.71E-05	-2.239	6.04E-08	-2.791	3.94E-09	-2.475	4.290E-18	-4.014	1.982E-22
Tef	2.613	1.01E-05	2.517	2.07E-07	2.278	7.12E-07	3.159	3.93E-09	2.098	5.22E-07	1.659	2.045E-12	1.621	5.422E-12
Tgfb1i1	-2.236	1.72E-05	-3.550	3.26E-08	-3.600	2.89E-08	-1.922	3.57E-07	-2.015	1.67E-07	-2.542	5.127E-18	-2.829	4.169E-19
Tgoln2	1.394	6.55E-03	1.889	3.80E-07	2.010	1.38E-07	1.106	7.38E-02	1.316	1.79E-04	2.030	1.183E-10	2.271	5.818E-12
Thbs2	-3.733	6.92E-07	-10.731	3.27E-10	-8.757	9.22E-10	-5.570	6.18E-07	-5.448	7.11E-07	-1.626	6.019E-11	-2.912	1.810E-18

Timeless	-1.875	3.94E-02	-1.926	1.52E-03	-2.239	2.98E-04	-3.165	3.99E-06	-3.225	3.38E-06	-1.998	4.312E-11	-2.684	2.254E-14
Tk1	-6.411	4.09E-03	-1.476	3.52E-02	-4.163	1.61E-06	-5.327	2.05E-04	-6.209	9.45E-05	-2.231	1.966E-11	-1.620	2.688E-07
Tmem158	-2.042	2.83E-03	-1.891	3.68E-03	-2.079	1.39E-03	-2.341	6.50E-06	-2.433	4.13E-06	-1.323	3.426E-05	-1.206	2.357E-03
Tmem164	-1.959	8.73E-04	-1.931	4.54E-04	-2.217	8.86E-05	-1.284	6.32E-02	-1.347	3.12E-02	-2.356	3.169E-17	-3.818	9.855E-22
Tmpo	-3.456	5.79E-05	-1.656	8.90E-03	-2.044	8.38E-04	-1.950	1.11E-06	-2.235	1.50E-07	-1.577	2.772E-13	-2.076	7.157E-18
Tmsb10	-3.567	3.24E-08	-6.694	5.97E-12	-7.693	2.59E-12	-2.171	2.80E-09	-2.247	1.70E-09	-1.240	8.639E-04	-2.890	7.255E-16
Tnc	-8.188	1.29E-03	-3.790	3.46E-06	-5.375	2.95E-07	-17.686	2.01E-11	-24.905	5.32E-12	-4.276	4.324E-13	-7.619	2.618E-16
Top2a	-2.852	3.53E-04	-3.711	5.05E-08	-6.962	5.83E-10	-3.622	1.18E-08	-3.558	1.38E-08	-2.980	1.022E-11	-3.055	6.412E-12
Tpbg	-11.444	7.58E-03	-2.466	3.82E-04	-3.334	2.92E-05	-2.108	5.85E-02	-4.437	1.28E-03	-1.391	4.035E-05	-3.315	1.475E-15
Tpm2	-2.418	3.88E-06	-3.711	6.23E-07	-3.825	4.88E-07	-3.089	9.02E-06	-2.543	5.57E-05	-1.473	1.853E-04	-3.735	1.071E-13
Trip13	-3.415	4.35E-04	-3.469	1.04E-06	-5.295	4.29E-08	-3.809	5.77E-08	-4.662	1.19E-08	-2.567	3.753E-15	-3.199	3.277E-17
Tspan6	-2.182	3.22E-06	-1.984	1.18E-06	-2.109	4.75E-07	-2.014	7.97E-08	-2.451	4.95E-09	-2.434	1.215E-21	-2.319	4.517E-21
Ttk	-3.368	3.42E-03	-2.648	1.39E-03	-5.437	1.11E-05	-2.493	7.07E-06	-2.705	2.96E-06	-2.441	1.194E-11	-2.257	7.853E-11
Tubb6	-2.289	2.88E-04	-12.645	3.23E-04	-19.023	8.82E-05	-3.577	2.29E-07	-3.292	4.76E-07	-2.181	4.274E-12	-4.524	1.786E-18
Ube2c	-5.480	3.22E-05	-3.657	2.36E-04	-8.321	2.17E-06	-5.153	9.59E-09	-5.520	6.02E-09	-2.367	2.266E-11	-2.648	1.757E-12
Uhrf1	-2.459	4.73E-04	-3.868	2.56E-06	-8.731	1.52E-08	-3.360	2.55E-07	-4.055	5.19E-08	-2.450	5.186E-12	-3.119	3.063E-14
Usp18	1.800	1.91E-04	1.462	7.26E-03	1.434	9.83E-03	2.029	5.73E-08	2.031	5.64E-08	5.836	7.123E-15	3.616	6.662E-12
Vangl2	-2.050	4.09E-03	-3.190	3.45E-06	-3.055	5.08E-06	-1.786	3.89E-05	-2.545	3.00E-07	-1.404	5.692E-06	-5.057	1.030E-19
Vash2	-5.799	2.65E-07	-3.863	6.96E-06	-2.763	1.05E-04	-4.967	7.54E-07	-6.219	1.83E-07	-3.270	8.317E-17	-2.493	2.820E-14
Wdhd1	-1.673	1.22E-02	-1.658	1.80E-03	-1.663	1.72E-03	-1.836	4.12E-06	-2.231	2.18E-07	-2.271	5.188E-10	-3.376	1.472E-13
Zfp423	-3.519	2.08E-03	-14.063	2.22E-06	-21.291	4.76E-07	-2.390	1.75E-01	-7.401	6.22E-03	-1.961	4.585E-12	-4.466	7.803E-20
Zfp618	-4.188	9.92E-03	-2.120	6.91E-05	-2.628	6.12E-06	-2.050	6.47E-03	-3.068	2.47E-04	-2.235	5.798E-14	-1.833	2.375E-11
Zfp704	-1.973	2.23E-03	-1.599	2.69E-05	-1.562	4.36E-05	-1.333	5.09E-05	-1.362	2.61E-05	-2.538	1.279E-19	-2.100	2.434E-17
Zfpm2	-1.272	1.47E-02	-1.784	8.23E-03	-2.422	4.14E-04	-2.763	3.26E-09	-3.757	1.54E-10	-3.171	6.149E-17	-2.407	2.825E-14
Zwilch	-2.722	1.97E-03	-2.774	3.29E-05	-3.997	1.54E-06	-3.561	9.23E-07	-5.492	3.75E-08	-2.425	9.555E-10	-2.542	3.489E-10

Table S2. Gene ontology analyses of these 316 age-regulated genes. Upregulated and downregulated groups were separately analyzed, using Ingenuity Pathway Analysis (IPA) 7.1. Genes in the 5 most overrepresented molecular, cellular, or physiological functions are tabulated.

Age-downregulated genes

Biological Function	*P*-value	No. of genes	Implicated genes
Cell Cycle	1.77×10^{-21}	73	*Afap1l2, Anln, Aspm, Aurka, Birc5, Brca1, Bub1, Bub1b , Ccna2, Ccnb1, Ccnb2, Ccnd2, Ccnf, Cdc20, Cdc2a, Cdca8, Cdk4, Cdkn1c, Cdt1, Cenpe, Cenpi, Chek1, Cks1b, Col1a1, Ect2, Espl1, Ezh2, Figf, Fn1, Foxm1, Gli2, Gpsm2, Grb10, H2afx, Igf2, Incenp, Kif22, Kif20a, Kif20b, Kif2c, Kntc1, Mad2l1, Maged1, Mcd2, Mcm7, Mdk, Mki67, Mxd3, Mycn, Ncapd2, Ncapg2, Ncaph, Ndc80, Nuf2, Nusap1, Plagl1, Pole, Prc1, Ptn, Racgap1, Rad51, Sgol1, Skp2, Smarcb1, Tacc3, Tcf3, Timeless, Tmpo, Top2a, Trip13, Ttk, Ube2c, Uhrf1*
Cellular Assembly & Organization	8.71×10^{-15}	63	*Atp7a, Aurka, Birc5, Brca1, Bub1, Bub1b , Ccna2, Ccnb1, Ccnb2, Cdc2a, Cdt1, Cenpe, Clip3, Col1a1, Col1a2, Col5a1, Col5a2, Cspg2, Csrp1, D10Ertd610e, Dbn1, Ect2, Espl1, Evl, Fgd1, Fn1, Fscn1, Gli2, Gpsm2, Hmgn2, Igf2, Incenp, Kif22, Kif20b, Kif2c, Mad2l1, Mcm4, Mdk, Mmp14, Mycn, Myh10, Ncapd2, Ncapg2, Ncaph, Ndc80, Ndn, Nuf2, Nusap1, Pdlim3, Pdlim7, Prc1, Prkg1, Ptn, Sema5a, Sgol1, Skp2, Smarca1, Tacc3, Timeless, Tmsb10, Tnc, Top2a, Uhrf1*
DNA Replication, Recombination & Repair	8.71×10^{-15}	62	*Aurka, Birc5, Brca1, Bub1, Bub1b , Ccna2, Ccnb1, Ccnb2, Ccnd2, Cdc20, Cdc2a, Cdk4, Cdkn1c, Cdt1, Cenpe, Chek1, Ect2, Espl1, Fn1, Foxm1, Gli2, Gpsm2, H2afx, Hmgb2, Igf2, Incenp, Kif22, Kif2c, Kntc1, Mad2l1, Mcm2, Mcm3, Mcm4, Mcm5, Mcm6, Mcm7, Mycn, Ncapd2, Ncapg2, Ncaph, Ndc80, Nuf2, Nusap1,*

			Pbk, Pole, Ptn, Rad51, Rad51ap1, Rfc3, Skp2, Smarcb1, Tacc3, Tdg, Thbs2, Timeless, Tmpo, Tnc, Top2a, Trip13, Ttk, Uhrf1, Zwilch
Cellular Movement	1.03×10^{-9}	23	*Anln, Aurka, Ccnb1, Cdc20, Col1a1, Ect2, Ezh2, Fn1, Foxm1, Incenp, Kif20a, Kif20b, Mdk, Mmp14, Myh10, Nusap1, Prc1, Ptn, Racgap1, Skp2, Tcf3, Thbs2, Top2a*
Cellular Growth & Proliferation	9.03×10^{-8}	92	*Anln, Aplnr, Aurka, B4galt2, Birc5, Brca1, Bub1, Bub1b, Cacna1g, Cacnb3, Ccna2, Ccnb1, Ccnd2, Ccnf, Cd276, Cdc2, Cdca7, Cdca8, Cdh11, Cdk4, Cdkn1c, Cdt1, Chek1, Cirbp, Cks1b, Col1a1, Cspg2, Dbn1, Dlk1, E2f8, Eif5a2, Eln, Espl1, Ezh2, Fbn1, Fbn2, Figf, Fn1, Foxm1, Fscn1, Gli2, Gpc3, Grb10, Igf2, Igf2bp3, Kif20a, Kif20b, Kif2c, Lamb1, Mad2l1, Maged1, Maged2, Marcksl1, Mcm2, Mcm3, Mcm5, Mcm7, Mdk, Meis1, Mest, Mki67, Mmp14, Mxd3, Mycn, Myh10, Ndn, Npas3, Pbk, Peg3, Plagl1, Plk4, Prc1, Prkg1, Ptn, Rrm1, Rrm2, Serpine2, Skp2, Smarcb1, Smo, Sox4, Tacc3, Tcf3, Tgfb1l1, Thbs2, Timeless, Tmsb10, Tnc, Tpm2, Ttk, Ube2c, Uhrf1*

Age-upregulated genes

Biological Function	*P*-value	No. of genes	Implicated genes
Hematological System Development & Function	5.35×10^{-10}	23	*B2m, C4b, Ccl5, Cd74, Clec7a, Ctss, Cxcl9, Cybb, Fas, Fgf1, H2-D1, H2-DMa, H2-Eb1, H2-T23, Ifi27, Igh-6, Irf7, Klf9, Psmb8, Psmb9, Sema4a, Spn, Stat1*
Cell-Cell Signaling & Interaction	5.35×10^{-10}	23	*Adra1a, Ar, B2m, C4b, Ccl5, Cd74, Clec7a, Cxcl9, Cybb, Fas, Fgf1, H2-D1, H2-DMa, H2-Eb1, Ifi27, Igh-6, Mapt, Nampt, Psmb8, Psmb9, Sema4a, Spn, Stat1*
Immune Cell Trafficking	5.35×10^{-10}	19	*B2m, C4b, Ccl5, Cd74, Clec7a, Ctss, Cxcl9, Cybb, Fas, Fgf1, H2-D1, H2-DMa, H2-Eb1, Igh-6, Psmb8, Psmb9, Sema4a, Spn, Stat1*
Cell-mediated Immune Response	9.42×10^{-9}	25	*B2m, C4b, Ccl5, Ccl6, Cd74, Clec7a, Ctss, Cxcl9, Cybb, Fas, Fgf1, H2-D1, H2-DMa, H2-Eb1, H2-T23, Ifi27, Igh-6, Irf7, Nupr1, Oas1, Psmb8, Psmb9, Sema4a, Spn, Stat1*
Humoral Immune Response	9.42×10^{-9}	25	*B2m, C4b, Ccl5, Ccl6, Cd74, Clec7a, Ctss, Cxcl9, Cybb, Fas, Fgf1, H2-D1, H2-DMa, H2-T23, Ifi27, Igh-6, Irf7, Klf9, Nupr1, Oas1, Psmb8, Psmb9, Sema4a, Spn, Stat1*

Table S3. Previously reported knockout phenotypes of genes showing uniform up- or down-regulation with age in mouse and rat organs. A gene was included only if it was uniformly up- or down-regulated with age (rat kidney and lung, 1 to 5 wk; mouse kidney and lung, 1 to 8 wk; mouse heart, 1 to 4 wk) at least 2.0 fold with $P < 0.05$ in all organs studied in both species and if a knockout has been characterized. References are listed as Pubmed ID numbers.

Age-downregulated genes

Gene Symbol (Mouse)	Growth Phenotype	Brief summary	Reference
Brca1	Decreased body size - embryonic	Embryo size of homozygous mutants was 50% of wild-type littermates as early as E4.5 due to reduced proliferation	9171368
Ccnb2	Decreased body size - embryonic	Body size of homozygous mutants was smaller than wild-type littermates at birth	9539739
Cks1b	Decreased body size - embryonic	Body mass of homozygous mutants was 80-90% of wild-type littermates at E13.5, and this ratio continued through adulthood	11463388
Dlk1	Decreased body size - embryonic	Body weight of paternally inherited heterozygous mutants was 81% of wild-type littermates at E18.5, but this difference eventually disappeared postnatally	12101250
E2f8	Decreased body size - embryonic	Homozygous mutants of E2f8 were normal, but E2f7 (homozygous) & E2f8 (heterozygous) double knockouts were growth retarded compared to wild-type littermates	18194653
Ezh2	Decreased body size - embryonic	Homozygous mutants were deformed and underdeveloped, lethal at E8.5	11390661
Fn1	Decreased body size - embryonic	Homozygous mutants were developmentally retarded and smaller than wild-type littermates at E8.0, lethal at E10.5	8306876
Gli2	Decreased body size - embryonic	Body size of homozygous mutants was smaller than wild-type littermates at E10.5, lethal before E18.5	9006072
Mad2l1	Decreased body size - embryonic	All homozyous mutants died at E6.5-7.5 and embryo size was smaller than wild-type littermates	10892650
Mcm4	Decreased body size - embryonic	Chaos3/- mutants (F391I mutation) were growth retarded compared to wild-type littermates and lethal before E14.5	17143284
Meis1	Decreased body size - embryonic	Most homozygous mutants died before E14.5 and embryo size was smaller than wild-type littermates	14713950, 15882575
Mycn	Decreased body size - embryonic	Homozygous mutants exhibited progressive embryonic growth retardation, and their body mass was 40% of wild-type littermates at E12.5	1459449
Plagl1	Decreased body size - embryonic	Body mass of paternally inherited heterozygous mutants was 77% of wild-type littermates at birth	17084362
Plk4	Decreased body size - embryonic	Most homozygous mutants died at E7.5-8.5 with an embryo size smaller than wild-type littermates	11301255
Rad51	Decreased body size - embryonic	Most homozygous mutants died at E5.5-7.5 with an embryo size smaller than wild-type littermates	8943369
Tacc3	Decreased body size - embryonic	Body size of homozygous mutants was smaller than wild-type littermates starting from E9, lethal at E15.5	17359303

Vangl2	Decreased body size - embryonic	Body size of homozygous mutants (G1391A mutation) was smaller than wild-type littermates at E14.5-19.5, and the reduction in size in different body parts was not even, the nervous system was disproportionately larger	14039372
Vcan	Decreased body size - embryonic	Insertional mutants (between exon 7 & 8) caused lethality at E10.5, and body size of mutants was smaller than wild-type littermates	9188753
Gjc1	Decreased body size - embryonic (secondary to heart failure)	Homozygous mutants have vascular and cardiac developmental defects, resulting in retarded growth and lethality at E10.5	10903175
Myh10	Decreased body size - embryonic (secondary to heart failure)	Body size of homozygous mutants was smaller than wild-type littermates at birth due to heart failure	9356462
Sox11	Decreased body size - embryonic (secondary to heart failure)	Body mass of homozygous mutants was 77% of wild-type and heterozygous littermates at birth	15254231
Bub1	Decreased body size - embryonic and postnatal	Body mass of homozygous mutants with C57BL6 background was normal at E18.5, but decreased to 84% of wild-type littermates at birth, with subsequent runting and failure to thrive postnatally, and is unrelated to nursing and ventilatory function	19117986
Cdkn1c	Decreased body size - embryonic and postnatal	Paternally inherited mutants were smaller at E18.5, showing developmental defects and lethality at birth, survivors were growth retarded postnatally	9144284, 9136926, 10731669
Igf2	Decreased body size - embryonic and postnatal	Body mass of paternally inherited heterozygotes was 61.5% of wild-type littermates at birth, and the ratio remained throughout adulthood	2330056
Mest	Decreased body size - embryonic and postnatal	Body mass of paternally inherited heterozygotes was 87.5% of wild-type littermates at E18.5, and further reduced to 65% of wild-type littermates at postnatal day 7	9771709
Npas3	Decreased body size - embryonic and postnatal	Body mass of homozygous mutants was 80% of wild-type littermates consistently throughout development (measured until postnatal day 50)	16190882
Peg3	Decreased body size - embryonic and postnatal	Body mass of paternally inherited heterozygous mutants was 86% of wild-type littermates at E17.5, 81% of wild-type at birth, and 65% of wild-type at 4 wk of age, proportionally in multiple organs	10195900
Skp2	Decreased body size - embryonic and postnatal	Body size of homozygous mutants was smaller than wild-type littermates from E18; heterozygous mutants were bigger than homozygous but smaller than wild-types	10790373
Bub1b	Decreased body size - postnatal	Homozygous null mutations were embryonal lethal; mice homozygous for hypomorphic mutations (insufficiency) were viable with decreased postnatal growth with body mass 50% of wild-types and heterozygotes at postnatal day 70	15208629
Cdk4	Decreased body size - postnatal	Body size of homozygous mutants was smaller than wild-type littermates at birth, more noticeble with age (up to 50% in adults), proportionately in all major organs	10319860
H2afx	Decreased body size - postnatal	Homozygous mutants were growth retarded postnatally, affecting both sexes; heterozygous mutants were bigger than homozygous but smaller than wild-types	11934988
Mdk	Decreased body size - postnatal	Homozygous Mdk knockout was normal, while Mdk and Ptn double knockout had normal body mass at birth but decreased postnatal growth (Body mass of double knockout was 50% of wild-type littermates at 4 wk and 75-80% of wild-type in adulthood)	17121547
Mmp14	Decreased body size - postnatal	Homozygous mutants had normal body mass at birth but were growth retarded postnatally with body mass 3.5-5 gram at weaning versus 12-16 gram for wild-type and heterozygous littermates, and subsequent weight gain was also decreased	10520996

Ptn	Decreased body size - postnatal	Homozygous Ptn knockout was normal, while Mdk and Ptn double knockout had normal body mass at birth but decreased postnatal growth (Body mass of double knockout was 50% of wild-type littermates at 4 wk and 75-80% of wild-type in adulthood)	17121547
Tcfe2a	Decreased body size - postnatal	Postnatal growth in homozygous mutants was slower than wild-type littermates without affecting appetite and feeding behavior, the effect was more prominent in females	8001124
Trip13	Decreased body size - postnatal	Homozygous mutants exhibited decrease in postnatal body mass compared to wild-type littermates	17696610
Zfp423	Decreased body size - postnatal	Homozygous mutants exhibited a significant decrease in postnatal body mass compared to wild-type littermates	16943432
Col1a1	Decreased body size - postnatal (secondary to known illness)	Body mass of homozygous mutants (G349C mutation) was 50% of wild-type littermates until 6 wk of age, after which body mass increased to 80% of wild-type	18248096, 10608859
Col1a2	Decreased body size - postnatal (secondary to known illness)	Body size of homozygous mutant (G3983 single deletion) was smaller than wild-type littermates postnatally	8446583
Col5a2	Decreased body size - postnatal (secondary to known illness)	Homozygous mutants gained weight more slowly than wild-type littermates due to poor nourishment (caused by inability to move), with body mass decreased to 50% of wild-type at 3 wk of age	7704020
Grb10	Increased body size - embryonic	Body mass of maternally inherited heterozygotes was greater than wild-type littermates from E10.5, and was 130% of wild-type at birth	12829789
Gpc3	Increased body size - embryonic and postnatal	Body mass of homozygous mutants was 130% of wild-type littermates at birth; heterozygous mutants were also bigger than wild-type but smaller than homozygotes, and effect was independent of Igf2	10402475, 11846487
Birc5	Embryonal lethality (without reporting size difference)	Homozygous mutants died before E4.5	12145814
Ccna2	Embryonal lethality (without reporting size difference)	Homozygous mutants died at E5.5 (implantation)	8988174
Ccnb1	Embryonal lethality (without reporting size difference)	Homozygous mutants died before E10	9539739
Ccnf	Embryonal lethality (without reporting size difference)	Homozygous mutants died at E10.5; proliferative defects were observed in vivo (placenta) & in vitro (using murine embryonal fibroblasts from the mutants)	14993286
Cdc20	Embryonal lethality (without reporting size difference)	Homozygous mutants died before E7.5	17325031
Cdc2a	Embryonal lethality (without reporting size difference)	Homozygous mutants of Cdc2a, homozygous Cdk2 knockin (which substituted Cdc2a with Cdk2), or Homozygous Cdk2 knockin & p53 -/- double knockout, were all lethal before E3.5	18787066
Cenpe	Embryonal lethality (without reporting size difference)	Homozygous mutants died before E7.5, with growth retarded inner cell mass and reduced cell number	12361599
Chek1	Embryonal lethality (without reporting size difference)	Homozygous mutants died at E3.5-7.5 due to aberrant ES cell proliferation; heterozygous mutants were unaffected	10859163
Col5a1	Embryonal lethality (without reporting size difference)	Homozygous mutants died at E10.5 due to cardiovascular insufficiency and lack of collagen fibril formation	15383546

Espl1	Embryonal lethality (without reporting size difference)	Homozygous mutants died at E3.5-9.5	16533944
Foxm1	Embryonal lethality (without reporting size difference)	75% of the homozygous mutants died before E17.5, and all homozygous mutants were dead by E18.5; defects in hepatoblast proliferation were reported	15531365
Fras1	Embryonal lethality (without reporting size difference)	Homozygous mutants died before birth due to hemorrhaging of embryonic blisters, kidney development severely delayed	12766769
Incenp	Embryonal lethality (without reporting size difference)	Homozygous mutants died before E8.5	10369859
Lamb1-1	Embryonal lethality (without reporting size difference)	Homozygous mutants died before E6.5	11242070
Ncapg2	Embryonal lethality (without reporting size difference)	Homozygous mutants died around E6 due to a failure of inner cell mass expansion, shortly after implantation	14729962
Ptk7	Embryonal lethality (without reporting size difference)	Homozygous mutants died perinatally with various developmental defects	15229603
Racgap1	Embryonal lethality (without reporting size difference)	Homozygous mutants died at the peri-implantation stage	11287179
Sema5a	Embryonal lethality (without reporting size difference)	Homozygous mutants died at E11.5-12.5	15743826
Smarcb1	Embryonal lethality (without reporting size difference)	Homozygous mutants died at E3.5-7.5 due to a defect in the hatching of the blastocyst	11313485
Smo	Embryonal lethality (without reporting size difference)	Homozygous mutants were severely deformed at E9.5	9636176
Sox4	Embryonal lethality (without reporting size difference)	Homozygous mutants died at E13.5-14.5, due to regurgitation of blood into the heart	18064674
Timeless	Embryonal lethality (without reporting size difference)	Homozygous mutants died at approximately the time of implantation	10903565
Zfpm2	Embryonal lethality (without reporting size difference)	Homozygous mutants exhibited cardiac defects, resulting in lethality at E12.5-15.5	10888889
Marcksl1	Neonatal lethality unrelated to growth	Homozygous mutants exhibited neural tube defects, resulting in anencephaly, tail malformations and neonatal lethality	8692805
Plxnd1	Neonatal lethality unrelated to growth	All homozygous mutants become cyanotic and died within 24 hours of birth	15239958
Robo1	Neonatal lethality unrelated to growth	Complete mortality of homozygous mice at birth (cause not reported)	16690755
Tcf21	Neonatal lethality unrelated to growth	Homozygous mutants died at birth due to respiratory failure	10944221
Tk1	Neonatal lethality unrelated to growth	Neonatal lethality with no obvious developmental abnormalities	8991081

Bcl6b	No reported effect on adult body size	N/A	N/A
Cacna1g	No reported effect on adult body size	N/A	N/A
Cacnb3	No reported effect on adult body size	N/A	N/A
Ccnd2	No reported effect on adult body size	N/A	N/A
Cd276	No reported effect on adult body size	N/A	N/A
Cry1	No reported effect on adult body size	N/A	N/A
Eln	No reported effect on adult body size	N/A	N/A
Emilin1	No reported effect on adult body size	N/A	N/A
Fbn1	No reported effect on adult body size	N/A	N/A
Fbn2	No reported effect on adult body size	N/A	N/A
Hmgb2	No reported effect on adult body size	N/A	N/A
Ndn	No reported effect on adult body size	N/A	N/A
Prkg1	No reported effect on adult body size	N/A	N/A
Thbs2	No reported effect on adult body size	N/A	N/A
Tnc	No reported effect on adult body size	N/A	N/A
Cdh11	No reported effect on adult body size	N/A	N/A
Evl	No reported effect on adult body size	N/A	N/A
Fbln2	No reported effect on adult body size	N/A	N/A
Figf	No reported effect on adult body size	N/A	N/A
Mxd3	No reported effect on adult body size	N/A	N/A
Pdlim3	No reported effect on adult body size	N/A	N/A
Serpine2	No reported effect on adult body size	N/A	N/A
Tead2	No reported effect on adult body size	N/A	N/A
Tmem158	No reported effect on adult body size	N/A	N/A

Age-upregulated genes

Gene Symbol (Mouse)	Growth Phenotype	Brief summary	Reference
Nr1d1	Decreased body size - postnatal	Body mass of homozygous mutants was 80% of wild-type littlermates at 3-5 months of age, possibly related to muscle function. A different study reported altered circadian behavior without commenting on body size difference	15374821, 12150932
Glul	Embryonal lethality (without reporting size difference)	Homozygous mutants died before E9.5 due to lack of L-glutamine.Culturing of mutant embryos with L-glutamine increased survival, with similar proliferation rate as wild-type embryos in culture	17557305
Nampt	Embryonal lethality (without reporting size difference)	Homozygous mutants died before E10.5	17983582
Abcb1a	No reported effect on adult body size	N/A	N/A
Adra1a	No reported effect on adult body size	N/A	N/A
Ar	No reported effect on adult body size	N/A	N/A
B2m	No reported effect on adult body size	N/A	N/A
C4b	No reported effect on adult body size	N/A	N/A
Ccl5	No reported effect on adult body size	N/A	N/A
Cd74	No reported effect on adult body size	N/A	N/A
Clec7a	No reported effect on adult body size	N/A	N/A
Cmah	No reported effect on adult body size	N/A	N/A
Cpeb1	No reported effect on adult body size	N/A	N/A
Ctss	No reported effect on adult body size	N/A	N/A
Cxcl9	No reported effect on adult body size	N/A	N/A
Cybb	No reported effect on adult body size	N/A	N/A
Cyp1a1	No reported effect on adult body size	N/A	N/A
Cyp2e1	No reported effect on adult body size	N/A	N/A
Ephx1	No reported effect on adult body size	N/A	N/A
Fas	No reported effect on adult body size	N/A	N/A
Gstm1	No reported effect on adult body size	N/A	N/A
H2-D1	No reported effect on adult body size	N/A	N/A
H2-DMa	No reported effect on adult body size	N/A	N/A
H2-T23	No reported effect on adult body size	N/A	N/A

Hspa4l	No reported effect on adult body size	N/A	N/A
Igh-6	No reported effect on adult body size	N/A	N/A
Irf7	No reported effect on adult body size	N/A	N/A
Klf9	No reported effect on adult body size	N/A	N/A
Mapt	No reported effect on adult body size	N/A	N/A
Nupr1	No reported effect on adult body size	N/A	N/A
Omd	No reported effect on adult body size	N/A	N/A
Psmb8	No reported effect on adult body size	N/A	N/A
Psmb9	No reported effect on adult body size	N/A	N/A
Sema4a	No reported effect on adult body size	N/A	N/A
Spn	No reported effect on adult body size	N/A	N/A
Stat1	No reported effect on adult body size	N/A	N/A
Tef	No reported effect on adult body size	N/A	N/A
Usp18	No reported effect on adult body size	N/A	N/A
Fgf1	No reported effect on adult body size	N/A	N/A
Hsd11b1	No reported effect on adult body size	N/A	N/A
Igtp	No reported effect on adult body size	N/A	N/A
Lims2	No reported effect on adult body size	N/A	N/A
Pcolce2	No reported effect on adult body size	N/A	N/A
Pim3	No reported effect on adult body size	N/A	N/A