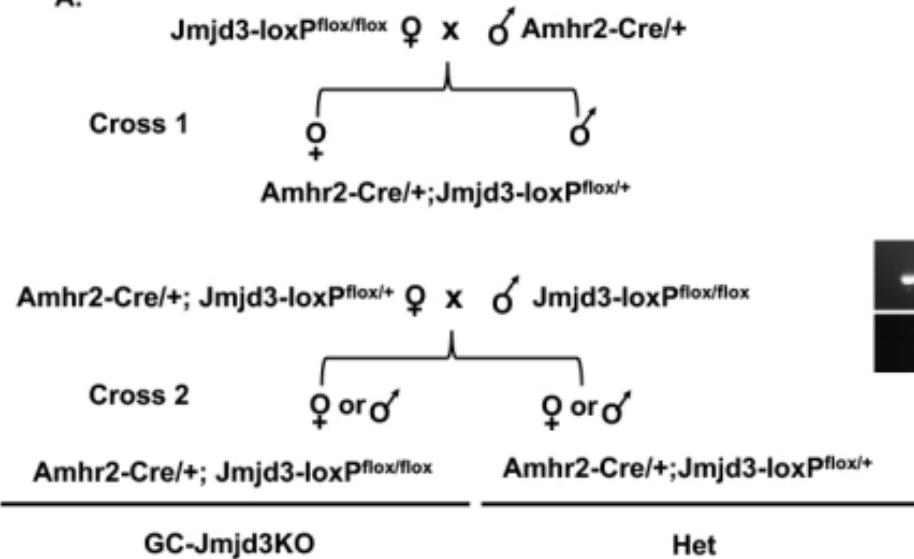


Fig S1.

A.



B. Genotyping

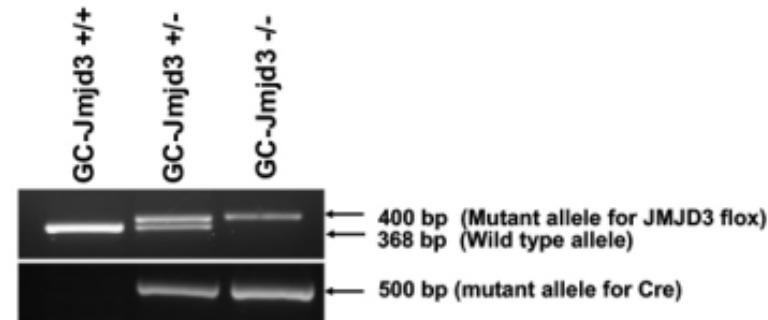
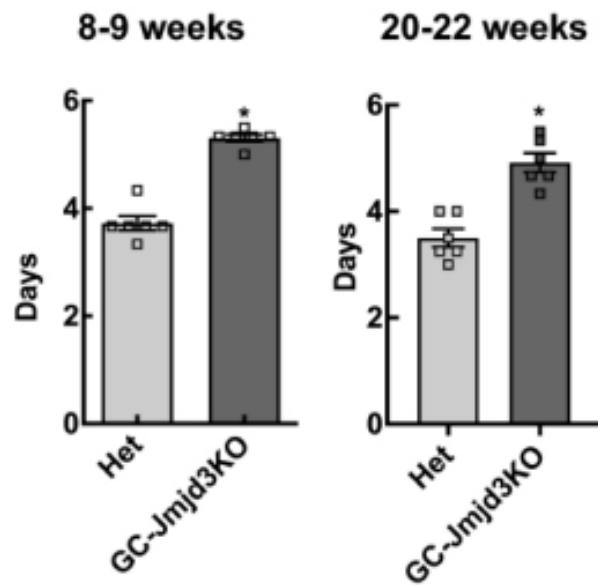


Figure S1. (A) Schematic diagram demonstrating the generation of GC-specific *Jmjd3* knockout (GC-Jmjd3KO) mouse. *Jmjd3*-loxP^{flox/flox} females were crossed with *Amhr2*-Cre males and thereafter, the *Amhr2*-Cre/+; *Jmjd3*-loxP^{flox/+} females were backcrossed with *Jmjd3*-loxP^{flox/flox} males to generate female heterozygous control *Amhr2*-Cre/+; *Jmjd3*-loxP^{flox/+} mice and *Amhr2*-Cre/+; *Jmjd3*-loxP^{flox/flox} mice conditionally deleted for *Jmjd3* in the GCs. (B) Floxed region in *Jmjd3* allele as well as *Cre* were detected by genomic DNA PCR. A biological replicate is shown for wild-type (Wt), heterozygous (Het) and GC-Jmjd3KO, using genomic DNA purified from granulosa cells of each mouse.

Fig S2.

A. Length of estrous cycle



B. Stages per cycle

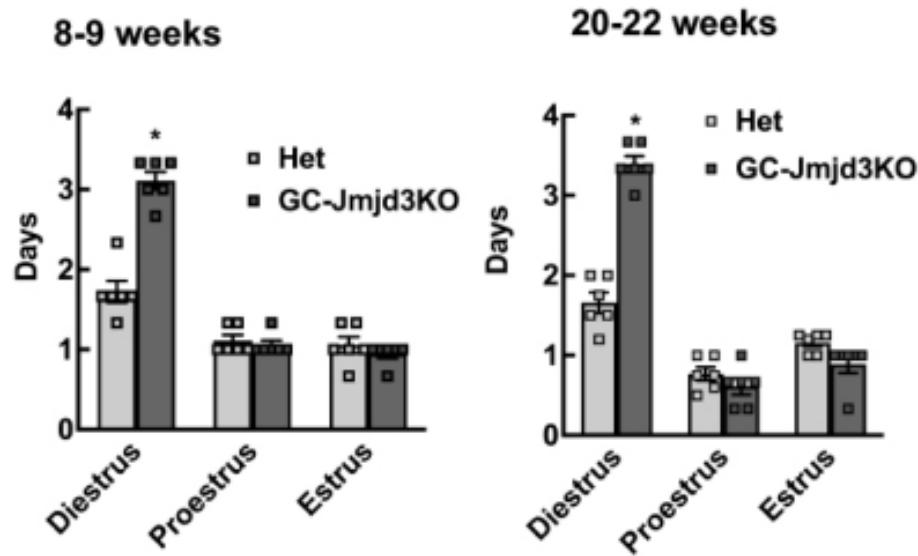


Figure S2. (A) Average length of estrous cycle determined by vaginal smears taken daily over a period of 2 weeks in 8-9 and 20-22 weeks old heterozygous (Het) and GC-Jmjd3KO mice. (C) Number of days heterozygous (Het) and GC-Jmjd3KO mice (8-9 and 20-22 weeks old) spent in each stage of estrous cycle. Data are represented as mean \pm SEM ($n = 6$ mice, * $p < 0.01$ vs Het, using Student's t test).

Fig S3.

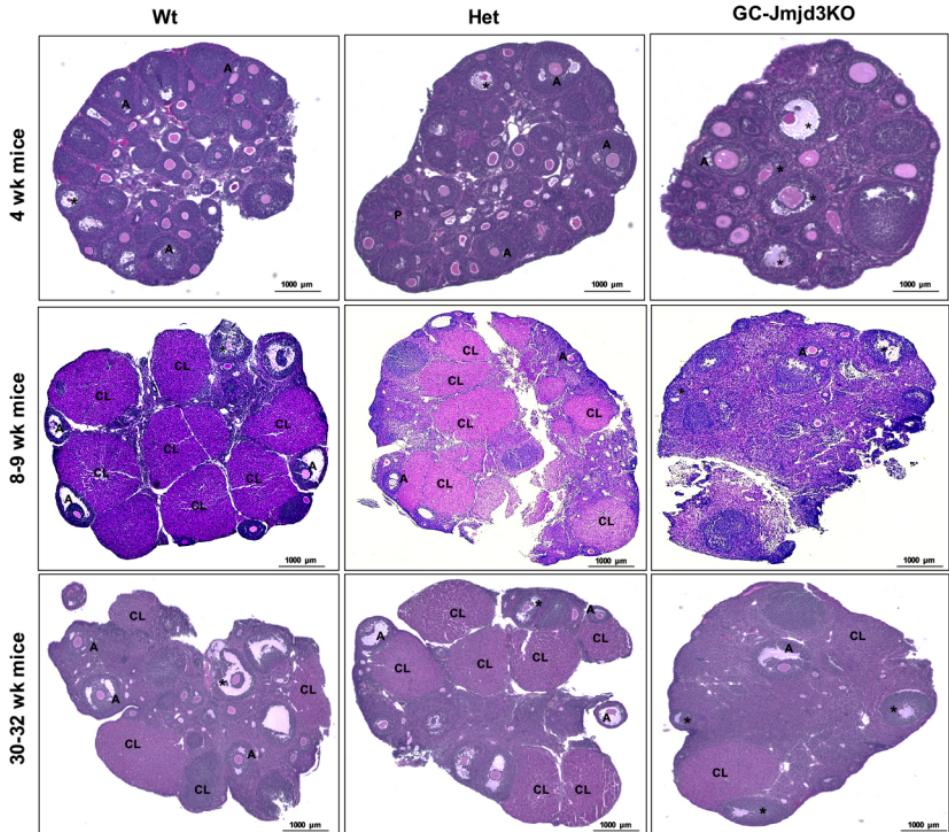
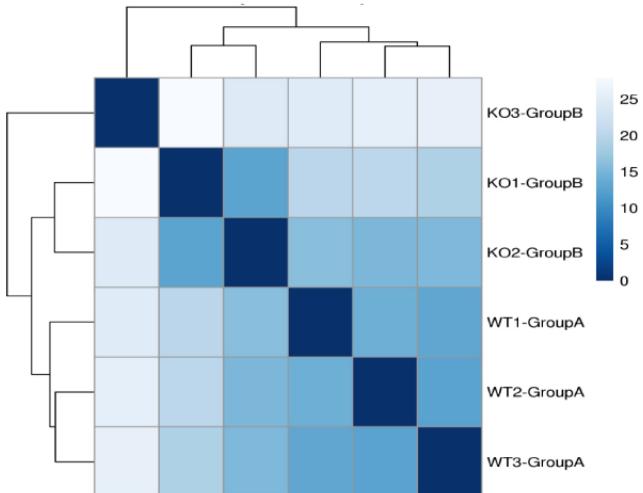


Fig S3: Ovarian Morphology. Representative hematoxylin and eosin-stained ovarian sections from 4, 8-9 and 30-32-weeks old Wt, heterozygous (Het) litter mate and GC-Jmj3KO mice ($n = 3$). 5 μ m paraffin-embedded ovarian sections were taken at 30 μ m intervals to determine ovarian morphology. A-Antral follicle, CL-Corpus luteum and * - Atretic follicles.

Fig S4.

A. Sample similarity assessment



B. Volcano plot

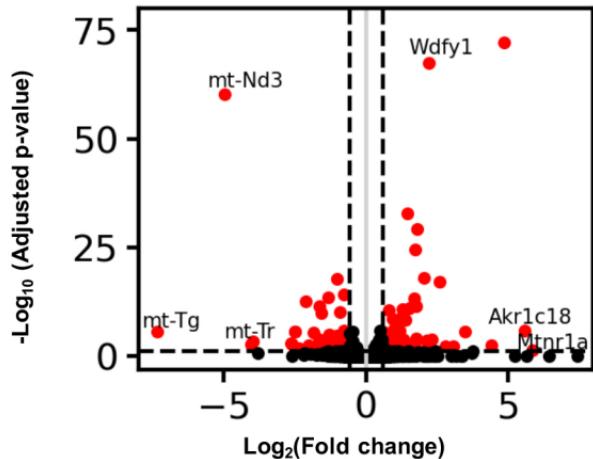
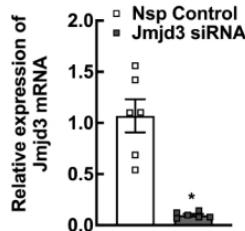


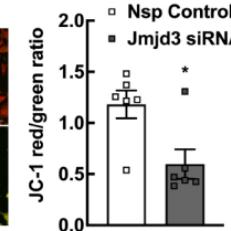
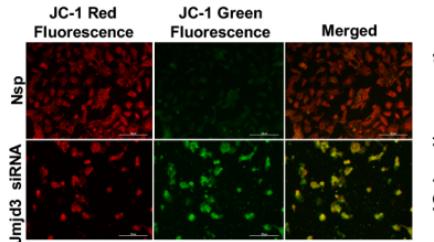
Fig S4: (A) Sample similarity assessment of RNA-Seq data in granulosa cells isolated from Wt and GC-Jmj3KO mice. **(B)** Volcano plot: Representing the global transcriptional change across the groups compared. Each data point in the scatter plot represents a gene. Genes with an adjusted $P \leq 0.05$ and a \log_2 fold change ≥ 1 and ≤ -1 are indicated by red dots.

Fig S5.

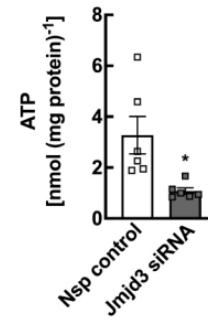
A.



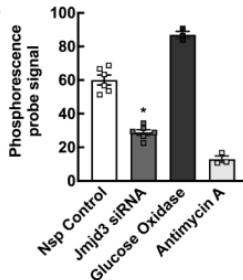
B.



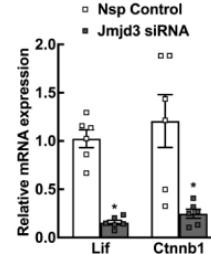
C.



D.



E.



F.

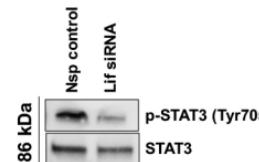


Figure S5. Knockdown of *Jmjd3* promotes mitochondrial dysfunction. (A) Relative expression of *Jmjd3* mRNA in granulosa cells treated with non-specific control siRNA (Nsp) or *Jmjd3* siRNA. The mRNA levels were measured by quantitative real-time PCR and normalized to *Rpl19* mRNA using the $\Delta\Delta Ct$ method. Results are represented as means \pm SEM ($n=6$; * $p<0.01$ vs Wt using Student's t-test). (B) Representative pictures primary granulosa cell cultures treated with non-specific control siRNA (Nsp) or *Jmjd3* siRNA and labeled with JC-1 dye to measure mitochondrial membrane potential (Scale bar = 100 μ m). Bar graph represents the quantification of the JC-1 red-to-green ratio. Data are represented as mean \pm SEM ($n=6$; * $p<0.05$ vs Nsp control using Student's t-test). (C) ATP levels were measured in GCs treated with non-specific control siRNA and *Jmjd3* siRNA. Data are represented as mean \pm SEM ($n=6$; * $p<0.01$ vs Nsp siRNA using Student's t-test). (D) Oxygen consumption rates (OCR) in granulosa cells treated with Nsp or *Jmjd3* siRNA. Glucose oxidase and Antimycin A were used as positive and negative controls, respectively. Data are represented as mean \pm SEM ($n=6$; * $p<0.01$ vs Nsp control using one-way ANOVA, followed by Dunnett's multiple comparison test). (E) Effect of siRNA-mediated knockdown of *Jmjd3* in primary mouse granulosa cell cultures on *Lif* and *Ctnnb1* mRNA levels. Data are displayed as mean \pm SEM ($n=6$ experiments and for each experiment granulosa cells isolated from 2 mice were pooled together) and normalized to *Rpl19* (* $p<0.01$ vs Nsp control using Student's t-test). (F) Representative Western blot of phosphorylated-STAT3 (p-STAT3, Tyr705) and total STAT3 levels in primary granulosa cell cultures from Wt mice treated with *Lif*-specific or non-specific (Nsp) siRNA ($n=3$).

Fig S6: List of (A) antibodies, (B) Taqman RT-PCR primers, (C) siRNAs and (D) ChIP primers used in this study.**A. Antibody list**

Target protein	Antibody name	Dilution	Manufacturer and Cat No.
JMJD3	Rabbit anti-JMJD3	1:1000 for WB 1:100 for IHC/IF	Sigma (SAB3500956)
GAPDH	Rabbit anti-GAPDH	1:1000	Cell Signal Technology(5174S)
Acetylated-Lysine Antibody	Rabbit anti-Acetylated-lysine	1:1000	Cell Signal Technology(9441S)
BAK	Rabbit anti-BAK	1:1000	Cell Signal Technology(6947S)
BAX	Rabbit anti-BAX	1:1000	Cell Signal Technology(2772S)
BMF	Rabbit anti-BMF	1:1000	Cell Signal Technology(5889S)
p53	Rabbit anti-p53	1:1000	Cell Signal Technology(9282S)
IgG	Rabbit-IgG antibody	1 µg per ChIP reaction	Invitrogen (49-2024)
p-STAT3(Tyr705)	Rabbit anti-pSTAT3	1:1000	Cell Signal Technology(9145S)
STAT3	Mouse anti-STAT3	1:1000	Cell Signal Technology(9139S)

B. TaqMan Gene Expression Assay primers list

Gene Name	Assay Identification Number
Jmjd3	Mm01332680_m1
Adcyap1	Mm00437433_m1
upk1a	Mm01176594_g1
Myl1	Mm00659043_m1
mt-nd3	Mm04225292_g1
mt-nd4l	Mm04225306_g1
Lif	Mm00434762_g1
Sirt3	Mm00452131_m1
Ctnnb1	Mm00483029_g1
Rpl19	Mm02601633_g1

C. siRNA list

Gene Name	Cat No.	Manufacturer
Mouse kdm6b (<i>Jmjd3</i>)	M-063799-01-0005	Dharmacon
Mouse <i>Lif</i> siRNA	M-047120-01-0005	Dharmacon
Mouse <i>Ctnnb1</i>	M-040628-00-0005	Dharmacon
Non targeting pool	D-001810-10-05	Dharmacon

D. ChIP primer list

Target	Sequence
H3K27me3 enrichment site - <i>Myl1</i>	F: 5'-CCCCAAGTTTCCACGAGCA-3' R: 5'-CGTGAAACAGCCCCCTGGTGAGA-3'
H3K27me3 enrichment site- <i>Upk1a</i>	F: 5'-TGCACCTTGCCCTCAATTCC-3' R: 5'-CTTTGGAGGCAGAGGGAGGA-3'
H3K27me3 enrichment site- <i>Adycap1</i>	F: 5'-TAGGGGACTAGGATGCTGACG-3' R: 5'-TGGTTGCACTTGCACTCC-3'
H3K27me3 enrichment site- <i>Lif</i>	F: 5'-ACCACCAAGGGACACAAAGGTAA-3' R: 5'-AGGGTCTCAGGGGATTCAAGAG-3'
H3K27me3 enrichment site- <i>Ctnnb1</i>	F: 5'-GCCCGCTCTGATTCCCTTTAG-3' R: 5'-GAAAGTAGTCCCCGCCAGTCC-3'

A	B	C	D	E	F	G	H	I	J	K
Dataset 1: List of differentially expressed genes WT vs KO										

ID	Gene name	log2 Fold Change	pvalue	padj	KO1	KO2	KO3	WT1	WT2	WT3
ENSMUSG0000054764	Mtnr1a	5.9	0.00042	0.03768	4.085	1.129	54.5	0.925	0	0
ENSMUSG0000021214	Akr1c18	5.6	2.52E-09	1.47E-06	40903	21766	3223	466.1	616.5	276.7
ENSMUSG0000101939	Gm28438	4.9	4.46E-77	8.07E-73	629.1	507.1	493.5	10.17	26.11	20.04
ENSMUSG0000032889	Gm6685	4.4	1.25E-05	0.00247	14.3	22.59	24.77	0	1.004	1.908
ENSMUSG0000101316	Gm12663	3.5	3.37E-09	1.85E-06	59.24	66.63	24.77	4.624	4.016	4.771
ENSMUSG0000045991	Onecut2	3.1	2.65E-05	0.00452	1162	795.1	185.3	109.1	81.33	62.97
ENSMUSG0000025475	Adgr a1	2.8	3.20E-05	0.00513	43.92	44.04	11.89	6.474	3.012	4.771

ENSMU SG0000 011038 6	Gm4 2031	2.6	3.44E-21	6.92E-18	131.7	151.3	158.5	17.57	27.11	28.62
ENSMU SG0000 002301 3	Aqp2	2.3	4.37E-07	0.00014	44.94	33.88	63.42	10.17	11.04	7.633
ENSMU SG0000 007364 3	Wdfy 1	2.2	3.16E-72	2.86E-68	2060	1821	1993	454.1	364.5	456.1
ENSMU SG0000 003382 5	Tpsb 2	2.2	0.00014	0.01616	127.7	80.18	19.82	13.87	15.06	21.95
ENSMU SG0000 000657 4	Slc4a 1	2.1	8.90E-07	0.00026	53.11	51.95	39.64	7.398	9.036	16.22
ENSMU SG0000 006636 1	Serpina3c	2	3.52E-22	9.10E-19	2381	1494	1419	378.2	525.1	380.7
ENSMU SG0000 004048 3	Xaf1	1.8	1.39E-33	5.04E-30	997.8	814.3	739.2	236.7	244	255.7
ENSMU SG0000 004013 3	Gpr1 76	1.8	0.0004	0.03691	108.3	94.87	23.78	20.35	25.1	20.99
ENSMU SG0000 002410 9	Nrxn 1	1.8	1.98E-15	2.56E-12	356.4	248.5	231.9	87.86	85.34	73.47
ENSMU SG0000 005037 0	Ch25 h	1.8	1.78E-07	6.46E-05	161.4	106.2	267.5	41.62	62.25	54.39

ENSMU SG0000 004428 5	Gm1 821	1.7	8.52E-29	2.57E-25	1309	1111	1437	309.8	422.7	417
ENSMU SG0000 006773 6	Gm1 0222	1.7	3.05E-06	0.00079	83.75	48.56	61.43	19.42	24.1	15.27
ENSMU SG0000 004155 0	Serpina5	1.7	3.24E-17	4.89E-14	9939	6543	6081	1887	2868	2223
ENSMU SG0000 010465 4	Gm4 3814	1.7	0.00028	0.0283	59.24	36.14	113	27.74	14.06	22.9
ENSMU SG0000 003656 0	Lgi4	1.7	0.00038	0.0352	48	44.04	41.62	6.474	24.1	11.45
ENSMU SG0000 003045 0	Oca2	1.5	8.29E-15	9.37E-12	852.8	566.9	676.8	219.2	302.2	212.8
ENSMU SG0000 002545 3	Nnt	1.5	3.51E-37	1.59E-33	6596	5355	5121	2073	2055	2015
ENSMU SG0000 010192 5	Gm2 8156	1.5	0.00054	0.04608	48	33.88	40.63	12.95	21.08	10.5
ENSMU SG0000 002179 2	Fam2 13a	1.4	4.53E-12	3.56E-09	10193	6416	5656	2453	3221	2815
ENSMU SG0000 010257 3	Gm7 265	1.4	0.00045	0.0399	48	56.47	31.71	18.5	16.06	17.17

ENSMU SG0000 002630 8	Klhl3 0	1.4	2.98E-05	0.00491	173.6	127.6	75.31	39.77	58.23	45.8
ENSMU SG0000 005789 7	Cam k2b	1.3	3.91E-07	0.00013	119.5	167.1	104	56.41	50.2	47.71
ENSMU SG0000 010540 3	Gm4 3618	1.3	2.98E-06	0.00078	86.81	72.28	82.24	33.29	29.12	35.3
ENSMU SG0000 001932 6	Aoc3	1.3	1.03E-14	1.10E-11	4446	3242	3330	1285	1821	1455
ENSMU SG0000 004204 1	2010 003K 11Ri k	1.2	8.08E-05	0.01096	84.77	65.5	61.43	30.52	29.12	33.39
ENSMU SG0000 004148 1	Serpina3g	1.2	2.73E-12	2.25E-09	1066	737.5	1010	356	463.9	417.9
ENSMU SG0000 003157 4	Star	1.2	1.65E-09	1.06E-06	55763	36462	29434	18374	16267	18848
ENSMU SG0000 004930 3	Syt12	1.2	1.52E-07	5.63E-05	548.4	428	792.7	213.6	276.1	290.1
ENSMU SG0000 006714 9	Jchain	1.1	2.12E-05	0.00381	309.5	208.9	175.4	80.46	133.5	103
ENSMU SG0000 009639 8	Gm2 3689	1.1	5.37E-06	0.00122	298.2	168.3	307.2	105.4	131.5	119.3

ENSMU SG0000 008966 1	Mia	1.1	3.64E-05	0.00574	125.6	79.05	108	44.39	51.21	49.62
ENSMU SG0000 010570 3	Gm4 3305	1.1	2.23E-11	1.68E-08	821.1	574.8	830.4	339.4	361.5	346.4
ENSMU SG0000 002424 7	Pkdc c	1.1	6.92E-11	5.01E-08	11683	7724	9539	3801	5238	4614
ENSMU SG0000 002275 5	Adgr g7	1.1	6.41E-07	0.0002	1276	769.1	731.3	388.4	492	457
ENSMU SG0000 007379 1	Efcab 7	1	5.73E-10	3.99E-07	337	325.3	315.1	177.6	127.5	167.9
ENSMU SG0000 009678 0	Tme m181 b-ps	1	6.23E-08	2.40E-05	509.6	511.6	615.3	291.3	194.8	315.8
ENSMU SG0000 001481 3	Stc1	1	1.01E-06	0.00029	2306	1521	1264	740.8	854.4	952.2
ENSMU SG0000 006422 5	Paqr 9	1	1.25E-09	8.39E-07	1347	875.3	1065	515.1	568.3	573.4
ENSMU SG0000 005166 9	AU02 1092	1	5.12E-06	0.00119	7642	4385	4156	2262	3059	2862
ENSMU SG0000 004679 4	Ppp1 r3b	1	5.59E-05	0.00803	231.8	251.8	414.2	167.4	156.6	140.3

ENSMU SG0000 002634 3	Gpr3 9	0.9	3.72E-05	0.0058	205.3	153.6	259.6	100.8	103.4	118.3
ENSMU SG0000 009234 1	Malat 1	0.9	4.12E-09	2.20E-06	61105	56519	77757	29454	31941	41255
ENSMU SG0000 007466 5	Bpifb 4	0.9	2.65E-12	2.25E-09	1498	1406	1141	681.6	768.1	677.4
ENSMU SG0000 002796 2	Vcam 1	0.9	8.12E-05	0.01096	1362	777	1638	566.9	771.1	655.5
ENSMU SG0000 001478 2	Plekh g4	0.9	9.58E-05	0.01212	1121	1106	675.8	686.2	449.8	434.1
ENSMU SG0000 002871 3	Cyp4 b1	0.9	9.07E-05	0.01171	251.2	188.6	175.4	89.71	118.5	128.8
ENSMU SG0000 003912 6	Prune e2	0.9	0.00042	0.03819	584.2	545.5	293.3	217.3	289.2	275.7
ENSMU SG0000 002757 7	Chrn a4	0.8	0.00029	0.02913	579.1	486.8	356.7	204.4	252	344.4
ENSMU SG0000 009625 5	Dynlt 1	0.8	1.85E-14	1.86E-11	930.4	873	917.6	550.3	507	489.5
ENSMU SG0000 003205 1	Fdx1	0.8	9.63E-06	0.00198	38730	34601	54380	21410	29099	24234

ENSMU SG0000 003024 7	Kcnj8	0.8	9.19E-05	0.01171	372.8	266.5	243.8	178.5	161.7	178.4
ENSMU SG0000 003877 6	Ephx 1	0.8	6.76E-05	0.00941	12706	9036	7616	4668	6439	6310
ENSMU SG0000 002466 5	Fads 2	0.7	6.82E-05	0.00942	9011	5858	5095	4226	3861	3873
ENSMU SG0000 003657 0	Fxyd 1	0.7	0.00028	0.0283	3621	2548	2070	1318	1909	1719
ENSMU SG0000 003010 3	Bhlh e40	0.7	1.27E-05	0.00248	2591	2782	3728	1557	2078	1933
ENSMU SG0000 004251 4	KlhI1 4	0.7	0.00058	0.04816	211.4	185.2	150.6	98.95	122.5	114.5
ENSMU SG0000 003359 7	Caskin1	0.7	2.41E-07	8.57E-05	1243	1161	1313	874.9	639.6	774.8
ENSMU SG0000 005327 9	Aldh 1a1	0.7	6.90E-07	0.00021	65901	46779	55543	31594	38757	33847
ENSMU SG0000 002844 4	Cntfr	0.7	8.65E-05	0.01134	607.7	452.9	458.8	276.5	356.4	328.2
ENSMU SG0000 000182 7	Folr1	0.7	9.72E-05	0.01222	5822	4119	4077	2413	3153	3309

ENSMU SG0000 007294 1	Sod3	0.7	0.0006	0.04951	6478	4695	3584	2688	3227	3426
ENSMU SG0000 003078 7	Lyve 1	0.7	0.00024	0.02542	558.7	443.8	360.7	271.9	308.2	285.3
ENSMU SG0000 004979 1	Fzd4	0.7	4.29E-05	0.00641	3877	3475	5450	2671	2626	2842
ENSMU SG0000 004969 0	Nckap5	0.6	4.13E-05	0.00628	1034	1014	1089	532.7	665.7	814.8
ENSMU SG0000 002177 0	Samd8	0.6	5.41E-06	0.00122	3950	3464	5001	2620	2809	2579
ENSMU SG0000 003176 0	Mt3	0.6	0.00012	0.0151	739.4	582.7	889.8	484.6	499	447.5
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ENSMU SG0000 004122 0	Elovl6	0.6	9.19E-05	0.01171	14503	12301	19378	10673	9559	10029
ENSMU SG0000 002683 6	Acvr1	0.6	2.64E-08	1.11E-05	3479	2863	3023	1961	2014	2197
ENSMU SG0000 000526 8	Prlr	0.6	1.52E-05	0.00289	43602	38836	30290	24073	23755	26848

ENSMU SG0000 006054 8	Tnfrsf 19	-0.6	3.08E-05	0.00502	618.9	659.5	529.1	783.3	922.7	1028
ENSMU SG0000 002450 0	Ppp2 r2b	-0.6	0.00026	0.0275	220.6	190.9	177.4	263.6	303.2	325.4
ENSMU SG0000 002782 7	Kcna b1	-0.6	0.0002	0.02199	610.7	606.5	453.8	704.7	899.6	958.9
ENSMU SG0000 007316 4	2410 018L 13Ri k	-0.6	0.00061	0.0496	129.7	144.6	113	181.3	206.8	206.1
ENSMU SG0000 010055 3	Gm1 7751	-0.6	0.00028	0.0283	134.8	122	125.8	189.6	188.8	209.9
ENSMU SG0000 004704 0	Prr15 I	-0.6	3.64E-05	0.00574	494.3	458.5	368.6	591.9	724.9	733.7
ENSMU SG0000 001358 4	Aldh 1a2	-0.6	3.88E-05	0.00599	3791	3336	2723	4178	5623	5554
ENSMU SG0000 002734 7	Rasg rp1	-0.6	0.00056	0.04717	259.4	273.3	172.4	364.4	356.4	377.8
ENSMU SG0000 008709 5	Emx2 os	-0.6	3.16E-05	0.00511	214.5	233.8	177.4	312.6	334.3	332
ENSMU SG0000 002869 9	Tspa n1	-0.7	0.00018	0.02078	652.6	578.2	463.7	708.4	947.8	1010

ENSMU SG0000 007372 1	Pram ef20	-0.7	0.00046	0.04007	185.9	177.3	252.7	278.4	353.4	340.6
ENSMU SG0000 004130 1	Cftr	-0.7	0.00037	0.0352	586.2	586.1	447.9	661.2	848.4	1046
ENSMU SG0000 005311 7	E330 013P 04Ri k	-0.7	0.00021	0.02261	193	181.8	138.7	266.3	251	292.9
ENSMU SG0000 004175 7	Plekha6	-0.7	1.20E-06	0.00034	451.4	472.1	408.2	617.8	704.8	807.2
ENSMU SG0000 005172 6	Kcnf1	-0.7	0.00034	0.0329	961	842.5	564.8	1056	1359	1428
ENSMU SG0000 007498 7	Wt1os	-0.7	2.68E-05	0.00453	190	172.8	196.2	255.2	319.3	346.4
ENSMU SG0000 001923 0	Lhx9	-0.7	9.33E-06	0.00196	1101	1134	764	1445	1700	1847
ENSMU SG0000 011037 3	Gm4 2303	-0.7	4.60E-08	1.81E-05	419.8	417.9	507.3	711.2	828.3	703.2
ENSMU SG0000 006869 6	Gpr8 8	-0.7	0.00058	0.04816	169.5	134.4	108	194.2	230.9	262.4
ENSMU SG0000 002289 9	Slc15 a2	-0.7	4.21E-06	0.00103	257.4	229.3	224.9	349.6	375.5	465.6

ENSMU SG0000 003184 4	Hsd1 7b2	-0.7	5.74E-05	0.00818	776.2	712.6	504.4	896.1	1204	1236
ENSMU SG0000 007907 1	Gm1 4085	-0.8	0.00014	0.01616	157.3	118.6	124.9	255.2	189.8	229.9
ENSMU SG0000 006721 9	Nipal 1	-0.8	2.94E-18	5.32E-15	1546	1600	1558	2635	2838	2534
ENSMU SG0000 007570 7	Dio3	-0.8	5.43E-05	0.00786	191	204.4	183.3	288.5	282.1	414.1
ENSMU SG0000 006021 2	Pcnx 2	-0.8	1.77E-05	0.0033	878.3	900.1	599.5	1136	1344	1577
ENSMU SG0000 005540 9	Nell1	-0.8	0.00024	0.02578	188.9	212.3	147.6	323.7	241	371.2
ENSMU SG0000 002505 6	Nr0b 1	-0.8	1.69E-09	1.06E-06	666.9	656.2	587.6	964.6	1234	1070
ENSMU SG0000 007974 1	Nlrp4 g	-0.8	3.66E-07	0.00012	467.8	425.8	561.8	759.3	773.1	964.6
ENSMU SG0000 005393 0	Shisa 6	-0.8	3.26E-08	1.34E-05	1951	2025	1412	3001	3008	3350
ENSMU SG0000 002797 1	Ndst 4	-0.9	0.00033	0.03225	55.15	85.83	60.44	106.4	127.5	142.2

ENSMU SG0000 006812 2	Agtr2	-0.9	7.41E-14	7.06E-11	351.3	361.4	386.4	760.2	666.7	653.6
ENSMU SG0000 009411 4	NA	-1	7.67E-08	2.89E-05	400.4	301.5	233.8	603	617.5	649.8
ENSMU SG0000 002898 9	Angp tl7	-1	6.77E-07	0.00021	447.3	414.5	397.3	602	1109	819.6
ENSMU SG0000 002304 7	Amhr 2	-1	7.35E-22	1.66E-18	6741	6108	6226	11402	12837	14099
ENSMU SG0000 004378 2	Bicdl 2	-1	0.00024	0.02542	46.98	57.6	35.67	82.31	91.37	110.7
ENSMU SG0000 001845 1	6330 403K 07Ri k	-1	3.55E-08	1.43E-05	116.4	89.22	114	208.1	238	208
ENSMU SG0000 001596 6	II17rb	-1	0.00032	0.03115	98.05	66.63	75.31	229.4	143.6	119.3
ENSMU SG0000 007312 5	Xlr3b	-1	2.76E-05	0.00463	89.87	57.6	115.9	185.9	181.7	175.6
ENSMU SG0000 004258 1	Thsd 7b	-1	2.44E-05	0.0042	96	147.9	95.12	199.8	200.8	297.7
ENSMU SG0000 004960 8	Gpr5 5	-1.1	9.99E-06	0.00201	67.41	80.18	52.52	117.4	144.6	158.4

ENSMU SG0000 005257 2	Dlg2	-1.1	4.63E-06	0.0011	48	60.99	57.47	99.88	134.5	126.9
ENSMU SG0000 010937 2	Gm1 9410	-1.2	2.17E-06	0.00058	52.09	55.34	53.51	96.18	135.5	129.8
ENSMU SG0000 007463 4	Tme m267	-1.2	4.91E-06	0.00115	115.4	97.12	54.5	199.8	214.9	189.9
ENSMU SG0000 007064 5	Ren1	-1.2	2.89E-05	0.00479	43.92	57.6	33.69	85.08	101.4	129.8
ENSMU SG0000 006181 6	Myl1	-1.3	0.00044	0.0395	44.94	40.66	16.85	91.56	70.28	83.01
ENSMU SG0000 002938 0	Cxcl1	-1.3	2.34E-08	1.01E-05	102.1	79.05	80.26	209	166.7	259.5
ENSMU SG0000 009361 0	Cyp2 c53- ps	-1.3	1.67E-06	0.00045	37.79	39.53	34.68	91.56	79.32	102.1
ENSMU SG0000 006368 1	Crb1	-1.3	2.18E-17	3.59E-14	192	213.4	204.1	459.6	588.4	467.5
ENSMU SG0000 002532 8	Padi 3	-1.4	8.17E-05	0.01096	19.4	19.2	15.85	55.49	44.18	46.75
ENSMU SG0000 002222 9	Atp1 2a	-1.5	1.22E-05	0.00242	98.05	45.17	101.1	135.9	272.1	278.6

ENSMU SG0000 011119 4	Gm4 7180	-1.6	1.37E-13	1.24E-10	83.75	88.09	107	229.4	258	331.1
ENSMU SG0000 006594 7	mt- Nd4I	-1.6	4.32E-07	0.00014	22.47	22.59	18.83	65.66	60.24	72.51
ENSMU SG0000 006345 8	Lrmd a	-1.7	2.55E-15	3.07E-12	82.73	118.6	72.33	295.9	260	301.5
ENSMU SG0000 002425 6	Adcy ap1	-1.9	7.69E-09	3.48E-06	72.51	107.3	116.9	258	249	567.7
ENSMU SG0000 000470 9	Cd24 4	-1.9	8.92E-05	0.01162	41.87	40.66	23.78	52.71	100.4	234.7
ENSMU SG0000 006674 9	Olfr8 77	-2	1.39E-05	0.00269	18.38	9.035	17.84	58.26	35.14	89.69
ENSMU SG0000 009676 8	Gm4 7283	-2.1	1.59E-16	2.21E-13	105.2	188.6	137.7	549.3	476.9	866.4
ENSMU SG0000 000498 8	Fxyd 4	-2.1	0.00049	0.04227	20.43	9.035	9.909	107.3	49.2	18.13
ENSMU SG0000 007483 2	2410 141K 09Ri k	-2.3	0.00057	0.04816	3.064	2.259	12.88	17.57	33.13	41.98
ENSMU SG0000 000631 3	Upk1 a	-2.3	8.28E-05	0.01103	27.58	7.905	14.86	160	68.27	28.62

ENSMU SG0000 008589 0	Tnfsf 13os	-2.5	3.30E-09	1.85E-06	18.38	14.68	4.954	62.89	67.27	83.01
ENSMU SG0000 009395 4	Gm1 6867	-2.5	4.45E-09	2.24E-06	10.21	12.42	5.945	56.41	48.19	56.29
ENSMU SG0000 003007 7	Chl1	-2.6	6.48E-06	0.00143	7.149	5.647	4.954	20.35	49.2	37.21
ENSMU SG0000 003086 2	Cpx m2	-2.6	4.17E-06	0.00103	186.9	192	122.9	693.6	563.3	1851
ENSMU SG0000 007521 7	4833 423E 24Ri k	-4	9.78E-07	0.00029	4.085	0	1.982	36.99	44.18	16.22
ENSMU SG0000 006436 1	mt-Tr	-4	9.18E-06	0.00195	2.043	0	1.982	29.59	16.06	21.95
ENSMU SG0000 006436 0	mt- Nd3	-5	1.10E-64	6.64E-61	12.26	18.07	13.87	360.7	523.1	508.6
ENSMU SG0000 006435 9	mt-Tg	-7.4	5.52E-09	2.63E-06	0	0	0	32.37	31.13	31.49