

## **SUPPLEMENTARY INFORMATION**

**A synthetic small molecule for rapid induction of multiple pluripotency genes in mouse embryonic fibroblasts**

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### **Cytotoxicity assay**

Colorimetric assays using WST-8 (Dojindo, Kumamoto, Japan) were carried out in 96-well plates with various concentrations of SAHA-PIP  $\delta$  as mentioned before<sup>2</sup>.

### **Microarray Analysis**

Microarray analysis was done by Medical & Biological Laboratories Co., Ltd with microarray chip that is manufactured by agilent technologies with UniGene number of genes. GeneSymbol, GeneName and sequences that were used as probes were given in supplementary table S1 and S2. For comparative method, 2-color method was chosen. In 2-color method, one sample is labeled with Cy3 and another is labeled with Cy5. By comparing fluorescence intensity of Cy3 and Cy5, expression levels were analyzed. Ratio of gene expression of DMSO over either SAHA or  $\delta$  treated MEFs were calculated using fold change to derive the regulation. The obtained raw data was the normalized to attain induction values of either SAHA or  $\delta$  treated MEF over DMSO.

### **Cell culture**

C57BL/6 mouse embryonic fibroblasts (MEFs) purchased from the American Type Culture Collection (ATCC) were used in all experiments. MEF cells were periodically cultured and maintained in Dulbecco's modified Eagle's medium (DMEM) that contains 15% heat-inactivated fetal bovine serum (FBS), 100 IU/ml penicillin, and 100  $\mu$ g/ml

streptomycin at 37 °C in a humidified atmosphere of 5% CO<sub>2</sub> in 95% air. MEFs were passaged by trypsin (Invitrogen). mES cell line R1 (a gift from Professor N. Nakatsuji, Kyoto University) were maintained on Mitomycin C-treated MEFs in complete mESC culture medium (Millipore) consisting of DMEM/F12 (80%), knockout serum replacement (10%), fetal bovine serum (10%), L-glutamine (1 mM), nonessential amino acids (1%), β-mercaptoethanol (0.1 mM) and Leukemia inhibitory factor (1000 U/mL). The medium was changed every day.

#### **Treatment of SAHA-PIPs against MEF**

MEF cells with in the passage P6 were trypsinized for 5 min at 37 °C, and were resuspended in the fresh DMEM medium to a concentration of  $2 \times 10^5$  cells/ml in a 35 mm plate and were grown for 24 h as mentioned before<sup>1, 3</sup>. The medium was then removed and replaced with 2 ml of fresh DMEM medium followed by the addition of 2 μl of the 100 μM of each individual SAHA-PIP **Q-Φ** shown in Figure 1 to achieve a final polyamide concentration of 100 nM in 0.1% DMSO and then were incubated in a 5% CO<sub>2</sub> atmosphere at 37 °C for 24 h. 0.1% DMSO treated cells were used as the control. Incubation time and the concentration of the PI polyamide SAHA conjugates were standardized based on the initial optimization experiments with varied incubation time and the treatment of MEF with various concentration of SAHA-PIPs as mentioned

before<sup>1,3</sup> to optimize 100 nM as the optimal concentration and 24 h as the optimal time for incubation.

### **Quantification of expression of marker genes in mouse embryonic fibroblasts treated with SAHA-PIP**

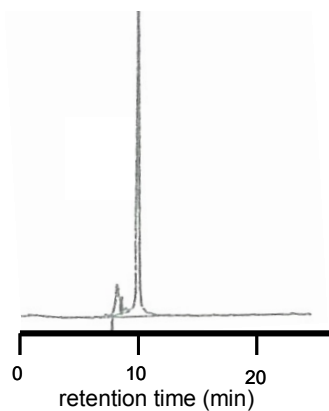
As mentioned in the previous report<sup>1</sup>, total RNA was extracted from PI polyamide SAHA conjugates treated MEF using an RNeasy Mini Kit, in accordance with the manufacturer's instructions. The amount of nucleic acid in the total RNA was determined by measuring the absorbance at 260 nm using a NanoDrop spectrophotometer, ND-1000 (Thermo Scientific, USA) as mentioned before<sup>1</sup>. cDNA was synthesized from 500 ng of total RNA using a ReverTra Ace qPCR RT kit (Toyobo, Japan) and used as a template for polymerase chain reaction (PCR). SYBR green real-time RT-PCR amplifications were carried out in triplicate with THUNDERBIRD SYBR qPCR Mix (TOYOBO, Japan) and the program as mentioned before<sup>1</sup>. Melting curve analysis of amplification products and the comparative cycle threshold (CT) method used to analyze the expression level of each gene was as carried out as mentioned before<sup>1</sup>. The average CT of the three determinations was used in calculations of relative expression level using DMSO treated cells as the internal control. The relative expression of genes was normalized against GAPDH. Primer pairs

of iPSC factors and actin that were used for RT-PCR analysis is as shown<sup>4</sup>. Other primer pairs used to analyze endogenous gene expression were listed in Table S4.

### **Chromatin immunoprecipitation (ChIP) analysis of promoter region of pluripotency genes**

Antibodies for acetylated histone H3 and normal rabbit IgG were purchased from Upstate Biotechnology Inc., USA and H3K14 was purchased from Abcam (ab10812, UK). ES cells were used as the positive control. After 24 h treatment of each of the cells individually with 100 nM of ***δ***, ***δ-OMe***, ***B***, SAHA and 0.1 % DMSO, ChIP assay was performed according to the protocol described in<sup>5</sup> and that in the kit manual (SimpleChIP™ Enzymatic Chromatin IP Kit, Cell Signaling Technology, USA). DNA fraction was then purified QIAquick PCR Purification Kit (Qiagen, USA) and analyzed with qRT-PCR as mentioned before. Input sample was used as the internal control and the GAPDH was used as the internal control primer pair. Details of the purchased primer pairs used for *Oct-3/4*, *Nanog*, *Rex1*, *Dppa4*, *Gapdh* and *Cdh1* were shown in Table S5.

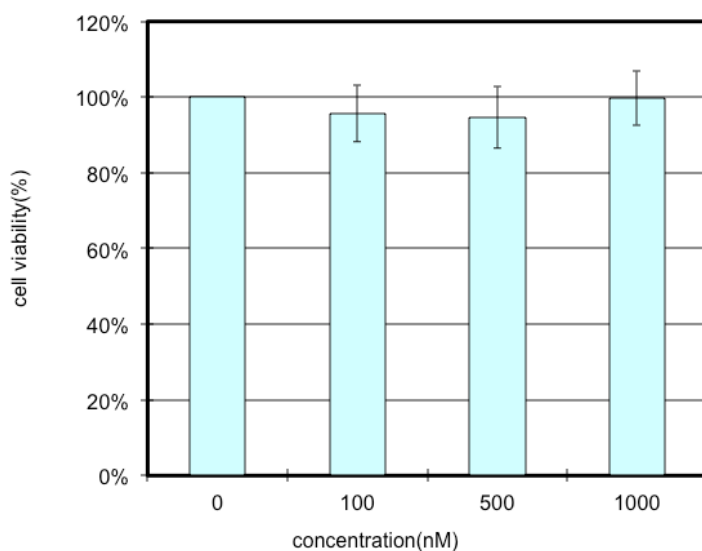
Figure S1



**Retention time: 10.4 min**

Figure S1 **HPLC chromatogram of  $\delta$** . The purities of the  $\delta$  were checked by HPLC (elution with trifluoroacetic acid and a 0-100% acetonitrile linear gradient (0-40 min) at a flow rate of 1.0 mL min<sup>-1</sup> under 254 nm).

Figure S2



**Figure S2.** Cytotoxicity assay of SAHA-PIP  $\delta$ . Cell viability of MEF was measured after 24 h treatment of the above effectors with various concentrations. Each bar represents mean  $\pm$  SD from 12 wells.

**Table S1****a) Up regulated genes in SAHA treated MEF**

No	ProbeName	Gene Symbol	Sequence	Fold change [SAHA] vs [DMSO3]
1	A_55_P2152009	Tesc	GTGGTGTGTGGGACTCCGATATTTTTATCTCTAATGGT GACAATAAAGGTTTCCTAATGA	23.539
2	A_52_P596595	Pnma2	TGACTCCACGTGGCATTATGTTCTGGGAATAGCTTTG CCGTTGACTTACCAACAGAAT	21.604
3	A_51_P368313	Vip	GGATAAAAGAGATATGTGGCAAAGGATTTTCAGAAT TGATTTCTCCAGTGATAGGTAC	15.784
4	A_55_P2004213	Gprasp2	TAAACATGTGGTCTCTGCTTGAGTCTGGGTTTTCAAT AAAGTTCGATGTTAAAGTTGCC	14.776
5	A_55_P2017600	Crmp1	GAGCAGGGCAGTCAGATTTTTAAAGTTTTGTACAGTTT TCCTTTGTATTCACCTCCATTT	11.216
6	A_51_P363187	Cxcl1	AGAAGTGCAGAGAGATAGAGTTTAGTATTATGTTTTGT ATGTATTAGGGTGAGGACATGT	10.696
7	A_55_P2114110	Cadm4	AAACACATTTTTGTACGGGGCGGGGAGGGGATAGGG AGGGGGTTTGCAATCCCACTAAC	8.946
8	A_55_P2146560	H2-Ab1	AATGTATGCTTATCCCCACCTAGATTACAAATAAACGA GACCCAGACTCTGGTTATTTGA	8.630
9	A_55_P1997756	Il6	CTGTTACCTAGCCAGATGGTTTCTTGAATGTATAAGT TTACCTCAATGAATTGCTAATT	8.301
10	A_55_P1965283	Wdr17	GTCTAAGAATAATAGGTTGGGAGGTGGTTTGATACTT GGAAGACAGAGGGAATAATATA	8.200
11	A_55_P2007500	Tmem151b	TCCAAGCGCAAAGATTGTACAAATCACACTGATGGAT AATAAAAGTGTGGATGACTCACT	8.194
12	A_52_P562676	Sult4a1	AGTACTGTACGGATGTTCTGGAACCCACACATGGTAATC TCTGCTTGCCTGCATCTTTAAT	7.730
13	A_51_P504354	Nrarp	TTTTTTGAATCTTGGTTATGAACCAATTTTAAAGGGC GTTGTATCCAGCGTTGTGAAGG	7.370
14	A_55_P1962747	H2-Ab1	TAGTAAACCAATGTATGCTTATCCCCACCTAGATTACA AATAAACGAGACTCAGACTCTG	7.308
15	A_51_P483159	Gchfr	CCGAGGACGAGGACAGTCCCTGGATCCTACACAGCTA ATCCAAGCCAATAAAGGGCTCTC	6.717
16	A_55_P1990032	Cxcl5	GCTGAGATATTTAGATGCTGTAGTGTGCTTTTTAAAG AGTGTGCTTTGTATAAAGGAGA	6.677
17	A_51_P428372	Ppbp	CTGGTCATGACCATGTTTTTCCAATTTCTTATCCCTAGA ATGTCTTGTTTCCAAGCAACC	6.467
18	A_51_P202050	Dtx1	TGAGGATTGGCTGCTGGGATGGAAGTCAGCCAAGCTT TAAAGGGACGCCAGCAATTGCTC	6.418
19	A_55_P2119633	Gnal	GATTGCAGCCATTAAGTAGTTGATTACTGTGTGATTT CAATACTCAAGAAAGCTTTCAG	6.392
20	A_51_P308048	Cmtm8	CCAGTGTCTTGTACAATTGAGCTGGATATTTACTTGG GGAGTGTGCGGCTTCTAATGA	6.352
21	A_55_P2085311	Nxph4	TCCTAACCTTGCTAAAGCAAAGTCTGATCAGGGGG CTCTGCCTGGCCCTGTGCTCTG	6.085
22	A_55_P2044684	Rsph1	CTCTAGCTGTTAAGTTGTTTTTCGGTTAACAAAATAA ATCTCCAGGTGTTCAAGTGTG	6.034
23	A_51_P204740	Cd34	CCAGAGATGAGAGGATTGGGTGTATTCTTCTTCTGAATA AACGTGATGAGTGAATGATG	5.987
24	A_55_P2032094		ATGTGTGATAATATTGGAACCAACAATTCGGTCATATT TTTAAAAGCTATTTGTGTGTGA	5.888
25	A_55_P1980204	LOC100044518	TTATAAACTAAACTCACGGTTTGACTTTTGTCTGACTCA GTGGAGGCTGTGGGGAAAAAG	5.883
26	A_55_P2047305	Adcy5	GCAAGAGGACACCAGGCAAGGAGCAGTGGCTCTGAG CAAAAGAAAATATTTATTAATAA	5.861

27	A_55_P2362877	LOC100044518	ACAGGCTAGGAATGGAGAAAGAAGCGCCTTTGTTTT CAATAAATGGTCAGGGCACTCAT	5.852
28	A_55_P2081785	Slc45a1	AGCCAGCCAGGCTTCTAGTGGGATGTAAATACGGGCT AAATAAACACAGCAGCAATCTT	5.723
29	A_55_P2137049	AA467197	CTGCATTAGCAAGTGAAGGTAGCACATAGTCTAAAT AGTTTTCTGTGTTTATTGGTGTA	5.654
30	A_51_P176352	Ndrp2	TCAGGAGAAGGTTTCTGGTGGGTCAGCGATCCTTAA TGTGATAGAAATATCCAGCATGT	5.609
31	A_55_P1984243	Naip2	TTCTAGTACATTTCACTCTAGACAGGCATGGTGAATC CTAGTACTTAGGAGCCTGAGCA	5.560
32	A_52_P220573	Serpini1	TGGTGTTAATTCAGTGTTACATTCTCTGTAAGAACA GTCTTTATCTGTATCCTTCT	5.555
33	A_55_P1997831	Dbndd1	TTTCATGTGCACAAAGACAAACACACTGGCTGCTCTGA CCACAAATCAAAGACTGTTTTG	5.548
34	A_55_P2072233	Zcchc12	GTGTTGTTCTATATGCTGTATTTTTACCAAACGAT GTTGTGGCCTCTTTGTCAAT	5.539
35	A_51_P397468	Rundc3a	GGACAGCGCTCATTCTGGTGGCTCTGAAGGCTGCC GGTTCCTCTGATTTCTCCACA	5.531
36	A_55_P2051313	Gstk1	ACAAGTGCCTTTGAAAAGCCTTAAATCTGCATTCCC ATAAAATAAAGTTGATGCCACC	5.495
37	A_55_P1966102	Nme5	AAGTTACCTTACTGTAAGAAGCCGCTCCCATGTTCTT ACATTAAGCATATATGTGT	5.472
38	A_55_P1976200	Lmtk3	AGCCTGGCCCTGGAGGGGCTCTGATTCAAACCTC GCGTGACATTTTACATTATT	5.409
39	A_51_P458778	Hpgd	AAGCTCCTTTACAATGGAATATTTAGTAATAAAAGCT TGTCGGGACCTGCAAGCGAAC	5.392
40	A_66_P135185	Etv1	TCACAGGCCAGTAGCATTTTATGTATCTGGTGCCATCC TGCTGTTTTGGTACTACAAATA	5.364
41	A_52_P533724	Ino80	ACTCGGCTCAAGTCTCAAGGACATAGGGTCTTATCTA CTCTCAGATGACCAGAATGATA	5.100
42	A_66_P125828	Gm6684	GTCGCCACCACGGTTCGCATGTGGATGGTAAACCT ACATGTCGCATGTGGATCTGA	5.033
43	A_66_P116998	Tro	CTATTCCCATCAGCTGAGTGAAACACTGAAAAATCTG CTGTTCTGCTTTGTGTTGCT	5.021
44	A_55_P2006093		TGCAAGTGAACATGGATATCCAGATATGCTTCGAGCC AAGAGGGCATCTGAAATCTACA	4.852
45	A_52_P49378	Kif1a	TGTGTACATAACCACCTGACGTAATGACTAGTATCCTGC TGTTTACACCCGAGTGTAGCT	4.829
46	A_66_P121288	Tceal6	ACCCAACTCCAGTCTCTGTCTTTTAGTACAGGATTT TCACCCATGTGCATGAAAAAT	4.777
47	A_55_P2169829	3632451O06Rik	GGTGCAATTTAGAACTCATAGGATACATGTTCAAGT GGAGATAGGTAGAATAAATATT	4.707
48	A_55_P2427377	3110068a07rik	CTTCATCTTTACAAAGCTTGTAGCTGCCATTGCTTCTCT GCTTTATTAATAAAGATACC	4.635
49	A_55_P2008987	Ch25h	TGCGTGAAGTCCAGAGAGCGATGCGCTGTACACTTGA TCCAGAAGAAGAAACAGACTTGA	4.630
50	A_55_P2004867	Serpib2	CATCATAAGTAAGCATGCTTACTTACACTGCTATCT GTTGTATAAAACTTAGCAATCC	4.617
51	A_55_P1982902	Tceal3	GCTCTGTCTTTTAGTACAGGATTTTACCCATGTGCA TGTACATTGTAATAACAAT	4.577
52	A_51_P270733	Syng1	ATGTGTAATCCCGCAGATCAGCAGTGTCAAGGACCG CAAGAAGGCCGTGCTCTGACA	4.564
53	A_51_P256246	Tspan13	AGTCAAGGGCAAAGGAAGATACCATTTGGGAAATGCT TTGGTGTGTAACATCTTCAAGCTC	4.510
54	A_55_P1953846	Abca8b	CACATCCCTTAGGACACTTATAGCCATAGTTCTGTAG AATGTTGAATAAACAGTACTT	4.498
55	A_55_P2048759	4930583H14Rik	CTTTCTTACTTTGTTCTATGTAAGACCAGATTACTGG GTTTGCTGTGAACACTTTAA	4.468
56	A_55_P2017710	lgsf9	CGCGCGCAAGCGCGCTTCGAAAGTGGTGTATTATG GTGTGGGTGCAGGTTCTTTTTT	4.444
57	A_51_P510418	Aldh1b1	AAATCTGATTTCAAGCTGAGTCCAGTGAAGTGTAC AAGAAGTGCAACCAATAAAGT	4.415



58	A_55_P2045642	Stmn4	GAGACCTGCCCTGCAGCGGGTGGGATAAGGTCTGTGT GCGTCTGTTTCATTGTCATCTTTT	4.376
59	A_55_P2048119	Slc29a4	CCTGTCTACCTGTGTGTTCTCTGACTACCGCACTGGCC ATTAATATGGCAGAGACTGCC	4.360
60	A_55_P2024463	Tbkbp1	CTCGGCCAGCCGATGGCAGTGAACGCCACTGTCCATC GAATGTGCCATTCTGATCCAAAT	4.331
61	A_55_P1962771	Cyfp2	GTACCTGTGTTGAGTCGATAAAACATTTTCATCTCCATT AAAACGTCTCCAAACCAGTT	4.327
62	A_55_P2042016	LOC100048058	ACCTGTGTGTTCTCTGACTACCGCACTGGCCATTAAAT ATGGCAGAGACTGCCACCCT	4.284
63	A_52_P482897	Areg	CTCAGAGGAGTATGATAATGAACCACAAATATCCGGC TATATTATAGATGATTCAGTCAG	4.263
64	A_55_P2123502	Jam2	TTCGTGATTTCTGTATGTGGCCTTGGCACATGCTATGC TCAGAGGAAAGGCTACTTTTCA	4.232
65	A_51_P182257	1700019N12Rik	CGGTCCTCGAACCAAGCTCAACCTCATCTGCATGGA ATTTGAATCCTAGAGAAATTA	4.210
66	A_51_P459108	Insl6	CAAACATCACTGGTGATAGAGATGTACAACTGTCGT AGGAACTATGCTCGCTTAATAAA	4.058
67	A_55_P2092296	Fbxo2	GGATCCCGCTCTTAGCATTGTGCCTGCCTCAAAGTG GGCACTCAATAAATATTTGTC	4.035
68	A_66_P119034	Pla2g7	TTACCCAAATAAGCATTTTTTAAATATACACTGTACTGT AGGATAGTGATGAACCCCTAG	3.963
69	A_55_P2208579	Onecut2	TCCAGCACTGTACCAAGCATGATGCAAGGACTCTCC ACCTGGGCACAAGTCATCTCCA	3.956
70	A_52_P63855	S100a7a	GTTCAAGTAAAGAAGTTTAGTTTTTATTATCAGGAACA TCGTTTTGGGCAGAAGACATGG	3.947
71	A_51_P399175	Ppm1j	GCAGTATGAGCACTGTCCAGATGATGTGCTGGTCTCG GGAACAGATGGCTGTGGGATGT	3.929
72	A_51_P389988	Slc40a1	TTCTAGAGCAACAATAGTCACAAAAGTTCCCTTTCAA TATCCCTGAGAAGAATAAAGAA	3.917
73	A_51_P469968	H2-M3	CCTTCTCGATAAAAGCTGTACTTCATGCTGTTAAAAGT GTAAGATTTGTACATTGGAAAG	3.907
74	A_51_P201785	Morn5	TGCTGGCCTGGGAACTGGCTGTAGTCTAGCTTCGA CTTAAGTTTCAGAATAAAGGTTT	3.893
75	A_52_P60353	Greb1l	GACTCTAAGCTGTCTTAACTTATGTCTACAGTATGTTCT TGTTCTTTTCATTTGGTGAATG	3.853
76	A_52_P476029	8430427H17Rik	GTCATAAGTATGTGGAATCCTTTTCTTTTGGACTGT ATATCATATACCAGACTGAATC	3.843
77	A_55_P2106901	Nkain4	CGGGGGACACTGCAGGACAGGGTGGCTACAACCTGTG AGTTTGTAATATCTTTCTTTTTT	3.841
78	A_55_P1953301	Sord	ATCATGGCCAGACCTGAGCTTCTCAAACCTGCTTCGC ATAATAAAGTGTGATGGTGTCT	3.840
79	A_55_P2109257	Nipal3	CATGTGTTATTTTGCAGAAGTGTGATACTGTGTGCAG ATAACATTGTAAGCGGTATTT	3.800
80	A_55_P2008889	Tmsb15b2	AGATCCATTTACTACCTGGCTGCAAAGGTCAGCATTT GCTATGAATCATTAAATTTTTT	3.733
81	A_55_P1977533	Eno3	CTTTCACAGGAAAGACACAGGCCTCAAGCCCTTCTCC CAGAAATAAAGACTGCCAAACC	3.729
82	A_55_P2169669	Csf1	CAGCTGCATCATATATTGTCATATGTTGAGCTGTAGT CTATTAACAAACCCAGTTCTAT	3.712
83	A_55_P2070199	Speer2	TGTGAATAGGAGGAAGCCAGTGTGATCTGATTCAG GGTGTGTTCCCTTTCATGTTCT	3.706
84	A_52_P282838	Spin2	CATTGTCTGTGTAAGAGATGAGTATGTTGGTGAATG GGATATGAAGAAACAGCTGTCA	3.697
85	A_52_P590396	Sort1	GTGTTAACTTTGACTGGTAATTTTCTGTATATTTGCA ATATTTGGGTTAGAAATAAAC	3.650
86	A_55_P2263877	8430436N08Rik	CTTTTCATTTCAAGCTGACTGTATTACTAGAATGAAAT AAAAGTGCTGTACTGGTCTGG	3.635
87	A_55_P2143219	Rasgrp2	TCTGTTAGACCAAGAAGGGAACCGCAGGCACAGCAGC CTCATCGACATCGAGAGTGTGTG	3.609
88	A_51_P230347	Sfrs13b	ATCTCATTACTAAAACACACTGTGAGTCCCTACAGCTA ATATTTATGCTGGAATACCTA	3.608

89	A_55_P2149500	Kifc2	CTATCTAGCAGAGACAACCCTTCTGGAGTAACCTAAT TAAAGCTGTGGGTTTTTCAGCAA	3.582
90	A_55_P2044582	Iglon5	GCCGTGTGTTCCAATTCATGGGGAGTGTGAGACCAC CACACCAATAAACGCCTTTTTCC	3.545
91	A_55_P2148688		CTGTGTGCAGATAACATTGTAAAGCGGTATTTAATTA AAATCCAAGCAGTCTTGCAGA	3.538
92	A_55_P2146214	Zcchc18	CTGTGTGCCTCGGTATATATGTATTGATAAAAGTGATC ACATATAAGTGCTGTTCTATAG	3.532
93	A_66_P119017	Smarca1	TTTACTTGTCCCATCTTCAAATGCTAATTACTACTTCC AGTGTATTCATGGTACTCTAA	3.517
94	A_51_P234881	Elovl4	TTTTTACACAGATTAATTTGTTATGGGCGTCACAGAGA GATCATATGGAAAGAGGAAATG	3.505
95	A_55_P2090070	Myh14	TCTGTGTGCTCATAGGGTAATGCTCATGGCCCTCATG CTCCAGACACTAAAGAAATAAA	3.466
96	A_52_P645862	Agtr1a	TCCTCCACATATATGTACATATGTATCTCTAAGCTGTCA TTTGATGAAGTTTTGGCAATG	3.465
97	A_55_P2047275	Tspan7	CTCTGTCTAGCATGCCAACAAGATGCATTGATATTGT GAACATTTGTGATACATGTATT	3.405
98	A_55_P2017914	Csf1	CGTGCGATTAAGATCACATTAGTTTTAACAGCTGCAT CATATATTGCATATGTTGAGC	3.399
99	A_52_P243391	Sema4f	ATGGCTTTCATCAGATTCTCAAGGCCCTTAATGAGGTTA AAGGACCACGGTCCATAGTCAC	3.391
100	A_55_P2082215	Ttbk1	CTGACACCAACACCTTGCAAGTCGCTGCACAACCTAGA TCGGGTCTCAGAAGGGAAAGTAG	3.391
101	A_51_P435339	Epor	GAACGGGATTGGTGAAGCCATACTTAAAGTCAGAGCT GACCTTGGCCCTCTGAGCAGGAA	3.378
102	A_51_P131164	Enkur	GCAGTGTGAAAGAATAGTTGAATTATTTGCTTGCTCT AGAGAAAATTTTCTCCTCCACT	3.361
103	A_55_P2147101	Sytl4	CCAGGCTCAGACTTGTCTTTGATATTCTACTTTAATAT GCATGTGTGTTTTCAATAAAGC	3.339
104	A_51_P509643	Snca	GTCTTGTGTGCTGTGGATATTGTTGTGGCTTCACACTT AAATTGTTAGAAGAACTTAAA	3.338
105	A_55_P2068673	Stmn2	TCTCTTGTATGTCATTGTGAGCAAGCTGTGATGAATA AAGAATTGGAGTTCTGTGAACT	3.316
106	A_55_P2024461	Tbkbp1	GAGAGGGCCAAGTGCTCTCTGAACAAGTTGAAAGTCC AAATAAACTTACCTGTCCATC	3.309
107	A_55_P2024841	Gstt1	ACTATAATCACTACTTTCCCTTGAGTCTGGGTAATAAA CTGGGGCTTGATTTGGGCTTT	3.266
108	A_51_P112223	Gsta4	GCTGGAGTGGAGTTTGAGGAAGAATTTCTTGAGACAA GGGAACAGTATGAGAAGATGCAA	3.259
109	A_66_P122086	9030619P08Rik	GCCCTACTGCGTGCAAAAAGATTCAGGGGCTGGAAT GCTACCAGTGTGTTGATGTCCCA	3.258
110	A_66_P129029	Taf10	GCATAATTCGGCTCATCTACTAGCTGCCAGAAATTC ATCTCAGATATTGCAATGATG	3.245
111	A_51_P460048	Cnrip1	AACATAAAGGTGGCACTAATACATACCCTTTAACTTGA ACTTTGTACAACCGTGTATGGA	3.234
112	A_55_P1959425	Slc16a3	CTGGGCAGTGGTCTGTTACCCTGAGTCCACCCTTTG TTAAATAACAACTGCTGATTC	3.227
113	A_55_P2123496		CTAAAGTCTGAAGTCTTAAATTGTTCAAGGCAATCGCT TAACTGTCAACCCTTATGTAAT	3.221
114	A_55_P2147083	Tnfaip6	AATTTATATTAGATTTAAGGTTGTTTTATAAATATTG CTGTAATAAATACTTTTGGAT	3.217
115	A_55_P2021704		ATTCTGCACCGTTTCTTGCTAACTTGAGGCTGTGGAT AATACAGCAGTTTACTTACTGA	3.211
116	A_55_P2126790	1500009L16Rik	CAGCATTTGAAAATGAACTCGTTAAATGTGCATGCTAT ACACATATGGATTAAGTCCTC	3.202
117	A_52_P365660	Lrrc4c	GCATGAACCGTTATTGATCCGAATGAACTCTAAAGACA ATGTACAAGAGACTCAGATATA	3.201
118	A_51_P344376	Gpr162	CCATCCAAGTGACCAGATACCCAACGCACCCGCTTCA CCCCTAGCAAAATGATTAATAAA	3.200
119	A_55_P2043200	LOC635905	AGTACAATTACGCAGTGTGAATAGGAGGAAGACAGTG AGCCAGCTGATTCAAGTGTGTT	3.198

120	A_52_P549827	Mgst1	AGAATTCTATATTTTCAGTGGATTCAAACCTTTTCTGA GGTTTTAATGCGTGAAAGGAG	3.195
121	A_55_P2129261	Arhgap36	TGATTGTTCAAACCTTCTCTGGCATTTCATCATTAAATAA CATCTGTGTGTGACAGCAGC	3.189
122	A_52_P151116	Kcnab3	GAAGACTTAAATCTAGAACTAGAGTCACACTTTGTGTT TACAGAGAGGGGATAAAGTTGG	3.187
123	A_55_P2015495	Abat	GGTGACCACGTGAACAGTTCATGAATTAATGTTTCC TGTGTTAATCAGTATTCTTAAA	3.186
124	A_55_P2141943		GTCATAGGCATGTCCAGATTTAAGTGTAAACATCTTA TTTTCCACTGATGAATCTCAAG	3.179
125	A_55_P2157033	Bace2	GACTGTATCTTGATTACTCTTGATTTCCAAGCTTTCAGA TCTTTTCTACTTCAGAGAGAA	3.171
126	A_55_P2183587	Gli1	GGGGCTGTATTTAGTCTATGTATGTTCCAGGAAAGAAC AAACTTTAATAATGACACAGTT	3.155
127	A_55_P2013043	Serpinb6b	CCTTCATCCTCTCTGCAGCAATACTGGGATCTCAATTT TTGGTTACTTAGTAATTTATT	3.142
128	A_55_P2104988	Accn2	TTTAGAGATCAGAACTCCCAGAAAGAAACAGGGCAA AGCTGAGAAATGTACACTGGCTG	3.127
129	A_51_P275454	Trim30	CATATTGCTTCTAGCAGATAGAAGGTATCAGATACTGT ATCTGTTAAGTTTTTCTACCC	3.105
130	A_52_P262219	Fos	GGACTTTATTTCCAGTAGATAGAAATCAATAGCTATA TCCATGTAAGTGTAGTCCCTCAG	3.105
131	A_55_P2067505	Slc16a3	GTGGTCTGTTCCACCTGAGTCCACCTTTGTTAAATA ACAACTGCTGATTCTTAAAAA	3.100
132	A_55_P1974645	Entpd2	AGAAAGGCAAGCACCAGAGACTACAGGCTAGGAGTC AGCTCCATGCCTACTTGTAAAAAA	3.095
133	A_51_P116601	A330021E22Rik	CGGGTGAAAGTGAAGCCACCACTGAATGATCCTAAAA AGAGCATCCCTACATGATGTGTT	3.086
134	A_55_P2162988	Tmem179	TGGTAGTGATGCCTCCGTGTGTCTGATCCTCAAGTCAA AATAAAATAAAGACGAAACATC	3.084
135	A_51_P429335	Prss16	AATGTAGGCAAATGATTACTGTCTTTGTAGGTAGTGA TATTCTGTATGGTAAATGTCAG	3.083
136	A_55_P2058671	Zfyve28	GGAGGTGGGAGAGTGTATAACAGAGGGGAATATTAT GTATTGAGATGATTTTTATTTTCT	3.080
137	A_55_P1955656	Ctla2a	AACACTGTGGTGTAAACTCTGAGGCACATTTCATGCAAT AAAACACTAGTTTTGGCAGTC	3.076
138	A_52_P387009	Egln3	ATCCCAGCATTTATTATGCACTATGTTTACTTCTTACTT GGGGAACCTAATTATCCAGAG	3.070
139	A_55_P2095899	2310057B04Rik	GTGGCTAAGTGGCTTCTGTACTTTGCACGTCTTGAA ATTATTGTTAATGAAATATTG	3.069
140	A_52_P138806	Dlgap3	CCACACCTGTGGCTGTTCCACATCCCTTTGAGTATCCC AGGAAAAATAAAACCCGAGAA	3.068
141	A_51_P271425	Lhfpl4	ATGTGTCTTAGATGTTCACTGTCCAATTTGGTAACATTT CTTTTGGTCCCGCCCTTCT	3.063
142	A_51_P401987	Tmem37	GTGCCTCTGTACGACGGCACAGTGAGCTGGATAGGTT AGTCATGCTATTAATAATCTCAAT	3.050
143	A_55_P1982404	Gpm6b	CTATCAGTGCCAAGGGCTTCTGTAGTCTATTCAAGT GTTACAATAAATATTTGTAGAT	3.041
144	A_52_P432919	Rab3d	CTATTCCTGACCAGACTCCCCTAAACACTATCTGACAT TTCATGGTCCAGGTGACAGAT	3.037
145	A_55_P2237432	Smarca1	TAAGGCAGTGTGTACGGAATGCTCCCAGTTTAGATTT GACTGGTTCATCAAGTCGAGAA	3.033
146	A_55_P2065364	Tdrkh	GGAGAAGTATCTTAGGAAATGTGTAACGTGTTACAA ATATGTGTCTGTATACACACAAC	3.032
147	A_55_P2021187	Malat1	CGTCTTATTACCTCTGAGTCGACACACCTCCTACTATTT ATTGAATACTTTGATTTTATG	3.029
148	A_55_P1991079	Phf21b	GGCTAGAGAAAGTGTGTTGCTTAAATATTCCAGTGTAG TTTTCTTCTGTATGATGCATT	3.024
149	A_55_P2049752	Pamr1	TGATCCTTTCCCTTTCCAATCTTCTGTACACATTTCAATA AAACAAGGTCTGCTCCCTGA	3.020
150	A_51_P265495	Ly6a	TATGAGTTATAGAAGCTCCAAGGTGGGAGTAGTGTGT GAAATACCATGTTTTGCCTTTAT	3.007

**b) Down regulated genes in SAHA treated MEF**

No	ProbeName	Gene Symbol	Sequence	Fold change [SAHA] vs [DMSO3]
1	A_51_P495780	Plin4	CAGCCTGTGGGTATGAGACCTGCCCTGAATCAGGTCT GGCTCCCTATACTGCTCATGGTA	10.405
2	A_51_P378051	Aoc3	GAAAAGCTAAAAATGAGTAGGCGATAAGTGTACATTT GTTTATTCTGCTGCATTCCTTG	6.298
3	A_51_P397437	Prss46	TTGAGCCATCTGAAGTTACCATGTTCTTGACTTTGACC AAAACCCCTTAGAGCACCTCCC	5.949
4	A_55_P1981681	Syt8	AGAAAATGGAAGAAGAGCAAAACATCTCCAAGAAA GGCAGGACTACCCCTACTTCAAC	5.535
5	A_55_P2093705	Meig1	GGCAATGCTCCTTTAAGAATTGGTTGTTTACATTCTCC ATCGTGAAATGCATTTTAC	5.039
6	A_55_P2052016	Crispld2	TGACAGGGCCACACTGGTTGTTGCTATGGTTTCAATA AAACGGATTTGATTTCTAACAC	4.843
7	A_52_P619248	Prl2c5	CAGTCCAGAACGGGGTTAATGCCCTCATGAGCACCAT GAATGGAGATGAAGAAAATAAGA	4.693
8	A_55_P2057380	Gm6745	AAATGTCAAACAGAACAGACTGAGAAAAAGCCAGATA CCTTTCACAATAGCCTGAAAAAA	4.679
9	A_66_P119376	Kctd12	AAAGCTCTTCTATATCCAAAGGGAAACAAAAACACAT GGATGAAATCTTTTCAGAGGTGC	4.649
10	A_55_P2004016	Crispld2	CGGTGAGTGCTAGCCAAACACAAACAGGGTTGCGTGC TCCAGCCAAATATTTCTTAGACC	4.607
11	A_55_P2004752	Prl2c5	GGTCTTGCAATCTGACAATGAAGATGCTCGCATTCTG TCTTCATATGGCATGATCAGCT	4.505
12	A_55_P2076866	Megf6	CAGCAAGTGGGATCAAGGGTTTTGTAACCCAGTGA GTTAAAGGCACAGTGGTGTCCCC	4.405
13	A_51_P235088	Dusp27	TGGGAAGATGTAGAAGAGTCATCTAAATCAGACTTCG CTGAGTTTGGGGCCAAGAGGAAA	4.186
14	A_55_P1994128	Tmem184a	AGAGTTGCCAGTGCCAGCCTACCAGCAACTATCTGC TTATTTATAGATAAACACCTTG	3.928
15	A_51_P352385	lsm1	GGGGTGGGTAGTAAGTGAATGTGCAGAGTCAAATCTA AGACATCGTTTTCAATGGCTTTA	3.858
16	A_55_P2040893	Tnni2	AAGCACCCAACATCCAGTCTGGGAGTACTTGGCCTCGC TCCAATAAAGGATTCACATCTC	3.832
17	A_55_P2172196	Thnsl1	GCCTGGGATACATGAGGTCCTGTTAAAAACAAACAA CAAACAAACAAACAAACAAACAA	3.737
18	A_55_P2385792	4933431K23Rik	CTACAAATCCTTTTGACAGATGGGCAAACTCACAATG TGGAATCCTTGAACATAAAAA	3.720
19	A_52_P382886	Gjb2	CAAGTTGAACCATTACCACTATGCCTTATGTGTATCCTA CAAGATGACAGTCAACAAATC	3.710
20	A_55_P2045571	Adam12	GACCTAAGATGAGATGTTTACTTTCTATTCAAGGCCTT ATCGGAAAATAGCTCCCCACCT	3.604
21	A_51_P205215	Klhl30	CCCTGGGGTGTGTCAAAGCTTGCTCCGGGGATATG CTGAGATGGGGTGGAGCTAACAT	3.577
22	A_55_P1960631	Col8a2	ATGGTCTCTACTCCACCGAGTACATCCATTCGCTCTCT CAGGATTCTTGCTCTGTCCCA	3.575
23	A_55_P2130032	Zfp599	ATGAATGTAAGGAGTGTGGGAAATCATTCTACCAGAA ATCAAACTCACTACATCAAA	3.549
24	A_55_P2083879	Vsig2	ACTTCTGATCGCTGAGGGTGGTGAGCGTCCATGTTAAT AATTAAGCCTAAACCATGCCA	3.517
25	A_51_P372393	Angpt4	TCTCCAACCTCAATGGCATCTACTATTCAAGTTCATCAGC ACTTGCACAAGATCAATGGCA	3.493

26	A_55_P1987430	Fam196a	GGATGACCCTTCTCCTGGAAAGATTGAGCTCAAAAGTT TCATACAAAATAAGTAAAAAA	3.467
27	A_55_P2130501	LOC100044727	AATGATTGGGATGTATTCCAGTCGACACACCATACCA TATGGGGATGCCCTAATTTC	3.444
28	A_66_P116372	Soat2	ACACGTTTGGTTCTTTCTGCTTCTCCAATGCAACAATA AAAATCTTAGTCTCGGACTGG	3.431
29	A_55_P2115851	9930013L23Rik	ATCTGAGAGTGGTTGGCTCCAGACCAGGATCTTTCAGC TTATGTTCACTCTGAGCAAATA	3.409
30	A_66_P123449	Gm847	CTTGCAACTTGAAAGACTTTCACAGAAGACATTGCTA CTAAAATAAAAACATCTGTATC	3.330
31	A_55_P2069659	9930013L23Rik	AGGGGAACCTCACCACACCAGAAACATGGGGAAGG CTTCTTCTGGAAGGTGATGGTCT	3.320
32	A_55_P2092551	LOC100044328	CCATTATATCTGTAGCATTGTGACTTCTGATGTTTCTTA ATAAAGCTTATATTCTGGGC	3.269
33	A_55_P2348126	1500032F14Rik	CATCGAGTCCAGGCCAGCCTCAAAAACAAAACAAA CAAAATAAAATGGCATTCAAATC	3.251
34	A_66_P103185	Olfr1418	AGAGAACTCAAGGATGCTTTGAGGAGAGTGATAATGA AATTGGTCTGATCCAAACACAA	3.248
35	A_55_P1968799	Krtap1-5	CTGCTAAGAAATAGGCCAGACCATTCTACACTTTTCCA CTGGATCCTTCTTATTTTTT	3.245
36	A_55_P1995473	Ptger1	CCTGCTCAAGCACACTCCAGTCCAGATGCACACAGAG GCTGAAAATGCATGTATGGAGT	3.228
37	A_55_P1995055	Prr7	AACTCTAGCCTGACTGCGAGGCTTTTTAAATGCTTCC CTTGACTGCAGGGAGGGGTGG	3.216
38	A_55_P2138718	Gm14483	CTACTAGCTGGGGAGCAAATCAAATATGCTATTA GCATCTAGATCAAACCCAAAAAA	3.215
39	A_51_P220150	Angptl7	TAACCTGAGGTCACTTAACCCATTTCCCTAACTGAG GCTTAGATGACACGAGGGAAAA	3.205
40	A_55_P2315747	4930571B16Rik	TGCTAGAAAGAGAGGTTGGAGTGTTAAGGAACCCTAA TAAAAGTAGGTTTCCAAAGATCT	3.187
41	A_52_P381484	Spon2	CCACAGGAGGAACAAACGAAGAGGGGCAGTTTTTCG AAACTTGGCCCTGTGTGTCGTG	3.182
42	A_55_P2128929	Cc2d2a	AACAAAGATGGAAGAGTACAGAACATCTCATCAGCAA TGGAAGCCTGGAGGAAAGCCCA	3.181
43	A_52_P89335	Tmie	ACCTGGCAGATACAAAGCTTTGAAAACAAGGTAACAG TGTGACAGACCTGAGGCCACTGA	3.152
44	A_55_P2121956	Gck	ACATCAGTGATCCGGGAAGAGAAGCAAGCCACCCACA GCATCTCTCCAGGAAACCACCA	3.151
45	A_51_P462271	Acan	ACAGGCTGGCTGAAGAGAAGCAGAGCCCTCTCCTAGG GACCTTTCATCTGGGTCAACCAA	3.143
46	A_52_P484956	Nnat	TGGATATATTCAACCAGTAATTGAATCCACCTTTACCA AAACAGTTCTCTAACCCTCG	3.105
47	A_55_P2344598	E330037I15Rik	GAGGAGTGCTACAAGTCTGAGGTACCATGATCTACTT AGCAACACCTTCTCTGAAAAA	3.092
48	A_51_P315890	Kcnk6	TGGGAAGTGATGACTATTCTGGTTCTGAAAGCAGAA CTCTGTGAGTTGAACCCTTGTC	3.054
49	A_55_P2452914	N4bp2	AATTGTCTCTGGAGTAGATACAGGCACTTGTAACCCAGA CTGAACCCCAAGATTTTGTCT	3.053
50	A_55_P2002903	Smoc2	GCTCATGTCAATGCTGTCTACAAACGAGTATGATCCTA ACTGTTTTGGATAATCTTTAT	3.044
51	A_51_P282616	4932425I24Rik	GGCTCTATTGAACTTAACTCTGCAATCTAAAAAATA AGACTATTGGTTATTTGGGGGG	3.019
52	A_51_P218653	Jph2	TCGGACCTAAAACCTTGCTCACATCCACTCCATGGACA TTTAAGGAGGCCTCCAGAGAGC	2.991
53	A_51_P507051	Bhlhe22	TTCCAAAAGGGGACCTATTTGCATTCCAAAACAGAAAA ACATCACAGCAATAGATTTTAC	2.983
54	A_55_P2197777	3110001N23Rik	AAGAGTCAGAGCACTCTTGCCCGAATTTATTTAGCAA ACAGAATTGGGCTTGATGACTC	2.976

55	A_52_P409769	Mrv1	CAGCCTTGTGTTTCCAGACGTAAGTGTGAAATGGAATA AAAGTTTCCCACTCAAGATGCC	2.975
56	A_52_P84027	Cyp7a1	TTGTTTTTAAAAACAAGTTTTATGACTCCCTGAACTGAAT GTATCCACATACCTTCCCATG	2.972
57	A_55_P2079732	Myo1h	TTTCAGGTGGCGCTGTATCTAGTCGCTTCTGAGAGCC AACCTAGAGTCTTCCCTGTCC	2.962
58	A_55_P1995104	Btbd19	ACTGGTGGTACGTGGGCAGGCTGCACCCTTTTCCACA GCACCTCGAAGCCTCATCAACAA	2.962
59	A_52_P283055	Slc5a3	GGCTTCAGTTTCAAAGAAAATAGAATTTGATATAAGCC AGGTTACTTCCATCTTGAAAGG	2.956
60	A_55_P1968618	LOC100045418	CTTTATGCTTAGATTAGTTGCCTTCTGTATTTTGTACA GTAACACGAAGCTAACCGTTT	2.947
61	A_52_P87763	Olf860	CTCCATTGTTAGAGTTCCTTCATCTGGGGGAAATGTA AAGCGTCTCTACTTGTGGATC	2.946
62	A_52_P657360	Tnni1	AGGTGTCCATGGATCTGCGGGCCAACTCAAGTCTGT GAAGAAAGAAGACACAGAAAAGG	2.930
63	A_55_P1997115		CTCTTACTGTCAGCAATTACAAAGTAGCTTCTGCCGA ATATTGTTGCAAAGCCCTGTAA	2.914
64	A_51_P208922	Stc2	AAGCAGTGAGTGGGAAGATGAACAGTCTGAGTATTCC GACATCCGGAGGTGAAATGAAAA	2.911
65	A_51_P302520	Myom1	AAGTCATCAGATCTTATTCTATAGATGAGGAGGCCA CCATTGAAGAACACATTAAGGG	2.888
66	A_55_P2049368	Olf1097	CAAAGAAGTAAAAGTGTGTTGTTAGAGTTATGAAG AAGAGAGAGTGCACCCAGAACT	2.882
67	A_52_P28960	Gdf6	CTAAAGTTACTGGAGGTGATTGATATACAAAACATTT TTACAGTATACCTTCTGGACG	2.882
68	A_55_P2080880	Clcnkb	TGACTTCTGGGGTTGCCTGCTGCTAACCAGGAGCTTCT GAGAAAATAAACTGATGTCT	2.866
69	A_51_P372550	Cgref1	CTTCAGTGGAAAGTAGGACTTTCTGTGCAGCTCAGGG AGACCATAAGCTGAGAAGCAGCT	2.865
70	A_55_P2028971	Odz3	AGGAGTTAATTTATGTAAAGTGTAAAAAGTTTATAC TTAAAAATAAAATGATAAAAAC	2.854
71	A_55_P2126363	Wnt10b	GGGTGGGAATGGATAATTTATTTTACTGAGATGTGTTT TTGGTCTCTGTTGAAACTAAA	2.850
72	A_52_P1011	Fgf14	GCTGGAGATGCACCTTAAAGATTTTCATGCAAAGTGTTC TATAACAGATATAAAAAGCTTC	2.840
73	A_66_P118600	Lama1	ATGTTGAACATAAGCCACACGGACAACAGATACCTCTA TTAAATGGTTTAAAACGTCAGT	2.840
74	A_52_P173442	Wscd2	TGGCCTCCTCTGGTACGAACTTCTGTTTGAAGATTC CTCAGGTCAACACTATCATTAA	2.838
75	A_52_P294514	4930542N07Rik	TTCTGGTTTTAGTGTGATAGCTTTCAGGATTAGCTGC ATGAAAGATCCATTCTAATGA	2.838
76	A_52_P249856	Cc2d2a	TGGTTAATATTCAACACCATGATTCTCCACTAAGGAT AAATTTTGATGTCACAAAGCCC	2.826
77	A_51_P501844	Cyp26b1	GTTCTGTGTCTCGTTGTTGTTAGCATTAAATGGGTGATG TAGTCTCACATTCCTAACTATT	2.807
78	A_55_P2143376	Gm6651	CCAAGGCACAATGCCTTGTGTTCTGGGAAAACCATAA ATTCACTTTTATATCCTTCTCC	2.804
79	A_55_P2037121	Tmem106a	TTCAACAGCAACTTCTATCCCATCACAGTGACACAGCT GACGGCCGAGGTGCTCCACCAG	2.803
80	A_55_P1980401	Cbx7	TTAGATGATTTATCTGATAGATGAGGCAAAAATTATTA AAAAATACATTAATGTCCTT	2.801
81	A_52_P505192	Ntn3	TGACCACAGATTTTCTTGACAGACCTGACTCAGTTCA GAAATAGTGTCTGTCCTTCTT	2.794
82	A_55_P2032853	Entpd1	CTAGGCTTTGTGTATGCACATGGATGTGTATGAGAGA GAAAAGTTTCAATTCATCTAAAT	2.792
83	A_55_P2027392	Gpr146	CAAAATTCTGTGAATGTGAAAAAGAACTACTGATGG GATCCACACTTCTGAAGACTATT	2.791

84	A_55_P2132323	Mthfr	AGTAACTACTGCGGCTTGAAACCATCTGCATATGA CCTGCTGCCAGCAGCACCCGGA	2.776
85	A_55_P2428514	Retn	ACTCACGTGCGGAATCCACACACAAGCACATACTT AAAAATAAAACAAAACAGGCTG	2.768
86	A_51_P304397	Cpm	AACAGGAAATAAATGGATGGGGAAGTGTCTCAGCTAC CGCTACAGACCTTCCAGAACGC	2.764
87	A_55_P2099650	Slc24a3	ACTTATCATCCATTGCGGTATGGTTTTCCAGTCCCTGT ACACATCCTGGTTGAATTGT	2.761
88	A_55_P2062627	2210411K11Rik	AATGTGGGCAGACTGAATCTGAGTGTAGACCACACAC TTCAAGAAAAGGTTTGGCAGTG	2.759
89	A_55_P2143832	Col4a4	GTACCCATGCAAACGCCACCCACAGACATACTCATA ACATAGAAAACAAAAGTAAATAA	2.755
90	A_55_P2141088		AAACCAGAAGTGATCCCGTGTAGCCTTCGTTGACAAAT AAAAGACTATTTGTGTTTAAA	2.750
91	A_55_P2086820	Zfp651	ACATGTGGCAAAGCCTTCAAGAACTGTGGTCTCTTCA TGAGCACAACAAGATAGTGCAC	2.749
92	A_55_P2068233	Phactr1	AACTCAATGAGTTTAAAGTACCGAGATGGAAGTCCA CGAGTTAAGTAGACACTTAACCA	2.743
93	A_55_P2141084	Odz4	TCGCCTTATGTTGTCCCACTGGGATAAGAGGATGTGT TCGTTAAGTCTCTTCTGATT	2.732
94	A_55_P1967643	Plb1	CCTGGGAGTTCATGATCTCTTTTTGGAAAGATAAAAA GAAAGAGAGGCCATACTCAGTG	2.699
95	A_55_P2107045	Myl4	GTTACTGTTACGGAGTATTGGACTCACATGGCTTCTCT GACCACAACCTCCCTGGAAA	2.694
96	A_55_P2019294		AGGACTAGTCCATCAGCAGAACCCACCCCAATGAA GCATGCATATATTCATCTTGAAC	2.693
97	A_55_P2333580	BC020402	TTTTTTTGTAGAAGTGTTAAGTTAAATGAAGGCATGT ATTAACAGCACTGGGACCCCC	2.693
98	A_51_P520849	Sfrp2	TCGGCATCTAAGTCTTCAAACATTTGTTGCTCGTTTTA TGCCCTCATGAGCTCTGACCA	2.687
99	A_55_P2160825		GATAATCAGATCTCCAGACAGTTTGTGAACCACTTCA AGTTCATAAACCTCTAGTCTGA	2.680
100	A_55_P1978047	Aven	ACTGGGATCGTATCAAGATACTGAAAAGGAGGTCAA TGGTGAAGTGGAGAATCTCAGC	2.673
101	A_55_P1961180	4930429B21Rik	CTTGTTTCATAGAAATGTAATCTCATGACAGAGAAAA TGGCCCCACAAATTAGAGCTTT	2.666
102	A_55_P2052690	Sym	GTTACTACGGCTGTGGCTCGTCATCTTATACTGTCA GAGATGTGCGGACTTATTTTT	2.664
103	A_55_P2277475	9330179D12Rik	GACTACCTGTAACACCTCACCCATTGCTATGTAATAAG CCTAATAAAGTCGTTGGTTTCC	2.664
104	A_52_P446457	Ly6g6f	CCAGGGTCTCGGGACAGAGAACCCTCAGTTCCTCATT TCAAGCCTGAAGTCCAGGTCTA	2.664
105	A_52_P498193	Aldh1l2	TAAATTGCCTTCCTAAGTTTTGCTTTTTGTTTCTGATT TCAGGATTTATATGGGGCGG	2.663
106	A_52_P362981		CAGGTTCTCATTGTAGATGGAGTGTTCGCTGTAGTA CACCAAGTTGACCAAAAACTAA	2.658
107	A_66_P105711	Ap4s1	CCAGTGCCATAACTTTTAAAGGATATTGCAAAGAACT GGGAAAGGGTAAAAAATGATC	2.650
108	A_55_P2145237	Gm7210	ATTTCAAATTCCTTCATCAGTGCCTGCAGGAGCCCAG GACTAGATCTCAAGCTTCTTA	2.639
109	A_55_P2133948	Olf1465	AGCATGAGGAACAAAGAAGTCAAGCGTGCAATCACAA ACGTTTTCCACAAAGCAAATAG	2.632
110	A_55_P2240823	Epb4.1	AACATCATGACAACAGAGAAGAGTTTAGCGGCTGAAG CTGAGAATTCTCAGCACCAGCAA	2.622
111	A_55_P2052416	lqsec1	GCAGAGCAAATCTGAGTCTGACTACTCAGATGGGGAC AATGACAGCATCAACAGCACCTC	2.614
112	A_52_P16356		CTGCCGTTAACCGTGCACATACTAATGTTCACTTGTGT GGGAATCCAATGAAAGAAAAA	2.600

113	A_51_P220135	Nfatc1	ATGCCCTTTAAAAATGAGGACAATAGCTTTGTTGCATT CTCAAACAAGGACATCAGTGAA	2.600
114	A_55_P2167236	Olf1184	ATTAAGGAATTACTCTGCAGAAGGAAGACACAAAGCC CTTCTACTCTGCATCTCATAT	2.581
115	A_51_P487555	Cd7	GGAGGTACCTGCCTTGAGCCGCTGGCCAGGAAAA TTAAATAAACACACAAATACATT	2.580
116	A_55_P2073694	Gm266	TTCTGGAAATCACGACCAAGAGCAAACGATGGTGG ACCGCGTGTTCACGAGGTGGTG	2.577
117	A_55_P2086785	Olf1362	TTGTTTATAGTCTCCGTAATAAGGATGTGAAAGGTGCC CTCCACAGACTACTGAGACAGG	2.573
118	A_55_P2302240	AU017834	TTTCTGGGTGCATTTTCTCAACACATTGGGTTGCACTC TTTCTTTAAAGCTCTCTCCC	2.569
119	A_51_P409010	Comp	CTGCGTACCGTTGCAATGATACAATCCCTGAGGACTA CGAGAGTACCGGCTGCAGAGA	2.567
120	A_51_P203182	Apob48r	GAGTTGGGGAACGTTGCCAGGAATCCAAGCACATA GGAGTAGAGAGGGTTCTGTGTG	2.560
121	A_55_P2081318	Gnas	ATGGGGGACATTGAAGGGATTTGCTGGAGCCATCCCC AACAAACAGCAAACATAAACATT	2.549
122	A_51_P456721	Azgp1	AGACTGAGTTCCTCTCAATGTCAGATCAATCACCTTG CCTTGTAACCTCTCTTGAT	2.546
123	A_66_P101724	Fam124a	CCATGTCATGACCCAAAGCCACACAGGGTGTCCAAG GCATGCTATTGCCTCCAACAACA	2.538
124	A_55_P2114626	Hiomt	GACATCGGCGGCGGGGAAGCGACATCACAGACAGGA AGTGAAGTCGGCACCCAGGACTGA	2.534
125	A_52_P103998	Htr1b	CATCATCTACCATGTCCAATGAGGACTTCAAACAAG CGTTCACAAAAGTATACGCTT	2.527
126	A_55_P2165199	Cxcr6	AATGTATAAAACAGAGCTTAAGACTTTAACAAATACAA GAGGACTCTGGTGGCTTTGCTC	2.524
127	A_55_P2034968		AGAACAAGACTCCTAACTGCCATGTGCCAGAATGAGA TGGTGAAAAACAAACAGATCTGC	2.523
128	A_55_P2089520	Col10a1	GCCCGGAGTATTTAATCTACTTGGTATTACGAAGCAAT AAAATGACATGAATAGACCTTT	2.523
129	A_51_P444822	Olf1574	TACATTATGAGGAGCCTTAGAGGAAGGTGGGCTAGAA GGAGACAGTTTTCCAGTACATGA	2.522
130	A_51_P204442	Phf19	GTCAATTTGTGGCTTCTGTTGGCTTCAGTGAACATG GCAACCTCCAACACGTGTTTTT	2.518
131	A_52_P386682		CCTAGGTGATGCTGTCTTACATACAGCCTAAGACAGTC CTCTGAAAATGGCTTACTCTGT	2.513
132	A_55_P2401624	C630004L07Rik	GGATGCCTTATTACTAAGAAGCACACACAGAATTG AAAACACTTAAATAAATGAGCA	2.510
133	A_55_P2009988	Trib3	GGTTAAGTGTGTATTTTCATCATGTGCCAATAAAAGA GAGCTGTGTGTTTGTATGTG	2.505
134	A_51_P148684	Pou6f2	AAAGACTTGCCCCAGTCATCATCTCCCTTGATGTAAA AGACTAAAAACAAAAACTAC	2.504
135	A_55_P2112142		CAGGAAAAACAAACATATGTTTCTCATTAAAGAGTGCC TTCCACTCCAACACAAAACC	2.501
136	A_51_P218953	Zfp536	CAGACTTGTGGTAAGTTTTAGAAATCCTCTTCTTCA GTTTCAATTTCCACAAAACGTC	2.494
137	A_51_P510882	Adam12	GAAAATCAAGTTAGCACTAATTACAAAATGCTTTTGAT GCAACTGAAATTTCCCAATGGC	2.494
138	A_51_P204247	C8a	GAACCTGGATGGACTTTTTAACAGATCAACATGGAGG AGACTTTTGAAATAGAAATCCAG	2.494
139	A_52_P495869	Mafb	GCCGCAACGCAACAGAAATGTTTTTAATTCATGTAA AATAAGGGATCAATTTCAACCC	2.491
140	A_55_P1961127	H19	TAGTCTGGAAGCAGTTCATCATAAAGTTCACATG CCCTACTTCATCCTTTGCCCT	2.485
141	A_55_P1963439	LOC100048608	ACAGTACCACCTTGAAGGGAACCTCTCTTAAGGCAA CAATGGTAAAGTTGGGACTCAT	2.478



142	A_65_P11603	Ldb3	GCATAGTGTTAAGATTAAGGCTGAATGTCGATAGGTT ACCATCACATCTTTACTAGTGCA	2.476
143	A_51_P519648	Mical3	AGAAACAAAAGATATCCACCTGGAAATGGAGAACATG GTGAATCCCGAACCCTCCCAA	2.475
144	A_51_P207706	Fam180a	CCTGGTAATGAGCAGACTTCTGAGATATACTTACACAC ATACCAAGAGTAGGGACTGAG	2.472
145	A_51_P207591	Anxa8	ATCCTCTGATCGTGGTCTCCGAGCCTGAAGAACATGAC AGAACTCTTCTCAATATTCGTT	2.468
146	A_55_P2052696	Sym	GTAAGCTAACACTGGAAAGGAAAATAGGTGCGTTTTT CTCTTCTCATCTTAAAAACA	2.464
147	A_55_P2107901	Dlk2	AAGACTTGTGAAGTGTCTACCTGCTCCAGAGCCTGC CTCAGTGGGCCACCCACAATG	2.463
148	A_55_P2054688		CCCACAGATTGCCACTACATATTCTATGAGTGTTAGGT CATGATGGAATTAAGAATAT	2.462
149	A_55_P2396370	A730056I06Rik	GTTTCATGATAGCCTGGGCTACAGCATGATACCCTGTC TGGAAAAAATAAAAAATAAC	2.461
150	A_55_P2122096	Gm2327	ATTCCTGAACTAACAGTCTCTAATCTGCTGAAAGGC AGCTGGCTAACTGCTGGTGTCT	2.446
151	A_52_P525183	Acot2	GGGGAAACCTCATATATATTATCACAATGTCAGTTCAG GTTAGTTCATTTGAACATATTC	2.437
152	A_55_P2119927	LOC100047419	AGCGCTTTCAGACACGAGAGACTTCAGAAGATAATAC TAAACAGAATAAACGCAAAAAA	2.435
153	A_55_P2172935		CTAACTCAGTTACTATGGATGGACAAGGTTTGCAGGTA ATGGATTCAAAGTTCAAATTAT	2.434
154	A_55_P2013630	LOC100046931	ACAGTCACTTTGAAAGCGGCAGACTGGCCAAAAGCGC AAGGCTCATGGAAGGTGCCCT	2.433
155	A_55_P1958597	Slc27a3	AGGGTTTTCGGGTATCTTTTGTATATGGAGTCATTATT TGTAATAAACAGCTGGAGCTT	2.432
156	A_55_P2131989		AGTTCGTAGGGCTCAGTGGTGAAAGCAGCTTATTC GCACCGAAAAACAACTACAAA	2.427
157	A_51_P302942	Rasl10a	GGACAGGTCAGTTTTACCTGAGACCTTATTGGGCATA AGCACAGATGAAAGGACTTGA	2.422
158	A_55_P2063312	Mgll	TATGATGAGCTGGCTCATATGTTGAAGGGGCTGGACA TGCTGGTATTTGCCATGACCAT	2.421
159	A_52_P622694	Adal	GAAGTTGGCATTGCATCTTGCCGAGATCCAAACAGG GAAAAAGAAAATCAGATGCTGCT	2.421
160	A_65_P19089	Esrrg	GGCAGTCTTATGTGCAAAGATCGTGAATGGACAAAA AAAAAATTAAGCTTACAATG	2.419
161	A_55_P2232325		GTCATCTAGGTATCTCAGCCACACGAAAAGGATTTTAA ATAAATTATACTGCTATTGGCC	2.417
162	A_55_P2144532	LOC100045235	AAACGAAACAACAATGATAAGAGCTACCCACACTGGG TCCACGGGCGAGAAAAACATATC	2.416
163	A_55_P2094434	Gm3906	AATTCACATCCCATCGAGCAGGCCAGATGTATCAGCAC ATGTTTTTAACCCAGCACTTG	2.416
164	A_55_P2431897	Thap6	GAAAAGAGAAAACTTCACTGTAGAAAAAATTCCTTC TCAAAACCTTCCCATCACCCA	2.414
165	A_55_P1990067		ATAATTTTGAAGACTCCTGTTGGCTCCAGAAGAGAT ATCCTGGTCTTGACCTAGGTGG	2.414
166	A_55_P1962209	Cxcr6	ACAGAGCTTAAGACTTTAACAAATACAAGAGGACTCT GGTGGCTTTGCTCATCTAAAAAA	2.414
167	A_55_P2297806	Mapkbp1	GTAAGACACCTTCGGCAGAGCAAAGTCACATCACCCG TCTCCTGAGAGACCTTCTCTC	2.413
168	A_51_P442964	Casc5	AGATGGACACTATCCTCAAGAAGATCAATAACTGTCTC GCTGAAGTGGAAACAGAACTA	2.412
169	A_55_P2206491	1810062O18Rik	CCACGAATAGTGACGGTGTTCACAGCATGTATTTTT AATATCTCATGAATACTAACAG	2.408
170	A_55_P2302290	E230012P03	GAGACCCTATGAGGGTGCCATGGGAGAAGGTATTTTC AGAATAAAAAGTTTTCTGTACTCC	2.407

171	A_52_P513123	Dna2	AACTACCAACTTCGGGTCTGATTCCCAAATCATACAAG TTACATTTAAACAGTCAGACAG	2.405
172	A_55_P2029962	Gm1998	CAGGTGAAAAGCCCTATCAATGTACAGAATGCAAGAA AGCATTTTTCTCCAAGAAACATC	2.402
173	A_51_P264495	Pgam2	ATGGGAACAGCCTTCGGGGCATTGTGAAACATCTGGA AGGGATGTCCGACCAGGCCATCA	2.398
174	A_55_P2014154	Cacna1c	TGACGCCTGCGACATGACAATAGAGGAGATGGAGAA CGCCGACAGACAACATCCTCAGTGG	2.397
175	A_51_P185593	Sym	AGTTCCTCTGAGATCAGAACTTTCCCTATAGGTTCAA ACTAGGAAGCATGCACTAACT	2.396
176	A_55_P2014144	Olftr830	AACAGGGATATGAAGGAGGCCCTGAAGAAAGTTATTG GTAGGACAGCTTCTTCTGTGA	2.395
177	A_51_P106799	Pparg	GCAGGAAAGTCCCACCGCTGACAACGTGTTCTTCTA TTGATTGCACTATTATTTTGGAG	2.391
178	A_55_P2079669	Bcat1	ACGATGGAGAATGGCCCAAGCTTGAAGTCAATCC TGGGAAAGCTGACTGATATCCAG	2.389
179	A_55_P2167733	U2af2	TTAAAGAGCTGCTGACATCCTTTGGGCCTCAAGGC CTTCAACTTGGTTAAGGATAGT	2.389
180	A_55_P2004179	Col2a1	GTCTACACAATGGTGCTATTCTGTGTCAAACACCTCT GTATTTTTTAAACATCAATTG	2.378
181	A_55_P1995060	EG667885	GACATGGAAGTCATCCTGATCTACGTCAAATTTGTTCA TGCTCAGAAAATTAATTTACG	2.375
182	A_52_P620448	Mab21l1	GAGACAGTGCAAACAATCTCTTCTTTAAAGGAGTAA CAACACAACATTTAACCATCAT	2.374
183	A_66_P119350	2310040G24Rik	TGCCATACAGGGAGAAGACAGTTCACAGATCATAATA AAACCTAAAAGGAAACCTATCTA	2.371
184	A_52_P19532	Fgd3	CAAGATATTGTGAAACCAAACGCAGCCTGCACGTTTCA CATAACAGGAAGAAAAAGTCC	2.371
185	A_55_P2083197	Maml2	AGGAAGGCTAGCAAACATGCTAAGGCTACAGTCGCGA CTGCCACTACCACAGCTCCTCCA	2.370
186	A_55_P2049717	Agrp	CTAGCCAATGGATGTTGTTGGGCAAAGGCAGGGGAT GAGAATAAAGGATGGGACGGTTT	2.368
187	A_55_P2011772	Oscp1	CAGGCCATTCTGGCTGCATAACAAGATAGATCTTTTAA AAAACCAAAACCAAAACAAAAC	2.364
188	A_51_P384693	Kirrel3	GACATGGTACATTCTGTTCTCCAAGGATTGGGGCTAC TTTGCAGAGGACCCTAGAAGTCTG	2.362
189	A_51_P163261	Gm6985	AAGGGGAAAGCCAATGCCAGTGAGGATGCAAATAAT CCTGCAGAAAATGGAGATGCCAAA	2.354
190	A_51_P213691	Scnn1a	TGGGTAGACTGAACTGTGCTCAGGGATGAGCTTTGCT CATTTTTGTATCCTCCGTTCTA	2.351
191	A_55_P2324425	5830403F22Rik	GTTGCCATGCCATTATGAATGTCCCCTCTGGAACCACA AGCCAAAATAAAGCCTTCTACA	2.350
192	A_55_P2074353	Sym	TGGCAAATCACAGTTATGAAGTGGCAATGGCGTGAT TTTATGGTTGGGGTCCAGCACA	2.350
193	A_55_P2120089	Zmynd11	GCTTGTAAACAAAATCAGCAGCAAAAACAAAATCAAA AGCCAAAACACTACCTGACTCAG	2.344
194	A_55_P1969977	Myo15	ACCAGGTACACATGTGATGCAGACATATGTGCAGGCA AAATACCCATATCCATAAATAAA	2.340
195	A_55_P1965584		GCCGCCTTTTCAGAAACCAAGAGAAAATGGTGGGAG GCGAAAAGAAAACAAATAAAA	2.336
196	A_51_P145511	Prl2a1	CTTTTCATCATATCTTCGCTGAGCCACTGCTTGATGAT ATATTGCTGTGAACTTCCTT	2.330
197	A_55_P1990066	LOC100045975	CAACAATGACTTGTGGTCTGGGAAAACATAACATTCAT TTTTATATCCTCTCCCCCTGT	2.324
198	A_55_P1976849	D130009I18Rik	ACTTTCATCTGTAACACAGACAGCTAAGTAAGA GGCTGACTGAAGTAGTCTTGG	2.323
199	A_55_P2257765	Gm7111	TCAGTAGATCATCTGATGTTTTCTAGCTTTGTTCTA CTGAGAAGCAAGTAGCAATCC	2.321

200	A_55_P2005549	Tnn	GTTTTCTGTAACCAAGTCAGTGACCTTTGAAGTAACTT AAATTCCTACTCAAGAAAAACAC	2.317
201	A_55_P2180944	Tmco4	AAGGACTGGGCCTTGGTAAGCATGGATTACATGAGGG GGGACCAATAAACTGATTATC	2.313
202	A_65_P04284	Erap1	ATGCAGAGTGCATTAGATCTGTATCAGAAATATCTCG TTTTAAGATATACTTGTGAGTC	2.312
203	A_52_P47126	Maml3	TTGCAGCATTCCAATCAGAGTGGAAATGGGCATCCCAC ACAACCAATCCCAGGGACCCAGG	2.311
204	A_55_P2094963	Gm10105	CAAAGCCAGGGCCCAAACCTAAAAAGGTCCCTACAAA GAAGGGAGAGAAGGTACCCAAGG	2.307
205	A_55_P1956752	Ska2l-ps	TGCAACAGAGCCATTAAGTCTCACATGCCGGACTGAT AAAAAGAATGTTAACGAGGAA	2.305
206	A_52_P167278	Mthfd1l	CTTTGCAAGAGTGTGAACTAAAAGCTAATGCTCCGTC TTTGAGATTTCTTTTCATCT	2.305
207	A_55_P2011560	1810009J06Rik	CCATTTCTTTTCTTATGCCTGAAATGAGGTTGAAA TAAATACATTTCTGCTGCTCT	2.303
208	A_55_P2234164	LOC100038760	CCAAAAGTTCTCCACACCTGAGAAAACCTGGCTCCCAA AATAAAGAACAGAGTTGTTAAA	2.299
209	A_55_P2112355		AGAAGAGCACTGGTTCCTTCTATAAAAGATTGTGGATC TTCATATGGATAATTCTGCCAT	2.298
210	A_51_P143805	Tmem42	ATAGTGCCTTGATTCTTGTGCACCAGGGAATATTGGAA GACTCTGTGATCATGGGTTACA	2.297
211	A_51_P389864	B3gnt9-ps	CTCATATTTCTCACTCCAGCTTCAAGGAAATCAACAG CTCACATTTTAGTACAAACAGC	2.293
212	A_55_P2184189	Ncf2-rs	GGAAATGTGGACTAACTTACCATTTCCCTATTTAAAT GAACCTGTACACGACAAAAAA	2.293
213	A_55_P2012146	Veph1	CTCTGCCATGATGGAAATATTTATCCTCTGAAACTGT AAACCTCCAATAAACTCTTTC	2.291
214	A_55_P2176025	Gm4532	TGCTCGGGGACAGGACCTAGAGACTGGGTACCAGAG ACAAAGAGATGTAGAAACAGATAA	2.290
215	A_55_P2174541	Dtx3l	GAAAGGGTTGGGCAAGGAGAGAGCTCGTTACACAA TACCAAGTTGCCGACAACTTTAA	2.290
216	A_55_P2002497	Srcap	GCCAAATCAAACCCGAGGCAAGAGCCGAAACTCACAG TTCCTCAAAGCCTATGGCCAGGT	2.289
217	A_55_P2156022	Fam132b	GGGGCTGGAGAACAGCAGCGAGCTTCCACCATCTCA GTAAATGGTGTCTCTATCTACA	2.288
218	A_55_P2162782	Ahnak	TCACCAGGGATTAATGTGGAAGCTCCTGATATTCATAT GAAGGCTCCAAGTCAAGGTG	2.287
219	A_55_P1992789		TTGTTAGGGGGCTATTCAGAGCCACTAATTCTGAGGA GTGTGTTTGTATCTGTCAGGTGT	2.286
220	A_55_P1960053	Hvcn1	AAAGGAACTGAAATCTAGAGAGAAATAACCTTTCATTC CAAGTAATAAACCTTTCCACC	2.285
221	A_55_P2022870		TGATCTCCTTGACAGATGTACCTCTTGATACCTATGTAA GCCAAACACAAACAGGTTGAC	2.281
222	A_51_P117581	Cables1	GTAAGACGCATGATTGGTGTCTTGTGGCTTTTGCAGCT GGGACAAACTACATTTCAAGCT	2.281
223	A_55_P2114863	Mgll	CTTTATGAAGGAGGGAGTATATTTTCTACACAGAGACT GTGTGGAAATATCCTTTGAATT	2.278
224	A_55_P2412859	5830468K08Rik	CAAACCAACCTTAGAAAGGCTACACACAATGGCTAC AATATTTCTAAAATGATACCTTA	2.277
225	A_55_P2205858	Gm7455	ATTACTTCCGAGACTTTAATAAGCTAAAGAATGTGGA TGTGAAGAAGAGAATGTTTCGT	2.274
226	A_51_P201982	Angpt2	ACCTATCTTGATGGCTTAGTTTTAATGGCTGGCTACTA TTTACTATATGGCAAAAATGC	2.273
227	A_55_P2113391		TCAGAGCCCAAACCATCTCCAAACCTGTAAGTGCATA TTGCTTTATAACAGTAAATAG	2.269
228	A_55_P2201020	AI790442	AAAGAAAAAGAAAAGGAGAAAAGAAAAGAAAACAA AAACCTAGTACCTTAGCAAAAAA	2.269

229	A_55_P2020461	Hmgn2	ACAAAACCAAGGTGAAGGACAAGCCACAAAGAAGAT CTGCAAGGTTGTCTGCTAACCTG	2.267
230	A_55_P2007356	lqcg	ATGTCCATCATCTGGATTTTAAAGACGTAAAGAAACCAA CCAAACCAACCAACCAAC	2.266
231	A_55_P2104422	Inadl	AATCTACTGAAGAATGCCTTCGGGCGCATTATCCTGCA GGTATTTTCGATCAATGGAGAAC	2.265
232	A_52_P87843	Aldh1a3	GGGGATTTTGATCTTAAGTTCAGATTGTGTTCAGCA ATGAAAAATAAAGTTGGACAC	2.265
233	A_51_P501656	Kdelc2	AACAAGAAGAAACCAGTTTTAATTATGCGGGAATGAA AGCTTTCATGACCAAAGGCACA	2.262
234	A_55_P2023285	A630075F10Rik	AAGCTCATCCGACTTTCGTCATGCTTACACATGTGTAT CCTTTCCGGAATGGACGGAA	2.261
235	A_55_P2062340	LOC100044039	CCTGGCTTGCGAGCATAAATGCAGGCAATACCGTGTA CTTAATAATAATAATAAATCTTTA	2.259
236	A_65_P05872		TCTGGGAGGATTCTGTATTGACTGTTACATTTCCCAA CTGAAGGTACCCAGGTTCTCT	2.258
237	A_52_P411430	Gm5914	AGACTCGCTTTGAATTCATGAGAAAGAAGAGTGTGAA ACAAGAAGCAAAGATCGGGTTGG	2.257
238	A_55_P2141866	9630025I21Rik	ACACTGTCTACTTTACAGAACACAAGTTTGTTCACTCT CTAGAGAAACTGTTGAAGTAG	2.257
239	A_55_P2094964	Gm10105	AAATCAAGGTGAAGGACAAGCCACAGAGAAGATCTTC AAGGTTGTCTGCTAAACCTGCTC	2.256
240	A_55_P1981291	Spink8	GGAGTGTTAAAAGAGAACAGCACCTTGAGAAAAACAT CTTGATATTAGAAGATACTTGA	2.251
241	A_55_P1978050	Aven	TGCTTACAGCAGCCAACACCTACCTCTGTGTTTGATGG CATCTGAATATATGTATGAGGC	2.248
242	A_52_P274496	Tspan18	TTGGAATTTGTAATGTCCCTTGCAAGTAGGAAACAGA GCTAATTTATCATTGTATCTCCC	2.247
243	A_55_P2160421	Gm8619	CTTCTTTAAACAGTCTCTTGTAACCATAACTGAAACT ATCTTGAAGCCTGAATACTCC	2.245
244	A_55_P2168497	Slc9a1	GGACAAGGAGGAAGAGATCCGCAAATCTTGAGGAG CAATCTGCAGAAAACCCGGCAACG	2.244
245	A_55_P2018697	Ldhd	AACTGAAGCACCTTCTCAAGCTGTTATGGTGACAAT AGAAATACAGATGAACCTAACCT	2.243
246	A_52_P81693	LOC100044247	TCAGAGACCTTCTCAGCCAGGAAACCATCAACCACCCC AGCATGGAAACAATGAACAGCC	2.240
247	A_52_P680751	Cux1	ATATCAGCAGAAGCCATACCCATCACAAAAACCATCG AGGAACTTGCCACACAACCTCAA	2.237
248	A_55_P1993789	Hmgn2	GAGCACTGGTTCCTTTTATAAAGGATTGTGGATCTTCA GATTGATAATTCTGCCAAAAG	2.237
249	A_51_P164393	Txndc2	AAGACATCATCCAATCCAAGAAAGAGGACAGGCCCAA GTCCTCAGAAGACATCATCCAAT	2.236
250	A_51_P358906	U2af2	CCTCTTGAAGAAGATGGGCGAGGAGTGACAGCCGA ATGACAGCCGGCAGCAACTGGAAT	2.230
251	A_55_P2196037	A630031M23Rik	ATAAGAGACGCAAGTCACACAGACACAGTATACTC TCACATAGACACGTCCACATACG	2.230
252	A_55_P1975315	Crygs	TCTGCTGTCTGGCTTGGTCCAAATAGACAACGTAAA TAAAAGCATTGGAATGCATCCC	2.229
253	A_55_P2109877	Gm4718	TGAGCTTGGGGCTTAAATCATTTAGGGTACAGATGATT TTAAGTTGTTTCAGCATAACGC	2.228
254	A_65_P15245	Nrp2	GGTTTCTGTGGCTGTCATTGTCATCTCCAGGTACCTA GACAAATAGAGACCATTGGGAA	2.228
255	A_66_P100586		ATGTAATAAAATGGGATTAGAGTAGACCAATTGGCAA ACCCTGGAACCCAGTGAGAGATT	2.226
256	A_55_P1989738	4930426L09Rik	CTCTCCTGTGTTGGAATAAGCATTATATTGTTGTTA ACCAGTTGGGAGTTCAATTAT	2.226
257	A_51_P210143	Syne2	GCAAGTGCCAAGTGGGAGCCGCTCCGTCATGAAATTT CTTGTATCTCCAACAACTAAAA	2.219

258	A_55_P2214408	A130049A11Rik	TGGGAGGTGGGGAAATCGGATCTTGGGAAGACAAGAA AAACAAAATAAACTTTTTGCGTC	2.214
259	A_55_P2114188	Gm5105	GTGCACACTCACATACCCTGACCCAGGCACATGTAAAT ATACAATAAAAATAAAATGTA	2.214
260	A_55_P1960157	Bcat1	GAGCAGGACACTTTGTTCTTTTGCTGGTGAGGTTCTT TTGTTTTTGTGGTTGTTT	2.213
261	A_55_P2065958	Gm3119	AAGAAGTCAAGAAGTCTCTGGGCTACTTACCCTTCAAC TCCATGTGTACTAGTGATGGC	2.210
262	A_51_P314107	Gsdma	CTAAGCCCATCTCTGATGCTTAAATCCTGAAGATACA GAATCATCAAACCCTTACTAC	2.209
263	A_55_P2114143	LOC100044698	CAGATGTGGTTAAAGGGCTTCTGCCTTTTTGTGACACA ATAAATTATAAACCTGGAAAGA	2.209
264	A_51_P233797	Adh7	CAGATGTGGCATGTAGAGATGTAGAAAATGAATTTTT CAAGAAATGACCATCAAACCAC	2.206
265	A_55_P2148961		CAGGTGGTGACAGACATACAAGCCTGCAAAGCACCC ATACACGTAATAATATATAATT	2.205
266	A_66_P117254		GTGACAGCCAAGCTTTGGAGGCATTGATGTCCCCTG GAATATCCCTGCAGCAAGGCTT	2.204
267	A_55_P1959525	Wbscr25	AGAATGCCAGGCTTGCCACACAAGGCACAGGACACCA AACACAACACACCAGGCACAACA	2.196
268	A_55_P1998912	Txnrd2	GCCCAGTTTTGAACCCTGGCATTCTAGAGCACTAAT AAAGAGGATGTTTTACTAAAGC	2.196
269	A_55_P2102998	Gm3893	AGTAAAGAAAATGTTGAAAGGGGTCTGCCTCAAGCCA AGAGCCCCACCAAGAAAATAAG	2.193
270	A_52_P507498	Plxnc1	GGATCCCATTAGCCAAATGCACAGAATGTCAAATTAG ATGTGTGCTGAAGACAATCAGT	2.193
271	A_55_P2094792	Pcdhga10	AATGATAACAGTCTGAGGTGACCATCACATCTCTCTT CAGTCCAGTGACAGAAGATTCG	2.193
272	A_66_P105526	Mamld1	AAGTCACATGGGTCATCAACTCTGAAGAAGCAGCAAA TCAACACCGGCCTTCCATTTCCC	2.192
273	A_51_P168613	Nuak1	CCAGCTGATTGTGTCTGTTTAGTATTTCCCACCATGCA GTTGACTCCATTAGGAAAACCA	2.192
274	A_55_P2157507	Gm3709	ACCAAGCCTCACAGGATCTACAACACCAGTCTCAAATA TCTTAGATTTTTCAGCAAAAAA	2.191
275	A_55_P2140449	B3galt4	AATGCAGGAAGCTTGAAGCTGGTGAGCGGCATGAA TGGGGAGAGGACTGCACCCTTTTG	2.188
276	A_55_P2046328	Gm6225	CAACATTCTTAGCCATCAGGGAAATGCAATCAGAAC AACTTTGAGATTCTATAGCCAAG	2.186
277	A_55_P2010364	Gm5116	ATGAAGAACTCGATGACATTGATGTACCAAAGTCC GTACCCTAACAAAGCCTGACAGA	2.185
278	A_55_P2102540	Olfml3	TTAGACGGCACCCAGAACGACACGGCTTTTGTCTTCCC AAGGCTGCGTGACTTCACCCTT	2.185
279	A_55_P2034033	Il12rb1	AGTTTTCCCTATTAGAGTATTGGGCACTTAATAAATGGG CCTTCCCAGAGACTGAGAAACT	2.180
280	A_55_P2144461	Suv420h1	GAGGTGGACGACTACAGTCAATATGAGGAGGACAGC ACAGATGAATCCTCATCTTCTGAG	2.178
281	A_55_P1995354	Btnl2	CACACATGTGGTACACAGACATAGATGTAGGCAAAAC ACCCATACATCTAAAATAAAAAT	2.175
282	A_55_P2084617	Fam78a	ATTTTGAGTTTTGAGATTAGATTGAGCGCTCTGACTG GGTCTGCAACCTCCATCCTTT	2.175
283	A_55_P2013928	Dhrs13	TAGGTAGTGAATTTACCCCATTTTTATGGAGGCGGAA TTGGGAAAGGACTAAGTCAGGG	2.174
284	A_55_P2104909	Pisd-ps2	CCAGAAAGCTGTATTGAGTGCACAGAGGAAAAAGAA ATCAGAAAGCAGTCACTACAAGC	2.169
285	A_66_P139618	Stfa2	ATCCCTAACCCCATTTGTAAGAGATGCGGCCATCAA TAAAGAAGCATTTTTGAAATAA	2.168
286	A_55_P2072631	Prr5l	CTCTGCAGAAACTCACAACCTAACTCCTTCTGGTTGT CTGTTTTCAAAATAGATACAA	2.166

287	A_55_P2233462	2700022O18Rik	AATTAGACTCCATTTCCACAACAAAAGGAGACAACCCT AACTTACAACCAGCCATTAAGC	2.166
288	A_55_P2107502	Fat1	CAATGGTCTTGTAAAGGTTTTACTGAAAATATCATT AGCCAGCCTTTCTACTGACAA	2.166
289	A_51_P279247	4930403N07Rik	TGAAGTAAATTTCTAACCAACAAAATAAGTGAGCTG AAGAGCATGAATGAAGTTCTGGG	2.161
290	A_52_P399095	9030224M15Rik	TTCTGAAGAAGGACCTTTCAACGCTAGCAGCTGTTA TACCTTGAGTTGGGTGAATACA	2.160
291	A_66_P105244	Tor1aip1	CCATTAAGAAGCCCAAGACTTGACTCAACATACCAAC AAATGGAAATACTAAAACGAAT	2.160
292	A_55_P1998995	Spep	TCCTGGCTGCTGAACGGGGCGATGCTGGTTTCTACAC ATGCAAGGCGGTCAACGAATATG	2.159
293	A_51_P160824	Cspg4	CTGACCCAGAACTATTGCAGTTTTGCCGGACACCCAAT CCTGCCCTCAGGAATGGCCAGT	2.158
294	A_55_P2085165	Gm5951	ATGTGGCTCCACTTCGAGGATTCATAGAAACAGCTGTT GTATTCAAGAAAACGGGGTGC	2.157
295	A_55_P2369191	Ggta1	GTCAAGGTAGCTTGGCAGACAAAAGAGTATAATTTGG TTAGAAATAATGTCTGACTTCAA	2.156
296	A_52_P298548	Nbn	GCTTTCTCCAATGAAATTTCTGTTGCAAATAAAAATA AGGATTGGACTTCTCAGCAGCA	2.153
297	A_52_P304128	Mmp14	GGACAGCGAGTACCCTAAAAACATCAAAGTCTGGGAA GGAATCCCTGAATCTCCAGGGG	2.152
298	A_55_P2063316	Mgll	AATTAATAAGAAGCCAATGTGCACTACAGCTCACCGT AATAAAAACCAGTCTTTGG	2.151
299	A_55_P2262560	5730471H19Rik	ACTTGCCATAAAGATAAGAGGCATGCAAGAACAATCT CTGGACAGGCCAGTTGAGATTG	2.151
300	A_52_P339791	Hdgp	GGATTGATGAGATGCCTGAGGCTGCAGTGAAGTCAAC AGCCAACAATACCAAGTCTTTT	2.150
301	A_55_P2162136	Hmgn2	GCTGACGCCGGAAGGATGCGAATAATCCTGCAGAAA ATGGAGATGCCAAAACAGACCAG	2.149
302	A_55_P2011490	Gm16510	AGTAAGGATGCGAATGTTCTGCAGAAAATGGAGATG CCAAAACAGACCAGGCACAGAAA	2.148
303	A_55_P2389818	A830035O19Rik	ATCCACTCCAGGGACTGTGCTCCTACGAATAAGAAATA CAAATAAAATATGGGGACAGCG	2.147
304	A_55_P2392972	K230015D01Rik	CTTCTCCAATGATGGATTATGATCTGGAAGGGTAAGA TGAAATAAACTTTTCTTCCC	2.146
305	A_51_P386829	Gm5577	GTGAGCTAGTGCATATTTTCACTAAACTTTAATCTTT GCTTGCACTTAAATGACGTGG	2.144
306	A_55_P2152069		TGCTCTGGATGAGGGAGAAGCAGGAAAGCAAAGAGC TCTTAATAAAAAGAAATGCCCTCCA	2.142
307	A_52_P117393	Tlr6	TTATGAAGTTAGCCTTAGTCAATGAGGATGATGTGAA AACTTGAACCTTGGGTTTCTAAC	2.142
308	A_55_P2163428	Foxm1	TTGTCTGGACACAATGAATGATAGCCTCAGCAAGATC CTTCTAGACATCAGTTCCCTG	2.140
309	A_55_P2039289	Hspb6	ACATTTCCCATCTCCGAGGCCTTCTACCATCAGTCCC CAATAAATGCACCTTGAGATTT	2.139
310	A_51_P482611	Dusp21	TCCTACATCAAGATAAAAAACAATGACCTTGGACCTATG GTTGGTTTAAAAACAGAAAGAG	2.139
311	A_55_P2005175		CCTGGCCTAGCAAGTAGACAACATACTTAATATTTAAC AGATATTTAATACAGAGACCTG	2.139
312	A_55_P1954331	Murc	TTGGAGAAGCTTGAGATCTGAGGTGGTGTACAGAGTT TGTGAGAACAAGACACACGACAA	2.137
313	A_55_P2006210	Fgf22	GCTCTGCTTTTTGAGTAGGTGATTTTAAATAGCTTTC CAGATAACACACATTTCCCTT	2.132
314	A_55_P2045903	LOC100044822	GTTATGGTCAACATTATGGTCAACAGTCTGGCTATGGT GGACAGCAACAAGCTATGGAC	2.130
315	A_55_P2081432	LOC635676	GTCTTCGACGCATCTGGTTTGTGTTTGTGTTTGTGTTT ACAGCTTCTTAATAAAATTG	2.130

316	A_55_P2019068	Flii	TATATGGGAAAAAGAACATCAAATTGGAGCCTGTGCC CCTCAAAGGCTCCTACTAGATC	2.129
317	A_51_P352381	Dhrs4	TTTCTTTGGAAATCTAATGGATGTCACAGAGGAGGTGT GGGACAAGTTTTGAGCATTAA	2.129
318	A_66_P111714	Utp20	TTGAAGAAACATAAAAATAAGAGTGAAGCAAAGAAG AGGAAGATAGAGTTCTCTGCGCCCC	2.126
319	A_55_P1958876	4833422C13Rik	GACCACCAAATAGATTCTACCAGAAAAGAAAATCCTCC CACCACATAATAATTAACAC	2.125
320	A_55_P2167070	Kif5a	TCAAAACCAACAGAAACATTTGCTAAAAAGCCCAAAT CTCATTATAGCCAACCCTGAC	2.122
321	A_55_P2169188	Ccdc23	GCCTTCTCATCTGCTGCTCACCCGGGGTTGGTAGGGAA ATGGCCAGGAAATGACTACTGT	2.117
322	A_51_P112762	Slc5a3	GAAGAGACTCCACAAGTAAAGTGATCCTAACATTG GACTTTTTGCTGTGTGTTCACTT	2.115
323	A_55_P1965876	Opn1mw	CATCAAAGCTTTGGCCATGTTTTACCTCCCTTCTCATCT ATCCTTGTAATAATAACATAA	2.113
324	A_52_P657123	Gm10270	TGGTAAGGATGCAAATAATCCTGCAGAAAATAGAGAT GCCAAAACAGACCAGACACAGAA	2.112
325	A_55_P2140162	Gm14725	ATGTTACCTTAGATATGGCCGGACGTTGTCTTCATACG ACCCATGCAGATACATCCTGAA	2.111
326	A_55_P1996742	Rbm14	TATGGGGCTCAAGCATCTATTGGCCTGTCAGGCTCATA TGGAGCTCAGTCTGCTGCTGCG	2.110
327	A_55_P1958906	Col17a1	GGCACAGTTGGTTTTTATTAAGCACTTCCACTGTCTA AAAACATTTGTATGTAACCTG	2.108
328	A_51_P207330	Tgm6	TTTCTGAAGCCATAAGACAAAGCAGAAACAAGTTGA GAACCAAGTGGTCCCCAACTCA	2.107
329	A_55_P2246235	Tpm3	AAGAAGCTGAAAGGGACAGAGGATGAGCTGGACAAG TATTCGGAAGCTTTAAAGGATGCT	2.107
330	A_52_P257502	Igfbp4	GAGAAGAGAAACCTCATTCTGGAGTGAGAGAGAAA GAAAGTGGTGAACATTGAACGCC	2.105
331	A_55_P1954985	Foxn3	CCAGTACCTGGCCTTCAAAGGTGACATTTTCAAGCTAA GGTTAAAAAACAAAAACAAAA	2.103
332	A_52_P502267	Epc2	TAATGGGATCATGAGCATGAAATGGGATCCTGCATCA CTTGTTTTAACTATTTATTTGTC	2.103
333	A_55_P2013143	Esrp2	ATGGTGTGACAGCCAGAAAACCTTCCATCTGTCTTTGG CCCTCAAATACTGAGTTTGAAG	2.102
334	A_55_P2176894	Gm2181	AAAGAAAGAAAGAAAGAGAGAAAACCTGGAATATCA ATCAACCAACCAACAATCAATCA	2.102
335	A_55_P1965338	Anxa8	GTATACCGCCACCTAGCATTACCTCTGAGCAAACGG AAACATCAACATGAAGAAAGAA	2.101
336	A_55_P2157423	Gm8784	ATTGTAGAGGACGTATGAGACGAGTGACGCAAGTATG GGCTGTCAAATCCATTGACATT	2.097
337	A_55_P2056493		TTGGGTGTGGCCGTCATTGGCATCGATGAGGGGCGAGT TTGTAAGTCAGCCTGCAGCATAA	2.096
338	A_51_P207622	Fmod	GGCAAGCGTGGTTTTCAAACATGAGAAAGAGCCTCT GCTCATCCTTTGGTCTAGTATGA	2.096
339	A_52_P681557		AGGGAGTCTAATGTAGACATGGAGACCTGATAAGGTT TTAGATAATTTTGAAGTATCTG	2.092
340	A_51_P430259	1700009P17Rik	TTTTAGAGACTGACCGAAATAGGTGAGACCCTGCCTGT ATTCAGAAATGTGGAACAGAGA	2.089
341	A_51_P451458	Mamdc2	ATGCAGTGTTTTATGGTAACAATTATTCTGGAAATAAG GTCGCCCATGGAGCCCCAGGA	2.089
342	A_51_P342926	Omd	TAAAGATCAGAAGCTGCGTTTAAAGATGTTGGTAAAAAT GGCTTACTTCATAAGCTTAGAG	2.088
343	A_55_P2026214	Gm5899	GATGCGAATAATCCTGCAGAAAATGGAGATGGCAAAA CAGACCAGGCACAGAAAGCATAA	2.087
344	A_55_P2000280	Mthfd1l	ACAGAAACGGAGCAAGTTAAAGGCTTGTCTAATGGA ATGAAACCCACAGGACTGGGCAA	2.086

345	A_55_P2168014	Prmt7	CACAGGCCTCTTGTCATGATGGCAGTTACTGCAGGG GCTGACTTCTGCTATGCTATCGA	2.086
346	A_51_P203653	4930417M19Rik	CATCTGGGAGAACAGCAGAGGCTACTATTTCCAGGCC TTTCTCCCATGGAAACATTATAT	2.082
347	A_55_P2133360	Gm4608	AAACGCAGACACGCTAAGGTTTAAACAGCATCCACCAA GCATTACTAAAATCCACCCGGAA	2.082
348	A_51_P121179	Fam132b	TGTGTCATATTGCTAGGCAGAATATTTTATGTAATGG ATCACACAAAGCCCTAACAAATG	2.081
349	A_55_P2096762	Arhgdig	TTGTGACTTCAGTGAGGAAGCACCAAGAGGAGCATT GGCAGCTGGCCTCTACGTGGTCA	2.080
350	A_55_P2044982	Zfp74	TGGAAGCTTTTCAGCCAAAAGTCACACCTTGCAGAC ACCAGAGAATCCACTACTA	2.080
351	A_52_P286002	Obsl1	ATGAACGTGCCTACTTTCACAGTTACCATCACAGATGTC TTCTCGTGATCGTCTACCCCA	2.080
352	A_55_P2031636	Igf1	AGAAATGTAATGGAATAAGAGGTCAGCTGACCATCC ACCTGCTTCCCAAGAAGGATACA	2.080
353	A_55_P2028496	Hmgn2l6	TCAGGGTCGGCTTGTAAGCTGTTAAAACAACATC CTTAATGTGAAATGCAACTCTC	2.080
354	A_52_P410685	Krt7	CAGCATCGCAGAGGCTGAGGAACAAGGGGAGCTGGC AATCAAGGATGCTCATGCTAAGCA	2.069
355	A_51_P281593	Ppapdc1b	GAAAATAAATGCAACACTTTCTGCCTTTGTTCAAAG AAATAAATGGCGCAACTAGAGG	2.068
356	A_55_P1983558	Tmed1	TCAAGGAACAGAGGGCATTGTCTGGGCACTGGAGT CAATAAATTATGGTCAGAAAGTT	2.067
357	A_55_P1962224	Afap1l2	GGCATTATTTCTGTATCATAAACACTTGGTGACCTTT ATCAAGTGGTGAGTTAGAATT	2.066
358	A_52_P132761	Stat6	CTAATTTCCAAGATGTCCCAAGAAAAGTCAACGGCT CTATGTTGACTTTCCACAACGC	2.065
359	A_51_P449995	C6	TTGTCTGGACATCAAGGTATACATGCAAGGAAGACTC CTGGACACCTCCCATTTCAAATT	2.064
360	A_51_P245275	H2afx	CTGTCTGGACTGAGCCTCTGGCTTCTGAACTGGAACCT TTGCAGCTATTACAAGTTTACA	2.063
361	A_55_P2037702	Gm10638	AGAGTTTTCTGGACTTCCCGGGGAGACCTTTTATCCA AAATAAATGAAGACCTCATCTC	2.062
362	A_51_P167292	Chi3l3	TGAACATCTTTTCTTCTGTAACCACCATGCTTGTT TCTTGCTCTACAATAAATTC	2.060
363	A_55_P1989524	Fndc1	ACTCAGACCTCGTCAGTGACCCATCTGCCATTGAGAA CTTGAAGCCAAACACAAGGTAT	2.059
364	A_55_P1997696	Plbd1	GATGACAGAAAGCTGCGAATAGGACACCAAAGGCACT CTTAGCTGTATTTCCCATCTGT	2.055
365	A_51_P475342	Chrnbl	CTCCAAGTGATTTTCTTTCCCTAAACTTAACAGGTTTC AGCCTGAATCATCTGCCCGG	2.053
366	A_55_P1974441	Pdgfb	ACTCCAGGCTGCAGGCTTCTTCTGACTCAAGAACCTG GAACAAGTGTGCAGGAGCCTTG	2.052
367	A_55_P2347073	Al662501	TCCTATGATCTGCCAGAAACGGATGCTTCAAGTTACT CTGACCTCGTTTAACTTCGAG	2.051
368	A_55_P2344608	D7Wsu130e	GGCCTTCACTCTGAGCCATCTGTGAGCTGCCAAGCT GAATTTTAAATAAAGCCATT	2.048
369	A_55_P1978241	Artn	ATATATACATATACATTGTAGTCGCGTTGCTGGACC AGCCTGTGCTGAAACCAGTCCC	2.048
370	A_55_P1988058	Tyw3	AGATCAAAATGCCAAGCCCTTTGTATAACGATGTTTAG GAATTTGAAGATAGCTACCACC	2.046
371	A_65_P06446	Tfrcl	TCCTGCTAGATGGAACATAGATTCTTATGTAAGCTGG AACTTTCACAGAATCAAATGT	2.043
372	A_66_P128199	Fzd5	AATTTCACTGGCTTCCACAAGACCTGTACACCTAGAT GCAGGACTCTGTGAAGGTCTTA	2.043
373	A_55_P2007708	Nanog	CCATGATGAACCGATGCCAGCTGGACTAGTTTAAACA AAATAAAACTAATTTTACCTT	2.042



374	A_55_P2148323	2810021J22Rik	AAAGAATGTAGCAAAGCATTTAGTGTCAAGTCCTATCT CACTATCCATCAGAAAACCTCAC	2.041
375	A_51_P225793	Prr5l	TAAATGGTGCCTTACCGTCACTCCAGTTTCAGGAACCA GCCACATTTCTGGTGTGTATAT	2.039
376	A_55_P1979863	Syne2	CAGGGGTTGGTAAAGAAAAGTGGAACTATTTGTGATA TGCAACTCAGATGTTTCTCATT	2.039
377	A_55_P2029046	Fgd3	TGTGAGGTTTCAGACGAGTTCTCTGTGGGCAGGTGC CATGCTTATCTGCATAAATAAAT	2.038
378	A_55_P2124331	LOC640017	AGAAGAAAAGAAAAGCTCTCACCGATACATCTTCGAC CCTCCAAGTACCTCAATTTCAA	2.035
379	A_55_P2384593	Gpc6	GCATTCTCTTAACATAACAACCTCACAAACAAACAAGTC AAGACAAAAAGAGAGAGAGGAT	2.031
380	A_55_P2200029	Dleu2	TTTCAGGTTTTGTAACAGTTTCAGTAGTTAAAAGCACTT GTGGGCTGGAGAGACACCTCGG	2.030
381	A_66_P132997	Ccdc15	CGCAACTCTCGAAATGCCATTTCGTAATTTTGCTTCTGC ACATAGACGGACTCCAAAACA	2.029
382	A_52_P630632	Rcvtb2	GTATCCTGTGTTCCGAGCTTTCCTGGAGTATCTATACA CAGATAACATCAGCCTATCTCC	2.029
383	A_51_P227345	Dpep1	AGCTCAGGGAAGACTGGACAAGCCCAGAGTTCTGTGTT GTCCGTGCAGAACCACACCCTTT	2.029
384	A_52_P152631	Tmem17	ATGTATGGCACTTCAGACGAAATTGCTTTGTTTCAGTGG AATCTCACCAAGTGTGACAACA	2.029
385	A_52_P233305	Adamts12	GCTCTCAGAAAAGAACCATTTCATTGCATCCCTCAGAA AACAGTACAACCTGAAGATCAAG	2.028
386	A_51_P389636	Kcnn4	GCCACATAGCTCCACATGAACTCACAGAAGAACCAGG CTAAGTACCAAGGACCGAGCTC	2.028
387	A_51_P332003	Aste1	TGAAGTGAAGAATTGATACAAATATCAAACATCAC CTGTTTATGCAAAGCAACTGCTC	2.026
388	A_55_P1966332	Plac9	GAACTGGCTTCAAACCTTCCCACAGGGCCCTTCAGCCC CAAACCTGACTTGCTTGAGAT	2.026
389	A_52_P586141	Adcy7	ACACTTCTGACAAAGTGATTGTTACTGTGTACTTCATA GATGACAGGTCAATGCTCCGA	2.026
390	A_52_P499299		TAACTCAGCAATTACGAATGTTTGCTTTCAAACATCCTT AAGAACAGGATGTCCTAACGA	2.025
391	A_55_P2120308	Cacna1a	GTCTGCTTGAATAACAAAAGAAAAAGAAAAAATT ACCACCATCACTGATTCCTTGC	2.023
392	A_51_P191782	Olfml3	TAAAGGACAACCAATTCTCAAGCCCCTGTGTTTATG CAGAACTCCAGATCCTGGGTAG	2.022
393	A_55_P1973941	Slc7a5	GTGGTTATAATGTCTTTTACTATTGTATTAATGGCTAGC CTGTTACATTAGACTGGGGGG	2.021
394	A_66_P140856	Gm4588	CGACTTTGCAATGAAAAAGCTGAAGAGGCAAAGAAA GACAAATCCAGATCGGAGAGTGAG	2.019
395	A_51_P198137	Ubxn8	GTCTTACTTGACTGGATGATGAAAGTTGGGTACCACAA ATCCCTATATAGACTTTCCACT	2.018
396	A_55_P2030771	Fnbp1	TACTCCTTAATCCTGCAGAGATTCAACCAGGAGCAATG GGAATACTACCATACCCACATC	2.018
397	A_55_P1962429	Maf	GAACAAGCCTTGGTTTACATTAGAATAACGTTATGATT ACAGTATTGAGCTCCACCCCCC	2.015
398	A_55_P2378486	Kcnma1	TGGGTGGGCAGTCAATGTATACATGTAAATCAAAG TCCTGTGAGTGAAGTATTTTTT	2.013
399	A_55_P1960298	Tmem80	GCAGCCTTTGTAGATGCCAAATGAATCTCATCTCCTGT TTTTCTTTTCTAGCCATTTT	2.008
400	A_55_P1966104	Il17d	GCGAACTCCAGCATGGACAAGCTGCTGCTGGGGCCCG CCGACAGGCCTGCGGGGCGCTGA	2.007
401	A_55_P2383877	2810040C05Rik	CATATACAAGACGGGGCAATCCAAAACAGCATAATAT AATTTTCTCCAACCTTGAGAA	2.007
402	A_55_P2133220	E130306D19Rik	CTACCTCTATGTTCTATAATTTATTTCCCACTGGATCT TAATAAAGGTTGTTTTTGC	2.007

403	A_55_P2144456	Suv420h1	CCCTCTTGCTCTGAGGGTTTGTGTGTTTCATGTGTATA CATGTAATTA AAAAGAAAATA	2.006
404	A_51_P162116	Mblac1	ACACAGTCAAGACAAGCAATATTTGTCACGTGCAGCTT TCTAGGAGGCAGCTTCAAACA	2.006
405	A_51_P256945	Opa3	GAGCCTTTATTACATCTCTGAAGACCCTTTTCTAAATG GAGACACACAGGCCCCAGGAT	2.006
406	A_55_P2071970	Nav2	ACACTGAAAATACTTCATGGGAAAGGATCCTCACTGTT GAAATATAAAGGGTTAAATGG	2.003
407	A_55_P2110703		ATGGTTAAACATTCATGACATAGGAATACAGACCACTG ACCACCTGTGACCACCTAGCAC	2.002
408	A_55_P2111825	1700001C02Rik	CCCAGGGAACCTTGGCCTGACCAGGCTGGCTTGCTTG TAATAAAATCTTCAGCCACAACC	2.002
409	A_52_P560146	Gm22	CCCCCAGGTTGTACTGTAAAAGCTACAGCTAATTTGT CTTTCAAATATATCCCACTA	2.001
410	A_52_P593037	Acsl5	GCAGCCAAGATCGGGGTAAAGGGATCATTTGAAGAAC TGTGCAAAAACCAATGTGTAAAG	2.001

**Table S2****a) Up regulated genes in  $\delta$ -treated MEF**

No	ProbeName	Gene Symbol	Sequence	Fold change [ $\sigma$ ] vs [DMSO]
1	A_51_P413376	Zfp42	TGTGCTATTGAAGGGGATGGGGACTTTTGCATA CGGCAGAAAATCAGTTATTTTAACTA	488.161
2	A_55_P2042297	Gm5250	GGATCCTTGCTGTGCATTCTGATGTGAATACCAG GTTACTACTCTAAATAAACATAAAA	155.015
3	A_55_P2067947	Dppa5b	TTCATTTACGGCTATCAAAGCATCAAGGTTCCGGG CTAAATGGTTGCTTCAGTCCATGGCT	123.400
4	A_55_P2003483	Gldc	CACTAATGTGCTGATCTGTCACAGCATAAGTGT CCTCCTTTCAGTGTGCGGACTTTTTT	122.181
5	A_55_P2028171	Dppa5a	CTGCGCATTCTGATGTGAATCCCAAGGTTACCAC TCTAAATAAAAAATAAAATTGAAGTG	94.802
6	A_51_P143712	Tdh	CACAAAGGCCAGAGAAATGAAGTCTGAGTGGT GGTGGCTATCTCTCGGGATCTGCAGCA	78.498
7	A_66_P114804	Gm7325	TGAGTACTTTCAAAGCTTGGTACGCAGCAGGTA GTCAATAAACGAGGACAGTGTGTTGTT	78.169
8	A_52_P537571	Trap1a	TGTAGGATGATTTATTTCTCCACGACCCTAATTT CCTGGTGTCTATACCAGTGAACCCT	69.488
9	A_55_P1978571	Otx2	TTTCAGGGCTGTGTGGATTGTGCGACTGATTGTC CTAGATGCACACTTTATTTAAAAA	58.380
10	A_55_P1971006	1190003J15Rik	GAAGATATTCTAGCTGCCCTGGAGTTTCATAATG GGAACTGTGACTTGGGTGTCAATAA	55.346
11	A_51_P491635	Ly6g6e	TACCCGAGGGTCTCAAGAACAGAGGGCTACCTT GGGAACCATAAAGAGTGTATTTAATA	54.093
12	A_55_P2137701	Gm13138	CTGTCAACATCTCCTTCTCATTGCCTGTAAATA AAGCTGAATATTTTAAACAAGGTAA	53.197
13	A_55_P1960342	Tcl1	GTGTGGGATTTTATGTGGTTCTATTTTAGAGATA CGGCTGGATTAATAAAGCTTTGTAG	52.202
14	A_55_P2027127	Triml2	CCCAAGATCAAAGAGACACAAAAATAAGATCC AGACTTTGTGAACACCACTTATGTAAT	51.429
15	A_55_P2101526	L1td1	GAAGAGACTGCAGGCTGACTGACTCAACAAGAT TACATTGCTTTATTATTTACTATTACA	46.675
16	A_51_P508580	Tcf15	CCATCCAGGCCTAGCTGGCCAGGGACAAGGCAG AAATTTTAGAAAACCAAAGACTATTTT	45.908
17	A_55_P2071349	Trh	GGGGTCACATCTTGATATAACCCTGCTCTTGTTA ATCTCAATGACAATAAAATATATCC	44.791
18	A_55_P2084332	Pigp	TATCGAGGTCTTCATTTGCGGCTCTCAAACAAC AAGGTTCCGGGCTAAATGGATGCTTCA	43.066
19	A_51_P137336	Cdh1	ACATTCTAACGGGAAAAAGGAGACAAGACCTTT GAGAGTTTTTCATTCAAATGCAAATCT	43.030
20	A_52_P633300	Morc1	AACGAAAAGCTAAAAACGTGTTTCAACCAGATCC AGAATATCTACATGGCTCAGTATGAG	42.882
21	A_55_P2007708	Nanog	CCATGATGAACCGATGCCAGCTGGACTAGTTTAA ACAAAATAAAACACTAATTTTACCTT	42.247
22	A_55_P1984655	Smtnl2	TGCCATCTATCCCTTAGATATTGGCAAATATATT ATGATAAAAAGTGGCCCAAAGTTGA	40.894

23	A_51_P269084	Chchd10	GCCTAACCCCTCACCGACAGCTTGATGGAAAGG AGAGGTTCCATGTGACTGGGAGTAAGG	36.728
24	A_51_P514449	Nr5a2	ATGCAAAGACAGTGATTCTGCATATGGCCTGGA AAGACAGGAAAGCCAGTCTCTACAAA	32.774
25	A_51_P245533	Tex19.1	TGACCTCACTGTCATAGGGGTCATATGCTTACTG TCTTAGGGTCAAGATACCTGATTTTA	31.948
26	A_51_P202340	Pou5f1	AAGTATTGAGTATTCCCAACGAGAAGAGTATGA GGCTACAGGACACCTTTCCAGGGGGG	31.537
27	A_66_P136102	Lefty2	AAGGGTGTACTGAGTCTTTCTGGCCATTGCCTG GCAGCTTTGCCCATGTCATTTATTGT	31.310
28	A_52_P175376	Tcfcp2l1	GTACCTGAAATAAAGCATATTTTGCACCTGTAAA TGAAAAATCTGTATGTGGGCTCTGTG	31.184
29	A_65_P16753	Bex1	AAGGATAGGCCAGGAGTAATGGAGTCCAAAGA TCAAGGCGTGAAAAATCTCAACATGGA	29.812
30	A_55_P2065549	Dppa4	CCAATGCTAAGAAGTACGAGGCAGTGCCAGCCG ATGCTTCGTCCTCATCAGAAGTCAAAG	28.775
31	A_55_P2150029		AAGCCAGGCCGTGTTTGAGCTGAAGAATCTGGA ATCTTCCAAACATACCGAGGTCTTAAT	27.322
32	A_52_P488501	Gtsf1l	GCGCCTACTGTCACCAATGTCGTCCTTAAGAG TTTTGTTCCCAAAAACCTGTTTGTG	26.557
33	A_51_P496720	Dnmt3l	ATGAAAGTCTTCTAGAACCCAGGGCAGATTTCT TCCTAAGGTCTTCCCTCCACAGTT	26.057
34	A_51_P494125	Alpl	CCTCTTTTGGTGTGGTTAAAAGGGAACACAAG ACATTTAAATAAAAACATCCCAAATAT	25.370
35	A_51_P376445	Rhox5	TGGAGTGAGATGGGGAGAAAGATGCCCTTTGC GACACCGAGATTTTGATTTGATCACAT	25.214
36	A_66_P137775	A830035A12Rik	TCACATCAGGCAGGTGAGCCAAGCCATATTTGA GCTGAAGAATCTGGAATCTTCTAAGA	23.447
37	A_51_P324814	Krt18	GGATGGCAGAGTGGTGTCCGAGACTAATGACAC CAGAGTTCTGAGGCACTGAGGCAGAGA	23.403
38	A_51_P368823	Grb7	CTGTACAGACTGAGAGGCCAGTTGATCTGCTCTG TTTTATACCAGTAACAATAAAGATTA	23.275
39	A_51_P354706	Lefty1	CTTTCATGCAAATCTGAAGTGCTCATTATACTGG GAGAGCTGGGGATTCTAACTCCCTAA	22.788
40	A_55_P2146254	Ifitm1	TGTGACACTCACAAATCTGTCCATGGTGGACTCA ATAAAGTGACAGTGCTGTGACTTTCT	21.932
41	A_55_P2011877	Eif2s3y	CTGTGCACCACTGAACCTTACAGTAAAGAAAGTTT TTCTTATGTTGAAGGATTGTTACTC	21.524
42	A_55_P2031021	Bex1	TTTTACTCGGCCTATAATTCTTTTGTAGCAGAA TTTATCAATTGCATGGGAAGATCCG	20.487
43	A_55_P2129498	Gm5712	AGATCAAGTATTGAGTATTCCCAACGAGAAAAGT ATGAGGCTTCCGGGGATGCCTTCG	20.487
44	A_55_P1983488	Lsr	GTCGGGAAAGTTTAGTCTGCTGATCCCACGTTTT GTTATGTAGCTTTTATACTTTTTTAA	20.401
45	A_55_P2183147	Tdgf1	TGATGCTCACAGTGAATCCCTAATGTTACCCCTC AAAACACTAACTAGGCCTTAGCTCTG	19.822
46	A_55_P2087265	Gm7676	ATGTGACACTCACAAATCTGTCCATGGTGGACTC AATAAAGTGACAGTGCTGTGAAAAAA	19.678
47	A_52_P307739	Sox2	TGGCAATCAAATGTCCATTGTTTATAAGCTGAGA ATTTGCCAATATTTTTCGAGGAAAGG	19.630

48	A_55_P1988368	Upp1	TTTCCGCCCCGAGAAGCCTCTGCAACTCTGGG CAATAAATCTATTTTTTCATAACACA	19.213
49	A_52_P270429	2200001115Rik	TGGAGAGAAGGCCATTAATGACGCCCTAAAGAA AGCCCAAGAATCAGGAGACAGGGTGGT	18.750
50	A_55_P1966749	Cyp2s1	TAGCTGACCTCTTTGTGACTTGAAGGTTCCCGTTT TGCAATAAAAGTTTGTCTTGCCCC	18.626
51	A_52_P648715	Triml1	AGAACCCGTGCATAAAGTTGGTGTGTTCTTGGAC TATGACTCTGGACACATAGCCTTCTA	18.592
52	A_55_P2015375	Tuba3a	TCTGGCTGGCGCCGTCCATTTATGTCTTCCCAC CATTGGAAATAAAGGATATATTATT	18.349
53	A_66_P118600	Lama1	ATGTTGAACTAAAGCCACACGGACAACAGATAC CTCTATTAATGGTTTAAACGTCAGT	17.736
54	A_66_P101192	Dppa4	ATAAGAACAAGATCTTGACTAAGAGCTCGAAG GATAAAGGACAGATCTCTTGTGAGC	17.493
55	A_52_P472302	Fxyd6	TTGGAACTAACCAAGCCACTGTGTACTGGGA CTGCTGATCTCTGTCTTGATCTAT	17.170
56	A_51_P109144	Grtp1	AAGCAGATCACCAAAGGGGACTTTGTGACAGAG TGTCACGCATTCATGCAGAAAATCTTT	16.755
57	A_55_P1998601	Slc17a9	CCTATTAGATTTTCTTATAGATGTGGTGAGTCTT GCCAGAGCCTTATTTAAGTAAAAC	16.526
58	A_51_P237668	Bex2	GTTTGTGATGTACTGTTGTAATTTCTGGTGCA CTTGTTCCTCCATGGGGCTCCAAC	16.267
59	A_51_P171999	Apoe	AAGATACAGGCCTCTGTGGCTACCAACCCCATCA TCACCCAGTGGCCAGGAGAATCAA	16.066
60	A_55_P2071691	Kank3	CTGGGTAATGCCATATCCCTCAACTCACTTCATG AAACATCCTAATAAAAGTATTTCTAC	16.053
61	A_55_P1960291	Tjp3	GCACTACCAGCGTGCCACAAGCCCTCAAGCTTC TGACCACTTAATAAATCTTAAAAAA	15.674
62	A_55_P2078960	Tdh	TTACACACTGCCTTTGTCTGTGCCTAAATTGGTC CAAGCACAAAGGCCAGAGAAATGAA	15.644
63	A_51_P417074	Arhgap8	AGACTGGAGATGCCCCCTTCAATCTAGGCATCT GTGTACTGTTGTCTTATGAACTTA	15.404
64	A_51_P346132	Rhox9	CACCAGTTCACCCACTCTCAGCTGCGTGATCTG GAGCGCCTTTTCCAAGAGAATCGCTT	15.227
65	A_51_P202050	Dtx1	TGAGGATTGGCTGCTGGGATGGAAGTCAGCCAA GCTTTAAAGGGACGCCAGCAATTGCTC	15.136
66	A_55_P2001628	Rps4y2	GGGGAAGGGCGTTTACGTTTGTATACTTAAA AGTTTTTAAAGCAGCATGTTGAATTA	14.705
67	A_55_P2169415	Cgn	CATGATTTAAAAGAAGATATTCTGCAGATCAGAT ATTTTCTCCAATCCAGCCTTGTTTT	14.469
68	A_66_P128079	Gm5604	CCATCCAAACCAATTGAGTTGATTTTCTAAAAT AAAGCCTCAGCTGGCTGTGCAACT	14.005
69	A_55_P2174601	LOC100047292	CTGTCTATTTTAACTAACTCCATATGCTGCCAGT ATCAACTTCATGACATTTGCCAAAA	13.962
70	A_55_P2129920	Chd7	GTCCTACTGTTTACACTCACAGTTAATGTTTCATAC CTAGTTTTATAAGCTGTTCTGTAAC	13.903
71	A_55_P1953341	Wfdc2	CGATGAAAGCATCTCCTTTTTCTAACCAATAAAGT GATCGCTTTCAGCAATGGAGAAGCT	13.226
72	A_51_P244950	Dpys	CAACCCCTGGAGAAACACCTGCTATTTCAACTCC CCAAGATCCTTAGGAAAAATCATTG	13.213

73	A_51_P359603	Itgb7	ATTTTTCAGAGTGACCTTCAGAGGGCAGCAGCCA TTCCACCACACGAAGGGCTGGTCCT	13.198
74	A_55_P1983733	Aldh1l1	AATCAGAAGTGGCTCCAAGTGGAGTGAGCAGTC ATGTCCCCATGAATAAAAATTGTGAG	13.171
75	A_51_P255657	2210011C24Rik	AACCACCTTTCTCCATAAAATTCTAGTCTTCCTT GGAAACCTGCAAAACCTATGAGT	13.162
76	A_51_P183894	Fbxo15	CGATGAATACTTCATTGTCAGACTGGACATTTAC CTCAGTGTAGCAAAATTACAACAATG	12.973
77	A_55_P1979126	Tuba3a	CGGCCGTCCATTTATGTCTTCCCACCATTGGAA ATAAAGGATATATTATTAATAATTCT	12.669
78	A_55_P2032543	Cblc	AAGGGAGCCTTGGGGCTGGAAGGAGTGACAAA GCAGAAATAAATTGAATCCTGATCTTTC	12.273
79	A_66_P112024	Gm6816	CTTTGCTACCCGCCTCTCCAACATCTTCATGATCT GGAAGGGCAAAAAGCCGTGGATCTC	12.077
80	A_55_P2174582	1190003J15Rik	GGAGTTAAAGTATGTGTTACCTGAAGAAAGCC ATCTATCTGCCTGTTTCTTCCAGAC	11.630
81	A_55_P2092661	Nup210	CCGAGAGCTGTTAATGGAGTCTCCCTGCATTTG TTTAATAAAGTTCTGTGTAGTTTCTT	11.325
82	A_55_P2090070	Myh14	TCTGTGTGCTCATAGGGTAATGCTCATGGCCCCT CATGCTCCAGACACTAAAGAAATAAA	11.160
83	A_55_P2096917	Mreg	CATGCTGTTTAAATTAGCCTGCAAATATTTTCAG TCACTTCTGTGGGCTATTAGAAGAT	11.056
84	A_55_P2151609	Sorl1	GTTGATGGTTTTATTTAAAGATGCACTTTGAGT TGCAATATGTTATTTTATATGGGCC	10.934
85	A_55_P2007703	Nanogpd	ACCCCAACAAGCCTTGAATTATTCCTGAACTACTC TGTGACTCCACCAGGTGAAATATGA	10.775
86	A_52_P138806	Dlgap3	CCACACCTGTGGCTGTCCACATCCCTTTGAGTA TCCCAGGAAAAATAAACCGCAGAA	10.726
87	A_51_P282144	Adam23	TAATGACTACAGAGCCTCAGATCTGAGAATTGG GATGGGGTACAAGACAAAGGTCCCTTT	10.532
88	A_55_P2086835	Gm5514	GGCTTGTGATGTTTGCCTAGGAGCTCCTGAT CAAATAAAGTTAGCAATTGCAAAAAA	10.384
89	A_55_P1954302	Esrrb	CATGCCCTGGGATTATCTCCATCCAGTCCCATGT ATCTGAAATCTAATAAATAAGGAAA	10.299
90	A_51_P103222	Slc39a4	CTCTGCTTACCTTCTTAAGCCACCTAATTGTTGG CCCCACTACGGGTAGCCAGAGGCTT	10.274
91	A_55_P2404484	1700001L05Rik	TTCTTTGCCAAGTGTTCCTTCTGTGGTGTTCAGT TTTGCTCAGGCCTACAGCCATAAG	10.226
92	A_55_P1962334	Trim71	AAAGGATTTACAAACCAACCACCAACAGGAA GTGTAGGACACAGTATATGTCTTTTTT	10.157
93	A_55_P1985351	Slc35f2	CAGCCACCAGAGTGCCGCCTTCAGAAAACCTTAT GTAAATTGTTTTGTATAAGAATAAT	10.111
94	A_55_P1954006	Ldhb	AGGCTTGTGATGTTTGCCTAGGAGCTCCTGA TCAAATAAAGTTAGCAATTGCAGCAT	10.103
95	A_55_P1975370	Apoc1	TCCACGTAATGTGCCAGGTCCCTTTCATCACAG ACCAATAAAAAACGTGTAGAAGGCAA	9.961
96	A_51_P486810	Gpx2	GGGCTCTAAGTCTGGGGTAGGTTCTGGGCCTTC ACAGAATGATGGCATCTTCTAAACCC	9.928
97	A_66_P124011	Spint2	AACCGGGAGTACAACCTGTGCTGTTTAAAAAGA GAGCAACTGCTTGCCTGAGATCATT	9.862

98	A_55_P2036086	Gm3761	GCAGGCGTCTGTCTATGGGAGAAGGTATATTTAA TAATAAAGCGTGCAATTCATAGAAAAAA	9.781
99	A_55_P2076085		TCTAGCAGGAGGAAGAGGGCTCTCGAATGCATG GATGGATTGTGCATCTCATCTGAATAA	9.755
100	A_52_P817257	Gm5480	GCAATGGTGTGGATAACTTGGCCCTGGAACCTTA ATGCTAACTTGCCTTGGCATGGGTC	9.752
101	A_55_P1989921	Eml2	GGGACGAATGGGCCACCATGCCTTGTGGGAGCC ATTGGTGTGGTTGGGTTGGGATTTTTT	9.695
102	A_51_P103397	Vwf	CAAGTGAGGCTGTGCAGCTACAGCGATTCTCT ACTGATACCCATGCTATGACCTGGCTA	9.694
103	A_55_P2027995	Rpl10l	ACCAAGCTGCAGAACAAGGAGCACGTGATCGAG GCCCTACGCCGAGCCAAATTCAGTTC	9.689
104	A_55_P2143219	Rasgrp2	TCTGTTAGACCAAGAAGGGAACCGCAGGCACAG CAGCCTCATCGACATCGAGAGTGTGTG	9.435
105	A_55_P1965233	Sh3tc1	ATTTTGTGAGGGTTGGGGGAACTGAAGGACC AAACAGTAGTAAATATTTTTCAGCAAC	9.399
106	A_55_P2180744	Clstn3	TGAGGGTAGGGGTGGGTGTGGTAAAGGAGGG CCGCACCCTAGGGTTTTCAATAAAACA	9.352
107	A_52_P23225	Gpc3	AAATGGTATCTTTATGAGGATGGTAAATTTAGT GGTAGGATAGATTGTCTTTTTCGAAA	9.133
108	A_55_P2037081	2610305D13Rik	CCCCCTTTTGTCTAGTCAACAACCTCTCACTAA TGTATTGTAAATAAAGCTGAATGAT	9.128
109	A_55_P1999511	Aurkc	AGGAAGCTCTCCAGGCTCTGTTTGTAGTCATG TGGATTGCTTGTCTCTTTTATGA	9.059
110	A_55_P2173188	Kank3	GCTCTGCATTACAGCGTGTCTCATGGGAATCTCG CCATTTCCAGCCTGCTACTGGATACA	9.043
111	A_51_P341108	Spint1	ATAGAAGGACCTGCTTATCCAAGAGCTGGAGAA AGTTGGTGTGGTGTCTTGTTCAAAG	8.863
112	A_51_P231946	1700029P11Rik	CGTATTTCTTCTGGAATCGGCCCTGGATTTTCAGAT TGCTGCCCGCTATGTTTCTTTTA	8.705
113	A_51_P112223	Gsta4	GCTGGAGTGGAGTTTGAGGAAGAATTTCTTGAG ACAAGGGAACAGTATGAGAAGATGCAA	8.637
114	A_55_P2140903	Vax2os2	ACTAAGGTTGGCGAGGCCCATGTTCCAGAA GTAATTCCAAATAAACTCCTTTGTTC	8.563
115	A_55_P1988384	Slc7a3	GGATATGAAATAATGCTCTGTATTTCTGTGAAA TGATGGCTATGTCTTGTGTTTCTC	8.474
116	A_66_P107379	Mdk	CTGCACCTCCAAGACCAAGTCAAAGACCAAAGCC AAGAAAGGAAAAGGAAAGGACTAAGT	8.464
117	A_55_P2143233	Rasgrp2	GTTTCTCATGATGCACCCCTGGTACATACCTTCT CTCAGCTGGCTTCGAAACTGCTCCA	8.276
118	A_55_P2199118	Bend4	CTAGAAGGCCACATGTTCTGTTGGGGTAAAATT GCACAATAAATGTCAAGTTACCTGTT	8.254
119	A_52_P338956	Aspg	CTGCTTCCAGCCTTTCCGCACGACAATCTGAAG GTCTTTGTTGAGAAGAATGTCAATAA	8.175
120	A_55_P2024366	Raver2	GCTGTGATTTTCTGTGTGCTAATGTTTGAA ATGCTTTTCAAGATGCAAGCTTAATA	8.158
121	A_55_P2123496		CTAAAGTCTGAAGTCTTAAATTGTTCAAGGCAAT CGCTTAACTGTCAACCTTATGTAAT	8.154
122	A_52_P236448	Ngfr	TCCAGCTGGCGACTATGAGATCCAGACCTTCTCA TGTTCCCTGACACTTCCCTTTGCAT	8.066

123	A_51_P125842	Tmem51	CCCCAAGTGCTGCTGGTTCTTTGAAGGTCTAAGG CCTGATGACCTTCAGCGTGCGACACA	8.015
124	A_55_P2143251		CTTCACATGGCTTCTGCATGTACAGTATTTGGGC AAAAACAAAAATAAAGTCCATTTG	7.852
125	A_55_P1968340	Plekhh1	ATGCTTGACACCCATGGCTGAAATGCTATGTATG TTTGTCAATAAACTGTCAGTGAACC	7.702
126	A_55_P2123502	Jam2	TTCGTGATTTCTGTATGTGGCCTTGGCACATGCT ATGCTCAGAGGAAAGGCTACTTTTCA	7.606
127	A_55_P2070992	Aldoc	TCCAGCCCTGACTCGTGCTCCTTATGCTCTGAGTA CATAGCAAATAAATGAGAGCAAAC	7.473
128	A_55_P2019054	Acacb	CCTGACCACTGGGTGCGCTGAAGAGGCTGCTG AAAGAGCTGCAAATAAACTATTTTTT	7.466
129	A_55_P2071811	Eml2	TGGTTTTCTGCTGACGACTTTGGCAAAGTGCACCT GTTGAGCTACCCCTGCTGTCAGCCGA	7.459
130	A_51_P472249	Slc7a7	CTCTTCTTTACAAGGGCCAACAATGCTCCAAAC TTGTCTCCTTCAGAGGAACACAAAA	7.384
131	A_52_P354744	Slc2a3	GTGCTTACACATTTAGACCCCTTAGGCAAACCC TTGCATAGAGTGGTAGAGCCATATCT	7.355
132	A_55_P2002572	Ephx2	TTTTGAAGCAGCTGATTGGAGAGTAAAGATTTT CATTCAATAAAGCTAAACCTCAGGGC	7.276
133	A_55_P2026982	2610019F03Rik	CTCCTCTCAGGAGGTGAAGATGCACTGTAAACCA GAAAGATTAATTACAATGATTTTTT	7.266
134	A_55_P2097340	Camkv	GGGCTAACTGTGTGCCTACTGAACCTGGCAAATA AACGTACCCTGCAAAGCCTCTGGCC	7.168
135	A_55_P2155504	Lck	AATCTTATGTCTCTGTGTGTTCTGTCTGGTGCCT AGCACACACCAGGAGCTCAATAAAA	7.105
136	A_55_P1954718	Cyb561	CTCCTGTGACGTACAGTGTGTTGTTGGTGCAACA GAGGAATCAATAAATGTCTACAGCTG	7.092
137	A_51_P273538	Syce2	AGGCATGCTGATATTGTTTTTATAGTTCTGTAAC CCAACACAAAGCCACCAATGCTCTT	7.088
138	A_55_P1955998	Nlrp1a	AACCTGCGGAGCCACACAGTGCACCTTTCTACT GGACCAGAGATTATTCGGCGGGAATC	7.070
139	A_55_P2067722	2310057J16Rik	AGCTCAGTCCCCTGTCTGCTCCTCCACTTTCTTGA ATAAAATAACTGAAAAGAGAAGCTG	7.049
140	A_51_P510418	Aldh1b1	AAATCTGATTTAGCCTGAGTCCAGTGAAGTG TTACAAGAAGTGTCAACCAATAAAGT	7.045
141	A_55_P1963002	Ppfia4	TGTGTGTGGCGTGAGCGGGTGTGTACGTACCA ATAAACATCCTGGTTTTAAGACAATGT	7.034
142	A_55_P1968231	Rbpms	AACCTTATATTTAAGGGGAGGGACCTTAGTTTGG AGGTAACCATTGCCTCAAGAGGAGCA	6.999
143	A_55_P1969392	Rpl39l	CTGTGCTTTAGTGAGTTCATTGAGCAGTTCAGTA ATAAATATGTGAAACCTTTGTTTCG	6.974
144	A_66_P107818	Gdf3	CTATCAGGATAGTGATAAGAACGTATTCTCCGA CATTATGAAGACATGGTAGTCGATGA	6.948
145	A_51_P282837	St14	CTCAGAGTCTTCCAAGTGGGACCCCTCAAGA GTTGGAGAGAGAACTTGCCTGCTAGC	6.925
146	A_55_P2037608	Acp5	CTTTCTGGGAACGGGCTTTCTTTCTCAGTCAAGTC TTACTGCTACTGCTATTCAATAAAA	6.773
147	A_55_P1957049	Bai1	GAAAGAAGCGGGTGGGAATCTATTTTTCTCT CCTTTCTTTCTTCAATAAAAAGAA	6.761



148	A_55_P1971244	Ndufa4l2	TGTCCTGGGGATCAAACAGAAGCAGCCGTGGG CAAAATACAATTTTCATTTAACAAATTG	6.674
149	A_55_P2102060	Gstm3	TCATGTACAATAAAGCCTGAAACACACTTGAAAC ACAATAAACACTGAACACTTGCTGTG	6.642
150	A_55_P1998943	Oas1a	TGCCACCTGTTGGAAGTTCTGTCTGACAAAGT CTGATCAACAATAAACACAGCAGGT	6.595
151	A_52_P379277	Enpp3	CCCACGTTTGAACCATTATTTGAATGAATGGAT GTATAAAGCCATTTGACAAAATGGGG	6.537
152	A_55_P2127934	Palm3	CCCTTCTGCAATGAAGCCTTTATACTTGAAAATTA AATGTTAAGGCACTCTGGCTTTAAG	6.463
153	A_51_P148612	Cox7a1	ACAACGTCCTGTACAGACTGACCATGACGCTGAC TCTGGGGGCACTGCCTACTGCTTAT	6.428
154	A_55_P2259125	LOC100303645	TATGGGAGCAACCAGTCCCTCAGCCTCCAAACA TGAATAATAAAGTCTTGTTCTCTTGA	6.415
155	A_55_P2097828	Gmfg	CCTTTGAGCCAGGGATTTGGAATCCTTACTTCTG AAGGCTCAGATTGATAGGATATGAAC	6.414
156	A_55_P2130535	Dnmt3b	GTGCAAAGATGACAGATGCCAGATTTACCTTT CTGGTTGATTAAGTTGATTTCTCT	6.291
157	A_55_P2052281	Rnf208	CTACCCTGCGTGGCATTGTCGCTGCAGCCAATT TGCCATTAATAACTCTTTGCCAAAGTT	6.261
158	A_55_P2428968	Lrrc2	CTTACTGCCCGTCTCTAAATCTTTGAATATGTG TTACCTCTTATTGGAATTGCGGCTT	6.241
159	A_66_P131110	Zfp473	GCACACAGGAAATGTTTCTATTGATGAAGTGT GGATGAGTGTCTAACTATCTAGTACAA	6.219
160	A_51_P486681	Ap3b2	CTTCTACCTGTTTCTATGGGTTCCCTAGTGACTT CCTAGGGGAAGACAGAAGCTGCTCC	6.138
161	A_51_P273609	Itpka	CCCGATCCATAATTGTACTTCACAGGTATATAGA CTTCTGGTCTAACTCTGCACTACA	6.125
162	A_52_P648601	Dusp9	CACTGAGACTCTTTGTACTGAGGGTGGTCAAAC TGCCACCGGAGGAGATAGGGTCTCAG	6.022
163	A_51_P438821	Pycard	ACCTGCAAGGACTCCCTCCTCCAGGCCTGAAGG AAATACATCCCTACTTGGTGATGGAC	6.011
164	A_55_P2170847	Fbxo27	GCCTAGAGTCCAGGCCCGATCATCAAAGATGTC TATATTGTATAATATTTAAAGTTATT	6.001
165	A_55_P2044439	Mfng	ATAGAAGGGTTTCTGGAATACATCCAGCCCAA GACCCCATCTTCTACTATGAATGTG	5.842
166	A_55_P1968178	Smagp	CCACTGTTCCCAATCAGCCTCAAACCTCTACTGT TTTTATCCTAATTAACCTTATGAAA	5.765
167	A_55_P1974019	Dapk1	CTGTCTGAGAAGCATGTCATGTTACCATATCAT CTGTACATATATATGCACTATGTA	5.737
168	A_55_P2075966	Spnb4	GGGCGGTGTGGCAGGCGCACACTGTATGTACCT ATAATAAACCTTTGGCTTTGACAGTC	5.701
169	A_55_P2088385	Tnnt1	CAGGAGCCACTGGAGCGTGCCCATCTGTAATC AAAATAAAGTGCCCCAGGCATCTGC	5.696
170	A_55_P1973578	Foxh1	AACAAGAGTATCTATGATGTGGGTGAGCCATC CTAGGGACCTGGCAGCTCCTGCCCA	5.647
171	A_51_P338443	Angptl4	ATGGTGCTGTTGTAGGTGCTGTGGATGCACAGG TGCTAACTGTGGTTCCAGGCACAGCT	5.594
172	A_55_P2052485	Ushbp1	CTGGCCTCTGCAGGCTCTGTACTAATGTTCCCTCA CACATGTAATTAGACAAAGTAACTT	5.562

173	A_51_P312949	Tdrd12	AGAGTGTTCCTGGTCGATTTTGCCAAGTATATT CCAGTAAATCTAAAAACATCCGAGT	5.555
174	A_52_P350786	Phlda2	ACCATTCCGTGTTAATATTTTTATACCATATTTTC ATTCCAAATAAACAATGTCACTTT	5.518
175	A_55_P1973447	Ybx2	TTTTATGAACTGTCATGTGCCACCTGAGCCTCCA GTAAAAACAAGCAGGCTTTCTTGT	5.494
176	A_52_P633560	Nodal	TTATTAGATTATAAACGAGCCATTTGGTTCTCCCT GCCTCAAGCTGTGGTAGGAAGACC	5.478
177	A_55_P2055324	Spint1	GGAGAAGGCCCAAGAGTCTGGAAGGAGCAGAG CAGCCTTGAGCCAGGAGTACTGTATATA	5.461
178	A_55_P2008722	Gm13157	TATCAAGGTGATTCTGAATCCCCCAATGTACA CCTTACAAAATAATCACAGCTCTCT	5.419
179	A_51_P487918	Rinl	AACGAACGGATGGGAACAAGAGAGACGGGAGA TGCTGGGCTACTCCAGGAAAGCTTCTCC	5.409
180	A_51_P270733	Syng1	ATGTGTACTTCCCGCAGATCAGCAGTGTCAAGGA CCGCAAGAAGGCCGTGCTCTCTGACA	5.404
181	A_51_P241769	Rhd	TTGGTTTCATGACAGAGACTATTAATACTTTGGG ATGAATACACCTCATTAAAGTTCTGG	5.392
182	A_55_P2144341	Gm7029	AGGAGGAGGCAGCTCTGGTCTCTGAGCATCTT CATAGACCACCTGTCCTTGTACTGAG	5.388
183	A_55_P2047461	Fcho1	TGGACAGGAACCCATTTTCAGCCTGGCTCAGCC AACTCTCCGTCCACAAGCAGGCCCT	5.355
184	A_52_P562676	Sult4a1	AGTACTGTACGGATGTTCTGGAACACACATGGT AATCTCTGCTGCCTGCATCTTTAAT	5.353
185	A_51_P451588	Plekhb1	AACCCCTCATGTGCCTGTCTATAGGTAGCAAGCA ATCTCTCATTTGATCCTGTTCCAAA	5.335
186	A_55_P2015687	D14Ert668e	CCATGGGTTTATGCTCACTATCATATCACATTGCC AATATTTAGCACACTTAATAAATGC	5.329
187	A_51_P280893	Pla2g1b	CGTACAACAAGGAATACAAAAACCTTGACACCG GGAAATTCTGTTAGCCTGTACCTCAC	5.316
188	A_55_P1995243	Cobl	TTAGTCACAGCTGTCTGCTTTTCTCTTAGTGCCA CAAATAAATGCAATCCAATGCTGT	5.281
189	A_55_P2035812	Rnf208	TGCGTGCCATTGTCGCTGCAGCCAACCTTGCCAT TAAAACCTTTGCCAAAGTAAAAAAA	5.276
190	A_55_P2047335	Capn5	GCCTCAGTGTGGAGGGCCCCAAAGAATCCC GTCTTGTTGGGGAGTTTTCTTGCCCTAA	5.246
191	A_51_P246317	Mt2	AGAAGCCTAGCCTTTTTGTACAACCCTGACTCG TTCTCCACAACCTTTTCTATAAAGCA	5.208
192	A_55_P2074371	Lin28a	TTCCTTCCCTTCTTCCCTGGGAAAATAAAGACT TATTGGTACTCCAGAGTTGGTACTG	5.206
193	A_51_P412914	Efs	GCTGAAGATGACAATGTAATAGTCTGAGAAACA CCAGAGAGCTTCTCCCTCACAAGTCA	5.201
194	A_55_P2080880	Clcnkb	TGACTTCTGGGGTTGCCTGCTGCTAACCAGGAGC TTCTGAGAAAAATAAACTGATGTCT	5.199
195	A_55_P1971897	Mdk	CCCTCTTTGTTCTCCACCTGATACTTGTATT AAGAAATGAATAAAATAAACTCAC	5.146
196	A_55_P2128501	Krt8	AGATCTCCGAGATGAACCGCAACATCAACCGCCT GCAGGCGGAGATTGAAGCCCTCAAAG	5.131
197	A_51_P208145	Si	ATCTCTGATACTAGGCATAGACTTAAGAAGCAGG GCTCAGTTTCCCAATGCCACATGGT	5.127

198	A_55_P2019694	1700061G19Rik	AAGAGGAAATCCAGAACTCTATGAGACTTCGA CCTCTAGGAACCCATTACCCTAAT	5.096
199	A_55_P2048119	Slc29a4	CCTGTCTACCTGTGTCTCTGACTACCGACTG GCCATTAAATATGGCAGAGACTGCC	5.050
200	A_51_P155755	Pld6	GGGGGAGCATGTTGGAGTAACAAGTCCTGATAT CCCCTTCTGGGCCACCCTTAGCCTCT	5.050
201	A_55_P2125963		GAATTCATACAGGAAAGAAACCTTACAAATGCA GTGAATGTGGGAAATGCTTTACTGACA	5.026
202	A_51_P154842	Oas1f	CCTGTCCACCTGTTGGGAGTTCTGTCCAATGTC TGATGCACAATAATAATACAGAGA	5.020
203	A_55_P2064538	Gm13154	GTGTGCTTCGAGTATCTACTAATCAGAATTCTTCT CAAATGCTTGTGTTGTCATTATAGGA	5.016
204	A_55_P2076462	Lnx1	ACGCTTGCCTGGCCAGGATGCTCAAGGAACTTAA AGGGAGAATTACTCTGACCATTGCTT	4.966
205	A_51_P498772	1700019D03Rik	CAAAGATGCTCTTGAAGTAGTCTCATTAAACACA GCTTGCCTTACCTGCCAAAGCTCTT	4.951
206	A_55_P1976734	Cacna2d2	TGTCAGCTGTCTCTGTGGGGCGTGTGTGTAA CTGTAGTGTAGTCAGGTGCTCAACGGA	4.927
207	A_55_P2015541	Hif3a	CAGAAACCACAAATGTCTCCAAAACCACCATAA AGACCTCTCCTTGTAGGCACCAGAG	4.907
208	A_55_P2091551	Arhgap9	GGTGATGCTTGTCTCAGTATTCCTTTATTGTCAG GAAACTGTGCATTATTAAGTTTG	4.906
209	A_55_P2097448	Rbpms	TTTGTACATATCAACCTACTGCAGACCAGCAGA GGGAGCTCCCGTGTGAATTTATTAG	4.902
210	A_51_P107020	Kif5a	AAATGTTGCATGCCGCGTGAAGACAAAACCA AACCGCACAAATCCAGTGTGTATTTA	4.833
211	A_55_P2088018	Fhod3	GTACACACATACAAGCACAGCTTGTTTACCAGTT GTGGATTTAGATGTACTAAATGTTT	4.809
212	A_51_P350332	Rbpms	CTCTCTGCTCCTCAAAAAGGAGCTATGTATTATT ATGTTGACCTCAGAATCCAGCTG	4.808
213	A_51_P145520	Sigirr	TTGCCTCTATCCCTGGGCCCTCAGGAAAGGAGT GTGGCCCGGGTGTCAAAAATAAA	4.727
214	A_55_P2148688		CTGTGTGCAGATAACATTGTAAAGCGGTATTTAA TTAAAATCCAAGCAGTCTTGCAGA	4.720
215	A_52_P97889	B4galnt4	TTTGGCCTCTTTGGGATCTACAAATCAGACTTTG ACAGAGTAGGAGGCATGAACACTGAG	4.642
216	A_55_P1995996	Gm13157	CGAAAATCCCATCTTGGTATTCATCAGAAAATTC ATACAGGAGAGAAACCTTACAAATAG	4.628
217	A_55_P2109257	Nipal3	CATGTGTTATTTTGCAGAAGTGTGTATACTGTGT GCAGATAACATTGTAAAGCGGTATTT	4.598
218	A_66_P110161	LOC626152	TTACAACTTTTCGTGTCTTCATGTCTTTTGATAAT AAATGAATTTCCGCTCTGTGGGG	4.576
219	A_55_P2103011	Sema4d	TTTCTACTTGGAACTGTACACATTTGAAAAGTACC CAAATAAACCAAGCTTTATCGTT	4.549
220	A_55_P2002849	Aifm3	GGACGATTTTCCAGCAAGCCCTTCAACATTAC CTTAAATTTAAACGCATGTCTCAGC	4.547
221	A_51_P181341	Necab2	TGTTCTCTACTTCCGTCCTCTGTGATGGCCCGCT ACCTAGTAGGAGCTGTGACCCTGTA	4.529
222	A_55_P2056774	Hsd17b14	TTAGTCTGGACTCTACCGATGCCTCTGGCTATA CTCTCCCTTATAGCTACAATAAAAGC	4.528

223	A_55_P2154914	Acap1	ATCTCGACATATTCCGAGACTTCTCCCTCATGGC GTCGGACGACCCAGAGAAACTGAGCC	4.501
224	A_55_P2035400	Ripk4	CTTGTGTA AACACGGGGACCATAGGAGATCTG TTTTATGTCAATAAAGGACTCCGCCTA	4.491
225	A_51_P414396	Mmrn2	ACTGTTTCTCAGAAGGAATGTCTACAGTGATGGG TTTGCCATGCAGAAAAGTCCCAGATT	4.452
226	A_51_P262515	Phf11	ACACTGATACCCTGGGTTTATGCTCACTATCATAC CAGATTGCCAATATTTAGCACACTT	4.444
227	A_55_P2137828	Gprc5b	CTGACCTCGTCTTAAGCCAGTACATCTGAGCTGA GTGTTTTAATAAATCTGATATTTCTC	4.443
228	A_51_P403814	Slc4a5	ATACCGAAAACATACAGCTTAAAATGCCACCCAC CATAGATATAACCTTTCTCGTGAAAA	4.388
229	A_55_P2045367	G630025P09Rik	AAATGACTATTGCCTTCGGTTTTTTCTAAGCAGGT TGCCCCACGGTAAATCGGTTACACT	4.379
230	A_52_P147803	AI428936	TCAGTTATGTCAATGGTCTCCCTCAATCTGAGCC CACCATCCAAGACACGTGCATTA	4.365
231	A_55_P2056719	AF067061	GTGTCTTTGTAGCCATCTGGGTTTTGGTTGTGTTT GTTTTATTTTTCGTTTGTTACAGC	4.364
232	A_55_P2048759	4930583H14Rik	CTTCTCTTACTTTGTTCTATGTAAGACCAGATTA CTGGGTTTGTGTGAACTCATTAA	4.348
233	A_55_P2175955	Ano9	GGATCCGTACAGCGGCAAACTTTTTACAAGCAA AATAAACCTGTGTGATTGATTCTG	4.347
234	A_55_P1974367	Fabp3	TTTATTTTTTAAAAGTATCAAAGGGTGCTCCA AGGTCAATAAAGCAGAACCAAGGCC	4.316
235	A_55_P2037717	Slc22a18	GACCACAAGGCCAGTACTTGCCAGTCCGG CAATAAACTTAAGAACCTCTCCTCTT	4.298
236	A_55_P2033780	Fabp3	TAAAAGTATCAAAGGGTGCTCAAGGTCAAT AAAGCAGAACCAAGGCCACCCAAAA	4.292
237	A_55_P2042016	LOC100048058	ACCTGTGTGTTCTGACTACCGCACTGGCCATT AAATATGGCAGAGACTGCCACCGCT	4.279
238	A_51_P391291	Gng3	CAAGCACCTTCTACTCTATCTATAAAGGGACCCC GCTAAACTGCCAAAATCCTGCCTGTT	4.270
239	A_55_P2022895	Slc12a8	CCAAATGTGGAGAATCAAACGAGATTTCTTATT CTAAGGGGCCAAAATAAACACTTCTT	4.239
240	A_55_P2158653	Cldn7	AAAGGCCTCCTGGCCACTCCACTCCAAACATCA TGTATAGTTTGCTTGGGGGAGGGCA	4.183
241	A_51_P176352	Ndrp2	TCAGGAGAAGGTTTGCTGGTGGGTGAGCGATCC TTAATGTGATAGAAATATCCAGCATGT	4.081
242	A_52_P683441	Capn5	AAGCCTTGAAGACTGGACAAGGGAGGACAGGG TGGAGCAGGGATAGCCGTGGCTTCATT	4.067
243	A_55_P2008889	Tmsb15b2	AGATCCATTTACTACCCTGGCTGAAAGGTCAGC ATTTGCTATGAATCATTAATTTTTT	4.016
244	A_52_P108850	St8sia1	CAGTTTCTACCTCCCTTCTGGAGAATATTTG GAAACGTACCCTGTGAATAAAATGG	3.982
245	A_52_P380369	D14Ert668e	AAGAAAGGCAAAGGCAGATGAAGAAGCAGCTT GAGGCACTGCAGACTTACAACAAACCT	3.973
246	A_55_P2173952	Myh6	GCACGACGAGGAATAACCTCTCAGCAGACCTC GCTGTGGCCAATACACAATAAACATA	3.945
247	A_55_P2005060		GTGTTGAAACATACGCTCACTATGGAGAGACTTG GCTGATCTTAAAATAATAGTGTGTTA	3.937

248	A_51_P518051	Dusp4	AATAACGGCGGTTTCCGCTGCCAGAGAAGACTT GGTTTCTGTGTCAGTTTTACTTTGCA	3.889
249	A_55_P1954277	Emid1	AAGTGCTGCTGCAGATGCCACGAGTCAATATGT ACAGGACAATAAACATCCCTGCTTGA	3.876
250	A_55_P2110351	Eppk1	GTCGGTGATTACAACCTCAGGGTATTACAACCTT TCGTGTCTTCATGTCTTTTGATAATA	3.868
251	A_52_P325116		CCTAGAAACACACAAGGCTATCCAGCCAAATCTT AATGTAAAGTAGCTAGAGCCATGGAA	3.862
252	A_55_P1961014	Selenbp1	TGTTTGTGCTTTTCTAAGTGAGCTCCTGGAAGC ACCAAGAAATAAAATGCTGAAACTTC	3.842
253	A_52_P167382	Tmem8	TAGCAGGCTGCTCAGCTGTATGAGGTCTGGCTCC AGAAGGCACACAATGCTCGCTAGTGT	3.828
254	A_55_P2173457	1700097N02Rik	CACTTCAATCTGTTGGCTGGCTTGCTTTGCTTTG CTAAATAAAGTCTCCATGCTGTC	3.819
255	A_52_P244702	Tcf7	TTTTTTCATTCTCGCTGTAGATAGCCTGAATCCAA AGAAAACCAAAAGGGGTATCCAAG	3.790
256	A_51_P139320	Pcbd1	GCCATGTTACTAATTTGAATAAGCTCTCCCTTT TTCTGTAGAGTCCAGCCTCAGTA	3.782
257	A_55_P2007986	Zscan4f	ATGTTGCAAGTAAATTGACTGTCCAATAATGA TATAACATGCTTGTGGATTGCCACTT	3.774
258	A_55_P2104769	Utf1	TGCCCCATCCCCATCTCAAACCTAGGTTCTTACC AAAATAAAGATTGTGTTTTCTACTT	3.772
259	A_55_P1975903	Dnmt3b	TGTTTGCCCCCTTGAAGGACCCTTTGCCTGTGA ATAGTTCTACCCAGGACTGGGGAGCT	3.750
260	A_55_P2072661	Prex1	GGCCAGGGCAGCATACTGGTTTATTTAAATGT ACAGATTCTTTTCATTAATTCATGA	3.746
261	A_55_P2136289		AACACGGGGACCATAGGAGATCTGTTTTATGTCA ATAAAGGACTCCGCCTACTTTTGAA	3.736
262	A_55_P1987761	Prkcz	TGATGAGGACGTCATAAAGAGGATCGACCAGTC CGAGTTTGAAGCTTTGAGTACATCAA	3.733
263	A_51_P440743	Celsr1	GTGTATTTACTGTTTCAGCACTGGATGGCAAC ACAGGTGAGATGATGCATCTATAATA	3.689
264	A_51_P300506	Cox6b2	GGAATTTCCCGGGCAAATATGACCTTGCACTT GAGCGTGCTCCCCTGGCGTCATCAA	3.685
265	A_55_P2194064	BC023969	TTGGATGATTGACCCTACATGCCAGCTGTATTT GAAGAATAAAAGTTCTGTGCTTTAC	3.652
266	A_55_P2182273	Bin2	TAATCCAGAACCAGCAGAAACCAGAGAAAAGGA AGGCGCTGGAAGTTCAGGCCAGAAGA	3.604
267	A_55_P2093665	Gm3950	TCCGAAGCCATCACGTGCTCACTGCTACTGGA CTCAGAGATTATTTGGTGGGAATCAG	3.602
268	A_55_P2154252	Gfpt2	CCCTGCTCTATTTAAAGCGTGCAATCAATGT ACTATGCAATTTACAATAAAGACAG	3.600
269	A_55_P2102857	Krtcap3	GCACGGGGCCCTGACCCTAGGGTGGTATAAAT AATTGTAATAAAAGAACTTGATTTTTG	3.568
270	A_52_P377576	Ap1s3	CTAAATGTAATACTTACATTCTGGATAATCCATA GTTGATCTTGCTAGGTTGCACAAG	3.552
271	A_55_P1956448	Ttyh1	CTCTAAATATGCTGCCAGAGACTGTGAATCACC AGCTATGTGAAAATAATAATAAACAA	3.543
272	A_51_P201338	Mtss1	GGAGATGCTGCCAGCGCAACGAACCTTTAATT AATAAAGCCTAATTTGTCTTGATCCA	3.522

273	A_55_P1961423	Gsta3	ATTCAGGCAACTATAAGTACATAGCCCCACAAA GCCAACCTTCTAAAATTTGCATCAC	3.514
274	A_55_P2151986	Gngt2	GTGTACTGGGATACCTAAGGACCAATGTTTTCTT CCTCTTAGACACAAATAAAGATGCTG	3.501
275	A_55_P1965416	Atp9a	GGCCCGTCTGAGGTTTGTGGGGTCACTGTGCAA GCTTCCTTATGGTTGAACCTCTTGTC	3.468
276	A_51_P399175	Ppm1j	GCAGTATGAGCACTGTCCAGATGATGTGCTGGT CCTGGGAACAGATGGCTTGTGGGATGT	3.405
277	A_55_P1954486	Mapt	ATGGTGGACTACCACAGCTTGCCACACTAGCCG ATGAAGTGTCTGCTTCTTGCCCAAG	3.402
278	A_51_P345792	Tmem180	AAAGCCCTGCAGGCCTCTAACTCTAAAGAGGTT CATCTCATCTCAAGTAAAGCCAGTCA	3.392
279	A_51_P297105	Ucp2	CTCAAAGAGCCCTAATGGCTGCCTACCAATCTC GGGAGGCACCTTCTGAGCCTCTCCA	3.389
280	A_55_P1977792	Folr1	GTGGTGGGGCTCTGACAGCCTTTAATAAACCA GACATTCACATGTGCCTTATGAATT	3.354
281	A_55_P2008874	Dnmt3b	TCAGGTCCCCAGAACCCCTAGTTCCTCATGAGA AGCTAGGACCAGAAGCACATCGTTCC	3.353
282	A_55_P2002103	Hmha1	GTAAAGGAGCTTCCACATGAACTCACAATTTTC TTGAAATAAACTTCTTAACCAACTGC	3.323
283	A_55_P1995924	Gm13157	TGTGAAATGTAGAAAGCCTTTCATGACACCTTT TACTTGTTCACCTCAAATGTTACAA	3.315
284	A_55_P2019533	Zscan4c	ATCCCAAGTCTTAGGGTTGCAAGTAAATGCATT GCCTTTCAGACATCTCATGCCATGT	3.306
285	A_55_P2029420	2610318N02Rik	CCAGTAACTCTTCCCAACAGACCATGCCCCAGG ACTGAATAAAGTTCATCCTGGTGTG	3.305
286	A_52_P73475	Fam78a	ACTCACTGTTTCTAGCAATAAGCACCAACTGCCT TGGTCACGGACAGTACTGTGAACAC	3.283
287	A_55_P1959305	Rbm47	CGTTCATACATTTCTAAAAGACTTGGCAGCCTC ACGCCTTAATGCCATCTCTAAAGTT	3.282
288	A_55_P1969477	Abcb1a	ACTCAGACATGGGCACCTGAGTTCAGATCCCTAC CACCTAAGTAAGCAGCAAGGTGTGGT	3.266
289	A_51_P214269	Epha1	TCAATCAGAACTCTGCCTTGAACCAAGGAGCCT TTGTTTATAAAGGGGGTGGATGGGTA	3.265
290	A_51_P230439	Ppfibp2	AAGAATCAAGTGCCTTAGGTTTGTGAGCCACAA AGTCTTGGCTGAGATCAAAGTGCCAA	3.233
291	A_55_P2139256	Rps6ka1	CTCAGCTGGTAACTCAGGGTTCATCTGTCCAAGG CCTTCTAATAAACTTACAATCCAGT	3.226
292	A_55_P2008427	Dnd1	CCCACCACTGTCCCTGGTTTGGGCTTACATGGTT TTTGTTTTCTATACTGGTTTTATT	3.187
293	A_66_P117578	Mtmr7	TGCAGGTTGCATTACGGAACCTTGACATTCCTTC TGCTTTACCAATATTTAAAAGAAA	3.186
294	A_55_P2128499	Mgl2	CGGGTCCCCTCCTCCTTCATAACTAGTGTCG CAACAATAAAATTTGAGCTTTAATC	3.164
295	A_55_P2003713	Zscan4e	AATTACCACAGATCTGACTGAAGTATCTAACATC CTCAGCAGAGACTGGTAGGGCTTCAG	3.143
296	A_52_P144297	Tspyl3	TGAGCCCTATTCCAACTGATCTGTTCCACATGG AGAAATGTTCTTTGTGAGTCAGAAG	3.140
297	A_51_P257743	Dnajc22	AGTCTTGAGTCAGCCCAAGAAGCCTAGAGCATCC TAGAGGTGAAAAGCAACCACTTGAGG	3.130

298	A_52_P370203	Jarid2	TGTTTTCCCTCACACTTAGAGCCACTAAGTCTGCA GTTCTTTTTGAATGTGAAACACATCT	3.077
299	A_55_P1970274	Zscan10	CCCACAGTTTACCTCTTCCCTTGACTCCAAGAATT TGTTTTTAAGTAAAGCTGCCTTCTC	3.068
300	A_55_P2091153	BC051142	TGTGAACAACCAGCTCCTTCTTCTCATCAGCA TCAGCATCAGCAGCAGCAGCAGCAG	3.065
301	A_55_P2178127	Sept1	CGCTCTCCCGGTTCCAATTGGGTTTTCTATTCT CTCCAAGTTCTCCATCTAATAAAAA	3.060
302	A_55_P1996963	1110012J17Rik	GTACCGTGTGACTGTTGCTGTTGGTCTCTGTAC CAGTAAGACAATGGCTCCATTTTT	3.051
303	A_55_P2071191	Prss8	CGAAATTGTTAAGGCCGTACTTTCTGCCACTT GGTCTGACCTGGCCTCTTGCTT	3.042
304	A_51_P388847	Stap2	CAGGCTCCAGGGATCAGTGGGCTATCTCTGGG TACAATAGTCTTCTCCAGCTCTATCC	3.029
305	A_55_P2111713	Spint2	TTGGTAGCTTCGCTGCTCTCTCCGGGGCCAGG TGCCAGCCGAGAACTAGACGTCCAC	3.029

## b) Down regulated genes in $\delta$ -treated MEF

No	ProbeName	Gene Symbol	Sequence	Fold change [ $\sigma$ ] vs [DMSO]
1	A_51_P406780	Serpib9b	GTAATTTAAATTTACAAACAAGTAAATTTAAA AATATAAAGGAAATTTAAGAGTGCT	24.702
2	A_55_P1964553	Gm13140	GGCTAATTATCAGACTAATCAGCCTAGCATAAAT CTGAATTCAAAATATGCTGTCAGTCT	14.603
3	A_55_P2063283		AGCAATGGGCATACAGAGGAGAACTACAAGGAC ACCGCACCAGTCTGGACTCTGACGGT	7.311
4	A_66_P102202	Gm648	CTACACTCAAGAGTGTGATCCTGCTGTTACAGTG GTCAGCAAGATTCAGCAAATAGTTCA	7.263
5	A_55_P2011163	BC061237	AACAAATAATTGTGGTTCCTGGAAGTAAGGCGG AGGCTGCTATGTCAAATCCATGTGCCT	6.644
6	A_55_P2001458		AGTAAACACCGAGAGACTCATACTCGAGAAAAG CTGCTGTCATAGTCAGTGCTTAAGCCA	6.471
7	A_52_P319093	Serpina3k	CAAGTTCTCATGATTCTGTCCAGGGCTCTGGGAC AGAGTCTGCATATGGATCTCTATATA	6.060
8	A_66_P109757	A430033K04Rik	GGCATCAGGGAATCCATGCGCCTGAGAAACCCT ACGAATGTAACGAATGTAAGAAATCTT	4.859
9	A_55_P2014352	Gm2494	GGAGGAGGAAAAACAAACAAACAAACAA ACAACATTAACCAACCAACCATGCTGG	4.786
10	A_55_P2425442	D030036P13Rik	CACACACAATAGCATGCACATGCATGTATACACA CACCCACAAATAAACAAACATAATTA	4.712
11	A_55_P2111114		GGGAAGACGCTGCTGCCTCACTTGTCTCCTTTA TCTCAGGTCGCAGCAACACTAGCTAG	4.670
12	A_55_P2030186	Ifna7	CTGAACATCTTACATCAAAGGACTCATCTGCTG CTTGGGATGGATCCCTCCTAGACTCA	4.637
13	A_55_P2058602	LOC674794	ACTCATGAACAACGAACAACCATGAAACAGAAC AGAACAGAACAGTCCCACTTCTCGAGG	4.461
14	A_55_P2125997	Grin2d	TCTTGGAGCCACCAGCTTTTTTAAACCCGAA AAGGGCTTTTTAACGTCACCTGATTG	4.140
15	A_52_P307749	Slc35a5	AAGGACAATGTGAAGGTAAGAGGTCCAGAACCA TTTCCAGGTAATAATGGAGTGGAAT	4.116

16	A_55_P1958876	4833422C13Rik	GACCACCAATAGATTCTACCAGAAAAGAAAATC CTCCCACCACATAATAATTAACACAC	4.083
17	A_52_P614207	LOC100047222	GCACTGGTACCAACAGAAACCAGGACAGCCACC CAAACCTCATCAAGTATGCATCAA	3.988
18	A_55_P2100197		GCAAACATATGGAGATCAGAACAGGAAACACACA CACACAATTTAACGAATTAACCTGTT	3.749
19	A_55_P2169227	AI836003	ATCCTTTCTTAGTGCTTTGCTTGATGTCAACCTTA ATAAAAAGGCACCATGTCCCTCTT	3.723
20	A_52_P101487	Ddn	TGAGCGCTTTCTGCCTCCATTCTTTTGCCTTAG GATTTTGTGAATAAGCGAGTAGAGA	3.417
21	A_51_P493117	Slc16a9	CAATGCAATAATGGGGCTCCAAGCACATGAGAC TTGTGTTCTACACTCAGACTTCTGGAA	3.354
22	A_55_P1959525	Wbscr25	AGAATGCCAGGCTTGCCACACAAGGCACAGGAC ACCAAACACAACACACCAGGCACAACA	3.329
23	A_55_P2213968	4933416M07Rik	TGGGAGGAAAGGAGGGAGGGGGAACCATGATC AAATACATTACATGAAAAACATTATTC	3.321
24	A_55_P2050169	Vmn1r197	GAGAATCATTCTACAGTACTATATGTTCCGGAGT TCCTAACCTTGGTTATGCAGTTCTC	3.275
25	A_55_P2420591	2010001M06Rik	CCCAAGGAAAATCCCGGGCCAAGGAAATAAGGG GGCTGGGGAATTCTCCACCCAAAAAA	3.237
26	A_55_P2162970	Gm3734	GCACAAAAGTGGTACACAGATACACACAGAAGC TAAACACCCATACACATAAAATAAAAA	3.233
27	A_55_P2061036		GAGAATTTGAGGCCATTCTGGCATAACAGGGAAC CCTGCCTCAAAAATCATTCTGCTCAC	3.232
28	A_55_P1995104	Btbd19	ACTGGTGGTACGTGGGCAGGCTGCACCTTTTCC ACAGCACTTGAAGCCTCATCAACAA	3.204
29	A_55_P2093053		AGTTGAAATTGGCCTGGTGGAAACCCATAGATCT GATGCCCAGGATGAAGAGAAACACTT	3.202
30	A_51_P202920	Wbscr17	ATACAACAACACTATCGCCTATGGGGAGCTTCGT AATAATAAGGCCAAGGACGTCTGTCT	3.191
31	A_55_P2058195		TTGGATATGATAAGTAAAGAATTGGAACAACCTTG AGCGCACAGCAGAGGAACAACGCTTA	3.144
32	A_55_P2044050		ACCCACGCCGGAACCGAATCAAACAGCACACCCT ACAGAGGGCAATGAACCAGCCATTTA	3.131
33	A_55_P2195077	1700066D14Rik	GGTTAATCGCCCCCTGGGAAAAATAAATTACCC ACCTTTTAAAAAATCTCAAAGGAA	3.092
34	A_52_P104658	Krt6a	AGCAAGAAGAGCTACAGGCAGTGAATTCTGTCA CCAAGAGCTTGTCTCTGGTCCAGATG	3.087
35	A_55_P2172196	Thns1	GCCTGGGATACATGAGGTCCTGTTTAAAACAAAC AAACAAACAAACAAACAAACAAACA	3.074
36	A_55_P2372528	4122401K19Rik	GTGAGAAAGGTGAGGTGATTCAACAAAATAAAT TTTGTCTGAAACTGCACAATAAAACC	3.043
37	A_55_P2014710	Naip7	GACCACACACTCATGCAAGCATACAACTGACT TAAATTTAACATCAAATCCTACTGG	3.038
38	A_55_P1959843	Gm2640	TTCTTGTGTGCCCTGAGAAACAAAGTTCAAATA ACCATTGTACAGCCAGCATCGCCAA	3.029
39	A_55_P2043033	Pla2g3	AGGAGTAAATGAATTAATCAACACACATACCACC CAGTAAACATTCTTCTTCTAACAC	3.014
40	A_55_P2091916	Gm8005	TAACATCTCATGCTCAGACTTGAAGGACGAG TCCATCAGCAAAAAACCCACACCAAT	3.010
41	A_55_P2431897	Thap6	GAAAAGAGAAAACTTCACTGTAGAAAAAATT CCTTCTCAAACCTTCCCATCACCCA	2.995
42	A_66_P136215	4921517L17Rik	GGTCGCCGGCGCTCATCGTCAAGAAGGGGCGAG ATGGGCAATAGCTTTTATTTCATCTAC	2.972
43	A_55_P2136970	Gm7269	TCAACATTCAAAATATGAGGAAGGAGGTGACA TGATTGAGCCCAAGCCTCCTTAAGCA	2.955
44	A_55_P2034968		AGAACAAGACTCCTAACTGCCATGTGCCAGAATG AGATGGTGAAAAACAAACAGATCTGC	2.949



45	A_55_P2032553	9430024F10Rik	CCGTGGGCACTTGCACTCATATGTACAAATCCAC ATACAGAAAACAAACACATTTAAAAAA	2.935
46	A_55_P2363040	1700007J24Rik	CATCCTTTCTTGCTACATCCCCTAAAAGTTGGCC AAGTGTACTTCACTATTATATATTA	2.841
47	A_55_P1994942	Rorc	TTGAGGTTGCAGCTCTGAGAAGCCTGAGGTTCTA ATTCATACAGGACACCAGAATTCATC	2.840
48	A_55_P2420694	AV074028	GCAGAGTGATATGGACAGCCATGACCTGAGAAA GTTCTTTCTAAAATAATAAACTCAAT	2.831
49	A_55_P2078143	Otop1	CACCAGCACTCACATGCAAGAGTGTGCTACCCCC ATGAATAATAAAAAATAATAATAATA	2.826
50	A_55_P2107632	BC030307	GTTTAGTAACAGCTCTTTCCTCCTAGTTGGGGTA AAACAAACAAACAAACAAACAAACA	2.811
51	A_55_P2151414	Gml	AGGAACAGCAGCAACAGCAAGAAGAACAAGGC CTCAAACCTTCAGCCAGAGGTCCCAGC	2.807
52	A_55_P2063618	Gm10818	ACAGGGAAGTGTGGGGGGCAGACAGAACAAG GCAAAGATGCCAGACAGTCCCCTCTAC	2.804
53	A_55_P2179074	Ciita	GCCCCATCTAATGCAAAACAAAACAAAACGAAA CAAAACAAAACAAAACAAAACAAAACA	2.779
54	A_55_P2200890	4933407G14Rik	TGCAACCACCAAGTTCTAATGAGCGGACCTCTCAC CCACCAATAAAGTAAATTTTAAAAAC	2.778
55	A_51_P347169	4921517D21Rik	AAGGCATACCTAACCTCAATACTCAAGAACCTCA TGAGCCCTGGCAATCTGCCCTTTCCA	2.776
56	A_55_P1985825	Gm2980	TAGACCTTAAAATTGATGTGGCCATGCCCTTGGA CTTCAGTAAAACCAGCTTTCTCGCCA	2.738
57	A_55_P2146122		AGGGAAGCTACTTCGTTCCAGGCCCTATCTTCA TGGGGTTAGTCTCACCTGGAACCTG	2.737
58	A_55_P2396370	A730056I06Rik	GTTTCATGATAGCCTGGGCTACAGCATGATACCC TGTCTGGAAAAATAAAAAATATAAC	2.734
59	A_55_P1985236	EG666692	ACAAACAGCTGCTAAGGGAGCAGATTGCATTGG AAGAATGCAACATAGAAACAAAACAC	2.728
60	A_55_P1961809	Adra1d	AGCAGTGTCCCTAAATGTTCCCAAGACGGGGC AGAGGCTGTCATCTGCCAGGCTTATGA	2.720
61	A_66_P105526	Mam1d1	AAGTCACATGGGTCATCAACTCTGAAGAAGCAG CAAATCAACACCGGCCTTCCATTCCC	2.695
62	A_51_P331288	Akr1b7	GAGATCCGTGCATGATAGATTCTTCGTCTCTCT AAAATCAACCTGGATGTAGGCTACCA	2.677
63	A_55_P2066240	Zufsp	CTCTCCAGTGAGAGAATATCAGCTGTAGAAGATT CCATAGATAATATGGACACAACAATC	2.661
64	A_55_P1973813	Gm7660	TAATATGACAGAAGAAAAGACCAATGCAATTGC ATGAGCCCTTGCCAGATTTCAAAAA	2.659
65	A_55_P2314657	4931403G20Rik	GACTGACCACCTACTTCTGACACTTTCTGATC CTTAGTAAACTGATAAAAGAGCATC	2.618
66	A_55_P2365902	LOC402769	TTCTGTTCAGAAGAGGGAGGAGGGGAGCCACA AAATACCATTCAACAAACACCTGAAA	2.615
67	A_55_P2011772	Oscp1	CAGGCCATTCTGGCTGCATAACAAGATAGATCTT TTAAAAAACCAAAACCAAAACAAAAC	2.605
68	A_51_P164393	Txndc2	AAGACATCATCCAATCCAAGAAAGAGGACAGGC CCAAGTCTCAGAAGACATCATCCAAT	2.555
69	A_55_P2146590	1810011O10Rik	ACAAAAGACAAGCTTCTCAGTTTCTCAAAGTGC GGAAATATTCCATCAAGGTACTGA	2.554
70	A_55_P2138718	Gm14483	CTACTAGCTGGGGAGCAAATCAAATATGCTATT AAAGCATCTAGATCAAACCAAAAAA	2.544
71	A_51_P257892	Adam25	TAGAACTACCTATGAGTGAAGAACCAAGTTCC CACCCAGAAAACAAAGAAGATACCA	2.540
72	A_55_P2037873	Gm10322	GGGAGGCTGAGGCAAAATTACAAGTTCTGGAG TACATAGTAAAAATTATCTCAAAAAA	2.502
73	A_55_P2201020	AI790442	AAAGAAAAAGAAAAGGAGAAAAGAAAAGAA ACAAAACCTAGCTACCCTAGCAAAAAA	2.498

74	A_55_P2115181		CTACCAGTCTGTGCCTTAGGTGAACTCTGTAAAA ATGGAATAAAAACAACTATCTTCATAA	2.483
75	A_52_P28582	Zmym2	CATCTTCAAAAAATGAAGAACTACAAGGAAACG ATCCCAAAATTTCTTCCTCATCGAAAG	2.482
76	A_55_P2412859	5830468K08Rik	CAAACCCAACCTTAGAAAGGCTACACACAATGGC TACAATTTTCTAAAATGATACCTTA	2.475
77	A_66_P128733	BC106175	GTAAAGTCTAGGAAAAGGCTCCAGAGTCAAAAC CCGGCAACCCAGGGACCAATTCAAATC	2.473
78	A_55_P2054703	Gm2659	AATATAAAGCATCTATAGGACCTAACACCCAATT ACATACCCTAATTCCTAACAGTC	2.472
79	A_66_P122377	Cd84	CTAATAGGCAGCAAAGCATAAGCAGGTCTCTTAC AAAAACATAACAGTAGATTCCTTATC	2.470
80	A_55_P1968325	Agbl3	TAAGCAGAGAATTCCTTACCTAACCAAAACCAGC AAGAAACCCAGTGAGAGTGATGGCCT	2.445
81	A_55_P2216988	A830021M18Rik	GCTCTCTCTAAAACCTAACGCCGCCACAGACAT ATGAAATTATATGCCACATCTCCCGC	2.444
82	A_52_P81693	LOC100044247	TCAGAGACCTTCTCAGCCAGGAAACCATCAACCA CCCCAGCATGGAAACAATGAACAGCC	2.440
83	A_55_P2004031	Ctrc	TCTCTTTCAGTACCTCAGGGATGACACTTGGAG GCACACCTGTGGGGCAGTCTCATCA	2.434
84	A_66_P135403		GCCTGAGCCTCAGAGATCATAATGGGAGGGCTT GGGACTTGACGGAGATCATATAAGAAC	2.416
85	A_55_P2367878	Ncrna00085	CCAAAGGAATCCAATAGAAAAGCACATACTA GGTACTGTTCAAAAACCTATAAGAAAC	2.410
86	A_55_P2017086	Ezh1	GCATTGGGATCTTTGCCAAGAGAGCAATTCAGG CTGGCGAAGAGCTCTCTTTGATTATA	2.406
87	A_55_P2401624	C630004L07Rik	GGATGCCTTATCTACTAAGAAGCACACACAGAG ATTGAAAACACTTAAATAAATGAGCA	2.403
88	A_55_P2054827	Rxfp3	CAGGAAAAGAAACCCTAACTAGGACATGCTCCA ATATACAAAATAAATAAAGGGTCAAC	2.398
89	A_55_P2005549	Tnn	GTTTTCTGTAACCAAGTCAGTGACCTTTGAAGTA ACTTAAATTCCTACTCAAGAAAACAC	2.394
90	A_55_P2183592	Rpl19-ps5	GAAACAACCTCCCTTACAATAGCCACATATAATA TAAAATATCTCAGGGTAACTCTAACC	2.393
91	A_55_P1954521	5430417L22Rik	AACGACCGCGGGGGCTGGACGAGGACGAAGAG GAAGCGGCCGAAGAGCCCCGGAGTCGTT	2.392
92	A_55_P2070510	Gas1	ATGGATGAGGACGCCATGCCAGAAGTGCGCGG AACTCGACAAACTTTCCAGCGGCC	2.387
93	A_55_P2162573	Art3	CCAACGGGTGCTAACCATCCAGACCTGCTTTGGA GTCGCGTGGGAAAGTTTCTTAATAA	2.385
94	A_55_P2175296	Gm9480	AATGAAAACCTGAGTCTTTCAAAGGAGACACC GAGAAGAAGTTCAAGACCCCAATGCA	2.377
95	A_55_P2073825	Ocm	AGCCCCATCTGGCAGACAAGGCCTTTAAAAATC ACCCAATAAATAATTTCTCATCATT	2.371
96	A_55_P2081452		GGAAAATGTAGAGCATTTGCCTAGCATAACATGA ACCCCAAGTTAATCCCAACATTGC	2.370
97	A_51_P209818	Prtn3	TTCCAGAACAATTACAACCCCGAGGAGAACCTCA ATGACGTGCTTCTCTCCAGCTAAAC	2.359
98	A_55_P1979950	LOC100046257	GTCCCTGCTAAGATAGAATATAGTCCCTCAAAC GTAAGCCAGAATAAACCTTCTCTCC	2.357
99	A_55_P2303868	5033421B08Rik	TAAGTTCCTGACGCCTTGACTTAACCCAGGATGA ACAATACCCTAAGCCATACAACCAA	2.349
100	A_55_P2022024	Olfr212	TTCCCTGTCTTTCTTAATGAACTGTAACCTGAA AGCCAAATAAACCTTTCTCTCCC	2.346
101	A_55_P1976744	Gm4324	GAAAAATACGTCTGCCACATCACAGAGATGAAC GAAAACAACCGCCAATCAGATCCATC	2.343
102	A_55_P2069550	Gm6750	GCTGAGAAAAGAAATTAGGGAAATGACACCTTCA CAATAGTCACAACAGTATAAAGTATC	2.338

103	A_55_P2123854	Zfhx2	CCAGAGGAATGAAGTAAAGAAAAACATAAACTT TGAATATACATAGAGAGAGAGAAAAA	2.328
104	A_55_P1971264	6530403M18Rik	ACACGATGGGATGGTGTAGTATAGAATAGAATT TATTC AAGGCATGGGGAGGGGAGTTAA	2.308
105	A_52_P459259	4930528A17Rik	CTTAACCTAAATATTGGAAAATGACTTTCTTGAA ATGTCAGTGAACAAAAAGAGTTAT	2.302
106	A_52_P125253	Olfr123	CCATGGGAAGTTCATCTCTCTTTTACACTGTTA TGACCCCGACCCTTAATCCCTCAT	2.299
107	A_52_P119060	Acpp	AGTCAAGTAAAAACAACACAACAGGTCACCTTTA TCCTGTGCTTCACTGTTTTTAATC	2.299
108	A_52_P628411	Far2	TCTGAAACGACAGCAAATTTTCCACTATAAATT TTCCAATTCATGTAACATGCCTGC	2.292
109	A_52_P578790	Dok3	AGCGGCCAGCCACTGCAGGACAGAGGTGATCAC CCAAGACCAGGAACAACCTCGAACATA	2.292
110	A_55_P2236622	Gm2763	AGAAGTTCATCTTTTAGGAAACGCTCCTTGCTTAA ATCTCCAGAATTCATCTGTTTCAA	2.290
111	A_51_P372702	Il16	AACAGTTCTGTGAGATGCACCCTGCCATGAAGAA CACATTCAAACACATAGAAGACTTTT	2.287
112	A_52_P186751	BC061237	AACGATTTGAATGACAGGATCACTTTGAGACAT TCATGCTTGAGATGCAACATAACCAG	2.282
113	A_66_P102853	Ccbe1	TCTGAAAACAAGATCACCACGACCAATACCCAT GTCTGAAGTCTTCGGGCGAGCTCACC	2.282
114	A_55_P2143832	Col4a4	GTACCCATGCAAACGCCACCCACAGACATACTC ATACACATAGAAACAAAAGTAAATAA	2.272
115	A_51_P224064	Klhl38	AAATGCCAGTGAATGCTTTTCAAAAATTCATCCT TACCCCTGAATCAATGTCAGAAAC	2.272
116	A_55_P1973417	LOC100041903	TGGAGTCCCTACAAACAATGACCAATAAACATG GTAAGGCGTACCAATAACAACCAGCA	2.271
117	A_55_P2171354	Gm7111	GAAACCCGTACGACAACAGTACGAAACCAACCC AGAGGACTGCTTTTCTGGACCAACCC	2.270
118	A_55_P1986691	Card6	AGACATCATTAATTACACTCAGTGGTTACCCAA ACCAAACCAAACCAAACCAAACCAA	2.270
119	A_55_P2139546	B3gnt3	CTCCCAACACCAGACAGGAGAGAAAAAGTAT AGAGGAAAGAAAAGAGATTACCCAATA	2.268
120	A_55_P2018215	Gm3859	CAAGAAACCCCTTATAATCTTCTTGAGTACCTGTG TACATGTGAATATACATACATACAC	2.267
121	A_55_P2098573	BC003267	GTAATGAGAGAAACCCTATAAATGGAGTCAAT ATTAGGAAGCCTTTTCTCAGAACAGTT	2.265
122	A_55_P2222437	D430040D24Rik	AAGCAAGAAGATCACAAGTTTAAAGCCAGCCAA GGCTGCTGCATAGAAAGAAAGCATCTC	2.260
123	A_55_P2078133	Gm7289	ACCCAGCCAAAAATTCGCAAAAAATCAAATAA AATGGAAAAGCAAGCAGCACCTTTAA	2.260
124	A_66_P128963	Cyp2d9	GCCATACTGGATAACCTGTTGACTGAGAATAGG ACCACCTGGGACCCTGTCCAAGCACCC	2.258
125	A_51_P308597	Gcm2	ACAGCATTTTGAACCTGCCACACCACACAGGC TATTCACCAGATGACACAAATTAATA	2.242
126	A_55_P2397854	4921518K17Rik	CTAGACCTTGGCCTGCCAGATGCCATATCTCTCT GCACTACCTTTATAAGACATTTTTT	2.238
127	A_55_P2173408	Gm2419	TAACCGCGTGAGAACACCTTCTAAGATAAGGA TATTCAAATAAAATACTACAACATCA	2.237
128	A_55_P2051199	Gm13710	GCAAAAGGAAGACCCTCAGACTGAGGTTGAGAG TACTAATTTATGTGAATAAATAAATT	2.233
129	A_55_P2167776	Gm2169	AAGTGGGAATGAAGAATAAAAAATTAAGAAC TCTTCTCACCCAGAGCCCAACCCCT	2.232
130	A_55_P2220092	D230035N22Rik	AAGGATACACAGAGAAATCCTGTCTTGAAAAACT AATAGAAGGGAAAAAATAGCACTCCC	2.226
131	A_66_P111163	Gm10896	ATGTAACCAGGAGGCCTTCAAGGATGCAGA TGTGTCTACAACACAATGACATCGTC	2.224

132	A_55_P2339760	C230006B20	GAGTTCTGCCTCAACTTCCCTGAATGAACCTGTA ATTAGAAATAAATCCTTACCTTCCCC	2.218
133	A_52_P496956	Acsbg1	TGACATCTCCAATGCCTTACGTGCAAGTAGTTT CAATTCTAACCACTGCTCCTGTTGAG	2.218
134	A_55_P2021330	Dynlt1d	AATAAGGAACAGGAAACCTTTGCTTACAGAGGA GTCCAGACACAAACAGATAGAAGGGGC	2.213
135	A_55_P2019294		AGGACTAGTCCATCAGCAGAACACCCACCCCAAT GAAGCATGCATATATTCATCTTGAAC	2.207
136	A_55_P2076545	F5	TGGGCAAAAGTGCTTGCTGCCAAAACAAAACAA CAACAGCAACACAACAAAAACAAACC	2.202
137	A_55_P2138744	LOC100045653	AAATCAGAGCGAAGCCACTGAAGTGCGACTGTG ACCGCCGCTTGAAGACCTACTACACCC	2.200
138	A_51_P449995	C6	TTGCTGGACCATCAAGGTATACATGCAAGGAAG ACTCCTGGACACCTCCATTTCAAATT	2.194
139	A_55_P2119613	Prss55	TTGACTGCTTAGAGCCTTGCCAACCTGGAATA AAACAATGCAGTCTCTGATCCACCCT	2.193
140	A_55_P2020242	LOC640683	TACAGTCCCTCTCCAACCTAAGGGTCACAGAACC TGCTTTGGGGACCATGCCATGGCAC	2.192
141	A_55_P2061879	Opn4	ACAGTCTTCTGCAGTCAGAACCTAGAAGATGGA GAACTCAAGGCCTCTCCAGCCCCCA	2.191
142	A_55_P2122300	Cir1	ACAGAAGAGCAAAAATAAACACAAAAAACGTAA AAACAATCCCCTTCTCTTCTCTCTC	2.189
143	A_52_P564413	Pik3c2g	TCTCCCCATCATCATTATCCTACTCAATAGACT CCATACCGAATAGAGAGAAAAGAAG	2.187
144	A_55_P2042452	Vgll1	AGATGTGGGCCCTTCAACATTTAGTCCAGCAAG ATAGATACAAAACCATCCTCTGGAA	2.186
145	A_55_P1974377	Defb26	CCTATCTATTCTGGGCCACTAACACTAAACCATT CACTATGATGCCTAATACTACTTAA	2.182
146	A_55_P2122075	Pdcd1lg2	ATCCTGGCAGCCTCTGAAGTTCTAATTAAGTGA AGCATTTAAGCAACACGTCAAGTGCC	2.174
147	A_55_P2278845	3830408C21Rik	GACCCCAATAAAAAGTCAAAGGACCAAAATGGA TGCAATGAGTATCTTAAACTTGATCA	2.174
148	A_55_P1954985	Foxn3	CCAGTACCTGGCCTTCAAAGGTGACATTTTCAAG CTAAGGTTAAAAACAAAAACAAAA	2.170
149	A_55_P2049323	Gm4755	GACTCTACACTGTGGAACACGCTTCTGGGAATT CAACAGCCTCCTTACACACACCACA	2.163
150	A_55_P2121716	Gm9513	GGGACTGTTATGATTGGAGATAAGACAGTAAAA ATGAACTGTTGCAACAACAAATCTTTC	2.162
151	A_55_P2051879	4930473A06Rik	GTGCAGGGATATGTCTACTTAAATAATGAAACAA CCCCTTTTTCTCCCTAAGTTTTAT	2.150
152	A_55_P1983523	Cd300ld	GTTCTAGGTCAGTCTGCTTTACAGAGTGAGTTAT AGGACTACACAGAGAAATCCAAAAAA	2.149
153	A_55_P2285669	Gm4250	AACTGTTGAAATAACAGAAAGAGCAGCAGACA GATCGGACCCTGGAATCAAGTTTGGTG	2.148
154	A_55_P2172001	Mrgpra2a	CAACATCTCCTCACTAAGTTTCTACCCCTC CTGAATAAAAAGCATTAAATCAGAAA	2.143
155	A_55_P2289707	Cacnb4	CGACATAGGCTTTGAGGCTGCCGAAACAAACAA ACAAACAAACAAACAAACATCATCTGT	2.141
156	A_55_P2138591		ATAAGCTGCACATAGTAAAAGGACAAGTCCAGG GCTAGCAAGATCCCTTTCAGCTAACA	2.140
157	A_55_P2111825	1700001C02Rik	CCCAGGGAACTTGGCCTGACCAGGCTGGCTTG CTTGAATAAAAATCTTACGCCACAACC	2.136
158	A_51_P229363	Rg9mtd3	AACACTCCTCTTATCCAAAACCTGAGCTCGTAG GTTTTAAGATTGTGGGAATTCTGTT	2.132
159	A_66_P110425	Kif6	GGGGGCGAGTGGAGGTGCAGAAATAGGTGCC AGAAATAATTACAGCTGAATAAAAATAC	2.131
160	A_55_P2122945	Olf41	CTGAGGAACAAGGATGTCAAGCTTGCCTGGGC AGAATCTTACCCTTTCTCACATTAA	2.124

161	A_55_P2102683	LOC100047543	GAGAGTCAAAGGTTTTCTTCGAGCACTAGGGAA ACAGCAGTAAAGGTAGAGAAGGAAAAA	2.123
162	A_55_P1996414	LOC100045477	ACAGCTGAAATTGCTCCACAACTGAGCTGGTG GAAGTAAAAAGTTCTGGATTACCCCA	2.117
163	A_52_P327610		GTCACACTCGGCGGGCCGGGAGAACCAGAACCC GCGGCTGGTGCTGCCACCCAGCAGCGC	2.113
164	A_55_P2348126	1500032F14Rik	CATCGAGTCCAGGCCAGCCTCAAAAAACAAAC AAAACAAAATAAAATGGCATTCAAATC	2.112
165	A_55_P1976204	Cdkn1a	TGGGGTAGTTTTCCATAGTGACCCGGGTCTTCTT GTGTTTCAGCCACAGGCACCATGTCC	2.103
166	A_55_P2088178	Cbln2	GGGGGCTCGGAGAGAAAAACAAAACAAAACAA AACAACAAAATTATGTTTCAGTCCTTGT	2.099
167	A_55_P2428514	Retn	ACTCAGTGCGCGAATCCACACACAAGCACACAT ACTTAAAAATAAAACAAAACAGGCTG	2.095
168	A_55_P2061243	LOC100048863	AATGTCTGTTGAAAGAAATTGCCTGCCATTAAC ACATTCATGGGACCTAACACTAC	2.095
169	A_55_P2117272		TGAGGTCTAATGTGCCAACTTCCCCTTAACATT TTACTTTACCTAAACAACCATTTTC	2.089
170	A_55_P2158324	Gm4958	AGGCACCACAGTGAGCCACACAGATCGCATAGA AGGCACAGCCATCATCGGCACAGCTAA	2.087
171	A_55_P1983828	Zbtb11	TATGCGGCAAAGATTTTATGAAAAAGCTTTATT CAGAAGACATGTAAGAAGGCCACCC	2.085
172	A_55_P2211937	E130101M22	AGGTAATCATGTGGTGCATAGATAAATGCAAG CAAATCATCCATACATAAAATCCCT	2.081
173	A_55_P1952684	LOC100048289	TGGAACATGAAAATCAAGAATTGTAATGCA ACAATAAGGGGGAAATGCAATTAATAA	2.078
174	A_55_P2036460	D930020E02Rik	AATTTCCAATATAAAAAACTGCCCAAGACTCCC CAGATGAGGACACCATTCTACATAA	2.071
175	A_55_P2022789	Zfp646	AAGGGTTTCTCAAACCTCATGTCCTCAAGAACC ACCGGCGCATCCATGCAGACCCTCGA	2.070
176	A_51_P519648	Mical3	AGAAACAAAAGATATCCACCTGGAATGGAGAA CATGGTGAATCCCCGAACCACTCCCAA	2.065
177	A_55_P2159573	Reep6	AATGTCCAGGCTCTGACAGTTCTTCAGACTCCC AGACAAAGACCACTGCAACCACAG	2.063
178	A_55_P2269289	Dgkg	TTTCTCTGAGGAGGAAAAGCCGTTCAAAGACTA AACAATATGCCAAACACCAGCTCTAC	2.058
179	A_52_P319726	LOC100047731	TTGCCCTAGGAGAAGCCTCACGTGAAGTAGGAA GTACTAATGGAAGGGTGGAGACATGTC	2.056
180	A_55_P2004457	Prrg1	CTCATTGCTACTGTAGACTCCCATACTCAAGA ATTTAGCCAAATCAAATCAAATC	2.056
181	A_55_P2121956	Gck	ACATCAGTGATCCGGGAAGAGAAGCAAGCCACC CACAGCATCTCTCCAGGAAACCACCA	2.053
182	A_55_P2032886	Pip5k1c	ATTCCAGCAGTGAATGGGCGGGGAGCGACTG CTCCTCCACATCGGGATCATTGATATT	2.049
183	A_55_P1999012	LOC100046875	GGCTCACAAGTCCACATACATAACTTACATAT ATCTGGATAAAACACTTAGACAGATA	2.047
184	A_55_P2394495	1700023A20Rik	CATACCAGGCATGTCCATCTCTCAGTGCAAAATA GTGCTTCCCAAATAAAGCCAATCTT	2.046
185	A_55_P2174945	Gm4615	TTAAAAGAAGCAGTGCAAGCTCAAAAATACTT CTTTCTCACTCAGGCAGGCACACCCT	2.046
186	A_55_P2164890	5830415F09Rik	TGAAGCTAAGACTGCTTTCACATCGTCAGGGGA AGAATATAATTGAAAACCTCCCAACC	2.045
187	A_55_P2410325	2610028D06Rik	GTAATTATACACACAGGTACACACAGACAGGCA CACATGAATAAAACCAATTTAAAAA	2.044
188	A_55_P2082376	Crybb2	TCATCATCTTCGAACAGGAGAACTCCAGGGCCA TTCCACAGCTCAGCGGGCCCTGCC	2.041
189	A_55_P2026734	Rgs4	GCTTCCGACGAAACACAAAATCTTAATGATGAC AGTAAATAAATGCTTCTCAAAAACA	2.041

190	A_55_P1965584		GCCGCCTCTTTCAGAAACCAAGAGAAAATGGTG GGAGGCGAAAAGAAAACTAAATAAAA	2.039
191	A_55_P2090909	Ptx4	GTCCATATGCCACACCGTGACTGTGTACACACA GTCAAGGCCATCAAGAACAAGCCTCA	2.032
192	A_55_P2008644	Gm6268	CCTACTAGCAAAATTCCTCCTCTAAATTTAACAT GGTTCATTCAAGTCCAAATGAAAC	2.028
193	A_55_P2323503	AA960618	GGTTAGGAAACTAGCACCCAAGCAGCAGAGAGG ACACAAGCTCATTCCCCTTACCCCAT	2.027
194	A_55_P2144296	LOC100046658	CAGGAGAGAAACCTTACAAATGTAATGAGTGTG AGAAATCTTTTACAAAGTCACACAAAC	2.026
195	A_55_P2096370	Gm3865	AGCCACAAGTCGCAGAATGTGATCCCGAACCAA ATCCTTCTAAAAATTAGCTTCGGGCAA	2.020
196	A_55_P2176894	Gm2181	AAAGAAAGAAAGAAAGAGAGAAAAGTGGAAAT ATCAATCAACCAACCAACAATCAATCA	2.016
197	A_52_P574759	Rbpjl	GAGCAGGAAGGAGAGAGATAGCTCACCTGACCT CAGGCCACTCACTGTCCTCAGACATAC	2.007
198	A_55_P2138966	Nab2	AGCTGAATAAGAAGCTGGCGCGGAGCGTGGGG CACATCTTTGAGATGGACGATCATGACG	2.005
199	A_51_P148684	Pou6f2	AAAGACTTGCCCCAGTCATCATCTCCCTTGATGT AAAAGACTAAAAACAATAAACTAC	2.001
200	A_65_P07627	Dach1	AGGATCGAAGACAAAAAGCTATCCACTATATGTT AAGAGACTCTTATTAACCTGTTGTAC	2.000

**Table S3. Induction of genes belonging to cellular reprogramming**

Phases in cellular reprogramming	Fold induction in MEF treated with	
	$\delta$	SAHA
Initiation		
<i>Cdh1</i>	43.3	1.13
<i>Esrp1</i>	2.8	1.07
<i>Cldn7</i>	4.31	0.9
<i>Alpl</i>	25.3	-
<i>Gdf3</i>	6.9	0.9
<i>Nanog</i>	42	1.2
Maturation		
<i>Utf1</i>	3.7	0.9
<i>Zfp42</i>	488	-
<i>Esrrb</i>	10.2	-
<i>Lin28</i>	5.2	1.13
<i>Prdm1</i>	2.3	1.5
<i>Dppa4</i>	20.2	-
Stabilization		
<i>Tcf7</i>	3.7	0.91
<i>Nodal</i>	5.478	1.232

Fold induction values in MEFs treated with either  $\delta$  or SAHA over DMSO treated MEFs

**Table S4. Primers for q-RT PCR analysis**

Gene	Endogenous primers
<i>Rex1</i>	F: CAGTCCTGCACACAGAAGA R: ACTGATCCGCAAACACCTG
<i>Cdh1</i>	F: CAGGTCTCCTCATGGCTTTGC R: CTTCCGAAAAGAAGGCTGTCC
<i>Snai1</i>	F: AAGATGCACATCCGAAGC R: ATCTCTTCACATCCGAGTGG
<i>Snai2</i>	F: TGATGCCCAGTCTAGGAAAT R: AGTGAGGGCAAGAGAAAGG
<i>Zeb2</i>	F: TAGCCGGTCCAGAAGAAATG R: GGCCATCTCTTCCTCCAGT
<i>Rex1</i>	F: AGGAAGTCAGCACCACCGTAGT R: AAGCAGGAAGAGGGCAATGGCT
FGF5	F: ACAAGAGAGGGAAAGCCAAGAG R: GAACAGTGACGGTGAAGGAAAG

**Table S5. Promoter primers for ChIP analysis**

Gene	Primers for ChIP analysis
<i>Oct-3/4</i>	F: ATCCGAGCAACTGGTTTGTG R: CAATCCCACCCTCTAGCCTT
<i>Nanog</i>	F: GGATGTCTTTAGATCAGAGGATGCCC R: CCACAGAAAGAGCAAGACACCAACC
<i>Dppa4</i>	F: GACCAGAAGGGGAGGGGAACGG R: ACCTTCTTGTCTCCAGCAGTCTCC
<i>Cdh1</i>	F: CATGCTGGGCTACATAGCAA R: TGGGCCTGGAATTGTCTTAG
<i>Rex1</i>	F: GCATCCTCTGCTTGTGTAATTC R: CTCAGTTATGCAAATGCCTCTTC
<i>Gapdh</i>	F: ACCAGGGAGGGCTGCAGTCC R: TCAGTTCGGAGCCCACACGC



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