rank = rank based on false discovery analysis
<FP> = false positive rate
FDR = false discovery rate
log2 (ko/wt) = log scale 2 (mean ko std chow / mean wt std chow)
log 2 (koro/ko) = log scale 2 (mean ko ro chow / mean ko std chow)
log 2 ttest ko/wt = unpaired t-test for wt std chow (log2 wt1, log2 wt2, log2 wt3, log2 wt4) versus ko std chow (log2 ko1, log2 ko2, log2 ko3, log2 ko4)
log 2 ttest koro/ko = unpaired t-test for ko ro chow (log2 koro1, log2 koro2, log2 koro3, log2 koro4) versus ko std chow (log2 ko1, log2 ko2, log2 ko3, log2 ko4)
Acc = GenBank Accession number
Description = GenBank description

rank	<FP>	FDR	log2 (ko/wt)	log2 (koro/ko)	log2 ttest ko/v	log2 ttest korc	Acc	Description
1	4.54E-11	4.54E-11	-2.63	1.40	0.00	0.03	NM_007823	cytochrome P450, family 4, subfamily b, polypeptide 1 (Cyp4b1)
2	1.19E-10	5.96E-11	-2.72	-0.31	0.00	0.03	NM_021050	cystic fibrosis transmembrane conductance regulator homolog (Cftr)
3	1.91E-09	6.35E-10	-1.87	-0.22	0.00	0.68	NM_029562	cytochrome P450, family 2, subfamily d, polypeptide 26 (Cyp2d26)
4	1.62E-07	4.05E-08	-1.48	0.20	0.00	0.30	NM_022434	cytochrome P450, family 4, subfamily f, polypeptide 14 (Cyp4f14)
5	2.03E-07	4.07E-08	-1.43	0.53	0.00	0.08	NM_025807	solute carrier family 16 (monocarboxylic acid transporters), member 9 (Slc16a9)
6	6.22E-07	1.04E-07	-1.35	-0.29	0.00	0.10	NM_029562	cytochrome P450, family 2, subfamily d, polypeptide 26 (Cyp2d26)
7	6.87E-07	9.81E-08	-1.36	-0.13	0.00	0.43	NM_019545	hydroxyacid oxidase (glycolate oxidase) 3 (Hao3)
8	9.13E-07	1.14E-07	-1.28	-0.01	0.00	0.99	NM_007819	cytochrome P450, family 3, subfamily a, polypeptide 13 (Cyp3a13)
9	1.57E-06	1.74E-07	-1.25	0.09	0.00	0.67	NM_007819	cytochrome P450, family 3, subfamily a, polypeptide 13 (Cyp3a13)
10	2.03E-06	2.03E-07	-1.25	0.06	0.00	0.71	NM_033603	amnionless (Amn)
11	2.14E-06	1.94E-07	-1.20	0.06	0.00	0.55	NM_011169	prolactin receptor (Prlr)
12	2.19E-06	1.82E-07	-1.28	0.37	0.00	0.07	NM_173404	bone morphogenetic protein 3 (Bmp3)
13	2.30E-06	1.77E-07	-1.18	0.15	0.00	0.45	NM_053078	DNA segment, human D4S114 (D0H4S114)
14	6.62E-06	4.73E-07	-1.21	0.29	0.01	0.27	NM_024435	neurotensin (Nts)
15	1.40E-05	9.30E-07	-1.29	0.18	0.00	0.34	NM_026716	syncollin (Sycn)
16	1.42E-05	8.33E-07	-1.22	-0.20	0.00	0.62	NM_133670	sulfotransferase family 1A, phenol-preferring, member 1 (Sult1a1)
17	1.42E-05	8.33E-07	-1.34	0.96	0.02	0.46	NM_010378	histocompatibility 2, class II antigen A, alpha (H2-Aa)
18	1.62E-05	9.02E-07	-1.31	0.31	0.01	0.37	NM_153506	C lectin-related protein A (Clra)
19	2.19E-05	1.15E-06	-0.98	0.04	0.00	0.71	NM_012033	tubulointerstitial nephritis antigen (Tinag)
20	2.32E-05	1.16E-06	-0.99	-0.45	0.02	0.27	NM_010005	cytochrome P450, family 2, subfamily d, polypeptide 10 (Cyp2d10)
21	2.41E-05	1.15E-06	-1.03	-0.42	0.00	0.12	NM_145146	afamin (Afm)
22	2.48E-05	1.13E-06	-1.09	-0.03	0.01	0.89	NM_145419	cDNA sequence BC016235 (BC016235)
23	4.19E-05	1.82E-06	-1.02	-0.07	0.00	0.77	NM_173735	RIKEN cDNA 2310044G17 gene (2310044G17Rik)
24	5.27E-05	2.19E-06	-1.05	0.27	0.01	0.26	NM_008100	glucagon (Gcg)
25	7.10E-05	2.84E-06	-1.39	-0.48	0.00	0.14	NM_011315	serum amyloid A 3 (Saa3)
26	7.55E-05	2.90E-06	-0.88	-0.08	0.00	0.61	NM_028270	aldehyde dehydrogenase 1 family, member B1 (Aldh1b1)
27	8.18E-05	3.03E-06	-1.10	-0.34	0.01	0.34	NM_008585	meprin 1 alpha (Mep1a)
28	1.04E-04	3.72E-06	-0.93	0.41	0.00	0.13	NM_009205	solute carrier family 3, member 1 (Slc3a1)
29	1.41E-04	4.87E-06	-0.99	0.70	0.01	0.37	NM_207105	histocompatibility 2, class II antigen A, beta 1 (H2-Ab1)
30	1.46E-04	4.87E-06	-0.89	0.14	0.00	0.33	NM_027286	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (Ace2)
31	1.66E-04	5.35E-06	-0.91	0.33	0.01	0.23	NM_007876	dipeptidase 1 (renal) (Dpep1)
32	1.67E-04	5.23E-06	-0.90	-0.15	0.00	0.42	NM_144930	expressed sequence AU018778 (AU018778)
33	1.77E-04	5.21E-06	-0.91	-0.48	0.00	0.01	NM_145079	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6)
34	1.77E-04	5.21E-06	-0.82	0.11	0.00	0.48	NM_009202	solute carrier family 22 (organic cation transporter), member 1 (Slc22a1)

35	1.97E-04	5.63E-06	-0.97	1.14	0.02	0.21	NM_207105	response to metastatic cancers 1 (Rmcs1)
36	2.16E-04	6.01E-06	-0.93	-0.11	0.05	0.93	NM_145932	RIKEN cDNA D630035O19 gene (D630035O19Rik)
37	2.52E-04	6.81E-06	-0.90	-0.03	0.01	0.99	NM_010893	neuraminidase 1 (Neu1)
38	2.76E-04	7.25E-06	-0.88	-0.46	0.00	0.02	NM_009178	sialyltransferase 4C (beta-galactoside alpha-2,3-sialytransferase) (Siat4c)
39	2.80E-04	7.17E-06	-1.01	1.28	0.02	0.21	NM_010545	Ia-associated invariant chain (Ii)
40	2.90E-04	7.07E-06	-0.95	-0.29	0.00	0.10	NM_021456	carboxylesterase 1 (Ces1)
41	2.90E-04	7.07E-06	-1.49	-0.37	0.01	0.27	NM_008630	metallothionein 2 (Mt2)
42	3.01E-04	7.16E-06	-0.84	1.01	0.02	0.19	NM_010379	histocompatibility 2, class II antigen A, beta 1 (H2-Ab1)
43	3.25E-04	7.56E-06	-0.91	-0.12	0.02	0.69	NM_007860	deiodinase, iodothyronine, type I (Dio1)
44	3.32E-04	7.54E-06	-0.76	0.33	0.03	0.23	NM_019823	cytochrome P450, family 2, subfamily d, polypeptide 22 (Cyp2d22)
45	4.10E-04	9.11E-06	-0.77	-0.08	0.00	0.63	NM_007410	alcohol dehydrogenase 5 (class III), chi polypeptide (Adh5)
46	4.46E-04	9.70E-06	-1.03	-0.23	0.02	0.68	NM_026085	RIKEN cDNA 3110049J23 gene (3110049J23Rik)
47	4.95E-04	1.05E-05	-0.83	0.72	0.00	0.00	NM_020043	neighbor of Punc E11 (Nope)
48	5.60E-04	1.17E-05	-0.88	-0.11	0.01	0.87	NM_011542	transcription elongation factor A (SII), 3 (Tcea3)
49	5.85E-04	1.19E-05	-0.81	0.87	0.01	0.13	NM_010382	histocompatibility 2, class II antigen E beta (H2-Eb1)
50	6.32E-04	1.26E-05	-0.83	-0.15	0.01	0.62	NM_020332	progressive ankylosis (Ank)
51	6.63E-04	1.30E-05	-0.81	-0.24	0.00	0.01	NM_007819	cytochrome P450, family 3, subfamily a, polypeptide 13 (Cyp3a13)
52	6.67E-04	1.28E-05	-0.87	-0.53	0.00	0.00	NM_201410	UDP glucuronosyltransferase 1 family, polypeptide A6B (Ugt1a6b)
53	8.19E-04	1.55E-05	-0.80	0.06	0.00	0.54	NM_011674	UDP-glucuronosyltransferase 8 (Ugt8)
54	1.07E-03	1.98E-05	-0.83	0.70	0.01	0.07	XM_131801	cytidine deaminase (Cda)
55	1.15E-03	2.10E-05	-1.58	-0.23	0.01	0.77	NM_009155	selenoprotein P, plasma, 1 (Sepp1)
56	1.21E-03	2.17E-05	-0.67	0.19	0.00	0.10	NM_146139	vav 3 oncogene (Vav3)
57	1.28E-03	2.25E-05	-0.75	-0.05	0.01	0.77	NM_029614	RIKEN cDNA 2310046G15 gene (2310046G15Rik)
58	1.32E-03	2.28E-05	-0.68	0.12	0.00	0.49	NM_028051	solute carrier family 39 (metal ion transporter), member 5 (Slc39a5)
59	1.49E-03	2.53E-05	-0.85	-0.10	0.02	0.89	NM_007472	aquaporin 1 (Aqp1)
60	1.57E-03	2.62E-05	-0.95	0.03	0.01	0.74	NM_013602	metallothionein 1 (Mt1)
61	1.99E-03	3.26E-05	-0.63	-0.14	0.00	0.32	NM_177870	solute carrier family 5 (sodium-dependent vitamin transporter), member 6 (Slc5a6)
62	2.09E-03	3.37E-05	-0.68	-0.27	0.00	0.01	NM_153598	expressed sequence AI788959 (AI788959)
63	2.13E-03	3.37E-05	-0.65	0.41	0.01	0.03	NM_177564	cDNA sequence BC022224 (BC022224)
64	2.29E-03	3.58E-05	-0.69	0.30	0.01	0.08	NM_133946	NACHT, leucine rich repeat and PYD containing 6 (Nalp6)
65	2.33E-03	3.58E-05	-0.68	-0.08	0.00	0.59	NM_133960	RIKEN cDNA 9130231C15 gene (9130231C15Rik)
66	2.39E-03	3.62E-05	-1.46	0.52	0.04	0.24	NM_008256	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (Hmgcs2)
67	2.44E-03	3.64E-05	-0.64	0.69	0.01	0.01	XM_355937	
68	2.55E-03	3.75E-05	-0.72	0.03	0.01	0.75	NM_007694	chromogranin B (Chgb)
69	2.95E-03	4.28E-05	-0.67	1.11	0.04	0.00	NM_009034	retinol binding protein 2, cellular (Rbp2)
70	4.22E-03	6.03E-05	-0.63	-0.36	0.00	0.01	NM_023383	arylacetamide deacetylase (esterase) (Aadac)
71	4.51E-03	6.35E-05	-0.65	-0.02	0.00	0.73	NM_172928	doublecortin-like kinase 3 (Dclk3)
72	4.83E-03	6.70E-05	-0.63	-0.12	0.01	0.58	NM_021719	claudin 15 (Cldn15)
73	4.90E-03	6.71E-05	-0.65	0.09	0.03	0.63	NM_015747	solute carrier family 20, member 1 (Slc20a1)
74	5.18E-03	7.00E-05	-0.86	0.27	0.05	0.40	NM_028089	cytochrome P450, family 2, subfamily c, polypeptide 55 (Cyp2c55)
75	5.20E-03	6.84E-05	-0.61	0.29	0.00	0.09	NM_010023	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase) (Dci)
76	5.20E-03	6.84E-05	-0.63	-0.04	0.01	0.77	NM_010239	ferritin heavy chain 1 (Fth1)
77	5.42E-03	7.04E-05	-0.82	-0.17	0.03	0.77	NM_007902	endothelin 2 (Edn2)
78	6.09E-03	7.81E-05	-0.69	0.29	0.01	0.22	NM_183251	RIKEN cDNA 1810020D17 gene (1810020D17Rik)
79	6.76E-03	8.55E-05	-0.86	0.15	0.02	0.38	NM_025655	RIKEN cDNA 2010002A20 gene (2010002A20Rik)
80	6.85E-03	8.56E-05	-0.62	-0.23	0.00	0.01	NM_012033	tubulointerstitial nephritis antigen (Tinag)

81	7.05E-03	8.70E-05	-0.82	-0.35	0.01	0.14	NM_011314	serum amyloid A 2 (Saa2)
82	7.91E-03	9.65E-05	-0.59	0.07	0.00	0.25	XM_130038	cubilin (intrinsic factor-cobalamin receptor) (Cubn)
83	8.30E-03	1.00E-04	-1.13	0.60	0.04	0.09	NM_009475	proline-rich acidic protein 1 (Prap1)
84	8.75E-03	1.04E-04	-0.58	-0.19	0.00	0.01	NM_007670	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (Cdkn2b)
85	8.80E-03	1.04E-04	-0.75	0.33	0.02	0.08	NM_011406	solute carrier family 8 (sodium/calcium exchanger), member 1 (Slc8a1)
86	9.88E-03	1.15E-04	-0.66	0.54	0.00	0.00	NM_007647	ectonucleoside triphosphate diphosphohydrolase 5 (Entpd5)
87	9.97E-03	1.15E-04	-0.91	-0.55	0.02	0.17	NM_009117	serum amyloid A 1 (Saa1)
88	1.00E-02	1.14E-04	-0.71	0.51	0.03	0.04	NM_007607	carbonic anhydrase 4 (Car4)
89	1.07E-02	1.20E-04	-0.71	-0.22	0.01	0.16	NM_008116	gamma-glutamyltransferase 1 (Ggt1)
90	1.20E-02	1.33E-04	-0.54	0.37	0.00	0.02	NM_026362	RIKEN cDNA 5033414D02 gene (5033414D02Rik)
91	1.34E-02	1.47E-04	-0.57	0.38	0.00	0.02	NM_172692	glucosidase beta 2 (Gba2)
92	1.36E-02	1.47E-04	-0.53	-0.11	0.01	0.55	NM_026752	zinc finger, FYVE domain containing 21 (Zfyve21)
93	1.37E-02	1.47E-04	-0.61	-0.03	0.01	0.88	NM_009421	Tnf receptor-associated factor 1 (Traf1)
94	1.38E-02	1.47E-04	-0.65	-0.40	0.00	0.00	NM_145558	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/ (Hadhb)
95	1.39E-02	1.46E-04	-0.56	0.18	0.00	0.13	NM_013670	small nuclear ribonucleoprotein N (Snrpn)
96	1.42E-02	1.48E-04	-0.73	0.61	0.01	0.00	NM_133732	RIKEN cDNA 4931406C07 gene (4931406C07Rik)
97	1.42E-02	1.47E-04	-0.67	-0.34	0.00	0.02	NM_145079	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6)
98	1.52E-02	1.56E-04	-0.70	0.48	0.02	0.01	NM_011905	toll-like receptor 2 (Tlr2)
99	1.53E-02	1.55E-04	-0.76	0.21	0.00	0.18	NM_023480	fumarylacetoacetate hydrolase domain containing 1 (Fahd1)
100	1.65E-02	1.63E-04	-0.74	0.45	0.00	0.05	NM_009504	vitamin D receptor (Vdr)
101	1.65E-02	1.63E-04	-0.68	0.96	0.00	0.00	NM_027239	RIKEN cDNA 1810065E05 gene (1810065E05Rik)
102	1.86E-02	1.83E-04	-0.51	0.00	0.03	0.95	NM_008918	pancreatic polypeptide (Ppy)
103	1.91E-02	1.85E-04	-0.49	-0.21	0.00	0.06	NM_023270	ring finger protein 128 (Rnf128)
104	2.01E-02	1.93E-04	-0.64	-0.84	0.01	0.00	NM_019769	RIKEN cDNA 1500003O03 gene (1500003O03Rik)
105	2.08E-02	1.98E-04	-0.75	0.31	0.01	0.16	NM_182805	glutamic pyruvic transaminase 1, soluble (Gpt1)
106	2.12E-02	2.00E-04	-0.64	0.25	0.01	0.05	NM_008509	lipoprotein lipase (Lpl)
107	2.19E-02	2.05E-04	-0.48	0.02	0.00	0.86	NM_025337	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase) (Akr7a5)
108	2.20E-02	2.04E-04	-0.52	0.40	0.10	0.16	NM_009944	cytochrome c oxidase, subunit VIIa 1 (Cox7a1)
109	2.21E-02	2.03E-04	-0.66	0.40	0.03	0.16	NM_019414	selenium binding protein 2 (Selenbp2)
110	2.29E-02	2.08E-04	-0.58	0.36	0.05	0.16	NM_138670	mercaptopyruvate sulfurtransferase (Mpst)
111	2.35E-02	2.12E-04	-0.74	0.51	0.01	0.00	NM_013467	aldehyde dehydrogenase family 1, subfamily A1 (Aldh1a1)
112	2.39E-02	2.13E-04	-0.75	-0.13	0.04	0.90	NM_009132	scinderin (Scin)
113	2.55E-02	2.25E-04	-0.61	0.17	0.02	0.39	XM_129951	RIKEN cDNA 2010001C14 gene (2010001C14Rik)
114	2.66E-02	2.33E-04	-0.66	-0.80	0.01	0.00	NM_019769	RIKEN cDNA 1500003O03 gene (1500003O03Rik)
115	3.64E-02	3.16E-04	-0.76	0.41	0.11	0.38	NM_011328	secretin (Sct)
116	3.82E-02	3.29E-04	-0.47	-0.28	0.08	0.23	NM_009366	transforming growth factor beta 1 induced transcript 4 (Tgfb1i4)
117	4.00E-02	3.42E-04	-0.57	-0.36	0.00	0.03	NM_033174	SNRPN upstream reading frame (Snurf)
118	4.13E-02	3.50E-04	-0.58	-0.07	0.01	0.72	NM_016710	nucleosome binding protein 1 (Nsbp1)
119	4.44E-02	3.73E-04	-0.51	0.08	0.02	0.55	NM_009215	somatostatin (Sst)
120	4.71E-02	3.92E-04	-0.49	0.41	0.02	0.02	NM_007408	adipose differentiation related protein (Adfp)
121	4.87E-02	4.03E-04	-0.72	0.54	0.02	0.00	NM_009705	arginase type II (Arg2)
122	4.90E-02	4.02E-04	-0.44	0.22	0.02	0.09	NM_024236	quininoid dihydropteridine reductase (Qdpr)
123	5.44E-02	4.43E-04	-0.87	0.38	0.04	0.18	NM_029360	transmembrane 4 superfamily member 5 (Tm4sf5)
124	5.96E-02	4.81E-04	-0.81	-0.03	0.03	0.88	NM_016771	sulfotransferase family 1D, member 1 (Sult1d1)
125	7.30E-02	5.84E-04	-0.51	-0.11	0.00	0.50	NM_027865	transmembrane protein 25 (Tmem25)
126	7.41E-02	5.88E-04	-0.50	0.45	0.03	0.06	NM_009876	cyclin-dependent kinase inhibitor 1C (P57) (Cdkn1c)

127	7.60E-02	5.98E-04	-0.65	-0.08	0.02	0.79	NM_007706	suppressor of cytokine signaling 2 (Socs2)
128	7.68E-02	6.00E-04	-0.60	0.76	0.06	0.01	NM_009366	transforming growth factor beta 1 induced transcript 4 (Tgfb1i4)
129	7.76E-02	6.02E-04	-0.69	0.15	0.04	0.47	NM_177016	RIKEN cDNA 9130214H05 gene (9130214H05Rik)
130	7.89E-02	6.07E-04	-0.59	0.06	0.06	0.64	NM_133969	cytochrome P450, family 4, subfamily v, polypeptide 3 (Cyp4v3)
131	8.33E-02	6.36E-04	-0.42	-0.11	0.00	0.12	NM_010195	G protein-coupled receptor 49 (Gpr49)
132	8.38E-02	6.35E-04	-0.48	-0.05	0.00	0.36	NM_008772	purinergic receptor P2Y, G-protein coupled 1 (P2ry1)
133	8.68E-02	6.52E-04	-0.46	0.08	0.00	0.19	NM_145558	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-t (Hadhb)
134	9.15E-02	6.83E-04	-0.70	0.35	0.02	0.11	NM_178711	phospholipid scramblase 4 (Plscr4)
135	9.60E-02	7.11E-04	-0.72	-0.19	0.01	0.20	NM_145519	FERM, RhoGEF and pleckstrin domain protein 2 (Farp2)
136	0.1	7.72E-04	-0.66	-0.21	0.05	0.59	NM_020268	kallikrein 27 (Klk27)
137	0.11	7.84E-04	-0.43	-0.03	0.00	0.67	NM_010074	dipeptidylpeptidase 4 (Dpp4)
138	0.11	7.92E-04	-0.43	0.18	0.07	0.31	NM_053122	inner mitochondrial membrane peptidase 2-like (S. cerevisiae) (Immp2l)
139	0.11	8.25E-04	-0.46	0.15	0.01	0.30	NM_024284	hydroxyacyl glutathione hydrolase (Hagh)
140	0.12	8.36E-04	-0.83	-0.07	0.01	0.88	NM_011170	prion protein (Prnp)
141	0.12	8.34E-04	-0.60	0.43	0.05	0.14	NM_009150	selenium binding protein 1 (Selenbp1)
142	0.13	8.95E-04	-0.75	0.22	0.08	0.47	NM_021481	trehalase (brush-border membrane glycoprotein) (Treh)
143	0.14	9.65E-04	-0.41	0.22	0.01	0.02	NM_011068	peroxisomal biogenesis factor 11a (Pex11a)
144	0.16	1.13E-03	-0.81	-0.06	0.12	0.90	NM_017474	chloride channel calcium activated 3 (Clca3)
145	0.17	1.14E-03	-0.38	-0.11	0.00	0.04	NM_019810	solute carrier family 5 (sodium/glucose cotransporter), member 1 (Slc5a1)
146	0.17	1.18E-03	-0.47	0.46	0.02	0.02	NM_201410	UDP glucuronosyltransferase 1 family, polypeptide A6B (Ugt1a6b)
147	0.18	1.25E-03	-0.39	-0.22	0.00	0.03	NM_013670	small nuclear ribonucleoprotein N (Snrpn)
148	0.18	1.25E-03	-0.37	0.21	0.01	0.03	NM_021534	peroxisomal membrane protein 4 (Pxmp4)
149	0.19	1.25E-03	-0.52	0.07	0.01	0.63	NM_011696	voltage-dependent anion channel 3 (Vdac3)
150	0.2	1.34E-03	-0.47	-0.19	0.01	0.16	NM_009752	galactosidase, beta 1 (Glb1)
151	0.22	1.44E-03	-0.54	0.63	0.02	0.01	NM_016772	enoyl coenzyme A hydratase 1, peroxisomal (Ech1)
152	0.22	1.47E-03	-0.49	0.46	0.02	0.03	NM_201642	UDP glucuronosyltransferase 1 family, polypeptide A7C (Ugt1a7c)
153	0.23	1.47E-03	-0.38	-0.12	0.00	0.08	NM_009302	SWAP complex protein (Swap70)
154	0.24	1.53E-03	-0.44	0.04	0.00	0.57	NM_177595	RIKEN cDNA 9430023B20 gene (9430023B20Rik)
155	0.25	1.59E-03	-0.40	0.15	0.00	0.08	NM_146466	olfactory receptor 165 (Olfr165)
156	0.25	1.58E-03	-0.38	0.17	0.01	0.18	NM_009202	solute carrier family 22 (organic cation transporter), member 1 (Slc22a1)
157	0.28	1.75E-03	-0.69	0.22	0.00	0.07	NM_008587	c-mer proto-oncogene tyrosine kinase (Mertk)
158	0.28	1.75E-03	-0.67	0.46	0.00	0.00	NM_172759	RIKEN cDNA 9030624L02 gene (9030624L02Rik)
159	0.29	1.80E-03	-0.67	-0.36	0.00	0.02	NM_008212	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain (Hadhsc)
160	0.29	1.79E-03	-0.92	-0.02	0.02	0.98	XM_150350	
161	0.29	1.78E-03	-0.43	0.44	0.04	0.02	NM_013535	gene rich cluster, C10 gene (Grcc10)
162	0.29	1.81E-03	-0.40	-0.04	0.04	0.90	NM_170689	ankyrin 3, epithelial (Ank3), transcript variant 4
163	0.29	1.80E-03	-0.57	-0.33	0.04	0.20	NM_177912	expressed sequence AI987692 (AI987692)
164	0.32	1.92E-03	-0.36	0.09	0.00	0.24	NM_013839	nuclear receptor subfamily 1, group H, member 3 (Nr1h3)
165	0.32	1.95E-03	-0.45	0.26	0.01	0.01	NM_026947	RIKEN cDNA 1810022C23 gene (1810022C23Rik)
166	0.32	1.94E-03	-0.41	-0.28	0.01	0.03	NM_007860	deiodinase, iodothyronine, type I (Dio1)
167	0.34	2.01E-03	-0.37	0.42	0.00	0.00	NM_053155	calmin (Clmn)
168	0.34	2.01E-03	-0.35	0.13	0.02	0.29	NM_053177	mucolipin 1 (Mcoln1)
169	0.34	2.01E-03	-0.68	0.61	0.02	0.01	XM_129243	cytochrome P450, family 2, subfamily c, polypeptide 66 (Cyp2c66)
170	0.36	2.12E-03	-0.51	0.37	0.01	0.00	NM_201641	UDP glycosyltransferase 1 family, polypeptide A10 (Ugt1a10)
171	0.37	2.19E-03	-0.56	0.49	0.01	0.02	NM_134007	DNA segment, Chr 10, ERATO Doi 214, expressed (D10Ertd214e)
172	0.42	2.42E-03	-0.48	0.66	0.02	0.00	NM_145079	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6)

173	0.52	3.01E-03	-0.35	-0.19	0.13	0.40	NM_009374	transglutaminase 3, E polypeptide (Tgm3)
174	0.53	3.05E-03	-0.40	0.20	0.02	0.17	NM_011353	small EDRK-rich factor 1 (Serf1)
175	0.55	3.15E-03	-0.38	0.01	0.02	0.86	NM_021304	abhydrolase domain containing 1 (Abhd1)
176	0.56	3.19E-03	-0.39	-0.06	0.00	0.48	NM_028493	Rho-related BTB domain containing 3 (Rhobtb3)
177	0.57	3.24E-03	-0.33	0.12	0.06	0.34	XM_128511	RIKEN cDNA 0610011F06 gene (0610011F06Rik)
178	0.6	3.35E-03	-0.95	0.37	0.02	0.20	XM_125703	RIKEN cDNA 2210404O07 gene (2210404O07Rik)
179	0.66	3.69E-03	-0.51	0.24	0.01	0.09	NM_027211	annexin A13 (Anxa13)
180	0.71	3.92E-03	-0.60	0.06	0.05	0.69	NM_008456	kallikrein 5 (Klk5)
181	0.78	4.32E-03	-0.43	0.30	0.03	0.01	NM_029643	G protein-coupled receptor 172B (Gpr172b)
182	0.8	4.38E-03	-0.37	-0.19	0.01	0.13	NM_009907	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) (Cln3)
183	0.81	4.44E-03	-0.65	0.08	0.05	0.60	NM_020268	kallikrein 27 (Klk27)
184	0.84	4.54E-03	-0.78	0.26	0.01	0.16	NM_009504	vitamin D receptor (Vdr)
185	0.84	4.54E-03	-0.45	-0.03	0.00	0.76	NM_172668	low density lipoprotein receptor-related protein 4 (Lrp4)
186	0.85	4.59E-03	-0.55	-0.08	0.02	0.76	NM_178779	ring finger protein 152 (Rnf152), transcript variant 1
187	0.89	4.75E-03	-0.42	0.20	0.01	0.32	NM_009735	beta-2 microglobulin (B2m)
188	0.9	4.76E-03	-0.40	-0.05	0.02	0.77	NM_025458	RIKEN cDNA 1810015P03 gene (1810015P03Rik)
189	0.9	4.76E-03	-0.39	0.11	0.01	0.18	NM_027227	RIKEN cDNA 2010001H14 gene (2010001H14Rik)
190	0.91	4.80E-03	-0.39	-0.15	0.00	0.04	NM_170755	cDNA sequence BC038286 (BC038286)
191	0.94	4.93E-03	-0.51	-0.02	0.03	0.91	NM_020277	transient receptor potential cation channel, subfamily M, member 5 (Trpm5)
192	0.94	4.91E-03	-0.40	0.30	0.15	0.24	NM_025469	colipase, pancreatic (Clps)
193	0.94	4.89E-03	-0.32	0.26	0.03	0.07	NM_198620	RUN domain containing 3B (Rundc3b)
194	0.99	5.10E-03	-0.33	0.22	0.00	0.01	NM_144801	RIKEN cDNA 2310076O21 gene (2310076O21Rik)
195	0.99	5.10E-03	-0.37	0.16	0.01	0.22	NM_178789	RIKEN cDNA B930062P21 gene (B930062P21Rik)
196	1.01	5.14E-03	-0.47	-0.09	0.03	0.59	NM_021281	cathepsin S (Ctss)
197	1.02	5.16E-03	-0.31	-0.07	0.00	0.35	NM_172881	hypothetical protein C730031G17 (C730031G17)
198	1.08	5.47E-03	-0.44	0.58	0.06	0.11	NM_008486	alanyl (membrane) aminopeptidase (Anpep)
199	1.08	5.45E-03	-0.30	-0.25	0.03	0.05	NM_010481	heat shock protein, A (Hspa9a)
200	1.15	5.73E-03	-0.36	-0.04	0.01	0.71	NM_019394	melanoma inhibitory activity 1 (Mia1)
201	1.18	5.89E-03	-0.33	-0.38	0.05	0.03	NM_178715	transmembrane protein 30B (Tmem30b)
202	1.23	6.09E-03	-0.49	0.08	0.01	0.37	NM_009049	regulated endocrine-specific protein 18 (Resp18)
203	1.24	6.11E-03	-0.36	0.20	0.01	0.05	NM_025412	pyrroline-5-carboxylate reductase-like (Pycrl)
204	1.26	6.16E-03	-0.42	0.25	0.01	0.02	XM_127929	RIKEN cDNA 4933421G18 gene (4933421G18Rik)
205	1.27	6.22E-03	-0.30	-0.11	0.00	0.13	NM_134054	RIKEN cDNA 1110002B05 gene (1110002B05Rik)
206	1.29	6.26E-03	-0.33	0.37	0.00	0.00	NM_008290	hydroxysteroid (17-beta) dehydrogenase 2 (Hsd17b2)
207	1.37	6.62E-03	-0.34	0.26	0.01	0.02	NM_030024	RIKEN cDNA E130201N16 gene (E130201N16Rik)
208	1.39	6.67E-03	-0.36	-0.22	0.02	0.11	NM_019758	mitochondrial carrier homolog 2 (C. elegans) (Mtch2)
209	1.41	6.77E-03	-0.34	-0.32	0.00	0.00	NM_134020	RIKEN cDNA 1110014L17 gene (1110014L17Rik)
210	1.42	6.76E-03	-0.39	0.01	0.02	0.97	NM_013813	erythrocyte protein band 4.1-like 3 (Epb4.1l3)
211	1.43	6.77E-03	-0.30	0.15	0.03	0.15	NM_031256	pleckstrin homology domain-containing, family A member 3 (Plekha3)
212	1.44	6.78E-03	-0.30	-0.25	0.00	0.00	NM_027194	RIKEN cDNA 2410018G23 gene (2410018G23Rik)
213	1.47	6.91E-03	-0.40	0.16	0.03	0.19	NM_008586	meprin 1 beta (Mep1b)
214	1.57	7.33E-03	-0.63	0.03	0.05	0.74	NM_010915	nerve growth factor, alpha (Ngfa)
215	1.65	7.67E-03	-0.29	0.14	0.01	0.06	NM_173742	DNA segment, Chr 11, Brigham & Womens Genetics 0434 expressed (D11Bwg0434e)
216	1.67	7.71E-03	-0.39	0.03	0.02	0.75	NM_175511	RIKEN cDNA A130092J06 gene (A130092J06Rik)
217	1.73	7.95E-03	-0.35	-0.17	0.09	0.27	NM_134021	expressed sequence AI415282 (AI415282)
218	1.84	8.42E-03	-0.31	0.13	0.00	0.03	NM_153417	transient receptor potential cation channel, subfamily M, member 6 (Trpm6)

219	1.85	8.44E-03	-0.30	0.21	0.03	0.02	NM_175274	tweety homolog 3 (Drosophila) (Ttyh3)
220	1.85	8.42E-03	-0.32	0.19	0.00	0.13	XM_129987	
221	1.85	8.39E-03	-0.36	0.10	0.02	0.33	NM_030004	crystallin, lamda 1 (Cryl1)
222	1.86	8.40E-03	-0.35	0.30	0.03	0.01	NM_028132	phosphoglucomutase 2 (Pgm2)
223	1.95	8.72E-03	-0.72	0.34	0.06	0.39	XM_128172	RIKEN cDNA 2010001J22 gene (2010001J22Rik)
224	1.97	8.78E-03	-0.31	0.05	0.01	0.48	NM_023608	glycerophosphodiester phosphodiesterase domain containing 2 (Gdpd2)
225	2	8.89E-03	-0.33	0.32	0.01	0.02	NM_015801	neuropathy target esterase (Nte)
226	2.02	8.95E-03	-0.40	0.21	0.02	0.21	NM_007405	adenylate cyclase 6 (Adcy6)
227	2.07	9.10E-03	-0.58	-0.15	0.01	0.41	NM_007382	acetyl-Coenzyme A dehydrogenase, medium chain (Acadm)
228	2.08	9.12E-03	-0.35	0.09	0.00	0.47	NM_021304	abhydrolase domain containing 1 (Abhd1)
229	2.09	9.15E-03	-0.34	-0.17	0.05	0.34	NM_010638	basic transcription element binding protein 1 (Bteb1)
230	2.16	9.40E-03	-0.52	0.84	0.03	0.01	NM_130864	acetyl-Coenzyme A acyltransferase 1A (Acaa1a)
231	2.2	9.54E-03	-0.30	0.19	0.14	0.22	XM_128511	RIKEN cDNA 0610011F06 gene (0610011F06Rik)
232	2.23	9.62E-03	-0.47	-0.04	0.01	0.88	NM_022433	sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae) (Sirt3)
233	2.28	9.80E-03	-0.29	-0.09	0.02	0.32	NM_019769	RIKEN cDNA 1500003O03 gene (1500003O03Rik)
234	2.31	9.89E-03	-0.45	-0.06	0.02	0.57	NM_009801	carbonic anhydrase 2 (Car2)
235	2.34	9.95E-03	-0.35	0.26	0.01	0.01	NM_145743	lactation elevated 1 (Lace1)
236	2.36	1.00E-02	-0.39	0.36	0.02	0.01	NM_026313	RIKEN cDNA 3300001P08 gene (3300001P08Rik)
237	2.41	1.02E-02	-0.45	-0.25	0.05	0.14	NM_134021	expressed sequence AI415282 (AI415282)
238	2.49	1.05E-02	-0.32	-0.16	0.01	0.12	XM_127323	RIKEN cDNA 1810073P09 gene (1810073P09Rik)
239	2.52	1.05E-02	-0.46	0.19	0.02	0.11	XM_134937	RIKEN cDNA 0610010I15 gene (0610010I15Rik)
240	2.56	1.06E-02	-0.40	0.54	0.01	0.00	NM_026633	RIKEN cDNA 9530058B02 gene (9530058B02Rik)
241	2.58	1.07E-02	-0.78	-0.86	0.01	0.00	XM_147230	eukaryotic translation initiation factor 4A2 (Eif4a2)
242	2.76	1.14E-02	-0.43	0.43	0.01	0.00	NM_011396	solute carrier family 22 (organic cation transporter), member 5 (Slc22a5)
243	2.81	1.15E-02	-0.64	0.23	0.01	0.29	NM_053109	osteoclast inhibitory lectin (Ocil)
244	2.86	1.17E-02	-0.58	0.26	0.03	0.16	NM_177470	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (Acaa2)
245	2.89	1.18E-02	-0.33	0.29	0.06	0.09	NM_010046	diacylglycerol O-acyltransferase 1 (Dgat1)
246	2.93	1.19E-02	-0.28	0.37	0.07	0.01	NM_009768	basigin (Bsg)
247	3.01	1.22E-02	-0.29	0.29	0.00	0.02	NM_025717	RIKEN cDNA 4921506I22 gene (4921506I22Rik)
248	3.03	1.22E-02	-0.53	0.13	0.01	0.42	NM_175105	aquaporin 11 (Aqp11)
249	3.09	1.24E-02	-0.28	-0.03	0.00	0.63	NM_146139	vav 3 oncogene (Vav3)
250	3.13	1.25E-02	-0.29	0.25	0.00	0.00	NM_026530	RIKEN cDNA E130307M08 gene (E130307M08Rik)
251	3.17	1.26E-02	-0.48	0.43	0.01	0.02	NM_016892	copper chaperone for superoxide dismutase (Ccs)
252	3.18	1.26E-02	-0.41	-0.06	0.02	0.76	NM_009856	CD83 antigen (Cd83)
253	3.19	1.26E-02	-0.31	0.00	0.01	0.87	XM_194020	activin A receptor, type IC (Acvr1c)
254	3.2	1.26E-02	-0.28	0.31	0.01	0.00	NM_016928	toll-like receptor 5 (Tlr5)
255	3.28	1.29E-02	-0.33	-0.05	0.00	0.35	NM_181066	EST AA881470 (AA881470)
256	3.38	1.32E-02	-0.32	-0.15	0.01	0.07	NM_010301	guanine nucleotide binding protein, alpha 11 (Gna11)
257	3.5	1.36E-02	-0.39	-0.51	0.11	0.03	NM_145474	cytochrome P450, family 2, subfamily d, polypeptide 34 (Cyp2d34)
258	3.53	1.37E-02	-0.39	0.05	0.08	0.68	NM_008457	kallikrein 8 (Klk8)
259	3.54	1.37E-02	-0.53	0.21	0.02	0.41	NM_010459	homeo box B4 (Hoxb4)
260	3.56	1.37E-02	-0.31	-0.10	0.00	0.10	NM_177206	RIKEN cDNA 9230101K24 gene (9230101K24Rik)
261	3.61	1.38E-02	-0.52	1.08	0.02	0.02	NM_023137	ubiquitin D (Ubd)
262	3.63	1.39E-02	-0.33	-0.16	0.01	0.23	NM_146133	RIKEN cDNA 2010204I15 gene (2010204I15Rik)
263	3.65	1.39E-02	-0.32	0.06	0.00	0.34	NM_177874	hypothetical protein F830003B07 (F830003B07)
264	3.75	1.42E-02	-0.46	-0.14	0.04	0.60	NM_130882	cytochrome P450, family 4, subfamily f, polypeptide 13 (Cyp4f13)

265	3.79	1.43E-02	-0.28	-0.01	0.01	0.93	NM_013889	zinc finger protein 292 (Zfp292)
266	3.79	1.42E-02	-0.39	0.30	0.07	0.10	NM_134147	RIKEN cDNA D930010J01 gene (D930010J01Rik)
267	3.82	1.43E-02	-0.31	-0.21	0.00	0.06	NM_008695	nidogen 2 (Nid2)
268	3.87	1.44E-02	-0.32	0.30	0.01	0.04	NM_009945	cytochrome c oxidase, subunit VIIa 2 (Cox7a2)
269	3.99	1.48E-02	-0.47	-0.52	0.02	0.00	XM_357113	
270	3.99	1.48E-02	-0.29	0.21	0.01	0.07	NM_011354	small EDRK-rich factor 2 (Serf2)
271	4.11	1.52E-02	-0.42	0.30	0.08	0.14	XM_129721	
272	4.11	1.51E-02	-0.26	0.26	0.04	0.07	NM_026680	RIKEN cDNA 0610012C01 gene (0610012C01Rik)
273	4.17	1.53E-02	-0.53	-0.16	0.02	0.30	NM_172607	RIKEN cDNA 9130210N20 gene (9130210N20Rik)
274	4.22	1.53E-02	-0.27	-0.20	0.01	0.03	XM_149387	
275	4.22	1.53E-02	-0.38	-0.08	0.00	0.42	NM_172607	RIKEN cDNA 9130210N20 gene (9130210N20Rik)
276	4.22	1.53E-02	-0.29	0.25	0.01	0.02	NM_145134	SPRY domain-containing SOCS box 4 (Ssb4)
277	4.23	1.53E-02	-0.48	0.35	0.01	0.01	NM_030706	tripartite motif protein 2 (Trim2)
278	4.33	1.56E-02	-0.36	0.01	0.01	0.88	NM_130884	isocitrate dehydrogenase 3 (NAD+) beta (Idh3b)
279	4.44	1.59E-02	-0.37	-0.23	0.02	0.13	NM_013935	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a (Ptpla)
280	4.6	1.64E-02	-0.31	-0.07	0.03	0.30	NM_026436	RIKEN cDNA 1810054O13 gene (1810054O13Rik)
281	4.72	1.68E-02	-0.32	0.32	0.02	0.00	NM_009849	ectonucleoside triphosphate diphosphohydrolase 2 (Entpd2)
282	4.74	1.68E-02	-0.27	0.36	0.00	0.00	NM_019730	expressed in non-metastatic cells 3 (Nme3)
283	4.76	1.68E-02	-0.43	0.13	0.01	0.27	XM_181343	
284	4.81	1.69E-02	-0.34	0.07	0.02	0.48	NM_139144	O-linked N-acetylglucosamine (GlcNAc) transferase(Ogt)
285	4.94	1.73E-02	-0.72	-0.07	0.01	0.79	NM_175316	solute carrier organic anion transporter family, member 2b1 (Slco2b1)
286	5.12	1.79E-02	-0.35	0.08	0.01	0.31	NM_008199	histocompatibility 2, blastocyst (H2-Bl)
287	5.14	1.79E-02	-0.42	0.24	0.00	0.11	NM_008129	glutamate-cysteine ligase , modifier subunit (Gclm)
288	5.24	1.82E-02	-0.44	0.07	0.04	0.63	NM_146083	splicing factor, arginine/serine-rich 7 (Sfrs7)
289	5.4	1.87E-02	-0.27	0.26	0.00	0.00	NM_008688	nuclear factor I/C (Nfic)
290	5.41	1.87E-02	-0.39	-0.62	0.03	0.00	NM_134079	adenosine kinase (Adk)
291	5.42	1.86E-02	-0.31	0.11	0.02	0.45	NM_019718	ADP-ribosylation factor-like 3 (Arl3)
292	5.44	1.86E-02	-0.32	0.19	0.01	0.00	NM_025697	RIKEN cDNA 6330409N04 gene (6330409N04Rik)
293	5.46	1.86E-02	-0.31	0.04	0.00	0.71	NM_177684	zinc finger protein 637 (Zfp637)
294	5.49	1.87E-02	-0.87	-0.03	0.01	0.95	NM_008278	hydroxyprostaglandin dehydrogenase 15 (NAD) (Hpgd)
295	5.62	1.91E-02	-0.41	0.37	0.02	0.02	NM_026159	RIKEN cDNA 0610039N19 gene (0610039N19Rik)
296	5.76	1.95E-02	-0.27	0.11	0.01	0.14	NM_023041	peroxisome biogenesis factor 19 (Pex19)
297	5.91	1.99E-02	-0.46	-0.24	0.01	0.10	NM_007860	deiodinase, iodothyronine, type I (Dio1)
298	5.96	2.00E-02	-0.83	-0.07	0.07	0.97	NM_025470	RIKEN cDNA 1810030J14 gene (1810030J14Rik)
299	6.08	2.03E-02	-0.32	0.05	0.01	0.56	NM_009478	uroporphyrinogen decarboxylase (Urod)
300	6.3	2.10E-02	-0.25	0.10	0.02	0.10	NM_010232	flavin containing monooxygenase 5 (Fmo5)
301	6.4	2.13E-02	-0.30	0.15	0.00	0.14	NM_133182	heterogeneous nuclear ribonucleoprotein methyltransferase-like 1 (S. cerevisiae) (Hrmt1l1)
302	6.41	2.12E-02	-0.27	0.30	0.01	0.01	NM_025457	RIKEN cDNA 1810008A14 gene (1810008A14Rik)
303	6.45	2.13E-02	-0.28	-0.22	0.00	0.00	XM_131162	sorting nexin 7 (Snx7)
304	6.63	2.18E-02	-0.30	-0.03	0.01	0.75	NM_011464	serine protease inhibitor, Kunitz type 2 (Spint2)
305	6.72	2.20E-02	-0.36	0.17	0.01	0.14	NM_172656	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 homolog (Als2cr2)
306	6.87	2.24E-02	-0.27	0.07	0.02	0.14	NM_023065	interferon gamma inducible protein 30 (Ifi30)
307	6.93	2.26E-02	-0.28	0.53	0.15	0.01	NM_009437	thiosulfate sulfurtransferase, mitochondrial (Tst)
308	7.3	2.37E-02	-0.59	0.60	0.04	0.00	XM_129243	cytochrome P450, family 2, subfamily c, polypeptide 65 (Cyp2c65)
309	7.3	2.36E-02	-0.24	0.34	0.01	0.44	NM_010387	histocompatibility 2, class II, locus Mb1 (H2-DMb1)
310	7.78	2.51E-02	-0.46	0.42	0.05	0.02	NM_009207	solute carrier family 4 (anion exchanger), member 2 (Slc4a2)

311	7.9	2.54E-02	-0.29	0.23	0.04	0.14	NM_025560	RIKEN cDNA 1810049H13 gene (1810049H13Rik)
312	7.91	2.54E-02	-0.52	0.02	0.01	0.87	NM_198037	RIKEN cDNA B430218L07 gene (B430218L07Rik)
313	7.92	2.53E-02	-0.29	0.25	0.03	0.05	NM_025661	ORM1-like 3 (S. cerevisiae) (Ormdl3)
314	8.14	2.59E-02	-0.70	0.39	0.02	0.18	NM_008289	hydroxysteroid 11-beta dehydrogenase 2 (Hsd11b2)
315	8.16	2.59E-02	-0.27	-0.07	0.00	0.16	NM_145125	WD repeat domain 9 (Wdr9)
316	8.19	2.59E-02	-0.30	0.18	0.00	0.00	NM_024442	cytochrome P450, family 4, subfamily f, polypeptide 16 (Cyp4f16)
317	8.63	2.72E-02	-0.27	0.09	0.00	0.17	NM_024464	RIKEN cDNA 2010319C14 gene (2010319C14Rik)
318	8.67	2.73E-02	-0.24	0.07	0.10	0.56	NM_019543	Down syndrome critical region homolog 5 (human) (Dscr5)
319	8.68	2.72E-02	-0.38	0.69	0.03	0.00	NM_026633	RIKEN cDNA 9530058B02 gene (9530058B02Rik)
320	8.75	2.73E-02	-0.29	0.32	0.07	0.03	NM_013677	surfeit gene 1 (Surf1)
321	8.77	2.73E-02	-0.49	0.08	0.02	0.62	NM_026159	RIKEN cDNA 0610039N19 gene (0610039N19Rik)
322	8.8	2.73E-02	-0.28	0.52	0.12	0.00	NM_007754	carboxypeptidase D (Cpd)
323	8.89	2.75E-02	-0.34	-0.11	0.03	0.36	NM_146141	RIKEN cDNA 1110013G13 gene (1110013G13Rik)
324	8.9	2.75E-02	-0.25	0.04	0.00	0.29	NM_145523	grancalcin (Gca)
325	9.27	2.85E-02	-0.27	0.24	0.02	0.04	NM_024192	CUE domain containing 2 (Cuedc2)
326	9.36	2.87E-02	-0.40	-0.09	0.06	0.56	XM_125538	sestrin 1 (Sesn1)
327	9.68	2.96E-02	-0.35	0.36	0.01	0.01	XM_204313	RIKEN cDNA 2300009A05 gene (2300009A05Rik)
328	9.73	2.97E-02	-0.39	0.23	0.06	0.12	NM_024186	single-stranded DNA binding protein 2 (Ssbp2)
329	9.78	2.97E-02	-0.26	0.61	0.01	0.00	NM_198415	creatine kinase, mitochondrial 2 (Ckmt2)
330	9.81	2.97E-02	-0.23	0.18	0.02	0.02	NM_010047	DiGeorge syndrome critical region gene 6 (Dgcr6)
331	10.06	3.04E-02	-0.29	-0.44	0.00	0.00	NM_011682	utrophin (Utrn)
332	10.09	3.04E-02	-0.47	0.23	0.01	0.08	XM_131643	
333	10.11	3.03E-02	-0.37	-0.03	0.02	0.65	NM_007693	chromogranin A (Chga)
334	10.36	3.10E-02	-0.25	0.22	0.00	0.01	NM_023374	succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (Sdhb)
335	10.54	3.15E-02	-0.73	-0.16	0.04	0.80	NM_029638	amiloride binding protein 1 (amine oxidase, copper-containing) (Abp1)
336	10.6	3.15E-02	-0.31	0.02	0.00	0.77	NM_022433	sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae) (Sirt3)
337	10.62	3.15E-02	-0.42	0.41	0.05	0.05	NM_145428	cDNA sequence BC003479 (BC003479)
338	10.64	3.15E-02	-0.32	0.07	0.04	0.61	NM_025455	RIKEN cDNA 1810010N17 gene (1810010N17Rik)
339	10.65	3.14E-02	-0.32	0.20	0.00	0.05	NM_146141	RIKEN cDNA 1110013G13 gene (1110013G13Rik)
340	10.7	3.15E-02	-0.26	0.26	0.08	0.08	NM_013889	zinc finger protein 292 (Zfp292)
341	10.75	3.15E-02	-0.28	0.03	0.00	0.84	NM_025835	propionyl Coenzyme A carboxylase, beta polypeptide (Pccb)
342	11.02	3.22E-02	-0.26	-0.08	0.00	0.31	NM_153574	RIKEN cDNA D430015B01 gene (D430015B01Rik)
343	11.11	3.24E-02	-0.26	0.17	0.05	0.20	NM_008813	ectonucleotide pyrophosphatase/phosphodiesterase 1 (Enpp1)
344	11.18	3.25E-02	-0.25	-0.34	0.01	0.03	NM_010422	hexosaminidase B (Hexb)
345	11.24	3.26E-02	-0.25	-0.25	0.01	0.01	NM_019396	cysteine and histidine rich 1 (Cyhr1)
346	11.31	3.27E-02	-0.23	0.07	0.05	0.39	NM_028048	RIKEN cDNA 1810012H11 gene (1810012H11Rik)
347	11.35	3.27E-02	-0.27	0.04	0.00	0.57	NM_009238	SRY-box containing gene 4 (Sox4)
348	11.54	3.31E-02	-0.23	-0.08	0.00	0.13	NM_009721	ATPase, Na+/K+ transporting, beta 1 polypeptide (Atp1b1)
349	11.82	3.39E-02	-0.27	-0.15	0.03	0.09	NM_008641	microtubule associated serine/threonine kinase 2 (Mast2)
350	11.92	3.41E-02	-0.38	-0.20	0.02	0.18	NM_013758	adducin 3 (gamma) (Add3)
351	11.97	3.41E-02	-0.34	-0.14	0.00	0.20	NM_144844	propionyl-Coenzyme A carboxylase, alpha polypeptide (Pcca)
352	12.02	3.42E-02	-0.25	0.18	0.00	0.00	NM_009239	trans-acting transcription factor 4 (Sp4)
353	12.06	3.42E-02	-0.28	-0.23	0.00	0.02	NM_008323	isocitrate dehydrogenase 3 (NAD+), gamma (Idh3g)
354	12.42	3.51E-02	-0.23	0.21	0.01	0.02	NM_026503	RIKEN cDNA 1110058L19 gene (1110058L19Rik)
355	12.75	3.59E-02	-0.27	0.13	0.00	0.06	NM_025515	RIKEN cDNA 2310015N07 gene (2310015N07Rik)
356	12.87	3.62E-02	-0.35	0.08	0.04	0.31	NM_018824	solute carrier family 23 (nucleobase transporters), member 2 (Slc23a2)

357	13.08	3.66E-02	-0.51	0.44	0.02	0.01	NM_025504	RIKEN cDNA 2310004L02 gene (2310004L02Rik)
358	13.43	3.75E-02	-0.24	0.20	0.01	0.02	NM_019443	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (Ndufa1)
359	13.47	3.75E-02	-0.67	-0.12	0.03	0.35	NM_008998	RAB17, member RAS oncogene family (Rab17)
360	13.83	3.84E-02	-0.47	-0.07	0.01	0.69	NM_019521	growth arrest specific 6 (Gas6)
361	13.96	3.87E-02	-0.49	0.00	0.02	0.95	NM_030676	nuclear receptor subfamily 5, group A, member 2 (Nr5a2)
362	14.09	3.89E-02	-0.39	-0.06	0.07	0.85	XM_126043	
363	14.3	3.94E-02	-0.24	-0.22	0.02	0.04	NM_013917	pituitary tumor-transforming 1 (Pttg1)
364	14.66	4.03E-02	-0.35	-0.15	0.02	0.24	NM_133710	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (Ctdspl)
365	14.8	4.05E-02	-0.53	0.13	0.02	0.34	NM_011218	protein tyrosine phosphatase, receptor type, S (Ptprs)
366	14.92	4.08E-02	-0.28	0.38	0.02	0.00	NM_078478	growth hormone inducible transmembrane protein (Ghitm)
367	14.99	4.08E-02	-0.42	0.46	0.05	0.03	NM_153807	cDNA sequence BC018371 (BC018371)
368	15.49	4.21E-02	-0.36	-0.19	0.04	0.08	NM_026420	polyadenylate-binding protein-interacting protein 2 (Paip2)
369	15.74	4.27E-02	-0.48	0.31	0.04	0.10	NM_177470	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (Acaa2)
370	15.9	4.30E-02	-0.37	0.07	0.02	0.54	XM_358776	
371	15.99	4.31E-02	-0.25	0.10	0.00	0.09	XM_134800	RIKEN cDNA 1810046K07 gene (1810046K07Rik)
372	16.07	4.32E-02	-0.29	0.17	0.02	0.04	NM_175128	RIKEN cDNA 4930430F08 gene (4930430F08Rik)
373	16.25	4.36E-02	-0.48	0.46	0.03	0.03	NM_144942	cysteine sulfinic acid decarboxylase (Csad)
374	16.37	4.38E-02	-0.23	-0.09	0.00	0.08	NM_021431	nudix (nucleoside diphosphate linked moiety X)-type motif 11 (Nudt11)
375	16.44	4.38E-02	-0.35	-0.04	0.04	0.78	NM_026229	
376	16.76	4.46E-02	-0.53	0.66	0.02	0.05	NM_025654	RAD52 homolog B (S. cerevisiae) (Rad52b)
377	17.41	4.62E-02	-0.31	0.33	0.02	0.02	XM_143732	
378	17.43	4.61E-02	-0.29	0.11	0.02	0.24	NM_138753	cardiac lineage protein 1 (Clp1)
379	17.66	4.66E-02	-0.23	-0.18	0.08	0.36	NM_007836	growth arrest and DNA-damage-inducible 45 alpha (Gadd45a)
380	17.71	4.66E-02	-0.37	-0.09	0.08	0.70	NM_015749	transcobalamin 2 (Tcn2)
381	17.86	4.69E-02	-0.22	0.03	0.01	0.74	NM_013909	F-box and leucine-rich repeat protein 6 (Fbxl6)
382	18.01	4.71E-02	-0.37	0.18	0.03	0.57	NM_011831	insulin-like 5 (Insl5)
383	18.54	4.84E-02	-0.24	0.14	0.01	0.16	NM_013764	deoxyguanosine kinase (Dguok)
384	18.72	4.88E-02	-0.42	-0.14	0.05	0.49	NM_007382	acetyl-Coenzyme A dehydrogenase, medium chain (Acadm)
385	18.94	4.92E-02	-0.24	-0.14	0.01	0.09	XM_135859	motile sperm domain containing 1 (Mospd1)
386	18.99	4.92E-02	-0.25	0.10	0.01	0.15	NM_178855	protease, serine, 7 (enterokinase) (Prss7)
387	19.24	4.97E-02	-0.27	-0.09	0.02	0.27	NM_133695	cytochrome P450, family 2, subfamily d, polypeptide 13 (Cyp2d13)
388	19.42	5.00E-02	-0.38	0.42	0.03	0.02	NM_145962	pantothenate kinase 3 (Pank3)