Supplemental Table 1

Gene/miRNA	Primers	Product length	Application
Rhesus-miR-375	RT:5'-GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTCACG-3' Forward:5'-TATTTGTTCGTTCGGCTCGC-3' Reverse:5'-CAGTGCAGGGTCCGAGGTAT-3'(universal reverse primer)	60 bp	qRT-PCR for miRNA
Rhesus-miR-96	RT:5'-GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGCAAA-3' Forward:5'-GCCGTTTGGCACTAGCACAT-3' Reverse:5'-CAGTGCAGGGTCCGAGGTAT-3'	62 bp	qRT-PCR for miRNA
Rhesus-miR-219-5p	RT:5'-GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACAGAAT-3' Forward:5'-CCGCTGATTGTCCAAAGCG-3' Reverse:5'-CAGTGCAGGGTCCGAGGTAT-3'	60 bp	qRT-PCR for miRNA
Rhesus-miR-423-5p	RT:5'-GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACAAAGT-3' Forward:5'-TGAGGGGCAGAGAGCGAG-3' Reverse:5'-CAGTGCAGGGTCCGAGGTAT-3'	59 bp	qRT-PCR for miRNA
Rhesus-miR-940	RT:5'-GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGGGGA-3' Forward:5'-ACAAGGCAGGGCCCCCG-3' Reverse:5'-CAGTGCAGGGTCCGAGGTAT-3'	59 bp	qRT-PCR for miRNA
Rhesus-miR-191	RT:5'-GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCAGCT-3' Forward:5'-GTCAACGGAATCCCAAAAGC-3' Reverse:5'-CAGTGCAGGGTCCGAGGTAT-3'	61 bp	qRT-PCR for miRNA
Rhesus-miR-708	RT:5'-GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCCCAG-3' Forward:5'-CCGCAAGGAGCTTACAATCT-3' Reverse:5'-CAGTGCAGGGTCCGAGGTAT-3'	63 bp	qRT-PCR for miRNA
Rhesus-miR-543	RT:5'-GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACAAGAA-3' Forward:5'-TAGCTCAAACATTCGCGGTG-3' Reverse:5'-CAGTGCAGGGTCCGAGGTAT-3'	64 bp	qRT-PCR for miRNA
Rhesus RGR(long)	Forward:5'-TTTAGAAGACTCCCACTG-3' Reverse:5'-TCACCTACAACTCCTCGT-3'	133 bp	qRT-PCR for mRNA
Rheus PGR(long+short)	Forward:5'-TACAGTGCCTGATAGGTAGGCG-3' Reverse:5'-CGATTGGGATGACGTTTGTG-3'	220 bp	qRT-PCR for mRNA
Rhesus lncRNA-PGR-3p	Forward:5'-CAGCTTGGGAGGATTTTTGG-3' Reverse:5'-AGGGCTACTCTGCCTACGGA-3'	125 bp	qRT-PCR for mRNA
Rhesus GAPDH	Forward:5'-GAAGGTGAAGGTCGGAGT-3' Reverse:5'-GATGGCAACAATATCCACTT-3'	94 bp	qRT-PCR for mRNA
Human-mir-96-target-PGR	Forward:5'-CCGTGTAATTCTAGAAGTTCTCATCTAGTCCTAGTAGCTT-3' Reverse:5'-TCGAAGCGGCCGGCCGAGCCAGTGCCAGGAGAACTGTCAGG-3'	422 bp	3'-UTR construct for luc assay
Mouse-mir-96-target-PGR	Forward:5'-CCGTGTAATTCTAGAAGATGCTTTAGAAATAGACAAGTCT-3' Reverse:5'-TCGAAGCGGCCGGCCTGTATGTTTATATGTTTGAGTTATT-3'	285 bp	3'-UTR construct for luc assay
Rhesus-mir-96-target-PGR	Forward:5'-AGTTCTAGACTAGTCCTAGTAGCTTTCGATGC-3' Reverse:5'-AGGGCCGGCCAGGACTGTCAGGCAC-3'	364 bp	3'-UTR construct for luc assay
Human-mir219-5p-target-PGR	Forward:5'-CCGTGTAATTCTAGAGATATTTATATGGAAGATTTGGCAT-3' Reverse:5'-TCGAAGCGGCCGGCCATAAACTTGGCTTCTTTCACTGTGG-3'	528 bp	3'-UTR construct for luc assay
Mouse-mir219-5p-target-PGR	Forward:5'-CCGTGTAATTCTAGAGCACAGCTCTCTAACAAACTGTATG-3' Reverse:5'-TCGAAGCGGCCGGCCTAGAGTATCCACCTTTGGATTTCTT-3'	552 bp	3'-UTR construct for luc assay
Rhesus-mir219-target-lnc-PGR-3p	Forward:5'-GCTCTCTAGATGGAAGATTTGGCATTAT-3' Reverse:5'-TTTGGCCGGCCTGCTTTCACTGTGGACTC-3'	485 bp	3'-UTR construct for luc assay
Human-mir375-target-PGR	Forward:5'-CCGTGTAATTCTAGAATGATCATAAACATGAAGAATTGTA-3' Reverse:5'-TCGAAGCGGCCGGCCAAATGGGCTTTGATGGAACTTGGTT-3'	578 bp	3'-UTR construct for luc assay
Mouse-mir375-target-PGR	Forward:5'-CCGTGTAATTCTAGATCATTTAACAGTGAGGAAATAGAGT-3' Reverse:5'-TCGAAGCGGCCGGCCGAGTCTCGGCAGTTGGAATTGTAGA-3'	285 bp	3'-UTR construct for luc assay
Rhesus-mir375-target-PGR	Forward:5'-GTGTCTAGAATGGTCATAAACACGAGGAGTTG-3' Reverse:5'-GTGGCCGGCCAAATGGGCTTTGATGGAAC-3'	570 bp	3'-UTR construct for luc assay
Rhesus-LncRNA-PGR-3p	Forward:5'-TACCGAGCTCGGATCCGTTTCTTTCTCCAGGTCTTCACTGG-3' Reverse:5'-GACTCGAGCGGCCGCCATGATCAGTGTGGAGAGAGCTACA-3'	3219 bp	3'-UTR construct for luc assay
Rhesus Pgr-RT-PCR	Forward:5'-AAATGAAAGCCAAGCCCTAA-3' Reverse:5'-GGATCTGCCACATGGTAAGG-3'	425 bp	Probe for Northern blot
Rhesus Genomic sequence	F3:5'-TAAACACGAGGAGTTGTAGGT-3' R3:5'-TTTCACTGTGGACTCCCTCTT-3'	3258 bp	RT-PCR for LncRNA-PGR-3p
Rhesus-LncRNA-PGR-3p	F2:5'-AGGAGAAAGGTCGGGTGC-3' R2:5'-AGGGCTACTCTGCCTACGG-3'	1637 bp	RT-PCR for LncRNA-PGR-3p
Rhesus Genomic sequence	F1:5'-AGTTTATTGGAGCAACAGCG-3' R1:5'-CAGGCAGATCACAAGGTAGG-3'	1673 bp	RT-PCR for LncRNA-PGR-3p

Supplemental Table 2

Name	Consevation	D15	D21	D15 (normalized, rpm)	D21 (normalized, rpm)	Folds (D21/D15)	Adjusted pvalue
mml-miR-874	mammal	8	2	0.97	0.28	0.29	1
mml-miR-128b	mammal	14863	10749	1803.43	1528.13	0.85	0
mml-miR-450a	mammal	152	191	18.44	27.15	1.47	0.055808354
mml-miR-128a	mammal	2963	1500	359.52	213.25	0.59	0
mml-miR-30c	mammal	1000	1930	121.34	274.38	2.26	1.36E-100
mml-miR-654-5p	mammal	38	31	4.61	4.41	0.96	1
mml-miR-455-5p	mammal	1153	361	139.90	51.32	0.37	0
mml-miR-486-3p	mammal	3	0	0.36	0.14	0.39	1
mml-miR-668	mammal	9	36	1.09	5.12	4.69	0.00079706
mml-miR-147b	mammal	1	1	0.12	0.14	1.17	1
mml-let-7f	mammal	512535	481089	62189.43	68393.83	1.10	0
mml-miR-934	primate	2	1	0.24	0.14	0.59	1
mml-miR-130b	mammal	5956	5662	722.68	804.94	1.11	1.00E-06
mml-miR-33a	mammal	201	311	24.39	44.21	1.81	4.15E-09
mml-miR-299-5p	mammal	1105	781	134.08	111.03	0.83	0.017361529
mml-miR-508	primate	1	0	0.12	0.14	1.17	1
mml-miR-582-5p	mammal	13	1	1.58	0.14	0.09	1
mml-miR-133c	mammal	1	4	0.12	0.57	4.69	1
mml-miR-190a	mammal	6	11	0.73	1.56	2.15	1
mml-miR-301b	mammal	6	8	0.73	1.14	1.56	1
mml-let-7b	mammal	781700	616708	94849.09	87674.06	0.92	0
mml-miR-17-5p	mammal	1847	225	224.11	31.99	0.14	0
mml-miR-23b	mammal	9895	9446	1200.63	1342.89	1.12	1.06E-12
mml-miR-454	primate	14	5	1.70	0.71	0.42	1
mml-miR-10a	mammal	44539	22620	5404.23	3215.76	0.60	0
mml-miR-942	primate	0	4	0.12	0.57	4.69	1
mml-miR-132	mammal	370	55	44.89	7.82	0.17	0
mml-miR-222	mammal	2958	806	358.91	114.58	0.32	0
mml-miR-375	mammal	363	789	44.05	112.17	2.55	1.64E-50
mml-miR-432	mammal	3858	778	468.12	110.60	0.24	0
mml-miR-636	primate	1	0	0.12	0.14	1.17	1
mml-miR-181a	mammal	14281	10196	1732.81	1449.51	0.84	0
mml-miR-576-3p	primate	5	1	0.61	0.14	0.23	1
mml-miR-937	mammal	1	1	0.12	0.14	1.17	1
mml-miR-423-5p	mammal	8170	31773	991.32	4517.00	4.56	0
mml-miR-142-5p	mammal	97	68	11.77	9.67	0.82	1
mml-miR-886-3p	primate	16	3	1.94	0.43	0.22	1
mml-miR-193b	mammal	403	465	48.90	66.11	1.35	0.001418194
mml-miR-369-3p	mammal	2192	936	265.97	133.07	0.50	0
mml-miR-590-3p	mammal	32	39	3.88	5.54	1.43	1
mml-miR-488	mammal	4	4	0.49	0.57	1.17	1
mml-miR-219-5p	mammal	14	43	1.70	6.11	3.60	0.000987781
mml-miR-323-5p	mammal	15	1	1.82	0.14	0.08	0.457705596
mml-miR-532-5p	mammal	3913	773	474.79	109.89	0.23	0
mml-miR-149	mammal	4	0	0.49	0.14	0.29	1
mml-miR-146b-5p	mammal	2103	6662	255.17	947.10	3.71	0
mml-miR-484	mammal	559	112	67.83	15.92	0.23	0
mml-miR-193a-5p	mammal	282	1300	34.22	184.81	5.40	1.48E-180
mml-miR-383	mammal	89	6	10.80	0.85	0.08	2.53E-12
mml-miR-31	mammal	256	1172	31.06	166.62	5.36	4.77E-162
mml-miR-7	mammal	201	200	24.39	28.43	1.17	1
mml-miR-708	mammal	7859	668	953.59	94.97	0.10	0
mml-miR-23a	mammal	15592	16449	1891.89	2338.47	1.24	2.06E-78
mml-miR-187	mammal	489	44	59.33	6.26	0.11	0
mml-miR-218	mammal	4	3	0.49	0.43	0.88	1
mml-miR-487b	mammal	2024	465	245.59	66.11	0.27	0
mml-miR-452	mammal	141	42	17.11	5.97	0.35	1.19E-07
mml-miR-25	mammal	38337	10308	4651.69	1465.43	0.32	0
mml-miR-96	mammal	32	220	3.88	31.28	8.06	3.21E-37

mml-miR-192	mammal	4722	2703	572.95	384.27	0.67	0
mml-miR-551b	mammal	3	5	0.36	0.71	1.95	1
mml-miR-214	mammal	1638	1152	198.75	163.77	0.82	0.00015004
mml-miR-411	mammal	14979	5945	1817.51	845.17	0.47	0
mml-miR-382	mammal	1618	688	196.32	97.81	0.50	0
mml-miR-496	mammal	76	98	9.22	13.93	1.51	1
mml-miR-379	mammal	848	791	102.89	112.45	1.09	1
mml-miR-320	mammal	82526	55467	10013.45	7885.44	0.79	0
mml-miR-337-3p	mammal	113	37	13.71	5.26	0.38	4.86E-05
mml-miR-323-3p	mammal	473	241	57.39	34.26	0.60	1.42E-08
mml-miR-584	primate	25	29	3.03	4.12	1.36	1
mml-miR-210	mammal	1783	4123	216.34	586.14	2.71	9.01E-292
mml-miR-425	mammal	850	143	103.14	20.33	0.20	0
mml-miR-665	mammal	2	0	0.24	0.14	0.59	1
mml-miR-135b	mammal	263	90	31.91	12.79	0.40	3.04E-12
mml-miR-129-3p	mammal	8	23	0.97	3.27	3.37	0.271642533
mml-miR-183	mammal	535	662	64.92	94.11	1.45	2.14E-08
mml-miR-455-3p	mammal	1605	731	194.75	103.92	0.53	0
mml-miR-203	mammal	1813	2679	219.98	380.86	1.73	2.00E-72
mml-miR-1	mammal	9494	21650	1151.97	3077.86	2.67	0
mml-miR-543	mammal	874	328	106.05	46.63	0.44	0
mml-miR-376a	mammal	283	33	34.34	4.69	0.14	0
mml-miR-224	mammal	18	10	2.18	1.42	0.65	1
mml-miR-107	mammal	73456	31151	8912.93	4428.57	0.50	0
mml-miR-181b	mammal	10051	8064	1219.56	1146.42	0.94	0.011315807
mml-miR-577	primate	1	3	0.12	0.43	3.51	1
mml-let-7c	mammal	122111	114613	14816.58	16293.91	1.10	7.21E-118
mml-miR-145	mammal	5964	2139	723.65	304.09	0.42	0
mml-miR-124a	mammal	5	8	0.61	1.14	1.87	1
mml-miR-150	mammal	229	62	27.79	8.81	0.32	0
mml-miR-542-5p	mammal	12	5	1.46	0.71	0.49	1
mml-miR-182	mammal	214	1208	25.97	171.73	6.61	3.33E-188
mml-miR-148a	mammal	57108	36541	6929.31	5194.84	0.75	0
mml-miR-22	mammal	7908	4184	959.53	594.82	0.62	0
mml-miR-500	mammal	27	8	3.28	1.14	0.35	1
mml-miR-181c	mammal	112	53	13.59	7.53	0.55	0.108182047
mml-miR-346	mammal	1	1	0.12	0.14	1.17	1
mml-miR-485-5p	mammal	2247	563	272.64	80.04	0.29	0
mml-miR-409-3p	mammal	1373	655	166.60	93.12	0.56	0
mml-miR-521	primate	1	0	0.12	0.14	1.17	1
mml-miR-376c	mammal	2840	566	344.60	80.47	0.23	0
mml-miR-877	mammal	119	165	14.44	23.46	1.62	0.007519
mml-miR-548e	primate	0	1	0.12	0.14	1.17	1
mml-miR-136	mammal	649	207	78.75	29.43	0.37	0
mml-miR-654-3p	mammal	227	101	27.54	14.36	0.52	9.69E-06
mml-miR-431	mammal	12	9	1.46	1.28	0.88	1
mml-miR-1224	mammal	0	1	0.12	0.14	1.17	1
mml-miR-423-3p	mammal	1327	399	161.01	56.72	0.35	0
mml-miR-30b	mammal	310	1324	37.61	188.23	5.00	7.68E-175
mml-miR-101	mammal	163649	142230	19856.67	20220.07	1.02	7.06E-05
mml-miR-549	primate	6	4	0.73	0.57	0.78	1
mml-miR-146a	mammal	120	154	14.56	21.89	1.50	0.121207844
mml-miR-542-3p	mammal	883	762	107.14	108.33	1.01	1
mml-miR-99a	mammal	106578	32613	12931.85	4636.41	0.36	0
mml-miR-628-3p	primate	3	0	0.36	0.14	0.39	1
mml-miR-34a	mammal	45	79	5.46	11.23	2.06	0.012962674
mml-miR-365	mammal	648	1040	78.63	147.85	1.88	1.83E-35
mml-miR-15a	mammal	3258	957	395.32	136.05	0.34	0
mml-miR-539	mammal	28	11	3.40	1.56	0.46	1
mml-miR-296-5p	mammal	102	40	12.38	5.69	0.46	0.006247198
mml-miR-148b	mammal	7014	4058	851.06	576.90	0.68	0
mml-miR-204	mammal	21	9	2.55	1.28	0.50	1
mml-miR-758	mammal	3	0	0.36	0.14	0.39	1

mml-miR-501	mammal	1	3	0.12	0.43	3.51	1
mml-miR-485-3p	mammal	5343	2920	648.30	415.12	0.64	0
mml-miR-223	mammal	2	7	0.24	1.00	4.10	1
mml-miR-329	mammal	37	20	4.49	2.84	0.63	1
mml-miR-135a	mammal	137	108	16.62	15.35	0.92	1
mml-miR-503	mammal	26868	8736	3260.08	1241.95	0.38	0
mml-miR-337-5p	mammal	99	82	12.01	11.66	0.97	1
mml-miR-34c-5p	mammal	1360	352	165.02	50.04	0.30	0
mml-miR-194	mammal	43	13	5.22	1.85	0.35	0.198109765
mml-miR-371-3p	mammal	3	0	0.36	0.14	0.39	1
mml-miR-24*	mammal	101	61	12.26	8.67	0.71	1
mml-miR-495	mammal	3752	1808	455.26	257.03	0.56	0
mml-miR-106a	mammal	110	27	13.35	3.84	0.29	2.02E-07
mml-miR-219-3p	mammal	7	2	0.85	0.28	0.33	1
mml-miR-32	mammal	179	141	21.72	20.05	0.92	1
mml-miR-451	mammal	667	399	80.93	56.72	0.70	5.37E-06
mml-miR-188	mammal	137	58	16.62	8.25	0.50	0.001606239
mml-miR-199a-5p	mammal	6407	1941	777.41	275.94	0.35	0
mml-let-7i	mammal	16309	10351	1978.88	1471.55	0.74	0
mml-miR-100	mammal	52451	19083	6364.24	2712.93	0.43	0
mml-miR-205	mammal	83	8	10.07	1.14	0.11	3.26E-10
mml-miR-376b	mammal	838	193	101.68	27.44	0.27	0
mml-miR-296-3p	mammal	49	52	5.95	7.39	1.24	1
mml-miR-410	mammal	1043	495	126.55	70.37	0.56	0
mml-miR-95	primate	474	1353	57.51	192.35	3.34	2.82E-125
mml-miR-200a	mammal	2438	4349	295.82	618.27	2.09	5.01E-193
mml-miR-191	mammal	201913	31454	24499.51	4471.65	0.18	0
mml-miR-541	mammal	744	1973	90.27	280.49	3.11	1.00E-167
mml-miR-889	primate	465	297	56.42	42.22	0.75	0.029295459
mml-miR-370	mammal	190	43	23.05	6.11	0.27	0
mml-miR-361-3p	mammal	173	73	20.99	10.38	0.49	8.39E-05
mml-miR-885-5p	primate	29	26	3.52	3.70	1.05	1
mml-miR-125a-3p	mammal	87	46	10.56	6.54	0.62	1
mml-miR-324-3p	mammal	12	8	1.46	1.14	0.78	1
mml-miR-18b	mammal	4	5	0.49	0.71	1.46	1
mml-miR-548b	primate	1	0	0.12	0.14	1.17	1
mml-miR-373	mammal	5	0	0.61	0.14	0.23	1
mml-miR-212	mammal	8	0	0.97	0.14	0.15	1
mml-miR-544	mammal	6	2	0.73	0.28	0.39	1
mml-miR-17-3p	mammal	246	156	29.85	22.18	0.74	1
mml-miR-155	mammal	389	95	47.20	13.51	0.29	0
mml-miR-28	mammal	1570	1348	190.50	191.64	1.01	1
mml-miR-660	primate	1004	797	121.82	113.31	0.93	1
mml-miR-106b	mammal	1226	965	148.76	137.19	0.92	1
mml-miR-30e	mammal	229	274	27.79	38.95	1.40	0.024446976
mml-miR-361-5p	mammal	1063	260	128.98	36.96	0.29	0
mml-miR-29c	mammal	3978	3090	482.68	439.29	0.91	0.027636171
mml-miR-129	mammal	1	5	0.12	0.71	5.86	1
mml-miR-338-5p	mammal	1	2	0.12	0.28	2.34	1
mml-miR-409-5p	mammal	3732	444	452.83	63.12	0.14	0
mml-miR-497	mammal	5412	2130	656.68	302.81	0.46	0
mml-miR-196a	mammal	4	1	0.49	0.14	0.29	1
mml-miR-26a	mammal	38545	25633	4676.93	3644.11	0.78	0
mml-miR-151-5p	mammal	2378	1218	288.54	173.16	0.60	0
mml-miR-139-5p	mammal	138	65	16.74	9.24	0.55	0.01979482
mml-miR-760	mammal	1	2	0.12	0.28	2.34	1
mml-miR-27a	mammal	9870	23714	1197.60	3371.29	2.82	0
mml-miR-299-3p	mammal	4470	3839	542.38	545.77	1.01	1
mml-miR-127	mammal	16951	18720	2056.78	2661.32	1.29	2.82E-129
mml-miR-324-5p	mammal	338	84	41.01	11.94	0.29	0
mml-miR-144	mammal	28	36	3.40	5.12	1.51	1
mml-miR-486-5p	mammal	175	51	21.23	7.25	0.34	4.62E-10
mml-miR-34c-3p	mammal	13	9	1.58	1.28	0.81	1

mml-miR-433	mammal	1970	1413	239.03	200.88	0.84	0.000191545
mml-miR-380	mammal	89	10	10.80	1.42	0.13	2.34E-10
mml-miR-18	mammal	179	57	21.72	8.10	0.37	4.87E-09
mml-miR-371-5p	mammal	82	58	9.95	8.25	0.83	1
mml-miR-940	primate	60	9	7.28	1.28	0.18	1.24E-05
mml-miR-181d	mammal	2674	1068	324.45	151.83	0.47	0
mml-miR-181a*	mammal	161	520	19.54	73.93	3.78	1.68E-54
mml-miR-19b	mammal	200	107	24.27	15.21	0.63	0.027097825
mml-miR-939	primate	0	3	0.12	0.43	3.51	1
mml-miR-342-3p	mammal	3843	515	466.30	73.21	0.16	0
mml-miR-449a	mammal	697	120	84.57	17.06	0.20	0
mml-miR-138	mammal	4	2	0.49	0.28	0.59	1
mml-miR-362-3p	mammal	402	248	48.78	35.26	0.72	0.017580721
mml-miR-199a-3p	mammal	3E+06	3095605	314949.82	440085.50	1.40	0
mml-miR-656	primate	97	90	11.77	12.79	1.09	1
mml-miR-137	mammal	1	1	0.12	0.14	1.17	1
mml-miR-450b-3p	mammal	8	0	0.97	0.14	0.15	1
mml-miR-139-3p	mammal	42	6	5.10	0.85	0.17	0.001015278
mml-miR-9	mammal	28	3	3.40	0.43	0.13	0.015809593
mml-miR-140-5p	mammal	67	12	8.13	1.71	0.21	1.22E-05
mml-let-7a	mammal	1E+06	1262243	178988.74	179446.29	1.00	1
mml-miR-197	mammal	299	209	36.28	29.71	0.82	1
mml-miR-671-3p	mammal	11	4	1.33	0.57	0.43	1
mml-miR-551a	mammal	50	56	6.07	7.96	1.31	1
mml-miR-624	primate	5	2	0.61	0.28	0.47	1
mml-miR-494	mammal	20	45	2.43	6.40	2.64	0.028839552
mml-miR-92a	mammal	6199	2974	752.17	422.80	0.56	0
mml-miR-513b	mammal	4	0	0.49	0.14	0.29	1
mml-miR-450b-5p	mammal	56	30	6.79	4.26	0.63	1
mml-miR-92b	mammal	6015	6369	729.84	905.45	1.24	4.57E-31
mml-miR-16	mammal	15531	3949	1884.48	561.41	0.30	0
mml-miR-424	mammal	147399	35287	17884.94	5016.56	0.28	0
mml-miR-185	mammal	25071	39259	3042.04	5581.24	1.83	0
mml-miR-125b	mammal	40301	12825	4890.00	1823.26	0.37	0
mml-miR-377	mammal	62	26	7.52	3.70	0.49	0.618508398
mml-miR-30a-3p	mammal	388	103	47.08	14.64	0.31	0
mml-miR-545	primate	1	0	0.12	0.14	1.17	1
mml-miR-374b	mammal	1989	648	241.34	92.12	0.38	0
mml-miR-221	mammal	31191	8880	3784.62	1262.42	0.33	0
mml-miR-330-5p	mammal	2	3	0.24	0.43	1.76	1
mml-miR-453	primate	2	0	0.24	0.14	0.59	1
mml-miR-29b	mammal	1211	958	146.94	136.19	0.93	1
mml-miR-30d	mammal	4625	7424	561.18	1055.43	1.88	1.45E-255
mml-miR-628-5p	mammal	64	10	7.77	1.42	0.18	6.41E-06
mml-let-7d	mammal	435408	105265	52831.08	14964.96	0.28	0
mml-miR-510	primate	13	2	1.58	0.28	0.18	1
mml-miR-592	mammal	5	0	0.61	0.14	0.23	1
mml-miR-133b	mammal	1	0	0.12	0.14	1.17	1
mml-miR-532-3p	mammal	4494	1026	545.29	145.86	0.27	0
mml-miR-504	mammal	707	124	85.79	17.63	0.21	0
mml-miR-576-5p	primate	1	2	0.12	0.28	2.34	1
mml-miR-675	mammal	64	83	7.77	11.80	1.52	1
mml-let-7g	mammal	63624	48225	7719.94	6855.89	0.89	0
mml-miR-516a-5p	primate	5	7	0.61	1.00	1.64	1
mml-miR-196b	mammal	27050	3507	3282.16	498.57	0.15	0
mml-miR-103	mammal	84116	21694	10206.38	3084.12	0.30	0
mml-miR-885-3p	primate	33	32	4.00	4.55	1.14	1
mml-miR-363	mammal	375	195	45.50	27.72	0.61	4.65E-06
mml-miR-448	mammal	7	1	0.85	0.14	0.17	1
mml-miR-605	primate	20	2	2.43	0.28	0.12	0.164834927
mml-miR-142-3p	mammal	45	51	5.46	7.25	1.33	1
mml-miR-193a-3p	mammal	1043	1331	126.55	189.22	1.50	1.96E-20
mml-miR-767-5p	mammal	13	15	1.58	2.13	1.35	1

mml-miR-130a	mammal	6343	5314	769.64	755.46	0.98	1
mml-miR-342-5p	mammal	272	79	33.00	11.23	0.34	0
mml-miR-140-3p	mammal	21280	22013	2582.05	3129.47	1.21	2.68E-87
mml-miR-490-3p	mammal	1	0	0.12	0.14	1.17	1
mml-miR-152	mammal	6471	2097	785.17	298.12	0.38	0
mml-miR-195	mammal	2802	972	339.99	138.18	0.41	0
mml-miR-362-5p	mammal	386	453	46.84	64.40	1.38	0.00063412
mml-miR-886-5p	primate	376	240	45.62	34.12	0.75	0.136016872
mml-miR-10b	mammal	49204	25912	5970.26	3683.77	0.62	0
mml-miR-98	mammal	1094	959	132.74	136.34	1.03	1
mml-miR-338-3p	mammal	9	9	1.09	1.28	1.17	1
mml-miR-339-5p	mammal	1209	184	146.70	26.16	0.18	0
mml-miR-151-3p	mammal	1217	850	147.67	120.84	0.82	0.002288866
mml-miR-27b	mammal	15126	19828	1835.34	2818.84	1.54	0
mml-miR-34b	mammal	37	21	4.49	2.99	0.66	1
mml-miR-331-3p	mammal	533	294	64.67	41.80	0.65	4.52E-07
mml-miR-20b	mammal	40	11	4.85	1.56	0.32	0.147562593
mml-miR-126	mammal	266	80	32.28	11.37	0.35	0
mml-miR-339-3p	mammal	850	713	103.14	101.36	0.98	1
mml-miR-429	mammal	4364	2978	529.51	423.37	0.80	0
mml-miR-369-5p	mammal	481	153	58.36	21.75	0.37	0
mml-miR-125a-5p	mammal	18744	6278	2274.34	892.51	0.39	0
mml-let-7e	mammal	141370	149313	17153.40	21227.03	1.24	0
mml-miR-19a	mammal	6	7	0.73	1.00	1.37	1
mml-miR-340	mammal	1401	1103	169.99	156.81	0.92	1
mml-miR-143	mammal	49689	34814	6029.11	4949.32	0.82	0
mml-miR-374a	mammal	3024	1142	366.92	162.35	0.44	0
mml-miR-99b	mammal	7867	5768	954.56	820.01	0.86	0
mml-miR-664	mammal	12	48	1.46	6.82	4.69	2.15E-05
mml-miR-30a-5p	mammal	7933	5363	962.57	762.43	0.79	0
mml-miR-502-3p	mammal	945	851	114.66	120.98	1.06	1
mml-miR-493	mammal	159	134	19.29	19.05	0.99	1
mml-miR-652	mammal	136	268	16.50	38.10	2.31	4.56E-14
mml-miR-491-5p	mammal	45	13	5.46	1.85	0.34	0.099380334
mml-miR-200c	mammal	98	45	11.89	6.40	0.54	0.152908653
mml-miR-20a	mammal	262	49	31.79	6.97	0.22	0
mml-miR-331-5p	mammal	4	5	0.49	0.71	1.46	1
mml-miR-215	mammal	6	13	0.73	1.85	2.54	1
mml-miR-216b	mammal	8	1	0.97	0.14	0.15	1
mml-miR-186	mammal	3403	6358	412.91	903.88	2.19	0
mml-miR-381	mammal	43	15	5.22	2.13	0.41	0.665209969
mml-miR-330-3p	mammal	638	736	77.41	104.63	1.35	3.67E-06
mml-miR-15b	mammal	9442	2406	1145.66	342.05	0.30	0
mml-miR-421	mammal	264	91	32.03	12.94	0.40	3.91E-12
mml-miR-93	mammal	92	24	11.16	3.41	0.31	1.39E-05
mml-miR-26b	mammal	4094	6336	496.75	900.76	1.81	3.21E-197
mml-miR-134	mammal	827	205	100.35	29.14	0.29	0
mml-miR-206	mammal	1	0	0.12	0.14	1.17	1
mml-miR-590-5p	mammal	6	2	0.73	0.28	0.39	1
mml-miR-449b	mammal	411	94	49.87	13.36	0.27	0
mml-miR-876-3p	mammal	24	26	2.91	3.70	1.27	1
mml-miR-887	primate	45	16	5.46	2.27	0.42	0.619357169
mml-miR-582-3p	mammal	114	133	13.83	18.91	1.37	1
mml-miR-671-5p	mammal	3	2	0.36	0.28	0.78	1
mml-miR-21	mammal	270158	115198	32780.15	16377.08	0.50	0
mml-miR-141	mammal	10	34	1.21	4.83	3.98	0.005291803
mml-miR-598	mammal	938	184	113.81	26.16	0.23	0
mml-miR-505	mammal	8	5	0.97	0.71	0.73	1
mml-miR-24	mammal	3897	1784	472.85	253.62	0.54	0
mml-miR-190b	mammal	1	6	0.12	0.85	7.03	1
mml-miR-154	mammal	544	212	66.01	30.14	0.46	0
mml-miR-33b	mammal	119	24	14.44	3.41	0.24	7.18E-10
mml-miR-184	mammal	1	4	0.12	0.57	4.69	1

mml-miR-29a	mammal	20760	58071	2518.95	8255.64	3.28	0
mml-miR-491-3p	mammal	5	0	0.61	0.14	0.23	1
mml-miR-522	primate	1	0	0.12	0.14	1.17	1
mml-miR-876-5p	mammal	27	46	3.28	6.54	2.00	0.592488395
mml-miR-378	mammal	4686	1339	568.58	190.36	0.33	0
mml-miR-122a	mammal	4	21	0.49	2.99	6.15	0.022916521
mml-miR-513a	primate	4	0	0.49	0.14	0.29	1
mml-miR-301a	mammal	51	52	6.19	7.39	1.19	1
mml-miR-211	mammal	6	0	0.73	0.14	0.20	1
mml-miR-499-5p	mammal	966	610	117.21	86.72	0.74	1.62E-06
mml-miR-372	primate	166	40	20.14	5.69	0.28	5.65E-12
mml-miR-499-3p	mammal	0	1	0.12	0.14	1.17	1
mml-miR-335	mammal	6533	1834	792.69	260.73	0.33	0
mml-miR-615-3p	mammal	1	0	0.12	0.142164618	1.17	1

Supplemental Table 3

Representative tag	Monkey gene	D15 (normalized, rpm)	D21 (normalized, rpm)	Folds (D21/D15)	Adjusted pvalue	Gene name
GATCCTTCAGACACGTGCTT	ENSMMUG00000010979	100.97	0.20	0.00	6.69E-110	S100A4
GATCAATGGACTCCTGGTGG	ENSMMUG00000002807	39.30	0.20	0.00	1.11E-41	NTHL1
GATCATTTTGGTTCGTGAGC	ENSMMUG00000017079	16.53	0.20	0.01	3.87E-16	GLRX5
GATCAGCCTCCGCCATTCCA	ENSMMUG00000007878	14.31	0.20	0.01	1.22E-13	PTPN1
GATCTTCTCTTCCCAACACC	ENSMMUG00000007544	13.30	0.20	0.01	7.57E-12	TROAP
GATCTTTTTTCAAATGGCTT	ENSMMUG00000000534	12.90	0.20	0.02	2.16E-11	KIAA1024
GATCCCCCTTTACTTCACTG	ENSMMUG00000000329	11.29	0.20	0.02	3.18E-10	SPRYD3
GATCATAAATTAATCAAGAT	ENSMMUG00000007081	21.97	0.39	0.02	5.83E-21	SGMS1
GATCTGAATCCCCCCAGAGT	ENSMMUG00000003115	51.19	0.98	0.02	9.30E-52	NLRP2
GATCCCACACTTCAGGCAGA	ENSMMUG00000023190	9.88	0.20	0.02	1.26E-08	TCIRG1
GATCCCGGTGGTCTTCCGCC	ENSMMUG00000020618	9.47	0.20	0.02	3.62E-08	ECSIT
GATCCAGGAATAAACCTTGT	ENSMMUG00000000488	17.53	0.39	0.02	5.57E-16	CLDN14
GATCATCAGCGCTAAGGCAG	ENSMMUG00000016921	42.52	0.98	0.02	4.41E-42	CYTL1
GATCAATTTGAAGTCCCTGT	ENSMMUG00000008761	8.46	0.20	0.02	2.28E-06	EXO1
GATCTAGAGCAAGTTAGCAC	ENSMMUG00000019290	8.26	0.20	0.02	3.86E-06	STK32A
GATCCAAGAACTCTCTCTCC	ENSMMUG00000023392	7.86	0.20	0.02	1.11E-05	P2RX5
GATCTGAGTGATTGAGATTC	ENSMMUG00000005853	13.91	0.39	0.03	6.73E-12	GSG2
GATCTTATGTACATACCCAT	ENSMMUG00000000902	41.72	1.17	0.03	1.45E-40	PLA1A
GATCCAGTTTAGGGTCAGGA	ENSMMUG00000021168	20.76	0.59	0.03	5.58E-19	UNC5CL
GATCTTTTCTCACTTCAATC	ENSMMUG00000009527	6.45	0.20	0.03	0.000452992	CLC
GATCGCCAGTCTAGTACAGT	ENSMMUG00000016018	12.70	0.39	0.03	1.55E-10	ESCO2
GATCAGAAGTTCGCATATAT	ENSMMUG00000001103	11.89	0.39	0.03	1.26E-09	GPR87
GATCCCAATCAGAGGGGTGG	ENSMMUG00000007973	10.28	0.39	0.04	8.32E-08	POLQ
GATCTTTCCAGAGGTCCAAG	ENSMMUG00000001936	9.88	0.39	0.04	2.38E-07	MAL
GATCTCAGCTCCCATTTCCC	ENSMMUG00000015851	13.30	0.59	0.04	1.30E-10	SFRP2
GATCTCTCGTGATTGATAAG	ENSMMUG00000018272	25.80	1.17	0.05	8.28E-23	GRIA2
GATCTCTTCCAAGCTTCAAC	ENSMMUG00000019642	41.92	1.95	0.05	2.15E-38	PDZK1
GATCCATGAGGTCCTGGCGC	ENSMMUG00000018524	234.19	11.12	0.05	7.82E-224	GSTP1
GATCGACCTGGTGGCCATCC	ENSMMUG00000000683	7.26	0.39	0.05	0.00022016	KCNG1
GATCCCCTACCCACGTGTCC	ENSMMUG00000019496	57.44	3.12	0.05	3.99E-52	SMPD3
GATCAATATTCTTTTCTTCT	ENSMMUG00000013666	21.16	1.17	0.06	1.20E-17	CPNE8
GATCCCCCTGGAGAGCTGCA	ENSMMUG00000018153	7.05	0.39	0.06	0.000372751	GOLGA7B
GATCCCAGCAGGCTGGACGA	ENSMMUG00000014542	9.88	0.59	0.06	9.23E-07	CHAC1
GATCCTACGCTCACGGCGCT	ENSMMUG00000001511	46.35	2.93	0.06	1.90E-40	KIF20A
GATCAGCCCAGGCCTGGCCT	ENSMMUG00000028951	9.07	0.59	0.06	7.43E-06	THEG
GATCCCAGAACCCCCCTGGA	ENSMMUG00000021556	242.65	15.99	0.07	5.15E-219	FSTL3
GATCCTTGGCAGTTCCTGGC	ENSMMUG00000001029	24.79	1.76	0.07	5.52E-20	ANO10
GATCGTTTTTATAACCATGG	ENSMMUG00000009274	419.60	31.01	0.07	0	CLDN11
GATCATGAAGTTCCAGAACC	ENSMMUG00000018070	33.46	2.54	0.08	2.39E-27	NCAPG
GATCTTTTGGCCCCATTTGT	ENSMMUG00000002057	66.51	5.07	0.08	1.45E-56	RRM2
GATCAGGGACCGACAAACCT	ENSMMUG00000015260	45.95	3.51	0.08	2.33E-38	PRSS12
GATCCCAGCTTTTTTTCCCC	ENSMMUG00000002712	7.66	0.59	0.08	0.00028621	SCN2A
GATCTCAAAGTTAAATAAAT	ENSMMUG00000000989	9.47	0.78	0.08	9.42E-06	IL1F9
GATCCCCCTCTTTGCACAGC	ENSMMUG00000000290	18.94	1.56	0.08	4.40E-14	RBP1
GATCTATCTTCAGAACGGAC	ENSMMUG00000021930	27.81	2.34	0.08	1.08E-21	SGOL2
GATCTTCTGTCCTGCCTCTG	ENSMMUG00000002621	32.04	2.73	0.09	2.88E-25	IQGAP3
GATCCTCGCCAAGCGGTATG	ENSMMUG00000006775	9.07	0.78	0.09	2.65E-05	PENK
GATCTAAGTTGCCTACCTTG	ENSMMUG00000013795	50.59	4.49	0.09	8.99E-41	UBE2T
GATCGCTTTGATTTTAAAGT	ENSMMUG00000003782	36.88	3.32	0.09	5.65E-29	MELK
GATCTTTAAAATTTTATATA	ENSMMUG00000012330	31.84	2.93	0.09	1.60E-24	ADAMTS14
GATCATTTTCTTCTTAGATT	ENSMMUG00000023151	12.70	1.17	0.09	2.92E-08	KIF15
GATCATAGTCCAACAGGGCC	ENSMMUG00000019042	16.93	1.56	0.09	7.23E-12	WSCD2
GATCTCTCATCTTTTGACTA	ENSMMUG00000006663	20.96	1.95	0.09	3.06E-15	DECR1
GATCTGTGTCATGGTTTTGT	ENSMMUG00000004869	69.53	6.63	0.10	1.17E-55	NPTXR
GATCGGCTGGTGTGCCTGCA	ENSMMUG00000011832	8.06	0.78	0.10	0.000349916	E2F2
GATCCTTGACGAGGAGAGAG	ENSMMUG00000023077	114.68	11.12	0.10	9.58E-93	PTTG1
GATCGATTGCAATAAATGTT	ENSMMUG00000021690	88.68	8.78	0.10	9.25E-71	C19orf12
GATCTGTATCAAGATAAAGA	ENSMMUG00000012323	66.10	6.63	0.10	5.93E-52	CDKN3
GATCCTTATGCATAAGTGTC	ENSMMUG00000021221	15.52	1.56	0.10	2.53E-10	HJURP
GATCTGACCTCCCGGGTGCC	ENSMMUG00000011191	48.17	4.88	0.10	4.02E-37	TACC3
GATCAGTTAGTGTAAATCAT	ENSMMUG00000000245	69.33	7.02	0.10	2.00E-54	ASPM
GATCTTGCCTCCCCACTGAT	ENSMMUG00000029628	24.79	2.54	0.10	7.10E-18	CCNB2
GATCGCACAGAAATCACTGT	ENSMMUG00000019533	13.30	1.37	0.10	2.08E-08	KIAA1210
GATCTCTAAGAAGAGGGTCT	ENSMMUG00000005127	64.29	6.63	0.10	5.37E-50	PLXNA4
GATCCCTACTGTTTTCCGTT	ENSMMUG00000021929	61.67	6.44	0.10	1.13E-47	KIF2C
GATCATTGAAATTCAATTTT	ENSMMUG00000012705	14.91	1.56	0.10	1.16E-09	UHRF1

GATCTCAACTCGTGGCACTA	ENSMMUG00000006027	12.90	1.37	0.11	5.74E-08	TTYH1
GATCATTTGTTGATGAGATG	ENSMMUG00000002746	14.31	1.56	0.11	5.29E-09	TRAT1
GATCACACAAATGATGAAAA	ENSMMUG00000029603	23.18	2.54	0.11	3.96E-16	KIAA0101
GATCCAGCAGGGAACAGGAC	ENSMMUG00000016727	10.68	1.17	0.11	4.79E-06	CDH16
GATCTTAGGTCTGCCCCCCC	ENSMMUG00000004706	10.68	1.17	0.11	4.79E-06	IGSF9
GATCAATGAAATTTGCCTTC	ENSMMUG00000002473	12.29	1.37	0.11	2.63E-07	AKR1CL2
GATCACATGCTTAGTCGTTT	ENSMMUG00000018720	61.07	7.02	0.11	1.52E-45	CKAP2
GATCTGTATCTCTTGTCTGA	ENSMMUG00000003855	15.12	1.76	0.12	2.21E-09	ZNF385B
GATCATGTATATATATCCAT	ENSMMUG00000018952	21.56	2.54	0.12	2.18E-14	NDC80
GATCGACTCTATCAATATTG	ENSMMUG00000014307	11.29	1.37	0.12	3.28E-06	MSTN
GATCACCCATGGCTAGACGC	ENSMMUG00000011333	30.43	3.71	0.12	5.30E-21	MBP
GATCTTCAAACAAGCATCAG	ENSMMUG00000000332	174.94	21.65	0.12	8.89E-131	TGFBI
GATCTGCTTGCCAGAGTCCT	ENSMMUG00000019385	51.39	6.44	0.13	1.14E-36	FOXM1
GATCCCAGTGGAGGGGTCTC	ENSMMUG00000014641	13.91	1.76	0.13	4.47E-08	IGLL1
GATCAAGAAAGACGAAAAGC	ENSMMUG00000005390	44.34	5.66	0.13	4.58E-31	MKI67
GATCATTTATTGATGATGAT	ENSMMUG00000021186	34.66	4.49	0.13	1.29E-23	ANLN
GATCATCACTGCAAACTTCT	ENSMMUG00000018767	23.58	3.12	0.13	4.09E-15	CDCA5
GATCCAGAAAAATGCAAGCA	ENSMMUG00000004755	9.88	1.37	0.14	0.000110051	CDC6
GATCCATTCGCCCCAAGGGG	ENSMMUG00000004154	20.96	2.93	0.14	8.51E-13	TCEAL5
GATCAACTTAACTAAAGAAG	ENSMMUG00000007996	17.94	2.54	0.14	1.64E-10	ZNF367
GATCTCTTTCCTACATTAGC	ENSMMUG00000005317	177.35	25.16	0.14	5.34E-125	ADAM28
GATCCGATTTTACCTTGGAC	ENSMMUG00000018956	16.32	2.34	0.14	2.94E-09	CAMK2N2
GATCCCATGGCCGCAGGGCT	ENSMMUG00000022864	16.32	2.34	0.14	2.94E-09	DDX11L8
GATCTGCTTATAAATAAACT	ENSMMUG00000004749	13.50	1.95	0.14	3.55E-07	PPARGC1B
GATCACTGAAGAAGAGCCTT	ENSMMUG00000017298	20.15	2.93	0.15	6.06E-12	TRIM59
GATCTACTACTGCAATGGCC	ENSMMUG00000011905	18.74	2.73	0.15	6.59E-11	TNFRSF21
GATCCGAGGCTCATGCTTGC	ENSMMUG00000013712	35.27	5.27	0.15	2.02E-22	CIZ1
GATCACTGTTGAAGGTGTTC	ENSMMUG00000020418	14.31	2.15	0.15	1.41E-07	DGKB
GATCCCTTTGCTGTGAGGGT	ENSMMUG00000000966	57.24	8.58	0.15	8.82E-38	TPX2
GATCAACAATAAACATAAGA	ENSMMUG00000015189	21.56	3.32	0.15	1.57E-12	RAD51AP1
GATCTGACCTCCGTCCTCTG	ENSMMUG00000029681	24.79	3.90	0.16	1.41E-14	PGA3
GATCACTCCAGCCTGCTGCT	ENSMMUG00000003247	11.89	1.95	0.16	1.79E-05	ASGR1
GATCTGTTTCTTTTTTTATT	ENSMMUG00000016596	105.81	17.36	0.16	1.99E-68	OLFM2
GATCACCCATTCCGGGTTCA	ENSMMUG00000002295	15.32	2.54	0.17	9.39E-08	CRABP2
GATCAGTGGGACTGCTTGAT	ENSMMUG00000019254	26.60	4.49	0.17	3.66E-15	PLA2G7
GATCCCTACTTGGGGCAGAA	ENSMMUG00000009101	20.56	3.51	0.17	4.76E-11	DERL3
GATCAAAAACCGTAGATGAC	ENSMMUG00000003720	22.77	3.90	0.17	1.73E-12	KIAA1644
GATCTAAATATGTATTTCAT	ENSMMUG00000018840	29.22	5.07	0.17	1.37E-16	SCN3A
GATCATGTAGTAAACGTAGG	ENSMMUG00000011040	28.82	5.07	0.18	3.54E-16	CRISPLD1
GATCTGTGTCTTTTCCTTTT	ENSMMUG00000010729	28.62	5.07	0.18	5.69E-16	RGS7
GATCTGGTTGCCGGTTACCT	ENSMMUG00000000862	86.26	15.41	0.18	1.12E-52	GNG4
GATCAGGAGCTGCTCCTGCC	ENSMMUG00000007556	13.10	2.34	0.18	7.06E-06	KNTC1
GATCTACTGAAATTAGCACT	ENSMMUG00000016019	37.89	6.83	0.18	1.06E-21	PBK
GATCTGTCTAGTTCCCATCC	ENSMMUG00000010582	42.12	7.61	0.18	2.34E-24	CDCA2
GATCTGTTTCCTATGAAAAC	ENSMMUG00000002330	69.93	12.68	0.18	6.88E-42	ENOX1
GATCTCCCTCCTGGGCCCAC	ENSMMUG00000005854	10.68	1.95	0.18	0.000327241	CPNE5
GATCTTTAATGATGTACAAC	ENSMMUG00000018726	21.36	3.90	0.18	4.84E-11	KIF24
GATCATTATTAATTTGAAAA	ENSMMUG00000016292	12.70	2.34	0.18	1.84E-05	PHACTR3
GATCCCCAGGGAGATGCTGA	ENSMMUG00000020973	17.94	3.32	0.18	8.94E-09	PTCH2
GATCTAAATAAGTGTGTCAA	ENSMMUG00000030704	13.50	2.54	0.19	7.05E-06	DIAPH3
GATCTTTCTGTAGTATTTAC	ENSMMUG00000015934	34.26	6.44	0.19	7.71E-19	CENPA
GATCCTCCAGGGCAGATGGC	ENSMMUG00000013990	40.71	7.80	0.19	1.58E-22	C6orf108
GATCCCTCCTCTTCTCGGAG	ENSMMUG00000013717	78.20	15.02	0.19	2.27E-45	DNM1
GATCAGGAGAACTGCCCCGA	ENSMMUG00000031415	3330.42	639.86	0.19	0	APOD
GATCACCTGGGCTGGGCTCG	ENSMMUG00000015448	93.31	17.94	0.19	1.57E-54	PARVB
GATCTGCTTATAATTAAACT	ENSMMUG00000005668	222.90	43.10	0.19	8.83E-133	KMO
GATCACCACATCCCCAAAGA	ENSMMUG00000006231	67.31	13.07	0.19	1.88E-38	FAM107A
GATCCAAGGGACTCAGTCCT	ENSMMUG00000001192	199.32	39.20	0.20	3.45E-117	LMNB2
GATCCTGGGCTTCCCCATCT	ENSMMUG00000014740	10.88	2.15	0.20	0.000521179	TRIP13
GATCAGTGCTGCCCACCTTG	ENSMMUG00000014699	27.01	5.46	0.20	1.55E-13	COL7A1
GATCAGTTTCTATTACTTTA	ENSMMUG00000004579	13.50	2.73	0.20	1.78E-05	RAD51
GATCAGCACTCTACCACAGC	ENSMMUG00000018142	61.47	12.48	0.20	8.19E-34	CCNB1
GATCCAAGGAGCTCCTGGGT	ENSMMUG00000006985	46.96	9.56	0.20	3.13E-25	ALPPL2
GATCCAGGCAGCCACTGGGA	ENSMMUG00000004063	25.80	5.27	0.20	1.01E-12	ARHGAP22
GATCTGTGACTTCCTCTATG	ENSMMUG00000015588	18.14	3.71	0.20	3.52E-08	RECQL4
GATCTGAGCCTAGAGCTTTA	ENSMMUG00000014639	15.12	3.12	0.21	2.57E-06	HLA-J
GATCTTTAATAGTGTTGAGT	ENSMMUG00000021689	15.12	3.12	0.21	2.57E-06	RACGAP1
GATCACAGGGGTCCAGCCCC	ENSMMUG00000007268	23.58	4.88	0.21	2.76E-11	THOP1
GATCTATGCATTTATTAAAT	ENSMMUG00000013960	107.42	22.23	0.21	5.71E-60	SLC24A4
GATCCAATAAACTTGGTAAC	ENSMMUG00000017923	507.88	105.51	0.21	1.22E-290	GNG8
GATCTCAAAGGAGTCTGAAA	ENSMMUG00000007047	672.53	140.80	0.21	0	CYB5R1

GATCTTACCTCCTGATAAAT	ENSMMUG00000017484	18.54	3.90	0.21	3.40E-08	SMAGP
GATCCACATTCTTGGGCTGA	ENSMMUG00000023089	78.40	16.58	0.21	1.78E-42	PHGDH
GATCCCACTGCTTCTCAGAC	ENSMMUG00000007432	14.71	3.12	0.21	6.51E-06	FAM70B
GATCTACATTAGGAAGAGTG	ENSMMUG00000011476	61.27	13.26	0.22	4.24E-32	SNX5
GATCCAGGCAAAAACACTTC	ENSMMUG00000019262	71.34	15.60	0.22	1.85E-37	CACNA1D
GATCTCTATCGCCACGGCAC	ENSMMUG00000002424	1072.59	236.56	0.22	0	FBLN1
GATCAGTTAAGGAGCTGTGC	ENSMMUG00000000070	29.83	6.63	0.22	4.78E-14	AURKA
GATCTTTTTTTTAATACTGT	ENSMMUG00000011810	65.70	14.63	0.22	8.00E-34	FAT4
GATCCAGCAAAGACTGGGAG	ENSMMUG00000012914	49.78	11.12	0.22	5.46E-25	PCNT
GATCCTTACCTAAATGAAAT	ENSMMUG00000016302	62.48	14.04	0.22	8.45E-32	L3MBTL4
GATCTGGGCAGTGGTTTCAC	ENSMMUG00000019276	18.14	4.10	0.23	2.02E-07	NR2E3
GATCTGGCAATGACTTTTTG	ENSMMUG00000019736	82.83	18.72	0.23	1.02E-42	SHANK2
GATCGACACATTCGCATCTG	ENSMMUG00000003148	41.92	9.56	0.23	2.68E-20	MPL
GATCGGGCCTAGCCCGGAAC	ENSMMUG00000011264	195.09	44.85	0.23	3.28E-102	MFSD2
GATCCTTGGCTTTCAGGATT	ENSMMUG00000020733	33.86	7.80	0.23	9.06E-16	CMYA5
GATCAGATGTGGTCAGACTC	ENSMMUG00000016476	15.92	3.71	0.23	5.49E-06	TRAIP
GATCCGGCCACCCCCTGATG	ENSMMUG00000011568	17.53	4.10	0.23	7.86E-07	RAD54L
GATCTGAACCTGGACCCTGG	ENSMMUG00000016732	89.28	20.87	0.23	5.88E-45	ANKRD35
GATCAGCGCTGAGATAGAGT	ENSMMUG00000017127	33.66	8.00	0.24	3.23E-15	CHST11
GATCACCATTATACTGCCTT	ENSMMUG00000019047	14.71	3.51	0.24	3.59E-05	SPARCL1
GATCTATGAGAGTGAACTCT	ENSMMUG00000006997	271.88	65.14	0.24	1.67E-138	TXNDC16
GATCCAAAGATGGCCCCTCT	ENSMMUG00000011688	46.35	11.12	0.24	1.07E-21	C1orf113
GATCGTTTTTGAAGCAGAAC	ENSMMUG00000022615	20.15	4.88	0.24	6.21E-08	EGFL6
GATCCTTGCCTGGGGAAACA	ENSMMUG00000022058	134.02	32.76	0.24	4.98E-66	GLI1
GATCGCTCTACTGCCCTCCA	ENSMMUG00000008364	17.53	4.29	0.24	1.79E-06	ZNF771
GATCAGGAGCAGCGGGCCCG	ENSMMUG00000009047	20.56	5.07	0.25	5.73E-08	MXD3
GATCGGGGGAGCAAGAATCA	ENSMMUG00000012485	55.83	14.04	0.25	1.83E-25	WDR51A
GATCCTGAACTGTTCCCTTA	ENSMMUG00000002997	23.18	5.85	0.25	4.47E-09	AURKB
GATCTCTTTTATTCTTTGTT	ENSMMUG00000008125	93.92	23.79	0.25	3.85E-44	IRF8
GATCCCGTGTAGCCTTCGTT	ENSMMUG00000021996	80.01	20.28	0.25	3.04E-37	ODZ4
GATCACATATTCTAGTGTAA	ENSMMUG00000022788	75.38	19.11	0.25	6.08E-35	TCF7
GATCCAAGTCCCCTGCCTGG	ENSMMUG00000014533	129.19	32.76	0.25	1.68E-61	TMEM132A
GATCATAGTCTTAGGAGTTC	ENSMMUG00000008934	802.53	203.80	0.25	0	MARCKS
GATCCCCGCCTGGCCAGGAG	ENSMMUG00000000835	40.51	10.34	0.26	1.48E-17	MSLN
GATCGAAGCCAAAGCAGCTC	ENSMMUG00000010682	18.34	4.68	0.26	1.50E-06	FBN2
GATCCGAGCGAGCTGTCAGT	ENSMMUG00000021942	358.94	91.66	0.26	1.34E-173	ANKH
GATCAAAGGCTACAAGGACA	ENSMMUG00000022251	12.90	3.32	0.26	0.000890882	TGM7
GATCGTTCCTTAAACTAGTG	ENSMMUG00000016072	15.92	4.10	0.26	2.78E-05	C3orf52
GATCTCACAAAAAATCATGA	ENSMMUG00000018360	36.28	9.36	0.26	2.77E-15	RCN1
GATCTCCTCCACCTTTCTGC	ENSMMUG00000001049	85.05	22.04	0.26	6.50E-39	SLC15A2
GATCTTGCAAACCTGCAGAT	ENSMMUG00000023566	22.57	5.85	0.26	1.66E-08	DYRK3
GATCACCTTTTAATAAAGAA	ENSMMUG00000011564	16.32	4.29	0.26	2.52E-05	TMC3
GATCTGCCAGCATTTCTTTT	ENSMMUG00000014377	18.54	4.88	0.26	2.11E-06	SAAL1
GATCCTTATAGAGTAAATGA	ENSMMUG00000023398	16.93	4.49	0.26	1.47E-05	COL16A1
GATCGCACCCTGCTGACTTT	ENSMMUG00000023216	21.97	5.85	0.27	6.11E-08	ASTN1
GATCTGAAGAAAAGGCTTCA	ENSMMUG00000005216	13.91	3.71	0.27	0.000470232	NEK2
GATCCGGCAGCGAAGCCGGC	ENSMMUG00000006009	48.97	13.07	0.27	9.16E-21	CDH24
GATCTGGCAAGCCTGCACAG	ENSMMUG00000019439	995.60	266.20	0.27	0	NKD2
GATCTGTGATTCCTGTAGCC	ENSMMUG00000004938	16.73	4.49	0.27	2.27E-05	PITRM1
GATCTGGAAGTCACCCTCCT	ENSMMUG00000009268	14.51	3.90	0.27	0.000273792	KIF5C
GATCCCTACTGCCCATGTTG	ENSMMUG00000017936	101.37	27.30	0.27	4.39E-45	SPEG
GATCTATGGCCTCTGGTGCT	ENSMMUG00000023383	318.23	86.39	0.27	4.52E-145	TRIB2
GATCTTTACAAAAAGACACT	ENSMMUG00000000809	20.76	5.66	0.27	3.80E-07	PLP1
GATCATACCCTGGTGAACCC	ENSMMUG00000013268	110.85	30.81	0.28	6.14E-48	BBS2
GATCTAAGAGCCAAGCGATT	ENSMMUG00000018588	58.04	16.19	0.28	6.66E-24	C17orf76
GATCCAGCTGAGCCCCGAGG	ENSMMUG00000008136	16.73	4.68	0.28	4.82E-05	GTSE1
GATCTGTACCTCTCTCCTTT	ENSMMUG00000004420	102.78	28.86	0.28	8.11E-44	INCENP
GATCCTGGTCCCGGCCAGGC	ENSMMUG00000000524	22.17	6.24	0.28	1.77E-07	SCNN1B
GATCTAATCTAAGTATTATT	ENSMMUG00000013989	48.97	13.85	0.28	1.75E-19	C4orf31
GATCTTTAAAGATGTGCTAA	ENSMMUG00000018574	225.32	63.77	0.28	6.74E-98	C5orf32
GATCTAGGTTTCAGACTGTG	ENSMMUG00000021927	16.53	4.68	0.28	7.38E-05	ITGA9
GATCCTCTCGCTCGTTCACT	ENSMMUG00000000567	60.46	17.36	0.29	3.33E-24	BAMBI
GATCTCGCGCTCCGGCCGCT	ENSMMUG00000020787	166.47	47.97	0.29	2.10E-70	PRR15
GATCCACCCATTTCCCTGTA	ENSMMUG00000002480	77.59	22.43	0.29	1.71E-31	ADAMTS19
GATCAGGAATTTCTCAGAGC	ENSMMUG00000015634	82.23	23.79	0.29	1.78E-33	CENPF
GATCGCTGAGCTGCTCAGGA	ENSMMUG00000014910	43.53	12.68	0.29	1.84E-16	DPEP1
GATCTAGCATGTGGATTTTA	ENSMMUG00000017014	23.38	6.83	0.29	1.23E-07	ECT2
GATCCTTCAGCAAGGGGCGC	ENSMMUG00000006059	66.71	19.50	0.29	2.12E-26	TTLL12
GATCGGGCGGCTGCTTAGAC	ENSMMUG00000015768	19.95	5.85	0.29	4.30E-06	C19orf26
GATCCCACCGGGCGTGGCCT	ENSMMUG00000012548	19.95	5.85	0.29	4.30E-06	INTS1
GATCCTGTATATGTGTTGAG	ENSMMUG00000011551	384.74	113.11	0.29	5.11E-162	SLC26A2

GATCAACTATTTTTAGCTTG	ENSMMUG00000022900	15.12	4.49	0.30	0.000692009	PDGFC
GATCCTGTTGAAGGTTAATA	ENSMMUG00000015443	22.77	6.83	0.30	4.30E-07	C14orf135
GATCTAAATGGAAGCATCTG	ENSMMUG00000014185	45.95	13.85	0.30	8.63E-17	NPY2R
GATCATGGTGAAATATTTTG	ENSMMUG00000019831	40.11	12.09	0.30	2.49E-14	NBEA
GATCACCTGCTTTGACATCA	ENSMMUG00000017326	64.69	19.70	0.30	2.53E-24	KIF26B
GATCAAATGCAACCTCACAA	ENSMMUG00000014601	376.07	114.67	0.30	4.58E-152	MYC
GATCTGCCTCTTGCCCCTGC	ENSMMUG00000008145	146.12	44.66	0.31	1.32E-57	S100A1
GATCCAAGAACTCCTGAAAT	ENSMMUG00000011217	498.40	152.51	0.31	2.12E-201	SERPINA5
GATCTGGGGCATGCTCTTGG	ENSMMUG00000001656	456.48	139.83	0.31	4.60E-184	FAM12B
GATCTCTTGCCTGCACCATC	ENSMMUG00000006265	290.42	90.10	0.31	1.18E-114	NES
GATCATAAAGACTTTTTTAC	ENSMMUG00000029416	85.65	26.72	0.31	5.11E-32	C6orf173
GATCCCACGTCTCCCTCCCT	ENSMMUG00000022989	47.76	15.02	0.31	1.30E-16	RAP1GAP2
GATCCCAGGGGCTTACCTCT	ENSMMUG00000021867	53.81	16.97	0.32	5.92E-19	TK1
GATCCTTTTCTCTAGGAATG	ENSMMUG00000005520	70.94	22.43	0.32	1.13E-25	CDH11
GATCAGTGTACGCGAAAAGG	ENSMMUG00000008546	435.32	138.46	0.32	6.60E-168	CCND2
GATCAGCGTCCTATACATTG	ENSMMUG00000003398	135.23	43.10	0.32	1.53E-50	BIRC3
GATCTGCATGGAGTGCTGTG	ENSMMUG00000009449	55.02	17.55	0.32	3.89E-19	MDFI
GATCCTGTGTTTCAAAACTA	ENSMMUG00000008795	24.39	7.80	0.32	4.89E-07	PKD2
GATCTGTGTCTCAGGCCCAC	ENSMMUG00000004703	133.62	42.90	0.32	1.88E-49	RNF24
GATCTGCCGTTCCATCCTGG	ENSMMUG00000022589	135.84	43.68	0.32	3.27E-50	PMEPA1
GATCATTATCTAAAGAATCT	ENSMMUG00000016520	130.80	42.12	0.32	3.53E-48	ATP7B
GATCAGGGATGAGTTAGAGT	ENSMMUG00000002022	31.44	10.14	0.32	1.07E-09	HCN1
GATCAACGTGCTGTACAACC	ENSMMUG00000006169	19.35	6.24	0.32	5.81E-05	TNNT1
GATCGAACAGTGTCTTGTGT	ENSMMUG00000004566	20.56	6.63	0.32	1.94E-05	ZNF124
GATCTTACTGGCCAAGCCAG	ENSMMUG00000020202	258.78	83.86	0.32	9.78E-97	MAGED4B
GATCGATACAGCTGCTTTGG	ENSMMUG00000021733	30.63	9.95	0.32	2.74E-09	PRICKLE1
GATCTCCAGACTGGGCTCAG	ENSMMUG00000008859	20.96	6.83	0.33	1.68E-05	C1orf88
GATCTCTGTCCCTCTATCCC	ENSMMUG00000007357	16.73	5.46	0.33	0.000782257	LRRC16B
GATCCGCTCGCGCCACGGCC	ENSMMUG00000002779	47.76	15.60	0.33	9.19E-16	CHST2
GATCCTAGTAATTGCCTAGA	ENSMMUG00000012321	3012.19	994.80	0.33	0	FN1
GATCCTACAGTAAATAAACC	ENSMMUG00000018986	24.18	8.00	0.33	1.40E-06	SEZ6L2
GATCAACCTGAGTTTTAAAA	ENSMMUG00000023785	29.42	9.75	0.33	1.54E-08	TUBB2B
GATCCACTTTCCTTCTGTGT	ENSMMUG00000002932	186.22	62.02	0.33	1.19E-66	DPT
GATCACTGGCTCCATCATAC	ENSMMUG00000018827	71.34	23.79	0.33	4.64E-24	MEGF10
GATCCCAGCCACCTTCTCCG	ENSMMUG00000008338	69.53	23.21	0.33	2.33E-23	WNT9A
GATCTTTTATTAAGCATACT	ENSMMUG00000012661	57.64	19.31	0.33	7.46E-19	PDZRN3
GATCCGAGCAAAAAGACTGG	ENSMMUG00000022366	25.60	8.58	0.34	5.99E-07	LRRC27
GATCATCACATCTTTTCCAA	ENSMMUG00000012534	44.74	15.02	0.34	4.87E-14	CKS2
GATCTTGGCTCAACCAAATC	ENSMMUG00000002394	45.14	15.21	0.34	4.18E-14	SNX26
GATCATCTGGAATGATACTT	ENSMMUG00000013205	32.04	10.92	0.34	4.19E-09	COL24A1
GATCTTCCTGGGGTTCTGAA	ENSMMUG00000006915	119.11	40.95	0.34	4.76E-40	WNT4
GATCCGTTTGCATCTTCTTT	ENSMMUG00000002634	223.71	77.03	0.34	4.89E-77	PTCH1
GATCGCTAATGAAAAAGGGA	ENSMMUG00000009817	151.56	52.27	0.34	2.27E-51	CCNA2
GATCACACACACCCGTCCGG	ENSMMUG00000010998	30.84	10.73	0.35	2.30E-08	TNFAIP8L1
GATCAGCAGGAGGGGAAAAG	ENSMMUG00000015825	87.27	30.42	0.35	3.74E-28	SCN5A
GATCCCACGGACATTTGGGG	ENSMMUG00000012895	145.91	50.90	0.35	1.35E-48	PYCR1
GATCATTAAAACGAAAGTAA	ENSMMUG00000020508	29.63	10.34	0.35	6.79E-08	ZNF8
GATCAATGACCCGTGCATGC	ENSMMUG00000020776	26.80	9.36	0.35	6.99E-07	PRKCQ
GATCATTCTTCACTCAGGAC	ENSMMUG00000004321	59.25	20.87	0.35	4.64E-18	LAMA3
GATCTTTTAGGCCTTCTTAT	ENSMMUG00000031041	40.91	14.43	0.35	1.15E-11	NIPSNAP1
GATCTTTCTCCCTTGAGGTG	ENSMMUG00000018341	19.35	6.83	0.35	0.000388786	PLCH1
GATCAAACAAGAGTCTGAGC	ENSMMUG00000004192	35.87	12.68	0.35	6.92E-10	CCDC37
GATCTGTTGAAGAACTCAGC	ENSMMUG00000018558	20.96	7.41	0.35	0.0001107	CAMTA1
GATCTTCTGTGGTGCTTAAG	ENSMMUG00000016872	24.18	8.58	0.35	9.04E-06	EFEMP1
GATCCACAGAGGACTGGGAC	ENSMMUG00000001153	48.17	17.16	0.36	5.91E-14	PDGFRL
GATCACATTAGCCAAATGCA	ENSMMUG00000018237	21.77	7.80	0.36	7.99E-05	PLXNC1
GATCTATTTGTATATAAGTC	ENSMMUG00000023310	106.41	38.22	0.36	2.32E-33	TSPAN12
GATCTGATTCCGTGGTCAAG	ENSMMUG00000018861	128.58	46.22	0.36	9.40E-41	HEYL
GATCTGAGGACACTGCCGAG	ENSMMUG00000009909	40.11	14.43	0.36	5.20E-11	CIB2
GATCAGGTTCTGTGGATGAG	ENSMMUG00000030915	44.34	15.99	0.36	2.17E-12	LAYN
GATCTGTATATTTTTTTTTC	ENSMMUG00000014983	44.74	16.19	0.36	1.84E-12	ANPEP
GATCACTGTGGGGTCAAGAA	ENSMMUG00000018866	41.32	15.02	0.36	3.18E-11	HPCAL4
GATCCTTCCTAAGGTACAGC	ENSMMUG00000021371	599.17	218.81	0.37	1.63E-193	GATA2
GATCAGCTAGACCTGCTTTT	ENSMMUG00000013172	134.83	49.34	0.37	1.01E-41	RFX5
GATCAGGGAGTGTGTCCAAG	ENSMMUG00000014409	35.07	12.87	0.37	5.61E-09	ANKRD13B
GATCAGACTGTTCAGCCTGC	ENSMMUG00000007802	30.23	11.12	0.37	2.35E-07	CENPT
GATCCAAGAGATATATTTGG	ENSMMUG00000015614	91.30	33.74	0.37	4.46E-27	TRPV2
GATCCGAGACTCTGCCAGGA	ENSMMUG00000005784	36.88	13.65	0.37	1.99E-09	TTC9
GATCACTCCACTGCTCCATG	ENSMMUG00000009054	21.56	8.00	0.37	0.000209811	GRIA3
GATCAGGACAGCAAGCAAGA	ENSMMUG00000015380	22.57	8.39	0.37	0.000102887	PSRC1
GATCCCCAGGCCCCATCCGG	ENSMMUG00000006348	173.12	64.36	0.37	6.02E-53	DENND1A

GATCAAAACAAATGATATTC	ENSMMUG00000020408	35.07	13.07	0.37	9.96E-09	HPGD
GATCTAAGAGTTGGATGGTT	ENSMMUG00000017438	76.79	28.67	0.37	5.03E-22	DCBLD2
GATCAGGCCCAGCAGGGGCA	ENSMMUG00000009712	285.18	106.48	0.37	4.64E-88	TMEM101
GATCGCTGCAGCCATGTTTT	ENSMMUG00000031463	615.90	232.46	0.38	1.54E-189	PUS1
GATCCGAGGAGGCGGAACAA	ENSMMUG00000017920	8023.04	3043.67	0.38	0	SPG7
GATCTGGGGCCCTCGGGCCC	ENSMMUG00000001420	182.19	69.23	0.38	5.63E-54	MFAP2
GATCGTGAGGGTTCCCTCAC	ENSMMUG00000023073	24.59	9.36	0.38	4.37E-05	CCNJL
GATCTTAAAAACAAGAATCT	ENSMMUG00000002003	32.25	12.29	0.38	1.78E-07	USF1
GATCAACGCATTTCATATGG	ENSMMUG00000011513	580.63	223.10	0.38	9.43E-174	VCAN
GATCCTCAGTAGAACAATCC	ENSMMUG00000003854	30.84	11.90	0.39	7.46E-07	SH3BP1
GATCACCAGTTGTACCAAAA	ENSMMUG00000000238	22.17	8.58	0.39	0.000378528	HECTD2
GATCCTGGAAATCAGGGTTA	ENSMMUG00000011269	24.18	9.36	0.39	9.08E-05	CFTR
GATCAAATGAATGCTTCAGG	ENSMMUG00000017255	47.36	18.33	0.39	7.80E-12	HELLS
GATCGGATGTGGGAACCTGG	ENSMMUG00000006616	108.63	42.12	0.39	3.17E-30	NEDD4L
GATCCTAGCATCCCTTTTCA	ENSMMUG00000016627	111.45	43.29	0.39	5.57E-31	TPMT
GATCCCCGTGTGCTGACCAG	ENSMMUG00000016207	32.85	12.87	0.39	3.12E-07	PASK
GATCAGAGGACCACCCGAGT	ENSMMUG00000006395	54.21	21.26	0.39	1.39E-13	H2AFY2
GATCTCCCCCACCCATGTCT	ENSMMUG00000008443	98.96	38.81	0.39	8.40E-27	TSKU
GATCTGGGAGGTGGAGGCCA	ENSMMUG00000007255	28.82	11.31	0.39	5.33E-06	MAP1A
GATCAGCAGAGGCTTGAGAT	ENSMMUG00000008625	39.70	15.60	0.39	3.16E-09	PPP1R3F
GATCCAGAAATAAAGTCTAA	ENSMMUG00000028729	765.24	301.70	0.39	1.55E-220	KLK4
GATCACAAAATCCAAGGTGC	ENSMMUG00000018728	128.58	50.71	0.39	3.33E-35	PRTFDC1
GATCCTCCTGAAGCCCTTTT	ENSMMUG00000009097	124.95	49.34	0.39	4.55E-34	MMP11
GATCTTCAAAAATAATGCCT	ENSMMUG00000006876	34.06	13.46	0.40	1.84E-07	TSPAN7
GATCGCCTGTGCTGCTGTTG	ENSMMUG00000007696	188.84	74.69	0.40	1.63E-52	PDIA5
GATCCAGTGGTGCGAGAAGC	ENSMMUG00000008661	71.95	28.47	0.40	1.59E-18	SLC7A1
GATCAGAATGGACCAGTCCC	ENSMMUG00000005902	39.90	15.80	0.40	3.79E-09	FRMPD1
GATCCTTATTCTTTAAGTCT	ENSMMUG00000011151	33.46	13.26	0.40	3.14E-07	KCNK13
GATCACTTGGCAAGCTGGGA	ENSMMUG00000013404	325.89	129.69	0.40	2.65E-91	SEC14L2
GATCAGGGGTAGTGAATGTT	ENSMMUG00000012287	126.36	50.32	0.40	5.45E-34	TMSB15A
GATCAATAAAATGATTTTTT	ENSMMUG00000017649	80.62	32.18	0.40	9.97E-21	E2F3
GATCAGACTCCAAGGGCCGT	ENSMMUG00000014174	428.27	171.23	0.40	9.83E-120	PLOD1
GATCTGGCCAAGGTCCCCAT	ENSMMUG00000021232	101.58	40.76	0.40	1.71E-26	HSPB8
GATCTGGCCAAGAATGAGGA	ENSMMUG00000015080	56.23	22.62	0.40	1.67E-13	PIK3R3
GATCACAGCCACCCTCACCC	ENSMMUG00000017546	38.29	15.41	0.40	2.21E-08	EMILIN2
GATCAGAAATGACTGTGTCA	ENSMMUG00000017234	409.53	165.38	0.40	1.64E-112	LRRC59
GATCCGCCAGCGCCATATCA	ENSMMUG00000022552	57.04	23.21	0.41	1.97E-13	RPS9
GATCCCAGACTAGCTTGGGA	ENSMMUG00000014230	43.13	17.55	0.41	1.55E-09	FMO4
GATCCCTTAGGGCACACAAC	ENSMMUG00000005123	25.39	10.34	0.41	0.000155869	ZNF114
GATCTGCTGATTTATACAGA	ENSMMUG00000004875	46.76	19.11	0.41	1.86E-10	MAD2L1
GATCAAGTCGAGACTGCAGG	ENSMMUG00000013863	61.07	24.96	0.41	1.99E-14	C14orf68
GATCTAATAATCAGATTGTT	ENSMMUG00000016949	134.22	55.00	0.41	1.80E-34	MAP9
GATCCATACTGAAAATTGAA	ENSMMUG00000008702	295.46	121.11	0.41	1.54E-78	SYNPO2
GATCGGGTACCGACCTTGCC	ENSMMUG00000012742	64.49	26.52	0.41	3.40E-15	SLC6A8
GATCATCTTGAATTACTGTG	ENSMMUG00000016994	54.42	22.43	0.41	2.25E-12	C12orf53
GATCTTATTGCATACATTTG	ENSMMUG00000028833	29.22	12.09	0.41	2.16E-05	ZNF506
GATCTTTCAGGAAAGACGGA	ENSMMUG00000014432	34.87	14.43	0.41	6.18E-07	PLAT
GATCTATATAATTTATGTAT	ENSMMUG00000011940	188.44	78.01	0.41	1.99E-48	VPS35
GATCACTGCCCTTTTTGAAA	ENSMMUG00000006171	28.22	11.70	0.41	4.39E-05	SLC16A1
GATCCAGGAGGAGCAGCAGC	ENSMMUG00000002167	258.57	107.26	0.41	4.83E-67	MRC2
GATCCCCAGTGTTTGGAACA	ENSMMUG00000001186	45.55	18.92	0.42	8.83E-10	PPRC1
GATCATGTGTGCTCAGGGTT	ENSMMUG00000018117	246.48	102.39	0.42	1.20E-63	GANAB
GATCTTGCAGCCCAGAACCA	ENSMMUG00000015215	79.00	32.96	0.42	1.21E-18	LHPP
GATCAGAAAGAAGATGAAGA	ENSMMUG00000001687	103.79	43.49	0.42	4.79E-25	NSBP1
GATCCTGAGACTGGCAGGAC	ENSMMUG00000003081	62.88	26.52	0.42	5.16E-14	GPSM1
GATCCAGGGGACCCCTTGCC	ENSMMUG00000004616	44.34	18.72	0.42	4.12E-09	PLAUR
GATCGTAGACTCACTAGCAT	ENSMMUG00000001722	27.61	11.70	0.42	0.000122886	FAM172A
GATCACTCAATAAATCTGAG	ENSMMUG00000005485	287.39	121.89	0.42	7.74E-72	MFRP
GATCCATGTAATCTGATGTC	ENSMMUG00000019339	55.02	23.40	0.43	9.81E-12	APBA2
GATCAGTGCTTTATTTTAGC	ENSMMUG00000007093	67.72	28.86	0.43	5.88E-15	LDLRAD3
GATCAAAATGAATGCAGTTG	ENSMMUG00000017806	127.98	54.61	0.43	2.29E-30	CD109
GATCTGCTTCACCCAGCATA	ENSMMUG00000018639	41.52	17.75	0.43	3.94E-08	MEX3B
GATCGCCAGACAGTCCTGCG	ENSMMUG00000015617	52.00	22.23	0.43	7.97E-11	PLSCR3
GATCCTCCTCCTTTCTTCTC	ENSMMUG00000008596	46.35	19.89	0.43	2.71E-09	TMEM176B
GATCTTATCTAGTAACTATG	ENSMMUG00000019068	30.43	13.07	0.43	3.39E-05	PTPLAD2
GATCCCTCACAGCATCCGAG	ENSMMUG00000023281	64.49	27.69	0.43	6.62E-14	SLMO1
GATCTGTAGTCCTGTCTTGT	ENSMMUG00000013461	707.60	305.01	0.43	9.31E-175	HOXA10
GATCCCCGCAGAGTCGCCGG	ENSMMUG00000005779	29.83	12.87	0.43	5.70E-05	GMDS
GATCATCTTTATTTTTTTTA	ENSMMUG00000021029	29.83	12.87	0.43	5.70E-05	RCBTB1
GATCGTGTCTTCAAGCAGTT	ENSMMUG00000004382	32.04	13.85	0.43	1.62E-05	ABHD3
GATCCCCTTAGCAGGGGCCT	ENSMMUG00000008430	62.68	27.11	0.43	3.09E-13	CACNB3

GATCCTGTATCTTGGTTAAT	ENSMMUG00000010842	90.09	39.00	0.43	4.61E-20	DPY19L3
GATCACCCTAGGTCTGGTCA	ENSMMUG00000031350	28.82	12.48	0.43	0.000115419	PHLDA3
GATCCCTTGGCCTCCGGCCC	ENSMMUG00000017256	90.89	39.39	0.43	3.20E-20	CACNA1G
GATCCATGGCTTCTTTCCAT	ENSMMUG00000022310	134.83	58.51	0.43	4.43E-31	PPPDE1
GATCGCCTTGTTTTAACCTG	ENSMMUG00000000802	25.60	11.12	0.43	0.000827427	RFX3
GATCCCACACAGCATGTCCG	ENSMMUG00000002536	32.25	14.04	0.44	1.88E-05	CABP1
GATCTGAGGAATAAAACGGC	ENSMMUG00000021645	181.18	78.98	0.44	3.49E-42	CHST10
GATCTTTGTGTGACCTCCAG	ENSMMUG00000006442	26.80	11.70	0.44	0.000473371	KCNB1
GATCTGCCCAAGGTCAGAGG	ENSMMUG00000006022	41.52	18.14	0.44	1.03E-07	VWA5B1
GATCCCTTATTTATTCCTTC	ENSMMUG00000022520	69.53	30.42	0.44	1.38E-14	KLC2
GATCTGTATTGGATGAGGAC	ENSMMUG00000013739	169.29	74.11	0.44	6.07E-39	RAI14
GATCTTTAAAATGCAAGGCC	ENSMMUG00000018677	135.84	59.48	0.44	9.11E-31	NCAPD2
GATCCACTCCTGTAAGGTGC	ENSMMUG00000017564	752.75	329.97	0.44	2.75E-180	TBCCD1
GATCAGGAATGGGTGATTGG	ENSMMUG00000015360	34.66	15.21	0.44	6.18E-06	MCM4
GATCCCTGTCCTCCTGGGCC	ENSMMUG00000011670	323.87	142.17	0.44	3.76E-76	PTK7
GATCTGGCCTGCTGTCCTGT	ENSMMUG00000002273	263.41	115.65	0.44	1.67E-61	ATP6V0E2
GATCTTTTAGGAAAAAAAAA	ENSMMUG00000004896	75.38	33.15	0.44	7.70E-16	CENPV
GATCCCGCCTCTGGATTCCC	ENSMMUG00000018051	26.60	11.70	0.44	0.000660145	FAT1
GATCTTAAGGTATGTACGGA	ENSMMUG00000004716	37.69	16.58	0.44	1.22E-06	NETO2
GATCCTGTGACTGAGGCTCC	ENSMMUG00000016595	43.73	19.31	0.44	4.74E-08	AXIN2
GATCTGGGGGAACCCTCATC	ENSMMUG00000010653	176.14	77.81	0.44	6.97E-40	C19orf28
GATCTTTATAAGGTGTTTTA	ENSMMUG00000019697	64.49	28.67	0.44	7.01E-13	ACPL2
GATCTGTTCCAAGTAGTCAC	ENSMMUG00000016131	37.28	16.58	0.44	2.34E-06	EDN3
GATCTGTGCTACCTTATTAA	ENSMMUG00000019974	95.13	42.32	0.44	3.85E-20	NARS
GATCTGACCGGCCGCGCCCG	ENSMMUG00000010956	40.31	17.94	0.45	4.61E-07	SOCS1
GATCTGTGCACTAGTCTGTG	ENSMMUG00000017852	189.65	84.64	0.45	3.08E-42	ZIM2
GATCAACATGGTGGAACAAA	ENSMMUG00000016029	108.23	48.36	0.45	5.01E-23	SLC4A4
GATCAATTTAGACAGATACC	ENSMMUG00000015246	225.52	100.83	0.45	1.76E-50	TBC1D9
GATCCTATCCTCTTATTAAA	ENSMMUG00000022158	3423.93	1533.24	0.45	0	RPL18
GATCTCTGAGTTGGAACTGA	ENSMMUG00000023420	146.92	65.92	0.45	7.55E-32	AGTR2
GATCCCGTCTTCCAGAGAAC	ENSMMUG00000012110	106.41	47.78	0.45	2.26E-22	SMO
GATCTCAATGATATTTGAGC	ENSMMUG00000007756	35.07	15.80	0.45	1.31E-05	MRAS
GATCTTAATTAAACCAGATT	ENSMMUG00000016402	185.82	83.86	0.45	2.10E-40	LHFPL2
GATCCTTGTTTTATTTTAAA	ENSMMUG00000023739	33.25	15.02	0.45	3.81E-05	CAMK2N1
GATCTGCTTTTCTCTGTGTT	ENSMMUG00000013858	34.46	15.60	0.45	2.17E-05	ABCA4
GATCCGACATTTTGGAGAGA	ENSMMUG00000013009	567.73	257.23	0.45	5.39E-127	MEIS3
GATCATCAGATTCCGCCTGG	ENSMMUG00000017946	380.71	172.79	0.45	3.68E-84	ROGDI
GATCAATTGTCATGCTTGAA	ENSMMUG00000014891	55.83	25.35	0.45	2.90E-10	CA2
GATCCTAGGTGCTTAGGCCT	ENSMMUG00000010677	52.80	23.99	0.45	1.46E-09	C10orf2
GATCTGTCTGAGCAAAGAAG	ENSMMUG00000020503	105.61	47.97	0.45	1.26E-21	ZSCAN18
GATCTGGATAGGTTGTTCGT	ENSMMUG00000006438	44.14	20.09	0.46	1.56E-07	CKAP4
GATCTGCTTCTCCCATGAGA	ENSMMUG00000005189	97.54	44.46	0.46	1.22E-19	GPR162
GATCCTAGGGGTGTCATACT	ENSMMUG00000015146	35.07	15.99	0.46	2.06E-05	FTH1
GATCTGACCTGTGACAAATC	ENSMMUG00000002227	140.67	64.16	0.46	2.39E-29	ENAH
GATCGCCCTTCCCTTCCTGT	ENSMMUG00000002407	139.67	63.97	0.46	7.34E-29	CLEC11A
GATCAAAACACTGGATTTAC	ENSMMUG00000002755	42.52	19.50	0.46	5.17E-07	KLHL5
GATCCACTCACTCTGCCTCC	ENSMMUG00000022518	42.52	19.50	0.46	5.17E-07	PACS1
GATCTGGGAACTCAGCCCCA	ENSMMUG00000017265	39.50	18.14	0.46	2.63E-06	CACNA2D4
GATCTGTGTGGTCCCCGACG	ENSMMUG00000006256	142.49	65.53	0.46	3.14E-29	TARS2
GATCATATTCTTGAAATTTT	ENSMMUG00000006771	28.82	13.26	0.46	0.000746208	DBF4
GATCAGTATCACTTTAAGTC	ENSMMUG00000014073	37.28	17.16	0.46	9.20E-06	ALPK1
GATCTAGAGGCCCCCAAATC	ENSMMUG00000017940	96.54	44.46	0.46	5.86E-19	GSS
GATCAGGCAGGGCACAGAAT	ENSMMUG00000002564	39.30	18.14	0.46	3.60E-06	FRAS1
GATCCTGCACGATAACACTC	ENSMMUG00000021516	140.67	65.14	0.46	2.14E-28	CLU
GATCGCTGGACGCTATGAGA	ENSMMUG00000014535	118.30	54.80	0.46	1.77E-23	SLC15A3
GATCATCTAATTTTTCTGCC	ENSMMUG00000003345	67.72	31.40	0.46	2.36E-12	ERMN
GATCGCTCAGCTGGCTGTGT	ENSMMUG00000001549	64.29	29.84	0.46	1.42E-11	ATAD3B
GATCCAAGCTCCCACATTTG	ENSMMUG00000010395	40.31	18.72	0.46	2.81E-06	GPR161
GATCGTAAACCGGTTTTATC	ENSMMUG00000032506	108.63	50.51	0.46	3.55E-21	DSEL
GATCACAGAGGCCACAGGGA	ENSMMUG00000020762	41.52	19.31	0.47	1.60E-06	BTD
GATCTAGTTCAGAAGGAAGC	ENSMMUG00000014049	344.63	160.50	0.47	5.29E-72	COL6A3
GATCAACTCCTGTCTGGACC	ENSMMUG00000032017	86.46	40.37	0.47	3.41E-16	C9orf16
GATCAAAGTGGCTGCAGCAG	ENSMMUG00000010858	141.48	66.11	0.47	5.41E-28	P4HA2
GATCCCCCCGTGGCAATGGT	ENSMMUG00000011665	149.74	70.40	0.47	2.33E-29	MMAB
GATCGTGCTACACAACCGGA	ENSMMUG00000008775	491.35	231.68	0.47	7.02E-101	RABL4
GATCACAGCGCTCGTGAGGA	ENSMMUG00000019676	201.74	95.17	0.47	4.63E-40	GPX7
GATCCAGGACACCATCATGG	ENSMMUG00000012841	9081.31	4289.26	0.47	0	KLK3
GATCCTTAGGTGCTCAATAA	ENSMMUG00000017489	86.66	40.95	0.47	9.06E-16	RASSF4
GATCCCTGGTCCAGAATTCC	ENSMMUG00000021120	1019.58	482.87	0.47	1.24E-209	MAGED1
GATCTGTGTATGCTCTATGG	ENSMMUG00000015581	40.71	19.31	0.47	5.55E-06	PHLDA1
GATCCCCACAACCTCACACT	ENSMMUG00000003304	43.94	20.87	0.47	1.23E-06	EPHB3

GATCTATGAGAATGCCATTG	ENSMMUG00000001604	178.56	84.83	0.48	1.24E-34	GPX8
GATCTGGACTTGAGGCCCAC	ENSMMUG00000015418	34.46	16.38	0.48	0.00012736	SLC25A20
GATCTATCCAAAGAGCCAGG	ENSMMUG00000002267	84.04	39.98	0.48	5.71E-15	LAMC3
GATCGGGGGCGTATCATCAT	ENSMMUG00000002368	115.48	55.00	0.48	1.96E-21	CCND1
GATCGGGTGCTGATATTACC	ENSMMUG00000022628	58.24	27.89	0.48	1.98E-09	MMD
GATCTCTGTGGCCTAGGTTT	ENSMMUG00000020040	56.43	27.11	0.48	5.66E-09	PHACTR1
GATCACTGCCTGCCTGGCCC	ENSMMUG00000031521	162.24	78.01	0.48	2.16E-30	FOXL2
GATCAATGCCACTGACCCTT	ENSMMUG00000019157	69.33	33.35	0.48	1.44E-11	ASNS
GATCCCCAGGAGGTCCCCAG	ENSMMUG00000014325	387.76	186.83	0.48	1.83E-75	CYBA
GATCACACATCGAGACTATC	ENSMMUG00000014011	2621.61	1265.09	0.48	0	IGFBP7
GATCTTGAATTTCCTTTCTA	ENSMMUG00000010277	43.94	21.26	0.48	2.86E-06	DTX4
GATCCCCTGCTTGTGGCACA	ENSMMUG00000000751	53.41	25.94	0.49	4.29E-08	NLE1
GATCTGCGTATTTGTAAATA	ENSMMUG00000011819	104.80	50.90	0.49	2.58E-18	CHSY1
GATCTTTTAGTTTCTATGTT	ENSMMUG00000014394	635.65	309.11	0.49	1.61E-122	DNAJC10
GATCAGGAGCGGAACTCCAC	ENSMMUG00000011663	32.85	15.99	0.49	0.000630191	MVK
GATCTCTGTCTGCAATGTAG	ENSMMUG00000011846	306.74	149.97	0.49	2.86E-57	PGR
GATCGTTCCCCTGTTCACTC	ENSMMUG00000004475	968.79	474.68	0.49	1.18E-184	MMP2
GATCTGGGAACTTTTTGCTG	ENSMMUG00000012644	46.56	22.82	0.49	1.56E-06	AKAP1
GATCACTTCCCGCAGTCCTT	ENSMMUG00000007102	72.76	35.69	0.49	1.24E-11	NCAPD3
GATCCCAGTCTCTGAAGACA	ENSMMUG00000013175	336.37	165.18	0.49	2.27E-62	WDR90
GATCAAGTTGTTTGATGCAA	ENSMMUG00000022766	47.97	23.60	0.49	9.93E-07	CDCA7L
GATCCTCGTCTTACAGCGAA	ENSMMUG00000014318	46.15	22.82	0.49	2.83E-06	PMS1
GATCATGGGCAAGAAGCCTG	ENSMMUG00000004675	189.24	93.61	0.49	1.71E-33	SMTN
GATCGCAGCTAAAAAGTCAG	ENSMMUG00000012684	819.66	406.23	0.50	7.75E-152	ALDH6A1
GATCCCAGCTGGCCCCTGTG	ENSMMUG00000005820	72.76	36.08	0.50	2.76E-11	AMPD2
GATCTGAACATTCAAAAGAA	ENSMMUG00000014466	410.94	204.19	0.50	1.36E-74	PGRMC1
GATCTGGCACACTGTGGATA	ENSMMUG00000014023	37.28	18.53	0.50	0.000177819	TLE3
GATCCCAGTTCCTAGACCTC	ENSMMUG00000016669	63.89	31.79	0.50	1.66E-09	ZNF385A
GATCTAATTAAGCTAAATTT	ENSMMUG00000023198	35.27	17.55	0.50	0.000457314	TET1
GATCTCCCTCCATCTTCATT	ENSMMUG00000030889	132.81	66.11	0.50	1.97E-22	H2AFX
GATCCAAAGACAGACCACAG	ENSMMUG00000018200	473.41	236.17	0.50	1.88E-85	C14orf166
GATCGAGGTCATGGAAGATG	ENSMMUG00000018446	44.94	22.43	0.50	7.40E-06	FGD5
GATCTGTTTTGTACTTTTTA	ENSMMUG00000009155	167.08	335.82	2.01	0	FAM60A
GATCCTGAGAAAGGGTTTGG	ENSMMUG00000018041	56.63	114.09	2.01	0	SPINT1
GATCCTTCTATCCAGTTTTC	ENSMMUG00000015876	17.13	34.52	2.02	0	RTN3
GATCCTGTTTGATATGCTAT	ENSMMUG00000020491	26.00	52.46	2.02	0	VWA5A
GATCTTGCACCAAGCCAATG	ENSMMUG00000011245	139.46	281.61	2.02	0	CRISPLD2
GATCACTAACACTGAATCTT	ENSMMUG00000019204	23.18	46.80	2.02	0	MARVELD3
GATCAGTAGCAATTAAATTG	ENSMMUG00000003914	13.70	27.69	2.02	0	KLHDC1
GATCACTGATATTTTAGTCA	ENSMMUG00000014784	71.55	144.70	2.02	0	DSP
GATCCCTGCTCGTGCAGGCC	ENSMMUG00000022685	58.85	119.16	2.02	0	SLC29A1
GATCATCAGTGTTCTTTTTA	ENSMMUG00000022303	251.12	508.61	2.03	0	SLC7A2
GATCCTGCCAGAAGAGGAGG	ENSMMUG00000011626	36.68	74.30	2.03	0	TBC1D17
GATCTGGGCTGTGGGGCCCT	ENSMMUG00000018034	60.26	122.28	2.03	0	ST14
GATCCCAGTGGTATCCGTGG	ENSMMUG00000009709	20.56	41.73	2.03	0	TMEM102
GATCTTTGTTTTTTTAAAGA	ENSMMUG00000020321	18.34	37.25	2.03	0	USP42
GATCGAGCCAAGAGCTGCAA	ENSMMUG00000029963	131.40	267.18	2.03	0	RND2
GATCCCCAGTCCAAGTCTCT	ENSMMUG00000014265	17.74	36.08	2.03	0	CD27
GATCCACCCTCCTATAATGT	ENSMMUG00000019696	22.77	46.41	2.04	0	GPD1L
GATCTTCGTAGTTTGTTCAT	ENSMMUG00000021164	44.94	91.66	2.04	0	WDFY3
GATCCTAGTTCTGTGTCATA	ENSMMUG00000018400	26.00	53.05	2.04	0	ADFP
GATCGCTGGCCTGTGCTAGG	ENSMMUG00000015689	72.35	148.02	2.05	0	GPR56
GATCAACAATGCATGGATTC	ENSMMUG00000007637	17.33	35.49	2.05	0	ENDOD1
GATCTTATTATATATTTTTA	ENSMMUG00000021532	24.18	49.54	2.05	0	BXDC1
GATCTAAATGTGAACAGTTT	ENSMMUG00000014940	236.00	483.45	2.05	0	PNRC1
GATCCCAACCTGCTGTCACT	ENSMMUG00000006248	51.39	105.31	2.05	0	WDR86
GATCCAGGCCTCCTTCTCCT	ENSMMUG00000015369	18.74	38.42	2.05	0	NKG7
GATCCTGTCTCCCACCTCCT	ENSMMUG00000016001	136.04	279.27	2.05	0	VAT1
GATCTGGTGAGCAGCCAGCA	ENSMMUG00000000976	33.05	68.26	2.07	0	KCNK12
GATCTGCAAGTGCAGAGTGT	ENSMMUG00000021696	17.94	37.05	2.07	0	EBF1
GATCTGATTTTTTTCCCCTT	ENSMMUG00000030250	267.44	552.88	2.07	0	NEK8
GATCCTGACACTGGAGGGCA	ENSMMUG00000018232	15.92	32.96	2.07	0	SESN1
GATCACACAAATTTTAGGGA	ENSMMUG00000003134	18.54	38.42	2.07	0	RNF217
GATCATGTTAGCTATCAGAG	ENSMMUG00000018265	19.75	40.95	2.07	0	PRR5L
GATCTCAGATTGTGTAGATA	ENSMMUG00000006035	22.98	47.78	2.08	0	THBS1
GATCAGAGTGGATGTAGAGC	ENSMMUG00000007845	109.84	228.56	2.08	0	CBX7
GATCAGGCAGAAAAGAAAAA	ENSMMUG00000014817	246.68	514.46	2.09	0	SLC18A2
GATCCTGACTGTGCTCTATA	ENSMMUG00000008748	10.28	21.45	2.09	0	DUOXA1
GATCGAGATGAAGGAAGGAC	ENSMMUG00000007085	38.29	79.96	2.09	0	ZBTB16
GATCCCCCAAACCTCAAGGT	ENSMMUG00000013579	24.18	50.51	2.09	0	SLC45A4
GATCCAGAAAGTGAACGAGA	ENSMMUG00000018578	20.36	42.51	2.09	0	LOH12CR1

GATCATTTTCTGCAACTGAG	ENSMMUG00000016970	47.97	100.24	2.09	0	SSR3
GATCCCTGGAGGGGCTGAAC	ENSMMUG00000003431	69.93	146.46	2.09	0	HNF1B
GATCTGTGCCAGCTGGGCGG	ENSMMUG00000013188	104.60	219.20	2.10	0	SERINC2
GATCTGGGACTTCGTGTGGT	ENSMMUG00000023748	103.99	218.03	2.10	0	HIST1H1E
GATCATCTTGAATGACAATG	ENSMMUG00000003868	15.52	32.57	2.10	0	B3GALT4
GATCCTGCATACTGAAAGCC	ENSMMUG00000001348	61.87	129.88	2.10	0	ERBB2
GATCGTGGAGGAGGTCTCTT	ENSMMUG00000015100	81.02	170.25	2.10	0	ABO
GATCTGTAGTTTTCATGCCT	ENSMMUG00000015885	22.17	46.61	2.10	0	MEGF9
GATCTCAGCCTCAGTTCTCT	ENSMMUG00000003457	111.45	234.41	2.10	0	PRKACB
GATCTGACACTTCCTTTCCA	ENSMMUG00000002203	142.08	298.97	2.10	0	FAM113B
GATCAAACATTGGCTTACTG	ENSMMUG00000007214	20.56	43.29	2.11	0	CCDC117
GATCTTTTTTTTCTTGGTAT	ENSMMUG00000008289	10.28	21.65	2.11	0	FAM45A
GATCTTACAGGAAAGGATAC	ENSMMUG00000005959	20.36	42.90	2.11	0	GK
GATCGAGGCCGCAGTAAGCT	ENSMMUG00000015545	11.29	23.79	2.11	0	ZDHHC4
GATCTATGCTCATGAATTAA	ENSMMUG00000014558	23.58	49.73	2.11	0	JAK2
GATCACACTCTGCAAATGCC	ENSMMUG00000021699	146.52	309.30	2.11	0	RNF145
GATCTTCTGTCTAGTACTTG	ENSMMUG00000018198	48.77	102.97	2.11	0	CCDC6
GATCTGGTTAAGTCGTGTAG	ENSMMUG00000000997	64.09	135.34	2.11	0	PERP
GATCTGCATTTATAAACGTG	ENSMMUG00000004712	39.50	83.47	2.11	0	LPL
GATCTGATAACATGTCAGAT	ENSMMUG00000010687	28.22	59.68	2.12	0	HEXA
GATCTCTCAACCTGCTTTCT	ENSMMUG00000006677	78.00	164.99	2.12	0	CREBL2
GATCTATAGTATAGAATGAA	ENSMMUG00000001051	75.17	160.70	2.14	0	MAP2K6
GATCAGCTATATAGTATTTA	ENSMMUG00000019457	356.12	764.09	2.15	0	VIL2
GATCTACTAGATGCATTATA	ENSMMUG00000006356	28.82	62.21	2.16	0	CORO2B
GATCACATTTGCTTCTAAAA	ENSMMUG00000005757	11.29	24.38	2.16	0	CST7
GATCTCTAAAAGGCTCTCTC	ENSMMUG00000017010	24.18	52.27	2.16	0	AADACL1
GATCTCAAAAAAGGAATTTT	ENSMMUG00000003707	18.14	39.20	2.16	0	ACVR1C
GATCTCCAATGTTTTGGGGA	ENSMMUG00000023169	15.32	33.15	2.16	0	EIF4EBP2
GATCTGTTGGGTTCTCTATT	ENSMMUG00000000073	9.27	20.09	2.17	0	CASS4
GATCGGGGTCACCGGAGCAA	ENSMMUG00000009674	36.08	78.20	2.17	0	ELANE
GATCTAACACTAACTGTATT	ENSMMUG00000021002	846.26	1839.04	2.17	0	HIF1A
GATCGAGAGCCGGTGAATGA	ENSMMUG00000012683	61.27	133.39	2.18	0	C14orf45
GATCAATTAAATTTTTTAAA	ENSMMUG00000003611	166.07	361.96	2.18	0	LDLR
GATCTTGGCTTCTGTTACTC	ENSMMUG00000015001	34.66	75.67	2.18	0	LIMK2
GATCAACGCGCTGGTGCAGG	ENSMMUG00000004676	274.29	599.69	2.19	0	SELM
GATCTCTTGTCAAATTGTTA	ENSMMUG00000004001	42.52	93.02	2.19	0	SYT2
GATCACTGAGATAAGAGCTG	ENSMMUG00000017872	29.02	63.58	2.19	0	MINA
GATCCAAGTGTGATTTGAAT	ENSMMUG00000017609	57.64	126.37	2.19	0	CTSL1
GATCATTTTTAAGAGAATAA	ENSMMUG00000003790	9.07	19.89	2.19	0	MED31
GATCTACGTTTCCATGGCTG	ENSMMUG00000010113	15.12	33.15	2.19	0	SRD5A3
GATCTTTCACTAGATATTTT	ENSMMUG00000023653	18.74	41.15	2.20	0	STEAP2
GATCAGAGTAGCCCATAGGC	ENSMMUG00000000306	823.28	1807.83	2.20	0	FAM82A2
GATCAGGAAGTGCATCTTCA	ENSMMUG00000008126	19.35	42.71	2.21	0	JHDM1D
GATCACAAGAAATACAAATC	ENSMMUG00000021153	58.45	129.30	2.21	0	SGK3
GATCAATCTTTGATGGTGAG	ENSMMUG00000001803	9.67	21.45	2.22	0	GJA5
GATCGGAGCCGCTTTGCACG	ENSMMUG00000009223	93.72	207.89	2.22	0	PPP1R15A
GATCTTCATGATGTGTGAGT	ENSMMUG00000001915	17.13	38.03	2.22	0	CLDN1
GATCTTCAATAGAAAGAGTC	ENSMMUG00000022585	10.68	23.79	2.23	0	SLC25A15
GATCTCATGCTGCTGTCTGG	ENSMMUG00000001347	18.54	41.34	2.23	0	PGAP3
GATCTGAACTCCTTGGCTTC	ENSMMUG00000015325	9.88	22.04	2.23	0	COL17A1
GATCACTCTACATAAAATAC	ENSMMUG00000029350	13.10	29.25	2.23	0	ERO1L
GATCCTGAAAGAGCTGCCTA	ENSMMUG00000020866	53.81	120.33	2.24	0	HOXB6
GATCAAAACCTTCCTTCCCT	ENSMMUG00000000669	14.71	32.96	2.24	0	GJB1
GATCCTGGTGACAAATTAAG	ENSMMUG00000003574	12.09	27.11	2.24	0	WDR51B
GATCAGTTTGCTAAATGAAC	ENSMMUG00000000874	96.13	215.69	2.24	0	CHST1
GATCCGTCTGTGCCCGTGTC	ENSMMUG00000016935	10.08	22.62	2.24	0	CLDN5
GATCTGGGGTGGGGGTAACA	ENSMMUG00000002031	103.19	231.68	2.25	0	PRSS8
GATCAGAAGAAGCAAAAGGG	ENSMMUG00000018386	9.27	20.87	2.25	0	SH3RF2
GATCACTTGTATTTCCCATC	ENSMMUG00000029908	10.48	23.60	2.25	0	HIST1H2BJ
GATCCTTTGTTTAATAAAGT	ENSMMUG00000004448	49.78	112.14	2.25	0	TMEM144
GATCTCAGGAATTACATTTT	ENSMMUG00000016880	15.12	34.13	2.26	0	SLC39A8
GATCCCCACTACAACTCCAA	ENSMMUG00000011719	46.76	106.09	2.27	0	SERPINB9
GATCCAGTAACGCTAGTCTT	ENSMMUG00000032579	9.27	21.06	2.27	0	KLK7
GATCCTCCAGATGGCATTCA	ENSMMUG00000013715	48.17	109.60	2.28	0	PAQR8
GATCAGCTTAGCTAGACCAT	ENSMMUG00000014746	21.77	49.54	2.28	0	BCL2L2
GATCTAGGTATTTTGTTCTC	ENSMMUG00000028907	14.31	32.57	2.28	0	INSR
GATCTTCTGAGCTTGTTTCC	ENSMMUG00000019743	56.43	128.52	2.28	0	KIAA1522
GATCGGAAACCAAGACGGAG	ENSMMUG00000018085	22.77	51.88	2.28	0	SLC37A1
GATCCAGGCCAGCTTGCCAC	ENSMMUG00000019535	130.60	297.60	2.28	0	NUPR1
GATCCTGAAATCTGCATCTG	ENSMMUG00000006093	16.93	38.61	2.28	0	EZH1
GATCTACAATGAAGCCCTCA	ENSMMUG00000008917	371.23	848.14	2.28	0	S100A6

GATCTGCATCCTCAGTGGGA	ENSMMUG00000008106	8.87	20.28	2.29	0	SLC25A17
GATCAGAGTCTCTTTTGGGC	ENSMMUG00000012671	123.54	282.58	2.29	0	SOCS2
GATCCTTGGAGGTCTGTAGA	ENSMMUG00000006731	116.29	266.20	2.29	0	CECR2
GATCAAGTTTGTCTTCCGCA	ENSMMUG00000008587	137.05	313.98	2.29	0	CAMK2D
GATCTGAAGGGTTTGGGGTG	ENSMMUG00000004313	14.11	32.37	2.29	0	PLCB1
GATCTTCATTGGGGGATTGA	ENSMMUG00000019771	90.29	207.31	2.30	0	PPP2R5A
GATCTTTCTGAAATTATGAA	ENSMMUG00000016674	8.06	18.53	2.30	0	B4GALT6
GATCCACTATGCCTTAATGG	ENSMMUG00000017745	9.07	20.87	2.30	0	ANGPT1
GATCTAAAAAGGTAATACGG	ENSMMUG00000015591	12.70	29.25	2.30	0	C4orf16
GATCAAGGGCTGGAAATAAA	ENSMMUG00000001819	8.46	19.50	2.30	0	ISG15
GATCCAGTACGCCTGCCTGC	ENSMMUG00000010198	52.80	121.69	2.30	0	CYB5R3
GATCTGGGAGCTCCTGTCTG	ENSMMUG00000003896	11.08	25.55	2.30	0	ARHGAP6
GATCAAAGGCCTCTCAGGGG	ENSMMUG00000001433	9.47	21.84	2.31	0	RAI2
GATCGCTACTACGACCCCAA	ENSMMUG00000002677	17.74	40.95	2.31	0	GAL3ST1
GATCAAGATGGAAAGAGACA	ENSMMUG00000014839	8.26	19.11	2.31	0	NPAS3
GATCTGCTGACAGTTTCAAT	ENSMMUG00000017981	8.67	20.09	2.32	0	PART1
GATCAACCCAGCCTAGCCCA	ENSMMUG00000007618	8.06	18.72	2.32	0	TMPRSS13
GATCATGCCAGAAATAGAGA	ENSMMUG00000010257	37.28	86.78	2.33	0	SLC5A6
GATCGCTGGTAGACAGGTTT	ENSMMUG00000017561	10.68	24.96	2.34	0	SLC43A2
GATCAGATGTGCTTTTCCTC	ENSMMUG00000020706	49.98	117.21	2.35	0	ETS1
GATCCACGCTGGGCCTAGGA	ENSMMUG00000004844	57.84	135.73	2.35	0	HPN
GATCATTGTATATTTTCTTT	ENSMMUG00000011850	37.08	87.17	2.35	0	CDH1
GATCTTTTGAATCCTGTCTC	ENSMMUG00000003529	85.65	201.65	2.35	0	FAM177A1
GATCATGCTTTACTCTGTGC	ENSMMUG00000008554	13.91	32.76	2.36	0	LAIR1
GATCCTAACGAACCTACATA	ENSMMUG00000008881	32.04	75.67	2.36	0	ING2
GATCATATTTTTTTATACAG	ENSMMUG00000002157	347.25	820.06	2.36	0	PIM3
GATCCCTCCTAATCAAATTC	ENSMMUG00000029682	8.67	20.48	2.36	0	KIAA0240
GATCGGGAAAAAATTCGGCC	ENSMMUG00000011848	240.03	569.46	2.37	0	C10orf116
GATCCAAAGTACTGTTTCTC	ENSMMUG00000019367	33.25	78.98	2.38	0	HLA-DPB1
GATCATCTTGTGAATTTGTT	ENSMMUG00000018930	11.89	28.28	2.38	0	PER2
GATCGCTGAGTGGGGTACTG	ENSMMUG00000008329	17.13	40.76	2.38	0	CHN2
GATCTGCTCTTTTTAAATTG	ENSMMUG00000001243	17.94	42.71	2.38	0	ADCY9
GATCATTTTAAATAAATGTA	ENSMMUG00000018688	26.00	62.21	2.39	0	XG
GATCTACATGTGTCTAGAGA	ENSMMUG00000016004	511.30	1224.33	2.39	0	ACPP
GATCCATCAGAGTCTAAAGG	ENSMMUG00000020016	8.06	19.31	2.39	0	APOL4
GATCTTAAACATGGTGAATT	ENSMMUG00000010163	11.89	28.67	2.41	0	ARHGEF3
GATCAGTCCAACGCATCCAC	ENSMMUG00000023808	11.29	27.30	2.42	0	CARD6
GATCTCTATTATTAGGCTAG	ENSMMUG00000019745	8.87	21.45	2.42	0	GPN1
GATCAAATTCATCATTATTT	ENSMMUG00000009322	8.46	20.48	2.42	0	ZNF24
GATCCGGTGAGCTGGGAAGC	ENSMMUG00000020989	42.52	102.97	2.42	0	GSTT1
GATCTTTCTCAAAGAAATAT	ENSMMUG00000016167	16.32	39.59	2.43	0	PTGER4
GATCCTCTCAAGGCAGCATC	ENSMMUG00000001866	11.89	28.86	2.43	0	MRGPRF
GATCCTTCACACAAGCACTT	ENSMMUG00000019657	66.71	162.06	2.43	0	ABHD14B
GATCACTCAGGAGGCTGTTC	ENSMMUG00000021900	26.40	64.16	2.43	0	UPK3A
GATCTGAGTGGGGCACTGGC	ENSMMUG00000012094	71.95	175.13	2.43	0	RAB17
GATCCCCGAATCCCAGGTCC	ENSMMUG00000004739	27.41	66.89	2.44	0	BIK
GATCTCCCTGAAATGGGCTT	ENSMMUG00000012770	45.14	110.38	2.45	0	SMAD7
GATCAAAATGTCAGGCTTGG	ENSMMUG00000000242	11.08	27.11	2.45	0	PPP1R3C
GATCTGTAAATGACTTTAAA	ENSMMUG00000014873	49.98	122.28	2.45	0	TOR1AIP1
GATCCCAACCCTCCCTCCTG	ENSMMUG00000000369	79.20	194.04	2.45	0	TP53I11
GATCTCTGCTTATTGAAGAT	ENSMMUG00000005353	10.08	24.77	2.46	0	PDGFD
GATCAGATGAGGACTCACTT	ENSMMUG00000023289	13.70	33.74	2.46	0	PLD1
GATCTTTGTTTTTATGTTTT	ENSMMUG00000022262	6.65	16.38	2.46	0	TNIK
GATCGCGGCGGAGCTGGCCC	ENSMMUG00000005688	48.37	119.16	2.46	0	JUNB
GATCATTGTGCAATAAAGCT	ENSMMUG00000011130	57.04	140.61	2.47	0	TRIM36
GATCGACCGAATGGTGAATC	ENSMMUG00000011286	46.76	115.84	2.48	0	DDIT3
GATCAAAATTCACCCAATAC	ENSMMUG00000018306	16.53	40.95	2.48	0	KIAA2026
GATCCAGCTCCTAGAGCTTG	ENSMMUG00000015324	18.94	47.19	2.49	0	SLK
GATCACTCTATCCAACCCCC	ENSMMUG00000022054	14.31	35.69	2.49	0	HIST1H2BH
GATCTTTCACTGTGGATGTT	ENSMMUG00000020236	17.53	43.88	2.50	0	ZNF610
GATCTTCCTGGAAATGAGCA	ENSMMUG00000010696	24.59	61.63	2.51	0	KLF6
GATCATCAACCTCGTGTCCA	ENSMMUG00000005507	13.30	33.54	2.52	0	PLXNA3
GATCACCCCAGCCACAACCC	ENSMMUG00000019803	26.60	67.28	2.53	0	TCN2
GATCATTTATTTAAAAGTAC	ENSMMUG00000019504	57.84	146.65	2.54	0	ALDH1A2
GATCTTGATATAGCTCATTC	ENSMMUG00000014055	204.96	519.92	2.54	0	AP1S2
GATCTTTGTCTTTTGTCATG	ENSMMUG00000018942	464.75	1180.06	2.54	0	IGFBP5
GATCATTTTATATTGGCATT	ENSMMUG00000003697	27.41	69.62	2.54	0	INPP4B
GATCATTACGTTGTATGTCT	ENSMMUG00000003799	16.93	43.10	2.55	0	FNBP1
GATCTGATTTTTTCACTATG	ENSMMUG00000001242	6.05	15.41	2.55	0	WDR72
GATCCTCTTGTACTGGGAGG	ENSMMUG00000013383	79.00	201.46	2.55	0	TOM1
GATCTGCAAATACTATCCAA	ENSMMUG00000022218	68.32	174.35	2.55	0	ANXA3

GATCCCTAAAGAAAACAAAC	ENSMMUG00000011607	7.26	18.53	2.55	0	NR4A2
GATCATAAAATGAATTCTTT	ENSMMUG00000004215	32.25	82.88	2.57	0	FAM84A
GATCCTGGACACGTCCCTTC	ENSMMUG00000009831	7.05	18.14	2.57	0	TBC1D2
GATCACCATGTGCTCAGGCC	ENSMMUG00000011915	41.32	106.29	2.57	0	LYST
GATCAAAATTGAACCATTGT	ENSMMUG00000010589	13.70	35.30	2.58	0	NEBL
GATCTTCTAGCCAGGAAAGG	ENSMMUG00000023275	42.32	109.02	2.58	0	MTF1
GATCTTTATTTATTACATGA	ENSMMUG00000011578	29.83	76.84	2.58	0	PAX8
GATCACCATCTTTAAATTTA	ENSMMUG00000020725	16.73	43.10	2.58	0	RIPK2
GATCCATTTCCCATGGATAA	ENSMMUG00000017266	7.86	20.28	2.58	0	KIAA1324
GATCACTTGGAGACTCTTTT	ENSMMUG00000002678	19.75	51.29	2.60	0	ITGB6
GATCATTAAGAAGAAAAGTG	ENSMMUG00000003608	23.58	61.24	2.60	0	LDB3
GATCGCACTGGAAGATTTTA	ENSMMUG00000003537	372.04	967.88	2.60	0	FAM100B
GATCCTCAGTGCAAAATGTC	ENSMMUG00000020865	58.24	152.31	2.62	0	HOXB5
GATCAGATCGAAAGGTTATA	ENSMMUG00000003890	16.12	42.51	2.64	0	CYFIP1
GATCTCAGGCTCCTGCAGTT	ENSMMUG00000008079	14.11	37.25	2.64	0	UPK1B
GATCGCCTACCATTTTATAG	ENSMMUG00000002865	36.28	95.95	2.64	0	ABI3BP
GATCAAGCATTGTTTTCCCC	ENSMMUG00000019979	6.25	16.58	2.65	0	PEX14
GATCCATGCAGCTTTTTTTG	ENSMMUG00000011520	26.20	69.82	2.66	0	FKBP5
GATCATGTCTGTTCCTGTTC	ENSMMUG00000002907	22.17	59.29	2.67	0	CTDSPL
GATCTGCTACTATTTAGTTT	ENSMMUG00000006305	87.67	234.61	2.68	0	WWP1
GATCATTCTGGCTAAAAATT	ENSMMUG00000005626	56.63	151.73	2.68	0	STK17B
GATCGGGCACTCTGCTCAGA	ENSMMUG00000010702	10.48	28.08	2.68	0	EEPD1
GATCTAGAGGAAGGAAGAAA	ENSMMUG00000007768	7.05	18.92	2.68	0	EN2
GATCAATCTGGTGAATCCTT	ENSMMUG00000016708	54.62	146.85	2.69	0	MFHAS1
GATCTTCTAATGGTCTAAAT	ENSMMUG00000001387	23.38	62.99	2.69	0	PAK1
GATCTGCTTGAAGAACATGT	ENSMMUG00000015725	95.53	258.01	2.70	0	CD24L4
GATCTTGGGAGAGGCCCAGA	ENSMMUG00000021400	15.72	42.51	2.70	0	RHOBTB1
GATCACCCTGTTGATACACA	ENSMMUG00000010323	5.04	13.65	2.71	0	ZC3H12A
GATCTATATATATCTTGAAT	ENSMMUG00000017549	20.96	56.95	2.72	0	ENPP3
GATCAAAGCACTGGGCTTGT	ENSMMUG00000007087	321.45	880.12	2.74	0	SLC22A5
GATCTGTATGTGTTCTATTC	ENSMMUG00000013884	855.73	2344.14	2.74	0	IVNS1ABP
GATCTGTCACAGCCAGTCCC	ENSMMUG00000016423	10.88	29.84	2.74	0	C9orf117
GATCACAGATGGATTTTGTT	ENSMMUG00000008140	105.40	289.02	2.74	0	SGK1
GATCTGTCATTAGTAATTTC	ENSMMUG00000013804	11.08	30.42	2.74	0	PPFIA2
GATCACCAGCCATGTGCCTT	ENSMMUG00000010093	91.10	250.41	2.75	0	CTSH
GATCTAGGAGGCTGGGGGAA	ENSMMUG00000004137	11.69	32.18	2.75	0	UBXN10
GATCCCATGTATCTTATTAT	ENSMMUG00000011553	75.98	209.65	2.76	0	TIGD6
GATCGAACAAGCAGCAACAC	ENSMMUG00000008269	9.47	26.33	2.78	0	PDE3A
GATCATGAGTTCATGCGATG	ENSMMUG00000016530	6.45	17.94	2.78	0	NEK3
GATCAAATCAGTAATTTTGT	ENSMMUG00000014047	9.07	25.35	2.80	0	BMX
GATCGTTGGCATGGTTAAAA	ENSMMUG00000004071	41.32	115.65	2.80	0	TGFB2
GATCGAGTTTTAAATTGATA	ENSMMUG00000017053	47.56	133.39	2.80	0	DAPK1
GATCAGGCAAAAATAGTTTC	ENSMMUG00000011687	11.49	32.37	2.82	0	DSC2
GATCCCCGGCACGGCAAGTA	ENSMMUG00000019628	21.77	61.43	2.82	0	TUBA1
GATCTTCAATTCCTTGAGTC	ENSMMUG00000018542	11.08	31.59	2.85	0	LNPEP
GATCTGCAATGAACTGGAAC	ENSMMUG00000020156	5.44	15.60	2.87	0	CD1D
GATCCCCAGTACCCAGCCAT	ENSMMUG00000007295	36.88	106.09	2.88	0	CYBRD1
GATCCATCTAAAAAGAAGCA	ENSMMUG00000012257	8.87	25.55	2.88	0	C1orf53
GATCACTCCCCTTTCTCGTG	ENSMMUG00000020212	40.71	117.40	2.88	0	SCNN1A
GATCTAGAAGGAAGAGGTTG	ENSMMUG00000023509	8.06	23.40	2.90	0	FGF1
GATCAGAGGGAGCTGCCGCC	ENSMMUG00000004179	5.04	14.63	2.90	0	LIMS2
GATCAACTTCCGGCTGAGGC	ENSMMUG00000008127	5.84	16.97	2.90	0	RAB11FIP4
GATCAGAACCTCCAAATACT	ENSMMUG00000007338	560.07	1627.24	2.91	0	TXNIP
GATCGCTCACCTCGACCTTC	ENSMMUG00000014369	61.27	178.64	2.92	0	ZBTB3
GATCTTTGAATGAGCTTTTA	ENSMMUG00000015374	9.88	28.86	2.92	0	LRMP
GATCCACGTTTCATCTTTAA	ENSMMUG00000020864	15.72	46.02	2.93	0	HOXB4
GATCATGCTCCATCCGGCCC	ENSMMUG00000020434	6.25	18.33	2.93	0	CSF3R
GATCGACGAGTTCTACTCCC	ENSMMUG00000002090	5.04	14.82	2.94	0	ATP6V1B1
GATCTCCAGCTGTGGTGAGC	ENSMMUG00000017871	7.46	22.04	2.96	0	CRYBG3
GATCCCCAAGGGATATGTAT	ENSMMUG00000014518	14.91	44.07	2.96	0	OSGIN2
GATCGTGACAAATCTTCCCT	ENSMMUG00000023104	20.15	59.87	2.97	0	ELMO1
GATCCTATGGTTTCTCCATC	ENSMMUG00000022626	149.34	448.16	3.00	0	HLA-DMB
GATCAGACTATCTGAATATA	ENSMMUG00000001250	119.92	360.01	3.00	0	PTPN3
GATCTGTTCTCAATAATTTA	ENSMMUG00000013080	9.67	29.06	3.00	0	TMEM184A
GATCTGCGCTGGCCACGTGC	ENSMMUG00000003360	107.22	323.34	3.02	0	CENPM
GATCCCGTCGTCTCGTAGAT	ENSMMUG00000018749	44.74	134.95	3.02	0	HAND2
GATCACATCTGTTAAATAGA	ENSMMUG00000022978	44.54	134.56	3.02	0	IL6R
GATCACACTACCATTATTTC	ENSMMUG00000008987	7.46	22.62	3.03	0	LYZ
GATCAGTATGCTGTTTTAAT	ENSMMUG00000005435	45.95	139.44	3.03	0	ICA1
GATCGGGGTGTTTAGCTGTG	ENSMMUG00000008752	167.08	509.98	3.05	0	DUOX1
GATCATCAACAAAGAAAGTC	ENSMMUG00000000476	9.07	27.69	3.05	0	FMO5

GATCAGAATTGAATTTAAGT	ENSMMUG00000004636	33.46	102.19	3.05	0	OMD
GATCATACCTATGACTTGTT	ENSMMUG00000005586	41.72	127.54	3.06	0	RPS6KA5
GATCAATGGGTTCTCCTAGA	ENSMMUG00000013102	15.92	48.75	3.06	0	TRPM6
GATCTCTTAAATAAACTTGC	ENSMMUG00000008120	46.35	142.17	3.07	0	AIM1
GATCCCCTCAAGTTTCTGTG	ENSMMUG00000000561	176.14	545.28	3.10	0	XDH
GATCCTGGGGACCAATAAAG	ENSMMUG00000029767	6.05	18.72	3.10	0	FN3K
GATCCACTTTCAGGCCCTGC	ENSMMUG00000020338	391.79	1215.75	3.10	0	IGFBP6
GATCCCGGCAGATGATGAGC	ENSMMUG00000020665	5.84	18.14	3.10	0	SDSL
GATCACTTTTAAATAACCAC	ENSMMUG00000001375	4.84	15.02	3.10	0	FAM134B
GATCTGGCCCAGTTCCCCGC	ENSMMUG00000001817	3.83	11.90	3.11	0	HES4
GATCAAGCTCAGAGACTGGC	ENSMMUG00000012138	16.93	52.85	3.12	0	RORC
GATCCTAAAGAAATTTAGTG	ENSMMUG00000022003	4.43	13.85	3.12	0	MMRN1
GATCAGTAAGGATTTCACCT	ENSMMUG00000012648	82.83	260.16	3.14	0	GPNMB
GATCTAGCCTGCCCTGCTTG	ENSMMUG00000001853	112.46	354.55	3.15	0	PMM1
GATCATTCTTACTCTAAATT	ENSMMUG00000017631	15.72	49.73	3.16	0	GPRC5A
GATCAGCGTGCGGGGCGTGA	ENSMMUG00000002456	19.75	62.60	3.17	0	MAPK8IP1
GATCATGTCTAATGCCCATT	ENSMMUG00000003696	5.84	18.53	3.17	0	SULT1C2
GATCACCTGACATGATTGGG	ENSMMUG00000002242	59.05	187.22	3.17	0	MDS1
GATCTGTAACATTTGTTTCA	ENSMMUG00000003118	18.74	59.87	3.19	0	ADCY7
GATCTCTTAAGTCCTGGCTG	ENSMMUG00000002853	12.50	40.17	3.22	0	CORO2A
GATCCACCAGCTCTTTCTGA	ENSMMUG00000019324	7.86	25.35	3.23	0	NEK10
GATCAATGGGATGATATAGG	ENSMMUG00000007633	24.39	78.79	3.23	0	LMO2
GATCTTCAGATATTCTTTGC	ENSMMUG00000000040	14.31	46.41	3.24	0	EGLN3
GATCCCCAAGTGTGAACAAA	ENSMMUG00000003057	17.74	57.53	3.24	0	KIT
GATCGAGATTGGACTGCCCA	ENSMMUG00000013557	7.46	24.38	3.27	0	MCC
GATCATTATGTTTGTTGTGC	ENSMMUG00000020919	57.44	188.19	3.28	0	SHROOM3
GATCAAGTTTGGCTCTCTTG	ENSMMUG00000005144	9.88	32.37	3.28	0	NEK11
GATCATTTTCTGTACTGTTT	ENSMMUG00000004851	3.43	11.31	3.30	0	FGD4
GATCTCTCCACAGGCCTTCA	ENSMMUG00000004917	5.24	17.36	3.31	0	PLXDC1
GATCAAAACTATAGATGGCT	ENSMMUG00000012151	3.22	10.73	3.33	0	GK5
GATCAACCACATGCACATCC	ENSMMUG00000002200	48.17	160.31	3.33	0	PPAP2B
GATCACGGAGGAGGCACCCC	ENSMMUG00000020426	46.76	156.02	3.34	0	SERPINA1
GATCTCTTAACATTGTTGGT	ENSMMUG00000003564	15.12	50.51	3.34	0	ITM2A
GATCTCAGTGGAAGAAGTGA	ENSMMUG00000031430	3.83	12.87	3.36	0	TATDN3
GATCTGATTCTTTGTTTGTG	ENSMMUG00000006702	99.96	336.02	3.36	0	BMPR1B
GATCAGCTCTGTGAATGCCA	ENSMMUG00000003653	5.84	19.70	3.37	0	PRTG
GATCAAGCAGCTCACGGAGG	ENSMMUG00000003834	3.22	10.92	3.39	0	BATF
GATCATTTTTGTTTGAAACT	ENSMMUG00000001527	6.85	23.21	3.39	0	CDC42SE2
GATCTATTTCCCCCAATAAA	ENSMMUG00000019737	18.74	63.97	3.41	0	NTN5
GATCAAGTCCTGGAGCCCGG	ENSMMUG00000007538	58.04	198.92	3.43	0	TRPM4
GATCCGTAACAAAATTATTA	ENSMMUG00000001147	106.82	367.42	3.44	0	C2orf29
GATCTCCAGGATGTTGGCTG	ENSMMUG00000000870	8.87	30.62	3.45	0	TLR5
GATCATGGATTTATTTTGTC	ENSMMUG00000016149	90.09	311.06	3.45	0	EMB
GATCATCTTGAATATTTGCT	ENSMMUG00000013039	37.49	130.47	3.48	0	SLC19A2
GATCGTTCAAGAGAATGATT	ENSMMUG00000016964	80.01	278.68	3.48	0	VTCN1
GATCTTTCCAAATGTGTTTT	ENSMMUG00000006967	7.66	26.72	3.49	0	LANCL3
GATCGCAAGCCTTTGTTTTC	ENSMMUG00000002843	14.91	52.27	3.50	0	RAB26
GATCAGATGTTTTAACTTGG	ENSMMUG00000020942	61.47	216.28	3.52	0	LGR5
GATCGTTCTTCCAGCGAAGG	ENSMMUG00000011127	34.26	121.11	3.53	0	TMEM37
GATCTGTAATGTTATTTCTA	ENSMMUG00000011711	28.22	100.83	3.57	0	CD55
GATCTGTTGCAACCATGTGA	ENSMMUG00000030902	15.52	55.58	3.58	0	FAM55B
GATCCTTTAAGGAAATATAC	ENSMMUG00000016431	4.43	15.99	3.61	0	LONRF3
GATCGTTAAAATAACTAGTG	ENSMMUG00000022906	99.16	358.45	3.61	0	VCAM1
GATCCGAAAATTCATCCATG	ENSMMUG00000010883	6.45	23.40	3.63	0	SPACA5B
GATCTCTCCCCGTCTCCCTC	ENSMMUG00000016421	15.12	55.00	3.64	0	STXBP1
GATCCATCCTGTATTTTGAT	ENSMMUG00000019472	7.86	28.86	3.67	0	MFAP3L
GATCATTGAACAGAAAAGGT	ENSMMUG00000019690	74.97	276.93	3.69	0	SESTD1
GATCCAAACCCACCCTCAGG	ENSMMUG00000007401	9.27	34.32	3.70	0	ARRDC2
GATCCTATTAGCTGTGTAAT	ENSMMUG00000014277	55.83	206.92	3.71	0	SSFA2
GATCATTTTCAGATTGTTCA	ENSMMUG00000009998	21.97	81.52	3.71	0	PVRL3
GATCGCCTACTACGAGACGA	ENSMMUG00000020218	10.08	37.44	3.72	0	AK5
GATCTTTTGGGAGATGCATC	ENSMMUG00000010657	5.04	18.72	3.72	0	PRAME
GATCAAACAGCAGTACAGGT	ENSMMUG00000022273	58.45	218.42	3.74	0	ST6GALNAC2
GATCTGGAGGAGGTGAAGGC	ENSMMUG00000016125	4.43	16.58	3.74	0	APOA4
GATCAGGGCAGCTTAAGTGG	ENSMMUG00000004379	23.18	86.98	3.75	0	DUSP10
GATCGTGTTTTAACTTTTTC	ENSMMUG00000014588	83.03	311.84	3.76	0	BHLHE40
GATCTCAATAAAAGAGCTGG	ENSMMUG00000023732	49.78	188.39	3.78	0	HIST1H1C
GATCTTGGGTATGGTTTTTA	ENSMMUG00000002573	2.82	10.73	3.80	0	LRRC16A
GATCTGGATTCTGCCTAATA	ENSMMUG00000004867	37.08	141.58	3.82	0	HBD
GATCTATTATGAATAATGTC	ENSMMUG00000017684	31.24	119.74	3.83	0	TNFAIP8
GATCTAATGAAAGTCAGTTA	ENSMMUG00000017401	22.17	85.42	3.85	0	LNX1

GATCCAGCTTCACCCACTGG	ENSMMUG00000015474	44.94	174.54	3.88	0	MYLIP
GATCTTAATAAACATTTGCT	ENSMMUG00000023308	6.05	23.60	3.90	0	KCND2
GATCTGGTGACTTGGTGACT	ENSMMUG00000013412	56.43	222.91	3.95	0	CYB561
GATCAATGGCTGCTGATTCC	ENSMMUG00000018226	6.45	25.55	3.96	0	KIF27
GATCAGTGGAAACTCCTGAA	ENSMMUG00000004647	195.69	778.13	3.98	0	RXFP1
GATCGGCTTCAGAGTGATGA	ENSMMUG00000005988	66.51	264.64	3.98	0	RASEF
GATCCCTACGCGACCTTACT	ENSMMUG00000007950	13.50	54.41	4.03	0	DCPS
GATCTGTTCACAGCCAGACT	ENSMMUG00000008387	2.42	9.75	4.03	0	DPP4
GATCAAAACTGGAAGAGTGA	ENSMMUG00000029276	4.23	17.16	4.05	0	ACOT6
GATCCGATTAAGTATAGTTC	ENSMMUG00000007379	46.35	188.97	4.08	0	TPTE2
GATCTTGTTTTGCTAGAGTT	ENSMMUG00000005775	5.44	22.23	4.09	0	PLA2G16
GATCCCAAATGGTGCTTATC	ENSMMUG00000010474	7.26	29.84	4.11	0	HMCN1
GATCCGACTTTAGAAGCCTA	ENSMMUG00000014691	103.39	425.92	4.12	0	ID4
GATCCATTATATCTGATTTT	ENSMMUG00000010712	2.22	9.17	4.13	0	SYT10
GATCAACAGGAAAACTAGGA	ENSMMUG00000001154	72.96	301.70	4.14	0	NUDT16
GATCAGACATCCTTTATAAA	ENSMMUG00000005882	53.81	223.88	4.16	0	CAPN9
GATCTTACCTAGTAACTATC	ENSMMUG00000018972	13.30	55.39	4.16	0	POLR3G
GATCTTTCATTCACATAAAA	ENSMMUG00000019892	25.19	105.12	4.17	0	MYOM1
GATCCTTGGTGTGTAGTTCA	ENSMMUG00000006340	18.14	76.25	4.20	0	SLC6A6
GATCTTTTCTAATATGGTAT	ENSMMUG00000005055	2.22	9.36	4.22	0	WASF3
GATCACTTTTTTTAGAGTGA	ENSMMUG00000021628	7.26	30.81	4.25	0	CADM1
GATCGCCCAACTTCACTGGG	ENSMMUG00000021378	3.43	14.63	4.27	0	RASL10A
GATCTCTTCGGGGAGACAGA	ENSMMUG00000023038	3.83	16.38	4.28	0	CALY
GATCTTTTGTGGATATGTGT	ENSMMUG00000018587	4.43	19.11	4.31	0	ABCA8
GATCCAGGTGATGTTACATG	ENSMMUG00000022040	150.55	649.81	4.32	0	MANEAL
GATCTGACCATTACAACTGC	ENSMMUG00000003796	74.37	321.78	4.33	0	DEFB1
GATCTGTACAACTGATTAAA	ENSMMUG00000010747	60.66	264.45	4.36	0	MFAP5
GATCTCTGGCTTTGCAAGGG	ENSMMUG00000016387	13.91	60.85	4.38	0	ADM
GATCGCTATATATGTATTGC	ENSMMUG00000022697	17.33	76.06	4.39	0	STEAP4
GATCCTGACTGCTGTCATGG	ENSMMUG00000031655	4.03	17.75	4.40	0	S100A3
GATCAGCAACACTCCTGGCT	ENSMMUG00000022044	11.89	52.46	4.41	0	SCARA5
GATCAGTGGGTTCCGGTGAT	ENSMMUG00000014808	65.90	292.33	4.44	0	GADD45A
GATCCTGGCGGCCTACCGGC	ENSMMUG00000021431	2.02	8.97	4.45	0	CLIC3
GATCATCCCTTTCCTCAAGG	ENSMMUG00000003155	2.02	8.97	4.45	0	RHOV
GATCACTGAAGAAACTTCTG	ENSMMUG00000019258	10.68	47.78	4.47	0	HLA-DRA
GATCAAATGTGAAATAAATA	ENSMMUG00000005316	15.52	69.43	4.47	0	ADRA2A
GATCTTGTTAACAAATCAGA	ENSMMUG00000014456	2.42	10.92	4.52	0	UGT8
GATCAAAGGGAATAAAGAGA	ENSMMUG00000004251	29.22	132.61	4.54	0	LPIN3
GATCACAGCTAACATTAAGA	ENSMMUG00000023575	2.02	9.17	4.55	0	C12orf35
GATCTGTTGCCTTAAATTGC	ENSMMUG00000018426	213.63	971.59	4.55	0	GCNT3
GATCTCTGCATGGTGTTGGG	ENSMMUG00000017483	20.96	97.51	4.65	0	EPS8L2
GATCAGAGAGAGAGGGAAAG	ENSMMUG00000018770	38.29	179.42	4.69	0	TCEAL2
GATCAAGGCAAAACAAATTA	ENSMMUG00000001168	2.62	12.29	4.69	0	HEG1
GATCAATTAAGTGAAGAAAT	ENSMMUG00000017640	3.43	16.19	4.72	0	GIMAP7
GATCTAATGAATGTGAACAT	ENSMMUG00000006779	7.26	34.32	4.73	0	MET
GATCCCGACACCATTGACAG	ENSMMUG00000000053	2.02	9.56	4.74	0	ANKRD20A4
GATCAGAAAATTTCTGACAT	ENSMMUG00000011671	6.45	30.81	4.78	0	LIN7A
GATCTACCAGGTGTGATGCT	ENSMMUG00000015605	6.45	31.01	4.81	0	SLC4A5
GATCTGGCAGGGGATTGACA	ENSMMUG00000017478	8.67	41.93	4.84	0	TESC
GATCTTTGGTGATTGAGAGA	ENSMMUG00000031747	14.31	70.01	4.89	0	HIST2H2BF
GATCATTTTTGTAACAAGGC	ENSMMUG00000005041	5.64	27.69	4.91	0	SRCIN1
GATCCTCCCTGCCCAACCCT	ENSMMUG00000000602	4.03	19.89	4.94	0	RGS11
GATCAGAAGACTTTAATTAT	ENSMMUG00000012667	599.37	3002.33	5.01	0	ANXA1
GATCATAATTGAAAGGTCAC	ENSMMUG00000010137	1.81	9.17	5.05	0	MCPH1
GATCACACTACGGGAGTCTC	ENSMMUG00000003406	1.81	9.17	5.05	0	SDC4
GATCAAGCTGGACTTGTGCA	ENSMMUG00000009842	55.83	282.58	5.06	0	FGF7
GATCATCATGATTTAAGTTG	ENSMMUG00000017129	13.10	67.67	5.17	0	SLC41A2
GATCTTACATTTGAAAGGTA	ENSMMUG00000001284	16.12	83.86	5.20	0	SLC28A2
GATCAGAATCATTTAAAAAT	ENSMMUG00000019256	95.33	497.11	5.21	0	ERRFI1
GATCCCCAGCGCCAGGAGTG	ENSMMUG00000013302	188.44	1007.08	5.34	0	FAM184A
GATCCATATAATTCTTTAAA	ENSMMUG00000008262	5.64	30.23	5.36	0	TMEM154
GATCTGACCTTCTTAGGGGT	ENSMMUG00000016376	8.67	47.58	5.49	0	MAP3K5
GATCACTTGCCCCGCAGCCA	ENSMMUG00000018577	4.43	24.96	5.63	0	MANSC1
GATCCTGCAGCTCCTGAAAG	ENSMMUG00000007669	66.71	381.85	5.72	0	ISG20
GATCCTGAAGTTAAATACCC	ENSMMUG00000015530	10.08	57.92	5.75	0	GALP
GATCCTAATATGTACATTGT	ENSMMUG00000002006	2.82	16.38	5.81	0	PVRL4
GATCAAAGGTTTAAAGTCTA	ENSMMUG00000009107	17.74	103.36	5.83	0	ALCAM
GATCCATTCCAGCGCCTTCC	ENSMMUG00000002529	19.75	117.40	5.94	0	CECR1
GATCATTTTGACATGAGGAT	ENSMMUG00000010977	1.21	7.22	5.97	0	TCEA3
GATCATTCTTCTCGCTTGCC	ENSMMUG00000008862	40.11	240.26	5.99	0	FGL1
GATCTTCCCCGAAAGGATTC	ENSMMUG00000017906	1.21	7.41	6.13	0	DNAJB1

GATCACGGGCCAGCCCAATA	ENSMMUG00000012608	4.84	30.23	6.25	0	ACE
GATCCATGTCTCCCTTGTGG	ENSMMUG00000014176	3.83	24.38	6.37	0	CYTIP
GATCAGTTTTTCAATAGAAC	ENSMMUG00000018058	8.26	52.66	6.37	0	ABCG1
GATCCAATCAGCTTGAGAAA	ENSMMUG00000001618	2.82	18.14	6.43	0	ATP6V0D2
GATCACATCACTGCACCAGC	ENSMMUG00000005222	20.36	133.59	6.56	0	DOC2B
GATCTCGTAGCCACACTAAA	ENSMMUG00000008685	31.24	205.36	6.57	0	SLC28A3
GATCTGGATTTCTGTAGCAA	ENSMMUG00000000358	1.01	6.83	6.77	0	PHF15
GATCGAGGTCTATGCATGGC	ENSMMUG00000006437	1.61	11.12	6.89	0	CA8
GATCTATTTTCTCTCAGTAG	ENSMMUG00000012406	9.88	70.40	7.13	0	PCOLCE2
GATCACTGTGGGCTGGAGAG	ENSMMUG00000007620	28.42	210.62	7.41	0	TMPRSS4
GATCGTGGAGACCATGATTG	ENSMMUG00000014632	1.61	12.29	7.62	0	BFSP1
GATCCAGAGGAGGAAGAGGA	ENSMMUG00000015344	2.42	18.92	7.82	0	CERKL
GATCTTTCCAAATACCCAAA	ENSMMUG00000022127	9.27	73.52	7.93	0	FXYD3
GATCCCCAACTAGGCACAGC	ENSMMUG00000006029	1.01	8.00	7.93	0	ODAM
GATCACACAGCCACTTACCA	ENSMMUG00000015865	10.48	83.47	7.96	0	ARG2
GATCATAATAAAAGTGAATC	ENSMMUG00000005518	3.22	25.74	7.98	0	CPB1
GATCTTCTCAACTGTGAGAG	ENSMMUG00000007612	19.15	155.63	8.13	0	LRP8
GATCCATCCAGCTAAATGGA	ENSMMUG00000021931	100.57	821.42	8.17	0	AOX1
GATCATCCCTTCTCACAGAG	ENSMMUG00000007595	7.26	60.85	8.39	0	CNNM4
GATCAAAGGCATATACTTCC	ENSMMUG00000016191	0.81	7.22	8.95	0	ABCA13
GATCCAGCCTTCCCTGCCGT	ENSMMUG00000007465	26.00	235.97	9.08	0	DHRS4
GATCTCACTGTAACATGGGA	ENSMMUG00000007684	4.03	36.66	9.10	0	SGPP2
GATCTAAACAAAATAGTTTC	ENSMMUG00000015966	22.77	207.89	9.13	0	ADH6
GATCCTAACCAGTGGGGAGC	ENSMMUG00000017133	1.21	11.12	9.19	0	C12orf45
GATCGAAAAACTACCTACCT	ENSMMUG00000009602	0.81	7.41	9.19	0	XAF1
GATCAGTGTTTATATCAGAG	ENSMMUG00000012801	1.21	11.12	9.19	0	ZNF235
GATCTTAGACAGCAAGCGAG	ENSMMUG00000029832	1.01	9.36	9.29	0	NT5C
GATCAGTAATGAAAAGCTGA	ENSMMUG00000010830	1876.12	17565.81	9.36	0	CRISP3
GATCCATCTCAGCTTCTTTG	ENSMMUG00000031146	0.60	5.85	9.68	0	C2orf72
GATCTGCTCTGTTTTATACC	ENSMMUG00000020775	23.38	226.42	9.68	0	GRB7
GATCCTGACAGACTGGGGAA	ENSMMUG00000003598	0.60	6.05	10.00	0	TRIM7
GATCGGACAGGGCTGGGAAC	ENSMMUG00000022656	1.21	12.48	10.32	0	PLIN4
GATCAGAGCAGTCTGTCCAG	ENSMMUG00000019407	5.24	54.80	10.46	0	RIMS2
GATCAGCCACCATCTGGAGT	ENSMMUG00000011822	0.60	6.44	10.64	0	PTGES
GATCTTCTCTTCTATCTCCA	ENSMMUG00000022608	13.70	146.65	10.70	0	ATP12A
GATCACTGTGTTGCTCTACA	ENSMMUG00000016831	2.42	26.33	10.89	0	DGKI
GATCCACACGAACACACGCC	ENSMMUG00000015590	2.22	24.96	11.26	0	SIAH2
GATCTTTTTTTTTGAAGATT	ENSMMUG00000030780	3.02	34.13	11.29	0	FOXO1
GATCTGGTTTCTAAGAGTTT	ENSMMUG00000012185	2.42	27.69	11.45	0	ATF3
GATCTGTCTTCATTGACTGA	ENSMMUG00000017377	1.41	16.38	11.61	0	HDHD1A
GATCTGATGTGTCTCTCACG	ENSMMUG00000019387	8.06	97.12	12.05	0	HLA-C
GATCTTCCTGTGGCTTGGGG	ENSMMUG00000000984	0.40	5.07	12.58	0	VILL
GATCATTTTGGTTGTTGCTC	ENSMMUG00000017919	1.21	15.80	13.06	0	CXCL17
GATCTGAAGTTGCAGGTTGC	ENSMMUG00000019891	1.21	16.19	13.39	0	AKR1CL1
GATCTTAAAGAAGATGATAT	ENSMMUG00000007473	1.21	16.19	13.39	0	DEFB104A
GATCCAGCCCTGCCCTTCAG	ENSMMUG00000007221	0.40	5.46	13.55	0	HMOX1
GATCATCCCAGCTGAACAAT	ENSMMUG00000001674	0.40	5.85	14.51	0	ERBB4
GATCTGGCGTCTGAGCTCGA	ENSMMUG00000010378	6.65	98.87	14.87	0	MT1E
GATCCAAGTTGAGATTTGAA	ENSMMUG00000022971	2.82	44.07	15.62	0	CTSL2
GATCAATAATCTAGTTTCAT	ENSMMUG00000014711	25.60	411.88	16.09	0	RBP4
GATCTTTCAATACTCTTAAA	ENSMMUG00000013342	6.65	111.55	16.77	0	HPSE
GATCAATTTGTACAGCGTAC	ENSMMUG00000008584	1.21	21.06	17.42	0	SLCO1A2
GATCTGGAATTGTAATGTAA	ENSMMUG00000021412	0.40	7.22	17.90	0	RNF128
GATCCCAGGAGACCTGGGGC	ENSMMUG00000013297	3.22	62.41	19.35	0	PRKCDBP
GATCGCCTTGTGACCGGAAA	ENSMMUG00000022529	0.40	7.80	19.35	0	RPRM
GATCACTAATTTATCTGCTG	ENSMMUG00000015498	0.40	8.00	19.84	0	C6orf132
GATCTGCTCCTATTCAAACA	ENSMMUG00000010579	1.21	24.57	20.32	0	AHNAK2
GATCAGTTTAGCAAATCTAC	ENSMMUG00000013738	1.81	37.83	20.86	0	C4BPA
GATCTCTTTGGCTGTAGCCG	ENSMMUG00000014927	0.20	4.29	21.29	0	ECH1
GATCACTGCGAGCAACTGAA	ENSMMUG00000023295	0.20	4.29	21.29	0	GJB6
GATCCCCTGGACCGCCCCAC	ENSMMUG00000010066	0.40	8.58	21.29	0	MERTK
GATCCTGCATTAAATTTTTA	ENSMMUG00000004758	0.20	4.29	21.29	0	TMEM56
GATCATAGACCAAAAACACA	ENSMMUG00000017087	0.60	13.65	22.58	0	SLIT3
GATCTACTCCATCCAGTCCT	ENSMMUG00000021987	1.41	32.57	23.09	0	GPX2
GATCAGAATATTACTGTTAT	ENSMMUG00000022269	0.20	4.68	23.22	0	C4orf40
GATCGCTGTAGTGCCTTGGA	ENSMMUG00000001389	2.62	61.24	23.37	0	IRX3
GATCGTAAAAAAATAGAAAA	ENSMMUG00000008858	5.44	131.05	24.08	0	STC1
GATCGCCCCACAATGGACCC	ENSMMUG00000023132	0.20	5.07	25.16	0	DUSP8
GATCTCAGATAAAGTGACCA	ENSMMUG00000015198	0.20	5.07	25.16	0	GAD1
GATCTTCATCTGACCATGAC	ENSMMUG00000017618	0.20	5.07	25.16	0	SLC26A3
GATCTGGTTCTTTCTTCAGA	ENSMMUG00000011449	10.28	265.03	25.79	0	SYT13

GATCCAACGCTACATGTATT	ENSMMUG00000002916	1.81	47.19	26.02	0	FLRT3
GATCCCAGCCCCTAGGTGGG	ENSMMUG00000031964	0.20	5.46	27.09	0	AQP5
GATCAGTTTTATTTCAATAA	ENSMMUG00000014640	0.20	5.66	28.06	0	RP1
GATCAACAGGAAGAAGAACA	ENSMMUG00000014522	0.20	6.05	30.00	0	ITIH3
GATCACAGACTCTTTCCCAC	ENSMMUG00000022068	1.41	43.29	30.69	0	SLC6A12
GATCCTTAAAGAAGATGTGG	ENSMMUG00000004771	2.22	68.45	30.88	0	CXCL14
GATCCGCGTGTGAGGCAGGC	ENSMMUG00000018148	0.20	6.24	30.96	0	CDC42EP4
GATCAGATAAAGCGTTCTTT	ENSMMUG00000018755	1.01	34.91	34.64	0	CPN1
GATCTCTGCAGTTTATCACA	ENSMMUG00000020034	0.20	7.02	34.84	0	MORN4
GATCTGTGTTAGAAGTGTTG	ENSMMUG00000008290	0.40	14.24	35.32	0	ABCC11
GATCCCCAAGCCTGGCAAGG	ENSMMUG00000008711	1.81	65.33	36.02	0	CHI3L1
GATCAGACTAAAAATCCTGG	ENSMMUG00000001365	0.20	8.78	43.54	0	C2CD4B
GATCCCCAACTGCTCCAGCC	ENSMMUG00000031123	225.12	10455.79	46.45	0	SCGB1A1
GATCCAAGAATATTCTTCAA	ENSMMUG00000015134	0.20	9.95	49.35	0	SLC5A8
GATCATGTCAAGTCAGTGAC	ENSMMUG00000004226	0.20	10.14	50.32	0	ACSM1
GATCTGAAGGACGAGGGATG	ENSMMUG00000016673	2.22	118.77	53.57	0	TTR
GATCATTTATTAGTAATGTA	ENSMMUG00000008233	1.21	85.03	70.32	0	C9orf71
GATCGCTTCTTTTCCTTTGC	ENSMMUG00000005876	0.20	14.63	72.57	0	ADRB3
GATCTCAAGTGAGTTCATGC	ENSMMUG00000009828	0.20	19.70	97.73	0	LRP11
GATCTTTGCACTGGCTCTGG	ENSMMUG00000018729	0.20	26.91	133.54	0	GAST
GATCGGTTTGCTATGTTCCT	ENSMMUG00000029122	0.20	27.69	137.41	0	MT1B
GATCTGCATCAGAAAATTTG	ENSMMUG00000029841	0.20	70.01	347.39	0	HLA-C