

Reviewers' comments:

Reviewer #1 (expert in GPCRs and vascular cells)

Remarks to the Author:

This was a study using microfluidic-based single-cell GPCR expression analysis in freshly isolated healthy and diseased VSMCs and ECs. Single cell RT-PCR and RNA sequencing was used to characterize selected GPCR expression in endothelial and smooth muscle cells. The authors found that RT-PCR was superior to RNA sequencing in this population, there was significant heterogeneity in the expression of GPCRs and they were also able to identify distinct cell populations, such as dedifferentiated SMCs. They observed changes in GPCR expression in the setting of sepsis and atherosclerosis. Earlier studies have studied the GPCR single expression primarily in the brain (Spaethling et al., FASEB J. 2014; Manteniotes et al., PLoS One 2013; Hanchate et al., Science 2015). I think the results of this study would be of interest to a wide audience. These findings, though, are primarily descriptive and do not provide significant insights into disease processes and it is unclear how heterogeneity contributes to the functions of these vascular cells (except for the case of the dedifferentiated smooth muscle cells where dedifferentiation were associated with binding of specific transcription factors). The limitations in mechanistic insight limit enthusiasm for the manuscript.

Reviewer #4 (expert in single cell transcriptomics)

Remarks to the Author:

The manuscript "Single-cell expression profiling reveals heterogeneity and functional patterning of GPCR expression in the vascular system" by Kaur et al analyzed the expression patterns of G-protein-coupled receptor (GPCR) in single vascular smooth muscle cells (SMC) and endothelial cells (EC) isolated from various sites on healthy and disease conditions by using a microfluidic-based single cell GPCR expression analysis. They found that GPCR expression is highly heterogeneous in all analyzed cell types. This was shown by both the single cell qPCR and single cell RNA-seq techniques, while the authors found that their single cell qPCR assay showed higher frequencies of expression than the single cell mRNA-seq assay. The authors found that different types of SMCs or ECs have distinct GPCR expression patterns. Further, the authors identified changes of GPCR expression patterns after inflammatory activation and they also identified and verified a dedifferentiating SMC subpopulations in healthy SMCs. In general, this study provides novel and valuable insights into the complex expression of GPCRs in EC and SMC at single cell resolution.

Major:

1. The authors mainly used a microfluidic-based single cell GPCR expression assay for analysis. They have also performed the single cell RNA-seq method and found their single qPCR assay showed higher frequencies of GPCR expression than the single cell mRNA-seq assay for nearly all GPCRs. The authors explained that the better performance of the single-cell RT-PCR may be due to its use of target-specific pre-amplification of mRNAs, while pre-amplification for mRNA sequencing is unbiased. However, the authors should exclude the possibility that the RT-PCR assay amplifies off-target sites, particularly that the sequences of different GPCRs genes may be highly similar. This is less possible to happen in the single RNA-seq method with its base-resolution character. The authors have verified the results of the RT-PCR assay by showing that the single cell qPCR results were consistent with the results of the GPCR reporter mice. However, they should directly address the off-target issue by sequencing (high throughput sequencing) the PCR product of the single-cell RT-PCR assay.
2. The authors found that different types of SMCs or ECs have distinct GPCR expression patterns and can be grouped into distinct clusters by clustering analysis. The authors should give a list to clearly show how many experiments and how many cells in each experiment have been analyzed for each

SMC and EC cell types. In Figure 3G and 4C, for a certain cluster, have the cells been analyzed by more than one independent experiments to exclude the batch effect?

3. The authors also found that GPCR expression was highly heterogeneous within each cell type. However, in most conditions, it seems that the authors have not identified functional cell subpopulations. I am not convinced that the intra-cell type heterogeneous GPCR expression has important biological functions in general. The authors should be careful to claim this. It can be helpful to verify the heterogeneous GPCR expression at the protein level if suitable antibodies are available. If you can detect the heterogeneously expressed GPCR gene at the protein level, it is more convincing that the gene could be functional.

4. The authors have identified a small subpopulation of dedifferentiating SMC from healthy SMao (Figure 8). They have also performed the single cell RNA-seq method for SMao. Could this small subpopulation also be identified from the single cell RNA-seq data and were the results between the single cell RT-PCR and single cell RNA-seq consistent?

Reviewer #4 (expert in single cell transcriptomics)

Remarks to the Author:

Major:

1. The authors mainly used a microfluidic-based single cell GPCR expression assay for analysis. They have also performed the single cell RNA-seq method and found their single qPCR assay showed higher frequencies of GPCR expression than the single cell mRNA-seq assay for nearly all GPCRs. The authors explained that the better performance of the single-cell RT-PCR may be due to its use of target-specific pre-amplification of mRNAs, while pre-amplification for mRNA sequencing is unbiased. However, the authors should exclude the possibility that the RT-PCR assay amplifies off-target sites, particularly that the sequences of different GPCRs genes may be highly similar. This is less possible to happen in the single RNA-seq method with its base-resolution character. The authors have verified the results of the RT-PCR assay by showing that the single cell qPCR results were consistent with the results of the GPCR reporter mice. However, they should directly address the off-target issue by sequencing (high throughput sequencing) the PCR product of the single-cell RT-PCR assay.

This is of course a valid point, and we sequenced the single-cell RT-PCR products of all GPCRs expressed in aortic smooth muscle cells at a frequency of more than 10% (as shown in Figures 2A and Suppl. Fig. 2 of the manuscript). Each amplicon was sequenced in forward and reverse direction, and the obtained sequences were aligned to the predicted amplicon sequence. Figure 1 of this letter shows an example of sequencing results and the corresponding alignment; the alignments for all sequences are shown in Table 1 of this letter.

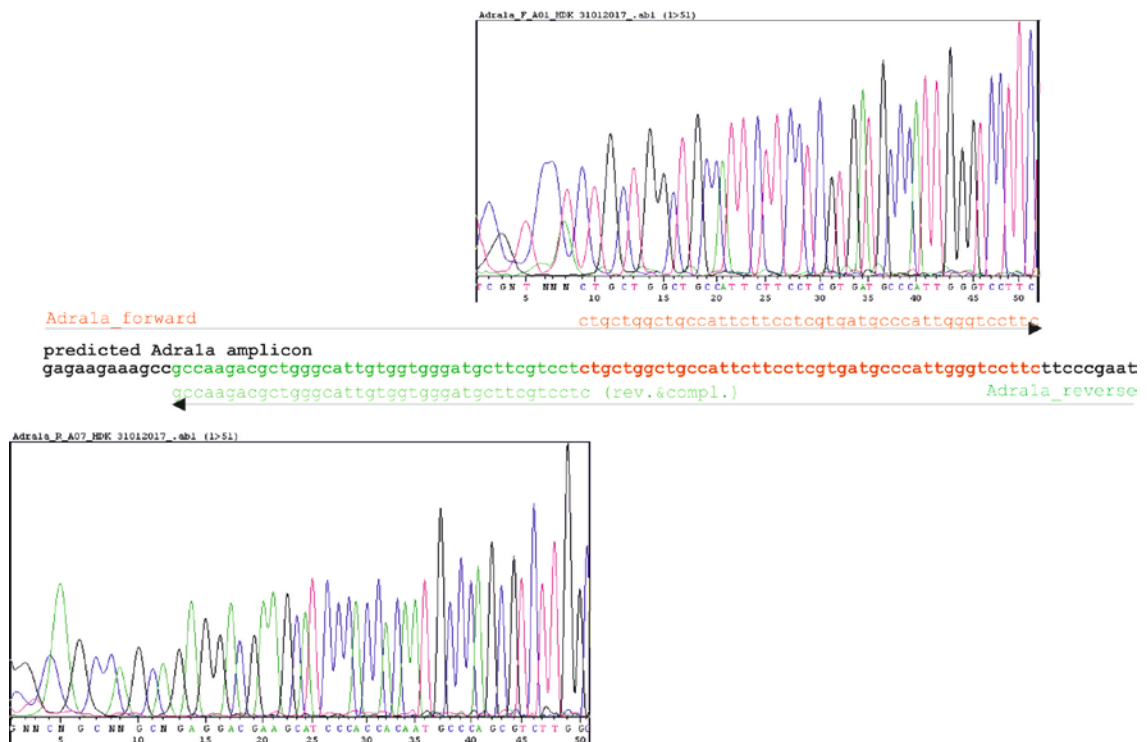


Figure 1: Exemplary analysis of results obtained by sequencing of single-cell amplicons (here for the alpha-1A adrenergic receptor Adra1a): Single-cell PCR products were sequenced with the same forward and reverse primers that were used for amplification, the respective chromatograms as well as the alignment of sequences to the predicted Adra1a amplicon are shown above (forward primer, matching base pairs in red) and below (reverse primer, matching base pairs in green) the aligned sequences. The sequence obtained from the reverse primer is for convenience shown reverse and complementary.

Table 1: Alignment of sequencing results

Adrala_F	-----ctgctggctgccattcttctcctcgtgatgccattgggtccttc-----
Amplicon	gagaagaaagccgccaagacgctgggcatttggtgggatgcttcgtcctctgctggctgccattcttctcctcgtgatgccattgggtccttccttcccgaat
Adrala_R	-----gccaaagacgctgggcatttggtgggatgcttcgtcctc-----
Adralb_F	-----ctccaacctaaagccccggacgccgtattcaaggtagtgttctggctgggc--
Amplicon	atggttgctcccttcttcatcgcctctcccacttggtccctggtctccaacctaaagccccggacgccgtattcaaggtagtgttctggctgggcta
Adralb_R	atggttgctccct-----
Adrald_F	-----ggttctctgttcctcagctgaaacctcag-----
Amplicon	ttcgtcctgtgctgggtccctttttcttcgtcctgcctctgggttctctgttcctcagctgaaacctcagagggcgctc
Adrald_R	ttcgtcctgtgctgggtccctttttct-----
Agtr1a_F	-----gtgtctgagaccaactcaaccaga
Amplicon	taactcacagcaaccctccaagaaagccatcacccagatcaagtgcattttgaacagtgtctgagaccaactcaaccaga
Agtrala_R	taactcacagcaaccctccaagaaagccatca-----
Bdkrb2_F	-----tgcccaccgggctcctttggcatcgaatggttcaacgtcaccac-----
Amplicon	aaatgcctgctcctggaagctactcgggtttctgtcggatgagcccatgcccaccgggctcctttggcatcgaatggttcaacgtcaccacacaag
Bdkrb2_R	--atgcctgctcctggaagctactcgggtttctgtcggatgagcccat-----
Calcr1_F	-----ctgggacggatggctatgctggaatgacgttg
Amplicon	atgcaggacccattcaacaagcagaaggcctttactgcaataggacctgggacggatggctatgctggaatgacgttg
Calcr1_R	atgcaggacccattcaacaagcaga-----
Ccr12_F	-----agcctccgatggataactacacagtggccc
Amplicon	caagcaacctgctcaaacgacgctgttttgtccggatgagcaaggacagcctccgatggataactacacagtggccc
Ccr12_R	caagcaacctgctcaaacgacgc-----
Cd97_F	-----ggacc-aaaggctggaattgatcaccaaggtggg
Amplicon	tgaccagctttgccatcctaattggctcagtaccatgtgcaaggacaaaggctggaattgatcaccaaggtggg
Cd97_R	tgaccagctttgccatcctaattggctcagtacc-----
Celsr2_F	-----tggtgacaactgtacaaatgtgtgtgacctgaacca
Amplicon	agcaatgactgggacagctattctttagctgtgttcttaggtactatggtgacaactgtacaaatgtgtgtgacctgaacca
Celsr2_R	agcaatgactgggacagctattctttag-----

Table 1 (cont.): Alignment of sequencing results

Cmklr1_F	-----ctcaaagagatggagtagcagcgttacaacgac
Amplicon	gtaacagaccagccaaggacca-ggactggagtctgttctacaacggtgaacagtgaaaggtctcaaagagatggagtagcagcgttacaacgac
Cmklr1_R	gtaacagaccagccnaggaccaaggacggag-----
Crhr2_F	-----tttcaggtccctacacctactgcaacacgaccttgg
Amplicon	gtggacacttttggagcagtactgccacaggaccacaactgggaatttttcaggtccctacacctactgcaacacgaccttgg
Crhr2_R	gtggacacttttggagcagtactgccacaggac-----
Cxcr7_F	-----caaaccacagcccaggaagccctgaggtcacttggctcctcctcaagac
Amplicon	aaaaactgctcagcactgaaggagcctgcagcgtcaccgtcaggaagcaaaccacagcccaggaagccctgaggtcacttggctcctcctcaagac
Cxcr7_R	aaaaactgctcagcactgaaggagcctgcagcgtcaccgtcaggaag-----
Ednra_F	-----gatgtgaaggactggtggctctt
Amplicon	cataggacctgcatgctcaacgccacgtccaagttcatggagttttaccaagatgtgaaggactggtggctctt
Ednra_R	cataggacctgcatgctcaacgccacgtccaagt-----
F2r_F	-----agaggacagatgctacggtga
Amplicon	gcggtcccttgtgtcttcccggctccctatgagccagccagaatcagagaggacagatgctacggtga
F2r_R	gcggtcccttgtgtcttcccgc-----
F2r11_F	-----ggaccgagaaccttgcaccgggacgcaacaacagtaaaggaagaagct-----
Amplicon	ggctgctgggaggtatcaccttctggcggcctcggtctcctgcagccggaccgagaaccttgcaccgggacgcaacaacagtaaaggaagaagcttattggcagat
F2r11_R	-----ctcggtctcctgcagccggaccgagaaccttgcaccgggacgcaacaaca-----
Gabbr1_F	-----tcgtgggacttttctatgagaccgaagccc
Amplicon	agatccagctgtgcctgttaaaaaacctgaagcgtcaagatgctcgaatcatcgtgggacttttctatgagaccgaagccc
Gabbr1_R	agagccagctgtgcctgntaaaaacctgaagcgtc-----
Gpr107_F	-----cgcagggctttccgattgaaggctgggctgttga
Amplicon	gtctctctcgttgggtgttccatgcaatcgactaccactacatctcctcgagggctttccgattgaaggctgggctgttga
Gpr107_R	gtctctctcgttgggtgttcca-gcaa-----
Gpr108_F	-----tcaactgtgatgatccgggagaagaatcca
Amplicon	tccacaactgtcacaactccatcccaggccaggagcagccattcgacctcaactgtgatgatccgggagaagaatcca
Gpr108_R	ccacaactgtcacaac-----

Table 1 (cont.): Alignment of sequencing results

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Gpr124_F      -----ttccttgcgtcactgctctggat
Amplicon     tcacgctcaccaactaccaaagggttgcagcgcgggtgggcatcactctgcactactttccttgcgtcactgctctggat
Gpr124_R     tcacgctcaccaactaccaaagggttgcag-----

Gpr125_F      -----ttattctacccttgccacggt
Amplicon     tgggaggaataaaccagaccagaaatgccagcgtctgtcaagcagttgggatcattcttcatattattctacccttgccacggt
Gpr125_R     tgggaggaataaaccagaccagaaatgccag-----

Gpr133_F      -----agaacggtgggt-----
Amplicon     tccgcttgcccaataaatccctctcagaggaaacggcgctgaacctcacagagaccttcttaagaacggtgggtgaggt
Gpr133_R     tccgcttgcccaataaatccctctcagag-----

Gpr137_F      -----ctctggcagttggtatggtgccatcgga
Amplicon     gctcctgggagcatagccggagtgagagcacccagcatgtccggcagcctgggctctggcagttggtatggtgccatcgga
Gpr137_R     gctcctgggagcatagccggagtgagagc-----

Gpr137b_F     -----cagtggtcaggtaactgccattggtgtcacogtcatctt-
Amplicon     tgtccctggccaacatctacttggagtcaaaagggtcatcagtggtcaggtaactgccattggtgtcacogtcatcttg
Gpr137b_R     -gtccctggccaacatctacttggagtcaaa-----

Gpr153_F      -----ccccgacatggtattggagcgctctctt
Amplicon     gccaacgacgaagattctgacaatgagaccagtcctagagggcagcatctccccgacatggtattggagcgctctctt
Gpr153_R     -ccaacgacgaagattctgacaatgagaccagtc-----

Gpr21_F      -----atgcagaatcacagctggtcagaggagactcattacaactcctgc-
Amplicon     gcattgcaaggctttcggttaaggatgtattgtggcttttgtttggatttcagcatgcagaatcacagctggtcagaggagactcattacaactcctgct
Gpr21_R     -----gcaaggctttcggttaaggatgtattgtggcttttgtttggatttcagca-----

Gpr4_F        -----tagcagtcgcagctctcaatgcagtggtgagtggaacaacttcatctccact
Amplicon     cgggaccaagtccagagacgccggctcgccagcccagccgaggagcaggcctagcaatctcagctctcaatgcagtcgtgagtggaacaacttcatctccactcctcag
Gpr4_R        -----agccgaggagcaggcctagcagtcgcagctctcaatgcagtggtgagtgga-----

Gpr64_F      -----tgtgtattctgggacttgggcagaa
Amplicon     gtgacagtcgcactgaaacacatcaacccaagtccggatgacttaactgtgaaatgtgtattctgggacttgggcagaa
Gpr64_R     gtgacagtcgcactgaaacacatcaacc-----

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Table 1 (cont.): Alignment of sequencing results

Gprc5b_F	-----ccgatcagcagtgggcttttccaatggaagcttggagcaaagatc-
Amplicon	cgggcctacatggagaacaaggccttctcaatggatgaacataacgcagctctccgatcagcagtgggcttttccaatggaagcttggagcaaagatct
Gprc5b_R	cgggcctacatggagaacaaggccttctcaatggatgaacataacgca-----
Htr2a_F	-----ggtaccggtggcctttgccagcaagctctgt
Amplicon	gctgctgggtttccttgtcatgcccggtccatgtaaccatcctgtatgggtaccggtggcctttgccagcaagctctgt
Htr2a_R	gctgctgggtttccttgtcatgcccggtccatgt-----
Lgr4_F	-----gtaattctatcttctgttatcccggatggagca-
Amplicon	ctcaggctattaaagcccttcccagccttaaagagctgggatttcacagtaattctatcttctgttatcccggatggagcat
Lgr4_R	ctcaggctattaaagcccttcccagccttaa-----
Lgr6_F	-----gctgcatctacataacaaccgcatccagcatg
Amplicon	tatccgccacatccctgactatgccttccagaacctcaccagtcttgtgggtgctgcatctacataacaaccgcatccagcatg
Lgr6_R	tatccgccacatccctgactatgccttccagaacc-----
Lpar1_F	-----gactgtggtcattgtgcttgggtgcctttattgtctgctggactccgg
Amplicon	agttctggaccaggaggaatcgggacaccatgatgagccttcgaaagactgtggtcattgtgcttgggtgcctttattgtctgctggactccgg
Lpar1_R	agttctggaccaggaggaatcgggacaccatgatgagccttc-----
Lpar4_F	-----ttctctcatctagcacactctttcttgggcaactcaattgaggaaac
Amplicon	agtgcgagttgccagtttacacgtttattagctaactatctacaggcatgagcacattctctcatctagcacactctttcttgggcaactcaattgaggaaactctctga
Lpar4_R	-----acgtttattagctaactatctacaggcatgagcacattctctcatctag-----
Lphn1_F	-----ggtgaaagttgtcttattctctacaacaacctgggcctcat
Amplicon	tctccgccaacacc-atcaagcagaacagccgcaacggtgtggtgaaagttgtcttattctctacaacaacctgggcctctt
Lphn1_R	tctccgccaacaccgatcaagcagaacagccgcaa-----
Lphn2_F	-----gacaaccttctgagagctgaggccttggaaatcctgga
Amplicon	gaagacatgcagggttaccttaaggcaattgtggacacggtagacaaccttctgagagctgaggccttggaaatcctgga
Lphn2_R	gaagacatgcagggttaccttaaggcaat-----
Mrgprf_F	-----tgtcctggatgagcgaggctcgga
Amplicon	agatggccggaactgttcatgggaagctcactccaccaaccagaacaagatgtgtcctggatgagcgaggctcgga
Mrgprf_R	aga_ggcccggaactgttcatgggaagctcagcgc-----

Table 1 (cont.): Alignment of sequencing results

Npy1r_F	-----aggagaaacaacatgatggacaagatccggg
Amplicon	ttcggcccactctgctttatattcatatgctacttcaagatatacattcgccttgaaaaggagaaacaacatgatggacaagatccggg
Npy1r_R	ttcggcccactctgctttatattcatatgctacttcaa-----
P2ry2_F	-----gacctggaaccctggaatagcacc
Amplicon	gagcatcctcaccacctcaagagcaggagctgatcaggtccagggcaatggcagcagacctggaaccctggaatagcacc
P2ry2_R	gagcatcctcaccacctcaagagcaggagctgatcag-----
P2ry6_F	-----cgagcataggaaaggctgacaggcag
Amplicon	ccaaatctggcacttcctcctaaaacatcttccatcttgcatgagacagactctccgagcataggaaaggctgacaggcag
P2ry6_R	ccaaatctggcacttcctcctaaaacatcttcc-----
Ptger3_F	-----ctattgataatgatggtgaaaatgatcttcaatcagatgtcggttgagc
Amplicon	cagctcatggggatcatgtgtgtgctgtccgtctgttggtcgccgctattgataatgatggtgaaaatgatcttcaatcagatgtcggttgagc
Ptger3_R	cagctcatggggatcatgtgtgtgctgtccgtctgttggtcgccgct-----
Ptgir_F	-----ccgaggcttcaactcaggccatcgcc
Amplicon	attctgctggccctcatgaccgcatcatggcgtgtgctccctgacctcatgatccgaggcttcaactcaggccatcgcc
Ptgir_R	attctgctggccctcatgaccgcatcatggcgtgtgc-----
Pth1r_F	-----ctcaacttcatcctctttatcaacatcatccgggtgct
Amplicon	tgggcacaagaagtggatcatccaggtgcccatcctggcatctggttgctcaacttcatcctctttatcaacatcatccgggtgct
Pth1r_R	tgggcacaagaagtggatcatccaggtgctcngatcc-----
Tbxa2r_F	-----ttcatcatgcagactttggtgcagacaccacct-
Amplicon	ttcagctcgtgggcatcatggtggtggccacggtgtgtggatgccttgctggcttcatcatgcagactttggtgcagacaccacctg
Tbx2ar_R	ttcagctcgtgggcatcatggtggtggccacggtgtgtggatgc-----

Table 1: Alignment of sequences obtained by sequencing of single-cell amplicons with forward (F) and reverse (R) primers. Non-matching base pairs are highlighted in yellow.

Table 1 shows that all sequences obtained from forward or reverse primers matched the predicted amplicon sequences, confirming that the correct mRNA was amplified. To furthermore exclude that mRNAs of highly similar GPCRs were amplified, we compared the sequencing results to the murine refseq_rna database (version mm10) using the Nucleotide BLAST tool (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). Table 2 shows for each of the sequencings the three best blast hits; the E-value indicates the likelihood that the respective match occurred by chance. For an extended list of blast results (limited to 20 hits per query), including start/end point of homology and hit sequence, please see the attached file “Supplemental Table 1 for Reviewers”.

Table 2: Blast analysis of single-cell transcript sequencing results.

Gene	Query	Hit	E-value	% match	length alignment
Adra1a	For	Mm_adrenergic_receptor_alpha_1a_(Adra1a),_mRNA	3,90E-17	100	43
		Mm_adrenergic_receptor_beta_1_(Adrb1),_mRNA	0,13	95,24	21
		Mm_leucine_rich_repeat_and_fibronectin_type_III_extracellular_1_(Elfn1),_mRNA	0,13	100	17
	Rev	Mm_adrenergic_receptor_alpha_1a_(Adra1a),_mRNA	8,10E-15	100	39
		Mm_trace_amine-associated_receptor_5_(Taar5),_mRNA	0,007	100	19
		PREDICTED: Mm_RIKEN_cDNA_4631423B10_gene_(4631423B10Rik),_miscRNA	0,43	100	16
Adra1b	For	Mm_adrenergic_receptor_alpha_1b_(Adra1b),_mRNA	2,21E-22	100	52
		Mm_RIKEN_cDNA_B430010I23_gene_(B430010I23Rik),_non-coding_RNA	0,67	100	16
		Mm_cAMP_responsive_element_binding_protein-like_2_(Crebl2),_mRNA	2,7	91,3	23
	Rev	Mm_adrenergic_receptor_alpha_1b_(Adra1b),_mRNA	0,58	100	14
		Mm_glutamate_receptor_ionotropic_AMPA3_(alpha_3)_(Gria3),_mRNA	2,3	100	13
		Mm_striatin_calmodulin_binding_protein_(Strn),_mRNA	2,3	100	13
Adra1d	For	Mm_adrenergic_receptor_alpha_1d_(Adra1d),_mRNA	3,35E-10	100	31
		Mm_arrestin_beta_2_(Arrb2),_mRNA	0,3	100	16
		Mm_small_nucleolar_RNA_C/D_box_1A_(Snord1a),_small_nucleolar_RNA	1,2	100	15
	Rev	Mm_adrenergic_receptor_alpha_1d_(Adra1d),_mRNA	1,68E-08	100	28
		Mm_adrenergic_receptor_alpha_2c_(Adra2c),_mRNA	0,001	92,86	28
		Mm_endothelin_receptor_type_A_(Ednra),_mRNA	0,24	95	20
Agtr1a	For	Mm_angiotensin_II_receptor_type_1a_(Agtr1a),_mRNA	7,97E-07	100	25
		Mm_NCK_interacting_protein_with_SH3_domain_(Nckipso),_mRNA	2,9	94,44	18
		Mm_UDP-N-acetyl-alpha-D-galactosamine:polypeptide_N-cetylgalactosaminyltransferase	2,9	100	14
	Rev	Mm_angiotensin_II_receptor_type_1a_(Agtr1a),_mRNA	9,01E-11	100	32
		Mm_ubiquitin_specific_peptidase_37_(Usp37),_mRNA	0,02	100	18
		Mm_histone_cluster_3_H2ba_(Hist3h2ba),_mRNA	0,08	100	17
Bdkrb2	For	Mm_bradykinin_receptor_beta_2_(Bdkrb2),_mRNA	7,02E-19	100	46
		PREDICTED: Mm_uncharacterized_LOC100862575_(LOC100862575),_miscRNA	2,2	100	15
		Mm_cytochrome_P450_family_11_subfamily_b_polypeptide_2_(Cyp11b2),_nuclear_g	2,2	100	15
	Rev	Mm_bradykinin_receptor_beta_2_(Bdkrb2),_mRNA	3,27E-21	100	50
		Mm_ankyrin_repeat_domain_29_(Ankr29),_mRNA	0,041	100	18
		PREDICTED: Mm_acetyl-CoA_carboxylase_1-like_(LOC100862524),_mRNA	0,64	100	16
Calcr1	For	Mm_calcitonin_receptor-like_(Calcr1),_mRNA	9,01E-11	100	32
		PREDICTED: Mm_predicted_gene_10847_(Gm10847),_miscRNA	5	100	14
		PREDICTED: Mm_predicted_gene_10847_(Gm10847),_miscRNA	5	100	14
	Rev	Mm_calcitonin_receptor-like_(Calcr1),_mRNA	2,22E-07	100	26
		Mm_coiled-coil_domain_containing_90A_(Ccdc90a),_mRNA	0,21	100	16
		Mm_transmembrane_and_coiled-coil_domains_4_(Tmco4),_mRNA	0,81	100	15
Ccr12	For	Mm_chemokine_(C-C_motif)_receptor-like_2_(Ccr12),_mRNA	1,24E-09	100	30
		PREDICTED: Mm_uncharacterized_LOC100048499_(LOC100048499),_miscRNA	1,1	100	15
		Mm_potassium_channel_tetramerisation_domain_containing_17_(Kctd17),_mRNA	1,1	100	15
	Rev	Mm_chemokine_(C-C_motif)_receptor-like_2_(Ccr12),_mRNA	2,83E-06	100	24
		Mm_T-box18_(Tbx18),_mRNA	2,6	100	14
		Mm_T-box_20_(Tbx20),_transcript_variant_1,_mRNA	2,6	100	14
Cd97	For	Mm_CD97_antigen_(Cd97),_transcript_variant_1,_mRNA	5,56E-09	100	29
		Mm_CD97_antigen_(Cd97),_transcript_variant_3,_mRNA	5,56E-09	100	29
		Mm_CD97_antigen_(Cd97),_transcript_variant_2,_mRNA	5,56E-09	100	29
	Rev	Mm_CD97_antigen_(Cd97),_transcript_variant_1,_mRNA	2,41E-11	100	33

		Mm_CD97_antigen_(Cd97),_transcript_variant_3,_mRNA	2,41E-11	100	33
		Mm_CD97_antigen_(Cd97),_transcript_variant_2,_mRNA	2,41E-11	100	33
Celsr2	For	Mm_cadherin_EGF_LAG_seven-pass_..._(Celsr2),_transcript_variant_1,_mRNA	1,15E-13	100	37
		Mm_cadherin_EGF_LAG_seven-pass_..._(Celsr2),_transcript_variant_2,_mRNA	1,15E-13	100	37
		Mm_MOB_kinase_activator_3C_(Mob3c),_mRNA	0,099	95,24	21
	Rev	Mm_cadherin_EGF_LAG_seven-pass_..._(Celsr2),_transcript_variant_1,_mRNA	4,58E-09	100	29
		Mm_cadherin_EGF_LAG_seven-pass_..._(Celsr2),_transcript_variant_2,_mRNA	4,58E-09	100	29
		Mm_centromere_protein_W_(Cenpw),_mRNA	0,26	100	16
Cmklr1	For	Mm_chemokine-like_receptor_1_(Cmklr1),_mRNA	6,45E-12	100	34
		Mm_expressed_sequence_AI646023_(AI646023),_mRNA	1,4	100	15
		Mm_PHD_finger_protein_16_(Phf16),_mRNA	1,4	100	15
	Rev	Mm_chemokine-like_receptor_1_(Cmklr1),_mRNA	0,005	95,45	22
		Mm_multiple_endocrine_neoplasia_1_(Men1),_transcript_variant_4,_mRNA	4,7	94,12	17
		Mm_multiple_endocrine_neoplasia_1_(Men1),_transcript_variant_2,_mRNA	4,7	94,12	17
Crhr2	For	Mm_corticotropin_releasing_hormone_receptor_2_(Crhr2),_mRNA	1,15E-13	100	37
		PREDICTED:_Mm_RIKEN_cDNA_D130079A08_gene_(D130079A08Rik),_miscRNA	1,6	100	15
		PREDICTED:_Mm_RIKEN_cDNA_D130079A08_gene_(D130079A08Rik),_miscRNA	1,6	100	15
	Rev	Mm_corticotropin_releasing_hormone_receptor_2_(Crhr2),_mRNA	2,41E-11	100	33
		Mm_RIKEN_cDNA_C030016D13_gene_(C030016D13Rik),_non-coding_RNA	0,34	91,67	24
		Mm_family_with_sequence_similarity_73,_member_B_(Fam73b),_transcript_variant_1,_	0,34	100	16
Cxcr7	For	Mm_chemokine_(C-X-C_motif)_receptor_7_(Cxcr7),_mRNA	8,51E-22	100	51
		Mm_glucocorticoid_receptor_DNA_binding_factor_1_(Grif1),_mRNA	0,17	100	17
		Mm_pleckstrin_homology_domain_containing,_family_N_member_1_(Plekhn1),_mRNA	0,17	100	17
	Rev	Mm_chemokine_(C-X-C_motif)_receptor_7_(Cxcr7),_mRNA	4,80E-20	100	48
		Mm_G-protein_coupled_receptor_12_(Gpr12),_transcript_variant_1,_mRNA	0,6	100	16
		Mm_armadillo_repeat_containing_3_(Armc3),_mRNA	0,6	100	16
Ednra	For	Mm_endothelin_receptor_type_A_(Ednra),_mRNA	2,83E-06	100	24
		Mm_family_with_sequence_similarity_13,_member_A_(Fam13a),_mRNA	0,043	100	17
		Mm_protein_phosphatase_1J_(Ppm1j),_mRNA	0,67	94,74	19
	Rev	Mm_endothelin_receptor_type_A_(Ednra),_mRNA	6,45E-12	100	34
		Mm_transmembrane_protein_132B_(Tmem132b),_mRNA	0,36	100	16
		Mm_zinc_finger_protein_382_(Zfp382),_mRNA	5,6	94,44	18
F2r	For	Mm_coagulation_factor_II_(thrombin)_receptor_(F2r),_mRNA	1,17E-04	100	21
		Mm_armadillo_repeat_containing_8_(Armc8),_transcript_variant_2,_mRNA	0,11	100	16
		Mm_armadillo_repeat_containing_8_(Armc8),_transcript_variant_1,_mRNA	0,11	100	16
	Rev	Mm_coagulation_factor_II_(thrombin)_receptor_(F2r),_mRNA	9,95E-06	100	23
		Mm_DNA_segment,_Chr_1,_ERATO_Doi_622,_expressed_(D1Erd622e),_mRNA	0,038	100	17
		Mm_small_nuclear_ribonucleoprotein_200_(U5)_(_Snrnp200),_mRNA	0,15	100	16
F2rl1	For	Mm_coagulation_factor_II_(thrombin)_receptor-like_1_(F2rl1),_mRNA	1,25E-20	100	49
		Mm_akirin_1_(Akirin1),_mRNA	0,62	100	16
		Mm_predicted_gene_5622_(Gm5622),_mRNA	2,4	94,74	19
	Rev	Mm_coagulation_factor_II_(thrombin)_receptor-like_1_(F2rl1),_mRNA	3,27E-21	100	50
		Mm_zinc_finger_protein_740_(Zfp740),_mRNA	0,64	100	16
		Mm_v-erb-erythroblastic_leukemia_viral_oncogene_homolog_2,_neuro/glioblastoma_	0,64	100	16
Gabbr1	For	Mm_gamma-aminobutyric_acid_(GABA)_B_receptor_1_(Gabbr1),_mRNA	3,35E-10	100	31
		Mm_calcium-sensing_receptor_(Casr),_mRNA	4,7	100	14
		Mm_B_lymphoid_kinase_(Blk),_mRNA	4,7	100	14
	Rev	Mm_gamma-aminobutyric_acid_(GABA)_B_receptor_1_(Gabbr1),_mRNA	2,45E-08	96,77	31
		Mm_beta_galactoside_alpha_2,6_sialyltransferase_1_(St6gal1),_transcript_variant_2,_m	1,4	100	15
		Mm_beta_galactoside_alpha_2,6_sialyltransferase_1_(St6gal1),_transcript_variant_1,_m	1,4	100	15
Gpr107	For	Mm_G_protein-coupled_receptor_107_(Gpr107),_mRNA	1,63E-12	100	35
		Mm_DiGeorge_syndrome_critical_region_gene_8_(Dgcr8),_mRNA	0,36	100	16
		Mm_GNAS_(guanine_nucleotide_binding_protein_alpha_stimulating)_complex_locus_(1,4	100	15
	Rev	Mm_G_protein-coupled_receptor_107_(Gpr107),_mRNA	1,94E-04	100	21
		PREDICTED:_Mm_predicted_gene_10775_(Gm10775),_miscRNA	2,9	94,44	18
		Mm_SMC_hinge_domain_containing_1_(Smchd1),_mRNA	2,9	100	14
Gpr108	For	Mm_G_protein-coupled_receptor_108_(Gpr108),_mRNA	4,58E-09	100	29
		Mm_a_disintegrin-like_and_metallopeptidase_(reprolysin_type)_with_thrombospondin	0,017	100	18
		Mm_adenosine_monophosphate_deaminase_3_(Ampd3),_mRNA	0,066	100	17
	Rev	Mm_G_protein-coupled_receptor_108_(Gpr108),_mRNA	0,056	100	16
		Mm_microRNA_1198_(Mir1198),_microRNA	3,5	100	13
		Mm_desmocollin_1_(Dsc1),_mRNA	3,5	100	13

Gpr124	For	Mm_G_protein-coupled_receptor_124_(Gpr124),_mRNA	2,83E-06	100	24
		Mm_twisted_gastrulation_homolog_1_(Drosophila)_(Twsg1),_mRNA	0,17	100	16
		Mm_RIKEN_cDNA_2310065F04_gene_(2310065F04Rik),_non-coding_RNA	0,17	100	16
	Rev	Mm_G_protein-coupled_receptor_124_(Gpr124),_mRNA	3,02E-07	100	26
		Mm_RNA_binding_protein,_fox-1_homolog_(C_elegans)_2_(Rbfox2),_transcript_variant	1,1	100	15
		Mm_RNA_binding_protein,_fox-1_homolog_(C_elegans)_2_(Rbfox2),_transcript_variant	1,1	100	15
Gpr125	For	Mm_G_protein-coupled_receptor_125_(Gpr125),_mRNA	1,17E-04	100	21
		Mm_chloride_intracellular_channel_4_(mitochondrial)_(Clic4),_nuclear_gene_encoding_	0,44	100	15
		Mm_RIKEN_cDNA_E130309D14_gene_(E130309D14Rik),_mRNA	1,8	100	14
	Rev	Mm_G_protein-coupled_receptor_125_(Gpr125),_mRNA	3,35E-10	100	31
		PREDICTED:_Mm_predicted_gene_16258_(Gm16258),_miscRNA	0,3	100	16
		PREDICTED:_Mm_predicted_gene_16258_(Gm16258),_miscRNA	0,3	100	16
Gpr133	For	Mm_G_protein-coupled_receptor_133_(Gpr133),_mRNA	9,1	100	12
		Mm_Kell_blood_group_precursor_(McLeod_phenotype)_homolog_(Xk),_mRNA	9,1	100	12
		PREDICTED:_Mm_predicted_gene_16244_(Gm16244),_miscRNA	9,1	100	12
	Rev	Mm_G_protein-coupled_receptor_133_(Gpr133),_mRNA	4,58E-09	100	29
		Mm_RIKEN_cDNA_0610007P08_gene_(0610007P08Rik),_transcript_variant_2,_mRNA	1	100	15
		Mm_cDNA_sequence_BC017643_(BC017643),_transcript_variant_5,_mRNA	4,1	100	14
Gpr137	For	Mm_G_protein-coupled_receptor_137_(Gpr137),_transcript_variant_1,_mRNA	1,68E-08	100	28
		Mm_G_protein-coupled_receptor_137_(Gpr137),_transcript_variant_2,_mRNA	1,68E-08	100	28
		Mm_G_protein-coupled_receptor_137_(Gpr137),_transcript_variant_4,_mRNA	1,68E-08	100	28
	Rev	Mm_G_protein-coupled_receptor_137_(Gpr137),_transcript_variant_1,_mRNA	4,58E-09	100	29
		Mm_G_protein-coupled_receptor_137_(Gpr137),_transcript_variant_2,_mRNA	4,58E-09	100	29
		Mm_G_protein-coupled_receptor_137_(Gpr137),_transcript_variant_4,_mRNA	4,58E-09	100	29
Gpr137b	For	Mm_G_protein-coupled_receptor_137B_(Gpr137b),_mRNA	5,64E-16	100	41
		Mm_G_protein-coupled_receptor_137B,_pseudogene_(Gpr137b-ps),_non-coding_RNA	5,64E-16	100	41
		PREDICTED:_Mm_uncharacterized_LOC100504746,_transcript_variant_1_(LOC10050474	7,3	100	14
	Rev	Mm_G_protein-coupled_receptor_137B_(Gpr137b),_mRNA	6,88E-05	96,67	30
		Mm_G_protein-coupled_receptor_137B,_pseudogene_(Gpr137b-ps),_non-coding_RNA	0,017	93,33	30
		Mm_ATPase,_class_V,_type_10B_(Atp10b),_mRNA	1	100	15
Gpr153	For	Mm_G_protein-coupled_receptor_153_(Gpr153),_mRNA	1,68E-08	100	28
		Mm_PRP38_pre-mRNA_processing_factor_38_(yeast)_domain_containing_B_(Prpf38b),	0,96	100	15
		Mm_retinoblastoma_binding_protein_8_(Rbbp8),_transcript_variant_3,_non-coding_R	3,8	100	14
	Rev	Mm_G_protein-coupled_receptor_153_(Gpr153),_mRNA	2,41E-11	100	33
		Mm_predicted_gene_11696_(Gm11696),_transcript_variant_1,_non-coding_RNA	0,34	100	16
		Mm_exonuclease_3'-5'_domain_containing_2_(Exd2),_mRNA	1,3	100	15
Gpr21	For	Mm_G_protein-coupled_receptor_21_(Gpr21),_mRNA	2,68E-18	100	45
		Mm_RIKEN_cDNA_9430014N10_gene_(9430014N10Rik),_non-coding_RNA	0,009	100	19
		Mm_patched_domain_containing_3_(Ptchd3),_mRNA	0,035	100	18
	Rev	Mm_G_protein-coupled_receptor_21_(Gpr21),_mRNA	3,27E-21	100	50
		Mm_zinc_finger_protein_317_(Zfp317),_mRNA	0,64	100	16
		Mm_glutamine_fructose-6-phosphate_transaminase_1_(Gfpt1),_mRNA	0,64	100	16
Gpr4	For	Mm_G_protein-coupled_receptor_4_(Gpr4),_mRNA	3,21E-15	94,23	52
		Mm_integrin_alpha_X_(Itgax),_mRNA	0,17	100	17
		PREDICTED:_Mms_predicted_gene_10723_(Gm10723),_miscRNA	0,67	100	16
	Rev	Mm_G_protein-coupled_receptor_4_(Gpr4),_mRNA	1,92E-13	93,88	49
		Mm_heat_shock_protein_5_(Hspa5),_transcript_variant_2,_mRNA	0,17	100	17
		PREDICTED:_Mm_predicted_gene_10723_(Gm10723),_miscRNA	0,65	100	16
Gpr64	For	Mm_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_4,_mRNA	7,97E-07	100	25
		Mm_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_3,_mRNA	7,97E-07	100	25
		Mm_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_2,_mRNA	7,97E-07	100	25
	Rev	Mm_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_4,_mRNA	1,68E-08	100	28
		Mm_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_3,_mRNA	1,68E-08	100	28
		Mm_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_2,_mRNA	1,68E-08	100	28
Gprc5b	For	Mm_G_protein-coupled_receptor,_family_C,_group_5,_member_B_(Gprc5b),_transcript	2,68E-18	100	45
		Mm_G_protein-coupled_receptor,_family_C,_group_5,_member_B_(Gprc5b),_transcript	2,68E-18	100	45
		Mm_nuclear_apoptosis_inducing_factor_1_(Naif1),_mRNA	0,54	100	16
	Rev	Mm_G_protein-coupled_receptor,_family_C,_group_5,_member_B_(Gprc5b),_transcript	4,80E-20	100	48
		Mm_G_protein-coupled_receptor,_family_C,_group_5,_member_B_(Gprc5b),_transcript	4,80E-20	100	48
		Mm_SNF_related_kinase_(Snrk),_transcript_variant_2,_mRNA	0,038	100	18
Htr2a	For	Mm_5-hydroxytryptamine_(serotonin)_receptor_2A_(Htr2a),_mRNA	9,01E-11	100	32
		Mm_Sec1_family_domain_containing_2_(Sctd2),_transcript_variant_b,_mRNA	0,02	100	18

		Mm_Sec1_family_domain_containing_2_(Scfd2),_transcript_variant_a,_mRNA	0,02	100	18
Rev		Mm_5-hydroxytryptamine_(serotonin)_receptor_2A_(Htr2a),_mRNA	1,63E-12	100	35
		PREDICTED:_Mm_predicted_gene_9930_(Gm9930),_miscRNA	1,4	100	15
		Mm_cDNA_sequence_BC027231_(BC027231),_mRNA	1,4	100	15
Lgr4	For	Mm_leucine-rich_repeat-containing_G_protein-coupled_receptor_4_(Lgr4),_mRNA	9,01E-11	100	32
		Mm_small_G_protein_signaling_modulator_2_(Sgsm2),_mRNA	0,32	100	16
		Mm_solute_carrier_family_16_(monocarboxylic_acid_transporters),_member_11_(Slc16	1,3	100	15
Rev		Mm_leucine-rich_repeat-containing_G_protein-coupled_receptor_4_(Lgr4),_mRNA	3,35E-10	100	31
		Mm_acyl-CoA_thioesterase_5_(Acot5),_mRNA	0,3	100	16
		Mm_acyl-CoA_thioesterase_3_(Acot3),_mRNA	0,3	100	16
Lgr6	For	Mm_leucine-rich_repeat-containing_G_protein-coupled_receptor_6_(Lgr6),_mRNA	9,01E-11	100	32
		Mm_phosphoinositide-3-kinase,_regulatory_subunit_5,_p101_(Pik3r5),_mRNA	1,3	100	15
		Mm_leucine-rich_repeat_containing_38_(Lrrc38),_mRNA	1,3	100	15
Rev		Mm_leucine-rich_repeat-containing_G_protein-coupled_receptor_6_(Lgr6),_mRNA	1,63E-12	100	35
		Mm_SCO_cytochrome_oxidase_deficient_homolog_1_(yeast)_(_Sco1),_nuclear_gene_enc	0,36	100	16
		PREDICTED:_Mms_predicted_gene_6934_(Gm6934),_mRNA	1,4	100	15
Lpar1	For	Mm_lyso-phosphatidic_acid_receptor_1_(Lpar1),_transcript_variant_2,_mRNA	1,84E-19	100	47
		Mm_lyso-phosphatidic_acid_receptor_1_(Lpar1),_transcript_variant_1,_mRNA	1,84E-19	100	47
		Mm_dopamine_receptor_D3_(Drd3),_mRNA	0,002	90,63	32
Rev		Mm_lyso-phosphatidic_acid_receptor_1_(Lpar1),_transcript_variant_2,_mRNA	3,90E-17	100	43
		Mm_lyso-phosphatidic_acid_receptor_1_(Lpar1),_transcript_variant_1,_mRNA	3,90E-17	100	43
		Mm_pyruvate_kinase_liver_and_red_blood_cell_(Pklr),_nuclear_gene_encoding_mitoch	0,13	100	17
Lpar4	For	Mm_lyso-phosphatidic_acid_receptor_4_(Lpar4),_mRNA	2,68E-18	100	45
		PREDICTED:_Mm_predicted_gene_13660_(Gm13660),_miscRNA	2,1	100	15
		Mm_interferon_(alpha_and_beta)_receptor_2_(Ifnar2),_transcript_variant_1,_mRNA	2,1	100	15
Rev		Mm_lyso-phosphatidic_acid_receptor_4_(Lpar4),_mRNA	1,25E-20	100	49
		Mm_additional_sex_combs_like_1_(Drosophila)_(_Asxl1),_mRNA	0,62	95	20
		Mm_ATPase_type_13A3_(Atp13a3),_transcript_variant_1,_mRNA	2,4	100	15
Lphn1	For	Mm_latrophilin_1_(Lphn1),_mRNA	2,32E-15	100	40
		PREDICTED:_Mm_predicted_gene_10644_(Gm10644),_miscRNA	2,32E-15	100	40
		PREDICTED:_Mm_predicted_gene_10644_(Gm10644),_miscRNA	2,32E-15	100	40
Rev		Mm_latrophilin_1_(Lphn1),_mRNA	9,69E-08	97,14	35
		PREDICTED:_Mm_predicted_gene_10644_(Gm10644),_miscRNA	9,69E-08	97,14	35
		PREDICTED:_Mm_predicted_gene_10644_(Gm10644),_miscRNA	9,69E-08	97,14	35
Lphn2	For	Mm_latrophilin_2_(Lphn2),_mRNA	2,68E-11	100	33
		Mm_tetratricopeptide_repeat_domain_16_(Ttc16),_mRNA	0,095	100	17
		Mm_sel-1_suppressor_of_lin-12-like_3_(C_elegans)_(_Sel1l3),_mRNA	0,37	100	16
Rev		Mm_latrophilin_2_(Lphn2),_mRNA	1,24E-09	100	30
		Mm_caspase_8_associated_protein_2_(Casp8ap2),_transcript_variant_2,_mRNA	1,1	94,74	19
		Mm_caspase_8_associated_protein_2_(Casp8ap2),_transcript_variant_1,_mRNA	1,1	94,74	19
Mrgprf	For	Mm_MAS-related_GPR,_member_F_(Mrgprf),_mRNA	2,22E-07	100	26
		Mm_copine_II_(Cpne2),_mRNA	0,052	100	17
		Mm_FERM,_RhoGEF_(Arhgef)_and_pleckstrin_domain_protein_1_(chondrocyte-derived	0,81	100	15
Rev		Mm_MAS-related_GPR,_member_F_(Mrgprf),_mRNA	2,45E-08	100	28
		Mm_lectin,_mannose-binding_2_(Lman2),_mRNA	0,36	100	16
		Mm_RIKEN_cDNA_9430015G10_gene_(9430015G10Rik),_transcript_variant_2,_mRNA	0,36	100	16
Npy1r	For	Mm_neuropeptide_Y_receptor_Y1_(Npy1r),_mRNA	3,35E-10	100	31
		Mm_collagen_type_XVIII,_alpha_1_(Col18a1),_transcript_variant_1,_mRNA	0,3	95	20
		Mm_collagen_type_XVIII,_alpha_1_(Col18a1),_transcript_variant_2,_mRNA	0,3	95	20
Rev		Mm_neuropeptide_Y_receptor_Y1_(Npy1r),_mRNA	3,06E-14	100	38
		Mm_PHD_finger_protein_23_(Phf23),_mRNA	0,41	100	16
		PREDICTED:_Mm_predicted_gene_5524_(Gm5524),_miscRNA	1,6	100	15
P2ry2	For	Mm_purinergic_receptor_P2Y,_G-protein_coupled_2_(P2ry2),_mRNA	2,83E-06	100	24
		Mm_cadherin-like_24_(Cdh24),_mRNA	0,67	100	15
		Mm_dehydrogenase/reductase_(SDR_family)_member_11_(Dhrs11),_mRNA	0,67	100	15
Rev		Mm_purinergic_receptor_P2Y,_G-protein_coupled_2_(P2ry2),_mRNA	1,15E-13	100	37
		PREDICTED:_Mm_myosin-6-like_(LOC100862557),_mRNA	1,6	100	15
		Mm_potassium_channel_subfamily_K,_member_7_(Kcnk7),_mRNA	1,6	100	15
P2ry6	For	Mm_pyrimidinergic_receptor_P2Y,_G-protein_coupled,_6_(P2ry6),_mRNA	2,22E-07	100	26
		Mm_nucleoporin_210-like_(Nup210l),_mRNA	0,21	100	16
		Mm_ribosomal_protein_L18A_(Rpl18a),_mRNA	0,81	100	15
Rev		Mm_pyrimidinergic_receptor_P2Y,_G-protein_coupled,_6_(P2ry6),_mRNA	2,41E-11	100	33

		PREDICTED: Mm_ring_finger_protein_213_(Rnf213),_mRNA	1,3	100	15
		Mm_SID1_transmembrane_family_member_1_(Sidt1),_transcript_variant_1,_mRNA	1,3	100	15
Ptger3	For	Mm_prostaglandin_E_receptor_3_(subtype_EP3)(Ptger3),_mRNA	1,25E-20	100	49
		Mm_solute_carrier_family_9_(sodium/hydrogen_exchanger),_member_9_(Slc9a9),_mRNA	0,04	100	18
		Mm_ATP-binding_cassette_sub-family_A_(ABC1),_member_15_(Abca15),_mRNA	0,62	95	20
	Rev	Mm_prostaglandin_E_receptor_3_(subtype_EP3)(Ptger3),_mRNA	1,84E-19	100	47
		Mm_component_of_oligomeric_golgi_complex_2_(Cog2),_mRNA	2,3	100	15
		Mm_solute_carrier_family_26_(sulfate_transporter),_member_1_(Slc26a1),_mRNA	2,3	100	15
Ptgir	For	Mm_prostaglandin_I_receptor_(IP)(Ptgir),_mRNA	7,97E-07	100	25
		Mm_SET_domain_containing_(lysine_methyltransferase)_7_(Setd7),_mRNA	0,19	95	20
		Mm_RIKEN_cDNA_4921511C10_gene_(4921511C10Rik),_non-coding_RNA	0,74	100	15
	Rev	Mm_prostaglandin_I_receptor_(IP)(Ptgir),_mRNA	8,10E-15	100	39
		Mm_solute_carrier_family_30_(zinc_transporter),_member_5_(Slc30a5),_mRNA	0,11	95,24	21
		Mm_nucleoporin_85_(Nup85),_mRNA	0,43	95	20
Pth1r	For	Mm_parathyroid_hormone_1_receptor_(Pth1r),_transcript_variant_3,_mRNA	3,06E-14	100	38
		Mm_parathyroid_hormone_1_receptor_(Pth1r),_transcript_variant_2,_mRNA	3,06E-14	100	38
		Mm_parathyroid_hormone_1_receptor_(Pth1r),_transcript_variant_1,_mRNA	3,06E-14	100	38
	Rev	Mm_parathyroid_hormone_1_receptor_(Pth1r),_transcript_variant_3,_mRNA	6,21E-09	100	29
		Mm_parathyroid_hormone_1_receptor_(Pth1r),_transcript_variant_2,_mRNA	6,21E-09	100	29
		Mm_parathyroid_hormone_1_receptor_(Pth1r),_transcript_variant_1,_mRNA	6,21E-09	100	29
Tbxa2r	For	Mm_thromboxane_A2_receptor_(Tbxa2r),_mRNA	2,68E-18	100	45
		Mm_prostaglandin_E_receptor_1_(subtype_EP1)(Ptger1),_mRNA	9,13E-06	100	24
		PREDICTED: Mm_RIKEN_cDNA_1700040D17_gene_(1700040D17Rik),_miscRNA	0,54	100	16
	Rev	Mm_thromboxane_A2_receptor_(Tbxa2r),_mRNA	2,41E-11	100	33
		Mm_glutamic-oxaloacetic_transaminase_1-like_1_(Got1l1),_mRNA	1,3	100	15
		Mm_a_disintegrin_and_metallopeptidase_domain_1a_(Adam1a),_mRNA	1,3	100	15

Table 2: List of blast hits for sequences obtained by sequencing of single-cell amplicons using forward (For) or reverse (Rev) primers (only the three highest ranking hits are shown per analysis). The E-value describes the number of hits expected to see by chance when searching a database of a comparable size. An E-value of 1 indicates that in a database of the current size one might expect to see 1 match with a similar score simply by chance. Mm, mus musculus.

To summarize these findings, we added the following paragraph on page 7, line 17-20 of the revised manuscript:

“We also sequenced single-cell RT-PCR amplicons to exclude off-target amplification or amplification of highly homologous GPCRs and found that the amplified sequences were in all cases specific for the targeted receptor (data not shown).”

We furthermore mention the amplicon sequencing results in the discussion on page 14, line 15.

2. The authors found that different types of SMCs or ECs have distinct GPCR expression patterns and can be grouped into distinct clusters by clustering analysis. The authors should give a list to clearly show how many experiments and how many cells in each experiment have been analyzed for each SMC and EC cell types. In Figure 3G and 4C, for a certain cluster, have the cells been analyzed by more than one independent experiments to exclude the batch effect?

Following the reviewer’s suggestion we assembled a table showing for each cell type the number of cells, mice, and independent experiments (Table 3).

Cell type	No. of cells	No. of mice	No. of exps
SMao	60	8	3
SMaoAged	32	6	2
SMaoApo0w	34	6	2
SMaoApo16w	50 (prev. vers.: 57)	6	2
SMsk	57 (prev. vers.: 66)	7	3
SMmes	29	8	5
SMub	25	8	4
ECsk	40	6	5
EClu	48	8	3
ECluLPS	25	4	2
ECbr	52	7	2
ECbrLPS	22	4	2
ECao	12	4	2
ECaoApo16w	16	6	2

Table 3: Overview of numbers of cells, mice, and independent experiments analyzed for the different cell types.

As shown in Table 3, data underlying cluster analyses in Figures 3G and 4C were generated in 2-5 independent experiments and 6-8 mice per group.

We added the total numbers of cells and mice to the respective Figure legends of the revised manuscript, in addition we attached Table 3 of this letter as Supplemental Figure 4 to the revised manuscript and refer to it on page 9, lines 1-2.

The numbers of SMsk and SMaoApo16w were unfortunately incorrect in the previous version of the manuscript, these mistakes have been corrected in Figure legends 1, 3 and 7 of the revised manuscript (for SMsk 57 instead of 66, for SMaoApo16w from 50 instead of 57).

3. The authors also found that GPCR expression was highly heterogeneous within each cell type. However, in most conditions, it seems that the authors have not identified functional cell subpopulations. I am not convinced that the intra-cell type heterogeneous GPCR expression has important biological functions in general. The authors should be careful to claim this. It can be helpful to verify the heterogeneous GPCR expression at the protein level if suitable antibodies are available. If you can detect the heterogeneously expressed GPCR gene at the protein level, it is more convincing that the gene could be functional.

We followed the reviewer's suggestion and investigated GPCR heterogeneity in aortic smooth muscle cells on the protein level by flow cytometry. To do so, aortae of wildtype mice were digested and permeabilized as described in the methods section, followed by incubation of single cell suspensions with antibodies directed against α SMA (PE or FITC) and APC-labelled antibodies directed against receptors Cmk1r1, Ccr12, Celsr2, and Cxcr7. For each GPCR-specific antibody the corresponding isotype control was used (Fig. 2A). We found that also on the protein level heterogeneity of GPCR was present within the SMao population, and that the percentages roughly matched the values obtained by single-cell RT-PCR (Fig. 2B).

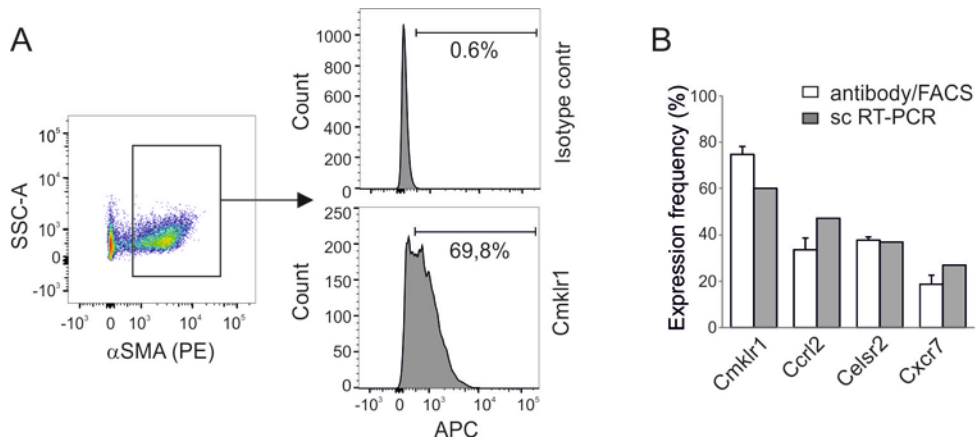


Figure 2: Flow cytometric analysis of GPCR expression. **A**, Example of the gating strategy. **B**, GPCR expression frequency in individual SMao as judged by single-cell flow cytometric analysis (antibody/FACS) or RT-PCR (sc RT-PCR).

We included these data in Suppl. Figures 2B and C and describe them on page 7, lines 20-23 of the revised manuscript as well as on page 22 of the revised Supplemental Material. We also mention these results in the discussion on page 14, lines 15 and 23.

4. The authors have identified a small subpopulation of dedifferentiating SMC from healthy SMao (Figure 8). They have also performed the single cell RNA-seq method for SMao. Could this small subpopulation also be identified from the single cell RNA-seq data and were the results between the single cell RT-PCR and single cell RNA-seq consistent?

We followed the reviewers' suggestion and investigated whether the small subpopulation of spontaneously dedifferentiating SMao was also found in the mRNAseq data. To do so, we applied the algorithm described by Grün et al¹ to the SMao mRNAseq data set, which led to the identification a subgroup of 14% of cells with distinct expression pattern (Fig.3A). This subgroup showed features indicative of a dedifferentiated state, such as expression of receptors or transcription factors that have been implicated in the regulation of smooth muscle (de-)differentiation, such as *Klf4*^{2, 3, 4, 5}, *Notch1*^{6, 7, 8}, or *FGF* receptors^{9, 10}. Furthermore, this population of cells showed a reduced expression of *Tagln2*, a homologue of the smooth muscle differentiation marker transgelin, also known as *Sm22a*¹¹ (Fig. 3B). Other markers typically changed in dedifferentiating smooth muscle cells, such as *Icam1* or *Vcam1*, were not enriched in these cells. This was probably due to the reduced detection frequency in mRNAseq compared to RTPCR: *Vcam1* was only detected in 2% of cells (RT-PCR: 10%) and *Icam1* not at all (RT-PCR: 8%). However, assuming that the above-mentioned subgroup represents a dedifferentiating subpopulation, we next investigated how their GPCR pattern differed. Cluster analysis identified only six GPCRs mRNAs that were significantly increased in the subpopulation (Fig. 3C): those encoding the orphan receptors *Gpr20* and *Mrgprh*, the olfactory receptors *Olfr558* and *Olfr78*, the corticotrophin releasing hormone receptors subtype 2 (*Crhr2*), and the endothelin receptor subtype A (*Ednra*). Three of these GPCRs were not included in the RT-PCR screen (*Gpr20*, *Olfr558*, *Mrgprh*); of the remaining three, *Ednra* and *Olfr78* were also in RT-PCR analysis enriched in dedifferentiating SMC (either spontaneous or atherosclerotic). However, the majority of GPCRs that were in RT-PCR found to be associated with a dedifferentiated state were not enriched in the putative SMaoDiff in mRNAseq. Again, this is most likely due differences in detection frequency, since all GPCRs identified in RT-PCR were, except for *Lgr6*, less efficiently detected in single-cell mRNAseq (Fig. 3D). We therefore conclude that the difference in detection frequency of low

abundance transcripts such as GPCRs hinders the direct comparison of data from single-cell RT-PCR and mRNAseq.

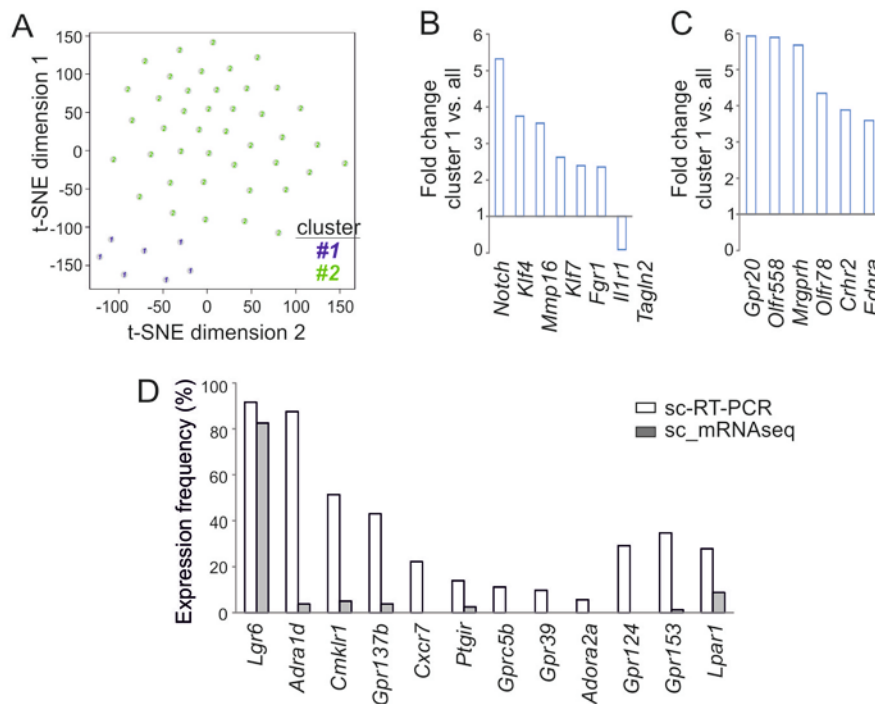


Figure 3: Functional subgroups within the SMao mRNAseq data set. **A**, T-SNE plot of k-means clustering data: cluster assignment is indicated by colored numbers (each dot one cell; distance between dots indicates degree of similarity). **B,C**, Fold change of gene expression in cluster 1 cells compared to the rest of SMao: genes indicative of differentiation state (B) and GPCRs (C). **D**, Comparison of the expression frequency in mRNAseq versus RT-PCR for those GPCRs that are according to single-cell RT-PCR enriched in dedifferentiating SMao.

Other changes

- We noted that the order of transcription factors in Figure 7F was incorrect, this has been remedied.
- The last sentence of paragraph 1 of the discussion (“However, it cannot be excluded that also with the RT-PCR method very low abundance transcripts escape detection”) was deleted since it was largely redundant with the sentence in lines 9-11 of the same paragraph.
- The number of function-defining genes included in the array has been corrected from 12 to 13 genes, since in the original version *Lyve1* (for lymphatic EC) was left out. Also the number of function-defining genes has been corrected to 36.
- Since the term “expression” was used twice in the title, we renamed the manuscript as follows: “Single-cell profiling reveals heterogeneity and functional patterning of GPCR expression in the vascular system” (instead of Single-cell expression profiling reveals heterogeneity and functional patterning of GPCR expression in the vascular system).

References

1. Grun D, *et al.* Single-cell messenger RNA sequencing reveals rare intestinal cell types. *Nature* **525**, 251-255 (2015).
2. Shankman LS, *et al.* KLF4-dependent phenotypic modulation of smooth muscle cells has a key role in atherosclerotic plaque pathogenesis. *Nat Med* **21**, 628-637 (2015).
3. Yoshida T, Kaestner KH, Owens GK. Conditional deletion of Kruppel-like factor 4 delays downregulation of smooth muscle cell differentiation markers but accelerates neointimal formation following vascular injury. *Circ Res* **102**, 1548-1557 (2008).
4. Yoshida T, Gan Q, Owens GK. Kruppel-like factor 4, Elk-1, and histone deacetylases cooperatively suppress smooth muscle cell differentiation markers in response to oxidized phospholipids. *Am J Physiol Cell Physiol* **295**, C1175-1182 (2008).
5. Liu Y, Sinha S, McDonald OG, Shang Y, Hoofnagle MH, Owens GK. Kruppel-like factor 4 abrogates myocardin-induced activation of smooth muscle gene expression. *J Biol Chem* **280**, 9719-9727 (2005).
6. Li Y, *et al.* Smooth muscle Notch1 mediates neointimal formation after vascular injury. *Circulation* **119**, 2686-2692 (2009).
7. Proweller A, Pear WS, Parmacek MS. Notch signaling represses myocardin-induced smooth muscle cell differentiation. *J Biol Chem* **280**, 8994-9004 (2005).
8. Boucher J, Gridley T, Liaw L. Molecular pathways of notch signaling in vascular smooth muscle cells. *Front Physiol* **3**, 81 (2012).
9. Chen PY, Qin L, Li G, Tellides G, Simons M. Fibroblast growth factor (FGF) signaling regulates transforming growth factor beta (TGFbeta)-dependent smooth muscle cell phenotype modulation. *Sci Rep* **6**, 33407 (2016).
10. Chen PY, Qin L, Li G, Tellides G, Simons M. Smooth muscle FGF/TGFbeta cross talk regulates atherosclerosis progression. *EMBO Mol Med* **8**, 712-728 (2016).
11. Robin YM, *et al.* Transgelin is a novel marker of smooth muscle differentiation that improves diagnostic accuracy of leiomyosarcomas: a comparative immunohistochemical reappraisal of myogenic markers in 900 soft tissue tumors. *Mod Pathol* **26**, 502-510 (2013).

Supplemental table 1

Query	Hit	E-value	% match	length	alignm	qstart	qend	Hit sequence
Adra1a	Adra1a_F	Mus_musculus_adrenergic_receptor_alpha_1a_(Adra1a)_mRNA	3.90E-17	100	43	1	43	CTCTGGCTGCATTCTCTCGTGATGCCCATTTGGGTCCTTC
	Mus_musculus_adrenergic_receptor_beta_1_(Adrb1)_mRNA	0.13	95.24	21	1	21	21	CTCTGGCTGCATTCTCTTC
	Mus_musculus_leucine_rich_repeat_and_fibronectin_type_III_extracellular_1_(Elf1)_mRNA	0.13	100	17	20	36	36	CTCTGGATGCCATTTGG
	Mus_musculus_inositol_polyphosphate_5_phosphatase_B_(Inpp5b)_nuclear_gene_encoding_mitochondrial_protein_mRNA	0.5	100	16	5	20	20	TGGCTGCATTTCTTC
	Mus_musculus_somatostatin_receptor_5_(Sstr5)_transcript_variant_1_mRNA	0.5	91.67	24	1	24	24	CTCTGGCTGCATTCTCTCTG
	Mus_musculus_somatostatin_receptor_5_(Sstr5)_transcript_variant_2_mRNA	0.5	91.67	24	1	24	24	CTCTGGCTGCATTCTCTCTG
	Mus_musculus_adrenergic_receptor_beta_3_(Adrb3)_mRNA	0.5	95	20	2	21	21	TGCTGGCTGCATTTCTTC
	Mus_musculus_Rap_guanine_nucleotide_exchange_factor_(GEF)_5_(Raggef5)_mRNA	2	100	15	8	22	22	CTGCATTTCTCTC
	Mus_musculus_RIKEN_cDNA_A330049M08_gene_(A330049M08RIK)_transcript_variant_3_mRNA	2	100	15	1	15	15	CTCTGGCTGCATT
	Mus_musculus_RIKEN_cDNA_A330049M08_gene_(A330049M08RIK)_transcript_variant_4_mRNA	2	100	15	1	15	15	CTCTGGCTGCATT
	Mus_musculus_RIKEN_cDNA_A330049M08_gene_(A330049M08RIK)_transcript_variant_6_mRNA	2	100	15	1	15	15	CTCTGGCTGCATT
	Mus_musculus_RIKEN_cDNA_A330049M08_gene_(A330049M08RIK)_transcript_variant_5_mRNA	2	100	15	1	15	15	CTCTGGCTGCATT
	Mus_musculus_RIKEN_cDNA_A330049M08_gene_(A330049M08RIK)_transcript_variant_2_mRNA	2	100	15	1	15	15	CTCTGGCTGCATT
	Mus_musculus_RIKEN_cDNA_A330049M08_gene_(A330049M08RIK)_transcript_variant_1_mRNA	2	100	15	1	15	15	CTCTGGCTGCATT
	Mus_musculus_RIKEN_cDNA_1190005F20_gene_(1190005F20RIK)_mRNA	2	100	15	25	39	39	GATGCCATTGGGTC
	Mus_musculus_adrenergic_receptor_beta_2_(Adrb2)_mRNA	2	94.74	19	1	19	19	CTCTGGCTGCATTCTTC
	PREDICTED: Mus_musculus_RIKEN_cDNA_4921528I07_gene_(4921528I07RIK)_mRNA	2	94.74	15	23	37	37	GTGATGCCATTGGG
	Mus_musculus_dopamine_receptor_D2_(Drd2)_mRNA	2	100	19	1	19	19	CTCTGGCTGCATTCTTC
	Mus_musculus_syntaxin_18_(Sxt18)_mRNA	2	100	15	14	28	28	TCTCTGCTGATTC
	PREDICTED: Mus_musculus_RIKEN_cDNA_9430032J07_gene_(9430032J07RIK)_miscRNA	7.9	100	14	3	16	16	CTCTGGCTGCATT
Adra1a_R	Mus_musculus_adrenergic_receptor_alpha_1a_(Adra1a)_mRNA	8.10E-15	100	39	1	39	39	GCCAAGACGCTGGGATTTGGTGGATGCTTCCTCCTCCT
	Mus_musculus_trace_amine-associated_receptor_5_(Taar5)_mRNA	0.007	100	19	1	19	19	GCCAAGACGCTGGGATTC
	PREDICTED: Mus_musculus_RIKEN_cDNA_4631423B10_gene_(4631423B10RIK)_miscRNA	0.43	100	16	9	24	24	GCTGGCATTGGTG
	PREDICTED: Mus_musculus_RIKEN_cDNA_4631423B10_gene_(4631423B10RIK)_miscRNA	0.43	100	16	9	24	24	GCTGGCATTGGTG
	Mus_musculus_periostin_osteoblast_specific_factor_(Postn)_transcript_variant_3_mRNA	0.43	100	16	7	22	22	ACGCTGGCATTGGG
	Mus_musculus_periostin_osteoblast_specific_factor_(Postn)_transcript_variant_5_mRNA	0.43	100	16	7	22	22	ACGCTGGCATTGGG
	Mus_musculus_periostin_osteoblast_specific_factor_(Postn)_transcript_variant_1_mRNA	0.43	100	16	7	22	22	ACGCTGGCATTGGG
	Mus_musculus_periostin_osteoblast_specific_factor_(Postn)_transcript_variant_2_mRNA	0.43	100	16	7	22	22	ACGCTGGCATTGGG
	Mus_musculus_HNF1b_homeobox_B_(Hnf1b)_mRNA	1.7	94.74	19	9	27	27	GCTGGCATTGGTGGGA
	Mus_musculus_dynein_axonemal_heavy_chain_2_(Dnahc2)_mRNA	1.7	100	15	9	23	23	GCTGGCATTGGTGT
	Mus_musculus_RIKEN_cDNA_2900052N01_gene_(2900052N01RIK)_non-coding_RNA	1.7	100	15	10	24	24	CTGGCATTGGTG
	Mus_musculus_OTU_domain_containing_7A_(Otu7a)_mRNA	1.7	100	15	3	17	17	CAAGACGCTGGGAT
	Mus_musculus_oculocutaneous_albinism_II_(Oca2)_mRNA	1.7	100	15	15	29	29	CATTGGTGGGATG
	Mus_musculus_myocyte_enhancer_factor_2D_(Mef2d)_mRNA	1.7	94.74	19	2	20	20	CCAAAGCTGGGATGTT
	Mus_musculus_coiled-coil_helix_coiled-coil_helix_domain_containing_5_(Chchd5)_mRNA	1.7	100	15	9	23	23	CTGGCATTGGTGT
	PREDICTED: Mus_musculus_predicted_gene_5067_(Gm5067)_miscRNA	6.7	100	14	20	33	33	TGTTGGATGCTTC
	PREDICTED: Mus_musculus_RIKEN_cDNA_5330417H12_gene_(5330417H12RIK)_miscRNA	6.7	100	14	4	17	17	AGACGCTGGGAT
	Mus_musculus_collagen_type_IV_alpha_5_(Col4a5)_transcript_variant_2_mRNA	6.7	100	14	11	24	24	TGGCATTGGTG
	Mus_musculus_collagen_type_IV_alpha_5_(Col4a5)_transcript_variant_1_mRNA	6.7	100	14	11	24	24	TGGCATTGGTG
	Mus_musculus_developmental_pluripotency_associated_4_(Dpp4)_transcript_variant_2_mRNA	6.7	100	14	26	39	39	GATGCTGCTCCT
	Mus_musculus_developmental_pluripotency_associated_4_(Dpp4)_transcript_variant_1_mRNA	6.7	100	14	26	39	39	GATGCTGCTCCT
Adra1b	Adra1b_F	Mus_musculus_adrenergic_receptor_alpha_1b_(Adra1b)_mRNA	2.21E-22	100	52	1	52	CTCCACCTAAAGCCCGAGCCGATTCACAGGTAGTGTCTGGCTGGC
	Mus_musculus_RIKEN_cDNA_B430010I23_gene_(B430010I23RIK)_non-coding_RNA	0.67	100	16	1	16	16	CTCCACCTAAAGCC
	Mus_musculus_cAMP_responsive_element_binding_protein-like_2_(Crebl2)_mRNA	2.7	91.3	23	29	51	51	TTCAAGTAGTGTCTGGCTGG
	Mus_musculus_kinase_non-catalytic_C-lobe_domain_(KIND)_containing_1_(Kndc1)_mRNA	2.7	100	15	37	51	51	AGTGTCTGGCTGG
	Mus_musculus_suppressor_of_Ty_5_homolog_(S_cerevisiae)_mRNA	2.7	100	15	38	52	52	GTGTCTGGCTGGC
Adra1b_R	Mus_musculus_adrenergic_receptor_alpha_1b_(Adra1b)_mRNA	0.58	100	14	1	14	14	ATGTTGCTCCCTC
	Mus_musculus_glutamate_receptor_ionotropic_AMPA3_alpha_3_(Gria3)_mRNA	2.3	100	13	1	13	13	ATGTTGCTCCCTC
	Mus_musculus_striatin_calmodulin_binding_protein_(Strn)_mRNA	2.3	100	13	2	14	14	TGTTGCTCCCTC
	Mus_musculus_centromere_protein_C1_(Cenpc1)_mRNA	2.3	100	13	2	14	14	TGTTGCTCCCTC
	Mus_musculusprofilin_2_(Pfn2)_mRNA	2.3	100	13	1	13	13	ATGTTGCTCCCTC
	PREDICTED: Mus_musculus_predicted_gene_10757_(Gm10757)_miscRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_RIKEN_cDNA_2610002M06_gene_(2610002M06RIK)_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_complement_component_2_(within_H_25)_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_transformation_related_protein_63_(Trp63)_transcript_variant_5_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_transformation_related_protein_63_(Trp63)_transcript_variant_6_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_transformation_related_protein_63_(Trp63)_transcript_variant_4_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_transformation_related_protein_63_(Trp63)_transcript_variant_2_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_transformation_related_protein_63_(Trp63)_transcript_variant_1_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_enoyl-Coenzyme_A_hydration/3-hydroxyacyl-Coenzyme_A_dehydrogenase_(Ehhadh)_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_NLR_family_CARD_domain_containing_3_(Nlr3)_mRNA	9.1	100	12	2	13	13	TGTTGCTCCCTC
	Mus_musculus_wingless-related_MMTV_integration_site_7B_(Wnt7b)_transcript_variant_2_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_wingless-related_MMTV_integration_site_7B_(Wnt7b)_transcript_variant_3_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
	Mus_musculus_wingless-related_MMTV_integration_site_7B_(Wnt7b)_transcript_variant_1_mRNA	9.1	100	12	1	12	12	ATGTTGCTCCCTC
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	Mus_musculus_tubulin_tyrosine_ligase-like_family_member_5_(Tll5)_mRNA	9.1	100	12	2	13	13	TGTTGCTCCCTC
Adra1d	Adra1d_F	Mus_musculus_adrenergic_receptor_alpha_1d_(Adra1d)_mRNA	3.35E-10	100	31	1	31	GGTTCCTGTTCCTCAGCTGAACCATCAG
	Mus_musculus_arrestin_beta_2_(Arb2)_mRNA	0.3	100	16	12	27	27	CCCTCAGCTGAACCA
	Mus_musculus_small_nucleolar_RNA_C/D_box_1A_(Snord1a)_small_nucleolar_RNA	1.2	100	15	10	24	24	TTCCCTCAGCTGAAA
	Mus_musculus_RIKEN_cDNA_1810032O08_gene_(1810032O08RIK)_transcript_variant_3_non-coding_RNA	1.2	100	15	10	24	24	TTCCCTCAGCTGAAA
	Mus_musculus_cullin_5_(Cul5)_transcript_variant_1_mRNA	1.2	100	15	16	30	30	CAGCTGAACCATCA
	Mus_musculus_cullin_5_(Cul5)_transcript_variant_2_mRNA	1.2	100	15	16	30	30	CAGCTGAACCATCA
	Mus_musculus_protein_kinase_N2_(Pkn2)_mRNA	1.2	100	15	5	19	19	CTCTGTTCCCTCAG
	PREDICTED: Mus_musculus_RIKEN_cDNA_B230314M03_gene_(B230314M03RIK)_miscRNA	4.7	100	14	5	18	18	CTCTGTTCCCTCAG
	Mus_musculus_NF-kappaB_repressing_factor_(Nkrf)_mRNA	4.7	100	14	5	18	18	CTCTGTTCCCTCAG
	Mus_musculus_sideroflexin_3_(Sfxn3)_transcript_variant_3_mRNA	4.7	100	14	5	18	18	CTCTGTTCCCTCAG
	Mus_musculus_sideroflexin_3_(Sfxn3)_transcript_variant_2_mRNA	4.7	100	14	5	18	18	CTCTGTTCCCTCAG
	Mus_musculus_sideroflexin_3_(Sfxn3)_transcript_variant_1_mRNA	4.7	100	14	5	18	18	CTCTGTTCCCTCAG
	Mus_musculus_SH3-binding_domain_glutamic_acid-rich_protein_(Sh3bgr)_mRNA	4.7	100	14	3	16	16	TCTGTTCCCTC
	Mus_musculus_microrchidia_3_(Mrc3)_mRNA	4.7	100	14	17	30	30	AGCTGAACCATCA
	Mus_musculus_class_II_transactivator_(Ctla)_transcript_variant_3_mRNA	4.7	100	14	10	23	23	TTCCCTCAGCTGAA
	Mus_musculus_class_II_transactivator_(Ctla)_transcript_variant_2_mRNA	4.7	100	14	10	23	23	TTCCCTCAGCTGAA
	Mus_musculus_class_II_transactivator_(Ctla)_transcript_variant_1_mRNA	4.7	100	14	10	23	23	TTCCCTCAGCTGAA
	Mus_musculus_F-box_protein_34_(Fbxo34)_transcript_variant_1_mRNA	4.7	100	14	8	21	21	TGTTCCCTCAGCTG
	Mus_musculus_F-box_protein_34_(Fbxo34)_transcript_variant_3_mRNA	4.7	100	14	8	21	21	TGTTCCCTCAGCTG
	Mus_musculus_F-box_protein_34_(Fbxo34)_transcript_variant_4_non-coding_RNA	4.7	100	14	8	21	21	TGTTCCCTCAGCTG
Adra1d_R	Mus_musculus_adrenergic_receptor_alpha_1d_(Adra1d)_mRNA	1.68E-08	100	28	1	28	28	TTCGCTGTGCTGGTCCCCTTTCT
	Mus_musculus_adrenergic_receptor_alpha_2c_(Adra2c)_mRNA	0.001	92.86	28	1	28	28	TTCGCTGTGCTGGTCCCCTTTCT
	Mus_musculus_endothelin_receptor_type_A_(Edra)_mRNA	0.24	95	20	1	20	20	TTCGCTGTGCTGGTCCC
	PREDICTED: Mus_musculus_CUB_and_Sushi_multiple_domains_2_(Csm2d)_mRNA	0.96	100	15	5	19	19	TCCTGTGCTGGTCCC
	PREDICTED: Mus_musculus_CUB_and_Sushi_multiple_domains_2_(Csm2d)_mRNA	0.96	100	15	5	19	19	TCCTGTGCTGGTCCC
	Mus_musculus_receptor_accessory_protein_5_(Reep5)_mRNA	0.96	94.74	19	5	23	23	TCTGTGCTGGTCCCCTT
	Mus_musculus_integrin_alpha_D_(Itgad)_mRNA	0.96	100	15	1	15	15	TTCGCTGTGCTGG
	Mus_musculus_shisa_homolog_7_(Xenopus_laevis)_mRNA	0.96	100	15	8	22	22	TGCTGTGCTCCCCT
	Mus_musculus_killer_cell_lectin-like_receptor_subfamily_C_member_1_(Klrc1)_transcript_variant_1_mRNA	0.96	100	15	5	19	19	TCCTGTGCTGGTCCC
	Mus_musculus_killer_cell_lectin-like_receptor_subfamily_C_member_1_(Klrc1)_transcript_variant_2_mRNA	0.96	100	15	5	19	19	TCTGTGCTGGTCCC
	PREDICTED: Mus_musculus_CUB_and_Sushi_multiple_domains_2_(Csm2d)_mRNA	0.96	100	15	5	19	19	TCTGTGCTGGTCCC
	Mus_musculus_Sec61_alpha_subunit_2_(S_cerevisiae)_mRNA	0.96	100	15	10	24	24	TGTTGCTGCCCTTT
	Mus_musculus_shughoshin-like_1_(S_pombe)_mRNA	3.8	100	14	12	25	25	TGTTGCTGCCCTTT
	Mus_musculus_phospholipase_A2_group_VI_(Pla2g6)_transcript_variant_2_mRNA	3.8	100	14	6	19	19	CTGTGCTGGTCCC
	Mus_musculus_phospholipase_A2_group_VI_(Pla2g6)_transcript_variant_3_mRNA	3.8	100	14	6	19	19	CTGTGCTGGTCCC
	Mus_musculus_phospholipase_A2_group_VI_(Pla2g6)_transcript_variant_1_mRNA	3.8	100	14	6	19	19	CTGTGCTGGTCCC
	Mus_musculus_phospholipase_A2_group_VI_(Pla2g6)_transcript_variant_4_mRNA	3.8	100	14	6	19	19	CTGTGCTGGTCCC
	Mus_musculus_prostaglandin_E_receptor_2_(subtype_EP2)_mRNA	3.8	100	14	7	20	20	CTGTGCTGGTCCC
	Mus_musculus_fidgetin-like_1_(Fglt1)_transcript_variant_1_mRNA	3.8	100	14	4	17	17	GTCTGTGCTGGTT
	Mus_musculus_fidgetin-like_1_(Fglt1)_transcript_variant_2_mRNA	3.8	100	14	4	17	17	GTCTGTGCTGGTT
Agtr1a	Agtr1a_F	Mus_musculus_angiotensin_II_receptor_type_1a_(Agtr1a)_mRNA	7.97E-07	100	25	1	25	GTGTGTGAGCAACTCAACCAGA
	Mus_musculus_NCK_interacting_protein_with_SH3_domain_(Nckippsd)_mRNA	2.9	94.44	18	5	22	22	GTGAGCAACTCAACC
	Mus_musculus_UDP-N-acetyl-alpha-D-galactosamine:polypeptide_N-acetylgalactosaminyltransferase_2_(Galt2)_mRNA	2.9	100	14	11	24	24	CCACTCAACCAG
	Mus_musculus_fibroblast_growth_factor_3_(Fgf3)_mRNA	2.9	100	14	4	17	17	TCTGAGCAACTCA
	Mus_musculus_heterogeneous_nuclear_ribonucleoprotein_F_(Hnmpf)_transcript_variant_7_mRNA	2.9	100	14	3	16	16	CTGAGCAACTCA
	Mus_musculus_serine_(or_cysteine)_peptidase_inhibitor_clade_B_member_5_(Serpinb5)_mRNA	2.9	100	14	12	25	25	CAACTCAACCAGA
	Mus_musculus_N(alpha)-acetyltransferase_30_NatC_catalytic_subunit_(Naa30)_mRNA	2.9	100	14	10			

Agtr1a_R	Mus_musculus_angiotensin_II_receptor_type_1a_(Agtr1a), mRNA	9.01E-11	100	32	1	32	TAACTCACAGCAACCCCTCAAGAAAGCCATCA	
	Mus_musculus_ubiquitin_specific_peptidase_37_(Usp37), mRNA	0.02	100	18	2	19	AACTCAGCAACCTCC	
	Mus_musculus_histone_cluster_3_H2ba_(Hist3h2ba), mRNA	0.08	100	17	16	32	CTCCAAGAAAGCCATCA	
	Mus_musculus_calmin_(Clmm)_transcript_variant_1_mRNA	1.3	100	15	10	24	GCAACCTCAAGAA	
	Mus_musculus_calmin_(Clmm)_transcript_variant_2_mRNA	1.3	100	15	10	24	GCAACCTCAAGAA	
	Mus_musculus_kelch-like_10_(Drosophila),(Klhl10), mRNA	1.3	100	15	2	16	AACTCAGCAACCC	
	Mus_musculus_myosin_heavy_polypeptide_4_skeletal_muscle_(Myh4), mRNA	1.3	100	15	18	32	CAAAGAAAGCCATCA	
	Mus_musculus_myosin_heavy_polypeptide_1_skeletal_muscle_adult_(Myh1), mRNA	1.3	100	15	18	32	CAAAGAAAGCCATCA	
	Mus_musculus_ring_finger_protein_130_(Rnf130), mRNA	1.3	100	15	18	32	CAAAGAAAGCCATCA	
	Mus_musculus_zinc_finger_protein_512_(Zfp512), mRNA	1.3	100	15	5	19	TCACAGCAACCTCC	
	Mus_musculus_mediator_complex_subunit_14_(Med14)_transcript_variant_2_mRNA	5	100	14	16	29	CTCCAAGAAAGCCA	
	Mus_musculus_mediator_complex_subunit_14_(Med14)_transcript_variant_1_mRNA	5	100	14	16	29	CTCCAAGAAAGCCA	
	Mus_musculus_PRR19/PSO4_pre-mRNA_processing_factor_19_homolog_(S_cerevisiae)(Prpf19)_transcript_variant_3_mRNA	5	100	14	3	16	ACTCAGCAACCC	
	Mus_musculus_PRR19/PSO4_pre-mRNA_processing_factor_19_homolog_(S_cerevisiae)(Prpf19)_transcript_variant_2_mRNA	5	100	14	3	16	ACTCAGCAACCC	
	Mus_musculus_PRR19/PSO4_pre-mRNA_processing_factor_19_homolog_(S_cerevisiae)(Prpf19)_transcript_variant_1_mRNA	5	100	14	3	16	ACTCAGCAACCC	
	Mus_musculus_metastasis_associated_lung_adenocarcinoma_transcript_1_(non-coding_RNA)(Malat1)_non-coding_RNA	5	100	14	12	25	AACTCAGCAAGAA	
	Mus_musculus_ATPase_class_I_type_8B_member_1_(Atp8b1), mRNA	5	100	14	19	32	CAAGAAGCCATCA	
	Mus_musculus_predicted_gene_10556_(Gm10556), non-coding_RNA	5	100	14	19	32	CAAGAAGCCATCA	
	Mus_musculus_[3]mbt-like_2_(Drosophila)(L3mbtl2), mRNA	5	100	14	16	29	CTCCAAGAAAGCCA	
	Mus_musculus_solute_carrier_family_1_(glial_high_affinity_glutamate_transporter)_member_3_(Slc1a3), mRNA	5	100	14	8	21	CAGCAACCTCCAA	
Bdkrb2	Bdkrb2_F	Mus_musculus_bradykinin_receptor_beta_2_(Bdkrb2), mRNA	7.02E-19	100	46	1	46	TGCCACCAGGCGCTCTTGGCATCAAATGTTCACGTCCACC
	PREDICTED: Mus_musculus_uncharacterized_LOC100862575_(LOC100862575), miscRNA	2.2	100	15	5	19	CACCGCGCTCTCT	
	Mus_musculus_cytochrome_P450_family_11_subfamily_b_polypeptide_2_(Cyp11b2)_nuclear_gene_encoding_mitochondrial_protein_mRNA	2.2	100	15	21	35	GGCATGAAATGTTC	
	Mus_musculus_endoplasmic_reticulum_metalloproteinase_1_(Ermp1), mRNA	8.8	100	14	4	17	CCACCGCGCTCC	
	Mus_musculus_mindbomb_homolog_1_(Drosophila)(Mib1), mRNA	8.8	100	14	13	26	CCTCTTGGGCATC	
	Mus_musculus_transmembrane_protein_63b_(Tmem63b), mRNA	8.8	100	14	32	45	GTCAACGTCACCA	
	Mus_musculus_lectin_mannose-binding_2_(Lman2), mRNA	8.8	100	14	12	25	GCCTCTTGGCATC	
	Mus_musculus_HECT_domain_containing_1_(Hectd1), mRNA	8.8	100	14	9	22	GGCGCTCTTGG	
	Mus_musculus_chromobox_homolog_4_(Drosophila_Pc_class)(Cbx4), mRNA	8.8	100	14	3	16	CCACCGCGCTCC	
	Mus_musculus_sterile_alpha_and_HEAT/Armadillo_motif_containing_1_(Sarm1)_transcript_variant_1_mRNA	8.8	100	14	12	25	GCCTCTTGGCATC	
	Mus_musculus_sterile_alpha_and_HEAT/Armadillo_motif_containing_1_(Sarm1)_transcript_variant_2_mRNA	8.8	100	14	12	25	GCCTCTTGGCATC	
	Mus_musculus_calcium/calmodulin-dependent_protein_kinase_II_beta_(Camk2b)_transcript_variant_2_mRNA	8.8	100	14	4	17	CACCGCGCTCC	
	Mus_musculus_ELOVL_family_member_5_(elongation_of_long_chain_fatty_acids_(yeast))(Elov5), mRNA	8.8	100	14	22	35	GATCGAAATGTT	
	Mus_musculus_dyrenin_axonemal_heavy_chain_10_(Dnaht10), mRNA	8.8	100	14	19	32	TTGGCATGAAATG	
	Mus_musculus_phosphatidylinositol-4-phosphate_5-kinase-like_1_(Pip5k1), mRNA	8.8	94.44	18	7	24	CGCGGCTCTTGGCA	
Bdkrb2_R	Mus_musculus_bradykinin_receptor_beta_2_(Bdkrb2), mRNA	3.27E-21	100	50	1	50	ATGCCCTGCTCTGGAAGCTACTCGGGTTCTGTGCGTGCATGACCCAT	
	Mus_musculus_ankyrin_repeat_domain_29_(Ankrd29), mRNA	0.041	100	18	2	19	GTCCCTGCTCTGGAAGC	
	PREDICTED: Mus_musculus_acetyl-CoA_carboxylase_1-like_(LOC100862524), mRNA	0.64	100	16	6	21	CTGCTCTGGAAGTCA	
	Mus_musculus_ferritin_mitochondrial(Fmtl)_nuclear_gene_encoding_mitochondrial_protein_mRNA	0.64	100	16	2	17	TCGCCCTGCTGGAAG	
	Mus_musculus_acetyl-Coenzyme_A_carboxylase_alpha_(Acaca), mRNA	0.64	100	16	6	21	CTGCTCTGGAAGTCA	
	Mus_musculus_translocase_of_inner_mitochondrial_membrane_13_homolog_(yeast)(Timm13)_nuclear_gene_encoding_mitochondrial_protein_mRNA	0.64	100	16	1	16	ATGCCCTGCTCTGGAAG	
	PREDICTED: Mus_musculus_RIKEN_cDNA_5730409K12_gene_(5730409K12Rik), miscRNA	0.64	95	20	5	24	CCTGCTCTGGAAGTACT	
	PREDICTED: Mus_musculus_RIKEN_cDNA_5730409K12_gene_(5730409K12Rik), miscRNA	0.64	95	20	5	24	CCTGCTCTGGAAGTACT	
	Mus_musculus_family_with_sequence_similarity_89_member_A_(Fam89a), mRNA	0.64	100	16	3	18	GCCTCTGCTGGAAG	
	Mus_musculus_zinc_finger_protein_518a_(Zfp518a), mRNA	2.5	100	15	13	27	TGGAAGTACTCGGG	
	Mus_musculus_RIKEN_cDNA_4930542C21_gene_(4930542C21Rik)_non-coding_RNA	2.5	100	15	6	20	CTGCTCTGGAAGT	
	Mus_musculus_Rho-associated_coiled-coil_containing_protein_kinase_2_(Rock2), mRNA	2.5	100	15	5	19	CTGCTCTGGAAGC	
	Mus_musculus_ligase_III_DNA_ATP-dependent_(Lig3)_nuclear_gene_encoding_mitochondrial_protein_mRNA	2.5	100	15	3	17	GCCTCTGCTGGAAG	
	Mus_musculus_olfactory_receptor_395_(Olf395), mRNA	2.5	100	15	1	15	ATGCCCTGCTCTGG	
	Mus_musculus_CUB_domain_containing_protein_1_(Cdcp1), mRNA	2.5	100	15	9	23	CTCTGGAAGTACT	
	Mus_musculus_single_stranded_DNA_binding_protein_4_(Ssbp4), mRNA	2.5	94.74	19	9	27	CTCTGGAAGTACTCGGG	
	Mus_musculus_purinergic_receptor_P2Y_G-protein_coupled_14_(P2ry14)_transcript_variant_1_mRNA	2.5	100	15	3	17	GCCTCTGCTGGAAG	
	Mus_musculus_purinergic_receptor_P2Y_G-protein_coupled_14_(P2ry14)_transcript_variant_2_mRNA	2.5	100	15	3	17	GCCTCTGCTGGAAG	
	Mus_musculus_transmembrane_protein_191C_(Tmem191c), mRNA	2.5	100	15	6	20	CTGCTCTGGAAGT	
	Mus_musculus_cytohesin_1_(Cyth1)_transcript_variant_3_mRNA	2.5	94.74	19	4	22	CCTGCTCTGGAAGTACT	
Calcr1	Calcr1_F	Mus_musculus_calcitonin_receptor-like_(Calcr1), mRNA	9.01E-11	100	32	1	32	CTGGAGCGGATGCTATCGGAATGACGTGG
	PREDICTED: Mus_musculus_predicted_gene_10847_(Gm10847), miscRNA	5	100	14	2	15	TGGAGCGATGGCT	
	PREDICTED: Mus_musculus_predicted_gene_10847_(Gm10847), miscRNA	5	100	14	2	15	TGGAGCGATGGCT	
	Mus_musculus_thyroid_hormone_receptor_interactor_11_(Trip11), mRNA	5	100	14	13	26	GCTATGCTGGAATG	
	Mus_musculus_VPS33B_interacting_protein_apical-basolateral_polarity_regulator_(Vpar)_transcript_variant_3_mRNA	5	100	14	19	32	CTGAATGACGTGG	
	Mus_musculus_VPS33B_interacting_protein_apical-basolateral_polarity_regulator_(Vpar)_transcript_variant_1_mRNA	5	100	14	19	32	CTGAATGACGTGG	
	Mus_musculus_VPS33B_interacting_protein_apical-basolateral_polarity_regulator_(Vpar)_transcript_variant_2_mRNA	5	100	14	19	32	CTGAATGACGTGG	
	Mus_musculus_solute_carrier_family_46_member_1_(Slc46a1), mRNA	5	94.44	18	7	24	CGGATGCTATGCTGGAA	
	Mus_musculus_neuron_navigator_3_(Nav3), mRNA	5	100	14	8	21	GGATGCTATGCTG	
	Mus_musculus_armadillo_repeat_containing_8_(Arm8c)_transcript_variant_2_mRNA	5	94.44	18	10	27	ATGGCTATGCTGGAATGA	
	Mus_musculus_glutamate_receptor_ionotropic_kainate_4_(Grik4), mRNA	5	100	14	10	23	ATGGCTATGCTGGA	
	Mus_musculus_a_disintegrin-like_and_metalloproteinase_(reprolysin_type)_with_thrombospondin_type_1_motif_17_(Adamt17), mRNA	5	100	14	9	22	GATGGCTATGCTGG	
	Mus_musculus_aristalexin-like_hormone_4_(Alx4), mRNA	5	100	14	11	24	TGGTATGCTGGAAG	
Calcr1_R	Mus_musculus_calcitonin_receptor-like_(Calcr1), mRNA	2.22E-07	100	26	1	26	ATGAGGAGCCCACTCAACAGCAGA	
	Mus_musculus_coiled-coil_domain_containing_90a_(Ccdc90a), mRNA	0.21	100	16	11	26	CCATTCAACAGCAGA	
	Mus_musculus_transmembrane_and_coiled-coil_domains_4_(Tmco4), mRNA	0.81	100	15	2	16	TGAGGAGCCCACTTC	
	Mus_musculus_WD_repeat_domain_13_(Wdr13)_transcript_variant_3_non-coding_RNA	3.2	100	14	11	24	CCATTCAACAGCA	
	Mus_musculus_WD_repeat_domain_13_(Wdr13)_transcript_variant_1_mRNA	3.2	100	14	11	24	CCATTCAACAGCA	
	Mus_musculus_protocadherin_beta_11_(Pcdhb11), mRNA	3.2	100	14	4	17	CAGGACCCCACTCA	
	Mus_musculus_active_BCR-related_gene_(Abr)_transcript_variant_1_mRNA	3.2	90.91	22	5	26	AGGACCCCACTCAACAGCAGA	
	Mus_musculus_active_BCR-related_gene_(Abr)_transcript_variant_3_mRNA	3.2	90.91	22	5	26	AGGACCCCACTCAACAGCAGA	
	Mus_musculus_active_BCR-related_gene_(Abr)_transcript_variant_2_mRNA	3.2	90.91	22	5	26	AGGACCCCACTCAACAGCAGA	
	Mus_musculus_exocyst_complex_component_8_(Exoc8), mRNA	3.2	100	14	2	15	TGAGGAGCCCACTTC	
	Mus_musculus_transmembrane_protein_200a_(Tmem200a), mRNA	3.2	94.44	18	4	21	CAGGACCCCACTCAACAA	
	Mus_musculus_forkhead_box_12_(Foxl2), mRNA	3.2	100	14	3	16	GCAGGACCCCACTTC	
	Mus_musculus_PNMA-like_1_(Pnma1), mRNA	3.2	100	14	5	18	AGGACCCCACTCA	
	Mus_musculus_RIKEN_cDNA_C330024D21_gene_(C330024D21Rik)_non-coding_RNA	3.2	100	14	11	24	CCATTCAACAGCA	
Ccr12	Ccr12_F	Mus_musculus_chemokine_(C-C_motif)_receptor-like_2_(Ccr12), mRNA	1.24E-09	100	30	1	30	AGCCTCGATGGAATCACTACAGTGGCC
	PREDICTED: Mus_musculus_uncharacterized_LOC100048499_(LOC100048499), miscRNA	1.1	100	15	13	27	ATAACTACACAGTGG	
	Mus_musculus_potassium_channel_tetramerisation_domain_containing_17_(Kctd17), mRNA	1.1	100	15	16	30	ACTACACAGTGGCC	
	Mus_musculus_microfibrillar-associated_protein_1A_(Mfap1a), mRNA	1.1	100	15	13	27	ATAACTACACAGTGG	
	PREDICTED: Mus_musculus_predicted_gene_12248_(Gm12248), miscRNA	4.4	94.44	18	9	26	ATGGATAACTACAGTGG	
	Mus_musculus_Pbx/knotted_1_homeobox_(Pknx1)_transcript_variant_1_mRNA	4.4	100	14	17	30	CTACACAGTGGCC	
	Mus_musculus_Pbx/knotted_1_homeobox_(Pknx1)_transcript_variant_2_non-coding_RNA	4.4	100	14	17	30	CTACACAGTGGCC	
	Mus_musculus_family_with_sequence_similarity_195_member_A_(Fam195a), mRNA	4.4	100	14	17	30	CTACACAGTGGCC	
	Mus_musculus_peroxisome_proliferator_activated_receptor_alpha_(Ppara)_transcript_variant_1_mRNA	4.4	100	14	17	30	CTACACAGTGGCC	
	Mus_musculus_peroxisome_proliferator_activated_receptor_alpha_(Ppara)_transcript_variant_2_mRNA	4.4	100	14	17	30	CTACACAGTGGCC	
	Mus_musculus_trafficking_particle_complex_9_(Trappc9)_transcript_variant_3_mRNA	4.4	100	14	17	30	CTACACAGTGGCC	
	Mus_musculus_spleen_tyrosine_kinase_(Syk)_transcript_variant_1_mRNA	4.4	94.44	18	13	30	ATAACTACACAGTGGCC	
	Mus_musculus_spleen_tyrosine_kinase_(Syk)_transcript_variant_2_mRNA	4.4	94.44	18	13	30	ATAACTACACAGTGGCC	
	PREDICTED: Mus_musculus_predicted_gene_12248_(Gm12248), miscRNA	4.4	94.44	18	9	26	ATGGATAACTACAGTGG	
	Mus_musculus_met_proto-oncogene_(Met), mRNA	4.4	100	14	15	28	AACTACACAGTGGC	
	Mus_musculus_RUN_domain_containing_3B_(Rundc3b), mRNA	4.4	100	14	15	28	AACTACACAGTGGC	
	Mus_musculus_RIKEN_cDNA_4933431E20_gene_(4933431E20Rik)_non-coding_RNA	4.4	100	14	17	30	CTACACAGTGGCC	
	Mus_musculus_interleukin_2_receptor_alpha_chain_(Il2ra), mRNA	4.4	100	14	16	29	AACTACACAGTGGC	
Ccr12_R	Mus_musculus_chemokine_(C-C_motif)_receptor-like_2_(Ccr12), mRNA	2.83E-06	100	24	1	24	CAAGCAAGTCTCTCAAACGCGC	
	Mus_musculus_T-box18_(Tbx18), mRNA	2.6	100	14	6	19	AACTCTCTCAAGC	
	Mus_musculus_T-box20_(Tbx20)_transcript_variant_1_mRNA	2.6	100	14	2	15	AGCAACTCTGCTC	
	Mus_musculus_ring_finger_protein_183_(Rnf183), mRNA	2.6	100	14	4	17	GCAACTCTCTCAA	
Cd97	Cd97_F	Mus_musculus_CD97_antigen_(Cd97)_transcript_variant_1_mRNA	5.56E-09	100	29	4	32	CAAAGGCTGGAATGATCAACAGGTGGG
	Mus_musculus_CD97_antigen_(Cd97)_transcript_variant_3_mRNA	5.56E-09	100	29	4	32	CAAAGGCTGGAATGATCAACAGGTGGG	
	Mus_musculus_CD97_antigen_(Cd97)_transcript_variant_2_mRNA	5.56E-09	100	29	4	32	CAAAGGCTGGAATGATCAACAGGTGGG	
	Mus_musculus_CD97_antigen_(Cd97)_transcript_variant_4_mRNA	5.56E-09	100	29	4	32	CAAAGGCTGGAATGATCAACAGGTGGG	
	Mus_musculus_protocadherin_beta_8_(Pcdhb8), mRNA	1.3	100	15	17	31	TGATCAAAGGTGG	

		Mus_musculus_receptor_transporter_protein_4_(Rtp4),_mRNA	1.3	100	15	15	29	ATTGATCAACAAGT
		Mus_musculus_transmembrane_protein_107_(Tmem107),_transcript_variant_1,_mRNA	1.3	100	15	1	15	GGACCAAGCTGGAA
		Mus_musculus_transmembrane_protein_107_(Tmem107),_transcript_variant_2,_mRNA	1.3	100	15	1	15	GGACCAAGCTGGAA
		Mus_musculus_kelch-like_ECH-associated_protein_1_(Keap1),_transcript_variant_1,_mRNA	1.3	100	15	10	24	CTGGAATGATCACC
		Mus_musculus_kelch-like_ECH-associated_protein_1_(Keap1),_transcript_variant_2,_mRNA	1.3	100	15	10	24	CTGGAATGATCACC
		Mus_musculus_kelch-like_ECH-associated_protein_1_(Keap1),_transcript_variant_3,_mRNA	1.3	100	15	10	24	CTGGAATGATCACC
		Mus_musculus_kelch-like_ECH-associated_protein_1_(Keap1),_transcript_variant_4,_mRNA	1.3	100	15	10	24	CTGGAATGATCACC
		Mus_musculus_snail_homolog_1_(Drosophila)_(Snai1),_mRNA	1.3	100	15	1	15	GGACCAAGCTGGAA
		Mus_musculus_biglycan_(Bgn),_mRNA	5	100	14	19	32	ATCACCAAGGTGG
		Mus_musculus_predicted_gene_608_(Gm608),_mRNA	5	100	14	17	30	TGATCACAAGGTG
		Mus_musculus_ubiquitin-conjugating_enzyme_E2_variant_2_(Ube2v2),_transcript_variant_1,_mRNA	5	100	14	4	17	CCAAGGTGGAAAT
		Mus_musculus_ubiquitin-conjugating_enzyme_E2_variant_2_(Ube2v2),_transcript_variant_2,_mRNA	5	100	14	4	17	CCAAGGTGGAAAT
		Mus_musculus_G_two_5_phase_expressed_protein_1_(Gtse1),_transcript_variant_2,_mRNA	5	100	14	1	14	GGACCAAGCTGGAA
		Mus_musculus_G_two_5_phase_expressed_protein_1_(Gtse1),_transcript_variant_3,_mRNA	5	100	14	1	14	GGACCAAGCTGGAA
		Mus_musculus_uncharacterized_A630020A06_(A630020A06),_non-coding_RNA	5	100	14	19	32	ATCACCAAGGTGG
Cd97_R		Mus_musculus_Cd97_antigen_(Cd97),_transcript_variant_1,_mRNA	2.41E-11	100	33	1	33	TGACCAGCTTGGCCTCAATGGCTCAGTACC
		Mus_musculus_Cd97_antigen_(Cd97),_transcript_variant_3,_mRNA	2.41E-11	100	33	1	33	TGACCAGCTTGGCCTCAATGGCTCAGTACC
		Mus_musculus_Cd97_antigen_(Cd97),_transcript_variant_2,_mRNA	2.41E-11	100	33	1	33	TGACCAGCTTGGCCTCAATGGCTCAGTACC
		Mus_musculus_Cd97_antigen_(Cd97),_transcript_variant_4,_mRNA	2.41E-11	100	33	1	33	TGACCAGCTTGGCCTCAATGGCTCAGTACC
		Mus_musculus_excision_repair_cross-complementing_rodent_repair_deficiency_complementation_group_4_(Erc44),_mRNA	1.3	100	15	5	19	CAGTCTGGCCATCT
		Mus_musculus_5'-nucleotidase_domain_containing_2_(Nt5dc2),_mRNA	1.3	100	15	4	18	CCAGCTTGGCCATCT
		Mus_musculus_folliculin_interacting_protein_1_(Fnip1),_mRNA	1.3	100	15	3	17	ACCAAGCTTGGCCATCT
		Mus_musculus_PAN3_polyA_specific_ribonuclease_subunit_homolog_(S_cerevisiae)_(Pan3),_mRNA	1.3	100	15	19	33	TAATGGCTCAGTACC
		Mus_musculus_Rap1_GTPase-activating_protein_(Rap1gap),_transcript_variant_2,_mRNA	1.3	100	15	3	17	ACCAAGCTTGGCCATCT
		Mus_musculus_Rap1_GTPase-activating_protein_(Rap1gap),_transcript_variant_1,_mRNA	1.3	100	15	3	17	ACCAAGCTTGGCCATCT
		Mus_musculus_Rap1_GTPase-activating_protein_(Rap1gap),_transcript_variant_3,_mRNA	1.3	100	15	3	17	ACCAAGCTTGGCCATCT
		PREDICTED: Mus_musculus_RIKEN_cDNA_4930547M16_gene_(4930547M16RIK),_miscRNA	5.3	100	14	13	26	CCATCTTAAGTCT
		Mus_musculus_oxyesterol_binding_protein-like_1A_(Osbp1a),_transcript_variant_7,_non-coding_RNA	5.3	100	14	3	16	ACCAAGCTTGGCCATCT
		Mus_musculus_oxyesterol_binding_protein-like_1A_(Osbp1a),_transcript_variant_5,_mRNA	5.3	100	14	3	16	ACCAAGCTTGGCCATCT
		Mus_musculus_oxyesterol_binding_protein-like_1A_(Osbp1a),_transcript_variant_6,_mRNA	5.3	100	14	3	16	ACCAAGCTTGGCCATCT
		Mus_musculus_oxyesterol_binding_protein-like_1A_(Osbp1a),_transcript_variant_4,_mRNA	5.3	100	14	3	16	ACCAAGCTTGGCCATCT
		Mus_musculus_oxyesterol_binding_protein-like_1A_(Osbp1a),_transcript_variant_3,_mRNA	5.3	100	14	3	16	ACCAAGCTTGGCCATCT
		Mus_musculus_oxyesterol_binding_protein-like_1A_(Osbp1a),_transcript_variant_2,_mRNA	5.3	100	14	3	16	ACCAAGCTTGGCCATCT
		Mus_musculus_oxyesterol_binding_protein-like_1A_(Osbp1a),_transcript_variant_1,_mRNA	5.3	100	14	9	22	TTTGGCCATCTCAAT
Celsr2	Celsr2_F	Mus_musculus_transmembrane_protein_232_(Tmem232),_mRNA	1.15E-13	100	37	1	37	TGGTGACAACCTGTACAATGTGTGACTGGAACCA
		Mus_musculus_cadherin_EGF_LAG_seven-pass_G_type_receptor_2_(flamingo_homolog_Drosophila)_(Celsr2),_transcript_variant_1,_mRNA	1.15E-13	100	37	1	37	TGGTGACAACCTGTACAATGTGTGACTGGAACCA
		Mus_musculus_cadherin_EGF_LAG_seven-pass_G_type_receptor_2_(flamingo_homolog_Drosophila)_(Celsr2),_transcript_variant_2,_mRNA	1.15E-13	100	37	1	37	TGGTGACAACCTGTACAATGTGTGACTGGAACCA
		Mus_musculus_MOB_kinase_activator_3C_(Mob3c),_mRNA	0.099	95.24	21	6	26	ACAACGTACAATGTGTG
		Mus_musculus_ubiquitin_specific_peptidase_30_(Usp30),_mRNA	0.39	100	16	3	18	GTGACACTGTACAAA
		Mus_musculus_zinc_finger_DHCH_domain_containing_17_(Zdhc17),_mRNA	1.6	100	15	7	21	CAACTGTACAATGT
		Mus_musculus_RAD54_like_2_(S_cerevisiae)_(Rad54l2),_mRNA	1.6	100	15	23	37	TGTGACTGACACCA
		PREDICTED: Mus_musculus_predicted_gene_4673_(Gm4673),_miscRNA	1.6	100	15	19	33	TGTGTGACTGAA
		PREDICTED: Mus_musculus_RIKEN_cDNA_C230062116_gene_(C230062116RIK),_mRNA	1.6	100	15	6	20	ACAACGTACAATGT
		Mus_musculus_SR-related_CTD-associated_factor_8_(Scaf8),_mRNA	1.6	100	15	4	18	TGACAACCTGTACAAA
		Mus_musculus_melanocyte_proliferating_gene_1_(Myg1),_mRNA	1.6	100	15	11	25	GTACAATGTGTG
		PREDICTED: Mus_musculus_predicted_gene_4673_(Gm4673),_miscRNA	1.6	100	15	19	33	TGTGTGACTGAA
		PREDICTED: Mus_musculus_RIKEN_cDNA_C230062116_gene_(C230062116RIK),_mRNA	1.6	100	15	6	20	ACAACGTACAATGT
		Mus_musculus_EH_domain_binding_protein_1-like_1_(Ehbp1l1),_transcript_variant_A,_mRNA	6.1	100	14	24	37	GTGACTGACACCA
		Mus_musculus_zinc_finger_protein_616_(Zfp616),_mRNA	6.1	100	14	8	21	AAGTGTGACAAATG
		Mus_musculus_ADAMTS-like_5_(Adamts5),_transcript_variant_2,_mRNA	6.1	100	14	17	30	AATGTGTGACT
		Mus_musculus_ADAMTS-like_5_(Adamts5),_transcript_variant_1,_mRNA	6.1	100	14	17	30	AATGTGTGACT
		PREDICTED: Mus_musculus_predicted_gene_19934_(Gm19934),_miscRNA	6.1	100	14	3	16	GTACAACCTGTACAAA
		Mus_musculus_methylenetetrahydrofolate_dehydrogenase_(NADP+-dependent)_2-like_(Mthfd2l),_mRNA	6.1	100	14	16	29	AATGTGTGACT
		Mus_musculus_protein_kinase_C_zeta_(Prkcz),_transcript_variant_2,_mRNA	6.1	100	14	11	24	TGTACAATGTGTG
		Mus_musculus_protein_kinase_C_zeta_(Prkcz),_transcript_variant_1,_mRNA	6.1	100	14	11	24	TGTACAATGTGTG
Celsr2_R		Mus_musculus_cadherin_EGF_LAG_seven-pass_G_type_receptor_2_(flamingo_homolog_Drosophila)_(Celsr2),_transcript_variant_1,_mRNA	4.58E-09	100	29	1	29	AGCAATGACTGGACAGCTATTCTGTAG
		Mus_musculus_cadherin_EGF_LAG_seven-pass_G_type_receptor_2_(flamingo_homolog_Drosophila)_(Celsr2),_transcript_variant_2,_mRNA	4.58E-09	100	29	1	29	AGCAATGACTGGACAGCTATTCTGTAG
		Mus_musculus_centromere_protein_W_(Cenpw),_mRNA	0.26	100	16	2	17	GCAATGACTGGACAG
		Mus_musculus_chromodomain_helicase_DNA_binding_protein_1_(Chd1),_mRNA	1	100	15	11	25	GGACAGCTATTCTT
		Mus_musculus_lethal_giant_larvae_homolog_2_(Drosophila)_(Llg2),_transcript_variant_1,_mRNA	1	100	15	4	18	AATGACTGGACAGC
		Mus_musculus_lethal_giant_larvae_homolog_2_(Drosophila)_(Llg2),_transcript_variant_2,_mRNA	1	100	15	4	18	AATGACTGGACAGC
		Mus_musculus_succinate_dehydrogenase_complex_assembly_factor_2_(Sdhaf2),_nuclear_gene_encoding_mitochondrial_protein,_mRNA	4.1	100	14	1	14	AGCAATGACTGGGA
		Mus_musculus_H2A_histone_family_member_Y3_(H2afy3),_non-coding_RNA	4.1	100	14	6	19	TGACTGGGACAGCT
		Mus_musculus_SEC23A_(S_cerevisiae)_(Sec23a),_mRNA	4.1	90.91	22	8	29	ACTGGGACAGCTATTCTGTAG
		Mus_musculus_trafficking_protein_particle_complex_4_(Trappc4),_mRNA	4.1	100	14	10	23	TGGGACAGCTATTCT
		Mus_musculus_cell_adhesion_molecule-related/down-regulated_by_oncogenes_(Cdon),_mRNA	4.1	100	14	4	17	AATGACTGGACAGC
		Mus_musculus_chromodomain_protein_Y_chromosome-like_2_(Cdy2l),_mRNA	4.1	94.44	18	6	23	TGACTGGGACAGCTATTCT
		Mus_musculus_NLR_family_pyrrin_domain_containing_9B_(Nlrp9b),_mRNA	4.1	100	14	3	16	CAATGACTGGGACA
		Mus_musculus_a_disintegrin-like_and_metalloproteinase_(reprolysin_type)_with_thrombospondin_type_1_motif_3_(Adamts3),_transcript_variant_1,_mRNA	4.1	94.44	18	1	18	AGCAATGACTGGGACAGC
		Mus_musculus_a_disintegrin-like_and_metalloproteinase_(reprolysin_type)_with_thrombospondin_type_1_motif_3_(Adamts3),_transcript_variant_2,_mRNA	4.1	94.44	18	1	18	AGCAATGACTGGGACAGC
		Mus_musculus_predicted_gene_11756_(Gm11756),_mRNA	4.1	100	14	13	26	GACAGCTATTCTT
		Mus_musculus_predicted_gene_13871_(Gm13871),_mRNA	4.1	100	14	13	26	GACAGCTATTCTT
		Mus_musculus_predicted_gene_11757_(Gm11757),_mRNA	4.1	100	14	13	26	GACAGCTATTCTT
		Mus_musculus_predicted_gene_11758_(Gm11758),_mRNA	4.1	100	14	13	26	GACAGCTATTCTT
		Mus_musculus_deleted_in_bladder_cancer_1_(human)_(Dbc1),_mRNA	4.1	100	14	2	15	GCAATGACTGGGAC
Cmk1r1	Cmk1r1_F	Mus_musculus_chemokine-like_receptor_1_(Cmk1r1),_mRNA	6.45E-12	100	34	1	34	CTCCAAGAGATGGAGTACACGACGCTTCAACGAC
		Mus_musculus_expressed_sequence_A1646023_(A1646023),_mRNA	1.4	100	15	2	16	TCCAAGAGATGGAG
		Mus_musculus_PHD_finger_protein_16_(Phf16),_mRNA	1.4	100	15	3	17	TCCAAGAGATGGAG
		Mus_musculus_tripartite_motif-containing_66_(Trim66),_transcript_variant_3,_mRNA	1.4	100	15	8	22	GAGATGGATGACAGC
		Mus_musculus_tripartite_motif-containing_66_(Trim66),_transcript_variant_1,_mRNA	1.4	100	15	8	22	GAGATGGATGACAGC
		Mus_musculus_tripartite_motif-containing_66_(Trim66),_transcript_variant_2,_mRNA	1.4	100	15	8	22	GAGATGGATGACAGC
		Mus_musculus_URB1_ribosome_biogenesis_1_homolog_(S_cerevisiae)_(Urb1),_mRNA	5.6	100	14	3	16	CCAAGAGATGGAG
		Mus_musculus_mediator_complex_subunit_15_(Med15),_transcript_variant_1,_mRNA	5.6	100	14	3	16	CCAAGAGATGGAG
		Mus_musculus_coiled-coil_domain_containing_129_(Ccdc129),_mRNA	5.6	100	14	2	15	TCCAAGAGATGGAG
		Mus_musculus_solute_carrier_family_43_member_1_(Slc43a1),_transcript_variant_3,_mRNA	5.6	100	14	3	16	CCAAGAGATGGAG
		Mus_musculus_glutamyl-prolyl-tRNA_synthetase_(Eprs),_mRNA	5.6	100	14	9	22	AGATGGATGACAGC
		Mus_musculus_parathyroid_hormone_2_receptor_(Ph2r),_mRNA	5.6	100	14	5	18	AAAGAGATGGAGTA
		PREDICTED: Mus_musculus_dynein_axonemal_heavy_chain_14_(Dnahc14),_mRNA	5.6	100	14	1	14	CTCCAAGAGATGG
		Mus_musculus_proline_dehydrogenase_(Prodh),_nuclear_gene_encoding_mitochondrial_protein,_mRNA	5.6	100	14	4	17	CAAGAGATGGAGT
		Mus_musculus_nidogen_1_(Nid1),_mRNA	5.6	100	14	2	15	TCCAAGAGATGGAG
		Mus_musculus_FAT_tumor_suppressor_homolog_2_(Drosophila)_(Fat2),_mRNA	5.6	100	14	3	16	CCAAGAGATGGAG
		Mus_musculus_solute_carrier_family_5_(sodium/glucose_cotransporter),_member_11_(Slc5a11),_mRNA	5.6	100	14	1	14	CTCCAAGAGATGG
		Mus_musculus_cytoplasmic_polyadenylation_element_binding_protein_1_(Cpeb1),_transcript_variant_1,_mRNA	5.6	100	14	1	14	CTCCAAGAGATGG
		Mus_musculus_cytoplasmic_polyadenylation_element_binding_protein_1_(Cpeb1),_transcript_variant_2,_mRNA	5.6	100	14	1	14	CTCCAAGAGATGG
		Mus_musculus_cytoplasmic_polyadenylation_element_binding_protein_1_(Cpeb1),_transcript_variant_3,_mRNA	5.6	100	14	1	14	CTCCAAGAGATGG
Cmk1r1_R		Mus_musculus_chemokine-like_receptor_1_(Cmk1r1),_mRNA	0.005	95.45	22	1	22	GTAACGACAGCCNAGGACCA
		Mus_musculus_multiple_endocrine_neoplasia_1_(Men1),_transcript_variant_4,_mRNA	4.7	94.12	17	11	27	AGCCNAGGACCAAGGAC
		Mus_musculus_multiple_endocrine_neoplasia_1_(Men1),_transcript_variant_2,_mRNA	4.7	94.12	17	11	27	AGCCNAGGACCAAGGAC
		Mus_musculus_multiple_endocrine_neoplasia_1_(Men1),_transcript_variant_3,_mRNA	4.7	94.12	17	11	27	AGCCNAGGACCAAGGAC
		Mus_musculus_multiple_endocrine_neoplasia_1_(Men1),_transcript_variant_1,_mRNA	4.7	94.12	17	11	27	AGCCNAGGACCAAGGAC
Cchr2	Cchr2_F	Mus_musculus_corticotropin_releasing_hormone_receptor_2_(Cchr2),_mRNA	1.15E-13	100	37	1	37	TTTCAAGCTTCCCTCACTCACTGCAACACGCTTGG
		PREDICTED: Mus_musculus_RIKEN_cDNA_D130079A08_gene_(D130079A08RIK),_miscRNA	1.6	100	15	1	15	TTTCAAGCTTCCCTCACTCACTGCAACACGCTTGG
		PREDICTED: Mus_musculus_RIKEN_cDNA_D130079A08_gene_(D130079A08RIK),_miscRNA	1.6	100	15	1	15	TTTCAAGCTTCCCTCACTCACTGCAACACGCTTGG
		Mus_musculus_Son_DNA_binding_protein_(Son),_transcript_variant_1,_mRNA	1.6	94.74	19	16	34	CACTGCAACACGCTT
		Mus_musculus_RIKEN_cDNA_1700017B05_gene_(1700017B05RIK),_mRNA	1.6	100	15	4	18	AGAGTCCCTCACT
		Mus_musculus_zinc_finger_MYM-type_3_(Zmy3),_transcript_variant_2,_mRNA	6.1	100	14	10	23	CTCACTCACTGCT
		Mus_musculus_zinc_finger_MYM-type_3_(Zmy3),_transcript_variant_1,_mRNA	6.1	100	14	10	23	CTCACTCACTGCT

		Mus_musculus_solute_carrier_family_43_member_2_(Slc43a2)_transcript_variant_3_mRNA	2.3	100	14	8	21	CTTGTCTCTCCC
		Mus_musculus_solute_carrier_family_43_member_2_(Slc43a2)_transcript_variant_2_mRNA	2.3	100	14	8	21	CTTGTCTCTCCC
		Mus_musculus_olfactory_receptor_986_(Olfr986)_mRNA	2.3	100	14	7	20	CCTTGCTCTTCC
		Mus_musculus_tyrosine_kinase_2_(Tyk2)_transcript_variant_1_mRNA	2.3	100	14	7	20	CCTTGCTCTTCC
		Mus_musculus_tyrosine_kinase_2_(Tyk2)_transcript_variant_2_mRNA	2.3	100	14	7	20	CCTTGCTCTTCC
		Mus_musculus_latrophilin_1_(Lphn1)_mRNA	2.3	100	14	4	17	GTCTCTGTCTCT
		Mus_musculus_tubulin_tyrosine_ligase-like_family_member_3_(Ttl3)_transcript_variant_2_mRNA	2.3	100	14	5	18	TCCTCTGTCTCT
		Mus_musculus_actin_related_protein_2/3_complex_subunit_4_(Arpc4)_transcript_variant_2_mRNA	2.3	100	14	5	18	TCCTCTGTCTCT
		Mus_musculus_actin_related_protein_2/3_complex_subunit_4_(Arpc4)_transcript_variant_3_mRNA	2.3	100	14	5	18	TCCTCTGTCTCT
		Mus_musculus_actin_related_protein_2/3_complex_subunit_4_(Arpc4)_transcript_variant_1_mRNA	2.3	100	14	5	18	TCCTCTGTCTCT
		Mus_musculus_WAS_protein_family_member_2_(Wasf2)_mRNA	2.3	94.44	18	4	21	GTCTCTGTCTCTCCC
		Mus_musculus_FH2_domain_containing_1_(Fhdci)_transcript_variant_1_mRNA	2.3	100	14	6	19	CCTTGCTCTTCC
F2r1l	F2r1l_F	Mus_musculus_coagulation_factor_1_(thrombin)_receptor-like_1_(F2r1l)_mRNA	1.25E-20	100	49	1	49	GGACCGAAGCTTGACCCGGACGCAACAACAGT
		Mus_musculus_akirin_1_(Akin1)_mRNA	0.62	100	16	27	42	AAAGGAGAAAGCT
		Mus_musculus_predicted_gene_5622_(Gm5622)_mRNA	2.4	94.74	19	27	45	AACAACGTAAGGAGAA
		PREDICTED: Mus_musculus_predicted_gene_7995_(Gm7995)_mRNA	2.4	94.74	19	27	45	AACAACGTAAGGAGAA
		Mus_musculus_chemokine_(C_C_motif)_ligand_9_(Ccl9)_mRNA	2.4	94.74	19	30	48	ACAACGTAAGGAGAACT
		Mus_musculus_vesicle-associated_membrane_protein_1_(Vamp1)_transcript_variant_1_mRNA	2.4	100	15	29	43	CAACGTAAGGAGAA
		Mus_musculus_vesicle-associated_membrane_protein_1_(Vamp1)_transcript_variant_2_mRNA	2.4	100	15	29	43	CAACGTAAGGAGAA
		Mus_musculus_tyrosine_3-monooxygenase/tryptophan_5-monooxygenase_activation_protein_gamma_polypeptide_(Ywhag)_mRNA	2.4	100	15	29	43	CAACGTAAGGAGAA
		Mus_musculus_myeloid_cell_leukemia_sequence_1_(Mcl1)_nuclear_gene_encoding_mitochondrial_protein_mRNA	2.4	100	15	29	43	CAACGTAAGGAGAA
		Mus_musculus_RIKEN_cDNA_2210018M11_gene_(2210018M11RIK)_mRNA	2.4	100	15	28	42	AACAACGTAAGGAGAA
		Mus_musculus_fibroblast_growth_factor_6_(Fgf6)_mRNA	2.4	100	15	30	44	AACAACGTAAGGAGAA
		Mus_musculus_CD1d2_antigen_(Cd1d2)_mRNA	9.6	100	14	36	49	AAAGGAGAAAGCT
		Mus_musculus_spermatogenesis_associated_13_(Spata13)_mRNA	9.6	100	14	5	18	CGAGAACCTTGAC
		Mus_musculus_tetratricopeptide_repeat_domain_18_(Ttc18)_transcript_variant_2_mRNA	9.6	100	14	33	46	AGTAAGGAGAAAG
		Mus_musculus_tetratricopeptide_repeat_domain_18_(Ttc18)_transcript_variant_1_mRNA	9.6	100	14	33	46	AGTAAGGAGAAAG
		Mus_musculus_tetratricopeptide_repeat_domain_18_(Ttc18)_transcript_variant_3_mRNA	9.6	100	14	33	46	AGTAAGGAGAAAG
		Mus_musculus_ubiquitin-conjugating_enzyme_E2N_(Ube2n)_mRNA	9.6	100	14	36	49	AAAGGAGAAAGCT
		Mus_musculus_CD1d2_antigen_(Cd1d2)_non-coding_RNA	9.6	100	14	36	49	AAAGGAGAAAGCT
		Mus_musculus_olfactory_receptor_1143_(Olfr1143)_mRNA	9.6	100	14	32	45	CAGTAAGGAGAA
		Mus_musculus_polycystic_kidney_and_hepatic_disease_1_(Pkhd1)_mRNA	9.6	100	14	34	47	GTAAAGGAGAAAGT
F2r1l	F2r1l_R	Mus_musculus_coagulation_factor_1_(thrombin)_receptor-like_1_(F2r1l)_mRNA	3.27E-21	100	50	1	50	CTGGTCTCTGACCGGACCGGAACTTGAC
		Mus_musculus_zinc_finger_protein_740_(Zfp740)_mRNA	0.64	100	16	15	30	CGGGACGCAACAACA
		b2_erythroblastic_leukemia_viral_oncogene_homolog_2_neuro/glioblastoma_derived_oncogene_homolog_(avian)_((Erbb2))_mRNA	0.64	100	16	1	16	CTGGTCTCTGACGAGC
		Mus_musculus_kinesin_family_member_17_(Kif17)_transcript_variant_1_mRNA	0.64	100	16	7	22	CTCTGACGCGGACC
		Mus_musculus_cadherin_EGF_LAG_seven-pass_G-type_receptor_2_(flamingo_homolog_Drosophila)_((Celsr2))_transcript_variant_1_mRNA	0.64	95	20	1	20	CTCGTCTCTGACGCGGA
		Mus_musculus_cadherin_EGF_LAG_seven-pass_G-type_receptor_2_(flamingo_homolog_Drosophila)_((Celsr2))_transcript_variant_2_mRNA	0.64	95	20	1	20	CTCGTCTCTGACGCGGA
		Mus_musculus_HEAT_repeat_containing_5A_(Heat5a)_mRNA	2.5	100	15	2	16	TCGGTCTCTGACGAGC
		Mus_musculus_trans-acting_transcription_factor_6_(Sp6)_mRNA	2.5	100	15	7	21	CTCTGACGCGGAC
		Mus_musculus_protein_phosphatase_1_regulatory_subunit_9B_(Ppp1r9b)_mRNA	2.5	100	15	5	19	GTCTCTGACCGCG
		Mus_musculus_ubiquitin_specific_peptidase_29_(Usp29)_mRNA	2.5	100	15	9	23	CTCTGACGCGGACG
		Mus_musculus_ORAI_calcium_release-activated_calcium_modulator_1_(Orai1)_mRNA	2.5	94.74	19	3	21	CGGTCTCTGACGCGGAC
		Mus_musculus_ATG2_autophagy_related_2_homolog_A_(S_cerevisiae)_((Atg2a))_mRNA	9.9	100	14	13	26	GACCGGACCGGAGA
		Mus_musculus_leucine-rich_PPR_motif_containing_(Lrpprc)_mRNA	9.9	100	14	6	19	TCTCTGACGCGCG
		Mus_musculus_histone_deacetylase_7_(Hdac7)_transcript_variant_2_mRNA	9.9	100	14	5	18	GTCTCTGACGCGC
		Mus_musculus_histone_deacetylase_7_(Hdac7)_transcript_variant_3_mRNA	9.9	100	14	5	18	GTCTCTGACGCGC
		Mus_musculus_histone_deacetylase_7_(Hdac7)_transcript_variant_1_mRNA	9.9	100	14	5	18	GTCTCTGACGCGC
		Mus_musculus_spermatogenesis_associated_13_(Spata13)_mRNA	9.9	100	14	22	35	CGAGAACCTTGAC
		Mus_musculus_elongation_factor_RNA_polymerase_II_2_(Eif2)_mRNA	9.9	94.44	18	1	18	CTGGTCTCTGACGCGC
		Mus_musculus_RIKEN_cDNA_4933426M11_gene_(4933426M11RIK)_transcript_variant_2_mRNA	9.9	100	14	4	17	GTCTCTGACGCGC
		Mus_musculus_RIKEN_cDNA_4933426M11_gene_(4933426M11RIK)_transcript_variant_1_mRNA	9.9	100	14	4	17	GTCTCTGACGCGC
Gabbr1_F	Gabbr1_F	Mus_musculus_gamma-aminobutyric_acid_(GABA)_B_receptor_1_(Gabbr1)_mRNA	3.35E-10	100	31	1	31	TGGTGGACTTTTCTATGACCGGAAGCCCG
		Mus_musculus_calcium_sensing_receptor_(Casr)_mRNA	4.7	100	14	4	17	TGGGACTTTCTAT
		Mus_musculus_B_lymphoid_kinase_(Btk)_mRNA	4.7	100	14	4	17	TGGGACTTTCTAT
		Mus_musculus_veriscan_(Vcan)_transcript_variant_1_mRNA	4.7	100	14	6	19	GGACTTTCTATGA
		Mus_musculus_veriscan_(Vcan)_transcript_variant_3_mRNA	4.7	100	14	6	19	GGACTTTCTATGA
		Mus_musculus_veriscan_(Vcan)_transcript_variant_2_mRNA	4.7	100	14	6	19	GGACTTTCTATGA
		Mus_musculus_veriscan_(Vcan)_transcript_variant_4_mRNA	4.7	100	14	6	19	GGACTTTCTATGA
		Mus_musculus_Bardet-Biedl_syndrome_10_(human)_((Bbs10))_mRNA	4.7	100	14	5	18	GGGACTTTTCTATG
		Mus_musculus_ATPase_Ca++_sequestering_(Atp2c1)_transcript_variant_2_mRNA	4.7	100	14	4	17	TGGGACTTTCTAT
		Mus_musculus_ATPase_Ca++_sequestering_(Atp2c1)_transcript_variant_3_mRNA	4.7	100	14	4	17	TGGGACTTTCTAT
		Mus_musculus_ATPase_Ca++_sequestering_(Atp2c1)_transcript_variant_1_mRNA	4.7	100	14	4	17	TGGGACTTTCTAT
		Mus_musculus_kinase_non_catalytic_C-lobe_domain_(KIND)_containing_1_(Kndc1)_mRNA	4.7	100	14	4	17	TGGGACTTTCTAT
		Mus_musculus_NADH_dehydrogenase_(ubiquinone)_1_beta_subcomplex_5_(Ndufb5)_nuclear_gene_encoding_mitochondrial_protein_mRNA	4.7	100	14	18	31	GAGCCGAGCCGCG
Gabbr1_R	Gabbr1_R	Mus_musculus_gamma-aminobutyric_acid_(GABA)_B_receptor_1_(Gabbr1)_mRNA	2.45E-08	96.77	31	5	35	CCAGCTGTGCTGNTAAACCTGAAGCGTC
		Mus_musculus_beta_galactoside_alpha_2,6_sialyltransferase_1_(St6gal1)_transcript_variant_2_mRNA	1.4	100	15	1	15	AGAGCCAGCTGTGCC
		Mus_musculus_beta_galactoside_alpha_2,6_sialyltransferase_1_(St6gal1)_transcript_variant_1_mRNA	1.4	100	15	1	15	AGAGCCAGCTGTGCC
		Mus_musculus_leucine_rich_repeat_containing_28_(Lrrc28)_transcript_variant_1_mRNA	1.4	100	15	2	16	GAGCCAGCTGTGCC
		Mus_musculus_leucine_rich_repeat_containing_28_(Lrrc28)_transcript_variant_3_non-coding_RNA	1.4	100	15	2	16	GAGCCAGCTGTGCC
		Mus_musculus_leucine_rich_repeat_containing_28_(Lrrc28)_transcript_variant_4_non-coding_RNA	1.4	100	15	2	16	GAGCCAGCTGTGCC
		Mus_musculus_DDB1_and_CUL4_associated_factor_17_(Dcaf17)_transcript_variant_1_mRNA	1.4	100	15	1	15	AGAGCCAGCTGTGCC
		Mus_musculus_secreted_frizzled-related_sequence_protein_5_(Sfrp5)_mRNA	5.5	100	14	3	16	AGCCAGCTGTGCC
		Mus_musculus_solute_carrier_family_9_(sodium/hydrogen_exchanger)_member_3_regulator_2_(Slc9a3r2)_transcript_variant_B_mRNA	5.5	100	14	4	17	GCCAGCTGTGCTGT
		Mus_musculus_solute_carrier_family_9_(sodium/hydrogen_exchanger)_member_3_regulator_2_(Slc9a3r2)_transcript_variant_A_mRNA	5.5	100	14	4	17	GCCAGCTGTGCTGT
		Mus_musculus_calcium_channel_voltage-dependent_alpha_11_subunit_(Cacna11)_mRNA	5.5	100	14	4	17	GCCAGCTGTGCTGT
		Mus_musculus_extended_synaptotagmin-like_protein_2_(Eyt2)_mRNA	5.5	100	14	1	14	AGAGCCAGCTGTGC
		Mus_musculus_phosphoribosyl_pyrophosphate_synthetase_1-like_1_(Prps11)_mRNA	5.5	100	14	1	14	AGAGCCAGCTGTGC
		Mus_musculus_FYVE_and_coiled-coil_domain_containing_1_(Fycy1)_transcript_variant_1_mRNA	5.5	100	14	4	17	GCCAGCTGTGCTGT
		Mus_musculus_KCNQ1_overlapping_transcript_1_(Kcnqtot1)_non-coding_RNA	5.5	100	14	4	17	GCCAGCTGTGCTGT
		Mus_musculus_olfactory_receptor_308_(Olfr308)_mRNA	5.5	100	14	1	14	AGAGCCAGCTGTGC
		Mus_musculus_zinc_finger_protein_109_(Zfp109)_mRNA	5.5	100	14	22	35	AAACTGGAAGCTG
		Mus_musculus_phosphatidylinositol_transfer_protein_membrane-associated_2_(Pitpm2)_mRNA	5.5	100	14	1	14	AGAGCCAGCTGTGC
Gpr107_F	Gpr107_F	Mus_musculus_G_protein-coupled_receptor_107_(Gpr107)_mRNA	1.63E-12	100	35	1	35	CGCAGGGCTTCCCATTGAAGCTGGCTGTTGTA
		Mus_musculus_DiGeorge_syndrome_critical_region_gene_8_(Dgcr8)_mRNA	0.36	100	16	19	34	AAGGCTGGGCTGTTG
		Mus_musculus_GNAS_(guanine_nucleotide_binding_protein_alpha_stimulating)_complex_locus_(Gnas)_transcript_variant_6_mRNA	1.4	100	15	20	34	AGGCTGGGCTGTTG
		Mus_musculus_GNAS_(guanine_nucleotide_binding_protein_alpha_stimulating)_complex_locus_(Gnas)_transcript_variant_5_mRNA	1.4	100	15	20	34	AGGCTGGGCTGTTG
		Mus_musculus_GNAS_(guanine_nucleotide_binding_protein_alpha_stimulating)_complex_locus_(Gnas)_transcript_variant_1_mRNA	1.4	100	15	20	34	AGGCTGGGCTGTTG
		Mus_musculus_GNAS_(guanine_nucleotide_binding_protein_alpha_stimulating)_complex_locus_(Gnas)_transcript_variant_1_mRNA	1.4	100	15	20	34	AGGCTGGGCTGTTG
		Mus_musculus_choline_dehydrogenase_(Chdh)_nuclear_gene_encoding_mitochondrial_protein_transcript_variant_2_mRNA	1.4	100	15	21	35	GGCTGGGCTGTGTA
		Mus_musculus_choline_dehydrogenase_(Chdh)_nuclear_gene_encoding_mitochondrial_protein_transcript_variant_3_mRNA	1.4	100	15	21	35	GGCTGGGCTGTGTA
		Mus_musculus_choline_dehydrogenase_(Chdh)_nuclear_gene_encoding_mitochondrial_protein_transcript_variant_1_mRNA	1.4	100	15	21	35	GGCTGGGCTGTGTA
		Mus_musculus_retina_and_anterior_neural_fold_homeobox_(Rax)_mRNA	5.5	100	14	3	16	CAGGGCTTCCGAT
		Mus_musculus_protocadherin_beta_22_(Pcdhb22)_mRNA	5.5	100	14	21	34	GGCTGGGCTGTTG
		Mus_musculus_protocadherin_beta_21_(Pcdhb21)_mRNA	5.5	100	14	21	34	GGCTGGGCTGTTG
		Mus_musculus_kelch-like_22_(Drosophila)_((Klhl22))_mRNA	5.5	100	14	17	30	TGAAGGCTGGGCTG
		Mus_musculus_clusterin_(Clu)_mRNA	5.5	100	14	18	31	GAAGGCTGGGCTG
		Mus_musculus_family_with_sequence_similarity_13_member_C_(Fam13c)_transcript_variant_2_mRNA	5.5	100	14	1	14	CGAGGCTTCCCG
		Mus_musculus_family_with_sequence_similarity_13_member_C_(Fam13c)_transcript_variant_1_mRNA	5.5	100	14	1	14	CGAGGCTTCCCG
		Mus_musculus_family_with_sequence_similarity_13_member_C_(Fam13c)_transcript_variant_3_mRNA	5.5	100	14	1	14	CGAGGCTTCCCG
		Mus_musculus_ubiquitin-like_7_(bone_marrow_stromal_cell-derived)_((Ubi7))_transcript_variant_2_mRNA	5.5	100	14	17	30	TGAAGGCTGGGCTG
		Mus_musculus_ubiquitin-like_7_(bone_marrow_stromal_cell-derived)_((Ubi7))_transcript_variant_1_mRNA	5.5	100	14	17	30	TGAAGGCTGGGCTG
		Mus_musculus_guanylate_cyclase_1_soluble_alpha_2_(Gucy1a2)_mRNA	5.5	100	14	16	29	TGAAGGCTGGGCTG
Gpr107_R	Gpr107_R	Mus_musculus_G_protein-coupled_receptor_107_(Gpr107)_mRNA	1.94E-04	100	21	1	21	CTTCTCTGTTGGTTTCA
		PREDICTED: Mus_musculus_predicted_gene_10775_(Gm10775)_miscRNA	2.9	94.44	18	7	24	CTTCTGGTGTCCAGCA
		Mus_musculus_SMC_hinge_domain_containing_1_(Smchd1)_mRNA	2.9	100	14	11	24	TGTGTTTCCAGCA

		PREDICTED: Mus musculus predicted gene 10775 (Gm10775)_miscRNA	2.9	94.44	18	7	24	CTGTTGGTTCACGA
		Mus musculus transient receptor potential cation channel_subfamily_V_member_1 (Trpv1)_mRNA	2.9	100	14	9	22	CGTTGGTTCACG
		Mus musculus coiled-coil domain containing_13 (Ccdc13)_mRNA	2.9	100	14	10	23	GTTGGTTCACG
		Mus musculus fibroblast growth factor_9 (Fgf9)_mRNA	2.9	100	14	3	16	CTCTCGTGGT
Gpr108_F	Gpr108_F	Mus musculus G protein-coupled receptor_108 (Gpr108)_mRNA	4.58E-09	100	29	1	29	TCACTGATGATCCGGGAGAAGATCCA
		Mus musculus metalloproteinase (reprolysin_type)_with thrombospondin_type_1_motif_19 (Adamts19)_mRNA	0.017	100	18	10	27	TGATCCGGGAGAAGATC
		Mus musculus adenosine monophosphate deaminase_3 (Ampd3)_mRNA	0.066	100	17	7	23	TGATGATCCGGGAGAAG
		Mus musculus cytochrome P450_family_27_subfamily_a_polypeptide_1 (Cyp27a1)_nuclear_gene_encoding_mitochondrial_protein_mRNA	0.066	100	17	4	20	CTGTGATGATCCGGGAG
		Mus musculus mitogen-activated protein kinase_kinase_kinase_1 (Map3k1)_mRNA	1	100	15	9	23	ATGATCCGGGAGAAG
		Mus musculus RIKEN_cDNA_6430571L13_gene_6430571L13Rik)_mRNA	1	100	15	1	15	TCAGTGTGATGATCC
		Mus musculus mucin_6_gastric (Muc6)_mRNA	1	100	15	7	21	TGATGATCCGGGAGA
		Mus musculus plexin_A4 (Plexn4)_mRNA	1	100	15	4	18	CTGTGATGATCCGGG
		Mus musculus YEATS_domain_containing_2 (Yeats2)_transcript_variant_2_mRNA	4.1	94.44	18	12	29	ATCCGGGAGAAGATCCA
		Mus musculus retinoic acid induced_12 (Rai12)_transcript_variant_3_mRNA	4.1	100	14	5	18	TGTGATGATCCGGG
		Mus musculus retinoic acid induced_12 (Rai12)_transcript_variant_1_mRNA	4.1	100	14	5	18	TGTGATGATCCGGG
		Mus musculus spectrin_beta_2 (Spnb2)_transcript_variant_2_mRNA	4.1	100	14	11	24	GATCCGGGAGAAGA
		Mus musculus spectrin_beta_2 (Spnb2)_transcript_variant_1_mRNA	4.1	100	14	11	24	GATCCGGGAGAAGA
		Mus musculus advillin (Avil)_mRNA	4.1	100	14	5	18	TGTGATGATCCGGG
		Mus musculus expressed sequence_C85492 (C85492)_mRNA	4.1	100	14	9	22	ATGATCCGGGAGAAG
		Mus musculus extended synaptotagmin-like protein_3 (Esl3)_mRNA	4.1	100	14	11	24	GATCCGGGAGAAGA
		Mus musculus sialic acid binding Ig-like lectin_E (Siglece)_mRNA	4.1	100	14	13	26	TCCGGGAGAAGAAT
		Mus musculus solute carrier_family_2_facilitated_glucose_transporter_member_1 (Slc2a1)_mRNA	4.1	94.44	18	8	25	GATGATCCGGGAGAAGA
		Mus musculus microtubule-associated protein_9 (Mtap9)_mRNA	4.1	100	14	1	14	TCACTGTGATGATC
Gpr108_R	Gpr108_R	Mus musculus G protein-coupled receptor_108 (Gpr108)_mRNA	0.056	100	16	2	17	CCACAAGTCCACAA
		Mus musculus microRNA_1198 (Mir1198)_microRNA	3.5	100	13	4	16	ACAAGTCCACAA
		Mus musculus desmocollin_1 (Dsc1)_mRNA	3.5	100	13	2	14	CCACAAGTCCAC
		Mus musculus laminin_alpha_1 (Lama1)_mRNA	3.5	100	13	5	17	CAACTGTCCACAC
		Mus musculus RIKEN_cDNA_4930444M15_gene_4930444M15Rik)_non-coding_RNA	3.5	100	13	3	15	CAACAAGTCCAC
		Mus musculus CD68 antigen (Cd68)_mRNA	3.5	100	13	2	14	CCACAAGTCCAC
		Mus musculus Smith-Magenis_syndrome_chromosome_region_candidate_8_homolog (human) (Smc8)_transcript_variant_1_mRNA	3.5	100	13	4	16	ACAAGTCCACAA
		Mus musculus neogenin (Neo1)_transcript_variant_1_mRNA	3.5	100	13	3	15	CAACAAGTCCAC
		Mus musculus neogenin (Neo1)_transcript_variant_2_mRNA	3.5	100	13	3	15	CAACAAGTCCAC
		Mus musculus solute carrier_family_7_cationic_amino_acid_transporter_yr_system_member_6 (Slc7a6)_mRNA	3.5	100	13	2	14	CCACAAGTCCAC
		Mus musculus caspase_3 (Casp3)_mRNA	3.5	100	13	4	16	ACAAGTCCACAA
		Mus musculus zinc_finger_protein_384 (Zfp384)_transcript_variant_1_mRNA	3.5	100	13	2	14	CCACAAGTCCAC
		Mus musculus zinc_finger_protein_384 (Zfp384)_transcript_variant_2_mRNA	3.5	100	13	2	14	CCACAAGTCCAC
		Mus musculus isoprenylcysteine_carboxyl_methyltransferase (lcmt)_transcript_variant_1_mRNA	3.5	100	13	3	15	CAACAAGTCCAC
		Mus musculus isoprenylcysteine_carboxyl_methyltransferase (lcmt)_transcript_variant_2_non-coding_RNA	3.5	100	13	3	15	CAACAAGTCCAC
		Mus musculus synaptopodin_2 (Synpo2)_mRNA	3.5	100	13	3	15	CAACAAGTCCAC
		Mus musculus nucleoporin_210-like (Nup210)_mRNA	3.5	100	13	2	14	CCACAAGTCCAC
		Mus musculus dispatched homolog_1 (Drosophila) (Disp1)_mRNA	3.5	100	13	5	17	CAACTGTCCACAC
		Mus musculus kelch-like_12 (Drosophila) (Kil12)_mRNA	3.5	100	13	4	16	ACAAGTCCACAA
Gpr124	Gpr124_F	Mus musculus G protein-coupled receptor_124 (Gpr124)_mRNA	2.83E-06	100	24	1	24	TTCTGTGTCAGTCTGTGGAT
		Mus musculus twisted gastrulation homolog_1 (Drosophila) (Twsg1)_mRNA	0.17	100	16	7	22	TGTCAGTCTGTGG
		Mus musculus RIKEN_cDNA_2310065F04_gene_2310065F04Rik)_non-coding_RNA	0.17	100	16	8	23	TGTCAGTCTGTGG
		Mus musculus cullin_5 (Cul5)_transcript_variant_1_mRNA	0.67	100	15	10	24	GTCAGTCTGTGG
		Mus musculus cullin_5 (Cul5)_transcript_variant_2_mRNA	0.67	100	15	10	24	GTCAGTCTGTGG
		Mus musculus WD_repeat_domain_38 (Wdr38)_mRNA	0.67	100	15	10	24	GTCAGTCTGTGG
		PREDICTED: Mus musculus predicted gene_19462 (Gm19462)_miscRNA	2.6	94.44	18	4	21	TTTGTGTCAGTCTGTG
		Mus musculus dynein_axonemal_light_chain_1 (Dnal1)_mRNA	2.6	100	14	9	22	GTCAGTCTGTGG
		Mus musculus regulatory associated protein_of_MTOR_complex_1 (Raptor)_mRNA	2.6	100	14	10	23	GTCAGTCTGTGG
		PREDICTED: Mus musculus predicted gene_19462 (Gm19462)_miscRNA	2.6	94.44	18	4	21	TTTGTGTCAGTCTGTG
		PREDICTED: Mus musculus protocadherin_beta_6 (Pcdhb6)_mRNA	2.6	100	14	11	24	TCAGTCTGTGGAT
		Mus musculus protocadherin_beta_10 (Pcdhb10)_mRNA	2.6	100	14	11	24	TCAGTCTGTGGAT
		Mus musculus protocadherin_beta_8 (Pcdhb8)_mRNA	2.6	100	14	11	24	TCAGTCTGTGGAT
		Mus musculus protocadherin_beta_6 (Pcdhb6)_mRNA	2.6	100	14	11	24	TCAGTCTGTGGAT
		Mus musculus POU_domain_class_5_transcription_factor_1 (Pou5f1)_transcript_variant_2_mRNA	2.6	100	14	9	22	GTCAGTCTGTGG
		Mus musculus POU_domain_class_5_transcription_factor_1 (Pou5f1)_transcript_variant_1_mRNA	2.6	100	14	9	22	GTCAGTCTGTGG
		Mus musculus synaptophysin-like protein (Synp)_transcript_variant_2_mRNA	2.6	100	14	8	21	TGTCAGTCTGTG
		Mus musculus synaptophysin-like protein (Synp)_transcript_variant_1_mRNA	2.6	100	14	8	21	TGTCAGTCTGTG
		Mus musculus CD28 antigen (Cd28)_mRNA	2.6	100	14	11	24	TCAGTCTGTGGAT
Gpr124_R	Gpr124_R	Mus musculus G protein-coupled receptor_124 (Gpr124)_mRNA	3.02E-07	100	26	1	26	TACGCTCAACCACTCAAAATGTT
		Mus musculus RNA binding protein_fox-1_homolog (C. elegans) 2 (Rbfox2)_transcript_variant_4_mRNA	1.1	100	15	5	19	GCTCAACAATACCA
		Mus musculus RNA binding protein_fox-1_homolog (C. elegans) 2 (Rbfox2)_transcript_variant_6_mRNA	1.1	100	15	5	19	GCTCAACAATACCA
		Mus musculus RNA binding protein_fox-1_homolog (C. elegans) 2 (Rbfox2)_transcript_variant_5_mRNA	1.1	100	15	5	19	GCTCAACAATACCA
		Mus musculus RNA binding protein_fox-1_homolog (C. elegans) 2 (Rbfox2)_transcript_variant_1_mRNA	1.1	100	15	5	19	GCTCAACAATACCA
		Mus musculus RNA binding protein_fox-1_homolog (C. elegans) 2 (Rbfox2)_transcript_variant_3_mRNA	1.1	100	15	5	19	GCTCAACAATACCA
		Mus musculus RNA binding protein_fox-1_homolog (C. elegans) 2 (Rbfox2)_transcript_variant_2_mRNA	1.1	100	15	5	19	GCTCAACAATACCA
		Mus musculus shisa_homolog_6 (Xenopus laevis) (Shisa6)_mRNA	4.4	100	14	8	21	CACCAACTCAAAA
		Mus musculus expressed sequence_A1317395 (A1317395)_mRNA	4.4	100	14	12	25	AACCAACAATGGT
		Mus musculus cDNA_sequence_BC048644 (BC048644)_mRNA	4.4	100	14	15	28	TACCAACTGGTGT
		PREDICTED: Mus musculus predicted gene_9615 (Gm9615)_miscRNA	4.4	100	14	2	15	CACGCTCACAAC
		PREDICTED: Mus musculus protein_FAM205A-like (LOC100862043)_mRNA	4.4	100	14	2	15	CACGCTCACAAC
		PREDICTED: Mus musculus protein_FAM205A-like (LOC100862324)_mRNA	4.4	100	14	2	15	CACGCTCACAAC
		PREDICTED: Mus musculus protein_FAM205A-like (LOC100861727)_miscRNA	4.4	100	14	2	15	CACGCTCACAAC
		Mus musculus predicted gene_13298 (Gm13298)_mRNA	4.4	100	14	2	15	CACGCTCACAAC
		PREDICTED: Mus musculus protein_FAM205A-like (LOC100862261)_mRNA	4.4	100	14	2	15	CACGCTCACAAC
		PREDICTED: Mus musculus protein_FAM205A-like (LOC100043920)_mRNA	4.4	100	14	2	15	CACGCTCACAAC
		Mus musculus signaling lymphocytic activation molecule family member_1 (Slamf1)_mRNA	4.4	94.44	18	2	19	CACCTCAACCACTACCA
Gpr125_F	Gpr125_F	Mus musculus G protein-coupled receptor_125 (Gpr125)_mRNA	1.17E-04	100	21	1	21	TTATTCACCTTGTCCAGGT
		Mus musculus chloride_intracellular_channel_4 (mitochondrial) (Clc4)_nuclear_gene_encoding_mitochondrial_protein_mRNA	0.44	100	15	3	17	TTTCACTCCCTGCCA
		Mus musculus RIKEN_cDNA_E130309D14Rik)_mRNA	1.8	100	14	4	17	TTCACCTTGTCCA
		Mus musculus platelet-activating factor acetylhydrolase_2 (Pafah2)_mRNA	1.8	100	14	4	17	TTCACCTTGTCCA
		Mus musculus special_AT-rich_sequence_binding_protein_1 (Satb1)_transcript_variant_1_mRNA	6.9	100	13	6	18	CTACCTTGTCCAC
		Mus musculus special_AT-rich_sequence_binding_protein_1 (Satb1)_transcript_variant_3_mRNA	6.9	100	13	6	18	CTACCTTGTCCAC
		Mus musculus special_AT-rich_sequence_binding_protein_1 (Satb1)_transcript_variant_2_mRNA	6.9	100	13	6	18	CTACCTTGTCCAC
		Mus musculus special_AT-rich_sequence_binding_protein_1 (Satb1)_transcript_variant_4_mRNA	6.9	100	13	6	18	CTACCTTGTCCAC
		Mus musculus AT_rich_interactive_domain_2 (ARID_RFX-like) (Arid2)_mRNA	6.9	100	13	5	17	TCTACCTTGTCCA
		Mus musculus somatostatin receptor_3 (Sstr3)_mRNA	6.9	100	13	6	18	CTACCTTGTCCAC
		Mus musculus WNT1_inducible_signaling_pathway_protein_1 (Wisp1)_mRNA	6.9	94.12	17	1	17	TTATTACCTTGTCCCA
		Mus musculus DPH3_homolog (KTI11_S_cerevisiae) (Dph3)_transcript_variant_1_mRNA	6.9	100	13	4	16	TTCACCTTGTCC
		Mus musculus DPH3_homolog (KTI11_S_cerevisiae) (Dph3)_transcript_variant_2_mRNA	6.9	100	13	4	16	TTCACCTTGTCC
		Mus musculus DEAD (Glu-Asp-Ala-Asp)_box_polypeptide_46 (Ddx46)_mRNA	6.9	100	13	4	16	TTCACCTTGTCC
		Mus musculus abhydrolase_domain_containing_15 (Abhd15)_mRNA	6.9	100	13	3	15	ATTCACTCTTGC
		Mus musculus R3H_domain_containing_2 (R3hdm2)_transcript_variant_2_mRNA	6.9	100	13	9	21	CCCTTGCCACGGT
		Mus musculus R3H_domain_containing_2 (R3hdm2)_transcript_variant_3_mRNA	6.9	100	13	9	21	CCCTTGCCACGGT
		Mus musculus R3H_domain_containing_2 (R3hdm2)_transcript_variant_1_mRNA	6.9	100	13	9	21	CCCTTGCCACGGT
		Mus musculus vomeronasal_1_receptor_51 (Vmn1r51)_mRNA	6.9	100	13	2	14	TATTTACCTTTG
		Mus musculus vomeronasal_1_receptor_45 (Vmn1r45)_mRNA	6.9	100	13	2	14	TATTTACCTTTG
Gpr125_R	Gpr125_R	Mus musculus G protein-coupled receptor_125 (Gpr125)_mRNA	3.35E-10	100	31	1	31	TGGGAGAAATACCAGACCAGAATGCCAG
		PREDICTED: Mus musculus predicted gene_16258 (Gm16258)_miscRNA	0.3	100	16	16	31	AGACAGAAATGCCAG
		PREDICTED: Mus musculus predicted gene_16258 (Gm16258)_miscRNA	0.3	100	16	16	31	AGACAGAAATGCCAG
		Mus musculus phosphodiesterase_12 (Pde12)_mRNA	1.2	100	15	10	24	TAACCCAGACAGAA
		Mus musculus cartilage_oligomeric_matrix_protein (Comp)_mRNA	1.2	100	15	9	23	ATAACCCAGACAGAA
		Mus musculus olfactory_receptor_503 (Olfr503)_mRNA	1.2	100	15	4	18	GAGGAATACCAGAA
		PREDICTED: Mus musculus protein_kinase_C-binding_protein_1-like (LOC546957)_miscRNA	1.2	100	15	12	26	ACCAGACAGAAAT
		PREDICTED: Mus musculus predicted gene_7340 (Gm7340)_miscRNA	4.7	100	14	5	18	AGGAATAACCCAGAA
		PREDICTED: Mus musculus predicted gene_7340 (Gm7340)_miscRNA	4.7	100	14	5	18	AGGAATAACCCAGAA
		Mus musculus adenomatous polyposis coli (Apc)_mRNA	4.7	100	14	18	31	AGCAAAATGCCAG
		Mus musculus mitogen-activated protein kinase_11 (Mapk11)_mRNA	4.7	100	14	14	27	CCAGACAGAAATG
		Mus musculus Rho_guanine_nucleotide_exchange_factor (GEF)_3 (Arhgef3)_mRNA	4.7	100	14	9	22	ATAACCCAGACCA
		Mus musculus T_cell_lymphoma_breakpoint_1 (Tcl1)_mRNA	4.7	100	14	7	20	GAATACCCAGACG
		Mus musculus adhesion molecule_with_Ig_like_domain_3 (Amigo3)_mRNA	4.7	100	14	11	24	AACCCAGACAGAA
		Mus musculus actinin_alpha_4 (Actn4)_mRNA	4.7	100	14	15	28	GACAGAGAATGC
		Mus musculus mitochondrial_translational_initiation_factor_3 (Mtfi3)_transcript_variant_1_mRNA	4.7	100	14	9	22	ATAACCCAGACCA
		Mus musculus mitochondrial_translational_initiation_factor_3 (Mtfi3)_nuclear_gene_encoding_mitochondrial_protein_transcript_variant_3_mRNA	4.7	100	14	9	22	ATAACCCAGACCA
		Mus musculus mitochondrial_translational_initiation_factor_3 (Mtfi3)_transcript_variant_2_mRNA	4.7	100	14	9	22	ATAACCCAGACCA
		Mus musculus mitochondrial_translational_initiation_factor_3 (Mtfi3)_transcript_variant_4_mRNA	4.7	100	14	9	22	ATAACCCAGACCA
		Mus musculus hydroxysteroid_11-beta_dehydrogenase_1 (Hsd11b1)_transcript_variant_2_mRNA	4.7	100	14	15	28	GACAGAGAATGC

Gpr133_F	Gpr133_F	Mus_musculus_G_protein-coupled_receptor_133_(Gpr133)_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		PREDICTED: Mus_musculus_predicted_gene_16244_(Gm16244)_miscRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_Bernardinelli-Seip_congenital_lipodystrophy_2_homolog_(human)_[Bsc12]_transcript_variant_2_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_Bernardinelli-Seip_congenital_lipodystrophy_2_homolog_(human)_[Bsc12]_transcript_variant_1_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_zinc_finger_and_BTb_domain_containing_38_(Zbtb38)_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_LSM4_homolog_U6_small_nuclear_RNA_associated_(S_cerevisiae)_[Lsm4]_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_Kell_blood_group_precursor_(McLeod_phenotype)_homolog_(Xk)_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_OCIA_domain_containing_1_(Ociad1)_transcript_variant_2_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_OCIA_domain_containing_1_(Ociad1)_transcript_variant_1_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_OCIA_domain_containing_1_(Ociad1)_transcript_variant_3_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_spindle_assembly_6_homolog_(C_elegans)_[Sass6]_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_golgi_phosphoprotein_3-like_(Golp3)_transcript_variant_2_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_golgi_phosphoprotein_3-like_(Golp3)_transcript_variant_1_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
		Mus_musculus_UDP-Gal4-beta1:Gal4-beta1-3-galactosyltransferase_polypeptide_1_(B3gal1)_mRNA	9.1	100	12	1	12	AGAAGCTGGGGT
Gpr133_R		Mus_musculus_G_protein-coupled_receptor_133_(Gpr133)_mRNA	4.58E-09	100	29	1	29	TCGCTTGGCCAAATAAATCCCTCCAGAG
		Mus_musculus_RIKEN_cDNA_O610007P08_gene_(O610007P08R1K)_transcript_variant_2_mRNA	1	100	15	12	26	ATAAATTCCTCTCA
		Mus_musculus_cDNA_sequence_BC017643_(BC017643)_transcript_variant_5_mRNA	4.1	100	14	8	21	GCCCAATAATCC
		Mus_musculus_cDNA_sequence_BC017643_(BC017643)_transcript_variant_1_mRNA	4.1	100	14	8	21	GCCCAATAATCC
		Mus_musculus_cDNA_sequence_BC017643_(BC017643)_transcript_variant_4_mRNA	4.1	100	14	8	21	GCCCAATAATCC
		Mus_musculus_cDNA_sequence_BC017643_(BC017643)_transcript_variant_2_mRNA	4.1	100	14	8	21	GCCCAATAATCC
		Mus_musculus_cDNA_sequence_BC017643_(BC017643)_transcript_variant_3_mRNA	4.1	100	14	8	21	GCCCAATAATCC
		Mus_musculus_RIKEN_cDNA_4930430J2_gene_(4930430J2R1K)_non-coding_RNA	4.1	100	14	16	29	AATCCCTCCAGAG
Gpr137	Gpr137_F	Mus_musculus_G_protein-coupled_receptor_137_(Gpr137)_transcript_variant_1_mRNA	1.68E-08	100	28	1	28	CTCTGGCAGTTGGTATGGTCCATCGGA
		Mus_musculus_G_protein-coupled_receptor_137_(Gpr137)_transcript_variant_2_mRNA	1.68E-08	100	28	1	28	CTCTGGCAGTTGGTATGGTCCATCGGA
		Mus_musculus_G_protein-coupled_receptor_137_(Gpr137)_transcript_variant_4_mRNA	1.68E-08	100	28	1	28	CTCTGGCAGTTGGTATGGTCCATCGGA
		Mus_musculus_G_protein-coupled_receptor_137_(Gpr137)_transcript_variant_3_mRNA	1.68E-08	100	28	1	28	CTCTGGCAGTTGGTATGGTCCATCGGA
		PREDICTED: Mus_musculus_spectrin_beta_5_(Spnb5)_mRNA	3.8	100	14	1	14	CTTGGCAGTTGGT
		Mus_musculus_bystin-like_(Bysl)_mRNA	3.8	100	14	3	16	CTGGCAGTTGGT
		Mus_musculus_ubiquitin_specific_peptidase_36_(Usp36)_mRNA	3.8	100	14	1	14	CTTGGCAGTTGGT
		Mus_musculus_hexamethylene_bis-acetamide_inducible_2_(Hexim2)_transcript_variant_1_mRNA	3.8	100	14	6	19	GCAGTTGGTATGGT
		Mus_musculus_hexamethylene_bis-acetamide_inducible_2_(Hexim2)_transcript_variant_2_mRNA	3.8	100	14	6	19	GCAGTTGGTATGGT
		Mus_musculus_hexamethylene_bis-acetamide_inducible_2_(Hexim2)_transcript_variant_3_mRNA	3.8	100	14	6	19	GCAGTTGGTATGGT
		Mus_musculus_cyclin-dependent_kinase_inhibitor_1C_(P57)_[Cdkn1c]_transcript_variant_1_mRNA	3.8	100	14	5	18	GGCAGTTGGTATGG
		Mus_musculus_cyclin-dependent_kinase_inhibitor_1C_(P57)_[Cdkn1c]_transcript_variant_2_mRNA	3.8	100	14	5	18	GGCAGTTGGTATGG
		PREDICTED: Mus_musculus_spectrin_beta_5_(Spnb5)_mRNA	3.8	100	14	1	14	CTTGGCAGTTGGT
Gpr137_R		Mus_musculus_G_protein-coupled_receptor_137_(Gpr137)_transcript_variant_1_mRNA	4.58E-09	100	29	1	29	GCTCTGGGAGCATAGCCGGATGAGAGC
		Mus_musculus_G_protein-coupled_receptor_137_(Gpr137)_transcript_variant_2_mRNA	4.58E-09	100	29	1	29	GCTCTGGGAGCATAGCCGGATGAGAGC
		Mus_musculus_G_protein-coupled_receptor_137_(Gpr137)_transcript_variant_4_mRNA	4.58E-09	100	29	1	29	GCTCTGGGAGCATAGCCGGATGAGAGC
		Mus_musculus_G_protein-coupled_receptor_137_(Gpr137)_transcript_variant_3_mRNA	4.58E-09	100	29	1	29	GCTCTGGGAGCATAGCCGGATGAGAGC
		Mus_musculus_RIKEN_cDNA_1700012A16_gene_(1700012A16R1K)_mRNA	0.26	100	16	3	18	TCTGGGAGCATAGCC
		Mus_musculus_glutamyl-peptide_cyclotransferase_(glutaminylicyclase)_[Qpc1]_mRNA	1	100	15	14	28	TACCCGGATGAGAG
		Mus_musculus_RIKEN_cDNA_1810013A23_gene_(1810013A23R1K)_non-coding_RNA	1	94.74	19	1	19	GCTCTGGGAGCATAGCCG
		Mus_musculus_mannoside_acetylglucosaminyltransferase_5_(Mgat5)_mRNA	1	100	15	15	29	AGCCGGATGAGAGC
		Mus_musculus_intersectin_1_(SH3_domain_protein_1A)_[Itsn1]_transcript_variant_1_mRNA	4.1	100	14	4	17	CTCTGGGAGCATAGC
		Mus_musculus_zinc_finger_protein_71_related_sequence_(Zfp71-rs1)_mRNA	4.1	100	14	2	15	CTCTGGGAGCATAGC
		Mus_musculus_histone_deacetylase_5_(Hdac5)_transcript_variant_1_mRNA	4.1	100	14	1	14	GCTCTGGGAGCATAGC
		Mus_musculus_histone_deacetylase_5_(Hdac5)_transcript_variant_2_mRNA	4.1	100	14	1	14	GCTCTGGGAGCATAGC
		Mus_musculus_RIMS_binding_protein_2_(Rimb2)_mRNA	4.1	94.44	18	3	20	TCTGGGAGCATAGCCG
Gpr137b	Gpr137b_F	Mus_musculus_G_protein-coupled_receptor_137b_(Gpr137b)_mRNA	5.64E-16	100	41	1	41	CAGTGTGTGAGTAACTGCATTCAGCCGCTC
		Mus_musculus_G_protein-coupled_receptor_137b_pseudogene_(Gpr137b-ps)_non-coding_RNA	5.64E-16	100	41	1	41	CAGTGTGTGAGTAACTGCATTCAGCCGCTC
		PREDICTED: Mus_musculus_uncharacterized_LOC100504746_transcript_variant_1_(LOC100504746)_miscRNA	7.3	100	14	6	19	TCTGAGTAATGTC
		PREDICTED: Mus_musculus_uncharacterized_LOC100504746_transcript_variant_2_(LOC100504746)_miscRNA	7.3	100	14	6	19	TCTGAGTAATGTC
		PREDICTED: Mus_musculus_fibrillin_2-like_(LOC100047082)_mRNA	7.3	94.44	18	11	28	GGTAACCTGCATTCGGT
		PREDICTED: Mus_musculus_predicted_gene_1966_(Gm1966)_mRNA	7.3	100	14	1	14	CAGTGTGTGAGTA
		Mus_musculus_fibrillin_2_(Fbn2)_mRNA	7.3	94.44	18	11	28	GGTAACCTGCATTCGGT
		Mus_musculus_peptidylprolyl_isomerase_(cyclophilin)-like_1_(Ppi1)_mRNA	7.3	100	14	16	29	CTGCAATGCTGTTG
		Mus_musculus_solute_carrier_family_9_member_10_(Sic9a10)_mRNA	7.3	100	14	12	25	GTAATGCTGCTGTTG
		Mus_musculus_F-box_and_leucine-rich_repeat_protein_20_(Fbxl20)_mRNA	7.3	100	14	1	14	CAGTGTGTGAGTA
		Mus_musculus_AT_rich_interactive_domain_3A_(BRIGHT-like)_[Arid3a]_mRNA	7.3	100	14	14	27	AACTGCTGCTGTTG
		Mus_musculus_CD109_antigen_(Cd109)_mRNA	7.3	100	14	17	30	TGCTGAGTGTGTA
		Mus_musculus_GDNF_family_receptor_alpha_like_(Gfral)_mRNA	7.3	100	14	9	22	CAGTAATGCTGTA
		PREDICTED: Mus_musculus_predicted_gene_1966_transcript_variant_1_(Gm1966)_mRNA	7.3	100	14	1	14	CAGTGTGTGAGTA
		PREDICTED: Mus_musculus_predicted_gene_1966_transcript_variant_2_(Gm1966)_mRNA	7.3	100	14	1	14	CAGTGTGTGAGTA
		PREDICTED: Mus_musculus_predicted_gene_1966_(Gm1966)_mRNA	7.3	100	14	1	14	CAGTGTGTGAGTA
		PREDICTED: Mus_musculus_predicted_gene_1966_(Gm1966)_mRNA	7.3	100	14	1	14	CAGTGTGTGAGTA
		Mus_musculus_interferon_regulatory_factor_3_(Irf3)_transcript_variant_1_mRNA	7.3	100	14	17	30	TGCTGAGTGTGTA
		Mus_musculus_interferon_regulatory_factor_3_(Irf3)_transcript_variant_2_non-coding_RNA	7.3	100	14	17	30	TGCTGAGTGTGTA
		Mus_musculus_RIKEN_cDNA_2700038G22_gene_(2700038G22R1K)_transcript_variant_2_non-coding_RNA	7.3	100	14	6	19	TCTGAGTAATGTC
Gpr137b_R		Mus_musculus_G_protein-coupled_receptor_137b_(Gpr137b)_mRNA	6.88E-05	96.67	30	1	29	GCTCTGGGAGCATAGCCGCTC
		Mus_musculus_G_protein-coupled_receptor_137b_pseudogene_(Gpr137b-ps)_non-coding_RNA	0.017	93.33	30	1	29	GCTCTGGGAGCATAGCCGCTC
		Mus_musculus_ATPase_class_V_type_10B_(Atp10b)_mRNA	1	100	15	14	28	ACTACTGAGGATCA
		Mus_musculus_SWI/SNF_related_matrix_associated_actin_dependent_regulator_of_chromatin_subfamily_a_member_4_(Smarca4)_transcript_variant_3_mRNA	1	100	15	3	17	CCCTGGCCAACTCT
		Mus_musculus_SWI/SNF_related_matrix_associated_actin_dependent_regulator_of_chromatin_subfamily_a_member_4_(Smarca4)_transcript_variant_2_mRNA	1	100	15	3	17	CCCTGGCCAACTCT
		Mus_musculus_SWI/SNF_related_matrix_associated_actin_dependent_regulator_of_chromatin_subfamily_a_member_4_(Smarca4)_transcript_variant_1_mRNA	1	100	15	3	17	CCCTGGCCAACTCT
		Mus_musculus_olfactory_receptor_633_(Olfr633)_mRNA	1	100	15	4	18	CTGCGCAACTCTA
		Mus_musculus_GTP_binding_protein_(gene_overexpressed_in_skeletal_muscle)_[Gem]_mRNA	1	100	15	3	17	CCCTGGCCAACTCT
		Mus_musculus_olfactory_receptor_1410_(Olfr1410)_mRNA	1	100	15	3	17	CCCTGGCCAACTCT
		Mus_musculus_myeloid/lymphoid_or_mixed-lineage_leukemia_2_(Mll2)_mRNA	4.1	100	14	13	26	CATCTACTGGAGTC
		Mus_musculus_L-2-hydroxyglutarate_dehydrogenase_(L2hgdh)_nuclear_gene_encoding_mitochondrial_protein_mRNA	4.1	100	14	4	17	CTGCGCAACTCTA
		Mus_musculus_additional_sex_combs_like_2_(Drosophila)_[Asx2]_mRNA	4.1	100	14	10	23	CAACTCTACTGGA
		Mus_musculus_translational_activator_of_mitochondrially_encoded_cytochrome_c_oxidase_1_(Taco1)_nuclear_gene_encoding_mitochondrial_protein_mRNA	4.1	100	14	4	17	CTGCGCAACTCTA
		Mus_musculus_tetratricopeptide_repeat_domain_19_(Ttc19)_transcript_variant_1_mRNA	4.1	100	14	5	18	CTGCGCAACTCTA
		Mus_musculus_tetratricopeptide_repeat_domain_19_(Ttc19)_transcript_variant_2_mRNA	4.1	100	14	5	18	CTGCGCAACTCTA
		Mus_musculus_RIKEN_cDNA_1700027J07_gene_(1700027J07R1K)_non-coding_RNA	4.1	100	14	2	15	TCCTGGCCAACTCT
		Mus_musculus_low_density_lipoprotein_receptor_(Ldlr)_transcript_variant_3_mRNA	4.1	100	14	10	23	CAACTCTACTGGA
		Mus_musculus_low_density_lipoprotein_receptor_(Ldlr)_transcript_variant_2_mRNA	4.1	100	14	10	23	CAACTCTACTGGA
		Mus_musculus_low_density_lipoprotein_receptor_(Ldlr)_transcript_variant_1_mRNA	4.1	100	14	10	23	CAACTCTACTGGA
		Mus_musculus_adenylate_cyclase_7_(Adcy7)_transcript_variant_3_mRNA	4.1	100	14	1	14	GCTCTGGCCACA
Gpr153	Gpr153_F	Mus_musculus_G_protein-coupled_receptor_153_(Gpr153)_mRNA	1.68E-08	100	28	1	28	CCCGCATGGTATGGAGCGCTCCTT
		Mus_musculus_PRP38_pre-mRNA_processing_factor_38_(yeast)_domain_containing_B_(Prpf38b)_mRNA	0.96	100	15	14	28	TTGAGCGCTCTCT
		Mus_musculus_retinoblastoma_binding_protein_8_(Rbbp8)_transcript_variant_3_non-coding_RNA	3.8	100	14	14	27	TTGAGCGCTCTCT
		Mus_musculus_retinoblastoma_binding_protein_8_(Rbbp8)_transcript_variant_1_mRNA	3.8	100	14	14	27	TTGAGCGCTCTCT
		Mus_musculus_retinoblastoma_binding_protein_8_(Rbbp8)_transcript_variant_4_non-coding_RNA	3.8	100	14	14	27	TTGAGCGCTCTCT
		Mus_musculus_retinoblastoma_binding_protein_8_(Rbbp8)_transcript_variant_2_mRNA	3.8	100	14	14	27	TTGAGCGCTCTCT
		Mus_musculus_RIKEN_cDNA_4930405A10_gene_(4930405A10R1K)_non-coding_RNA	3.8	100	14	6	19	ACATGATTGGAGC
		Mus_musculus_golgi_associated_PDZ_and_coiled-coil_motif_containing_(Gopc)_transcript_variant_1_mRNA	3.8	100	14	7	20	CATGATTGGAGC
		Mus_musculus_golgi_associated_PDZ_and_coiled-coil_motif_containing_(Gopc)_transcript_variant_2_mRNA	3.8	100	14	7	20	CATGATTGGAGC
Gpr153_R		Mus_musculus_G_protein-coupled_receptor_153_(Gpr153)_mRNA	2.41E-11	100	33	1	33	CAAACGCAAGATTGCAACATGAGACAGTC
		Mus_musculus_predicted_gene_11696_(Gm11696)_transcript_variant_1_non-coding_RNA	0.34	100	16	10	25	AGATTCTGACAATGA
		Mus_musculus_exonuclease_3'-5'_domain_containing_2_(Exd2)_mRNA	1.3	100	15	16	30	CTGACATGAGACCA
		Mus_musculus_TSPY-like_2_(Tspy2)_mRNA	1.3	100	15	16	30	CTGACATGAGACCA
		Mus_musculus_coagulation_factor_VIII_(F8)_transcript_variant_1_mRNA	5.3	100	14	9	22	GAAGATTCTGACAA
		Mus_musculus_coagulation_factor_VIII_(F8)_transcript_variant_2_mRNA	5.3	100	14	9	22	GAAGATTCTGACAA
		Mus_musculus_coagulation_factor_VIII_(F8)_transcript_variant_3_mRNA	5.3	100	14	9	22	GAAGATTCTGACAA
		Mus_musculus_thioredoxin-related_transmembrane_protein_1_(Trm1)_mRNA	5.3	100	14	9	22	GAAGATTCTGACAA
		Mus_musculus_serine_incorporator_1_(Serinc1)_mRNA	5.3	100	14	9	22	GAAGATTCTGACAA
		Mus_musculus_praja1_RING-H2_motif_containing_(Praja1)_transcript_variant_1_mRNA	5.3	94.44	18	4	21	ACGACGAAGATTCTGACA
		Mus_musculus_praja1_RING-H2_motif_containing_(Praja1)_transcript_variant_2_mRNA	5.3	94.44	18	4	21	ACGACGAAGATTCTGACA
		Mus_musculus_RAN_binding_protein_3_(Ranbp3)_transcript_variant_3_mRNA	5.3	94.44	18	9	26	GAAGATTCTGCAATGAG
		Mus_musculus_RAN_binding_protein_3_(Ranbp3)_transcript_variant_2_mRNA	5.3	94.44	18	9	26	GAAGATTCTGCAATGAG
		Mus_musculus_RAN_binding_protein_3_(Ranbp3)_transcript_variant_4_non-coding_RNA	5.3	94.44	18	9	26	GAAGATTCTGCAATGAG
		Mus_musculus_RAN_binding_protein_3_(Ranbp3)_transcript_variant_1_mRNA	5.3	94.44	18	9	26	GAAGATTCTGCAATGAG
		Mus_musculus_carnitine_palmitoyltransferase_1b_muscle_(Cpt1b)_nuclear_gene_encoding_mitochondrial_protein_mRNA	5.3	94.44	18	16	33	CTGACATGAGACAGTC
		Mus_musculus_cDNA_sequence_BC090627_(BC090627)_non-coding_RNA	5.3	94.44	18	16	33	CTGACATGAGACAGTC

		Mus_musculus_small_nuclear_ribonucleoprotein_polypeptide_A_(Snrp1),_mRNA	5.3	100	14	14	27	TTCTGACAATGAGA
Gpr21	Gpr21_F	Mus_musculus_G_protein-coupled_receptor_21_(Gpr21),_mRNA	2.68E-18	100	45	1	45	ATGCAGAACTACACGCTGTTCAGAGAGACTCATTACA CAACTCTCGC TCACAGCTGTTCAGAGGAG CACAGCTGTTCAGAGGAG GAGGAGACTCATTACA ATCACAGCTGTTCAGA TCAGAGGAGACTCATTACAA GAATCACAGCTGTTC GAATCACAGCTGTTC GAATCACAGCTGTTC GAATCACAGCTGTTC GAATCACAGCTGTTC CTCATCACACTCTC AATCACAGCTGTTCAGAGG AGCTCATTCACAC ATGCAGAACTACAC CAGAACTACACGCT TCACAGCTGTTCAG TCGTTCAGAGGAG CACAGCTGTTCAGA AGCTCATTCACAC GACTCATTCAGAGGAG
		Mus_musculus_RIKEN_cDNA_9430014N10_gene_(9430014N10R1K),_non-coding_RNA	0.009	100	19	9	27	
		Mus_musculus_patched_domain_containing_3_(Pchd3),_mRNA	0.035	100	18	10	27	
		Mus_musculus_UHRF1_(ICBP90)_binding_protein_1_(Uhrf1bp1),_mRNA	0.54	100	16	22	37	
		Mus_musculus_GTF2I_repeat_domain_containing_2_(Gtf2ird2),_mRNA	0.54	100	16	8	23	
		Mus_musculus_coiled-coil_domain_containing_141_(Ccdc141),_mRNA	0.54	95	20	19	38	
		Mus_musculus_AT_rich_interactive_domain_5A_(MRF1-like)_([Arid5a]),_transcript_variant_2,_mRNA	0.54	100	16	6	21	
		Mus_musculus_AT_rich_interactive_domain_5A_(MRF1-like)_([Arid5a]),_transcript_variant_3,_mRNA	0.54	100	16	6	21	
		Mus_musculus_AT_rich_interactive_domain_5A_(MRF1-like)_([Arid5a]),_transcript_variant_4,_non-coding_RNA	0.54	100	16	6	21	
		Mus_musculus_AT_rich_interactive_domain_5A_(MRF1-like)_([Arid5a]),_transcript_variant_1,_mRNA	0.54	100	16	6	21	
		Mus_musculus_myeloblastosis_oncogene-like_1_(Mybl1),_mRNA	2.1	100	15	29	43	
		Mus_musculus_testis_expressed_gene_2_(Tex2),_mRNA	2.1	94.74	19	7	25	
		PREDICTED: Mus_musculus_RIKEN_cDNA_9930038818_gene_(9930038818R1K),_miscRNA	8.5	100	14	26	39	
		Mus_musculus_cytoplasmic_polyadenylation_element_binding_protein_3_(Cpeb3),_mRNA	8.5	100	14	1	14	
		Mus_musculus_predicted_gene_10556_(Gm10556),_non-coding_RNA	8.5	100	14	4	17	
		Mus_musculus_carboxypeptidase_N_polypeptide_2_(Cpn2),_mRNA	8.5	100	14	9	22	
		Mus_musculus_leucine-rich_repeat_immunoglobulin-like_and_transmembrane_domains_2_(Lrit2),_mRNA	8.5	100	14	15	28	
		Mus_musculus_DEK_oncogene_(DNA_binding)_([Dek]),_mRNA	8.5	100	14	10	23	
		PREDICTED: Mus_musculus_RIKEN_cDNA_9930038818_gene_(9930038818R1K),_miscRNA	8.5	100	14	26	39	
		Mus_musculus_hepatic_leukemia_factor_(Hlf),_mRNA	8.5	100	14	14	27	
Gpr21	R	Mus_musculus_G_protein-coupled_receptor_21_(Gpr21),_mRNA	3.27E-21	100	50	1	50	GCAAGCTTCGGTAAAGATGTATTGGCTTTG TTGGATTTCAGCA GTGATTGGGCTTTG TGTGGCTTTTGGTGG TGTCGTTTGTGGTGG PREDICTED: Mus_musculus_uncharacterized_LOC100862313,_transcript_variant_2_(LOC100862313),_miscRNA PREDICTED: Mus_musculus_uncharacterized_LOC100862313,_transcript_variant_1_(LOC100862313),_miscRNA Mus_musculus_family_with_sequence_similarity_70,_member_A_(Fam70a),_mRNA Mus_musculus_developmental_pluripotency_associated_4_(Dppa4),_transcript_variant_2,_mRNA Mus_musculus_developmental_pluripotency_associated_4_(Dppa4),_transcript_variant_1,_mRNA Mus_musculus_apolipoprotein_D_(ApoD),_mRNA Mus_musculus_odz/Odz/ten-m_homolog_2_(Drosophila)_([Odz2]),_mRNA Mus_musculus_ankyrin_repeat_and_SOCS_box-containing_7_(Asb7),_transcript_variant_2,_non-coding_RNA Mus_musculus_ankyrin_repeat_and_SOCS_box-containing_7_(Asb7),_transcript_variant_1,_mRNA Mus_musculus_interferon_induced_with_helicase_C_domain_1_(Ifih1),_transcript_variant_1,_mRNA Mus_musculus_interferon_induced_with_helicase_C_domain_1_(Ifih1),_transcript_variant_2,_mRNA PREDICTED: Mus_musculus_predicted_gene_20179,_transcript_variant_1_(Gm20179),_miscRNA PREDICTED: Mus_musculus_predicted_gene_20179,_transcript_variant_2_(Gm20179),_miscRNA PREDICTED: Mus_musculus_G_protein-coupled_receptor_112_(Gpr112),_partial_mRNA PREDICTED: Mus_musculus_predicted_gene_12758_(Gm12758),_miscRNA PREDICTED: Mus_musculus_predicted_gene_20179,_transcript_variant_1_(Gm20179),_miscRNA PREDICTED: Mus_musculus_G_protein-coupled_receptor_112_(Gpr112),_partial_mRNA
Gpr4	Gpr4_F	Mus_musculus_G_protein-coupled_receptor_4_(Gpr4),_mRNA	3.21E-15	94.23	52	1	52	TAGCAGCTCAGCTCAATGAGTGTGAGTGG ACAACATCACTCCACT ACAACATCACTCCAC TCGCAGCTCAATGC AGTTGGAAGTGAACA TCGCAGCTCAATGC CGCAGCTCAATGC Mus_musculus_integrin_alpha_X_(Itgax),_mRNA PREDICTED: Mus_musculus_predicted_gene_10723_(Gm10723),_miscRNA Mus_musculus_v-ras_leukemia_viral_oncogene_1_(Raf1),_mRNA PREDICTED: Mus_musculus_predicted_gene_10723_(Gm10723),_miscRNA Mus_musculus_ATP_synthase_H+_transporting_mitochondrial_F0_complex_subunit_5_(Atp5s)_nuclear_gene_encoding_mito chondrial_protein,_mRNA Mus_musculus_regulator_of_G-protein_signaling_17_(Rgs17),_transcript_variant_1,_mRNA Mus_musculus_regulator_of_G-protein_signaling_17_(Rgs17),_transcript_variant_2,_mRNA Mus_musculus_Rho_guanine_nucleotide_exchange_factor_(GEF)_10_(Arhgef10),_transcript_variant_2,_mRNA Mus_musculus_Rho_guanine_nucleotide_exchange_factor_(GEF)_10_(Arhgef10),_transcript_variant_1,_mRNA Mus_musculus_tropomyosin_3_gamma_(Tpm3),_transcript_variant_4,_mRNA Mus_musculus_tropomyosin_3_gamma_(Tpm3),_transcript_variant_3,_mRNA Mus_musculus_tropomyosin_3_gamma_(Tpm3),_transcript_variant_1,_mRNA Mus_musculus_tubulin_beta_1_class_VI_(Tubb1),_mRNA Mus_musculus_family_with_sequence_similarity_23,_member_A_(Fam23a),_mRNA
		Mus_musculus_G_protein-coupled_receptor_4_(Gpr4),_mRNA	1.92E-13	93.88	49	1	49	AGCCGGAGGAGCGCTAGCAGTCGACCTCTCAA TCGAGTGTGGAGTG CGGAGCGGCTAGCAG TCGCAGCTCAATGC TCGCAGCTCAATGC CGCAGCTCAATGC CGCAGCTCAATGC Mus_musculus_heat_shock_protein_5_(Hspa5),_transcript_variant_2,_mRNA PREDICTED: Mus_musculus_predicted_gene_10723_(Gm10723),_miscRNA PREDICTED: Mus_musculus_predicted_gene_10723_(Gm10723),_miscRNA Mus_musculus_ATP_synthase_H+_transporting_mitochondrial_F0_complex_subunit_5_(Atp5s)_nuclear_gene_encoding_mito chondrial_protein,_mRNA Mus_musculus_olfactory_receptor_781_(Olfr781),_mRNA Mus_musculus_de-ethylated_homolog_1_(Arabidopsis)_([Det1]),_mRNA Mus_musculus_tubulin_beta_1_class_VI_(Tubb1),_mRNA Mus_musculus_tropomyosin_3_gamma_(Tpm3),_transcript_variant_4,_mRNA Mus_musculus_tropomyosin_3_gamma_(Tpm3),_transcript_variant_3,_mRNA Mus_musculus_tropomyosin_3_gamma_(Tpm3),_transcript_variant_1,_mRNA Mus_musculus_cleavage_stimulation_factor_3_pre-RNA_subunit_3_(Cstf3),_transcript_variant_3,_mRNA Mus_musculus_cleavage_stimulation_factor_3_pre-RNA_subunit_3_(Cstf3),_transcript_variant_2,_mRNA Mus_musculus_cleavage_stimulation_factor_3_pre-RNA_subunit_3_(Cstf3),_transcript_variant_1,_mRNA Mus_musculus_family_with_sequence_similarity_23,_member_A_(Fam23a),_mRNA
Gpr64	Gpr64_F	Mus_musculus_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_4,_mRNA Mus_musculus_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_3,_mRNA Mus_musculus_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_2,_mRNA Mus_musculus_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_1,_mRNA PREDICTED: Mus_musculus_predicted_gene_19613_(Gm19613),_miscRNA PREDICTED: Mus_musculus_predicted_gene_19613_(Gm19613),_miscRNA Mus_musculus_predicted_gene_12505_(Gm12505),_non-coding_RNA PREDICTED: Mus_musculus_RIKEN_cDNA_E030047D23_gene_(E030047D23R1K),_miscRNA PREDICTED: Mus_musculus_RIKEN_cDNA_E030047D23_gene_(E030047D23R1K),_miscRNA Mus_musculus_protease_serine_8_(prolactin)_([Prss8]),_mRNA Mus_musculus_branched_chain_ketoadid_dehydrogenase_kinase_(Bckdk)_nuclear_gene_encoding_mitochondrial_protein,m RNA Mus_musculus_synaptotagmin-like_3_(Sytl3),_transcript_variant_3,_mRNA Mus_musculus_synaptotagmin-like_3_(Sytl3),_transcript_variant_5,_mRNA Mus_musculus_synaptotagmin-like_3_(Sytl3),_transcript_variant_1,_mRNA PREDICTED: Mus_musculus_predicted_gene_2808_(Gm2808),_mRNA Mus_musculus_RIKEN_cDNA_4933400C5_gene_(4933400C5R1K),_mRNA Mus_musculus_Vac14_homolog_(S_cerevisiae)_([Vac14]),_mRNA Mus_musculus_solute_carrier_family_38_member_7_(Slc38a7),_mRNA Mus_musculus_coiled-coil_domain_containing_129_(Ccdc129),_mRNA PREDICTED: Mus_musculus_ring_finger_protein_213_(Rnf213),_mRNA						
		Mus_musculus_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_4,_mRNA Mus_musculus_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_3,_mRNA Mus_musculus_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_2,_mRNA Mus_musculus_G_protein-coupled_receptor_64_(Gpr64),_transcript_variant_1,_mRNA Mus_musculus_T_cell_leukemia_homeobox_3_(Tlx3),_mRNA Mus_musculus_flavin_containing_monoxygenase_5_(Fmo5),_transcript_variant_3,_mRNA Mus_musculus_flavin_containing_monoxygenase_5_(Fmo5),_transcript_variant_1,_mRNA Mus_musculus_flavin_containing_monoxygenase_5_(Fmo5),_transcript_variant_2,_mRNA Mus_musculus_2-oxoglutarate_and_iron-dependent_oxygenase_domain_containing_1_(Ogof1),_transcript_variant_2,_mRNA Mus_musculus_2-oxoglutarate_and_iron-dependent_oxygenase_domain_containing_1_(Ogof1),_transcript_variant_1,_mRNA Mus_musculus_makorin_ring_finger_protein_2_(Mkrn2),_mRNA Mus_musculus_prion_protein_duplicate_(Prnd),_transcript_variant_1,_mRNA Mus_musculus_serine_(or_cysteine)_peptidase_inhibitor_c1ade_E_member_2_(Serpin2),_mRNA PREDICTED: Mus_musculus_cDNA_sequence_BC067074_(BC067074),_miscRNA PREDICTED: Mus_musculus_cDNA_sequence_BC067074_(BC067074),_miscRNA						
Gprc5b	Gprc5b_F	Mus_musculus_G_protein-coupled_receptor_family_C_group_5_member_B_(Gprc5b),_transcript_variant_2,_mRNA Mus_musculus_G_protein-coupled_receptor_family_C_group_5_member_B_(Gprc5b),_transcript_variant_1,_mRNA Mus_musculus_nuclear_apoptosis_inducing_factor_1_(Naf1),_mRNA Mus_musculus_RIKEN_cDNA_2410075B13_gene_(2410075B13R1K),_transcript_variant_2,_mRNA Mus_musculus_RIKEN_cDNA_2410075B13_gene_(2410075B13R1K),_transcript_variant_1,_mRNA Mus_musculus_N-acetylated_alpha-linked_acidic_dipeptidase_2_(Naalad2),_mRNA Mus_musculus_titin_(Ttn),_transcript_variant_N2-A,_mRNA Mus_musculus_titin_(Ttn),_transcript_variant_N2-B,_mRNA PREDICTED: Mus_musculus_uncharacterized_LOC100861939,_transcript_variant_2_(LOC100861939),_miscRNA PREDICTED: Mus_musculus_uncharacterized_LOC100861939,_transcript_variant_1_(LOC100861939),_miscRNA						

		PREDICTED: Mus_musculus_predicted_gene_10278 (Gm10278)_miscRNA	8.5	94.44	18	22	39	CAATGGAAGCTTGGAGCA
		Mus_musculus_ephrin_B1_(Efnb1)_mRNA	8.5	94.44	18	20	37	TCCAATGGAAGCTTGGAG
		Mus_musculus_protein_kinase_X-linked_(Prkx)_mRNA	8.5	100	14	4	17	ATCAGCAGTGGGCT
		Mus_musculus_CBP80/20-dependent_translation_initiation_factor_(Ctif)_mRNA	8.5	94.44	18	5	22	TGAGCAGTGGGCTTTCC
		Mus_musculus_CDC23_(cell_division_cycle_23_23_23_23_23_23)_mRNA	8.5	100	14	11	24	GTGGGCTTTCCAA
		Mus_musculus_calcium/calmodulin-dependent_protein_kinase_IV_(Camk4)_mRNA	8.5	100	14	15	28	GCTTTTCCAAATGGA
		Mus_musculus_solute_carrier_family_8_(sodium/calcium_exchanger)_member_1_(Slc8a1)_transcript_variant_A_mRNA	8.5	94.44	18	25	42	TGGAAGCTTGGAGCAAA
		Mus_musculus_solute_carrier_family_8_(sodium/calcium_exchanger)_member_1_(Slc8a1)_transcript_variant_B_mRNA	8.5	94.44	18	25	42	TGGAAGCTTGGAGCAAA
		Mus_musculus_solute_carrier_family_45_member_2_(Slc45a2)_mRNA	8.5	100	14	6	19	CAGCAGTGGGCTTT
		Mus_musculus_nucleoporin_155_(Nup155)_mRNA	8.5	100	14	8	21	CAGTGGGCTTTTC
Gprc5b_R		Mus_musculus_G_protein-coupled_receptor_family_C_group_5_member_5_(Gprc5b)_transcript_variant_2_mRNA	4.80E-20	100	48	1	48	CGGGCTCATGGAGAACCAAGGCTTCTCAATGGA
		Mus_musculus_G_protein-coupled_receptor_family_C_group_5_member_5_(Gprc5b)_transcript_variant_1_mRNA	4.80E-20	100	48	1	48	TGAACATAACGCA
		Mus_musculus_SNF_related_kinase_(Snrk)_transcript_variant_2_mRNA	0.038	100	18	11	28	TGAGACAAGGCTTCT
		Mus_musculus_SNF_related_kinase_(Snrk)_transcript_variant_1_mRNA	0.038	100	18	11	28	TGAGACAAGGCTTCT
		Mus_musculus_asparagine-linked_glycosylation_9_homolog_(yeast_alpha_1_2_mannosyltransferase_(Alg9)_transcript_variant_2_non-coding_RNA	0.038	100	18	5	22	CCTACATGAGAACAAGG
		Mus_musculus_asparagine-linked_glycosylation_9_homolog_(yeast_alpha_1_2_mannosyltransferase_(Alg9)_transcript_variant_1_mRNA	0.038	100	18	5	22	CCTACATGAGAACAAGG
		Mus_musculus_aarF_domain_containing_kinase_1_(Adck1)_mRNA	0.6	100	16	2	17	GGGCTACATGGAGAA
		Mus_musculus_Dnaj_(Hsp40)_homolog_subfamily_A_member_2_(Dnaj2)_mRNA	0.6	100	16	10	25	ATGGAGAAACAGGCTT
		Mus_musculus_predicted_gene_6588_(Gm6588)_mRNA	0.6	100	16	13	28	GAGAACAAAGGCTTCT
		Mus_musculus_nuclear_factor_of_activated_T_cells_cytoplasmic_calcineurin_dependent_2_(Nfat2)_transcript_variant_2_mRNA	0.6	100	16	6	21	TCATCGAGAACAAAG
		Mus_musculus_nuclear_factor_of_activated_T_cells_cytoplasmic_calcineurin_dependent_2_(Nfat2)_transcript_variant_3_mRNA	0.6	100	16	6	21	TCATCGAGAACAAAG
		Mus_musculus_nuclear_factor_of_activated_T_cells_cytoplasmic_calcineurin_dependent_2_(Nfat2)_transcript_variant_d_mRNA	0.6	100	16	6	21	TCATCGAGAACAAAG
		Mus_musculus_nuclear_factor_of_activated_T_cells_cytoplasmic_calcineurin_dependent_2_(Nfat2)_transcript_variant_1_mRNA	0.6	100	16	6	21	TCATCGAGAACAAAG
		Mus_musculus_leucine_rich_repeat_containing_58_(Lrrc58)_mRNA	2.4	100	15	32	46	TGGATGAACATAACG
		Mus_musculus_RIKEN_cDNA_4921513D23_gene_(4921513D23Rik)_mRNA	2.4	100	15	7	21	TACATGGAGAACAAAG
		Mus_musculus_UDP-N-acetyl-alpha-D-galactosamine:polypeptide_N-acetylgalactosaminyltransferase_6_(Galnt6)_transcript_variant_3_mRNA	2.4	100	15	23	37	CCTTCTCAATGGATG
		Mus_musculus_UDP-N-acetyl-alpha-D-galactosamine:polypeptide_N-acetylgalactosaminyltransferase_6_(Galnt6)_transcript_variant_1_mRNA	2.4	100	15	23	37	CCTTCTCAATGGATG
		Mus_musculus_UDP-N-acetyl-alpha-D-galactosamine:polypeptide_N-acetylgalactosaminyltransferase_6_(Galnt6)_transcript_variant_2_mRNA	2.4	100	15	23	37	CCTTCTCAATGGATG
		Mus_musculus_dehydrogenase/reductase_member_2_(Dhrs2)_mRNA	2.4	100	15	5	19	CCATCATGGAGAACA
		Mus_musculus_RIKEN_cDNA_1700094J05_gene_(1700094J05Rik)_non-coding_RNA	2.4	100	15	8	22	CAATGGAGAACAAAG
Htr2a	Htr2a_F	Mus_musculus_5-hydroxytryptamine_(serotonin)_receptor_2A_(Htr2a)_mRNA	9.01E-11	100	32	1	32	GSTACGGTGGCTTCCGCCAGGCTCTGT
		Mus_musculus_Sec1_family_domain_containing_2_(Scfd2)_transcript_variant_b_mRNA	0.02	100	18	9	26	TGGCCTTGGCCAGCAAG
		Mus_musculus_Sec1_family_domain_containing_2_(Scfd2)_transcript_variant_a_mRNA	0.02	100	18	9	26	TGGCCTTGGCCAGCAAG
		Mus_musculus_trinucleotide_repeat_containing_18_(Trnc18)_transcript_variant_A_mRNA	0.08	100	17	16	32	TGCCACGAAGCTCTGT
		Mus_musculus_FLYWCH-type_zinc_finger_1_(Flywh1)_mRNA	0.32	100	16	10	25	GGCCTTGGCCAGCAA
		Mus_musculus_androgen_binding_protein_alpha_(Abpa)_mRNA	0.32	100	16	8	23	GTGGCTTGGCCAGCA
		Mus_musculus_peroxisomal_testis_specific_1_(Pxt1)_mRNA	1.3	100	15	15	29	TTGCCAGCAAGCTC
		Mus_musculus_Fas_(TNFRSF6)_binding_factor_1_(Fbf1)_mRNA	1.3	100	15	15	29	TTGCCAGCAAGCTC
		Mus_musculus_sema_domain_immunoglobulin_domain_(lg)_short_basic_domain_secreted_(semaphorin)_3F_(Sema3f)_mRNA	1.3	100	15	1	15	GTACCGTGGCTT
		Mus_musculus_predicted_gene_12776_(Gm12776)_mRNA	1.3	100	15	8	22	GTGGCTTGGCCAGCA
		Mus_musculus_complement_component_1_r_subcomponent-like_(C1r)_mRNA	1.3	94.74	19	14	32	TTTGCCAGCAAGCTCTGT
		Mus_musculus_K_voltage-gated_channel_subfamily_S_1_(Kcns1)_mRNA	1.3	100	15	16	30	TGCCAGCAAGCTCT
		Mus_musculus_carbohydrate_(keratan_sulfate_Gal6)_sulfotransferase_1_(Cst1)_mRNA	1.3	100	15	8	22	GTGGCTTGGCCAGCA
		PREDICTED: Mus_musculus_mothers_against_decapentaplegic_homolog_5-like_(LOC676358)_miscRNA	5	100	14	18	31	CCAGCAAGCTCTGT
		Mus_musculus_clusterin_associated_protein_1_(Cluap1)_mRNA	5	100	14	13	26	CTTGGCCAGCAAG
		Mus_musculus_fibroblast_growth_factor_14_(Fgf14)_transcript_variant_1_mRNA	5	100	14	11	24	GCTTGGCCAGCAAG
		Mus_musculus_fibroblast_growth_factor_14_(Fgf14)_transcript_variant_2_mRNA	5	100	14	11	24	GCTTGGCCAGCAAG
		Mus_musculus_opsin_4_(melanopsin_(Opn4))_transcript_variant_1_mRNA	5	94.44	18	7	24	GGTGGCTTGGCCAGCA
		Mus_musculus_opsin_4_(melanopsin_(Opn4))_transcript_variant_2_mRNA	5	94.44	18	7	24	GGTGGCTTGGCCAGCA
		Mus_musculus_cardiomyopathy_associated_5_(Cmya5)_mRNA	5	100	14	11	24	GCTTGGCCAGCAAG
Htr2a_R		Mus_musculus_5-hydroxytryptamine_(serotonin)_receptor_2A_(Htr2a)_mRNA	1.63E-12	100	35	1	35	GCTGGTGGTCTTGTTCATGCCGCTGCTCAATGT
		PREDICTED: Mus_musculus_predicted_gene_9930_(Gm9930)_miscRNA	1.4	100	15	3	17	TGCTGGGTTCTCTTG
		Mus_musculus_cDNA_sequence_BC027231_(BC027231)_mRNA	1.4	100	15	2	16	CTGCTGGGTTCTCTT
		Mus_musculus_platelet-activating_factor_acetylhydrolase_isoform_1b_subunit_1_(Pafah1b1)_transcript_variant_2_non-coding_RNA	1.4	100	15	1	15	GCTGGTGGTCTCTT
		Mus_musculus_platelet-activating_factor_acetylhydrolase_isoform_1b_subunit_1_(Pafah1b1)_transcript_variant_1_mRNA	1.4	100	15	1	15	GCTGGTGGTCTCTT
		PREDICTED: Mus_musculus_predicted_gene_9930_(Gm9930)_miscRNA	1.4	100	15	3	17	TGCTGGGTTCTCTTG
		Mus_musculus_exophilin_5_(Exph5)_mRNA	1.4	100	15	3	17	TGCTGGGTTCTCTTG
		Mus_musculus_leucine_rich_repeat_and_fibronectin_type_III_extracellular_1_(Efn1)_mRNA	1.4	100	15	1	15	GCTGGTGGTCTCTT
		Mus_musculus_transcription_elongation_factor_A_(SII)-like_8_(Tceal8)_transcript_variant_1_mRNA	5.5	100	14	4	17	GCTGGGTTCTCTTG
		Mus_musculus_transcription_elongation_factor_A_(SII)-like_8_(Tceal8)_transcript_variant_2_mRNA	5.5	100	14	4	17	GCTGGGTTCTCTTG
		Mus_musculus_transcriptional_regulating_factor_1_(Tref1)_transcript_variant_2_mRNA	5.5	100	14	17	30	GTACGCCGCTGTC
		Mus_musculus_transcriptional_regulating_factor_1_(Tref1)_transcript_variant_1_mRNA	5.5	100	14	17	30	GTACGCCGCTGTC
		Mus_musculus_myosin_light_polypeptide_kinase_(Mylk)_mRNA	5.5	100	14	2	15	CTGGTGGTCTCTT
		Mus_musculus_mitogen-activated_protein_kinase_kinase_kinase_9_(Map3k9)_transcript_variant_2_mRNA	5.5	100	14	5	18	CTGGGTTCTCTTG
		Mus_musculus_G_protein-coupled_receptor_33_(Gpr33)_mRNA	5.5	100	14	3	16	TGCTGGGTTCTCTT
		Mus_musculus_Rho-associated_coiled-coil_containing_protein_kinase_2_(Rock2)_mRNA	5.5	100	14	3	16	TGCTGGGTTCTCTT
		Mus_musculus_v-erb-b2_erythroblastic_leukemia_viral_oncogene_homolog_3_(avian_(ErbB3))_mRNA	5.5	100	14	3	16	TGCTGGGTTCTCTT
		Mus_musculus_OTU_domain_containing_4_(Otu4)_transcript_variant_2_mRNA	5.5	100	14	5	18	CTGGGTTCTCTTG
		Mus_musculus_OTU_domain_containing_4_(Otu4)_transcript_variant_1_mRNA	5.5	100	14	5	18	CTGGGTTCTCTTG
		Mus_musculus_protein-L-isoaspartate_(D-aspartate)_O-methyltransferase_domain_containing_2_(Pcmt2d)_mRNA	5.5	100	14	12	25	TCCTGTCTATGCC
Lgr4	Lgr4_F	Mus_musculus_leucine_rich_repeat-containing_G_protein-coupled_receptor_4_(Lgr4)_mRNA	9.01E-11	100	32	1	32	GTAATCTATTCTGTTATCCCGATGGAGCA
		Mus_musculus_small_G_protein_signaling_modulator_2_(Sgsm2)_mRNA	0.32	100	16	5	20	TTCTATTTCTGTATC
		Mus_musculus_solute_carrier_family_16_(monocarboxylic_acid_transporters)_member_11_(Slc16a11)_transcript_variant_3_mRNA	1.3	100	15	17	31	TATCCGGATGGAGC
		PREDICTED: Mus_musculus_uncharacterized_LOC100861772_(LOC100861772)_miscRNA	5	100	14	4	17	ATTCTATTCTGTT
		PREDICTED: Mus_musculus_predicted_gene_10305_(Gm10305)_miscRNA	5	100	14	5	18	TTCTATTCTGTAT
		Mus_musculus_cytochrome_P450_family_2_subfamily_c_polypeptide_44_(Cyp2c44)_transcript_variant_1_mRNA	5	100	14	2	15	TAATCTATTCTCTG
		Mus_musculus_poly(A)_binding_protein_cytoplasmic_6_(Pabpc6)_mRNA	5	100	14	7	20	CTATTCTGTTATC
		Mus_musculus_BRCA1_interacting_protein_C-terminal_helicase_1_(Brip1)_mRNA	5	100	14	1	14	GTAATCTATTCTT
		Mus_musculus_HEAT_repeat_containing_6_(Heatr6)_mRNA	5	100	14	9	22	ATTCTGTTATCC
		PREDICTED: Mus_musculus_uncharacterized_LOC100861772_(LOC100861772)_miscRNA	5	100	14	4	17	ATTCTATTCTGTT
		Mus_musculus_replication_protein_A1_(Rpa1)_transcript_variant_1_mRNA	5	100	14	4	17	ATTCTATTCTGTT
		Mus_musculus_replication_protein_A1_(Rpa1)_transcript_variant_2_mRNA	5	100	14	4	17	ATTCTATTCTGTT
		Mus_musculus_fibroblast_growth_factor_3_(Fgf3)_mRNA	5	100	14	18	31	ATCCCGATGGAGC
		Mus_musculus_RIKEN_cDNA_9530036O11Rik_(9530036O11Rik)_non-coding_RNA	5	100	14	3	16	AATCTATTCTGT
		PREDICTED: Mus_musculus_predicted_gene_10305_(Gm10305)_miscRNA	5	100	14	5	18	TTCTATTCTGTAT
		Mus_musculus_RIKEN_cDNA_E130309F12_gene_(E130309F12Rik)_mRNA	5	100	14	5	18	TTCTATTCTGTAT
		Mus_musculus_zinc_finger_protein_704_(Zfp704)_mRNA	5	100	14	3	16	AATCTATTCTGT
		Mus_musculus_homeobox_D13_(Hoxd13)_mRNA	5	100	14	1	14	GTAATCTATTCTT
Lgr4_R		Mus_musculus_leucine_rich_repeat-containing_G_protein-coupled_receptor_4_(Lgr4)_mRNA	3.55E-10	100	31	1	31	CTAGGCTATAAGCCCTCCAGCCTTAA
		Mus_musculus_acyl-CoA_thioesterase_5_(Aco5)_mRNA	0.3	100	16	12	27	AAAGCCCTCCAGCC
		Mus_musculus_acyl-CoA_thioesterase_3_(Aco3)_mRNA	0.3	100	16	12	27	AAAGCCCTCCAGCC
		Mus_musculus_acyl-CoA_thioesterase_1_(Aco1)_mRNA	0.3	100	16	12	27	AAAGCCCTCCAGCC
		Mus_musculus_acyl-CoA_thioesterase_2_(Aco2)_nuclear_gene_encoding_mitochondrial_protein_mRNA	0.3	100	16	12	27	AAAGCCCTCCAGCC
		PREDICTED: Mus_musculus_predicted_gene_10091_(Gm10091)_miscRNA	1.2	100	15	15	29	GCCCTCCAGCCTT
		PREDICTED: Mus_musculus_predicted_gene_10091_(Gm10091)_miscRNA	1.2	100	15	15	29	GCCCTCCAGCCTT
		PREDICTED: Mus_musculus_predicted_gene_16244_(Gm16244)_miscRNA	1.2	100	15	15	29	GCCCTCCAGCCTT
		Mus_musculus_pleckstrin_homology_domain_containing_family_G_(with_RhoGef_domain)_member_1_(Plekhh1)_transcript_variant_2_mRNA	1.2	100	15	12	26	AAAGCCCTCCAGCC
		Mus_musculus_pleckstrin_homology_domain_containing_family_G_(with_RhoGef_domain)_member_1_(Plekhh1)_transcript_variant_1_mRNA	1.2	100	15	12	26	AAAGCCCTCCAGCC
		Mus_musculus_upstream_binding_protein_1_(Ubp1)_transcript_variant_2_mRNA	1.2	100	15	11	25	TAAAGCTTCCAGC
		Mus_musculus_upstream_binding_protein_1_(Ubp1)_transcript_variant_1_mRNA	1.2	100	15	11	25	TAAAGCTTCCAGC
		Mus_musculus_ubiquitin_ligase_E3A_(Ube3a)_transcript_variant_3_mRNA	1.2	100	15	6	20	GCTATAAAGCCCTT
		Mus_musculus_ubiquitin_ligase_E3A_(Ube3a)_transcript_variant_2_mRNA	1.2	100	15	6	20	GCTATAAAGCCCTT
		Mus_musculus_ubiquitin_ligase_E3A_(Ube3a)_transcript_variant_1_mRNA	1.2	100	15	6	20	GCTATAAAGCCCTT

		Mus_musculus_carbamoyl-phosphate_synthetase_2_aspartate_transcarbamylase_and_dihydroorotase_(Cad)_mRNA	1.2	94.74	19	1	19	CTCAGGCTATTAAGGCTCT
		Mus_musculus_regulator_of_calineurin_3_(Rcan3)_mRNA	1.2	100	15	14	28	AGCCCTTCCAGCCT
		PREDICTED: Mus_musculus_uncharacterized_LOC100861680_(LOC100861680)_miscRNA	4.7	100	14	18	31	CTCCAGGACTTAA
		Mus_musculus_claudin_17_(Cldn17)_mRNA	4.7	100	14	12	25	AAAGCCTTCCAG
		Mus_musculus_DIP2_disc-interacting_protein_2_homolog_B_(Drosophila)_Dip2b_transcript_variant_2_mRNA	4.7	100	14	16	29	CCCTCCAGGCTCT
Lgr6	Lgr6_F	Mus_musculus_leucine-rich_repeat-containing_G_protein-coupled_receptor_6_(Lgr6)_mRNA	9.01E-11	100	32	1	32	GCTGACTACATACAACCGCATCCAGCATG
		Mus_musculus_phosphoinositide-3_kinase_regulatory_subunit_5_p101_(Pik3r5)_mRNA	1.3	100	15	18	32	ACCGCATCCAGCATG
		Mus_musculus_leucine-rich_repeat-containing_38_(Lrrc38)_mRNA	1.3	100	15	16	30	CAACCGATCCAGCA
		Mus_musculus_heterogeneous_nuclear_ribonucleoprotein_L_(Hnrnp1)_mRNA	5	100	14	17	30	AACCGATCCAGCA
		Mus_musculus_leucine-rich_repeat-containing_G_protein-coupled_receptor_4_(Lgr4)_mRNA	5	94.44	18	1	18	GCTGACTACATACA
		Mus_musculus_leucine-rich_repeat-containing_G_protein-coupled_receptor_6_(Lgr6)_mRNA	1.63E-12	100	35	1	35	TATCGCCACATCCGACTATGCCTCCAGAACC
		Mus_musculus_SCO_cytochrome_oxidase_deficient_homolog_1_(yeast)_Sco1_nuclear_gene_encoding_mitochondrial_protein_mRNA	0.36	100	16	3	18	TCCGCACATCCCTGA
		PREDICTED: Mus_musculus_predicted_gene_6934_(Gm6934)_mRNA	1.4	100	15	4	18	CCGCACATCCCTGA
		Mus_musculus_multiple_C2_domains_transmembrane_2_(Mctp2)_mRNA	1.4	100	15	20	34	TATGCCTTCCAGAAC
		Mus_musculus_CLK4-associating_serine/arginine-rich_protein_(Clarsp)_transcript_variant_L_mRNA	1.4	100	15	7	21	CCACATCCCTGACTA
		PREDICTED: Mus_musculus_predicted_gene_19422_(Gm19422)_miscRNA	5.5	100	14	12	25	CCCTGACTACTTC
		PREDICTED: Mus_musculus_predicted_gene_11483_(Gm11483)_miscRNA	5.5	100	14	21	34	ATCCCTTCCAGAAC
		Mus_musculus_opsin_1_(cone_pigments)_medium-wave-sensitive_(color_blindness_deutan)_Opn1mw_mRNA	5.5	94.44	18	13	30	CCCTGACTGCTCCCTCA
		Mus_musculus_NLR_family_CARD_domain_containing_4_(Nlr4)_mRNA	5.5	100	14	9	22	ACATCCCTGACTAT
		Mus_musculus_protein_phosphatase_2_formerly_2A_regulatory_subunit_A_(PR_65)_alpha_isoform_(Ppp2r1a)_mRNA	5.5	100	14	22	35	TGCCTCCAGAAC
		PREDICTED: Mus_musculus_predicted_gene_19422_(Gm19422)_miscRNA	5.5	100	14	12	25	TCCCTGACTATGCC
		Mus_musculus_vesicle_amine_transport_protein_1_homolog_(T_californica)_Vat1_mRNA	5.5	100	14	6	19	GCCACATCCCTGAC
		Mus_musculus_chondroadherin_(Chad)_mRNA	5.5	90.91	22	10	31	CATCCCTGACTACTCCCTCAAG
		Mus_musculus_neurofibromatosis_1_(Nf1)_mRNA	5.5	100	14	11	24	ATCCCTGACTATGC
		Mus_musculus_alkB_alkylation_repair_homolog_5_(E_coli)_AlkBh5_mRNA	5.5	100	14	20	33	TATGCTTCCAGAA
		Mus_musculus_aquaporin_9_(Aqp9)_mRNA	5.5	100	14	20	33	TATGCTTCCAGAA
		Mus_musculus_eukaryotic_translation_initiation_factor_3_subunit_K_(Eif3k)_mRNA	5.5	100	14	20	33	TATGCTTCCAGAA
		Mus_musculus_uncharacterized_LOC30324_(6430584L05)_non-coding_RNA	5.5	100	14	22	35	TGCCTCCAGAAC
		Mus_musculus_glutamate_receptor_ionotropic_kainate_3_(Grik3)_mRNA	5.5	100	14	21	26	CCCTGACTATGCT
		Mus_musculus_24-dehydrocholesterol_reductase_(Dhcr24)_mRNA	5.5	100	14	22	35	TGCCTCCAGAAC
Lpar1	Lpar1_F	Mus_musculus_lyso-phosphatidic_acid_receptor_1_(Lpar1)_transcript_variant_2_mRNA	1.84E-19	100	47	1	47	GACTGTGGTCAATGGCTGGTCTTATTGTCTG
		Mus_musculus_lyso-phosphatidic_acid_receptor_1_(Lpar1)_transcript_variant_1_mRNA	1.84E-19	100	47	1	47	CTGGACTCCGG
		Mus_musculus_dopamine_receptor_D3_(Drd3)_mRNA	0.002	90.63	32	5	36	GTGGTCAATGGCTGGTCTTATTGTCTG
		Mus_musculus_syntaxin_12_(Sxt12)_mRNA	0.009	100	19	22	40	TGCCTTATTGTCTGGG
		Mus_musculus_caspase_8_associated_protein_2_(Casp8ap2)_transcript_variant_2_mRNA	0.037	100	18	6	23	TGCTCATTTGCTTGGTG
		Mus_musculus_caspase_8_associated_protein_2_(Casp8ap2)_transcript_variant_1_mRNA	0.037	100	18	6	23	GTGGTCAATGGCTGGTG
		Mus_musculus_opioid_receptor_mu_1_(Oprm1)_mRNA	0.15	100	17	26	42	TTTATGTCTCTGGAC
		Mus_musculus_Gem-interacting_protein_(Gimp)_mRNA	0.15	100	17	31	47	TGCTGCTGGACTCCGG
		Mus_musculus_NIPA-like_domain_containing_2_(Nipal2)_mRNA	2.3	100	15	2	16	ACTGTGTCTATTGTG
		Mus_musculus_zinc_finger_protein_828_(Zfp828)_mRNA	2.3	94.74	19	1	19	GACTGTGGTCAATGGCTCT
		Mus_musculus_RIKEN_cDNA_4930571K23_gene_(4930571K23Rik)_mRNA	2.3	100	15	11	25	ATTGTGTGGTGCT
		Mus_musculus_general_transcription_factor_IIIH_polypeptide_3_(Gtf2h3)_mRNA	2.3	100	15	12	26	TTGCTTGGTCCCT
		PREDICTED: Mus_musculus_RIKEN_cDNA_A430010I10_gene_(A430010I10Rik)_miscRNA	2.3	100	15	22	36	TGCCTTATTGTCTG
		Mus_musculus_a_disintegrin_and_metalloproteinase_domain_7_(Adam7)_mRNA	2.3	100	15	6	20	GTGCTATTGCTGCTG
		Mus_musculus_natural_killer_tumor_recognition_sequence_(Nkr)_mRNA	2.3	100	15	14	28	GTGCTTGGTCTT
		Mus_musculus_pyruvate_kinase_muscle_(Pkm2)_transcript_variant_1_mRNA	2.3	100	15	4	18	TGTGCTATTGTGCT
		Mus_musculus_pyruvate_kinase_muscle_(Pkm2)_transcript_variant_2_mRNA	2.3	100	15	4	18	TGTGCTATTGTGCT
		PREDICTED: Mus_musculus_RIKEN_cDNA_A430010I10_gene_(A430010I10Rik)_miscRNA	2.3	100	15	22	36	TGCCTTATTGTCTG
		Mus_musculus_family_with_sequence_similarity_123_member_B_(Fam123b)_mRNA	9.1	100	14	26	39	TTTATTGTCTGCTG
		Mus_musculus_RIKEN_cDNA_4930474N09_gene_(4930474N09Rik)_non-coding_RNA	9.1	94.44	18	7	24	GGTCAATGGCTTGGTC
		Mus_musculus_lyso-phosphatidic_acid_receptor_1_(Lpar1)_transcript_variant_2_mRNA	3.90E-17	100	43	1	43	AGTTTGGACCAGGAGGAATCGGGACCATCATG
		Mus_musculus_lyso-phosphatidic_acid_receptor_1_(Lpar1)_transcript_variant_1_mRNA	3.90E-17	100	43	1	43	GAGCCTTC
		Mus_musculus_pyruvate_kinase_liver_and_red_blood_cell_(Pklr)_nuclear_gene_encoding_mitochondrial_protein_transcript_variant_2_mRNA	0.13	100	17	7	23	AGTTTGGACCAGGAGGAATCG
		Mus_musculus_pyruvate_kinase_liver_and_red_blood_cell_(Pklr)_nuclear_gene_encoding_mitochondrial_protein_transcript_variant_1_mRNA	0.13	100	17	7	23	GGACCCAGGAGGAATCG
		Mus_musculus_Fas_apoptotic_inhibitory_molecule_2_(Faim2)_transcript_variant_1_mRNA	0.5	100	16	2	17	GTTCGGACCAGGAG
		Mus_musculus_Fas_apoptotic_inhibitory_molecule_2_(Faim2)_transcript_variant_2_mRNA	0.5	100	16	2	17	GTTCGGACCAGGAG
		Mus_musculus_leucine-rich_repeat_containing_26_(Lrrc26)_mRNA	0.5	100	16	4	19	TCTGGACCAGGAGGA
		PREDICTED: Mus_musculus_predicted_gene_7489_(Gm7489)_mRNA	2	100	15	3	17	TCTGGACCAGGAG
		Mus_musculus_PQ_loop_repeat_containing_1_(Pqlc1)_transcript_variant_3_mRNA	2	100	15	3	17	TCTGGACCAGGAG
		Mus_musculus_PQ_loop_repeat_containing_1_(Pqlc1)_transcript_variant_1_mRNA	2	100	15	3	17	TCTGGACCAGGAG
		Mus_musculus_PQ_loop_repeat_containing_1_(Pqlc1)_transcript_variant_4_mRNA	2	100	15	3	17	TCTGGACCAGGAG
		Mus_musculus_PQ_loop_repeat_containing_1_(Pqlc1)_transcript_variant_2_mRNA	2	100	15	3	17	TCTGGACCAGGAG
		Mus_musculus_DENN/MADD_domain_containing_3_(Denn3)_mRNA	2	100	15	17	31	GGAATCGGACACCA
		PREDICTED: Mus_musculus_predicted_gene_7489_(Gm7489)_mRNA	2	100	15	3	17	TCTGGACCAGGAG
		Mus_musculus_phosphoribosylformylglycinamide_synthase_(FGAR_amidotransferase_(Pfas))_mRNA	2	100	15	5	19	CTGGACCAGGAGGA
		Mus_musculus_calcium_channel_voltage-dependent_P/Q_type_alpha_1A_subunit_(Cacna1a)_transcript_variant_2_mRNA	2	100	15	5	19	TCTGGACCAGGAGGA
		Mus_musculus_calcium_channel_voltage-dependent_P/Q_type_alpha_1A_subunit_(Cacna1a)_transcript_variant_4_mRNA	2	100	15	5	19	CTGGACCAGGAGGA
		Mus_musculus_calcium_channel_voltage-dependent_P/Q_type_alpha_1A_subunit_(Cacna1a)_transcript_variant_3_mRNA	2	100	15	5	19	CTGGACCAGGAGGA
		Mus_musculus_calcium_channel_voltage-dependent_P/Q_type_alpha_1A_subunit_(Cacna1a)_mRNA	2	100	15	5	19	CTGGACCAGGAGGA
		Mus_musculus_S100_calcium_binding_protein_A14_(S100a14)_transcript_variant_3_mRNA	2	100	15	3	17	TTCTGGACCAGGAG
Lpar4	Lpar4_F	Mus_musculus_lyso-phosphatidic_acid_receptor_4_(Lpar4)_mRNA	2.68E-18	100	45	1	45	TTCTCTCATCTAGCAACTCTTTCTGGGCACTCAAT
		PREDICTED: Mus_musculus_predicted_gene_13660_(Gm13660)_miscRNA	2.1	100	15	3	17	TGAGGAAC
		Mus_musculus_interferon_alpha_and_beta_receptor_2_(Ifnar2)_transcript_variant_1_mRNA	2.1	100	15	12	26	AGCACATCTTCTTT
		Mus_musculus_polybromo_1_(Pbrn1)_mRNA	2.1	100	15	15	29	ACACTCTTCTTTGGG
		Mus_musculus_zinc_finger_protein_366_(Zfp366)_mRNA	2.1	100	15	20	34	CTTCTTTGGGCACT
		Mus_musculus_odd_Oz/ten-m_homolog_2_(Drosophila)_Odd2_mRNA	2.1	100	15	19	33	CTTCTTTGGGCACT
		PREDICTED: Mus_musculus_predicted_gene_13660_(Gm13660)_miscRNA	2.1	100	15	3	17	CTCTCATCTAGCA
		PREDICTED: Mus_musculus_RIKEN_cDNA_A13005007_gene_(A13005007Rik)_miscRNA	8.5	100	14	12	25	AGCACACTTTTCT
		Mus_musculus_ubiquitin-like_4_(Ubl4)_transcript_variant_1_mRNA	8.5	100	14	12	25	AGCACACTTTTCT
		Mus_musculus_ubiquitin-like_4_(Ubl4)_transcript_variant_2_non-coding_RNA	8.5	100	14	12	25	AGCACACTTTTCT
		Mus_musculus_transferrin_receptor_(Tfrc)_mRNA	8.5	100	14	12	25	AGCACACTTTTCT
		Mus_musculus_RIKEN_cDNA_A830093I24Rik_gene_(A830093I24Rik)_mRNA	8.5	100	14	21	34	TTTCTGGGCACT
		Mus_musculus_protein-L-isoaspartate_(D-aspartate)_O-methyltransferase_1_(Pcmt1)_mRNA	8.5	94.44	18	21	38	TTTCTGGGCACTCAAT
		Mus_musculus_sema_domain_immunoglobulin_domain_(lg)_short_basic_domain_secreted_(semaphorin)_3B_(Sema3b)_transcript_variant_2_mRNA	8.5	100	14	18	31	CTCTTTCTGGGCA
		Mus_musculus_sema_domain_immunoglobulin_domain_(lg)_short_basic_domain_secreted_(semaphorin)_3B_(Sema3b)_transcript_variant_1_mRNA	8.5	100	14	18	31	CTCTTTCTGGGCA
		Mus_musculus_coiled-coil_domain_containing_144B_(Ccd144b)_mRNA	8.5	100	14	28	41	GGCACTCAATTGAG
		PREDICTED: Mus_musculus_RIKEN_cDNA_A13005007_gene_(A13005007Rik)_miscRNA	8.5	100	14	12	25	AGCACACTTTTCT
		Mus_musculus_RIKEN_cDNA_D030040B21_gene_(D030040B21Rik)_non-coding_RNA	8.5	100	14	4	17	TCTCATGACCA
		Mus_musculus_lyso-phosphatidic_acid_receptor_4_(Lpar4)_mRNA	1.25E-20	100	49	1	49	ACGTTTATTAGCTAACTACTACAGGCATGAGCACA
		Mus_musculus_additional_sex_combs_like_1_(Drosophila)_Asx1_mRNA	0.62	95	20	7	26	TTTCTCATCTAGCA
		Mus_musculus_ATPase_type_13A3_(Atp13a3)_transcript_variant_1_mRNA	2.4	100	15	4	18	TTTATTAGTAACCTA
		Mus_musculus_ATPase_type_13A3_(Atp13a3)_transcript_variant_2_mRNA	2.4	100	15	4	18	TTTATTAGTAACCTA
		Mus_musculus_metallophosphoesterase_domain_containing_2_(Mpped2)_transcript_variant_2_mRNA	2.4	100	15	20	34	CTACAGGATGAGCA
		Mus_musculus_metallophosphoesterase_domain_containing_2_(Mpped2)_transcript_variant_1_mRNA	2.4	100	15	20	34	CTACAGGATGAGCA
		Mus_musculus_guanine_nucleotide_binding_protein-like_3_(nucleolar)-like_(Gnli3)_transcript_variant_2_mRNA	9.6	100	14	27	40	CATGAGCACTTCT
		Mus_musculus_guanine_nucleotide_binding_protein-like_3_(nucleolar)-like_(Gnli3)_transcript_variant_1_mRNA	9.6	100	14	27	40	CATGAGCACTTCT
		Mus_musculus_glycerol-3-phosphate_acyltransferase_mitochondrial_(Gpam)_nuclear_gene_encoding_mitochondrial_protein_mRNA	9.6	100	14	29	42	TGAGCACTTCTCT
		Mus_musculus_rhesus_blood_group-associated_A_glycoprotein_(Rhag)_mRNA	9.6	100	14	3	16	GTTTATTAGCTAAC
		Mus_musculus_tripartite_motif-containing_35_(Trim35)_mRNA	9.6	100	14	18	31	ACTACAGGATGACT
		PREDICTED: Mus_musculus_RIKEN_cDNA_2610027K06Rik_gene_(2610027K06Rik)_miscRNA	9.6	100	14	20	33	CTACAGGATGAGC
		Mus_musculus_vomeriasal_2_receptor_84_(Vmn2r84)_mRNA	9.6	100	14	27	40	CATGAGCACTTCT
		Mus_musculus_pregnancy_specific_glycoprotein_16_(Psg16)_mRNA	9.6	100	14	20	33	CTACAGGATGAGC
		Mus_musculus_inaD-like_(Drosophila)_InaD)_transcript_variant_4_mRNA	9.6	100	14	21	34	TACAGGATGAGCA
		Mus_musculus_complement_component_factor_1_(Cfi)_mRNA	9.6	100	14	34	47	ACATTTCTCTACT

		Mus_musculus_SH3_domain_protein_D19_(Sh3d19),_mRNA	9.6	100	14	16	29	CTATCTACAGGAT
		Mus_musculus_ubiquitin_protein_ligase_E3_component_n_recognin_1_(Ubr1),_mRNA	9.6	100	14	28	41	ATGAGCACATCTCT
		Mus_musculus_sodium_channel_voltage_gated_type_IX_alpha_(Scn9a),_mRNA	9.6	100	14	32	45	GCACATTCCTCTCAT
		Mus_musculus_threonine_synthase-like_1_(bacterial)_([ThnS1]),_transcript_variant_2,_mRNA	9.6	100	14	8	21	TTAGCTAACTATCT
Lphn1	Lphn1_F	Mus_musculus_latrophilin_1_(Lphn1),_mRNA	2.32E-15	100	40	1	40	GGTGAAGTGTCTTCATTCTACAAACAACCTGGG
		PREDICTED:_Mus_musculus_predicted_gene_10644_(Gm10644),_miscRNA	2.32E-15	100	40	1	40	CCTC
		PREDICTED:_Mus_musculus_predicted_gene_10644_(Gm10644),_miscRNA	2.32E-15	100	40	1	40	GGTGAAGTGTCTTCATTCTACAAACAACCTGGG
		Mus_musculus_transient_receptor_potential_cation_channel_subfamily_M_member_6_(Trpm6),_mRNA	0.12	100	17	17	33	ATTCCTACAAACCT
		Mus_musculus_ryanodine_receptor_2_cardiac_(Ryr2),_mRNA	0.49	100	16	21	36	CTCAACAACCTGGG
		Mus_musculus_tubulin_gamma_complex_associated_protein_5_(Tubgp5),_mRNA	1.9	100	15	9	23	TTGTCTTCATCTCT
		Mus_musculus_RIKEN_cDNA_4933407H18_gene_(4933407H18RIK),_mRNA	1.9	100	15	8	22	GTGTCTTCATCTCT
		PREDICTED:_Mus_musculus_predicted_gene_4454_(Gm4454),_mRNA	1.9	100	15	24	38	ACAACAACCTGGCC
		PREDICTED:_Mus_musculus_predicted_gene_7061_(Gm7061),_mRNA	1.9	100	15	19	19	GGTGAAGTGTCTTCATT
		PREDICTED:_Mus_musculus_predicted_gene_7061_(Gm7061),_mRNA	1.9	100	15	19	19	GGTGAAGTGTCTTCATT
		Mus_musculus_proteasome_prosome_mascropain_subunit_beta_type_1_(Psmb1),_mRNA	1.9	100	15	19	19	GGTGAAGTGTCTTCATT
		Mus_musculus_tetratricopeptide_repeat_domain_8_(Ttc8),_transcript_variant_2,_mRNA	1.9	100	15	25	39	CAACAACCTGGGCT
		Mus_musculus_tetratricopeptide_repeat_domain_8_(Ttc8),_transcript_variant_1,_mRNA	1.9	100	15	25	39	CAACAACCTGGGCT
		Mus_musculus_forkhead_box_B1_(Foxb1),_mRNA	1.9	100	15	2	16	GTGAAGTGTCTCTC
		Mus_musculus_glycogen_synthase_1_muscle_(Gys1),_mRNA	1.9	100	15	21	35	TCTACAACAACCTGG
		Mus_musculus_predicted_gene_5592_(Gm5592),_mRNA	1.9	100	15	24	38	ACAACAACCTGGCC
		PREDICTED:_Mus_musculus_predicted_gene_2128_(Gm2128),_mRNA	1.9	100	15	24	38	ACAACAACCTGGCC
		Mus_musculus_predicted_gene_5114_(Gm5114),_mRNA	1.9	100	15	24	38	ACAACAACCTGGCC
		PREDICTED:_Mus_musculus_uncharacterized_LOC100861686_(LOC100861686),_mRNA	1.9	100	15	24	38	ACAACAACCTGGCC
		PREDICTED:_Mus_musculus_predicted_gene_6605_(Gm6605),_mRNA	1.9	100	15	24	38	ACAACAACCTGGCC
Lphn1_R		Mus_musculus_latrophilin_1_(Lphn1),_mRNA	9.69E-08	97.14	35	1	35	TCTCCGCAACACCGATCAAGCAGAACCGCCAA
		PREDICTED:_Mus_musculus_predicted_gene_10644_(Gm10644),_miscRNA	9.69E-08	97.14	35	1	35	TCTCCGCAACACCGATCAAGCAGAACCGCCAA
		PREDICTED:_Mus_musculus_predicted_gene_10644_(Gm10644),_miscRNA	9.69E-08	97.14	35	1	35	TCTCCGCAACACCGATCAAGCAGAACCGCCAA
		Mus_musculus_transmembrane_protein_164_(Tmem164),_transcript_variant_3,_mRNA	1.4	100	15	6	20	GCACAACCGATCAA
		Mus_musculus_armadillo_repeat_containing_Xlinked_5_(Armcx5),_mRNA	1.4	100	15	17	31	TCAAGCAGAACAGCC
		Mus_musculus_sperm_antigen_with_calponin_homology_and_coiled-coil_domains_1_(Speck1),_mRNA	1.4	100	15	16	30	ATCAAGCAGAACAGCC
		Mus_musculus_cytochrome_P450_family_2_subfamily_c_polypeptide_50_(Cyp2c50),_transcript_variant_3,_mRNA	5.5	100	14	16	29	ATCAAGCAGAACAG
		Mus_musculus_cytochrome_P450_family_2_subfamily_c_polypeptide_50_(Cyp2c50),_transcript_variant_1,_mRNA	5.5	100	14	16	29	ATCAAGCAGAACAG
		Mus_musculus_t-complex_11_(mouse)_like_2_(Tcp112),_mRNA	5.5	100	14	17	30	TCAAGCAGAACAGCC
		Mus_musculus_copine_II_(Cpne2),_mRNA	5.5	100	14	2	15	CTCCGCAACACCC
		Mus_musculus_predicted_gene_3414_(Gm3414),_non-coding_RNA	5.5	100	14	17	30	TCAAGCAGAACAGCC
		PREDICTED:_Mus_musculus_predicted_gene_16892_(Gm16892),_miscRNA	5.5	100	14	1	14	TCTCCGCAACACC
		PREDICTED:_Mus_musculus_ring_finger_protein_213_(Rnf213),_mRNA	5.5	100	14	15	28	GATCAAGCAGAAC
		PREDICTED:_Mus_musculus_predicted_gene_16892_(Gm16892),_miscRNA	5.5	100	14	1	14	TCTCCGCAACACC
		Mus_musculus_expressed_sequence_AU022754_(AU022754),_non-coding_RNA	5.5	100	14	18	31	CAAGCAGAACAGCC
		PREDICTED:_Mus_musculus_RIKEN_cDNA_6030426L16_gene_(6030426L16RIK),_miscRNA	5.5	100	14	18	31	CAAGCAGAACAGCC
		PREDICTED:_Mus_musculus_predicted_gene_19924_(Gm19924),_miscRNA	5.5	100	14	18	31	CAAGCAGAACAGCC
		PREDICTED:_Mus_musculus_ring_finger_protein_213_(Rnf213),_mRNA	5.5	100	14	15	28	GATCAAGCAGAAC
		Mus_musculus_microtubule-associated_protein_7_domain_containing_1_(Mtap7d1),_transcript_variant_1,_mRNA	5.5	100	14	4	17	CCGCAACACCGAT
		Mus_musculus_microtubule-associated_protein_7_domain_containing_1_(Mtap7d1),_transcript_variant_2,_mRNA	5.5	100	14	4	17	CCGCAACACCGAT
Lphn2	Lphn2_F	Mus_musculus_latrophilin_2_(Lphn2),_mRNA	2.68E-11	100	33	4	36	ACCTTGTGAGGCTGAGGCTTTGGAATCTGGA
		Mus_musculus_tetratricopeptide_repeat_domain_16_(Ttc16),_mRNA	0.095	100	17	9	25	CTGAGAGCTGAGGCTTT
		Mus_musculus_sel-1_suppressor_of_lin-12-like_3_(C_elegans)_([Sel13]),_mRNA	0.37	100	16	13	28	GAGCTGAGGCTTTGGA
		Mus_musculus_plastin_3_(T-isoform)_([Pls3]),_transcript_variant_3,_mRNA	1.5	100	15	19	33	AGGCTTTGGAATCT
		Mus_musculus_plastin_3_(T-isoform)_([Pls3]),_transcript_variant_1,_mRNA	1.5	100	15	19	33	AGGCTTTGGAATCT
		Mus_musculus_plastin_3_(T-isoform)_([Pls3]),_transcript_variant_2,_mRNA	1.5	100	15	19	33	AGGCTTTGGAATCT
		Mus_musculus_zinc_finger_protein_236_(Zfp236),_mRNA	1.5	100	15	6	20	CTTCTGAGAGCTGAG
		Mus_musculus Centrosomal_protein_192_(Cep192),_mRNA	1.5	100	15	19	33	AGGCTTTGGAATCT
		Mus_musculus_epsin_2_(Epn2),_transcript_variant_1,_mRNA	1.5	91.3	23	6	28	CTTCTGAGAGCTGAGGCTTTGGA
		Mus_musculus_epsin_2_(Epn2),_transcript_variant_2,_mRNA	1.5	91.3	23	6	28	CTTCTGAGAGCTGAGGCTTTGGA
		Mus_musculus_epsin_2_(Epn2),_transcript_variant_3,_mRNA	1.5	91.3	23	6	28	CTTCTGAGAGCTGAGGCTTTGGA
		Mus_musculus_tet_methylcytosine_dioxygenase_1_(Tet1),_transcript_variant_1,_mRNA	1.5	100	15	6	20	CTTCTGAGAGCTGAG
		Mus_musculus_tet_methylcytosine_dioxygenase_1_(Tet1),_transcript_variant_2,_mRNA	1.5	100	15	6	20	CTTCTGAGAGCTGAG
		Mus_musculus_transforming_acidic_coiled-coil_containing_protein_2_(Tacc2),_transcript_variant_3,_mRNA	1.5	94.74	19	5	23	CTTCTGAGAGCTGAGGCT
		PREDICTED:_Mus_musculus_putative_PFRAME_family_member_24-like_(LOC100861603),_mRNA	1.5	94.74	19	9	27	CTGAGAGCTGAGGCTTTGG
		PREDICTED:_Mus_musculus_PFRAME_family_member_12-like_(LOC100038995),_mRNA	1.5	94.74	19	9	27	CTGAGAGCTGAGGCTTTGG
		PREDICTED:_Mus_musculus_PFRAME_family_member_12-like_(LOC100038995),_mRNA	1.5	94.74	19	9	27	CTGAGAGCTGAGGCTTTGG
		PREDICTED:_Mus_musculus_PFRAME_family_member_12-like_(LOC100038995),_mRNA	1.5	94.74	19	9	27	CTGAGAGCTGAGGCTTTGG
		PREDICTED:_Mus_musculus_PFRAME_family_member_12-like_(LOC100039010),_mRNA	1.5	94.74	19	9	27	CTGAGAGCTGAGGCTTTGG
		PREDICTED:_Mus_musculus_PFRAME_family_member_12-like_(LOC100039010),_mRNA	1.5	94.74	19	9	27	CTGAGAGCTGAGGCTTTGG
Lphn2_R		Mus_musculus_latrophilin_2_(Lphn2),_mRNA	1.24E-09	100	30	1	30	GAAGCATCGAGGCTTACCTAAGGCAAT
		Mus_musculus_caspase_8_associated_protein_2_(Casp8ap2),_transcript_variant_2,_mRNA	1.1	94.74	19	1	19	GAAGCATCGAGGCTTAC
		Mus_musculus_caspase_8_associated_protein_2_(Casp8ap2),_transcript_variant_1,_mRNA	1.1	94.74	19	1	19	GAAGCATCGAGGCTTAC
		Mus_musculus_aquaporin_6_(Aqp6),_mRNA	4.4	100	14	9	22	GCAGGCTTACTCT
		Mus_musculus_cytoplasmic_FMR1_interacting_protein_2_(Cyfip2),_transcript_variant_3,_mRNA	4.4	100	14	1	14	GAAGCATCGAGGG
		Mus_musculus_cytoplasmic_FMR1_interacting_protein_2_(Cyfip2),_transcript_variant_1,_mRNA	4.4	100	14	1	14	GAAGCATCGAGGG
		Mus_musculus_cytoplasmic_FMR1_interacting_protein_2_(Cyfip2),_transcript_variant_2,_mRNA	4.4	100	14	1	14	GAAGCATCGAGGG
		Mus_musculus_WD_repeat_domain_6_(Wdr6),_mRNA	4.4	100	14	1	14	GAAGCATCGAGGG
		Mus_musculus_mitogen-activated_protein_kinase_kinase_10_(Map3k10),_mRNA	4.4	100	14	9	22	GCAGGCTTACTCT
		Mus_musculus_chaperonin_containing_Tcp1_subunit_6a_(zeta)_([Ct6a]),_mRNA	4.4	100	14	4	17	GACATCGAGGCTT
Mrgprf	Mrgprf_F	Mus_musculus_MAS-related_GPR_member_F_(Mrgprf),_mRNA	2.22E-07	100	26	1	26	TGTCTGGTATGAGGAGGCTCGGGGA
		Mus_musculus_copine_II_(Cpne2),_mRNA	0.052	100	17	10	26	ATGAGCAGGCTCGGGA
		Mus_musculus_FERM_RhoGEF_(ArhGEF)_and_pleckstrin_domain_protein_1_(chondrocyte-derived)_([Farp1]),_mRNA	0.81	100	15	1	15	TGTCTGGTATGAGC
		Mus_musculus_Max_interacting_protein_1_(Mxi1),_transcript_variant_2,_mRNA	3.2	100	14	13	26	AGCGAGGCTCGGGA
		Mus_musculus_olfactory_receptor_171_(Olfr171),_mRNA	3.2	100	14	6	19	TGGTATGAGCGAGG
		Mus_musculus_olfactory_receptor_170_(Olfr170),_mRNA	3.2	100	14	6	19	TGGTATGAGCGAGG
		Mus_musculus_olfactory_receptor_169_(Olfr169),_mRNA	3.2	100	14	6	19	TGGTATGAGCGAGG
		Mus_musculus_zinc_and_ring_finger_1_(Znrf1),_transcript_variant_3,_mRNA	3.2	100	14	13	26	ACCGAGGCTCGGGA
		Mus_musculus_zinc_and_ring_finger_1_(Znrf1),_transcript_variant_2,_mRNA	3.2	100	14	13	26	ACCGAGGCTCGGGA
		Mus_musculus_zinc_and_ring_finger_1_(Znrf1),_transcript_variant_1,_mRNA	3.2	100	14	13	26	ACCGAGGCTCGGGA
		Mus_musculus_thymidine_kinase_2_mitochondrial_(Tk2)_nuclear_gene_encoding_mitochondrial_protein_transcript_variant_1,_mRNA	3.2	100	14	1	14	TGTCTGGTATGAG
		Mus_musculus_thymidine_kinase_2_mitochondrial_(Tk2)_transcript_variant_2,_non-coding_RNA	3.2	100	14	1	14	TGTCTGGTATGAG
		Mus_musculus_citron_(Cit),_mRNA	3.2	100	14	1	14	TGTCTGGTATGAG
		Mus_musculus_RIKEN_cDNA_2610301B20_gene_(2610301B20RIK),_mRNA	3.2	100	14	13	26	ACCGAGGCTCGGGA
Mrgprf_R		Mus_musculus_MAS-related_GPR_member_F_(Mrgprf),_mRNA	2.45E-08	100	28	4	31	GGCGGAACATGCTCATGGGAAGCTCAC
		Mus_musculus_lectin_mannose-binding_2_(Lman2),_mRNA	0.36	100	16	7	22	CGGAACTGTCATGG
		Mus_musculus_RIKEN_cDNA_9430015G10_gene_(9430015G10RIK),_transcript_variant_2,_mRNA	0.36	100	16	13	28	CTGTCATGGGAAGCT
		Mus_musculus_RIKEN_cDNA_9430015G10_gene_(9430015G10RIK),_transcript_variant_1,_mRNA	0.36	100	16	13	28	CTGTCATGGGAAGCT
		PREDICTED:_Mus_musculus_SCO-spondin-like,_transcript_variant_4_(LOC100505089),_mRNA	1.4	100	15	14	28	TGTTATGGGAAGCT
		PREDICTED:_Mus_musculus_SCO-spondin-like,_transcript_variant_1_(LOC100505089),_mRNA	1.4	100	15	14	28	TGTTATGGGAAGCT
		PREDICTED:_Mus_musculus_SCO-spondin-like,_transcript_variant_2_(LOC100505089),_mRNA	1.4	100	15	14	28	TGTTATGGGAAGCT
		Mus_musculus_SCO-spondin_(Sspo),_mRNA	1.4	100	15	14	28	TGTTATGGGAAGCT
		Mus_musculus_high_mobility_group_20A_(Hmg20a),_mRNA	1.4	100	15	14	28	TGTTATGGGAAGCT
		Mus_musculus_shroom_family_member_2_(Shroom2),_mRNA	5.6	94.44	18	2	19	GAGCGGAAACTGTTCA
		Mus_musculus_BCL6_co-repressor-like_1_(Bcorl1),_mRNA	5.6	100	14	9	22	GAACTGTTCTATGG
		Mus_musculus_oncostatin_M_receptor_(Osmr),_mRNA	5.6	100	14	12	25	ACTGTTCTATGGGA
		Mus_musculus_RIKEN_cDNA_2310005E17_gene_(2310005E17RIK),_non-coding_RNA	5.6	100	14	9	22	GAACTGTTCTATGG
		Mus_musculus_Parkinson_disease_7_domain_containing_1_(Pdc1),_mRNA	5.6	100	14	12	25	ACTGTTCTATGGGA
		Mus_musculus_TBC1_domain_family_member_10b_(Tbc10b),_mRNA	5.6	100	14	3	16	AGCGCGAAACTGTT
		Mus_musculusGRAM_domain_containing_1A_(Gram1a),_mRNA	5.6	100	14	6	19	CGGAAACTGTTCA
		Mus_musculus_hyaluronoglucosaminidase_6_(Hyal6),_mRNA	5.6	100	14	10	23	AAACTGTTCTATGG
		Mus_musculus_nebulin_(Neb),_mRNA	5.6	100	14	10	23	AAACTGTTCTATGG
		Mus_musculus_striatin_caldesmon_binding_protein_(Strn),_mRNA	5.6	94.44	18	10	27	AAACTGTTCTATGGGAAGC
		Mus_musculus_ankyrin_repeat_domain_10_(Ankrd10),_transcript_variant_5,_non-coding_RNA	5.6	100	14	10	23	AAACTGTTCTATGG
Npy1r	Npy1r_F	Mus_musculus_neuropeptide_Y_receptor_Y1_(Npy1r),_mRNA	3.35E-10	100	31	1	31	AGGAAACCAACATGATGAGCAAGATCCGGG
		Mus_musculus_collagen_type_XVIII_alpha_1_(Col18a1),_transcript_variant_1,_mRNA	0.3	95	20	12	31	CATGATGGACAAAGTCCGGG
		Mus_musculus_collagen_type_XVIII_alpha_1_(Col18a1),_transcript_variant_2,_mRNA	0.3	95	20	12	31	CATGATGGACAAAGTCCGGG
		Mus_musculus_toll-like_receptor_13_(Tlr13),_mRNA	1.2	100	15	2	16	GGAGAAACAACATGA

		Mus_musculus_protein_phosphatase_1_regulatory_inhibitor_subunit_14B_Ppp1r14b_mRNA	1.2	100	15	17	31	TGGACAAGTCCGGG
		Mus_musculus_zinc_finger_protein_36_C3H_type-like_2_Zfp362i_mRNA	1.2	94.74	19	7	25	AACAACATGATGGACAAGA
		Mus_musculus_RIKEN_cDNA_4934346101_gene_4934346101Rik_mRNA	4.7	100	14	5	18	GAACAACATGATG
		Mus_musculus_RIKEN_cDNA_241012717_gene_241012717Rik_mRNA	4.7	100	14	17	30	TGGACAAGTCCGG
		Mus_musculus_SID1_transmembrane_family_member_1_Sid1i1_transcript_variant_1_mRNA	4.7	100	14	11	24	ACATGATGGACAAG
		Mus_musculus_SID1_transmembrane_family_member_1_Sid1i1_transcript_variant_2_mRNA	4.7	100	14	11	24	ACATGATGGACAAG
		Mus_musculus_RIKEN_cDNA_1700024P04_gene_1700024P04Rik_mRNA	4.7	100	14	1	14	AGGAGAAACAACAT
		Mus_musculus_gastric_inhibitory_polypeptide_Gip_mRNA	4.7	100	14	16	29	ATGGACAAGATCCG
		Mus_musculus_RIKEN_cDNA_2810442I21_gene_2810442I21Rik_non-coding_RNA	4.7	100	14	3	16	GAGAAACAACATG
		Mus_musculus_integrin_beta_1_binding_protein_3_Igfbp3_mRNA	4.7	100	14	1	14	AGGAGAAACAACAT
		Mus_musculus_RIKEN_cDNA_1810043G02_gene_1810043G02Rik_mRNA	4.7	100	14	3	16	GAGAAACAACATG
		Mus_musculus_laminin_alpha_4_Lama4_mRNA	4.7	100	14	3	16	GAGAAACAACATG
		Mus_musculus_pericentriolar_material_1_Pcm1_mRNA	4.7	100	14	4	17	AGAAACAACATGAT
		Mus_musculus_SRY-box_containing_gene_6_Sox6_transcript_variant_3_mRNA	4.7	100	14	4	17	AGAAACAACATGAT
		Mus_musculus_SRY-box_containing_gene_6_Sox6_transcript_variant_3_mRNA	4.7	100	14	4	17	AGAAACAACATGAT
		Mus_musculus_SRY-box_containing_gene_6_Sox6_transcript_variant_2_mRNA	4.7	100	14	4	17	AGAAACAACATGAT
Npy1r_R		Mus_musculus_neuropeptide_Y_receptor_Y1_Npy1r_mRNA	3.06E-14	100	38	1	38	TTGGCCCACTCTGTTATATTCATGCTACTTCA
		Mus_musculus_PHD_finger_protein_23_Phf23_mRNA	0.41	100	16	5	20	GCCCACTCTGTTTAT
		PREDICTED: Mus_musculus_predicted_gene_5524_Gm5524_miscRNA	1.6	100	15	20	34	TATTCATGTACTACT
		PREDICTED: Mus_musculus_predicted_gene_5524_Gm5524_miscRNA	1.6	100	15	20	34	TATTCATGTACTACT
		PREDICTED: Mus_musculus_predicted_gene_9938_Gm9938_miscRNA	6.4	100	14	17	30	TTATATTATATG
		PREDICTED: Mus_musculus_uncharacterized_LOC100861964_LOC100861964_miscRNA	6.4	100	14	5	18	GCCCACTCTGTTT
		PREDICTED: Mus_musculus_predicted_gene_9938_Gm9938_miscRNA	6.4	100	14	17	30	TTATATTATATG
		Mus_musculus_RIKEN_cDNA_6430571L13_gene_6430571L13Rik_mRNA	6.4	100	14	6	19	CCCATCTGCTTTA
		Mus_musculus_RIKEN_cDNA_2700050L05_gene_2700050L05Rik_mRNA	6.4	100	14	19	32	ATATTCATATGCTA
		Mus_musculus_vomeronal_1_receptor_73_Vmn173_mRNA	6.4	90.91	22	17	38	TTATATTATATGCTACTTCAA
		Mus_musculus_transmembrane_protein_64_Tmem64_mRNA	6.4	100	14	13	26	TGCTTTATATTCAT
		PREDICTED: Mus_musculus_uncharacterized_LOC100861964_LOC100861964_miscRNA	6.4	100	14	5	18	GCCCACTCTGTTT
		PREDICTED: Mus_musculus_predicted_gene_20158_Gm20158_miscRNA	6.4	100	14	15	28	TTTATATTATCAT
		Mus_musculus_serine_or_cysteine_peptidase_inhibitor_clade_A_alpha_1_antiproteinase_antitrypsin_member_7_Serpina7_mRNA	6.4	100	14	16	29	TTTATATTATCAT
		Mus_musculus_predicted_gene_10474_Gm10474_non-coding_RNA	6.4	100	14	13	26	TGCTTTATATTCAT
		Mus_musculus_structural_maintenance_of_chromosomes_6_Smc6_mRNA	6.4	100	14	13	26	TGCTTTATATTCAT
		Mus_musculus_unkempt_homolog_Drosophila_Unk_mRNA	6.4	100	14	5	18	GCCCACTCTGTTT
		Mus_musculus_vacuolar_protein_sorting_35_Vps35_mRNA	6.4	100	14	21	34	ATTCATATGCTACT
		Mus_musculus_importin_8_Ipo8_mRNA	6.4	100	14	16	29	TTTATATTATCAT
		PREDICTED: Mus_musculus_predicted_gene_20158_Gm20158_miscRNA	6.4	100	14	15	28	TTTATATTATCAT
P2ry2	P2ry2_F	Mus_musculus_purinergic_receptor_P2Y_G-protein_coupled_2_P2ry2_mRNA	2.83E-06	100	24	1	24	GACCTGGAACCTGGAAATAGCACC
		Mus_musculus_cadherin-like_24_Cdh24_mRNA	0.67	100	15	1	15	ACCTTGGAACTCTGG
		Mus_musculus_dehydrogenase/reductase_SDR_family_member_11_Dhrs11_mRNA	0.67	100	15	2	16	ACCTTGGAACTCTGG
		Mus_musculus_stromal_antigen_1_Stag1_mRNA	2.6	100	14	6	19	GGAACCTGGAAAT
		Mus_musculus_olfactory_receptor_701_Olf701_mRNA	2.6	100	14	5	18	TGGAACCTGGAAAT
		Mus_musculus_phosphoglucomutase_2-like_1_Pgm21_mRNA	2.6	100	14	5	18	TGGAACCTGGAAAT
		Mus_musculus_zinc_finger_MYM-type_4_Zmy4_mRNA	2.6	100	14	3	16	CCTGGAACCTGGGA
		Mus_musculus_cyclin-dependent_kinase_18_Cdk18_mRNA	2.6	94.44	18	1	18	ACCTTGGAACTCTGG
		Mus_musculus_collagen_type_III_alpha_1_Col3a1_mRNA	2.6	100	14	8	21	AACCTTGGAACTCTGG
		PREDICTED: Mus_musculus_uncharacterized_LOC100862473_LOC100862473_mRNA	2.6	100	14	10	23	CCCTGGAATAGCACC
		Mus_musculus_deleted_in_colorectal_carcinoma_Dcc_mRNA	2.6	100	14	2	15	ACCTGGAACCTGGG
		Mus_musculus_transmembrane_protein_106C_Tmem106C_transcript_variant_2_mRNA	2.6	100	14	2	15	ACCTGGAACCTGGG
		Mus_musculus_transmembrane_protein_106C_Tmem106C_transcript_variant_1_mRNA	2.6	100	14	2	15	ACCTGGAACCTGGG
		Mus_musculus_predicted_gene_3415_Gm3415_mRNA	2.6	100	14	4	17	CTGGAACCTGGAA
		Mus_musculus_predicted_gene_3409_Gm3409_mRNA	2.6	100	14	4	17	CTGGAACCTGGAA
		Mus_musculus_predicted_gene_3404_Gm3404_mRNA	2.6	100	14	4	17	CTGGAACCTGGAA
		Mus_musculus_predicted_gene_3402_Gm3402_mRNA	2.6	100	14	4	17	CTGGAACCTGGAA
		Mus_musculus_RIKEN_cDNA_4930449I24_gene_4930449I24Rik_mRNA	2.6	100	14	4	17	CTGGAACCTGGAA
		Mus_musculus_predicted_gene_6370_Gm6370_mRNA	2.6	100	14	4	17	CTGGAACCTGGAA
		Mus_musculus_predicted_gene_6408_Gm6408_mRNA	2.6	100	14	4	17	CTGGAACCTGGAA
P2ry2_R		Mus_musculus_purinergic_receptor_P2Y_G-protein_coupled_2_P2ry2_mRNA	1.15E-13	100	37	1	37	GAGCATCTCCACCCTCAAGGACGAGCTGATC
		PREDICTED: Mus_musculus_myosin-6-like_LOC100862557_mRNA	1.6	100	15	20	34	AGAGCAGGAGCTGAT
		Mus_musculus_potassium_channel_subfamily_K_member_7_Kcnk7_mRNA	1.6	100	15	2	16	AGCATCTCACCACC
		Mus_musculus_proteasome_prosome_macropain_265_subunit_non-ATPase_2_Psm22_transcript_variant_2_non-coding_RNA	1.6	100	15	19	33	AAAGCAGGAGCTGTA
		Mus_musculus_myosin_heavy_polypeptide_7_cardiac_muscle_beta_Myh7_mRNA	1.6	100	15	20	34	AGAGCAGGAGCTGAT
		Mus_musculus_myosin_heavy_polypeptide_6_cardiac_muscle_alpha_Myh6_transcript_variant_1_mRNA	1.6	100	15	20	34	AGAGCAGGAGCTGAT
		Mus_musculus_myosin_heavy_polypeptide_6_cardiac_muscle_alpha_Myh6_transcript_variant_2_mRNA	1.6	100	15	20	34	AGAGCAGGAGCTGAT
		Mus_musculus_golgi_autoantigen_golgin_subfamily_a_4_Golga4_mRNA	1.6	100	15	19	33	AAAGCAGGAGCTGTA
		Mus_musculus_zinc_finger_protein_704_Zfp704_mRNA	1.6	100	15	22	36	ACGAGGAGCTGATCA
		Mus_musculus_histone_deacetylase_4_Hdac4_mRNA	1.6	100	15	18	32	CAAGGACGAGGCTG
		PREDICTED: Mus_musculus_acetyl-CoA_carboxylase_1-like_LOC100862524_mRNA	6.1	100	14	4	17	CATCTCACCACCT
		PREDICTED: Mus_musculus_cDNA_sequence_BC106175_BC106175_miscRNA	6.1	100	14	8	21	CTCACCACTCAAG
		PREDICTED: Mus_musculus_fibrous_sheath-interacting_protein_2_Fsip2_mRNA	6.1	100	14	6	19	TCTCACCACTCA
		Mus_musculus_adipocyte-related_X-chromosome_expressed_sequence_1_Arxes1_mRNA	6.1	100	14	3	16	GATCTCTCACCACC
		Mus_musculus_adipocyte-related_X-chromosome_expressed_sequence_2_Arxes2_mRNA	6.1	100	14	3	16	GATCTCTCACCACC
		Mus_musculus_E74-like_factor_4_ets_domain_transcription_factor_Eif4_mRNA	6.1	94.44	18	15	32	CCTCAAGACGAGGAGCTG
		Mus_musculus_coiled-coil_domain_containing_22_Ccdc22_mRNA	6.1	100	14	16	29	CTCAAGGACGAGG
		Mus_musculus_lysyl_oxidase-like_4_Lox4_mRNA	6.1	100	14	20	33	AGAGCAGGAGCTGTA
		Mus_musculus_olfactory_receptor_1461_Olf1461_mRNA	6.1	100	14	16	29	CTCAAGGACGAGG
		Mus_musculus_immunoglobulin_mu_binding_protein_2_Ighmbp2_mRNA	6.1	100	14	2	15	AGCATCTCACCACC
P2ry6_F	P2ry6_F	Mus_musculus_pyrimidinergic_receptor_P2Y_G-protein_coupled_6_P2ry6_mRNA	2.22E-07	100	26	1	26	CGAGCAGTAAAGGCTCAGCAGGCAG
		Mus_musculus_nucleoporin_210-like_Nup210_mRNA	0.21	100	16	8	23	AGGAAAGGCTGACAGG
		Mus_musculus_ribosomal_protein_L18A_Rpl18a_mRNA	0.81	100	15	12	26	AAGGCTGACAGGCG
		Mus_musculus_transmembrane_protein_86B_Tmem86B_mRNA	0.81	100	15	6	20	ATAGGAAAGGCTGAC
		Mus_musculus_C1q_and_tumor_necrosis_factor_related_protein_4_C1qtnf4_mRNA	0.81	100	15	12	26	AAGGCTGACAGGCG
		Mus_musculus_myosin_IIIB_Myo3b_mRNA	0.81	100	15	7	21	TAGGAAAGGCTGACA
		Mus_musculus_olfactory_receptor_426_Olf426_mRNA	3.2	100	14	6	19	ATAGGAAAGGCTGACA
		Mus_musculus_collagen_type_IV_alpha_5_Col4a5_mRNA	3.2	94.44	18	7	24	TAGGAAAGGCTGACAGGC
		Mus_musculus_C2_calcium-dependent_domain_containing_2_C2cd2_mRNA	3.2	100	14	9	22	GGAAGGCTGACAGG
		Mus_musculus_arfGAP_with_coiled-coil_ankyrin_repeat_and_PH_domains_2_Acap2_mRNA	3.2	100	14	12	25	AAGGCTGACAGGCA
		PREDICTED: Mus_musculus_predicted_gene_4583_Gm4583_mRNA	3.2	100	14	3	16	AGCATAGGAAAGGCG
		Mus_musculus_mitogen-activated_protein_kinase_8_Mapk8_mRNA	3.2	100	14	12	25	AAGGCTGACAGGCA
		Mus_musculus_zinc_finger_FYVE_domain_containing_16_Zfyve16_mRNA	3.2	100	14	13	26	AGGCTGACAGGCG
		Mus_musculus_serine_or_cysteine_peptidase_inhibitor_clade_A_member_3B_Serpina3b_mRNA	3.2	94.44	18	2	19	GAGCATAGGAAAGGCTGTA
		Mus_musculus_kelch-like_29_Drosophila_Klhl29_mRNA	3.2	100	14	13	26	AGGCTGACAGGCG
		Mus_musculus_genetic_suppressor_element_1_Gse1_transcript_variant_2_mRNA	3.2	100	14	12	25	AAGGCTGACAGGCA
		Mus_musculus_genetic_suppressor_element_1_Gse1_transcript_variant_3_mRNA	3.2	100	14	12	25	AAGGCTGACAGGCA
		Mus_musculus_genetic_suppressor_element_1_Gse1_transcript_variant_1_mRNA	3.2	100	14	12	25	AAGGCTGACAGGCA
		Mus_musculus_negative_regulator_of_ubiquitin-like_proteins_1_Nub1_mRNA	3.2	100	14	11	24	AAAGGCTGACAGGCG
		Mus_musculus_apoptosis-inducing_TAF9-like_domain_1_Ap1td1_mRNA	3.2	100	14	4	17	CGATGAAAGGCTG
P2ry6_R		Mus_musculus_pyrimidinergic_receptor_P2Y_G-protein_coupled_6_P2ry6_mRNA	2.41E-11	100	33	1	33	CCAATCTGGCACTCTCCTCAAAACATCTCC
		PREDICTED: Mus_musculus_ring_finger_protein_213_Rnf213_mRNA	1.3	100	15	6	20	TCTGGCACTCTCCC
		Mus_musculus_SID1_transmembrane_family_member_1_Sid1i1_transcript_variant_1_mRNA	1.3	100	15	5	19	ATCTGGCACTCTCCC
		Mus_musculus_SID1_transmembrane_family_member_1_Sid1i1_transcript_variant_2_mRNA	1.3	100	15	5	19	ATCTGGCACTCTCCC
		Mus_musculus_predicted_gene_10485_Gm10485_non-coding_RNA	1.3	100	15	7	21	CTGGCACTCTCCC
		PREDICTED: Mus_musculus_ring_finger_protein_213_Rnf213_mRNA	1.3	100	15	6	20	TCTGGCACTCTCCC
		Mus_musculus_thiamine_pyrophosphokinase_Tpk1_mRNA	1.3	100	15	4	18	AATCTGGCACTCTCT
		Mus_musculus_NEDD4_binding_protein_2-like_2_N4bp2i2_mRNA	1.3	100	15	11	25	CACCTCTCTCAAAA
		Mus_musculus_doublecortin_Dcx_transcript_variant_1_mRNA	5.3	94.44	18	4	21	AATCTGGCACTCTCTCT
		Mus_musculus_doublecortin_Dcx_transcript_variant_2_mRNA	5.3	94.44	18	4	21	AATCTGGCACTCTCTCT
		Mus_musculus_doublecortin_Dcx_transcript_variant_3_mRNA	5.3	94.44	18	4	21	AATCTGGCACTCTCTCT
		Mus_musculus_doublecortin_Dcx_transcript_variant_4_mRNA	5.3	94.44	18	4	21	AATCTGGCACTCTCTCT
		Mus_musculus_ankyrin_repeat_domain_29_Ankd29_mRNA	5.3	100	14	4	17	AATCTGGCACTCTCT
		Mus_musculus_LIM_domain_containing_preferred_translocation_partner_in_lipoma_Lpp_transcript_variant_3_mRNA	5.3	100	14	9	22	GGCATCTCTCTCA
		Mus_musculus_LIM_domain_containing_preferred_translocation_partner_in_lipoma_Lpp_transcript_variant_2_mRNA	5.3	100	14	9	22	GGCATCTCTCTCA
		Mus_musculus_LIM_domain_containing_preferred_translocation_partner_in_lipoma_Lpp_transcript_variant_1_mRNA	5.3	100	14	9	22	GGCATCTCTCTCA
		Mus_musculus_Dnaj_Hsp40_homolog_subfamily_C_member_3_Dnajc3_mRNA	5.3	100	14	8	21	TGGCACTCTCTCTCT
		Mus_musculus_nei_like_2_E_coli_Nei2_mRNA	5.3	100	14	15	28	CTCTCTAAACAT
		Mus_musculus_EFR3_homolog_B_5_cerevisiae_Efr3b_mRNA	5.3	100	14	7	20	TCTGGCACTCTCTCT
		Mus_musculus_RIKEN_cDNA_4930430F08_gene_4930430F08Rik_mRNA	5.3	100	14	12	25	ACTCTCTCTAAAA
Ptger3_F	Ptger3_F	Mus_musculus_prostaglandin_E_receptor_3_subtype_EP3_Ptger3_mRNA	1.25E-20	100	49	1	49	CTATTGATGATGTTGAAATGATCTCAATCAG
		Mus_musculus_solute_carrier_family_9_sodium_hydrogen_exchanger_member_9_Slc9a9_mRNA	0.04	100	18	14	31	TGTTGAAATGATCTTCA
		Mus_musculus_ATP-binding_cassette_subfamily_A_Abc1_member_15_Abca15_mRNA	0.62	95	20	6	25	GATATGATGTTGAAATGAT

		Mus_musculus_zinc_finger_protein_518B_(Zfp518b)_transcript_variant_1_mRNA	0.62	100	16	10	25	ATGATGTTGAAAATGA
		Mus_musculus_zinc_finger_protein_518B_(Zfp518b)_transcript_variant_2_mRNA	0.62	100	16	10	25	ATGATGTTGAAAATGA
		PREDICTED: Mus_musculus_dynein_axonemal_heavy_chain_14_(Dnahc14)_mRNA	2.4	100	15	22	36	ATGATCTCAATCAG
		Mus_musculus_guanosine_monophosphate_reductase_2_(Gmpr2)_mRNA	2.4	100	15	2	16	TATGATAATGATG
		Mus_musculus_protein_tyrosine_phosphatase_receptor_type_K_(Ptkrk)_mRNA	2.4	94.74	19	18	36	GAAAATGATCTCAATCAG
		Mus_musculus_protein_phosphatase_2_regulatory_subunit_B'_alpha_(Ppp2r3a)_transcript_variant_2_mRNA	2.4	100	15	12	26	GATGTGAAAATGAT
		Mus_musculus_protein_phosphatase_2_regulatory_subunit_B'_alpha_(Ppp2r3a)_transcript_variant_1_mRNA	2.4	100	15	12	26	GATGTGAAAATGAT
		Mus_musculus_olfactory_receptor_901_(Olf901)_mRNA	2.4	100	15	13	27	ATGTGAAAATGATC
		PREDICTED: Mus_musculus_KRA8_box_and_zinc_finger_C2H2_type_domain_containing_protein-like_(LOC627901)_mRNA	2.4	94.74	19	16	34	TTGAAAATGATCTCAATC
		Mus_musculus_predicted_gene_14295_(Gm14295)_mRNA	2.4	94.74	19	16	34	TTGAAAATGATCTCAATC
		Mus_musculus_predicted_gene_100043387_(100043387)_mRNA	2.4	94.74	19	16	34	TTGAAAATGATCTCAATC
		Mus_musculus_predicted_gene_14308_(Gm14308)_mRNA	2.4	94.74	19	16	34	TTGAAAATGATCTCAATC
		Mus_musculus_predicted_gene_14334_(Gm14334)_mRNA	2.4	94.74	19	16	34	TTGAAAATGATCTCAATC
		PREDICTED: Mus_musculus_zinc_finger_protein_709_like_(LOC628147)_partial_miscRNA	2.4	94.74	19	16	34	TTGAAAATGATCTCAATC
		Mus_musculus_RIKEN_cDNA_0610010808_gene_(0610010808Rik)_mRNA	2.4	94.74	19	16	34	TTGAAAATGATCTCAATC
		Mus_musculus_predicted_gene_6710_(Gm6710)_mRNA	2.4	94.74	19	16	34	TTGAAAATGATCTCAATC
		PREDICTED: Mus_musculus_predicted_gene_2007_(Gm2007)_mRNA	2.4	94.74	19	16	34	TTGAAAATGATCTCAATC
Ptger3_R		Mus_musculus_prostaglandin_E_receptor_3_(subtype_EP3)_Ptger3_mRNA	1.84E-19	100	47	1	47	CAGCTCATGGGATCATGTGTGTGCTGCCGCTGT TGCTGCCCT
		Mus_musculus_component_of_oligomeric_goleg_complex_2_(Cog2)_mRNA	2.3	100	15	17	31	TGTGTGTGCTGCCG
		Mus_musculus_solute_carrier_family_26_(sulfate_transporter)_member_1_(Slc26a1)_mRNA	2.3	100	15	10	24	GGGATCATGTGTG
		Mus_musculus_G_protein-coupled_receptor_20_(Gpr20)_mRNA	2.3	94.74	19	11	29	GGGATCATGTGTGCTGTC
		Mus_musculus_protein_phosphatase_1_regulatory_(inhibitor)_subunit_8_(Ppp1r8)_mRNA	2.3	100	15	28	42	TGCTGTGTGCTG
		PREDICTED: Mus_musculus_cytochrome_P450_family_2_subfamily_a_polypeptide_5_(Cyp2a5)_partial_mRNA	9.1	100	14	6	19	CATGGGATCATGT
		Mus_musculus_pyruvate_carboxylase_(Pcx)_nuclear_gene_encoding_mitochondrial_protein_transcript_variant_2_mRNA	9.1	100	14	17	30	TGTGTGTGCTGTC
		Mus_musculus_pyruvate_carboxylase_(Pcx)_nuclear_gene_encoding_mitochondrial_protein_transcript_variant_1_mRNA	9.1	100	14	17	30	TGTGTGTGCTGTC
		Mus_musculus_family_with_sequence_similarity_167_member_A_(Fam167a)_mRNA	9.1	100	14	1	14	CAGCTCATGGGAT
		Mus_musculus_SRY_box_containing_gene_9_(Sox9)_mRNA	9.1	100	14	22	35	TGCTGTCCGCTG
		Mus_musculus_low_density_lipoprotein_receptor-related_protein_1_(Lrp1)_mRNA	9.1	100	14	7	20	ATGGGGATCATGTG
		Mus_musculus_Fras1_related_extracellular_matrix_protein_3_(Frem3)_mRNA	9.1	100	14	30	43	CGCTGTGTGCTG
		Mus_musculus_odd_Oz/ten-m_homolog_4_(Drosophila)_Od24_mRNA	9.1	100	14	17	30	TGTGTGTGCTGTC
		Mus_musculus_tubulin_tyrosine_ligase-like_family_member_13_(Ttl13)_mRNA	9.1	94.44	18	1	18	CAGCTCATGGGATCATG
		Mus_musculus_cytochrome_P450_family_2_subfamily_a_polypeptide_5_(Cyp2a5)_mRNA	9.1	100	14	6	19	CATGGGATCATGT
		Mus_musculus_Rho_GTPase_activating_protein_29_(Rhgap29)_mRNA	9.1	100	14	17	30	TGTGTGTGCTGTC
		Mus_musculus_cytoskeleton-associated_protein_5_(Ckap5)_transcript_variant_2_mRNA	9.1	100	14	15	28	CATGTGTGTGCTG
		Mus_musculus_cytoskeleton-associated_protein_5_(Ckap5)_transcript_variant_1_mRNA	9.1	100	14	15	28	CATGTGTGTGCTG
		Mus_musculus_nuclear_receptor_subfamily_4_group_A_member_2_(Nr4a2)_transcript_variant_1_mRNA	9.1	100	14	19	32	TGTGTGTGCTGCT
		Mus_musculus_nuclear_receptor_subfamily_4_group_A_member_2_(Nr4a2)_transcript_variant_2_mRNA	9.1	100	14	19	32	TGTGTGTGCTGCT
Ptgir	Ptgir_F	Mus_musculus_prostaglandin_I_receptor_(IP)_Ptgir_mRNA	7.97E-07	100	25	1	25	CCGAGCTTCACCTAGGCCATCGCC
		Mus_musculus_SET_domain_containing_(lysine_methyltransferase)_7_(Setd7)_mRNA	0.19	95	20	4	23	AGCTTCATCAGGCCATCG
		Mus_musculus_RIKEN_cDNA_4921511C10_gene_(4921511C10Rik)_non-coding_RNA	0.74	100	15	6	20	CGCTTCATCAGGCCA
		Mus_musculus_cytoplasmic_polyadenylation_element_binding_protein_1_(Cpeb1)_transcript_variant_1_mRNA	0.74	100	15	8	22	TTCACTCAGGCCATC
		Mus_musculus_cytoplasmic_polyadenylation_element_binding_protein_1_(Cpeb1)_transcript_variant_2_mRNA	0.74	100	15	8	22	TTCACTCAGGCCATC
		Mus_musculus_cytoplasmic_polyadenylation_element_binding_protein_1_(Cpeb1)_transcript_variant_3_mRNA	0.74	100	15	8	22	TTCACTCAGGCCATC
		Mus_musculus_uncharacterized LOC434825_(LOC434825)_non-coding_RNA	2.9	100	14	9	22	TCACCTCAGGCCATC
		Mus_musculus_mex3_homolog_B_(C_elegans)_Mex3b_mRNA	2.9	100	14	9	22	TCACCTCAGGCCATC
		Mus_musculus_protein_kinase_C_zeta_(Prkcz)_transcript_variant_2_mRNA	2.9	100	14	12	25	CTCAGGCCATCGCC
		Mus_musculus_protein_kinase_C_zeta_(Prkcz)_transcript_variant_1_mRNA	2.9	100	14	12	25	CTCAGGCCATCGCC
		Mus_musculus_talin_1_(Tln1)_mRNA	2.9	100	14	9	22	TCACCTCAGGCCATC
		Mus_musculus_alkylglycerol_monooxygenase_(Agmo)_mRNA	2.9	100	14	7	20	CTTCACTCAGGCCA
		Mus_musculus_NIPA-like_domain_containing_3_(Nipal3)_mRNA	2.9	100	14	3	16	GAGGCTCACTCAG
		Mus_musculus_ADP-ribosylation_factor_guanine_nucleotide-exchange_factor_1(brefeldin_A_inhibited)_Arfgef1_mRNA	2.9	100	14	1	14	CCGAGGCTCACTC
Ptgir_R		Mus_musculus_prostaglandin_I_receptor_(IP)_Ptgir_mRNA	8.10E-15	100	39	1	39	ATTCTGCTGCCCTCATGACCTCATCATGCCGCTG TGC
		Mus_musculus_solute_carrier_family_30_(zinc_transporter)_member_5_(Slc30a5)_mRNA	0.11	95.24	21	17	37	TGACCGTTCATGCCGCTGT
		Mus_musculus_nucleoporin_85_(Nup85)_mRNA	0.43	95	20	2	21	TTCTGCTGCCCTCATGCC
		Mus_musculus_polycystic_kidney_disease_(polycystin)_and_REJ_(sperm_receptor_for_egg_jelly_homolog_sea_urchin_(Pkdre))_mRNA	1.7	94.74	19	8	26	TGGCCCTCATGCGCTG
		Mus_musculus_G_protein-coupled_receptor_179_(Gpr179)_mRNA	1.7	100	15	6	20	GCTGGCCCTCATGAC
		Mus_musculus_solute_carrier_family_23_(nucleobase_transporters)_member_1_(Slc23a1)_mRNA	1.7	94.74	19	5	23	TGCTGCCCTCATGCCGT
		Mus_musculus_glutamate_receptor_ionotropic_N-methyl_D-aspartate-associated_protein_1_(glutamate_binding)_Grin1_mRNA	1.7	100	15	22	36	GTCCATCATGCCGCTG
		Mus_musculus_olfactory_receptor_30_(Olf30)_mRNA	1.7	100	15	4	18	CTGCTGCCCTCATG
		Mus_musculus_muscle_skeletal_receptor_tyrosine_kinase_(Musk)_transcript_variant_5_mRNA	1.7	100	15	15	29	CATGACGCTCATCT
		Mus_musculus_muscle_skeletal_receptor_tyrosine_kinase_(Musk)_transcript_variant_4_mRNA	1.7	100	15	15	29	CATGACGCTCATCT
		Mus_musculus_muscle_skeletal_receptor_tyrosine_kinase_(Musk)_transcript_variant_3_mRNA	1.7	100	15	15	29	CATGACGCTCATCT
		Mus_musculus_muscle_skeletal_receptor_tyrosine_kinase_(Musk)_transcript_variant_2_mRNA	1.7	100	15	15	29	CATGACGCTCATCT
		Mus_musculus_muscle_skeletal_receptor_tyrosine_kinase_(Musk)_transcript_variant_1_mRNA	1.7	100	15	15	29	CATGACGCTCATCT
		PREDICTED: Mus_musculus_SET_domain_containing_1B_(Setd1b)_mRNA	6.7	100	14	4	17	CTGCTGCCCTCAT
		PREDICTED: Mus_musculus_spectrin_beta_5_(Spn5b)_mRNA	6.7	100	14	4	17	CTGCTGCCCTCAT
		Mus_musculus_testis_expressed_gene_22_(Tex22)_mRNA	6.7	100	14	3	16	CTGCTGCCCTCAT
		Mus_musculus_trinucleotide_repeat_containing_18_(Trnc18)_transcript_variant_A_mRNA	6.7	100	14	5	18	TGCTGCCCTCATG
		PREDICTED: Mus_musculus_SET_domain_containing_1B_(Setd1b)_mRNA	6.7	100	14	4	17	CTGCTGCCCTCAT
		Mus_musculus_preferentially_expressed_antigen_in_melanoma_like_5_(Prmel5)_mRNA	6.7	100	14	16	29	ATGACCTCATCAT
		Mus_musculus_protein_tyrosine_phosphatase_receptor_type_F_(Ptprf)_mRNA	6.7	100	14	4	17	CTGCTGCCCTCAT
Pth1r_F	Pth1r_F	Mus_musculus_parathyroid_hormone_1_receptor_(Pth1r)_transcript_variant_3_mRNA	3.06E-14	100	38	1	38	CTCAACTCATCTCTTTTCAACATCATCCGGGCTG T
		Mus_musculus_parathyroid_hormone_1_receptor_(Pth1r)_transcript_variant_2_mRNA	3.06E-14	100	38	1	38	CTCAACTCATCTCTTTTCAACATCATCCGGGCTG T
		Mus_musculus_parathyroid_hormone_1_receptor_(Pth1r)_transcript_variant_1_mRNA	3.06E-14	100	38	1	38	CTCAACTCATCTCTTTTCAACATCATCCGGGCTG T
		Mus_musculus_vasoactive_intestinal_peptide_receptor_1_(Vipr1)_mRNA	0.1	89.66	29	4	32	AACCTCATCTCTTTATCAACATCATCCG
		Mus_musculus_BRCA2_and_CDKN1A_interacting_protein_(Bccip)_mRNA	0.41	100	16	2	17	CTCAACTCATCTCTT
		Mus_musculus_RNA_polymerase_II_associated_protein_1_(Rpap1)_transcript_variant_1_mRNA	0.41	100	16	6	21	CTTCACTCTCTTATC
		Mus_musculus_RNA_polymerase_II_associated_protein_1_(Rpap1)_transcript_variant_2_mRNA	0.41	100	16	6	21	CTTCACTCTCTTATC
		PREDICTED: Mus_musculus_predicted_gene_10535_(Gm10535)_miscRNA	1.6	100	15	3	17	CAACTCATCTCTT
		Mus_musculus_vacuolar_protein_sorting_41_(yeast)_Vps41_mRNA	1.6	100	15	15	29	CTTATCAACATCAT
		Mus_musculus_serrate_RNA_effector_molecule_homolog_(Arabidopsis)_Srrt1_transcript_variant_1_mRNA	1.6	100	15	20	34	TCAACATCATCCGG
		Mus_musculus_serrate_RNA_effector_molecule_homolog_(Arabidopsis)_Srrt1_transcript_variant_2_mRNA	1.6	100	15	20	34	TCAACATCATCCGG
		Mus_musculus_serrate_RNA_effector_molecule_homolog_(Arabidopsis)_Srrt1_transcript_variant_3_mRNA	1.6	100	15	20	34	TCAACATCATCCGG
		Mus_musculus_leucine-rich_repeats_and_IQ_motif_containing_3_(Lrrq3)_mRNA	1.6	100	15	16	30	TTTATCAACATCATC
		Mus_musculus_cytochrome_b_561_domain_containing_1_(Cyb561d1)_transcript_variant_1_mRNA	1.6	100	15	17	31	TTATCAACATCATCC
		Mus_musculus_cytochrome_b_561_domain_containing_1_(Cyb561d1)_transcript_variant_2_mRNA	1.6	100	15	17	31	TTATCAACATCATCC
		Mus_musculus_ryanodine_receptor_3_(Ryr3)_mRNA	1.6	100	15	3	17	CAACTCATCTCTT
		PREDICTED: Mus_musculus_predicted_gene_10535_(Gm10535)_miscRNA	1.6	100	15	3	17	CAACTCATCTCTT
		Mus_musculus_NOP58_ribonucleoprotein_homolog_(yeast)_Nop58_mRNA	1.6	100	15	7	21	TTCACTCTTTTATC
		PREDICTED: Mus_musculus_NLR_family_pyrrin_domain_containing_1B_(Nlrp1b)_partial_mRNA	1.6	94.44	18	18	35	TATCAACATCATCCGGG
		Mus_musculus_cytochrome_b_245_beta_polypeptide_(Cyb245)_mRNA	6.4	100	14	11	24	TCTTCTTATCAAC
Pth1r_R		Mus_musculus_parathyroid_hormone_1_receptor_(Pth1r)_transcript_variant_3_mRNA	6.21E-09	100	29	1	29	TGGGCAAGAAGTGGATCATCCAGGTGC
		Mus_musculus_parathyroid_hormone_1_receptor_(Pth1r)_transcript_variant_2_mRNA	6.21E-09	100	29	1	29	TGGGCAAGAAGTGGATCATCCAGGTGC
		Mus_musculus_parathyroid_hormone_1_receptor_(Pth1r)_transcript_variant_1_mRNA	6.21E-09	100	29	1	29	TGGGCAAGAAGTGGATCATCCAGGTGC
		Mus_musculus_adenosine_monophosphate_deaminase_3_(Ampd3)_mRNA	0.36	100	16	14	29	TGGATCATCCAGGTG
		Mus_musculus_phosphoribosyl_pyrophosphate_synthetase_1-like_3_(Prps13)_mRNA	1.4	94.74	19	11	29	AAGTGGATCATCCAGGTGC
		Mus_musculus_MYB_binding_protein_(P160)_1a_(Mybbp1a)_mRNA	1.4	100	15	10	24	GAGTGGATCATCA
		Mus_musculus_X-linked_lymphocyte-regulated_5B_(Xlr5b)_mRNA	5.5	100	14	13	26	GTGGATCATCCAGG
		Mus_musculus_X-linked_lymphocyte-regulated_5A_(Xlr5a)_mRNA	5.5	100	14	13	26	GTGGATCATCCAGG
		Mus_musculus_raffin_lipid_raff linker_1_(Rfln1)_mRNA	5.5	100	14	8	21	ABGAAGTGGATCAT
		Mus_musculus_zinc_finger_CCH2_type_containing_7B_(Zc3h7b)_mRNA	5.5	100	14	3	16	GSCACAGAATGGG
		Mus_musculus_aldo-keto_reductase_family_1_member_C20_(Akr1c20)_mRNA	5.5	94.44	18	7	24	CAAGAATGGATCATCA
		Mus_musculus_purine_rich_element_binding_protein_B_(Purb)_mRNA	5.5	100	14	1	14	TGGGCAAGAAGT
		Mus_musculus_predicted_gene_17296_(Gm17296)_mRNA	5.5	100	14	7	20	CAAGAATGGATCAT
		Mus_musculus_folate_receptor_2_(fetal)_Folr2_mRNA	5.5	100	14	1	14	TGGGCAAGAAGT
		Mus_musculus_Eph_receptor_A7_(Epha7)_transcript_variant_2_mRNA	5.5	100	14	15	28	GGATCATCCAGGTG
		Mus_musculus_Eph_receptor_A7_(Epha7)_transcript_variant_1_mRNA	5.5	100	14	15	28	GGATCATCCAGGTG
Tbxa2r_R	Tbxa2r_R	Mus_musculus_thromboxane_A2_receptor_(Tbxa2r)_mRNA	2.68E-18	100	45	1	45	TTCACTGCTGGGCATCATGTGTGGCCAGGTG TGTTGGATG
		Mus_musculus_prostaglandin_E_receptor_1_(subtype_EP1)_Ptger1_mRNA	9.13E-06	100	24	3	26	CAGCTGTGGGCATCATGGTGGT
		PREDICTED: Mus_musculus_RIKEN_cDNA_1700040D17_gene_(1700040D17Rik)_miscRNA	0.54	100	16	20	35	GGGTGTGGCCATGTC

	Mus_musculus_shroom_family_member_4_(Shroom4),_mRNA	0.54	100	16	17	32	CATGGTGGTGGCCAGC
	Mus_musculus_chemokine_(C-C_motif)_receptor_9_(Ccr9),_transcript_variant_2,_mRNA	0.54	100	16	9	24	GTGGGCATCATGGTGG
	Mus_musculus_chemokine_(C-C_motif)_receptor_9_(Ccr9),_transcript_variant_1,_mRNA	0.54	100	16	9	24	GTGGGCATCATGGTGG
	PREDICTED:_Mus_musculus_RIKEN_cDNA_1700040D17_gene_(1700040D17Rik),_miscRNA	0.54	100	16	20	35	GGTGGTGGCCACGGTG
	PREDICTED:_Mus_musculus_predicted_pseudogene_5958_(Gm5958),_mRNA	2.1	100	15	16	30	TCATGGTGGTGGCCCA
	PREDICTED:_Mus_musculus_cell_division_cycle_20_homolog_B_(S_cerevisiae)_(Cdc20b),_mRNA	2.1	94.74	19	14	32	CATCATGGTGGTGGCCACG
	PREDICTED:_Mus_musculus_predicted_pseudogene_5958_(Gm5958),_mRNA	2.1	100	15	16	30	TCATGGTGGTGGCCCA
	PREDICTED:_Mus_musculus_cell_division_cycle_20_homolog_B_(S_cerevisiae)_(Cdc20b),_mRNA	2.1	94.74	19	14	32	CATCATGGTGGTGGCCACG
	Mus_musculus_zinc_finger_protein_748_(Zfp748),_transcript_variant_2,_mRNA	2.1	100	15	17	31	CATGGTGGTGGCCAC
	Mus_musculus_zinc_finger_protein_748_(Zfp748),_transcript_variant_1,_mRNA	2.1	100	15	17	31	CATGGTGGTGGCCAC
	PREDICTED:_Mus_musculus_predicted_gene_9837_(Gm9837),_miscRNA	2.1	100	15	23	37	GGTGGCCACGGTGTG
	Mus_musculus_gap_junction_protein_delta_3_(Gjd3),_mRNA	2.1	91.3	23	13	35	GCATCATGGTGGTGGCCACGGTG
	Mus_musculus_heparan_sulfate_(glucosamine)_3-O-sulfotransferase_3B1_(Hs3st3b1),_mRNA	2.1	100	15	6	20	CTCGTGGGCATCATG
	PREDICTED:_Mus_musculus_predicted_gene_9837_(Gm9837),_miscRNA	2.1	100	15	23	37	GGTGGCCACGGTGTG
	Mus_musculus_SRY-box_containing_gene_6_(Sox6),_transcript_variant_1,_mRNA	2.1	100	15	17	31	CATGGTGGTGGCCAC
	Mus_musculus_multiple_EGF-like_domains_9_(Megf8),_mRNA	2.1	100	15	24	38	GTGGCCACGGTGTGT
	Mus_musculus_contactin_associated_protein-like_2_(Cntnap2),_transcript_variant_1,_mRNA	2.1	100	15	25	39	TGGCCACGGTGTGT
Tbxa2r_F	Mus_musculus_thromboxane_A2_receptor_(Tbxa2r),_mRNA	2.41E-11	100	33	1	33	TTCATGCAGACTTTGTGCAGACCCACCT
	Mus_musculus_glutamic-oxaloacetic_transaminase_1-like_1_(Got1l1),_mRNA	1.3	100	15	5	19	TCATGCAGACTTTGT
	Mus_musculus_a_disintegrin_and_metalloproteinase_domain_1a_(Adam1a),_mRNA	1.3	100	15	6	20	CATGCAGACTTTGT
	Mus_musculus_nucleolar_and_spindle_associated_protein_1_(Nusap1),_transcript_variant_2,_mRNA	1.3	100	15	10	24	CAGACTTTGTGCAG
	Mus_musculus_nucleolar_and_spindle_associated_protein_1_(Nusap1),_transcript_variant_1,_mRNA	1.3	100	15	10	24	CAGACTTTGTGCAG
	Mus_musculus_regulatory_factor_X_3_(influences_HLA_class_II_expression)_(Rfx3),_transcript_variant_2,_mRNA	5.3	100	14	3	16	CATCATGCAGACTT
	Mus_musculus_regulatory_factor_X_3_(influences_HLA_class_II_expression)_(Rfx3),_transcript_variant_1,_mRNA	5.3	100	14	3	16	CATCATGCAGACTT
	Mus_musculus_fatty_acid_desaturase_3_(Fads3),_mRNA	5.3	100	14	17	30	TGTTGCAGACACCA
	Mus_musculus_Notch_gene_homolog_3_(Drosophila)_(Notch3),_mRNA	5.3	100	14	19	32	TTGCAGACACACC
	Mus_musculus_transmembrane_protein_55b_(Tmem55b),_mRNA	5.3	100	14	18	31	GTTCAGACACACC
	Mus_musculus_vomerinasal_1_receptor_200_(Vmn1r200),_mRNA	5.3	100	14	6	19	CATGCAGACTTTGT
	Mus_musculus_calmodulin_1_(Calm1),_mRNA	5.3	100	14	6	19	CATGCAGACTTTGT
	Mus_musculus_HEAT_repeat_containing_6_(Heatr6),_mRNA	5.3	100	14	15	28	TTTGTGCAGACAC
	Mus_musculus_RIKEN_cDNA_D930048N14_gene_(D930048N14Rik),_non-coding_RNA	5.3	100	14	1	14	TTCATCATGCAGAC
	Mus_musculus_netrin_4_(Ntn4),_mRNA	5.3	100	14	16	29	TTTGTGCAGACACC
	Mus_musculus_CD164_antigen_(Cd164),_mRNA	5.3	100	14	4	17	ATCATGCAGACTTT
	Mus_musculus_proprotein_convertase_subtilisin/kexin_type_7_(Pcsk7),_mRNA	5.3	100	14	2	15	TCATCATGCAGACTT
	Mus_musculus_phosphatidylinositol_glycan_anchor_biosynthesis_class_Y-like_(Pigy1),_mRNA	5.3	100	14	20	33	TGCAGACACACCT
	Mus_musculus_piwi-like_homolog_4_(Drosophila)_(Pwi4),_mRNA	5.3	100	14	5	18	TCATGCAGACTTTG
	Mus_musculus_arginine/serine-rich_coiled-coil_2_(Rsrc2),_transcript_variant_3,_mRNA	5.3	100	14	16	29	TTTGTGCAGACACC

REVIEWERS' COMMENTS:

Reviewer #4 (Remarks to the Author):

My questions have mostly been answered. Just that the authors verified the protein-level expression of several GPCR receptors by flow cytometry. From my point of view, immunostaining is better that can directly see the in situ heterogeneity.