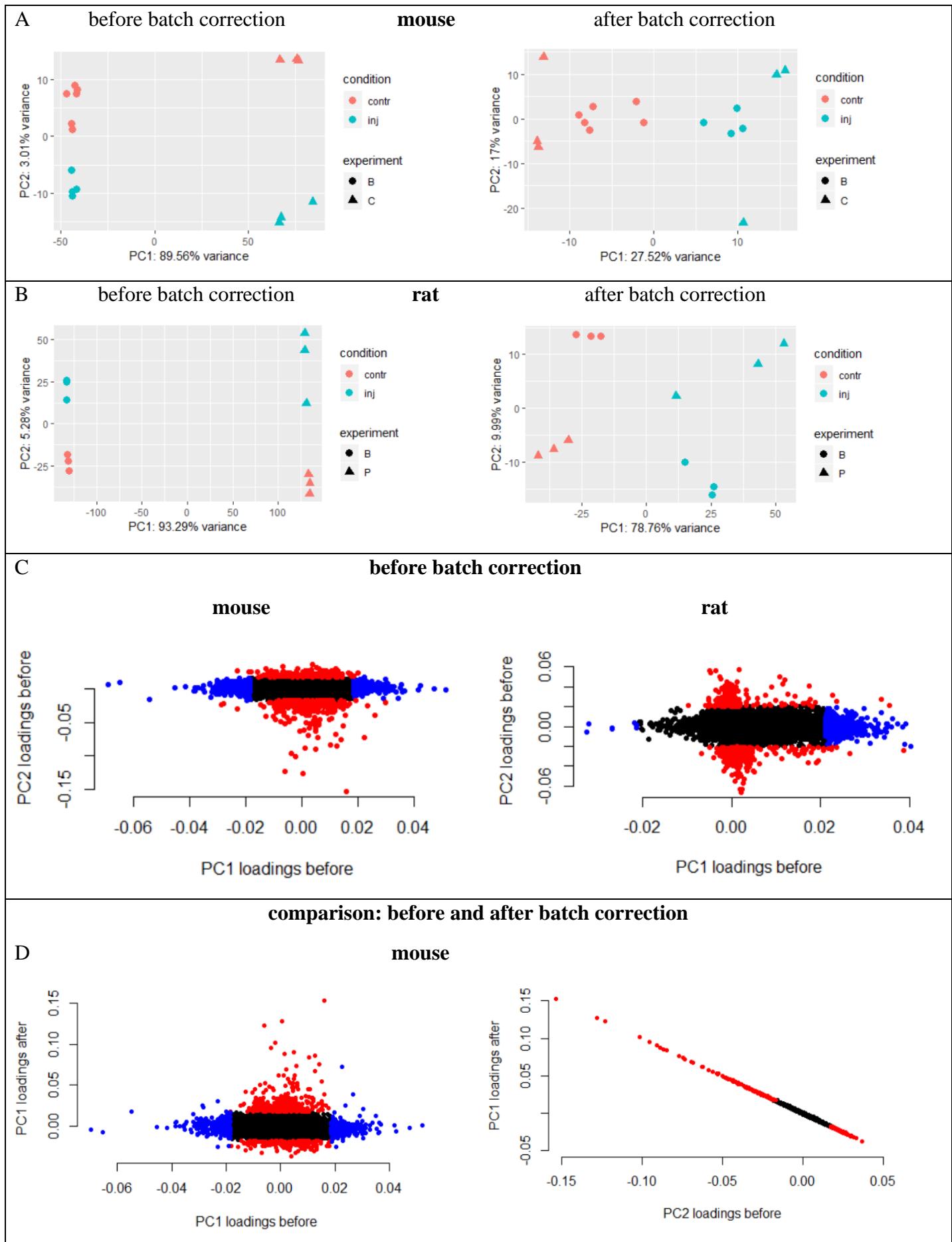
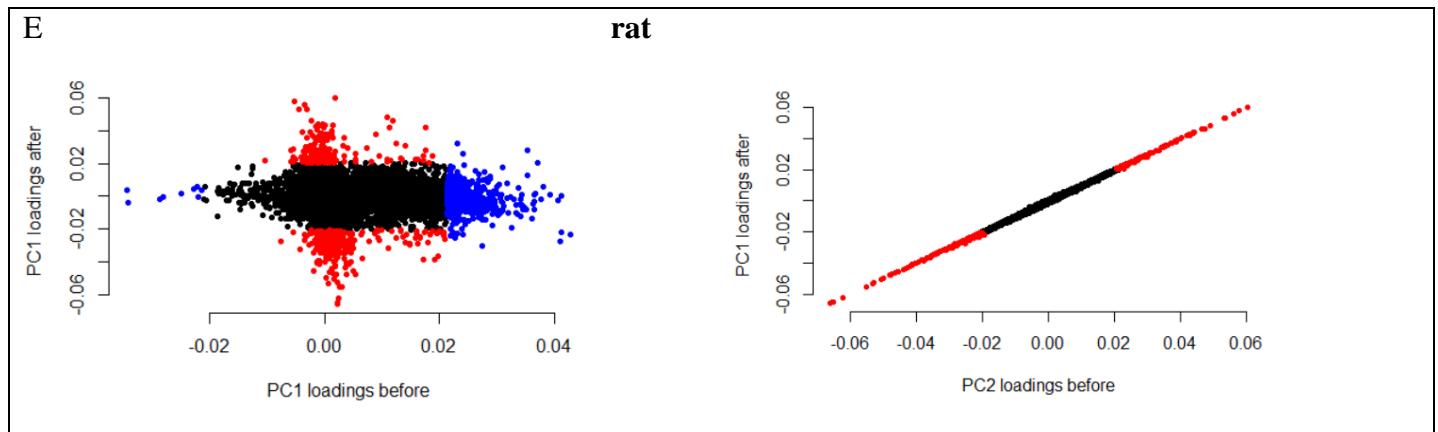
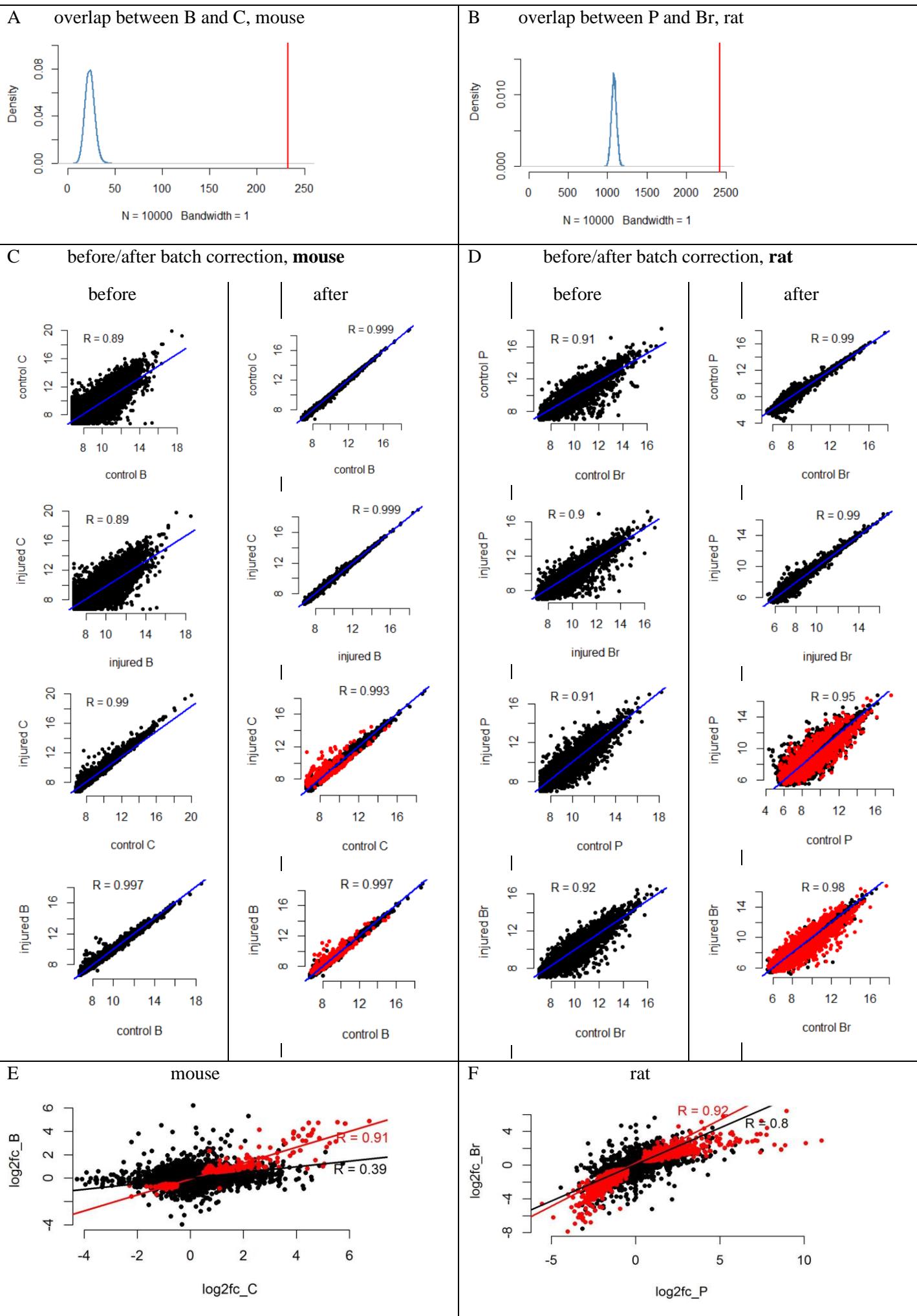


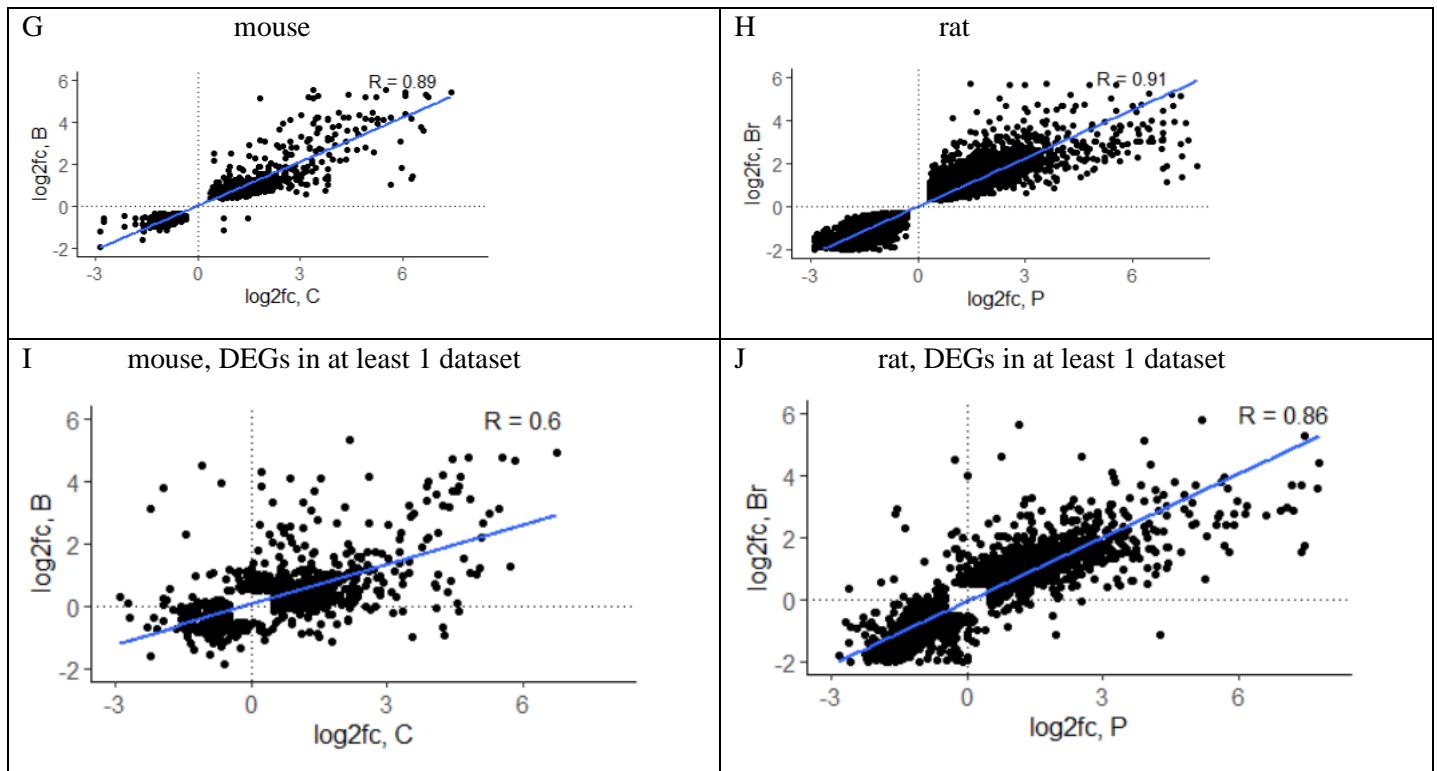
## Supplementary Figures





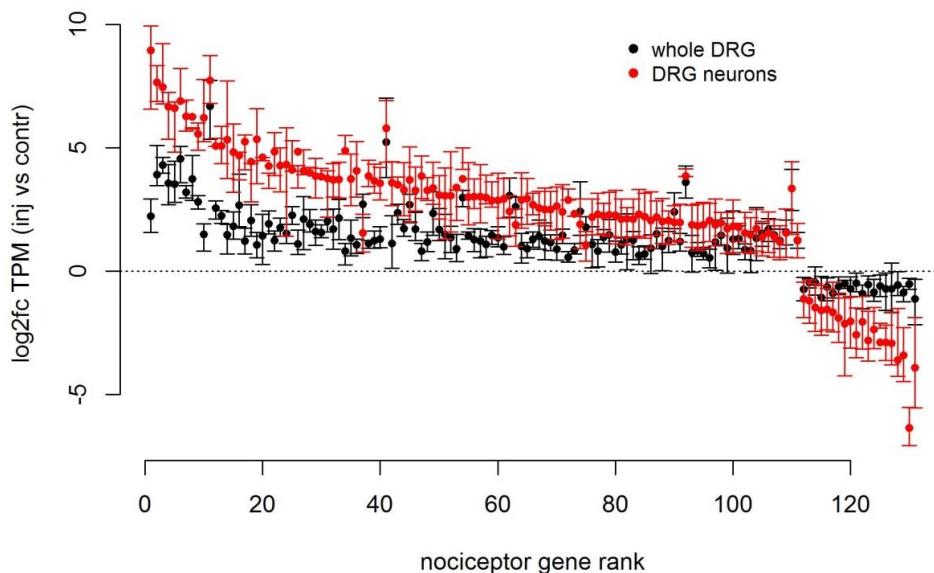
**Figure S1. PCA plots of rodent samples and the effects of batch correction.** **A,B.** PCA plots of variance-stabilized transformed counts of mouse (A) and rat (B) datasets before and after batch correction. Batch correction was done internally by Deseq2 and illustrated using the removeBatchEffect function from limma. **C.** Gene loadings on top PCs before batch correction for mouse (left) and rat (right). All genes - black, top 500 genes with highest loading on PC1 and PC2 are shown by blue and red dots, respectively. **D,E.** Gene loadings on top PCs before and after batch correction. All genes - black, top 500 PC1 genes before the correction - blue and top 500 PC1 genes after the correction - red (left). Right panel shows linear correlation of the top 500 PC2 genes before the correction and PC1 genes after the correction.



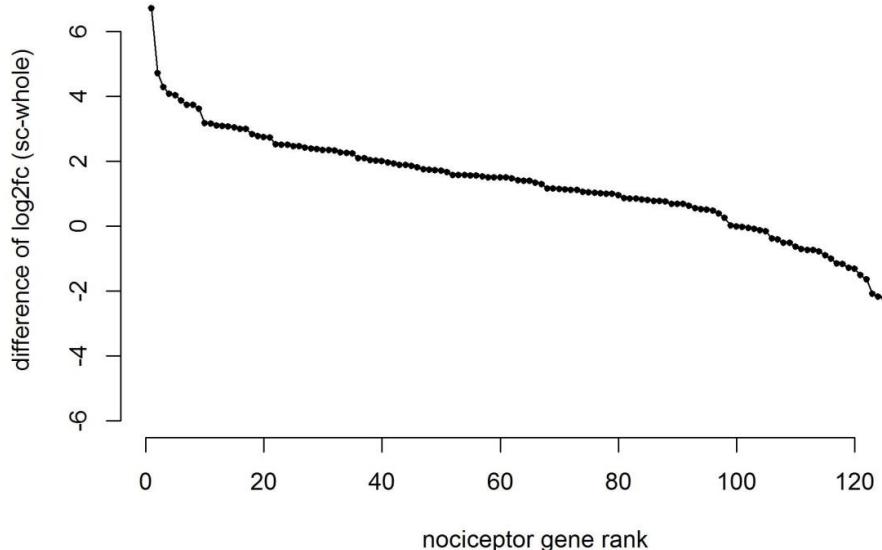


**Figure S2. Gene overlap and correlation between samples.** **A,B.** Expected number of overlapping genes between mouse (A) and rat (B) datasets. The figures show the probability densities calculated by random sampling from all expressed genes (19,312 for A and 13,940 for B). Sampling sizes were equal to the respective sizes of DEG sets: 966 genes for Cobos (C) and 474 for Baskozos (Br) mouse datasets (A); 5154 for Perkins (P) and 2950 for Baskozos (Br) rat datasets (B). Red lines correspond to the size of the observed overlap ( $p \sim 4 \cdot 10^{-184}$ ). **C,D.** Effects of the correction of technical variations on the linear correlation of vst-normalized mean expression between datasets/batches or treatments (injury vs control). DEGs are marked by red on the panels with injured vs control after the correction. **E,F.** The linear correlation between  $\log_{2}fc$  in the expression of the common mouse (E) or rat (F) DEGs (red) and between all expressed genes (black). Red and black labels show correlation coefficients for DEGs and the whole transcriptome, respectively. **G,H.** The linear correlation between  $\log_{2}fc$  in the expression of the common mouse (E) or rat (F) DEGs, taking into account the spread of the  $\log_{2}fc$  between replicates. For each gene four data points were plotted, corresponding to pairwise comparison between low and upper bounds of  $\log_{2}fc$  ( $\log_{2}fc \pm \text{lfcSE}$ , where lfcSE is a standard error of  $\log_{2}fc$ ). **I,J.** The linear correlation between  $\log_{2}fc$  of genes identified as DEGs in at least one dataset for mouse (I) or rat (J).

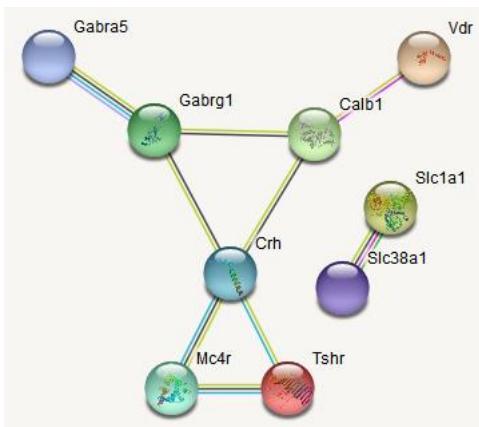
A



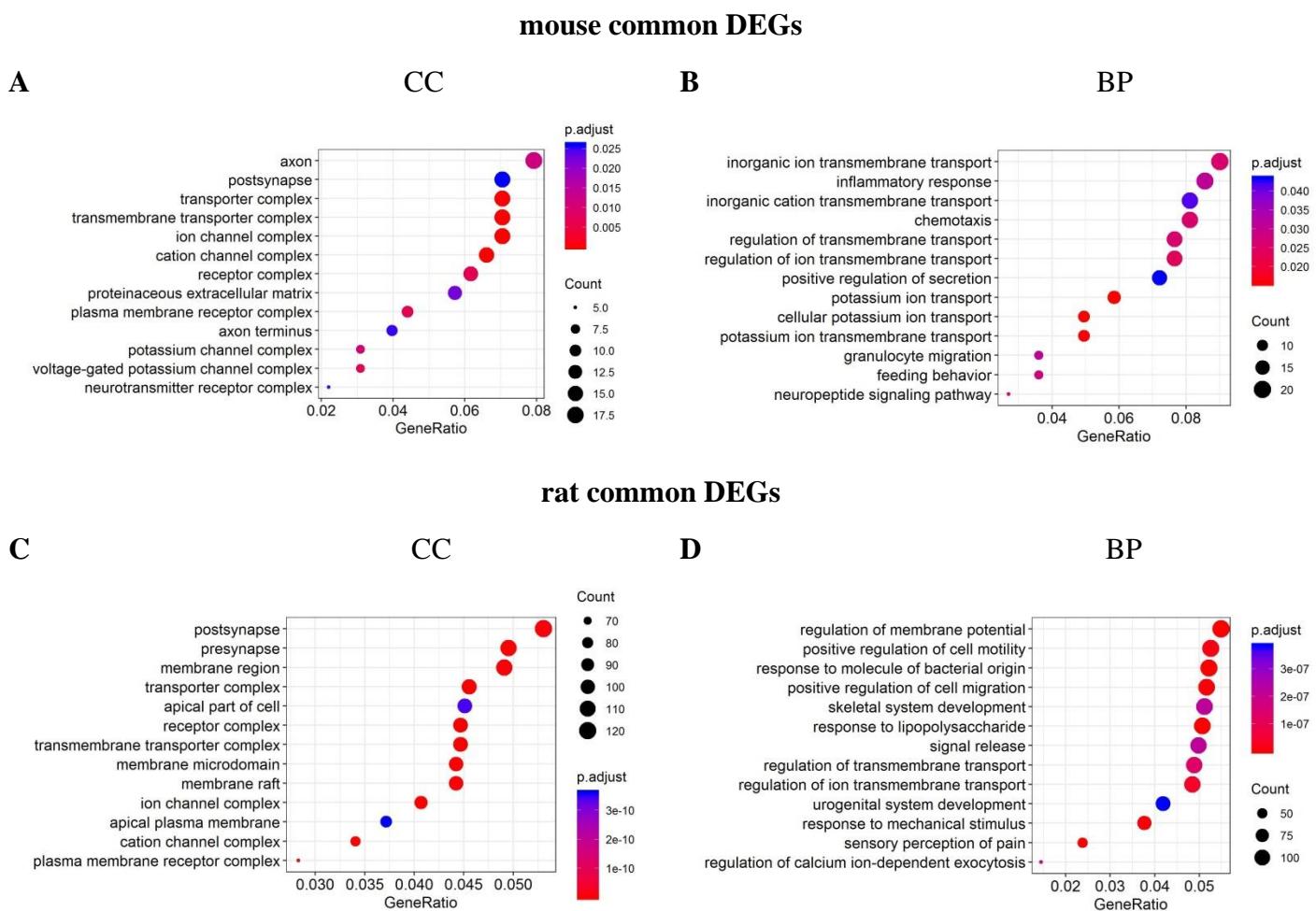
B



**Figure S3. Comparison of single cell and bulk expression of the common mouse neuronal DEGs. A.** Mean expression changes (log<sub>2</sub>fc of transcripts per million, TPM) of 131 common mouse DEGs. For single cell dataset (red) the values were taken from [17], for all sensory neurons. For the whole DRG (black) the Cobos dataset was used, as it represents to early changes after the injury (day 7), comparable to the single cell dataset (day 3). For each gene the error bars show the spread of the expression changes (min to max). For the single cell dataset the lower and upper bounds of log<sub>2</sub>fc TPM were taken from [17], for all sensory neurons expressing the gene. For the bulk dataset error bars show min and max values of log<sub>2</sub>fc TPM, based on all replicates of the Cobos dataset. **B.** The differences between the mean expression changes of single cell and whole DRG datasets, calculated from A. The genes were ranked by the expression changes in single cell dataset multiplied to the differences in expression changes between single cell and the whole DRG dataset (for A) or by the differences in expression changes between single cell and the whole DRG dataset (for B).

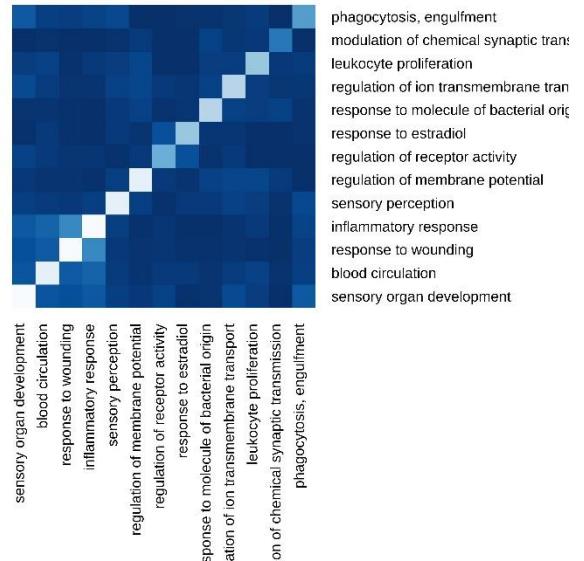
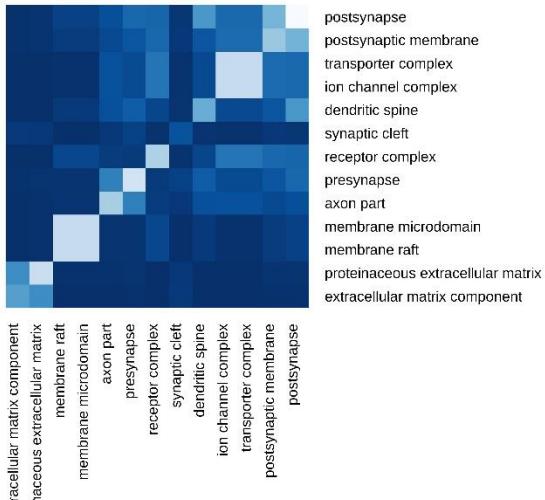


**Figure S4. STRING analysis for biological interactions within anti-correlated genes between rat and mouse SNT models (Table S5).** Only interacting genes, which are potentially involved in nociception are shown, with medium confidence of interactions (score 0.4). The line colour indicates the type of interaction evidence.



**overlap between gene sets of top GO terms for rat/mouse common DEGs (from Fig. 2 A,B)**

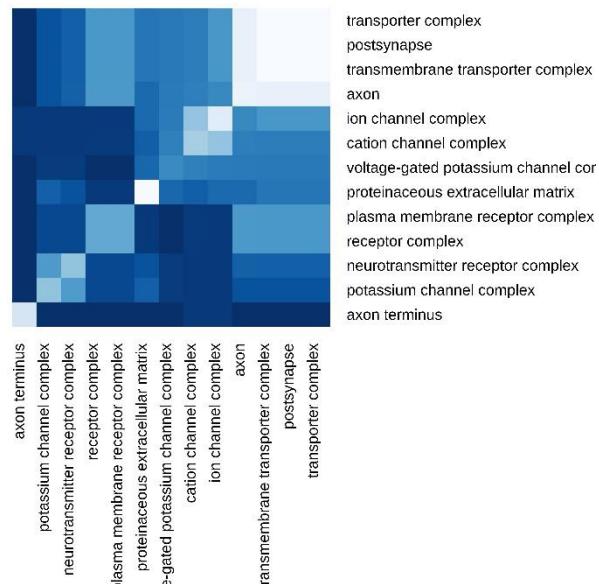




**overlap between gene sets of top GO terms for mouse common DEGs (from A,B)**

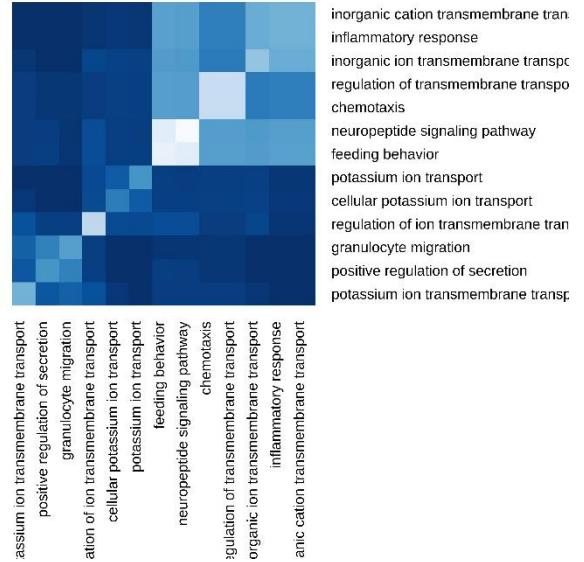
**G**

**CC**



**H**

**BP**



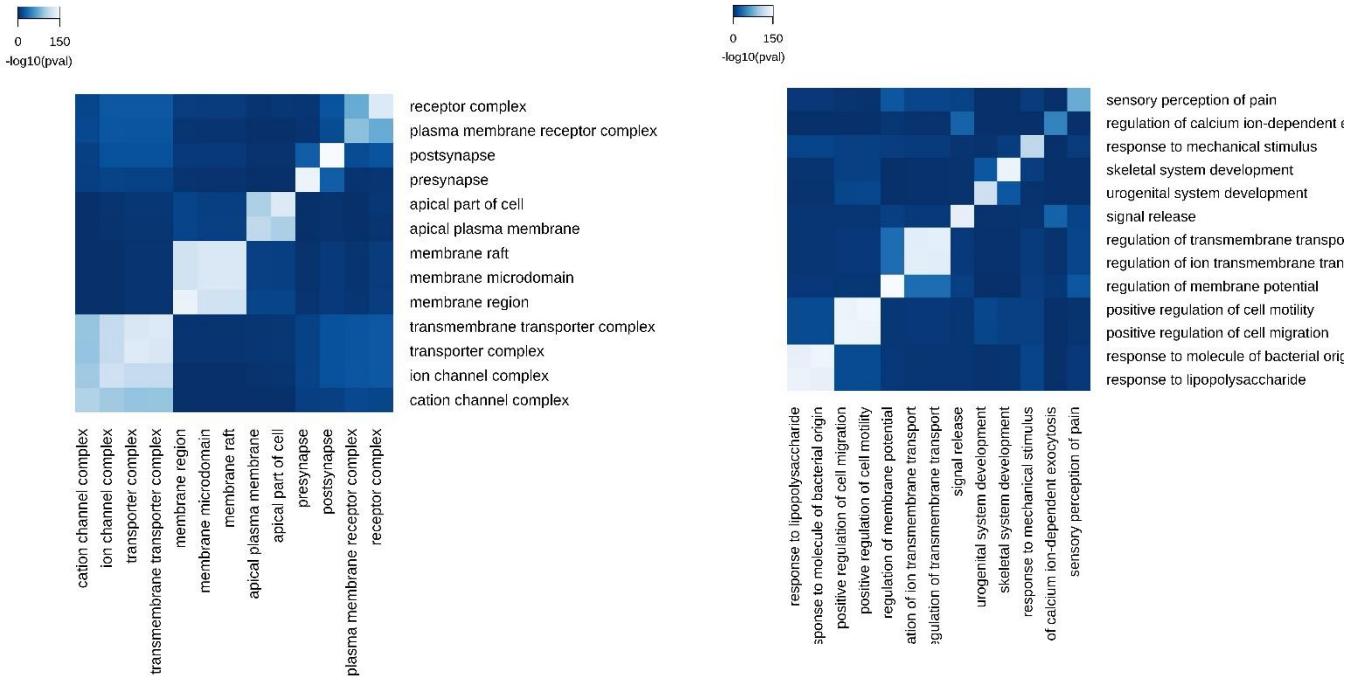
**overlap between gene sets of top GO terms for rat common DEGs (from C,D)**

**I**

**CC**

**J**

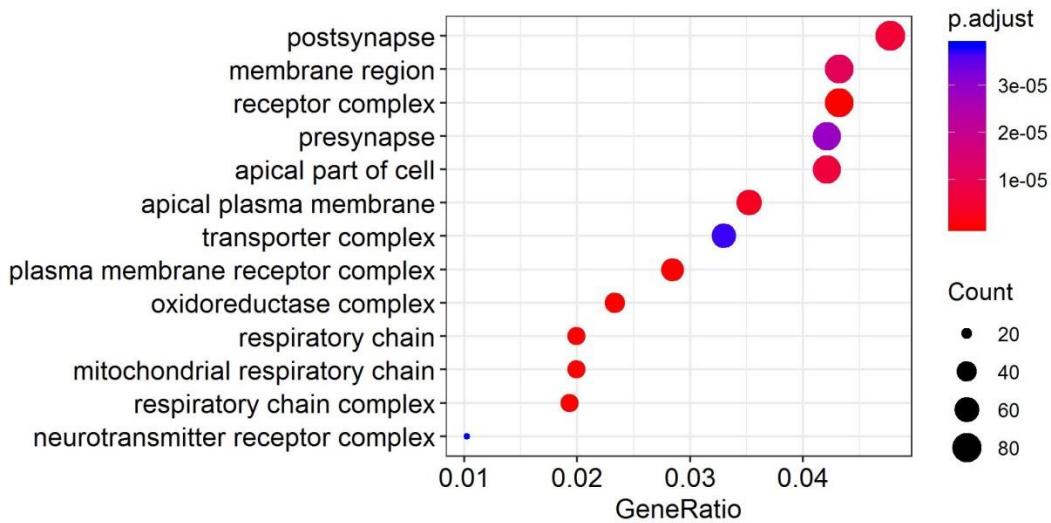
**BP**



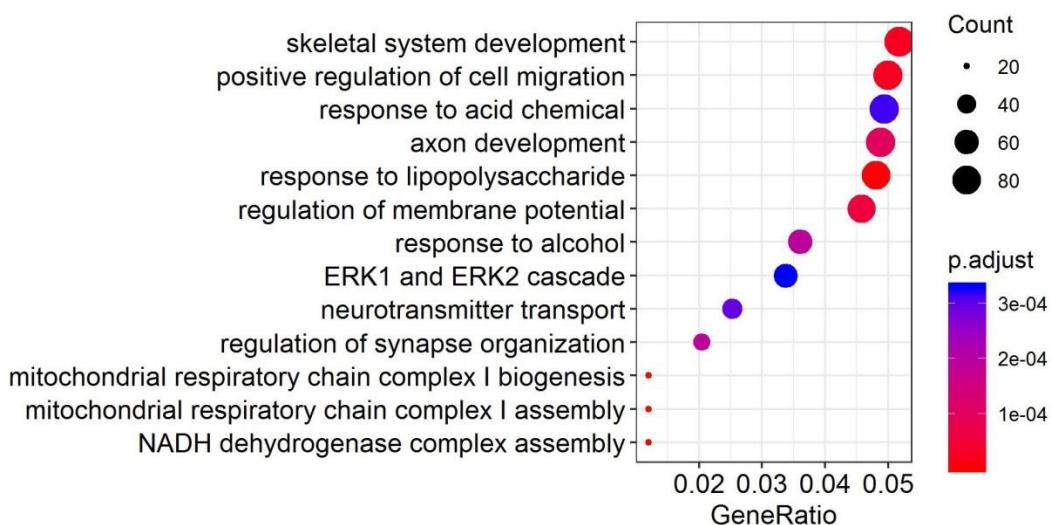
**Figure S5. The enrichment analysis of the common mouse (Table S2) and rat (Table S3) DEGs.**

Analysis of the significantly enriched GO terms within mouse (A,B) and rat (C,D) genes using ClusterProfiler with FDR adjusted  $P \leq 0.05$ . GO terms are shown for the cell component, (A,C) and biological processes (B,D) categories. E-J. Similarity matrices for the enriched sets of DEGs from the top GO terms shown on Fig. 2, Fig. S5A-D, showing the significance of the overlap (-log<sub>10</sub> of  $P$  value) between each pair of gene sets.  $P$  values of the overlaps were calculated using hypergeometric distribution, with total number of drawn genes equal to 18,270 (the number of all genes used in ClusterProfiler, R-3.5.1).

A

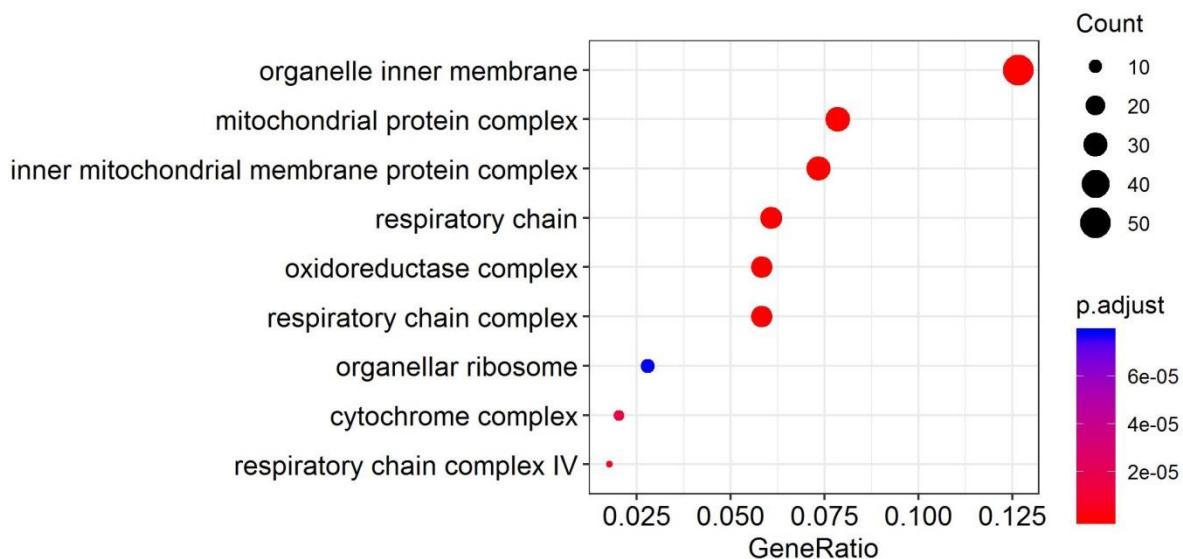


B

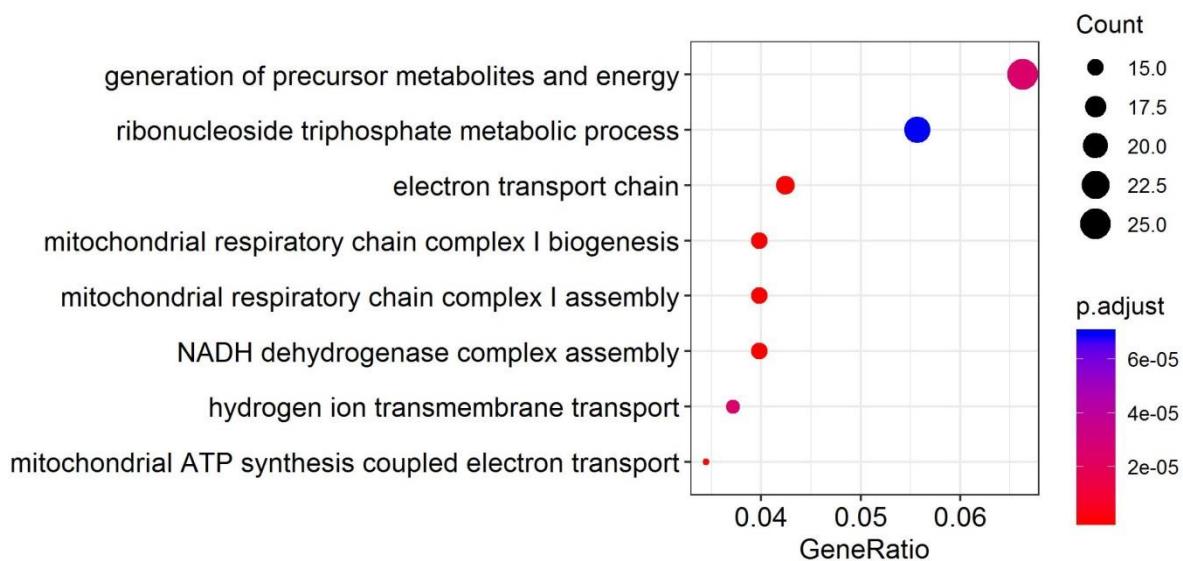


**Figure S6. The enrichment analysis of the common rat DEGs (Table S3), excluding genes classified as sensory neurons - related with the mouse classification from [17].** The ClusterProfiler analysis of significantly enriched GO terms within the cell component (A) and biological processes (B) categories; FDR adjusted  $P \leq 0.05$ .

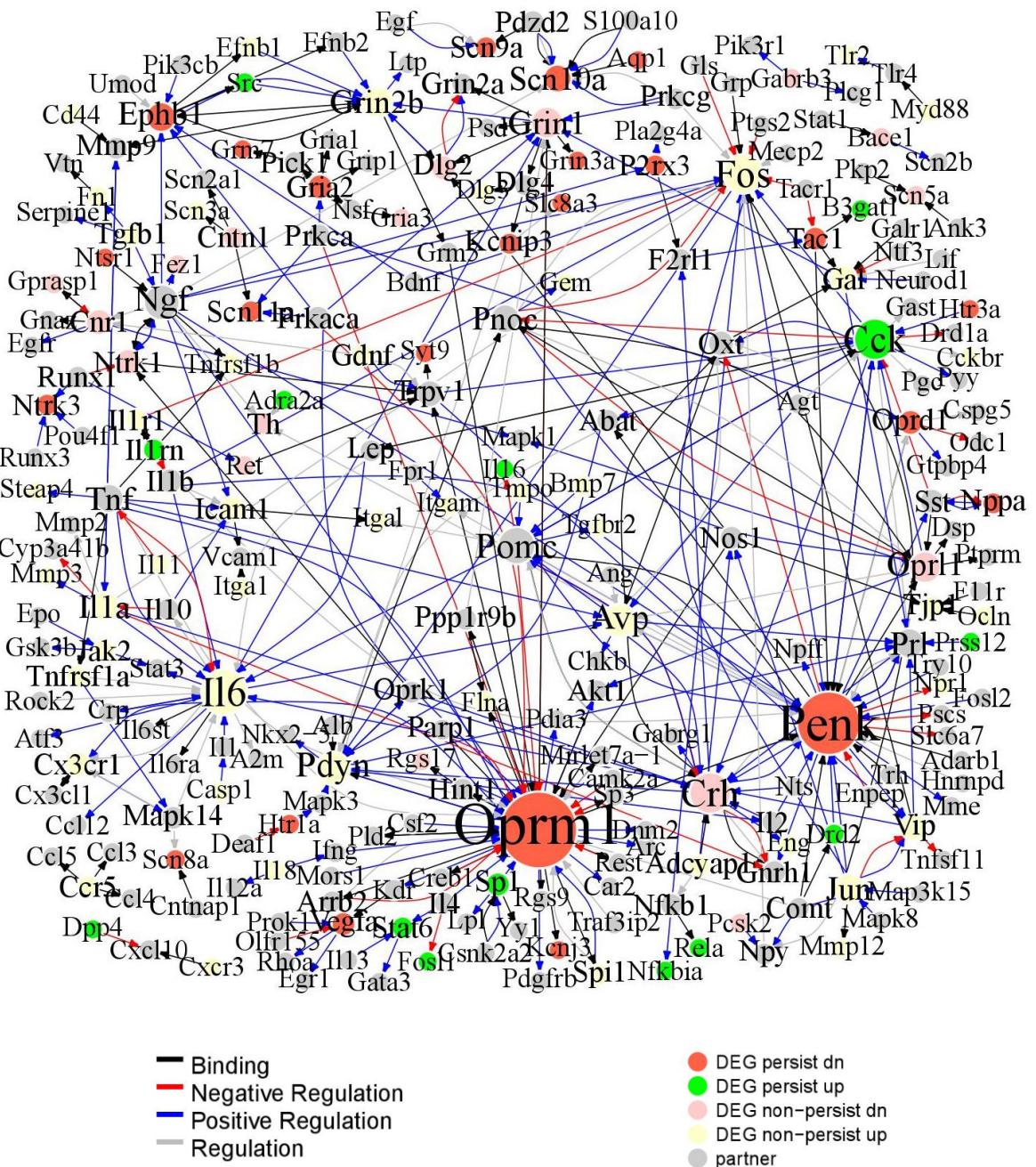
A



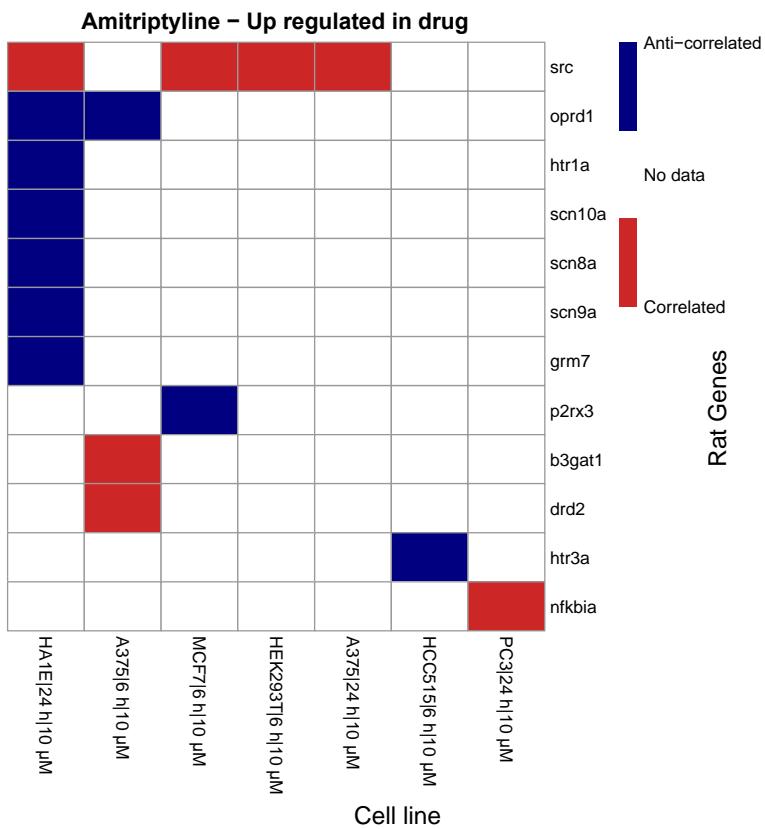
B



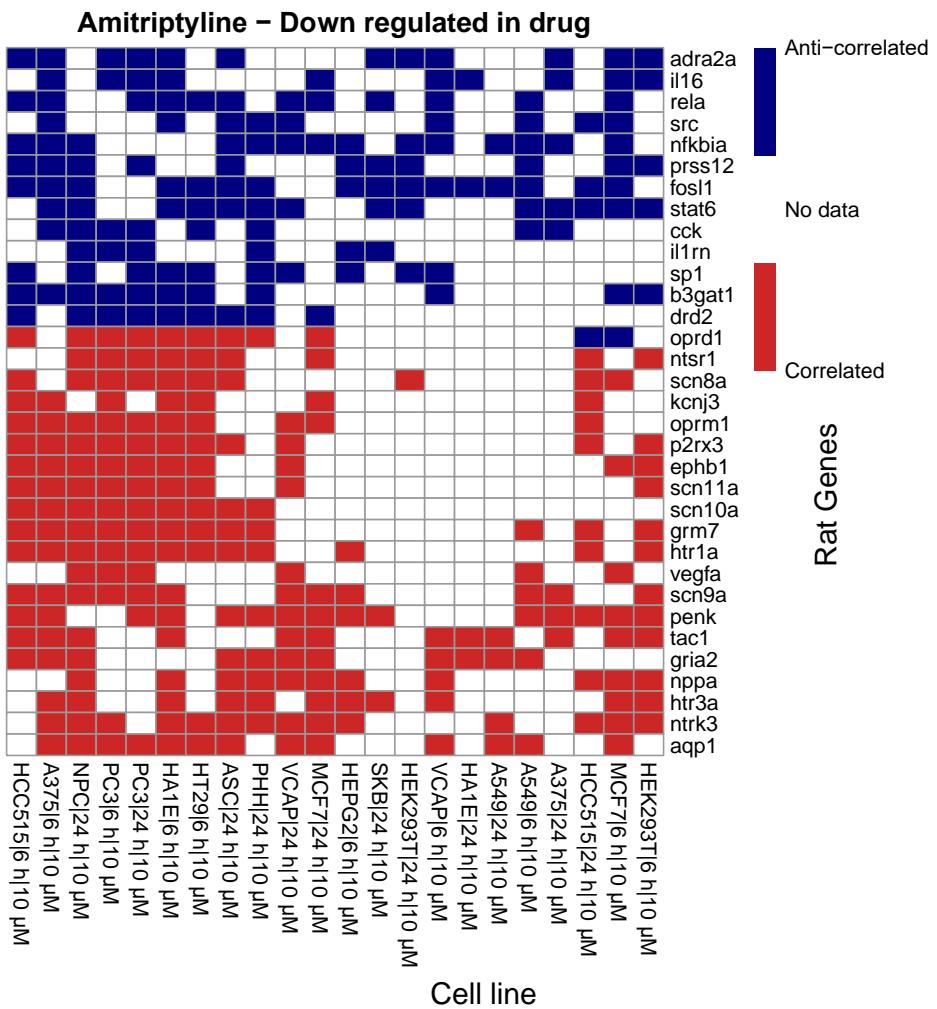
**Figure S7. The enrichment analysis of the persistent rat DEGs, which are not present in the mouse dataset of sensory neurons from [17].** Only gene with relatively low expression changes ( $0.5 \leq |\log_{2}fc| < 1$ ) (432 genes) were analysed with ClusterProfiler within the biological processes (A) and cell component (B); FDR adjusted  $P \leq 0.05$ . Analysis of genes with  $|\log_{2}fc| \geq 1$  is shown on Fig. 4A,B.



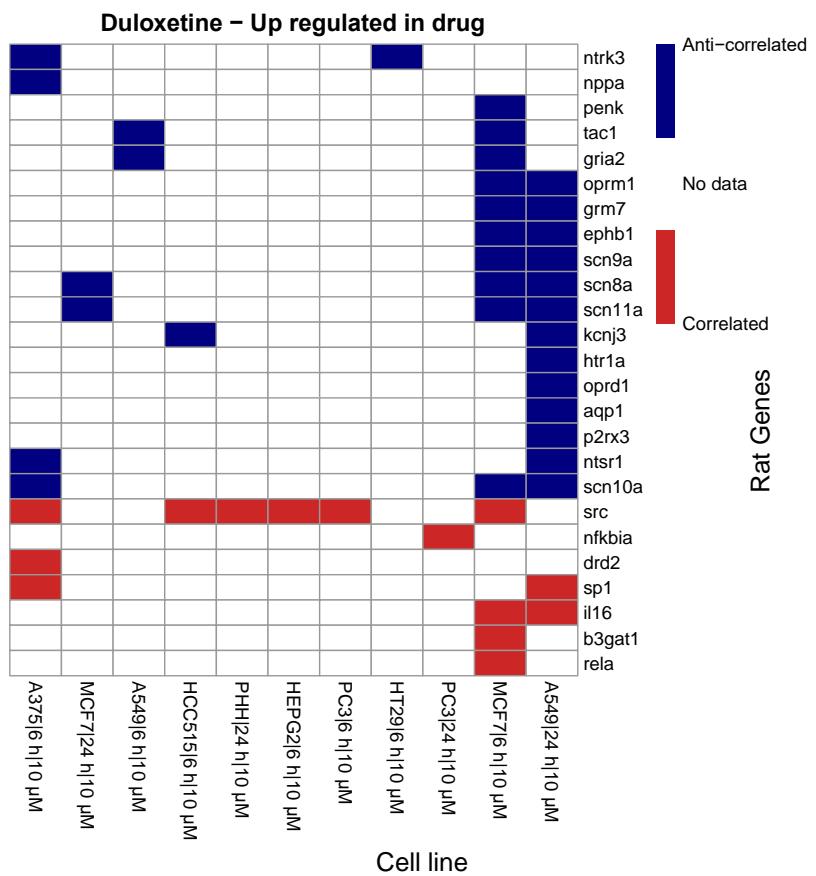
**Figure S8. The pain-related PPI network of the common rat DEGs.** The networks were built based on pain interactome, using the common rat DEGs, together with neighbours from the pain interactome network. The coloured arrows mark the type and direction of interactions; coloured nodes mark the expression changes in rat datasets (up/down/persistent/non-persistent/non-DEG partner), as explained in the legend.



**Figure S9. Persistent rat genes from the pain network of Fig. 5 that are either anti-correlated or correlated with respect to an up-regulated signature from the treatment of amitriptyline.** Only the cell lines with up-regulated genes in response to drugs are shown. The comparison of the direction of the drug effect with the direction of expression changes during nerve injury is shown by colour; white indicates no data available. The column names show *cell lines | time of the exposure to drug | drug concentration*. The row names show gene names in low case, for compactness.

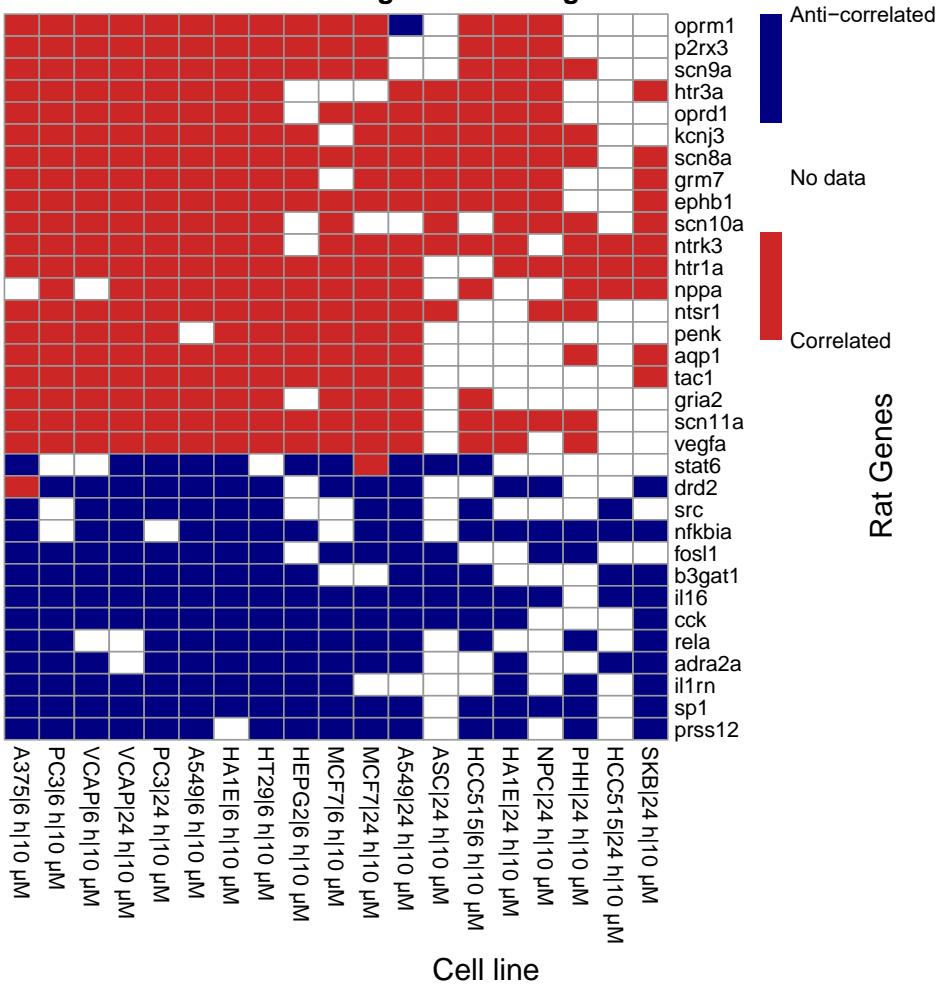


**Figure S10. Persistent rat genes from pain network of Fig. 5 that are either anti-correlated or correlated with respect to a down-regulated signature from the treatment of amitriptyline.** Only the cell lines with down-regulated genes in response to drugs are shown. See the legend of Fig. S9 for other details.

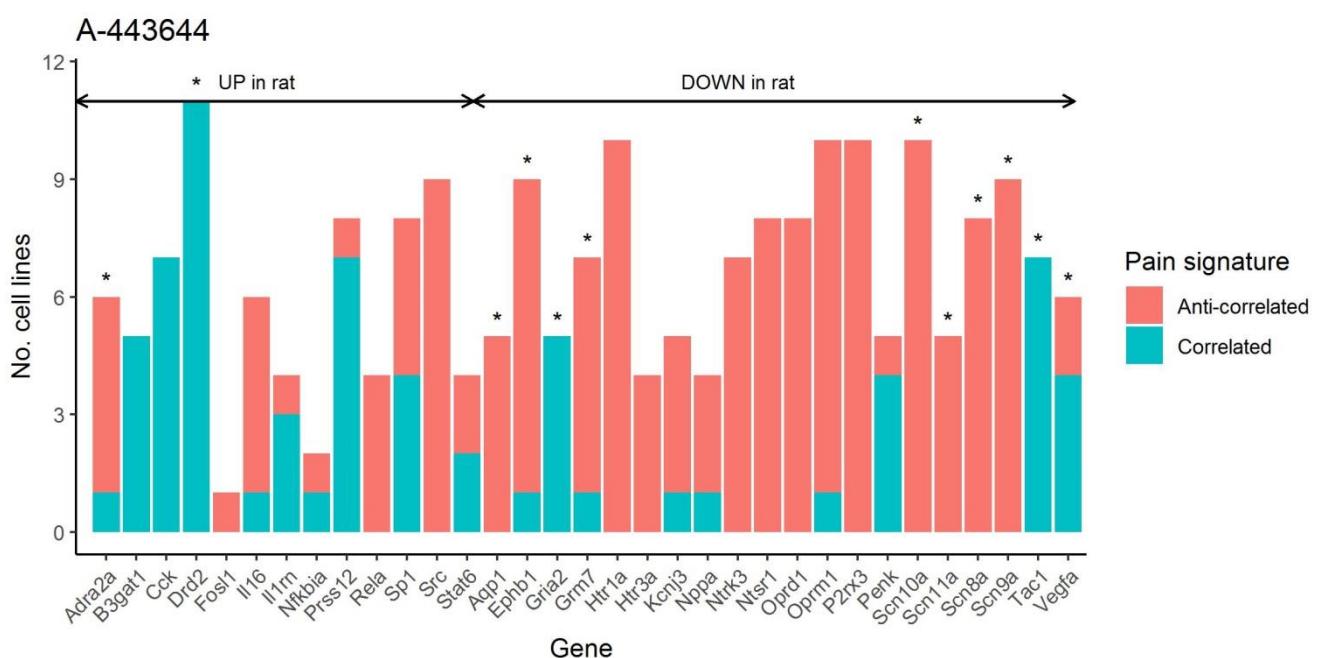


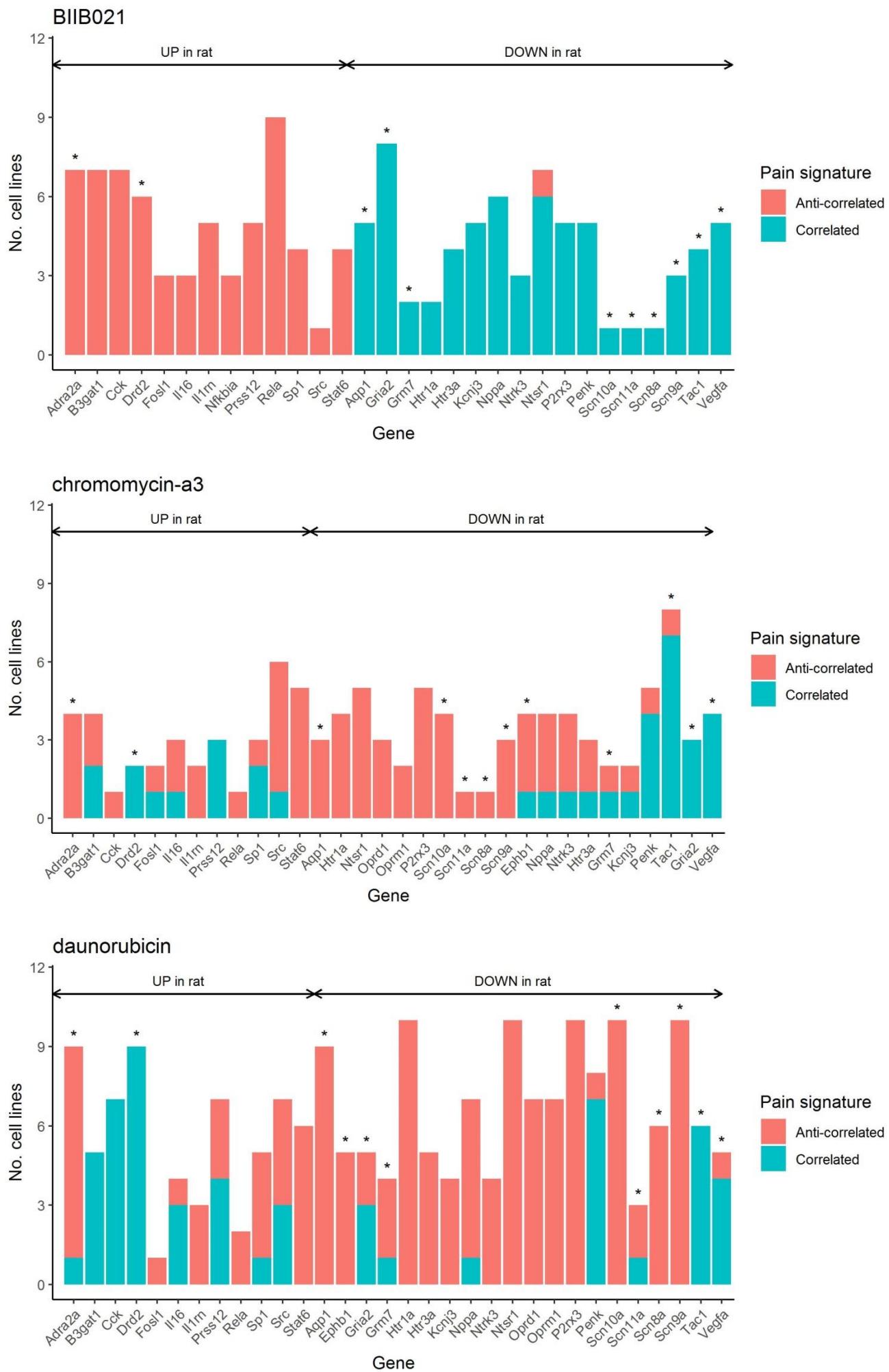
**Figure S11. Persistent rat genes from pain network of Fig. 5 that are either anti-correlated or correlated with respect to an up-regulated signature from the treatment of duloxetine. See the legend of Fig. S9 for details.**

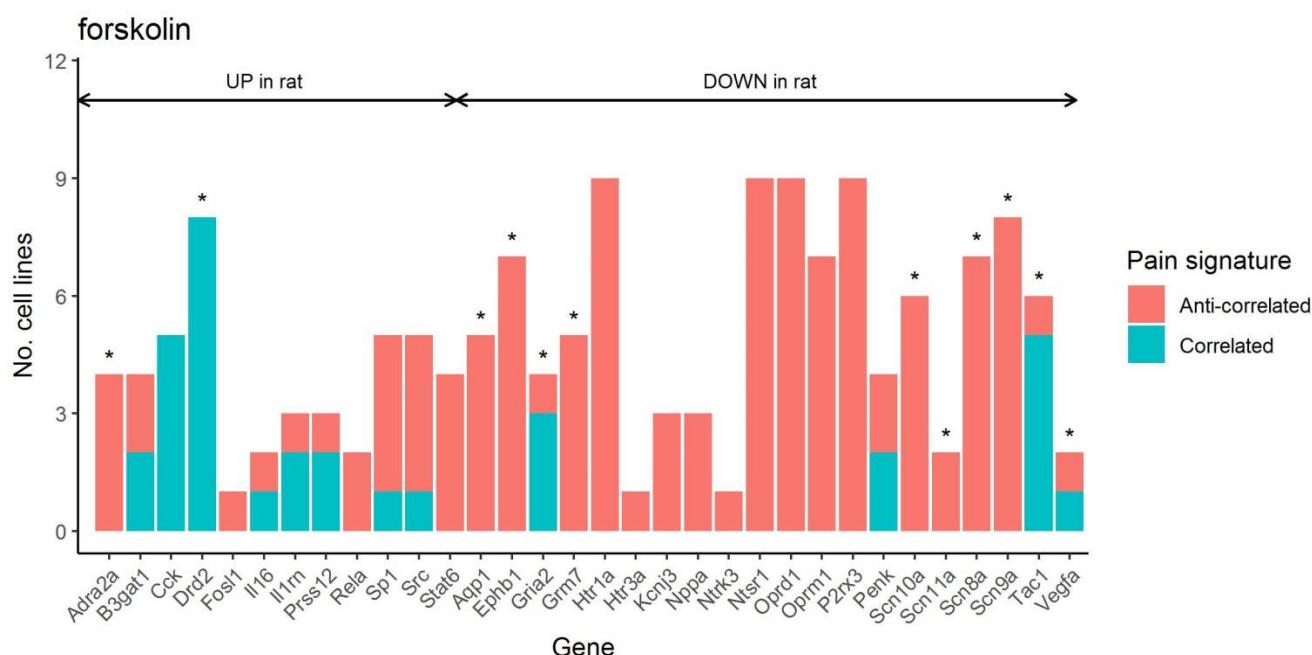
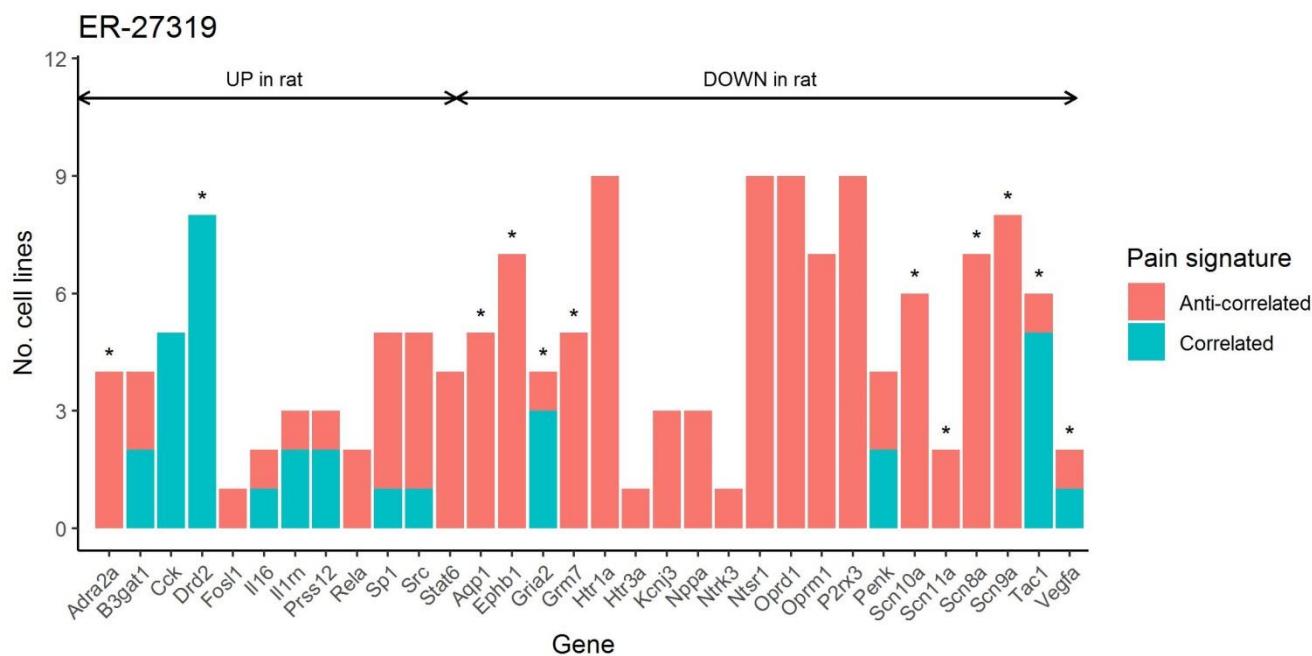
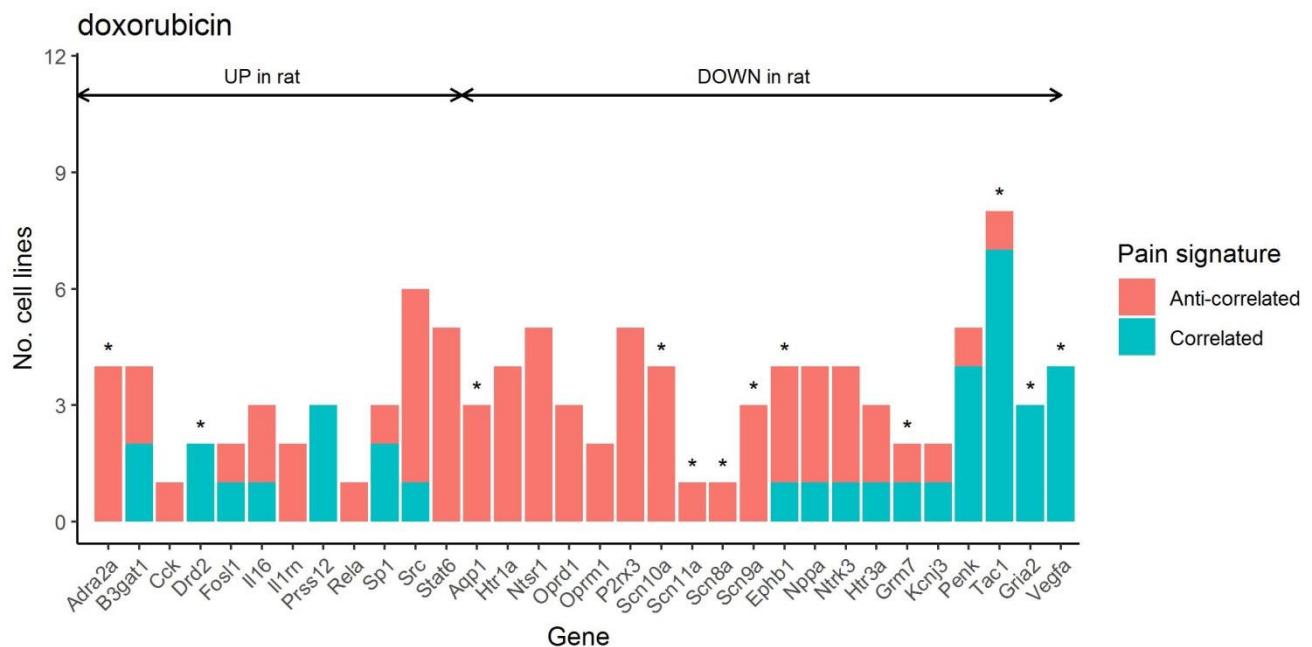
### Duloxetine – Down regulated in drug

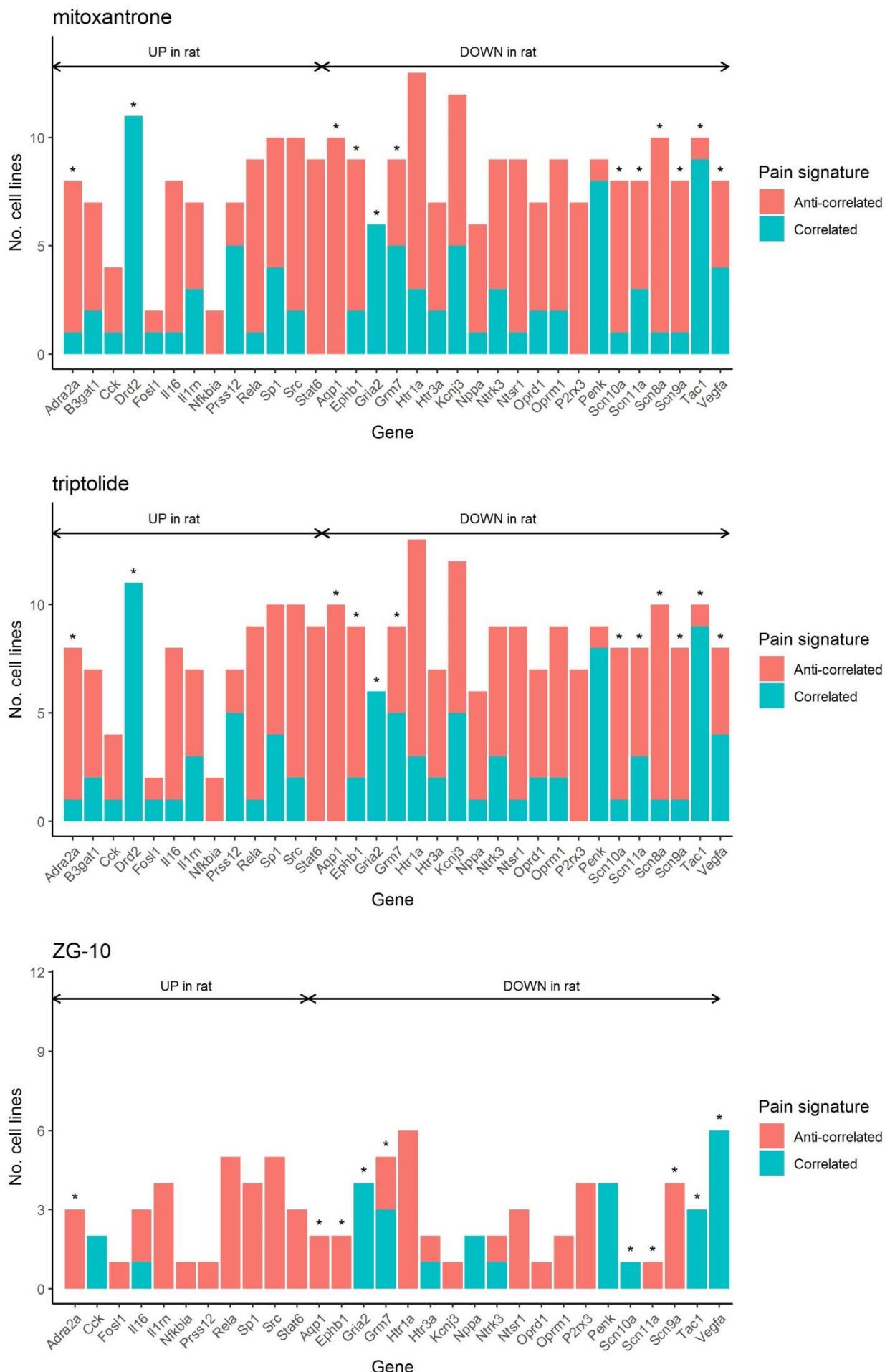


**Figure S12. Persistent rat genes from pain network of Fig. 5 that are either anti-correlated or correlated with respect to a down-regulated signature from the treatment of duloxetine. See the legend of Fig. S9 for details.**









**Figure S13. Rat gene correlation distributions on cell line response to drugs.** Transcriptional signatures were generated from the persistent rat list in the absence of genes with anti-nociceptor effects (\*).

**Table S1. Percent of variance explained by PC1, PC2 and lists of top 500 genes with highest loadings on PC1, PC2 before and after batch correction (related to Fig. S1).**

mouse	PC1	PC2
before correction	89.33	3.04
after correction	27.25	16.75
rat	PC1	PC2
before correction	93.67	4.95
after correction	78.33	9.97

mouse							
before correction				after correction			
gene	PC1	gene	PC2	gene	PC1	gene	PC2
Rpph1	-0.069	Sprr1a	-0.153	Sprr1a	0.152	Myh4	0.084
Rmrp	-0.065	Atf3	-0.127	Atf3	0.127	Ttn	0.083
Hbb-b1	-0.054	Gal	-0.122	Gal	0.123	Atp2a1	0.056
Cdr1	0.052	Nts	-0.101	Nts	0.101	Xirp2	0.054
Zbed6	0.047	Npy	-0.096	Npy	0.096	Acta1	0.054
Snrpn	-0.045	Gpr151	-0.091	Gpr151	0.091	Tnnt3	0.051
Slc3a1	0.042	Ecel1	-0.089	Ecel1	0.088	Myh1	0.051
Adnp	0.042	Sox11	-0.086	Sox11	0.085	Neb	0.045
Gapdh	-0.041	Sez6l	-0.084	Sez6l	0.083	Myh2	0.043
Eno1	-0.039	Flrt3	-0.076	Flrt3	0.075	Ryr1	0.040
Ppia	-0.038	Lmo7	-0.073	Lmo7	0.073	Mybpc2	0.037
Rplp1	-0.038	Sema6a	-0.072	Sema6a	0.071	Xist	-0.036
Ubb	-0.037	Cckbr	-0.070	Cckbr	0.069	Tnnnc2	0.033
Gm16907	0.037	Mmp16	-0.067	Mmp16	0.067	Tnni2	0.031
Gm11149	0.037	Slfn9	-0.063	Slc6a4	0.063	Mybpc1	0.031
Akap2	0.036	Slc6a4	-0.063	Slfn9	0.062	Myot	0.030
Palm2	0.036	Fst	-0.062	Fst	0.062	Ckm	0.029
Gpx4	-0.036	Lipn	-0.059	Igfn1	0.059	Smim12	0.029
Megf11	0.036	Igfn1	-0.059	Lipn	0.059	Tppp3	0.029
Gm15772	-0.036	Chl1	-0.055	Chl1	0.054	Trdn	0.029
Fbxl22	0.035	Glis3	-0.053	Glis3	0.053	Dbi	0.028
Oaz1	-0.035	Csf1	-0.053	Gadd45a	0.053	Sh3bgrl3	0.028

A730008H23Rik	-0.035	Gadd45a	-0.053	Csf1	0.053	Cfl1	0.028
A830010M20Rik	0.035	Loxl2	-0.053	Anxa1	0.053	Apoe	0.028
Rpl10	-0.035	Anxa1	-0.052	Loxl2	0.052	Mylpf	0.027
AF357425	0.034	Adam8	-0.050	Sdc1	0.050	Aldoa	0.027
Rabac1	-0.033	Acvr1c	-0.050	Adam8	0.050	Rps5	0.026
Map3k15	0.033	Sdc1	-0.050	Acvr1c	0.049	Tuba1a	0.026
Nptxr	-0.033	Fln	-0.048	Fln	0.048	Gng3	0.025
Myo1h	0.033	Stmn4	-0.048	Stmn4	0.048	Pmp2	0.025
Clip3	0.032	Slfn10-ps	-0.048	Slfn10-ps	0.047	Arhgdia	0.025
Hba-a1	-0.032	Xdh	-0.047	Xdh	0.047	Tuba1c	0.025
Rpl19	-0.032	Cyp1b1	-0.046	Serpinc1a	0.045	Ldha	0.024
Rpl34	-0.032	Abca1	-0.045	Tnc	0.045	Pctp	0.024
Rps27	-0.032	Tnc	-0.045	Cyp1b1	0.045	S100a6	0.024
Evi2b	0.031	Serpinc1a	-0.045	Ctss	0.044	Tuba1b	0.024
Fam166a	0.031	Tnik	-0.045	Abca1	0.044	Lamtor1	0.024
Hnrnpa1	-0.031	Ctss	-0.044	Tnik	0.044	Sncg	0.024
Rps14	-0.031	Gap43	-0.043	Gap43	0.043	Atp5o	0.024
Fau	-0.031	Rhoq	-0.042	Rhoq	0.042	Apod	0.024
Zfhx3	0.031	Itga7	-0.041	Itga7	0.041	Rpsa	0.024
Igf2bp3	0.031	Dsp	-0.041	Dsp	0.041	Slc25a4	0.024
Rps21	-0.031	Anxa10	-0.040	Lyz2	0.040	Tubb4b	0.023
2410021H03Rik	0.031	Lyz2	-0.040	Anxa10	0.040	Ndufs8	0.023
Tubb3	-0.030	Neto1	-0.040	Ly6a	0.039	Dio2	-0.023
Rpl7a	-0.030	Cacna2d1	-0.039	Neto1	0.039	Tubb3	0.023
Scarna13	-0.030	Ly6a	-0.039	Smim3	0.039	Lmod3	0.023
Rims3	-0.030	Smim3	-0.039	Cacna2d1	0.039	Tmsb4x	0.023
Sncg	-0.030	Satb2	-0.037	Kcnh7	-0.036	Ndufa4	0.023
Pdzk1	0.030	Hrk	-0.037	Hrk	0.036	Cyc1	0.023
Tuba1c	0.030	Mpeg1	-0.037	Satb2	0.036	Rpl7	0.023
Rpl9	-0.030	Kcnh7	0.036	Mpeg1	0.036	Ptgds	0.023
Acat3	0.030	Fyb	-0.036	Fyb	0.035	Capns1	0.023
Pclo	0.030	Top2a	-0.035	Lgals3	0.035	Calm2	0.023
Stmn3	-0.030	4930544M13Rik	-0.035	Top2a	0.035	Tpi1	0.022

Rpsa	-0.030	Tex16	-0.035	Tex16	0.035	Ndufaf3	0.022
Nme7	0.030	Rasgrf2	-0.035	4930544M13Rik	0.035	Pvalb	0.022
Cox6b1	-0.030	Lgals3	-0.035	Col5a3	0.035	Ndufa10	0.022
4930473A02Rik	0.029	Ildr2	-0.035	Pkhd1	0.034	Fxyd2	0.022
Ckb	-0.029	Pkhd1	-0.035	Fgf3	0.034	Dcn	0.022
4930480K15Rik	0.029	Col5a3	-0.035	Ildr2	0.034	Ftl1	0.022
Rpl13	-0.029	Fgf3	-0.034	Rasgrf2	0.034	Cend1	0.022
Actg1	-0.029	Tecta	-0.034	Fosl2	0.034	Rpl14	0.022
H2-T24	0.029	Fosl2	-0.034	Tecta	0.034	Klh31	0.022
Ctnnd1	0.029	Myo10	-0.034	Plin2	0.034	Nedd8	0.022
Rps19	-0.029	Draxin	-0.034	Draxin	0.034	Gstm5	0.022
Ass1	-0.029	Pappa2	-0.034	Ltbp1	0.033	Ckb	0.022
Apoe	-0.029	Ltbp1	-0.033	Myo10	0.033	Ctsd	0.022
Fitm2	-0.029	Htr3a	0.033	Pappa2	0.033	Atp5b	0.022
Rpl17	-0.029	Plin2	-0.033	Jun	0.033	A730018C14Rik	0.022
Pkd2l2	0.029	Cd109	-0.033	Htr3a	-0.033	Cd63	0.022
Rpl12	-0.029	Bach1	-0.033	Cd109	0.033	Rrp1	0.022
Tubb2b	-0.029	Jun	-0.033	Bach1	0.033	Pygm	0.022
Cox5b	-0.029	Il13ra1	-0.032	Csf1r	0.032	Dctn3	0.021
Rpl3	-0.028	Man1a	-0.032	Il13ra1	0.032	Rps11	0.021
Uqcr11	-0.028	Csf1r	-0.032	Man1a	0.032	Ngp	0.021
Amd1	-0.028	Tmprss11f	-0.032	Lancl3	-0.032	Cd9	0.021
Masp2	0.028	Chst2	-0.032	Tmprss11f	0.032	Cd151	0.021
Myl6	-0.028	Scpep1	-0.032	Pkd2l1	0.032	Islr	0.021
Gm7457	0.028	Lancl3	0.032	Scpep1	0.032	Tusc2	0.021
Rps8	-0.028	Galnt6	-0.032	Chst2	0.031	Ly86	0.021
Rpl38	-0.028	Pkd2l1	-0.032	Galnt6	0.031	Csnk2b	0.021
Lgals1	-0.028	Mcoln2	-0.032	Mcoln2	0.031	Kbtbd8	-0.021
Tppp3	-0.028	Star	-0.031	Star	0.031	Them6	0.021
B430010I23Rik	0.028	Il17ra	-0.031	Il17ra	0.031	Skp1a	0.021
Rpl11	-0.028	Car1	-0.031	Car1	0.031	Tubb5	0.021
Mir568	0.028	Slc4a8	-0.031	Cntn4	-0.030	Tcap	0.021
Srgap1	0.028	Pde1a	-0.031	Xist	0.030	Prelid1	0.021

Map1lc3a	-0.028	Adcyap1	-0.030	Scn1a	-0.030	Cenpe	-0.021
Mxd4	-0.027	Cntn4	0.030	Cdh12	-0.030	Arpc3	0.021
Rab1b	-0.027	S100a11	-0.030	Adcyap1	0.030	Akr1a1	0.021
Mia2	-0.027	Lgi3	0.030	Sertm1	0.030	Tmem176a	0.021
Camta1	0.027	Xist	-0.030	S100a11	0.030	Cacna2d1	-0.021
Rps29	-0.027	Scn1a	0.030	Pde1a	0.030	Slc15a2	-0.021
Glrx3	-0.027	Sertm1	-0.030	Slc4a8	0.030	Mapk3	0.021
Rps12	-0.027	C4b	-0.030	C4b	0.030	Cox7b	0.021
Ncoa6	0.027	Cdh12	0.030	Stab1	0.030	Atp6ap1	0.021
Gnb2	-0.027	Stab1	-0.030	Lgi3	-0.029	Tuba4a	0.021
Rpl14	-0.027	Il1r1	-0.030	C1qc	0.029	Myl12b	0.021
Zmat3	0.027	Mrc1	-0.030	Tmem43	0.029	Chchd2	0.021
Speer4b	0.027	Nefh	0.029	Mrc1	0.029	Tagln2	0.021
Zc3h11a	0.027	Tubb6	-0.029	Srxn1	0.029	S100b	0.021
Apbb1	-0.027	Cyp4b1	-0.029	Cx3cr1	0.029	Pcp4	0.021
Gucy1a2	0.027	Tmem43	-0.029	Il1r1	0.029	Hspb8	0.021
Ftl1	-0.027	Il4ra	-0.029	Il4ra	0.029	Clec2l	0.021
Pcbp4	-0.027	C1qc	-0.029	Tubb6	0.029	Cox6a1	0.021
Ap2s1	-0.027	Srxn1	-0.029	Cyp4b1	0.029	Eif2s3y	0.021
Syn3	0.027	A630023A22Rik	-0.029	Ndst4	-0.029	Chl1	-0.021
Tpt1	-0.026	Inhbb	-0.029	Rnase4	0.029	Uchl1	0.021
Syn1	0.026	Cx3cr1	-0.029	A630023A22Rik	0.029	Ctsl	0.021
Spryd3	-0.026	Cenpf	-0.029	Nefh	-0.029	Fbxo2	0.021
Scg5	-0.026	Rnase4	-0.029	Inhbb	0.029	1110032A03Rik	0.021
Prss48	0.026	Antxrl	-0.029	Cenpf	0.028	4930521E06Rik	-0.020
Neto1	0.026	Ndst4	0.029	Antxrl	0.028	Lin37	0.020
Fxyd2	-0.026	Fcrls	-0.028	Fcrls	0.028	Nrap	0.020
Zfp871	0.026	Siglec1	-0.028	Siglec1	0.028	Tprgl	0.020
Faxc	0.026	Pik3cg	-0.028	Vgf	0.028	Atp6v0e2	0.020
Rps23	-0.026	Rin1	-0.028	Rin1	0.028	Tubb2a	0.020
4930419G24Rik	0.026	Cd33	-0.028	Slco5a1	-0.028	Sox11	-0.020
Rpl41	-0.026	Vgf	-0.028	Esrrg	-0.028	Psmc3	0.020
Rpl6	-0.026	Prokr2	-0.028	Pik3cg	0.028	Cstb	0.020

4931403E22Rik	0.026	Fam151a	-0.027	Kcnh5	-0.028	Txn1	0.020
Rpl23	-0.026	Cd84	-0.027	Cd33	0.028	Fbxw5	0.020
Rpl37a	-0.025	Slco5a1	0.027	Fgd3	0.027	Mrfap1	0.020
Tmsb10	-0.025	Vamp1	0.027	Cd84	0.027	Cmya5	0.020
Eif2s3y	0.025	Kcnh5	0.027	Nfil3	0.027	Zkscan8	-0.020
Nav1	0.025	Fgd3	-0.027	Vwc2l	-0.027	Nefl	0.020
Arpc3	-0.025	Nfil3	-0.027	Ptpro	0.027	E130308A19Rik	-0.020
Rpl35	-0.025	Esrrg	0.027	Fam151a	0.027	6330403K07Rik	0.020
Atp5h	-0.025	Ptpro	-0.027	S100a8	0.027	Aplp1	0.020
Fkbp8	-0.025	Pappa	-0.027	Apod	0.027	Slc10a1	-0.020
Pla2g4b	0.025	Vwc2l	0.027	Prokr2	0.027	Uqcrc1	0.020
Muc15	0.025	Klf6	-0.027	Frmpd4	-0.027	Ndufb11	0.020
Eef1a2	-0.025	Hsd17b7	-0.027	Oprd1	-0.027	Prph	0.020
Srrm2	0.025	Mki67	-0.027	Klf6	0.027	Amotl1	-0.020
Gabarap	-0.025	Phlda1	-0.027	Vamp1	-0.027	Mdh1	0.020
Rps7	-0.025	Clec2l	0.027	Pappa	0.027	Pnkd	0.020
Brd4	0.025	Prc1	-0.027	Camk1	0.027	Itm2c	0.020
Stxbp5l	0.025	Oprd1	0.027	Frrs1l	-0.027	Frem3	-0.020
Rps10	-0.025	Gfra1	-0.026	Phlda1	0.026	Tecr	0.020
Raph1	0.025	S100a8	-0.026	Sectm1b	0.026	Pak3	-0.020
Atp5g1	-0.025	Ptprc	-0.026	Prc1	0.026	Capzb	0.020
B3gat2	0.025	Frrs1l	0.026	Gfra1	0.026	Calca	0.020
Rps16	-0.025	Sectm1b	-0.026	Hsd17b7	0.026	Grik3	-0.020
4833422C13Rik	0.025	Frmpd4	0.026	Mki67	0.026	Wdr74	0.020
Rpl23a	-0.025	Apod	-0.026	Pxdc1	0.026	Taf10	0.020
Rps2	-0.025	Camk1	-0.026	Ptprc	0.026	Gabarap	0.020
Lrtm1	0.025	Pigf	-0.026	Tgfb1	0.026	Atp6v1e1	0.020
Lrrc71	0.025	Pxdc1	-0.026	Rnf122	0.026	Tubb4a	0.020
Hint1	-0.025	Zfp697	-0.026	Kcnc3	-0.026	Myoz1	0.020
Cox8a	-0.025	Rnf122	-0.026	Zfp697	0.026	Clpp	0.020
Calm3	-0.024	Tnfrsf1b	-0.026	Tnfrsf1b	0.026	Dok4	0.020
Fzd3	0.024	Nefm	0.026	C3	0.026	Psmc5	0.020
Rtl1	0.024	Cyp24a1	-0.026	Pigf	0.026	Cuta	0.020

Ap1s1	-0.024	Tgfb1	-0.026	Nefm	-0.026	Acot7	0.020
Gm12709	0.024	Ckmt1	0.026	Clec2l	-0.026	Myl1	0.020
Cd82	-0.024	Prdm1	-0.026	Cdkn1a	0.026	Serpina3n	0.020
Ndufa13	-0.024	Cdkn1a	-0.026	Ccr5	0.025	BC107364	-0.020
Rpl7	-0.024	Ccr5	-0.025	Tubb2b	0.025	B2m	0.019
Rpl8	-0.024	C3	-0.025	Gabrb2	-0.025	Psmc4	0.019
Rpl37	-0.024	Podxl	-0.025	Igfbp3	0.025	Cyb5r3	0.019
Flywch1	-0.024	D430019H16Rik	-0.025	Cyp24a1	0.025	Ctbp1	0.019
Rpl18	-0.024	Kcnc3	0.025	Snap25	-0.025	Fibp	0.019
Bsn	0.024	Vmn2r78	-0.025	Gria2	-0.025	Hspa8	0.019
S100a6	-0.024	Snap25	0.025	Podxl	0.025	Grina	0.019
Mt3	-0.024	Srrm4	-0.025	Trp53i11	0.025	Ifi203	-0.019
Psmb3	-0.024	Igfbp3	-0.025	Vmn2r78	0.025	Cacna1s	0.019
Aff2	0.024	Fam19a2	0.025	Prdm1	0.025	Mpv17	0.019
Ak1	-0.024	Runx2	-0.025	Rgs7bp	-0.025	Clu	0.019
Nron	0.024	Irs2	-0.025	D430019H16Rik	0.025	Themis	-0.019
Rpl30	-0.024	Trp53i11	-0.025	Cckar	0.025	Cct5	0.019
Atp6v1f	-0.024	Pvalb	0.025	Atp2b3	-0.025	Grn	0.019
Lypla2	-0.024	Lama5	-0.025	Lama5	0.025	Map1lc3b	0.019
Fam78b	0.024	Cckar	-0.025	Fam19a2	-0.025	Actn3	0.019
Rpl36	-0.024	C3ar1	-0.025	Irs2	0.025	Pappa2	-0.019
Ndufb8	-0.024	Gria2	0.025	Oxr1	-0.025	Abca1	-0.019
Gm10532	0.024	Tmc5	-0.025	Sbno2	0.025	Taldo1	0.019
1110002L01Rik	0.024	Fam111a	-0.025	Ckmt1	-0.025	Rab7	0.019
Cox4i1	-0.024	Gabrb2	0.025	Etv1	-0.025	Atp5a1	0.019
Trim43c	0.024	Oxr1	0.025	Tmc5	0.025	Degs1	0.019
Hist1h4d	-0.024	Calb2	0.025	S100a9	0.025	Mdp1	0.019
Arl6ip5	-0.024	Chrna7	0.025	C3ar1	0.025	Fkbp4	0.019
Gm11837	0.024	Ntrk1	0.025	Runx2	0.025	Mpdu1	0.019
Aldoc	-0.024	Sbno2	-0.025	Unc80	-0.025	Actb	0.019
Rfx7	0.024	Atp2b3	0.025	Pnpla3	-0.025	H2-Ab1	0.019
Degs2	0.024	Pnpla3	0.025	Calb2	-0.025	Smpd1	0.019
Rplp2	-0.024	Mapk6	-0.025	Opcml	-0.025	Pink1	0.019

Ppp2r5b	-0.024	Tubb2b	-0.025	Rras2	0.024	Tspan3	0.019
Gm16982	0.024	Rgs7bp	0.024	Fam111a	0.024	Thy1	0.019
Dnm3os	0.024	Map7d2	0.024	Srrm4	0.024	Igfbp5	-0.019
Srrm4	0.024	Rras2	-0.024	Chrna7	-0.024	Rpl41	0.019
Tonsl	-0.023	Kndc1	0.024	Epha6	-0.024	Cpe	0.019
Ndufs5	-0.023	Laptm5	-0.024	Sv2b	-0.024	Eno3	0.019
Fis1	-0.023	Sv2b	0.024	Kndc1	-0.024	Pmp22	0.019
Rps13	-0.023	Smad1	-0.024	Laptm5	0.024	Cfdp1	0.019
Mlf2	-0.023	Epha6	0.024	Mapk6	0.024	Pebp1	0.019
Rps9	-0.023	S100a9	-0.024	Pvalb	-0.024	Trove2	-0.019
Nfia	0.023	Liph	-0.024	Map7d2	-0.024	Ergic3	0.019
Aamp	-0.023	Opcml	0.024	Btc	0.024	Prdx2	0.019
Prdx5	-0.023	Nrip1	-0.024	Liph	0.024	Abhd4	0.019
Ccdc73	0.023	Unc80	0.024	Akr1b8	0.024	Trappc1	0.019
Itm2c	-0.023	Etv1	0.024	Smad1	0.024	Slc5a5	0.019
Eps8l3	0.023	Btc	-0.024	Postn	0.024	Mvd	0.019
Cox6c	-0.023	Asic1	0.024	Ntrk1	-0.024	Ckmt1	0.019
Orc3	0.023	Pcp4l1	0.024	Kcnb2	-0.024	Ufc1	0.019
Usmg5	-0.023	Nat8l	0.024	Mettl7a3	0.024	Prdx5	0.019
Gca	0.023	Gm765	0.024	Asic1	-0.024	Vsnl1	0.019
Hivep3	0.023	Mettl7a3	-0.024	Nat8l	-0.024	Slc25a1	0.019
Clec2l	-0.023	Postn	-0.024	Gm765	-0.024	Mrpl9	0.019
Rps24	-0.023	Vstm2b	0.024	Spock1	-0.024	Rab3a	0.019
Hspb1	-0.023	Akr1b8	-0.024	AI593442	-0.024	Adra1a	-0.019
Cenpb	-0.023	Fam81a	0.023	Vstm2b	-0.023	Cox8a	0.019
Rps27a	-0.023	Rgs6	0.023	Pcp4l1	-0.023	Phactr2	-0.019
Xist	-0.023	Kcnk1	0.023	Ankrd34c	-0.023	Pkm	0.019
1700010K23Rik	0.023	Kcnb2	0.023	Fam81a	-0.023	Htr3a	0.019
Ptma	-0.023	Tmem229b	0.023	Nrip1	0.023	Gabarapl1	0.019
Prrc2c	0.023	Ankrd34c	0.023	Slitrk3	-0.023	Actg1	0.019
Rps28	-0.023	Wdr63	-0.023	Rgs6	-0.023	Muc15	-0.019
Usp5	-0.023	Zfp488	-0.023	Cntn1	-0.023	Alb	0.019
Gm15713	0.023	Shisa9	-0.023	Ifi202b	0.023	Cplx1	0.019

Atp6v0b	-0.023	Spock1	0.023	Slc6a19	0.023	Kctd12	-0.019
Zmiz1	0.023	Ifi202b	-0.023	Fam13a	-0.023	Stk33	0.018
4930599N23Rik	0.023	Slc6a19	-0.023	Tmem229b	-0.023	Sqstm1	0.018
Fcgbp	-0.023	Fam13a	0.023	Zfp488	0.023	Smim1	0.018
H2-Ea-ps	-0.023	Slitrk3	0.023	Kcnk1	-0.023	Raph1	-0.018
Atp6v1e1	-0.023	Ccr2	-0.023	Wdr63	0.023	Stmn1	0.018
Rpl28	-0.023	AI593442	0.023	C1qb	0.023	Celsr2	-0.018
Wipf3	0.023	Cntn1	0.023	Scn8a	-0.023	Creb1	-0.018
Prpf19	-0.023	Col5a2	-0.023	Shisa9	0.023	Hsp90ab1	0.018
Zfhx4	0.023	Kcng4	0.023	Col5a2	0.023	Rpl4	0.018
Myh6	0.022	Palld	-0.023	Tenm1	-0.023	1700030C10Rik	-0.018
AU040972	0.022	C1qb	-0.023	Lgals1	0.023	Cst3	0.018
Rps17	-0.022	Acvr1	-0.023	Plat	0.023	Eno2	0.018
Ptgds	-0.022	Sema3c	-0.023	Cd74	0.023	Fkbp1b	0.018
Zfp609	0.022	Vash2	-0.023	Ccr2	0.023	Rhof	0.018
Dnm3	0.022	Cdcp1	-0.023	Slc4a1	0.023	Fth1	0.018
Glcci1	0.022	Slc1a7	-0.022	Slc1a7	0.023	Pmvk	0.018
Eif4a1	-0.022	Ppef1	-0.022	Cdcp1	0.023	Rras	0.018
Sema6a	0.022	Tenm1	0.022	Abcd2	-0.023	Dazap2	0.018
Bcam	-0.022	Dock2	-0.022	Dock2	0.023	Map9	-0.018
Gfer	0.022	Hapl4	0.022	Rnd1	0.022	Med16	0.018
Abhd8	-0.022	Abcd2	0.022	Rab31	0.022	Psma7	0.018
Ube2m	-0.022	Plat	-0.022	Tmem159	0.022	Sumo3	0.018
Gm6994	0.022	4933403008Rik	-0.022	Ogfrl1	-0.022	Scg2	0.018
Hist1h4h	-0.022	Itgam	-0.022	Palld	0.022	1110059G10Rik	0.018
Calr	-0.022	Colec10	-0.022	Hapl4	-0.022	Eef1a1	0.018
6330415B21Rik	0.022	Plxna4	-0.022	Sema3c	0.022	Atp5g3	0.018
Ptms	-0.022	Syk	-0.022	Kcng4	-0.022	Slc1a2	-0.018
Prrxl1	-0.022	Cttnbp2	-0.022	Syk	0.022	Use1	0.018
4930533B01Rik	0.022	Rab31	-0.022	Ppef1	0.022	Il17rd	-0.018
Laptm4a	-0.022	Scn8a	0.022	Sphkap	-0.022	Slc4a10	-0.018
Igfbp6	-0.022	Rnd1	-0.022	Kcnj3	-0.022	Paqr4	0.018
Akr1b3	-0.022	Slc4a1	-0.022	Vash2	0.022	Mettl4	-0.018

Psap	-0.022	Tmem159	-0.022	4933403O08Rik	0.022	Rfx3	-0.018
Cblb	0.022	Nefl	0.022	Colec10	0.022	Siah1b	0.018
Kcna1	0.022	Ogfrl1	0.022	Pros1	0.022	Syt5	0.018
Crip1	-0.022	Cd74	-0.022	Trim10	0.022	Ccdc92	0.018
Klf12	0.022	Pros1	-0.022	B3galt5	-0.022	Dtd1	0.018
Fbxl17	0.022	Kcnj3	0.022	Ctsc	0.022	Aes	0.018
Rpl27	-0.022	Gm16551	0.022	Acvr1	0.022	Spag7	0.018
Dohh	-0.022	Speer4a	-0.022	Gria4	-0.022	Obscn	0.018
Hba-a2	-0.022	Cyth4	-0.022	Lamb3	0.022	Srgap1	-0.018
Onecut2	0.022	Cplx2	0.022	Cplx2	-0.022	Arl6	0.018
Ndufb2	-0.022	Sphkap	0.022	Gm16551	-0.022	P4hb	0.018
Sema5a	0.022	Cybb	-0.022	Stat5a	0.022	Stub1	0.018
Tead1	0.022	Ctsc	-0.022	Itgam	0.022	Pcbp1	0.018
Dynll2	-0.022	Faim2	0.022	Cyth4	0.022	Mt2	0.018
Atp6v0e2	-0.022	Aifm3	0.022	Creg2	-0.022	Fam180a	0.018
Map1b	0.022	Lamb3	-0.022	Car3	0.022	S100a10	0.018
Cpne1	0.022	Trim10	-0.022	Rph3a	-0.022	Hars	0.018
Cdkn1b	-0.022	B3galt5	0.022	Esd	0.022	Rpn1	0.018
Lzts1	-0.022	Stat5a	-0.022	Speer4a	0.022	Lmcd1	0.018
Atn1	0.022	Lgals1	-0.022	Asah2	-0.022	Ptgir	0.018
Rpl39	-0.022	Dtnbp1	-0.022	Pcdh7	-0.022	S100a8	0.018
Rpl21	-0.022	Inpp5j	0.022	Arap2	-0.022	Hopx	0.018
Spr	-0.022	Ddr2	-0.022	Cd52	0.022	Plag1	-0.018
B3gnt2	0.022	Gria4	0.022	Cybb	0.022	Psmd8	0.018
Mif	-0.021	Emp1	-0.022	Emp1	0.022	Cyb5r1	0.018
4930565N06Rik	0.021	Rph3a	0.022	Inpp5j	-0.022	Drg2	0.018
Atp5k	-0.021	Cd52	-0.022	Aifm3	-0.022	Hyi	-0.018
Tpi1	-0.021	Asah2	0.022	Dtnbp1	0.022	Scamp3	0.018
Id3	-0.021	Tes	-0.022	Sorl1	-0.022	Inpp4b	-0.018
Slc24a5	0.021	Creg2	0.022	Tes	0.022	Yars	0.018
Osbpl6	0.021	Gnpda2	-0.022	Cttnbp2	0.022	Praf2	0.018
Actb	-0.021	Pcnx	-0.021	Nefl	-0.022	Gm10373	-0.018
Nbea	0.021	Esd	-0.021	Plxna4	0.021	Pgm2l1	-0.018

D10Jhu81e	-0.021	Fads3	-0.021	Gnpda2	0.021	Nmb	0.018
Rps3	-0.021	Sorl1	0.021	Ttl7	-0.021	Actr1a	0.018
C130083M11Rik	0.021	Vsnl1	0.021	Fads3	0.021	Zfp169	-0.018
1700071M16Rik	0.021	Car3	-0.021	Vsnl1	-0.021	Ctse	0.018
Urm1	-0.021	Wisp1	-0.021	Cntn3	-0.021	Mpz	0.018
Fads6	-0.021	Arap2	0.021	L3mbtl1	-0.021	Mrpl43	0.018
Chpf2	-0.021	Pcdh7	0.021	Ddr2	0.021	Gpx1	0.018
Igsf10	0.021	Stk32b	-0.021	Faim2	-0.021	Zim1	-0.018
Rmnd1	-0.021	Chrm2	0.021	Chrm2	-0.021	Epha3	-0.018
Cpeb2	0.021	Htr3b	0.021	Vav1	0.021	Ndufb9	0.018
Atp5e	-0.021	Crlf1	-0.021	Crlf1	0.021	Npc2	0.018
Arf5	-0.021	Vav1	-0.021	Apba2	0.021	Lyz2	0.017
4930405J17Rik	0.021	6430571L13Rik	0.021	Kcna2	-0.021	Sema6a	-0.017
Fxr2	-0.021	Gabrg1	-0.021	Stk32b	0.021	Pde1c	-0.017
Psmb6	-0.021	Syt2	0.021	Tpm4	0.021	Slc4a5	-0.017
Oaz3	0.021	Tet3	-0.021	Htr3b	-0.021	Nrn1	0.017
Pkm	-0.021	Ttl7	0.021	Trf	0.021	Bola1	0.017
Cst3	-0.021	Apba2	-0.021	Wisp1	0.021	Slc22a29	-0.017
Ccdc88a	0.021	Fgl2	-0.021	Zfp804a	-0.021	Trmt61a	0.017
Serinc4	0.021	Cntn3	0.021	Gabrg1	0.021	Psmb5	0.017
Apc	0.021	Aspm	-0.021	Sla	0.021	Mbps2	-0.017
Hipk2	0.021	Tpm4	-0.021	Wfdc3	0.021	Arhgap42	-0.017
Bckdha	-0.021	L3mbtl1	0.021	Syt2	-0.021	Gng8	0.017
Cd247	0.021	Col27a1	-0.021	Pls1	-0.021	Bsg	0.017
Nfat5	0.021	Syne2	-0.021	Tgif1	0.021	Gabrb2	-0.017
Gm10578	0.021	Sla	-0.021	6430571L13Rik	-0.021	Got2	0.017
Eif5a	-0.021	Ache	0.021	Pcnx	0.021	Zcchc3	0.017
Ylpm1	0.021	Trf	-0.021	Col27a1	0.021	Nlgn1	-0.017
Prdx2	-0.021	Csf2rb2	-0.021	Fgl2	0.021	Anxa6	0.017
Scn1b	-0.021	Dio2	-0.021	Fam126b	-0.021	Sult4a1	0.017
Timm13	-0.021	Kcna2	0.021	Tet3	0.021	Rnf187	0.017
Gsk3b	0.021	Scn4b	0.021	Oas1e	0.021	Tkt	0.017
Cntd1	0.021	Cd53	-0.021	Fstl5	-0.021	Tmem50a	0.017

Muc6	0.021	Tmtc4	-0.021	Aspm	0.021	Prps1	0.017
Sos1	0.021	Tgif1	-0.021	Cd53	0.021	Kif14	-0.017
Serinh1	-0.021	Wfdc3	-0.021	Dpp10	-0.021	Slc22a17	0.017
Rps4x	-0.021	Myo1f	-0.021	Myo1f	0.021	Ndufa11	0.017
Scarb2	-0.021	Oas1e	-0.021	Tifa	0.021	Ahsa1	0.017
Wnk1	0.021	Pls1	0.021	Rnf157	-0.020	Rpl13a	0.017
Coro1a	-0.021	Slc15a3	-0.021	Tmem47	-0.020	Rps25	0.017
Eml5	0.021	Tifa	-0.020	Pfkfb4	0.020	Cpeb2	-0.017
Gabbrb3	0.021	Tuba1c	-0.020	Atp2b2	-0.020	Lonrf3	-0.017
Phxr4	0.021	Zfp804a	0.020	Ano3	-0.020	Thsd7a	-0.017
Ndufa7	-0.021	Dpp10	0.020	Slc15a3	0.020	Tac1	0.017
Qser1	0.021	Epn3	0.020	Kcnmb1	-0.020	2900011O08Rik	0.017
Glul	-0.021	Fstl5	0.020	Csf2rb2	0.020	Dbpht2	-0.017
Prg4	0.021	Wdr72	0.020	Pcdh11x	-0.020	Cisd1	0.017
Uqcrc1	-0.021	Rnf157	0.020	Pmaip1	0.020	Zdhhc21	-0.017
Nyap1	-0.020	Kcnmb1	0.020	Dio2	0.020	L3mbtl1	-0.017
Gpc1	-0.020	Ifi204	-0.020	Casp3	0.020	Arpc1b	0.017
Brat1	-0.020	Pfkfb4	-0.020	Scn4b	-0.020	Ywhah	0.017
Ccdc39	0.020	Nkain1	-0.020	Ngp	0.020	Rplp0	0.017
Hist1h4c	-0.020	Marcks	-0.020	Tmtc4	0.020	Sparc	0.017
Kdm5d	0.020	Tmem47	0.020	Syne2	0.020	Pag1	-0.017
Fndc9	0.020	Pmaip1	-0.020	Marcks	0.020	Pnpla2	0.017
Mybph	0.020	Met	-0.020	Tuba1c	0.020	Fam213a	0.017
Pcyt2	-0.020	Arhgef4	0.020	Trem2	0.020	Rab3c	-0.017
Mafg	-0.020	Fam126b	0.020	Ctla2a	0.020	Bloc1s1	0.017
Vps37a	0.020	Prss12	-0.020	Wdr72	-0.020	Lrrc34	-0.017
Rpl18a	-0.020	Fndc5	0.020	Ache	-0.020	Cndp2	0.017
Fmn2	0.020	Casp3	-0.020	Ifi204	0.020	Map2	-0.017
Rps25	-0.020	Tmem88b	-0.020	Nkain1	0.020	Lum	0.017
Ahsa1	-0.020	Pcdh11x	0.020	Epn3	-0.020	Slc25a5	0.017
Cox7c	-0.020	Galnt9	-0.020	Galnt9	0.020	Pfn4	-0.017
1110008P14Rik	-0.020	Ms4a7	-0.020	Rimkla	-0.020	Cox6b1	0.017
Psmb4	-0.020	Atp2b2	0.020	Lrrn1	-0.020	Vamp1	0.017

Tmem242	-0.020	Rimkla	0.020	Prss12	0.020	Klhdc9	0.017
Crebbp	0.020	Tuba4a	0.020	Actn2	0.020	Ubxn6	0.017
D330041H03Rik	0.020	Actn2	-0.020	Acsl6	-0.020	Atp10a	-0.017
Etv1	0.020	Corin	-0.020	Met	0.020	Rgs10	0.017
Cdkn2d	-0.020	Slco2b1	-0.020	Cited2	0.020	Wars2	-0.017
Iqck	0.020	Cited2	-0.020	Smad9	-0.020	Arpc4	0.017
Snord17	-0.020	Ano3	0.020	Ms4a7	0.020	Cers2	0.017
C1qa	-0.020	Trem2	-0.020	Corin	0.020	Dusp28	0.017
Mkl2	0.020	Acsl6	0.020	Trpm1	0.020	Mrps34	0.017
Slc18a2	0.020	Igfsf21	0.020	Tmem88b	0.020	H2afx	0.017
Srgap3	0.020	Galm	0.020	Slco2b1	0.020	Ndufs7	0.017
1700007J10Rik	0.020	Trpm1	-0.020	Galm	-0.020	Trnp1	0.017
Raver1	0.020	Ngp	-0.020	Zfp365	-0.020	Cryab	0.017
Pcm1	0.020	Ctla2a	-0.020	Fndc5	-0.020	Sep-05	0.017
Mdga2	0.020	Myadm	-0.020	Fcgr2b	0.020	Sema3b	0.017
Hist4h4	-0.020	Lrrn1	0.020	Arhgef4	-0.020	Syp	0.017
Impdh1	-0.020	Kcns1	0.020	Lcp1	-0.020	Gcsam	0.017
Eif1ax	-0.020	Fcgr2b	-0.020	F13a1	0.020	Fam160a2	-0.017
Orc1	0.020	Pou2f1	-0.020	Igfsf21	-0.019	Fbl1	0.017
4933413L06Rik	0.020	Msr1	-0.020	Atp8b1	0.019	AW549877	-0.017
Tex261	-0.020	Lcp1	0.020	Msr1	0.019	Acrv1	0.017
Cmip	0.020	Susd4	0.020	Glb1l2	-0.019	Sdhc	0.017
9930021J03Rik	0.020	Opnl1	0.020	Kcns1	-0.019	Zfp354c	-0.017
Metrn	-0.020	Nav2	-0.020	Inpp5d	0.019	Maged1	0.017
Akt1s1	-0.020	Itpr1	-0.019	Myadm	0.019	Rell2	0.017
Kcnma1	0.020	Qrfpr	-0.019	Qrfpr	0.019	Lox	-0.017
Rps15	-0.020	Kcnip1	0.019	Kcnip1	-0.019	B3galnt1	0.017
S100a10	-0.020	F13a1	-0.019	Agtr1b	-0.019	Mdh2	0.017
Pcdhgb1	0.020	Zfp365	0.019	Trpm8	-0.019	Hist1h2bc	0.017
Ccpq1	0.020	Smad9	0.019	Gm7271	-0.019	Dgkb	-0.017
Raly	-0.020	Glb1l2	0.019	Cntn5	-0.019	Acadvl	0.017
Otub1	-0.020	Atp8b1	-0.019	Opnl1	-0.019	Zkscan14	0.017
Dnase1	0.020	Agtr1b	0.019	Tuba4a	-0.019	Adh5	0.017

Lpp	0.020	Inpp5d	-0.019	Galnt5	-0.019	Calm3	0.017
Epas1	0.020	Igf1	-0.019	Susd4	-0.019	Syngr3	0.017
Pom121	0.020	Fgf1	0.019	Kcnc1	-0.019	Pcolce	0.017
Atp5j2	-0.020	Vcam1	-0.019	Scrt1	-0.019	Plcd2	-0.017
Ap2m1	-0.020	Lrrc49	0.019	Vcam1	0.019	Rasgrf2	-0.017
Ep300	0.020	Necab3	0.019	Mc4r	0.019	Tmed8	-0.017
Rere	0.020	Cntn5	0.019	Fgf1	-0.019	Pdzd11	0.016
Gps1	-0.020	Scrt1	0.019	Itpr1	0.019	Lmf2	0.016
Sqstm1	-0.020	Fbxo31	0.019	Odc1	0.019	Hagh	0.016
Runx1	0.019	Mc4r	-0.019	Fgf12	-0.019	Jmj8	0.016
Cfl1	-0.019	Trpm8	0.019	Edil3	-0.019	Kbtbd4	0.016
Ddit4	-0.019	1700025G04Rik	-0.019	Cpne4	-0.019	Ifitm2	0.016
Cd151	-0.019	Galnt5	0.019	Galnt13	-0.019	Insr	-0.016
Haghl	-0.019	Spock3	0.019	St8sia1	-0.019	Anxa5	0.016
Cd47	0.019	Gm7271	0.019	Slitrk4	-0.019	D17H6S53E	0.016
Mapk8ip1	-0.019	Jph3	0.019	Pou2f1	0.019	Dpy19l4	-0.016
2210416O15Rik	-0.019	Fgf12	0.019	Prokr1	-0.019	Pde1a	-0.016
Igfbp4	-0.019	Axl	-0.019	Ar	-0.019	Pcp4l1	0.016
Rpl10a	-0.019	Cpne4	0.019	Nav2	0.019	Fez1	0.016
Morf4l1	-0.019	Bin2	-0.019	Axl	0.019	Ifitm7	0.016
Mgst3	-0.019	Gabrg2	0.019	Csmd3	-0.019	Mlip	0.016
Tagln2	-0.019	Mdga1	-0.019	Bin2	0.019	Mmp16	-0.016
Purg	0.019	Aoah	-0.019	Astn2	-0.019	Cd74	0.016
Sycp3	0.019	Astn2	0.019	Gfra3	0.019	Chmp4b	0.016
Arid1a	0.019	Odc1	-0.019	Fbxo31	-0.019	2210016L21Rik	0.016
Atf2	0.019	Ar	0.019	Spock3	-0.019	Tnfrsf1a	0.016
Rab3d	-0.019	Csf3r	-0.019	Gabrg2	-0.019	Rccd1	0.016
Uty	0.019	Kcnc1	0.019	Cpeb3	-0.019	Kcnk1	0.016
Phactr2	0.019	Kcns3	0.019	Lrrc49	-0.019	Ndn	0.016
Drap1	-0.019	Rab37	0.019	Ltf	0.019	Abcb1a	-0.016
Rock2	0.019	Eps8	-0.019	Slc2a1	0.019	Nrip1	-0.016
Zfhx2	0.019	Slfn8	-0.019	1700025G04Rik	0.019	Dnaic2	0.016
Galnt2	0.019	D130043K22Rik	0.019	Necab3	-0.019	Pnrc1	0.016

Ctif	0.019	Nap1l5	0.019	Csf3r	0.019	Atp6v1g1	0.016
Park7	-0.019	Prokr1	0.019	Kcnv1	-0.019	Ch25h	0.016
Mbd5	0.019	Gfra3	-0.019	Igf1	0.019	Znhit3	0.016
Arl1	-0.019	Wdfy4	-0.019	Tnfrsf12a	0.019	Lin7a	-0.016
Hnrnpk	-0.019	Edil3	0.019	Kcns3	-0.019	Rnasek	0.016
Jund	-0.019	Tmem132e	0.019	D130043K22Rik	-0.019	Tpm2	0.016
Ddx3y	0.019	Slitrk4	0.019	Ank1	-0.019	Dynlrb1	0.016
Htr2b	0.019	Mcm6	-0.019	Aoah	0.019	Htra1	0.016
Egln2	-0.019	Dab2	-0.019	Jph3	-0.019	Tmem28	0.016
H19	-0.019	Amotl1	-0.019	Eps8	0.019	Lmbrd2	-0.016
Rab3a	-0.019	Ncald	0.019	Eif5a2	-0.019	Fam166a	0.016
Srp54c	-0.019	Tnfrsf12a	-0.018	Mdga1	0.018	Mrps26	0.016
Rps3a1	-0.019	Kcnv1	0.018	Wdfy4	0.018	Nalcn	-0.016
Mecp2	0.019	Grb10	-0.018	B3galt1	-0.018	Por	0.016
Chchd10	-0.019	Crem	-0.018	Dzank1	-0.018	Fsd1l	-0.016
Gpld1	0.019	Gas7	-0.018	Rab37	-0.018	Ccndbp1	0.016
Nxpe2	0.019	Galnt13	0.018	Hist1h1d	0.018	Ostc	0.016
Ncor2	0.019	Kcnip3	0.018	Gadd45g	0.018	Cep290	-0.016
Ankrd12	0.019	Slc2a1	-0.018	Fam163a	0.018	Herc6	-0.016
Tmem131	0.019	Rnf112	0.018	Kcnk16	0.018	Zfp322a	-0.016
Uqcrb	-0.019	Csmd3	0.018	Tmem132e	-0.018	Psmc2	0.016
Map1a	0.019	Ltf	-0.018	Kcnip3	-0.018	Zbtb41	-0.016
Nova2	0.019	Doc2b	-0.018	Doc2b	0.018	Gtf2f1	0.016
Tmem233	-0.019	Kcnk16	-0.018	Carhsp1	0.018	Pla2g4b	-0.016
Rhoc	-0.019	Angel1	0.018	Nap1l5	-0.018	Mrps16	0.016
Tpr	0.019	Baalc	-0.018	Mcm6	0.018	Mmachc	0.016
Ntrk1	-0.019	Flna	-0.018	Cntnap2	-0.018	Arhgap11a	-0.016
Ndufb7	-0.019	Ank1	0.018	Slfn8	0.018	Fndc5	0.016
Rac3	-0.019	Fam163a	-0.018	Flna	0.018	Psap	0.016
Swi5	-0.019	St8sia1	0.018	Baalc	0.018	Eif2b5	0.016
Aes	-0.019	Mtus2	-0.018	Gas7	0.018	Klhl15	-0.016
Smim12	-0.019	Prdm9	-0.018	Hecw1	-0.018	Serpingle1	0.016
Nudt21	-0.019	Ntm	0.018	Crem	0.018	Mfap3l	-0.016

Vat1	-0.019	Hist1h1d	-0.018	Ncald	-0.018	Rock2	-0.016
Rps11	-0.019	Nckap1l	-0.018	Atp11a	-0.018	Epha5	-0.016
Ppp6r1	-0.019	Eif5a2	0.018	Angel1	-0.018	Cep97	-0.016
Eef1a1	-0.019	Chrna3	-0.018	Stear4	0.018	Tnik	-0.016
Snhg11	0.019	Slc22a23	-0.018	Coro6	-0.018	Grb10	-0.016
Rpl36a	-0.019	Gadd45g	-0.018	Nckap1l	0.018	Tmem106b	-0.016
Ank3	0.019	Sh2d1b2	-0.018	Ntm	-0.018	Cox4i1	0.016
Vdac1	-0.019	Cpeb3	0.018	Cnnm1	-0.018	Fam192a	0.016
9430069I07Rik	0.019	Coro6	0.018	Grb10	0.018	Idh3g	0.016
Ywhaz	0.019	Ldhb	0.018	Dab2	0.018	Ubxn1	0.016
Atp9a	-0.019	Cntnap5a	0.018	Mtus2	0.018	Cybrd1	-0.016
Prcaa2	0.019	Carhsp1	-0.018	Tmem255a	-0.018	Ankrd28	-0.016
Ppargc1a	0.019	Atp1a1	0.018	Wipf3	-0.018	Rimbp3	-0.016
Amy1	0.019	Cnnm1	0.018	Cntnap5a	-0.018	Osbpl8	-0.016
Asb14	0.019	B3galt1	0.018	Sh3bp2	0.018	Ogt	-0.016
Pin1	-0.019	Ms4a6d	-0.018	Hapl1	-0.018	Col25a1	-0.016
Fmn1	0.019	Hao1	-0.018	Ms4a6d	0.018	Arhgap5	-0.016
Synj1	0.019	Nt5c1b	-0.018	Kif26b	-0.018	Znhit1	0.016
1700094D03Rik	-0.019	Stear4	-0.018	Tmem56	-0.018	Kat5	0.016
Sema3g	-0.019	Cmah	-0.018	Amotl1	0.018	Gstt3	0.016
Dgkk	0.019	Cfh	-0.018	Six4	-0.018	Mylk4	0.016
Rrp7a	-0.019	Cxadr	-0.018	Sh2d1b2	0.018	Tm9sf1	0.016
Dimt1	0.019	Bambi	0.018	Cfh	0.018	Synj1	-0.016
Ntn3	-0.019	Lhfpl4	0.018	Prdm9	0.018	Tmem229a	-0.016
Cd63	-0.019	Trim58	-0.018	Hao1	0.018	Igfbp4	0.016
Kcnrg	0.019	Kif26b	0.018	Sh2d1b1	0.018	Tram1l1	0.016
Cep290	0.019	Sh3bp2	-0.018	Lhfpl4	-0.018	Ube2ql1	0.016
Ubqln2	0.019	Cntnap2	0.018	Nrg1	-0.018	Flrt2	-0.016
Eif3j1	-0.019	Sh2d1b1	-0.018	Rnf112	-0.018	Anxa2	0.016
Mrps25	0.019	Mapkbp1	-0.018	S100a10	0.018	Nap1l5	0.016
Zfp462	0.019	Tmem255a	0.018	Cttn	0.018	Bbox1	-0.016
G530011O06Rik	0.019	Atp11a	0.018	Slc22a23	0.018	Bglap3	-0.016
Qsox1	-0.019	Elf4	-0.018	Bambi	-0.018	Kat6a	-0.016

Rprm	-0.019	Phactr2	-0.018	Chrna3	0.018	Mtfp1	0.016
Aldh2	-0.019	Rnf152	-0.018	Trim58	0.018	Tubg1	0.016
4930563F08Rik	0.019	Adam11	0.018	Mapkbp1	0.018	Eif2b4	0.016
Rps20	-0.019	Hs3st2	0.018	Igsf9b	0.018	Crip2	0.016
Rps18	-0.019	Dzank1	0.018	Cmah	0.018	Brip1	0.016
Ipw	-0.019	Fam196a	-0.018	Cxadr	0.018	Gstp1	0.016
Ston2	0.019	Bcan	0.018	Fermt3	0.018	Cd24a	0.016
St8sia1	0.018	Kcnab2	0.018	Rasgrp1	-0.018	Clock	-0.016
Aldoa	-0.018	Hecw1	0.018	Hist1h2bn	0.018	Adam20	-0.016
Fxyd7	-0.018	Itgb2	-0.018	Necab1	-0.018	Uprrt	-0.016
Tcte1	0.018	Fermt3	-0.018	Tlr13	0.018	Cct7	0.016
Mcrs1	-0.018	Sema4f	-0.018	Ntng1	-0.018	Amy1	-0.016
1700080N15Rik	0.018	Hapln1	0.018	Rnh1	0.018	Dnajc13	-0.016
4932702P03Rik	0.018	Ccna2	-0.018	Itgb2	0.018	Car3	0.016
Rpl32	-0.018	Hist1h2bn	-0.018	Kcnb1	-0.018	Rps9	0.016
Wasf1	0.018	Ctnn	-0.018	Dgkh	-0.018	Uhmk1	-0.016

**rat**

before correction				after correction			
gene	PC1	gene1	PC2	gene	PC1	gene1	PC2
Nefm	0.040	Htr3b	-0.066	Htr3b	-0.066	Crisp1	0.080
Mpz	0.039	Htr3a	-0.066	Htr3a	-0.066	Htr3b	0.078
Nefh	0.039	Scn11a	-0.063	Scn11a	-0.063	Cxcl14	0.077
Nefl	0.039	Kcns1	-0.063	Kcns1	-0.063	Pvalb	0.076
Pmp22	0.038	Gpnmb	0.057	Gpnmb	0.057	Stac2	0.069
Tubb3	0.037	Vip	0.057	Vip	0.057	Atf3	0.066
Sparc	0.036	Chrna3	-0.057	Chrna3	-0.057	Tgm1	0.065
Mbp	0.036	Gal	0.056	Gal	0.056	Dpp10	-0.062
Vim	0.035	Hapln1	-0.055	Hapln1	-0.055	Nrn1	-0.062
Ctsb	0.035	Csrp3	0.054	Csrp3	0.055	Mrgprx1	0.059
Sptbn1	0.035	Scg2	-0.053	Scg2	-0.053	Calca	0.059
Psap	0.035	Tmem255a	-0.050	Tmem255a	-0.050	Nptx1	-0.058
Zwint	0.035	Thbs2	0.050	Thbs2	0.050	Kcns1	0.054
Rtn4	0.035	Scn10a	-0.050	Scn10a	-0.050	Cd68	0.053

Ndrg4	0.034	Crisp1	0.050	Crisp1	0.049	Chrnb3	-0.053
Col1a1	0.034	Kcnh7	-0.049	Kcnh7	-0.049	Cyct	0.053
Apod	0.034	Mrgprb4	-0.048	Mrgprb4	-0.048	LOC100134871	0.052
Cltc	0.034	Ptprh	0.048	Ptprh	0.048	Hbb-b1	0.052
Uchl1	0.033	Plcd4	-0.047	Plcd4	-0.048	Hapln1	0.052
Sncg	0.033	Cxcl14	0.047	Nmb	-0.047	Cldn4	0.051
Pafah1b1	0.033	Nmb	-0.047	Cxcl14	0.047	Htr3a	0.050
Tubb5	0.033	Vsnl1	-0.046	Vsnl1	-0.046	Col18a1	0.050
S100b	0.033	Kcns3	-0.046	Kcns3	-0.046	Crlf1	0.050
Spp1	0.033	Reg3b	0.045	Calca	-0.045	Hbb	0.050
Serinc1	0.033	Calca	-0.045	Reg3b	0.045	Vsnl1	0.049
Hspa8	-0.033	Serpina3n	0.045	Serpina3n	0.045	Grik1	-0.048
Ywhah	0.033	Necab1	-0.045	Pvalb	-0.044	Chrna3	0.048
Actb	0.032	Pvalb	-0.044	Necab1	-0.044	Rgs4	-0.047
Reep5	0.032	Ecel1	0.043	Ecel1	0.043	Spock3	-0.047
Actg1	-0.032	Stac2	0.043	Postn	0.043	Gabra1	-0.046
Dpysl2	0.032	Postn	0.043	Stac2	0.042	Rnf112	-0.046
Atp1b1	0.032	Clec2l	-0.042	Clec2l	-0.042	Sst	-0.046
Canx	0.032	Pltp	0.042	Pltp	0.042	Hpd	0.045
Fstl1	0.031	Clec7a	0.042	Ppef1	-0.042	Gabrg2	-0.045
Pea15	0.031	Ppef1	-0.042	Clec7a	0.042	Gfap	0.044
Ywhag	0.031	Sptlc3	-0.041	Sptlc3	-0.041	Clec2l	0.044
Ywhae	0.030	Atf3	0.041	Gpr22	-0.041	Casr	-0.044
Itgb1	0.030	Gpr22	-0.041	Mpeg1	0.041	Necab1	0.043
Anxa6	0.030	Mpeg1	0.041	Hs3st2	-0.041	Scn11a	0.043
Eif4a2	0.030	Hs3st2	-0.041	Kcnd3	-0.041	Mmp9	-0.043
Gas7	0.030	Kcnab1	-0.041	Kcnab1	-0.041	Apod	0.043
Ndfip1	0.030	Kcnd3	-0.040	Atf3	0.040	Serpina3n	0.042
App	0.030	Calcb	-0.040	Calcb	-0.040	Nefl	-0.042
Clu	0.030	Siglec1	0.040	Cntn4	-0.040	Serpine1	0.042
Ttc3	0.030	Cntn4	-0.040	Siglec1	0.040	Chrna6	-0.042
Cplx1	0.029	Tgm1	0.040	Nap1l5	-0.040	Sptlc3	0.041
Hba1	0.029	Nap1l5	-0.040	Lhfpl1	-0.040	Cd55	-0.041

Itgb4	0.029	Lhfpl1	-0.040	Lilrb4	0.040	Mrgprb4	0.041
Skp1	0.029	Lilrb4	0.040	Mmp12	0.040	Plcd4	0.041
Dynll2	0.029	Mmp12	0.040	Ankrd1	0.040	Col2a1	-0.041
Syt4	0.029	Ankrd1	0.040	Tgm1	0.039	Rit2	-0.041
Calr	0.029	Scn1a	-0.039	Scn1a	-0.039	Vamp1	0.040
Itm2b	0.029	C1qa	0.039	C1qa	0.039	Kcnh7	0.040
Tppp3	0.029	Kcnip3	-0.039	Kcnip3	-0.039	Kcns3	0.040
Ngfr	0.029	Col7a1	0.039	Col7a1	0.039	Rtn4rl1	-0.040
Acly	0.029	Vamp1	-0.038	Vamp1	-0.038	Cd74	0.040
Ap2m1	0.029	Frmpd4	-0.038	Dpp10	-0.038	Grem2	-0.040
Arhgdia	0.029	Avil	-0.038	Kcnc3	-0.038	Kcna4	0.040
Gabbr1	0.028	Kcnc3	-0.037	Frmpd4	-0.038	Tmem255a	0.039
Pfkp	0.028	Sprr1a	0.037	Nrn1	-0.038	Lgi3	-0.039
Ddx5	0.028	Unc13c	-0.037	Avil	-0.037	RT1-Da	0.039
Slc25a4	0.028	Myo1a	-0.037	Sprr1a	0.037	Trpv1	-0.039
Fasn	0.028	Flrt3	0.037	Flrt3	0.037	C2	0.039
Lamp1	0.028	C1qb	0.037	Unc13c	-0.037	Itgb6	0.039
Spock2	0.028	Kcnv1	-0.037	Myo1a	-0.037	Cdh3	-0.038
Cd164	0.028	Dpp6	-0.037	C1qb	0.037	Scg2	0.038
Atp11a	0.028	Il31ra	-0.037	Kcnv1	-0.037	Nrsn1	-0.038
Atp6v1b2	0.028	Slitrk3	-0.037	Slitrk3	-0.037	Ncf1	0.038
Abhd4	0.028	Dpp10	-0.037	Dpp6	-0.037	Scn10a	0.038
Dync1li2	0.028	Lyz2	0.037	Il31ra	-0.037	Phyhipl	-0.038
Spag9	0.028	Nrn1	-0.037	Lyz2	0.037	Cdkn1a	0.038
Agtpbp1	0.028	Arg1	0.037	Arg1	0.037	Serpinc2	0.038
Col4a1	0.028	Ctss	0.037	Ctss	0.036	Fcer1g	0.038
Kifap3	0.028	Trem2	0.036	Trem2	0.036	Cck	-0.037
Lamc1	0.028	Tmem151b	-0.036	Tmem151b	-0.036	Arap2	-0.037
Sqstm1	0.028	Cthrc1	0.036	Cthrc1	0.036	Parm1	-0.037
Cyfip2	0.028	Tspan8	-0.036	Entpd3	-0.036	Dok4	-0.037
Timp2	0.028	Entpd3	-0.036	Tspan8	-0.036	Mrgprd	0.037
Atp2a2	0.028	Pou3f1	0.035	Nptx1	-0.036	Arl11	0.037
Aatk	0.027	Kcna4	-0.035	Pou3f1	0.035	Ppef1	0.037

Capn2	0.027	Atp2b3	-0.035	Kcna4	-0.035	Unc13c	0.036
Kif5b	0.027	Fn1	0.035	Atp2b3	-0.035	RT1-Db1	0.036
Cnp	0.027	Nptx1	-0.035	Fn1	0.035	RT1-Ba	0.036
Cpe	0.027	Gpr149	-0.034	Gpr149	-0.035	Calml4	0.036
Susd2	0.027	Syt9	-0.034	Flnc	0.034	Il24	0.036
Nfasc	0.027	Flnc	0.034	Syt9	-0.034	Kcnip4	-0.036
Atp1a2	0.027	Sdc1	0.034	Atp1a1	-0.034	Nat8l	-0.036
Mdh1	0.027	Atp1a1	-0.034	Sdc1	0.034	Acsl6	-0.036
Hspa4	0.027	Mrgprd	-0.034	Kirrel3	-0.034	Rem2	-0.036
Ccng1	0.027	Kirrel3	-0.034	Mrgprd	-0.034	Cxcl10	0.036
Gap43	0.027	Galnt5	-0.034	Hoxd1	-0.034	Nefm	-0.036
Mbnl2	0.027	Myof	0.034	Galnt5	-0.034	Cntnap4	-0.036
Tsc22d1	0.027	Hoxd1	-0.034	Myof	0.034	Rph3a	-0.036
Vps41	0.027	Htr1d	-0.034	Htr1d	-0.034	Cd300a	0.035
Myl6l	-0.027	Chga	-0.034	C1qc	0.034	Iapp	0.035
Gpr158	0.027	C1qc	0.034	Chga	-0.034	Rbfox3	-0.035
Gapdh	-0.027	Fabp3	-0.034	Kcng1	-0.034	Nmb	0.035
Tacc1	0.027	Tmem25	-0.034	Fabp3	-0.034	Plau	0.035
Pank3	0.027	Kcng1	-0.034	Tmem25	-0.034	Itgb2	0.035
Mapk8ip3	0.027	Trpa1	-0.033	Cpne4	-0.034	Doc2a	0.035
Lcp1	0.027	Cpne4	-0.033	Trpa1	-0.033	Kcnj6	-0.035
Ndrg2	0.027	Plekhd1	-0.033	Plekhd1	-0.033	Tmem150c	-0.035
Hspf1	0.027	Chrnb4	-0.033	Chrnb4	-0.033	Pla2g3	-0.035
Add1	0.027	Gria2	-0.033	Gria2	-0.033	Lypd1	-0.035
Akap11	0.027	Isl2	-0.033	Hebp2	-0.033	Slc30a3	-0.035
Stat3	0.027	Hebp2	-0.033	Isl2	-0.033	Tspy14	-0.035
Gdi2	0.027	Acpp	-0.033	Acpp	-0.033	Calb2	-0.035
Hnrnpu	0.027	Cd68	0.033	Thbs4	0.033	Ache	-0.035
Rgs4	0.027	Doc2a	-0.033	Doc2a	-0.033	Stmn4	0.034
Synj1	0.026	Thbs4	0.033	Gadd45a	0.033	Ibsp	0.034
Aldoc	0.026	Gbp2	0.033	Gbp2	0.033	Alas2	0.034
Vps35	0.026	Cd8a	0.033	Lrrn1	-0.033	Fgf12	-0.034
Ccdc92	0.026	Gadd45a	0.033	Scn8a	-0.033	P2rx6	-0.034

Gng2	0.026	Scn8a	-0.033	Chrb3	-0.033	Piwi2	-0.034
Prkar1b	0.026	Vwc2l	-0.033	Vwc2l	-0.032	Mmp10	-0.034
Ank3	0.026	Lrrn1	-0.033	Cd8a	0.032	Mt3	-0.034
Mtmr6	0.026	Calml4	-0.032	Calml4	-0.032	Susd4	-0.034
Aars	0.026	Lamp5	-0.032	Lamp5	-0.032	Robo2	-0.034
Map1lc3b	0.026	Chrb3	-0.032	Cd68	0.032	Nefh	-0.033
Mprip	0.026	Tac1	-0.032	Tac1	-0.032	Ifi30	0.033
Mrfap1	0.026	Amigo1	-0.032	Cuedc2	0.032	Pacsin1	-0.033
Sparcl1	0.026	Cuedc2	0.032	Amigo1	-0.032	Hk3	0.033
Wdr1	0.026	Col18a1	0.031	Tyrp1	-0.031	Kcnh6	-0.033
P4hb	0.026	Cldn4	0.031	Fam57b	-0.031	Lhfpl1	0.033
Cct8	0.026	Tyrp1	-0.031	Scube1	0.031	Esrrg	-0.033
Rufy3	0.026	Hhatl	-0.031	Hhatl	-0.031	Csf1r	0.033
Atp6v0c	0.026	Scube1	0.031	Rprm	-0.031	Top2a	0.033
Tubb2b	0.026	Fam57b	-0.031	Cldn4	0.031	Fxyd7	0.033
Csrp1	0.026	Rprm	-0.031	RGD1307461	-0.031	Klh14	-0.033
Nsf	0.026	Crlf1	0.031	Oprm1	-0.031	Tac1	0.032
Psmd2	0.026	Oprm1	-0.031	Kcnc1	-0.031	Igfbp3	0.032
Nars	0.026	RGD1307461	-0.031	Mmp19	0.030	Cmtm3	0.032
Hspb1	0.026	Kcnc1	-0.031	Sv2b	-0.030	Lix1	0.032
Rnf14	0.026	Mmp19	0.031	Itgb6	-0.030	Vim	0.032
Tagln2	0.026	Sv2b	-0.030	Abcd2	-0.030	Jph3	-0.032
Mapt	0.026	Itgb6	-0.030	Col18a1	0.030	Aifm3	-0.032
Itfg1	0.026	Abcd2	-0.030	Sphkap	-0.030	Pde6b	0.032
Usp14	0.026	Sphkap	-0.030	Crlf1	0.030	Cfh	0.032
Glul	0.026	Syt6	-0.030	Syt6	-0.030	Cntn4	0.032
Tns3	0.026	Cdh9	-0.030	Cdh9	-0.030	Acan	-0.032
Vat1	0.026	Syt3	-0.030	Syt3	-0.030	Nrg1	-0.031
Apc	0.026	Iapp	-0.030	Iapp	-0.030	Slfn13	0.031
Cadm3	0.026	Galnt18	-0.030	Cntn3	-0.030	Tubb6	0.031
Rnf187	0.026	Cntn3	-0.030	Galnt18	-0.030	C3	-0.031
Hk1	0.026	Itgal	0.030	Cckbr	0.030	Igf2bp2	0.031
Atp6v0d1	0.026	Cckbr	0.030	Hs6st2	-0.030	Pirt	-0.031

Marcks	0.026	Prrg4	0.030	Grik1	-0.030	Cysitr2	-0.031
Son	0.026	Hs6st2	-0.029	Itgal	0.030	Msln	0.031
Camsap2	0.026	Mctp2	-0.029	Prrg4	0.029	Socs3	0.031
Wdfy3	0.026	B3gat2	-0.029	B3gat2	-0.029	Caskin1	-0.031
Vamp2	0.025	Hamp	0.029	Hamp	0.029	Rab3a	-0.031
Dusp3	0.025	Ppp4r4	-0.029	Mctp2	-0.029	Myo1a	0.031
Vdac3	0.025	Fgf13	-0.029	Ppp4r4	-0.029	RT1-Bb	0.031
Eprs	0.025	Ptpn5	0.029	Fgf13	-0.029	Tnfrsf19	0.031
Prpf8	0.025	Cacna2d1	0.029	Cacna2d1	0.029	Tmem88	0.031
Ntrk2	0.025	Synm	-0.029	Smad9	-0.029	Vgf	0.031
Myh10	0.025	Lix1	-0.029	Synm	-0.029	Dbp	-0.031
Ccdc47	0.025	Cntn6	-0.029	Ptpn5	0.029	Dnm3	-0.031
Atp6v0a1	0.025	Grik1	-0.029	Lix1	-0.029	Thsd7b	-0.030
Ppp1r2	0.025	Lin7b	-0.029	Cntn6	-0.029	Adora1	-0.030
Ogdh	0.025	Dpysl4	-0.029	C3	0.029	Aif1	0.030
Prkar1a	0.025	C3	0.029	Spock3	-0.029	Slfn2	0.030
Scoc	0.025	Glb1l2	-0.029	Glb1l2	-0.029	Vwa5b2	-0.030
Prrc2a	0.025	Smad9	-0.029	Dpysl4	-0.029	Ripk3	0.030
Psme4	0.025	Ucn2	0.029	Rgs4	-0.029	Fads6	-0.030
Got2	0.025	Glrb	-0.029	Lin7b	-0.029	Adamts4	0.030
Actr3	0.025	Tnik	0.029	Tnik	0.029	LOC300308	0.030
Mycbp2	0.025	Sox11	0.029	Sox11	0.029	Mmp13	-0.030
Tbc1d9b	0.025	Chrna7	-0.029	Ucn2	0.029	Cenpf	0.030
Prdx2	0.025	Emp1	0.028	Glrb	-0.029	Rasd1	0.030
Ranbp2	0.025	Cybb	0.028	Cybb	0.029	Tmem151b	0.030
Rnf10	0.025	Csf1	0.028	Chrna7	-0.028	Faim2	0.030
Itpr3	0.025	Csrp2	0.028	Csrp2	0.028	Rgs10	0.030
Tnpo2	0.025	Tbxas1	0.028	Itgam	0.028	Ptprc	0.030
Epdr1	0.025	Itgam	0.028	Tbxas1	0.028	Fstl1	-0.030
Eif4h	0.025	Igfsf10	0.028	Csf1	0.028	Mmd	0.030
Fermt2	0.025	Rab32	0.028	Emp1	0.028	Chchd10	-0.029
Ccni	0.025	Ndst4	-0.028	Ntng1	-0.028	Stbd1	-0.029
RGD1304884	0.025	Dlgap3	-0.028	Igfsf10	0.028	Tgfb1	0.029

Glud1	0.025	Cbln4	-0.028	Rab32	0.028	Camk2a	-0.029
Usp32	0.025	Ntng1	-0.028	Cbln4	-0.028	Litaf	0.029
Csnk1d	0.025	Kcnk18	-0.028	Dlgap3	-0.028	Prkg2	-0.029
Pi4ka	0.025	Ass1	-0.028	Ndst4	-0.028	Irf8	0.029
Myoc	0.025	Spock3	-0.028	Ass1	-0.028	Ablim2	-0.029
Calm2	0.025	Slc9a9	-0.028	Slc9a9	-0.028	Tnfrsf12a	0.029
Hsbp1	0.025	Hpd	0.028	Kcnk18	-0.028	Hecw1	-0.029
Pcp4	0.025	LOC365985	-0.028	LOC365985	-0.028	Kcnv1	0.029
Slc12a2	0.025	Apod	0.028	Rnf112	-0.028	Cacna2d3	-0.029
Cpne6	0.025	Plbd1	0.028	Gabra1	-0.028	Rrm2	-0.029
Alcam	0.025	Tspo	0.028	Tspo	0.028	Grm4	-0.029
Cox4i1	0.025	Kcnab2	-0.028	Sst	-0.028	Atp2b4	0.029
Pebp1	0.025	Sptssb	-0.028	Plbd1	0.028	Lin7b	0.029
Ubl3	0.025	Gfap	0.028	Sptssb	-0.028	Nid2	0.029
Ncoa4	0.025	Fos	0.028	Kcnab2	-0.028	Slc51a	-0.029
Cct4	0.025	Chgb	-0.028	Hpd	0.028	Kcnf1	0.029
Vcl	0.025	Rgs4	-0.027	Chgb	-0.028	Adam11	-0.029
Sep-05	0.025	Slc24a2	-0.027	Fos	0.028	Stard13	0.029
Cdh1	0.025	Galnt14	-0.027	Slc24a2	-0.028	Gadd45g	0.029
Evi5	0.025	Ppp1r1c	-0.027	Galnt14	-0.028	Inhbb	-0.029
Myo18a	0.025	Tyrobp	0.027	Gabrg2	-0.027	Calcb	0.028
Adam19	0.025	Sst	-0.027	Ppp1r1c	-0.027	Cdk1	0.028
Mdh2	0.025	Prc1	0.027	Six4	-0.027	Fat3	0.028
Arl8a	0.025	Six4	-0.027	Lrrc49	-0.027	Dgkg	-0.028
Mtch1	0.024	Lrrc49	-0.027	Adcyap1	0.027	Pik3r5	0.028
Nsg2	0.024	Adcyap1	0.027	Tyrobp	0.027	Cyba	0.028
Aff4	0.024	Rnf112	-0.027	Prc1	0.027	Ccl9	0.028
Clip2	0.024	Necab3	-0.027	Sbsn	0.027	Hes5	0.028
Msmo1	0.024	Gabra1	-0.027	Necab3	-0.027	C4b	0.028
Tkt	0.024	Sbsn	0.027	Faim2	-0.027	Mmp2	0.028
Rplp0	0.024	Apobec1	0.027	Apobec1	0.027	Ifi47	0.028
Nacad	0.024	Faim2	-0.027	Fxyd7	-0.027	Slc9a3	-0.028
Glg1	0.024	Kcna2	-0.027	Gfap	0.027	Nfil3	0.028

Mmp15	0.024	Fxyd7	-0.027	Col27a1	0.027	Nudt6	0.028
Tfrc	0.024	Col27a1	0.027	Rgs7bp	-0.027	Cntn3	0.028
Ppp3r1	0.024	Gabrg2	-0.027	Casr	-0.027	Arpc1b	0.028
Ptpn11	0.024	Kcnq5	-0.027	Kcnq5	-0.027	P2rx7	0.028
Hspb8	0.024	Sgpp2	-0.027	Cacng2	-0.027	Bmp1	0.028
Anapc5	0.024	Rgs7bp	-0.026	Kcna2	-0.026	Atp11a	-0.027
Supt6h	0.024	Cacng2	-0.026	Sbno2	0.026	Hist2h3c2	-0.027
Bnip3l	0.024	Ccnd1	0.026	Ccnd1	0.026	Gm2a	0.027
Copa	0.024	Acp5	0.026	Acp5	0.026	Cdh9	0.027
Ankrd17	0.024	Sbno2	0.026	Sgpp2	-0.026	Rhbdf2	0.027
Ank1	0.024	Col16a1	0.026	Col16a1	0.026	Galnt5	0.027
Srsf1	0.024	Rab3c	-0.026	Apod	0.026	Btc	0.027
Sod1	0.024	Casr	-0.026	Abca1	0.026	Plcx2	-0.027
Fkbp8	0.024	Caly	-0.026	Cx3cr1	0.026	Cadps	-0.027
Cadps	0.024	St8sia1	-0.026	Gyg1	-0.026	Myh8	-0.027
Kpnb1	0.024	Cx3cr1	0.026	Caly	-0.026	Rgs8	-0.027
Atp9b	0.024	Gyg1	-0.026	Sh3gl2	-0.026	Gas7	0.027
Gtf2i	0.024	Serpine1	0.026	Rab3c	-0.026	Smpd13a	0.027
Dbi	0.024	Bcan	-0.026	Myo1f	0.026	Rap1gap2	-0.027
Ghitm	0.024	Myt1l	-0.026	St8sia1	-0.026	Msr1	0.027
Cfbf	0.024	Myo1f	0.026	Bcan	-0.026	Epn3	-0.027
Abcc5	0.024	Rgs6	-0.026	Kif22	0.026	Tspan8	0.027
Sucla2	0.024	Abca1	0.026	Rgs6	-0.026	Amdhd1	0.026
Npepps	0.024	Igsf21	-0.026	Igsf21	-0.026	Trim37	-0.026
Mtmr4	0.024	Cdhr5	0.026	Myt1l	-0.026	B3gat2	0.026
Tubb2a	0.024	Camkv	-0.026	Camkv	-0.026	Olfml2b	0.026
Trim35	0.024	Sh3gl2	-0.026	Cdhr5	0.026	Inpp5j	-0.026
Ncor2	0.024	Kif22	0.026	F2rl2	-0.026	Fbn2	0.026
Dpysl3	0.024	F2rl2	-0.026	C1s	0.026	Frmpd4	0.026
Abr	0.024	Arpp21	-0.026	RGD1306941	-0.026	Slamf9	0.026
Cntnap1	0.024	Runx2	0.026	Arpp21	-0.026	Dmrtc1a	0.026
Tgfb1	0.024	RGD1306941	-0.026	Ucn	0.026	Fcgr2b	0.026
Tbcd	0.024	Pclo	-0.026	Pclo	-0.026	Adra2c	-0.026

Nsg1	0.024	C1s	0.026	Nefl	-0.026	Ybx1	-0.026
Igfbp7	0.024	Ucn	0.026	Runx2	0.026	Grn	0.026
Ppp1cc	0.024	Ptgfr	-0.026	Ptgfr	-0.026	Scn1a	0.026
Gas6	0.024	Extl2	-0.026	Pygb	-0.026	Coro6	-0.026
Adipor1	0.024	Pygb	-0.026	Extl2	-0.026	Entpd3	0.026
Plbd2	0.024	Smim17	-0.026	LOC100125362	-0.026	Mag	-0.026
Nfat5	0.024	Cd74	0.025	Rab9b	-0.026	Car12	0.026
Nat8l	0.024	Rab9b	-0.025	Serpine1	0.025	Dnase2	0.026
Cd74	0.024	Jun	0.025	Mmp16	0.025	Gzmb	0.025
LOC294154	0.023	Mmp16	0.025	Jun	0.025	Fgf9	-0.025
Usp34	0.023	Cnnm1	-0.025	Cnnm1	-0.025	Cdh22	-0.025
Ociad1	0.023	LOC100125362	-0.025	Chrna6	-0.025	Entpd4	-0.025
Fam13b	0.023	Nell1	-0.025	Smim17	-0.025	Aurkb	0.025
Asah1	0.023	Smagp	0.025	Nell1	-0.025	Syt2	-0.025
Cox6a1	0.023	Btbd16	0.025	Cd55	-0.025	Gch1	0.025
Tm9sf2	0.023	Tgfbr1	0.025	Btbd16	0.025	Ier5	0.025
Fdft1	0.023	LOC100910996	-0.025	Smagp	0.025	Lilrb3	-0.025
Ubqln1	0.023	Lrfn5	-0.025	Tgfbr1	0.025	Nkiras1	-0.025
Tpr	0.023	PVR	0.025	LOC100910996	-0.025	Ciita	0.025
Rab1a	0.023	Prmt8	-0.025	Rit2	-0.025	Mcm6	0.025
Flot2	0.023	Chrna6	-0.025	Lrfn5	-0.025	Syk	0.025
Rab3a	0.023	RT1-Da	0.025	Prmt8	-0.025	Dpp6	0.025
Gnao1	0.023	Serpding1	0.025	PVR	0.025	Cdh7	-0.025
Zdhhc2	0.023	Clrn1	-0.025	LOC688459	0.025	Col8a1	0.025
Dnm1l	0.023	Anpep	0.025	Clrn1	-0.025	Cxcl9	0.025
Cd48	0.023	Amdhd1	-0.025	Kcnf1	-0.025	Flt3	-0.025
Slc22a23	0.023	Folr2	0.025	Serpding1	0.025	Fcgr3a	0.025
Mink1	0.023	LOC688459	0.025	Sertm1	-0.024	Dsc2	0.025
Sep-08	0.023	Kcnf1	-0.025	Amdhd1	-0.024	Cd38	0.025
Cyb5r1	0.023	Apba1	-0.024	Apba1	-0.024	Gabrg1	-0.025
Psmc5	0.023	Igfbp2	-0.024	Folr2	0.024	Hs6st2	0.025
Bicd2	0.023	Tmem72	-0.024	Padi3	0.024	Pcp4l1	-0.025
Kif3a	0.023	Sertm1	-0.024	Rtn4rl1	-0.024	Csf2ra	0.025

Lgals3	0.023	Padi3	0.024	Anpep	0.024	Pbk	0.025
Slc22a17	0.023	Ifitm1	0.024	Gabbr2	-0.024	Vwc2l	0.025
Lasp1	0.023	Ppm1j	-0.024	Cyth4	0.024	Mrc1	0.025
Pkd1	0.023	Vcan	0.024	Vcan	0.024	Ugt1a1	-0.025
Jup	0.023	C2	0.024	Ppm1j	-0.024	Cacng5	-0.025
Golgb1	0.023	Cyth4	0.024	Fndc5	-0.024	Cntn6	0.025
Git1	0.023	Fndc5	-0.024	Igfbp2	-0.024	Krt28	-0.025
Dnajc7	0.023	Gabbr2	-0.024	Tmem72	-0.024	Arhgap30	0.025
Rundc3a	0.023	Slc16a12	-0.024	Grem2	-0.024	Galnt18	0.024
H3f3b	0.023	Lancl3	-0.024	Cd74	0.024	Kcnt2	-0.024
Arpc1a	0.023	Rit2	-0.024	Cd4	0.024	Grid2ip	-0.024
Tmem130	0.023	Cd55	-0.024	Ifitm1	0.024	Marcks	0.024
Arhgef40	0.023	Arid5a	0.024	Slc16a12	-0.024	Emp2	0.024
Agpat3	0.023	Cd4	0.024	Arid5a	0.024	Ank1	-0.024
Plxna2	0.023	Gpr34	0.024	Lingo1	-0.024	Sh2b3	0.024
Ctnna1	0.023	Rarres1	-0.024	Lancl3	-0.024	Ryr2	-0.024
Wdr26	0.023	Lingo1	-0.024	Rarres1	-0.024	Abca5	-0.024
Lars	0.023	Fndc1	0.024	Gpr34	0.024	Cd300lf	0.024
Ube2l3	0.023	Slc17a7	-0.024	Slc8a2	-0.024	Kcnip3	0.024
Flli	0.023	Isl1	-0.024	Slc17a7	-0.024	Mir675	-0.024
Nf1	0.023	Slc8a2	-0.024	Fndc1	0.024	Kcnd3	0.024
Uso1	0.023	Entpd2	0.024	Entpd2	0.024	Fabp4	-0.024
Pcm1	0.023	Asic1	-0.024	Elovl7	-0.024	C4a	0.024
Gna12	0.023	Met	0.024	Met	0.024	Tex15	-0.024
Mapk9	0.023	Elovl7	-0.024	Asic1	-0.024	Man1a1	0.024
Cntn2	0.023	Nefl	-0.024	Lgi3	-0.024	Mapk10	-0.024
Ankfy1	0.023	Sipa1	0.024	Ccdc126	-0.024	Nsg2	-0.024
Serpinb1a	0.023	Ccdc126	-0.024	Isl1	-0.024	Cntn2	-0.024
Vdac2	0.023	Cfd	0.024	Sipa1	0.024	Egr2	0.024
Nbr1	0.023	Dync1i1	-0.024	Trpv1	-0.024	Rhobtb2	-0.024
Atp6v1g2	0.023	Pld4	0.024	Cfd	0.024	Bcl2l11	-0.024
Fbxw11	0.023	Cst12	-0.024	RT1-Da	0.024	Aebp1	0.024
Psmc6	0.023	Rtn4rl1	-0.024	Pld4	0.024	Adamts1	0.024

Qdpr	0.023	Syt12	-0.024	Dync1i1	-0.024	Chrm2	0.024
lvns1abp	0.023	Grem2	-0.024	Cst12	-0.024	Ptchd1	-0.024
Col18a1	0.023	Csf2rb	0.024	Syt12	-0.024	Angptl4	0.024
Art3	0.023	Tmem54	-0.024	Csf2rb	0.024	Cxadr	0.024
Elov12	0.023	Sorcs3	-0.023	Cdh3	-0.024	P2rx5	-0.023
Col6a2	0.023	Htr2b	0.023	Tmem54	-0.024	Lyrm7	-0.023
Fytd1	0.023	Kcnb1	-0.023	C2	0.023	Tlr5	0.023
Bin1	0.023	Ncf1	0.023	Ntrk1	-0.023	Cox7a2	0.023
Fxr2	0.023	Cdkn1a	0.023	Sorcs3	-0.023	Chrne	-0.023
Rac1	0.023	Slc16a14	-0.023	Kcnb1	-0.023	Nos1	0.023
Sec63	0.023	Ntrk1	-0.023	Kcnc2	-0.023	Anxa3	0.023
Rph3a	0.023	Kcnc2	-0.023	Slc16a14	-0.023	Ppic	0.023
Ctbp1	0.023	Tsc22d3	-0.023	Plcd1	0.023	Tnni3k	0.023
Tecr	0.023	Plcd1	0.023	Etv1	-0.023	Slc18a2	-0.023
Brox	0.023	Bcl2a1	0.023	Htr2b	0.023	Rab27b	-0.023
Egfl8	0.023	Etv1	-0.023	Tsc22d3	-0.023	Col6a2	0.023
Plat	0.023	Mki67	0.023	Mki67	0.023	Kcnab1	0.023
Ube2z	0.023	Serpinb2	0.023	Nrsn1	-0.023	Cpne9	-0.023
Syt2	0.023	Fcer1g	0.023	Lama5	0.023	Scml4	-0.023
Abce1	0.023	Zdhhc22	-0.023	Bcl2a1	0.023	Mcm5	0.023
Synpr	0.022	Lama5	0.023	Zdhhc22	-0.023	Adap2	0.023
Ppp2cb	0.022	C1r	0.023	C1r	0.023	Mybph	-0.023
Flot1	0.022	Cdh3	-0.023	Rdh16	0.023	Omg	-0.023
Ndel1	0.022	Rims1	-0.023	Rims1	-0.023	Amigo1	0.023
Lgals3bp	0.022	Cnr1	-0.023	Cnr1	-0.023	Colec12	0.023
Anxa11	0.022	Rdh16	0.023	Mum1l1	-0.023	RGD1307443	-0.023
Dhx9	0.022	Pcsk9	-0.023	Vtcn1	0.023	Slitrk1	-0.023
MAST1	0.022	Ttc39b	-0.023	Pianp	-0.023	Fzd2	0.023
Cdc42bpa	0.022	Mum1l1	-0.023	Hpca	-0.023	Dmgdh	0.023
Tmed2	0.022	Vtcn1	0.023	Serpinb2	0.023	Metrn	0.023
Lgi3	0.022	Trpv1	-0.023	Ttc39b	-0.023	Nxpe3	-0.023
S1pr3	0.022	Fez1	-0.023	Pcsk9	-0.023	Gap43	0.023
Acaca	0.022	Hpca	-0.023	Fez1	-0.023	Pou4f3	-0.023

Spop	0.022	Eepd1	-0.023	Phyhipl	-0.023	Slc16a12	0.023
Ube2b	0.022	RT1-Db1	0.023	Grin1	-0.023	Npr3	-0.023
Pitpna	0.022	Crbn	-0.023	Cdkn1a	0.023	S100a13	0.023
Psmd6	0.022	Iqgap3	0.023	Crbn	-0.023	Tox3	-0.023
Wbp2	0.022	RT1-Ba	0.023	Eepd1	-0.023	Cbln4	0.023
Klf6	0.022	Lgi3	-0.023	Iqgap3	0.023	Smim17	0.023
Tmed7	0.022	Grin1	-0.023	St14	0.023	Pqlc1	-0.023
Napg	0.022	St14	0.023	Ncf1	0.023	Ly6g6c	0.023
Rpl18a	0.022	Pianp	-0.023	Scrt1	-0.023	Gnao1	-0.023
Rbfox1	0.022	Has1	0.023	Has1	0.023	Btbd16	-0.023
Pitpnm2	0.022	Vstm2b	-0.023	Tbx18	0.023	Tmem14a	0.023
Ndfip2	0.022	Gna14	-0.023	Gna14	-0.023	Lcp2	0.023
Lrrc59	0.022	Tbx18	0.023	Thbs1	0.023	Kirrel3	0.023
Fnta	0.022	Khk	-0.023	Arap2	-0.023	Ncf2	0.022
Ulk2	0.022	Nrsn1	-0.023	Vstm2b	-0.023	Dleu7	-0.022
Actr2	0.022	Cxcl10	0.023	Mal2	-0.023	Pdgfra	0.022
Entpd4	0.022	Ets1	0.023	Parm1	-0.023	Cntnap1	-0.022
Optn	0.022	Ubash3b	-0.023	Dok4	-0.023	Cxcl16	0.022
Arf4	0.022	Scrt1	-0.023	Panx2	-0.023	Pitpnm2	-0.022
Ubb	0.022	Mal2	-0.023	Khk	-0.023	Pla2g4a	0.022
Nsd1	0.022	Spi1	0.022	Fcer1g	0.023	Sfrp2	0.022
Sec14l1	0.022	Cyp2s1	0.022	Spi1	0.023	B3galt5	-0.022
Wsb2	0.022	Zcchc12	-0.022	Rcan2	-0.023	Ldb2	-0.022
Mapk10	0.022	Arl11	0.022	Zcchc12	-0.023	Sgsm1	-0.022
Cdh2	0.022	Thbs1	0.022	Cyp2s1	0.022	Fabp7	-0.022
Limk1	0.022	Rcan2	-0.022	Ets1	0.022	Hcls1	0.022
Fgfr1	0.022	Clcn4	-0.022	Col5a2	0.022	Fkbp10	0.022
Elmo1	0.022	Col5a2	0.022	Clcn4	-0.022	Fras1	-0.022
Adam9	0.022	Il24	0.022	Cck	0.022	Acyp2	-0.022
Mmp2	0.022	Thbd	0.022	Fbn1	0.022	Ppp1r3c	0.022
Robo2	0.022	Bin2	0.022	Rdh10	0.022	RT1-Db2	0.022
Pttg1ip	0.022	Cck	0.022	Ubash3b	-0.022	Dscam	-0.022
Opa1	0.022	Mafb	0.022	Kcnd1	-0.022	Cd14	0.022

Trim37	0.022	Panx2	-0.022	Bin2	0.022	Mdh1	-0.022
Srsf2	0.022	Slpi	0.022	Prkce	-0.022	Ppp1r18	0.022
Trrap	0.022	Herc3	-0.022	Herc3	-0.022	Gpr22	0.022
Igfbp4	0.022	Lyn	0.022	Thbd	0.022	Mme	-0.022
Bcl2l2	0.022	P2ry6	0.022	Mafb	0.022	Hspf1	-0.022
Tmem50b	0.022	Vav1	0.022	P2ry6	0.022	Cd86	0.022
Rps4x	-0.022	Fbn1	0.022	Lyn	0.022	Junb	0.022
Grsf1	0.022	Pcsk2	-0.022	Vav1	0.022	Tk1	0.022
Bag6	0.022	Kcnd1	-0.022	Kcnj3	-0.022	Sh3bp2	0.022
Dock9	0.022	Rdh10	0.022	Slpi	0.022	Fry	-0.022
Tpm4	0.022	Prkce	-0.022	Tmem45b	-0.022	Limk1	-0.022
Cacybp	0.022	Blnk	0.022	Paqr9	-0.022	Cyp2d3	-0.022
Dbn1	0.022	Paqr9	-0.022	Pcsk2	-0.022	Aqp4	-0.022
Larp4b	0.022	Cd53	0.022	Il24	0.022	Gprc5c	-0.022
Snn	0.022	Tmem45b	-0.022	Blnk	0.022	Pou3f1	-0.022
Ube3b	0.022	Kcnj3	-0.022	RT1-Db1	0.022	Cdo1	-0.022
Rabep1	0.022	Fam198b	0.022	Arl11	0.022	Ppm1j	0.022
Adss	0.022	Fam81a	-0.022	Fam81a	-0.022	Glrb	0.022
Ndufs2	0.022	Stmn4	0.022	RT1-Ba	0.022	Casp3	0.022
Fat1	0.022	Tnfaip6	0.022	Cxcl10	0.022	Rara	0.022
RGD1309748	0.022	Ar	-0.022	Plekha7	0.022	Per3	-0.022
Cmip	0.022	Gpr88	0.022	Fam198b	0.022	Egfr	0.021
Trappc10	0.022	Phyhipl	-0.022	Cd53	0.022	Slc7a11	-0.021
Wrb	0.022	Steap4	0.022	Kcnip4	-0.022	Pcolce	0.021
Xpo1	0.022	Arap2	-0.022	Rem2	-0.022	Cabp1	-0.021
Cnot1	0.022	Ptpro	0.022	Ltbp1	0.022	Lfng	0.021
Pcbp3	0.022	Ezh2	0.022	Tnfaip6	0.022	Scara5	0.021
Idi1	0.022	Ltbp1	0.022	Fermt3	0.022	Parp9	0.021
Slc30a9	0.022	Plau	0.022	Steap4	0.022	Asphd2	-0.021
Gabra2	0.022	Asah2	-0.022	Acsl6	-0.022	Chrnb4	0.021
Sorcs2	0.022	Tlr8	0.022	Nat8l	-0.022	Csmd1	-0.021
Iscu	0.022	Fermt3	0.022	Gpr88	0.022	Mctp2	0.021
Sgcb	0.022	Cxxc4	-0.022	Ptpro	0.022	Spire2	-0.021

Tsnax	0.022	Parm1	-0.022	Ar	-0.022	Baiap2l1	-0.021
Atp1b2	0.022	Irak3	0.022	Fgf2	0.022	Galr1	-0.021
Phyhipl	0.022	Cd300a	0.022	Cxxc4	-0.022	Tmem132e	-0.021
Pdhb	0.022	Itgb2	0.022	Ezh2	0.022	Cebpd	0.021
Ppp1r9b	0.022	Ramp1	0.022	Tlr8	0.022	Lama5	-0.021
Cbln2	0.022	Scn9a	-0.022	Asah2	-0.022	Asic2	-0.021
Eif3b	0.022	Fgf2	0.022	Cntnap4	-0.022	Ifi27l2b	0.021
Supt16h	0.022	Dok4	-0.022	Ahr	0.022	Nlrp3	0.021
Gpr37l1	0.022	Stra6	0.022	Nefm	-0.022	Vwa7	-0.021
Mmp14	0.022	Gna15	0.022	Stra6	0.022	Ccdc28a	0.021
Txnl1	0.022	Ahr	0.022	Rph3a	-0.022	Ass1	0.021
Glo1	0.022	Tle3	0.022	Irak3	0.022	Bex1	0.021
Cltb	0.022	Cd8b	0.022	Gna15	0.022	Gria2	0.021
Clcn3	0.022	Plekha7	0.021	Ramp1	0.022	Tyrp1	0.021
Nploc4	0.022	Kcnip4	-0.021	Scn9a	-0.022	Gpr149	0.021
Tbc1d9	0.022	Rgs10	-0.021	Tmem178b	-0.022	Rbm11	-0.021
Wdr7	0.022	Ankrd13d	-0.021	Rgs10	-0.022	Tmem45b	0.021
Txndc5	0.022	Rem2	-0.021	Rbfox3	-0.021	Nog	-0.021
Tgfbr3	0.022	Parvg	0.021	Axl	0.021	Fxyd2	0.021
Htt	0.022	Cd276	0.021	Parvg	0.021	Pcdh9	-0.021
Atg12	0.022	Tmem178b	-0.021	Ap1s2	-0.021	Ndrg4	-0.021
Parp1	0.022	Axl	0.021	Tle3	0.021	Atp8b1	0.021
Nid2	0.022	Lhfpl4	-0.021	Ankrd13d	-0.021	Pla2g4c	-0.021
Riok3	0.022	Mgp	0.021	Cd8b	0.021	Anxa5	0.021
Gmfb	0.022	Ibsp	0.021	Lhfpl4	-0.021	Stk10	0.021
Mtus1	0.022	Ap1s2	-0.021	Kcnh2	-0.021	Camk1g	-0.021
Cpd	0.022	Fxyd5	0.021	Cd276	0.021	Olfml2a	-0.021
Prkaca	0.022	Kcnh2	-0.021	Kcnj6	-0.021	Zfp365	-0.021
Dnm3	0.022	Tgfb1	0.021	Tmem150c	-0.021	Slc4a4	-0.021
Gm2a	0.022	Tspan11	0.021	Htr2c	-0.021	Selp	0.021
LOC680039	0.022	Htr2c	-0.021	Fstl5	-0.021	Gabra2	-0.021
Nfe2l1	0.022	Cntnap4	-0.021	Lypd1	-0.021	Gngt2	0.021
Pds5b	0.022	Mag	0.021	Tcte1	-0.021	Kcnma1	-0.021

Aebp1	0.022	Gldn	0.021	Slc46a2	-0.021	Amph	-0.021
Nudt3	0.022	Slc46a2	-0.021	Cd300a	0.021	Tnc	0.021
Ppp2r2b	0.021	Dusp6	0.021	Tspan11	0.021	Cdh15	-0.021
Ppp2r5b	-0.021	Fstl5	-0.021	Dusp6	0.021	Ppp1r2	-0.021
Vps4b	0.021	Hes5	-0.021	Fes	0.021	Bst2	0.021
Rpl37a	-0.021	Vim	0.021	Pla2g3	-0.021	Hoxb8	-0.021
Cldnd1	0.021	Slc25a33	-0.021	Plau	0.021	Hebp2	0.021
Tnfaip1	0.021	Fes	0.021	Tgfb1	0.021	Eif4ebp1	0.021
Emp2	0.021	Cadm1	-0.021	Fxyd5	0.021	Scn8a	0.020
Iars	0.021	Cpxm1	0.021	Gldn	0.021	Mospd1	0.020
Dusp26	0.021	Fkbp1b	-0.021	Smad3	0.021	Trim47	0.020
Golga7	0.021	Bmp7	0.021	Slc25a33	-0.021	Stear3	-0.020
Ublcp1	0.021	Smad3	0.021	Cpxm1	0.021	Khk	0.020
Rab3gap2	0.021	Tecta	0.021	Gpc3	0.021	Loxl2	0.020
Ap1b1	0.021	Gpc3	0.021	Bmp7	0.021	Rnase4	0.020
Psmd3	0.021	Psd4	0.021	Mag	0.021	Rarres1	0.020
Kctd10	0.021	Tcte1	-0.021	Stmn4	0.021	Pnp	0.020
Bpnt1	0.021	Scg5	-0.021	Tspyl4	-0.021	Clic1	0.020
Mx2	0.021	Cp	0.021	Psd4	0.021	Tubb2b	0.020
Ap1s1	0.021	Tmem86a	0.021	Mgp	0.021	Cdkl2	-0.020
Uba6	0.021	Tlr7	0.021	Hes5	-0.021	Kcnk1	-0.020
Myo9b	0.021	Fblim1	0.021	Scg5	-0.021	Cd8a	0.020
Tpcn1	0.021	Acsl6	-0.021	Ache	-0.021	Ppp4r4	0.020
Aldh3a2	0.021	Ssc5d	0.021	Tecta	0.021	Ckap2	0.020
Ddx39b	0.021	Clec4a3	0.021	Itgb2	0.021	Ap1s2	0.020
Rps27a	-0.021	Lypd1	-0.021	Itgb8	0.021	Pou4f2	-0.020
Scarb2	0.021	Kcnj6	-0.021	Calb2	-0.021	RGD1302996	-0.020
Zmiz1	0.021	Ankr34c	-0.021	Cp	0.021	Col1a1	0.020
Dcaf7	0.021	Clec12a	0.021	Cadm1	-0.021	Kif18b	0.020
Ssr1	0.021	Rbfox3	-0.021	Tlr7	0.021	Nrp2	-0.020
Cd200	0.021	Ctsc	0.021	Tmem86a	0.021	Cryga	0.020
Gaa	0.021	Itgb8	0.021	Fblim1	0.021	Scrg1	-0.020
Pfn1	0.021	Rgs3	-0.021	Ibsp	0.021	Cyp26b1	-0.020

Xpo7	0.021	Ifi30	0.021	Piwil2	-0.021	RT1-T24-3	0.020
Fgf1	0.021	Nat8l	-0.021	Ankrd34c	-0.021	Dnah1	0.020
Sec24c	0.021	Gdap1	-0.021	Fkbp1b	-0.021	Kazn	-0.020
Camta2	0.021	Tnfaip8l2	0.021	Clec4a3	0.021	Nsf	-0.020
Nus1	0.021	Mrgprf	0.021	Rgs3	-0.021	Chrna7	0.020
Cndp2	0.021	Csf1r	0.021	Gdap1	-0.021	Fcho1	-0.020
Ubxn4	0.021	Cadm4	0.021	RGD1563349	-0.021	Clec10a	0.020
Hsd17b4	0.021	Rhoq	0.021	Fgf12	-0.021	Fabp3	0.020
Hspa9	0.021	Col5a1	0.021	Clec12a	0.021	Abcb9	-0.020
Csnk1a1	0.021	Pla2g3	-0.021	Col5a1	0.021	Kifc1	0.020
Maea	0.021	RGD1563349	-0.021	P2rx6	-0.021	Elov12	-0.020
Impact	0.021	Atp2b2	-0.021	Ctsc	0.021	Lsamp	-0.020
Ncor1	0.021	Ptprt	0.021	Ssc5d	0.021	Eif5a2	0.020
Zcchc24	0.021	Arhgap8	-0.021	Cadm4	0.021	Jph4	-0.020
Eif1	0.021	Rph3a	-0.021	Dhfr	0.021	Il1rap	0.020
Dnaja2	0.021	Laptm5	0.020	Mrgprf	0.021	Igtp	0.020
Atp6v1a	0.021	Tmem150c	-0.020	Tnfaip8l2	0.021	Sep-04	-0.020
Tpt1	0.021	Trim9	-0.020	Atp2b2	-0.021	Ccnf	0.020
Cdh19	0.021	Capg	0.020	Rhoq	0.021	Camkk1	-0.020
Appbp2	0.021	Dhfr	0.020	Ly49si1	0.021	Npl	0.020
Klhl24	0.021	Cd63	0.020	Arhgap8	-0.021	Gfod1	-0.020
Usp7	0.021	Epb41l4b	0.020	Susd4	-0.021	Krt19	0.020
Degs1	0.021	Ly49si1	0.020	Ptprt	0.021	Homer3	0.020
Gab1	0.021	Piwil2	-0.020	Mt3	-0.021	Slc46a2	0.020

**Table S2. Common differentially expressed genes in mouse models of injury pain.** The DEGs, common between Baskozos (B) and Cobos (C) datasets. The names of the known pain genes (based on pain databases and literature curation, Table S6) are marked in bold. The names of genes, which are present in three main types of sensory neurons NP, PEP, LM (based on single cell classification of sensory neuron - related genes in SNT injury model in mice) are marked by blue, magenta and green colours, respectively. Genes expressed in both PEP and NP are coloured by purple; in both NP and LM - by brown. Genes expressed in all 3 neuron types are marked as red. Additionally, genes expressed in the dataset of pooled sensory neurons from DRG of SNI-injured mouse [17] are marked by light blue. Log2 fold changes compared to control, non-injured DRG are shown. Genes were considered to be differentially expressed in B and C based on p adjusted FDR  $\leq 0.05$  and log2 fold changes  $\geq 0.5$ .

gene name	description	log2fc_B	log2fc_C
<b>Sprr1a</b>	small proline-rich protein 1A; neuronal regeneration [20]	4.88	6.75
<b>Npy</b>	neuropeptide Y; endocrine; GPCR binding; neuron projection development; negative regulation of blood pressure [58]	4.67	5.84
Anxa10	annexin A10	4.77	5.55
Tex16	testis expressed gene 16	3.13	5.49
<b>Wdr63</b>	WD repeat domain 63	2.98	5.25
<b>Slc6a4</b>	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	2.66	5.14
<b>Rnd1</b>	Rho family GTPase 1	1.23	5.05
Mc4r	melanocortin 4 receptor	1.01	5
4933403O08Rik	RIKEN cDNA 4933403O08 gene	3.41	4.86
<b>Pkd2l1</b>	polycystic kidney disease 2-like 1; subunit of calcium channel; involved in sensory functions and pain [18]	4.73	4.82
Lamb3	laminin, beta 3	1.53	4.72
<b>Gal</b>	Galanin; hormone of nervous systems activating GPCRs; produced in pituitary gland; mechanical and thermal nociception [24]; axon regeneration [16]	4.13	4.63
Tmprss11f	transmembrane protease, serine 11f	3.84	4.58
<b>Ecel1</b>	endothelin converting enzyme-like 1	3.66	4.54
<b>Lipn</b>	lipase, family member N	4.72	4.47
<b>Cckbr</b>	cholecystokinin B receptor; GPCR protein signalling; positive regulation of synaptic transmission	3.67	4.45
Trem2	triggering receptor expressed on myeloid cells 2; involved in chronic inflammation [37]	0.82	4.41
<b>Atf3</b>	activating transcription factor 3; apoptosis, stress, regeneration [42; 49]	3.18	4.36
Vmn2r78	vomeronasal 2, receptor 78	4.2	4.25
4930544M13Rik	RIKEN cDNA 4930544M13 gene	3.21	4.23
<b>Slfn10-ps</b>	schlafen 10, pseudogene	2.37	4.14
<b>Slc1a7</b>	solute carrier family 1 (glutamate transporter), member 7	3.6	4.08
<b>Gpr151</b>	G protein-coupled receptor 151, involved in pain [31]	3.96	3.9
<b>Car1</b>	carbonic anhydrase 1	2.21	3.9
<b>Kcnk16</b>	potassium channel, subfamily K, member 16	3.39	3.89
Pkhd1	polycystic kidney and hepatic disease 1	3.83	3.89
<b>Hao1</b>	hydroxyacid oxidase 1, liver	2.17	3.87
<b>Fst</b>	follistatin	1.91	3.76
<b>Nts</b>	Neurotensin; neuropeptide hormone activity; vesicle transport; analgesic [13]	2.96	3.59

<b>Oas1e</b>	2'-5' oligoadenylate synthetase 1E	3.22	3.51
<b>Mcoln2</b>	mucolipin 2	0.95	3.34
<b>Sez6l</b>	seizure related 6 homolog like	1.72	3.28
<b>Acvr1c</b>	activin A receptor, type IC; differentiation, apoptosis	1.39	3.28
<b>A630023A22Rik</b>	RIKEN cDNA A630023A22 gene	2.15	3.27
<b>Sifn9</b>	schlafen 9	2.61	3.01
<b>Sox11</b>	SRY (sex determining region Y)-box 11; transcription factor involved in neuronal regeneration [20]	1.52	3.01
<b>Stmn4</b>	stathmin-like 4; promote microtubule assemble [19]	1.7	2.88
<b>Lmo7</b>	LIM domain only 7	0.96	2.85
<b>Tnni1</b>	troponin I, skeletal, slow 1	0.93	2.78
<b>Liph</b>	lipase, member H	1.76	2.73
<b>Sectm1b</b>	secreted and transmembrane 1B	1.11	2.62
<b>Speer4a</b>	spermatogenesis associated glutamate (E)-rich protein 4A	4.13	2.6
<b>Colec10</b>	collectin sub-family member 10; lectin	2.67	2.59
<b>Rin1</b>	Ras and Rab interactor 1; neuronal plasticity	1.31	2.58
<b>Glis3</b>	GLIS family zinc finger 3	1.72	2.58
<b>Pmaip1</b>	phorbol-12-myristate-13-acetate-induced protein 1	0.84	2.57
<b>Sema6a</b>	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A; axon growth inhibitor [46]	1.19	2.53
<b>Loxl2</b>	lysyl oxidase-like 2	1.59	2.35
<b>Gadd45a</b>	growth arrest and DNA-damage-inducible 45 alpha; anti-apoptosis [26]	1.07	2.35
<b>Mmp16</b>	matrix metallopeptidase 16; remodelling	1.25	2.34
<b>Csf1</b>	colony stimulating factor 1 (macrophage)	0.85	2.3
<b>Anxa1</b>	annexin A1; anti-apoptotic, neuroinflammation [33]	1.06	2.24
<b>Smim3</b>	small integral membrane protein 3	1.36	2.22
<b>Flrt3</b>	fibronectin leucine rich transmembrane protein 3; promotes neurite outgrowth [52]	1.78	2.22
<b>Shisa9</b>	shisa family member 9; involved in synaptic plasticity	0.97	2.19
<b>FlnC</b>	filamin C, gamma	1.02	2.16
<b>Sdc1</b>	syndecan 1	1.05	2.14
<b>Corin</b>	corin	1.99	2.14
<b>Draxin</b>	dorsal inhibitory axon guidance protein	1.7	2.11
<b>S100a11</b>	S100 calcium binding protein A11, differentiation	0.86	2.04
<b>Ctss</b>	cathepsin S; induce pain and itch during inflammatory pain [62]; microglia-specific lysosomal cysteine protease	0.99	2.04

<b>Lgals3</b>	lectin, galactose binding, soluble 3; inflammation	0.86	2
<b>Adam8</b>	a disintegrin and metallopeptidase domain 8	1.32	1.94
<b>Cyp4b1</b>	cytochrome P450, family 4, subfamily b, polypeptide 1	1	1.92
<b>Galnt6</b>	polypeptide N-acetylgalactosaminyltransferase 6	0.97	1.92
<b>Hrk</b>	harakiri, BCL2 interacting protein (contains only BH3 domain)	2.64	1.91
<b>Ccr5</b>	chemokine (C-C motif) receptor 5	0.84	1.89
<b>Nfil3</b>	nuclear factor, interleukin 3, regulated; axon growth inhibition [32]	0.73	1.84
<b>C5ar2</b>	complement component 5a receptor 2	1.4	1.84
<b>Krt19</b>	keratin 19	1.59	1.81
<b>Tmc5</b>	transmembrane channel-like gene family 5	0.7	1.79
<b>Xdh</b>	xanthine dehydrogenase	1.08	1.78
<b>Cx3cr1</b>	chemokine (C-X3-C motif) receptor 1	0.95	1.77
<b>Chl1</b>	cell adhesion molecule L1-like	0.99	1.65
<b>Tnfrsf1b</b>	tumor necrosis factor receptor superfamily, member 1b; involved in neuro-inflammation [15; 47]	0.57	1.61
<b>Tmem159</b>	transmembrane protein 159	0.68	1.6
<b>Gm9866</b>	predicted gene 9866	0.58	1.56
<b>Il17ra</b>	interleukin 17 receptor A	0.72	1.54
<b>Itga7</b>	integrin alpha 7, promote neurite outgrowth [56]	0.56	1.54
<b>Cd84</b>	CD84 antigen	0.89	1.53
<b>Fyb</b>	FYN binding protein	0.76	1.53
<b>Hhip1</b>	hedgehog interacting protein-like 1	0.64	1.53
<b>Cyp1b1</b>	cytochrome P450, family 1, subfamily b, polypeptide 1	0.83	1.51
<b>Cd109</b>	CD109 antigen	0.77	1.5
<b>Tecta</b>	tectorin alpha	0.65	1.49
<b>Sh3bp2</b>	SH3-domain binding protein 2	0.69	1.47
<b>Serpinb1a</b>	serine (or cysteine) peptidase inhibitor, clade B, member 1a; inflammatory component of neuropathic pain [43]	0.88	1.45
<b>Pik3cg</b>	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma; immunity [48]	0.78	1.42
<b>Gap43</b>	growth associated protein 43; nerve growth; microtubule assemble [44]	0.78	1.42
<b>5930412G12Rik</b>	RIKEN cDNA 5930412G12 gene	0.78	1.42
<b>Rhoq</b>	ras homolog family member Q; remodelling	0.64	1.41
<b>Abca1</b>	ATP-binding cassette, sub-family A (ABC1), member 1; cholesterol transport	0.72	1.41
<b>Sertm1</b>	serine rich and transmembrane domain containing 1	0.86	1.4

Il13ra1	interleukin 13 receptor, alpha 1	0.74	1.39
Ltbp1	latent transforming growth factor beta binding protein 1	0.57	1.37
Man1a	mannosidase 1, alpha	0.54	1.37
Slc15a3	solute carrier family 15, member 3	1.68	1.36
Akr1b8	aldo-keto reductase family 1, member B8	1.15	1.36
Fam163a	family with sequence similarity 163, member A	0.86	1.34
Csrnp1	cysteine-serine-rich nuclear protein 1	0.63	1.33
Bach1	BTB and CNC homology 1, basic leucine zipper transcription factor 1; axon growth inhibitor [21]	0.52	1.31
Tnik	TRAF2 and NCK interacting kinase	0.98	1.26
Pxdc1	PX domain containing 1	0.71	1.25
Plin2	perilipin 2	0.73	1.24
Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1; target of the neuropathic pain drug, gabapentin [5]	0.69	1.23
Ildr2	immunoglobulin-like domain containing receptor 2	0.56	1.23
Pappa2	pappalysin 2	0.71	1.23
Mpeg1	macrophage expressed gene 1	0.92	1.22
Tgif1	TGFB-induced factor homeobox 1	0.63	1.2
Jun	jun proto-oncogene; axon regeneration [6; 39]	0.55	1.18
Fosl2	fos-like antigen 2; transcriptional regulator	0.89	1.18
Cckar	cholecystokinin A receptor; nociceptor marker [24]	0.59	1.18
Camk1	calcium/calmodulin-dependent protein kinase I; promote nerve regeneration [12]	0.63	1.17
Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	0.81	1.16
Il4ra	interleukin 4 receptor, alpha	0.67	1.15
Vash2	vasohibin 2	0.74	1.13
B230319C09Rik	RIKEN cDNA B230319C09 gene	-0.87	1.11
Star	steroidogenic acute regulatory protein	1.54	1.11
Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	1.16	1.11
Al427809	expressed sequence Al427809	0.61	1.09
Chst2	carbohydrate sulfotransferase 2	0.53	1.08
Casp3	caspase 3	0.77	1.07
Fam111a	family with sequence similarity 111, member A	0.62	1.05
Col5a3	collagen, type V, alpha 3	0.78	1.04
Stat5a	signal transducer and activator of transcription 5A	0.53	1.04

<b>Adcyap1</b>	adenylate cyclase activating polypeptide 1; pituitary adenylate cyclase-activating polypeptide (PACAP); axon regeneration [1]	0.71	1.03
<b>Ier5</b>	immediate early response 5	0.52	0.99
<b>Ephb2</b>	Eph receptor B2; axon guidance	0.5	0.98
<b>Plat</b>	plasminogen activator, tissue; remodelling	0.56	0.92
<b>Wisp1</b>	WNT1 inducible signaling pathway protein 1	0.73	0.92
<b>Pip5kl1</b>	phosphatidylinositol-4-phosphate 5-kinase-like 1	0.53	0.92
<b>Lgals1</b>	lectin, galactose binding, soluble 1	0.63	0.91
<b>Lama5</b>	laminin, alpha 5; remodelling	0.65	0.9
<b>C4b</b>	complement component 4B (Chido blood group)	0.76	0.89
<b>Pappa</b>	pregnancy-associated plasma protein A	0.59	0.86
<b>Emp1</b>	epithelial membrane protein 1	0.61	0.85
<b>Fam196a</b>	family with sequence similarity 196, member A	0.91	0.83
<b>Atp8b1</b>	ATPase, class I, type 8B, member 1	0.73	0.82
<b>Rgs20</b>	regulator of G-protein signaling 20	0.81	0.81
<b>Rab31</b>	RAB31, member RAS oncogene family; vesiculation	0.52	0.79
<b>Tes</b>	testis derived transcript	0.81	0.78
<b>Tubb6</b>	tubulin, beta 6 class V; microtubules assembly [41]	1.05	0.77
<b>Csf2rb</b>	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	0.64	0.72
<b>Ly6a</b>	lymphocyte antigen 6 complex, locus A	2.33	0.72
<b>Pros1</b>	protein S (alpha)	0.61	0.7
<b>Runx2</b>	runt related transcription factor 2	1.03	0.69
<b>Casp4</b>	caspase 4, apoptosis-related cysteine peptidase	0.58	0.68
<b>Trf</b>	transferrin	0.57	0.61
<b>Met</b>	met proto-oncogene	0.82	0.61
<b>Acvr1</b>	activin A receptor, type 1	0.75	0.6
<b>Bmp1</b>	bone morphogenetic protein 1	0.55	0.55
<b>Ahr</b>	aryl-hydrocarbon receptor	0.52	0.5
<b>AI593442</b>	expressed sequence AI593442	-0.58	-0.51
<b>Zfp804a</b>	zinc finger protein 804A	-0.6	-0.52
<b>Gm19461</b>	predicted gene, 19461	-0.72	-0.52
<b>Sphkap</b>	SPHK1 interactor, AKAP domain containing	-0.54	-0.55
<b>Map7d2</b>	MAP7 domain containing 2	-0.57	-0.55

Tmem229b	transmembrane protein 229B	-0.62	-0.56
Nefm	neurofilament, medium polypeptide	-0.6	-0.56
Unc80	unc-80, NALCN activator, regulation of cation channel	-0.51	-0.57
Htr1b	5-hydroxytryptamine (serotonin) receptor 1B	-0.55	-0.57
Vsnl1	visinin-like 1	-0.59	-0.58
Gm765	predicted gene 765	-0.58	-0.58
Opcml	opioid binding protein/cell adhesion molecule-like	-0.54	-0.58
Pls1	plastin 1 (I-isoform)	-0.64	-0.59
Slco5a1	solute carrier organic anion transporter family, member 5A1	-0.75	-0.59
Frmpd4	FERM and PDZ domain containing 4; stimulates dendritic morphogenesis; required for synaptic transmission	-0.68	-0.6
Etv1	ets variant 1	-0.58	-0.61
Kcns1	K+ voltage-gated channel, subfamily S, 1	-0.66	-0.62
Cntn6	contactin 6	-0.61	-0.62
Epn3	epsin 3	-0.71	-0.62
Nefh	neurofilament, heavy polypeptide	-0.72	-0.63
Cnnm1	cyclin M1; metal transporter	-0.56	-0.63
Hs3st2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	-0.58	-0.63
Ndst4	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4	-0.77	-0.63
Snap25	synaptosomal-associated protein 25; t-SNARE involved in neurotransmitter release	-0.53	-0.63
Hapln4	hyaluronan and proteoglycan link protein 4	-0.78	-0.64
Arhgef4	Rho guanine nucleotide exchange factor (GEF) 4	-0.51	-0.64
Kcnip1	Kv channel-interacting protein 1	-0.56	-0.67
Gria2	glutamate receptor, ionotropic, AMPA2 (alpha 2)	-0.54	-0.67
Epha6	Eph receptor A6	-0.54	-0.68
Galm	galactose mutarotase	-0.78	-0.69
Glb1l2	galactosidase, beta 1-like 2	-0.88	-0.7
Vamp1	vesicle-associated membrane protein 1	-0.62	-0.7
Coro6	coronin 6	-0.59	-0.7
Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	-0.59	-0.71
Asic1	acid-sensing (proton-gated) ion channel 1	-0.61	-0.71
Hrasls	HRAS-like suppressor; phospholipase activity	-0.65	-0.72
Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	-0.79	-0.73

Pcp4l1	Purkinje cell protein 4-like 1	-0.53	-0.73
Frrs1l	ferric-chelate reductase 1 like; (glutamate signaling)	-0.63	-0.73
Esrsg	estrogen-related receptor gamma	-0.78	-0.73
Kcnk1	potassium channel, subfamily K, member 1	-0.59	-0.74
Fam19a2	family with sequence similarity 19, member A2	-0.68	-0.75
Scn1a	sodium channel, voltage-gated, type I, alpha	-0.59	-0.77
Scrt1	scratch family zinc finger 1; neural differentiation	-0.51	-0.77
Ankrd34c	ankyrin repeat domain 34C	-0.72	-0.77
Fndc5	fibronectin type III domain containing 5	-0.54	-0.79
Onecut1	one cut domain, family member 1; transcriptional activator	-0.77	-0.8
Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	-0.54	-0.82
Cpb1	carboxypeptidase B1 (tissue)	-0.55	-0.83
Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	-0.53	-0.83
Rgs6	regulator of G-protein signaling 6	-0.78	-0.86
Lancl3	LanC lantibiotic synthetase component C-like 3 (bacterial)	-0.85	-0.86
Gabrb2	gamma-aminobutyric acid (GABA) A receptor, subunit beta 2	-0.55	-0.86
Kcnh7	potassium voltage-gated channel, subfamily H (eag-related), member 7	-0.73	-0.89
Gm16551	predicted gene 16551	-0.82	-0.9
Cdh12	cadherin 12	-0.97	-0.91
Chrm2	cholinergic receptor, muscarinic 2, cardiac	-0.5	-0.92
Kndc1	kinase non-catalytic C-lobe domain (KIND) containing 1; negative regulation of dendrite growth	-0.5	-0.93
Kcnh5	potassium voltage-gated channel, subfamily H (eag-related), member 5	-0.53	-0.94
Aifm3	apoptosis-inducing factor, mitochondrion-associated 3	-0.63	-0.95
Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	-0.71	-0.96
Hs3st4	heparan sulfate (glucosamine) 3-O-sulfotransferase 4	-0.53	-0.96
Lgi3	leucine-rich repeat LGI family, member 3	-0.69	-0.98
Fam81a	family with sequence similarity 81, member A	-0.55	-0.99
Inpp5j	inositol polyphosphate 5-phosphatase J	-0.53	-1
Wdr72	WD repeat domain 72	-0.86	-1.02
Agtr1b	angiotensin II receptor, type 1b; GPCR	-0.66	-1.03
Cntn4	contactin 4; neurite outgrowth	-0.73	-1.05
Vwc2l	von Willebrand factor C domain-containing protein 2-like; neurogenesis	-0.62	-1.07

<b>Oprl1</b>	opioid receptor-like 1; nociception	-0.56	-1.08
B3gat1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	-0.83	-1.1
<b>Htr3a</b>	5-hydroxytryptamine (serotonin) receptor 3A; chronic inflammatory pain [53]	-0.64	-1.17
Kcng4	potassium voltage-gated channel, subfamily G, member 4	-0.75	-1.19
<b>Oprd1</b>	opioid receptor, delta 1	-0.72	-1.23
<b>Htr3b</b>	5-hydroxytryptamine (serotonin) receptor 3B	-0.76	-1.24
Vstm2b	V-set and transmembrane domain containing 2B	-1.37	-1.28
<b>Igsf21</b>	immunoglobulin superfamily, member 21	-0.72	-1.33
Gm13446	predicted gene 13446	-0.73	-1.5
Fbxo40	F-box protein 40	-0.71	-1.65
Zswim2	zinc finger SWIM-type containing 2	-1.57	-2.22
6430571L13Rik	RIKEN cDNA 6430571L13 gene	-0.64	-2.3

**Table S3. Common differentially expressed genes between two rat datasets on nerve injury.** The common DEGs between Baskozos, rat (Br) and Perkins (P) datasets are shown together with log2 fold changes relative to control, non-injured DRG.

gene name	description	log2fc_Br	log2fc_P
Sprr1a	small proline-rich protein 1A	2.91	11.03
Hamp	hepcidin antimicrobial peptide	2.62	10.09
Mmp12	matrix metallopeptidase 12	6.43	8.95
Csrp3	cysteine and glycine rich protein 3	2.37	8.88
Il1a	interleukin 1 alpha	1.85	8.63
Ly49si1	immunoreceptor Ly49si1	2.43	8.24
Lce1f	late cornified envelope 1F	4.41	7.79
Tacstd2	tumor-associated calcium signal transducer 2	3.59	7.77
Mmp7	matrix metallopeptidase 7	5.24	7.47
RGD1305807	hypothetical LOC298077	3.69	7.41
Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	1.52	7.4
Ptprh	protein tyrosine phosphatase, receptor type, H	2.88	7.22
Vip	vasoactive intestinal peptide	3.66	7.19
Ucn2	urocortin 2	2.96	7.1
Serpina1f	serine (or cysteine) peptidase inhibitor, clade A, member 1F	2.84	6.93
Ucn	urocortin	2.73	6.62
Cd8b	CD8b molecule	3.03	6.21
Vtcn1	V-set domain containing T cell activation inhibitor 1	2.76	6.15
Reg3b	regenerating family member 3 beta	3.18	5.97
Ankrd1	ankyrin repeat domain 1	2.76	5.9
RGD1308878	similar to arylacetamide deacetylase	3.59	5.78
Il6	interleukin 6	2.38	5.72
Gdnf	glial cell derived neurotrophic factor	3.92	5.71
Pglyrp4	peptidoglycan recognition protein 4	3.77	5.62
Cd8a	CD8a molecule	2.76	5.61
Gal	galanin and GMAP prepropeptide	2.68	5.57
Nps	neuropeptide S	2.41	5.5
Htr2b	5-hydroxytryptamine receptor 2B	2.04	5.29

Lipn	lipase, family member N	5.8	5.2
Col7a1	collagen type VII alpha 1 chain	2.46	5.06
Lilrb4	leukocyte immunoglobulin like receptor B4	3.69	5.04
Gpnmb	glycoprotein nmb	3.14	5
Arg1	arginase 1	2.4	4.99
Nccrp1	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	2.74	4.93
Rhcg	Rh family, C glycoprotein	3.4	4.8
Ecel1	endothelin converting enzyme-like 1	2.9	4.79
Gpr101	G protein-coupled receptor 101	3.78	4.58
Cxcr3	C-X-C motif chemokine receptor 3	1.68	4.45
Dusp9	dual specificity phosphatase 9	2.71	4.41
Trem2	triggering receptor expressed on myeloid cells 2	1.7	4.4
Mmp3	matrix metallopeptidase 3	3.38	4.35
LOC497796	hypothetical protein LOC497796	2.88	4.24
Siglec1	sialic acid binding Ig like lectin 1	2.2	4.21
Sdcbp2	syndecan binding protein 2	1.1	4.19
Ugt1a1	UDP glucuronosyltransferase family 1 member A1	1.51	4.15
Thbs2	thrombospondin 2	2.26	4.13
Cthrc1	collagen triple helix repeat containing 1	1.65	4.09
Olr434	olfactory receptor 434	4.34	4.07
Clec7a	C-type lectin domain containing 7A	2.45	4.04
Mcoln3	mucolipin 3	2.14	3.96
Cckbr	cholecystokinin B receptor	3.16	3.92
Cidec	cell death-inducing DFFA-like effector c	2.34	3.91
Slc30a3	solute carrier family 30 member 3	5.12	3.9
Ly49s6	Ly49 stimulatory receptor 6	3.67	3.86
Pltp	phospholipid transfer protein	1.84	3.75
Apobec1	apolipoprotein B mRNA editing enzyme catalytic subunit 1	1.63	3.73
Col17a1	collagen type XVII alpha 1 chain	1.43	3.7
Slpi	secretory leukocyte peptidase inhibitor	1.34	3.66
Amn	amnion associated transmembrane protein	1.92	3.65
Mlph	melanophilin	3.26	3.6
Tbxas1	thromboxane A synthase 1	1.55	3.57
Cd3e	CD3e molecule	2.65	3.55
Hao1	hydroxyacid oxidase 1	1.62	3.54
Postn	periostin	2.76	3.5
C1qa	complement C1q A chain	2.06	3.48
Cdhr5	cadherin-related family member 5	2.23	3.48
Avp	arginine vasopressin	2.88	3.47
Abcb1b	ATP-binding cassette, subfamily B (MDR/TAP), member 1B	0.96	3.45
Has1	hyaluronan synthase 1	2.35	3.44
Apoc4	apolipoprotein C4	1.78	3.44
LOC688459	hypothetical protein LOC688459	2	3.42
Cyp27b1	cytochrome P450, family 27, subfamily b, polypeptide 1	1.46	3.42
Slc4a5	solute carrier family 4 member 5	1.88	3.4
C1qb	complement C1q B chain	1.9	3.35
Pdyn	prodynorphin	2.16	3.33
Cck	cholecystokinin	3.76	3.28
Clec2d	C-type lectin domain family 2, member D	3.96	3.25
Padi3	peptidyl arginine deiminase 3	2.45	3.24
Troap	trophinin associated protein	1.61	3.22
Prlhr	prolactin releasing hormone receptor	3.06	3.21
Clcf1	cardiotrophin-like cytokine factor 1	1.39	3.19
LOC689757	similar to osteoclast inhibitory lectin	2.43	3.19
Folr2	folate receptor beta	1.31	3.16

Sstr3	somatostatin receptor 3	2.88	3.13
Lrat	lecithin retinol acyltransferase	1.56	3.12
P2ry6	pyrimidinergic receptor P2Y6	1.6	3.12
Sdc1	syndecan 1	2.24	3.12
Plbd1	phospholipase B domain containing 1	1.84	3.11
Sox11	SRY box 11	2.19	3.06
Cx3cr1	C-X3-C motif chemokine receptor 1	1.68	3.02
Neurl3	neuralized E3 ubiquitin protein ligase 3	1.8	3
Rab32	RAB32, member RAS oncogene family	1.33	2.99
Gpr34	G protein-coupled receptor 34	1.62	2.99
Fln	filamin C	1.74	2.98
Sbsn	suprabasin	1.52	2.98
Kif22	kinesin family member 22	1.65	2.98
Cfd	complement factor D	1.66	2.98
Cyp4b1	cytochrome P450, family 4, subfamily b, polypeptide 1	1.78	2.97
Tnfaip6	TNF alpha induced protein 6	1.49	2.96
C1qc	complement C1q C chain	1.77	2.94
Smagp	small cell adhesion glycoprotein	2.49	2.93
Epcam	epithelial cell adhesion molecule	1.48	2.91
Klrk1	killer cell lectin like receptor K1	1.92	2.9
Fn1	fibronectin 1	1.29	2.88
Btbd16	BTB domain containing 16	2.73	2.88
Fblim1	filamin binding LIM protein 1	1.93	2.87
Clspn	claspin	1.47	2.87
Gna15	G protein subunit alpha 15	1.46	2.86
Mmp19	matrix metallopeptidase 19	1.74	2.86
Lyz2	lysozyme 2	1.9	2.86
Tecta	tectorin alpha	2.28	2.86
Wdr63	WD repeat domain 63	2.52	2.85
St14	suppression of tumorigenicity 14	1.91	2.85
C2cd4c	C2 calcium-dependent domain containing 4C	1.53	2.82
Myof	myoferlin	1.77	2.8
Bcl2a1	BCL2-related protein A1	2.05	2.79
Itgam	integrin subunit alpha M	1.71	2.78
Plcb2	phospholipase C, beta 2	1.55	2.78
Rdh16	retinol dehydrogenase 16 (all-trans)	2.16	2.77
Tnfrsf18	TNF receptor superfamily member 18	2.32	2.77
Gadd45a	growth arrest and DNA-damage-inducible, alpha	1.92	2.77
Tnfrsf8	TNF receptor superfamily member 8	3.15	2.75
Gbp2	guanylate binding protein 2	1.54	2.75
Itgal	integrin subunit alpha L	1.92	2.75
Clec2dl1	C-type lectin domain family 2 member D-like 1	2.11	2.74
Cdh17	cadherin 17	2.32	2.74
Csf2rb	colony stimulating factor 2 receptor beta common subunit	1.67	2.74
Ccrl2	C-C motif chemokine receptor like 2	1.99	2.72
Ptpn5	protein tyrosine phosphatase, non-receptor type 5	2.15	2.72
Fos	Fos proto-oncogene, AP-1 transcription factor subunit	1.41	2.71
Thbs4	thrombospondin 4	1.33	2.71
Cd180	CD180 molecule	1.78	2.71
Rbpjl	recombination signal binding protein for immunoglobulin kappa J region-like	1.44	2.7
Gapt	Grb2-binding adaptor protein, transmembrane	2.71	2.7
Ctsw	cathepsin W	1.89	2.69
Tyrobp	Tyro protein tyrosine kinase binding protein	1.57	2.68
Tfec	transcription factor EC	1.77	2.65

Cst7	cystatin F	1.95	2.65
Il2rb	interleukin 2 receptor subunit beta	1.92	2.64
Cd3d	CD3d molecule	2.32	2.64
Chrna1	cholinergic receptor nicotinic alpha 1 subunit	2.66	2.63
Csf1	colony stimulating factor 1	1.69	2.63
Stra6	stimulated by retinoic acid 6	1.18	2.63
Ccr6	C-C motif chemokine receptor 6	1.91	2.63
Icos	inducible T-cell co-stimulator	2.41	2.62
Fgf2	fibroblast growth factor 2	1.63	2.61
Igsgf10	immunoglobulin superfamily, member 10	1.89	2.6
Olr1	oxidized low density lipoprotein receptor 1	1.64	2.6
C3ar1	complement C3a receptor 1	1.58	2.6
Cd3g	CD3g molecule	1.82	2.58
Prc1	protein regulator of cytokinesis 1	1.66	2.58
Cd27	CD27 molecule	1.94	2.58
Runx2	runt-related transcription factor 2	1.77	2.57
Sapcd2	suppressor APC domain containing 2	1.48	2.55
Myo1f	myosin IF	1.42	2.55
Rorb	RAR-related orphan receptor B	1	2.54
Clec12a	C-type lectin domain family 12, member A	1.56	2.54
Il18	interleukin 18	1.03	2.54
Scube1	signal peptide, CUB domain and EGF like domain containing 1	1.85	2.54
Atp6v0d2	ATPase H+ transporting V0 subunit D2	4.61	2.54
Parvg	parvin, gamma	1.36	2.53
Batf	basic leucine zipper ATF-like transcription factor	2.2	2.53
Bin2	bridging integrator 2	1.57	2.53
Cyp2s1	cytochrome P450, family 2, subfamily s, polypeptide 1	1.55	2.5
Wnt10b	Wnt family member 10B	2.84	2.49
Tnik	TRAF2 and NCK interacting kinase	1.65	2.48
Kcnk13	potassium two pore domain channel subfamily K member 13	1.05	2.47
Spi1	Spi-1 proto-oncogene	1.55	2.47
Cuedc2	CUE domain containing 2	2.19	2.47
Acp5	acid phosphatase 5, tartrate resistant	2.89	2.47
Cebpa	CCAAT/enhancer binding protein alpha	1.66	2.44
Rrm2	ribonucleotide reductase regulatory subunit M2	2.24	2.44
Vav1	vav guanine nucleotide exchange factor 1	1.54	2.44
Fam83d	family with sequence similarity 83, member D	1.25	2.42
Ifitm1	interferon induced transmembrane protein 1	0.98	2.42
PVR	poliovirus receptor	1.68	2.42
Prrg4	proline rich and Gla domain 4	1.67	2.42
Arid5a	AT-rich interaction domain 5A	1.6	2.42
Met	MET proto-oncogene, receptor tyrosine kinase	1.79	2.41
Iqgap3	IQ motif containing GTPase activating protein 3	1.35	2.4
Apobec3b	apolipoprotein B mRNA editing enzyme catalytic subunit 3B	1.29	2.4
Tlr7	toll-like receptor 7	1.43	2.4
Clec4a3	C-type lectin domain family 4, member A3	1.38	2.39
Cybb	cytochrome b-245 beta chain	1.93	2.39
Myo7a	myosin VIIA	1.18	2.39
Bhlhe22	basic helix-loop-helix family, member e22	1.43	2.39
Gpr31	G protein-coupled receptor 31	1.53	2.39
Csrp2	cysteine and glycine-rich protein 2	2.17	2.38
Tspo	translocator protein	1.86	2.38
Anpep	alanyl aminopeptidase, membrane	1.45	2.37
Kif2c	kinesin family member 2C	1.63	2.37
SrpX2	sushi-repeat-containing protein, X-linked 2	1.19	2.37

Dlk1	delta like non-canonical Notch ligand 1	3.2	2.36
Cyth4	cytohesin 4	1.14	2.35
Adcyap1	adenylate cyclase activating polypeptide 1	1.73	2.34
Akr1b8	aldo-keto reductase family 1, member B8	1.21	2.34
Cacna2d1	calcium voltage-gated channel auxiliary subunit alpha2delta 1	1.92	2.33
Mafb	MAF bZIP transcription factor B	1.5	2.33
Emp1	epithelial membrane protein 1	1.17	2.33
Gprc5a	G protein-coupled receptor, class C, group 5, member A	2.55	2.33
Sstr4	somatostatin receptor 4	2.51	2.32
Defb36	defensin beta 36	1.66	2.32
Cryba2	crystallin, beta A2	1.94	2.32
Il11	interleukin 11	1.35	2.32
Fes	FES proto-oncogene, tyrosine kinase	1.35	2.31
Xcr1	X-C motif chemokine receptor 1	1.88	2.3
Il1r2	interleukin 1 receptor type 2	1.96	2.29
Clec4a	C-type lectin domain family 4, member A	1.45	2.29
Tshr	thyroid stimulating hormone receptor	2.14	2.29
Uhrf1	ubiquitin-like with PHD and ring finger domains 1	1.71	2.28
Fermt3	fermitin family member 3	1.4	2.28
Tnfaip8l2	TNF alpha induced protein 8 like 2	1.32	2.27
Tlr8	toll-like receptor 8	1.65	2.25
Abca1	ATP binding cassette subfamily A member 1	1.27	2.25
Mmp16	matrix metallopeptidase 16	1.77	2.25
Cep55	centrosomal protein 55	1.13	2.24
Steap1	STEAP family member 1	1.21	2.23
Cd6	Cd6 molecule	1.77	2.22
Blnk	B-cell linker	1.57	2.22
Oscar	osteoclast associated, immunoglobulin-like receptor	1.3	2.22
Sbno2	strawberry notch homolog 2	1.63	2.21
Tgfb1	transforming growth factor, beta receptor 1	1.11	2.21
Tbx18	T-box18	0.98	2.21
Cysltr1	cysteinyl leukotriene receptor 1	2.04	2.21
Ankrd33b	ankyrin repeat domain 33B	1.37	2.21
Ect2	epithelial cell transforming 2	1.21	2.2
Angpt4	angiopoietin 4	1.5	2.2
Nusap1	nucleolar and spindle associated protein 1	1.5	2.19
Col27a1	collagen type XXVII alpha 1 chain	1.74	2.18
Tpbg	trophoblast glycoprotein	1.39	2.17
Cdca3	cell division cycle associated 3	1.42	2.17
Csrnp1	cysteine and serine rich nuclear protein 1	1.62	2.17
Cdc20	cell division cycle 20	1.36	2.16
B3gnt7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	1.48	2.16
Peg12	paternally expressed 12	1.79	2.16
Rdh10	retinol dehydrogenase 10	1.12	2.16
Lilrb3	leukocyte immunoglobulin like receptor B3	2.89	2.15
Psd4	pleckstrin and Sec7 domain containing 4	1.64	2.15
Tmem86a	transmembrane protein 86A	1.4	2.15
Clec4a1	C-type lectin domain family 4, member A1	1.31	2.14
Fam46a	family with sequence similarity 46, member A	1.32	2.14
C3	complement C3	2.52	2.14
Cpg1	candidate plasticity gene 1	1.53	2.12
Pld4	phospholipase D family, member 4	1.47	2.12
Bmp7	bone morphogenetic protein 7	1.25	2.12
Ramp1	receptor activity modifying protein 1	1.13	2.12
Hcst	hematopoietic cell signal transducer	1.17	2.11

Kif15	kinesin family member 15	1.41	2.11
Itga10	integrin subunit alpha 10	2.04	2.1
C1s	complement C1s	1.22	2.1
Sla	src-like adaptor	1.79	2.1
Tlr2	toll-like receptor 2	1.21	2.1
Arhgap9	Rho GTPase activating protein 9	1.3	2.1
Vcan	versican	1.01	2.09
Col16a1	collagen type XVI alpha 1 chain	1.36	2.07
Melk	maternal embryonic leucine zipper kinase	1.37	2.07
Frem1	Fras1 related extracellular matrix 1	1.27	2.06
Des	desmin	1.1	2.05
Cd53	Cd53 molecule	1.08	2.04
Bmp2	bone morphogenetic protein 2	1.27	2.03
Ccnd1	cyclin D1	1.47	2.03
Ptafr	platelet-activating factor receptor	1.11	2.03
Grin2b	glutamate ionotropic receptor NMDA type subunit 2B	1.63	2.03
Gpr88	G-protein coupled receptor 88	1.64	2.02
Kif23	kinesin family member 23	1.01	2.02
Il21r	interleukin 21 receptor	1.23	2.01
Arntl2	aryl hydrocarbon receptor nuclear translocator-like 2	1.45	2.01
Psrc1	proline and serine rich coiled-coil 1	1.67	1.99
Pycard	PYD and CARD domain containing	1.44	1.99
Tgfb1	transforming growth factor, beta 1	1.22	1.99
Aldh1l2	aldehyde dehydrogenase 1 family, member L2	1.42	1.99
Fap	fibroblast activation protein, alpha	0.97	1.99
Irak3	interleukin-1 receptor-associated kinase 3	1.23	1.98
Plekha7	pleckstrin homology domain containing A7	1.27	1.98
Stx11	syntaxin 11	1.46	1.98
Fst	follistatin	2.01	1.97
RGD1565785	similar to chromosome X open reading frame 21	1.61	1.97
Tfp1i2	tissue factor pathway inhibitor 2	1.44	1.97
Thbd	thrombomodulin	1.01	1.97
MGC105649	hypothetical LOC302884	1.52	1.96
Dapp1	dual adaptor of phosphotyrosine and 3-phosphoinositides 1	1.51	1.96
Pmf1	polyamine-modulated factor 1	0.74	1.95
Nox4	NADPH oxidase 4	0.84	1.95
Lyn	LYN proto-oncogene, Src family tyrosine kinase	1.35	1.94
Plcd1	phospholipase C, delta 1	1.44	1.94
Cd4	Cd4 molecule	1.65	1.94
Ccr5	chemokine (C-C motif) receptor 5	1.78	1.93
Knstrn	kinetochore-localized astrin/SPAG5 binding protein	1.16	1.93
Serpinc1	serpin family G member 1	1.17	1.92
Jun	Jun proto-oncogene, AP-1 transcription factor subunit	1.73	1.92
Il1r1	interleukin 1 receptor type 1	1.16	1.91
Il18r1	interleukin 18 receptor 1	1.87	1.91
Ajap1	adherens junctions associated protein 1	1.58	1.9
Cpa4	carboxypeptidase A4	2.19	1.9
Ier5l	immediate early response 5-like	1.43	1.9
Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2	1.27	1.9
Ezh2	enhancer of zeste 2 polycomb repressive complex 2 subunit	1.45	1.9
Ltbp1	latent transforming growth factor beta binding protein 1	1.05	1.89
Neu2	neuraminidase 2	1.85	1.89
Cnr2	cannabinoid receptor 2	1.35	1.89
Sipa1	signal-induced proliferation-associated 1	1.4	1.89
Aldh1a3	aldehyde dehydrogenase 1 family, member A3	1.06	1.88

Mcm3	minichromosome maintenance complex component 3	1.24	1.88
Pole2	DNA polymerase epsilon 2, accessory subunit	1.52	1.88
Gem	GTP binding protein overexpressed in skeletal muscle	1.12	1.87
Mybl2	MYB proto-oncogene like 2	1.21	1.87
Bcl3	B-cell CLL/lymphoma 3	1.15	1.86
Cd2	Cd2 molecule	1.5	1.86
Plk1	polo-like kinase 1	1.45	1.86
Slc15a3	solute carrier family 15 member 3	1.39	1.85
Fgr	FGR proto-oncogene, Src family tyrosine kinase	1.39	1.85
Ptpro	protein tyrosine phosphatase, receptor type, O	1.56	1.85
Slc11a1	solute carrier family 11 member 1	1.07	1.84
Mmp23	matrix metallopeptidase 23	1.24	1.84
Bcl2l11	BCL2 like 11	1.71	1.84
Pou2f2	POU class 2 homeobox 2	1.37	1.84
Icam1	intercellular adhesion molecule 1	1.18	1.84
Ccna2	cyclin A2	1.07	1.84
Kif11	kinesin family member 11	1.09	1.83
Ephb2	Eph receptor B2	1.4	1.83
Rbl1	RB transcriptional corepressor like 1	1.1	1.83
Sh3bp1	SH3-domain binding protein 1	1.01	1.83
Cpxm1	carboxypeptidase X (M14 family), member 1	1.19	1.82
Cd276	Cd276 molecule	1.13	1.82
Stear4	STEAP4 metalloreductase	0.93	1.82
Il1rn	interleukin 1 receptor antagonist	2.37	1.82
Zc3h12d	zinc finger CCCH type containing 12D	1.37	1.81
Unc93b1	unc-93 homolog B1, TLR signaling regulator	1.1	1.81
Maff	MAF bZIP transcription factor F	1.24	1.8
Dsn1	DSN1 homolog, MIS12 kinetochore complex component	1.05	1.8
Tnfrsf14	TNF receptor superfamily member 14	1.64	1.79
Slc1a5	solute carrier family 1 member 5	1.23	1.79
Epb41l4b	erythrocyte membrane protein band 4.1 like 4B	1.22	1.79
Rnaset2	ribonuclease T2	0.9	1.78
Il10ra	interleukin 10 receptor subunit alpha	1.29	1.78
Fosl1	FOS like 1, AP-1 transcription factor subunit	2.4	1.78
Rhoq	ras homolog family member Q	1.14	1.78
Smad3	SMAD family member 3	1.32	1.77
Dhfr	dihydrofolate reductase	1.7	1.77
Fbn1	fibrillin 1	1.04	1.77
Phldb3	pleckstrin homology-like domain, family B, member 3	1.7	1.77
Mki67	marker of proliferation Ki-67	1.64	1.76
Ptpn6	protein tyrosine phosphatase, non-receptor type 6	1.31	1.76
C1r	complement C1r	1.28	1.75
Thbs1	thrombospondin 1	1.08	1.75
Ssc5d	scavenger receptor cysteine rich family member with 5 domains	1.42	1.74
Cnksr3	Cnksr family member 3	1.3	1.74
Fxyd5	FXYD domain-containing ion transport regulator 5	1.47	1.73
Lag3	lymphocyte activating 3	1.31	1.73
Arhgap11a	Rho GTPase activating protein 11A	1.13	1.72
Tspan11	tetraspanin 11	1.32	1.72
Cd101	CD101 molecule	1.31	1.72
Lama5	laminin subunit alpha 5	1.83	1.72
Itga4	integrin subunit alpha 4	1.29	1.71
Cmtm7	CKLF-like MARVEL transmembrane domain containing 7	1.17	1.71
Adamtsl5	ADAMTS-like 5	1.43	1.71
Satb2	SATB homeobox 2	1.57	1.71

Baz1a	bromodomain adjacent to zinc finger domain, 1A	1.1	1.71
Xdh	xanthine dehydrogenase	1.08	1.7
Fcgr1a	Fc fragment of IgG receptor Ia	1.11	1.7
Nckap1l	NCK associated protein 1 like	1.18	1.7
Ctbp2	C-terminal binding protein 2	1.08	1.69
Gbp5	guanylate binding protein 5	1.31	1.69
Il2rg	interleukin 2 receptor subunit gamma	1.36	1.69
Fam198b	family with sequence similarity 198, member B	1.2	1.69
Was	Wiskott-Aldrich syndrome	1.66	1.69
C1rl	complement C1r subcomponent like	1.32	1.68
Ncf4	neutrophil cytosolic factor 4	1.16	1.68
Dusp6	dual specificity phosphatase 6	1.2	1.68
Col5a2	collagen type V alpha 2 chain	1.11	1.68
Slc4a8	solute carrier family 4 member 8	0.96	1.68
Tead1	TEA domain transcription factor 1	1.24	1.67
Eya4	EYA transcriptional coactivator and phosphatase 4	1.52	1.67
Tmprss6	transmembrane protease, serine 6	1.97	1.67
Fadd	Fas associated via death domain	1.1	1.67
Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	1.59	1.66
Cxcr6	C-X-C motif chemokine receptor 6	1.94	1.66
Il6r	interleukin 6 receptor	1.07	1.66
Ptprt	protein tyrosine phosphatase, receptor type, T	1.66	1.66
Myd88	myeloid differentiation primary response 88	0.9	1.66
Gpc3	glypican 3	0.89	1.65
Lpar4	lysophosphatidic acid receptor 4	0.88	1.65
Il1rl1	interleukin 1 receptor-like 1	1.37	1.65
Acvr1c	activin A receptor type 1C	1.9	1.65
Serpina1	serpin family A member 1	1.09	1.65
Itga5	integrin subunit alpha 5	0.89	1.65
Fut4	fucosyltransferase 4	1.08	1.65
RGD1305464	similar to human chromosome 15 open reading frame 39	1.46	1.65
Ahr	aryl hydrocarbon receptor	1.58	1.65
Cp	ceruloplasmin	1.02	1.64
Casp7	caspase 7	1.26	1.64
Ets1	ETS proto-oncogene 1, transcription factor	1.54	1.64
Ctsc	cathepsin C	1.12	1.64
Ptpn22	protein tyrosine phosphatase, non-receptor type 22	1.55	1.64
Crabp2	cellular retinoic acid binding protein 2	1.29	1.64
Tmem144	transmembrane protein 144	1.15	1.64
Lsp1	lymphocyte-specific protein 1	0.99	1.64
Rgma	repulsive guidance molecule family member A	1.11	1.64
Axl	Axl receptor tyrosine kinase	1.23	1.64
Cd44	CD44 molecule (Indian blood group)	1.04	1.63
Espl1	extra spindle pole bodies like 1, separase	1.44	1.63
Trem1	triggering receptor expressed on myeloid cells 1	2.89	1.63
Cd63	Cd63 molecule	0.95	1.62
Tnfrsf1b	TNF receptor superfamily member 1B	1.14	1.61
Itgb8	integrin subunit beta 8	1.1	1.61
Trib3	tribbles pseudokinase 3	0.86	1.61
Fam111a	family with sequence similarity 111, member A	1	1.61
Sucnr1	succinate receptor 1	1.26	1.61
Itpkc	inositol-trisphosphate 3-kinase C	1.04	1.61
Bard1	BRCA1 associated RING domain 1	1.17	1.6
Rab13	RAB13, member RAS oncogene family	0.85	1.6
Slc28a2	solute carrier family 28 member 2	1.13	1.6

Tpx2	TPX2, microtubule nucleation factor	0.86	1.6
Gpr171	G protein-coupled receptor 171	1.41	1.6
Irf5	interferon regulatory factor 5	1.32	1.6
Nkdc2	naked cuticle homolog 2	1.06	1.59
Xkr7	XK related 7	1.32	1.59
Hck	HCK proto-oncogene, Src family tyrosine kinase	0.87	1.59
Klra1	killer cell lectin-like receptor, subfamily A, member 1	1.15	1.58
Dock8	dedicator of cytokinesis 8	1.21	1.57
LOC691141	hypothetical protein LOC691141	1.08	1.57
Tle3	transducin-like enhancer of split 3	1.49	1.57
Myc	MYC proto-oncogene, bHLH transcription factor	1.33	1.56
Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	0.53	1.56
Parp3	poly (ADP-ribose) polymerase family, member 3	1.1	1.56
Mob3c	MOB kinase activator 3C	1.06	1.56
Osr2	odd-skipped related transcription factor 2	1.04	1.56
Ube2c	ubiquitin-conjugating enzyme E2C	1.22	1.56
Mrgprf	MAS related GPR family member F	1.63	1.56
Pdlim1	PDZ and LIM domain 1	0.99	1.55
Ifitm3	interferon induced transmembrane protein 3	1.05	1.55
Rbp1	retinol binding protein 1	1.06	1.55
Bmf	Bcl2 modifying factor	1.23	1.55
Sytl4	synaptotagmin-like 4	1.08	1.55
Col15a1	collagen type XV alpha 1 chain	1.39	1.54
Ccnd3	cyclin D3	1.2	1.54
Ndc80	NDC80 kinetochore complex component	1.15	1.54
Odf3l1	outer dense fiber of sperm tails 3-like 1	1.71	1.54
Rspo1	R-spondin 1	1.01	1.53
Themis2	thymocyte selection associated family member 2	1.12	1.53
Gldn	gliomedin	1.22	1.53
Fbxo32	F-box protein 32	1	1.53
Hk2	hexokinase 2	1.25	1.53
Skap2	src kinase associated phosphoprotein 2	0.99	1.53
Cd3eap	CD3e molecule associated protein	1.23	1.53
Fam105a	family with sequence similarity 105, member A	0.65	1.53
Sp110	SP110 nuclear body protein	1.09	1.52
Fam110a	family with sequence similarity 110, member A	1.03	1.52
Col5a1	collagen type V alpha 1 chain	1.15	1.52
Dusp16	dual specificity phosphatase 16	1.44	1.52
Cd37	CD37 molecule	1.19	1.52
Cfp	complement factor properdin	0.7	1.52
Tgif1	TGFB-induced factor homeobox 1	1.13	1.51
Smoc2	SPARC related modular calcium binding 2	1.07	1.51
Tnfaip2	TNF alpha induced protein 2	1.3	1.51
Pdgfc	platelet derived growth factor C	0.83	1.51
Laptm5	lysosomal protein transmembrane 5	1.2	1.51
Foxs1	forkhead box S1	1.03	1.51
Tln1	talin 1	1.23	1.51
Sash3	SAM and SH3 domain containing 3	1.4	1.5
Rab38	RAB38, member RAS oncogene family	0.85	1.5
Cyp7b1	cytochrome P450 family 7 subfamily B member 1	0.94	1.49
Dab2	DAB2, clathrin adaptor protein	0.77	1.49
Eva1b	eva-1 homolog B	1.12	1.49
Rac2	Rac family small GTPase 2	1.68	1.48
Nfkcb2	nuclear factor kappa B subunit 2	1.2	1.48
Plaur	plasminogen activator, urokinase receptor	0.77	1.48

Ocln	occludin	1.1	1.48
Meis3	Meis homeobox 3	1	1.48
Ston2	stonin 2	1.24	1.47
Efemp2	EGF containing fibulin extracellular matrix protein 2	0.83	1.47
Cadm4	cell adhesion molecule 4	1.23	1.47
Lhx6	LIM homeobox 6	2.21	1.46
St18	ST18, C2H2C-type zinc finger	1.45	1.46
Anxa1	annexin A1	0.77	1.46
Scnn1b	sodium channel epithelial 1 beta subunit	2.16	1.46
Pde8a	phosphodiesterase 8A	1.19	1.46
Btg1	BTG anti-proliferation factor 1	1.2	1.45
PCOLCE2	procollagen C-endopeptidase enhancer 2	1.51	1.45
Nradd	neurotrophin receptor associated death domain	0.9	1.45
Glipr1	GLI pathogenesis-related 1	1.21	1.45
Map3k6	mitogen-activated protein kinase kinase kinase 6	1.25	1.44
Stom	stomatin	1.03	1.44
Nck2	NCK adaptor protein 2	1.01	1.44
Sp140	SP140 nuclear body protein	1.03	1.44
Mfap2	microfibril associated protein 2	1.25	1.43
Syt17	synaptotagmin 17	1.33	1.43
Plk5	polo-like kinase 5	0.84	1.42
H6pd	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	1.04	1.42
Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2	0.91	1.42
Tnfrsf26	tumor necrosis factor receptor superfamily, member 26	0.94	1.42
Myl12a	myosin light chain 12A	0.98	1.42
Rai14	retinoic acid induced 14	0.84	1.42
Elk3	ELK3, ETS transcription factor	1.22	1.42
Gsdmd	gasdermin D	0.96	1.41
Fam129b	family with sequence similarity 129, member B	1.17	1.41
Usp18	ubiquitin specific peptidase 18	1.04	1.4
Slc9a3	solute carrier family 9 member A3	2.24	1.39
Micb	MHC class I polypeptide-related sequence B	0.81	1.39
Foxm1	forkhead box M1	1.13	1.39
Cytip	cytohesin 1 interacting protein	1.51	1.38
Fhl3	four and a half LIM domains 3	0.88	1.38
Mgst2	microsomal glutathione S-transferase 2	1.07	1.38
Adamts7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	1.13	1.38
Mms22l	MMS22-like, DNA repair protein	0.8	1.37
Hhex	hematopoietically expressed homeobox	1.02	1.37
Tlr9	toll-like receptor 9	1.04	1.37
S100a11	S100 calcium binding protein A11	0.92	1.36
Baalc	BAALC, MAP3K1 and KLF4 binding	0.8	1.36
Rnd3	Rho family GTPase 3	1.07	1.36
Loxl1	lysyl oxidase-like 1	0.84	1.36
Lum	lumican	0.9	1.36
Iqgap1	IQ motif containing GTPase activating protein 1	0.89	1.36
Syt1	synaptotagmin-like 1	1.14	1.36
Pabpc1	poly(A) binding protein, cytoplasmic 1	0.9	1.36
Dchs1	dachsous cadherin-related 1	0.85	1.36
Epha2	Eph receptor A2	1.42	1.35
Rhoc	ras homolog family member C	1.03	1.35
Dkk2	dickkopf WNT signaling pathway inhibitor 2	1.13	1.35
Chst14	carbohydrate sulfotransferase 14	0.95	1.35
Ptgs1	prostaglandin-endoperoxide synthase 1	0.76	1.34
Plscr1	phospholipid scramblase 1	1.29	1.34

Mex3b	mex-3 RNA binding family member B	1.18	1.34
Pik3ap1	phosphoinositide-3-kinase adaptor protein 1	1.13	1.34
Bzw2	basic leucine zipper and W2 domains 2	0.92	1.34
Ctsk	cathepsin K	1.72	1.34
Slc22a18	solute carrier family 22, member 18	0.91	1.33
Phyhd1	phytanoyl-CoA dioxygenase domain containing 1	0.65	1.33
Ms4a7	membrane spanning 4-domains A7	1.38	1.33
Lmna	lamin A/C	0.96	1.33
Jak2	Janus kinase 2	0.96	1.33
Lat	linker for activation of T cells	1.17	1.33
Gabra5	gamma-aminobutyric acid type A receptor alpha 5 subunit	1.25	1.33
Eef1a1	eukaryotic translation elongation factor 1 alpha 1	0.83	1.33
Mgp	matrix Gla protein	1.49	1.32
Tbc1d10c	TBC1 domain family, member 10C	1.69	1.32
Ppp2r1b	protein phosphatase 2 scaffold subunit A beta	0.92	1.32
Nabp1	nucleic acid binding protein 1	0.67	1.32
Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	0.75	1.31
Syne3	spectrin repeat containing, nuclear envelope family member 3	1.06	1.31
Celf3	CUGBP, Elav-like family member 3	1.38	1.31
Cdh22	cadherin 22	2.69	1.31
Ankrd44	ankyrin repeat domain 44	1.08	1.31
Casp8	caspase 8	0.72	1.31
Il13ra1	interleukin 13 receptor subunit alpha 1	1.03	1.3
Calhm2	calcium homeostasis modulator family member 2	0.69	1.3
Arse	arylsulfatase E	0.74	1.3
Zfp36l1	zinc finger protein 36, C3H type-like 1	1.01	1.3
Ezr	ezrin	0.99	1.29
Prr18	proline rich 18	1.54	1.29
Kank2	KN motif and ankyrin repeat domains 2	1.09	1.29
Adam17	ADAM metallopeptidase domain 17	0.83	1.29
Lck	LCK proto-oncogene, Src family tyrosine kinase	1.09	1.29
Cdkn2c	cyclin-dependent kinase inhibitor 2C	0.94	1.29
Synj2	synaptojanin 2	0.73	1.29
Tmem43	transmembrane protein 43	0.93	1.28
Hspa2	heat shock protein family A member 2	1.3	1.28
C1qtnf6	C1q and TNF related 6	1.27	1.28
Lima1	LIM domain and actin binding 1	0.9	1.28
Trip13	thyroid hormone receptor interactor 13	0.96	1.28
Cdca8	cell division cycle associated 8	0.76	1.28
Ptma	prothymosin alpha	0.94	1.28
Triobp	TRIO and F-actin binding protein	1.15	1.28
Klf10	Kruppel-like factor 10	0.91	1.28
Casp1	caspase 1	1.05	1.27
Tmem123	transmembrane protein 123	1.09	1.27
Vwa1	von Willebrand factor A domain containing 1	1.11	1.27
Adcy6	adenylate cyclase 6	1.04	1.27
P2ry13	purinergic receptor P2Y13	1.41	1.27
Emilin1	elastin microfibril interfacer 1	0.88	1.27
Aspg	asparaginase	0.69	1.27
Zfp36	zinc finger protein 36	1.07	1.27
Reln	reelin	1.01	1.26
Ldlrap1	low density lipoprotein receptor adaptor protein 1	0.9	1.26
Tp53i11	tumor protein p53 inducible protein 11	1.09	1.26
Bgn	biglycan	0.76	1.26
Apoibr	apolipoprotein B receptor	1.1	1.26

Uap1l1	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1	0.92	1.26
Mag	myelin-associated glycoprotein	1.93	1.26
Ltbp4	latent transforming growth factor beta binding protein 4	1.26	1.25
Erf	Ets2 repressor factor	1.24	1.25
Olfml2a	olfactomedin-like 2A	1.57	1.25
Nr2f2	nuclear receptor subfamily 2, group F, member 2	0.88	1.25
Ptprcap	protein tyrosine phosphatase, receptor type, C-associated protein	2.04	1.25
Ptpn18	protein tyrosine phosphatase, non-receptor type 18	0.78	1.25
Col3a1	collagen type III alpha 1 chain	1.29	1.25
Clec9a	C-type lectin domain containing 9A	1.17	1.25
Slc6a6	solute carrier family 6 member 6	1.22	1.25
Pnpla7	patatin-like phospholipase domain containing 7	0.78	1.25
Plxnb2	plexin B2	0.87	1.24
Lctl	lactase-like	1.64	1.24
Sned1	sushi, nidogen and EGF-like domains 1	0.92	1.24
Gja4	gap junction protein, alpha 4	0.63	1.24
Arhgdb	Rho GDP dissociation inhibitor beta	1.25	1.24
Rps6ka1	ribosomal protein S6 kinase A1	1.12	1.23
Tgfb2	transforming growth factor, beta receptor 2	1.2	1.23
Npc2	NPC intracellular cholesterol transporter 2	0.63	1.23
Phldb1	pleckstrin homology-like domain, family B, member 1	1.09	1.23
Egflam	EGF-like, fibronectin type III and laminin G domains	0.84	1.23
Il20rb	interleukin 20 receptor subunit beta	1.12	1.22
Sdc4	syndecan 4	0.81	1.22
Zeb2	zinc finger E-box binding homeobox 2	1.16	1.22
Txnip	thioredoxin interacting protein	1.02	1.21
Ick	intestinal cell kinase	0.8	1.21
Ptpkj	protein tyrosine phosphatase, receptor type, J	0.94	1.21
Map4k1	mitogen activated protein kinase kinase kinase kinase 1	1.28	1.21
Mov10	Mov10 RISC complex RNA helicase	0.79	1.21
Procr	protein C receptor	0.91	1.21
Ccnd2	cyclin D2	1.33	1.21
Cox6b2	cytochrome c oxidase subunit 6B2	1.07	1.2
Dok1	docking protein 1	1.25	1.2
Tmem140	transmembrane protein 140	0.59	1.2
Slco2b1	solute carrier organic anion transporter family, member 2b1	0.73	1.2
Sh3d21	SH3 domain containing 21	0.97	1.19
Ggn	gametogenitin	1	1.19
Arhgap4	Rho GTPase activating protein 4	0.73	1.19
Rab31	RAB31, member RAS oncogene family	0.97	1.19
Rfx2	regulatory factor X2	1.27	1.19
Timeless	timeless circadian regulator	0.94	1.19
Mcm2	minichromosome maintenance complex component 2	0.77	1.18
Ccdc172	coiled-coil domain containing 172	0.76	1.18
Zbtb42	zinc finger and BTB domain containing 42	1.25	1.18
Sigirr	single Ig and TIR domain containing	0.58	1.18
Fnbp1l	formin binding protein 1-like	0.98	1.17
Enc1	ectodermal-neural cortex 1	1.01	1.17
Hexb	hexosaminidase subunit beta	0.6	1.17
Ppp1r36	protein phosphatase 1, regulatory subunit 36	0.87	1.17
Lmo2	LIM domain only 2	0.64	1.17
Meox2	mesenchyme homeobox 2	0.93	1.17
Pla2g2d	phospholipase A2, group IID	1.36	1.17
Tgm2	transglutaminase 2	0.64	1.16
Lpxn	leupaxin	0.77	1.16

Cdkn2b	cyclin-dependent kinase inhibitor 2B	1.12	1.16
RGD1561958	similar to RIKEN cDNA 2010106E10	1.06	1.16
Lbh	limb bud and heart development	0.9	1.16
Card10	caspase recruitment domain family, member 10	1.02	1.16
Slc6a11	solute carrier family 6 member 11	1.49	1.15
Lrrkip1	LRR binding FLII interacting protein 1	0.74	1.15
Fmo5	flavin containing monooxygenase 5	0.99	1.15
Sh3gl3	SH3 domain containing GRB2 like 3, endophilin A3	0.84	1.15
Adamts12	ADAM metallopeptidase with thrombospondin type 1 motif, 12	0.77	1.15
Nr4a2	nuclear receptor subfamily 4, group A, member 2	1.03	1.15
Lrrc17	leucine rich repeat containing 17	0.72	1.15
Gpc1	glypican 1	1.08	1.14
Nr1h3	nuclear receptor subfamily 1, group H, member 3	0.78	1.14
Mfng	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	1.02	1.14
Dhrs3	dehydrogenase/reductase 3	0.79	1.14
Phf19	PHD finger protein 19	0.66	1.14
Sox18	SRY box 18	1.12	1.13
Prickle3	prickle planar cell polarity protein 3	0.92	1.13
Chsy1	chondroitin sulfate synthase 1	0.72	1.13
Birc3	baculoviral IAP repeat-containing 3	0.72	1.13
Kcnmb4	potassium calcium-activated channel subfamily M regulatory beta subunit 4	1.27	1.13
Gpx7	glutathione peroxidase 7	0.88	1.13
Eng	endoglin	0.89	1.12
Grin2d	glutamate ionotropic receptor NMDA type subunit 2D	0.92	1.12
Mtmr11	myotubularin related protein 11	0.84	1.12
Erbb3	erb-b2 receptor tyrosine kinase 3	1.21	1.12
Cdca4	cell division cycle associated 4	0.57	1.12
Rab3il1	RAB3A interacting protein-like 1	0.71	1.12
Lrrc10b	leucine rich repeat containing 10B	2.02	1.11
Arl4a	ADP-ribosylation factor like GTPase 4A	0.84	1.11
Ecm1	extracellular matrix protein 1	0.99	1.11
Rad51	RAD51 recombinase	0.68	1.11
Nes	nestin	0.82	1.11
Gli1	GLI family zinc finger 1	0.84	1.11
Wnt10a	Wnt family member 10A	1.74	1.11
Scamp2	secretory carrier membrane protein 2	0.93	1.11
Ifih1	interferon induced with helicase C domain 1	0.56	1.11
Hjurp	Holliday junction recognition protein	1.23	1.11
Olfml3	olfactomedin-like 3	0.97	1.11
Ptbp1	polypyrimidine tract binding protein 1	0.88	1.11
Efnb1	ephrin B1	0.8	1.11
Lrtm2	leucine-rich repeats and transmembrane domains 2	1.1	1.1
Gfpt1	glutamine fructose-6-phosphate transaminase 1	0.69	1.1
Sidt2	SID1 transmembrane family, member 2	0.87	1.1
Pbxip1	PBX homeobox interacting protein 1	0.91	1.1
Ccdc125	coiled-coil domain containing 125	0.66	1.1
Depdc7	DEP domain containing 7	0.84	1.09
Stard5	StAR-related lipid transfer domain containing 5	0.62	1.09
Ppp1r14b	protein phosphatase 1, regulatory (inhibitor) subunit 14B	0.71	1.09
Shroom4	shroom family member 4	1.04	1.09
Sema4a	semaphorin 4A	0.86	1.08
Cpne9	copine family member 9	1.64	1.08
Tmem202	transmembrane protein 202	0.94	1.08
Emp3	epithelial membrane protein 3	0.73	1.08

Slc39a1	solute carrier family 39 member 1	0.73	1.08
Pros1	protein S	0.56	1.08
Rab15	RAB15, member RAS oncogene family	1.1	1.08
Akna	AT-hook transcription factor	1.1	1.08
Elf4	E74 like ETS transcription factor 4	0.97	1.08
Pid1	phosphotyrosine interaction domain containing 1	0.98	1.08
Nedd1	neural precursor cell expressed, developmentally down-regulated 1	0.88	1.08
Mvp	major vault protein	0.69	1.08
Mdk	midkine	0.74	1.08
Prcp	prolylcarboxypeptidase	0.65	1.07
Dennd2c	DENN domain containing 2C	0.98	1.07
Slc17a9	solute carrier family 17 member 9	1.3	1.07
Zfp217	zinc finger protein 217	0.65	1.07
Wfdc2	WAP four-disulfide core domain 2	1.05	1.07
Tm4sf1	transmembrane 4 L six family member 1	0.78	1.07
Pcgf5	polycomb group ring finger 5	0.57	1.07
Kcnn4	potassium calcium-activated channel subfamily N member 4	0.81	1.07
Ptpn1	protein tyrosine phosphatase, non-receptor type 1	0.82	1.07
Klf11	Kruppel-like factor 11	0.83	1.06
Wwtr1	WW domain containing transcription regulator 1	1.18	1.06
Tia1	TIA1 cytotoxic granule-associated RNA binding protein	0.58	1.06
Gng12	G protein subunit gamma 12	0.86	1.06
Lrp4	LDL receptor related protein 4	0.76	1.06
Sema4f	ssemaphorin 4F	1.18	1.06
Plekha1	pleckstrin homology domain containing A1	0.98	1.05
Trim34	tripartite motif-containing 34	0.84	1.05
Acsl4	acyl-CoA synthetase long-chain family member 4	0.73	1.05
Clic4	chloride intracellular channel 4	1.18	1.05
Ppp1r12a	protein phosphatase 1, regulatory subunit 12A	0.79	1.04
Oplah	5-oxoprolinase (ATP-hydrolysing)	0.62	1.04
Plagl2	PLAG1 like zinc finger 2	0.68	1.04
Fign	fidgetin, microtubule severing factor	1.07	1.04
Frmd8	FERM domain containing 8	0.87	1.04
Serpinh1	serpin family H member 1	0.89	1.04
Mycn	MYCN proto-oncogene, bHLH transcription factor	0.8	1.04
F3	coagulation factor III, tissue factor	0.71	1.04
Ctnbp2nl	CTTNBP2 N-terminal like	0.85	1.04
S1pr2	sphingosine-1-phosphate receptor 2	0.8	1.04
Plekha4	pleckstrin homology domain containing A4	1.15	1.03
Myo10	myosin X	0.6	1.03
Nab2	Ngfi-A binding protein 2	1.18	1.03
E2f7	E2F transcription factor 7	0.95	1.03
Tnfrsf1a	TNF receptor superfamily member 1A	0.89	1.03
Cdk2	cyclin dependent kinase 2	0.89	1.03
Insc	INSC, spindle orientation adaptor protein	0.64	1.03
Fbxo5	F-box protein 5	1.03	1.03
Camk2d	calcium/calmodulin-dependent protein kinase II delta	0.95	1.03
Irf7	interferon regulatory factor 7	1.05	1.02
Sostdc1	sclerostin domain containing 1	1.08	1.02
Trim5	tripartite motif-containing 5	0.74	1.02
Rad54l2	RAD54 like 2	1.04	1.02
Parp16	poly (ADP-ribose) polymerase family, member 16	0.88	1.02
Mob1a	MOB kinase activator 1A	0.56	1.02
Fkbp9	FK506 binding protein 9	0.79	1.02
Panx1	Pannexin 1	1.42	1.02

Frmd6	FERM domain containing 6	1.06	1.02
Rcn3	reticulocalbin 3	0.85	1.01
Renbp	renin binding protein	0.6	1.01
Hsd3b7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	0.63	1.01
Tcf3	transcription factor 3	0.93	1.01
Foxp1	forkhead box P1	0.87	1.01
Bcl2l12	BCL2 like 12	0.86	1.01
Gtse1	G-2 and S-phase expressed 1	0.89	1.01
Rela	RELA proto-oncogene, NF-kB subunit	1.09	1.01
Pdcl3	phosducin-like 3	0.66	1.01
Recql4	RecQ like helicase 4	0.79	1.01
Etv6	ets variant 6	0.88	1
Dpp4	dipeptidylpeptidase 4	1.02	1
P2ry14	purinergic receptor P2Y14	0.94	1
Cd40	CD40 molecule	0.94	1
Flna	filamin A	0.79	1
Sspn	sarcospan	0.75	1
Spn	sialophorin	0.97	0.99
Id2	inhibitor of DNA binding 2	1.16	0.99
Il18bp	interleukin 18 binding protein	0.77	0.99
Nr4a1	nuclear receptor subfamily 4, group A, member 1	1.09	0.99
Fam210b	family with sequence similarity 210, member B	0.68	0.99
Irak2	interleukin-1 receptor-associated kinase 2	0.79	0.99
Rpia	ribose 5-phosphate isomerase A	0.67	0.99
Irak4	interleukin-1 receptor-associated kinase 4	0.55	0.98
Glb1l	galactosidase, beta 1-like	0.56	0.98
Itga6	integrin subunit alpha 6	1.2	0.98
Itgb7	integrin subunit beta 7	1.14	0.98
Il17ra	interleukin 17 receptor A	0.79	0.98
Zdhhc12	zinc finger, DHHC-type containing 12	0.88	0.98
Mtbp	MDM2 binding protein	0.84	0.98
Sh3pxd2a	SH3 and PX domains 2A	1.18	0.98
Tmem198b	transmembrane protein 198b	0.74	0.98
Wasf2	WAS protein family, member 2	0.92	0.98
Il16	interleukin 16	1.1	0.97
Scn3a	sodium voltage-gated channel alpha subunit 3	0.81	0.97
Creb3l2	cAMP responsive element binding protein 3-like 2	1.03	0.97
Prkd3	protein kinase D3	0.76	0.97
Zdhhc21	zinc finger, DHHC-type containing 21	0.81	0.97
Slco2a1	solute carrier organic anion transporter family, member 2a1	0.61	0.97
Slc50a1	solute carrier family 50 member 1	0.71	0.97
Agrn	agrin	0.83	0.97
Capn12	calpain 12	1.14	0.97
Lilra5	leukocyte immunoglobulin like receptor A5	1.19	0.96
Atad2	ATPase family, AAA domain containing 2	0.7	0.96
Rassf3	Ras association domain family member 3	0.81	0.96
Rftn1	raftlin lipid raft linker 1	0.83	0.96
Dusp7	dual specificity phosphatase 7	1.03	0.96
Arhgap15	Rho GTPase activating protein 15	1.06	0.96
Tmod3	tropomodulin 3	0.64	0.95
Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase type 1 beta	1.29	0.95
Ror1	receptor tyrosine kinase-like orphan receptor 1	0.72	0.95
Ptpn21	protein tyrosine phosphatase, non-receptor type 21	0.81	0.95
Slc2a10	solute carrier family 2 member 10	0.97	0.95

Tjp1	tight junction protein 1	0.78	0.95
Apaf1	apoptotic peptidase activating factor 1	0.72	0.95
Dot1l	DOT1 like histone lysine methyltransferase	0.89	0.94
Sema4c	semaphorin 4C	1.14	0.94
Ccdc134	coiled-coil domain containing 134	0.51	0.94
Plxnb3	plexin B3	1.09	0.94
Bcor	BCL6 co-repressor	1.14	0.94
Dnaaf3	dynein, axonemal, assembly factor 3	0.81	0.94
Dhcr24	24-dehydrocholesterol reductase	0.87	0.94
Marcks1	MARCKS-like 1	1.15	0.94
Acvr1	activin A receptor type 1	0.65	0.93
Dnmt1	DNA methyltransferase 1	0.81	0.93
Loxl3	lysyl oxidase-like 3	0.73	0.93
Tle2	transducin-like enhancer of split 2	0.98	0.93
Pld1	phospholipase D1	0.61	0.93
Cdc42se1	CDC42 small effector 1	0.84	0.93
Sema3c	semaphorin 3C	0.99	0.93
Dgka	diacylglycerol kinase, alpha	0.82	0.93
Creb5	cAMP responsive element binding protein 5	0.99	0.93
Dock1	dedicator of cyto-kinesis 1	0.59	0.93
Acvrl1	activin A receptor like type 1	0.94	0.93
Clmn	calmin	0.55	0.93
Rap2b	RAP2B, member of RAS oncogene family	0.71	0.93
Arhgap20	Rho GTPase activating protein 20	0.58	0.92
Fnip2	folliculin interacting protein 2	0.8	0.92
Sox10	SRY box 10	1.14	0.92
Syt13	synaptotagmin 13	1	0.92
Furin	furin (paired basic amino acid cleaving enzyme)	0.8	0.92
Shh	sonic hedgehog	0.6	0.92
Cdk4	cyclin-dependent kinase 4	0.63	0.92
Ccdc120	coiled-coil domain containing 120	0.71	0.92
Grasp	general receptor for phosphoinositides 1 associated scaffold protein	0.66	0.92
Tmpo	thymopoietin	0.64	0.92
Peli3	pellino E3 ubiquitin protein ligase family member 3	0.88	0.92
Lrp1	LDL receptor related protein 1	0.79	0.91
Aen	apoptosis enhancing nuclease	0.65	0.91
Tjp2	tight junction protein 2	1.06	0.91
Ak4	adenylate kinase 4	0.72	0.91
Itga1	integrin subunit alpha 1	0.8	0.91
Sulf2	sulfatase 2	0.73	0.91
Card9	caspase recruitment domain family, member 9	0.96	0.91
Nin	ninein	0.71	0.91
Atf1	activating transcription factor 1	0.58	0.91
Ltbr	lymphotoxin beta receptor	0.77	0.91
Shisa7	shisa family member 7	0.75	0.91
Lpin3	lipin 3	0.54	0.91
Antxr1	anthrax toxin receptor 1	1.06	0.91
Plp2	proteolipid protein 2	0.54	0.9
Tor4a	torsin family 4, member A	0.87	0.9
Il17rc	interleukin 17 receptor C	0.87	0.9
Nav2	neuron navigator 2	0.63	0.9
Suv39h1	suppressor of variegation 3-9 homolog 1 (Drosophila)	0.54	0.9
Maoa	monoamine oxidase A	0.69	0.9
Rpl18	ribosomal protein L18	0.55	0.9
Sertad1	SERTA domain containing 1	0.68	0.9

Serinc5	serine incorporator 5	1.05	0.9
Anp32b	acidic nuclear phosphoprotein 32 family member B	0.89	0.9
Lhfpl2	LHFPL tetraspan subfamily member 2	0.74	0.9
Dpy19l1	dpy-19 like C-mannosyltransferase 1	0.5	0.9
Tmbim1	transmembrane BAX inhibitor motif containing 1	0.79	0.9
Ano6	anoctamin 6	0.76	0.9
Rab43	RAB43, member RAS oncogene family	0.89	0.9
Apol3	apolipoprotein L, 3	0.6	0.89
Zfp641	zinc finger protein 641	0.66	0.89
Wipf1	WAS/WASL interacting protein family, member 1	0.92	0.89
Spr	sepiapterin reductase	0.7	0.88
Sirpa	signal-regulatory protein alpha	0.97	0.88
Dap	death-associated protein	0.77	0.88
Nln	neurolysin	0.69	0.88
Rbm43	RNA binding motif protein 43	0.5	0.87
Scnn1a	sodium channel epithelial 1 alpha subunit	0.91	0.87
Slc30a7	solute carrier family 30 member 7	0.58	0.87
Mutyh	mutY DNA glycosylase	0.56	0.87
Il1rl2	interleukin 1 receptor-like 2	0.68	0.87
Prss12	protease, serine 12	1.13	0.87
Fat4	FAT atypical cadherin 4	0.69	0.87
Aldh3b1	aldehyde dehydrogenase 3 family, member B1	0.69	0.87
Akap2	A-kinase anchoring protein 2	1.02	0.87
Fam126a	family with sequence similarity 126, member A	0.75	0.87
Lgi4	leucine-rich repeat LGI family, member 4	0.89	0.87
Ifngr1	interferon gamma receptor 1	0.77	0.87
Midn	midnolin	1.12	0.87
Zc3h12a	zinc finger CCCH type containing 12A	0.98	0.86
Podxl	podocalyxin-like	0.81	0.86
Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	1.1	0.86
Adra2a	adrenoceptor alpha 2A	1.36	0.86
Efhd1	EF-hand domain family, member D1	0.9	0.86
Anks4b	ankyrin repeat and sterile alpha motif domain containing 4B	0.7	0.86
Sox2	SRY box 2	0.79	0.86
Rin2	Ras and Rab interactor 2	0.63	0.86
Vkorc1	vitamin K epoxide reductase complex, subunit 1	0.68	0.85
Dnmt3b	DNA methyltransferase 3 beta	0.77	0.85
Impdh2	inosine monophosphate dehydrogenase 2	0.62	0.85
Rassf1	Ras association domain family member 1	0.62	0.85
Mreg	melanoregulin	0.64	0.85
Lmbr1l	limb development membrane protein 1-like	0.79	0.85
Casp2	caspase 2	0.51	0.85
Snx33	sorting nexin 33	0.73	0.85
Tie1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	0.83	0.85
Fabp5	fatty acid binding protein 5	0.64	0.85
Man1c1	mannosidase, alpha, class 1C, member 1	0.86	0.85
Cdk5rap2	CDK5 regulatory subunit associated protein 2	0.6	0.85
Spry1	sprouty RTK signaling antagonist 1	0.82	0.85
Ano1	anoctamin 1	0.79	0.85
Glb1	galactosidase, beta 1	0.51	0.85
Fstl3	follistatin like 3	0.78	0.84
Ppp4r1	protein phosphatase 4, regulatory subunit 1	0.66	0.84
Prss53	protease, serine, 53	1.16	0.84
Osmr	oncostatin M receptor	0.52	0.84

Abcd1	ATP binding cassette subfamily D member 1	0.73	0.84
Rarg	retinoic acid receptor, gamma	0.89	0.84
Stard8	StAR-related lipid transfer domain containing 8	0.96	0.84
Plk2	polo-like kinase 2	0.95	0.83
Nono	non-POU domain containing, octamer-binding	0.55	0.83
Bcas1	breast carcinoma amplified sequence 1	0.97	0.83
Scrib	scribbled planar cell polarity protein	1.06	0.83
Ehd2	EH-domain containing 2	0.7	0.83
Zc3hav1	zinc finger CCCH-type containing, antiviral 1	0.55	0.83
St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	0.67	0.83
Angptl2	angiopoietin-like 2	0.94	0.82
Fbxl6	F-box and leucine-rich repeat protein 6	0.56	0.82
Itga7	integrin subunit alpha 7	0.56	0.82
Rras	RAS related	0.67	0.82
Nr4a3	nuclear receptor subfamily 4, group A, member 3	1.59	0.82
Synpo2	synaptopodin 2	0.92	0.82
Slc2a5	solute carrier family 2 member 5	0.56	0.82
Shroom2	shroom family member 2	0.9	0.82
Manba	mannosidase beta	0.66	0.82
Ankrd39	ankyrin repeat domain 39	0.86	0.81
Tpp1	tripeptidyl peptidase 1	0.51	0.81
B3gat1	beta-1,3-glucuronyltransferase 1	1.4	0.81
Fbln1	fibulin 1	0.55	0.81
Inmt	indolethylamine N-methyltransferase	0.68	0.81
Galt	galactose-1-phosphate uridylyltransferase	0.65	0.81
Tbx15	T-box 15	0.79	0.81
Zbed3	zinc finger, BED-type containing 3	0.88	0.81
Efhed2	EF-hand domain family, member D2	0.84	0.8
Ptprn	protein tyrosine phosphatase, receptor type, N	0.93	0.8
Plekhg2	pleckstrin homology and RhoGEF domain containing G2	0.97	0.8
LOC100151767	hypothetical LOC100151767	0.52	0.8
Card6	caspase recruitment domain family, member 6	0.59	0.8
Mecom	MDS1 and EVI1 complex locus	0.72	0.8
Scn3b	sodium voltage-gated channel beta subunit 3	0.62	0.8
Hexa	hexosaminidase subunit alpha	0.57	0.8
Lzts2	leucine zipper tumor suppressor 2	1.04	0.79
Arrb1	arrestin, beta 1	0.65	0.79
Vangl1	VANGL planar cell polarity protein 1	0.71	0.79
Zbtb2	zinc finger and BTB domain containing 2	0.69	0.79
Tfeb	transcription factor EB	0.93	0.79
Zfp579	zinc finger protein 579	0.72	0.79
Sardh	sarcosine dehydrogenase	0.71	0.79
Fyco1	FYVE and coiled-coil domain containing 1	0.75	0.79
Crtac1	cartilage acidic protein 1	0.76	0.79
Efna4	ephrin A4	1.08	0.78
Eif3f	eukaryotic translation initiation factor 3, subunit F	0.81	0.78
Rassf8	Ras association domain family member 8	0.86	0.78
Tcirg1	T-cell immune regulator 1, ATPase H+ transporting V0 subunit A3	0.7	0.78
Plekhn1	pleckstrin homology domain containing N1	1.06	0.78
Shisa5	shisa family member 5	0.66	0.78
Hs2st1	heparan sulfate 2-O-sulfotransferase 1	0.64	0.78
Fli1	Fli-1 proto-oncogene, ETS transcription factor	0.71	0.78
Npr1	natriuretic peptide receptor 1	0.74	0.78
Pak4	p21 (RAC1) activated kinase 4	0.78	0.78
Tmem179b	transmembrane protein 179B	0.55	0.78

Rras2	RAS related 2	0.51	0.78
Acy1	aminoacylase 1	0.63	0.78
Pfkfb4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	0.89	0.78
Mad2l2	mitotic arrest deficient 2 like 2	0.73	0.78
Plekhf2	pleckstrin homology and FYVE domain containing 2	0.57	0.77
Pyroxd2	pyridine nucleotide-disulphide oxidoreductase domain 2	0.74	0.77
Hps1	HPS1, biogenesis of lysosomal organelles complex 3 subunit 1	0.68	0.77
Map3k1	mitogen-activated protein kinase kinase kinase 1	1	0.77
Tmem136	transmembrane protein 136	0.51	0.77
Lpcat1	lysophosphatidylcholine acyltransferase 1	0.67	0.77
Ppfibp1	PPFIA binding protein 1	0.55	0.76
Ch25h	cholesterol 25-hydroxylase	1.15	0.76
Acp6	acid phosphatase 6, lysophosphatidic	0.64	0.76
Hrh1	histamine receptor H 1	0.52	0.76
Lamb2	laminin subunit beta 2	0.66	0.76
Pax9	paired box 9	0.66	0.76
Ptk2	protein tyrosine kinase 2	0.54	0.76
Ccdc17	coiled-coil domain containing 17	0.71	0.76
Sppl2b	signal peptide peptidase-like 2B	0.78	0.76
Zfp513	zinc finger protein 513	0.72	0.76
Mxra8	matrix remodeling associated 8	0.69	0.76
Dlgap4	DLG associated protein 4	0.87	0.75
Zmynd8	zinc finger, MYND-type containing 8	0.76	0.75
Phf10	PHD finger protein 10	0.61	0.75
Zdhhc18	zinc finger, DHHC-type containing 18	0.82	0.75
Necap2	NECAP endocytosis associated 2	0.71	0.75
Tcf12	transcription factor 12	0.62	0.75
Fgfr2	fibroblast growth factor receptor 2	0.66	0.74
Col14a1	collagen type XIV alpha 1 chain	0.84	0.74
Zcchc11	zinc finger CCHC-type containing 11	0.51	0.74
Stag1	stromal antigen 1	0.59	0.74
Pou3f2	POU class 3 homeobox 2	0.8	0.74
Rab12	RAB12, member RAS oncogene family	0.75	0.74
Mchr1	melanin-concentrating hormone receptor 1	1.03	0.73
Foxp4	forkhead box P4	0.83	0.73
Calb1	calbindin 1	0.65	0.73
Plekhg5	pleckstrin homology and RhoGEF domain containing G5	1.09	0.73
Zfp202	zinc finger protein 202	0.74	0.73
Gar1	GAR1 ribonucleoprotein	0.52	0.73
Map4k4	mitogen-activated protein kinase kinase kinase 4	0.78	0.73
Ttc12	tetratricopeptide repeat domain 12	0.5	0.73
Ndor1	NADPH dependent diflavin oxidoreductase 1	0.59	0.73
Cdkn1c	cyclin-dependent kinase inhibitor 1C	0.52	0.73
Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	1.3	0.72
Lix1l	limb and CNS expressed 1 like	0.63	0.72
B4galnt2	beta-1,4-galactosyltransferase 2	0.91	0.72
Chst10	carbohydrate sulfotransferase 10	0.53	0.72
Lrrn4cl	LRRN4 C-terminal like	0.65	0.72
Mllt1	MLLT1, super elongation complex subunit	0.84	0.72
Efna2	ephrin A2	1.27	0.72
Mxd1	max dimerization protein 1	0.67	0.71
Phc1	polyhomeotic homolog 1	0.61	0.71
Kdelr1	KDEL endoplasmic reticulum protein retention receptor 1	0.51	0.71
Stk17b	serine/threonine kinase 17b	0.66	0.71
Eef2	eukaryotic translation elongation factor 2	0.67	0.71

Foxn3	forkhead box N3	0.7	0.71
Mta2	metastasis associated 1 family, member 2	0.72	0.71
Cenpm	centromere protein M	0.58	0.71
Akap13	A-kinase anchoring protein 13	0.57	0.71
Ctsh	cathepsin H	0.56	0.71
Trerf1	transcriptional regulating factor 1	0.93	0.71
Akt2	AKT serine/threonine kinase 2	0.58	0.7
Rab33b	RAB33B, member RAS oncogene family	0.83	0.7
Apba3	amyloid beta precursor protein binding family A member 3	0.77	0.7
Tbc1d20	TBC1 domain family, member 20	0.64	0.7
Rcc1	regulator of chromosome condensation 1	0.55	0.7
Ifrd2	interferon-related developmental regulator 2	0.63	0.7
Bcl7c	BCL tumor suppressor 7C	0.74	0.7
Nav3	neuron navigator 3	0.62	0.69
Ryk	receptor-like tyrosine kinase	0.52	0.69
Tram1	translocation associated membrane protein 1	0.53	0.69
Serinc2	serine incorporator 2	0.97	0.69
Src	SRC proto-oncogene, non-receptor tyrosine kinase	0.93	0.69
Dclk1	doublecortin-like kinase 1	0.87	0.69
Mical3	microtubule associated monooxygenase, calponin and LIM domain containing 3	0.8	0.69
Cldn19	claudin 19	1	0.69
Nxf1	nuclear RNA export factor 1	0.54	0.69
Prss23	protease, serine, 23	1.33	0.69
Lrp12	LDL receptor related protein 12	0.65	0.69
Bok	BOK, BCL2 family apoptosis regulator	0.72	0.68
Myrf	myelin regulatory factor	1.14	0.68
Map3k11	mitogen-activated protein kinase kinase kinase 11	0.94	0.68
Pard3b	par-3 family cell polarity regulator beta	0.57	0.68
Os9	OS9, endoplasmic reticulum lectin	0.59	0.68
Pear1	platelet endothelial aggregation receptor 1	0.58	0.68
Mcam	melanoma cell adhesion molecule	0.86	0.68
Tek	TEK receptor tyrosine kinase	0.81	0.68
Fbxl12	F-box and leucine-rich repeat protein 12	0.64	0.68
Slc1a1	solute carrier family 1 member 1	0.76	0.68
Acrbp	acrosin binding protein	0.67	0.68
Dhh	desert hedgehog	0.74	0.67
Rbms2	RNA binding motif, single stranded interacting protein 2	0.53	0.67
Dnajb5	DnaJ heat shock protein family (Hsp40) member B5	0.68	0.67
Fam214a	family with sequence similarity 214, member A	0.59	0.67
Arhgef1	Rho guanine nucleotide exchange factor 1	0.81	0.67
Fam109b	family with sequence similarity 109, member B	0.89	0.67
Arid1a	AT-rich interaction domain 1A	0.77	0.67
Inpp1l	inositol polyphosphate phosphatase-like 1	0.79	0.67
Rem1	RRAD and GEM like GTPase 1	1.02	0.67
Isg20l2	interferon stimulated exonuclease gene 20-like 2	0.7	0.67
Ctu1	cytosolic thiouridylase subunit 1	0.51	0.67
Cdkn1b	cyclin-dependent kinase inhibitor 1B	0.78	0.67
Crocc	ciliary rootlet coiled-coil, rootletin	0.63	0.66
Gadd45b	growth arrest and DNA-damage-inducible, beta	0.57	0.66
Gstcd	glutathione S-transferase, C-terminal domain containing	0.6	0.66
Rnf19b	ring finger protein 19B	0.59	0.66
Slc44a1	solute carrier family 44 member 1	0.68	0.66
Dyrk2	dual specificity tyrosine phosphorylation regulated kinase 2	0.5	0.66
Fads3	fatty acid desaturase 3	0.75	0.66

Pold1	DNA polymerase delta 1, catalytic subunit	0.96	0.66
Calcr1	calcitonin receptor like receptor	0.71	0.65
Vldlr	very low density lipoprotein receptor	0.5	0.65
Limd1	LIM domains containing 1	0.58	0.65
Rnls	renalase, FAD-dependent amine oxidase	0.66	0.65
Drd2	dopamine receptor D2	1.33	0.65
Qser1	glutamine and serine rich 1	0.5	0.65
Csnk1e	casein kinase 1, epsilon	0.7	0.65
Hmgn2	high mobility group nucleosomal binding domain 2	0.6	0.65
Szrd1	SUZ RNA binding domain containing 1	0.57	0.64
Herpud2	HERPUD family member 2	0.53	0.64
Amotl2	angiomotin like 2	0.88	0.64
Ston1	stonin 1	0.66	0.64
Inpp5d	inositol polyphosphate-5-phosphatase D	0.56	0.64
Pmepa1	prostate transmembrane protein, androgen induced 1	0.59	0.64
Sp1	Sp1 transcription factor	0.64	0.64
Sema3b	semaphorin 3B	1.04	0.64
Duox2	dual oxidase 2	1	0.64
Col11a1	collagen type XI alpha 1 chain	0.71	0.64
Raver2	ribonucleoprotein, PTB-binding 2	1.11	0.64
Phactr2	phosphatase and actin regulator 2	0.53	0.64
Mroh7	maestro heat-like repeat family member 7	0.75	0.64
Pleckhh1	pleckstrin homology, MyTH4 and FERM domain containing H1	0.68	0.63
Dnmt3a	DNA methyltransferase 3 alpha	0.75	0.63
Mertk	MER proto-oncogene, tyrosine kinase	0.71	0.63
Itpripl1	ITPRIP like 1	0.88	0.63
Marveld1	MARVEL domain containing 1	0.97	0.63
Pa2g4	proliferation-associated 2G4	0.53	0.63
Pcif1	PDX1 C-terminal inhibiting factor 1	0.81	0.63
Add3	adducin 3	0.56	0.63
Rcl1	RNA terminal phosphate cyclase-like 1	0.75	0.62
Cnppd1	cyclin Pas1/PHO80 domain containing 1	0.5	0.62
Zbtb38	zinc finger and BTB domain containing 38	0.73	0.62
Aebp2	AE binding protein 2	0.77	0.62
Hnrnpul1	heterogeneous nuclear ribonucleoprotein U-like 1	0.67	0.62
Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	0.6	0.62
Gpr160	G protein-coupled receptor 160	0.71	0.62
Mbd6	methyl-CpG binding domain protein 6	0.66	0.62
Fam212a	family with sequence similarity 212, member A	0.8	0.62
Fam181b	family with sequence similarity 181, member B	0.86	0.61
Hmg20b	high mobility group 20 B	0.55	0.61
Sox17	SRY box 17	0.75	0.61
Stk36	serine/threonine kinase 36	0.66	0.61
Npepl1	aminopeptidase-like 1	0.67	0.61
Ahnak	AHNAK nucleoprotein	0.61	0.61
Notch1	notch 1	0.71	0.61
Isoc2b	isochorismatase domain containing 2b	0.69	0.61
Slc2a1	solute carrier family 2 member 1	0.52	0.6
Foxo4	forkhead box O4	0.55	0.6
Tyk2	tyrosine kinase 2	0.61	0.6
Dlg3	discs large MAGUK scaffold protein 3	0.53	0.6
Epha10	EPH receptor A10	1.16	0.6
Rhob	ras homolog family member B	0.75	0.6
Tjap1	tight junction associated protein 1	0.7	0.6

Fxyd6	FXYD domain-containing ion transport regulator 6	0.7	0.6
Ccne2	cyclin E2	0.58	0.6
Cspg4	chondroitin sulfate proteoglycan 4	0.75	0.6
Thap4	THAP domain containing 4	0.67	0.59
Spon1	spondin 1	0.58	0.59
Tm7sf3	transmembrane 7 superfamily member 3	0.55	0.59
Rhog	ras homolog family member G	0.65	0.59
Nfyα	nuclear transcription factor Y subunit alpha	0.58	0.59
Zyx	zyxin	0.72	0.59
Myadm	myeloid-associated differentiation marker	0.66	0.59
Fxyd1	FXYD domain-containing ion transport regulator 1	0.69	0.59
Nhlrc2	NHL repeat containing 2	0.52	0.59
Actr5	ARP5 actin-related protein 5 homolog	0.56	0.59
Spint1	serine peptidase inhibitor, Kunitz type 1	1.33	0.58
Ppp1r15a	protein phosphatase 1, regulatory subunit 15A	0.58	0.58
Nnt	nicotinamide nucleotide transhydrogenase	0.56	0.58
Bcorl1	BCL6 co-repressor-like 1	0.74	0.58
Strn4	striatin 4	0.76	0.58
Hyal2	hyaluronoglucosaminidase 2	0.56	0.58
Agap2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	1.04	0.58
Swap70	SWAP switching B-cell complex 70	0.65	0.58
Tnfrsf25	TNF receptor superfamily member 25	0.84	0.58
Arnt	aryl hydrocarbon receptor nuclear translocator	0.52	0.58
Tpcn2	two pore segment channel 2	0.52	0.57
Rfx5	regulatory factor X5	0.61	0.57
Fbxo46	F-box protein 46	0.69	0.57
Lifr	LIF receptor alpha	0.61	0.57
Fgf7	fibroblast growth factor 7	0.69	0.57
Zfp111	zinc finger protein 111	0.56	0.56
Hdac1	histone deacetylase 1	0.5	0.56
Slc18a2	solute carrier family 18 member A2	1.68	0.56
RGD1560108	similar to RIKEN cDNA 2700081O15	0.6	0.56
Npr3	natriuretic peptide receptor 3	1.35	0.56
Bcl9l	B-cell CLL/lymphoma 9-like	0.65	0.56
Prickle1	prickle planar cell polarity protein 1	0.6	0.55
Plscr4	phospholipid scramblase 4	0.67	0.55
Tbc1d2b	TBC1 domain family, member 2B	0.51	0.55
RGD1308428	similar to RIKEN cDNA 4931406P16	0.6	0.55
Matk	megakaryocyte-associated tyrosine kinase	0.6	0.55
Csk	C-terminal Src kinase	0.9	0.55
Mknk2	MAP kinase-interacting serine/threonine kinase 2	0.59	0.55
Rnf38	ring finger protein 38	0.54	0.54
Sh3kbp1	Sh3kbp1 binding protein 1	0.67	0.54
Map4	microtubule-associated protein 4	0.64	0.54
Rps6ka4	ribosomal protein S6 kinase A4	0.7	0.54
Zbtb8a	zinc finger and BTB domain containing 8a	0.8	0.54
Srsf4	serine and arginine rich splicing factor 4	0.51	0.54
Pkdcc	protein kinase domain containing, cytoplasmic	0.55	0.54
Cad	carbamoyl-phosphate synthetase 2, aspartate carbamylase, and dihydroorotase	0.73	0.53
Map7d1	MAP7 domain containing 1	0.85	0.53
Dkc1	dyskerin pseudouridine synthase 1	0.71	0.53
Srf	serum response factor	0.57	0.53
Khsrp	KH-type splicing regulatory protein	0.8	0.53
Cyp2u1	cytochrome P450, family 2, subfamily u, polypeptide 1	0.53	0.52

Vps72	vacuolar protein sorting 72 homolog	0.52	0.52
Stat6	signal transducer and activator of transcription 6	0.56	0.52
Toe1	target of EGR1, exonuclease	0.55	0.52
Spint2	serine peptidase inhibitor, Kunitz type, 2	0.8	0.52
Col5a3	collagen type V alpha 3 chain	0.66	0.52
Cdc42ep1	CDC42 effector protein 1	0.95	0.52
Zhx2	zinc fingers and homeoboxes 2	0.7	0.52
Fus	FUS RNA binding protein	0.58	0.51
Arhgef28	Rho guanine nucleotide exchange factor 28	0.61	0.51
Mfge8	milk fat globule-EGF factor 8 protein	0.55	0.51
Nfkbia	NFKB inhibitor alpha	0.7	0.51
Cish	cytokine inducible SH2-containing protein	0.79	0.51
Galnt16	polypeptide N-acetylgalactosaminyltransferase 16	0.53	0.51
Raver1	ribonucleoprotein, PTB-binding 1	0.58	0.51
Wnt6	Wnt family member 6	0.79	0.5
Chst1	carbohydrate sulfotransferase 1	0.95	0.5
Reck	reversion-inducing-cysteine-rich protein with kazal motifs	0.56	0.5
Maged1	MAGE family member D1	0.55	0.5
Zfp772	zinc finger protein 772	-0.95	-0.5
Sept7	septin 7	-0.65	-0.5
Tmem30a	transmembrane protein 30A	-0.55	-0.5
Zfp40	zinc finger protein 40	-0.66	-0.51
Psma3	proteasome subunit alpha 3	-0.65	-0.51
Abcf2	ATP binding cassette subfamily F member 2	-0.51	-0.51
Acyp1	acylphosphatase 1	-0.67	-0.51
Armc8	armadillo repeat containing 8	-0.58	-0.51
Cox7a2l	cytochrome c oxidase subunit 7A2 like	-0.69	-0.51
Gmcl1	germ cell-less, spermatogenesis associated 1	-0.51	-0.51
Mpzl3	myelin protein zero-like 3	-0.69	-0.51
Atp2c1	ATPase secretory pathway Ca2+ transporting 1	-0.59	-0.51
Polr3g	RNA polymerase III subunit G	-0.54	-0.51
Ifi27l2b	interferon, alpha-inducible protein 27 like 2B	-1.12	-0.51
Cox8a	cytochrome c oxidase subunit 8A	-0.51	-0.51
Smm12	small integral membrane protein 12	-0.56	-0.51
Rmdn2	regulator of microtubule dynamics 2	-0.54	-0.51
Ggh	gamma-glutamyl hydrolase	-0.61	-0.51
Gnl3l	G protein nucleolar 3 like	-0.53	-0.51
Chchd5	coiled-coil-helix-coiled-coil-helix domain containing 5	-0.56	-0.51
Phactr3	phosphatase and actin regulator 3	-0.51	-0.52
Acad9	acyl-CoA dehydrogenase family, member 9	-0.57	-0.52
Ifi27	interferon, alpha-inducible protein 27	-1.02	-0.52
Slc35b4	solute carrier family 35 member B4	-0.51	-0.52
Pls3	plastin 3	-0.67	-0.52
Ccpg1	cell cycle progression 1	-0.5	-0.52
Asns	asparagine synthetase (glutamine-hydrolyzing)	-0.6	-0.52
Gpd2	glycerol-3-phosphate dehydrogenase 2	-0.54	-0.52
Mrpl44	mitochondrial ribosomal protein L44	-0.58	-0.52
Acot8	acyl-CoA thioesterase 8	-0.75	-0.52
Tax1bp1	Tax1 binding protein 1	-0.62	-0.52
Trpt1	tRNA phosphotransferase 1	-0.62	-0.52
Cpt2	carnitine palmitoyltransferase 2	-0.57	-0.52
Fdx1l	ferredoxin 1-like	-0.55	-0.52
Uqcr11	ubiquinol-cytochrome c reductase, complex III subunit XI	-0.56	-0.52
Dnajc10	DnaJ heat shock protein family (Hsp40) member C10	-0.55	-0.52
Ecsit	ECSIT signalling integrator	-0.61	-0.52

Psmb7	proteasome subunit beta 7	-0.6	-0.53
Cops5	COP9 signalosome subunit 5	-0.69	-0.53
Tpd52l2	tumor protein D52-like 2	-0.73	-0.53
Xrcc5	X-ray repair cross complementing 5	-0.81	-0.53
Dctn5	dynactin subunit 5	-0.75	-0.53
Atp6v1c2	ATPase H+ transporting V1 subunit C2	-1.1	-0.53
Tspan12	tetraspanin 12	-0.76	-0.53
Ndufaf4	NADH:ubiquinone oxidoreductase complex assembly factor 4	-0.65	-0.53
Lamtor2	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	-0.74	-0.53
Ccdc127	coiled-coil domain containing 127	-0.61	-0.53
Snx7	sorting nexin 7	-0.56	-0.53
Fam19a4	family with sequence similarity 19 member A4, C-C motif chemokine like	-0.57	-0.53
Hps3	HPS3, biogenesis of lysosomal organelles complex 2 subunit 1	-0.64	-0.53
Siae	sialic acid acetylesterase	-0.67	-0.53
Tc2n	tandem C2 domains, nuclear	-0.84	-0.54
Sub1	SUB1 homolog, transcriptional regulator	-0.78	-0.54
Ndufa11	NADH:ubiquinone oxidoreductase subunit A11	-0.6	-0.54
Usp9x	ubiquitin specific peptidase 9, X-linked	-0.5	-0.54
Ndufa7	NADH:ubiquinone oxidoreductase subunit A7	-0.64	-0.54
Crebl2	cAMP responsive element binding protein-like 2	-0.57	-0.54
Sdcbp	syndecan binding protein	-0.89	-0.54
Rrm2b	ribonucleotide reductase regulatory TP53 inducible subunit M2B	-0.53	-0.54
Blvra	biliverdin reductase A	-0.74	-0.54
Hbs1l	HBS1-like translational GTPase	-0.59	-0.54
Zcchc17	zinc finger CCHC-type containing 17	-0.63	-0.54
Usp45	ubiquitin specific peptidase 45	-0.56	-0.55
Thyn1	thymocyte nuclear protein 1	-0.71	-0.55
Gpcpd1	glycerophosphocholine phosphodiesterase 1	-0.54	-0.55
Elp6	elongator acetyltransferase complex subunit 6	-0.6	-0.55
Napa	NSF attachment protein alpha	-0.52	-0.55
Aqp1	aquaporin 1	-0.89	-0.55
Stx12	syntaxin 12	-0.76	-0.55
Dnaja1	DnaJ heat shock protein family (Hsp40) member A1	-0.78	-0.55
Slrpl	SRA stem-loop interacting RNA binding protein	-0.87	-0.55
Stoml2	stomatin like 2	-0.67	-0.55
Mrpl16	mitochondrial ribosomal protein L16	-0.61	-0.55
Lipe	lipase E, hormone sensitive type	-0.59	-0.55
Farsb	phenylalanyl-tRNA synthetase, beta subunit	-0.68	-0.56
Nudt22	nudix hydrolase 22	-0.55	-0.56
Exoc6	exocyst complex component 6	-0.73	-0.56
Pex7	peroxisomal biogenesis factor 7	-0.59	-0.56
Slc25a20	solute carrier family 25 member 20	-0.72	-0.56
Dph5	diphthamide biosynthesis 5	-0.56	-0.56
Insrr	insulin receptor-related receptor	-0.77	-0.56
Scfd1	sec1 family domain containing 1	-0.66	-0.56
Vegfa	vascular endothelial growth factor A	-0.65	-0.57
Naa20	N(alpha)-acetyltransferase 20, NatB catalytic subunit	-0.88	-0.57
Pnlip	pancreatic lipase	-1.61	-0.57
Snx19	sorting nexin 19	-0.53	-0.57
Ypel3	yippee-like 3	-0.54	-0.57
Gria3	glutamate ionotropic receptor AMPA type subunit 3	-0.56	-0.57
Vcpip1	valosin containing protein interacting protein 1	-0.51	-0.57
Aifm1	apoptosis inducing factor, mitochondria associated 1	-0.72	-0.57
Uba3	ubiquitin-like modifier activating enzyme 3	-0.73	-0.57

Morn2	MORN repeat containing 2	-1.21	-0.57
Rnf13	ring finger protein 13	-0.65	-0.57
Prkar2b	protein kinase cAMP-dependent type 2 regulatory subunit beta	-0.73	-0.58
S100a1	S100 calcium binding protein A1	-0.69	-0.58
Pecr	peroxisomal trans-2-enoyl-CoA reductase	-0.65	-0.58
Immt	inner membrane mitochondrial protein	-0.6	-0.58
St6galnac3	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	-0.9	-0.58
Chchd3	coiled-coil-helix-coiled-coil-helix domain containing 3	-0.66	-0.58
Mrpl35	mitochondrial ribosomal protein L35	-0.85	-0.58
Cab39	calcium binding protein 39	-0.59	-0.58
Layn	layilin	-0.65	-0.58
Ndufaf6	NADH:ubiquinone oxidoreductase complex assembly factor 6	-0.61	-0.58
Ric3	RIC3 acetylcholine receptor chaperone	-0.68	-0.58
Tmem18	transmembrane protein 18	-0.76	-0.58
Aasdhppt	amino adipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	-0.63	-0.59
Polr3k	RNA polymerase III subunit K	-0.73	-0.59
Copg2	coatomer protein complex, subunit gamma 2	-0.67	-0.59
Nup155	nucleoporin 155	-0.53	-0.59
Mtx2	metaxin 2	-0.57	-0.59
Hspe1	heat shock protein family E member 1	-0.92	-0.59
Klh14	kelch-like family member 4	-1.14	-0.59
Kbtbd2	kelch repeat and BTB domain containing 2	-0.64	-0.59
Pde4dip	phosphodiesterase 4D interacting protein	-0.54	-0.59
Zfp458	zinc finger protein 458	-0.61	-0.59
Gprasp1	G protein-coupled receptor associated sorting protein 1	-0.56	-0.6
RGD1559786	similar to RIKEN cDNA 0610037L13	-0.68	-0.6
Tsfrm	Ts translation elongation factor, mitochondrial	-0.52	-0.6
Mrrf	mitochondrial ribosome recycling factor	-0.65	-0.6
Nckap1	NCK-associated protein 1	-0.58	-0.6
Ndufa6	NADH:ubiquinone oxidoreductase subunit A6	-0.82	-0.6
Klhdc2	kelch domain containing 2	-0.68	-0.6
Chka	choline kinase alpha	-0.55	-0.6
Ocrl	OCRL, inositol polyphosphate-5-phosphatase	-0.61	-0.6
Nans	N-acetylneuraminate synthase	-0.63	-0.6
Otud6b	OTU domain containing 6B	-0.62	-0.61
Ift80	intraflagellar transport 80	-0.53	-0.61
Rfesd	Rieske (Fe-S) domain containing	-0.58	-0.61
Dync1li1	dynein cytoplasmic 1 light intermediate chain 1	-0.59	-0.61
Ano4	anoctamin 4	-0.54	-0.61
Eps8l2	EPS8-like 2	-1.2	-0.61
Aldoa	aldolase, fructose-bisphosphate A	-0.53	-0.61
Mrpl48	mitochondrial ribosomal protein L48	-0.81	-0.61
Mrps10	mitochondrial ribosomal protein S10	-0.72	-0.61
Orc4	origin recognition complex, subunit 4	-0.61	-0.61
Rb1cc1	RB1-inducible coiled-coil 1	-0.65	-0.62
Ccp110	centriolar coiled-coil protein 110	-0.67	-0.62
Mrpl49	mitochondrial ribosomal protein L49	-0.73	-0.62
Vopp1	vesicular, overexpressed in cancer, prosurvival protein 1	-0.61	-0.62
Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12	-0.75	-0.62
Tmem126b	transmembrane protein 126B	-0.85	-0.62
Ndufs8	NADH:ubiquinone oxidoreductase core subunit S8	-0.65	-0.62
Dnajc21	DnaJ heat shock protein family (Hsp40) member C21	-0.74	-0.62
Ntrk3	neurotrophic receptor tyrosine kinase 3	-0.66	-0.62
Gemin7	gem (nuclear organelle) associated protein 7	-0.73	-0.62

Nudcd1	NudC domain containing 1	-0.83	-0.62
Atmin	ATM interactor	-0.5	-0.62
Wdr47	WD repeat domain 47	-0.64	-0.62
E2f6	E2F transcription factor 6	-0.53	-0.62
Ephb1	Eph receptor B1	-0.85	-0.62
Chchd6	coiled-coil-helix-coiled-coil-helix domain containing 6	-0.66	-0.62
Lancl2	LanC like 2	-0.55	-0.62
Tmem176b	transmembrane protein 176B	-0.92	-0.63
Prkaa1	protein kinase AMP-activated catalytic subunit alpha 1	-0.82	-0.63
Cep290	centrosomal protein 290	-0.66	-0.63
Fbln5	fibulin 5	-0.9	-0.63
Hint3	histidine triad nucleotide binding protein 3	-0.76	-0.63
Mrpl2	mitochondrial ribosomal protein L2	-0.51	-0.63
Atl2	atlastin GTPase 2	-0.56	-0.63
Ptn	pleiotrophin	-0.62	-0.63
Cox6c	cytochrome c oxidase subunit 6C	-0.87	-0.63
Ppm1a	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> dependent, 1A	-0.54	-0.63
Hddc2	HD domain containing 2	-0.63	-0.64
Mettl5	methyltransferase like 5	-0.55	-0.64
Bbs5	Bardet-Biedl syndrome 5	-0.73	-0.64
Mrpl47	mitochondrial ribosomal protein L47	-0.84	-0.64
Tpd52l1	tumor protein D52-like 1	-0.83	-0.64
RGD1560065	similar to RIKEN cDNA 2410004B18	-0.71	-0.64
Lage3	L antigen family, member 3	-0.69	-0.64
Mtch2	mitochondrial carrier 2	-0.78	-0.64
Prdx5	peroxiredoxin 5	-0.67	-0.64
Tmem141	transmembrane protein 141	-0.75	-0.64
Malsu1	mitochondrial assembly of ribosomal large subunit 1	-0.62	-0.64
Actr6	ARP6 actin-related protein 6 homolog	-0.88	-0.64
Cby1	chibby family member 1, beta catenin antagonist	-0.68	-0.64
Gskip	GSK3B interacting protein	-0.82	-0.64
B3gat3	beta-1,3-glucuronyltransferase 3	-0.57	-0.64
Arhgap5	Rho GTPase activating protein 5	-0.5	-0.64
Hcn1	hyperpolarization-activated cyclic nucleotide-gated potassium channel 1	-0.69	-0.64
Ralgapa1	Ral GTPase activating protein catalytic alpha subunit 1	-0.51	-0.65
Dctn3	dynactin subunit 3	-0.77	-0.65
Psmd14	proteasome 26S subunit, non-ATPase 14	-0.84	-0.65
Mcts1	MCTS1, re-initiation and release factor	-0.82	-0.65
Phospho2	phosphatase, orphan 2	-0.69	-0.65
Usp15	ubiquitin specific peptidase 15	-0.73	-0.65
Btbd6	BTB domain containing 6	-0.5	-0.65
Calm1	calmodulin 1	-0.64	-0.65
Hadhb	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta	-0.77	-0.65
Atp5b	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, beta polypeptide	-0.56	-0.65
Cdpt	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	-0.66	-0.66
Prr15	proline rich 15	-0.76	-0.66
Arfgef2	ADP ribosylation factor guanine nucleotide exchange factor 2	-0.61	-0.66
Cox5b	cytochrome c oxidase subunit 5B	-0.68	-0.66
C2cd5	C2 calcium-dependent domain containing 5	-0.63	-0.66
Abo	ABO, alpha 1-3-N-acetylgalactosaminyltransferase and alpha 1-3-galactosyltransferase	-0.52	-0.66
Cacnb4	calcium voltage-gated channel auxiliary subunit beta 4	-0.7	-0.66

Chordc1	cysteine and histidine rich domain containing 1	-0.85	-0.66
Glx5	glutaredoxin 5	-0.72	-0.66
Rom1	retinal outer segment membrane protein 1	-0.69	-0.66
Zfp956	zinc finger protein 956	-0.62	-0.66
Zfhx4	zinc finger homeobox 4	-0.61	-0.66
Mob4	MOB family member 4, phocean	-0.81	-0.67
Usp8	ubiquitin specific peptidase 8	-0.63	-0.67
Vps39	VPS39 HOPS complex subunit	-0.58	-0.67
Bcap31	B-cell receptor-associated protein 31	-0.85	-0.67
Mapk11	mitogen-activated protein kinase 11	-0.74	-0.67
Daam1	dishevelled associated activator of morphogenesis 1	-0.72	-0.67
Ret	ret proto-oncogene	-0.63	-0.67
Usp33	ubiquitin specific peptidase 33	-0.65	-0.67
Hibch	3-hydroxyisobutyryl-CoA hydrolase	-0.64	-0.67
Elmod1	ELMO domain containing 1	-0.64	-0.67
Eif2b2	eukaryotic translation initiation factor 2B subunit beta	-0.76	-0.67
Syt11	synaptotagmin 11	-0.62	-0.68
Rundc3b	RUN domain containing 3B	-0.73	-0.68
Tfb1m	transcription factor B1, mitochondrial	-0.6	-0.68
Atp5l	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G	-0.89	-0.68
Osbpl9	oxysterol binding protein-like 9	-0.84	-0.68
Ube2j1	ubiquitin-conjugating enzyme E2, J1	-0.59	-0.68
Fam204a	family with sequence similarity 204, member A	-0.56	-0.68
Ddx10	DEAD-box helicase 10	-0.74	-0.68
Idh3g	isocitrate dehydrogenase 3 (NAD), gamma	-0.75	-0.68
Hsd17b10	hydroxysteroid (17-beta) dehydrogenase 10	-0.82	-0.68
Ndufb5	NADH:ubiquinone oxidoreductase subunit B5	-0.76	-0.68
Sdhb	succinate dehydrogenase complex subunit D	-0.85	-0.68
Mkks	McKusick-Kaufman syndrome	-0.75	-0.69
Tmem41b	transmembrane protein 41B	-0.73	-0.69
Alg2	ALG2, alpha-1,3/1,6-mannosyltransferase	-0.6	-0.69
Bbs10	Bardet-Biedl syndrome 10	-0.63	-0.69
Col4a3bp	collagen type IV alpha 3 binding protein	-0.61	-0.69
Ighmbp2	immunoglobulin mu binding protein 2	-0.52	-0.69
Myo9a	myosin IXA	-0.6	-0.69
Mgll	monoglyceride lipase	-0.52	-0.69
RGD1305014	similar to RIKEN cDNA 2310057M21	-0.6	-0.69
Prcaa2	protein kinase AMP-activated catalytic subunit alpha 2	-0.79	-0.69
Yipf6	Yip1 domain family, member 6	-0.83	-0.69
Sirt3	sirtuin 3	-0.75	-0.69
Ahcyl2	adenosylhomocysteinase-like 2	-0.5	-0.69
Serpina11	serpin family A member 11	-0.85	-0.69
Morn1	MORN repeat containing 1	-0.52	-0.7
Chm	CHM, Rab escort protein 1	-0.76	-0.7
Gabrb3	gamma-aminobutyric acid type A receptor beta 3 subunit	-0.66	-0.7
Mkrn1	makorin ring finger protein 1	-0.6	-0.7
Pdha1	pyruvate dehydrogenase E1 alpha 1 subunit	-0.63	-0.7
Cops2	COP9 signalosome subunit 2	-0.94	-0.7
Gale	UDP-galactose-4-epimerase	-0.8	-0.7
Tmem126a	transmembrane protein 126A	-0.83	-0.7
Efr3a	EFR3 homolog A	-0.76	-0.7
Lactb2	lactamase, beta 2	-0.83	-0.7
Pkig	cAMP-dependent protein kinase inhibitor gamma	-0.72	-0.7
Zfyve9	zinc finger FYVE-type containing 9	-0.55	-0.7
Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily C, member 3	-0.72	-0.7

	chromatin, subfamily d, member 3		
Fam45a	family with sequence similarity 45, member A	-0.79	-0.7
Mrpl50	mitochondrial ribosomal protein L50	-0.79	-0.7
Tdrd7	tudor domain containing 7	-0.55	-0.7
Pdhx	pyruvate dehydrogenase complex, component X	-0.72	-0.71
Ciao1	cytosolic iron-sulfur assembly component 1	-0.68	-0.71
Slc20a1	solute carrier family 20 member 1	-0.74	-0.71
Ttc33	tetratricopeptide repeat domain 33	-0.85	-0.71
Armc1	armadillo repeat containing 1	-0.71	-0.71
Lztf1	leucine zipper transcription factor-like 1	-0.86	-0.71
Mrpl41	mitochondrial ribosomal protein L41	-0.87	-0.71
Ndufs4	NADH:ubiquinone oxidoreductase subunit S4	-0.76	-0.71
Atp5s	ATP synthase, H <sup>+</sup> transporting, mitochondrial Fo complex, subunit s (factor B)	-0.71	-0.71
P2rx3	purinergic receptor P2X 3	-1.11	-0.72
Mpc1	mitochondrial pyruvate carrier 1	-0.9	-0.72
Eps15	epidermal growth factor receptor pathway substrate 15	-0.59	-0.72
Ubl4a	ubiquitin-like 4A	-0.57	-0.72
Ndufc2	NADH:ubiquinone oxidoreductase subunit C2	-0.8	-0.72
Ndufb9	NADH:ubiquinone oxidoreductase subunit B9	-0.89	-0.72
Dnajc24	DnaJ heat shock protein family (Hsp40) member C24	-1.07	-0.72
Musk	muscle associated receptor tyrosine kinase	-0.8	-0.72
Asnsd1	asparagine synthetase domain containing 1	-0.88	-0.72
Slc4a1ap	solute carrier family 4 member 1 adaptor protein	-0.63	-0.72
Vps11	VPS11 CORVET/HOPS core subunit	-0.75	-0.72
Dnajc5	DnaJ heat shock protein family (Hsp40) member C5	-0.68	-0.72
Ddx1	DEAD-box helicase 1	-0.73	-0.72
Pde4d	phosphodiesterase 4D	-0.81	-0.73
Yaf2	YY1 associated factor 2	-0.79	-0.73
Aox1	aldehyde oxidase 1	-1.12	-0.73
Preb	prolactin regulatory element binding	-0.6	-0.73
Tpd52	tumor protein D52	-0.82	-0.73
Atp6v1d	ATPase H <sup>+</sup> transporting V1 subunit D	-0.87	-0.73
Unc79	unc-79 homolog, NALCN channel complex subunit	-0.83	-0.73
Gpr68	G protein-coupled receptor 68	-0.93	-0.73
Lipa	lipase A, lysosomal acid type	-0.69	-0.73
Eea1	early endosome antigen 1	-0.64	-0.73
Eml2	echinoderm microtubule associated protein like 2	-0.53	-0.73
Idh3a	isocitrate dehydrogenase 3 (NAD <sup>+</sup> ) alpha	-0.61	-0.73
Pmpca	peptidase, mitochondrial processing alpha subunit	-0.57	-0.73
Tmem223	transmembrane protein 223	-0.86	-0.74
Dync1i2	dynein cytoplasmic 1 intermediate chain 2	-0.95	-0.74
Mrps15	mitochondrial ribosomal protein S15	-0.8	-0.74
Stmn3	stathmin 3	-0.58	-0.74
Pin1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	-0.56	-0.74
Chac1	ChaC glutathione-specific gamma-glutamylcyclotransferase 1	-1.08	-0.74
Rnf7	ring finger protein 7	-1.15	-0.74
Trpc1	transient receptor potential cation channel, subfamily C, member 1	-0.7	-0.74
Ssu72	SSU72 homolog, RNA polymerase II CTD phosphatase	-0.87	-0.75
Tmem169	transmembrane protein 169	-0.69	-0.75
Serhl2	serine hydrolase-like 2	-0.77	-0.75
Lancl1	LanC like 1	-0.58	-0.75
Stap2	signal transducing adaptor family member 2	-1.09	-0.75
Tdrkh	tudor and KH domain containing	-0.68	-0.75
Uqcrc2	ubiquinol cytochrome c reductase core protein 2	-0.88	-0.75

Rab11a	RAB11a, member RAS oncogene family	-0.85	-0.75
Klc1	kinesin light chain 1	-0.56	-0.75
Lmbrd1	LMBR1 domain containing 1	-0.75	-0.76
Ypel5	yippee-like 5	-0.97	-0.76
Tce2a	transcription elongation factor A2	-0.59	-0.76
Dld	dihydrolipoamide dehydrogenase	-0.91	-0.76
Osgepl1	O-sialoglycoprotein endopeptidase-like 1	-0.77	-0.76
Pfn2	profilin 2	-0.52	-0.76
Ech1	enoyl-CoA hydratase 1	-0.69	-0.76
Fam213b	family with sequence similarity 213, member B	-0.77	-0.76
Ppm1h	protein phosphatase, Mg2+/Mn2+ dependent, 1H	-0.79	-0.76
Icmt	isoprenylcysteine carboxyl methyltransferase	-0.71	-0.76
Rbp4	retinol binding protein 4	-0.55	-0.76
Arl6ip1	ADP-ribosylation factor like GTPase 6 interacting protein 1	-0.93	-0.76
Timm8b	translocase of inner mitochondrial membrane 8 homolog B	-0.92	-0.76
Kif1b	kinesin family member 1B	-0.51	-0.76
Esrra	estrogen related receptor, alpha	-0.58	-0.77
Znhit2	zinc finger, HIT-type containing 2	-0.76	-0.77
Osbpl6	oxysterol binding protein-like 6	-0.52	-0.77
Xk	X-linked Kx blood group	-0.8	-0.77
Coro2a	coronin 2A	-0.78	-0.77
Syndig1	synapse differentiation inducing 1	-0.54	-0.77
Usmg5	up-regulated during skeletal muscle growth 5 homolog (mouse)	-0.93	-0.77
Casc4	cancer susceptibility 4	-0.95	-0.77
Hspa4l	heat shock protein family A (Hsp70) member 4 like	-0.74	-0.77
Lrrc28	leucine rich repeat containing 28	-0.85	-0.77
Gabarapl1	GABA type A receptor associated protein like 1	-0.79	-0.77
Ndufa9	NADH:ubiquinone oxidoreductase subunit A9	-0.73	-0.77
Nrcam	neuronal cell adhesion molecule	-0.88	-0.77
Ap3s2	adaptor-related protein complex 3, sigma 2 subunit	-0.8	-0.77
Atp6v1h	ATPase H+ transporting V1 subunit H	-0.82	-0.77
Pdk3	pyruvate dehydrogenase kinase 3	-0.8	-0.77
RGD1309079	similar to Ab2-095	-0.85	-0.77
Gpr155	G protein-coupled receptor 155	-0.68	-0.78
Rtn3	reticulon 3	-0.63	-0.78
Cox7c	cytochrome c oxidase subunit 7C	-1.06	-0.78
Uqcrh	ubiquinol-cytochrome c reductase hinge protein	-1.12	-0.78
Tceal1	transcription elongation factor A like 1	-1.02	-0.79
Ccsrer1	coiled-coil serine-rich protein 1	-0.6	-0.79
Moap1	modulator of apoptosis 1	-0.71	-0.79
Crip2	cysteine-rich protein 2	-0.73	-0.79
Mnat1	MNAT1, CDK activating kinase assembly factor	-0.89	-0.79
Atl1	atlastin GTPase 1	-0.8	-0.79
Zdhhc17	zinc finger, DHHC-type containing 17	-0.76	-0.79
Jkamp	JNK1/MAPK8-associated membrane protein	-0.76	-0.79
Bace1	beta-secretase 1	-0.69	-0.79
Kif5a	kinesin family member 5A	-0.62	-0.79
Uqcrb	ubiquinol-cytochrome c reductase binding protein	-0.74	-0.79
Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	-0.97	-0.79
Cmas	cytidine monophosphate N-acetylneuraminic acid synthetase	-0.7	-0.79
Atp5g3	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)	-0.72	-0.79
Svip	small VCP interacting protein	-0.58	-0.79
Ebf3	early B-cell factor 3	-0.62	-0.79
Ppp3ca	protein phosphatase 3 catalytic subunit alpha	-0.7	-0.8

LOC500475	similar to hypothetical protein 4933430I17	-0.81	-0.8
Syt5	synaptotagmin 5	-0.6	-0.8
Hmgcs2	3-hydroxy-3-methylglutaryl-CoA synthase 2	-1.05	-0.8
Mrps36	mitochondrial ribosomal protein S36	-0.89	-0.8
Tmem143	transmembrane protein 143	-0.59	-0.8
Shank2	SH3 and multiple ankyrin repeat domains 2	-0.65	-0.8
Cpm	carboxypeptidase M	-1.17	-0.8
Emc4	ER membrane protein complex subunit 4	-0.84	-0.8
Tspan33	tetraspanin 33	-0.55	-0.8
Vav2	vav guanine nucleotide exchange factor 2	-0.63	-0.8
Kctd17	potassium channel tetramerization domain containing 17	-0.7	-0.8
Mns1	meiosis-specific nuclear structural 1	-1.05	-0.8
Ppfia3	PTPRF interacting protein alpha 3	-0.58	-0.8
Ndufa4	NDUFA4, mitochondrial complex associated	-1.06	-0.8
Pqlc3	PQ loop repeat containing 3	-1.06	-0.8
Snhg11	small nucleolar RNA host gene 11	-1.05	-0.8
Gpx4	glutathione peroxidase 4	-0.93	-0.81
Parvb	parvin, beta	-1.1	-0.81
Ctnna2	catenin alpha 2	-0.63	-0.81
Gstm4	glutathione S-transferase mu 4	-0.61	-0.81
Nmrk1	nicotinamide riboside kinase 1	-1.04	-0.81
Fastkd2	FAST kinase domains 2	-0.95	-0.81
Acvr1b	activin A receptor type 1B	-0.52	-0.81
Dnaja4	Dnaj heat shock protein family (Hsp40) member A4	-0.86	-0.81
Spats2	spermatogenesis associated, serine-rich 2	-0.77	-0.81
Ttbk2	tau tubulin kinase 2	-0.72	-0.82
Slc38a1	solute carrier family 38, member 1	-0.63	-0.82
Tmx4	thioredoxin-related transmembrane protein 4	-0.74	-0.82
Dkk3	dickkopf WNT signaling pathway inhibitor 3	-1.01	-0.82
Spryd3	SPRY domain containing 3	-0.74	-0.82
Lrriq3	leucine-rich repeats and IQ motif containing 3	-0.85	-0.82
Tmem60	transmembrane protein 60	-0.79	-0.82
Fhdc1	FH2 domain containing 1	-0.63	-0.82
Oxct1	3-oxoacid CoA transferase 1	-0.74	-0.82
Tubb4b	tubulin, beta 4B class IVb	-0.54	-0.82
Atp6v1e1	ATPase H+ transporting V1 subunit E1	-0.77	-0.82
Pdzd7	PDZ domain containing 7	-0.73	-0.82
Mospd1	motile sperm domain containing 1	-1.31	-0.82
Lrpprc	leucine-rich pentatricopeptide repeat containing	-0.73	-0.82
Dffa	DNA fragmentation factor subunit alpha	-0.65	-0.83
Slc35f2	solute carrier family 35, member F2	-0.71	-0.83
Cpeb1	cytoplasmic polyadenylation element binding protein 1	-0.57	-0.83
Trim23	tripartite motif-containing 23	-1.02	-0.83
Actr10	actin-related protein 10 homolog	-1.04	-0.83
Pex14	peroxisomal biogenesis factor 14	-0.69	-0.83
Tanc1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	-0.54	-0.83
Slc8a3	solute carrier family 8 member A3	-0.83	-0.83
Stk32c	serine/threonine kinase 32C	-0.55	-0.83
Phgdh	phosphoglycerate dehydrogenase	-0.67	-0.83
Atp13a2	ATPase 13A2	-0.5	-0.83
Ndufa8	NADH:ubiquinone oxidoreductase subunit A8	-0.85	-0.83
Htatip2	HIV-1 Tat interactive protein 2	-1.12	-0.83
Sdha	succinate dehydrogenase complex flavoprotein subunit A	-0.78	-0.83
Gpr89b	G protein-coupled receptor 89B	-0.89	-0.83
Kcnn3	potassium calcium-activated channel subfamily N member 3	-0.7	-0.83

Usp20	ubiquitin specific peptidase 20	-0.8	-0.84
Cyc1	cytochrome c-1	-0.69	-0.84
Hey2	hes-related family bHLH transcription factor with YRPW motif 2	-0.89	-0.84
Klhl17	kelch-like family member 17	-0.52	-0.84
Larp1b	La ribonucleoprotein domain family, member 1B	-0.93	-0.84
Grid2	glutamate ionotropic receptor delta type subunit 2	-0.57	-0.84
Pgm2l1	phosphoglucomutase 2-like 1	-0.74	-0.84
Aak1	AP2 associated kinase 1	-0.56	-0.84
Wipf3	WAS/WASL interacting protein family, member 3	-1.44	-0.84
Ndufs3	NADH:ubiquinone oxidoreductase core subunit S3	-1	-0.84
Apoo	apolipoprotein O	-0.93	-0.84
Atp1b3	ATPase Na+/K+ transporting subunit beta 3	-1.02	-0.84
Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A	-0.59	-0.84
Calm3	calmodulin 3	-0.58	-0.85
Ndufb8	NADH:ubiquinone oxidoreductase subunit B8	-0.86	-0.85
Atp6v1c1	ATPase H+ transporting V1 subunit C1	-0.99	-0.85
Elov5	ELOVL fatty acid elongase 5	-0.75	-0.85
Cacnb3	calcium voltage-gated channel auxiliary subunit beta 3	-0.7	-0.85
Gfm1	G elongation factor, mitochondrial 1	-0.95	-0.85
Tomm34	translocase of outer mitochondrial membrane 34	-0.8	-0.85
Fundc1	FUN14 domain containing 1	-1.24	-0.85
Arhgap35	Rho GTPase activating protein 35	-0.51	-0.86
Nlgn1	neuroligin 1	-0.89	-0.86
Abhd12	abhydrolase domain containing 12	-0.94	-0.86
Fam126b	family with sequence similarity 126, member B	-0.9	-0.86
Tmem205	transmembrane protein 205	-0.92	-0.86
Dlg2	discs large MAGUK scaffold protein 2	-0.56	-0.86
Sec23a	Sec23 homolog A, coat complex II component	-0.71	-0.86
Cox4i2	cytochrome c oxidase subunit 4i2	-0.85	-0.86
Aco2	aconitase 2	-0.69	-0.86
Map2	microtubule-associated protein 2	-0.86	-0.87
Nipa1	non imprinted in Prader-Willi/Angelman syndrome 1	-0.87	-0.87
Kcna3	potassium voltage-gated channel subfamily A member 3	-0.67	-0.87
Ift27	intraflagellar transport 27	-0.92	-0.87
Morn5	MORN repeat containing 5	-1.89	-0.87
Rnf32	ring finger protein 32	-0.59	-0.87
Hdac9	histone deacetylase 9	-0.57	-0.87
Bckdhb	branched chain keto acid dehydrogenase E1 subunit beta	-0.6	-0.87
Agl	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	-0.69	-0.87
Fam110b	family with sequence similarity 110, member B	-0.7	-0.87
Ppp1r3d	protein phosphatase 1, regulatory subunit 3D	-0.77	-0.87
Gstm1	glutathione S-transferase mu 1	-0.74	-0.88
Prkcz	protein kinase C, zeta	-0.73	-0.88
Oscp1	organic solute carrier partner 1	-0.72	-0.88
Ttl1	tubulin tyrosine ligase like 1	-0.73	-0.88
Tmod1	tropomodulin 1	-0.91	-0.88
Trappc2	trafficking protein particle complex 2	-1.22	-0.88
Ndufb6	NADH:ubiquinone oxidoreductase subunit B6	-0.81	-0.88
Stip1	stress-induced phosphoprotein 1	-0.93	-0.88
Fbxl4	F-box and leucine-rich repeat protein 4	-0.61	-0.89
Slc25a34	solute carrier family 25, member 34	-1.32	-0.89
Tmem230	transmembrane protein 230	-0.93	-0.89
Dtd1	D-tyrosyl-tRNA deacylase 1	-0.9	-0.89
Sacm1l	SAC1 like phosphatidylinositide phosphatase	-1.03	-0.89
Nudt14	nudix hydrolase 14	-0.88	-0.89

Scrn3	secernin 3	-1.2	-0.89
Fbxo2	F-box protein 2	-0.86	-0.89
Suclg1	succinate-CoA ligase, alpha subunit	-0.75	-0.89
Fpgt	fucose-1-phosphate guanylyltransferase	-0.96	-0.89
Pigy	phosphatidylinositol glycan anchor biosynthesis, class Y	-0.88	-0.89
Thsd7a	thrombospondin type 1 domain containing 7A	-0.64	-0.89
Pcdh11x	protocadherin 11 X-linked	-0.8	-0.89
Ngrn	neugrin, neurite outgrowth associated	-0.82	-0.9
Phtf1	putative homeodomain transcription factor 1	-0.85	-0.9
Necap1	NECAP endocytosis associated 1	-0.73	-0.9
Pdzd4	PDZ domain containing 4	-0.73	-0.9
Sgtb	small glutamine rich tetratricopeptide repeat containing beta	-0.83	-0.9
Fitm2	fat storage-inducing transmembrane protein 2	-0.69	-0.9
Tspan7	tetraspanin 7	-0.88	-0.9
Sord	sorbitol dehydrogenase	-0.76	-0.9
Scamp1	secretory carrier membrane protein 1	-0.87	-0.9
Dpcd	deleted in primary ciliary dyskinesia	-0.96	-0.9
Trim46	tripartite motif-containing 46	-0.77	-0.91
Gipc2	GIPC PDZ domain containing family, member 2	-1.04	-0.91
Ttc9	tetratricopeptide repeat domain 9	-0.77	-0.91
Fkbp3	FK506 binding protein 3	-1.16	-0.91
Aplp2	amyloid beta precursor like protein 2	-0.92	-0.91
Trappc4	trafficking protein particle complex 4	-0.8	-0.91
Ntm	neurotrimin	-0.75	-0.91
Gas2	growth arrest-specific 2	-0.87	-0.91
Ubac1	UBA domain containing 1	-0.71	-0.91
Stard10	StAR-related lipid transfer domain containing 10	-0.6	-0.91
RGD1359108	similar to RIKEN cDNA 3110043O21	-0.92	-0.91
Mfsd6	major facilitator superfamily domain containing 6	-0.94	-0.92
Elavl2	ELAV like RNA binding protein 2	-1.16	-0.92
Gsta3	glutathione S-transferase alpha 3	-5.18	-0.92
Mid1ip1	MID1 interacting protein 1	-0.64	-0.92
Cox7b	cytochrome c oxidase subunit 7B	-1.25	-0.92
Ankrd46	ankyrin repeat domain 46	-0.85	-0.92
Gla	galactosidase, alpha	-1.07	-0.92
Tram1l1	translocation associated membrane protein 1-like 1	-0.63	-0.92
Rab39a	RAB39A, member RAS oncogene family	-0.99	-0.92
St13	ST13, Hsp70 interacting protein	-0.85	-0.93
Gys1	glycogen synthase 1	-0.6	-0.93
Arg2	arginase 2	-0.94	-0.93
Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	-0.7	-0.93
Gria4	glutamate ionotropic receptor AMPA type subunit 4	-0.65	-0.93
Emb	embigin	-1.21	-0.93
Chp2	calcineurin-like EF hand protein 2	-1.06	-0.93
Zfp483	zinc finger protein 483	-0.74	-0.93
Strbp	spermatid perinuclear RNA binding protein	-0.8	-0.93
Actr3b	ARP3 actin related protein 3 homolog B	-0.93	-0.93
Mapk12	mitogen-activated protein kinase 12	-0.76	-0.94
Tmem179	transmembrane protein 179	-0.82	-0.94
Nckipsd	NCK interacting protein with SH3 domain	-0.82	-0.94
Madd	MAP-kinase activating death domain	-0.54	-0.94
Rnf144a	ring finger protein 144A	-0.67	-0.94
Sqle	squalene epoxidase	-0.72	-0.94
Pde1a	phosphodiesterase 1A	-0.59	-0.94

Abhd2	abhydrolase domain containing 2	-0.67	-0.94
Jakmip3	janus kinase and microtubule interacting protein 3	-0.87	-0.94
Chn2	chimerin 2	-0.82	-0.94
Map1b	microtubule-associated protein 1B	-0.95	-0.94
Prdx3	peroxiredoxin 3	-0.99	-0.94
Ndufab1	NADH:ubiquinone oxidoreductase subunit AB1	-0.76	-0.95
Slit1	slit guidance ligand 1	-0.89	-0.95
Amigo2	adhesion molecule with Ig like domain 2	-0.79	-0.95
Fam69b	family with sequence similarity 69, member B	-0.64	-0.95
Sult2b1	sulfotransferase family 2B member 1	-0.84	-0.95
Ndufaf1	NADH:ubiquinone oxidoreductase complex assembly factor 1	-0.93	-0.95
RGD1305645	similar to RIKEN cDNA 1500015O10	-1.05	-0.95
Fbxo36	F-box protein 36	-1.06	-0.96
Mcm8	minichromosome maintenance 8 homologous recombination repair factor	-0.78	-0.96
Tcaim	T cell activation inhibitor, mitochondrial	-0.86	-0.96
Dtd2	D-tyrosyl-tRNA deacylase 2	-0.91	-0.96
Plcl1	phospholipase C-like 1	-0.69	-0.96
Cdk5	cyclin-dependent kinase 5	-0.81	-0.96
Tle4	transducin-like enhancer of split 4	-0.61	-0.96
Cep70	centrosomal protein 70	-0.99	-0.96
Pak1	p21 (RAC1) activated kinase 1	-0.85	-0.96
Adam23	ADAM metallopeptidase domain 23	-0.56	-0.96
Kcna1	potassium voltage-gated channel subfamily A member 1	-0.64	-0.96
Tmem218	transmembrane protein 218	-0.86	-0.97
Slc29a1	solute carrier family 29 member 1	-1.15	-0.97
Slc25a14	solute carrier family 25 member 14	-0.85	-0.97
Lrrk2	leucine-rich repeat kinase 2	-0.69	-0.97
Ndufb3	NADH:ubiquinone oxidoreductase subunit B3	-1	-0.97
Gnb5	G protein subunit beta 5	-1.04	-0.97
Ogfrl1	opioid growth factor receptor-like 1	-1.1	-0.97
Ica1l	islet cell autoantigen 1-like	-1.07	-0.97
Ndufv2	NADH:ubiquinone oxidoreductase core subunit V2	-1.19	-0.98
Tmeff1	transmembrane protein with EGF-like and two follistatin-like domains 1	-0.66	-0.98
Ctnnd2	catenin delta 2	-0.68	-0.98
Pdzd8	PDZ domain containing 8	-0.75	-0.98
Gstk1	glutathione S-transferase kappa 1	-0.95	-0.98
Insig1	insulin induced gene 1	-0.61	-0.98
Cpne3	copine 3	-0.91	-0.98
Gchfr	GTP cyclohydrolase I feedback regulator	-1.18	-0.98
Sh3glb2	SH3 domain-containing GRB2-like endophilin B2	-0.82	-0.98
Rasgrp1	RAS guanyl releasing protein 1	-0.87	-0.98
Dnajc6	DnaJ heat shock protein family (Hsp40) member C6	-0.74	-0.98
Pcdh18	protocadherin 18	-0.84	-0.98
Lysmd2	LysM domain containing 2	-0.94	-0.98
Ndufa5	NADH:ubiquinone oxidoreductase subunit A5	-1.07	-0.99
Ndufaf5	NADH:ubiquinone oxidoreductase complex assembly factor 5	-1.14	-0.99
Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	-0.67	-0.99
Tmem56	transmembrane protein 56	-0.92	-0.99
Ccl27	C-C motif chemokine ligand 27	-0.74	-0.99
Map3k10	mitogen activated protein kinase kinase kinase 10	-0.54	-0.99
Ndufaf7	NADH:ubiquinone oxidoreductase complex assembly factor 7	-1.02	-0.99
Rhpn2	rhophilin, Rho GTPase binding protein 2	-1.18	-0.99
LOC500300	similar to hypothetical protein MGC6835	-1.42	-1

Idh3B	isocitrate dehydrogenase 3 (NAD+) beta	-1.04	-1
Fam103a1	family with sequence similarity 103, member A1	-1.17	-1
Mab21l3	mab-21 like 3	-0.93	-1
Dynlt3	dynein light chain Tctex-type 3	-1.34	-1
Cela1	chymotrypsin-like elastase family, member 1	-0.99	-1
Pnkd	paroxysmal nonkinesigenic dyskinesia	-0.71	-1
Ncald	neurocalcin delta	-1.05	-1
Tmem196	transmembrane protein 196	-1.04	-1.01
Neu3	neuraminidase 3	-0.66	-1.01
Timm10	translocase of inner mitochondrial membrane 10	-1.05	-1.01
Tmem70	transmembrane protein 70	-0.71	-1.01
Cntn1	contactin 1	-0.97	-1.01
Tm7sf2	transmembrane 7 superfamily member 2	-0.58	-1.01
Ptpnu	protein tyrosine phosphatase, receptor type, U	-0.64	-1.01
Kcnt1	potassium sodium-activated channel subfamily T member 1	-1.07	-1.01
Gpr61	G protein-coupled receptor 61	-0.87	-1.01
Tbxa2r	thromboxane A2 receptor	-0.94	-1.02
Rapgef5	Rap guanine nucleotide exchange factor 5	-1.02	-1.02
Lrsam1	leucine rich repeat and sterile alpha motif containing 1	-0.77	-1.02
Klhdc1	kelch domain containing 1	-1.08	-1.02
Atp6v0e2	ATPase, H+ transporting V0 subunit e2	-0.93	-1.02
Sv2c	synaptic vesicle glycoprotein 2c	-0.9	-1.02
Pja2	praia ring finger ubiquitin ligase 2	-0.79	-1.02
Fxyd2	FXYD domain-containing ion transport regulator 2	-1.47	-1.02
Pex3	peroxisomal biogenesis factor 3	-1.04	-1.02
Hpcal1	hippocalcin-like 1	-0.7	-1.03
Cyp51	cytochrome P450, family 51	-0.77	-1.03
Map1a	microtubule-associated protein 1A	-0.73	-1.03
Hmgcs1	3-hydroxy-3-methylglutaryl-CoA synthase 1	-0.69	-1.03
Syn1	synapsin I	-0.56	-1.03
Resp18	regulated endocrine-specific protein 18	-0.89	-1.03
Fbxo44	F-box protein 44	-0.72	-1.03
Tasp1	taspase 1	-0.68	-1.03
Ldhb	lactate dehydrogenase B	-1.12	-1.03
Slc13a3	solute carrier family 13 member 3	-0.54	-1.03
Cds2	CDP-diacylglycerol synthase 2	-1.22	-1.03
Folh1	folate hydrolase 1	-0.96	-1.03
Kcna5	potassium voltage-gated channel subfamily A member 5	-0.78	-1.03
Btbd3	BTB domain containing 3	-0.64	-1.04
Fgfbp3	fibroblast growth factor binding protein 3	-1.19	-1.04
Entpd6	ectonucleoside triphosphate diphosphohydrolase 6	-0.99	-1.04
Luzp1	leucine zipper protein 1	-0.89	-1.04
Them6	thioesterase superfamily member 6	-1.19	-1.04
Dnajb4	DnaJ heat shock protein family (Hsp40) member B4	-0.87	-1.04
Slc40a1	solute carrier family 40 member 1	-0.75	-1.04
Tmx2	thioredoxin-related transmembrane protein 2	-1.16	-1.04
Ccdc28a	coiled-coil domain containing 28A	-1.56	-1.05
Gabra3	gamma-aminobutyric acid type A receptor alpha3 subunit	-1.2	-1.05
Fbxo9	f-box protein 9	-1.18	-1.05
Prepl	prolyl endopeptidase-like	-0.96	-1.05
Larp6	La ribonucleoprotein domain family, member 6	-0.71	-1.05
Pak7	p21 (RAC1) activated kinase 7	-0.84	-1.05
Bola3	bola family member 3	-1.47	-1.05
Rnf180	ring finger protein 180	-0.75	-1.05
Endog	endonuclease G	-0.84	-1.05

Tmem229a	transmembrane protein 229A	-0.61	-1.06
Sema7a	semaphorin 7A (John Milton Hagen blood group)	-0.8	-1.06
Ttl	tubulin tyrosine ligase	-0.94	-1.06
Cmpk2	cytidine/uridine monophosphate kinase 2	-1.36	-1.06
Sfrp5	secreted frizzled-related protein 5	-0.68	-1.06
Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	-1.07	-1.06
Ahrr	aryl-hydrocarbon receptor repressor	-1.97	-1.06
Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1	-0.85	-1.06
Sfxn5	sideroflexin 5	-0.72	-1.06
Ranbp6	RAN binding protein 6	-1.01	-1.06
Tmem229b	transmembrane protein 229B	-0.97	-1.07
Stxbp1	syntaxin binding protein 1	-0.76	-1.07
Oprl1	opioid related nociceptin receptor 1	-0.88	-1.07
Rab3ip	RAB3A interacting protein	-0.94	-1.07
Aass	amino adipate-semialdehyde synthase	-1.03	-1.07
Snapc5	small nuclear RNA activating complex, polypeptide 5	-1.3	-1.07
Slc3a1	solute carrier family 3 member 1	-1.32	-1.07
Grik4	glutamate ionotropic receptor kainate type subunit 4	-1	-1.08
Tusc2	tumor suppressor candidate 2	-0.98	-1.08
Gpr162	G protein-coupled receptor 162	-1.32	-1.08
Sema3f	semaphorin 3F	-0.67	-1.08
Tst	thiosulfate sulfurtransferase	-1.03	-1.08
Pim3	Pim-3 proto-oncogene, serine/threonine kinase	-0.84	-1.08
Pdgfd	platelet derived growth factor D	-1.11	-1.09
Six1	SIX homeobox 1	-0.7	-1.09
Nceh1	neutral cholesterol ester hydrolase 1	-1.03	-1.09
Rbm46	RNA binding motif protein 46	-1.07	-1.09
Acot1	acyl-CoA thioesterase 1	-1.17	-1.09
Olfm1	olfactomedin 1	-0.76	-1.09
Apbb1	amyloid beta precursor protein binding family B member 1	-0.86	-1.09
Etfα	electron transfer flavoprotein alpha subunit	-1.19	-1.1
Gpr137	G protein-coupled receptor 137	-0.77	-1.1
Dmgdh	dimethylglycine dehydrogenase	-2.32	-1.11
Macrod1	MACRO domain containing 1	-0.98	-1.11
Ndufs1	NADH:ubiquinone oxidoreductase core subunit S1	-1.16	-1.11
Rbm20	RNA binding motif protein 20	-0.61	-1.12
Scn4b	sodium voltage-gated channel beta subunit 4	-1.09	-1.12
B3gnt8	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8	-0.66	-1.12
LOC691215	hypothetical protein LOC691215	-1.46	-1.12
Ola1	Obg-like ATPase 1	-1.3	-1.12
Syp	synaptophysin	-0.96	-1.13
Armcx6	armadillo repeat containing, X-linked 6	-0.92	-1.13
Coq3	coenzyme Q3 methyltransferase	-1.05	-1.13
Dlgap1	DLG associated protein 1	-1.04	-1.13
Triqk	triple QxxK/R motif containing	-1.25	-1.13
Ubxn2a	UBX domain protein 2A	-1.11	-1.13
Napb	NSF attachment protein beta	-1	-1.13
Pak3	p21 (RAC1) activated kinase 3	-0.88	-1.13
Dtnb	dystrobrevin, beta	-0.78	-1.13
Dgkz	diacylglycerol kinase zeta	-1.31	-1.14
Lrp11	LDL receptor related protein 11	-0.96	-1.14
Ntsr2	neurotensin receptor 2	-1.34	-1.14
Gclm	glutamate cysteine ligase, modifier subunit	-1.13	-1.14
Bex2	brain expressed X-linked 2	-0.88	-1.14
Thy1	Thy-1 cell surface antigen	-0.88	-1.15

Epb41l3	erythrocyte membrane protein band 4.1-like 3	-0.93	-1.15
Slco5a1	solute carrier organic anion transporter family, member 5A1	-1.25	-1.15
Zdhhc15	zinc finger, DHHC-type containing 15	-1.3	-1.15
Kif9	kinesin family member 9	-1.08	-1.15
Slc25a25	solute carrier family 25 member 25	-1.11	-1.15
S100a13	S100 calcium binding protein A13	-1.54	-1.16
Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	-1.16	-1.16
Sbk1	SH3 domain binding kinase 1	-2.03	-1.16
Abhd1	abhydrolase domain containing 1	-1.03	-1.16
Slc16a4	solute carrier family 16, member 4	-1.59	-1.16
Usp31	ubiquitin specific peptidase 31	-1	-1.16
Gpr26	G protein-coupled receptor 26	-0.97	-1.16
Vstm5	V-set and transmembrane domain containing 5	-1.53	-1.16
Rims3	regulating synaptic membrane exocytosis 3	-0.77	-1.16
Bnip3	BCL2 interacting protein 3	-1.41	-1.16
Gipr	gastric inhibitory polypeptide receptor	-1.64	-1.16
Anxa5	annexin A5	-1.54	-1.16
Ralyl	RALY RNA binding protein-like	-0.95	-1.16
Tmem47	transmembrane protein 47	-1.27	-1.16
Pir	pirin	-1.07	-1.17
Bmpr1b	bone morphogenetic protein receptor type 1B	-0.89	-1.17
Rps6ka6	ribosomal protein S6 kinase A6	-0.95	-1.17
Crabp1	cellular retinoic acid binding protein 1	-1.3	-1.17
Cpvl	carboxypeptidase, vitellogenin-like	-1.36	-1.17
Slc6a17	solute carrier family 6 member 17	-0.84	-1.18
Scn1b	sodium voltage-gated channel beta subunit 1	-0.66	-1.18
Pex5l	peroxisomal biogenesis factor 5-like	-1.21	-1.18
Tmem246	transmembrane protein 246	-0.88	-1.18
Slc27a3	solute carrier family 27 member 3	-0.67	-1.18
Eif5a2	eukaryotic translation initiation factor 5A2	-1.52	-1.18
Mlf1	myeloid leukemia factor 1	-2.06	-1.19
Bend6	BEN domain containing 6	-1.17	-1.19
Syt1	synaptotagmin 1	-0.98	-1.19
Hapl2	hyaluronan and proteoglycan link protein 2	-1.04	-1.19
Fam189b	family with sequence similarity 189, member B	-0.73	-1.19
Lrfn2	leucine rich repeat and fibronectin type III domain containing 2	-1.01	-1.2
Med12l	mediator complex subunit 12-like	-0.93	-1.2
Got1	glutamic-oxaloacetic transaminase 1	-0.99	-1.2
Dnajc27	DnaJ heat shock protein family (Hsp40) member C27	-1.1	-1.2
Cldn20	claudin 20	-1.14	-1.2
Epha7	Eph receptor A7	-1.24	-1.2
Syt7	synaptotagmin 7	-1.27	-1.21
Pfkm	phosphofructokinase, muscle	-0.9	-1.21
Alkbh3	alkB homolog 3, alpha-ketoglutarate-dependent dioxygenase	-1.08	-1.21
Trpm8	transient receptor potential cation channel, subfamily M, member 8	-1.13	-1.21
Ptprk	protein tyrosine phosphatase, receptor type, K	-1.22	-1.22
Sptb	spectrin, beta, erythrocytic	-1.02	-1.22
Astn2	astrotactin 2	-1.09	-1.22
Gpr3	G protein-coupled receptor 3	-1.39	-1.22
Elavl4	ELAV like RNA binding protein 4	-1	-1.22
Crispld1	cysteine-rich secretory protein LCCL domain containing 1	-0.86	-1.22
Frzb	frizzled-related protein	-0.92	-1.23
Lrp3	LDL receptor related protein 3	-0.81	-1.23
Srsf12	serine and arginine rich splicing factor 12	-0.83	-1.23

Sfxn4	sideroflexin 4	-1.24	-1.23
Tm6sf1	transmembrane 6 superfamily member 1	-1.39	-1.23
Atcay	ATCAY, caytaxin	-0.93	-1.23
Dgkb	diacylglycerol kinase, beta	-1.04	-1.23
Ndufs5	NADH:ubiquinone oxidoreductase subunit S5	-0.93	-1.24
Slc24a3	solute carrier family 24 member 3	-0.84	-1.24
Il1rapl1	interleukin 1 receptor accessory protein-like 1	-0.91	-1.24
Map7	microtubule-associated protein 7	-1.25	-1.24
Ccdc32	coiled-coil domain containing 32	-1.26	-1.24
S100a9	S100 calcium binding protein A9	-1.47	-1.24
Lrrc4c	leucine rich repeat containing 4C	-1.04	-1.24
RGD1563714	RGD1563714	-1.57	-1.24
Nrarp	Notch-regulated ankyrin repeat protein	-1.47	-1.25
Grin3a	glutamate ionotropic receptor NMDA type subunit 3A	-1.4	-1.25
Mypop	Myb-related transcription factor, partner of profilin	-0.65	-1.25
St6gal2	ST6 beta-galactoside alpha-2,6-sialyltransferase 2	-2.26	-1.25
Acsbg1	acyl-CoA synthetase bubblegum family member 1	-0.89	-1.25
Nrsn2	neurensin 2	-1.7	-1.25
Slc4a11	solute carrier family 4 member 11	-1.49	-1.25
Samd12	sterile alpha motif domain containing 12	-1.1	-1.25
Fkbp4	FK506 binding protein 4	-1.2	-1.25
Lrrn3	leucine rich repeat neuronal 3	-1.03	-1.26
Ddx25	DEAD-box helicase 25	-1.3	-1.26
Pls1	plastin 1	-1.01	-1.26
Scn9a	sodium voltage-gated channel alpha subunit 9	-1.46	-1.26
Lurap1l	leucine rich adaptor protein 1-like	-1.15	-1.26
Diras1	DIRAS family GTPase 1	-0.67	-1.26
Nell2	neural EGFL like 2	-1.03	-1.27
Klhdc8b	kelch domain containing 8B	-1.03	-1.27
Rtn4rl2	reticulon 4 receptor-like 2	-1.17	-1.27
Mir331	microRNA 331	-0.93	-1.27
Lgi1	leucine-rich, glioma inactivated 1	-1.31	-1.27
Gls2	glutaminase 2	-1.34	-1.27
Galnt13	polypeptide N-acetylgalactosaminyltransferase 13	-1.07	-1.28
Tctex1d1	Tctex1 domain containing 1	-1.83	-1.28
Gucy1a2	guanylate cyclase 1 soluble subunit alpha 2	-0.85	-1.28
Cacna2d2	calcium voltage-gated channel auxiliary subunit alpha2delta 2	-1.06	-1.28
Gpr150	G protein-coupled receptor 150	-1.03	-1.28
Ebf4	early B-cell factor 4	-1.1	-1.29
P2ry1	purinergic receptor P2Y1	-0.57	-1.29
Zc2hc1a	zinc finger, C2HC-type containing 1A	-1.32	-1.31
Fam217b	family with sequence similarity 217, member B	-1.06	-1.31
Oxr1	oxidation resistance 1	-1.34	-1.31
Rlbp1	retinaldehyde binding protein 1	-1.61	-1.31
Plcd3	phosphatidylinositol-specific phospholipase C, X domain containing 3	-1.28	-1.31
Srgap3	SLIT-ROBO Rho GTPase activating protein 3	-1.15	-1.31
Cdkl1	cyclin dependent kinase like 1	-1.49	-1.31
Tmem30b	transmembrane protein 30B	-1.33	-1.31
Kcnk4	potassium two pore domain channel subfamily K member 4	-1.02	-1.32
Elov14	ELOVL fatty acid elongase 4	-1.19	-1.32
RGD1560028	similar to RIKEN cDNA C130060K24 gene	-0.65	-1.33
Syngr1	synaptogyrin 1	-0.86	-1.33
Slc26a7	solute carrier family 26 member 7	-1.23	-1.34
Cadm1	cell adhesion molecule 1	-1.37	-1.34
Chrna5	cholinergic receptor nicotinic alpha 5 subunit	-1.41	-1.34

Ica1	islet cell autoantigen 1	-1.21	-1.34
Scg5	secretogranin V	-1.49	-1.34
Spag1	sperm associated antigen 1	-1.24	-1.34
Myo3b	myosin IIIB	-1.43	-1.34
Lrrc9	leucine rich repeat containing 9	-1.23	-1.34
Clip4	CAP-GLY domain containing linker protein family, member 4	-1.54	-1.35
Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	-1.68	-1.35
Amer1	APC membrane recruitment protein 1	-0.97	-1.35
Rgs10	regulator of G-protein signaling 10	-2.07	-1.36
Aox4	aldehyde oxidase 4	-1.49	-1.36
Pcyt1b	phosphate cytidylyltransferase 1, choline, beta	-1.27	-1.36
Mlc1	megalencephalic leukoencephalopathy with subcortical cysts 1	-2.06	-1.37
Cdk5r2	cyclin-dependent kinase 5 regulatory subunit 2	-1.01	-1.37
Adhfe1	alcohol dehydrogenase, iron containing, 1	-0.91	-1.37
Nap1l3	nucleosome assembly protein 1-like 3	-1.3	-1.37
Gna14	G protein subunit alpha 14	-1.69	-1.37
Gdap1	ganglioside-induced differentiation-associated-protein 1	-1.39	-1.38
Nacc2	NACC family member 2	-0.99	-1.38
Gdpd2	glycerophosphodiester phosphodiesterase domain containing 2	-1.53	-1.38
Dock11	dedicator of cytokinesis 11	-1.34	-1.38
Vwa5b1	von Willebrand factor A domain containing 5B1	-1.66	-1.39
Rgn	regucalcin	-0.84	-1.39
Rcor2	REST corepressor 2	-1.25	-1.39
Kbtbd3	kelch repeat and BTB domain containing 3	-1.5	-1.39
Grm7	glutamate metabotropic receptor 7	-1.47	-1.39
Hcn2	hyperpolarization activated cyclic nucleotide gated potassium and sodium channel 2	-1.02	-1.39
Pth1r	parathyroid hormone 1 receptor	-1.54	-1.4
Rgs3	regulator of G-protein signaling 3	-1.25	-1.4
Hdac11	histone deacetylase 11	-1.28	-1.4
Impdh1	inosine monophosphate dehydrogenase 1	-1.2	-1.4
Lrrc24	leucine rich repeat containing 24	-1.24	-1.4
Snrpn	small nuclear ribonucleoprotein polypeptide N	-1.3	-1.41
Esr1	estrogen receptor 1	-1.25	-1.41
Perp	PERP, TP53 apoptosis effector	-1.88	-1.41
Bhmt2	betaine-homocysteine S-methyltransferase 2	-3.11	-1.41
Hnmt	histamine N-methyltransferase	-1.65	-1.41
Slc25a40	solute carrier family 25, member 40	-1.47	-1.41
Atp2b2	ATPase plasma membrane Ca2+ transporting 2	-1.05	-1.41
Hndl	4-hydroxyphenylpyruvate dioxygenase-like	-0.96	-1.41
Lrrc55	leucine rich repeat containing 55	-1.64	-1.41
Mest	mesoderm specific transcript	-1.23	-1.41
Timp4	TIMP metallopeptidase inhibitor 4	-1.51	-1.42
Ccdc148	coiled-coil domain containing 148	-1.63	-1.42
Slco4c1	solute carrier organic anion transporter family, member 4C1	-1.85	-1.42
Akr7a3	aldo-keto reductase family 7 member A3	-1.85	-1.42
Herc3	HECT and RLD domain containing E3 ubiquitin protein ligase 3	-1.43	-1.43
Ahsp	alpha hemoglobin stabilizing protein	-1.54	-1.43
Fam13a	family with sequence similarity 13, member A	-1.14	-1.44
Spdya	speedy/RINGO cell cycle regulator family member A	-1.83	-1.44
Angel1	angel homolog 1	-1.37	-1.44
Tcf15	transcription factor 15	-2.34	-1.44
Abcc8	ATP binding cassette subfamily C member 8	-0.94	-1.44
RGD1563349	similar to RIKEN cDNA 9330182L06	-1.29	-1.44
Lhfpl4	LHFPL tetraspan subfamily member 4	-1.44	-1.45

Ntrk1	neurotrophic receptor tyrosine kinase 1	-1.44	-1.45
Aqp11	aquaporin 11	-1.1	-1.45
Crhr2	corticotropin releasing hormone receptor 2	-1.57	-1.46
Mgmt	O-6-methylguanine-DNA methyltransferase	-1.26	-1.46
Kcnd1	potassium voltage-gated channel subfamily D member 1	-1.33	-1.46
Rcan2	regulator of calcineurin 2	-1.27	-1.48
Ubash3b	ubiquitin associated and SH3 domain containing, B	-1.28	-1.48
Rbp2	retinol binding protein 2	-1.93	-1.48
Rnf208	ring finger protein 208	-0.74	-1.49
Abcg8	ATP binding cassette subfamily G member 8	-2.94	-1.49
Mpped2	metallophosphoesterase domain containing 2	-1.58	-1.49
Magee1	MAGE family member E1	-0.82	-1.49
Ttc39b	tetratricopeptide repeat domain 39B	-1.64	-1.49
Ttc9b	tetratricopeptide repeat domain 9B	-0.97	-1.49
Sh2d1a	SH2 domain containing 1A	-1.3	-1.5
Ntsr1	neurotensin receptor 1	-2.02	-1.5
Ceacam16	carcinoembryonic antigen-related cell adhesion molecule 16	-1.47	-1.5
Fez1	fasciculation and elongation protein zeta 1	-1.42	-1.5
Fkbp1b	FK506 binding protein 1B	-1.05	-1.5
Ankrd13d	ankyrin repeat domain 13D	-1.47	-1.51
Bex1	brain expressed, X-linked 1	-1.82	-1.51
Pank1	pantothenate kinase 1	-1.57	-1.51
Olfm3	olfactomedin 3	-1.55	-1.52
Ppm1j	protein phosphatase, Mg2+/Mn2+ dependent, 1J	-1.87	-1.52
Asic1	acid sensing ion channel subunit 1	-1.36	-1.52
Dync1i1	dynein cytoplasmic 1 intermediate chain 1	-1.47	-1.53
Fxyd7	FXYD domain-containing ion transport regulator 7	-2.36	-1.53
Slc5a11	solute carrier family 5 member 11	-2.76	-1.53
Pla2g7	phospholipase A2 group VII	-1.44	-1.53
Crbn	cereblon	-1.68	-1.53
Tmem45b	transmembrane protein 45b	-2.16	-1.54
Clic3	chloride intracellular channel 3	-1.82	-1.54
Elov17	ELOVL fatty acid elongase 7	-1.66	-1.55
Asah2	N-acylsphingosine amidohydrolase 2	-1.76	-1.55
Grin1	glutamate ionotropic receptor NMDA type subunit 1	-1.33	-1.55
Chst15	carbohydrate sulfotransferase 15	-1.34	-1.55
B3galt1	Beta-1,3-galactosyltransferase 1	-1.48	-1.55
Pcsk2	proprotein convertase subtilisin/kexin type 2	-1.29	-1.56
Clcn4	chloride voltage-gated channel 4	-1.37	-1.56
Paqr5	progesterin and adipQ receptor family member 5	-1.21	-1.56
RGD1564053	similar to hypothetical protein	-1.32	-1.56
Rims1	regulating synaptic membrane exocytosis 1	-1.69	-1.56
S100a5	S100 calcium binding protein A5	-2.49	-1.57
Eepd1	endonuclease/exonuclease/phosphatase family domain containing 1	-1.3	-1.57
Trpc3	transient receptor potential cation channel, subfamily C, member 3	-1.17	-1.57
Itga11	integrin subunit alpha 11	-1.61	-1.57
Slc17a7	solute carrier family 17 member 7	-1.47	-1.57
Rgs17	regulator of G-protein signaling 17	-0.88	-1.57
Nrxn3	neurexin 3	-0.97	-1.58
Trhde	thyrotropin-releasing hormone degrading enzyme	-1.35	-1.58
Opcml	opioid binding protein/cell adhesion molecule-like	-1.08	-1.58
Tmem14a	transmembrane protein 14A	-1.97	-1.59
Ube2ql1	ubiquitin-conjugating enzyme E2Q family-like 1	-0.83	-1.6
Nhlh2	nescient helix loop helix 2	-1.43	-1.6
Pdzrn4	PDZ domain containing RING finger 4	-1.8	-1.6

Panx2	pannexin 2	-1.42	-1.61
Grm8	glutamate metabotropic receptor 8	-1.71	-1.61
Kcnj3	potassium voltage-gated channel subfamily J member 3	-1.61	-1.61
Tsc22d3	TSC22 domain family, member 3	-1.5	-1.62
Cdh10	cadherin 10	-1.69	-1.62
A4galt	alpha 1,4-galactosyltransferase	-1.36	-1.62
Ppcs	phosphopantethoylcysteine synthetase	-1.55	-1.62
Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	-1.11	-1.62
Kcnh2	potassium voltage-gated channel subfamily H member 2	-0.96	-1.63
Apba1	amyloid beta precursor protein binding family A member 1	-1.3	-1.63
Slc24a2	solute carrier family 24 member 2	-1.83	-1.63
Trim9	tripartite motif-containing 9	-1.26	-1.64
Tac1	tachykinin, precursor 1	-2.45	-1.64
Rarres1	retinoic acid receptor responder 1	-1.86	-1.64
Abcc2	ATP binding cassette subfamily C member 2	-1.77	-1.64
Ndst3	N-deacetylase and N-sulfotransferase 3	-2.04	-1.65
Slc25a33	solute carrier family 25 member 33	-1.57	-1.65
Kcnb1	potassium voltage-gated channel subfamily B member 1	-1.44	-1.65
Egln3	egl-9 family hypoxia-inducible factor 3	-1.24	-1.65
Zbtb8b	zinc finger and BTB domain containing 8b	-1.15	-1.66
Slc35g2	solute carrier family 35, member G2	-1.81	-1.66
Csdc2	cold shock domain containing C2	-0.85	-1.66
Fstl5	follistatin-like 5	-1.63	-1.66
Rab9b	RAB9B, member RAS oncogene family	-1.67	-1.67
Rragd	Ras-related GTP binding D	-1.61	-1.67
LOC501038	Ab2-060	-1.92	-1.67
Shox2	short stature homeobox 2	-0.93	-1.67
Kcnq5	potassium voltage-gated channel subfamily Q member 5	-1.93	-1.67
Ccdc126	coiled-coil domain containing 126	-1.89	-1.68
Gabbr2	gamma-aminobutyric acid type B receptor subunit 2	-1.18	-1.68
Nppa	natriuretic peptide A	-2.34	-1.68
Etv1	ets variant 1	-1.34	-1.68
Pygb	glycogen phosphorylase B	-1.51	-1.68
Gpr165	G protein-coupled receptor 165	-1.62	-1.68
Acot4	acyl-CoA thioesterase 4	-1.61	-1.69
Pnma1	PNMA family member 1	-0.81	-1.69
Mst1r	macrophage stimulating 1 receptor	-1.06	-1.69
Chrna4	cholinergic receptor nicotinic alpha 4 subunit	-1.74	-1.69
Zcchc12	zinc finger CCHC-type containing 12	-1.91	-1.7
Dusp5	dual specificity phosphatase 5	-2.06	-1.7
Paqr9	progestin and adiponectin receptor family member 9	-1.37	-1.7
LOC100125362	hypothetical protein LOC100125362	-1.58	-1.7
Cnr1	cannabinoid receptor 1	-1.61	-1.71
Penk	proenkephalin	-2.5	-1.71
Mab21l2	mab-21 like 2	-1.4	-1.71
Kcnab2	potassium voltage-gated channel subfamily A regulatory beta subunit 2	-1.83	-1.72
Extl2	exostosin-like glycosyltransferase 2	-1.78	-1.72
Tmie	transmembrane inner ear	-1.98	-1.73
LRRTM1	leucine rich repeat transmembrane neuronal 1	-1.3	-1.73
Gyg1	glycogenin 1	-1.87	-1.74
Glrb	glycine receptor, beta	-2.05	-1.74
Nell1	neural EGFL like 1	-1.55	-1.74
Ankrd55	ankyrin repeat domain 55	-1.49	-1.75
Trpc5	transient receptor potential cation channel, subfamily C, member 5	-1.51	-1.75

Bcan	brevican	-1.87	-1.75
Rbp7	retinol binding protein 7	-2.96	-1.75
Scrt2	scratch family transcriptional repressor 2	-1.2	-1.76
Ppp1r1c	protein phosphatase 1, regulatory (inhibitor) subunit 1C	-1.79	-1.76
Isl1	ISL LIM homeobox 1	-1.56	-1.77
Faim2	Fas apoptotic inhibitory molecule 2	-2.85	-1.77
Fgf13	fibroblast growth factor 13	-1.8	-1.77
Kcna2	potassium voltage-gated channel subfamily A member 2	-1.64	-1.77
Sorcs3	sortilin-related VPS10 domain containing receptor 3	-1.64	-1.78
Gal3st3	galactose-3-O-sulfotransferase 3	-2.59	-1.78
Hspb3	heat shock protein family B (small) member 3	-2.24	-1.78
Khk	ketohexokinase	-2.05	-1.78
Pik3c2g	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	-2.15	-1.78
Tmem72	transmembrane protein 72	-1.82	-1.78
Lrrc49	leucine rich repeat containing 49	-1.84	-1.8
Lin7a	lin-7 homolog A, crumbs cell polarity complex component	-1.97	-1.8
Myt1l	myelin transcription factor 1-like	-1.88	-1.81
Gstm6	glutathione S-transferase, mu 6	-1.92	-1.81
RGD1306941	similar to CG31122-PA	-2.01	-1.81
Rab3c	RAB3C, member RAS oncogene family	-1.58	-1.81
Six4	SIX homeobox 4	-1.72	-1.82
Igfbp2	insulin-like growth factor binding protein 2	-1.73	-1.82
Wnt7a	Wnt family member 7A	-2.32	-1.82
Lrfn5	leucine rich repeat and fibronectin type III domain containing 5	-1.53	-1.82
Cxxc4	CXXC finger protein 4	-1.71	-1.82
Sertm1	serine-rich and transmembrane domain containing 1	-1.77	-1.82
Slc9a9	solute carrier family 9 member A9	-1.67	-1.83
Fndc7	fibronectin type III domain containing 7	-1.5	-1.83
March11	membrane associated ring-CH-type finger 11	-1.92	-1.83
Lingo1	leucine rich repeat and Ig domain containing 1	-1.46	-1.84
Galnt14	polypeptide N-acetylgalactosaminyltransferase 14	-2.02	-1.84
Efhc2	EF-hand domain containing 2	-1.88	-1.84
Ust	uronyl-2-sulfotransferase	-1.12	-1.84
Synm	synemin	-1.55	-1.85
Sh3gl2	SH3 domain containing GRB2 like 2, endophilin A1	-1.78	-1.85
Pgf	placental growth factor	-1.57	-1.86
Chgb	chromogranin B	-1.76	-1.86
Dpysl4	dihydropyrimidinase-like 4	-2.03	-1.86
Magee2	MAGE family member E2	-1.69	-1.86
Fgf21	fibroblast growth factor 21	-2.56	-1.87
Tcerg1l	transcription elongation regulator 1-like	-2.3	-1.87
Scn8a	sodium voltage-gated channel alpha subunit 8	-2.15	-1.88
Igfbpl1	insulin-like growth factor binding protein-like 1	-2.9	-1.88
Chrna7	cholinergic receptor nicotinic alpha 7 subunit	-2.14	-1.88
Kcnc2	potassium voltage-gated channel subfamily C member 2	-2.1	-1.89
Stk31	serine threonine kinase 31	-1.83	-1.89
Arpp21	cAMP regulated phosphoprotein 21	-1.95	-1.9
Syndig1l	synapse differentiation inducing 1-like	-1.41	-1.91
Sgpp2	sphingosine-1-phosphate phosphatase 2	-1.76	-1.91
Tox2	TOX high mobility group box family member 2	-2.54	-1.91
Kcnf1	potassium voltage-gated channel modifier subfamily F member 1	-3.37	-1.91
Calca	calcitonin-related polypeptide alpha	-3.46	-1.92
Clrn1	clarin 1	-1.67	-1.92
Scrt1	scratch family transcriptional repressor 1	-1.36	-1.92

Fndc5	fibronectin type III domain containing 5	-1.72	-1.93
Ppp4r4	protein phosphatase 4, regulatory subunit 4	-2.32	-1.93
Mctp2	multiple C2 and transmembrane domain containing 2	-2.17	-1.93
Cnnm1	cyclin and CBS domain divalent metal cation transport mediator 1	-1.7	-1.93
Galnt18	polypeptide N-acetylgalactosaminyltransferase 18	-2.32	-1.93
Sphkap	SPHK1 interactor, AKAP domain containing	-2.16	-1.94
Agbl4	ATP/GTP binding protein-like 4	-1.79	-1.94
Lrrc73	leucine rich repeat containing 73	-1.41	-1.94
Necab3	N-terminal EF-hand calcium binding protein 3	-1.5	-1.94
Zdhhc22	zinc finger, DHHC-type containing 22	-1.67	-1.95
Aldh1b1	aldehyde dehydrogenase 1 family, member B1	-2.05	-1.96
St8sia1	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 1	-2.28	-1.97
R3hdml	R3H domain containing-like	-3.96	-1.97
Tyrp1	tyrosinase-related protein 1	-2.03	-1.99
LOC365985	similar to adenylate kinase 5 isoform 1	-1.77	-1.99
Fam81a	family with sequence similarity 81, member A	-2.31	-1.99
Car8	carbonic anhydrase 8	-1.73	-1.99
Syt12	synaptotagmin 12	-2.12	-2
Tmc2	transmembrane channel-like 2	-1.61	-2
Crb3	crumbs 3, cell polarity complex component	-5.02	-2
Tacr3	tachykinin receptor 3	-2.38	-2
Tuba8	tubulin, alpha 8	-2.41	-2.01
Mrgprx3	MAS related GPR family member X3	-1.72	-2.02
Ndst4	N-deacetylase and N-sulfotransferase 4	-1.8	-2.02
Trpc4	transient receptor potential cation channel, subfamily C, member 4	-2.56	-2.03
Ptgfr	prostaglandin F receptor	-1.95	-2.03
Scx	scleraxis bHLH transcription factor	-1.7	-2.03
Odf3b	outer dense fiber of sperm tails 3B	-3.53	-2.03
Tmem54	transmembrane protein 54	-2.13	-2.04
Atp1a1	ATPase Na+/K+ transporting subunit alpha 1	-2.08	-2.05
Rgs6	regulator of G-protein signaling 6	-1.86	-2.05
Ly6h	lymphocyte antigen 6 family member H	-3.47	-2.06
Lrguk	leucine-rich repeats and guanylate kinase domain containing	-1.8	-2.06
Mal2	mal, T-cell differentiation protein 2	-2.25	-2.06
Vamp1	vesicle-associated membrane protein 1	-3	-2.06
Smpx	small muscle protein, X-linked	-1.26	-2.07
Flrt1	fibronectin leucine rich transmembrane protein 1	-2.31	-2.08
Scn5a	sodium voltage-gated channel alpha subunit 5	-1.58	-2.08
Gpr45	G protein-coupled receptor 45	-2.61	-2.08
Fam57b	family with sequence similarity 57, member B	-2.06	-2.08
Amigo1	adhesion molecule with Ig like domain 1	-2.27	-2.08
Lingo4	leucine rich repeat and Ig domain containing 4	-3.11	-2.09
Ar	androgen receptor	-1.84	-2.09
Lrrn1	leucine rich repeat neuronal 1	-2.02	-2.09
Acpp	acid phosphatase, prostate	-2.34	-2.09
Kcnj5	potassium voltage-gated channel subfamily J member 5	-1.39	-2.11
Pvalb	parvalbumin	-4.94	-2.12
Slc8a2	solute carrier family 8 member A2	-1.74	-2.12
Krt75	keratin 75	-3.06	-2.13
Gria2	glutamate ionotropic receptor AMPA type subunit 2	-2.45	-2.13
Abcd2	ATP binding cassette subfamily D member 2	-2.26	-2.14
Tmc3	transmembrane channel-like 3	-2.43	-2.15
Hrh3	histamine receptor H3	-2.06	-2.15
Mgat4c	MGAT4 family, member C	-2.27	-2.15
Sstr1	somatostatin receptor 1	-2.41	-2.15

Arhgap8	Rho GTPase activating protein 8	-2.89	-2.15
Kcng3	potassium voltage-gated channel modifier subfamily G member 3	-3.41	-2.15
Ntng1	netrin G1	-2.23	-2.16
Pate2	prostate and testis expressed 2	-2.14	-2.17
Asb18	ankyrin repeat and SOCS box-containing 18	-3.62	-2.17
Syt3	synaptotagmin 3	-2.1	-2.18
Smim17	small integral membrane protein 17	-2.32	-2.18
Cpne4	copine 4	-2.19	-2.18
Si	sucrase-isomaltase	-1.97	-2.19
Gpr149	G protein-coupled receptor 149	-2.75	-2.19
Plekhd1	pleckstrin homology and coiled-coil domain containing D1	-1.98	-2.19
Ngb	neuroglobin	-1.67	-2.19
Msx3	msh homeobox 3	-3.28	-2.2
Hebp2	heme binding protein 2	-2.35	-2.2
Clca5	chloride channel calcium activated 5	-1.4	-2.2
C1qtnf4	C1q and TNF related 4	-1.94	-2.2
Atp2b3	ATPase plasma membrane Ca2+ transporting 3	-2.45	-2.2
Oprd1	opioid receptor, delta 1	-2.24	-2.2
Dpp6	dipeptidyl peptidase like 6	-2.53	-2.2
Hal	histidine ammonia lyase	-2.04	-2.21
Slc12a1	solute carrier family 12 member 1	-1.92	-2.21
Tmem25	transmembrane protein 25	-2.45	-2.21
Pianp	PILR alpha associated neural protein	-1.82	-2.21
Dlgap3	DLG associated protein 3	-1.87	-2.22
Unc13c	unc-13 homolog C	-3.48	-2.22
Gpihbp1	glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	-2.24	-2.23
Hhatl	hedgehog acyltransferase-like	-2.16	-2.23
Chga	chromogranin A	-2.25	-2.23
Grip2	glutamate receptor interacting protein 2	-1.67	-2.23
Mpped1	metallophosphoesterase domain containing 1	-2.6	-2.24
Htr7	5-hydroxytryptamine (serotonin) receptor 7, adenylate cyclase-coupled	-2.18	-2.24
Onecut1	one cut homeobox 1	-2.28	-2.24
Entpd3	ectonucleoside triphosphate diphosphohydrolase 3	-2.69	-2.24
Htr5a	5-hydroxytryptamine receptor 5A	-3.18	-2.25
Avil	advillin	-2.04	-2.25
Tspan8	tetraspanin 8	-2.55	-2.25
Myl3	myosin light chain 3	-1.74	-2.25
Kcna4	potassium voltage-gated channel subfamily A member 4	-3.35	-2.25
F2rl2	coagulation factor II (thrombin) receptor-like 2	-2.94	-2.26
Cyp2a3	cytochrome P450, family 2, subfamily a, polypeptide 3	-2.09	-2.26
Hs6st2	heparan sulfate 6-O-sulfotransferase 2	-3.07	-2.26
Rxfp1	relaxin/insulin-like family peptide receptor 1	-2.59	-2.28
Vstm2b	V-set and transmembrane domain containing 2B	-1.74	-2.28
Hes5	hes family bHLH transcription factor 5	-3.43	-2.29
Kirrel3	kirre like nephrin family adhesion molecule 3	-2.98	-2.29
Scn1a	sodium voltage-gated channel alpha subunit 1	-2.69	-2.31
Clec2l	C-type lectin domain family 2, member L	-3.52	-2.32
Kcnmb2	potassium calcium-activated channel subfamily M regulatory beta subunit 2	-2.22	-2.32
Frmpd4	FERM and PDZ domain containing 4	-2.88	-2.34
Tnni3k	TNNI3 interacting kinase	-3.69	-2.34
Hpca	hippocalcin	-3.1	-2.35
Scn10a	sodium voltage-gated channel alpha subunit 10	-3.28	-2.35

Cacng2	calcium voltage-gated channel auxiliary subunit gamma 2	-2.37	-2.36
Isl2	ISL LIM homeobox 2	-2.43	-2.38
Abra	actin-binding Rho activating protein	-3.44	-2.39
Lamp5	lysosomal-associated membrane protein family, member 5	-2.52	-2.39
Kcnd3	potassium voltage-gated channel subfamily D member 3	-3.02	-2.39
Slc25a18	solute carrier family 25 member 18	-2.73	-2.4
Dmrt1	DMRT-like family A1	-5.37	-2.4
Cntn3	contactin 3	-3.9	-2.4
Ppef1	protein phosphatase with EF-hand domain 1	-3.31	-2.41
Rprm	reproto, TP53 dependent G2 arrest mediator homolog	-2.17	-2.41
Galnt5	polypeptide N-acetylgalactosaminyltransferase 5	-2.99	-2.42
Oprm1	opioid receptor, mu 1	-2.93	-2.43
Slitrk3	SLIT and NTRK-like family, member 3	-2.6	-2.43
S100g	S100 calcium binding protein G	-3.9	-2.43
Cdh9	cadherin 9	-3.88	-2.43
Syt9	synaptotagmin 9	-2.59	-2.44
Ass1	argininosuccinate synthase 1	-2.97	-2.45
Calcb	calcitonin-related polypeptide, beta	-2.8	-2.45
Syt6	synaptotagmin 6	-2.57	-2.48
Ctxn2	cortexin 2	-3.07	-2.48
Vsnl1	visinin-like 1	-4.07	-2.48
Nap1l5	nucleosome assembly protein 1-like 5	-2.41	-2.48
Kcnab1	potassium voltage-gated channel subfamily A member regulatory beta subunit 1	-2.74	-2.49
Slc16a12	solute carrier family 16, member 12	-3.07	-2.49
Caly	calcyon neuron-specific vesicular protein	-3.15	-2.49
Prmt8	protein arginine methyltransferase 8	-2.99	-2.5
Kcnc3	potassium voltage-gated channel subfamily C member 3	-2.56	-2.53
Vwc2l	von Willebrand factor C domain-containing protein 2-like	-3.02	-2.53
Tcte1	t-complex-associated testis expressed 1	-3.92	-2.53
Scg2	secretogranin II	-3.76	-2.54
Calml4	calmodulin-like 4	-4.91	-2.55
RGD1307461	similar to RIKEN cDNA 6430571L13 gene; similar to g20 protein	-2.63	-2.55
Tmem151b	transmembrane protein 151B	-3.65	-2.57
Akr1b7	aldo-keto reductase family 1, member B7	-3.11	-2.58
Mum1l1	MUM1 like 1	-2.75	-2.59
Htr2c	5-hydroxytryptamine receptor 2C	-3.44	-2.59
Necab1	N-terminal EF-hand calcium binding protein 1	-3.63	-2.6
Npas4	neuronal PAS domain protein 4	-2.64	-2.6
Rpe65	RPE65, retinoid isomerohydrolase	-3.31	-2.62
Fabp3	fatty acid binding protein 3	-2.72	-2.63
Kcnk9	potassium two pore domain channel subfamily K member 9	-4.14	-2.66
Syt10	synaptotagmin 10	-3.4	-2.66
Car12	carbonic anhydrase 12	-6.78	-2.66
B3gat2	beta-1,3-glucuronyltransferase 2	-3.94	-2.67
Kcns3	potassium voltage-gated channel, modifier subfamily S, member 3	-3.69	-2.67
Kcnc1	potassium voltage-gated channel subfamily C member 1	-3.17	-2.68
Il31ra	interleukin 31 receptor A	-2.56	-2.7
Cbln4	cerebellin 4 precursor	-5.81	-2.71
Camkv	CaM kinase-like vesicle-associated	-4.66	-2.71
Cntn4	contactin 4	-3.84	-2.71
Kcnip3	potassium voltage-gated channel interacting protein 3	-2.91	-2.73
Kcnk18	potassium two pore domain channel subfamily K member 18	-3.64	-2.73
Grm3	glutamate metabotropic receptor 3	-3.85	-2.74
Plcd4	phospholipase C, delta 4	-4.19	-2.74

Capsl	calcypbosine-like	-2.83	-2.74
Cntn6	contactin 6	-4.01	-2.75
Pcsk9	proprotein convertase subtilisin/kexin type 9	-2.31	-2.75
Crh	corticotropin releasing hormone	-2.55	-2.75
Lix1	limb and CNS expressed 1	-4.5	-2.76
Scn11a	sodium voltage-gated channel alpha subunit 11	-4.41	-2.77
Smad9	SMAD family member 9	-3.98	-2.78
Slc16a14	solute carrier family 16, member 14	-2.2	-2.78
Itgb6	integrin beta 6	-4.6	-2.78
Lin7b	lin-7 homolog B, crumbs cell polarity complex component	-4.12	-2.8
Ankrd34c	ankyrin repeat domain 34C	-3.23	-2.81
Astl	astacin like metalloendopeptidase	-4.34	-2.82
Esrrb	estrogen-related receptor beta	-3.16	-2.82
C1ql4	complement C1q like 4	-5.66	-2.83
Slc30a2	solute carrier family 30 member 2	-3.47	-2.83
Th	tyrosine hydroxylase	-1.79	-2.85
Mep1a	meprin A subunit alpha	-3.79	-2.88
Kcnj4	potassium voltage-gated channel subfamily J member 4	-2.88	-2.88
Kcnh7	potassium voltage-gated channel subfamily H member 7	-3.99	-2.9
Ankrd34a	ankyrin repeat domain 34A	-2.28	-2.9
Igfsf21	immunoglobulin superfamily, member 21	-5.69	-2.9
Lancl3	LanC like 3	-2.1	-2.91
Prlr	prolactin receptor	-4.42	-2.93
Sptlc3	serine palmitoyltransferase, long chain base subunit 3	-3.98	-2.94
Hcrtr2	hypocretin receptor 2	-5.11	-2.96
Mrgprd	MAS related GPR family member D	-6.76	-2.98
Srd5a2	steroid 5 alpha-reductase 2	-3.88	-2.99
Tdo2	tryptophan 2,3-dioxygenase	-3.94	-2.99
Gjd2	gap junction protein, delta 2	-2.58	-3.02
Nmb	neuromedin B	-4.36	-3.06
Glb1l2	galactosidase, beta 1-like 2	-4.39	-3.07
Htr1d	5-hydroxytryptamine receptor 1D	-3.52	-3.11
Chrna3	cholinergic receptor nicotinic alpha 3 subunit	-6.51	-3.12
Slc46a2	solute carrier family 46, member 2	-6.21	-3.12
Ky	kyphoscoliosis peptidase	-2.03	-3.15
Bpifb2	BPI fold containing family B, member 2	-3.73	-3.18
Cpn1	carboxypeptidase N subunit 1	-5.79	-3.19
Slc17a8	solute carrier family 17 member 8	-4.55	-3.22
Htr3a	5-hydroxytryptamine receptor 3A	-6.23	-3.26
Sptssb	serine palmitoyltransferase, small subunit B	-4.52	-3.32
Krt81	keratin 81	-2.44	-3.33
Doc2a	double C2 domain alpha	-5.83	-3.33
Plscr5	phospholipid scramblase family, member 5	-4.85	-3.38
Gja10	gap junction protein, alpha 10	-3.1	-3.4
Htr1a	5-hydroxytryptamine receptor 1A	-6.19	-3.41
Slc30a8	solute carrier family 30 member 8	-4.75	-3.52
Hapln1	hyaluronan and proteoglycan link protein 1	-6.92	-3.6
Cst12	cystatin 12	-5.48	-3.63
Clrn3	clarin 3	-3.01	-3.7
Cyp11b2	cytochrome P450, family 11, subfamily b, polypeptide 2	-3.83	-3.71
Edn2	endothelin 2	-4.99	-3.81
Gnmt	glycine N-methyltransferase	-3.47	-4.01
Iapp	islet amyloid polypeptide	-7.87	-4.03
Il1rapl2	interleukin 1 receptor accessory protein-like 2	-6.19	-4.89
Ern2	endoplasmic reticulum to nucleus signaling 2	-4.58	-5.55

**Table S4. Core rodent genes, which are differentially expressed in 2 rat and 2 mouse DRG datasets on nerve injury pain.** Log2 fold changes in expression compared to control are shown for mouse (Baskozos, B; Cobos, C) and for rat (Perkins, P; Baskozos, Br). The names of the known pain genes (Table S6) are marked in bold. The gene names of NP, PEP, LM sensory neurons (based on the classification from [17]) are marked by blue, magenta and green colours, respectively. Genes expressed in both PEP and NP are coloured by purple; in both NP and LM - by brown. Genes expressed in all 3 types of sensory neurons are marked by red. Gene expressed in Hu dataset of pooled sensory neurons are marked by light blue.

gene name	description	log2fc_B	log2fc_C	log2fc_P	log2fc_Br
Lipn	lipase, family member N	4.72	4.47	5.2	5.8
Cckbr	cholecystokinin B receptor; GPCR protein signalling; positive regulation of synaptic transmission	3.67	4.45	3.92	3.16
<b>Sprr1a</b>	small proline-rich protein 1A; neuronal regeneration [20]	4.88	6.75	11.03	2.91
Ecel1	endothelin converting enzyme-like 1	3.66	4.54	4.79	2.9
<b>Gal</b>	Galanin; hormone of nervous systems activating GPCRs; produced in pituitary gland; mechanical and thermal nociception [24]; axon regeneration [16]	4.13	4.63	5.57	2.68
Wdr63	WD repeat domain 63	2.98	5.25	2.85	2.52
Tecta	tectorin alpha	0.65	1.49	2.86	2.28
Sdc1	syndecan 1	1.05	2.14	3.12	2.24
<b>Sox11</b>	SRY (sex determining region Y)-box 11; transcription factor involved in neuronal regeneration [20]	1.52	3.01	3.06	2.19
Fst	follistatin	1.91	3.76	1.97	2.01
<b>Gadd45a</b>	growth arrest and DNA-damage-inducible 45 alpha; anti-apoptosis [26]	1.07	2.35	2.77	1.92
<b>Cacna2d1</b>	calcium channel, voltage-dependent, alpha2/delta subunit 1; target of the neuropathic pain drug, gabapentin (Bauer 09)	0.69	1.23	2.33	1.92
Acvr1c	activin A receptor, type IC; differentiation, apoptosis	1.39	3.28	1.65	1.9
Lama5	laminin, alpha 5; remodelling	0.65	0.9	1.72	1.83
Met	met proto-oncogene	0.82	0.61	2.41	1.79
<b>Cyp4b1</b>	cytochrome P450, family 4, subfamily b, polypeptide 1	1	1.92	2.97	1.78
<b>Ccr5</b>	chemokine (C-C motif) receptor 5	0.84	1.89	1.93	1.78
Runx2	runt related transcription factor 2	1.03	0.69	2.57	1.77
<b>Mmp16</b>	matrix metallopeptidase 16; remodelling	1.25	2.34	2.25	1.77
<b>FlnC</b>	filamin C, gamma	1.02	2.16	2.98	1.74
<b>Adcyap1</b>	adenylate cyclase activating polypeptide 1; pituitary adenylate cyclase-activating polypeptide (PACAP); axon regeneration [1]	0.71	1.03	2.34	1.73
<b>Jun</b>	jun proto-oncogene; axon regeneration [6; 39]	0.55	1.18	1.92	1.73
Trem2	triggering receptor expressed on myeloid cells 2;	0.82	4.41	4.4	1.7

	involved in chronic inflammation [37]				
Csf1	colony stimulating factor 1 (macrophage)	0.85	2.3	2.63	1.69
Cx3cr1	chemokine (C-X3-C motif) receptor 1	0.95	1.77	3.02	1.68
Csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	0.64	0.72	2.74	1.67
Tnik	TRAF2 and NCK interacting kinase	0.98	1.26	2.48	1.65
Hao1	hydroxyacid oxidase 1, liver	2.17	3.87	3.54	1.62
Csrnp1	cysteine-serine-rich nuclear protein 1	0.63	1.33	2.17	1.62
Ahr	aryl-hydrocarbon receptor	0.52	0.5	1.65	1.58
Ephb2	Eph receptor B2	0.5	0.98	1.83	1.4
B3gat1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	-0.83	-1.1	0.81	1.4
Slc15a3	solute carrier family 15, member 3	1.68	1.36	1.85	1.39
Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	1.16	1.11	1.33	1.38
Abca1	ATP-binding cassette, sub-family A (ABC1), member 1; cholesterol transport	0.72	1.41	2.25	1.27
Akr1b8	aldo-keto reductase family 1, member B8	1.15	1.36	2.34	1.21
Emp1	epithelial membrane protein 1	0.61	0.85	2.33	1.17
Rhoq	ras homolog family member Q; remodelling	0.64	1.41	1.78	1.14
Tnfrsf1b	tumor necrosis factor receptor superfamily, member 1b; involved in neuro-inflammation [15; 47]	0.57	1.61	1.61	1.14
Tgif1	TGFB-induced factor homeobox 1	0.63	1.2	1.51	1.13
Xdh	xanthine dehydrogenase	1.08	1.78	1.7	1.08
Ltbp1	latent transforming growth factor beta binding protein 1	0.57	1.37	1.89	1.05
Il13ra1	interleukin 13 receptor, alpha 1	0.74	1.39	1.3	1.03
Fam111a	family with sequence similarity 111, member A	0.62	1.05	1.61	1
Rab31	RAB31, member RAS oncogene family; vesiculation	0.52	0.79	1.19	0.97
S100a11	S100 calcium binding protein A11, differentiation	0.86	2.04	1.36	0.92
Il17ra	interleukin 17 receptor A	0.72	1.54	0.98	0.79
Anxa1	annexin A1; anti-apoptotic, neuroinflammation [33]	1.06	2.24	1.46	0.77
Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	-0.79	-0.73	0.68	0.76
Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	0.83	1.51	1.31	0.75
Col5a3	collagen, type V, alpha 3	0.78	1.04	0.52	0.66

<b>Acvr1</b>	activin A receptor, type 1	0.75	0.6	0.93	0.65
<b>Pros1</b>	protein S (alpha)	0.61	0.7	1.08	0.56
<b>Itga7</b>	integrin alpha 7, promote neurite outgrowth [56]	0.56	1.54	0.82	0.56
<b>Htr3a</b>	5-hydroxytryptamine (serotonin) receptor 3A; chronic inflammatory pain [53]	-0.64	-1.17	-3.26	-6.23
<b>Igfsf21</b>	immunoglobulin superfamily, member 21	-0.72	-1.33	-2.9	-5.69
<b>Glb1l2</b>	galactosidase, beta 1-like 2	-0.88	-0.7	-3.07	-4.39
<b>Vsnl1</b>	visinin-like 1	-0.59	-0.58	-2.48	-4.07
<b>Cntn6</b>	contactin 6	-0.61	-0.62	-2.75	-4.01
<b>Kcnh7</b>	potassium voltage-gated channel, subfamily H (eag-related), member 7	-0.73	-0.89	-2.9	-3.99
<b>Cntn4</b>	contactin 4; neurite outgrowth	-0.73	-1.05	-2.71	-3.84
<b>Ankrd34c</b>	ankyrin repeat domain 34C	-0.72	-0.77	-2.81	-3.23
<b>Vwc2l</b>	von Willebrand factor C domain-containing protein 2-like; neurogenesis	-0.62	-1.07	-2.53	-3.02
<b>Vamp1</b>	vesicle-associated membrane protein 1	-0.62	-0.7	-2.06	-3
<b>Frmpd4</b>	FERM and PDZ domain containing 4; stimulates dendritic morphogenesis; required for synaptic transmission	-0.68	-0.6	-2.34	-2.88
<b>Scn1a</b>	sodium channel, voltage-gated, type I, alpha	-0.59	-0.77	-2.31	-2.69
<b>Kcnc3</b>	potassium voltage gated channel, Shaw-related subfamily, member 3	-0.71	-0.96	-2.53	-2.56
<b>Gria2</b>	glutamate receptor, ionotropic, AMPA2 (alpha 2)	-0.54	-0.67	-2.13	-2.45
<b>Fam81a</b>	family with sequence similarity 81, member A	-0.55	-0.99	-1.99	-2.31
<b>Onecut1</b>	one cut domain, family member 1; transcriptional activator	-0.77	-0.8	-2.24	-2.28
<b>Abcd2</b>	ATP-binding cassette, sub-family D (ALD), member 2	-0.59	-0.71	-2.14	-2.26
<b>Oprd1</b>	opioid receptor, delta 1	-0.72	-1.23	-2.2	-2.24
<b>Sphkap</b>	SPHK1 interactor, AKAP domain containing	-0.54	-0.55	-1.94	-2.16
<b>Lancl3</b>	LanC lantibiotic synthetase component C-like 3 (bacterial)	-0.85	-0.86	-2.91	-2.1
<b>Rgs6</b>	regulator of G-protein signaling 6	-0.78	-0.86	-2.05	-1.86
<b>Ndst4</b>	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4	-0.77	-0.63	-2.02	-1.8
<b>Sertm1</b>	serine rich and transmembrane domain containing 1	0.86	1.4	-1.82	-1.77
<b>Vstm2b</b>	V-set and transmembrane domain containing 2B	-1.37	-1.28	-2.28	-1.74
<b>Fndc5</b>	fibronectin type III domain containing 5	-0.54	-0.79	-1.93	-1.72

Cnnm1	cyclin M1	-0.56	-0.63	-1.93	-1.7
<b>Kcnj3</b>	potassium inwardly-rectifying channel, subfamily J, member 3	-0.54	-0.82	-1.61	-1.61
Scrt1	scrach family zinc finger 1; neural differentiation	-0.51	-0.77	-1.92	-1.36
<b>Asic1</b>	acid-sensing (proton-gated) ion channel 1	-0.61	-0.71	-1.52	-1.36
<b>Etv1</b>	ets variant 1	-0.58	-0.61	-1.68	-1.34
Slco5a1	solute carrier organic anion transporter family, member 5A1	-0.75	-0.59	-1.15	-1.25
Opcml	opioid binding protein/cell adhesion molecule-like	-0.54	-0.58	-1.58	-1.08
Pls1	plastin 1 (I-isoform)	-0.64	-0.59	-1.26	-1.01
Tmem229b	transmembrane protein 229B	-0.62	-0.56	-1.07	-0.97
<b>Oprl1</b>	opioid receptor-like 1; nociception	-0.56	-1.08	-1.07	-0.88

**Table S5. Common DEGs between at least one mouse and one rat DRG dataset.** The DEGs, which are common between mouse (B or C) and rat (Br, P) datasets are shown, together with log 2 fold changes compared to control, non-injured DRG (mouse: log2fc\_B for Baskozos, log2fc\_C for Cobos); rat: log2fc\_P, for Perkins, log2fc\_Br for Baskozos). Genes, which are anti-correlated between mouse and rat models are shown at the bottom of the Table as indicated by thick borders.

SYMBOL	description	log2fc_B	log2fc_C	log2fc_P	log2fc_Br
Lipn	lipase, family member N	4.72	4.47	5.2	5.8
Cckbr	cholecystokinin B receptor	3.67	4.45	3.92	3.16
Sprr1a	small proline-rich protein 1A	4.88	6.75	11.03	2.91
Ecel1	endothelin converting enzyme-like 1	3.66	4.54	4.79	2.9
Gal	galanin	4.13	4.63	5.57	2.68
Wdr63	WD repeat domain 63	2.98	5.25	2.85	2.52
Tecta	tectorin alpha	0.65	1.49	2.86	2.28
Sdc1	syndecan 1	1.05	2.14	3.12	2.24
Sox11	SRY (sex determining region Y)-box 11	1.52	3.01	3.06	2.19
Fst	follistatin	1.91	3.76	1.97	2.01
Gadd45a	growth arrest and DNA-damage-inducible 45 alpha	1.07	2.35	2.77	1.92
Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	0.69	1.23	2.33	1.92
Acvr1c	activin A receptor, type IC	1.39	3.28	1.65	1.9
Lama5	laminin, alpha 5	0.65	0.9	1.72	1.83
Met	met proto-oncogene	0.82	0.61	2.41	1.79

Cyp4b1	cytochrome P450, family 4, subfamily b, polypeptide 1	1	1.92	2.97	1.78
Ccr5	chemokine (C-C motif) receptor 5	0.84	1.89	1.93	1.78
Mmp16	matrix metallopeptidase 16	1.25	2.34	2.25	1.77
Runx2	runt related transcription factor 2	1.03	0.69	2.57	1.77
FlnC	filamin C, gamma	1.02	2.16	2.98	1.74
Jun	jun proto-oncogene	0.55	1.18	1.92	1.73
Adcyap1	adenylate cyclase activating polypeptide 1	0.71	1.03	2.34	1.73
Trem2	triggering receptor expressed on myeloid cells 2	0.82	4.41	4.4	1.7
Csf1	colony stimulating factor 1 (macrophage)	0.85	2.3	2.63	1.69
Cx3cr1	chemokine (C-X3-C motif) receptor 1	0.95	1.77	3.02	1.68
Csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	0.64	0.72	2.74	1.67
Tnik	TRAF2 and NCK interacting kinase	0.98	1.26	2.48	1.65
Hao1	hydroxyacid oxidase 1, liver	2.17	3.87	3.54	1.62
Csrnp1	cysteine-serine-rich nuclear protein 1	0.63	1.33	2.17	1.62
Ahr	aryl-hydrocarbon receptor	0.52	0.5	1.65	1.58
Ephb2	Eph receptor B2	0.5	0.98	1.83	1.4
Slc15a3	solute carrier family 15, member 3	1.68	1.36	1.85	1.39
Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	1.16	1.11	1.33	1.38
Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	0.72	1.41	2.25	1.27
Akr1b8	aldo-keto reductase family 1, member B8	1.15	1.36	2.34	1.21
Emp1	epithelial membrane protein 1	0.61	0.85	2.33	1.17
Tnfrsf1b	tumor necrosis factor receptor superfamily, member 1b	0.57	1.61	1.61	1.14
Rhoq	ras homolog family member Q	0.64	1.41	1.78	1.14
Tgif1	TGFB-induced factor homeobox 1	0.63	1.2	1.51	1.13
Xdh	xanthine dehydrogenase	1.08	1.78	1.7	1.08
Ltbp1	latent transforming growth factor beta binding protein 1	0.57	1.37	1.89	1.05

Il13ra1	interleukin 13 receptor, alpha 1	0.74	1.39	1.3	1.03
Fam111a	family with sequence similarity 111, member A	0.62	1.05	1.61	1
Rab31	RAB31, member RAS oncogene family	0.52	0.79	1.19	0.97
S100a11	S100 calcium binding protein A11	0.86	2.04	1.36	0.92
Il17ra	interleukin 17 receptor A	0.72	1.54	0.98	0.79
Anxa1	annexin A1	1.06	2.24	1.46	0.77
Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	0.83	1.51	1.31	0.75
Col5a3	collagen, type V, alpha 3	0.78	1.04	0.52	0.66
Acvr1	activin A receptor, type 1	0.75	0.6	0.93	0.65
Itga7	integrin alpha 7	0.56	1.54	0.82	0.56
Pros1	protein S (alpha)	0.61	0.7	1.08	0.56
Opnl1	opioid receptor-like 1	-0.56	-1.08	-1.07	-0.88
Tmem229b	transmembrane protein 229B	-0.62	-0.56	-1.07	-0.97
Pls1	plastin 1 (I-isoform)	-0.64	-0.59	-1.26	-1.01
Opcml	opioid binding protein/cell adhesion molecule-like	-0.54	-0.58	-1.58	-1.08
Slco5a1	solute carrier organic anion transporter family, member 5A1	-0.75	-0.59	-1.15	-1.25
Etv1	ets variant 1	-0.58	-0.61	-1.68	-1.34
Asic1	acid-sensing (proton-gated) ion channel 1	-0.61	-0.71	-1.52	-1.36
Scrt1	scratch family zinc finger 1	-0.51	-0.77	-1.92	-1.36
Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	-0.54	-0.82	-1.61	-1.61
Cnnm1	cyclin M1	-0.56	-0.63	-1.93	-1.7
Fndc5	fibronectin type III domain containing 5	-0.54	-0.79	-1.93	-1.72
Vstm2b	V-set and transmembrane domain containing 2B	-1.37	-1.28	-2.28	-1.74
Ndst4	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4	-0.77	-0.63	-2.02	-1.8
Rgs6	regulator of G-protein signaling 6	-0.78	-0.86	-2.05	-1.86
Lancl3	LanC lantibiotic synthetase component C-like 3 (bacterial)	-0.85	-0.86	-2.91	-2.1
Sphkap	SPHK1 interactor, AKAP domain containing	-0.54	-0.55	-1.94	-2.16

Oprd1	opioid receptor, delta 1	-0.72	-1.23	-2.2	-2.24
Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	-0.59	-0.71	-2.14	-2.26
Onecut1	one cut domain, family member 1	-0.77	-0.8	-2.24	-2.28
Fam81a	family with sequence similarity 81, member A	-0.55	-0.99	-1.99	-2.31
Gria2	glutamate receptor, ionotropic, AMPA2 (alpha 2)	-0.54	-0.67	-2.13	-2.45
Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	-0.71	-0.96	-2.53	-2.56
Scn1a	sodium channel, voltage-gated, type I, alpha	-0.59	-0.77	-2.31	-2.69
Frmpd4	FERM and PDZ domain containing 4	-0.68	-0.6	-2.34	-2.88
Vamp1	vesicle-associated membrane protein 1	-0.62	-0.7	-2.06	-3
Vwc2l	von Willebrand factor C domain-containing protein 2-like	-0.62	-1.07	-2.53	-3.02
Ankrd34c	ankyrin repeat domain 34C	-0.72	-0.77	-2.81	-3.23
Cntn4	contactin 4	-0.73	-1.05	-2.71	-3.84
Kcnh7	potassium voltage-gated channel, subfamily H (eag-related), member 7	-0.73	-0.89	-2.9	-3.99
Cntn6	contactin 6	-0.61	-0.62	-2.75	-4.01
Vsnl1	visinin-like 1	-0.59	-0.58	-2.48	-4.07
Glb1l2	galactosidase, beta 1-like 2	-0.88	-0.7	-3.07	-4.39
Igfsf21	immunoglobulin superfamily, member 21	-0.72	-1.33	-2.9	-5.69
Htr3a	5-hydroxytryptamine (serotonin) receptor 3A	-0.64	-1.17	-3.26	-6.23
Kcnh5	potassium voltage-gated channel, subfamily H (eag-related), member 5	-0.53	-0.94	-	-1.1
Chrm2	cholinergic receptor, muscarinic 2, cardiac	-0.5	-0.92	-	-1.23
Npy	neuropeptide Y	4.67	5.84	3.68	-
Lamb3	laminin, beta 3	1.53	4.72	1.93	-
Atf3	activating transcription factor 3	3.18	4.36	5.06	-
Stmn4	stathmin-like 4	1.7	2.88	2.59	-
Lmo7	LIM domain only 7	0.96	2.85	1.2	-
Tnni1	troponin I, skeletal, slow 1	0.93	2.78	2.11	-

Sectm1b	secreted and transmembrane 1B	1.11	2.62	3.45	-
Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1	0.84	2.57	1.35	-
Loxl2	lysyl oxidase-like 2	1.59	2.35	1.56	-
Smim3	small integral membrane protein 3	1.36	2.22	0.68	-
Lgals3	lectin, galactose binding, soluble 3	0.86	2	1.27	-
Nfil3	nuclear factor, interleukin 3, regulated	0.73	1.84	2.4	-
Krt19	keratin 19	1.59	1.81	2.23	-
Cd84	CD84 antigen	0.89	1.53	1.42	-
Sh3bp2	SH3-domain binding protein 2	0.69	1.47	1.92	-
Gap43	growth associated protein 43	0.78	1.42	1.65	-
Bach1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	0.52	1.31	1.5	-
Pxdc1	PX domain containing 1	0.71	1.25	0.57	-
Plin2	perilipin 2	0.73	1.24	0.79	-
Vash2	vasohibin 2	0.74	1.13	1.83	-
Casp3	caspase 3	0.77	1.07	1.64	-
Stat5a	signal transducer and activator of transcription 5A	0.53	1.04	0.89	-
Ier5	immediate early response 5	0.52	0.99	1.9	-
Plat	plasminogen activator, tissue	0.56	0.92	1.2	-
C4b	complement component 4B (Chido blood group)	0.76	0.89	2.58	-
Atp8b1	ATPase, class I, type 8B, member 1	0.73	0.82	2.19	-
Tes	testis derived transcript	0.81	0.78	0.56	-
Tubb6	tubulin, beta 6 class V	1.05	0.77	2.3	-
Casp4	caspase 4, apoptosis-related cysteine peptidase	0.58	0.68	0.79	-
Bmp1	bone morphogenetic protein 1	0.55	0.55	1.87	-
Nefm	neurofilament, medium polypeptide	-0.6	-0.56	-1.99	-
Epn3	epsin 3	-0.71	-0.62	-1.78	-
Nefh	neurofilament, heavy polypeptide	-0.72	-0.63	-1.88	-
Kcnip1	Kv channel-interacting protein 1	-0.56	-0.67	-1.04	-
Coro6	coronin 6	-0.59	-0.7	-1.84	-
Hrasls	HRAS-like suppressor	-0.65	-0.72	-0.83	-

Esrrg	estrogen-related receptor gamma	-0.78	-0.73	-2.19	-
Pcp4l1	Purkinje cell protein 4-like 1	-0.53	-0.73	-1.96	-
Kcnk1	potassium channel, subfamily K, member 1	-0.59	-0.74	-1.32	-
Gabrb2	gamma-aminobutyric acid (GABA) A receptor, subunit beta 2	-0.55	-0.86	-1.64	-
Aifm3	apoptosis-inducing factor, mitochondrion-associated 3	-0.63	-0.95	-2.18	-
Lgi3	leucine-rich repeat LGI family, member 3	-0.69	-0.98	-2.27	-
Inpp5j	inositol polyphosphate 5-phosphatase J	-0.53	-1	-1.72	-
Agtr1b	angiotensin II receptor, type 1b	-0.66	-1.03	-2.68	-
Ucn	urocortin	4.11	-	6.62	2.73
Ucn2	urocortin 2	3.95	-	7.1	2.96
Slc30a3	solute carrier family 30 (zinc transporter), member 3	3.81	-	3.9	5.12
Kcnh4	potassium voltage-gated channel, subfamily H (eag-related), member 4	2.77	-	1.93	-
Gdnf	glial cell line derived neurotrophic factor	2.61	-	5.71	3.92
Btc	betacellulin, epidermal growth factor family member	2.55	-	3.27	-
Tgm1	transglutaminase 1, K polypeptide	2.49	-	8.52	-
Fosl1	FOS like 1, AP-1 transcription factor subunit	2.2	-	1.78	2.4
Tnc	tenascin C	2.05	-	1.19	-
Fgd3	FYVE, RhoGEF and PH domain containing 3	1.94	-	1.22	-
Crlf1	cytokine receptor-like factor 1	1.92	-	3.78	-
Pde6b	phosphodiesterase 6B, cGMP, rod receptor, beta polypeptide	1.85	-	3.35	-
Wt1	Wilms tumor 1 homolog	1.79	-	5.91	-
Rorb	RAR-related orphan receptor beta	1.73	-	2.54	1
Prc1	protein regulator of cytokinesis 1	1.57	-	2.58	1.66
Havcr2	hepatitis A virus cellular receptor 2	1.37	-	2.4	-
Slitrk6	SLIT and NTRK-like family, member 6	1.33	-	1.67	-
Wnt10b	wingless-type MMTV integration site family, member 10B	1.25	-	2.49	2.84
Kif22	kinesin family member 22	1.17	-	2.98	1.65

Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	1.17	-	2.54	-
Cxcl14	chemokine (C-X-C motif) ligand 14	1.12	-	7.32	-
Cenpf	centromere protein F	1.11	-	2.51	-
S100a4	S100 calcium binding protein A4	1.11	-	1.52	-
Timp1	tissue inhibitor of metalloproteinase 1	1.09	-	1.81	-
Clcf1	cardiotrophin-like cytokine factor 1	1.05	-	3.19	1.39
Cxcl10	chemokine (C-X-C motif) ligand 10	1.05	-	2.89	-
Il21r	interleukin 21 receptor	1.04	-	2.01	1.23
Rgs16	regulator of G-protein signaling 16	1.03	-	1.69	-
Syt17	synaptotagmin XVII	1.03	-	1.43	1.33
Lrrc10b	leucine rich repeat containing 10B	1.02	-	1.11	2.02
Postn	periostin, osteoblast specific factor	1.01	-	3.5	2.76
P2ry13	purinergic receptor P2Y, G-protein coupled 13	1.01	-	1.27	1.41
Fos	FBJ osteosarcoma oncogene	1	-	2.71	1.41
Mmp19	matrix metallopeptidase 19	0.99	-	2.86	1.74
Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2	0.99	-	1.42	0.91
Tnfaip6	tumor necrosis factor alpha induced protein 6	0.97	-	2.96	1.49
Piwil4	piwi-like RNA-mediated gene silencing 4	0.97	-	2.13	-
Tpbg	trophoblast glycoprotein	0.96	-	2.17	1.39
Lrrc17	leucine rich repeat containing 17	0.95	-	1.15	0.72
Mcm6	minichromosome maintenance complex component 6	0.93	-	2.11	-
Mchr1	melanin-concentrating hormone receptor 1	0.9	-	0.73	1.03
Pcdh15	protocadherin 15	0.87	-	1.71	-
Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	0.86	-	1.66	1.59
Col27a1	collagen, type XXVII, alpha 1	0.81	-	2.18	1.74
Foxm1	forkhead box M1	0.8	-	1.39	1.13
Rhoc	ras homolog family member C	0.8	-	1.35	1.03
Kif20a	kinesin family member 20A	0.8	-	1.18	-
Apobec1	apolipoprotein B mRNA editing enzyme,	0.78	-	3.73	1.63

	catalytic polypeptide 1				
Col18a1	collagen, type XVIII, alpha 1	0.77	-	3.4	-
Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2	0.76	-	2.84	-
Col5a2	collagen, type V, alpha 2	0.73	-	1.68	1.11
Gpnmb	glycoprotein (transmembrane) nmb	0.68	-	5	3.14
Igtp	interferon gamma induced GTPase	0.66	-	1.48	-
Mcm3	minichromosome maintenance complex component 3	0.65	-	1.88	1.24
Gas7	growth arrest specific 7	0.65	-	1.78	-
Thbs2	thrombospondin 2	0.64	-	4.13	2.26
Nkd2	naked cuticle 2	0.64	-	1.59	1.06
Ptpn5	protein tyrosine phosphatase, non-receptor type 5	0.63	-	2.72	2.15
Creb5	cAMP responsive element binding protein 5	0.63	-	0.93	0.99
Casp6	caspase 6	0.61	-	1.19	-
Socs3	suppressor of cytokine signaling 3	0.6	-	3.02	-
Nckap1l	NCK associated protein 1 like	0.6	-	1.7	1.18
Mrgprf	MAS-related GPR, member F	0.6	-	1.56	1.63
Cnksr3	Cnksr family member 3	0.59	-	1.74	1.3
Fam109b	family with sequence similarity 109, member B	0.58	-	0.67	0.89
Gfra3	glial cell line derived neurotrophic factor family receptor alpha 3	0.57	-	0.86	-
Arhgap25	Rho GTPase activating protein 25	0.57	-	0.78	-
Apod	apolipoprotein D	0.56	-	2.85	-
Zbtb42	zinc finger and BTB domain containing 42	0.56	-	1.18	1.25
Srpx2	sushi-repeat-containing protein, X-linked 2	0.55	-	2.37	1.19
P2ry14	purinergic receptor P2Y, G-protein coupled, 14	0.55	-	1	0.94
Ccnd1	cyclin D1	0.54	-	2.03	1.47
Arid5a	AT rich interactive domain 5A (MRF1-like)	0.53	-	2.42	1.6
Col5a1	collagen, type V, alpha 1	0.52	-	1.52	1.15

Cdh19	cadherin 19, type 2	0.52	-	0.51	-
Tbx18	T-box18	0.51	-	2.21	0.98
Tax1bp3	Tax1 (human T cell leukemia virus type I) binding protein 3	0.51	-	1.11	-
Lgi4	leucine-rich repeat LGI family, member 4	0.5	-	0.87	0.89
Hebp2	heme binding protein 2	-0.51	-	-2.2	-2.35
Hhatl	hedgehog acyltransferase-like	-0.51	-	-2.23	-2.16
P2rx6	purinergic receptor P2X, ligand-gated ion channel, 6	-0.51	-	-2.25	-
Calml4	calmodulin-like 4	-0.51	-	-2.55	-4.91
Rem2	rad and gem related GTP binding protein 2	-0.51	-	-2.76	-
Rcor2	REST corepressor 2	-0.52	-	-1.39	-1.25
Scx	scleraxis bHLH transcription factor	-0.52	-	-2.03	-1.7
Epha10	Eph receptor A10	-0.55	-	0.6	1.16
Ly6h	lymphocyte antigen 6 complex, locus H	-0.55	-	-2.06	-3.47
Siah3	siah E3 ubiquitin protein ligase family member 3	-0.57	-	-3.13	-
Pctp	phosphatidylcholine transfer protein	-0.58	-	-1.7	-
Fgf9	fibroblast growth factor 9	-0.59	-	-1.88	-
Kcnj11	potassium inwardly rectifying channel, subfamily J, member 11	-0.6	-	-1.35	-
Chst9	carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 9	-0.6	-	-1.94	-
Caln1	calneuron 1	-0.6	-	-2.22	-
Chchd10	coiled-coil-helix-coiled-coil-helix domain containing 10	-0.61	-	-1.92	-
Syt3	synaptotagmin III	-0.61	-	-2.18	-2.1
Tshr	thyroid stimulating hormone receptor	-0.63	-	2.29	2.14
Hoxb9	homeobox B9	-0.63	-	-1.5	-
Cacng2	calcium channel, voltage-dependent, gamma subunit 2	-0.64	-	-2.36	-2.37
B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	-0.68	-	-1.56	-
Tmem196	transmembrane protein 196	-0.7	-	-1.01	-1.04
Tll1	tolloid-like	-0.7	-	-1.15	-

Scn4a	sodium channel, voltage-gated, type IV, alpha	-0.73	-	-1.4	-
Fam57b	family with sequence similarity 57, member B	-0.73	-	-2.08	-2.06
Evpl	envoplakin	-0.76	-	-0.98	-
Slc34a2	solute carrier family 34 (sodium phosphate), member 2	-0.76	-	-1.38	-
Tpd52l1	tumor protein D52-like 1	-0.78	-	-0.64	-0.83
Lingo4	leucine rich repeat and Ig domain containing 4	-0.78	-	-2.09	-3.11
Olfm3	olfactomedin 3	-0.8	-	-1.52	-1.55
Wnt7a	wingless-type MMTV integration site family, member 7A	-0.8	-	-1.82	-2.32
Myadml2	myeloid-associated differentiation marker-like 2	-0.81	-	-1.72	-
Rassf6	Ras association (RalGDS/AF-6) domain family member 6	-0.83	-	-1.98	-
Myo5b	myosin VB	-0.87	-	-0.76	-
Clec2l	C-type lectin domain family 2, member L	-0.87	-	-2.32	-3.52
Omg	oligodendrocyte myelin glycoprotein	-0.91	-	-1.63	-
Esrrb	estrogen related receptor, beta	-0.92	-	-2.82	-3.16
Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1	-0.94	-	-2.41	-
Chst5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	-0.95	-	-1.68	-
Smpx	small muscle protein, X-linked	-1.04	-	-2.07	-1.26
Gjd2	gap junction protein, delta 2	-1.08	-	-3.02	-2.58
Best3	bestrophin 3	-1.31	-	-2.06	-
Calb2	calbindin 2	-3.27	-	-2.08	-
Duoxa1	dual oxidase maturation factor 1	3.1	-	-	0.69
Tuba1c	tubulin, alpha 1C	0.85	-	-	0.52
Hist2h3c2	histone cluster 2, H3c2	0.81	-	-	1.22
Slc44a5	solute carrier family 44, member 5	0.79	-	-	2.04
Nudt17	nudix (nucleoside diphosphate linked moiety X)-type motif 17	0.76	-	-	0.88
Mrgprx1	MAS-related GPR, member X1	-0.54	-	-	-5.71
Bnc1	basonuclin 1	-0.81	-	-	-2.91

Siglec1	sialic acid binding Ig-like lectin 1, sialoadhesin	-	2.22	4.21	2.2
Sdcbp2	syndecan binding protein (syntenin) 2	-	1.73	4.19	1.1
Clec7a	C-type lectin domain family 7, member a	-	1.41	4.04	2.45
Dsc2	desmocollin 2	-	2.23	3.57	-
C1qb	complement component 1, q subcomponent, beta polypeptide	-	1.48	3.35	1.9
Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	-	1.19	3.3	-
Clec2d	C-type lectin domain family 2, member D	-	0.94	3.25	3.96
Plau	plasminogen activator, urokinase	-	1.19	2.97	-
C1qc	complement component 1, q subcomponent, C chain	-	2.76	2.94	1.77
Msr1	macrophage scavenger receptor 1	-	1.6	2.9	-
Irf8	interferon regulatory factor 8	-	1.29	2.89	-
Ripk3	receptor-interacting serine-threonine kinase 3	-	2.36	2.88	-
Lyz2	lysozyme 2	-	1.14	2.86	1.9
Itgam	integrin alpha M	-	1.18	2.78	1.71
Plcb2	phospholipase C, beta 2	-	1.53	2.78	1.55
Tnfrsf8	tumor necrosis factor receptor superfamily, member 8	-	2.36	2.75	3.15
Fcgr2b	Fc receptor, IgG, low affinity IIb	-	1.57	2.73	-
Aoah	acyloxyacyl hydrolase	-	1.42	2.68	-
Fgf2	fibroblast growth factor 2	-	0.74	2.61	1.63
C3ar1	complement component 3a receptor 1	-	1.64	2.6	1.58
Bin2	bridging integrator 2	-	1.93	2.53	1.57
Vav1	vav guanine nucleotide exchange factor 1	-	1.51	2.44	1.54
Cenpt	centromere protein T	-	0.73	2.4	-
Cyth4	cytohesin 4	-	1.6	2.35	1.14
Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	-	1.74	2.34	-
Vgf	VGF nerve growth factor inducible	-	1.71	2.32	-
Ptx3	pentraxin related gene	-	1.81	2.29	-

Aif1	allograft inflammatory factor 1	-	1.95	2.26	-
Cyba	cytochrome b-245, alpha polypeptide	-	4.35	2.23	-
Stear1	six transmembrane epithelial antigen of the prostate 1	-	2.34	2.23	1.21
Igfbp3	insulin-like growth factor binding protein 3	-	1.55	2.22	-
Csf1r	colony stimulating factor 1 receptor	-	1.62	2.21	-
Cysltr1	cysteinyl leukotriene receptor 1	-	1.47	2.21	2.04
Sbno2	strawberry notch 2	-	0.95	2.21	1.63
C5ar1	complement component 5a receptor 1	-	2.25	2.18	-
Cd14	CD14 antigen	-	3.21	2.17	-
C3	complement component 3	-	1.39	2.14	2.52
Ticam2	toll-like receptor adaptor molecule 2	-	1.86	2.12	-
Sla	src-like adaptor	-	1.38	2.1	1.79
Cd38	CD38 antigen	-	0.82	2.08	-
Cd53	CD53 antigen	-	1.14	2.04	1.08
Ptprc	protein tyrosine phosphatase, receptor type, C	-	0.85	2.01	-
Irak3	interleukin-1 receptor-associated kinase 3	-	0.67	1.98	1.23
Gpr65	G-protein coupled receptor 65	-	1.9	1.95	-
Tgfb1i	transforming growth factor, beta induced	-	0.83	1.93	-
Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	-	1.39	1.92	-
Il1r1	interleukin 1 receptor, type I	-	1.18	1.91	1.16
Ptpro	protein tyrosine phosphatase, receptor type, O	-	1.28	1.85	1.56
Bcl2l11	BCL2-like 11 (apoptosis facilitator)	-	0.64	1.84	1.71
Icam1	intercellular adhesion molecule 1	-	1.59	1.84	1.18
Slc11a1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	-	1.25	1.84	1.07
Sox7	SRY (sex determining region Y)-box 7	-	1.84	1.84	-
Stear4	STEAP family member 4	-	0.66	1.82	0.93
Cxadr	coxsackie virus and adenovirus receptor	-	0.71	1.81	-

Prdm1	PR domain containing 1, with ZNF domain	-	2.3	1.81	-
Il10ra	interleukin 10 receptor, alpha	-	1.74	1.78	1.29
Tlr1	toll-like receptor 1	-	1.09	1.77	-
Lipk	lipase, family member K	-	1.36	1.75	-
Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	-	1.2	1.74	-
Mrc1	mannose receptor, C type 1	-	1.17	1.74	-
Satb2	special AT-rich sequence binding protein 2	-	2.87	1.71	1.57
Il2rg	interleukin 2 receptor, gamma chain	-	1.2	1.69	1.36
Slc4a8	solute carrier family 4 (anion exchanger), member 8	-	1.27	1.68	0.96
Fadd	Fas (TNFRSF6)-associated via death domain	-	1.06	1.67	1.1
Adamts1	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1	-	0.53	1.66	-
Ctsc	cathepsin C	-	1	1.64	1.12
Adcy4	adenylate cyclase 4	-	1.07	1.63	-
Slc28a2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	-	1.96	1.6	1.13
Marcks	myristoylated alanine rich protein kinase C substrate	-	0.71	1.58	-
Dock8	dedicator of cytokinesis 8	-	0.56	1.57	1.21
Parp3	poly (ADP-ribose) polymerase family, member 3	-	0.73	1.56	1.1
Cdkn3	cyclin-dependent kinase inhibitor 3	-	0.97	1.55	-
Tmem173	transmembrane protein 173	-	0.94	1.54	-
Fam105a	family with sequence similarity 105, member A	-	0.68	1.53	0.65
Rspo1	R-spondin 1	-	0.72	1.53	1.01
Sp110	Sp110 nuclear body protein	-	1.07	1.52	1.09
Laptm5	lysosomal-associated protein transmembrane 5	-	1.57	1.51	1.2
Dab2	disabled 2, mitogen-responsive phosphoprotein	-	0.71	1.49	0.77
Tubb2b	tubulin, beta 2B class IIB	-	1.22	1.46	-

Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	-	0.6	1.45	-
Stom	stomatin	-	0.68	1.44	1.03
Fam129b	family with sequence similarity 129, member B	-	0.57	1.41	1.17
Psmb8	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	-	0.98	1.41	-
Rnase4	ribonuclease, RNase A family 4	-	1.47	1.4	-
Smad1	SMAD family member 1	-	0.84	1.4	-
Klhl6	kelch-like 6	-	1	1.38	-
Clic1	chloride intracellular channel 1	-	0.74	1.34	-
Oas2	2'-5' oligoadenylate synthetase 2	-	1.28	1.34	-
Dtnbp1	dystrobrevin binding protein 1	-	0.99	1.32	-
Plcg2	phospholipase C, gamma 2	-	0.75	1.3	-
Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	-	0.72	1.28	-
Klf10	Kruppel-like factor 10	-	0.51	1.28	0.91
Tmem43	transmembrane protein 43	-	1.26	1.28	0.93
Triobp	TRIO and F-actin binding protein	-	0.51	1.28	1.15
Tmem98	transmembrane protein 98	-	1.51	1.27	-
Apoibr	apolipoprotein B receptor	-	2.38	1.26	1.1
Rps6ka1	ribosomal protein S6 kinase polypeptide 1	-	0.66	1.23	1.12
Zfp367	zinc finger protein 367	-	1.03	1.23	-
Ptprj	protein tyrosine phosphatase, receptor type, J	-	0.53	1.21	0.94
Tpm4	tropomyosin 4	-	0.59	1.21	-
Hr	hairless	-	0.72	1.2	-
Slco2b1	solute carrier organic anion transporter family, member 2b1	-	0.87	1.2	0.73
Scpep1	serine carboxypeptidase 1	-	1.56	1.18	-
Pla2g2d	phospholipase A2, group IID	-	4.56	1.17	1.36
Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	-	0.9	1.16	1.12
Lbh	limb-bud and heart	-	0.53	1.16	0.9

Zmynd15	zinc finger, MYND-type containing 15	-	1.44	1.16	-
Crem	cAMP responsive element modulator	-	0.74	1.12	-
Adrb2	adrenergic receptor, beta 2	-	1.03	1.11	-
Gypc	glycophorin C	-	0.66	1.11	-
Klf6	Kruppel-like factor 6	-	0.89	1.1	-
Rgs12	regulator of G-protein signaling 12	-	0.57	1.09	-
Elf4	E74-like factor 4 (ets domain transcription factor)	-	1.01	1.08	0.97
Mvp	major vault protein	-	0.62	1.08	0.69
Tm4sf1	transmembrane 4 superfamily member 1	-	0.72	1.07	0.78
Sema4f	sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain	-	0.65	1.06	1.18
S1pr2	sphingosine-1-phosphate receptor 2	-	0.9	1.04	0.8
Tnfaip8	tumor necrosis factor, alpha-induced protein 8	-	1.27	1.04	-
Myo10	myosin X	-	1.21	1.03	0.6
Nfatc1	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 1	-	0.62	1.03	-
Btg2	B cell translocation gene 2, anti-proliferative	-	0.95	1.01	-
Nrip1	nuclear receptor interacting protein 1	-	0.87	1.01	-
Carhsp1	calcium regulated heat stable protein 1	-	0.61	1	-
Flna	filamin, alpha	-	0.53	1	0.79
Fam210b	family with sequence similarity 210, member B	-	0.79	0.99	0.68
Kpna2	karyopherin (importin) alpha 2	-	0.75	0.97	-
Metrnl	meteordin, glial cell differentiation regulator-like	-	0.56	0.97	-
Lilra5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	-	1.87	0.96	1.19
Apaf1	apoptotic peptidase activating factor 1	-	0.56	0.95	0.72
H3f3b	H3 histone, family 3B	-	0.52	0.94	-
Marcks1	MARCKS-like 1	-	1.77	0.94	1.15
Prkab1	protein kinase, AMP-activated, beta 1	-	0.77	0.93	-

	non-catalytic subunit				
Rap2b	RAP2B, member of RAS oncogene family	-	0.88	0.93	0.71
Sema3c	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	-	0.84	0.93	0.99
Phlda1	pleckstrin homology like domain, family A, member 1	-	1.52	0.92	-
Nav2	neuron navigator 2	-	0.54	0.9	0.63
Ets2	E26 avian leukemia oncogene 2, 3' domain	-	0.73	0.88	-
Pou2f1	POU domain, class 2, transcription factor 1	-	0.7	0.87	-
Prss12	protease, serine 12 neurotrypsin (motopsin)	-	0.7	0.87	1.13
Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	-	1.48	0.86	1.1
Podxl	podocalyxin-like	-	1.09	0.86	0.81
Rassf1	Ras association (RalGDS/AF-6) domain family member 1	-	0.57	0.85	0.62
Ppp4r1	protein phosphatase 4, regulatory subunit 1	-	0.67	0.84	0.66
Tnfsf10	tumor necrosis factor (ligand) superfamily, member 10	-	0.58	0.81	-
Syt4	synaptotagmin IV	-	0.53	0.79	-
Mad2l2	MAD2 mitotic arrest deficient-like 2	-	1.08	0.78	0.73
Pfkfb4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	-	1.02	0.78	0.89
Rras2	related RAS viral (r-ras) oncogene 2	-	1.4	0.78	0.51
Prdm9	PR domain containing 9	-	1.2	0.77	-
Fzd6	frizzled class receptor 6	-	0.54	0.76	-
Il33	interleukin 33	-	1.15	0.76	-
Ccl7	chemokine (C-C motif) ligand 7	-	2.51	0.75	-
Fam43a	family with sequence similarity 43, member A	-	1.09	0.73	-
Lrrn4cl	LRRN4 C-terminal like	-	1.26	0.72	0.65
Arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2	-	0.69	0.7	-

Ifrd2	interferon-related developmental regulator 2	-	2.09	0.7	0.63
Rcc1	regulator of chromosome condensation 1	-	0.82	0.7	0.55
Slc38a6	solute carrier family 38, member 6	-	0.6	0.69	-
Dnajb5	DnaJ heat shock protein family (Hsp40) member B5	-	0.76	0.67	0.68
Fads3	fatty acid desaturase 3	-	0.81	0.66	0.75
Rnf19b	ring finger protein 19B	-	0.64	0.66	0.59
Drd2	dopamine receptor D2	-	1.59	0.65	1.33
Arhgef15	Rho guanine nucleotide exchange factor (GEF) 15	-	0.71	0.64	-
Dhrs1	dehydrogenase/reductase (SDR family) member 1	-	0.6	0.64	-
Duox2	dual oxidase 2	-	4.86	0.64	1
Inpp5d	inositol polyphosphate-5-phosphatase D	-	0.83	0.64	0.56
Phactr2	phosphatase and actin regulator 2	-	0.58	0.64	0.53
Tapbpl	TAP binding protein-like	-	0.53	0.62	-
Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	-	1.13	0.61	-
Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	-	0.85	0.6	0.52
Mettl9	methyltransferase like 9	-	0.76	0.59	-
Myadm	myeloid-associated differentiation marker	-	0.69	0.59	0.66
Sec61b	Sec61 beta subunit	-	1.82	0.59	-
Tmem88b	transmembrane protein 88B	-	1.21	0.58	-
Mknk2	MAP kinase-interacting serine/threonine kinase 2	-	0.72	0.55	0.59
Zfp655	zinc finger protein 655	-	0.56	0.55	-
Abract	ABRA C-terminal like	-	0.78	0.53	-
Fndc3a	fibronectin type III domain containing 3A	-	0.51	0.53	-
Slc25a24	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	-	0.66	0.53	-
Crmp1	collapsin response mediator protein 1	-	0.53	0.52	-

Gmip	Gem-interacting protein	-	0.52	0.52	-
Zhx2	zinc fingers and homeoboxes 2	-	0.57	0.52	0.7
Tifa	TRAF-interacting protein with forkhead-associated domain	-	1.22	0.51	-
Hyal3	hyaluronoglucosaminidase 3	-	-1.3	-0.52	-
Nek11	NIMA (never in mitosis gene a)-related expressed kinase 11	-	-1.44	-0.56	-
Spock1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1	-	-0.62	-0.63	-
Slc5a6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	-	-0.68	-0.67	-
Suox	sulfite oxidase	-	-0.81	-0.67	-
Tuba4a	tubulin, alpha 4A	-	-0.55	-0.67	-
Bloc1s5	biogenesis of lysosomal organelles complex-1, subunit 5, muted	-	-0.63	-0.74	-
Rassf5	Ras association (RalGDS/AF-6) domain family member 5	-	-0.58	-0.75	-
Ech1	enoyl coenzyme A hydratase 1, peroxisomal	-	-0.56	-0.76	-0.69
Esrra	estrogen related receptor, alpha	-	-0.83	-0.77	-0.58
Klhdc8a	kelch domain containing 8A	-	-1	-0.77	-
Lmln	leishmanolysin-like (metallopeptidase M8 family)	-	-0.56	-0.78	-
Fbxo31	F-box protein 31	-	-0.54	-0.79	-
Lrrk3	leucine-rich repeats and IQ motif containing 3	-	-1.32	-0.82	-0.85
Wipf3	WAS/WASL interacting protein family, member 3	-	-0.57	-0.84	-1.44
Fam126b	family with sequence similarity 126, member B	-	-0.6	-0.86	-0.9
Nfic	nuclear factor I/C	-	-0.54	-0.87	-
Rab4a	RAB4A, member RAS oncogene family	-	-0.65	-0.87	-
Pcdh11x	protocadherin 11 X-linked	-	-0.68	-0.89	-0.8
Cdh8	cadherin 8	-	-0.51	-0.9	-
Sord	sorbitol dehydrogenase	-	-0.59	-0.9	-0.76
Brsk1	BR serine/threonine kinase 1	-	-0.66	-0.91	-

Ntm	neurotrimin	-	-0.98	-0.91	-0.75
Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)	-	-0.5	-0.93	-0.65
Mycbpap	MYCBP associated protein	-	-0.91	-0.94	-
Pde1a	phosphodiesterase 1A, calmodulin-dependent	-	1.37	-0.94	-0.59
Fam69b	family with sequence similarity 69, member B	-	-0.71	-0.95	-0.64
Ogfrl1	opioid growth factor receptor-like 1	-	-0.6	-0.97	-1.1
Lhfpl5	lipoma HMGIC fusion partner-like 5	-	-0.79	-0.98	-
Rasgrp1	RAS guanyl releasing protein 1	-	-0.55	-0.98	-0.87
Lrfn1	leucine rich repeat and fibronectin type III domain containing 1	-	-1.36	-0.99	-
Ncald	neurocalcin delta	-	-0.68	-1	-1.05
Cntn1	contactin 1	-	-0.53	-1.01	-0.97
Ldhb	lactate dehydrogenase B	-	-0.54	-1.03	-1.12
Usp29	ubiquitin specific peptidase 29	-	-0.72	-1.03	-
Rpa1	replication protein A1	-	-0.66	-1.04	-
Rnf180	ring finger protein 180	-	-0.52	-1.05	-0.75
Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1	-	-0.58	-1.06	-0.85
Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A	-	-0.53	-1.06	-0.8
Lrrn2	leucine rich repeat protein 2, neuronal	-	-0.74	-1.08	-
Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	-	-0.67	-1.08	-0.67
Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1	-	-0.52	-1.09	-0.86
Scn4b	sodium channel, type IV, beta	-	-0.6	-1.12	-1.09
Slc6a7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	-	-1.57	-1.12	-
Armcx6	armadillo repeat containing, X-linked 6	-	-1.55	-1.13	-0.92
Cplx2	complexin 2	-	-0.81	-1.16	-
Ankrd29	ankyrin repeat domain 29	-	-0.59	-1.17	-
Bmpr1b	bone morphogenetic protein receptor,	-	-0.87	-1.17	-0.89

	type 1B				
Pir	pirin	-	-0.61	-1.17	-1.07
Trpm8	transient receptor potential cation channel, subfamily M, member 8	-	-0.64	-1.21	-1.13
Astn2	astrotactin 2	-	-0.79	-1.22	-1.09
Abhd8	abhydrolase domain containing 8	-	-1.35	-1.25	-
Fkbp4	FK506 binding protein 4	-	-0.55	-1.25	-1.2
Lurap1l	leucine rich adaptor protein 1-like	-	-0.73	-1.26	-1.15
Vwa7	von Willebrand factor A domain containing 7	-	-0.51	-1.26	-
Cacna2d2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	-	-0.52	-1.28	-1.06
P2ry1	purinergic receptor P2Y, G-protein coupled 1	-	-0.62	-1.29	-0.57
Tmem132e	transmembrane protein 132E	-	-0.62	-1.3	-
Oxr1	oxidation resistance 1	-	-0.67	-1.31	-1.34
Ank1	ankyrin 1, erythroid	-	-0.51	-1.37	-
Nap1l3	nucleosome assembly protein 1-like 3	-	-0.56	-1.37	-1.3
Slc9a5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	-	-0.72	-1.37	-
Gdpd2	glycerophosphodiester phosphodiesterase domain containing 2	-	-0.95	-1.38	-1.53
Hcn2	hyperpolarization-activated, cyclic nucleotide-gated K+ 2	-	-0.84	-1.39	-1.02
Atp2b2	ATPase, Ca++ transporting, plasma membrane 2	-	-0.53	-1.41	-1.05
Zfp365	zinc finger protein 365	-	-0.54	-1.42	-
Angel1	angel homolog 1	-	-0.81	-1.44	-1.37
Fam13a	family with sequence similarity 13, member A	-	-0.92	-1.44	-1.14
Hpse	heparanase	-	-1.32	-1.45	-
Ntrk1	neurotrophic tyrosine kinase, receptor, type 1	-	-0.86	-1.45	-1.44
Gpr156	G protein-coupled receptor 156	-	-0.58	-1.47	-
Syt2	synaptotagmin II	-	-0.53	-1.47	-
Ankrd13d	ankyrin repeat domain 13 family,	-	-0.63	-1.51	-1.47

	member D				
Asah2	N-acylsphingosine amidohydrolase 2	-	-0.61	-1.55	-1.76
Grin1	glutamate receptor, ionotropic, NMDA1 (zeta 1)	-	-0.52	-1.55	-1.33
Paqr5	progestin and adiponectin receptor family member V	-	-0.6	-1.56	-1.21
Asphd2	aspartate beta-hydroxylase domain containing 2	-	-0.71	-1.57	-
Eepd1	endonuclease/exonuclease/phosphatase family domain containing 1	-	-0.57	-1.57	-1.3
Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	-	-0.58	-1.57	-1.47
Trhde	TRH-degrading enzyme	-	-0.82	-1.58	-1.35
Tusc5	tumor suppressor candidate 5	-	-0.54	-1.58	-
Gprc5c	G protein-coupled receptor, family C, group 5, member C	-	-0.68	-1.6	-
Fstl5	follistatin-like 5	-	-0.55	-1.66	-1.63
Adam11	a disintegrin and metalloproteinase domain 11	-	-0.71	-1.69	-
Extl2	exostosin-like glycosyltransferase 2	-	-0.54	-1.72	-1.78
Bcan	brevican	-	-0.67	-1.75	-1.87
Faim2	Fas apoptotic inhibitory molecule 2	-	-0.74	-1.77	-2.85
Kcna2	potassium voltage-gated channel, shaker-related subfamily, member 2	-	-0.57	-1.77	-1.64
Khk	ketohexokinase	-	-0.64	-1.78	-2.05
Caskin1	CASK interacting protein 1	-	-0.52	-1.79	-
Cxxc4	CXXC finger 4	-	-0.53	-1.82	-1.71
Scml4	Scm polycomb group protein like 4	-	-0.71	-1.83	-
Lingo1	leucine rich repeat and Ig domain containing 1	-	-0.55	-1.84	-1.46
Tcerg1l	transcription elongation regulator 1-like	-	-0.54	-1.87	-2.3
Chrna7	cholinergic receptor, nicotinic, alpha polypeptide 7	-	-0.89	-1.88	-2.14
Scn8a	sodium channel, voltage-gated, type VIII, alpha	-	-0.55	-1.88	-2.15
Jph3	junctophilin 3	-	-0.63	-1.89	-

P2rx5	purinergic receptor P2X, ligand-gated ion channel, 5	-	-0.81	-1.91	-
Agbl4	ATP/GTP binding protein-like 4	-	-0.8	-1.94	-1.79
Necab3	N-terminal EF-hand calcium binding protein 3	-	-0.76	-1.94	-1.5
Aldh1b1	aldehyde dehydrogenase 1 family, member B1	-	3.36	-1.96	-2.05
Galr1	galanin receptor 1	-	-0.77	-1.98	-
Rph3a	rabphilin 3A	-	-0.68	-1.98	-
Shank1	SH3 and multiple ankyrin repeat domains 1	-	-0.78	-1.99	-
Susd4	sushi domain containing 4	-	-0.71	-2.01	-
Ache	acetylcholinesterase	-	-0.91	-2.03	-
Nat8l	N-acetyltransferase 8-like	-	-0.64	-2.04	-
Kcnn2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	-	-0.66	-2.05	-
Adra2c	adrenergic receptor, alpha 2c	-	-1.25	-2.06	-
Lrguk	leucine-rich repeats and guanylate kinase domain containing	-	-0.85	-2.06	-1.8
Ar	androgen receptor	-	-0.77	-2.09	-1.84
Lrrn1	leucine rich repeat protein 1, neuronal	-	-0.59	-2.09	-2.02
Fgf12	fibroblast growth factor 12	-	-0.56	-2.13	-
Ntng1	netrin G1	-	-0.58	-2.16	-2.23
Cpne4	copine IV	-	-0.57	-2.18	-2.19
Atp2b3	ATPase plasma membrane Ca2+ transporting 3	-	-0.79	-2.2	-2.45
Thsd7b	thrombospondin, type I, domain containing 7B	-	-0.63	-2.22	-
Kcna4	potassium voltage-gated channel, shaker-related subfamily, member 4	-	-0.53	-2.25	-3.35
Hs6st2	heparan sulfate 6-O-sulfotransferase 2	-	-0.51	-2.26	-3.07
Arap2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	-	-0.52	-2.3	-
Nefl	neurofilament, light polypeptide	-	-0.56	-2.34	-
Cntn3	contactin 3	-	-0.78	-2.4	-3.9
Rtn4rl1	reticulon 4 receptor-like 1	-	-0.61	-2.41	-

Galnt5	polypeptide N-acetylgalactosaminyltransferase 5	-	-0.59	-2.42	-2.99
Slitrk3	SLIT and NTRK-like family, member 3	-	-0.69	-2.43	-2.6
Nap1l5	nucleosome assembly protein 1-like 5	-	-0.51	-2.48	-2.41
Prmt8	protein arginine N-methyltransferase 8	-	-0.69	-2.5	-2.99
Gabrg2	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 2	-	-0.59	-2.64	-
Rnf112	ring finger protein 112	-	-0.97	-2.64	-
Kcns3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	-	-0.68	-2.67	-3.69
Kcnip3	Kv channel interacting protein 3, calsenilin	-	-0.56	-2.73	-2.91
Gabra1	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1	-	-0.52	-2.82	-
Th	tyrosine hydroxylase	-	-0.72	-2.85	-1.79
Ankrd34a	ankyrin repeat domain 34A	-	-1.44	-2.9	-2.28
Dpp10	dipeptidylpeptidase 10	-	-0.66	-3.18	-
Cps1	carbamoyl-phosphate synthetase 1	-	-3.96	-3.35	-
Htr1a	5-hydroxytryptamine (serotonin) receptor 1A	-	-1.21	-3.41	-6.19
Ush1g	USH1 protein network component sans	-	-1.33	-3.58	-
Hapl1	hyaluronan and proteoglycan link protein 1	-	-0.71	-3.6	-6.92
Ern2	endoplasmic reticulum (ER) to nucleus signalling 2	-	-4.09	-5.55	-4.58
Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	-	-0.65	-	-0.53
Basp1	brain abundant, membrane attached signal protein 1	-	0.52	-	0.67
Cyth2	cytohesin 2	-	0.53	-	0.53
Gpr153	G protein-coupled receptor 153	-	0.68	-	1.03
Prokr2	prokineticin receptor 2	-	1.15	-	0.69
Rab33a	RAB33A, member RAS oncogene family	-	1.15	-	0.57
Tmc7	transmembrane channel-like gene family 7	-	0.57	-	0.51
Tmem132a	transmembrane protein 132A	-	0.99	-	0.6
B3gat1	beta-1,3-glucuronyltransferase 1	-0.83	-1.1	0.81	1.4

	(glucuronosyltransferase P)				
Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	-0.79	-0.73	0.68	0.76
Sertm1	serine rich and transmembrane domain containing 1	0.86	1.4	-1.82	-1.77
Mc4r	melanocortin 4 receptor	1.01	5	-1.74	-
Car1	carbonic anhydrase 1	2.21	3.9	-2.16	-
Sez6l	seizure related 6 homolog like	1.72	3.28	-1.01	-
Corin	corin	1.99	2.14	-1.95	-
Fam163a	family with sequence similarity 163, member A	0.86	1.34	-0.95	-
Crh	corticotropin releasing hormone	3.34	-	-2.75	-2.55
Wif1	Wnt inhibitory factor 1	0.95	-	-0.8	-
Layn	layilin	0.58	-	-0.58	-0.65
Arc	activity regulated cytoskeletal-associated protein	0.54	-	-0.56	-
Amz1	archaelysin family metallopeptidase 1	0.54	-	-0.77	-
Ibsp	integrin binding sialoprotein	-0.66	-	3.46	-
Gabra5	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 5	-0.69	-	1.33	1.25
Slc2a5	solute carrier family 2 (facilitated glucose transporter), member 5	-0.72	-	0.82	0.56
Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9	-0.75	-	0.68	-
Qprt	quinolinate phosphoribosyltransferase	-0.8	-	1.54	-
Il17re	interleukin 17 receptor E	-0.85	-	0.98	-
Pmfbp1	polyamine modulated factor 1 binding protein 1	-0.93	-	1.59	-
Fam151a	family with sequence simliarity 151, member A	3.82	-	-	-0.95
Gfral	GDNF family receptor alpha like	1.61	-	-	-4.7
Slc25a45	solute carrier family 25, member 45	0.52	-	-	-0.52
Rasgrp4	RAS guanyl releasing protein 4	-0.54	-	-	1.09
Myh7b	myosin, heavy chain 7B, cardiac muscle, beta	-0.96	-	-	0.66

Vdr	vitamin D (1,25-dihydroxyvitamin D3) receptor	-0.96	-	-	1.07
Scin	scinderin	-	-0.98	3.12	-
Ifitm2	interferon induced transmembrane protein 2	-	-1.07	1.21	-
Sh3gl3	SH3-domain GRB2-like 3	-	-0.78	1.15	0.84
Cdc45	cell division cycle 45	-	-0.89	1.14	-
Sh3bp5	SH3-domain binding protein 5 (BTK-associated)	-	-0.51	1.1	-
Bambi	BMP and activin membrane-bound inhibitor	-	-1.24	1.03	-
Gtse1	G two S phase expressed protein 1	-	-2.89	1.01	0.89
Spr	sepiapterin reductase	-	-1.52	0.88	0.7
Manba	mannosidase, beta A, lysosomal	-	-0.72	0.82	0.66
Calb1	calbindin 1	-	-0.54	0.73	0.65
Chst10	carbohydrate sulfotransferase 10	-	-0.84	0.72	0.53
Kdrlr1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	-	-0.66	0.71	0.51
Crocc	ciliary rootlet coiled-coil, rootletin	-	-0.79	0.66	0.63
Pold1	polymerase (DNA directed), delta 1, catalytic subunit	-	-1.04	0.66	0.96
Col11a1	collagen, type XI, alpha 1	-	-0.55	0.64	0.71
Notch4	notch 4	-	-0.83	0.64	-
Prickle1	prickle planar cell polarity protein 1	-	-0.59	0.55	0.6
Cyp2u1	cytochrome P450, family 2, subfamily u, polypeptide 1	-	-0.96	0.52	0.53
Asns	asparagine synthetase	-	0.54	-0.52	-0.6
Ptrhd1	peptidyl-tRNA hydrolase domain containing 1	-	0.64	-0.55	-
Rtn2	reticulon 2 (Z-band associated protein)	-	0.5	-0.64	-
Elmod1	ELMO/CED-12 domain containing 1	-	0.62	-0.67	-0.64
Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	-	1.09	-0.67	-
Anxa8	annexin A8	-	2.16	-0.71	-
Galnt9	polypeptide N-acetylgalactosaminyltransferase 9	-	0.82	-0.72	-
Chac1	ChaC, cation transport regulator 1	-	1.9	-0.74	-1.08

Slc38a1	solute carrier family 38, member 1	-	0.57	-0.82	-0.63
B3gnt8	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8	-	1.23	-1.12	-0.66
Atp13a4	ATPase type 13A4	-	2.86	-1.17	-
Chrna5	cholinergic receptor, nicotinic, alpha polypeptide 5	-	2.22	-1.34	-1.41
Gabrg1	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 1	-	1	-1.57	-
Adra1a	adrenergic receptor, alpha 1a	-	0.91	-1.73	-
Mgat4c	MGAT4 family, member C	-	0.99	-2.15	-2.27
Inhbb	inhibin beta-B	-	1.99	-2.29	-
Ppef1	protein phosphatase with EF hand calcium-binding domain 1	-	0.91	-2.41	-3.31
Grem2	gremlin 2, DAN family BMP antagonist	-	1.07	-2.45	-
Gamt	guanidinoacetate methyltransferase	-	-0.81	-	0.75
Rinl	Ras and Rab interactor-like	-	-1.89	-	1.18

**Table S6. List of 486 know pain-related genes.** The list is based on pain databases <http://www.painnetworks.org/> [38] and <http://www.jbldesign.com/jmogil/enter.html> [23] (437 genes) and additional curation of the existing literature.

N	gene name	description
1	A530088H08Rik	RIKEN cDNA A530088H08 gene
2	Abcb1a	ATP-binding cassette, sub-family B (MDR/TAP), member 1A
3	Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
4	Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
5	Accn1	acid-sensing (proton-gated) ion channel 2
6	Accn2	acid-sensing (proton-gated) ion channel 1
7	Accn3	acid-sensing (proton-gated) ion channel 3
8	Ache	acetylcholinesterase
9	Acpp	acid phosphatase, prostate
10	Adam11	a disintegrin and metallopeptidase domain 11
11	Adamts5	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2)
12	Adcy1	adenylate cyclase 1
13	Adcy5	adenylate cyclase 5
14	Adcy8	adenylate cyclase 8
15	Adcyap1	adenylate cyclase activating polypeptide 1; pituitary adenylate cyclase-activating polypeptide (PACAP); axon regeneration [1]
16	Adcyap1r1	adenylate cyclase activating polypeptide 1 receptor 1
17	Adm	adrenomedullin
18	Adora1	adenosine A1 receptor
19	Adora2a	adenosine A2a receptor
20	Adora2b	adenosine A2b receptor; hub gene in nociception [24]
21	Adora3	adenosine A3 receptor

22	Adra1d	adrenergic receptor, alpha 1d
23	Adra2a	adrenergic receptor, alpha 2a
24	Adra2c	adrenergic receptor, alpha 2c
25	Adrb2	adrenergic receptor, beta 2
26	Adrbk1	G protein-coupled receptor kinase 2
27	Adrbk2	G protein-coupled receptor kinase 3
28	Ager	advanced glycosylation end product-specific receptor
29	Agtr2	angiotensin II receptor, type 2
30	Alox12	arachidonate 12-lipoxygenase
31	Alox5	arachidonate 5-lipoxygenase
32	Ano1	anoctamin 1, calcium activated chloride channel; heat sensing [9]
33	Anxa1	annexin A1; anti-apoptotic, neuroinflammation [33]
34	Anxa2	annexin A2
35	Apoe	apolipoprotein E
36	Aqp1	aquaporin 1
37	Aqp4	aquaporin 4
38	Arrb2	arrestin, beta 2
39	Asic3	acid-sensing (proton-gated) ion channel 3; temperature sensitivity [24]
40	Atf3	activating transcription factor 3; apoptosis, stress, regeneration [42; 49]
41	Avpr1a	arginine vasopressin receptor 1A
42	Bace1	beta-site APP cleaving enzyme 1
43	Bach1	BTB and CNC homology 1, basic leucine zipper transcription factor 1; axon growth inhibitor [21]
44	Bambi	BMP and activin membrane-bound inhibitor
45	Bbs1	Bardet-Biedl syndrome 1 (human)
46	Bbs4	Bardet-Biedl syndrome 4 (human)
47	Bdkrb1	bradykinin receptor, beta 1
48	Bdkrb2	bradykinin receptor, beta 2
49	Bdnf	brain derived neurotrophic factor
50	Bhlhe22	basic helix-loop-helix family, member e22
51	Bloc1s6	biogenesis of lysosomal organelles complex-1, subunit 6, pallidin
52	C5ar1	complement component 5a receptor 1
53	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
54	Cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit
55	Cacna1e	calcium channel, voltage-dependent, R type, alpha 1E subunit
56	Cacna1g	calcium channel, voltage-dependent, T type, alpha 1G subunit
57	Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit
58	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1; target of the neuropathic pain drug, gabapentin [5]
59	Cacnb3	calcium channel, voltage-dependent, beta 3 subunit
60	Cacng2	calcium channel, voltage-dependent, gamma subunit 2
61	Calb1	calbindin 1; modulator of synaptic plasticity [25]; neuron marker, low threshold mechanoreceptors [53]
62	Calca	calcitonin/calcitonin-related polypeptide, alpha; Ca regulation; vasodilator
63	Calcb	calcitonin-related polypeptide, beta; paralog of CALCA with similar function [40]; Ca regulation; vasodilator
64	Camk1	calcium/calmodulin-dependent protein kinase I; promote nerve regeneration [12]
65	Camk2a	calcium/calmodulin-dependent protein kinase II alpha
66	Camk4	calcium/calmodulin-dependent protein kinase IV
67	Casp1	caspase 1
68	Casp6	caspase 6

69	Ccdc68	coiled-coil domain containing 68; nociceptor marker [24]
70	Cckar	cholecystokinin A receptor; nociceptor marker [24]
71	Cckbr	cholecystokinin B receptor; GPCR protein signalling; positive regulation of synaptic transmission
72	Ccl2	C-C motif chemokine ligand 2; inflammatory and pain mediator [57]
73	Ccl21a	chemokine (C-C motif) ligand 21A (serine)
74	Ccl5	chemokine (C-C motif) ligand 5
75	Ccr2	chemokine (C-C motif) receptor 2
76	Ccr5	chemokine (C-C motif) receptor 5
77	Ccr7	chemokine (C-C motif) receptor 7
78	Cd14	CD14 antigen
79	Cd274	CD274 antigen
80	Cd38	CD38 antigen
81	Cd4	CD4 antigen
82	Cd40	CD40 antigen
83	Cd55	CD55 molecule, decay accelerating factor for complement ; nociceptor marker [24]
84	Cdk5	cyclin-dependent kinase 5
85	Cdk5r1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
86	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21); Cip1;axon regeneration [51]
87	Chrm1	cholinergic receptor, muscarinic 1, CNS
88	Chrm2	cholinergic receptor, muscarinic 2, cardiac; neurotransmission [35]
89	Chrna4	cholinergic receptor, nicotinic, alpha polypeptide 4
90	Chrna5	cholinergic receptor, nicotinic, alpha polypeptide 5; involved in inflammation and pain [2]
91	Chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6; potentially involved in mechanical allodynia [40]
92	Chrna7	cholinergic receptor, nicotinic, alpha polypeptide 7
93	Chrnbg2	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)
94	Chrnbg4	cholinergic receptor, nicotinic, beta polypeptide 4
95	Clock	circadian locomotor output cycles kaput
96	Cnga3	cyclic nucleotide gated channel alpha 3
97	Cnr1	cannabinoid receptor 1 (brain)
98	Cnr2	cannabinoid receptor 2 (macrophage)
99	Col9a1	collagen, type IX, alpha 1
100	Comt	catechol-O-methyltransferase
101	Comt1	catechol-O-methyltransferase 1
102	Cpne6	copine VI; marker of large neurons [24]
103	Crip2	cysteine rich protein 2
104	Csf2	colony stimulating factor 2 (granulocyte-macrophage)
105	Csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
106	Csk	c-src tyrosine kinase
107	Ctsb	cathepsin B
108	Ctss	cathepsin S; induce pain and itch during inflammatory pain [62]
109	Cttn	cortactin; promotes neurite outgrowth [50]
110	Ctxn3	cortexin 3; nociceptor marker [24]
111	Cx3cr1	chemokine (C-X3-C motif) receptor 1
112	Cxcr3	chemokine (C-X-C motif) receptor 3
113	Cybb	cytochrome b-245, beta polypeptide
114	Cyp19a1	cytochrome P450, family 19, subfamily a, polypeptide 1
115	Dab1	disabled 1
116	Dao	D-amino acid oxidase

117	Dbh	dopamine beta hydroxylase
118	Dicer1	dicer 1, ribonuclease type III
119	Disc1	disrupted in schizophrenia 1
120	Dlg2	discs large MAGUK scaffold protein 2; involved in perception of chronic pain via NMDA signalling; synaptic transmission [22]
121	Dlg4	discs large MAGUK scaffold protein 4
122	Dpp4	dipeptidylpeptidase 4
123	Drd1a	dopamine receptor D1
124	Drd2	dopamine receptor D2
125	Drd3	dopamine receptor D3
126	Dtnbp1	dystrobrevin binding protein 1; targets membrane proteins into vesicles; involved in BDNF action [61]
127	Dusp6	dual specificity phosphatase 6
128	Ece2	endothelin converting enzyme 2
129	Edn1	endothelin 1
130	Ednra	endothelin receptor type A
131	Ednrb	endothelin receptor type B
132	Efnb1	ephrin B1
133	Efnb2	ephrin B2
134	Egr1	early growth response 1
135	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2
136	Ephx2	epoxide hydrolase 2, cytoplasmic
137	Esr1	estrogen receptor 1 (alpha)
138	Esr2	estrogen receptor 2 (beta)
139	F2r	coagulation factor II (thrombin) receptor
140	F2rl1	coagulation factor II (thrombin) receptor-like 1
141	F2rl3	coagulation factor II (thrombin) receptor-like 3
142	Faah	fatty acid amide hydrolase
143	Fabp7	fatty acid binding protein 7, brain; found in satellite cells [24]
144	Fam19a4	family with sequence similarity 19, member A4
145	Flrt3	fibronectin leucine rich transmembrane protein 3; promotes neurite outgrowth [52]
146	Fmr1	fragile X mental retardation syndrome 1
147	Fosb	FBJ osteosarcoma oncogene B
148	Foxn1	forkhead box N1
149	Frmpd4	FERM and PDZ domain containing 4
150	Fstl1	follistatin-like 1
151	Fxyd7	FXYD domain-containing ion transport regulator 7; nociceptor marker [24]
152	Fyn	Fyn proto-oncogene
153	Gabbr1	gamma-aminobutyric acid (GABA) B receptor, 1
154	Gabbr2	gamma-aminobutyric acid (GABA) B receptor, 2
155	Gabbr3	gamma-aminobutyric acid (GABA) A receptor, subunit beta 3
156	Gabrd	gamma-aminobutyric acid (GABA) A receptor, subunit delta
157	Gabrg2	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 2
158	Gabrr1	gamma-aminobutyric acid (GABA) C receptor, subunit rho 1
159	Gad2	glutamic acid decarboxylase 2
160	Gadd45a	growth arrest and DNA-damage-inducible 45 alpha; anti-apoptosis [26]
161	Gal	galanin; hormone of nervous systems activating GPCRs; produced in pituitary gland; mechanical and thermal nociception [24]; axon regeneration [16]
162	Galr1	galanin receptor 1
163	Galr2	galanin receptor 2
164	Gap43	growth associated protein 43; nerve growth; microtubule assemble [44]

165	Gfap	glial fibrillary acidic protein
166	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2
167	Gja1	gap junction protein, alpha 1
168	Gla	galactosidase, alpha
169	Glra2	glycine receptor, alpha 2 subunit
170	Glra3	glycine receptor, alpha 3 subunit
171	Gnao1	guanine nucleotide binding protein, alpha O
172	Gnaq	guanine nucleotide binding protein, alpha q polypeptide
173	Gnaz	guanine nucleotide binding protein, alpha z subunit
174	Gpr151	G protein-coupled receptor 151, involved in pain [31]
175	Gpr3	G-protein coupled receptor 3
176	Gpr55	G protein-coupled receptor 55
177	Gpr84	G protein-coupled receptor 84
178	Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein
179	Gria1	glutamate receptor, ionotropic, AMPA1 (alpha 1)
180	Gria2	glutamate receptor, ionotropic, AMPA2 (alpha 2)
181	Grik1	glutamate receptor, ionotropic, kainate 1; involved in itch [11]
182	Grin1	glutamate receptor, ionotropic, NMDA1 (zeta 1)
183	Grin2a	glutamate receptor, ionotropic, NMDA2A (epsilon 1)
184	Grin2b	glutamate receptor, ionotropic, NMDA2B (epsilon 2)
185	Grin2d	glutamate receptor, ionotropic, NMDA2D (epsilon 4)
186	Grin3a	glutamate receptor ionotropic, NMDA3A
187	Grk5	G protein-coupled receptor kinase 5
188	Grk6	G protein-coupled receptor kinase 6; endocytosis; involved in migration of dendritic cells [45]
189	Grm2	glutamate receptor, metabotropic 2
190	Grm4	glutamate receptor, metabotropic 4
191	Grm5	glutamate receptor, metabotropic 5
192	Grn	granulin
193	Gucy1b3	guanylate cyclase 1, soluble, beta 3
194	H2-Ab1	histocompatibility 2, class II antigen A, beta 1
195	Hcn1	hyperpolarization-activated, cyclic nucleotide-gated K+ 1
196	Hcn2	hyperpolarization-activated, cyclic nucleotide-gated K+ 2
197	Hcrt	hypocretin
198	Hdac4	histone deacetylase 4
199	Hdc	histidine decarboxylase
200	Hint1	histidine triad nucleotide binding protein 1
201	Hmox2	heme oxygenase 2
202	Hn1	Jupiter microtubule associated homolog 1; hemopoietic- and neurologic-expressed sequence-1; nerve regeneration [63]
203	Hoxb8	homeobox B8
204	Hrh1	histamine receptor H1
205	Hrh2	histamine receptor H2
206	Hrh3	histamine receptor H3
207	Hspb1	heat shock protein 1; neuron regeneration [17]
208	Htr1a	5-hydroxytryptamine (serotonin) receptor 1A
209	Htr1b	5-hydroxytryptamine (serotonin) receptor 1B
210	Htr2a	5-hydroxytryptamine (serotonin) receptor 2A
211	Htr3a	5-hydroxytryptamine (serotonin) receptor 3A; 5-HT3 ligand gated ion channel [29]
212	Iapp	islet amyloid polypeptide
213	Ica1	islet cell autoantigen 1

214	Ido1	indoleamine 2,3-dioxygenase 1
215	Ifng	interferon gamma
216	Ifngr1	interferon gamma receptor 1
217	Ikbke	inhibitor of kappaB kinase epsilon
218	Il1	interleukin 1 complex
219	Il10	interleukin 10
220	Il17a	interleukin 17A
221	Il18	interleukin 18
222	Il1r1	interleukin 1 receptor, type I
223	Il1rap	interleukin 1 receptor accessory protein
224	Il1rl1	interleukin 1 receptor-like 1
225	Il31ra	interleukin 31 receptor A; mediates each [7]
226	Il4	interleukin 4
227	Il6	interleukin 6
228	Il6st	interleukin 6 signal transducer
229	Irf8	interferon regulatory factor 8
230	Itga7	integrin alpha 7, promote neurite outgrowth [56]
231	Itpr1	inositol 1,4,5-trisphosphate receptor 1
232	Jun	jun proto-oncogene; axon regeneration [6; 39]
233	Kcna1	potassium voltage-gated channel, shaker-related subfamily, member 1
234	Kcna2	potassium voltage-gated channel, shaker-related subfamily, member 2; downregulated in pain [17]
235	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2
236	Kcnip3	Kv channel interacting protein 3, calsenilin
237	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3
238	Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5
239	Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6
240	Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9
241	Kcnk10	potassium channel, subfamily K, member 10
242	Kcnk18	potassium channel, subfamily K, member 18
243	Kcnk2	potassium channel, subfamily K, member 2
244	Kcnk3	potassium channel, subfamily K, member 3
245	Kcnk9	potassium channel, subfamily K, member 9
246	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2
247	Kcnt1	potassium channel, subfamily T, member 1
248	Kif1a	kinesin family member 1A
249	Kit	KIT proto-oncogene receptor tyrosine kinase
250	Klf11	Kruppel-like factor 11
251	Klf6	Kruppel-like factor 6; axon regeneration [54]
252	Klf7	Kruppel-like factor 7 (ubiquitous)
253	L1cam	L1 cell adhesion molecule
254	Lama4	laminin, alpha 4
255	Lcn2	lipocalin 2
256	Lep	leptin
257	Lepr	leptin receptor
258	Lgals1	lectin, galactose binding, soluble 1
259	Lmx1b	LIM homeobox transcription factor 1 beta
260	Lpar1	lysophosphatidic acid receptor 1
261	Lpar3	lysophosphatidic acid receptor 3; nociceptor marker [24]
262	Lpar5	lysophosphatidic acid receptor 5; market of neuropathic pain [53]
263	Lrp1	low density lipoprotein receptor-related protein 1

264	Ltb4r1	leukotriene B4 receptor 1
265	Lxn	latexin
266	Lyn	LYN proto-oncogene, Src family tyrosine kinase
267	Lynx1	Ly6/neurotoxin 1; nociceptor marker [24]
268	Lyst	lysosomal trafficking regulator
269	Map2k1	mitogen-activated protein kinase kinase 1
270	Map2k3	mitogen-activated protein kinase kinase 3
271	Map3k8	mitogen-activated protein kinase kinase kinase 8
272	Mapk1	mitogen-activated protein kinase 1
273	Mapk10	mitogen-activated protein kinase 10
274	Mapk3	mitogen-activated protein kinase 3
275	Mapk8	mitogen-activated protein kinase 8
276	Mapk9	mitogen-activated protein kinase 9
277	Mapt	microtubule-associated protein tau
278	Mc1r	melanocortin 1 receptor
279	Mgll	monoglyceride lipase
280	Mif	macrophage migration inhibitory factor (glycosylation-inhibiting factor)
281	Mme	membrane metallo endopeptidase
282	Mmp24	matrix metallopeptidase 24
283	Mmp9	matrix metallopeptidase 9
284	Mrgprb4	MAS-related GPR, member B4; sensing touch [27]
285	Mrgprd	MAS-related GPR, member D; temperature sensitivity [24]
286	Mrgpre	MAS-related GPR, member E
287	Mtap6	microtubule-associated protein 6
288	Myd88	myeloid differentiation primary response gene 88
289	Nav2	neuron navigator 2
290	Nbl1	neuroblastoma, suppression of tumorigenicity 1
291	Ncam1	neural cell adhesion molecule 1
292	Ndn	necdin
293	Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like
294	Nefh	neurofilament, heavy polypeptide; nociceptor marker [24]
295	Nf1	neurofibromin 1
296	Nfe2l2	nuclear factor, erythroid derived 2, like 2
297	Nfil3	nuclear factor, interleukin 3, regulated; axon growth inhibition [32]
298	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105
299	Ngf	nerve growth factor
300	Ngfr	nerve growth factor receptor (TNFR superfamily, member 16); neuronal survival [8]; can mediate neuron survival; marker of neuropathic pain [3]
301	Nlgn2	neuroligin 2
302	Nmu	neuromedin U
303	Nmur2	neuromedin U receptor 2
304	Nos1	nitric oxide synthase 1, neuronal
305	Nos2	nitric oxide synthase 2, inducible
306	Nos3	nitric oxide synthase 3, endothelial cell
307	Nox1	NADPH oxidase 1
308	Nox4	NADPH oxidase 4
309	Npb	neuropeptide B
310	Npepps	aminopeptidase puromycin sensitive
311	Nppc	natriuretic peptide type C
312	Nptx1	neuronal pentraxin 1
313	Npy	neuropeptide Y; endocrine; GPCR binding; neuron projection development;

		negative regulation of blood pressure [58]
314	Npy1r	neuropeptide Y receptor Y1
315	Nr2c2	nuclear receptor subfamily 2, group C, member 2
316	Nr2f6	nuclear receptor subfamily 2, group F, member 6
317	Nrg1	neuregulin 1
318	Nt5e	5' nucleotidase, ecto
319	Ntf5	neurotrophin 5
320	Ntrk1	neurotrophic tyrosine kinase, receptor, type 1
321	Ntrk3	neurotrophic tyrosine kinase, receptor, type 3; survival, differentiation; marker of myelinated neurons [53]
322	Nts	Neurotensin; neuropeptide hormone activity; vesicle transport
323	Ntsr1	neurotensin receptor 1
324	Ntsr2	neurotensin receptor 2
325	Oprd1	opioid receptor, delta 1
326	Oprk1	opioid receptor, kappa 1
327	Oprl1	opioid receptor-like 1
328	Oprm1	opioid receptor, mu 1
329	Oprs1	sigma non-opioid intracellular receptor 1
330	Osm	oncostatin M
331	Oxt	oxytocin
332	P2rx2	purinergic receptor P2X, ligand-gated ion channel, 2
333	P2rx3	purinergic receptor P2X, ligand-gated ion channel, 3
334	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4
335	P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7
336	P2ry1	purinergic receptor P2Y, G-protein coupled 1; heat and mechanical sensitivity [30]
337	P2ry12	purinergic receptor P2Y, G-protein coupled 12
338	P2ry2	purinergic receptor P2Y, G-protein coupled 2
339	Pak7	p21 protein (Cdc42/Rac)-activated kinase 7
340	Pcsk2	proprotein convertase subtilisin/kexin type 2
341	Pcsk6	proprotein convertase subtilisin/kexin type 6
342	Pdyn	prodynorphin
343	Penk	preproenkephalin
344	Per1	period circadian clock 1
345	Per2	period circadian clock 2
346	Pick1	protein interacting with C kinase 1
347	Pik3cg	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma; immunity [48]
348	Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha
349	Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma
350	Pirt	phosphoinositide-interacting regulator of transient receptor potential channels
351	Pkd2l1	polycystic kidney disease 2-like 1; subunit of calcium channel; involved in sensory functions and pain [18]
352	Plaur	plasminogen activator, urokinase receptor; marker of large neurons [24]
353	Plcb1	phospholipase C, beta 1
354	Plcb3	phospholipase C, beta 3
355	Plcb4	phospholipase C, beta 4
356	Plcl1	phospholipase C-like 1
357	Pldn	pallidin
358	Plp1	proteolipid protein (myelin) 1
359	Pmp22	peripheral myelin protein 22
360	Pnoc	prepronociceptin

361	Pomc	pro-opiomelanocortin-alpha
362	Por	P450 (cytochrome) oxidoreductase
363	Ppara	peroxisome proliferator activated receptor alpha
364	Ppp1r9b	protein phosphatase 1, regulatory subunit 9B
365	Prcaa2	protein kinase, AMP-activated, alpha 2 catalytic subunit
366	Prkar1b	protein kinase, cAMP dependent regulatory, type I beta
367	Prkca	protein kinase C, alpha
368	Prkcb	protein kinase C, beta
369	Prkcc	protein kinase C, gamma
370	Prkcd	protein kinase C, delta
371	Prkce	protein kinase C, epsilon
372	Prkcg	protein kinase C, gamma
373	Prkg1	protein kinase, cGMP-dependent, type I
374	Prl	prolactin
375	Prlhr	prolactin releasing hormone receptor
376	Prlr	prolactin receptor
377	Prnp	prion protein
378	Prok2	prokineticin 2
379	Prokr1	prokineticin receptor 1; involved in nociception and inflammatory pain [36]
380	Prrxl1	paired related homeobox protein-like 1
381	Prx	periaxin
382	Ptafr	platelet-activating factor receptor; regulates neuro-inflammation [60]
383	Ptgdr	prostaglandin D receptor; marker of chronic inflammatory pain [53]
384	Ptgds	prostaglandin D2 synthase (brain)
385	Ptger1	prostaglandin E receptor 1 (subtype EP1); marker of chronic inflammatory pain [53]; sensitivity to heat [24]
386	Ptger2	prostaglandin E receptor 2 (subtype EP2)
387	Ptger3	prostaglandin E receptor 3 (subtype EP3)
388	Ptger4	prostaglandin E receptor 4 (subtype EP4)
389	Ptges	prostaglandin E synthase
390	Ptgfr	prostaglandin F receptor
391	Ptgir	prostaglandin I receptor (IP)
392	Ptgs1	prostaglandin-endoperoxide synthase 1
393	Ptgs2	prostaglandin-endoperoxide synthase 2
394	Pth2	parathyroid hormone 2
395	Pth2r	parathyroid hormone 2 receptor
396	Ptn	Pleiotrophin; mediates microglia-mediated inflammation [14]
397	Ptpn6	protein tyrosine phosphatase, non-receptor type 6
398	Ptprz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1
399	Rabggt1a	Rab geranylgeranyl transferase, a subunit
400	Rag1	recombination activating gene 1
401	Rag2	recombination activating gene 2
402	Ramp1	receptor (calcitonin) activity modifying protein 1
403	Rasd2	RASD family, member 2
404	Reln	reelin
405	Ret	ret proto-oncogene
406	Rgs4	regulator of G-protein signaling 4
407	Rgs9	regulator of G-protein signaling 9
408	Rps6ka3	ribosomal protein S6 kinase polypeptide 3
409	Rsk2	ribosomal protein S6 kinase polypeptide 3
410	Rtn4	reticulon 4; axon growth inhibition [55]

411	Runx1	runt related transcription factor 1
412	S100a10	S100 calcium binding protein A10 (calpactin)
413	S100b	S100 protein, beta polypeptide, neural
414	S1pr3	sphingosine-1-phosphate receptor 3
415	Scg3	secretogranin III; nociceptor marker [24]
416	Scn10a	sodium channel, voltage-gated, type X, alpha [40]
417	Scn11a	sodium channel, voltage-gated, type XI, alpha
418	Scn2b	sodium channel, voltage-gated, type II, beta; modulates response to pain [28]
419	Scn9a	sodium channel, voltage-gated, type IX, alpha
420	Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A; axon growth inhibitor [46]
421	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N
422	Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a; inflammatory component of neuropathic pain [43]
423	Sesn2	sestrin 2
424	Shc1	src homology 2 domain-containing transforming protein C1
425	Shisa9	shisa family member 9, AMPAR-associated; axon growth [43]
426	Sigmar1	sigma non-opioid intracellular receptor 1
427	Slc12a2	solute carrier family 12, member 2
428	Slc12a5	solute carrier family 12, member 5
429	Slc12a6	solute carrier family 12, member 6
430	Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2
431	Slc17a6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6
432	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7
433	Slc17a8	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 8
434	Slc32a1	solute carrier family 32 (GABA vesicular transporter), member 1
435	Slc6a1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1
436	Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2
437	Slc6a4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4
438	Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6
439	Sod2	superoxide dismutase 2, mitochondrial
440	Sox11	SRY (sex determining region Y)-box 11; transcription factor involved in neuronal regeneration [20]
441	Sparc	secreted acidic cysteine rich glycoprotein
442	Spp1	secreted phosphoprotein 1
443	Sprr1a	small proline-rich protein 1A; neuronal regeneration [20]
444	Srd5a1	steroid 5 alpha-reductase 1
445	Srr	serine racemase
446	Sstr4	somatostatin receptor 4
447	St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
448	Stard13	StAR-related lipid transfer (START) domain containing 13
449	Stk39	serine/threonine kinase 39
450	Stmn4	stathmin-like 4; promote microtubule assemble (Iwata 02)
451	Stoml3	stomatin (Epb7.2)-like 3
452	Stx1a	syntaxin 1A (brain)
453	SYMBOL	description
454	Syn2	synapsin II
455	Synpr	Synaptoporin; nociceptor marker [24]
456	Tac1	tachykinin 1

457	Tac4	tachykinin 4
458	Tacr1	tachykinin receptor 1
459	Th	tyrosine hydroxylase; marker of small neurons
460	Thbs4	thrombospondin 4
461	Tlr2	toll-like receptor 2
462	Tlr3	toll-like receptor 3
463	Tlr4	toll-like receptor 4
464	Tlr5	toll-like receptor 5
465	Tlr9	toll-like receptor 9
466	Tmem88b	transmembrane protein 88B; potentially involved in sensory functions [59]
467	Tnf	tumor necrosis factor
468	Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a; survival, apoptosis, and inflammation; marker of neuropathic pain [53]
469	Tnfrsf1b	tumor necrosis factor receptor superfamily, member 1b; involved in neuro-inflammation [15; 47]
470	Trpa1	transient receptor potential cation channel, subfamily A, member 1; sensitivity to cold and chemicals [4; 34]
471	Trpc3	transient receptor potential cation channel, subfamily C, member 3; might contribute to sensitivity to heat and mechanic stimuli [24]
472	Trpm2	transient receptor potential cation channel, subfamily M, member 2
473	Trpm3	transient receptor potential cation channel, subfamily M, member 3
474	Trpm8	transient receptor potential cation channel, subfamily M, member 8; sensitivity to cold [4; 34]
475	Trpv1	transient receptor potential cation channel, subfamily V, member 1; temperature sensitivity [4; 10]
476	Trpv3	transient receptor potential cation channel, subfamily V, member 3
477	Trpv4	transient receptor potential cation channel, subfamily V, member 4
478	Tuba4a	tubulin, alpha 4A; nociceptor marker [24]
479	Tubb6	tubulin, beta 6 class V; microtubules assembly [41]
480	Tyrp1	tyrosinase-related protein 1
481	Uchl1	ubiquitin carboxy-terminal hydrolase L1
482	Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)
483	Vip	vasoactive intestinal polypeptide
484	Wld	wallerian degeneration
485	Yy1	YY1 transcription factor
486	Zeb2	zinc finger E-box binding homeobox 2

**Table S7. Significantly enriched GO terms associated with common 655 rat/mouse genes (Table S5) in injury models.**

GO term	score	genes	term name
GO.0005615	1.41E-10	Abca1, Abhd8, Ache, Adcyap1, Akr1b8, Anxa1, Anxa8, Apaf1, Apobr, Apod, Atp2b2, B3gnt8, Basp1, Bcan, Bmp1, Btc, Btg2, C1qb, C1qc, C3, C4b, Cacna2d1, Calb1, Car1, Carhsp1, Ccl7, Cd14, Cd38, Cd53, Cd84, Clcf1, Clic1, Ctnn1, Col11a1, Col18a1, Col5a1, Col5a2, Col5a3, Cpne4, Creb5, Crh, Crlf1, Crocc, Csf1, Ctsc, Cxadr, Cxcl10, Cxcl14, Dab2, Dsc2, Duox2, Ech1, Entpd2, EphA10, Epn3, Evpl, Extl2, Fgf2, Fam129b, Fgf9, Fam151a, Fkbp4, Flna, Fst, Gabrb2, Gal, Gamt, Gcnt1, Gdnf, Gprc5c,	extracellular space

		Grem2,H3f3b,Havcr2,Hebp2,Hist2h3c2,Hs6st2,Ibsp,Icam1,Igfbp3,Il1r1,Il33,Inhbb,Itgam,Khk,Krt19,Lama5,Ldhb,Lgals3,Lgi4,Lilra5,Lingo1,Loxl2,Lrfn1,Lrrc17,Lrrn1,Lrrn2,Ltbp1,Lyz2,Manba,Marcks1,Met,Metrnl,Mmp19,Mrgprf,Msr1,Mthfd2,Mvp,Myadm,Myo5b,Ncald,Nckap1l,Npy,Ntm,Olfm3,Omg,Opcml,Pcdh11x,Pcdh15,Plat,Plau,Plcg2,Pls1,Postn,Pros1,Psmb8,Ptprc,Ptprj,Ptpro,Ptrhd1,Ptx3,Qprt,Rab4a,Rap2b,Rhoc,Rhoq,Rnase4,Rras2,Rspo1,Rtn4rl1,Scin,S100a4,Scpep1,Sdc1,Sdcbp2,Sema3c,Sema3f,Sema4f,Sh3gl3,Slc1a1,Slc2a1,Slc2a5,Slc38a1,Sord,Sphkap,Spock1,Spr,Srp2,Stom,Steap4,Tax1bp3,Tecta,Tgfb1,Tgm1,Thbs2,Timp1,Tmem132a,Tnc,Tnfaip6,Tnfrsf8,Tnfsf10,Tnik,Trhde,Tuba4a,Tubb6,Ucn2,Vgf,Vwc2l,Wnt10b,Wnt7a,Xdh,Zmynd15	
GO.0005887	2.72E-10	Abca1,Abcc3,Acvr1,Acvr1c,Adra1a,Adra2c,Adrb2,Asic1,Atp13a4,Atp2b2,Atp2b3,C3ar1,C5ar1,Cacng2,Cd53,Chrm2,Chrna5,Chrna7,Clec2d,Corin,Cyba,Cysltr1,Dab2,Dpp10,Drd2,Ecel1,Epha10,Ephb2,Fcgr2b,Gabra1,Gabrb2,Gabrg2,Galr1,Gpnmb,Gpr65,Gria2,Gria4,Grin1,Gypc,Hcn2,Htr1a,Icam1,Il17ra,Il17re,Itga7,Itgam,Kcna2,Kcna4,Kcnc3,Kcnh4,Kcnh5,Kcnh7,Kcnip1,Kcnip3,Kcnj11,Kcnj3,Kcnj9,Kcnk1,Kcns3,Laptm5,Mmp16,Mrc1,Mrgprf,Mrgprx1,Ntrk1,Olfm3,Oprd1,Opri1,P2rx5,P2rx6,P2ry13,P2ry14,Pcdh15,Ptprc,Scn1a,Scn4a,Scn4b,Scn8a,Sectm1b,Shank1,Slc1a1,Slc28a2,Slc2a1,Slc2a5,Slc38a1,Slc38a6,Slc4a8,Slc6a7,Slco2b1,Slco5a1,Slitrk6,Stom,Steap1,Steap4, Ticam2,Tlr1,Tm4sf1,Tnfrsf1b,Tnfrsf8,Tshr,Vwc2l	integral component of plasma membrane
GO.0005886	2.93E-09	Abca1,Abcc3,Ache,Acvr1,Acvr1c,Adcy4,Adra1a,Adra2c,Adrb2,Agtr1b,Aif1,Ank1,Ankrd13d,Anxa1,Anxa8,Ap2s1,Apbb1,Apoibr,Ar,Arc,Arhgap25,Arhgef2,Asah2,Asic1,Atp13a4,Atp2b2,Atp2b3,Atp8b1,Bambi,Basp1,Best3,Bin2,Bmpr1b,Btc,C3ar1,C5ar1,Cacna2d1,Cacna2d2,Cacng2,Caln1,Casp3,Casp4,Cckbr,Ccr5,Cd14,Cd38,Cd53,Cd84,Cdh8,Chrm2,Chrna5,Chrna7,Clec2d,Clic1,Cnnm1,Cntn1,Cntn3,Cntn4,Cntn6,Corin,Crocc,Csf1,Csf1r,Cx3cr1,Cxadr,Cxcl10,Cyba,Cysltr1,Cyth2,Cyth4,Dab2,Dock8,Dpp10,Drd2,Dsc2,Dtnbp1,Duox2,Duoxa1,Ecel1,Emp1,Entpd2,Epha10,Ephb2,Epn3,Ets2,Evpl,Fadd,Faim2,Fam126b,Fam129b,Fcgr2b,Flna,Flnc,Fndc5,Fosl1,Fzd6,Gabra1,Gabra5,Gabrb2,Gabrg1,Gabrg2,Galr1,Gap43,	plasma membrane

		Gdpd2,Gfra3,Gfral,Gjd2,Gpnmb,Gpr153,Gpr156,Gpr65,Gprc5c, Gria2,Gria4,Grid2ip,Grin1,Gypc,Havcr2,Hcn2,Hsd17b7,Htr1a, Htr3a,Icam1,Iftm2,Il10ra,Il17ra,Il17re,Il1r1,Il2rg,Inpp5d,Inpp5j, Itga7,Itgam,Jph3,Kcna2,Kcna4,Kcnc3,Kcnh4,Kcnh5,Kcnh7,Kcnip1, Kcnip3,Kcnj11,Kcnj3,Kcnj9,Kcnk1,Kcnn2,Kcns3,Krt19,Lancl3,Laptm5, Lgals3,Lhfpl5,Lingo1,Lmo7,Lrfn1,Ly6h,Marcksl1,Mc4r,Mchr1,Met, Mmp16,Mmp19,Mrc1,Mrgprf,Mrgprx1,Msr1,Myadm,Myo10,Nav2, Nkd2,Notch4,Ntm,Ntng1,Ntrk1,Olfm3,Omg,Oprd1,Oprl1,P2rx5, P2rx6,P2ry1,P2ry13,P2ry14,Paqr5,Pcdh15,Plcb2,Plcg2,Plin2,Podxl, Prc1,Prmt8,Prokr2,Prss12,Ptpcr,Ptpcr,Ptpro,Rab33a,Rab4a,Rap2b, Rasgrp1,Rasgrp4,Rem2,Rgs12,Rgs16,Rgs6,Rhoc,Rhoq,Ripk3,Rph3a, Rras2,Rtn2,Rtn4rl1,S1pr2,Scn1a,Scn4a,Scn4b,Scn8a,Sdc1,Sdcbp2, Sectm1b,Sema4f,Sema7a,Sez6l,Shank1,Siglec1,Sla,Slc11a1,Slc1a1, Slc28a2,Slc2a1,Slc2a5,Slc30a3,Slc34a2,Slc38a1,Slc38a6,Slc4a8, Slc5a6,Slc6a7,Slc9a5,Slco2b1,Slco5a1,Slitrk6,Spr,Sprr1a,Srpox2, Steap1,Steap4,Stom,Syt17,Syt2,Syt3,Syt4,Tapbpl,Tax1bp3,Tecta, Tes,Th,Ticam2,Tlr1,Tm4sf1,Tmem173,Tnfrsf12a,Tnfrsf1b,Tnfrsf8, Tnik,Tpbg,Trem2,Trhde,Trpm8,Tshr,Tusc5,Ush1g,Vdr,Vstm2b, Vwc2l,Zbtb42	
GO.0043025	5.36E-07	Ache,Adrb2,Aif1,Apbb1,Apod,Ar,Arhgef2,Atp2b2,C4b,Calb1,Casp4, Chrna5,Chrna7,Cnnm1,Cplx2,Crh,Crmp1,Cx3cr1,Cyba,Drd2,Dtnbp1, Ephb2,Fbxo31,Fkbp4,Flna,Gabra5,Gal,Gria2,Gria4,Grin1,Hcn2, Htr1a,Htr3a,Kcna2,Kcnc3,Kcnip1,Kcnj11,Kcnn2,Ltbp1,Met,Myo10, Myo5b,Nefh,Nefm,Npy,Ntrk1,P2rx6,Pde1a,Ptpn5,Ptx3,Rgs12, Scn1a,Scn8a,Sez6l,Slc4a8,Syt4,Th,Tnfrsf1b,Ucn,Vgf	neuronal cell body
GO.0016021	1.90E-06	Abca1,Abcc3,Abcd2,Acvr1,Acvr1c,Adam11,Adcy4,Adra1a,Adra2c, Adrb2,Agtr1b,Armcx6,Asah2,Asic1,Asphd2,Astn2,Atp13a4,Atp2b2, Atp2b3,Atp8b1,B3galt5,B3gat1,B3gnt8,Bambi,Best3,Bmpr1b,Btc, C3,C3ar1,C5ar1,Cacna2d1,Cacna2d2,Cacng2,Caln1,Cckbr,Ccr5, Cd14,Cd38,Cd53,Cd84,Cdh8,Chrm2,Chrna5,Chrna7,Chst10,Chst5, Chst9,Clec2d,Clec2l,Clic1,Cnnm1,Corin,Csf1,Csf1r,Csf2rb,Cx3cr1, Cxadr,Cyba,Cyp2u1,Cysltr1,Dab2,Dpp10,Drd2,Dsc2,Duoxa1,Ecel1, Emp1,Entpd2,Epha10,Ephb2,Ern2,Extl2,Fads3,Faim2,Fam151a, Fam163a,Fam210b,Fam57b,Fam69b,Fcgr2b,Fndc3a,Fndc5,Fzd6,	integral component of membrane

		Gabra1,Gabra5,Gabrb2,Gabrg1,Gabrg2,Gal,Galnt5,Galnt9,Galr1, Gcnt1,Gdpd2,Gfral,Gjd2,Gpnmb,Gpr153,Gpr156,Gpr65,Gprc5c, Gria2,Gria4,Grin1,Gypc,Havcr2,Hcn2,Hhatl,Hrasls,Hs6st2,Hsd17b7, Htr1a,Htr3a,Icam1,Ifitm2,Il10ra,Il13ra1,Il17ra,Il17re,Il1r1,Il21r, Il2rg,Itga7,Itgam,Jph3,Kcna2,Kcna4,Kcnc3,Kcnh4,Kcnh5,Kcnh7, Kcnip1,Kcnip3,Kcnj11,Kcnj3,Kcnj9,Kcnk1,Kcnn2,Kcns3,Kdelr1, Laptm5,Layn,Lhfpl5,Lingo1,Lingo4,Lrfn1,Lrrn1,Lrrn4cl,Mc4r,Mchr1, Met,Mgat4c,Mmp16,Mrc1,Mrgprf,Mrgprx1,Msr1,Myadm, Myadml2,Nat8l,Nckap1l,Ndst4,Notch4,Ntrk1,Olfm3,Oprd1, Oprl1,P2rx5,P2rx6,P2ry1,P2ry13,P2ry14,Paqr5,Pcdh15,Podxl, Prokr2,Ptpn5,Ptprc,Ptprj,Ptpro,Rnf112,Rnf180,Rnf19b,Rtn2, Rtn4rl1,S1pr2,Scn1a,Scn4a,Scn4b,Scn8a,Sdc1,Sec61b,Sectm1b, Sema4f,Sertm1,Sez6l,Shank1,Siglec1,Slc11a1,Slc15a3,Slc17a7, Slc1a1,Slc25a24,Slc25a45,Slc28a2,Slc2a1,Slc2a5,Slc30a3,Slc34a2, Slc38a1,Slc38a6,Slc44a5,Slc4a8,Slc5a6,Slc6a7,Slco2b1,Slco5a1, Slitrk3,Slitrk6,Smim3,Spr,Steap1,Steap4,Stom,Susd4,Syt2,Syt3,Syt4, Tapbpl,Thsd7b,Ticam2,Tlr1,Tm4sf1,Tmc7,Tmem132a,Tmem132e, Tmem173,Tmem229b,Tmem43,Tmem88b,Tmem98,Tnfrsf12a, Tnfrsf1b,Tnfrsf8,Tnfsf10,Tpbpg,Trem2,Trhde,Trpm8,Tshr,Tusc5, Vamp1,Vstm2b,Vwc2l,Zmynd15	
GO.0045211	3.77E-06	Ache,Ank1,Apbb1,Arc,Atp2b2,Cacng2,Chrm2,Chrna5,Chrna7, Dtnbp1,Faim2,Gabra1,Gabra5,Gabrb2,Gabrg1,Gabrg2,Gpr156, Gria2,Gria4,Grid2ip,Grin1,Htr3a,Kcna4,Lrfn1,Met,Oprd1,P2ry1, Sdcbp2,Sema4f,Shank1	postsynaptic membrane
GO.0030054	1.14E-05	Ache,Anxa1,Arc,Arhgef2,Atp2b2,Basp1,Brsk1,Cacng2,Calb2,Ccnd1, Cd53,Chrm2,Chrna5,Chrna7,Cxadr,Cyba,Cyth2,Dab2,Dsc2,Dtnbp1, Evpl,Faim2,Fam129b,Flna,Flnc,Gabra1,Gabra5,Gabrb2,Gabrg1, Gabrg2,Gap43,Gjd2,Gpr156,Gria2,Gria4,Grid2ip,Grin1,Gypc,Havcr2, Htr3a,Icam1,Itga7,Kcna2,Kcnc3,Kcnj11,Kcnk1,Lgi3,Lmln,Lmo7,Lrfn1, Myadm,Olfm3,P2rx6,Plau,Podxl,Ptprc,Ptprj,Rap2b,Rgs12,Rph3a, Ras2,Scin,Scn1a,Scn4b,Sdcbp2,Shank1,Slc17a7,Slc2a1,Slc30a3, Smpx,Srpx2,Syt2,Syt4,Tes,Tgm1,Tnc,Triobp,Vamp1,Vav1,Vwc2l	cell junction
GO.0009986	1.94E-05	Abca1,Ache,Acvr1c,Anxa1,Asic1,C5ar1,Ccr5,Cd14,Cd38,Cd53, Chrna7,Clec2d,Corin,Csf1r,Cxcl10,Entpd2,Fcgr2b,Gfra3,Gria2,Grin1,	cell surface

		Havcr2,Htr3a,Icam1,Il1r1,Il2rg,Itga7,Itgam,Kcna4,Kcnh5,Kcnj3, Lgals3,Lrfn1,Met,Mrc1,Notch4,Ntm,Ntrk1,P2ry1,Plat,Plau,Ptpcr, Ptprj,Rhoc,Rtn4rl1,Sdc1,Sema7a,Slitrk6,Spr,Srpx2,Tnfrsf12a,Tpbg, Trpm8,Vamp1,Wnt7a	
GO.0043197	2.61E-05	Adrb2,Apbb1,Ar,Asic1,Calb1,Chrna7,Drd2,Dtnbp1,Fcgr2b,Frmpd4, Gria2,Gria4,Grid2ip,Grin1,Kcna4,Kcnn2,Myo5b,P2rx6,Ptpro,Shank1	dendritic spine
GO.0043083	3.27E-05	Ache,Cdh8,Grin1,Lama5,Prss12	synaptic cleft
GO.0005583	5.78E-05	Col11a1,Col27a1,Col5a1,Col5a2,Col5a3	fibrillar collagen trimer
GO.0030425	5.83E-05	Ache,Adcy4,Adrb2,Apbb1,Apod,Ar,Arhgef15,Arhgef2,Asic1,Atp2b2, Bcan,C4b,Calb1,Chrna5,Chrna7,Cnnm1,Cplx2,Crmp1,Ctla2a,Cyba, Drd2,Dtnbp1,Ephb2,Fcgr2b,Flna,Frmpd4,Gabra5,Gabrg2,Gria2, Gria4,Grid2ip,Grin1,Hcn2,Inpp5j,Kcna2,Kcna4,Kcnc3,Kcnip1,Kcnip3, Kcnn2,Ltbp1,Met,Myo5b,Ntrk1,Oprd1,P2rx6,P2ry1,Prss12,Ptpn5, Ptpro,Rgs12,Scn8a,Sdcbp2,Shank1,Spr,Syt4,Th,Ucn	dendrite
GO.0031225	6.51E-05	Ache,Bcan,Cd14,Cntn1,Cntn3,Cntn4,Cntn6,Gfra3,Ly6h,Mmp19,Ntm, Ntng1,Omg,Rtn4rl1,Sema7a,Tecta	anchored component of membrane
GO.0005576	7.40E-05	Abca1,Abhd8,Ache,Adamts1,Adcyap1,Akr1b8,Anxa1,Anxa8,Aoah, Apaf1,Apoibr,Apod,Atp2b2,Atp2b3,B3gat1,B3gnt8,Basp1,Bcan, Bmp1,Btc,Btg2,C1qb,C1qc,C3,C4b,Cacna2d1,Calb1,Car1,Carhsp1, Casp4,Ccl7,Cd14,Cd38,Cd53,Cd84,Cdh8,Clf1,Clic1,Cntn1,Cntn4, Col11a1,Col18a1,Col27a1,Col5a1,Col5a2,Col5a3,Corin,Cpne4,Creb5, Crh,Crlf1,Crocc,Csf1,Ctla2a,Ctsc,Cxadr,Cxcl10,Cxcl14,Dab2,Dsc2, Duox2,Ech1,Entpd2,Epha10,Epn3,Evpl,Extl2,Fam129b,Fam151a, Fcgr2b,Fgf2,Fgf9,Fkbp4,Flna,Fndc5,Fst,Fstl5,Gabrb2,Gal,Gamt, Gcnt1,Gdnf,Glb1l2,Gprc5c,Grem2,Gria4,Grin1,H3f3b,Hapl1, Havcr2,Hebp2,Hist2h3c2,Hpse,Hs6st2,Hyal3,Ibsp,Icam1,Igfbp3, Igfsf21,Il17re,Il1r1,Il33,Inhbb,Itgam,Khk,Krt19,Lama5,Lamb3,Ldhb, Lgals3,Lgi3,Lgi4,Lilra5,Lingo1,Lipk,Lipn,Loxl2,Lrfn1,Lrrc17,Lrrn1, Lrrn2,Ltbp1,Lyz2,Manba,Marcks1l,Met,Metrnl,Mmp16, Mmp19,Mrgprf,Msr1,Mthfd2,Mvp,Myadm,Myo5b,Nav2,Ncald, Nckap1l,Npy,Ntm,Olfm3,Omg,Opcml,Pcdh11x,Pcdh15,Pla2g2d,Plat, Plau,Plcg2,Pls1,Postn,Pros1,Prss12,Psmb8,Ptpcr,Ptprj,Ptpro,Ptrhd1, Ptx3,Qprt,Rab4a,Rap2b,Rhoc,Rhoq,Rnase4,Rras2,Rspo1,Rtn4rl1,	extracellular region

		S100a4,Scin,Scpep1,Sdc1,Sdcbp2,Sectm1b,Sema3c,Sema3f,Sema4f, Sh3gl3,Siglec1,Slc1a1,Slc2a1,Slc2a5,Slc38a1,Sord,Sphkap,Spock1, Spr,Srpx2,Steap4,Stom,Syt4,Tax1bp3,Tecta,Tgfb1,Tgm1,Thbs2, Tim1,Tll1,Tmem132a,Tnc,Tnfaip6,Tnik,Tnfrsf8,Tnfsf10,Trem2, Trhde,Tuba4a,Tubb6,Ucn,Ucn2,Vash2,Vgf,Vwa7,Vwc2l,Wif1, Wnt10b,Wnt7a,Xdh,Zmynd15	
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**Table S8. GO terms associated with BP and CC categories from enrichment analysis with ClusterProfiler of the common rat DEGs, excluding genes classified as nociceptor-related with the mouse classification of [17].**

GO term	term name	gene ratio	p_adj	genes
<b>CC terms</b>				
GO:1990204	oxidoreductase complex	41/1758	1.79E-11	Rrm2/Cybb/Nox4/Ncf4/Gpd2/Ndufa11/Ndufa7/Rrm2b/Ndufa6/Ndufs8/Idh3g/Ndufb5/Sdhd/Pdha1/Pdhx/Ndufs4/Ndufc2/Ndufb9/Idh3a/Uqcrc2/Dld/Ndufa9/Uqcrh/Uqcrb/Mrps36/Ndufa4/Ndufa8/Sdha/Cyc1/Ndufs3/Ndufb8/Bckdhb/Ndufb6/Ndufab1/Ndufb3/Ndufv2/Ndufa5/Ndufa10/Idh3B/Ndufs1/Ndufs5
GO:0005746	mitochondrial respiratory chain	35/1758	4.42E-11	MGC105649/Cox7a2l/Cox8a/Ndufa11/Ndufa7/Ndufa6/Ndufs8/Cox6c/Cox5b/Ndufb5/Sdhd/Ndufs4/Ndufc2/Ndufb9/Uqcrc2/Ndufa9/Cox7c/Uqcrh/Uqcrb/Ndufa4/Ndufa8/Sdha/Cyc1/Ndufs3/Ndufb8/Cox4i2/Ndufb6/Cox7b/Ndufab1/Ndufb3/Ndufv2/Ndufa5/Ndufa10/Ndufs1/Ndufs5
GO:0043235	receptor complex	76/1758	4.42E-11	Il6/Gdnf/Gpr101/Cd3e/Itgam/Itgal/Cd3d/Chrna1/Olr1/Cd3g/Tlr7/Tshr/Cd6/Tgfb1/Ramp1/Itga10/Tlr2/Bmp2/Grin2b/Smad3/Ptpn6/Itga4/Il6r/Dab2/Gabra5/Emilin1/Nr1h3/Eng/Grin2d/Lrp4/Cd40/Itga6/Itgb7/Ror1/Lrp1/Itga1/Shisa7/Osmr/Scrib/Npr1/Notch1/Dlg3/Lifr/Sdcbp/Stoml2/Ntrk3/Ret/Gabrb3/P2rx3/Musk/Trpc1/Shank2/Acvr1b/Grid2/Nlgn1/Abhd12/Dlg2/Sacm1l/Gabra3/Olfm1/Grin3a/Chrna5/Grm7/Ph1r/Ntrk1/Abcg8/Olfm3/Grin1/Itga11/Kcnh2/Chrna4/Dlgap3/Vwc2l/Itgb6/Chrna3/Htr3a
GO:0098803	respiratory chain complex	34/1758	4.79E-11	MGC105649/Cox8a/Ndufa11/Ndufa7/Ndufa6/Ndufs8/Cox6c/Cox5b/Ndufb5/Sdhd/Ndufs4/Ndufc2/Ndufb9/Uqcrc2/Ndufa9/Cox7c/Uqcrh/Uqcrb/Ndufa4/Ndufa8/Sdha/Cyc1/Ndufs3/Ndufb8/Cox4i2/Ndufb6/Cox7b/Ndufab1/Ndufb3/Ndufv2/Ndufa5/Ndufa10/Ndufs1/Ndufs5
GO:0098802	plasma membrane receptor complex	50/1758	1.17E-10	Il6/Cd3e/Itgam/Itgal/Cd3d/Chrna1/Cd3g/Cd6/Tgfb1/Ramp1/Itga10/Tlr2/Bmp2/Grin2b/Ptpn6/Itga4/Il6r/Dab2/Emilin1/Grin2d/Cd40/Itga6/Itgb7/Itga1/Shisa7/Osmr/Scrib/Dlg3/Sdcbp/Stoml2/Shank2/Acvr1b/Grid2/Nlgn1/Abhd12/Dlg2/Sacm1l/Olfm1/Grin3a/Chrna5/Olfm3/Grin1/Itga11/Kcnh2/Chrna4/Dlgap3/Vwc2l/Itgb6/Chrna3/Htr3a
GO:0070469	respiratory chain	35/1758	1.84E-10	MGC105649/Cox7a2l/Cox8a/Ndufa11/Ndufa7/Ndufa6/Ndufs8/Cox6c/Cox5b/Ndufb5/Sdhd/Ndufs4/Ndufc2/Ndufb9/Uqcrc2/Ndufa9/Cox7c/Uqcrh/Uqcrb/Ndufa4/Ndufa8/Sdha/Cyc1/Ndufs3/Ndufb8/Cox4i2/Ndufb6/Cox7b/Ndufab1/Ndufb3/Ndufv2/Ndufa5/Ndufa10/Ndufs1/Ndufs5

				ufs5
GO:0016 324	apical plasma membrane	62/1758	3.00E-06	Rhcg/Amn/Cdhr5/Abcb1b/P2ry6/Epcam/Fn1/Atp6v0d2/Myo7a/Tgfbr1/Nox4/Ajap1/Ii6r/Syt14/Dab2/Ocln/Scnn1b/Slc9a3/Tlr9/Ezr/Adam17/Slco2b1/Shroom4/Dpp4/Tjp1/Pld1/Scnn1a/Ano1/Osmr/Slc2a5/Shrom2/Tcigr1/Ptk2/Tek/Slc1a1/Amotl2/Duox2/Notch1/Hyal2/Sept7/Tmem30a/Aqp1/Prkaa1/Prkaa2/Eps15/Hsp90aa1/Shank2/Atp6v1e1/Cacnb3/Prkcz/Kcna1/Kcna5/Mlc1/Pth1r/Abcg8/Slc5a11/Abcc2/Kcnc2/Si/Slc12a1/Gpihbp1/S100g
GO:0098 794	postsynapse	84/1758	5.68E-06	Cd3e/Chrna1/Met/Grin2b/Myd88/Gabra5/Grin2d/Lrp4/Sema4f/Sema4c/Grasp/Ifngr1/Bcas1/Scrib/Ptk2/Zmynd8/Calb1/Src/Drd2/Add3/Dlg3/Strn4/Map4/Fus/Stx12/Mob4/Usp8/Syt11/Gabrb3/P2rx3/Musk/Rab11a/Syndig1/Shank2/Ctnna2/Cpeb1/Tanc1/Slc8a3/Khlh17/Grid2/Nlgn1/Dlg2/Map2/Fbxo2/Map1b/Cdk5/Ctnnd2/Pja2/Map1a/Syn1/Gabra3/Stxbp1/Apbb1/Dlgap1/Epb41l3/Lrfn2/Epha7/Grin3a/Chrna5/Grm7/Magee1/Ntsr1/Grin1/Rims1/Slc17a7/Grm8/Chrna4/LRRTM1/Glrb/Faim2/Kcnc2/Slc8a2/Dlgap3/Grip2/Frmpd4/Hpca/Cdh9/Kcnc3/Npas4/Grm3/Lin7b/Kcnj4/Chrna3/Htr3a
GO:0045 177	apical part of cell	74/1758	6.34E-06	Hamp/Reg3b/Rhcg/Amn/Cdhr5/Abcb1b/P2ry6/Epcam/Fn1/Sapcd2/Atp6v0d2/Myo7a/Tgfbr1/Fap/Nox4/Ajap1/Epb41l4b/Ii6r/Syt14/Dab2/Ocln/Scnn1b/Slc9a3/Tlr9/Dchs1/Ezr/Adam17/Slco2b1/Shroom4/Nedd1/Insc/Dpp4/Tjp1/Pld1/Nin/Scnn1a/Ano1/Osmr/Slc2a5/Shroom2/Tcigr1/Ptk2/Tek/Slc1a1/Amotl2/Duox2/Notch1/Hyal2/Sept7/Tmem30a/Usp9x/Aqp1/Prkaa1/Prkaa2/Eps15/Hsp90aa1/Shank2/Atp6v1e1/Atp6v1c1/Cacnb3/Prkcz/Kcna1/Kcna5/Mlc1/Pth1r/Abcg8/Slc5a11/Abcc2/Kcnc2/Crb3/Si/Slc12a1/Gpihbp1/S100g
GO:0098 589	membrane region	76/1758	1.08E-05	Cd8a/Cdhr5/Myof/Itgam/Olr1/Tshr/Tgfbr1/Tlr2/Cd4/Cd2/Icam1/Fcgr1a/Fadd/Hck/Dab2/Iqgap1/Plscr1/Jak2/Ppp2r1b/Casp8/Ezr/Adam17/Lck/Adcy6/Ldlrap1/Mag/Birc3/Efnb1/Lrp4/Dpp4/Rftn1/Furin/Shh/Itga1/Ehd2/Efhd2/Necap2/Eef2/Src/Tek/Inpp5d/Ahnak/Hyal2/Csk/Stat6/Lamtor2/Sdcbp/Aqp1/Stx12/Stoml2/Ocrl/Ephb1/Atp5b/Ret/P2rx3/Eps15/Trpc1/Bace1/Aak1/Kcna3/Prkcz/Necap1/Cntn1/Ldhb/Kcna5/Trpm8/Lrp3/Rtn4rl2/Mlc1/Ntsr1/Cnr1/Faim2/Trpc4/Si/Atp2b3/Chrna3
GO:0098 793	presynapse	74/1758	2.89E-05	Slc30a3/Pdyn/Cck/Grin2b/Fosl1/Syt14/Syt17/Syt1/Sema4c/Syt13/Shh/Scrib/Ptprn/Calb1/Drd2/Slc18a2/Cad/Sept7/Cops5/Napa/Aqp1/Stx12/Hcn1/Calm1/Syt11/Gabrb3/P2rx3/Dnajc5/Pfn2/Syndig1/Zdhhc17/Syt5/Shank2/Ppfia3/Tanc1/Aak1/Calm3/Nlgn1/Tmem230/Scamp1/Trappc4/Madd/Kcna1/Sv2c/Syn1/Stxbp1/Apbb1/Rims3/Anxa5/Got1/Ica1/Grm7/Esr1/Crhr2/Ntsr1/Grin1/Rims1/Slc17a7/Grm8/Trim9/Cnr1/Wnt7a/Kcnc2/Syt3/Unc13c/Cdh9/Kcnc3/Kcnk9/Syt10/Grm3/Lin7b/Th/Slc17a8/Doc2a
GO:1990 351	transporter complex	58/1758	3.72E-05	Chrna1/Grin2b/Scnn1b/Gabra5/Hspa2/Grin2d/Scn3a/Shisa7/Scnn1a/Scrib/Scn3b/Dlg3/Ppm1a/Hcn1/Calm1/Gabrb3/Uqcrc2/Uqcrh/Uqcrb/Shank2/Pex14/Cyc1/Grid2/Calm3/Cacnb3/Nlgn1/Abhd12/Dlg2/Kcna3/Sacm1l/Kcna1/Timm10/Kcna5/Gabra3/Olfm1/Scn1b/Grin3a/Kcnk4/Chrna5/Hcn2/Lrrc55/Abcg8/Olfm3/Clic3/Grin1/Kcnh2/Chrna4/Glrb/Scn8a/Kcnc2/Trpc4/Kcnj5/Dlgap3/Kcnmb2/Kcnc3/Vwc2l/Chrna3/Htr3a
GO:0098	neurotrans	18/1758	3.84E-	Grin2b/Grin2d/Shisa7/Scrib/Dlg3/Shank2/Grid2/Nlgn1/Abhd12/Dlg2/

878	mitter receptor complex		05	Sacm1l/Olfm1/Grin3a/Olfm3/Grin1/Dlgap3/Vwc2l/Htr3a
GO:0098552	side of membrane	80/1758	3.84E-05	Cd8b/Vtcn1/Ii6/Cd8a/Cxcr3/Cd3e/Folr2/Klrk1/Gna15/Itgam/Tnfrsf18/Itgal/Ii2rb/Icos/Cd27/Scube1/Anpep/Dlk1/Fes/Tlr8/Sla/Tlr2/Cd4/Ccr5/Ajap1/Cnr2/Gem/Cd2/Fgr/Icam1/Tnfrsf14/Thbs1/Lag3/Itga4/Fcgr1a/Ii2rg/Ii1rl1/Ptpn22/Hck/Scnn1b/Micb/Iqgap1/Jak2/Ezr/Lck/Tmem123/Ldlrap1/Eng/Shroom4/Gng12/Cd40/Spn/Itga6/Itga1/Scnn1a/Ano1/Osmr/Ptk2/Sppl2b/Src/Tyk2/Hyal2/Matk/Csk/Musk/Nlgn1/Chp2/Genb5/Sema7a/Anxa5/Trpm8/Rtn4rl2/Ntsr1/Chrna4/Rgs6/Kcnj5/Gpihb1/Htr2c/Itgb6/Th
GO:1902495	transmembrane transporter complex	56/1758	7.98E-05	Chrna1/Grin2b/Scnn1b/Gabra5/Hspa2/Grin2d/Scn3a/Shisa7/Scnn1a/Scrib/Scn3b/Dlg3/Ppm1a/Hcn1/Calm1/Gabrb3/Uqcrc2/Uqcrh/Uqcrb/Shank2/Cyc1/Grid2/Calm3/Cacnb3/Nlgn1/Abhd12/Dlg2/Kcna3/Sacm1l/Kcna1/Kcna5/Gabra3/Olfm1/Scn1b/Grin3a/Kcnk4/Chrna5/Hcn2/Lrrc55/Abcg8/Olfm3/Clic3/Grin1/Kcnh2/Chrna4/Glrb/Scn8a/Kcnc2/Trpc4/Kcnj5/Dlgap3/Kcnmb2/Kcnc3/Vwc2l/Chrna3/Htr3a
GO:0009897	external side of plasma membrane	53/1758	9.61E-05	Cd8b/Vtcn1/Ii6/Cd8a/Cxcr3/Cd3e/Folr2/Klrk1/Itgam/Tnfrsf18/Itgal/Ii2rb/Icos/Cd27/Scube1/Anpep/Dlk1/Tlr8/Tlr2/Cd4/Ccr5/Cd2/Icam1/Tnfrsf14/Thbs1/Lag3/Itga4/Fcgr1a/Ii2rg/Ii1rl1/Scnn1b/Micb/Tmem123/Eng/Cd40/Spn/Itga6/Itga1/Scnn1a/Ano1/Osmr/Hyal2/Musk/Nlgn1/Sema7a/Anxa5/Trpm8/Rtn4rl2/Chrna4/Kcnj5/Gpihb1/Htr2c/Itgb6
GO:0043204	perikaryon	34/1758	0.000134	Cck/Cnr2/Reln/Itga1/Ptpn/Efna2/Drd2/Fus/Kif5a/Slc8a3/Map1b/Cdk5/Kcna1/Ctnnd2/Resp18/Endog/Pcmt1/Olfm1/Ntsr2/Anxa5/Nell2/Rtn4rl2/Esr1/Crhr2/Ntsr1/Glrb/Kcnc2/Slc8a2/Ngb/Htr5a/Hpca/Kcnc3/Th/Slc17a8
GO:0070069	cytochrome complex	13/1758	0.000153	Ugt1a1/MGC105649/Cox8a/Cox6c/Cox5b/Uqcrc2/Cox7c/Uqcrh/Uqcrb/Ndufa4/Cyc1/Cox4i2/Cox7b
GO:0030133	transport vesicle	54/1758	0.000649	Slc30a3/Lyz2/Grin2b/Sipa1/Nkd2/Hck/Syt14/Syt1/Ldlrap1/Bgn/Scamp2/Sspn/Sema4c/Syt13/Furin/Shh/Ptpn/Plekhf2/Drd2/Slc18a2/Tmem30a/Atp2c1/Cops5/Stx12/Calm1/Syt11/Dnajc5/Rab11a/Syt5/Atp13a2/Calm3/Sec23a/Tmem230/Scamp1/Trappc4/Madd/RGD1305645/Sv2c/Syn1/Anxa5/Nrsn2/Ica1/Grin1/Slc17a7/Trim9/Clrn1/Syt3/Unc13c/Kcnk9/Syt10/Th/Slc17a8/Doc2a/Slc30a8
GO:0045277	respiratory chain complex IV	9/1758	0.001218	MGC105649/Cox8a/Cox6c/Cox5b/Uqcrc2/Cox7c/Ndufa4/Cox4i2/Cox7b
GO:0005911	cell-cell junction	69/1758	0.001366	Hamp/Cd3e/Abcb1b/Smagp/Epcam/Itgal/Sapcd2/Vav1/Tgfb1/Ect2/Cdca3/Des/Cd53/Ccnd1/Plekha7/Ajap1/Cd2/Sh3bp1/Epb41l4b/Ptpn6/Itga4/Was/Rab13/Ocln/Cadm4/Iqgap1/Lat/Adam17/Lck/Gja4/Ptprj/Panx1/Dpp4/Itga6/WASF2/Tjp1/Cdk4/Tjp2/Scrib/Shroom2/Pak4/Ptk2/Plekhg5/Cldn19/Tek/Amot12/Add3/Ahnak/Dlg3/Tjp1/Csk/Ctnna2/Prkcz/Stard10/Ptpnu/Kcna5/Epb41l3/Anxa5/Tmem47/Scn1b/Cldn20/Ptpnk/Mlc1/Abcc2/Trpc4/Flrt1/Lin7b/Gjd2/Gja10
GO:0044306	neuron projection terminus	38/1758	0.00164	Pdyn/Cck/Grin2b/Ptbp1/Fstl3/Ptpn/Calb1/Drd2/Slc18a2/Cad/Sept7/Napa/Aqp1/Hcn1/Syt11/Gabrb3/P2rx3/Dnajc5/Pfn2/Tanc1/Aak1/Scamp1/Kcna1/Syn1/Stxbp1/Anxa5/Got1/Grm7/Esr1/Crhr2/Ntsr1/Grin1

				/Kcnc2/Flrt1/Unc13c/Kcnc3/Th/Slc17a8
GO:0015 629	actin cytoskeleton	66/1758	0.0029 33	Mlph/Abcb1b/Fblim1/Gbp2/Myo1f/Bin2/Myo7a/Fermt3/Nox4/Fgr/ Was/Hck/Bmf/Rac2/Myl12a/Fhl3/Iqgap1/Eef1a1/Ezr/Adam17/Triobp/ Lpxn/Shroom4/Gng12/Ppp1r12a/Cttnbp2nl/Sh3pxd2a/Ror1/Wipf1/ Scnn1a/Synpo2/Shroom2/Ptk2/Sppl2b/Stk17b/Akap13/Src/Tek/Croc c/Inpp5d/Ahnak/Sept7/Pls3/Stoml2/Nckap1/Aldoa/Lancl2/Dctn3/Da am1/Myo9a/Vps11/Coro2a/Actr10/Klh17/Arhgap35/Map2/Prkcz/Ac tr3b/Kif9/Pls1/Myo3b/Gdpd2/Mst1r/Cnr1/Myl3/Abra
GO:0045 239	tricarboxyli c acid cycle enzyme complex	7/1758	0.0033 89	Idh3g/Idh3a/Dld/Mrps36/Bckdhb/Suclg1/Idh3B
GO:0030 659	cytoplasmic vesicle membrane	53/1758	0.0054 35	Slc30a3/Rab32/Smagp/Slc11a1/Rab13/Syt14/Rab38/Dab2/Scnn1b/Ldl rap1/Sema4c/Rab43/Snx33/Ptprn/Necap2/Kdelr1/Acrbp/Drd2/Slc18 a2/Tmem30a/Stx12/Copg2/Ocrl/Vopp1/Calm1/Syt11/Gabrb3/Eps15/ Kif1b/Gabarapl1/RGD1309079/Zdhhc17/Bace1/Syt5/Calm3/Sec23a/ Necap1/Scamp1/Sv2c/Syn1/Ica1/Slc17a7/Syt3/Unc13c/Lamp5/Caly/S yt10/Camkv/Th/Kcnj4/Slc17a8/Doc2a/Slc30a8
GO:0045 178	basal part of cell	15/1758	0.0056 06	Tacstd2/Rhcg/Met/Fap/Ldlrap1/Phldb1/Shroom4/Prcp/Itga6/Itga1/T ek/Aqp1/Eps15/Oscp1/Clrn1
GO:0012 506	vesicle membrane	56/1758	0.0065 72	Slc30a3/Rab32/Smagp/Anpep/Slc11a1/Was/Rab13/Syt14/Rab38/Dab 2/Scnn1b/Ldlrap1/Sema4c/Rab43/Snx33/Ptprn/Necap2/Kdelr1/Acrb p/Drd2/Slc18a2/Tmem30a/Stx12/Copg2/Ocrl/Vopp1/Calm1/Syt11/G abrb3/Eps15/Kif1b/Gabarapl1/RGD1309079/Zdhhc17/Bace1/Syt5/At p13a2/Calm3/Sec23a/Necap1/Scamp1/Sv2c/Syn1/Ica1/Slc17a7/Syt3/ Unc13c/Lamp5/Caly/Syt10/Camkv/Th/Kcnj4/Slc17a8/Doc2a/Slc30a8
GO:0098 984	neuron to neuron synapse	43/1758	0.0070 05	Met/Grin2b/Myd88/Lrp4/Sema4c/Ifngr1/Bcas1/Scrib/Src/Drd2/Add3/ Dlg3/Map4/Usp8/Syt11/Syndig1/Shank2/Ctnna2/Cpeb1/Tanc1/Klh 17/Grid2/Nlgn1/Dlg2/Map2/Map1b/Cdk5/Ctnnd2/Pja2/Map1a/Syn1/ Dlgap1/Epb41l3/Grin3a/Grm7/Ntsr1/Grin1/Rims1/Dlgap3/Grip2/Gr m3/Lin7b/Chrna3
GO:0043 209	myelin sheath	36/1758	0.0070 46	Eef1a1/Ezr/Hspa2/Mag/Serinc5/Scrib/Sept7/Napa/Immt/Aldoa/Calm 1/Atp5b/Cox5b/Pdha1/Idh3a/Uqcrc2/Dld/Fam213b/Hsp90aa1/Tubb 4b/Sdha/Ndufs3/Calm3/Aco2/Prkcz/Stip1/Gnb5/Ndufv2/Ndufa10/Cn tn1/Syn1/Ldhb/Stxbp1/Ndufs1/Napb/Hrh3
GO:0060 076	excitatory synapse	11/1758	0.0076 74	Met/Srp2/Fgfr2/Syt11/Syndig1/Nlgn1/Ntm/Grin1/Slc17a7/LRRTM1/ Slc17a8
GO:0044 420	extracellular matrix component	24/1758	0.0096 76	Col7a1/Thbs2/Fn1/Thbs4/Col27a1/Frem1/Fbn1/Adamts15/Col5a2/Co l15a1/Col5a1/Smoc2/Mfap2/Loxl1/Lum/Emilin1/Spn/Itga6/Agrn/Fbln 1/Lamb2/Col11a1/Vegfa/Ptn
<b>BP terms</b>				
GO:0010 257	NADH dehydroge nase complex	20/1663	2.17E- 06	Acad9/Ndufa11/Aifm1/Ndufaf6/Ndufs8/Ndufb5/Ndufs4/Ndufc2/Ndu fb9/Ndufa9/Ndufa8/Ndufb8/Ndufab1/Ndufb3/Ndufa5/Nduf af5/Ndufa10/Ndufaf7/Ndufs5

	assembly			
GO:0032981	mitochondrial respiratory chain complex I assembly	20/1663	2.17E-06	Acad9/Ndufa11/Aifm1/Ndufaf6/Ndufs8/Ndufb5/Ndufs4/Ndufc2/Ndufb9/Ndufa9/Ndufa8/Ndufb8/Ndufb6/Ndufab1/Ndufb3/Ndufa5/Ndufaf5/Ndufa10/Ndufaf7/Ndufs5
GO:0097031	mitochondrial respiratory chain complex I biogenesis	20/1663	2.17E-06	Acad9/Ndufa11/Aifm1/Ndufaf6/Ndufs8/Ndufb5/Ndufs4/Ndufc2/Ndufb9/Ndufa9/Ndufa8/Ndufb8/Ndufb6/Ndufab1/Ndufb3/Ndufa5/Ndufaf5/Ndufa10/Ndufaf7/Ndufs5
GO:0032496	response to lipopolysaccharide	80/1663	4.09E-06	Hamp/Ill1a/Serpina3n/Ankrd1/Ill6/Trem2/Mmp3/Ugt1a1/Sipi/Abcb1b/Cyp27b1/Klrk1/Fn1/Tnfrsf18/Tnfrsf8/Gbp2/Csf2rb/Fos/Cd180/Cd27/Acp5/Tspo/Cd6/Tlr2/Ptafr/Pycard/Tgfb1/Thbd/Ccr5/Cnr2/Slc11a1/Icam1/Ill1rn/Tnfrsf14/Ill10ra/Ill6r/Myd88/Serpina1/Ptpn22/Nfkb2/Nrad/Tnfrsf26/Mgst2/Tlr9/Lox11/Plscr1/Jak2/Casp8/Adam17/Casp1/Zfp36/Nr1h3/Gng12/Trim5/Tcf3/Foxp1/Cd40/Ill18bp/Irak2/Tjp1/Dnmt1/Cdk4/Ltbr/Zc3h12a/Fgfr2/Zcchc11/Src/Notch1/Tnfrsf25/Hdac1/Nfkbia/Aloda/Cpeb1/Tbxa2r/S100a9/Timp4/Abcc2/Cnr1/Ptgfr/Th
GO:0030335	positive regulation of cell migration	83/1663	2.35E-05	Ill1a/Mmp3/P2ry6/Fn1/Tnfrsf18/Thbs4/Ccr6/Fgf2/C3ar1/Myo1f/Acp5/Met/SrpX2/Fermt3/Tgfb1/Angpt4/Bmp7/Tlr2/Bmp2/Ptafr/Pycard/Tgfb1/Nox4/Ccr5/Fgr/Icam1/Tnfrsf14/Epb41l4b/Smad3/Thbs1/Itga4/Nckap1l/Fadd/Ets1/Dock8/Myc/Pdgfc/Dab2/Rac2/Iqgap1/Jak2/Adam17/Reln/Ptprj/Gli1/Foxp1/Itga6/Pld1/Sema3c/Dock1/Furin/Shh/Zc3h12a/Synpo2/Fbln1/Rras2/Ptk2/Ctsh/Akt2/Src/Tek/Notch1/Foxo4/Rhob/Swap70/Fgf7/Sdcbp/Elp6/Aqp1/Vegfa/Ntrk3/Arhgap5/Atp5b/Ret/Rab11a/Acvr1b/Cpeb1/Hdac9/Ccl27/Pdgfd/Wnt7a/Onecut1/Edn2
GO:0001501	skeletal system development	86/1663	2.60E-05	Tyrobp/Fgf2/Runx2/Wnt10b/Acp5/Dlk1/Tgfb1/Col27a1/Bmp7/Vcan/Frem1/Bmp2/Tgfb1/Smad3/Fbn1/Ptpn6/Thbs1/Col5a2/Myc/Osr2/Pdgfc/Adamts7/Lum/Dchs1/Epha2/Mgp/Adamts12/Lrrc17/Dhrs3/Chsy1/Eng/Plekha1/Mycn/Nab2/Foxp1/Recql4/WASF2/Creb3l2/Shh/Tjp2/Sulf2/Vkorc1/Tbx15/Hexa/Fli1/Fgfr2/Cdkn1c/Cyp26b1/Foxn3/Akap13/Rab33b/Ryk/Src/Tek/Inpp1l/Sp1/Col11a1/Hyal2/Npr3/Pkdcc/Srf/Pls3/Pex7/Vegfa/Snx19/Mkks/Gpr68/Rbp4/Esr1a/Six1/Bmpr1b/Hapl2/Amer1/Rgn/Pth1r/Esr1/Tcf15/Shox2/Bcan/Six4/Wnt7a/Scx/Hes5/Smad9/Srd5a2/Hapl1
GO:0042391	regulation of membrane potential	76/1663	5.84E-05	Ill6/Nps/Cck/Chrna1/Kcnk13/Met/Tspo/Grin2b/Gpr88/Cnr2/Ill1rn/Myc/Casp1/Reln/Grin2d/Pid1/S1pr2/Scn3a/Agrn/Ano1/Scn3b/Zmynd8/Akt2/Src/Cldn19/Bok/Tpcn2/Fam19a4/Stoml2/Nup155/Ptn/Mtch2/Hcn1/Gabrb3/P2rx3/Dld/Nrcam/Slc8a3/Grid2/Cacnb3/Nlgn1/Prkcz/Cdk5/Kcna1/Kcna5/Tusc2/Ndufs1/Ntsr2/Gclm/Rims3/Scn1b/Grin3a/Kcnk4/Slc26a7/Chrna5/Hcn2/Ntsr1/Asic1/Grin1/Rims1/Slc17a7/Kcnh2/Slc25a33/Nppa/Chrna4/Cnr1/Glrb/Wnt7a/Scn8a/Kcnc2/Kcnj5/Kcnmb2/Npas4/Kcnk9/Gjd2/Chrna3
GO:0061	axon	81/1663	9.78E-	Cck/Fn1/Tnfrsf8/Bhlhe22/Tspo/Bmp7/Vcan/Ccr5/Ephb2/Dhfr/Crabp

564	development		05	2/Rgma/Tnfrsf26/Tlr9/Jak2/Adam17/Rein/Mag/Arhgap4/Nr4a2/Efnb1/Lrp4/Sema4f/Foxp1/Agrn/Sema3c/Shh/Nin/Nr4a3/Crtac1/Efna4/Lamb2/Ptk2/Fgfr2/Pou3f2/Efna2/Ryk/Drd2/Notch1/Agap2/Srf/Arhgef28/Sept7/Usp9x/Vegfa/Ntrk3/Ephb1/Ret/Usp33/Eif2b2/Rab11a/Nrcam/Atl1/Kif5a/Ctnna2/Arhgap35/Map2/Trim46/Map1b/Slit1/Cdk5/Sema7a/Ttl/Stxbp1/Olfm1/Abpb1/Bmpr1b/Scn1b/Lrfn2/Epha7/Lrrc4c/Lrrc55/Ntrk1/Grin1/Shox2/Cnr1/Wnt7a/Lingo4/Ntng1/Slitrk3/Cntn4
GO:0050807	regulation of synapse organization	34/1663	0.000191	Thbs2/Srpx2/Tpbg/Cdc20/Tlr2/Ephb2/I110ra/Rein/Lrp4/Agrn/Ptk2/Zmynd8/Drd2/Ntrk3/Ephb1/Ptn/Musk/Syndig1/Ctnna2/Grid2/Nlgn1/Slit1/Six1/Epha7/Lrrc24/Ntrk1/Grin1/LRRTM1/Six4/Wnt7a/Flrt1/Lingo4/Frmpd4/Slitrk3
GO:0097305	response to alcohol	60/1663	0.000191	Hamp/Ugt1a1/Apobec1/Tbxas1/Avp/Cyp27b1/P2ry6/Fn1/Cd27/Spi1/Acp5/Cybb/Tgfbr1/Ccnd1/Grin2b/Tgfb1/Ccr5/Neu2/Icam1/I6r/Serpin1a1/Myc/H6pd/Casp8/Adcy6/Rein/Ccnd2/Rad51/Cdk2/Tjp1/Dnmt1/Shh/Fgfr2/Eef2/Drd2/Dnmt3a/Ggh/Ntrk3/Lancl2/Prcaa1/Psmd14/Prcaa2/Unc79/Rbp4/Kif5a/Atp5g3/Oxct1/Tbxa2r/Hmgcs1/Pcmt1/S100a9/Grin3a/Mlc1/Ntrk1/Mgmt/Grin1/Cnr1/Kcnc2/Th/Htr3a
GO:0006836	neurotransmitter transport	42/1663	0.000295	Gdnf/Pdyn/Syt14/Syt17/Syt11/Slc6a11/Syt13/Scrib/Drd2/Slc18a2/Napa/Calm1/Syt11/Pfn2/Syt5/Ppfia3/Calm3/Nlgn1/Sv2c/Syn1/Prepl/Stxbp1/Napb/Rims3/Ica1/Asic1/Rims1/Slc17a7/Nrxn3/Grm8/Trim9/Wnt7a/Syt3/Unc13c/Kcnc3/Htr2c/Syt10/Lin7b/Th/Chrna3/Slc17a8/Doc2a
GO:0001101	response to acid chemical	82/1663	0.000316	Hamp/I11a/Reg3b/I16/Mmp3/Tbxas1/Abcb1b/Cyp27b1/P2ry6/Fn1/Rorb/Wnt10b/Acp5/Cybb/Tgfbr1/Tlr2/Bmp2/Ptafr/Grin2b/Sipa1/Icam1/Dhfr/Col5a2/Tead1/Serpina1/Myc/Pdgfc/Ptgs1/Adcy6/Rein/Pid1/Foxp1/Dnmt1/Shh/Cdk4/Zc3h12a/Sox2/Dnmt3b/Tie1/Fgfr2/Cyp26b1/Phc1/Eef2/Ctsh/Src/Tek/Dnmt3a/Xrcc5/Lamtor2/Aqp1/Vegfa/Aifm1/Ntrk3/Lancl2/Prcaa1/Ptn/Hcn1/Abo/Ret/Prcaa2/Rbp4/Pdk3/Cpeb1/Pdgfd/Six1/Lrp11/Gclm/Gipr/Map7/Kcnk4/Gdap1/Mest/Ntrk1/Mgmt/Grin1/Abcc2/Rragd/Glrb/Fgf21/Ptgfr/Hpca/Th
GO:0070371	ERK1 and ERK2 cascade	56/1663	0.000328	I11a/I16/Htr2b/Trem2/Avp/Fn1/Fgf2/Fam83d/C3/Tlr2/Bmp2/Pycard/Tgfb1/Nox4/Cd4/Icam1/Ephb2/Ptpn6/Cnksr3/Dusp6/Ptpn22/Myc/Pdgfc/Dab2/Pde8a/Epha2/Tbc1d10c/Zfp36l1/Ezr/Spry1/Rras/Fbln1/Fgfr2/Ctsh/Src/Tek/Drd2/Csk/Vegfa/Ephb1/Pin1/Prkcz/Fgfbp3/Sema7a/Pdgfd/Ntsr2/Rps6ka6/Dnajc27/Epha7/Esr1/Ntrk1/Crhr2/Fgf21/Arhgap8/Htr2c/C1ql4
GO:0099531	presynaptic process involved in chemical synaptic transmission	35/1663	0.000364	Gdnf/Pdyn/Syt14/Syt17/Syt11/Syt13/Scrib/Drd2/Napa/Calm1/Syt11/Pfn2/Syt5/Ppfia3/Calm3/Nlgn1/Syn1/Prepl/Stxbp1/Napb/Rims3/Asic1/Rims1/Nrxn3/Grm8/Trim9/Wnt7a/Syt3/Unc13c/Kcnc3/Htr2c/Syt10/Lin7b/Chrna3/Doc2a
GO:0099504	synaptic vesicle cycle	32/1663	0.000364	Syt14/Syt17/Syt11/Sh3gl3/Syt13/Scrib/Slc18a2/Napa/Calm1/Syt11/Eps15/Pfn2/Syndig1/Syt5/Calm3/Nlgn1/Cdk5/Syn1/Prepl/Stxbp1/Napb/Rims3/Ap1s2/Rims1/Slc17a7/Trim9/Sh3gl2/Syt3/Unc13c/Syt10/Th/Doc2a
GO:0050	regulation of synapse	34/1663	0.0003	Thbs2/Srpx2/Tpbg/Cdc20/Tlr2/Ephb2/I110ra/Rein/Lrp4/Agrn/Ptk2/Zmynd8/Drd2/Ntrk3/Ephb1/Ptn/Musk/Syndig1/Ctnna2/Grid2/Nlgn1/S

803	structure or activity		64	lit1/Six1/Epha7/Lrrc24/Ntrk1/Grin1/LRRTM1/Six4/Wnt7a/Flrt1/Lingo4/Frmpd4/Slitrk3
GO:0051963	regulation of synapse assembly	25/1663	0.000374	Thbs2/Srpox2/Tpbg/Tlr2/Ephb2/Agrn/Ptk2/Ntrk3/Ephb1/Musk/Syndig1/Grid2/Nlgn1/Slit1/Six1/Epha7/Lrrc24/Ntrk1/Grin1/LRRTM1/Six4/Wnt7a/Flrt1/Lingo4/Slitrk3
GO:0007416	synapse assembly	35/1663	0.000414	Thbs2/Srpox2/Tpbg/Tlr2/Ephb2/Lrp4/Agrn/Ptk2/Drd2/Ntrk3/Ephb1/Musk/Syndig1/Shank2/Grid2/Nlgn1/Map1b/Slit1/Cdk5/Six1/Epha7/Lrrc24/Ntrk1/Grin1/Nrxn3/LRRTM1/Six4/Wnt7a/Flrt1/Lingo4/Kirrel3/Slitrk3/Cdh9/Npas4/Gja10
GO:0007613	memory	32/1663	0.000491	Cebpa/Grin2b/I1rn/Cyp7b1/Ptgs1/Casp1/Reln/Ccnd2/Mdk/Hrh1/Cab1/B4galt2/Chst10/Drd2/Srf/Musk/Shank2/Slc8a3/Prkcz/Pja2/Pak7/Kcnk4/Grm7/Asic1/Grin1/Slc17a7/Slc24a2/Cnr1/Slc8a2/Hrh3/Npas4/Th
GO:0050808	synapse organization	53/1663	0.000491	Gdnf/Thbs2/Chrna1/Srpox2/Tpbg/Cdc20/Tlr2/Ephb2/I10ra/Reln/Lrp4/Agrn/Lamb2/Ptk2/Zmynd8/Fgfr2/Drd2/Ntrk3/Ephb1/Ptn/Musk/Pin1/Syndig1/Shank2/Ctnna2/Grid2/Cacnb3/Nlgn1/Map1b/Slit1/Cdk5/Ctnnd2/Six1/Dlgap1/Epha7/Lrrc24/Ntrk1/Grin1/Nrxn3/LRRTM1/Glrb/Six4/Wnt7a/Flrt1/Lingo4/Kirrel3/Frmpd4/Slitrk3/Cdh9/Npas4/Ky/Gja10/Htr1a
GO:0051650	establishment of vesicle localization	42/1663	0.000491	Mlph/Myo7a/Kif23/Itga4/Syt14/Syt17/Syt1/Fnbp1l/Sh3gl3/Syt13/Mr1eg/Scrib/Shroom2/Fyco1/Fgfr2/Napa/Calm1/Syt11/Eps15/Preb/Rab11a/Pfn2/Ap3s2/Syt5/Calm3/Nlgn1/Prkcz/Tmem230/Trim46/Cdk5/Prepl/Stxbp1/Napb/Rims3/Ap1s2/Rims1/Trim9/Sh3gl2/Syt3/Unc13c/Syt10/Doc2a
GO:0042773	ATP synthesis coupled electron transport	20/1663	0.000491	Cox8a/Ndufa7/Mtch2/Cox5b/Sdhb/Ndufc2/Ndufb9/Dld/Cox7c/Uqcrh/Uqcrb/Ndufa8/Sdha/Cyc1/Ndufb8/Cox4i2/Ndufb6/Ndufv2/Ndufa10/Ndufs1
GO:0001667	ameboidal-type cell migration	61/1663	0.000491	Mmp12/Tacstd2/Gdnf/Htr2b/Has1/Ccr6/Fgf2/Met/Srpox2/Tgfbr1/Angpt4/Bmp7/Tgfb1/Fap/Ccr5/Sh3bp1/Epb41l4b/Thbs1/Itga4/Ets1/Rab13/Epha2/Nr2f2/Arhdib/Arhgap4/Meox2/Sox18/Efnb1/Prcp/Foxp1/Dpp4/Nr4a1/Itgb7/Wasf2/Sema3c/Dock1/Acvrl1/Shh/Zc3h12a/Ptk2/Plekhg5/Mta2/Ctsh/Src/Tek/Sox17/Notch1/Rhob/Hyal2/Fgf7/Srf/Aqp1/Vegfa/Nckap1/Atp5b/Ret/Rab11a/Pfn2/Acvr1b/Hdac9/Wnt7a
GO:0007269	neurotransmitter secretion	33/1663	0.000491	Pdyn/Syt14/Syt17/Syt1/Syt13/Scrib/Napa/Calm1/Syt11/Pfn2/Syt5/Ppfia3/Calm3/Nlgn1/Syn1/Prepl/Stxbp1/Napb/Rims3/Asic1/Rims1/Nrxn3/Grm8/Trim9/Wnt7a/Syt3/Unc13c/Kcnc3/Htr2c/Syt10/Lin7b/Chrna3/Doc2a
GO:0099643	signal release from synapse	33/1663	0.000491	Pdyn/Syt14/Syt17/Syt1/Syt13/Scrib/Napa/Calm1/Syt11/Pfn2/Syt5/Ppfia3/Calm3/Nlgn1/Syn1/Prepl/Stxbp1/Napb/Rims3/Asic1/Rims1/Nrxn3/Grm8/Trim9/Wnt7a/Syt3/Unc13c/Kcnc3/Htr2c/Syt10/Lin7b/Chrna3/Doc2a
GO:0002443	leukocyte mediated immunity	56/1663	0.000532	I16/Cd8a/C1qa/C1qb/C1qc/Klrk1/Itgam/Gapt/Ccr6/Myo1f/Batf/Vav1/PVR/Fes/C3/C1s/Tlr2/Ptafr/Tgfb1/Serpine1/Bcl3/Fgr/Slc11a1/Pou2f2/Icam1/Ptpn6/C1r/Lag3/Fcgr1a/Was/C1rl/Fadd/Myd88/Trem1/Sash3/Rac2/Tlr9/Lat/I120rb/Irf7/Dpp4/Cd40/Spn/Irak4/Rftn1/Nr4a3/Kdelr1

				/Ctsh/Rnf19b/Inpp5d/Swap70/Stat6/Prkcz/Stxbp1/Tusc2/Sh2d1a
GO:0051 648	vesicle localization	44/1663	0.0005 91	Mlph/Myo7a/Kif23/Itga4/Syt14/Syt17/Syt1l/Fnbp1l/Sh3gl3/Syt13/Mreg/Scrib/Shroom2/Fyco1/Fgfr2/Napa/Calm1/Syt11/Eps15/Preb/Rab11a/Pfn2/Syndig1/Ap3s2/Syt5/Calm3/Nlgn1/Prkcz/Tmem230/Trim46/Cdk5/Syn1/Prepl/Stxbp1/Napb/Rims3/Ap1s2/Rims1/Trim9/Sh3gl2/Syt3/Unc13c/Syt10/Doc2a
GO:0009 612	response to mechanical stimulus	54/1663	0.0005 91	Csrp3/Mmp7/Ankrd1/Ii6/Mmp3/Tnfrsf8/Fos/Stra6/Tlr7/Tlr8/Bmp2/Grin2b/Tgfb1/Fosl1/Thbs1/Fadd/Myd88/Ets1/Myc/Mgp/Casp8/Lck/Casp1/Reln/Mag/Eng/Cd40/Ltbr/Sox2/Casp2/Ptk2/Src/Drd2/Col11a1/Nfkbia/Aqp1/Mkks/P2rx3/Pdzd7/Abhd12/Strbp/Map1b/Kcna1/Kcna5/Endog/Lrp11/Kcnk4/Ntrk1/Grm8/Nppa/Tmc2/Scx/Kcnj4/Cyp11b2
GO:0019 233	sensory perception of pain	32/1663	0.0005 91	Ii1a/Vip/Cck/Ptafr/Grin2b/Cnr2/Ii1rn/Ptgs1/Grin2d/Scn3a/Ano1/Scn3b/Fam19a4/Aqp1/Ephb1/P2rx3/Dlg2/Cdk5/Kcna1/Oprl1/Kcnk4/Ntrk1/Crhr2/Ntsr1/Asic1/Grin1/Grm8/Chrna4/Cnr1/Htr2c/Grm3/lapp
GO:0002 250	adaptive immune response	55/1663	0.0006 22	Cd8b/Vtcn1/Ii6/Cd8a/C1qa/C1qb/C1qc/Klrk1/Gapt/Ccr6/C3ar1/Batf/PVR/Clec4a/C3/C1s/Pycard/Tgfb1/Cd4/Serpine1/Ii18r1/Bcl3/Slc11a1/Pou2f2/Icam1/Ptpn6/C1r/Fcgr1a/Was/C1rl/Fadd/Myd88/Ii1rl1/Sash3/Nfk2/Jak2/Lat/Adam17/Ii20rb/Irf7/Dpp4/Cd40/Spn/Ii18bp/Rftn1/Loxl3/Kdelr1/Ctsh/Inpp5d/Swap70/Csk/Stat6/Vegfa/Prkcz/Sh2d1a
GO:0002 460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	46/1663	0.0006 22	Ii6/Cd8a/C1qa/C1qb/C1qc/Gapt/Ccr6/C3ar1/Batf/PVR/C3/C1s/Tgfb1/Cd4/Serpine1/Ii18r1/Bcl3/Slc11a1/Pou2f2/Icam1/Ptpn6/C1r/Fcgr1a/Was/C1rl/Fadd/Myd88/Ii1rl1/Sash3/Nfk2/Adam17/Ii20rb/Irf7/Dpp4/Cd40/Spn/Ii18bp/Rftn1/Loxl3/Kdelr1/Ctsh/Inpp5d/Swap70/Stat6/Vegfa/Prkcz
GO:0017 158	regulation of calcium ion-dependent exocytosis	21/1663	0.0006 22	Syt14/Syt17/Syt1l/Syt13/Notch1/Napa/Calm1/Pfn2/Syt5/Calm3/Nlgn1/Cdk5/Prepl/Stxbp1/Napb/Rims3/Rims1/Trim9/Syt3/Syt10/Doc2a
GO:0018 212	peptidyl-tyrosine modification	61/1663	0.0006 67	Ii6/Gdnf/Trem2/Cd3e/Cck/Tnfrsf18/Thbs4/Met/Gprc5a/Ii11/Fes/Angpt4/Sla/Melk/Tgfb1/Cd4/Fgr/Icam1/Ephb2/Tnfrsf14/Ptpn6/Ii6r/Ptpn22/Hck/Pdgfc/Iqgap1/Epha2/Jak2/Adam17/Lck/Reln/Lrp4/Cd40/Argn/Tie1/Ptk2/Fgfr2/Src/Tek/Dyrk2/Mertk/Tyk2/Hyal2/Fgf7/Hdac1/Matk/Csk/Pkdcc/Vegfa/Ntrk3/Ephb1/Ret/Musk/Prkcz/Cntn1/Ttl/Pdgfd/Epha7/Ntrk1/Mst1r/Hes5
GO:0001 505	regulation of neurotransmitter	40/1663	0.0007 57	Gdnf/Pdyn/Syt14/Syt17/Syt1l/Syt13/Maoa/Scrib/Drd2/Napa/Calm1/Syt11/Pfn2/Syt5/Ppfia3/Calm3/Nlgn1/Syn1/Prepl/Stxbp1/Napb/Rims3/Hnmt/Asic1/Rims1/Slc17a7/Nrxn3/Grm8/Trim9/Wnt7a/Hrh3/Syt3/

	levels			Unc13c/Kcnc3/Htr2c/Syt10/Lin7b/Th/Chrna3/Doc2a
GO:0032 355	response to estradiol	46/1663	0.0007 96	Reg3b/Iil6/Mmp3/Ugt1a1/Sstr3/C3/Bmp7/Ccnd1/Tgfb1/Cd4/Ezh2/Ccna2/Fcgr1a/Serpina1/Ets1/Myc/Casp8/Nr2f2/Ccnd2/Cdk2/Dnmt1/Shh/Dnmt3b/Ptk2/Eef2/Dhh/Dnmt3a/Ifi27/Vegfa/Aifm1/Ptn/Esrra/Gpx4/Map2/Ntm/Map1b/Endog/Stxbp1/Oprl1/Esr1/Wnt7a/Tacr3/Ptgfr/Ar/Htr5a/Th
GO:0031 960	response to corticosteroid	55/1663	0.0008 23	Serpina3n/Ucn2/Iil6/Gdnf/Ugt1a1/C1qb/Sstr3/Fn1/Fos/Cebpa/Cybb/Sstr4/C3/Ccnd1/Ptafr/Grin2b/Tgfb1/Icam1/Iil1rn/Fosl1/Iil6r/Fbxo32/Slc9a3/Ptgs1/Jak2/Mgp/Zfp36l1/Zfp36/Reln/Eng/Mdk/Dnmt3b/Glb1/Akap13/Src/Notch1/Slc18a2/Cad/Aqp1/Vegfa/Aifm1/Ntrk3/Usp8/Bckdhb/Agl/Ptpru/Got1/Hcn2/Hnmt/Crhr2/Abcc2/Si/Npas4/Th/Cpn1
GO:0022 900	electron transport chain	23/1663	0.0008 64	Cox8a/Ndufa7/Mtch2/Cox5b/Sdhd/Ndufs4/Ndufc2/Ndufb9/Dld/Cox7c/Uqcrh/Uqcrb/Ndufa8/Sdha/Cyc1/Ndufb8/Cox4i2/Ndufb6/Ndufb3/Ndufv2/Ndufa5/Ndufa10/Ndufs1
GO:0001 819	positive regulation of cytokine production	66/1663	0.0009 3	Mmp12/Iil1a/Vtcn1/Iil6/Htr2b/Cd3e/Klrk1/Tnfrsf8/C3ar1/Tlr7/Cybb/Dlk1/Tlr8/Cd6/C3/Tlr2/Ptafr/Pycard/Tgfb1/Ccr5/Iil18r1/Agpat2/Bcl3/Cd2/Fgr/Slc11a1/Unc93b1/Tnfrsf14/Smad3/Thbs1/Gbp5/Fadd/Iil6r/Myd88/Iil1rl1/Ptpn22/Sash3/Gsdmd/Tlr9/Lum/Jak2/Adam17/Casp1/Cle9a/Iil20rb/Irfih1/Irf7/Panx1/Cd40/Spn/Sulf2/Card9/Iil1rl2/Nr4a3/Zcccc11/Src/Tek/Drd2/Hyal2/Arnt/Hdac1/Mapk11/Prkcz/Sema7a/Tusc2/Crhr2
GO:0072 657	protein localization to membrane	72/1663	0.0009 3	Trem2/Amn/Rab32/Itgam/Itgal/Ramp1/Grin2b/Tgfb1/Ephb2/Itga4/Rab13/Nkd2/Rab38/Dab2/Myl12a/Dchs1/Epha2/Syne3/Ezr/Adcy6/Reln/Ldlrap1/Pid1/Lrp4/Itgb7/Agrn/Rftn1/Lrp1/Fam126a/Scrib/Ehd2/Scn3b/Zmynd8/Akt2/Dlg3/Rhog/Csk/Pkdcc/Nup155/Ptn/Mtch2/Calm1/Chm/Efr3a/Lztfl1/Ubl4a/Musk/Rab11a/Arl6ip1/Moap1/Hsp90aa1/Tspan33/Calm3/Cacnb3/Nlgn1/Dlg2/Prkcz/Cdk5/Timm10/Pex3/Stxbp1/Rab3ip/Epb41l3/Map7/Pls1/Glrb/Crb3/Ar/Slc12a1/Hpca/Lin7b/Htr1a
GO:0048 489	synaptic vesicle transport	31/1663	0.0010 56	Syt14/Syt17/Syt11/Sh3gl3/Syt13/Scrib/Fgfr2/Napa/Calm1/Syt11/Eps15/Pfn2/Ap3s2/Syt5/Calm3/Nlgn1/Tmem230/Trim46/Cdk5/Prepl/Stxbp1/Napb/Rims3/Ap1s2/Rims1/Trim9/Sh3gl2/Syt3/Unc13c/Syt10/Doc2a
GO:0099 003	vesicle-mediated transport in synapse	31/1663	0.0010 56	Syt14/Syt17/Syt11/Sh3gl3/Syt13/Scrib/Fgfr2/Napa/Calm1/Syt11/Eps15/Pfn2/Ap3s2/Syt5/Calm3/Nlgn1/Tmem230/Trim46/Cdk5/Prepl/Stxbp1/Napb/Rims3/Ap1s2/Rims1/Trim9/Sh3gl2/Syt3/Unc13c/Syt10/Doc2a
GO:0050 663	cytokine secretion	40/1663	0.0010 56	Mmp12/Iil1a/Vtcn1/Iil6/Htr2b/Fn1/Tlr8/Tlr2/Pycard/Ccr5/Cd2/Fgr/Unc93b1/Tnfrsf14/Ssc5d/Gbp5/Iil1rl1/Ptpn22/Trem1/Gsdmd/Tlr9/Ezr/Casp1/Clec9a/Ifh1/Panx1/Foxp1/Zc3h12a/Fbln1/Src/Tek/Rnf19b/Drd2/Notch1/Hyal2/Mapk11/Syt11/Prkcz/S100a13/Itgb6
GO:0019 221	cytokine-mediated signaling pathway	62/1663	0.0012 56	Mmp12/Iil1a/Iil6/Cxcr3/Trem2/Tnfrsf18/Tnfrsf8/Csf2rb/Ccrl2/Iil2rb/Ccr6/Cd27/Xcr1/Iil21r/Pycard/Cd4/Ccr5/Iil18r1/Iil1rn/Tnfrsf14/Iil10ra/Iil2rg/Fadd/Cxcr6/Iil6r/Myd88/Iil1rl1/St18/Nradd/Tnfrsf26/Jak2/Casp1/Bgn/Iil20rb/SigIRR/Irf7/Cd40/Irak2/Irak4/Peli3/Tjp2/Ltbr/Iil1rl2/Ifngr1/Osmr/Ptprn/Zcchc11/Akt2/Duo2/Tnfrsf25/Lifr/Rps6ka4/Stat6/Nfkbia/Mkks/Lrrc4c/Rtn4rl2/LRRTM1/Flrt1/Prlr/Edn2/Iil1rapl2

GO:1902 600	hydrogen ion transmembrane transport	25/1663	0.0020 26	Atp6v0d2/MGC105649/Slc9a3/Tcirg1/Cox7a2l/Cox8a/Uqcr11/Atp6v1c2/Stoml2/Cox6c/Atp5b/Cox5b/Atp5l/Atp6v1h/Cox7c/Uqcrh/Uqcrb/Atp5g3/Ndufa4/Atp6v1e1/Cyc1/Atp6v1c1/Cox4i2/Cox7b/Atp6v0e2
GO:0050 778	positive regulation of immune response	76/1663	0.0021 77	Mmp12/Ii6/Pglyrp4/Lilrb4/Clec7a/Cd3e/C1qa/C1qb/Cfd/C1qc/Kirk1/tgam/Cd180/C3ar1/Vav1/PVR/Tlr7/Tlr8/C3/C1s/Tlr2/Ptafr/Pycard/Tgfb1/Cd4/Serping1/Fgr/Slc11a1/Unc93b1/Tnfrsf14/Ptpn6/C1r/Lag3/Fcgr1a/Nckap1l/Gbp5/C1rl/Fadd/Myd88/Ptpn22/Themis2/Skap2/Sash3/Tlr9/Plscr1/Pik3ap1/Ezr/Lck/Ptprj/Lpxn/Nr1h3/Birc3/Ifih1/Plekha1/Irf7/Trim5/Cd40/Irak2/Irak4/Rftn1/Peli3/Card9/Nr4a3/Tek/Csk/Stat6/Nfkbia/Xrcc5/Stoml2/Cacnb3/Prkcz/Sema7a/Stxbp1/Esr1/Sh2d1a/Cnr1
GO:0003 013	circulatory system process	72/1663	0.0024 25	Csrp3/Vip/Htr2b/Tbxas1/Avp/Slc4a5/C3ar1/Met/Anpep/Cysltr1/Ptafr/Tgfb1/Icam1/Smad3/Ptgs1/Jak2/Adcy6/Nr2f2/Ptprj/Eng/Prcp/Agrn/Tjp1/Acvrl1/Itga1/Scnn1a/Zc3h12a/Slc2a5/Scn3b/Fli1/Npr1/Hrh1/Ptk2/Akap13/Src/Slc1a1/Rnls/Drd2/Npr3/Vegfa/S100a1/Nup155/Calm1/Mkks/Hsp90aa1/Hey2/Calm3/Arhgap35/Tbxa2r/Kcna5/Fgfbp3/Oprl1/Gclm/Scn1b/Crhr2/Ntsr1/Trhde/Kcnh2/Nppa/Cnr1/Tacr3/Ar/Kcnj5/Hrh3/Grip2/Myl3/Tnni3k/Htr2c/Th/Htr1a/Cyp11b2/Edn2
GO:0009 167	purine ribonucleoside monophosphate metabolic process	47/1663	0.0028 07	Tspo/Tgfb1/Myc/Hk2/Pid1/Impdh2/Scrib/Galt/Tcirg1/Dlg3/Cox7a2l/Cox8a/Ndufa7/Stoml2/Aldoa/Prcaa1/Mtch2/Atp5b/Cox5b/Atp5l/Sdhd/Prcaa2/Atp5s/Ndufc2/Ndufb9/Dld/Cox7c/Uqcrh/Uqcrb/Atp5g3/Ndufa8/Sdha/Cyc1/Ndufb8/Dlg2/Cox4i2/Ndufb6/Ndufv2/Ndufa10/Ndufaf7/Ndufs1/Ola1/Slc25a25/Impdh1/Slc25a33/LOC365985/Esrbb
GO:1905 114	cell surface receptor signaling pathway involved in cell-cell signaling	74/1663	0.0028 23	Cthrc1/Chrna1/Fgf2/Wnt10b/Met/Tbx18/Tlr2/Bmp2/Ccnd1/Grin2b/Smad3/Nkd2/Tle3/Myc/Rspo1/Dab2/Hhex/Dkk2/Reln/Grin2d/Gli1/Wnt10a/Wwtr1/Lrp4/S1pr2/Tle2/Shh/Lrp1/Sulf2/Sox2/Zbed3/Lzts2/Mad2l2/Zmynd8/Fgfr2/Ryk/Src/Drd2/Csnk1e/Amotl2/Sox17/Notch1/Hdac1/Bcl9l/Prickle1/Atp6v1c2/Prcaa1/Ppm1a/Cby1/Gskip/Prcaa2/Gabrb3/P2rx3/Pin1/Grid2/Nlgn1/Prkcz/Cdk5/Tle4/Ctnnd2/Ptpru/Nrap/Grin3a/Chrna5/Amer1/Ntsr1/Grin1/Rims1/Slc17a7/Chrna4/Glrb/Wnt7a/Npas4/Chrna3
GO:0043 281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	39/1663	0.0030 27	Ii6/Avp/Cck/Cd27/Pycard/Smad3/Thbs1/Myc/St18/Jak2/Casp8/Lck/Ptma/Casp1/Rps6ka1/Birc3/Bcl2l12/Nr4a1/Apaf1/Anp32b/Dap/Sox2/Ctsh/Akt2/Src/Bok/Ifi27/Aqp1/Vegfa/Aifm1/Mtch2/Prdx5/Bcap31/Ret/Arl6ip1/Epha7/S100a9/Mgmt/Egln3
GO:0090 132	epithelium migration	43/1663	0.0048 65	Tacstd2/Ccr6/Fgf2/Met/Srpx2/Tgfb1/Angpt4/Tgfb1/Fap/Ccr5/Sh3bp1/Epb41l4b/Thbs1/Ets1/Rab13/Epha2/Nr2f2/Meox2/Sox18/Prcp/Foxp1/Dpp4/Nr4a1/Dock1/Acvrl1/Shh/Zc3h12a/Ptk2/Plekhg5/Ctsh/Src/Tek/Notch1/Rhob/Fgf7/Srf/Aqp1/Vegfa/Atp5b/Rab11a/Pfn2/Hdac9/Wnt7a

GO:0050804	modulation of chemical synaptic transmission	62/1663	0.004993	Gdnf/Nps/Pdyn/Met/Cdc20/Cpg1/Grin2b/Cnr2/Ephb2/Reln/S1pr2/Shisa7/Hrh1/Ptk2/Zmynd8/Calb1/Drd2/Srf/Napa/Ptn/Calm1/P2rx3/Musk/Rab11a/Pfn2/Bace1/Shank2/Ppfia3/Cpeb1/Slc8a3/Grid2/Calm3/Nlgn1/Prkcz/Map1b/Cdk5/Ctnnd2/Prepl/Stxbp1/Napb/Rims3/Grm7/Ntrk1/Crhr2/Ntsr1/Asic1/Grin1/Rims1/Grm8/Slc24a2/Chrna4/Cnr1/LRRTM1/Bcan/Wnt7a/Slc8a2/Unc13c/Kcnc3/Htr2c/Npas4/Grm3/Chrn a3
GO:1903829	positive regulation of cellular protein localization	62/1663	0.00572	Il6/Trem2/Itgam/Tlr7/Tgfb1/Ect2/Tlr2/Tgfb1/Iil18r1/Ephb2/Smad3/Ptpn22/Nkd2/Ndc80/Dab2/Rac2/Tlr9/Iqgap1/Epha2/Ctsk/Jak2/Ezr/Slc17a9/Lrp4/Plagl2/Shh/Lrp1/Sulf2/Anp32b/Wipf1/Zc3h12a/Snx33/Zbed3/Akt2/Src/Tek/Crocc/Rhog/Hyal2/Dkc1/Tmem30a/Gnl3l/Vegfa/Cep290/Ptn/Ppm1a/B3gat3/Bcap31/Syt11/Musk/Vps11/Rab11a/Hsp90aa1/Kcnn3/Oscp1/Chp2/Cdk5/Gpr26/Pls1/Tmem30b/Hnmt/Hpca
GO:0050890	cognition	53/1663	0.005871	Vip/Nps/Fos/Stra6/Cebpa/Tlr2/Grin2b/Gpr88/Ephb2/Iil1rn/Fosl1/Cyp7b1/Ptgs1/Gabra5/Casp1/Reln/Ccnd2/Shroom4/Mdk/Hrh1/Calb1/B4galt2/Chst10/Drd2/Srf/Ptn/Musk/Shank2/Tanc1/Slc8a3/Prkcz/Cdk5/Ctnnd2/Pja2/Pak7/Abpbb1/Elavl4/Kcnk4/Ap1s2/Grm7/Ntrk1/Ntsr1/Asic1/Grin1/Slc17a7/Nrxn3/Slc24a2/Chrna4/Cnr1/Slc8a2/Hrh3/Npas4/Th
GO:0006091	generation of precursor metabolites and energy	54/1663	0.005871	Myc/Hk2/Gfpt1/Nr4a3/Galt/Akt2/Dyrk2/Cox7a2l/Cox8a/Chchd5/Ndufa7/Aldoa/Rb1cc1/Prkaa1/Mtch2/Cox5b/Idh3g/Sdh/Prkaa2/Pdha1/Ndufs4/Ndufc2/Ndufb9/Idh3a/Dld/Cox7c/Uqcrh/Uqcrb/Fastkd2/Ndufa8/Sdha/Cyc1/Ndufs3/Ndufb8/Cox4i2/Aco2/Agl/Ppp1r3d/Ndufb6/Suclg1/Gys1/Ndufb3/Ndufv2/Ndufa5/Ndufa10/Idh3B/Aass/Ndufs1/Slc25a25/Slc25a33/Pygb/Gyg1/Esrbb/Gnmt
GO:0050707	regulation of cytokine secretion	34/1663	0.005922	Mmp12/Iil1a/Vtcn1/Iil6/Htr2b/Fn1/Tlr2/Pycard/Ccr5/Cd2/Fgr/Unc93b1/Tnfrsf14/Ssc5d/Iil1rl1/Ptpn22/Gsdmd/Tlr9/Ezr/Casp1/Clec9a/Iifi1/Panx1/Foxp1/Zc3h12a/Fbln1/Src/Tek/Drd2/Hyal2/Mapk11/Syt1/Prkcz
GO:0007492	endoderm development	20/1663	0.005922	Col7a1/Fn1/Tgfb1/Smad3/Itga4/Dusp6/Col5a2/Col5a1/Dab2/Hhex/Zfp36l1/Sox2/Pax9/Col11a1/Sox17/Notch1/Hdac1/Nckap1/Dusp5/Onecut1
GO:0048871	multicellular organismal homeostasis	57/1663	0.006013	Hamp/Iil1a/Iil6/Avp/Lyz2/Acp5/Met/Dlk1/Nox4/Ccr5/Slc11a1/Iil1rn/Slc28a2/Sash3/Rac2/Scnn1b/Tlr9/Ctsk/Adcy6/Iil20rb/Prcp/Scnn1a/Nr4a3/Tpp1/Lpcat1/Col14a1/Cyp26b1/Ctsh/Src/Crocc/Drd2/Inpp5d/Hyal2/Fgf7/Csk/Srf/Aqp1/Vegfa/Prkaa1/Cep290/Prdx5/Mkks/Bbs10/Prkaa2/Lipa/Rbp4/Map1a/Pth1r/Ntsr1/Nppa/Cnr1/Clrn1/Scx/Rpe65/Esrbb/Edn2/Iapp
GO:0031346	positive regulation of cell projection organization	65/1663	0.00642	Ankrd1/Iil6/Fn1/Met/Fes/Tgfb1/Bmp7/Ezh2/Crabp2/Rgma/Rac2/Syt17/Plk5/Iqgap1/Eef1a1/Reln/Fnbp1l/Enc1/Ptbp1/Wasf2/Agrn/Nin/Atf1/Zmynd8/Nav3/Src/Crocc/Srf/Sept7/Tmem30a/Aqp1/Vegfa/Nckap1/Eps8l2/Ccp110/Ntrk3/Atmin/Ptn/Ret/Eif2b2/Rab11a/Hsp90aa1/Kctd17/Mns1/Ttbk2/Cpeb1/Arhgap35/Nlgn1/Nckipsd/Map1b/Cntn1/Sema7a/Abpbb1/Scn1b/Elavl4/S100a9/Myo3b/Ntrk1/Grin1/Rims1/Shox2/Cnr1/Clrn1/Syt3/Avil
GO:0033627	cell adhesion mediated	15/1663	0.00642	Fermt3/Icam1/Fbn1/Ptpn6/Nckap1l/Epha2/Adam17/Lpxn/Dpp4/Itga6/Ptk2/Swap70/Ret/Itga11/Itgb6

	by integrin			
GO:0045 428	regulation of nitric oxide biosyntheti c process	17/1663	0.0064 2	Il6/Klrk1/Acp5/Tspo/Tlr2/Icam1/Smad3/Jak2/Zc3h12a/Hrh1/Akt2/Kh srp/Hsp90aa1/Gla/Gchfr/Rgn/Esr1
GO:0022 407	regulation of cell-cell adhesion	60/1663	0.0068 08	Vtcn1/Il6/Lilrb4/Cd3e/Epcam/Itgal/Icos/Cd27/Fermt3/Tnfaip8l2/Cd6 /Tbx18/Bmp7/Bmp2/Ptafr/Pycard/Tgfb1/Cd4/Ccr5/Icam1/Il1rn/Zc3h 12d/Tnfrsf14/Ptpn6/Lag3/Itga4/Nckap1l/Il2rg/Fadd/Ets1/Ptpn22/Do ck8/Sash3/Rac2/Mex3b/Jak2/Lat/Lck/Il20rb/Efnb1/Dpp4/Spn/Itga6/L oxl3/Shh/Il1rl2/Sox2/Fstl3/Nr4a3/Mad2l2/Ptk2/Cyp26b1/Src/Swap7 0/Spint2/Vegfa/Prkcz/Epha7/Nrarp/Slc46a2
GO:0071 229	cellular response to acid chemical	44/1663	0.0071 02	Hamp/Reg3b/Mmp3/Abcb1b/P2ry6/Fn1/Rorb/Wnt10b/Cybb/Ptafr/ Grin2b/Sipa1/Col5a2/Tead1/Myc/Pdgfc/Adcy6/Pid1/Foxp1/Dnmt1/C dk4/Zc3h12a/Dnmt3b/Fgfr2/Cyp26b1/Phc1/Src/Dnmt3a/Xrcc5/Lamt or2/Aqp1/Ntrk3/Lancl2/Prkaa1/Ret/Prkaa2/Pdk3/Cpeb1/Pdgfd/Six1/ Gclm/Kcnk4/Rragd/Ptgfr
GO:0071 384	cellular response to corticoster oid stimulus	25/1663	0.0075 59	Serpina3n/Ucn2/Il6/Gdnf/Ugt1a1/Sstr3/Sstr4/Grin2b/Tgfb1/Icam1/F bxo32/Jak2/Zfp36l1/Zfp36/Reln/Dnmt3b/Akap13/Aqp1/Vegfa/Aifm1 /Usp8/Hcn2/Crhr2/Abcc2/Npas4
GO:0036 293	response to decreased oxygen levels	64/1663	0.0076 35	Mmp12/Il1a/Ucn2/Ankrd1/Mmp3/Abcb1b/Cybb/Tgfbr1/Angpt4/Tlr2 /Bmp2/Grin2b/Tgfb1/Nox4/Icam1/Ccna2/Smad3/Serpina1/Ets1/Myc /Scnn1b/Zfp36l1/Adam17/Casp1/Nr4a2/Eng/Dpp4/Apaf1/Acvrl1/Shh /Suv39h1/Dnmt3b/Src/Tek/Drd2/Dnmt3a/Notch1/Ppp1r15a/Arnt/Sr f/Aqp1/Scfd1/Vegfa/Aifm1/Aldoa/Prkaa1/Ptn/Sdhb/P2rx3/Trpc1/Pdk 3/Cpeb1/Slc8a3/Fundc1/Cox4i2/Kcna5/Endog/Pcmt1/Egln3/Nppa/Ch rna4/Ngb/Smad9/Th
GO:0120 034	positive regulation of plasma membrane bounded cell projection assembly	22/1663	0.0078 35	Tgfbr1/Rac2/Fnbp1l/WASF2/Agrn/Zmynd8/Crocc/Srf/Sept7/Aqp1/Nc kap1/Eps8l2/Ccp110/Atmin/Hsp90aa1/Kctd17/Mns1/Ttbk2/Arhgap3 5/Nlgn1/Myo3b/Clrn1
GO:2000 377	regulation of reactive oxygen species metabolic process	34/1663	0.0081 69	Il6/Mmp3/Klrk1/Itgam/Acp5/Tspo/Tlr2/Tgfb1/Nox4/Icam1/Smad3/D hfr/Thbs1/Hk2/Foxm1/Jak2/Eef1a1/Birc3/Pid1/Prcp/Mycn/Zc3h12a/ Hrh1/Akt2/Khsrp/Pdk3/Hsp90aa1/Gla/Gchfr/Tusc2/Rgn/Esr1/Grin1/ Slc25a33
GO:0014 075	response to amine	17/1663	0.0081 98	Htr2b/Grin2b/Cnr2/Icam1/Nr4a2/Drd2/Hdac1/Slc18a2/Cad/Rrm2b/C alm1/Calm3/Hdac9/Hnmt/Grin1/Kcnc2/Th
GO:0042 035	regulation of cytokine	21/1663	0.0084 13	Il1a/Il6/Cd3e/Tnfrsf8/Tlr7/Cybb/Tlr2/Ptafr/Bcl3/Thbs1/Lag3/My d88/Tlr9/Zfp36/SigIRR/Tia1/Spn/Card9/Inpp5d/Ube2j1

	biosynthetic process			
GO:0002274	myeloid leukocyte activation	34/1663	0.0087 13	Hamp/Kirk1/Itgam/Tyrobp/Myo1f/Batf/Spi1/Tlr7/Fes/Tlr8/Tlr2/Ptafr/Pycard/Tgfb1/Cnr2/Fgr/Slc11a1/Thbs1/I1rl1/Cd37/Rac2/Tlr9/Plscr1/Lat/Casp1/Nr1h3/Foxp1/Spn/Ltbr/Nr4a3/Hyal2/Stxbp1/Cnr1/Edn2
GO:0045785	positive regulation of cell adhesion	59/1663	0.0087 13	Vtcn1/I6/Lilrb4/Cd3e/Fn1/Tnfrsf18/Itgal/Icos/Cd27/Vav1/Cd6/Tbx18/Bmp7/Ptafr/Pycard/Tgfb1/Cd4/Ccr5/Icam1/Epb41l4b/Smad3/Ptpn6/Thbs1/Itga4/Nckap1l/I2rg/Fadd/Ets1/Ptpn22/Dock8/Smoc2/Sash3/Dab2/Iqgap1/Mex3b/Jak2/Lck/Triobp/Emilin1/Ptpnj/Tgm2/Efnb1/Dpp4/Spn/Itga6/Dock1/Shh/I1rl2/Sox2/Fstl3/Nr4a3/Fbln1/Ptk2/Src/Tek/Vegfa/Ptn/Ret/Prkcz
GO:0010718	positive regulation of epithelial to mesenchymal transition	13/1663	0.0092 72	Tgfbr1/Bmp7/Bmp2/Tgfb1/Ezh2/Smad3/Dab2/Eng/Wwtr1/Notch1/Blcl9l/Sdcbp/Olfm1
GO:0071356	cellular response to tumor necrosis factor	37/1663	0.0094 29	Hamp/Reg3b/Ankrd1/I6/Abcb1b/Tnfrsf18/Tnfrsf8/Cd27/Cebpa/Pycard/Icam1/Tnfrsf14/Thbs1/Oclin/St18/Nradd/Tnfrsf26/Adamts7/Jak2/Zfp36l1/Casp1/Zfp36/Adamts12/Birc3/Pid1/Foxp1/Cd40/I18bp/Peli3/Tjp2/Ltbr/Zc3h12a/Hyal2/Tnfrsf25/Hdac1/Nfkbia/Abcc2
GO:0060828	regulation of canonical Wnt signaling pathway	33/1663	0.0094 43	Cthrc1/Fgf2/Wnt10b/Tbx18/Bmp2/Nkd2/Rspo1/Dab2/Dkk2/Gli1/Wwtr1/Lrp4/Tle2/Shh/Sulf2/Sox2/Zbed3/Lzts2/Mad2l2/Fgfr2/Src/Csnk1e/Sox17/Notch1/Hdac1/Prickle1/Cby1/Gskip/Pin1/Ctnnd2/Nrarp/Amer1/Wnt7a
GO:0042107	cytokine metabolic process	23/1663	0.0094 43	I1a/I6/Cd3e/Tnfrsf8/Tlr7/Cybb/Tlr8/Tlr2/Ptafr/Bcl3/Thbs1/Lag3/Myd88/Trem1/Tlr9/Zfp36/Sigirr/Tia1/Irf7/Spn/Card9/Inpp5d/Ube2j1
GO:0010463	mesenchymal cell proliferation	15/1663	0.0094 43	Tbx18/Bmp7/Bmp2/Myc/Dchs1/Mycn/Foxp1/Shh/Fgfr2/Fgf7/Vegfa/Ptn/Arhgap5/Six1/Shox2
GO:0032680	regulation of tumor necrosis factor production	26/1663	0.0094 43	Tnfrsf8/Acp5/Cybb/Tspo/Tlr2/Ptafr/Pycard/Ccr5/Bcl3/Cd2/Thbs1/Fadd/Myd88/Ptpn22/Sash3/Tlr9/Jak2/Zfp36/Ifh1/Foxp1/Spn/Card9/Zc3h12a/Hdac1/Syt11/Ube2j1
GO:0050678	regulation of epithelial cell proliferation	53/1663	0.0094 83	Mmp12/Tacstd2/Vip/I6/Htr2b/Cxcr3/Thbs4/Fgf2/Wnt10b/Tgfbr1/Tbx18/Bmp2/Ccnd1/Tgfb1/Smad3/Thbs1/Myc/Osr2/Cyp7b1/Dab2/Zfp36l1/Zfp36/Nr2f2/Ccnd2/Cdkn2b/Eng/Gli1/Foxp1/Nr4a1/Avrl1/Shh/Sulf2/Sox2/Nr4a3/Ptpn/Fgfr2/Cdkn1c/Notch1/Agap2/Fgf7/Vegfa/Ptn/Six1/Ptpnk/Nrarp/Rgn/Esr1/Six4/Wnt7a/Ar/Hrh3/Hes5/Scg2

	n					
GO:0006809	nitric oxide biosynthetic process	18/1663	0.009665	Il6/Klrk1/Acp5/Tspo/Tlr2/Icam1/Smad3/Jak2/Spr/Zc3h12a/Hrh1/Akt2/Khsrp/Hsp90aa1/Gla/Gchfr/Rgn/Esr1		
GO:0034612	response to tumor necrosis factor	40/1663	0.009665	Hamp/Reg3b/Ankrd1/Il6/Mmp3/Abcb1b/Tnfrsf18/Tnfrsf8/Cd27/Cebpa/Pycard/Icam1/Tnfrsf14/Thbs1/OcIn/St18/Nradd/Tnfrsf26/Adamts7/Jak2/Casp8/Zfp36l1/Casp1/Zfp36/Adamts12/Birc3/Pid1/Foxp1/Cd40/Il18bp/Peli3/Tjp2/Ltbr/Zc3h12a/Hyal2/Tnfrsf25/Hdac1/Nfkbia/Endog/Abcc2		

**Table S9. List of the common rodent DEGs with absolute expression changes not decreasing with time.** The genes were chosen from the common DEGs between two mouse (C, B; Table S2) or two rat (P, Br; Table S3) datasets, based on the requirement than absolute log2fc at later time-point is not smaller than at earlier time point  $|\log_{2}fc_B| \geq |\log_{2}fc_C|$  for mouse or  $|\log_{2}fc_{Br}| \geq |\log_{2}fc_P|$  for rat. For DEGs, which are common for all 4 datasets (top of the Table) both conditions were true. Only correlated genes, up- or down-regulated in all compared datasets, were used. For the rat datasets there were 949 DEGs with persistent changes with time; the Table shows only 37 of them, which are present in the pain interactome network (Fig. 5).

gene	description	log2fc_B	log2fc_C	log2fc_P	log2fc_Br
Lipn	lipase, family member N	4.72	4.47	5.2	5.8
Ms4a7	membrane spanning 4-domains A7	1.16	1.11	1.33	1.38
Slco5a1	solute carrier organic anion transporter family, member 5A1	-0.75	-0.59	-1.15	-1.25
Frmpd4	FERM and PDZ domain containing 4	-0.68	-0.6	-2.34	-2.88
Vsnl1	visinin-like 1	-0.59	-0.58	-2.48	-4.07
Glb1l2	galactosidase, beta 1-like 2	-0.88	-0.7	-3.07	-4.39

#### mouse common persistent

gene	description	log2fc_B	log2fc_C
Gpr151	G protein-coupled receptor 151	3.96	3.9
Speer4a	spermatogenesis associated glutamate (E)-rich protein 4A	4.13	2.6
Colec10	collectin sub-family member 10	2.67	2.59
Hrk	harakiri, BCL2 interacting protein (contains only BH3 domain)	2.64	1.91
Slc15a3	solute carrier family 15, member 3	1.68	1.36
Star	steroidogenic acute regulatory protein	1.54	1.11
Fam196a	family with sequence similarity 196, member A	0.91	0.83

Rgs20	regulator of G-protein signaling 20	0.81	0.81
Tes	testis derived transcript	0.81	0.78
Tubb6	tubulin, beta 6 class V	1.05	0.77
Ly6a	lymphocyte antigen 6 complex, locus A	2.33	0.72
Runx2	runt related transcription factor 2	1.03	0.69
Met	met proto-oncogene	0.82	0.61
Acvr1	activin A receptor, type 1	0.75	0.6
Bmp1	bone morphogenetic protein 1	0.55	0.55
Ahr	aryl-hydrocarbon receptor	0.52	0.5
AI593442	expressed sequence AI593442	-0.58	-0.51
Zfp804a	zinc finger protein 804A	-0.6	-0.52
Gm19461	predicted gene, 19461	-0.72	-0.52
Map7d2	MAP7 domain containing 2	-0.57	-0.55
Tmem229b	transmembrane protein 229B	-0.62	-0.56
Nefm	neurofilament, medium polypeptide	-0.6	-0.56
Gm765	predicted gene 765	-0.58	-0.58
Pls1	plastin 1 (I-isoform)	-0.64	-0.59
Kcns1	K+ voltage-gated channel, subfamily S, 1	-0.66	-0.62
Epn3	epsin 3	-0.71	-0.62
Nefh	neurofilament, heavy polypeptide	-0.72	-0.63
Ndst4	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4	-0.77	-0.63
Hapln4	hyaluronan and proteoglycan link protein 4	-0.78	-0.64
Galm	galactose mutarotase	-0.78	-0.69
Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	-0.79	-0.73
Esrrg	estrogen-related receptor gamma	-0.78	-0.73
Cdh12	cadherin 12	-0.97	-0.91
Vstm2b	V-set and transmembrane domain containing 2B	-1.37	-1.28

**rat common persistent from the pain interactome network**

SYMBOL	description	log2fc_Br	log2fc_P
Cck	cholecystokinin	3.76	3.28
Il1rn	interleukin 1 receptor antagonist	2.37	1.82

Fosl1	FOS like 1, AP-1 transcription factor subunit	2.4	1.78
Rela	RELA proto-oncogene, NF-kB subunit	1.09	1.01
Il16	interleukin 16	1.1	0.97
Prss12	protease, serine 12	1.13	0.87
Adra2a	adrenoceptor alpha 2A	1.36	0.86
B3gat1	beta-1,3-glucuronyltransferase 1	1.4	0.81
Src	SRC proto-oncogene, non-receptor tyrosine kinase	0.93	0.69
Drd2	dopamine receptor D2	1.33	0.65
Sp1	Sp1 transcription factor	0.64	0.64
Stat6	signal transducer and activator of transcription 6	0.56	0.52
Nfkbia	NFKB inhibitor alpha	0.7	0.51
Aqp1	aquaporin 1	-0.89	-0.55
Vegfa	vascular endothelial growth factor A	-0.65	-0.57
Ntrk3	neurotrophic receptor tyrosine kinase 3	-0.66	-0.62
Ephb1	Eph receptor B1	-0.85	-0.62
P2rx3	purinergic receptor P2X 3	-1.11	-0.72
Slc8a3	solute carrier family 8 member A3	-0.83	-0.83
Grin3a	glutamate ionotropic receptor NMDA type subunit 3A	-1.4	-1.25
Scn9a	sodium voltage-gated channel alpha subunit 9	-1.46	-1.26
Grm7	glutamate metabotropic receptor 7	-1.47	-1.39
Ntsr1	neurotensin receptor 1	-2.02	-1.5
Kcnj3	potassium voltage-gated channel subfamily J member 3	-1.61	-1.61
Tac1	tachykinin, precursor 1	-2.45	-1.64
Nppa	natriuretic peptide A	-2.34	-1.68
Penk	proenkephalin	-2.5	-1.71
Scn8a	sodium voltage-gated channel alpha subunit 8	-2.15	-1.88
Gria2	glutamate ionotropic receptor AMPA type subunit 2	-2.45	-2.13
Oprd1	opioid receptor, delta 1	-2.24	-2.2
Scn10a	sodium voltage-gated channel alpha subunit 10	-3.28	-2.35
Oprm1	opioid receptor, mu 1	-2.93	-2.43
Syt9	synaptotagmin 9	-2.59	-2.44

Kcnip3	potassium voltage-gated channel interacting protein 3	-2.91	-2.73
Scn11a	sodium voltage-gated channel alpha subunit 11	-4.41	-2.77
Htr3a	5-hydroxytryptamine receptor 3A	-6.23	-3.26
Htr1a	5-hydroxytryptamine receptor 1A	-6.19	-3.41

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