Gene Microarray Integrated with iTRAQ-Based Proteomics for the Discovery of NLRP3 in LPS-Induced Inflammatory Response of Bovine Mammary Epithelial Cells

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SUPPLEMENTARY FILE

Supplementary Material & Methods

RNA isolation and microarray assay

Total RNA was extracted from BMECs using Trizol reagent (Hoffmann-La Roche Ltd., Shanghai, China) according to the manufacturer instructions. The gene chip used in the Bovine Genome Array was generated by a service provider (SBC Co., Ltd., Shanghai); the chip included 45,220 probes that contained 43,711 transcripts of 11,542 BMEC genes. The total RNAs of the NT and LPS-treated BMECs were individually hybridized with gene chips. In brief, in the first-strand cDNA synthesis reaction, 500 ng total RNA (in a 10 µ*l* volume) was combined with 10 µ*l* of reaction solution and T7-oligo (dT) promoter primer. The double-stranded cDNA was then synthesized from the first-strand cDNA using RNase H. After purification of the resulting DNA, an *in vitro* transcription reaction was carried out to produce biotin-labeled cRNA using the MEGA Script T7 Kit (Ambion, Inc., Houston, TX, USA). After the biotin-labeled cRNA was cleaned and fragmented, the cRNA was hybridized to the probe array at 45 °C for 16 h. The probe array was then washed and stained on a fluidics station and the microarrays were scanned using a GeneChip Scanner 3000 (Affymetrix, San Diego, CA). Affymetrix Micro Array Suite 5.0-Specific Terms GCOS v1.4 was used for quantity analysis of the hybridization gene expression levels; those with ≥ 2-fold difference between the groups were checked and further analyzed (Affymetrix microarray analysis followed by RMA normalization method). The Molecule Annotation System (http://david.abcc.ncifcrf.gov/) was used to analyze the differentially expressed genes, using the Kyoto encyclopedia of genes and genomes (KEGG) public pathway resource and the gene ontology (GO) consortium.

Protein extraction, quantification and digestion

Prepared samples were first frozen to a dry powder with a vacuum freeze drier. The freeze-dried powder was dissolved in 200 µ*l* L3 dissolution buffer and 800 µ*l* cold acetone containing 10 mmol/*l* dithiothreitol (DTT) and the resuspended powder was incubated for approximately 2 h. After centrifugation at 17370×g for 20 min at 15 °C, the precipitate was collected and mixed with 800 µ*l* cold acetone containing a solution of 10 mmol/*l* DTT for 1 h at 56 °C to break the protein disulfide bonds. Again, centrifugation at 17370 ×g for 20 min at 15 °C, the precipitate was collected and then dried and then stored at -80 °C for later use.

Total protein concentration was measured using the Bradford method. For each sample, 100 µg of protein was dissolved to 500 μ*l* in a dissolution buffer and then diluted with 500 μ*l* NH_4HCO_3 (50 mmol/*l*). After being reduced and alkylated, 2 μg trypsin was added before incubation overnight at 37 °C for protein digestion. After protein digestion, equal volumes of 0.1% Formamide (FA) was added to acidify the solution. Peptides were purified on a Strata–X C18 pillar three times, washed with 0.1% FA + 5% Acetonitrile (ACN) twice, and eluted with 1 m*l* 0.1% FA + 80% ACN. Eluted peptides were dried with a vacuum concentration meter. The dried peptide powder was redissolved in 20 μ*l* of 0.5 mol/L Triethylamine borane (TEAB) for peptide labeling.

LC-MS/MS and data analysis

Liquid chromatography electrospray ionization tandem mass spectrometry LC-ESI-MS/MS analysis was performed on an AB Sciex nano LC-MS/MS (Triple TOF 5600 plus) system. Samples were chromate graphed using a 120 min gradient from 2% to 35% (buffer A 0.1% (v/v) formic acid, 2% (v/v) acetonitrile; buffer B 0.1% (v/v) formic acid, 90% (v/v) acetonitrile)) after direct injection onto a 20 cm PicoFrit emitter (New Objective, Woburn, USA) packed to 20 cm with Magic C18 AQ 3 lm 200-Astationary phase. MS1 spectra were collected in the range 360–1460 m/z for 250 ms. The 20 most intense precursors with charge state 2–5 were selected for fragmentation and MS2 spectra were collected in the range 50–2000 m/z for 100 ms; precursor ions were excluded from reselection for 15 s.

The original MS/MS file data were submitted to Protein Pilot Software v4.5 (Applied Biosystems, Foster City, CA, USA) for data analysis. For protein identification, the Paragon algorithmintegrated into Protein Pilot was employed against the SwissProt bovine database from Uniprot website (http://www.uniprot.org) using Mascot software version 2.3.02 (Matrix Science, London, UK). Trypsin was chosen as the cleavage specificity with a maximum number of allowed missed cleavages of two. Carbamidomethylation (C) and iTRAQ 8-plex label were set as fixed modifications. The searches were performed using a peptide and product ion tolerance of 0.05 Da. Scaffold was used to further filter the database search results by the decoy database method. The following filter was used in this study: 1% false positive rate at the protein level and two unique peptides for each protein. After filtering the results, the peptide abundances in the different reporter ion channels of MS/MS scan were normalized. For differentially expressed protein (DEP) determination, fold changes were calculated as the average comparison pairs among biological replicates. Proteins with a fold change larger than 1.3 and P-value < 0.05 were considered to be significantly differentially expressed. The Molecule Annotation System (http://david.abcc.ncifcrf.gov/) was used to analyze the differentially expressed proteins. The Gene Ontology (GO) terms of biological process in DAVID were employed to categorize enriched biological themes in differentially expressed protein lists.

Supplementary Table S1. Primers used for RT-Qpcr

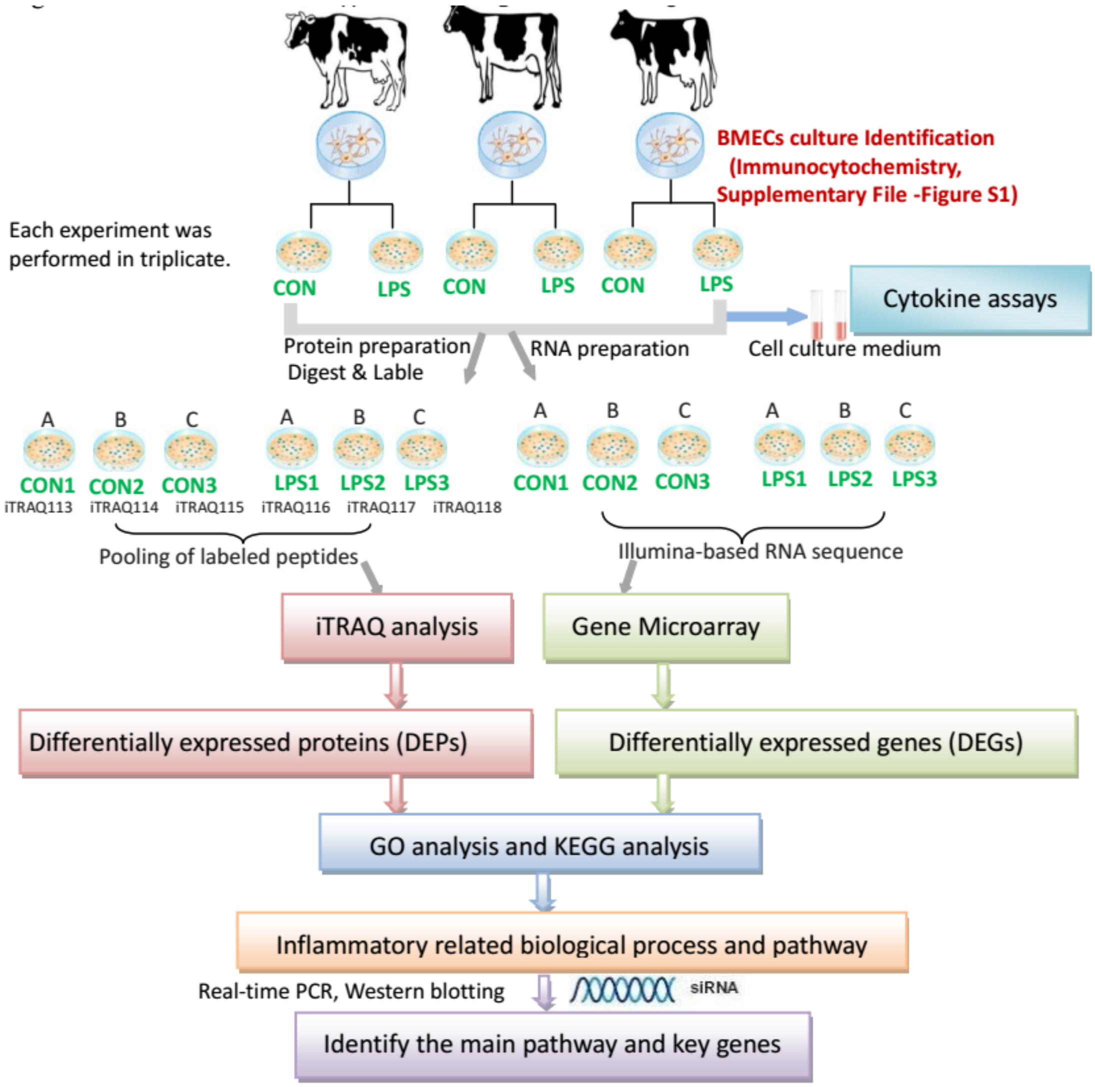
Gene symbol	Accession No.	Product size (bp)	Primer sequence (5’ → 3’)
NLRP3	NM_001102219.1	123	F: TGTCTTTGAGCCTTCTCGGT R: GCAGAAGGACCATCAGCAAG
IL-1β	NM_174093.1	264	F:CGTCTTCCTGGGACATTTTCG R: GTCTGAGGATGGGCTC TGGG
COX-2	NM_174445.2 213	213	F: CCAGAGCTCTTCCTCCTGTG R: AAGCTGGTCCTCGTTCAAAA
CXCL10	NM_001046551	117	F: CTCGAACACGGAAAGAGGCA R: TCCACGGACAATTAGGGCTT
COL4A5	AC_000187.1	121	F: CTGACATTTAGACATGATGAG R: ACTGACCGAGATGGGAGCAT
LTF	AC_000179.1	119	F: GCAACAACGAGAATGAGAACAAGT R: GACATCTTTCACAAATGCAACGTC
CATHL5	NM_174510	176	F: TGGTCACTGTGGCTACTGC R: GGGTTCTCATCGTCCTCC
18S rRNA	AC_000182	116	F:TCCAGCCTTCCTTCCTGGGCAT R:GGACAGCACCGTGTTGGCGTAGA

Supplementary Table S2. siRNA sequences of NLRP3 that were used in this study

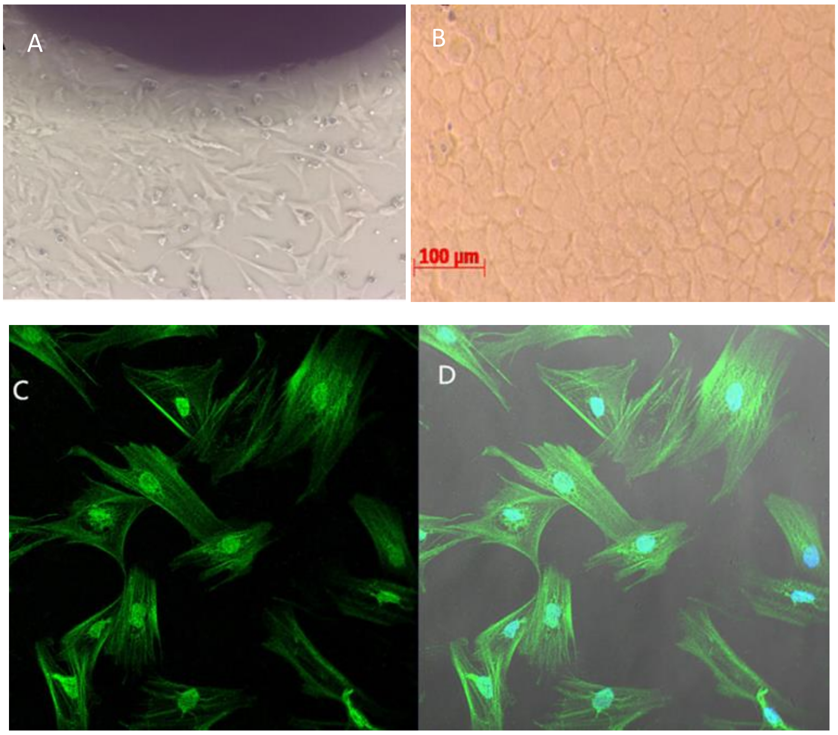
Genes	Forward	Reverse
siRNA-1	5′-CCUGGAAGACAUAGACUUUTT-3′	5′-AAAGUCUAUGUCUUCCAGGTT-3′
siRNA-2	5′-GCGAGAAAUUCUACAGCUUTT-3′	5′-AAGCUGUAGAAUUUCUCGCTT-3′
siRNA-3	5′-CCACACUUCUAACUUCUAATT-3′	5′-UUAGAAGUUAGAAGUGUGGTT-3′
Negative control	5′- UUCUCGACGUCACGUTT-3′	5′- ACGUGACACGUUAGGATT-3′

Supplementary Table S3. The biological processes of DEGs and DEPs

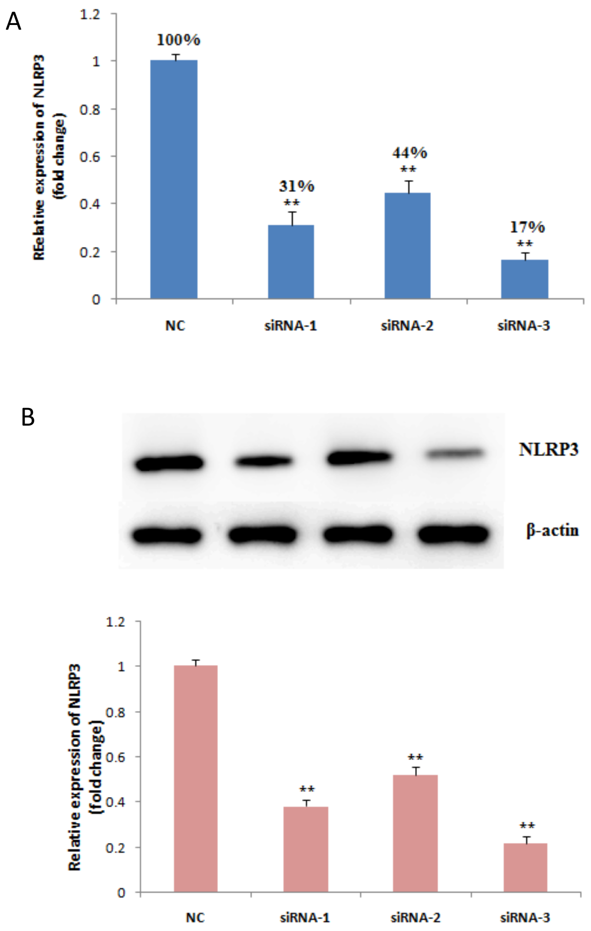
Processs	DEGs	DEPs
Response to stimulus	GO:0032496~response to lipopolysaccharide GO:0071222~cellular response to lipopolysaccharide GO:0009617~response to bacterium GO:0002237~response to molecule of bacterial origin GO:0009605~response to external stimulus GO:0006953~acute-phase response GO:0032101~regulation of response to external stimulus GO:0071216~cellular response to biotic stimulus GO:0043207~response to external biotic stimulus GO:0006950~response to stress GO:0009607~response to biotic stimulus GO:0009719~response to endogenous stimulus GO:0070887~cellular response to chemical stimulus GO:0050896~response to stimulus GO:0071495~cellular response to endogenous stimulus	GO:0009605~response to external stimulus GO:0009991~response to extracellular stimulus
Immune process	GO:0002376~immune system process GO:0006955~immune response GO:0042092~type 2 immune response GO:0006952~defense response	GO:0006952~defense response
Inflammatory process	GO:0031663~lipopolysaccharide-mediated signaling pathway GO:0006954~inflammatory response GO:0002526~acute inflammatory response	GO:0006954~inflammatory response GO:0002526~acute inflammatory response



Supplementary Figure S1. Experimental design based on iTRAQ and gene Microarrays, overall workflow and overview of key data outputs across the study.



Supplementary Figure S2. Primary bovine mammary epithelial cell (BMEC) isolation and identification. (A) Polygon-like aggregates of BMEC emerged from the tissue edges; magnification ×100. **(B)** Purified epithelial cells obtained over three passages; magnification ×200. **(C-D)** Immunofluorescence of cytokeratin 18; magnification ×300.



Supplementary Figure S3 The mRNA expression and protein levels were detected by real-time RT-PCR(**A**), and Western blot (B) after transfection of BMECs with three different pairs of siRNA siRNA-1, siRNA-2, and siRNA-3 represent different sequences of siNLRP3. ***p*<0.01.

Abbreviation: NC, negative control.

Supplementary Full Microarray Dataset

1019 differentially expressed genes (fold change ≥ 2 or ≤0.5, P-value < 0.05)

GeneSymbol	foldchange(LPS *vs*.CONTROL)	P Val(LPS *vs*.CONTROL)
GNGT1	57.59214334	0.02760187
SBK2	51.14841051	0.032322101
PRKAG3	48.51202512	0.04185709
EOMES	48.45816483	3.35E-23
ADAMTS16	44.4953293	0.006224534
BAP1	42.54388796	0.028324209
STAC2	42.11115695	0.03855117
BEX2	42.01598229	0.02302786
SOX13	39.66220493	0.01532008
UGT2B10	39.58382955	0.000542625
SERPINA3-7	39.09510776	0.01497817
RNF169	39.02170707	0.0259407
ABRA	38.43834683	0.005719196
PGLYRP3	37.28293801	9.71E-03
HOXA2	35.31198011	0.000222348
RERG	34.65058935	0.000955699
SLC10A6	34.41055979	0.003351011
GDF9	34.33482289	0.003811733
NDUFA11	34.2800994	0.000144632
MXRA5	33.50041329	0.0141383
GHRL	32.94067124	0.006817644
COL6A6	32.51144297	0.047077801
NEUROD6	32.41016057	0.0385276
FGFBP3	31.8636511	0.01198754
CD8B	31.5132886	0.01051581
KIF17	31.06443466	0.02961511
CACNA2D3	30.66426889	6.05E-06
GPM6A	30.52878924	0.042854119
PDE1C	30.42045881	0.018094361
PAPPA	30.2292188	0.000221016
CD34	29.88819614	0.000574379
AHSG	29.64683969	2.00E-05
CRYAA	29.29252775	0.02139847
MRGPRX2	28.94630057	0.000923668
FMO1	28.77375327	0.00754943
HERC3	28.64530633	3.10E-03
SLC30A10	28.57828654	0.00503333
EPX	28.49933299	2.19E-23

ZNF389	28.43879652	0.001971208
CCDC149	28.20780896	0.02116137
IL18RAP	28.10249429	0.002349729
IGFBP1	27.96316424	0.017301129
FOXO3	27.79089354	2.44201E-06
TM4SF18	27.58228163	0.000129244
CATHL4	27.54867401	0.006817644
PDE1A	27.52113933	0.0051078
CRYBA2	27.44402798	0.03922425
ALDOB	27.43322034	0.000591218
KCNK5	27.3730282	5.60E-03
TAP1	27.13291948	0.001189154
GABRR1	27.11120454	0.000761227
FSTL4	26.56682801	1.60E-02
HAND1	26.45000064	2.04E-09
FGB	26.4220481	0.0385276
SPDEF	26.29952806	0.004335132
ZNF555	26.293733	0.03240518
CTAGE5	25.78039704	1.93E-07
ABI3	25.59932331	6.85E-06
DCST2	25.58334723	3.57E-72
ADAM18	25.49212938	0.001260774
KEL	25.4533969	0.000146972
BBS10	25.44076248	0.000730592
OR2M3	25.43584447	0.04285171
DOCK8	24.96435465	0.000356341
CHGB	23.96900328	0.001178271
CCDC70	23.94032571	0.000366613
PHYHIP	22.84169352	0.000140447
CYP2C18	22.58546703	0.00858301
PDZD3	22.43998784	0.00299693
CEP97	21.70767931	0.000174135
ABAT	21.5846682	0.01169324
ARPP21	21.42952688	5.78496E-06
NOX3	21.25005714	0.0125528
LRRC18	20.92233126	8.89293E-05
STAB2	20.80790174	0.00773904
ARID3B	20.66560098	0.000367495
PTPRK	20.63735669	0.01308586
OPALIN	20.60873844	0.002975108
FGB	20.59574341	0.004299686
C18H16	20.50979218	0.038681939
SATL1	20.48490499	0.04703338

IL22RA1	20.12601932	1.29E-105
FHIT	19.93986456	0.01159536
AGAP2	19.92549697	0.003017498
PPM1L	19.87100736	0.000496291
VAT1L	19.12168809	0.000996824
CNGB1	18.75846394	0.000229839
AOAH	18.74621455	0.01389586
CSF2RB	18.26014357	0.002481728
OR2Y1	18.04643937	0.000350212
FASTKD3	17.88709256	0.003311035
BOSTAUV1R404	17.75007	0.00298394
OR10A6	17.69372863	0.040009879
C3AR1	17.2500305	0.00143529
C11H9orf9	17.23209864	0.01198
FAM82B	16.90672726	0.001048235
SYNE4	16.31945769	0.01404001
SLC8A1	16.09190926	0.0055955
CDH9	15.94244954	0.02212307
CCL20	15.49166181	0.017410271
TAF6L	15.27927933	5.36279E-05
VILL	15.18962869	0.02000911
FMO1	15.02018322	0.02710004
CYP2C87	14.89217425	3.44811E-11
SLC10A4	14.81578124	0.006928992
ZNF740	14.80167895	0.01230794
GBF1	14.61745962	0.003202281
BMP7	14.58693427	3.90671E-05
SLC22A20	14.42771078	0.01410362
PTPN22	14.2759049	0.033077259
CCL20	14.25114569	0.000356341
SLC18A3	14.15032519	1.17211E-07
CCDC68	13.83702311	2.30721E-06
CBLN1	13.82499839	1.13169E-05
TCP11L2	13.73130179	0.003103429
CA8	13.57642004	0.000426883
TNRC6B	13.51976531	0.005294728
CSF3	13.43870858	8.93467E-07
STAT2	13.43493007	4.4053E-11
LCN6	13.39255862	0.004951362
ECM2	13.39022877	3.51174E-08
RABGAP1L	13.22803902	0.025482509
KCTD20	12.76815178	0.01128111
PKN1	12.6674788	0.031609669

FAM162B	12.65511581	5.15061E-06
CCL20	12.62132533	8.93654E-06
GCM2	12.62079855	0.002551326
ARPP21	12.33250014	0.033094499
MORN3	12.31474544	0.003033679
CSRNP3	12.20510409	2.89787E-07
NUMBL	12.066895	0.036266141
PEG11AS	12.06527502	0.000367495
C13H20orf112	11.95118357	0.018094361
KLHL38	11.89221632	7.6875E-06
GFRA1	11.87019153	0.003811733
VPS13D	11.66858734	0.036455661
CAMSAP1	11.54653759	5.78496E-06
CXCL13	11.14946279	0.019581299
PRKCZ	11.11774816	0.000146972
NCOA2	11.09141559	0.000444094
SULT6B1	11.00438509	0.036614291
TNNC2	10.94594651	0.006818983
NRXN2	10.70955928	7.41331E-08
ADCY6	10.51160021	0.01043122
TYRP1	10.49574015	0.003640894
CNNM1	10.4324883	0.002774426
PHKA2	10.2823235	0.0051078
QRICH2	10.26506955	0.034207489
C3H1orf141	10.11139747	0.003146521
BOLA-DQA5	9.96841617	0.049978182
SLC8A3	9.755683159	0.023572469
RASA3	9.604052572	3.77112E-05
ZNF407	9.600256826	6.87172E-08
DUSP23	9.562877521	6.76499E-05
WDR86	9.415563897	0.031738348
RAPGEF3	9.320829205	0.009074424
IPO13	9.319393075	6.21303E-12
NUDT11	9.283338348	0.01197931
TNNI3K	9.215183548	0.002347769
ELAVL3	9.205472705	0.003443727
ATP10D	9.176786207	1.29808E-09
EMILIN2	9.067622941	0.002082329
FOXO4	9.035383293	8.89293E-05
PVRL1	8.917549417	0.009232295
GSDMC	8.839136259	0.00454695
TBC1D10C	8.836536456	0.01158283
APLNR	8.819598594	0.002975108

ABCB1	8.662807178	1.45301E-09
PEX13	8.561337519	3.7927E-05
SULT1C2	8.533925383	0.00079272
GDPD4	8.502266062	2.64274E-10
KLHDC9	8.470104702	0.01515232
OCLN	8.34227173	0.041758489
FGB	8.207532718	0.01222101
SLC1A7	8.202150395	5.51654E-08
ATAD1	8.137452973	0.04417843
STARD9	8.007282463	0.0055955
DYNC2LI1	7.84891153	0.011368
MLIP	7.796714455	0.003817958
DCDC2C	7.726339126	0.017931361
SLC37A2	7.709947281	0.008014595
KIRREL3	7.691349232	0.046758778
AMT	7.67464332	3.56197E-05
BAG6	7.613622311	0.03074313
SPARCL1	7.609547136	0.006946657
TFCP2	7.60446946	0.048405111
CHSY1	7.603779519	0.02217098
FIBIN	7.591333324	0.001669685
ASZ1	7.523578368	0.042854119
CXCL10	7.512036104	0.01169324
MSTO1	7.455367121	0.003997674
IL1B	7.426515171	0.039712571
ZNF181	7.398837964	0.003311035
ARHGEF9	7.30667328	0.036479801
C1H3orf52	7.285360193	0.0187211
EMC3	7.141371636	0.01073254
LPHN2	7.103862721	0.007204999
LPAR3	7.094514714	0.000174135
TJP1	7.076605056	0.002533916
CXCL10	7.003127737	6.33705E-09
CFTR	7.002473407	0.03484831
NTM	6.758053161	0.000563325
MRAP2	6.730259362	0.03213216
BIK	6.713322287	0.041420508
AMZ1	6.709662497	0.040300399
CDHR1	6.706443072	0.020218261
BCHE	6.697411446	0.040506139
KCNJ10	6.693235151	0.021684529
AKAP5	6.671113097	0.001045697
PIGS	6.624127316	1.64704E-10

CCL11	6.608253364	0.02190616
ASGR2	6.529741129	0.003930275
TRIM63	6.500028301	0.005541831
CXCL10	6.451426977	0.019441471
ACE3	6.432502892	0.003794501
ESRRG	6.396449387	0.004450682
ZNF555	6.307782003	0.000730592
TM4SF18	6.3022422	0.042926561
HEPACAM	6.146669869	0.008372493
IL6	6.118313362	0.033792861
UPK3B	6.111845178	0.016639819
NFAM1	6.107228831	0.01051581
Mar	6.094712627	0.02791624
ART3	6.091795463	0.03733696
NYAP2	6.065671632	0.003790005
CD8B	6.057471448	0.02747196
DBC1	6.026307968	1.58857E-05
CATSPER4	6.004955265	4.58922E-07
OLR1	5.992887952	0.02460333
C5H12orf54	5.870870761	0.008341776
CACHD1	5.85901847	0.036187802
TKTL2	5.838292924	0.046104372
SCMH1	5.826204744	0.00143529
TLN2	5.816272254	2.68606E-05
MAGEE2	5.728246991	0.002917996
PIK3CB	5.716389803	0.02266632
LAMA1	5.678928317	0.009560845
GREB1	5.67141883	0.006006601
IL6	5.666307919	7.10407E-06
SERINC2	5.626931114	0.002872616
MDP-1	5.606781321	0.02827381
PCDHA11	5.588331086	0.001070434
CSF2	5.562156754	0.02139847
SLC4A1	5.542614997	0.01935255
IL1A	5.486611015	0.042541619
SIAH1	5.484875229	0.008139121
PLG	5.464735238	0.018297231
GPR155	5.456256239	0.00032166
WRN	5.39182474	7.24999E-06
MTMR2	5.365477983	0.00216046
INPP4B	5.35321761	0.023119681
WDR64	5.338945776	0.01337965
SPAG6	5.302557656	0.007222672

CD1E	5.295050345	0.037911341
IL1A	5.29372408	0.02116137
PTGS2	5.289502373	0.01134212
BDH2	5.268656042	0.000213935
CCL11	5.254908352	0.000691943
PLEKHG1	5.243214253	0.01189747
AKAP6	5.235968448	0.044186249
GSS	5.232071651	0.01077593
OR2A12	5.219232613	0.000534804
CACNA1E	5.20708949	0.022265069
PCIF1	5.12661727	0.01159536
C13H20orf195	5.030303327	0.022350829
GRM1	5.025826971	0.026851909
RHOBTB2	4.994585669	0.00299693
TTC6	4.960642879	0.01241356
GIGYF1	4.953341185	2.2284E-05
EML3	4.944412125	0.016244199
GLIS1	4.94287287	5.17752E-05
JHDM1D	4.940450502	0.020684
MYO3B	4.912775803	0.00773904
NEUROG2	4.895723225	0.025242999
ZDHHC14	4.879680879	0.02319606
ARHGAP20	4.830836754	0.000299061
CCL2	4.775272295	0.01517996
KIF12	4.762611284	0.03583806
DNAJC18	4.661785417	0.01308586
P2RY12	4.639159666	0.019495141
PLCXD1	4.631912498	0.036780652
PTPRH	4.615278166	0.041165389
CNPY3	4.515401572	0.041414991
CUL5	4.511851852	3.60329E-08
EXOC8	4.49037832	0.01100258
TRMT61A	4.482684613	0.01286099
CYP2A13	4.481790467	0.019501621
C15H11orf88	4.435699709	0.02447582
CAPS	4.406284047	0.038821299
RAB20	4.346624302	0.01340431
CEP89	4.332529282	0.000869049
FAM65A	4.291688598	0.02961511
GAN	4.161792964	4.07475E-05
MYOM1	4.161411619	0.00082158
RND1	4.149187919	0.023750089
DIS3	4.146348849	0.002481728

MUC19	4.122785201	0.043234561
NPBWR2	4.089641841	0.0254777
CCL2	4.076525382	0.00754943
NCAM1	4.061705676	0.03668623
FGF12	4.033799285	0.016381221
C28H10orf10	4.025745577	0.025442651
ZFP62	3.994744402	0.049514908
CCRL2	3.987478393	0.0464045
PRSS16	3.981526339	0.002575187
ZNF184	3.952969982	0.01117369
ATG4B	3.946546646	3.33249E-05
CSN2	3.922006431	2.14984E-12
LRRC16B	3.876399603	0.004931632
UNC119B	3.837302768	8.93296E-11
RAB40B	3.824017959	0.01389586
KIAA0895L	3.771539934	2.44201E-06
GIT2	3.77123224	0.001849319
TEX12	3.732172578	2.00982E-05
USP2	3.718163476	0.02040871
PCED1A	3.70661944	7.3032E-05
ATP6V1B1	3.691797193	0.02000911
RELA	3.682014728	0.02710004
PCP4	3.664018784	3.44811E-11
CCRL2	3.663540848	0.006928992
SYK	3.615005147	0.003202281
PUS10	3.612529572	3.90671E-05
FAM170A	3.607008698	0.01410362
MPPE1	3.582548418	0.033077259
PTGS2	3.582343306	0.000356341
C20H5orf22	3.576628811	1.17211E-07
UTP18	3.576460728	2.30721E-06
RSAD2	3.547254891	1.13169E-05
EPS8L2	3.53860812	0.003103429
BCL6	3.51617774	0.000426883
PBX2	3.510779036	0.005294728
PTPN7	3.509191789	8.93467E-07
NDP	3.505224139	4.4053E-11
SLC46A1	3.493733589	0.004951362
ANKRD34B	3.47174552	3.51174E-08
RNASEH2A	3.460953598	0.025482509
C18H16orf70	3.455864129	0.01128111
CXCL2	3.402938315	0.031609669
DDX31	3.39472568	5.15061E-06

ELF2	3.377392613	8.93654E-06
MOB1A	3.364976201	0.002551326
C17H22orf25	3.322462689	0.033094499
PHF20	3.317961164	0.003033679
MAPK8	3.312013373	2.89787E-07
NRD1	3.300158697	0.036266141
CXCL2	3.294309264	0.000367495
COL5A3	3.282946183	0.018094361
HTR2A	3.272299055	7.6875E-06
ATP2A3	3.265377987	0.003811733
TIMP4	3.249733928	0.036455661
SAA3	3.249146961	5.78496E-06
ZNF672	3.219943786	0.019581299
LTF	3.211059505	0.000146972
M-SAA3.2	3.202699635	0.000444094
SAA2	3.188514847	0.006818983
CCDC120	3.18774737	7.41331E-08
M-SAA3.2	3.172257758	0.01043122
SLC25A44	3.16561542	0.003640894
GALNT4	3.122538591	0.002774426
SAA3	3.11374241	0.0051078
ENTPD5	3.110746211	0.034207489
EHMT2	3.109366339	0.003146521
APBB3	3.097288348	0.049978182
SLC46A2	3.091624923	0.023572469
CCR7	3.08537404	3.77112E-05
FGF22	3.082972885	6.87172E-08
FRY	3.060391239	6.76499E-05
TRPV2	3.053581603	0.031738348
GDF10	3.044364285	0.009074424
GCNT2	3.044052629	6.21303E-12
IL8	3.040155252	0.01197931
DHX38	3.038193587	0.002347769
LIF	3.024574715	0.003443727
SAA3	3.009646404	1.29808E-09
TNFAIP3	3.007001737	0.002082329
HAS2	3.004323146	8.89293E-05
TMEM200C	3.002319475	0.009232295
SEMA6A	3.001670045	0.00454695
SAA3	2.990019718	0.01158283
MAML3	2.989073767	0.002975108
SAA3	2.989031292	1.45301E-09
SAA3	2.987898833	3.7927E-05

PTX3	2.987166598	0.00079272
CA4	2.953805841	2.64274E-10
PARP8	2.951275083	0.01515232
KRT82	2.915615348	0.041758489
TAP	2.908015582	0.01222101
GIN1	2.902918363	5.51654E-08
PAG11	2.900000599	0.04417843
LIFR	2.897841325	0.0055955
BAP1	2.885237336	0.011368
PTGS2	2.876905836	0.003817958
GRO1	2.8681908	0.017931361
IL8	2.865562773	0.008014595
C17H4orf45	2.85371745	0.046758778
SRPX2	2.820988918	3.56197E-05
PTGER2	2.814669637	0.03074313
TMTC1	2.808543208	0.006946657
ZNF385B	2.788782461	0.048405111
PTGFRN	2.787393146	0.02217098
IRX6	2.782818273	0.001669685
ABCC2	2.782229639	0.042854119
SIRT6	2.771434672	0.01169324
CLDN1	2.762524003	0.003997674
KCNJ15	2.76108366	0.039712571
SALL4	2.756709412	0.003311035
TCF20	2.751367781	0.036479801
NHS	2.750680927	0.0187211
HAS2	2.749637249	0.01073254
BAG6	2.747145835	0.007204999
C10H15orf59	2.728010508	0.000174135
CIST1	2.715063985	0.002533916
IL8	2.709694109	6.33705E-09
CXCL3	2.691590624	0.03484831
ZBTB8B	2.669929413	0.000563325
SETMAR	2.65243427	0.03213216
PMS1	2.647792376	0.041420508
C3H2orf54	2.623305814	0.040300399
AKAP8L	2.616058855	0.020218261
SLC46A2	2.612955403	0.040506139
PTX3	2.611905136	0.021684529
CBX8	2.604035292	0.001045697
ABCA7	2.602800976	1.64704E-10
CLDN1	2.587832966	0.02190616
CDA	2.572934445	0.003930275

DDIT4L	2.55449533	0.005541831
HMGB3	2.546191096	0.019441471
P2RX5	2.529066197	0.003794501
TPRG1	2.513242008	0.004450682
ADRBK1	2.505005722	0.000730592
XIST	2.496191124	0.042926561
SLC39A8	2.493760126	0.008372493
LETM2	2.486157164	0.033792861
ART3	2.48309335	0.016639819
MX2	2.471541277	0.01051581
TUBGCP3	2.458781267	0.02791624
ITCH	2.444745691	0.03733696
AMH	2.417113638	0.003790005
ALS2	2.416638035	0.02747196
CA4	2.402834029	1.58857E-05
REEP6	2.398709255	4.58922E-07
OBFC1	2.370494426	0.02460333
RHOH	2.368290407	0.008341776
C16H1orf129	2.35817045	0.036187802
LTF	2.356548709	0.046104372
PTGS1	2.353001109	0.00143529
FCHO2	2.344746574	2.68606E-05
NFKBIA	2.332891157	0.002917996
CYP3A5	2.324809494	0.02266632
SFTPC	2.298064674	0.009560845
ZNF180	2.295395893	0.006006601
B3GNT5	2.289038137	7.10407E-06
USP24	2.287840696	0.002872616
FMNL1	2.271415917	0.02827381
THBD	2.262522279	0.001070434
CYP3A4	2.25817767	0.02139847
PLA2G4A	2.254675795	0.01935255
MMP12	2.254349656	0.042541619
RAMP1	2.253625665	0.008139121
NRAS	2.252408186	0.018297231
C15H11orf70	2.250576181	0.00032166
PSMB10	2.244937684	7.24999E-06
RALGAPA1	2.242718582	0.00216046
ZNF770	2.23634877	0.023119681
PNKD	2.234499156	0.01337965
JSP.1	2.232299651	0.007222672
RPRM	2.230120556	0.037911341
GGT5	2.222505206	0.02116137

ADPRH	2.221518263	0.01134212
ADI1	2.217827257	0.000213935
SLC39A8	2.214932908	0.000691943
KIF2A	2.200693914	0.01189747
PF4	2.195506186	0.044186249
HES5	2.193813522	0.01077593
C8H9orf91	2.193634249	0.000534804
FEV	2.192473946	0.022265069
FAM102A	2.190767528	0.01159536
BIN1	2.189447718	0.022350829
SAMSN1	2.188479698	0.026851909
SH2D3A	2.187488904	0.00299693
MYOF	2.180741852	0.01241356
SERPINB2	2.166646817	2.2284E-05
MAFF	2.16439543	0.016244199
LRRC25	2.163131395	5.17752E-05
IGF2	2.159982313	0.020684
IL1B	2.149699492	0.00773904
DNAJB4	2.145738549	0.025242999
METTL15	2.144423275	0.02319606
GAS8	2.143843063	0.000299061
STAU2	2.137718961	0.01517996
CIB3	2.13359744	0.03583806
SLX4	2.129708091	0.01308586
PRDM1	2.129036966	0.019495141
TNIP2	2.121475915	0.036780652
RSBN1	2.118389682	0.041165389
SPP2	2.098604057	0.041414991
ZNF784	2.094141604	3.60329E-08
BHLHE41	2.092838522	0.01100258
NLRP3	2.0900702	0.01286099
DUS3L	2.089963141	0.019501621
XPC	2.085065493	0.02447582
C10H15orf48	2.082717118	0.038821299
UNC5B	2.08119248	0.01340431
KLHL12	2.072467387	0.000869049
SOD2	2.066122797	0.02961511
NFKBIA	2.065067587	4.07475E-05
CYP3A4	2.058807582	0.00082158
CYP3A5	2.049870828	0.023750089
STC1	2.048140947	0.002481728
NCALD	2.045971431	0.043234561
CHAF1B	2.045132052	0.0254777

CYP3A4	2.042712264	0.00754943
NOS2	2.041404388	0.03668623
ALG13	2.036272302	0.016381221
CHD1	2.034341669	0.025442651
C15H11orf96	2.031514977	0.049514908
BIVM	2.024872403	0.0464045
PIF1	2.022266313	0.002575187
APOA5	2.021226921	0.000289109
CHRNA1	2.020338036	0.001459269
IL11	2.020168457	1.12634E-11
ALOX12E	2.019629983	0.02760187
S100G	2.018898526	0.023452541
RRAD	2.01704462	0.02437005
DDA1	2.016709104	0.03467378
ADAMTS5	2.01647707	0.007965421
CFB	2.016363857	0.000117263
ZRANB3	2.016054585	0.02999136
CA3	2.014067869	0.000370896
SCGB1A1	2.010142811	7.68735E-06
GGT5	2.009963635	0.01848289
RNF4	2.00761635	0.01450318
PRDM1	2.004019434	0.001354806
AKR1C4	2.003716361	0.042175949
SERPINF2	2.00203001	0.02089061
RELB	2.001247778	0.034144819
WIPF1	0.496367238	0.003289841
C26H10orf122	0.496182239	0.001588506
TSC22D3	0.493964306	0.02300084
ERAP2	0.492027447	0.002570762
OGN	0.491027592	0.01242267
CENPE	0.490676132	0.048496019
C11H2orf42	0.486338261	0.02262033
CNKSR1	0.485122232	0.02138591
GJA5	0.48416688	0.01106099
PRKAA1	0.484163525	0.027726529
FAH	0.481551633	0.0125528
FPGT	0.481335688	0.0259407
KIAA0528	0.481182907	0.000113187
POSTN	0.481179472	0.02212307
GADD45GIP1	0.480507948	7.08273E-05
CCDC173	0.478764803	0.033305518
MAPK3	0.477666101	0.026002521
MTHFD1L	0.477552947	0.0141383

GLRB	0.476642103	0.01493896
CALM3	0.475914066	0.00068201
VPS13D	0.475323291	0.001189154
MYH9	0.473798849	0.001417227
MCM3AP	0.473604174	0.002739107
KRT4	0.47313474	0.004335132
NFKBID	0.468559057	0.000221016
WHSC2	0.468410428	6.21774E-05
GAS7	0.46832193	0.001806159
TNNC1	0.4659432	0.001836406
DGKE	0.464207488	0.004299686
SLC38A10	0.463206049	0.038434099
EMX2	0.462878995	0.006192105
RGL1	0.462628804	0.003044358
MEOX1	0.460489766	0.001670022
MED18	0.459300736	0.02913622
EPM2A	0.459148743	0.000140447
DMC1	0.458772303	0.040009879
GRB14	0.45867526	0.02124464
ZNF462	0.458035239	0.002349729
IGF2BP3	0.458009618	0.03355208
MGC134577	0.457770024	0.024211841
GPR161	0.457395571	0.031295501
OR2Z1	0.456443755	0.017410271
KIF13A	0.454687233	0.000785313
RING1	0.450136139	0.041080989
GPATCH3	0.44905467	0.01353239
SYNPO2	0.447256793	0.007076628
MEI1	0.447202544	0.0308327
MAP4K5	0.446950108	0.02690281
DUSP8	0.443950275	0.0474713
UNC5B	0.443302284	0.009524952
ZNF710	0.439345828	0.001809
SLC12A2	0.438674059	0.000996824
MS4A8B	0.436990766	0.01198754
CAPN1	0.436786842	0.03655155
MEF2C	0.435478863	0.047077801
DUS4L	0.431134674	0.0110282
SP6	0.429343216	0.01404001
CES1	0.426329118	0.001094311
OTOP1	0.426241213	0.002036634
COL4A5	0.426102966	0.006206541
ARPC4	0.42520221	4.8115E-05

HCST	0.423836929	0.005565139
EVX1	0.423512131	0.00927037
EMC1	0.422938735	0.000839021
ATRIP	0.421554043	0.02534222
C17H4orf29	0.420615815	0.003130677
PPP3CA	0.42052661	0.001971208
GCC1	0.419294846	0.0265554
AMT	0.418990634	0.030711779
PIK3R1	0.417767828	0.003377477
FAM149B1	0.417120262	0.008560696
ABI2	0.416840627	0.04766307
GGA3	0.414802933	0.0372006
SMARCD1	0.41258984	0.004641809
FCGR3A	0.412515033	0.000390322
TCN1	0.411268163	0.048354141
ARHGAP20	0.407744042	0.017301129
LRRC16B	0.406036239	0.0153699
LPIN3	0.405018104	0.000663659
DKK2	0.404371605	0.022418579
OGN	0.403773323	0.008364874
SLC2A10	0.402888072	0.00385624
TTC14	0.401905437	0.003259917
PTRF	0.401473175	0.000615534
LAMP3	0.40015607	0.001929455
NAA25	0.399643242	0.00298394
PIDD	0.399146343	0.01198
RTKN2	0.397151952	0.047763959
SIX1	0.39633017	0.01073631
BOLA1	0.396120426	0.000943544
BPIFC	0.395820435	0.044737879
GAL	0.39345226	0.016874099
RCC1	0.391761492	0.000234225
PIK3R2	0.391500946	0.000258406
NCOA6	0.388314235	0.003017498
NRXN3	0.387541093	2.69494E-05
ACTA1	0.386986327	0.034296051
UBE4B	0.386267741	0.000291141
NPBWR1	0.385576706	0.001048235
TBCEL	0.380444576	0.000229839
PRPF31	0.377635422	0.018461689
KIAA0753	0.377211797	0.01229956
SIX2	0.376793452	0.021243419
GFAP	0.374778475	0.039387502

MAD2L1BP	0.37348329	0.039913431
ICOSLG	0.373001852	0.043128882
C17H22orf39	0.372487289	1.50506E-07
CD163L1	0.372122802	0.027261719
KANK1	0.37147247	0.017122921
EPB41L1	0.369756932	0.016307009
CGN	0.369456803	0.003324616
EEPD1	0.366156878	0.00037865
SMC1A	0.365387251	0.003626406
USP38	0.362695311	4.94814E-05
C11H2orf43	0.361939558	0.000128063
DEPDC7	0.359218859	0.003809233
C2CD3	0.358363771	0.000149925
DYNLRB1	0.356189847	0.036614291
MFSD6L	0.356139238	0.034828018
MIS18BP1	0.351951783	2.25438E-05
BRWD1	0.350527564	0.001571613
SYNPO2	0.345624885	0.000350212
TBC1D5	0.344961079	0.01120027
COX18	0.338900648	0.000846585
GATSL2	0.338782087	0.01152621
ZFAT	0.338230578	0.01118644
ZNF638	0.337948894	0.02645845
CATHL5	0.337051675	0.000496291
ABCA4	0.336016504	0.004347253
WISP1	0.334853047	0.039567601
MARVELD1	0.33436448	0.001501482
SERPINB9	0.33370664	4.26954E-05
CITED1	0.333597874	0.000591218
GAS7	0.331441371	1.54676E-12
SPERT	0.328097521	0.00845671
EXTL1	0.327009624	0.00503333
GNRH1	0.325192412	0.004289629
USP36	0.323788466	2.33792E-06
FBXO10	0.321453909	0.002930052
FBXO45	0.320673157	2.95558E-06
CAMP	0.319836036	0.000103728
ENPP1	0.317500771	0.000222434
TAB3	0.316243076	1.94726E-05
CD163L1	0.312623384	9.19358E-06
KDM5C	0.311702947	0.01911103
CDK19	0.311447522	0.0090994
SCIN	0.30858728	0.018275781

SNX22	0.307740345	0.001118317
SMC5	0.306129504	0.008060192
KLC3	0.306001578	0.027429949
KERA	0.305266186	0.02199159
STIM2	0.305225563	0.000222348
LPHN1	0.304841368	0.001260774
HGS	0.304452486	0.000210719
ZNF280D	0.302507538	2.58499E-06
COG2	0.301736431	0.001390666
CORO7	0.299740057	0.003722836
ZBTB7B	0.296348775	0.001974508
KIF18A	0.295478364	0.005719196
PDE10A	0.293815416	0.007728219
PTCH2	0.293282725	7.4829E-14
EPB41L5	0.288549953	0.03111822
CA5B	0.286932144	5.77946E-08
SLC16A13	0.283941908	0.00093542
DNASE1L1	0.282784804	0
LRRC20	0.282556973	0.01493793
CECR5	0.282410317	0.000144632
NID1	0.281383083	0.001176487
LRIG3	0.280522559	0.020058971
PDE4C	0.279931278	6.342E-06
C3H1	0.279226738	0.001522411
VWA1	0.277015921	0.001178271
GJA10	0.275403519	0.000955699
SLC16A13	0.275202599	0.02786422
NBEAL1	0.274168038	5.36279E-05
FGF12	0.271768057	1.19904E-14
MOBP	0.27013036	1.14121E-06
ING2	0.269937179	2.27187E-06
LHFPL3	0.268394684	0.008635683
TPM2	0.266453761	0.02511419
FGFRL1	0.265784412	0.02626721
LRRC58	0.263067312	0.03702921
ATP6AP1	0.261378612	0.016739121
CP	0.254535485	0.01292261
DIRAS3	0.252102565	0.044950619
SLC22A18	0.250351048	0.022234291
LYZL6	0.24811707	0.03485183
HOXB4	0.245384495	0.038681939
HIST1H2BD	0.24394706	0.04860748
SLC22A15	0.243791444	0.007232118

CCDC57	0.239899258	0.009685407
CBX1	0.238423608	0.02891532
EXOC4	0.23810569	0.01197548
POLE	0.237154311	0.02719376
ANKRD1	0.235592089	0.042985741
MYOM2	0.233867777	0.01061664
ANKRD1	0.232105063	0.01889924
NGP	0.231815076	0.021365451
WHSC1	0.230016618	0.01348344
ALKBH2	0.227595762	0.02514787
EPS8	0.226775674	0.001573622
OR10R2	0.225729801	0.01278181
LIFR	0.224943955	0.042348959
NOSTRIN	0.223856172	0.01532008
LTBP3	0.223592949	0.02745145
ZFYVE26	0.223529167	1.26968E-10
ARMC4	0.223349666	0.01062912
RALGAPA1	0.221795392	0.00322726
PARS2	0.220564315	0.007422611
ANKRD1	0.219508696	0.004421348
MIOS	0.21777931	0.01261566
CCL28	0.216008202	0.0331733
ZNF227	0.214480486	2.71124E-05
GTPBP10	0.214457206	0.01192693
POU2F1	0.214448555	0.005450147
MFSD9	0.214203105	0.049605709
FUT5	0.212925627	0.026755679
SPARCL1	0.210946302	0.01430092
C24H18orf34	0.20875204	0.009919097
CRABP2	0.204903708	0.01545066
MOG	0.204884961	0.00594828
CIB3	0.204119795	0.01388586
RASGRP3	0.203969169	0.002271621
EXPH5	0.201815348	0.046719249
RXFP3	0.200158682	0.02973469
DLGAP3	0.199920082	0.04904709
ACTN2	0.199611563	0.04514987
LMNB2	0.199458512	0.001679147
ZSWIM4	0.19595822	0.001230624
UOX	0.195580725	1.81246E-05
C11H9orf167	0.195466381	0.00517816
ABO	0.195441169	0.01295421
IPO4	0.195013499	0.00170417

SLC36A2	0.19460685	0.020961151
ITGA9	0.193865703	0.000594083
CDH5	0.193656107	0.002696097
KIAA1530	0.193343571	0.03682578
SHD	0.193080517	0.01629973
NR1I3	0.192071185	0.01105613
FHIT	0.192027056	0.003925795
PPP1R16A	0.191507354	4.78793E-07
TBC1D13	0.191046006	0.033531729
GLRB	0.190987537	0.03568954
USP11	0.190127629	0.03897455
PDE4B	0.189557652	1.58942E-05
OTC	0.188485572	0.008619026
PTRF	0.187894013	0.007008385
RPS6KL1	0.187471514	0.01242633
RAD1	0.187191431	0.007663802
KIAA1161	0.187141016	0.01218763
RHAG	0.186869134	2.27882E-05
SAMD3	0.186849382	0.027115559
RICTOR	0.18567127	0.001620575
KCNA2	0.185421122	0.00130404
OR1D5	0.18478019	3.42E-06
ARHGAP44	0.184686331	0.0182609
TNFRSF11A	0.183825269	0.025758641
SLC6A11	0.183036554	0.023518199
PAX6	0.181969139	0.006396028
RNF31	0.179519268	0.008992802
SAMD10	0.179351001	0.000592207
PLCB3	0.177964871	0.048533428
EDEM1	0.177535618	3.74533E-05
IL17RD	0.177115368	0.043810569
KCNG2	0.175183463	0.01186606
CCDC99	0.173047859	0.004170773
IRGC	0.172366379	0.00612262
TLR5	0.171441229	0.001406179
ITGB2	0.170713411	0.008000961
MGAT4C	0.170150772	1.56039E-06
ARHGAP36	0.169174719	0.000190589
TTC12	0.168990494	0.027901299
TMEM2	0.166721076	0.008704969
ACP5	0.166095743	0.01892918
PAG6	0.165803182	0
OR4D6	0.162967547	0.017580399

CNKSR2	0.162719674	4.68392E-05
OSBP2	0.161521789	0.027197899
TNRC6A	0.159026974	0.02428229
PRKCQ	0.158894016	0.02598834
ADCYAP1R1	0.157515183	0.001143172
PFKFB2	0.156178796	0.002855319
CCK	0.155833326	0.03667983
TNNI3K	0.155465051	0.028324209
CAMSAP3	0.154100879	0.0108014
SH2D2A	0.15263686	0.02388739
MMP15	0.150886956	0.000266535
GRAP	0.149811056	0.02381557
USP49	0.14954522	0.00628467
VIL1	0.149141225	0.007898995
GATA2	0.14884782	0.01300344
PLA2G12A	0.148340393	0.000837033
AP4E1	0.144755142	0.019279029
TULP2	0.144197224	0.01535467
PLCL1	0.143861046	0.021214381
RGS6	0.143711389	0.03195104
CACNB4	0.143405504	0.041874271
EXOC3L1	0.143153783	0.01544829
SPON1	0.14218245	0.0123515
HEPH	0.14139987	0.000556027
EHBP1L1	0.140674623	0.025220379
SEZ6L	0.138670258	0.02006101
MATN3	0.138553465	0.01451696
CLOCK	0.137616523	0.01321304
PRRC2A	0.136322348	0.02244373
ZNF37A	0.135689689	0.01594316
AQP12B	0.13403895	0.001022305
CLPTM1	0.133622013	0.003032094
CHST4	0.133291621	0.017709039
HOOK1	0.133191784	0.049609311
TAAR6	0.132639787	1.64971E-05
GPRASP1	0.130842959	0.001831131
SPEG	0.130235964	0.002473044
DNAJC6	0.129665448	0.04548284
REST	0.129398213	0.037505869
ABCG5	0.127515718	0.02239494
AMY2A	0.127140229	0.017575361
KCNMB1	0.125375669	0.00792306
PIP5K1C	0.124726731	0.0233007

LTF	0.124328272	0.031827811
CEPT1	0.123725519	0.009879077
FHL5	0.123443143	0.01357834
BRS3	0.12335459	0.017153781
SLC2A4	0.123042447	0.01317778
KIAA0232	0.122947508	0.003739432
PIK3AP1	0.122064983	0.03878421
RNF125	0.120916497	0.01694496
MAPK7	0.120227781	0.01607451
PDLIM5	0.119571063	0.000784667
PCDH9	0.119155628	0.008806715
BATF	0.118944973	0.001927979
HEATR7A	0.11858406	0.02604449
GSG1L	0.117091885	0.0155302
WDR19	0.116596477	0.002799731
ZNF382	0.11587637	0.000114884
ZFP62	0.114406871	0.033343881
SHANK1	0.11341038	0.002010007
S100Z	0.112978292	0.000847769
CNR1	0.111863633	0.01446471
KCNV1	0.110070365	0.005117949
IGF2	0.108988189	0.01990198
RHBDD1	0.107742295	0.006825017
FBXO47	0.106432186	0.008520544
ST6GAL1	0.105615384	0.02692475
PIKFYVE	0.105328977	0.006036988
LUZP1	0.105317421	4.07927E-07
BOSTAUV1R403	0.103809739	0.032621451
HCK	0.102705632	0.029349741
KRT20	0.10259657	0.001421284
MYOT	0.102513229	0.034928411
HSD11B2	0.099634839	0.038375579
SP1	0.09885303	0.004932478
PLAGL1	0.098772011	0.002174085
HSD17B13	0.096499816	6.66134E-15
HBB	0.09477361	0.03263247
CDH13	0.093928872	0.029933469
METTL4	0.092463129	0.004392964
ZNF295	0.089314771	2.34082E-08
BVES	0.087947062	0.009932947
CLIC2	0.085542815	0.001512696
IQCA1	0.084312065	0.008603265
FETUB	0.084149762	0.001421903

SOX6	0.082997075	0.019829631
WDR33	0.082577915	0.003823845
OPN4	0.081636905	0.000182135
ENTPD8	0.080955623	0.001230232
DAAM2	0.07864654	0.0222723
FA2H	0.077734444	1.1981E-07
CDH26	0.07739358	0.001448595
PGM1	0.07647871	0.01404094
KREMEN1	0.074108282	0.02066345
NXPH4	0.073896011	0.001509099
EPHB1	0.072980457	0.028439561
CCDC172	0.072753224	0.00016164
COL4A3	0.07169805	1.43066E-08
MTMR3	0.071212549	0.016507849
LEMD3	0.070561977	0.0395879
HHIP	0.069939515	0.00186809
PLXNA4	0.069863043	0.024821959
FEZF1	0.068772743	0.008232813
ZDHHC22	0.068523345	0.00533589
FRMPD4	0.067770156	0.01069044
HSD11B2	0.065071274	0.01138304
MATN1	0.064209105	0.01100132
TRAF3IP3	0.063932233	0.01396289
DEF6	0.06283068	0.01392081
POLL	0.062498484	0.003611821
MGP	0.061903174	0.041141789
CNGB1	0.060811353	0.000381721
PEX6	0.058960068	0.000372113
LA-DQB	0.058797136	0.03436406
GPR182	0.057935037	0.01568496
REG3G	0.057203086	0.000288849
PAX6	0.057024868	0.000102869
PNPLA1	0.056287341	0.017334851
HSPB3	0.05532578	0.001844633
NCAM1	0.055216502	4.05279E-06
BLOC1S3	0.054580442	8.75966E-13
PGBD1	0.054149608	0.000629056
PAG1	0.052677763	0.035715759
BOLA-DOB	0.052216298	0.021110229
CD200R1L	0.052150153	0.000763004
C19H17	0.051878404	0.000661151
PRRG2	0.050797271	0.001068492
RELL2	0.050008204	2.56564E-05

LSAMP	0.049663223	0.000424642
IL21	0.049510921	0.003324936
DYSF	0.04759391	0.040659841
CACNA1D	0.047124865	0.02315612
ADIG	0.047057213	2.02376E-05
HACE1	0.047002018	0.04049591
PTPRD	0.046069498	0.004756795
ZNF527	0.046010132	0.01158038
HPS3	0.04533534	0.03499715
SOX6	0.044260084	0.004893277
CCR2	0.043323773	0.01216884
HTR1B	0.04286605	0.000756185
CCDC158	0.042697384	0.004618463
CBLN4	0.042204587	0.006132877
MGC152281	0.042094425	4.73703E-06
GP1BA	0.040606993	0.02457951
GJD4	0.040263042	0.000565785
NAV2	0.039470968	1.05881E-05
GPM6A	0.039412471	4.59605E-08
ADTRP	0.037996122	0.01495092
ZNF292	0.03365937	0.003254189
FCGR3A	0.033449241	0.008946785
FAM160B2	0.03236742	0.02302786
SALL1	0.028334312	0.001734596
HTR1E	0.028134174	0.01246072
DEFB124	0.027126426	0.000626829
MRCL	0.026997732	2.83289E-05
ORAI1	0.026892107	1.34771E-09
CYP2E1	0.026831922	0.000676116
MPTX	0.026780058	0.000486804
OR52H1	0.026671242	0.002479264
ZNF674	0.025522226	0.004677762
KIAA0895L	0.025033087	0.019331429
KCNMB4	0.024738201	0.0334436
TMOD4	0.024669102	1.88173E-05
OSBP2	0.024554513	1.37535E-05
DYNC1I1	0.024419958	0.000117759
CLASP2	0.024061695	0.00012145
KCNMB2	0.02381853	0.02349182
FOXE3	0.023799598	0.000778162
RPL37	0.022870706	8.84566E-06
ZBTB11	0.022479258	8.48097E-05
ODZ3	0.022322328	3.00611E-09

SELK	0.021976082	0.03473511
SBSN	0.021428154	0.03912311
CHAT	0.020921707	0.007765132
CNTN3	0.020652464	0.01357757
CD37	0.020640432	0.000109945
CAMTA1	0.020153796	3.56836E-05
MYO3B	0.019595098	0.006772469
ATP1B4	0.019135614	0.02149724
CCDC105	0.019060857	0.035698269
PTGER3	0.018803395	0.047208689
SIRPD	0.018335879	0.003147802
KCTD8	0.017744324	0.003487152
FER1L6	0.017374645	0.001262189
KIF21A	0.016590622	0.000114719
SLC26A7	0.016533363	0.018185141
SLCO1A2	0.01562706	0.003139251
TRGV7-1	0.014944396	0.035254229
OR5M9	0.0138544	0.003031163
SERTAD4	0.012970867	0.003624395
CBY3	0.011926857	0.000267819
BTK	0.011453283	0.018805999
GRM7	0.011348728	0.00483168
ZNF689	0.01118954	0.003890621
RAB42	0.01095935	0.001145273
TDH	0.010464268	0.00444242
PAG19	0.010414414	0.03338816
SGIP1	0.009042523	2.54515E-05
GRAP2	0.008806861	0.021449121
SLC22A2	0.007391868	4.56944E-06
C8H9	0.007018176	0.005374438
CCDC73	0.006462374	0.01100785
MCOLN3	0.005719576	0.000523485
GAP43	0.004075127	0.036204681
LY6D	0.004053888	0.00328065
PHACTR1	0.003747372	0.046327569

Biological Process of DEGs

Term	Count
GO:0048731~system development	200
GO:0007275~multicellular organism development	213
GO:0009617~response to bacterium	39
GO:0006952~defense response	80

GO:0044707~single-multicellular organism process	249
GO:0032496~response to lipopolysaccharide	26
GO:0044767~single-organism developmental process	234
GO:1902578~single-organism localization	154
GO:0044765~single-organism transport	145
GO:0048856~anatomical structure development	233
GO:0006954~inflammatory response	40
GO:0032502~developmental process	236
GO:0002237~response to molecule of bacterial origin	26
GO:0009605~response to external stimulus	105
GO:1990266~neutrophil migration	15
GO:0030593~neutrophil chemotaxis	14
GO:0006953~acute-phase response	9
GO:0051179~localization	238
GO:0070098~chemokine-mediated signaling pathway	12
GO:0071222~cellular response to lipopolysaccharide	17
GO:0002376~immune system process	111
GO:0097530~granulocyte migration	15
GO:0060326~cell chemotaxis	24
GO:0065008~regulation of biological quality	153
GO:0051239~regulation of multicellular organismal process	125
GO:0007399~nervous system development	100
GO:0071219~cellular response to molecule of bacterial origin	17
GO:0032501~multicellular organismal process	277
GO:0071621~granulocyte chemotaxis	14
GO:0032101~regulation of response to external stimulus	49
GO:0071216~cellular response to biotic stimulus	18
GO:0051707~response to other organism	51
GO:0043207~response to external biotic stimulus	51
GO:0071347~cellular response to interleukin-1	12
GO:0097529~myeloid leukocyte migration	17
GO:0006950~response to stress	148
GO:0070555~response to interleukin-1	13
GO:0030154~cell differentiation	163
GO:0050900~leukocyte migration	24
GO:0048869~cellular developmental process	176
GO:0006935~chemotaxis	36
GO:0002682~regulation of immune system process	64
GO:0042330~taxis	36
GO:0006928~movement of cell or subcellular component	84
GO:0048513~animal organ development	139
GO:0022610~biological adhesion	74
GO:0002684~positive regulation of immune system process	45

GO:0009607~response to biotic stimulus	51
GO:0009893~positive regulation of metabolic process	129
GO:0007155~cell adhesion	73
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	51
GO:0044763~single-organism cellular process	472
GO:0051234~establishment of localization	184
GO:0044699~single-organism process	516
GO:0030595~leukocyte chemotaxis	18
GO:1902624~positive regulation of neutrophil migration	7
GO:0006810~transport	177
GO:1901701~cellular response to oxygen-containing compound	43
GO:0002526~acute inflammatory response	11
GO:0002687~positive regulation of leukocyte migration	13
GO:0042592~homeostatic process	78
GO:0006955~immune response	63
GO:0050808~synapse organization	18
GO:0035556~intracellular signal transduction	116
GO:2000026~regulation of multicellular organismal development	83
GO:1901700~response to oxygen-containing compound	57
GO:0046631~alpha-beta T cell activation	13
GO:0022008~neurogenesis	72
GO:0048468~cell development	95
GO:0051249~regulation of lymphocyte activation	25
GO:0002690~positive regulation of leukocyte chemotaxis	11
GO:0002520~immune system development	50
GO:0009653~anatomical structure morphogenesis	120
GO:1902622~regulation of neutrophil migration	7
GO:0007015~actin filament organization	25
GO:0010628~positive regulation of gene expression	74
GO:0002685~regulation of leukocyte migration	15
GO:0032879~regulation of localization	106
GO:0090023~positive regulation of neutrophil chemotaxis	6
GO:0010604~positive regulation of macromolecule metabolic process	118
GO:0045935~positive regulation of nucleobase-containing compound metabolic process	73
GO:0071624~positive regulation of granulocyte chemotaxis	6
GO:0035710~CD4-positive, alpha-beta T cell activation	9
GO:0006811~ion transport	60
GO:0051049~regulation of transport	76
GO:0048534~hematopoietic or lymphoid organ development	47
GO:0046634~regulation of alpha-beta T cell activation	9

GO:0007416~synapse assembly	11
GO:0050864~regulation of B cell activation	12
GO:0009891~positive regulation of biosynthetic process	75
GO:0050869~negative regulation of B cell activation	6
GO:0009719~response to endogenous stimulus	59
GO:0042991~transcription factor import into nucleus	10
GO:0032103~positive regulation of response to external stimulus	19
GO:0040011~locomotion	71
GO:0098609~cell-cell adhesion	50
GO:0071622~regulation of granulocyte chemotaxis	7
GO:0060538~skeletal muscle organ development	15
GO:0031328~positive regulation of cellular biosynthetic process	73
GO:0071310~cellular response to organic substance	83
GO:0001944~vasculature development	36
GO:0050921~positive regulation of chemotaxis	12
GO:0090022~regulation of neutrophil chemotaxis	6
GO:0034097~response to cytokine	34
GO:0046632~alpha-beta T cell differentiation	10
GO:0048870~cell motility	63
GO:0051674~localization of cell	63
GO:0070887~cellular response to chemical stimulus	99
GO:0031663~lipopolysaccharide-mediated signaling pathway	6
GO:0072358~cardiovascular system development	49
GO:0072359~circulatory system development	49
GO:0045064~T-helper 2 cell differentiation	5
GO:0002688~regulation of leukocyte chemotaxis	11
GO:0042092~type 2 immune response	6
GO:0051173~positive regulation of nitrogen compound metabolic process	74
GO:0048878~chemical homeostasis	49
GO:0098742~cell-cell adhesion via plasma-membrane adhesion molecules	15
GO:0016477~cell migration	57
GO:1903706~regulation of hemopoiesis	22
GO:1900076~regulation of cellular response to insulin stimulus	8
GO:0006820~anion transport	23
GO:0033993~response to lipid	33
GO:0050896~response to stimulus	321
GO:0071495~cellular response to endogenous stimulus	50
GO:0001775~cell activation	44
GO:0048699~generation of neurons	63

GO:0006690~icosanoid metabolic process	9
GO:0002694~regulation of leukocyte activation	25
GO:0046649~lymphocyte activation	35
GO:0048584~positive regulation of response to stimulus	81
GO:0050793~regulation of developmental process	93
GO:0046058~cAMP metabolic process	11
GO:0048871~multicellular organismal homeostasis	20
GO:0065007~biological regulation	433
GO:0019369~arachidonic acid metabolic process	6
GO:0051704~multi-organism process	81
GO:0007519~skeletal muscle tissue development	14
GO:0042990~regulation of transcription factor import into nucleus	9
GO:0048518~positive regulation of biological process	201
GO:0001568~blood vessel development	33
GO:0050865~regulation of cell activation	26
GO:2000514~regulation of CD4-positive, alpha-beta T cell activation	6
GO:0051241~negative regulation of multicellular organismal process	49
GO:0010033~response to organic substance	98
GO:0051240~positive regulation of multicellular organismal process	65
GO:0099536~synaptic signaling	29
GO:0007268~chemical synaptic transmission	29
GO:0098916~anterograde trans-synaptic signaling	29
GO:0099537~trans-synaptic signaling	29
GO:0022409~positive regulation of cell-cell adhesion	15
GO:0008154~actin polymerization or depolymerization	15
GO:0030182~neuron differentiation	57
GO:0022407~regulation of cell-cell adhesion	22
GO:0002293~alpha-beta T cell differentiation involved in immune response	7
GO:0002287~alpha-beta T cell activation involved in immune response	7
GO:0031347~regulation of defense response	32
GO:0031325~positive regulation of cellular metabolic process	112
GO:0001709~cell fate determination	6
GO:0006140~regulation of nucleotide metabolic process	14
GO:0032970~regulation of actin filament-based process	21
GO:0030097~hemopoiesis	42
GO:0080134~regulation of response to stress	55
GO:0045981~positive regulation of nucleotide metabolic process	10

GO:0061041~regulation of wound healing	11
GO:0070423~nucleotide-binding oligomerization domain containing signaling pathway	4
GO:0070431~nucleotide-binding oligomerization domain containing 2 signaling pathway	4
GO:0051531~NFAT protein import into nucleus	4
GO:0045165~cell fate commitment	18
GO:0001708~cell fate specification	9
GO:1902680~positive regulation of RNA biosynthetic process	58
GO:0015711~organic anion transport	17
GO:0048771~tissue remodeling	12
GO:0016337~single organismal cell-cell adhesion	38
GO:0042221~response to chemical	137
GO:0048863~stem cell differentiation	10
GO:0072006~nephron development	12
GO:0007610~behavior	30
GO:0010557~positive regulation of macromolecule biosynthetic process	66
GO:0048666~neuron development	46
GO:0008286~insulin receptor signaling pathway	9
GO:2000553~positive regulation of T-helper 2 cell cytokine production	3
GO:2000551~regulation of T-helper 2 cell cytokine production	3
GO:0032691~negative regulation of interleukin-1 beta production	4
GO:0035872~nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	4
GO:0060536~cartilage morphogenesis	4
GO:0045628~regulation of T-helper 2 cell differentiation	4
GO:0051251~positive regulation of lymphocyte activation	16
GO:1903508~positive regulation of nucleic acid-templated transcription	57
GO:0045893~positive regulation of transcription, DNA-templated	57
GO:0043462~regulation of ATPase activity	6
GO:0009187~cyclic nucleotide metabolic process	13
GO:0071214~cellular response to abiotic stimulus	16
GO:0051254~positive regulation of RNA metabolic process	59
GO:0002828~regulation of type 2 immune response	5
GO:0002292~T cell differentiation involved in immune response	7
GO:0070486~leukocyte aggregation	26
GO:0071396~cellular response to lipid	23
GO:0071345~cellular response to cytokine stimulus	28
GO:0009628~response to abiotic stimulus	41

GO:0042063~gliogenesis	15
GO:0045321~leukocyte activation	37
GO:0051094~positive regulation of developmental process	51
GO:0002830~positive regulation of type 2 immune response	4
GO:0034114~regulation of heterotypic cell-cell adhesion	4
GO:0072538~T-helper 17 type immune response	4
GO:0019221~cytokine-mediated signaling pathway	22
GO:0051963~regulation of synapse assembly	8
GO:0048583~regulation of response to stimulus	137
GO:0046903~secretion	44
GO:0009888~tissue development	77
GO:0007517~muscle organ development	20
GO:0090596~sensory organ morphogenesis	18
GO:0030155~regulation of cell adhesion	32
GO:0061061~muscle structure development	30
GO:0009887~organ morphogenesis	47
GO:0050920~regulation of chemotaxis	14
GO:0044057~regulation of system process	22
GO:0030217~T cell differentiation	15
GO:1903037~regulation of leukocyte cell-cell adhesion	17
GO:0031665~negative regulation of lipopolysaccharide-mediated signaling pathway	3
GO:0023035~CD40 signaling pathway	3
GO:2000739~regulation of mesenchymal stem cell differentiation	3
GO:0070372~regulation of ERK1 and ERK2 cascade	16
GO:0043367~CD4-positive, alpha-beta T cell differentiation	7
GO:0071498~cellular response to fluid shear stress	4
GO:0060707~trophoblast giant cell differentiation	4
GO:0035994~response to muscle stretch	4
GO:0045597~positive regulation of cell differentiation	39
GO:0048514~blood vessel morphogenesis	27
GO:0046637~regulation of alpha-beta T cell differentiation	6
GO:1900544~positive regulation of purine nucleotide metabolic process	9
GO:0007159~leukocyte cell-cell adhesion	27
GO:0031349~positive regulation of defense response	17
GO:0009611~response to wounding	23
GO:1903034~regulation of response to wounding	11
GO:0050863~regulation of T cell activation	16
GO:0098602~single organism cell adhesion	39
GO:0060706~cell differentiation involved in embryonic placenta development	5
GO:0050871~positive regulation of B cell activation	8

GO:0030801~positive regulation of cyclic nucleotide metabolic process	8
GO:0042742~defense response to bacterium	15
GO:0010243~response to organonitrogen compound	27
GO:0070509~calcium ion import	11
GO:0030799~regulation of cyclic nucleotide metabolic process	10
GO:0032495~response to muramyl dipeptide	4
GO:1901652~response to peptide	16
GO:0071702~organic substance transport	95
GO:0006357~regulation of transcription from RNA polymerase II promoter	71
GO:0014706~striated muscle tissue development	20
GO:0042093~T-helper cell differentiation	6
GO:0043370~regulation of CD4-positive, alpha-beta T cell differentiation	5
GO:0003231~cardiac ventricle development	10
GO:0019882~antigen processing and presentation	10
GO:0030193~regulation of blood coagulation	8
GO:1900046~regulation of hemostasis	8
GO:0002696~positive regulation of leukocyte activation	16
GO:0050801~ion homeostasis	32
GO:1901653~cellular response to peptide	13
GO:0008104~protein localization	94
GO:0055085~transmembrane transport	47
GO:0032940~secretion by cell	38
GO:0015758~glucose transport	9
GO:0098542~defense response to other organism	29
GO:0001660~fever generation	3
GO:0021796~cerebral cortex regionalization	3
GO:0045630~positive regulation of T-helper 2 cell differentiation	3
GO:0002634~regulation of germinal center formation	3
GO:0001696~gastric acid secretion	3
GO:0035745~T-helper 2 cell cytokine production	3
GO:0072497~mesenchymal stem cell differentiation	3
GO:0051336~regulation of hydrolase activity	43
GO:0002294~CD4-positive, alpha-beta T cell differentiation involved in immune response	6
GO:0035690~cellular response to drug	6
GO:0001890~placenta development	11
GO:0042127~regulation of cell proliferation	62
GO:0032692~negative regulation of interleukin-1 production	4
GO:0070233~negative regulation of T cell apoptotic process	4

GO:1900542~regulation of purine nucleotide metabolic process	12
GO:0071417~cellular response to organonitrogen compound	20
GO:0045785~positive regulation of cell adhesion	20
GO:0048522~positive regulation of cellular process	177
GO:0070232~regulation of T cell apoptotic process	5
GO:0071356~cellular response to tumor necrosis factor	10
GO:0045580~regulation of T cell differentiation	9
GO:0001816~cytokine production	31
GO:0098771~inorganic ion homeostasis	30
GO:0051641~cellular localization	98
GO:0007599~hemostasis	13
GO:0050817~coagulation	13
GO:0050708~regulation of protein secretion	19
GO:0044708~single-organism behavior	21
GO:0044087~regulation of cellular component biogenesis	38
GO:1903556~negative regulation of tumor necrosis factor superfamily cytokine production	6
GO:0046635~positive regulation of alpha-beta T cell activation	6
GO:0051046~regulation of secretion	30
GO:1902105~regulation of leukocyte differentiation	15
GO:0030278~regulation of ossification	13
GO:0034504~protein localization to nucleus	21
GO:0046456~icosanoid biosynthetic process	5
GO:2000736~regulation of stem cell differentiation	5
GO:0015749~monosaccharide transport	9
GO:0008645~hexose transport	9
GO:0032102~negative regulation of response to external stimulus	16
GO:0050867~positive regulation of cell activation	16
GO:0070489~T cell aggregation	24
GO:0042110~T cell activation	24
GO:0001676~long-chain fatty acid metabolic process	6
GO:0006812~cation transport	38
GO:0071593~lymphocyte aggregation	24
GO:0033559~unsaturated fatty acid metabolic process	8
GO:0050818~regulation of coagulation	8
GO:0055080~cation homeostasis	29
GO:0045595~regulation of cell differentiation	66
GO:0033555~multicellular organismal response to stress	7
GO:0048568~embryonic organ development	24
GO:1902533~positive regulation of intracellular signal transduction	41
GO:1901342~regulation of vasculature development	15

GO:0033036~macromolecule localization	105
GO:0071363~cellular response to growth factor stimulus	27
GO:0002819~regulation of adaptive immune response	10
GO:0050789~regulation of biological process	402
GO:0007596~blood coagulation	12
GO:0045765~regulation of angiogenesis	14
GO:0048701~embryonic cranial skeleton morphogenesis	6
GO:0035743~CD4-positive, alpha-beta T cell cytokine production	3
GO:0034116~positive regulation of heterotypic cell-cell adhesion	3
GO:1903046~meiotic cell cycle process	13
GO:0009306~protein secretion	22
GO:0050727~regulation of inflammatory response	16
GO:0008064~regulation of actin polymerization or depolymerization	12
GO:0070374~positive regulation of ERK1 and ERK2 cascade	12
GO:0030832~regulation of actin filament length	12
GO:0048705~skeletal system morphogenesis	15
GO:0030099~myeloid cell differentiation	20
GO:0008015~blood circulation	21
GO:0051250~negative regulation of lymphocyte activation	9
GO:0046717~acid secretion	4
GO:0034123~positive regulation of toll-like receptor signaling pathway	4
GO:0032753~positive regulation of interleukin-4 production	4
GO:0008643~carbohydrate transport	10
GO:0034613~cellular protein localization	67
GO:0042060~wound healing	19
GO:0060537~muscle tissue development	20
GO:0048665~neuron fate specification	5
GO:0071375~cellular response to peptide hormone stimulus	12
GO:0055074~calcium ion homeostasis	19
GO:0001764~neuron migration	10
GO:0021700~developmental maturation	16
GO:0032846~positive regulation of homeostatic process	13
GO:0003013~circulatory system process	21
GO:0030029~actin filament-based process	32
GO:0030041~actin filament polymerization	11
GO:0030833~regulation of actin filament polymerization	11
GO:0070848~response to growth factor	27
GO:0045619~regulation of lymphocyte differentiation	10
GO:0001892~embryonic placenta development	8
GO:0032651~regulation of interleukin-1 beta production	5

GO:0001817~regulation of cytokine production	28
GO:0045652~regulation of megakaryocyte differentiation	4
GO:0072273~metanephric nephron morphogenesis	4
GO:1900078~positive regulation of cellular response to insulin stimulus	4
GO:0070727~cellular macromolecule localization	67
GO:0031623~receptor internalization	7
GO:0030814~regulation of cAMP metabolic process	8
GO:0051272~positive regulation of cellular component movement	22
GO:0005513~detection of calcium ion	3
GO:0051014~actin filament severing	3
GO:0051532~regulation of NFAT protein import into nucleus	3
GO:0021554~optic nerve development	3
GO:0034612~response to tumor necrosis factor	10
GO:0051270~regulation of cellular component movement	36
GO:0018108~peptidyl-tyrosine phosphorylation	15
GO:0023052~signaling	232
GO:0098660~inorganic ion transmembrane transport	27
GO:0050730~regulation of peptidyl-tyrosine phosphorylation	13
GO:0007528~neuromuscular junction development	5
GO:0072507~divalent inorganic cation homeostasis	20
GO:0031175~neuron projection development	36
GO:0060249~anatomical structure homeostasis	18
GO:0071887~leukocyte apoptotic process	8
GO:0030048~actin filament-based movement	7
GO:0042493~response to drug	11
GO:1901699~cellular response to nitrogen compound	22
GO:0006936~muscle contraction	15
GO:0030335~positive regulation of cell migration	21
GO:0071804~cellular potassium ion transport	10
GO:0071805~potassium ion transmembrane transport	10
GO:0032869~cellular response to insulin stimulus	10
GO:0009411~response to UV	10
GO:0007166~cell surface receptor signaling pathway	93
GO:2000516~positive regulation of CD4-positive, alpha-beta T cell activation	4
GO:0045622~regulation of T-helper cell differentiation	4
GO:0032956~regulation of actin cytoskeleton organization	17
GO:0018212~peptidyl-tyrosine modification	15
GO:0006874~cellular calcium ion homeostasis	18
GO:0072503~cellular divalent inorganic cation homeostasis	19
GO:0035821~modification of morphology or physiology of other organism	8

GO:1903530~regulation of secretion by cell	27
GO:0006873~cellular ion homeostasis	26
GO:0070371~ERK1 and ERK2 cascade	14
GO:0040017~positive regulation of locomotion	22
GO:0051716~cellular response to stimulus	261
GO:1902593~single-organism nuclear import	16
GO:0006606~protein import into nucleus	16
GO:0044744~protein targeting to nucleus	16
GO:0051050~positive regulation of transport	38
GO:0051960~regulation of nervous system development	34
GO:0008217~regulation of blood pressure	10
GO:0002822~regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	9
GO:0072210~metanephric nephron development	5
GO:0003012~muscle system process	17
GO:0007154~cell communication	233
GO:0030010~establishment of cell polarity	8
GO:0051170~nuclear import	16
GO:0006816~calcium ion transport	16
GO:0001525~angiogenesis	21
GO:0001501~skeletal system development	25
GO:0002764~immune response-regulating signaling pathway	15
GO:0034405~response to fluid shear stress	4
GO:0002832~negative regulation of response to biotic stimulus	4
GO:0048703~embryonic viscerocranium morphogenesis	3
GO:0032291~axon ensheathment in central nervous system	3
GO:0003337~mesenchymal to epithelial transition involved in metanephros morphogenesis	3
GO:0034162~toll-like receptor 9 signaling pathway	3
GO:0022010~central nervous system myelination	3
GO:0071404~cellular response to low-density lipoprotein particle stimulus	3
GO:0030036~actin cytoskeleton organization	28
GO:1902531~regulation of intracellular signal transduction	67
GO:0019220~regulation of phosphate metabolic process	68
GO:0046822~regulation of nucleocytoplasmic transport	13
GO:0032835~glomerulus development	6
GO:0050764~regulation of phagocytosis	6
GO:0034113~heterotypic cell-cell adhesion	5
GO:0046626~regulation of insulin receptor signaling pathway	5
GO:1900047~negative regulation of hemostasis	5
GO:0030195~negative regulation of blood coagulation	5

GO:0051174~regulation of phosphorus metabolic process	68
GO:0007204~positive regulation of cytosolic calcium ion concentration	12
GO:0046942~carboxylic acid transport	12
GO:0048519~negative regulation of biological process	165
GO:0044700~single organism signaling	229
GO:0010001~glial cell differentiation	11
GO:0002521~leukocyte differentiation	26
GO:0051962~positive regulation of nervous system development	20
GO:0007264~small GTPase mediated signal transduction	27
GO:0048708~astrocyte differentiation	6
GO:0003281~ventricular septum development	6
GO:0051965~positive regulation of synapse assembly	6
GO:0048663~neuron fate commitment	7
GO:0032368~regulation of lipid transport	7
GO:2000147~positive regulation of cell motility	21
GO:1903039~positive regulation of leukocyte cell-cell adhesion	11
GO:0072577~endothelial cell apoptotic process	5
GO:0042993~positive regulation of transcription factor import into nucleus	5
GO:0030834~regulation of actin filament depolymerization	5
GO:0019827~stem cell population maintenance	9
GO:0032673~regulation of interleukin-4 production	4
GO:0001893~maternal placenta development	4
GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	4
GO:0030001~metal ion transport	30
GO:0043434~response to peptide hormone	13
GO:0050776~regulation of immune response	27
GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	10
GO:0032989~cellular component morphogenesis	58
GO:0023051~regulation of signaling	112
GO:0055065~metal ion homeostasis	24
GO:1903708~positive regulation of hemopoiesis	11
GO:0009967~positive regulation of signal transduction	56
GO:0006366~transcription from RNA polymerase II promoter	63
GO:0017038~protein import	18
GO:0072028~nephron morphogenesis	7
GO:0031589~cell-substrate adhesion	17
GO:0030816~positive regulation of cAMP metabolic process	6
GO:0050807~regulation of synapse organization	8
GO:0048704~embryonic skeletal system morphogenesis	8

GO:0030098~lymphocyte differentiation	19
GO:0023056~positive regulation of signaling	60
GO:0002757~immune response-activating signal transduction	14
GO:1901698~response to nitrogen compound	30
GO:0032611~interleukin-1 beta production	5
GO:0071402~cellular response to lipoprotein particle stimulus	3
GO:0021781~glial cell fate commitment	3
GO:0051345~positive regulation of hydrolase activity	25
GO:0098727~maintenance of cell number	9
GO:0045087~innate immune response	27
GO:0007389~pattern specification process	23
GO:0043112~receptor metabolic process	10
GO:0032868~response to insulin	11
GO:0048709~oligodendrocyte differentiation	6
GO:1904888~cranial skeletal system development	6
GO:0001659~temperature homeostasis	4
GO:0048661~positive regulation of smooth muscle cell proliferation	4
GO:0003338~metanephros morphogenesis	4
GO:2000352~negative regulation of endothelial cell apoptotic process	4
GO:0046627~negative regulation of insulin receptor signaling pathway	4
GO:0007156~homophilic cell adhesion via plasma membrane adhesion molecules	9
GO:0015850~organic hydroxy compound transport	10
GO:0001776~leukocyte homeostasis	7
GO:0002224~toll-like receptor signaling pathway	7
GO:0015698~inorganic anion transport	8
GO:0030837~negative regulation of actin filament polymerization	5
GO:0032652~regulation of interleukin-1 production	5
GO:0070231~T cell apoptotic process	5
GO:0050819~negative regulation of coagulation	5
GO:0009416~response to light stimulus	15
GO:0007417~central nervous system development	35
GO:0040012~regulation of locomotion	34
GO:0002695~negative regulation of leukocyte activation	9
GO:0010646~regulation of cell communication	110
GO:0019932~second-messenger-mediated signaling	12
GO:0007010~cytoskeleton organization	50
GO:0051321~meiotic cell cycle	13
GO:0051693~actin filament capping	4

GO:1900077~negative regulation of cellular response to insulin stimulus	4
GO:0001662~behavioral fear response	4
GO:0021602~cranial nerve morphogenesis	4
GO:0042992~negative regulation of transcription factor import into nucleus	4
GO:0002209~behavioral defense response	4
GO:0021871~forebrain regionalization	4
GO:0034067~protein localization to Golgi apparatus	4
GO:0051258~protein polymerization	14
GO:0060485~mesenchyme development	14
GO:0042391~regulation of membrane potential	18
GO:0042471~ear morphogenesis	9
GO:0010647~positive regulation of cell communication	59
GO:0021545~cranial nerve development	5
GO:0032720~negative regulation of tumor necrosis factor production	5
GO:0048247~lymphocyte chemotaxis	5
GO:0014013~regulation of gliogenesis	6
GO:0072283~metanephric renal vesicle morphogenesis	3
GO:2000738~positive regulation of stem cell differentiation	3
GO:0031649~heat generation	3
GO:0019373~epoxygenase P450 pathway	3
GO:0035729~cellular response to hepatocyte growth factor stimulus	3
GO:0035728~response to hepatocyte growth factor	3
GO:0072074~kidney mesenchyme development	3
GO:0072539~T-helper 17 cell differentiation	3
GO:0002700~regulation of production of molecular mediator of immune response	8
GO:0050714~positive regulation of protein secretion	11
GO:0051051~negative regulation of transport	20
GO:0097168~mesenchymal stem cell proliferation	2
GO:0003422~growth plate cartilage morphogenesis	2
GO:0019371~cyclooxygenase pathway	2
GO:0021564~vagus nerve development	2
GO:0034155~regulation of toll-like receptor 7 signaling pathway	2
GO:0034146~toll-like receptor 5 signaling pathway	2
GO:0034157~positive regulation of toll-like receptor 7 signaling pathway	2
GO:1902732~positive regulation of chondrocyte proliferation	2

GO:0034242~negative regulation of syncytium formation by plasma membrane fusion	2
GO:0048608~reproductive structure development	21
GO:0048523~negative regulation of cellular process	153
GO:0048646~anatomical structure formation involved in morphogenesis	51
GO:0033554~cellular response to stress	69
GO:0051223~regulation of protein transport	31
GO:0002250~adaptive immune response	16
GO:0022600~digestive system process	6
GO:0035914~skeletal muscle cell differentiation	6
GO:0030334~regulation of cell migration	31
GO:0030042~actin filament depolymerization	5
GO:0090280~positive regulation of calcium ion import	5
GO:0034121~regulation of toll-like receptor signaling pathway	5
GO:0045937~positive regulation of phosphate metabolic process	44
GO:0010562~positive regulation of phosphorus metabolic process	44
GO:0001656~metanephros development	7
GO:0042552~myelination	7
GO:0070229~negative regulation of lymphocyte apoptotic process	4
GO:0002753~cytoplasmic pattern recognition receptor signaling pathway	4
GO:0045746~negative regulation of Notch signaling pathway	4
GO:0007126~meiotic nuclear division	11
GO:1902580~single-organism cellular localization	42
GO:0050794~regulation of cellular process	380
GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	12
GO:0050803~regulation of synapse structure or activity	12
GO:0060627~regulation of vesicle-mediated transport	21
GO:0034220~ion transmembrane transport	32
GO:0009725~response to hormone	25
GO:0001819~positive regulation of cytokine production	19
GO:0030003~cellular cation homeostasis	24
GO:0046427~positive regulation of JAK-STAT cascade	6
GO:0009408~response to heat	6
GO:0046323~glucose import	6
GO:0003014~renal system process	6
GO:0009063~cellular amino acid catabolic process	6
GO:1904894~positive regulation of STAT cascade	6
GO:0032271~regulation of protein polymerization	11
GO:0061458~reproductive system development	21

GO:0030534~adult behavior	10
GO:0055082~cellular chemical homeostasis	28

KEGG PATHWAY of DEGs

Term	Count
bta04062:Chemokine signaling pathway	28
bta04668:TNF signaling pathway	21
bta04024:cAMP signaling pathway	24
bta04750:Inflammatory mediator regulation of TRP channels	16
bta04921:Oxytocin signaling pathway	18
bta04611:Platelet activation	16
bta04621:NOD-like receptor signaling pathway	10
bta04068:FoxO signaling pathway	16
bta04022:cGMP-PKG signaling pathway	18
bta04662:B cell receptor signaling pathway	11
bta04664:Fc epsilon RI signaling pathway	10
bta04514:Cell adhesion molecules (CAMs)	16
bta04060:Cytokine-cytokine receptor interaction	21
bta04020:Calcium signaling pathway	18
bta04370:VEGF signaling pathway	9
bta00591:Linoleic acid metabolism	7
bta04620:Toll-like receptor signaling pathway	12
bta04064:NF-kappa B signaling pathway	11
bta04660:T cell receptor signaling pathway	12
bta04924:Renin secretion	9
bta04931:Insulin resistance	12
bta04261:Adrenergic signaling in cardiomyocytes	14
bta05332:Graft-versus-host disease	7
bta05231:Choline metabolism in cancer	11
bta05321:Inflammatory bowel disease (IBD)	9
bta04666:Fc gamma R-mediated phagocytosis	10
bta04912:GnRH signaling pathway	10

Table S2-Proteomics data

340 differentially expressed proteins (fold change ≥ 1.3 or ≤ 0.77, P-value < 0.05)

Protein name	GN(GENE NAME)	lps:control
Uncharacterized protein (Fragment)	DNER	3.5055271
Keratin 31	KRT31	3.3762804
Solute carrier family 2 (Facilitated glucose transporter), member 3	SLC2A3	2.8079994

Uncharacterized protein	IL6ST	2.6726478
Alpha-2-macroglobulin variant 20	A2M	2.4199478
Inositol monophosphatase 3	IMPAD1	2.4154071
Uncharacterized protein	BACE2	2.4040972
Amino acid transporter	SLC1A5	2.3783241
Ragulator complex protein LAMTOR1	LAMTOR1	2.2316044
Optineurin	OPTN	2.2186657
Uncharacterized protein	SEC24C	2.1545038
Keratin, type II cuticular Hb3	KRT83	2.1395003
Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1	2.1156622
Integral membrane protein 2B	ITM2B	2.0276484
Prostaglandin G/H synthase 2	PTGS2	1.9924835
Peptidyl-prolyl cis-trans isomerase C	PPIC PE	1.9736044
Enhancer of rudimentary homolog	ERH	1.9593234
Uncharacterized protein (Fragment)		1.952397
Uncharacterized protein	ABHD14A	1.9183799
Uncharacterized protein (Fragment)	EIF4G1	1.9110797
Stromal cell-derived factor 2	SDF	1.8540163
Interleukin enhancer binding factor 2, 45kDa	ILF2	1.8501684
V-type proton ATPase subunit d 1	ATP6V0D1	1.8224434
39S ribosomal protein L16, mitochondrial	MRPL16	1.821085
40S ribosomal protein S15a	RPS15A	1.8207698
39S ribosomal protein L14, mitochondrial	MRPL14	1.8161348
Uncharacterized protein	AHNAK	1.807321
Alpha-2-macroglobulin	A2M	1.8044048
40S ribosomal protein S10	RPS10	1.7994055
Heme oxygenase 1	HMOX1	1.7958408
LRP10 protein	LRP10	1.7747299
Uncharacterized protein	SERPINB2	1.774334
Protein-glutamine gamma-glutamyltransferase E	TGM3	1.7719362
DNA topoisomerase 2	TOP2A	1.7652771
Uncharacterized protein	LOC506828	1.7602827
Small nuclear ribonucleoprotein E (Fragment)	SNRPE	1.7592501
40S ribosomal protein S4	RPS4Y1	1.7550535
Uncharacterized protein	SLC30A1	1.7444763
Ribose-phosphate pyrophosphokinase 1	PRPS1	1.7318545
C-X-C motif chemokine 6	CXCL6	1.7073636
RRAS2 protein	RRAS2	1.705438
FAR1 protein	FAR1	1.7003418
Transthyretin	TTR	1.6817219
Chromosome 15 open reading frame 24 ortholog	C10H15orf24	1.6689639
ATP synthase subunit g, mitochondrial	ATP5L	1.6594936
Ubiquitin carboxyl-terminal hydrolase 10	USP10	1.6570494

Uncharacterized protein (Fragment)	FAM129B	1.6504881
Uncharacterized protein (Fragment)		1.6498496
Collagen triple helix repeat containing 1	CTHRC1	1.6485703
UBAC2 protein	UBAC2	1.6475101
AP-1 complex subunit beta-1	AP2B1	1.6445845
Phospholipase D3	PLD3	1.6361292
SPTLC2 protein	SPTLC2	1.6310166
60S acidic ribosomal protein P0	RPLP0	1.6140131
Synaptosomal-associated protein	SNAP23	1.6116778
Myosin regulatory light polypeptide 9	MYL9	1.6105479
Uncharacterized protein	EREG	1.607108
Receptor protein-tyrosine kinase	EPHA4	1.5899111
Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	1.586983
Malate dehydrogenase, cytoplasmic	MDH1	1.5844263
GLRX5 protein	GLRX5	1.5791589
Elongation factor G, mitochondrial	GFM1	1.5765192
39S ribosomal protein L22, mitochondrial	MRPL22	1.5761878
Uncharacterized protein (Fragment)	NDFIP1	1.5745797
Uncharacterized protein (Fragment)	FADS1	1.5740171
General vesicular transport factor p115	USO1	1.5722695
Small nuclear ribonucleoprotein-associated protein	SNRPB	1.5677379
28S ribosomal protein S2, mitochondrial	MRPS2	1.556134
MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	1.5559222
Probable ATP-dependent RNA helicase DDX47	DDX47	1.5534147
Endoplasmic reticulum resident protein 29	ERP29	1.5530029
Histone H2A	HIST1H2AD	1.5500037
Histone H2A	H4	1.5408691
Acetyltransferase component of pyruvate dehydrogenase complex	DLAT	1.5400352
Dihydroorotate dehydrogenase (quinone), mitochondrial (Fragment)	DHODH	1.5310927
Zinc transporter ZIP14	SLC39A14	1.5144977
Myosin light polypeptide 6	MYL6	1.5104411
Proliferating cell nuclear antigen	PCNA	1.504787
Leucine-rich repeat-containing protein 59	LRRC59	1.5036199
60S ribosomal protein L12	RPL12	1.5028298
L-lactate dehydrogenase A chain	LDHA	1.4952119
Uncharacterized protein	NT5DC2	1.4932443
Importin subunit alpha	KPNA2	1.4876403
UPF0556 protein C19orf10 homolog		1.4872172
Uncharacterized protein	SRBD1	1.4814838
Pyrin domain containing 3	NLRP3	1.4754234
Trifunctional purine biosynthetic protein adenosine-3	GART	1.4650471
Pre-mRNA-splicing factor RBM22	RBM22	1.4633505
Uncharacterized protein (Fragment)	FLII	1.460274

Transmembrane protein 120A	TMEM120A	1.4586244
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	1.458312
Eukaryotic translation elongation factor 1 gamma (Fragment)	EEF1G	1.4484279
STX6 protein	STX6	1.447891
Metalloproteinase inhibitor 3	TIMP3	1.4461426
Apolipoprotein O (Fragment)	APOO	1.4456516
Mitochondrial import inner membrane translocase subunit Tim23	TIMM23	1.4447696
Uncharacterized protein	GLS	1.443624
40S ribosomal protein S9	RPS9	1.4413443
Calponin-1	CNN1	1.4265432
Ras-related protein Rab-18	RAB18	1.4230901
Vimentin	VIM	1.421169
Uncharacterized protein	RANGAP1	1.4157211
Uncharacterized protein	P4HA2	1.4149289
Uncharacterized protein	SNRPD3	1.412785
Inter-alpha-trypsin inhibitor heavy chain H3	ITIH3	1.4125176
ADP/ATP translocase 2 (Fragment)	SLC25A5	1.411398
Vesicle-associated membrane protein-associated protein B	VAPB	1.4071984
AP-1 complex subunit sigma-2	AP1S2	1.4048789
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	DUFB5	1.4044776
Uncharacterized protein (Fragment)	CDCP1	1.3992025
Reticulocalbin-3	RCN3	1.3979677
Polypyrimidine tract-binding protein	PTBP1	1.3974684
Uncharacterized protein	HNRPDL	1.3946836
DNA replication licensing factor MCM7	MCM7	1.3928565
39S ribosomal protein L15, mitochondrial	MRPL15	1.3925481
CCAAT/enhancer-binding protein beta	CEBPB	1.3921581
60S ribosomal protein L11	RPL11	1.3895947
Importin subunit alpha-7 (Fragment)	KPNA6	1.3852792
Uncharacterized protein	TFRC	1.381345
Transaldolase	TALDO1	1.37934
Heat shock 70 kDa protein 13	HSPA13	1.3790213
Transgelin	TAGLN	1.3780802
ATP synthase subunit f, mitochondrial	ATP5J2	1.3715032
Uncharacterized protein		1.3713791
GLI pathogenesis-related 2	GLIPR2	1.3697195
Cathepsin D	CTSD	1.3627142
PGRMC2 protein	PGRMC2	1.362074
Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	1.3555222
T-complex protein 1 subunit gamma	CCT3	1.3539486
ERO1-like protein alpha	ERO1L	1.3538299
DDX21 protein	DDX21	1.3530129

Ras-related protein Rab-8A	RAB8A	1.3529322
Rho-related GTP-binding protein RhoB	RHOB	1.3507159
Probable ATP-dependent RNA helicase DDX27	DDX27	1.3493542
NOL6 protein	NOL6	1.3484398
60S ribosomal protein L7a	RPL7A	1.3480527
CD276 antigen (Fragment)	Cd276	1.3403559
SQRDL protein	SQRDL	1.3397635
mRNA export factor	RAE1	1.3370393
40S ribosomal protein S13	RPS13	1.3359374
UTP--glucose-1-phosphate uridylyltransferase	UGP2	1.33264
PDZ and LIM domain protein 4	PDLIM4	1.3313991
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	1.3309769
Eukaryotic translation initiation factor 3 subunit C	EIF3C	1.3309352
60S ribosomal protein L10a	RPL10A	1.3305446
Ras-related protein Rab-7a	RAB7A	1.3301083
Myosin regulatory light polypeptide 9	MYL9	1.3265501
Derlin-1	DERL1	1.3251261
Protein S100-A4	S100A4	1.3223324
Peptidyl-prolyl cis-trans isomerase B	PPIB	1.3208823
ADP-dependent glucokinase	ADPGK	1.3202362
PICALM protein	PICALM	1.3173957
RAB9A, member RAS oncogene family	RAB9A	1.3167716
Endoglin	ENG	1.3141051
Sulfide dehydrogenase like	SQRDL	1.3128952
DDX5 protein (Fragment)	DDX5	1.3121691
SKIV2L2 protein	SKIV2L2	1.3121117
Non-muscle caldesmon	CALD1	1.3117356
Perilipin	PLIN2	1.310518
Serpin H1	SERPINH1	1.3085991
Alpha-actinin-1	ACTN1	1.3047541
Platelet-derived growth factor receptor beta	PDGFRB	1.3015839
C4b-binding protein alpha-like	LOC510860	0.7682395
Uncharacterized protein (Fragment)	ITGA1	0.7665625
Uncharacterized protein	LMNA	0.7626132
ATPase inhibitor, mitochondrial	ATPIF1	0.7620617
Purine nucleoside phosphorylase	PNP	0.7604938
Fibrillin-1	FBN1	0.7577941
Glycoprotein 2 (Zymogen granule membrane)	GP2	0.7574946
Serine--tRNA ligase, cytoplasmic	SARS	0.7556222
Uncharacterized protein	GLG1	0.7547996
H/ACA ribonucleoprotein complex subunit 2	NHP2	0.7543999
Intercellular adhesion molecule 1	ICAM1	0.7519776

Cytochrome P450	CYP1A2	0.7517885
Actin-related protein 2/3 complex subunit 5-like protein	ARPC5L	0.7514047
Proliferation-associated 2G4, 38kDa	PA2G4	0.751145
Gamma-interferon-inducible lysosomal thiol reductase	IFI30	0.74812
Platelet glycoprotein 4	CD36	0.7393343
Aminopeptidase N	ANPEP	0.7374173
Decorin	DCN	0.7362643
Alpha-S1-casein	CSN1S1	0.735016
Uncharacterized protein	NID2	0.7319771
Pyridoxal kinase	PDXK	0.7310117
Lysosome-associated membrane glycoprotein 1	LAMP1	0.7301395
Uncharacterized protein (Fragment)	MAGT1	0.7293947
Hepatitis A virus cellular receptor 1 N-terminal domain containing protein	MGC137099	0.7293909
Thy-1 cell surface antigen	THY1	0.7292645
Clusterin	CLU	0.723396
Metastasis associated 1 family, member 2	MTA2	0.7209269
Annexin	ANXA3	0.719472
Prostaglandin E synthase 3	PTGES3	0.7186465
Cytokine induced protein 29 kDa	CIP29	0.7183021
Caveolin-1	CAV1	0.7120392
Uncharacterized protein	PGAM5	0.7119205
Protein kinase C delta-binding protein	PRKCDBP	0.7114394
Plasminogen	PLG	0.7094091
Thioredoxin-like 1	TXNL1	0.707845
Fatty acid synthase	FASN	0.7058096
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC	0.7043136
FabG-like protein	HKE6	0.698575
Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	0.6983873
Eukaryotic translation initiation factor 3 subunit E	EIF3E	0.6979684
Uncharacterized protein	NADK2	0.6957003
Lactoferrin (Fragment)		0.6939648
Acyl-CoA synthetase family member 2, mitochondrial	ACSF2 P	0.6918617
Kininogen-1	KNG1	0.6906329
NADPH:adrenodoxin oxidoreductase, mitochondrial	FDXR	0.686268
Pancreatic trypsin inhibitor		0.6843868
Uncharacterized protein (Fragment)	PTGFRN P	0.6834234
Apolipoprotein A-IV	APOA4	0.6828258
Galactokinase	GALK1	0.6823135
Uncharacterized protein	LAMC2	0.6809427
Proteasome (Prosome, macropain) activator subunit 1 (PA28 alpha)	PSME1	0.6804481
Cathelicidin-1	CATHL1	0.6801281
IGL@ protein	IGL@	0.6779251

Lumican	LUM	0.6779076
Uncharacterized protein	GGT1	0.6761827
D-beta-hydroxybutyrate dehydrogenase, mitochondrial	BDH1	0.6743149
LOC539596 protein	LOC539596	0.6742949
Uncharacterized protein (Fragment)	UBE2J1	0.6742296
EH-domain containing 2	EHD2	0.6735665
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NDUFB3	0.6719494
Apolipoprotein A-I preproprotein	APOA1	0.67175
Fascin	FSCN1	0.6670382
Uncharacterized protein	ABCB7	0.6633746
Uncharacterized protein	LEMD	0.6608588
Protein S100-A16	S100A16	0.6603176
RCN1 protein	RCN	0.6598738
Sulfotransferase 1A1	SULT1A1	0.6585682
Uncharacterized protein	LOC784932	0.6579487
Mimecan	OGN	0.656949
Uncharacterized protein	LAMB3	0.6562647
EIF2AK3 protein	EIF2AK3	0.6558292
Collectin-12	COLEC12	0.6522783
Uncharacterized protein (Fragment)	IGHM	0.6519643
Pro-cathepsin H	CTSH	0.6518162
Proline/arginine-rich end leucine-rich repeat protein	PRELP	0.650857
SNTB2 protein	SNTB2	0.6469267
Dermatopontin	DPT	0.6457229
Vacuolar protein sorting-associated protein 29 (Fragment)	VPS29	0.6378942
Isocitrate dehydrogenase [NADP] cytoplasmic	IDH	0.6373423
Chitinase-3-like protein 1	CHI3L1	0.6315615
B-cell receptor-associated protein 31	BCAP31	0.6297422
3 beta-hydroxy-delta 5-C27-steroid oxidoreductase	HSD3B7	0.6278431
Transmembrane protein 65	TMEM65	0.623235
NID1 protein	NID1	0.6224485
2,4-dienoyl CoA reductase 1, mitochondrial	DECR1	0.6217104
Aldehyde dehydrogenase	ALDH3A2	0.6202617
Uncharacterized protein	LAMA4	0.6172859
SCARB2 protein	SCARB2	0.6133953
PCYT1A protein	PCYT1A	0.6127167
Uncharacterized protein	LAMB2	0.6123021
Monoacylglycerol lipase ABHD6	ABHD6	0.6115747
Uncharacterized protein	COL7A1	0.6113042
Minichromosome maintenance complex component 4	MCM4	0.6087412
Quinone oxidoreductase-like protein 2		0.6082311
Uncharacterized protein (Fragment)	LAMA3	0.607939
Uncharacterized protein	CENPV	0.6077706

Amine oxidase	AOC3	0.6065046
Uncharacterized protein (Fragment)	HSPG2	0.6059634
14-3-3 protein epsilon	YWHAE	0.6048398
Uncharacterized protein	COL18A1	0.6040671
Uncharacterized protein (Fragment)	ARID1	0.6037305
Integrin alpha-3	ITGA3	0.6032513
Beta-1,4-galactosyltransferase 1	B4GALT1	0.6032022
Annexin A7	ANXA7	0.6018109
Uncharacterized protein	MCM3AP	0.6001957
Uncharacterized protein (Fragment)		0.5963972
KRT15 protein	KRT15	0.5945608
Uncharacterized protein	COL6A2	0.5922599
Mitogen-activated protein kinase	MAPK14	0.591092
Vitamin D binding protein		0.5886662
Matrix Gla protein	MGP	0.5884236
Sulfite oxidase	SUOX	0.5865385
Uncharacterized protein	CYP3A4	0.5854272
Uncharacterized protein (Fragment)	SFT2D3	0.5829548
Uncharacterized protein	PML	0.5828217
C-reactive protein	CRP	0.5821957
Interstitial collagenase	MMP1	0.5801134
ATP-binding cassette, sub-family G (WHITE), member 2	ABCG2	0.5791456
Hemoglobin fetal subunit beta		0.5782399
Vitamin K-dependent protein S	PROS1	0.5777401
Protein AMBP	AMBP	0.5754501
Protein-glutamine gamma-glutamyltransferase 2	TGM2	0.575174
Uncharacterized protein	COL15A1	0.5672746
Uncharacterized protein	DSP	0.5651918
Embryo-specific fibronectin 1 transcript variant	FN1	0.5643275
Uncharacterized protein (Fragment)	LAMA5	0.5640172
Metalloendopeptidase	BMP1	0.5614944
Annexin A8	ANXA8	0.5584191
Uncharacterized protein	VTN	0.5579866
Uncharacterized protein	COL6A3	0.5549548
Ezrin	EZR	0.5531285
Keratin, type II cytoskeletal 8	KRT8	0.5529988
Alpha-1-acid glycoprotein	agp	0.5499853
Aldehyde dehydrogenase, mitochondrial	ALDH2	0.5492163
Microfibril-associated glycoprotein 4	MFAP4	0.5455819
Integrin alpha-2 (Fragment)	ITGA2	0.5396497
Collagen alpha-5(IV) chain (Fragment)	COL4A5	0.5365115
Uncharacterized protein	COL6A1	0.535646
Serine protease HTRA1	HTRA1	0.5327572

Uncharacterized protein	LAMC1	0.5317004
Coagulation factor IX (Fragment)	F9	0.5263428
Integrin beta	ITGB4	0.5231634
Thiosulfate sulfurtransferase	TST	0.5228332
Uncharacterized protein	RBM12B	0.5179861
Uncharacterized protein	ECH1	0.5174627
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	BCKDHB	0.5113372
UMP-CMP kinase	CMPK1	0.50903
Hemoglobin subunit alpha	HBA	0.5055684
KRT18 protein (Fragment)	KRT18	0.5046081
Phospholipase D2	PLD2	0.5033316
Uncharacterized protein	TRIM29	0.5013397
Uncharacterized protein	ITGA6	0.4949501
Glutathione peroxidase	GPX3	0.4906709
Uncharacterized protein	SYNM	0.4836227
Adiponectin	ADIPOQ	0.467492
Kappa-casein	CSN3	0.4665879
Tetraspanin (Fragment)	TSPAN3	0.4645828
Hemoglobin beta	HBB	0.4548057
Keratin, type II cytoskeletal 7	KRT7	0.4541651
Keratin, type I cytoskeletal 19	KRT19	0.4355429
ADAMTSL4 protein	ADAMTSL4	0.4149428
Uncharacterized protein	TINAGL	0.4101077
Keratin, type I cytoskeletal 14	KRT14	0.402087
Uncharacterized protein	EMILIN1	0.3754576
Obg-like ATPase 1	OLA1	0.3735223
Uncharacterized protein	KRT6A	0.3645515
Uncharacterized protein (Fragment)		0.3337162
Keratin, type II cytoskeletal 5	KRT5	0.3289413
Uncharacterized protein (Fragment)		0.321749
Apolipoprotein E	APOE	0.3147554
Keratin, type I cytoskeletal 17	KRT17	0.2976483
Uncharacterized protein	EXOG	0.2793937
LOC615589 protein	LOC615589	0.2793015
Uncharacterized protein	KRT2	0.2380918
Plakophilin-1	PKP1	0.2339252
Uncharacterized protein (Fragment)	MAP4K4	0.1532083
A disintegrin and metalloproteinase with thrombospondin motifs 5	ADAMTS5	0.1106262
Uncharacterized protein	PNPLA6	0.0352654

Biological Process of DEPs

Term	Count

GO:0035987~endodermal cell differentiation	6
GO:0007155~cell adhesion	13
GO:0098609~cell-cell adhesion	8
GO:0010951~negative regulation of endopeptidase activity	7
GO:0033627~cell adhesion mediated by integrin	4
GO:0050873~brown fat cell differentiation	5
GO:0007229~integrin-mediated signaling pathway	7
GO:0009396~folic acid-containing compound biosynthetic process	3
GO:0030855~epithelial cell differentiation	6
GO:0055114~oxidation-reduction process	15
GO:0051260~protein homooligomerization	9
GO:0001525~angiogenesis	9
GO:0031102~neuron projection regeneration	3
GO:0007160~cell-matrix adhesion	6
GO:0018149~peptide cross-linking	4
GO:0006412~translation	10
GO:0010873~positive regulation of cholesterol esterification	3
GO:0034372~very-low-density lipoprotein particle remodeling	3
GO:0048333~mesodermal cell differentiation	3
GO:0034380~high-density lipoprotein particle assembly	3
GO:0000387~spliceosomal snRNP assembly	4
GO:0006695~cholesterol biosynthetic process	4
GO:0043588~skin development	4
GO:0046470~phosphatidylcholine metabolic process	3
GO:0070208~protein heterotrimerization	3
GO:0042632~cholesterol homeostasis	5
GO:0050821~protein stabilization	7
GO:0032570~response to progesterone	3
GO:0043691~reverse cholesterol transport	3
GO:0070125~mitochondrial translational elongation	6
GO:0031623~receptor internalization	4
GO:0006886~intracellular protein transport	9
GO:0033700~phospholipid efflux	3
GO:0030155~regulation of cell adhesion	4
GO:0045109~intermediate filament organization	3
GO:0006879~cellular iron ion homeostasis	4
GO:0042157~lipoprotein metabolic process	3
GO:0006006~glucose metabolic process	4
GO:0000470~maturation of LSU-rRNA	3
GO:0019433~triglyceride catabolic process	3
GO:1902235~regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	2
GO:0006221~pyrimidine nucleotide biosynthetic process	2

GO:0007409~axonogenesis	5
GO:0005977~glycogen metabolic process	3
GO:0010501~RNA secondary structure unwinding	4
GO:0071353~cellular response to interleukin-4	3
GO:0030198~extracellular matrix organization	5
GO:0051289~protein homotetramerization	4
GO:0050900~leukocyte migration	3
GO:0010629~negative regulation of gene expression	5
GO:0006508~proteolysis	8
GO:0031581~hemidesmosome assembly	2
GO:0060355~positive regulation of cell adhesion molecule production	2
GO:0010628~positive regulation of gene expression	7
GO:0042130~negative regulation of T cell proliferation	3
GO:0006914~autophagy	4
GO:0006364~rRNA processing	4
GO:0032092~positive regulation of protein binding	4
GO:0070124~mitochondrial translational initiation	5
GO:0042147~retrograde transport, endosome to Golgi	4
GO:0010952~positive regulation of peptidase activity	2
GO:0045110~intermediate filament bundle assembly	2
GO:0009299~mRNA transcription	2
GO:0022614~membrane to membrane docking	2
GO:0050713~negative regulation of interleukin-1 beta secretion	2
GO:0070508~cholesterol import	2
GO:0007596~blood coagulation	4
GO:2001244~positive regulation of intrinsic apoptotic signaling pathway	3
GO:0033344~cholesterol efflux	3
GO:0030324~lung development	4
GO:0051017~actin filament bundle assembly	3
GO:0019915~lipid storage	3
GO:0050728~negative regulation of inflammatory response	4
GO:0006012~galactose metabolic process	2
GO:1903494~response to dehydroepiandrosterone	2
GO:0030300~regulation of intestinal cholesterol absorption	2
GO:0097186~amelogenesis	2
GO:0051346~negative regulation of hydrolase activity	2
GO:0035878~nail development	2
GO:1903496~response to 11-deoxycorticosterone	2
GO:0034115~negative regulation of heterotypic cell-cell adhesion	2
GO:0090336~positive regulation of brown fat cell differentiation	2
GO:0071276~cellular response to cadmium ion	2

KEGG PATHWAY of DEPs

Term	Count	%	PValue
bta04512:ECM-receptor interaction	20	0.040298	1.82E-13
bta04510:Focal adhesion	23	0.046343	6.42E-09
bta03010:Ribosome	15	0.030224	4.85E-06
bta04151:PI3K-Akt signaling pathway	20	0.040298	8.80E-04
bta05205:Proteoglycans in cancer	13	0.026194	0.004341
bta00920:Sulfur metabolism	4	0.00806	0.004396
bta04974:Protein digestion and absorption	8	0.016119	0.004532
bta04810:Regulation of actin cytoskeleton	13	0.026194	0.006298
bta01100:Metabolic pathways	44	0.088656	0.011716
bta01130:Biosynthesis of antibiotics	12	0.024179	0.01279
bta00620:Pyruvate metabolism	5	0.010075	0.013742
bta04640:Hematopoietic cell lineage	7	0.014104	0.025746
bta05200:Pathways in cancer	17	0.034253	0.037807
bta05410:Hypertrophic cardiomyopathy (HCM)	6	0.012089	0.047087
bta05414:Dilated cardiomyopathy	6	0.012089	0.060757
bta00010:Glycolysis / Gluconeogenesis	5	0.010075	0.069352
bta00670:One carbon pool by folate	3	0.006045	0.071478