## *SUPPLEMENTARY "PATIENTS AND METHODS"*

# "Gene expression signature for biliary atresia and a role for Interleukin-8 in pathogenesis of experimental disease"

**Bessho K, et al.**

## PATIENTS AND METHODS

**Patients.** Liver biopsies, serum samples and clinical data were obtained from infants with cholestasis enrolled into a prospective study (ClinicalTrials.gov Identifier: NCT00061828) of the NIDDK-funded Childhood Liver Disease Research and Education Network (www.childrennetwork.org) or from infants evaluated at Cincinnati Children's Hospital Medical Center. For subjects with biliary atresia (BA), liver biopsies were obtained from 64 infants during the preoperative workup or at the time of intraoperative cholangiogram, with ages ranging from 22-169 days after birth (Supplementary Table 7). For subjects with intrahepatic cholestasis (serving as diseased controls, and referred to as non-BA), liver biopsy samples were obtained percutaneously or intraoperatively from 14 infants at the time of diagnostic evaluation, with ages ranging from 19-189 days. Their diagnosis were Alagille syndrome (N=1), multidrug resistance protein-3 deficiency (N=2), alpha-1-antitrypsin deficiency (N=2) and cholestasis with unknown etiology (N=9) (Supplementary Table 7). Representative liver biopsy photomicrographs are shown in Supplementary Figure 6A-D. A third group of normal controls (NC) consisted of liver biopsy samples obtained from 7 deceased-donor children aged 22-42 months as described previously (1). This group serves as a reference cohort, with the median levels of gene expression used to normalize gene expression across all patients in the BA and non-BA groups. This greatly facilitates the visual identification of key differences in gene expression levels between BA and non-BA groups. Further, the ability to compare these experimental groups with normal controls separately enables the discoveries of profiles that are unique for BA and non-BA groups individually. We also obtained a liver biopsy from an infant at 75 days of age being evaluated for hypotonia. The infant had normal bilirubin levels and normal synthetic function, with normal liver histology and electron microscopy.

Serum samples were obtained from 81 subjects at the time of diagnosis of biliary atresia (ages: 10-116 days), and 66 patients with other causes of intrahepatic cholestasis (ages: 2-118 days). Serum samples were also obtained from 5 healthy age-matched controls. All samples were obtained after informed consent from patients' parents/legal guardians. The study protocols were approved by the human research review boards of all participating institutions.

**Mouse model of experimental biliary atresia.** BALB/c mice carrying the genetic inactivation of *Cxcr2* (C.129S2[B6]-Cxcr2$^{tm1Mwm/J}$; *Cxcr2*$^{-/-}$ mice) were purchased from Jackson Laboratory (Bar Harbor, ME). Newborn mice were injected with $1.5 \times 10^6$ fluorescent-forming units of rhesus rotavirus (RRV) or 0.9% NaCl (saline) intraperitoneally within 24 hours of birth, and were examined daily for the development of cholestasis as described previously (2, 3). The extrahepatic bile ducts and gallbladder were microdissected en bloc (here collectively referred to as extrahepatic bile ducts) at 3, 7 and 14 days after RRV or saline injection, and snap frozen in liquid nitrogen or embedded in paraffin. Livers were harvested using snap frozen in liquid nitrogen, embedded in paraffin or subjected to protocols to purify mononuclear cells for flow cytometric analysis, as described previously (2, 3). All mice were maintained under specific pathogen–free conditions and diet that contained trimethoprim-sulfamethoxazole. The Institutional Animal Care and Use Committee of Cincinnati Children's Hospital Medical Center approved the experimental protocols.

To generate genome-wide expression datasets for extrahepatic bile ducts of mice, 3 sets of total RNA samples were generated for each time point and experimental and control groups, with each set containing 2-6 extrahepatic bile ducts depending on their sizes to make sure enough RNA was available for processing and hybridization to GeneChip® Mouse Gene ST 1.0 Arrays (Affymetrix) following the same experimental protocols as described above for human samples (data also deposited in GEO: GSE46995.

**Quantitative PCR and detection of IL8 protein.** Quantitative PCR was performed as reported previously (2), with all primers are listed in the Supplementary Table 8. Sections of frozen liver biopsies fixed in paraformaldehyde were dual stained with anti-cytokeratin antibody (polyclonal rabbit anti-cytokeratin, DAKO, Carpinteria, CA; to stain cholangiocytes) simultaneously with anti-human IL8 antibody (Human CXCL8/IL-8 polyclonal antibody, goat IgG, R&D Systems, Minneapolis, MN), followed by incubation with fluorescence-labeled species-specific secondary antibodies, and DAPI counterstaining, as described previously (4). Serum IL8 concentrations were measured using the Luminex Technology Platform according to the instruction supplied by the manufacturer (Millipore Co., Bedford, MA)**.**

**Cell isolation and flow cytometric analysis.** Single-cell suspensions from neonatal livers and cellular phenotyping by flow activated cell sorting (FACS) were performed using protocols and antibodies as described previously (1, 2, 4); isotype-matched controls were used for all FACS acquisitions and analyses.

## REFERENCES

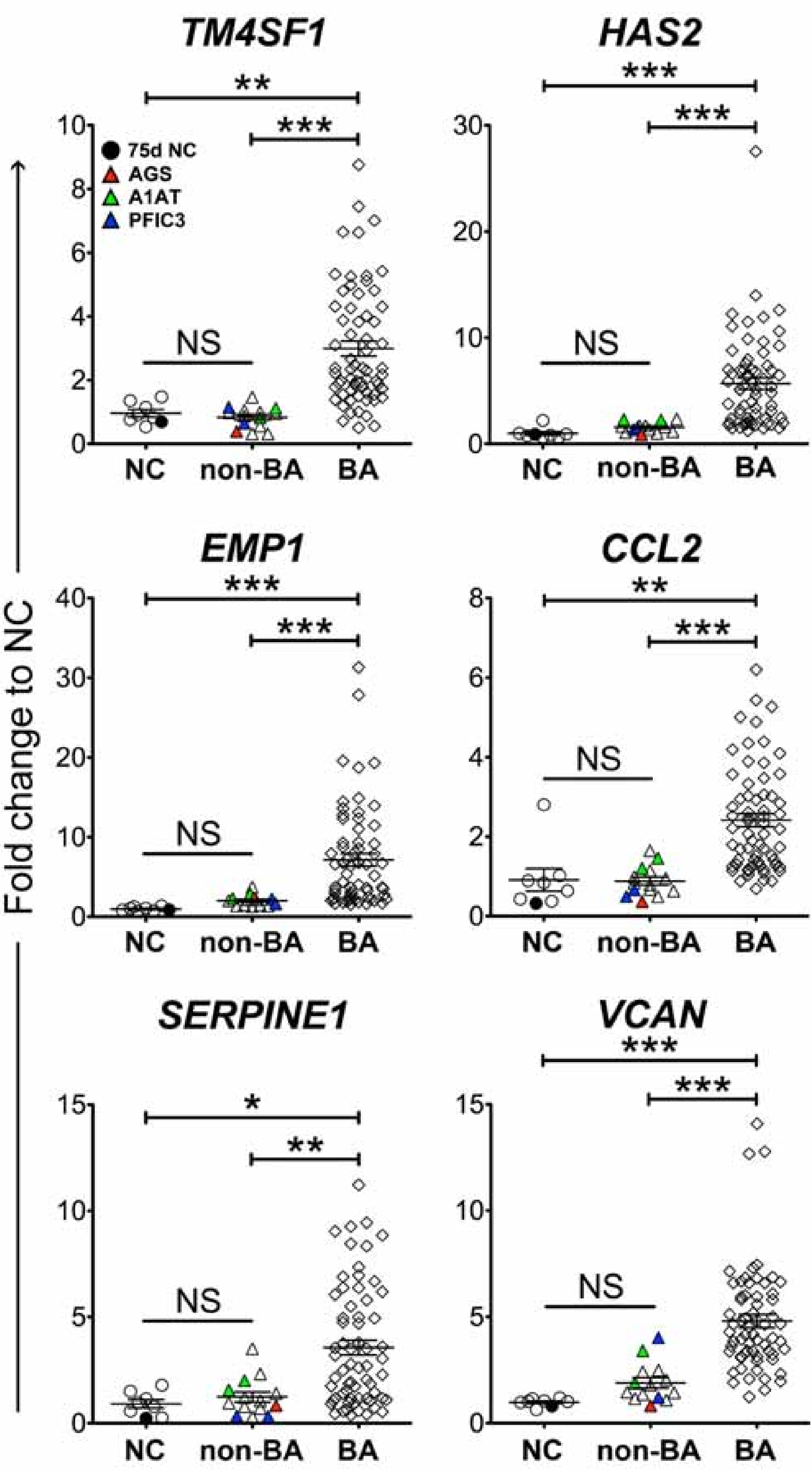
1. Li J, Bessho K, Shivakumar P, Mourya R, Mohanty SK, Dos Santos JL, Miura IK, et al. Th2 signals induce epithelial injury in mice and are compatible with the biliary atresia phenotype. J Clin Invest 2011;121:4244-4256.

2. Shivakumar P, Campbell KM, Sabla GE, Miethke A, Tiao G, McNeal MM, Ward RL, et al. Obstruction of extrahepatic bile ducts by lymphocytes is regulated by IFN-gamma in experimental biliary atresia. J Clin Invest 2004;114:322-329.

3. Carvalho E, Liu C, Shivakumar P, Sabla G, Aronow B, Bezerra JA. Analysis of the biliary transcriptome in experimental biliary atresia. Gastroenterology 2005;129:713-717.

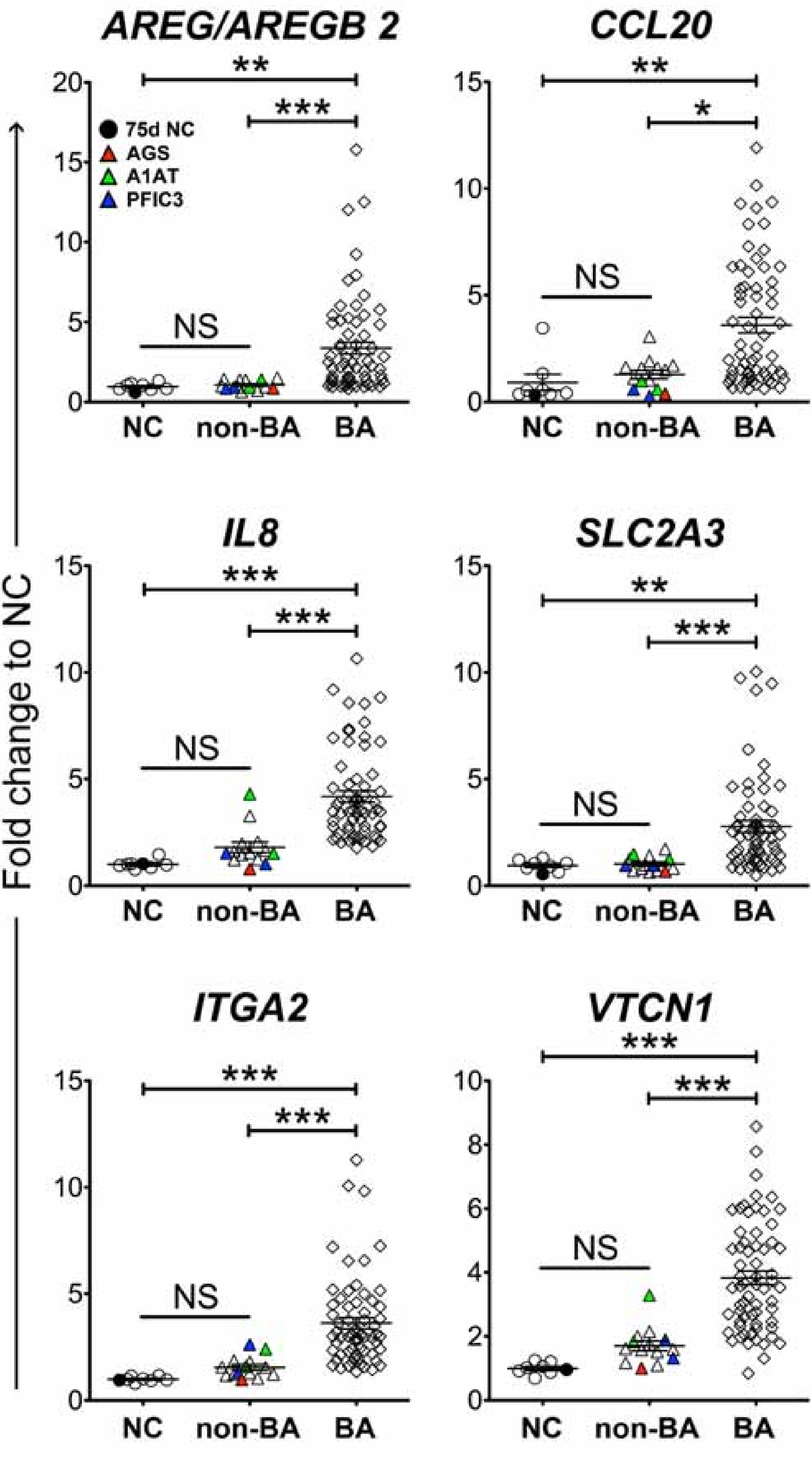
4. Shivakumar P, Sabla GE, Whitington P, Chougnet CA, Bezerra JA. Neonatal NK cells target the mouse duct epithelium via Nkg2d and drive tissue-specific injury in experimental biliary atresia. J Clin Invest 2009;119:2281-2290.

Supplementary Figure 1A



**Supplementary Figure 1. Hepatic expression levels of the 24 genes enriched in biliary atresia.** The expression levels of individual genes in 64 subjects with biliary atresia (BA), 7 normal controls (NC) and 14 non-biliary atresia (non-BA). The genes are shown in panels A-D. Gene expression is depicted as fold change to NC. $^*P < 0.05$; $^{**}P < 0.01$, $^{***}P < 0.001$ by Kruskal Wallis test between the groups. NS; not significant. Standard deviation is shown as horizontal lines for each group.

Supplementary Figure 1B



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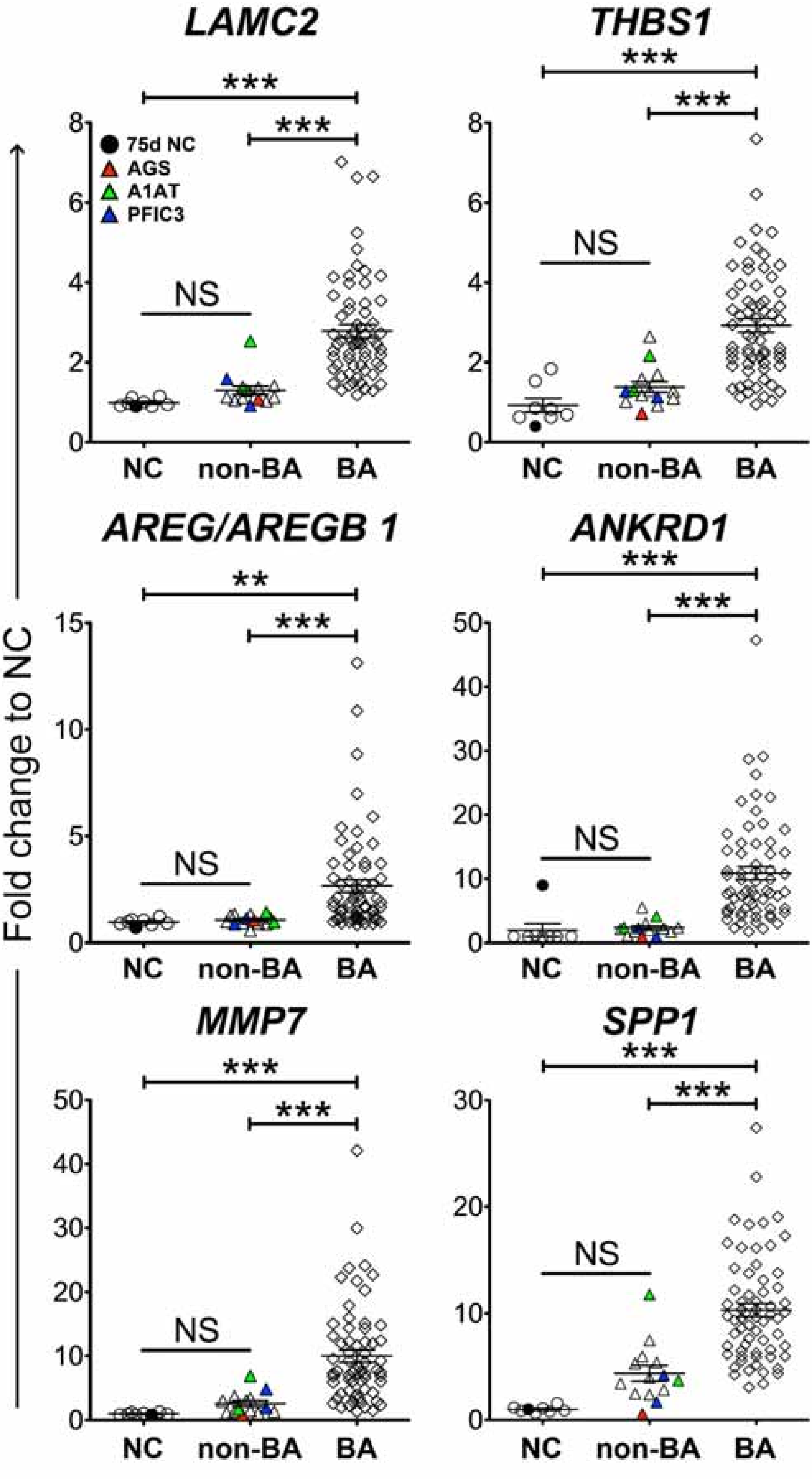
# Supplementary Figure 1C



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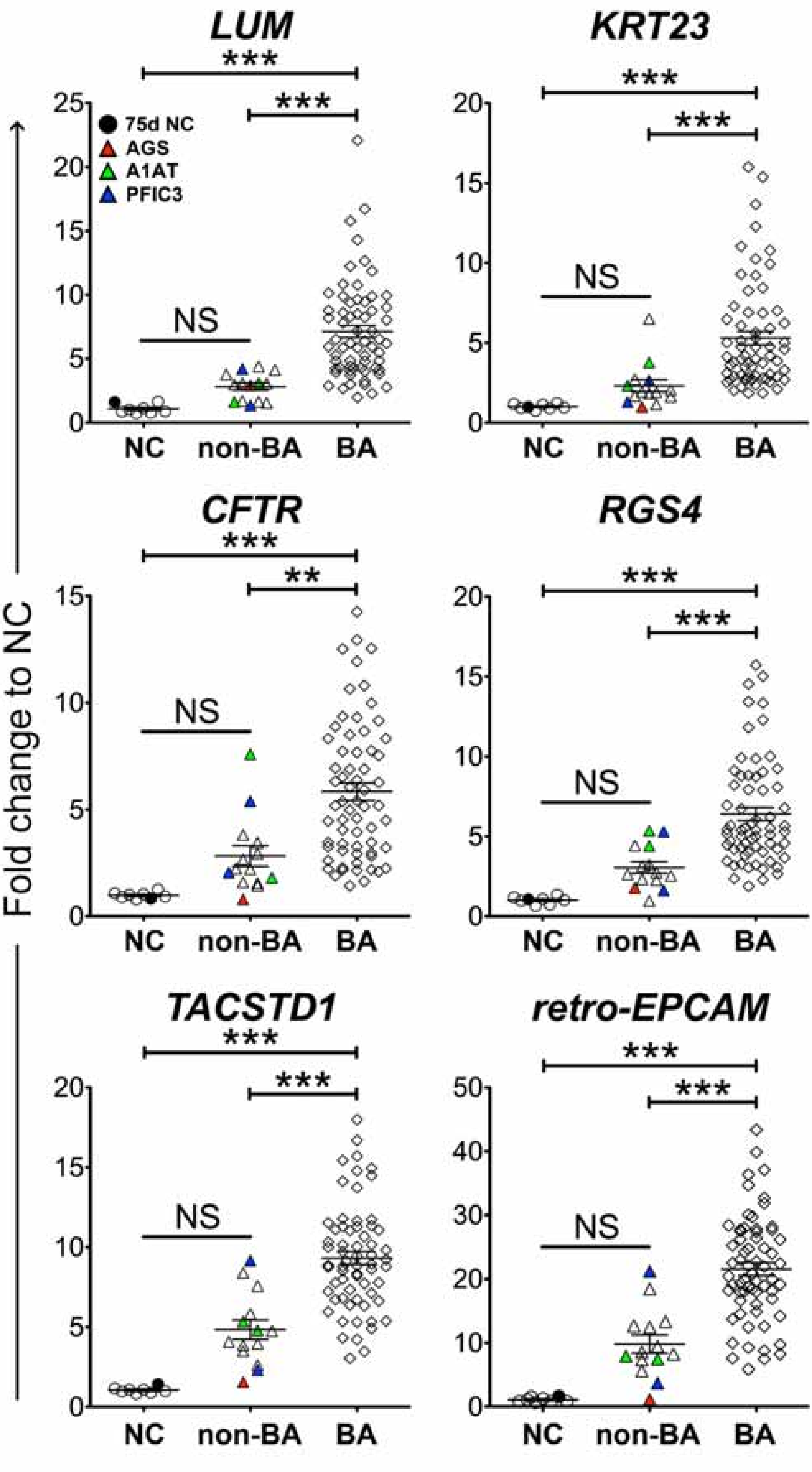
# Supplementary Figure 1D



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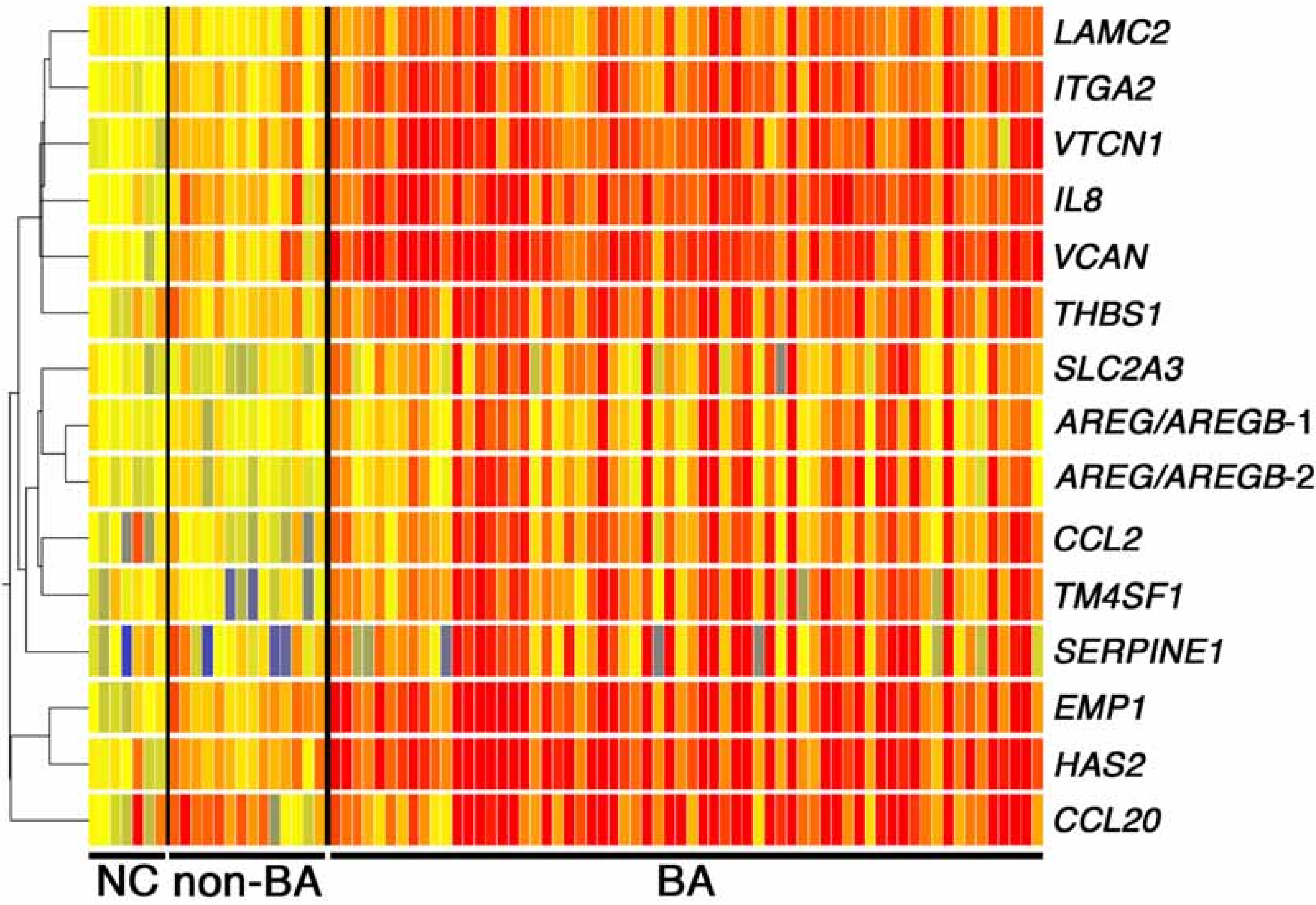
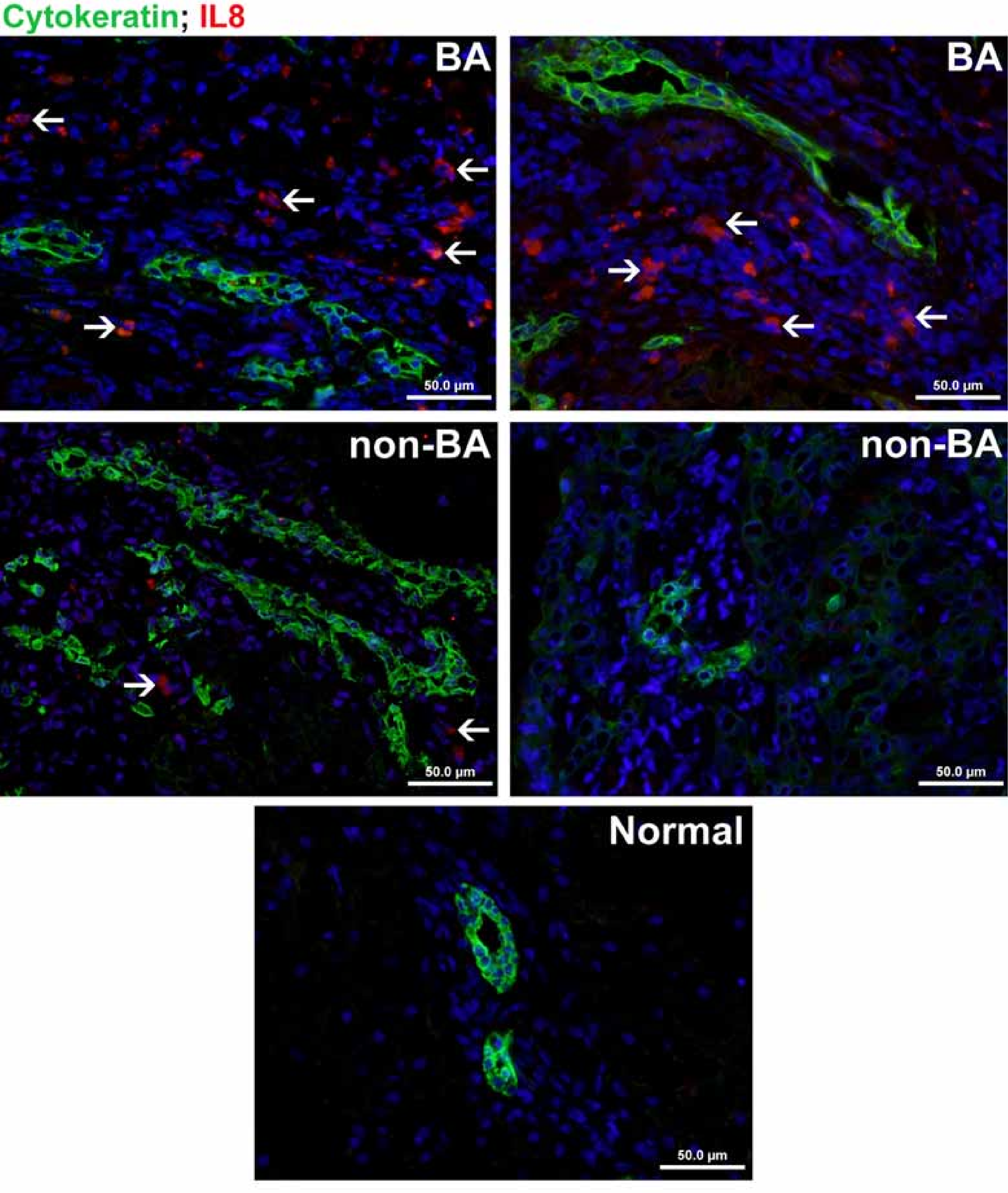
# Supplementary Figure 2



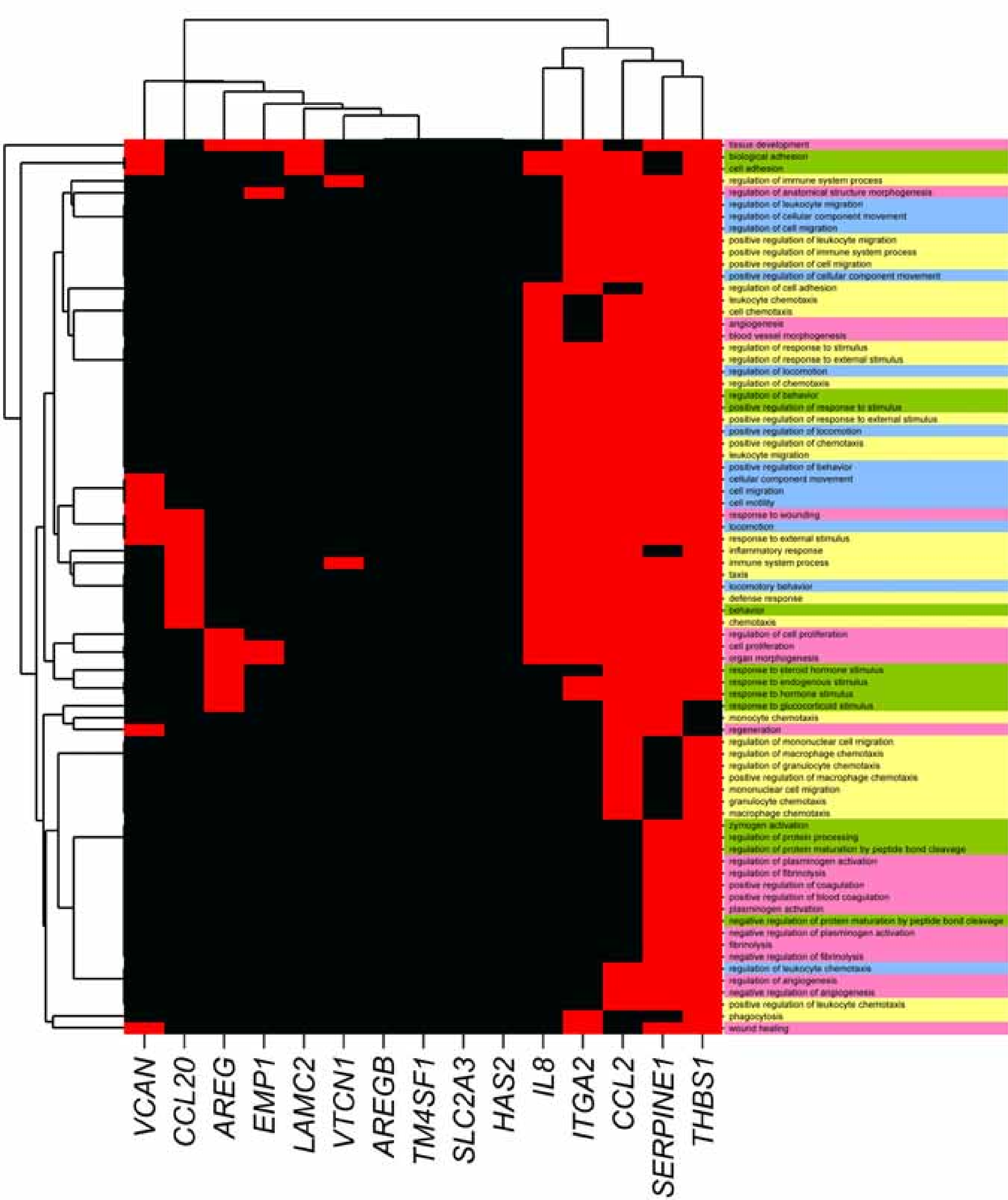
**Supplementary Figure 2. Hierarchical cluster analysis of 15 genes enriched for biliary atresia.** Hierarchical clustering of 15 genes/probe sets in 64 subjects with biliary atresia (BA), 7 normal controls (NC) and 14 non-biliary atresia (non-BA). Each column represents samples and the expression level is depicted by color variation from red (high expression) to blue (low expression); yellow indicates expression level of the median of 7 NC.

# Supplementary Figure 3



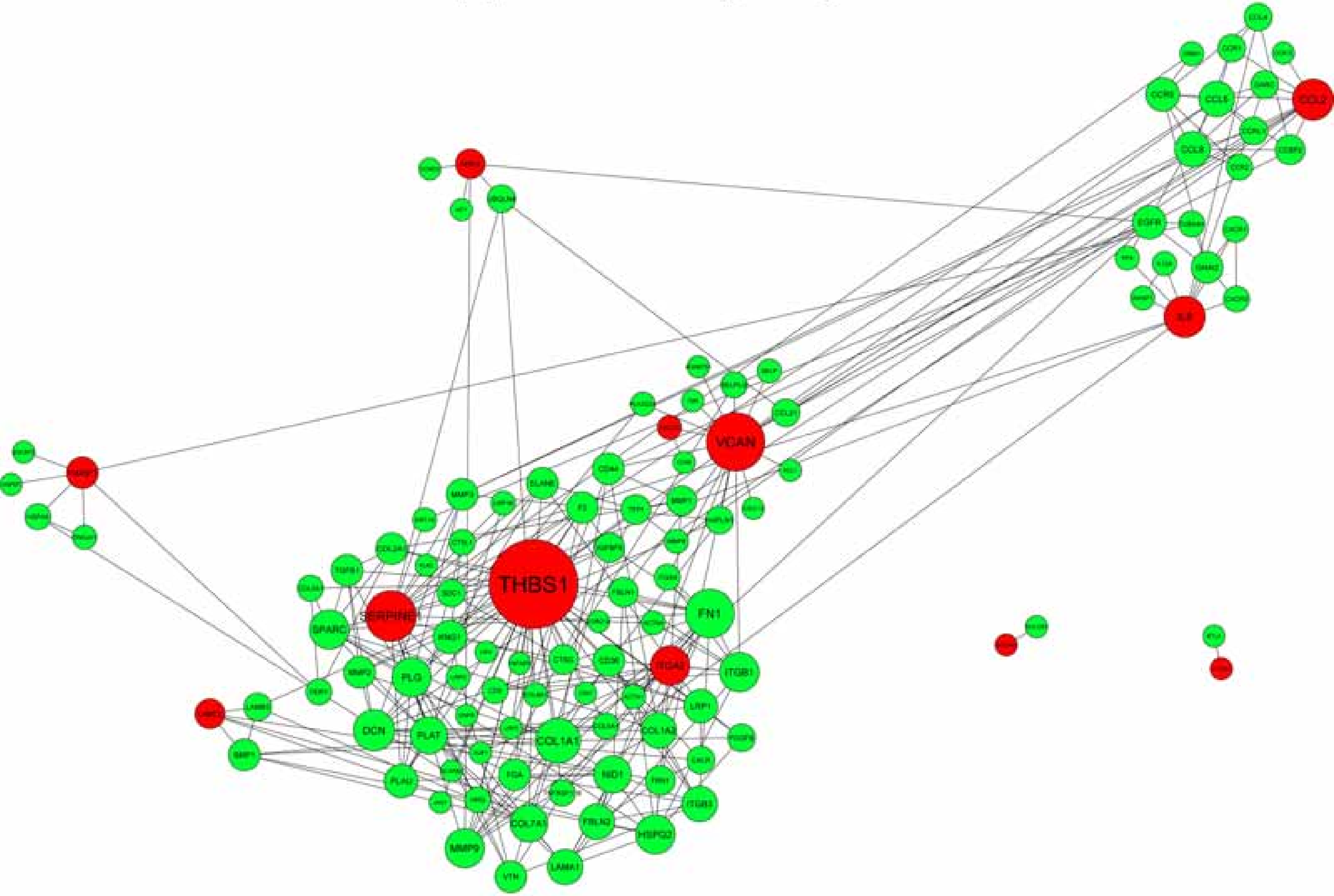
**Supplementary Figure 3. IL8 expression in portal tracts.** Immunostaining of cytokeratin (green) and IL8 (red) in frozen liver sections of infants with biliary atresia (BA), non-biliary atresia (non-BA), and normal control (NC) in infants 2-4 months of age.

# Supplementary Figure 4



**Supplementary Figure 4. Details of the functional enrichment heatmap depicted in Figure 4A.** Functional enrichment analysis of the 15 genes depicted as a 2-way condition tree for individual genes and biological processes (from Gene Ontology), classified into 4 functional categories, which are detailed in individual rows as the right vertical axis. The red area in the heat map indicates the closely related biological processes that are shared by the subgroup of genes shown in the horizontal axis.

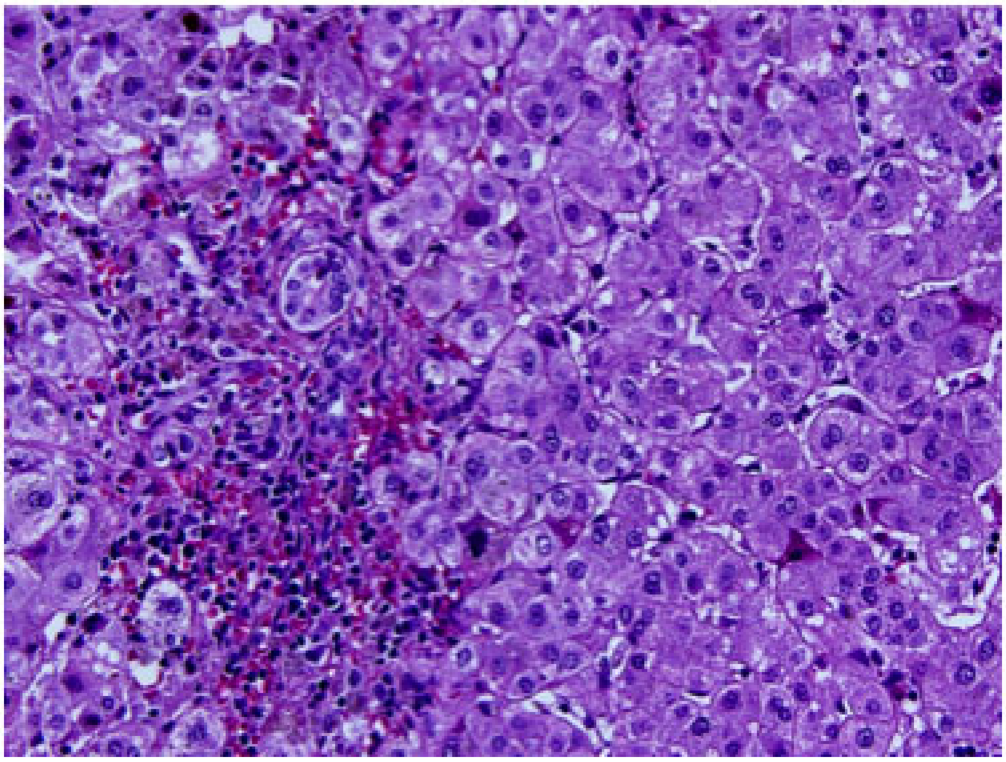
# Supplementary Figure 5



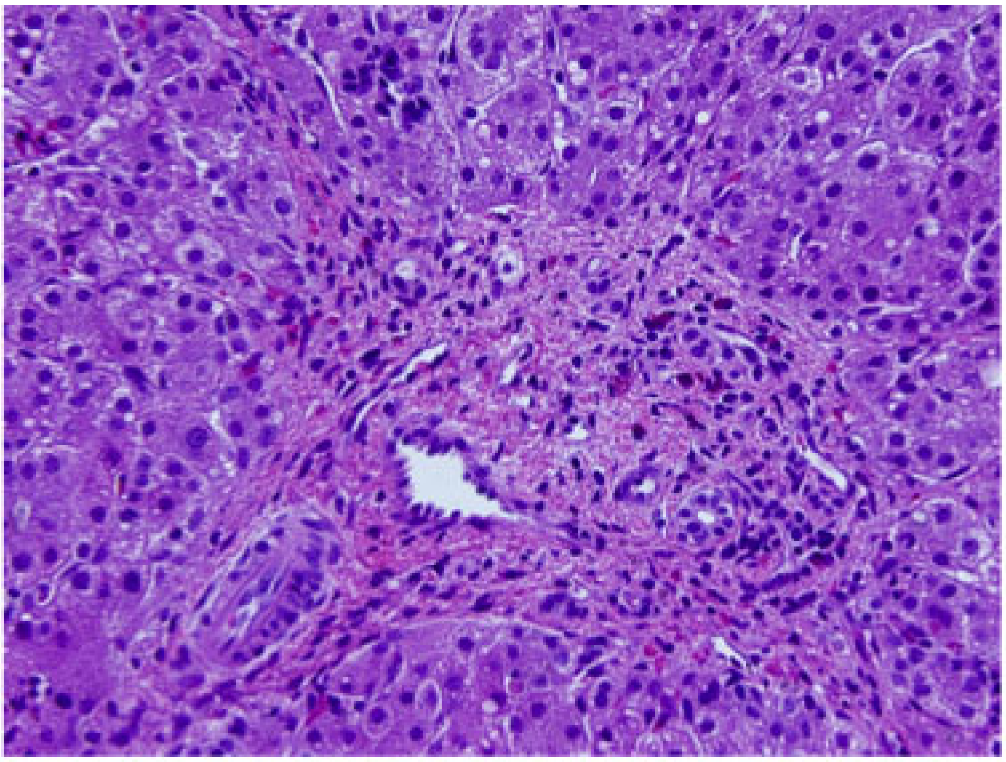
**Supplementary Figure 5. Details of the protein-protein interaction network depicted in Figure 4B.** Protein-protein interaction network of the 15 genes and their accessory proteins, with red nodes indicate original seed proteins and green nodes indicate accessory proteins that are known to directly bind to one of the original 15 proteins. The size of the nodes is proportional to the number of edges connected to the node.

# Supplementary Figure 6A

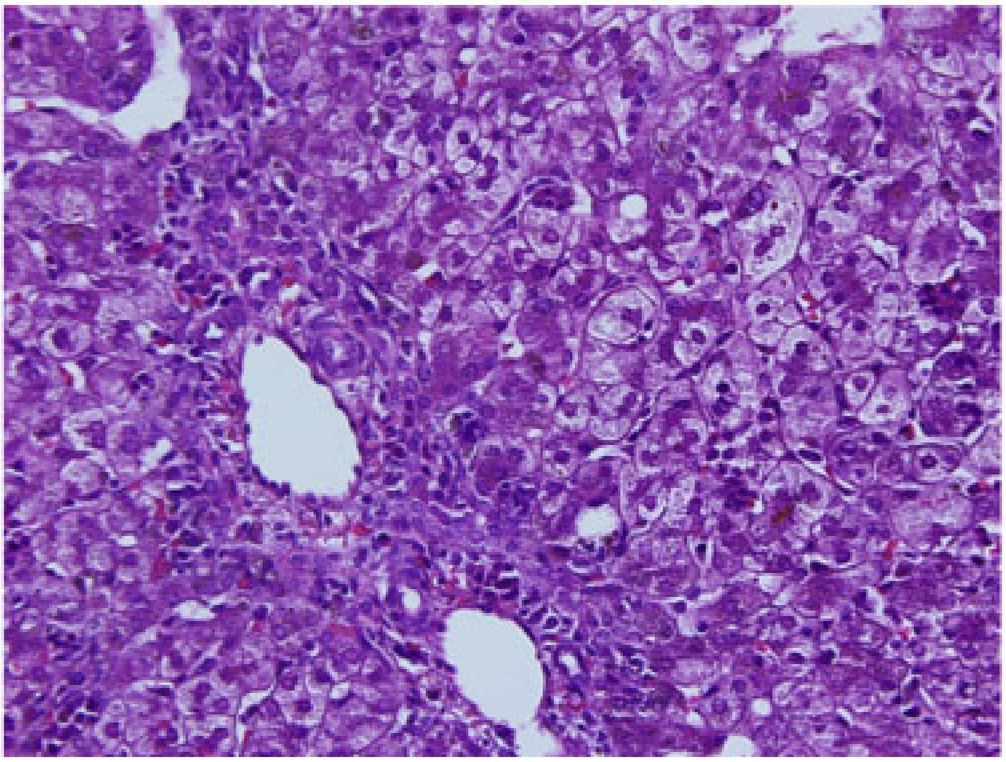
## Liver Biopsies from non-BA



Patient 1: Normal number of interlobular bile duct



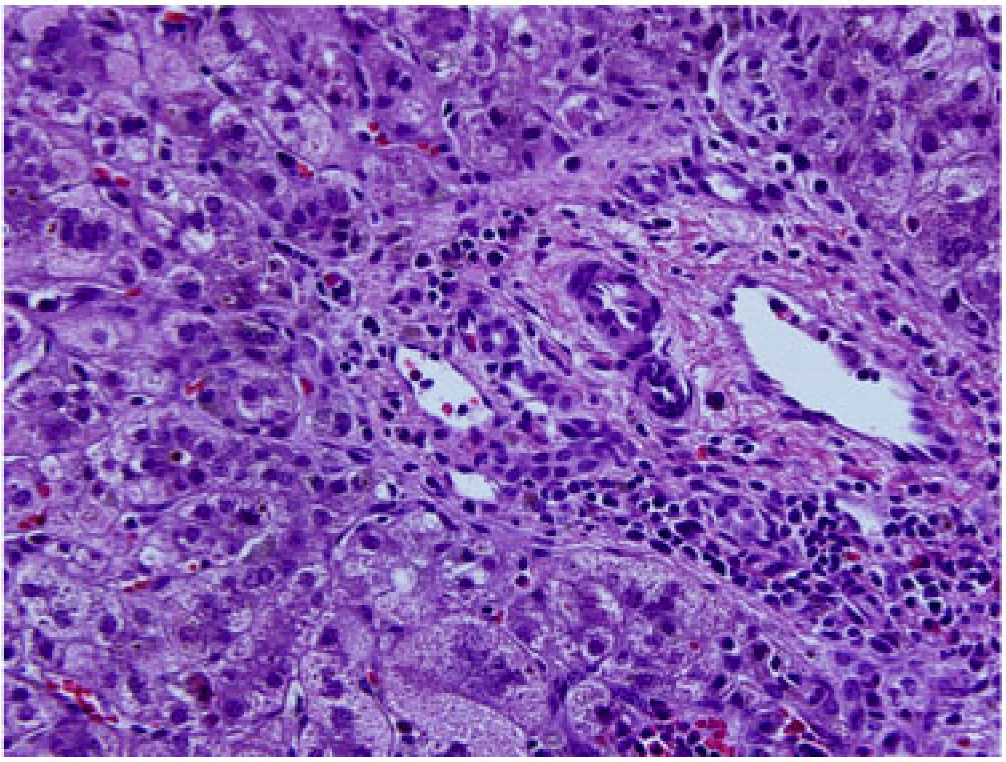
Patient 2: Normal number of interlobular bile duct



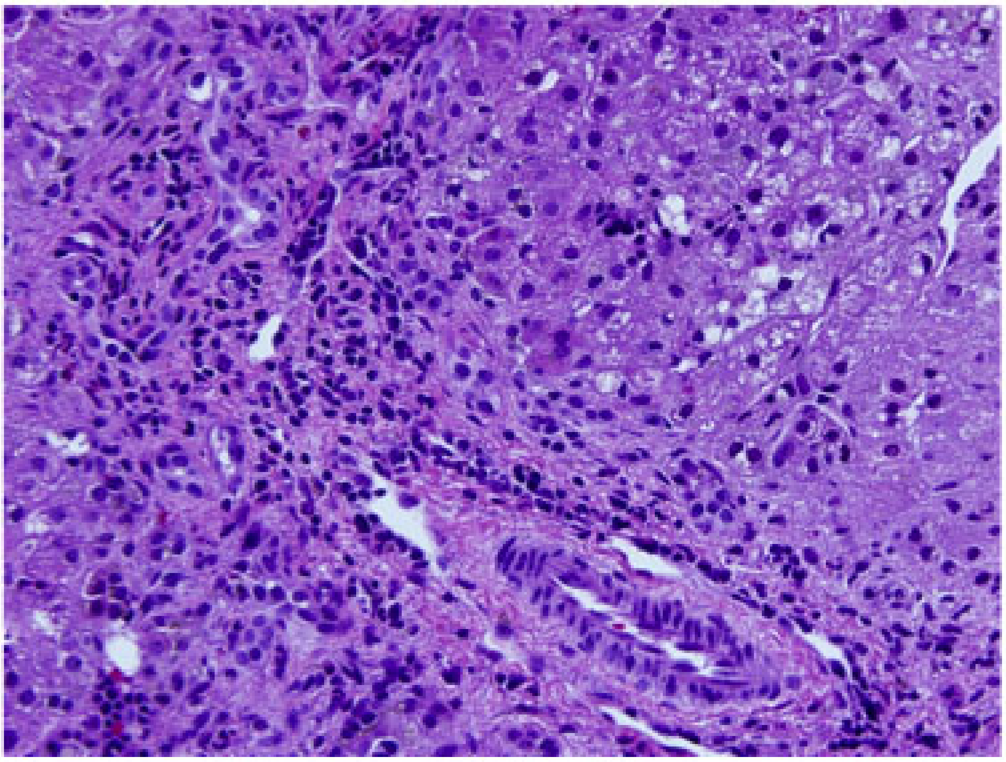
Patient 3: Normal number of interlobular bile duct

# Supplementary Figure 6B

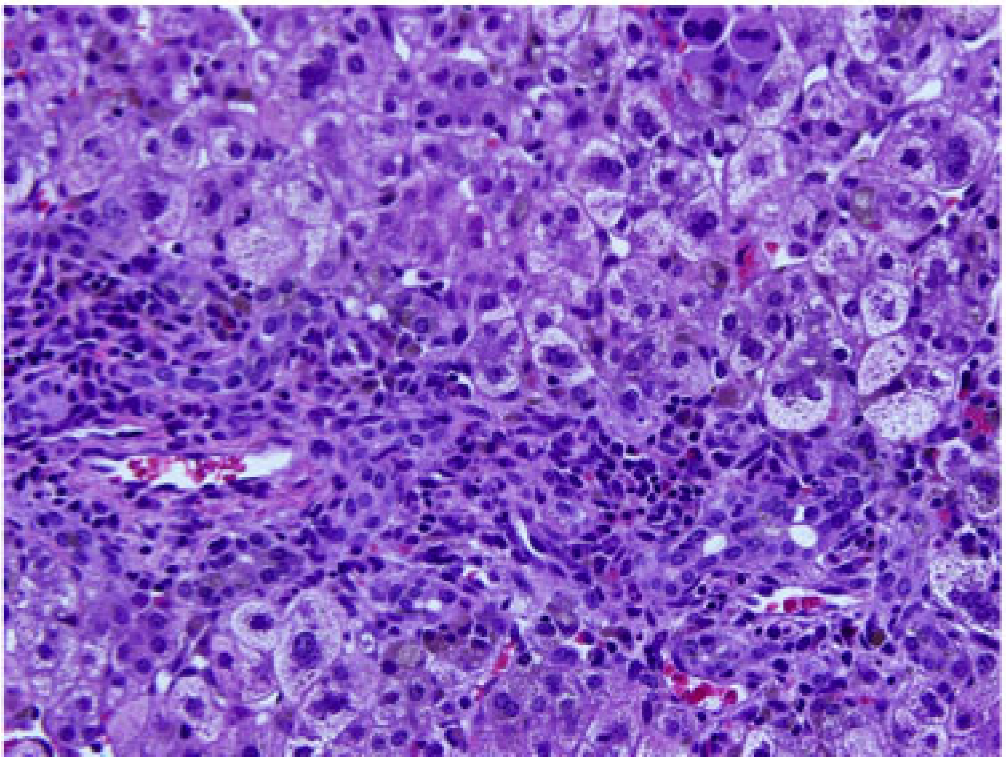
Liver Biopsies from non-BA



Patient 4: Normal number of interlobular bile duct



Patient 5: Normal number of interlobular bile duct

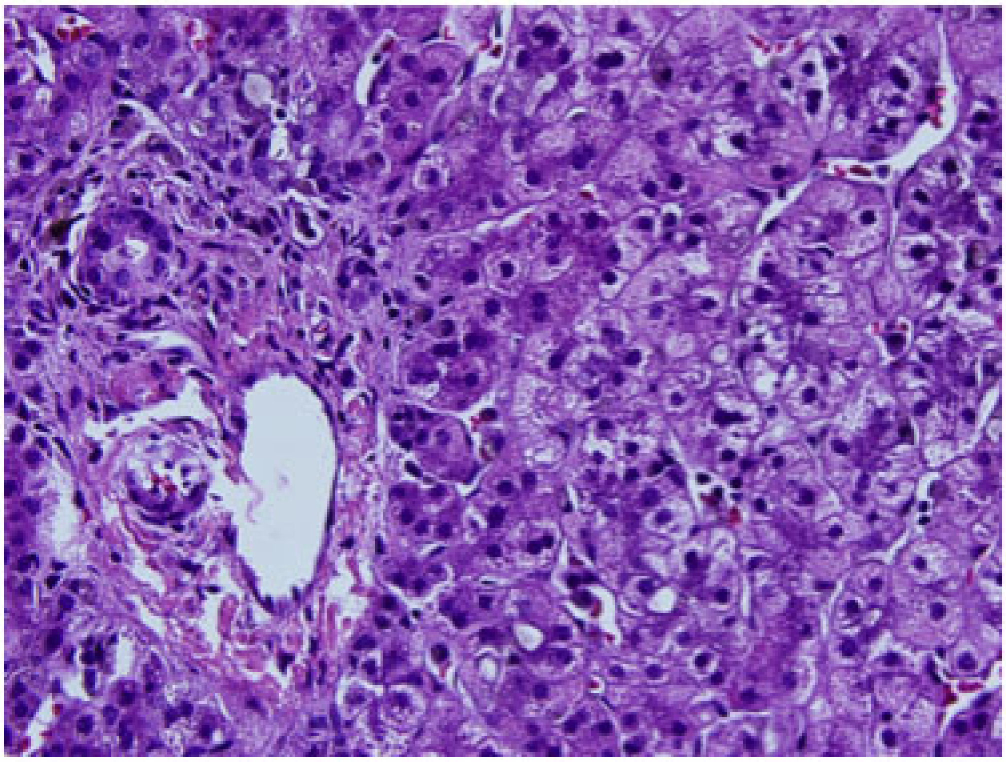


Patient 6: Mild increase in the number of interlobular bile ducts

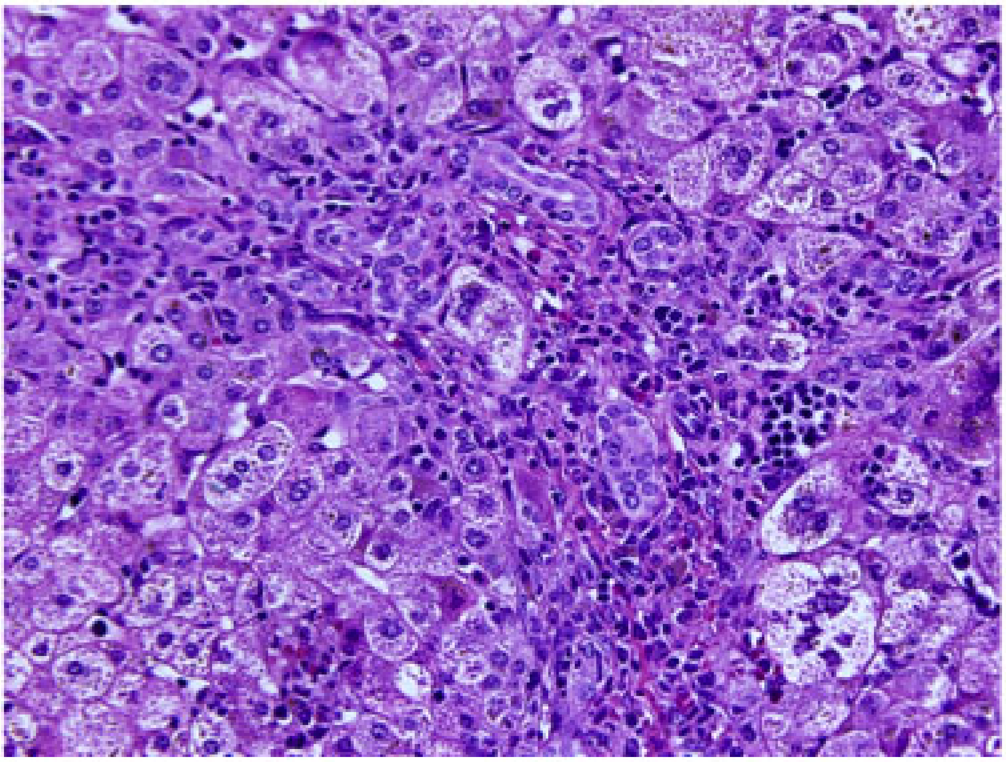
# Supplementary Figure 6C

## Liver Biopsies from non-BA

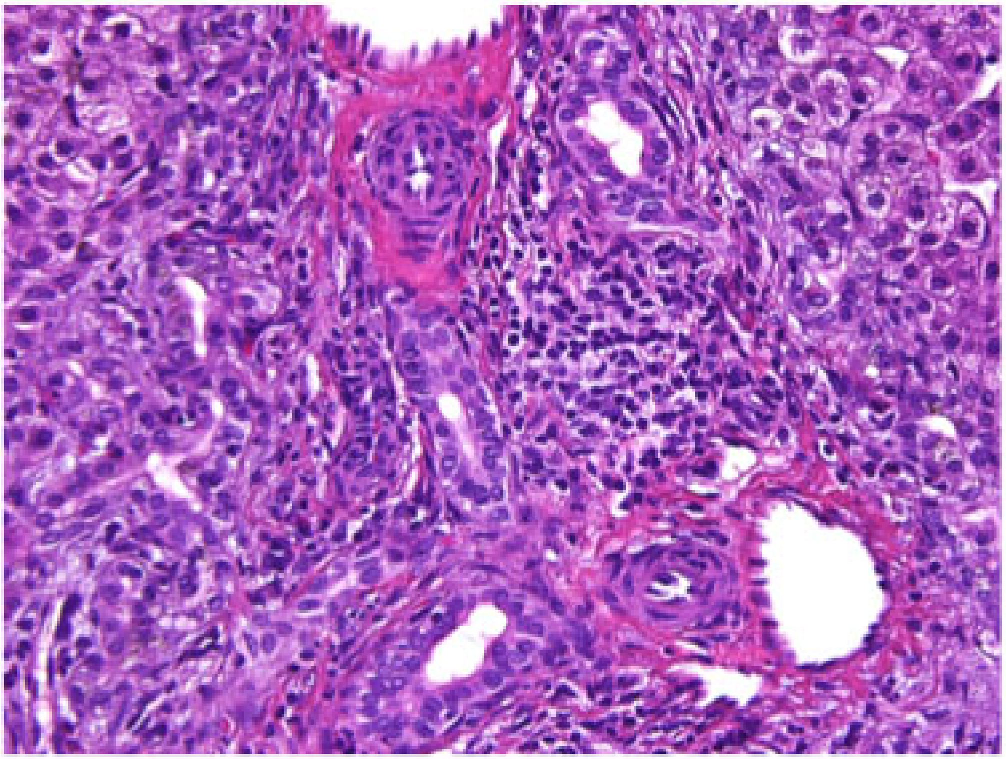
Patient 7: Normal number of interlobular bile duct



Patient 8: Proliferation of interlobular bile duct

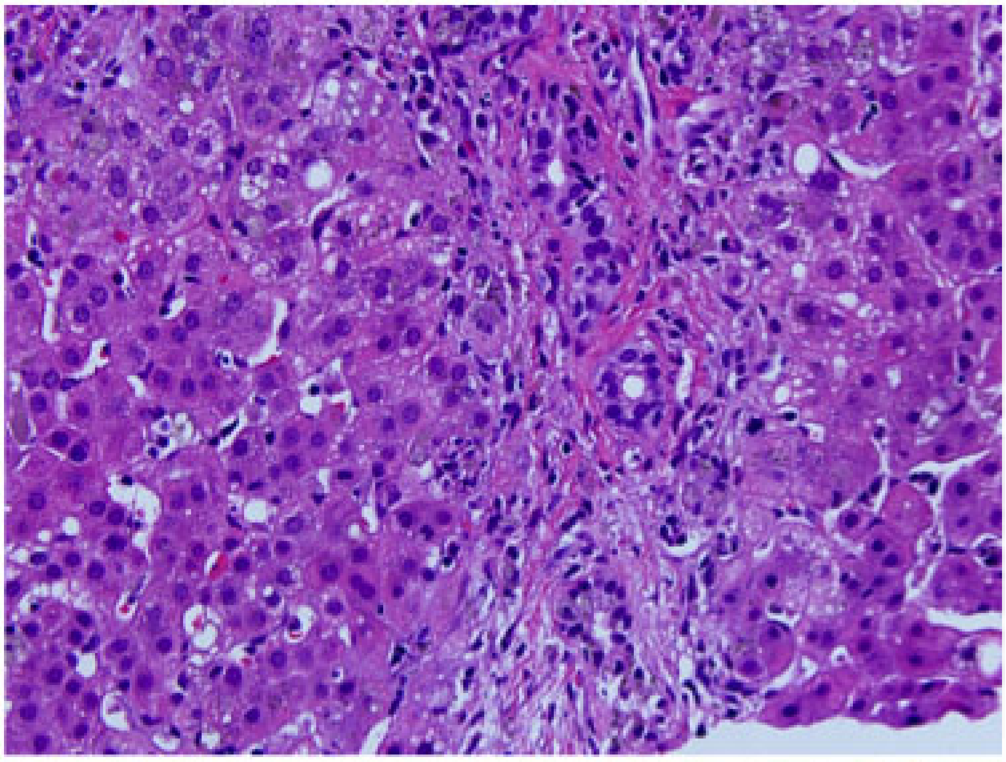


Patient 9: Proliferation of interlobular bile duct

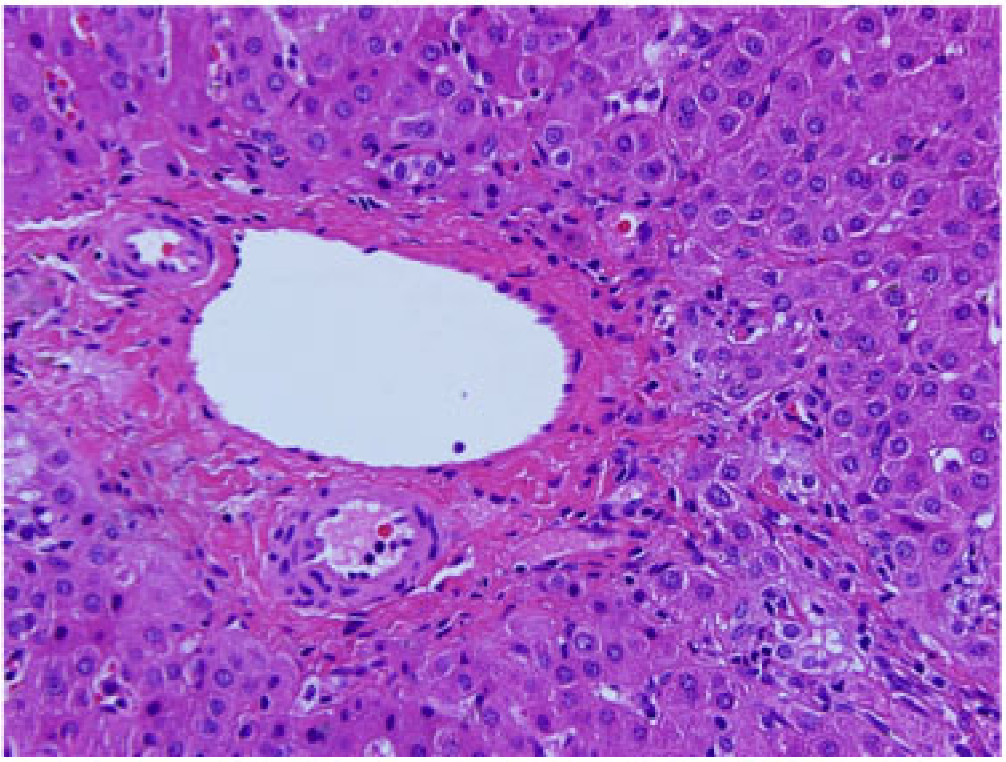


# Supplementary Figure 6D

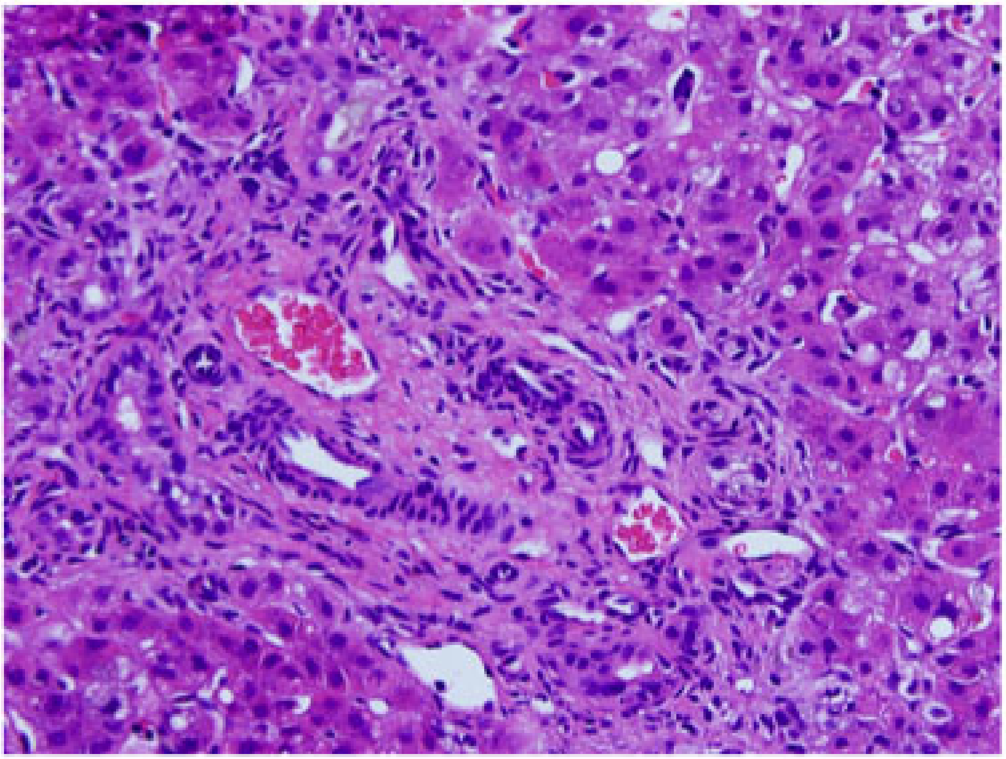
## Liver Biopsies from non-BA



Patient 10: Proliferation of interlobular bile duct



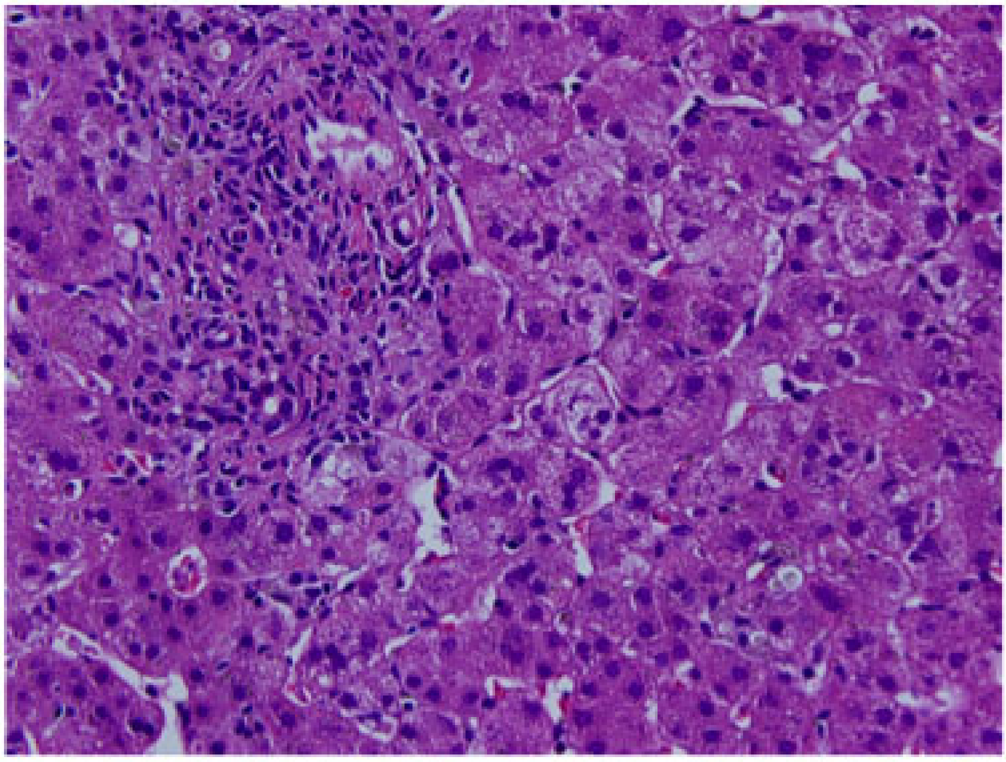
Patient 11: Paucity of intrahepatic bile duct



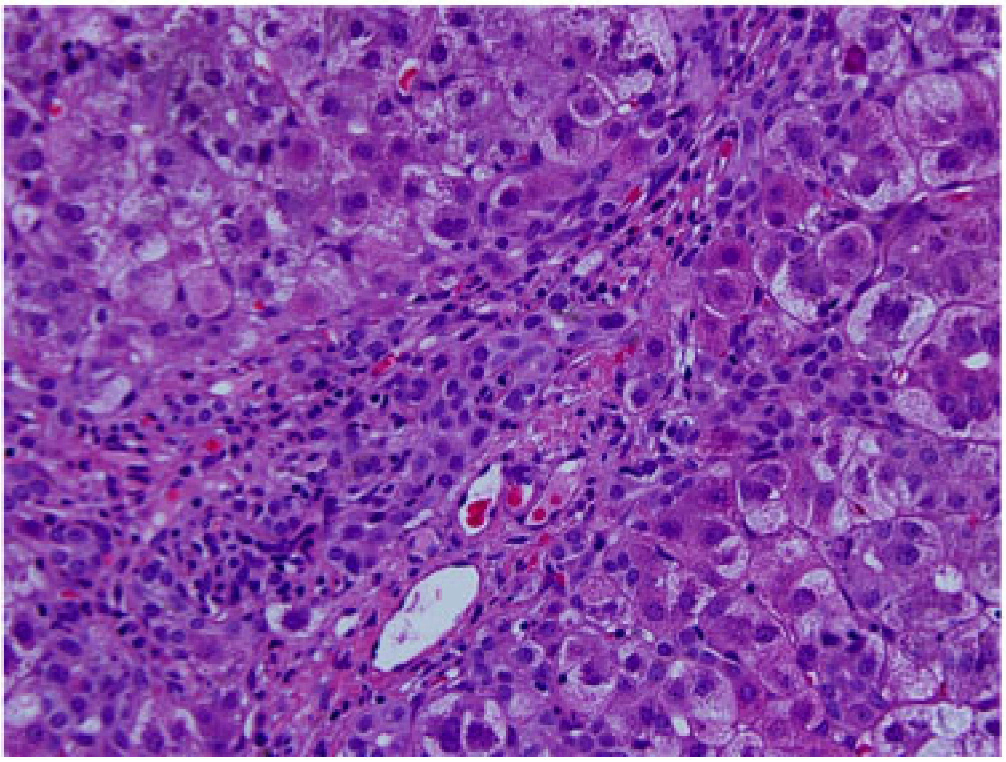
Patient 12: Normal number of interlobular bile duct

# Supplementary Figure 6E

## Liver Biopsies from non-BA



Patient 13: Normal number of interlobular bile duct



Patient 14: Proliferation of interlobular bile duct

# Supplementary Table 1

List of regulated probe sets differing by more than 2-fold change among the 3 conditions (BA, DC and NC).
The probe sets in red font constitute the molecular signature of biliary atresia.
Corrected P value equals to P value with Benjamini-Hochberg multiple testing correction (false discovery rate [FDR] 0.05).

## 574 probe sets regulated by more than at least 2-fold between biliary atresia (BA) and normal control (NC)

| Transcripts Cluster ID | Gene Symbol | Gene Description | Entrezgene ID | Fold change BA vs NC | Regulation in BA | Corrected P value |
|---|---|---|---|---|---|---|
| 8175234 | GPC3 | glypican 3 | 2719 | 54.44 | up | 1.37E-18 |
| 8098439 | | | | 20.67 | up | 1.26E-09 |
| 8131844 | GPNMB | glycoprotein (transmembrane) nmb | 10457 | 10.12 | up | 5.49E-07 |
| 8096301 | SPP1 | secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) | 6696 | 9.56 | up | 8.01E-09 |
| 8016646 | COL1A1 | collagen, type I, alpha 1 | 1277 | 8.92 | up | 1.39E-06 |
| 8041853 | TACSTD1 | tumor-associated calcium signal transducer 1 | 4072 | 8.79 | up | 4.08E-15 |
| 7934979 | ANKRD1 | ankyrin repeat domain 1 (cardiac muscle) | 27063 | 8.61 | up | 3.58E-16 |
| 8134263 | COL1A2 | collagen, type I, alpha 2 | 1278 | 8.31 | up | 2.15E-06 |
| 8104663 | CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | 1004 | 7.97 | up | 3.58E-16 |
| 7951217 | MMP7 | matrix metallopeptidase 7 (matrilysin, uterine) | 4316 | 7.70 | up | 2.16E-12 |
| 8124196 | DCDC2 | doublecortin domain containing 2 | 51473 | 7.37 | up | 6.55E-13 |
| 8124650 | UBD\|GABBR1 | ubiquitin D \| gamma-aminobutyric acid (GABA) B receptor, 1 | 10537 \| 2550 | 7.10 | up | 2.07E-04 |
| 8178295 | UBD\|GABBR1 | ubiquitin D \| gamma-aminobutyric acid (GABA) B receptor, 1 | 10537 \| 2550 | 6.70 | up | 2.39E-04 |
| 7965403 | LUM | lumican | 4060 | 6.49 | up | 2.76E-08 |
| 8174201 | BEX1 | brain expressed, X-linked 1 | 55859 | 6.33 | up | 4.64E-11 |
| 8107769 | SLC12A2 | solute carrier family 12 (sodium/potassium/chloride transporters), member 2 | 6558 | 6.23 | up | 5.08E-14 |
| 7927681 | BICC1 | bicaudal C homolog 1 (Drosophila) | 80114 | 6.18 | up | 4.36E-15 |
| 8101126 | CXCL10 | chemokine (C-X-C motif) ligand 10 | 3627 | 6.09 | up | 2.11E-04 |
| 7906919 | RGS4 | regulator of G-protein signaling 4 | 5999 | 5.81 | up | 1.64E-08 |
| 8126784 | PLA2G7 | phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) | 7941 | 5.76 | up | 1.40E-05 |

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|---|---|---|---|---|---|---|
| 8046922 | COL3A1 | collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) | 1281 | 5.72 | up | 1.42E-05 |
| 8029693 | FOSB | FBJ murine osteosarcoma viral oncogene homolog B | 2354 | 5.62 | up | 4.84E-12 |
| 8104079 | FAT |  | 2195 | 5.54 | up | 1.53E-06 |
| 7954090 | EMP1 | epithelial membrane protein 1 | 2012 | 5.28 | up | 5.72E-08 |
| 8130867 | THBS2 | thrombospondin 2 | 7058 | 5.20 | up | 1.63E-06 |
| 8177222 | CD24 |  | 934 | 5.16 | up | 1.77E-06 |
| 7976812 | SNORD113-4 | small nucleolar RNA, C/D box 113-4 | 767564 | 5.03 | up | 3.95E-07 |
| 8135661 | CFTR | cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7) | 1080 | 5.02 | up | 2.81E-12 |
| 7935553 | LOXL4 | lysyl oxidase-like 4 | 84171 | 5.02 | up | 2.78E-12 |
| 8152617 | HAS2 | hyaluronan synthase 2 | 3037 | 4.85 | up | 2.70E-06 |
| 7938366 | WEE1 |  | 7465 | 4.83 | up | 6.35E-05 |
| 8136336 | AKR1B10 | aldo-keto reductase family 1, member B10 (aldose reductase) | 57016 | 4.79 | up | 0.045463 |
| 7976814 | SNORD114-2 | small nucleolar RNA, C/D box 114-2 | 767578 | 4.77 | up | 2.96E-09 |
| 8049425 | SPP2 | secreted phosphoprotein 2, 24kDa | 6694 | 4.71 | up | 7.52E-06 |
| 7946048 | HBG1\|HBG2 | hemoglobin, gamma A \| hemoglobin, gamma G | 3047 \| 3048 | 4.64 | up | 9.38E-09 |
| 7946054 | HBG1\|HBG2 | hemoglobin, gamma A \| hemoglobin, gamma G | 3047 \| 3048 | 4.63 | up | 9.38E-09 |
| 8059905 | COL6A3 | collagen, type VI, alpha 3 | 1293 | 4.63 | up | 1.54E-07 |
| 8126954 | PKHD1 | polycystic kidney and hepatic disease 1 (autosomal recessive) | 5314 | 4.57 | up | 6.95E-12 |
| 8015133 | KRT23 | keratin 23 (histone deacetylase inducible) | 25984 | 4.57 | up | 1.79E-10 |
| 8044225 | SULT1C4 | sulfotransferase family, cytosolic, 1C, member 4 | 27233 | 4.47 | up | 6.13E-13 |
| 8106743 | VCAN | versican | 1462 | 4.36 | up | 7.01E-09 |
| 7945680 | H19 |  | 283120 | 4.30 | up | 0.0047741 |
| 7981990 | SNRPN\|SNORD116-21\|SNORD116@ | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-21 \| small nucleolar RNA, C/D box 116 cluster | 6638 \| 100033432 \| 692236 | 4.22 | up | 6.23E-07 |
| 7972750 | COL4A1 | collagen, type IV, alpha 1 | 1282 | 4.21 | up | 3.98E-08 |
| 8057620 | COL5A2 | collagen, type V, alpha 2 | 1290 | 4.16 | up | 5.72E-10 |
| 7976810 | SNORD113-3 | small nucleolar RNA, C/D box 113-3 | 767563 | 4.06 | up | 2.45E-09 |
| 7938364 | WEE1 |  | 7465 | 4.03 | up | 9.65E-06 |
| 8006594 | CCL18 | chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) | 6362 | 3.91 | up | 1.29E-12 |
| 8056257 | FAP | fibroblast activation protein, alpha | 2191 | 3.82 | up | 6.13E-13 |

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|---|---|---|---|---|---|---|
| 8095680 | IL8 | interleukin 8 | 3576 | 3.81 | up | 1.79E-08 |
| 8089544 | CCDC80 | coiled-coil domain containing 80 | 151887 | 3.80 | up | 6.72E-09 |
| 8134339 | PEG10 | paternally expressed 10 | 23089 | 3.80 | up | 0.0020475 |
| 7976795 | MEG3\|LOC100131839 | maternally expressed 3 \| hypothetical protein LOC100131839 | 55384 \| 100131839 | 3.80 | up | 1.43E-10 |
| 8020847 | DTNA | dystrobrevin, alpha | 1837 | 3.78 | up | 3.12E-12 |
| 7961514 | MGP | matrix Gla protein | 4256 | 3.74 | up | 3.14E-05 |
| 7982084 | SNRPN\|SNORD115-11\|SNORD115-12\|SNORD115-26\|SNORD115-29\|SNORD115-36\|SNORD115-39\|SNORD115-43\|SNORD115-9\|SNORD115-41\|SNORD115-22\|SNORD115-16\|SNORD115-14\|SNORD115-6\|SNORD115-38\|SNORD115-44\|SNORD115-30 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-38 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-30 | 6638 \| 100033448 \| 100033449 \| 100033802 \| 100033803 \| 100033810 \| 100033813 \| 100033817 \| 100033446 \| 100033815 \| 100033799 \| 100033454 \| 100033451 \| 100033443 \| 100033812 \| 100033818 \| 100033440 \| 100033804 | 3.73 | up | 4.26E-05 |
| 8112274 | ELOVL7 | ELOVL family member 7, elongation of long chain fatty acids (yeast) | 79993 | 3.71 | up | 2.53E-12 |
| 8112668 | GCNT4 | glucosaminyl (N-acetyl) transferase 4, core 2 (beta-1,6-N-acetylglucosaminyltransferase) | 51301 | 3.69 | up | 1.17E-06 |
| 8048864 | CCL20 | chemokine (C-C motif) ligand 20 | 6364 | 3.66 | up | 0.0045863 |
| 7988767 | CYP19A1 | cytochrome P450, family 19, subfamily A, polypeptide 1 | 1588 | 3.64 | up | 5.66E-10 |
| 8162394 | ASPN | asporin | 54829 | 3.59 | up | 3.66E-05 |

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| 7982058 | SNORD115-1\|SNRPN\|SNORD115-26\|SNORD115-11\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-5\|SNORD115-22\|SNORD115-39\|SNORD115-41\|SNORD115-16\|SNORD115-44\|SNORD115-34\|SNORD115-6\|HBII-52-24\|SNORD115-7 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-6 \| HBII-52-24 snoRNA \| small nucleolar RNA, C/D box 115-7 | 338433 \| 6638 \| 100033802 \| 100033448 \| 100033803 \| 100033810 \| 100033817 \| 100033442 \| 100033799 \| 100033813 \| 100033815 \| 100033440 \| 100033454 \| 100033818 \| 100033808 \| 100033443 \| 100036563 \| 100033444 | 3.57 | up | 1.35E-05 |
| 8099476 | PROM1 | prominin 1 | 8842 | 3.56 | up | 6.42E-07 |

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| 7982064 | SNORD115-1\|SNRPN\|SNORD115-11\|SNORD115-12\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-5\|SNORD115-9\|SNORD115-26\|SNORD115-22\|SNORD115-20\|SNORD115-39\|SNORD115-41\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-16\|SNORD115-40\|SNORD115-44\|SNORD115-34\|SNORD115-42\|SNORD115-6\|SNORD115-10\|SNORD115-14\|SNORD115-15\|SNORD115-21\|HBII-52-24\|SNORD115-7 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| HBII-52-24 snoRNA \| small nucleolar RNA, C/D box 115-7 | 338433 \| 6638 \| 100033448 \| 100033449 \| 100033803 \| 100033810 \| 100033817 \| 100033442 \| 100033446 \| 100033802 \| 100033799 \| 100033460 \| 100033813 \| 100033440 \| 100033815 \| 100033455 \| 100033456 \| 100033458 \| 100033450 \| 100033454 \| 100033814 \| 100033818 \| 100033808 \| 100033441 \| 100033816 \| 100033443 \| 100033447 \| 100033451 \| 100033453 \| 100033603 \| 100036563 \| 100033444 | 3.56 | up | 1.46E-05 |

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| 7982078 | SNORD115-1\|SNRPN\|SNORD115-11\|SNORD115-12\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-5\|SNORD115-9\|SNORD115-26\|SNORD115-22\|SNORD115-20\|SNORD115-39\|SNORD115-41\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-16\|SNORD115-40\|SNORD115-44\|SNORD115-34\|SNORD115-42\|SNORD115-6\|SNORD115-10\|SNORD115-14\|SNORD115-15\|HBII-52-24\|SNORD115-7 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| HBII-52-24 snoRNA \| small nucleolar RNA, C/D box 115-7 | 338433 \| 6638 \| 100033448 \| 100033449 \| 100033803 \| 100033810 \| 100033817 \| 100033442 \| 100033446 \| 100033802 \| 100033799 \| 100033460 \| 100033813 \| 100033440 \| 100033815 \| 100033455 \| 100033456 \| 100033458 \| 100033450 \| 100033454 \| 100033814 \| 100033818 \| 100033808 \| 100033441 \| 100033816 \| 100033443 \| 100033447 \| 100033451 \| 100033453 \| 100036563 \| 100033444 | 3.55 | up | 1.53E-05 |

<table>
<tr><td>7982092</td><td>SNORD115-1|SNRPN|SNORD115-11|SNORD115-12|SNORD115-29|SNORD115-36|SNORD115-43|SNORD115-5|SNORD115-9|SNORD115-26|SNORD115-22|SNORD115-20|SNORD115-39|SNORD115-41|SNORD115-17|SNORD115-18|SNORD115-19|SNORD115-13|SNORD115-16|SNORD115-40|SNORD115-44|SNORD115-34|SNORD115-6|SNORD115-10|HBII-52-24|SNORD115-7</td><td>small nucleolar RNA, C/D box 115-1 | small nuclear ribonucleoprotein polypeptide N | small nucleolar RNA, C/D box 115-11 | small nucleolar RNA, C/D box 115-12 | small nucleolar RNA, C/D box 115-29 | small nucleolar RNA, C/D box 115-36 | small nucleolar RNA, C/D box 115-43 | small nucleolar RNA, C/D box 115-5 | small nucleolar RNA, C/D box 115-9 | small nucleolar RNA, C/D box 115-26 | small nucleolar RNA, C/D box 115-22 | small nucleolar RNA, C/D box 115-20 | small nucleolar RNA, C/D box 115-39 | small nucleolar RNA, C/D box 115-3 | small nucleolar RNA, C/D box 115-41 | small nucleolar RNA, C/D box 115-17 | small nucleolar RNA, C/D box 115-18 | small nucleolar RNA, C/D box 115-19 | small nucleolar RNA, C/D box 115-13 | small nucleolar RNA, C/D box 115-16 | small nucleolar RNA, C/D box 115-40 | small nucleolar RNA, C/D box 115-44 | small nucleolar RNA, C/D box 115-34 | small nucleolar RNA, C/D box 115-6 | small nucleolar RNA, C/D box 115-10 | HBII-52-24 snoRNA | small nucleolar RNA, C/D box 115-7</td><td>338433 | 6638 | 100033448 | 100033449 | 100033803 | 100033810 | 100033817 | 100033442 | 100033446 | 100033802 | 100033799 | 100033460 | 100033813 | 100033440 | 100033815 | 100033455 | 100033456 | 100033458 | 100033450 | 100033454 | 100033814 | 100033818 | 100033808 | 100033443 | 100033447 | 100036563 | 100033444</td><td>3.55</td><td>up</td><td>1.44E-05</td></tr>
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| 7982028 | SNORD115-1\|SNRPN\|SNORD115-11\|SNORD115-12\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-5\|SNORD115-9\|SNORD115-26\|SNORD115-22\|SNORD115-20\|SNORD115-39\|SNORD115-41\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-16\|SNORD115-40\|SNORD115-44\|SNORD115-34\|SNORD115-42\|SNORD115-6\|SNORD115-10\|SNORD115-14\|SNORD115-15\|SNORD115-21\|HBII-52-24\|SNORD115-7 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| HBII-52-24 snoRNA \| small nucleolar RNA, C/D box 115-7 | 338433 \| 6638 \| 100033448 \| 100033449 \| 100033803 \| 100033810 \| 100033817 \| 100033442 \| 100033446 \| 100033802 \| 100033799 \| 100033460 \| 100033813 \| 100033440 \| 100033815 \| 100033455 \| 100033456 \| 100033458 \| 100033450 \| 100033454 \| 100033814 \| 100033818 \| 100033808 \| 100033441 \| 100033816 \| 100033443 \| 100033447 \| 100033451 \| 100033453 \| 100033603 \| 100036563 \| 100033444 | 3.55 | up | 1.56E-05 |
| 8155849 | ANXA1 | annexin A1 | 301 | 3.54 | up | 9.79E-06 |
| 7946033 | HBB | hemoglobin, beta | 3043 | 3.53 | up | 0.0217883 |

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| 7982050 | SNRPN\|SNORD115-11\|SNORD115-12\|SNORD115-22\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-9\|SNORD115-26\|SNORD115-39\|SNORD115-41\|SNORD115-16\|SNORD115-44\|SNORD115-34\|SNORD115-6\|SNORD115-7 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-7 | 6638 \| 100033448 \| 100033449 \| 100033799 \| 100033803 \| 100033810 \| 100033817 \| 100033446 \| 100033802 \| 100033440 \| 100033813 \| 100033815 \| 100033454 \| 100033818 \| 100033808 \| 100033443 \| 100033444 | 3.52 | up | 1.42E-05 |
| 7982016 | SNORD115-1\|SNRPN\|SNORD115-12\|SNORD115-5\|SNORD115-9\|SNORD115-20\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-25\|SNORD115-40\|SNORD115-42\|SNORD115-10\|SNORD115-14\|SNORD115-15\|SNORD115-21\|HBII-52-24\|SNORD115-7 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-25 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| HBII-52-24 snoRNA \| small nucleolar RNA, C/D box 115-7 | 338433 \| 6638 \| 100033449 \| 100033442 \| 100033446 \| 100033460 \| 100033455 \| 100033456 \| 100033458 \| 100033450 \| 100033801 \| 100033814 \| 100033441 \| 100033816 \| 100033447 \| 100033451 \| 100033453 \| 100033603 \| 100036563 \| 100033444 | 3.51 | up | 1.21E-05 |

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| 7982024 | SNORD115-1\|SNRPN\|SNORD115-12\|SNORD115-5\|SNORD115-9\|SNORD115-11\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-22\|SNORD115-20\|SNORD115-39\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-16\|SNORD115-25\|SNORD115-40\|SNORD115-44\|SNORD115-34\|SNORD115-42\|SNORD115-6\|SNORD115-10\|SNORD115-14\|SNORD115-15\|SNORD115-21\|HBII-52-24 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-25 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| HBII-52-24 snoRNA | 338433 \| 6638 \| 100033449 \| 100033442 \| 100033446 \| 100033448 \| 100033803 \| 100033810 \| 100033817 \| 100033799 \| 100033460 \| 100033813 \| 100033455 \| 100033456 \| 100033458 \| 100033440 \| 100033450 \| 100033454 \| 100033801 \| 100033814 \| 100033818 \| 100033808 \| 100033441 \| 100033816 \| 100033443 \| 100033447 \| 100033451 \| 100033453 \| 100033603 \| 100036563 | 3.51 | up | 1.18E-05 |
| 7918936 | VTCN1 | V-set domain containing T cell activation inhibitor 1 | 79679 | 3.51 | up | 2.89E-08 |

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| 7982030 | SNORD115-1\|SNRPN\|SNORD115-12\|SNORD115-5\|SNORD115-9\|SNORD115-11\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-22\|SNORD115-20\|SNORD115-39\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-16\|SNORD115-25\|SNORD115-40\|SNORD115-44\|SNORD115-34\|SNORD115-42\|SNORD115-6\|SNORD115-10\|SNORD115-14\|SNORD115-15\|SNORD115-21\|HBII-52-24 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-25 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| HBII-52-24 snoRNA | 338433 \| 6638 \| 100033449 \| 100033442 \| 100033446 \| 100033448 \| 100033803 \| 100033810 \| 100033817 \| 100033799 \| 100033460 \| 100033813 \| 100033455 \| 100033456 \| 100033458 \| 100033440 \| 100033450 \| 100033454 \| 100033801 \| 100033814 \| 100033818 \| 100033808 \| 100033441 \| 100033816 \| 100033443 \| 100033447 \| 100033451 \| 100033453 \| 100033603 \| 100036563 | 3.51 | up | 1.20E-05 |
| 7975779 | FOS | v-fos FBJ murine osteosarcoma viral oncogene homolog | 2353 | 3.51 | up | 0.0076882 |
| 7988467 | FBN1 | fibrillin 1 | 2200 | 3.50 | up | 6.76E-07 |
| 7948420 | FABP5\|FABP5L7 | fatty acid binding protein 5 (psoriasis-associated) \| fatty acid binding protein 5-like 7 | 2171 \| 728641 | 3.49 | up | 2.79E-06 |
| 8162373 | OGN | osteoglycin | 4969 | 3.46 | up | 2.59E-07 |
| 7991762 | HBA1\|HBA2 | hemoglobin, alpha 1 \| hemoglobin, alpha 2 | 3039 \| 3040 | 3.42 | up | 0.0042486 |
| 7991766 | HBA1\|HBA2 | hemoglobin, alpha 1 \| hemoglobin, alpha 2 | 3039 \| 3040 | 3.42 | up | 0.004258 |
| 7908388 | RGS1 | regulator of G-protein signaling 1 | 5996 | 3.42 | up | 1.63E-06 |
| 8152719 | ANXA13 | annexin A13 | 312 | 3.41 | up | 3.64E-12 |

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|---|---|---|---|---|---|---|
| 7957023 | LYZ | lysozyme (renal amyloidosis) | 4069 | 3.41 | up | 9.74E-06 |
| 8147049 | FABP5\|FABP5L7 | fatty acid binding protein 5 (psoriasis-associated) \| fatty acid binding protein 5-like 7 | 2171 \| 728641 | 3.40 | up | 3.69E-06 |
| 8021685 | CCDC102B | coiled-coil domain containing 102B | 79839 | 3.39 | up | 2.74E-07 |
| 7970033 | COL4A2 | collagen, type IV, alpha 2 | 1284 | 3.38 | up | 2.50E-11 |
| 8042439 | ANTXR1 | anthrax toxin receptor 1 | 84168 | 3.36 | up | 1.25E-10 |
| 8112980 | EDIL3 | EGF-like repeats and discoidin I-like domains 3 | 10085 | 3.34 | up | 6.91E-11 |
| 8151816 | GEM | GTP binding protein overexpressed in skeletal muscle | 2669 | 3.34 | up | 4.91E-05 |
| 8095646 | AFP | alpha-fetoprotein | 174 | 3.33 | up | 1.85E-06 |
| 8053801 | ANKRD36B\|FLJ40330\|LOC400986 | ankyrin repeat domain 36B \| hypothetical LOC645784 \| protein immuno-reactive with anti-PTH polyclonal antibodies | 57730 \| 645784 \| 400986 | 3.33 | up | 1.57E-04 |
| 7908204 | HMCN1 | hemicentin 1 | 83872 | 3.27 | up | 4.00E-10 |
| 7957570 | PLXNC1 | plexin C1 | 10154 | 3.25 | up | 4.39E-06 |
| 8053797 | | | | 3.24 | up | 1.57E-04 |
| 8108217 | TGFBI | transforming growth factor, beta-induced, 68kDa | 7045 | 3.23 | up | 1.82E-07 |
| 8105267 | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | 3673 | 3.21 | up | 6.91E-11 |
| 8059376 | SERPINE2 | serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 | 5270 | 3.19 | up | 1.60E-06 |
| 7976816 | SNORD114-3 | small nucleolar RNA, C/D box 114-3 | 767579 | 3.18 | up | 2.64E-08 |
| 8175531 | CDR1 | cerebellar degeneration-related protein 1, 34kDa | 1038 | 3.17 | up | 1.28E-06 |
| 8055465 | CXCR4 | chemokine (C-X-C motif) receptor 4 | 7852 | 3.14 | up | 4.13E-05 |
| 7914580 | FNDC5 | fibronectin type III domain containing 5 | 252995 | 3.14 | up | 1.16E-10 |
| 8021376 | NEDD4L | neural precursor cell expressed, developmentally down-regulated 4-like | 23327 | 3.14 | up | 6.42E-07 |
| 7926368 | VIM | vimentin | 7431 | 3.13 | up | 1.75E-07 |
| 7992828 | IL32 | interleukin 32 | 9235 | 3.10 | up | 0.0011185 |
| 8148070 | COL14A1 | collagen, type XIV, alpha 1 | 7373 | 3.10 | up | 2.24E-05 |
| 8008151 | IGF2BP1 | insulin-like growth factor 2 mRNA binding protein 1 | 10642 | 3.09 | up | 2.00E-08 |
| 7976783 | DLK1 | delta-like 1 homolog (Drosophila) | 8788 | 3.09 | up | 1.37E-06 |
| 8083301 | TM4SF4 | transmembrane 4 L six family member 4 | 7104 | 3.08 | up | 4.26E-05 |
| 8089835 | FSTL1 | follistatin-like 1 | 11167 | 3.07 | up | 2.68E-05 |
| 8046861 | ITGAV | integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) | 3685 | 3.07 | up | 4.04E-06 |
| 7937772 | IGF2 | insulin-like growth factor 2 (somatomedin A) | 3481 | 3.05 | up | 1.37E-06 |

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|---|---|---|---|---|---|---|
| 8129573 | MOXD1 | monooxygenase, DBH-like 1 | 26002 | 3.03 | up | 6.13E-13 |
| 8014974 | TOP2A | topoisomerase (DNA) II alpha 170kDa | 7153 | 3.02 | up | 0.0064491 |
| 8115327 | SPARC | secreted protein, acidic, cysteine-rich (osteonectin) | 6678 | 3.01 | up | 1.61E-05 |
| 7996837 | CDH1 | cadherin 1, type 1, E-cadherin (epithelial) | 999 | 2.99 | up | 3.57E-04 |
| 8138466 | 7A5 | putative binding protein 7a5 | 346389 | 2.99 | up | 1.90E-13 |
| 8044212 | SULT1C2 | sulfotransferase family, cytosolic, 1C, member 2 | 6819 | 2.97 | up | 6.73E-07 |
| 8043697 | ANKRD36B\|FLJ40330\|LOC400986 | ankyrin repeat domain 36B \| hypothetical LOC645784 \| protein immuno-reactive with anti-PTH polyclonal antibodies | 57730 \|<br>645784 \|<br>400986 | 2.95 | up | 2.26E-04 |
| 8123388 | UNC93A | unc-93 homolog A (C. elegans) | 54346 | 2.94 | up | 8.73E-05 |
| 8084206 | B3GNT5 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 | 84002 | 2.91 | up | 1.45E-09 |
| 7957458 | NTS | neurotensin | 4922 | 2.91 | up | 7.84E-10 |
| 7981982 | SNRPN\|SNORD116-17\|SNORD116-19\|SNORD116-15\|SNORD116-16\|SNORD116-18\|SNORD116-21\|SNORD116-22\|SNORD116-14\|SNORD116-20 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-17 \| small nucleolar RNA, C/D box 116-19 \| small nucleolar RNA, C/D box 116-15 \| small nucleolar RNA, C/D box 116-16 \| small nucleolar RNA, C/D box 116-18 \| small nucleolar RNA, C/D box 116-21 \| small nucleolar RNA, C/D box 116-22 \| small nucleolar RNA, C/D box 116-14 \| small nucleolar RNA, C/D box 116-20 | 6638 \|<br>100033429 \|<br>727708 \|<br>100033427 \|<br>100033428 \|<br>100033430 \|<br>100033432 \|<br>100033433 \|<br>100033426 \|<br>100033431 | 2.90 | up | 5.44E-05 |
| 7981986 | SNRPN\|SNORD116-17\|SNORD116-19\|SNORD116-15\|SNORD116-16\|SNORD116-18\|SNORD116-21\|SNORD116-22\|SNORD116-14\|SNORD116-20 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-17 \| small nucleolar RNA, C/D box 116-19 \| small nucleolar RNA, C/D box 116-15 \| small nucleolar RNA, C/D box 116-16 \| small nucleolar RNA, C/D box 116-18 \| small nucleolar RNA, C/D box 116-21 \| small nucleolar RNA, C/D box 116-22 \| small nucleolar RNA, C/D box 116-14 \| small nucleolar RNA, C/D box 116-20 | 6638 \|<br>100033429 \|<br>727708 \|<br>100033427 \|<br>100033428 \|<br>100033430 \|<br>100033432 \|<br>100033433 \|<br>100033426 \|<br>100033431 | 2.90 | up | 5.53E-05 |
| 8054054 | ANKRD36B\|FLJ40330 | ankyrin repeat domain 36B \| hypothetical LOC645784 | 57730 \|<br>645784 | 2.89 | up | 9.25E-05 |
| 8135069 | SERPINE1 | serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 | 5054 | 2.88 | up | 0.0044532 |
| 8013341 | MFAP4 | microfibrillar-associated protein 4 | 4239 | 2.87 | up | 1.26E-05 |
| 7982597 | THBS1 | thrombospondin 1 | 7057 | 2.86 | up | 1.12E-04 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 7982090 | SNORD115-1\|SNRPN\|SNORD115-42\|SNORD115-6\|SNORD115-30\|SNORD115-34\|SNORD115-15\|SNORD115-21\|SNORD115-12\|SNORD115-13\|SNORD115-40\|SNORD115-5\|SNORD115-9\|SNORD115-10\|SNORD115-14\|HBII-52-24 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-30 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| HBII-52-24 snoRNA | 338433 \| 6638 \| 100033816 \| 100033443 \| 100033441 \| 100033804 \| 100033808 \| 100033453 \| 100033603 \| 100033449 \| 100033450 \| 100033814 \| 100033442 \| 100033446 \| 100033447 \| 100033451 \| 100036563 | 2.86 | up | 1.20E-05 |
| 8052355 | EFEMP1 | EGF-containing fibulin-like extracellular matrix protein 1 | 2202 | 2.85 | up | 1.12E-05 |
| 7982032 | SNORD115-1\|SNRPN\|SNORD115-13\|SNORD115-16\|SNORD115-11\|SNORD115-12\|SNORD115-29\|SNORD115-36\|SNORD115-39\|SNORD115-40\|SNORD115-43\|SNORD115-5\|SNORD115-9\|SNORD115-10\|SNORD115-14\|SNORD115-21\|SNORD115-42 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-21 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 | 338433 \| 6638 \| 100033450 \| 100033454 \| 100033448 \| 100033449 \| 100033803 \| 100033810 \| 100033813 \| 100033814 \| 100033817 \| 100033442 \| 100033446 \| 100033447 \| 100033451 \| 100033603 \| 100033441 \| 100033816 | 2.83 | up | 5.28E-06 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 7982018 | SNORD115-1\|SNRPN\|SNORD115-6\|SNORD115-42\|SNORD115-30\|SNORD115-34\|SNORD115-15\|SNORD115-21\|SNORD115-11\|SNORD115-16\|SNORD115-26\|SNORD115-29\|SNORD115-36\|SNORD115-39\|SNORD115-41\|SNORD115-43\|SNORD115-14\|HBII-52-24 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-30 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-14 \| HBII-52-24 snoRNA | 338433 \| 6638 \| 100033443 \| 100033816 \| 100033441 \| 100033804 \| 100033808 \| 100033453 \| 100033603 \| 100033448 \| 100033454 \| 100033802 \| 100033803 \| 100033810 \| 100033813 \| 100033815 \| 100033817 \| 100033451 \| 100036563 | 2.82 | up | 1.00E-05 |
| 7982038 | SNORD115-1\|SNRPN\|SNORD115-13\|SNORD115-16\|SNORD115-11\|SNORD115-12\|SNORD115-26\|SNORD115-29\|SNORD115-36\|SNORD115-39\|SNORD115-40\|SNORD115-41\|SNORD115-43\|SNORD115-9\|SNORD115-21\|SNORD115-34\|SNORD115-6 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-21 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-6 | 338433 \| 6638 \| 100033450 \| 100033454 \| 100033448 \| 100033449 \| 100033802 \| 100033803 \| 100033810 \| 100033813 \| 100033814 \| 100033815 \| 100033817 \| 100033446 \| 100033603 \| 100033808 \| 100033443 | 2.82 | up | 5.38E-06 |
| 7982008 | SNORD115-1\|SNRPN\|SNORD115-13\|SNORD115-16\|SNORD115-26\|SNORD115-41\|SNORD115-5 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-5 | 338433 \| 6638 \| 100033450 \| 100033454 \| 100033802 \| 100033815 \| 100033442 | 2.82 | up | 5.07E-06 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 7926545 | PLXDC2 | plexin domain containing 2 | 84898 | 2.82 | up | 3.93E-08 |
| 7908917 | BTG2 | BTG family, member 2 | 7832 | 2.81 | up | 0.0304549 |
| 8000480 | | | | 2.79 | up | 1.67E-07 |
| 7981943 | PAR5\|SNRPN\|SNORD64\|PAR-SN | Prader-Willi/Angelman syndrome-5 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 64 \| paternally expressed transcript PAR-SN | 8123 \| 6638 \| 347686 \| 347746 | 2.79 | up | 1.74E-06 |
| 8030866 | FPR3 | formyl peptide receptor 3 | 2359 | 2.78 | up | 3.54E-06 |
| 7909789 | TGFB2 | transforming growth factor, beta 2 | 7042 | 2.78 | up | 9.65E-08 |
| 7938348 | WEE1 | | 7465 | 2.78 | up | 9.66E-06 |
| 7902074 | LEPR\|LEPROT | leptin receptor \| leptin receptor overlapping transcript | 3953 \| 54741 | 2.76 | up | 2.68E-05 |
| 8099850 | TMEM156 | transmembrane protein 156 | 80008 | 2.76 | up | 7.41E-09 |
| 8081081 | EPHA3 | EPH receptor A3 | 2042 | 2.75 | up | 2.19E-06 |
| 7957861 | TMEM16D | transmembrane protein 16D | 121601 | 2.74 | up | 7.03E-14 |
| 7952268 | THY1 | Thy-1 cell surface antigen | 7070 | 2.73 | up | 1.20E-15 |
| 7981976 | SNRPN\|SNORD116-14 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-14 | 6638 \| 100033426 | 2.71 | up | 5.44E-05 |
| 8161945 | RASEF | RAS and EF-hand domain containing | 158158 | 2.71 | up | 1.82E-09 |
| 7918323 | SORT1 | sortilin 1 | 6272 | 2.71 | up | 0.0035538 |
| 8068383 | CLIC6 | chloride intracellular channel 6 | 54102 | 2.69 | up | 2.35E-09 |
| 8113504 | C5orf13 | chromosome 5 open reading frame 13 | 9315 | 2.69 | up | 9.69E-04 |
| 7981996 | SNRPN\|SNORD116-24 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-24 | 6638 \| 100033435 | 2.69 | up | 1.61E-04 |
| 8008885 | MIRN21 | microRNA 21 | 406991 | 2.66 | up | 0.0010457 |
| 7981988 | SNRPN\|SNORD116-20\|SNORD116@ | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-20 \| small nucleolar RNA, C/D box 116 cluster | 6638 \| 100033431 \| 692236 | 2.66 | up | 3.41E-04 |
| 8169836 | XPNPEP2 | X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound | 7512 | 2.64 | up | 0.0141963 |
| 8099326 | SLC2A9 | solute carrier family 2 (facilitated glucose transporter), member 9 | 56606 | 2.63 | up | 1.43E-07 |
| 7903507 | FAM102B | family with sequence similarity 102, member B | 284611 | 2.63 | up | 1.22E-10 |
| 8115099 | PDGFRB | platelet-derived growth factor receptor, beta polypeptide | 5159 | 2.63 | up | 5.24E-06 |
| 7982098 | SNRPN\|SNORD109A\|SNORD109B | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 109A \| small nucleolar RNA, C/D box 109B | 6638 \| 338428 \| 338429 | 2.63 | up | 9.09E-06 |
| 7981947 | SNRPN\|SNORD109A\|SNORD109B | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 109A \| small nucleolar RNA, C/D box 109B | 6638 \| 338428 \| 338429 | 2.63 | up | 8.76E-06 |
| 8088919 | ROBO1 | roundabout, axon guidance receptor, homolog 1 (Drosophila) | 6091 | 2.62 | up | 1.56E-07 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 7934936 | SLC16A12 | solute carrier family 16, member 12 (monocarboxylic acid transporter 12) | 387700 | 2.62 | up | 1.94E-06 |
| 7927998 | HKDC1 | hexokinase domain containing 1 | 80201 | 2.61 | up | 0.0129315 |
| 8006433 | CCL2 | chemokine (C-C motif) ligand 2 | 6347 | 2.61 | up | 2.66E-04 |
| 8101757 | GPRIN3 | GPRIN family member 3 | 285513 | 2.61 | up | 0.0054822 |
| 7981978 | SNRPN\|SNORD116-15 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-15 | 6638 \| 100033427 | 2.60 | up | 6.52E-04 |
| 8091411 | TM4SF1 | transmembrane 4 L six family member 1 | 4071 | 2.60 | up | 2.00E-05 |
| 8157216 | UGCG | UDP-glucose ceramide glucosyltransferase | 7357 | 2.60 | up | 1.03E-04 |
| 7982046 | SNRPN\|SNORD115-25\|SNORD115-20\|SNORD115-12\|SNORD115-5\|SNORD115-9\|SNORD115-11\|SNORD115-22\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-39\|SNORD115-10\|SNORD115-14\|SNORD115-15\|SNORD115-21 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-25 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 | 6638 \| 100033801 \| 100033460 \| 100033449 \| 100033442 \| 100033446 \| 100033448 \| 100033799 \| 100033803 \| 100033810 \| 100033817 \| 100033455 \| 100033456 \| 100033458 \| 100033440 \| 100033813 \| 100033447 \| 100033451 \| 100033453 \| 100033603 | 2.59 | up | 1.33E-06 |
| 8149448 | MSR1 | macrophage scavenger receptor 1 | 4481 | 2.58 | up | 2.84E-05 |
| 8114263 | LECT2 | leukocyte cell-derived chemotaxin 2 | 3950 | 2.58 | up | 0.0013685 |
| 7963946 | MMP19 | matrix metallopeptidase 19 | 4327 | 2.58 | up | 7.45E-08 |
| 8097692 | EDNRA | endothelin receptor type A | 1909 | 2.56 | up | 2.70E-06 |
| 7913869 | STMN1 | stathmin 1/oncoprotein 18 | 3925 | 2.55 | up | 0.0019989 |
| 7908072 | LAMC2 | laminin, gamma 2 | 3918 | 2.55 | up | 4.30E-11 |
| 7999909 | GPRC5B | G protein-coupled receptor, family C, group 5, member B | 51704 | 2.54 | up | 5.50E-08 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 8095744 | AREG\|LOC727738 | amphiregulin (schwannoma-derived growth factor) \| similar to Amphiregulin precursor (AR) (Colorectum cell-derived growth factor) (CRDGF) | 374 \| 727738 | 2.53 | up | 3.67E-06 |
| 8171297 | MID1 | midline 1 (Opitz/BBB syndrome) | 4281 | 2.53 | up | 1.83E-07 |
| 8178193 | HLA-DRA | major histocompatibility complex, class II, DR alpha | 3122 | 2.52 | up | 0.0018063 |
| 8019842 | TYMS | thymidylate synthetase | 7298 | 2.52 | up | 0.0313901 |
| 8046380 | ITGA6 | integrin, alpha 6 | 3655 | 2.52 | up | 8.39E-05 |
| 8147030 | STMN2 | stathmin-like 2 | 11075 | 2.52 | up | 3.97E-12 |
| 7903144 | SLC44A3 | solute carrier family 44, member 3 | 126969 | 2.51 | up | 3.10E-05 |
| 8094301 | SLIT2 | slit homolog 2 (Drosophila) | 9353 | 2.50 | up | 1.45E-09 |
| 7995681 | MMP2 | matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) | 4313 | 2.50 | up | 1.90E-12 |
| 8122265 | TNFAIP3 | tumor necrosis factor, alpha-induced protein 3 | 7128 | 2.50 | up | 3.82E-05 |
| 8118548 | HLA-DRA | major histocompatibility complex, class II, DR alpha | 3122 | 2.50 | up | 0.0015005 |
| 8179481 | HLA-DRA | major histocompatibility complex, class II, DR alpha | 3122 | 2.49 | up | 0.0019278 |
| 8095688 | CXCL6 | chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2) | 6372 | 2.48 | up | 1.83E-07 |
| 8022666 | CHST9 | carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 | 83539 | 2.48 | up | 3.78E-05 |
| 7951077 | SESN3 | sestrin 3 | 143686 | 2.47 | up | 0.0010338 |
| 8001800 | CDH11 | cadherin 11, type 2, OB-cadherin (osteoblast) | 1009 | 2.46 | up | 3.39E-07 |
| 8138824 | SCRN1 | secernin 1 | 9805 | 2.45 | up | 4.07E-07 |
| 7981964 | SNRPN\|SNORD116-8\|SNORD116-3\|SNORD116-9 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-8 \| small nucleolar RNA, C/D box 116-3 \| small nucleolar RNA, C/D box 116-9 | 6638 \| 100033420 \| 100033415 \| 100033421 | 2.44 | up | 0.0046185 |
| 8064978 | JAG1 | jagged 1 (Alagille syndrome) | 182 | 2.44 | up | 3.04E-07 |
| 8145134 | | | | 2.44 | up | 1.47E-05 |
| 8037387 | | | | 2.44 | up | 0.0034721 |
| 7955613 | KRT7 | keratin 7 | 3855 | 2.43 | up | 1.47E-09 |
| 8057394 | SESTD1 | SEC14 and spectrin domains 1 | 91404 | 2.41 | up | 3.65E-09 |
| 8131666 | ITGB8 | integrin, beta 8 | 3696 | 2.40 | up | 5.08E-10 |
| 8105828 | CCNB1 | cyclin B1 | 891 | 2.39 | up | 0.0010547 |
| 7973101 | RNASE6 | ribonuclease, RNase A family, k6 | 6039 | 2.37 | up | 4.32E-11 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 7982056 | SNRPN\|SNORD115-25 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-25 | 6638 \| 100033801 | 2.36 | up | 1.16E-04 |
| 7968800 | DGKH | diacylglycerol kinase, eta | 160851 | 2.36 | up | 1.51E-06 |
| 7981919 | SNRPN\|SNURF | small nuclear ribonucleoprotein polypeptide N \| SNRPN upstream reading frame | 6638 \| 8926 | 2.35 | up | 1.79E-09 |
| 8126839 | TNFRSF21 | tumor necrosis factor receptor superfamily, member 21 | 27242 | 2.35 | up | 1.25E-08 |
| 8146000 | ADAM9 | ADAM metallopeptidase domain 9 (meltrin gamma) | 8754 | 2.34 | up | 7.36E-04 |
| 8138566 | IGF2BP3 | insulin-like growth factor 2 mRNA binding protein 3 | 10643 | 2.34 | up | 6.42E-07 |
| 7916609 | JUN | jun oncogene | 3725 | 2.34 | up | 0.0031225 |
| 8053834 | ANKRD36B | ankyrin repeat domain 36B \| ankyrin repeat domain 36 | 57730 \| 375248 | 2.34 | up | 1.02E-04 |
| 7973336 | MMP14 | matrix metallopeptidase 14 (membrane-inserted) | 4323 | 2.33 | up | 7.51E-10 |
| 7959893 | GPR133 | G protein-coupled receptor 133 | 283383 | 2.33 | up | 1.90E-05 |
| 8047097 | GLS | glutaminase | 2744 | 2.33 | up | 3.51E-07 |
| 7981960 | SNRPN\|SNORD116-6 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-6 | 6638 \| 100033418 | 2.33 | up | 5.53E-05 |
| 8015349 | KRT19 | keratin 19 | 3880 | 2.32 | up | 1.65E-07 |
| 8120279 | LRRC1 | leucine rich repeat containing 1 | 55227 | 2.32 | up | 3.90E-06 |
| 8117594 | HIST1H2BM | histone cluster 1, H2bm | 8342 | 2.32 | up | 0.0096238 |
| 8053417 | CAPG | capping protein (actin filament), gelsolin-like | 822 | 2.32 | up | 9.38E-09 |
| 7989335 | ANXA2 | annexin A2 | 302 | 2.32 | up | 3.45E-04 |
| 8140709 | KIAA1324L | KIAA1324-like | 222223 | 2.31 | up | 1.74E-07 |
| 8144726 | TUSC3 | tumor suppressor candidate 3 | 7991 | 2.30 | up | 1.52E-05 |
| 8113073 | ARRDC3 | arrestin domain containing 3 | 57561 | 2.30 | up | 0.0062773 |
| 8023528 | ALPK2 | alpha-kinase 2 | 115701 | 2.30 | up | 1.32E-05 |
| 8123936 | NEDD9 | neural precursor cell expressed, developmentally down-regulated 9 | 4739 | 2.29 | up | 4.23E-05 |
| 8056222 | DPP4 | dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2) | 1803 | 2.28 | up | 0.0363338 |
| 8104022 | PDLIM3 | PDZ and LIM domain 3 | 27295 | 2.28 | up | 8.31E-08 |
| 8168589 | ZNF711 | zinc finger protein 711 | 7552 | 2.28 | up | 1.99E-05 |
| 7903358 | VCAM1 | vascular cell adhesion molecule 1 | 7412 | 2.28 | up | 0.0019205 |

<table>
<tr><td>8180022</td><td>HLA-DQB1|LOC100133484|LOC100133583|LOC100133661|LOC100133811|HLA-DQB2|HLA-DRB1|HLA-DRB2|HLA-DRB3|HLA-DRB4|HLA-DRB5|ZNF749|RNASE2|LOC730415|hCG_1998957</td><td>major histocompatibility complex, class II, DQ beta 1 | similar to Major histocompatibility complex, class II, DR beta 4 | similar to major histocompatibility complex, class II, DQ beta 1 | similar to HLA class II histocompatibility antigen, DR-W53 beta chain | similar to hCG1992647 | major histocompatibility complex, class II, DQ beta 2 | major histocompatibility complex, class II, DR beta 1 | major histocompatibility complex, class II, DR beta 2 (pseudogene) | major histocompatibility complex, class II, DR beta 3 | major histocompatibility complex, class II, DR beta 4 | major histocompatibility complex, class II, DR beta 5 | zinc finger protein 749 | ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) | hypothetical protein LOC730415</td><td>3119 | 100133484 | 100133583 | 100133661 | 100133811 | 3120 | 3123 | 3124 | 3125 | 3126 | 3127 | 388567 | 6036 | 730415 | 731247</td><td>2.27</td><td>up</td><td>6.46E-04</td></tr>
<tr><td>8178826</td><td>HLA-DQB1|LOC100133484|LOC100133583|LOC100133661|LOC100133811|HLA-DQB2|HLA-DRB1|HLA-DRB2|HLA-DRB3|HLA-DRB4|HLA-DRB5|ZNF749|RNASE2|LOC730415|hCG_1998957</td><td>major histocompatibility complex, class II, DQ beta 1 | similar to Major histocompatibility complex, class II, DR beta 4 | similar to major histocompatibility complex, class II, DQ beta 1 | similar to HLA class II histocompatibility antigen, DR-W53 beta chain | similar to hCG1992647 | major histocompatibility complex, class II, DQ beta 2 | major histocompatibility complex, class II, DR beta 1 | major histocompatibility complex, class II, DR beta 2 (pseudogene) | major histocompatibility complex, class II, DR beta 3 | major histocompatibility complex, class II, DR beta 4 | major histocompatibility complex, class II, DR beta 5 | zinc finger protein 749 | ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) | hypothetical protein LOC730415</td><td>3119 | 100133484 | 100133583 | 100133661 | 100133811 | 3120 | 3123 | 3124 | 3125 | 3126 | 3127 | 388567 | 6036 | 730415 | 731247</td><td>2.27</td><td>up</td><td>6.72E-04</td></tr>
<tr><td>8104758</td><td>C5orf23</td><td>chromosome 5 open reading frame 23</td><td>79614</td><td>2.27</td><td>up</td><td>1.92E-05</td></tr>
<tr><td>7927732</td><td>ARID5B</td><td>AT rich interactive domain 5B (MRF1-like)</td><td>84159</td><td>2.27</td><td>up</td><td>5.48E-05</td></tr>
<tr><td>7980891</td><td>TC2N</td><td>tandem C2 domains, nuclear</td><td>123036</td><td>2.27</td><td>up</td><td>3.03E-04</td></tr>
<tr><td>7924526</td><td>TP53BP2</td><td>tumor protein p53 binding protein, 2</td><td>7159</td><td>2.26</td><td>up</td><td>1.85E-05</td></tr>
<tr><td>7976850</td><td></td><td></td><td></td><td>2.25</td><td>up</td><td>8.53E-06</td></tr>
<tr><td>8117054</td><td>CAP2</td><td>CAP, adenylate cyclase-associated protein, 2 (yeast)</td><td>10486</td><td>2.25</td><td>up</td><td>2.08E-04</td></tr>
<tr><td>8043100</td><td>TMSB10</td><td>thymosin beta 10</td><td>9168</td><td>2.25</td><td>up</td><td>3.22E-05</td></tr>
<tr><td>8168749</td><td>SRPX2</td><td>sushi-repeat-containing protein, X-linked 2</td><td>27286</td><td>2.25</td><td>up</td><td>1.12E-05</td></tr>
<tr><td>8149551</td><td>PSD3</td><td>pleckstrin and Sec7 domain containing 3</td><td>23362</td><td>2.25</td><td>up</td><td>6.24E-05</td></tr>
<tr><td>7981945</td><td></td><td></td><td></td><td>2.25</td><td>up</td><td>1.50E-07</td></tr>
<tr><td>7986512</td><td></td><td></td><td></td><td>2.24</td><td>up</td><td>1.50E-06</td></tr>
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|---|---|---|---|---|---|---|
| 7986527 | C15orf51 | chromosome 15 open reading frame 51 | 196968 | 2.24 | up | 1.44E-06 |
| 7986509 | LOC441734 | similar to hypothetical protein DKFZp434I1020 | 441734 | 2.24 | up | 1.50E-06 |
| 7984079 | TPM1 | tropomyosin 1 (alpha) | 7168 | 2.24 | up | 2.58E-04 |
| 8092177 | AADACL1 | arylacetamide deacetylase-like 1 | 57552 | 2.23 | up | 1.06E-07 |
| 7981966 | SNRPN\|SNORD116-3\|SNORD116-9\|SNORD116-5\|SNORD116-7\|SNORD116-8 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-3 \| small nucleolar RNA, C/D box 116-9 \| small nucleolar RNA, C/D box 116-5 \| small nucleolar RNA, C/D box 116-7 \| small nucleolar RNA, C/D box 116-8 | 6638 \| 100033415 \| 100033421 \| 100033417 \| 100033419 \| 100033420 | 2.23 | up | 0.0149408 |
| 8041383 | LTBP1 | latent transforming growth factor beta binding protein 1 | 4052 | 2.23 | up | 4.51E-07 |
| 7981953 | SNRPN\|SNORD116-3\|SNORD116-9\|SNORD116-5\|SNORD116-7\|SNORD116-8 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-3 \| small nucleolar RNA, C/D box 116-9 \| small nucleolar RNA, C/D box 116-5 \| small nucleolar RNA, C/D box 116-7 \| small nucleolar RNA, C/D box 116-8 | 6638 \| 100033415 \| 100033421 \| 100033417 \| 100033419 \| 100033420 | 2.23 | up | 0.0149527 |
| 7958262 | TCP11L2 | t-complex 11 (mouse)-like 2 | 255394 | 2.23 | up | 1.34E-04 |
| 7908041 | LAMC1 | laminin, gamma 1 (formerly LAMB2) | 3915 | 2.22 | up | 1.14E-06 |
| 7965541 | FGD6 | FYVE, RhoGEF and PH domain containing 6 | 55785 | 2.22 | up | 6.38E-15 |
| 7960865 | SLC2A3 | solute carrier family 2 (facilitated glucose transporter), member 3 | 6515 | 2.22 | up | 2.84E-05 |
| 8112803 | LHFPL2 | lipoma HMGIC fusion partner-like 2 | 10184 | 2.22 | up | 8.18E-06 |
| 7972557 | EBI2 | Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) | 1880 | 2.22 | up | 1.35E-05 |
| 7933877 | JMJD1C | jumonji domain containing 1C | 221037 | 2.22 | up | 1.66E-04 |
| 7936734 | FGFR2 | fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) | 2263 | 2.21 | up | 2.03E-05 |
| 8125530 | HLA-DMB | major histocompatibility complex, class II, DM beta | 3109 | 2.21 | up | 5.58E-04 |
| 7929047 | IFIT2 | interferon-induced protein with tetratricopeptide repeats 2 | 3433 | 2.21 | up | 1.55E-04 |
| 7951351 | PDGFD | platelet derived growth factor D | 80310 | 2.21 | up | 1.45E-07 |
| 8104746 | NPR3 | natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C) | 4883 | 2.20 | up | 2.06E-06 |
| 8147019 | C8orf70 | chromosome 8 open reading frame 70 | 51101 | 2.19 | up | 2.33E-09 |
| 7925525 | CEP170 | centrosomal protein 170kDa | 9859 | 2.19 | up | 3.31E-04 |
| 8026490 | UCA1 | urothelial cancer associated 1 | 652995 | 2.18 | up | 7.38E-07 |

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|---|---|---|---|---|---|---|
| 8056545 | STK39 | serine threonine kinase 39 (STE20/SPS1 homolog, yeast) | 27347 | 2.18 | up | 6.11E-05 |
| 8117018 | | | | 2.17 | up | 0.045068 |
| 8057744 | STAT1 | signal transducer and activator of transcription 1, 91kDa | 6772 | 2.17 | up | 4.55E-04 |
| 8180078 | HLA-DMB | major histocompatibility complex, class II, DM beta | 3109 | 2.17 | up | 5.12E-04 |
| 7958253 | OCC-1 | overexpressed in colon carcinoma-1 | 387882 | 2.17 | up | 2.44E-07 |
| 8146788 | | | | 2.16 | up | 5.52E-05 |
| 8012896 | PMP22 | peripheral myelin protein 22 | 5376 | 2.16 | up | 8.64E-05 |
| 8053025 | NAT8 | N-acetyltransferase 8 | 9027 | 2.16 | up | 0.005342 |
| 8083166 | TRPC1 | transient receptor potential cation channel, subfamily C, member 1 | 7220 | 2.16 | up | 3.14E-10 |
| 8018966 | TIMP2 | TIMP metallopeptidase inhibitor 2 | 7077 | 2.16 | up | 6.92E-07 |
| 8096116 | AGPAT9 | 1-acylglycerol-3-phosphate O-acyltransferase 9 | 84803 | 2.16 | up | 0.0021156 |
| 7989501 | CA12 | carbonic anhydrase XII | 771 | 2.16 | up | 3.31E-06 |
| 7963054 | TUBA1A | tubulin, alpha 1a | 7846 | 2.15 | up | 3.03E-04 |
| 8180100 | HLA-DPA1 | major histocompatibility complex, class II, DP alpha 1 | 3113 | 2.15 | up | 0.0071934 |
| 7995128 | ITGAX | integrin, alpha X (complement component 3 receptor 4 subunit) | 3687 | 2.15 | up | 6.16E-05 |
| 7909708 | CENPF | centromere protein F, 350/400ka (mitosin) | 1063 | 2.15 | up | 1.75E-05 |
| 7919349 | RNU1A\|RNU1A3\|RNU1C1\|RNU1C2\|RNU1D2\|RNU1F1\|RNU1G3\|ATG9B | RNA, U1A small nuclear \| RNA, U1A3 small nuclear \| RNA, U1C1 small nuclear \| RNA, U1C2 small nuclear \| RNA, U1D2 small nuclear \| RNA, U1F1 small nuclear \| RNA, U1G3 small nuclear \| ATG9 autophagy related 9 homolog B (S. cerevisiae) | 6060 \| 26871 \| 26870 \| 26869 \| 26868 \| 26866 \| 26863 \| 285973 | 2.14 | up | 0.0103011 |
| 7919269 | RNU1A\|RNU1A3\|RNU1C1\|RNU1C2\|RNU1D2\|RNU1F1\|RNU1G3\|ATG9B | RNA, U1A small nuclear \| RNA, U1A3 small nuclear \| RNA, U1C1 small nuclear \| RNA, U1C2 small nuclear \| RNA, U1D2 small nuclear \| RNA, U1F1 small nuclear \| RNA, U1G3 small nuclear \| ATG9 autophagy related 9 homolog B (S. cerevisiae) | 6060 \| 26871 \| 26870 \| 26869 \| 26868 \| 26866 \| 26863 \| 285973 | 2.14 | up | 0.0103137 |
| 8128991 | LAMA4 | laminin, alpha 4 | 3910 | 2.14 | up | 8.01E-07 |
| 8007429 | G6PC | glucose-6-phosphatase, catalytic subunit | 2538 | 2.14 | up | 0.0235771 |
| 7980908 | FBLN5 | fibulin 5 | 10516 | 2.14 | up | 0.006287 |
| 8121949 | LAMA2 | laminin, alpha 2 (merosin, congenital muscular dystrophy) | 3908 | 2.13 | up | 1.05E-05 |
| 8094278 | NCAPG | non-SMC condensin I complex, subunit G | 64151 | 2.13 | up | 0.0251385 |
| 8113790 | 3-Mar | membrane-associated ring finger (C3HC4) 3 | 115123 | 2.13 | up | 8.90E-05 |
| 8125556 | HLA-DPA1 | major histocompatibility complex, class II, DP alpha 1 | 3113 | 2.13 | up | 0.0047546 |
| 8178891 | HLA-DPA1 | major histocompatibility complex, class II, DP alpha 1 | 3113 | 2.13 | up | 0.0048425 |
| 7965410 | DCN | decorin | 1634 | 2.13 | up | 0.0031465 |

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|---|---|---|---|---|---|---|
| 8129562 | CTGF | connective tissue growth factor | 1490 | 2.12 | up | 2.65E-04 |
| 8084929 | OSTalpha | organic solute transporter alpha | 200931 | 2.12 | up | 1.33E-04 |
| 7976818 | SNORD114-6 | small nucleolar RNA, C/D box 114-6 | 767582 | 2.12 | up | 1.48E-07 |
| 8020779 | DSG2 | desmoglein 2 | 1829 | 2.12 | up | 1.59E-04 |
| 8142194 | LAMB1 | laminin, beta 1 | 3912 | 2.12 | up | 0.0017519 |
| 8077499 | LOH3CR2A | loss of heterozygosity, 3, chromosomal region 2, gene A | 29931 | 2.12 | up | 3.22E-09 |
| 7982004 | SNRPN\|SNORD116-28 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-28 | 6638 \| 100033820 | 2.12 | up | 1.57E-10 |
| 7929065 | IFIT1 | interferon-induced protein with tetratricopeptide repeats 1 | 3434 | 2.12 | up | 0.0132655 |
| 8123104 | FNDC1 | fibronectin type III domain containing 1 | 84624 | 2.12 | up | 2.81E-11 |
| 8022310 | C18orf58 | chromosome 18 open reading frame 58 | 284222 | 2.11 | up | 1.33E-06 |
| 8039607 | PEG3\|ZIM2 | paternally expressed 3 \| zinc finger, imprinted 2 | 5178 \| 23619 | 2.11 | up | 3.35E-10 |
| 8031047 | MYADM | myeloid-associated differentiation marker | 91663 | 2.11 | up | 5.30E-05 |
| 8146863 | SULF1 | sulfatase 1 | 23213 | 2.11 | up | 6.97E-06 |
| 7953878 | CLEC2D | C-type lectin domain family 2, member D | 29121 | 2.11 | up | 2.64E-05 |
| 7931810 | KLF6 | Kruppel-like factor 6 | 1316 | 2.11 | up | 0.0045004 |
| 8158317 | SPTAN1 | spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) | 6709 | 2.10 | up | 2.06E-07 |
| 8162117 | GOLM1 | golgi membrane protein 1 | 51280 | 2.10 | up | 0.0032997 |
| 8123920 | ELOVL2 | elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 | 54898 | 2.10 | up | 9.65E-05 |
| 7981958 | SNRPN\|SNORD116-5\|SNORD116-7\|SNORD116-3\|SNORD116-9 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-5 \| small nucleolar RNA, C/D box 116-7 \| small nucleolar RNA, C/D box 116-3 \| small nucleolar RNA, C/D box 116-9 | 6638 \| 100033417 \| 100033419 \| 100033415 \| 100033421 | 2.10 | up | 0.0149044 |
| 7923086 | ASPM | asp (abnormal spindle) homolog, microcephaly associated (Drosophila) | 259266 | 2.10 | up | 0.0019181 |
| 7963567 | KRT8 | keratin 8 | 3856 | 2.10 | up | 1.27E-04 |
| 7981962 | SNRPN\|SNORD116-5\|SNORD116-7\|SNORD116-3\|SNORD116-9 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-5 \| small nucleolar RNA, C/D box 116-7 \| small nucleolar RNA, C/D box 116-3 \| small nucleolar RNA, C/D box 116-9 | 6638 \| 100033417 \| 100033419 \| 100033415 \| 100033421 | 2.10 | up | 0.0148883 |
| 7935058 | FER1L3 | fer-1-like 3, myoferlin (C. elegans) | 26509 | 2.10 | up | 2.84E-05 |
| 8054846 | SCTR | secretin receptor | 6344 | 2.10 | up | 1.38E-06 |

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|---|---|---|---|---|---|---|
| 7926037 | PFKFB3 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 | 5209 | 2.09 | up | 1.60E-06 |
| 8121563 | MARCKS | myristoylated alanine-rich protein kinase C substrate | 4082 | 2.09 | up | 1.74E-06 |
| 8124166 | MBOAT1 | membrane bound O-acyltransferase domain containing 1 | 154141 | 2.09 | up | 4.66E-04 |
| 8095736 | AREG\|LOC727738 | amphiregulin (schwannoma-derived growth factor) \| similar to Amphiregulin precursor (AR) (Colorectum cell-derived growth factor) (CRDGF) | 374 \| 727738 | 2.09 | up | 3.69E-06 |
| 7986520 | | | | 2.09 | up | 1.80E-05 |
| 8149555 | PSD3 | pleckstrin and Sec7 domain containing 3 | 23362 | 2.09 | up | 1.02E-05 |
| 7902127 | SGIP1 | SH3-domain GRB2-like (endophilin) interacting protein 1 | 84251 | 2.09 | up | 3.29E-08 |
| 7901293 | CYP4A22 | cytochrome P450, family 4, subfamily A, polypeptide 22 | 284541 | 2.08 | up | 1.15E-04 |
| 8027002 | GDF15 | growth differentiation factor 15 | 9518 | 2.08 | up | 0.0090521 |
| 8099721 | KIAA0746\|SERINC2 | KIAA0746 protein \| serine incorporator 2 | 23231 \| 347735 | 2.08 | up | 5.65E-06 |
| 8116992 | UNQ9364 | FLFF9364 | 100130515 | 2.08 | up | 4.98E-08 |
| 8022283 | FAM38B | family with sequence similarity 38, member B | 63895 | 2.08 | up | 6.62E-07 |
| 7981949 | SNRPN\|SNORD116-1 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-1 | 6638 \| 100033413 | 2.07 | up | 0.0094026 |
| 8172270 | | | | 2.07 | up | 1.20E-05 |
| 8175121 | IGSF1 | immunoglobulin superfamily, member 1 | 3547 | 2.07 | up | 1.17E-10 |
| 8060963 | SNAP25 | synaptosomal-associated protein, 25kDa | 6616 | 2.06 | up | 9.65E-06 |
| 8006906 | ERBB2 | v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) | 2064 | 2.06 | up | 3.95E-07 |
| 7997642 | CRISPLD2 | cysteine-rich secretory protein LCCL domain containing 2 | 83716 | 2.06 | up | 9.66E-06 |
| 8054064 | ANKRD36B | ankyrin repeat domain 36B | 57730 | 2.05 | up | 0.0059245 |
| 8096704 | NPNT | nephronectin | 255743 | 2.05 | up | 5.09E-08 |
| 8152041 | RNF19A | ring finger protein 19A | 25897 | 2.05 | up | 9.43E-06 |
| 8170648 | BGN | biglycan | 633 | 2.05 | up | 2.57E-04 |
| 8140463 | FGL2 | fibrinogen-like 2 | 10875 | 2.05 | up | 5.75E-06 |
| 7986517 | | | | 2.05 | up | 2.07E-04 |
| 7986522 | | | | 2.05 | up | 2.06E-04 |
| 8114920 | DPYSL3 | dihydropyrimidinase-like 3 | 1809 | 2.04 | up | 1.58E-11 |
| 7968789 | C13orf15 | chromosome 13 open reading frame 15 | 28984 | 2.04 | up | 2.38E-05 |
| 8083282 | HPS3 | Hermansky-Pudlak syndrome 3 | 84343 | 2.04 | up | 5.97E-06 |
| 8150509 | PLAT | plasminogen activator, tissue | 5327 | 2.04 | up | 2.59E-09 |

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|---|---|---|---|---|---|---|
| 8007919 | LRRC37A2\|LRRC37A4 | leucine rich repeat containing 37, member A2 \| leucine rich repeat containing 37A \| leucine rich repeat containing 37, member A4 (pseudogene) | 474170 \| 9884 \| 55073 | 2.04 | up | 2.98E-05 |
| 8043363 | C2orf59\|LOC541471 | chromosome 2 open reading frame 59 \| hypothetical LOC541471 | 112597 \| 541471 | 2.03 | up | 4.34E-05 |
| 8092552 | IGF2BP2 | insulin-like growth factor 2 mRNA binding protein 2 | 10644 | 2.03 | up | 5.23E-11 |
| 7916584 | TACSTD2 | tumor-associated calcium signal transducer 2 | 4070 | 2.02 | up | 3.03E-07 |
| 8067040 | NFATC2 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 | 4773 | 2.02 | up | 1.19E-04 |
| 8014115 | MYO1D | myosin ID | 4642 | 2.02 | up | 4.51E-04 |
| 8092021 | LRRC31 | leucine rich repeat containing 31 | 79782 | 2.01 | up | 6.84E-06 |
| 7961142 | OLR1 | oxidized low density lipoprotein (lectin-like) receptor 1 | 4973 | 2.01 | up | 8.82E-11 |
| 8016245 | LRRC37A4\|LRRC37A3\|LOC652203\|LRRC37A2 | leucine rich repeat containing 37, member A4 (pseudogene) \| leucine rich repeat containing 37, member A3 \| hypothetical protein LOC652203 \| leucine rich repeat containing 37, member A2 | 55073 \| 374819 \| 652203 \| 474170 | 2.01 | up | 2.33E-05 |
| 8146243 | HOOK3 | hook homolog 3 (Drosophila) | 84376 | 2.01 | up | 1.60E-06 |
| 8150225 | RAB11FIP1 | RAB11 family interacting protein 1 (class I) | 80223 | 2.01 | up | 1.93E-05 |
| 8049540 | LRRFIP1 | leucine rich repeat (in FLII) interacting protein 1 | 9208 | 2.01 | up | 1.24E-04 |
| 8159142 | COL5A1 | collagen, type V, alpha 1 | 1289 | 2.01 | up | 9.31E-09 |
| 8113709 | LOX | lysyl oxidase | 4015 | 2.01 | up | 1.18E-05 |
| 7961075 | CD69 | | 969 | 2.00 | up | 2.21E-04 |
| 8054611 | C2orf59\|LOC541471 | chromosome 2 open reading frame 59 \| hypothetical LOC541471 | 112597 \| 541471 | 2.00 | up | 7.66E-06 |
| 8043687 | ANKRD36 | ankyrin repeat domain 36 | 375248 | 2.00 | up | 0.0103723 |
| 7976073 | FLRT2 | fibronectin leucine rich transmembrane protein 2 | 23768 | 2.00 | up | 2.06E-06 |
| 7961829 | BCAT1 | branched chain aminotransferase 1, cytosolic | 586 | 2.00 | up | 5.59E-08 |
| 7979307 | DLG7 | discs, large homolog 7 (Drosophila) | 9787 | 2.00 | up | 4.96E-04 |
| 7982094 | SNRPN\|SNORD115-44 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-44 | 6638 \| 100033818 | 2.00 | up | 4.85E-04 |
| 7901732 | C8A | complement component 8, alpha polypeptide | 731 | 2.00 | down | 1.95E-04 |
| 7926786 | APBB1IP | amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein | 54518 | 2.01 | down | 1.39E-05 |
| 8171435 | PIR | pirin (iron-binding nuclear protein) | 8544 | 2.01 | down | 0.037316 |
| 7956658 | SLC16A7 | solute carrier family 16, member 7 (monocarboxylic acid transporter 2) | 9194 | 2.01 | down | 8.59E-04 |

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|---|---|---|---|---|---|---|
| 8167305 | EBP | emopamil binding protein (sterol isomerase) | 10682 | 2.02 | down | 2.78E-05 |
| 7939056 | BBOX1 | butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 | 8424 | 2.02 | down | 0.0046943 |
| 7942613 | DGAT2 | diacylglycerol O-acyltransferase homolog 2 (mouse) | 84649 | 2.02 | down | 4.02E-04 |
| 7997188 | HP | haptoglobin | 3240 | 2.03 | down | 7.86E-14 |
| 7904433 | PHGDH | phosphoglycerate dehydrogenase | 26227 | 2.03 | down | 0.0068264 |
| 8070557 | ZNF295 | zinc finger protein 295 | 49854 | 2.03 | down | 2.91E-04 |
| 8001457 | CES1 | carboxylesterase 1 (monocyte/macrophage serine esterase 1) | 1066 | 2.03 | down | 0.0019101 |
| 8019280 | PCYT2 | phosphate cytidylyltransferase 2, ethanolamine | 5833 | 2.04 | down | 1.59E-04 |
| 8013804 | DHRS13 | dehydrogenase/reductase (SDR family) member 13 | 147015 | 2.04 | down | 0.0130115 |
| 7956401 | SHMT2 | serine hydroxymethyltransferase 2 (mitochondrial) | 6472 | 2.05 | down | 3.89E-04 |
| 7914075 | FCN3 | ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen) | 8547 | 2.05 | down | 3.80E-05 |
| 8111864 | C6 | complement component 6 | 729 | 2.05 | down | 1.70E-06 |
| 8073890 | GRAMD4 | GRAM domain containing 4 | 23151 | 2.05 | down | 1.59E-04 |
| 7975167 | GPHN | gephyrin | 10243 | 2.06 | down | 4.27E-06 |
| 7985636 | SLC28A1 | solute carrier family 28 (sodium-coupled nucleoside transporter), member 1 | 9154 | 2.06 | down | 0.0011369 |
| 8113214 | GLRX | glutaredoxin (thioltransferase) | 2745 | 2.07 | down | 2.43E-04 |
| 7905986 | FDPS | farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase) | 2224 | 2.08 | down | 3.38E-06 |
| 7931754 | IDI1 | isopentenyl-diphosphate delta isomerase 1 | 3422 | 2.08 | down | 1.98E-05 |
| 7898655 | CDA | cytidine deaminase | 978 | 2.08 | down | 2.34E-07 |
| 7959205 | KIAA0152 | | 9761 | 2.08 | down | 2.89E-04 |
| 8051998 | MCFD2 | multiple coagulation factor deficiency 2 | 90411 | 2.09 | down | 0.013714 |
| 8019778 | PCYT2 | phosphate cytidylyltransferase 2, ethanolamine | 5833 | 2.09 | down | 1.32E-04 |
| 7927082 | HSD17B7P2 | hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2 | 158160 | 2.09 | down | 0.0031844 |
| 7952145 | HYOU1 | hypoxia up-regulated 1 | 10525 | 2.09 | down | 0.0332143 |
| 8113491 | STARD4 | StAR-related lipid transfer (START) domain containing 4 | 134429 | 2.09 | down | 2.31E-05 |
| 7940775 | RARRES3 | retinoic acid receptor responder (tazarotene induced) 3 | 5920 | 2.09 | down | 9.49E-04 |
| 7958565 | MVK | mevalonate kinase | 4598 | 2.09 | down | 1.44E-08 |
| 8165817 | GYG2 | glycogenin 2 | 8908 | 2.09 | down | 9.11E-04 |
| 7944656 | SC5DL | sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like | 6309 | 2.10 | down | 2.32E-05 |
| 7960757 | C1RL | complement component 1, r subcomponent-like | 51279 | 2.10 | down | 5.28E-05 |

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|---|---|---|---|---|---|---|
| 7928944 | PAPSS2 | 3'-phosphoadenosine 5'-phosphosulfate synthase 2 | 9060 | 2.10 | down | 0.0016682 |
| 7960730 | MBOAT5 | membrane bound O-acyltransferase domain containing 5 | 10162 | 2.10 | down | 6.28E-04 |
| 8111019 | DNAH5 | dynein, axonemal, heavy chain 5 | 1767 | 2.10 | down | 0.0011046 |
| 7946167 | HPX | hemopexin | 3263 | 2.10 | down | 6.00E-14 |
| 8056102 | CD302 | | 9936 | 2.11 | down | 4.70E-05 |
| 8147132 | CA2 | carbonic anhydrase II | 760 | 2.11 | down | 2.79E-06 |
| 8013112 | RASD1 | RAS, dexamethasone-induced 1 | 51655 | 2.12 | down | 0.0019838 |
| 8102249 | AGXT2L1 | alanine-glyoxylate aminotransferase 2-like 1 | 64850 | 2.13 | down | 0.0143308 |
| 7901696 | PCSK9 | proprotein convertase subtilisin/kexin type 9 | 255738 | 2.13 | down | 4.50E-05 |
| 7934755 | MAT1A | methionine adenosyltransferase I, alpha | 4143 | 2.13 | down | 1.82E-09 |
| 7918558 | KCND3 | potassium voltage-gated channel, Shal-related subfamily, member 3 | 3752 | 2.14 | down | 8.90E-05 |
| 7940160 | DTX4 | deltex 4 homolog (Drosophila) | 23220 | 2.14 | down | 4.11E-04 |
| 8063177 | SLC2A10 | solute carrier family 2 (facilitated glucose transporter), member 10 | 81031 | 2.15 | down | 0.0053374 |
| 8066214 | TGM2 | transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) | 7052 | 2.15 | down | 3.62E-04 |
| 8080212 | GLYCTK | glycerate kinase | 132158 | 2.15 | down | 1.18E-05 |
| 8003332 | MVD | mevalonate (diphospho) decarboxylase | 4597 | 2.16 | down | 0.0011452 |
| 8020183 | IMPA2 | inositol(myo)-1(or 4)-monophosphatase 2 | 3613 | 2.16 | down | 0.0025857 |
| 8144669 | FDFT1 | farnesyl-diphosphate farnesyltransferase 1 | 2222 | 2.17 | down | 2.01E-05 |
| 8175492 | ATP11C | ATPase, class VI, type 11C | 286410 | 2.18 | down | 5.04E-05 |
| 8070632 | CBS | cystathionine-beta-synthase | 875 | 2.20 | down | 4.72E-05 |
| 7961710 | ABCC9 | ATP-binding cassette, sub-family C (CFTR/MRP), member 9 | 10060 | 2.20 | down | 0.0046689 |
| 8062461 | LBP | lipopolysaccharide binding protein | 3929 | 2.20 | down | 2.87E-04 |
| 8013788 | FLOT2 | flotillin 2 | 2319 | 2.21 | down | 1.06E-04 |
| 7954344 | LST-3TM12\|SLCO1B1\|SLCO1B3 | organic anion transporter LST-3b \| solute carrier organic anion transporter family, member 1B1 \| solute carrier organic anion transporter family, member 1B3 | 338821 \| 10599 \| 28234 | 2.21 | down | 0.0441345 |
| 8142120 | NAMPT | nicotinamide phosphoribosyltransferase | 10135 | 2.22 | down | 3.37E-11 |
| 7936871 | OAT | ornithine aminotransferase (gyrate atrophy) | 4942 | 2.22 | down | 0.0132995 |
| 8121838 | TPD52L1 | tumor protein D52-like 1 | 7164 | 2.23 | down | 0.0017903 |
| 7995838 | MT1X | metallothionein 1X | 4501 | 2.23 | down | 4.26E-06 |
| 7933084 | NAMPT | nicotinamide phosphoribosyltransferase | 10135 | 2.25 | down | 1.04E-10 |

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|---|---|---|---|---|---|---|
| 7995803 | MT1JP\|MT1M | metallothionein 1J (pseudogene) \| metallothionein 1M | 4498 \| 4499 | 2.25 | down | 7.40E-04 |
| 8126760 | RCAN2 | regulator of calcineurin 2 | 10231 | 2.25 | down | 0.005563 |
| 7931863 | ASB13 | ankyrin repeat and SOCS box-containing 13 | 79754 | 2.25 | down | 0.0090872 |
| 8140840 | STEAP4 | STEAP family member 4 | 79689 | 2.25 | down | 0.0106021 |
| 8078956 | | | | 2.26 | down | 0.0032253 |
| 7997192 | HPR | haptoglobin-related protein | 3250 | 2.26 | down | 1.79E-09 |
| 7912975 | ALDH4A1 | aldehyde dehydrogenase 4 family, member A1 | 8659 | 2.27 | down | 1.70E-06 |
| 7919984 | SELENBP1 | selenium binding protein 1 | 8991 | 2.27 | down | 1.50E-05 |
| 8126153 | KCNK5 | potassium channel, subfamily K, member 5 | 8645 | 2.28 | down | 0.0101595 |
| 8126770 | CYP39A1 | cytochrome P450, family 39, subfamily A, polypeptide 1 | 51302 | 2.28 | down | 0.0023213 |
| 7976496 | SERPINA3 | serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 | 12 | 2.28 | down | 8.78E-07 |
| 8101893 | ADH1C | alcohol dehydrogenase 1C (class I), gamma polypeptide | 126 | 2.29 | down | 5.40E-04 |
| 8099897 | UGDH | UDP-glucose dehydrogenase | 7358 | 2.29 | down | 0.0379411 |
| 8062844 | C20orf121 | chromosome 20 open reading frame 121 | 79183 | 2.29 | down | 0.0019838 |
| 8103695 | MFAP3L | microfibrillar-associated protein 3-like | 9848 | 2.29 | down | 2.14E-05 |
| 8024323 | REEP6 | receptor accessory protein 6 | 92840 | 2.29 | down | 3.15E-12 |
| 7928308 | DDIT4 | DNA-damage-inducible transcript 4 | 54541 | 2.30 | down | 0.0013198 |
| 7991846 | DECR2 | 2,4-dienoyl CoA reductase 2, peroxisomal | 26063 | 2.30 | down | 8.29E-13 |
| 8145122 | SLC39A14 | solute carrier family 39 (zinc transporter), member 14 | 23516 | 2.30 | down | 1.29E-05 |
| 8152278 | | | | 2.31 | down | 0.0130115 |
| 8172905 | HSD17B10 | hydroxysteroid (17-beta) dehydrogenase 10 | 3028 | 2.32 | down | 4.30E-11 |
| 7940135 | GLYATL1 | glycine-N-acyltransferase-like 1 | 92292 | 2.33 | down | 1.25E-04 |
| 7946977 | SAA4 | serum amyloid A4, constitutive | 6291 | 2.33 | down | 3.65E-07 |
| 8161174 | GNE | glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase | 10020 | 2.34 | down | 7.25E-06 |
| 7995806 | MT1A | metallothionein 1A | 4489 | 2.35 | down | 7.20E-04 |
| 8137526 | INSIG1 | insulin induced gene 1 | 3638 | 2.35 | down | 0.0038548 |
| 8101852 | ADH4 | alcohol dehydrogenase 4 (class II), pi polypeptide | 127 | 2.36 | down | 0.0036862 |
| 8057004 | PDE11A | phosphodiesterase 11A | 50940 | 2.36 | down | 1.66E-04 |
| 8002629 | PKD1L3 | polycystic kidney disease 1-like 3 | 342372 | 2.36 | down | 0.0146214 |
| 7946972 | SAA3P | serum amyloid A3 pseudogene | 6290 | 2.37 | down | 1.75E-04 |
| 8005839 | TMEM97 | transmembrane protein 97 | 27346 | 2.38 | down | 1.92E-05 |

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|---|---|---|---|---|---|---|
| 8013135 | SREBF1 | sterol regulatory element binding transcription factor 1 | 6720 | 2.39 | down | 0.0024022 |
| 7995729 | CES4\|CES1\|LOC652708 | carboxylesterase 4-like \| carboxylesterase 1 (monocyte/macrophage serine esterase 1) \| similar to Liver carboxylesterase 1 precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1) (Triacylglycerol hydrolase) (TGH) (Egasyn)... | 51716 \| 1066 \| 652708 | 2.39 | down | 0.0140703 |
| 8153474 | TSTA3 | tissue specific transplantation antigen P35B | 7264 | 2.40 | down | 4.15E-04 |
| 8144866 | NAT2 | N-acetyltransferase 2 (arylamine N-acetyltransferase) | 10 | 2.41 | down | 0.0070346 |
| 7904396 | HAO2 | hydroxyacid oxidase 2 (long chain) | 51179 | 2.41 | down | 0.0043701 |
| 8124365 | SLC17A2 | solute carrier family 17 (sodium phosphate), member 2 | 10246 | 2.42 | down | 0.0073506 |
| 7939590 | SLC35C1 | solute carrier family 35, member C1 | 55343 | 2.43 | down | 0.0010173 |
| 7993126 | ABAT | 4-aminobutyrate aminotransferase | 18 | 2.43 | down | 9.65E-06 |
| 7906904 | HSD17B7\|HSD17B7P2 | hydroxysteroid (17-beta) dehydrogenase 7 \| hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2 | 51478 \| 158160 | 2.44 | down | 5.21E-05 |
| 8156706 | TMOD1 | tropomodulin 1 | 7111 | 2.45 | down | 0.0014733 |
| 8095705 | MTHFD2L | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like | 441024 | 2.45 | down | 7.48E-04 |
| 8148572 | LY6E | lymphocyte antigen 6 complex, locus E | 4061 | 2.46 | down | 9.32E-05 |
| 7906458 | APCS | amyloid P component, serum | 325 | 2.47 | down | 3.78E-07 |
| 7909318 | C4BPA | complement component 4 binding protein, alpha | 722 | 2.48 | down | 4.02E-07 |
| 7906465 | OR10J6P | olfactory receptor, family 10, subfamily J, member 6 pseudogene | 401973 | 2.48 | down | 3.38E-06 |
| 7921492 | IGSF9 | immunoglobulin superfamily, member 9 | 57549 | 2.49 | down | 0.0065589 |
| 8100798 | SULT1B1 | sulfotransferase family, cytosolic, 1B, member 1 | 27284 | 2.49 | down | 0.0133791 |
| 8123137 | ACAT2 | acetyl-Coenzyme A acetyltransferase 2 | 39 | 2.49 | down | 2.75E-07 |
| 7981051 | SERPINA10 | serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10 | 51156 | 2.50 | down | 1.16E-04 |
| 7901513 | SCP2 | sterol carrier protein 2 | 6342 | 2.50 | down | 2.22E-08 |
| 7934997 | PPP1R3C | protein phosphatase 1, regulatory (inhibitor) subunit 3C | 5507 | 2.50 | down | 0.002102 |
| 7948612 | FADS1\|FADS3 | fatty acid desaturase 1 \| fatty acid desaturase 3 | 3992 \| 3995 | 2.50 | down | 5.89E-05 |
| 7972650 | FGF14 | fibroblast growth factor 14 | 2259 | 2.52 | down | 2.86E-05 |
| 8035083 | CYP4F2 | cytochrome P450, family 4, subfamily F, polypeptide 2 | 8529 | 2.53 | down | 1.74E-06 |
| 7991374 | IDH2 | isocitrate dehydrogenase 2 (NADP+), mitochondrial | 3418 | 2.53 | down | 5.58E-05 |
| 8090314 | ALDH1L1 | aldehyde dehydrogenase 1 family, member L1 | 10840 | 2.53 | down | 0.0100982 |

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|---|---|---|---|---|---|---|
| 8091243 | PCOLCE2 | procollagen C-endopeptidase enhancer 2 | 26577 | 2.53 | down | 9.65E-06 |
| 7909306 | C4BPB | complement component 4 binding protein, beta | 725 | 2.54 | down | 2.57E-04 |
| 8013660 | ALDOC | aldolase C, fructose-bisphosphate | 230 | 2.55 | down | 1.53E-04 |
| 7970793 | SLC46A3 | solute carrier family 46, member 3 | 283537 | 2.55 | down | 2.01E-04 |
| 8021741 | CNDP1 | carnosine dipeptidase 1 (metallopeptidase M20 family) | 84735 | 2.56 | down | 0.0033179 |
| 8019357 | DCXR | dicarbonyl/L-xylulose reductase | 51181 | 2.56 | down | 1.28E-04 |
| 7925939 | AKR1C4 | aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4) | 1109 | 2.58 | down | 7.64E-04 |
| 8025303 | CLEC4M | C-type lectin domain family 4, member M | 10332 | 2.58 | down | 8.20E-04 |
| 8103706 | AADAT | aminoadipate aminotransferase | 51166 | 2.59 | down | 3.18E-04 |
| 8111941 | HMGCS1 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble) | 3157 | 2.63 | down | 2.96E-05 |
| 8148280 | SQLE | squalene epoxidase | 6713 | 2.63 | down | 2.49E-06 |
| 8070961 | LSS | lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) | 4047 | 2.66 | down | 6.95E-08 |
| 7956271 | HSD17B6 | hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse) | 8630 | 2.67 | down | 3.52E-06 |
| 7908312 | PRG4 | proteoglycan 4 | 10216 | 2.68 | down | 3.59E-07 |
| 8102342 | ELOVL6 | ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast) | 79071 | 2.69 | down | 0.0017808 |
| 7963826 | PPP1R1A | protein phosphatase 1, regulatory (inhibitor) subunit 1A | 5502 | 2.69 | down | 1.41E-05 |
| 8113369 | SLCO4C1 | solute carrier organic anion transporter family, member 4C1 | 353189 | 2.70 | down | 8.98E-04 |
| 7936322 | GPAM | glycerol-3-phosphate acyltransferase, mitochondrial | 57678 | 2.70 | down | 1.15E-04 |
| 7936494 | GFRA1 | GDNF family receptor alpha 1 | 2674 | 2.71 | down | 6.76E-07 |
| 7954330 | SLCO1B3\|SLCO1B1\|LST-3TM12 | solute carrier organic anion transporter family, member 1B3 \| solute carrier organic anion transporter family, member 1B1 \| organic anion transporter LST-3b | 28234 \| 10599 \| 338821 | 2.75 | down | 8.71E-05 |
| 8013243 | SHMT1 | serine hydroxymethyltransferase 1 (soluble) | 6470 | 2.77 | down | 4.85E-07 |
| 8044793 | STEAP3 | STEAP family member 3 | 55240 | 2.82 | down | 5.86E-05 |
| 7942603 | MOGAT2 | monoacylglycerol O-acyltransferase 2 | 80168 | 2.84 | down | 7.69E-06 |
| 8113232 | | | | 2.87 | down | 0.0033106 |
| 8099612 | GPR125 | G protein-coupled receptor 125 | 166647 | 2.87 | down | 7.85E-10 |
| 8151042 | TTPA | tocopherol (alpha) transfer protein | 7274 | 2.87 | down | 2.97E-06 |
| 8020955 | MOCOS | molybdenum cofactor sulfurase | 55034 | 2.90 | down | 4.04E-04 |
| 7935169 | CYP2C8 | cytochrome P450, family 2, subfamily C, polypeptide 8 | 1558 | 2.91 | down | 0.0023986 |
| 8098195 | SC4MOL | sterol-C4-methyl oxidase-like | 6307 | 2.98 | down | 2.96E-09 |

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|---|---|---|---|---|---|---|
| 8078933 | MYRIP | myosin VIIA and Rab interacting protein | 25924 | 3.05 | down | 7.08E-05 |
| 8088642 | LRIG1 | leucine-rich repeats and immunoglobulin-like domains 1 | 26018 | 3.11 | down | 1.14E-04 |
| 7943867 | BCO2 | beta-carotene oxygenase 2 | 83875 | 3.14 | down | 0.0072235 |
| 8075390 | SEC14L4 | SEC14-like 4 (S. cerevisiae) | 284904 | 3.14 | down | 8.37E-05 |
| 8157450 | ORM2 | orosomucoid 2 | 5005 | 3.19 | down | 4.57E-11 |
| 7995787 | MT1M | metallothionein 1M | 4499 | 3.26 | down | 0.0014687 |
| 8094361 | GBA3 | glucosidase, beta, acid 3 (cytosolic) | 57733 | 3.26 | down | 4.96E-05 |
| 8123232 | SLC22A1 | solute carrier family 22 (organic cation transporter), member 1 | 6580 | 3.27 | down | 7.63E-04 |
| 8157446 | ORM1 | orosomucoid 1 | 5004 | 3.28 | down | 3.77E-13 |
| 8111757 | C9 | complement component 9 | 735 | 3.29 | down | 1.04E-12 |
| 7964292 | RDH16 | retinol dehydrogenase 16 (all-trans) | 8608 | 3.30 | down | 1.70E-04 |
| 7965873 | IGF1 | insulin-like growth factor 1 (somatomedin C) | 3479 | 3.30 | down | 5.95E-04 |
| 7948987 | HRASLS3 | HRAS-like suppressor 3 | 11145 | 3.34 | down | 3.75E-05 |
| 8106999 | C5orf27 | chromosome 5 open reading frame 27 | 202299 | 3.36 | down | 3.67E-06 |
| 8111474 | AGXT2 | alanine-glyoxylate aminotransferase 2 | 64902 | 3.36 | down | 6.33E-06 |
| 8081288 | TMEM45A | transmembrane protein 45A | 55076 | 3.42 | down | 1.83E-07 |
| 8119620 | GNMT | glycine N-methyltransferase | 27232 | 3.42 | down | 0.0019784 |
| 8019392 | FASN | fatty acid synthase | 2194 | 3.55 | down | 3.99E-05 |
| 8130608 | LPA | lipoprotein, Lp(a) | 4018 | 3.56 | down | 0.006898 |
| 8035095 | CYP4F11 | cytochrome P450, family 4, subfamily F, polypeptide 11 | 57834 | 3.57 | down | 8.18E-07 |
| 8136459 | AKR1D1 | aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) | 6718 | 3.61 | down | 0.0150441 |
| 8025522 | LOC388503 | similar to Complement C3 precursor | 388503 | 3.63 | down | 6.65E-04 |
| 8007454 | RND2 | Rho family GTPase 2 | 8153 | 3.63 | down | 2.58E-04 |
| 8051030 | SLC5A6 | solute carrier family 5 (sodium-dependent vitamin transporter), member 6 | 8884 | 3.67 | down | 3.80E-05 |
| 8028963 | CYP2B6 | cytochrome P450, family 2, subfamily B, polypeptide 6 | 1555 | 3.72 | down | 0.0205225 |
| 8091863 | SLITRK3 | SLIT and NTRK-like family, member 3 | 22865 | 3.78 | down | 1.96E-04 |
| 8028955 | CYP2B7P1 | cytochrome P450, family 2, subfamily B, polypeptide 7 pseudogene 1 | 1556 | 3.80 | down | 0.0379944 |
| 8062041 | ACSS2 | acyl-CoA synthetase short-chain family member 2 | 55902 | 3.86 | down | 2.88E-08 |
| 7997179 | DHODH | dihydroorotate dehydrogenase | 1723 | 3.92 | down | 1.65E-06 |
| 7929466 | CYP2C18\|CYP2C19 | cytochrome P450, family 2, subfamily C, polypeptide 18 \| cytochrome P450, family 2, subfamily C, polypeptide 19 | 1562 \| 1557 | 3.94 | down | 3.22E-05 |

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|---|---|---|---|---|---|---|
| 8149885 | ADRA1A | adrenergic, alpha-1A-, receptor | 148 | 4.10 | down | 1.73E-12 |
| 7909446 | HSD11B1 | hydroxysteroid (11-beta) dehydrogenase 1 | 3290 | 4.12 | down | 4.09E-06 |
| 7995739 | GNAO1 | guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O | 2775 | 4.14 | down | 6.19E-05 |
| 7929478 | CYP2C19 | cytochrome P450, family 2, subfamily C, polypeptide 19 | 1557 | 4.17 | down | 0.0020065 |
| 8027819 | HAMP | hepcidin antimicrobial peptide | 57817 | 4.38 | down | 5.12E-11 |
| 8101637 | HSD17B13 | hydroxysteroid (17-beta) dehydrogenase 13 | 345275 | 4.40 | down | 0.0219071 |
| 7958466 | ACACB | acetyl-Coenzyme A carboxylase beta | 32 | 4.55 | down | 1.20E-12 |
| 8154135 | SLC1A1 | solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1 | 6505 | 4.58 | down | 2.05E-05 |
| 7990839 | STARD5 | StAR-related lipid transfer (START) domain containing 5 | 80765 | 4.71 | down | 5.86E-05 |
| 7960984 | PZP | pregnancy-zone protein | 5858 | 4.72 | down | 0.0022229 |
| 7913216 | PLA2G2A | phospholipase A2, group IIA (platelets, synovial fluid) | 5320 | 4.82 | down | 0.0010423 |
| 7943998 | NNMT | nicotinamide N-methyltransferase | 4837 | 4.96 | down | 1.44E-08 |
| 7921449 | CRP | C-reactive protein, pentraxin-related | 1401 | 4.99 | down | 1.92E-05 |
| 7908499 | CFHR5 | complement factor H-related 5 | 81494 | 5.14 | down | 7.35E-06 |
| 8032834 | LRG1 | leucine-rich alpha-2-glycoprotein 1 | 116844 | 5.31 | down | 3.90E-06 |
| 7898693 | ALPL | alkaline phosphatase, liver/bone/kidney | 249 | 5.45 | down | 7.40E-07 |
| 7988990 | WDR72 | WD repeat domain 72 | 256764 | 5.46 | down | 4.03E-06 |
| 8156043 | PSAT1 | phosphoserine aminotransferase 1 | 29968 | 5.81 | down | 5.48E-06 |
| 7979658 | GPX2 | glutathione peroxidase 2 (gastrointestinal) | 2877 | 5.94 | down | 1.91E-05 |
| 7908492 | CFHR4 | complement factor H-related 4 | 10877 | 6.09 | down | 9.06E-06 |
| 7964142 | APOF | apolipoprotein F | 319 | 6.15 | down | 5.47E-08 |
| 7964660 | AVPR1A | arginine vasopressin receptor 1A | 552 | 6.17 | down | 3.06E-04 |
| 7990391 | CYP1A1 | cytochrome P450, family 1, subfamily A, polypeptide 1 | 1543 | 6.40 | down | 0.0061888 |
| 8114964 | SPINK1 | serine peptidase inhibitor, Kazal type 1 | 6690 | 7.25 | down | 9.91E-06 |
| 7900365 | MFSD2 | major facilitator superfamily domain containing 2 | 84879 | 7.33 | down | 3.77E-09 |
| 8047300 | AOX1 | aldehyde oxidase 1 | 316 | 9.31 | down | 9.48E-15 |
| 7942793 | THRSP | thyroid hormone responsive (SPOT14 homolog, rat) | 7069 | 10.39 | down | 5.36E-07 |
| 7984862 | CYP1A2 | cytochrome P450, family 1, subfamily A, polypeptide 2 | 1544 | 13.86 | down | 3.96E-04 |
| 8103769 | HPGD | hydroxyprostaglandin dehydrogenase 15-(NAD) | 3248 | 24.26 | down | 7.01E-09 |
| 7946986 | SAA1 | serum amyloid A1 | 6288 | 34.36 | down | 8.92E-08 |
| 7946983 | SAA2\|SAA1 | serum amyloid A2 \| serum amyloid A1 | 6289 \| 6288 | 49.12 | down | 1.31E-12 |

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|---|---|---|---|---|---|---|
| 7938758 | SAA1\|SAA2 | serum amyloid A1 \| serum amyloid A2 | 6288 \| 6289 | 53.44 | down | 6.00E-14 |

## 32 probe sets regulated by more than at least 2-fold between biliary atresia (BA) and disease control (DC)

| Transcripts Cluster ID | Gene Symbol | Gene Description | Entrezgene ID | Fold change BA vs NC | Regulation in BA | Corrected P value |
|---|---|---|---|---|---|---|
| 7934979 | ANKRD1 | ankyrin repeat domain 1 (cardiac muscle) | 27063 | 4.13 | up | 3.58E-16 |
| 7951217 | MMP7 | matrix metallopeptidase 7 (matrilysin, uterine) | 4316 | 3.62 | up | 2.16E-12 |
| 8091411 | TM4SF1 | transmembrane 4 L six family member 1 | 4071 | 3.27 | up | 2.00E-05 |
| 8152617 | HAS2 | hyaluronan synthase 2 | 3037 | 2.94 | up | 2.70E-06 |
| 7954090 | EMP1 | epithelial membrane protein 1 | 2012 | 2.66 | up | 5.72E-08 |
| 8096301 | SPP1 | secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) | 6696 | 2.59 | up | 8.01E-09 |
| 8006433 | CCL2 | chemokine (C-C motif) ligand 2 | 6347 | 2.59 | up | 2.66E-04 |
| 8135069 | SERPINE1 | serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 | 5054 | 2.56 | up | 0.0044532 |
| 8106743 | VCAN | versican | 1462 | 2.50 | up | 7.01E-09 |
| 8098439 | | | | 2.44 | up | 1.26E-09 |
| 8095744 | AREG\|LOC727738 | amphiregulin (schwannoma-derived growth factor) \| similar to Amphiregulin precursor (AR) (Colorectum cell-derived growth factor) (CRDGF) | 374 \| 727738 | 2.42 | up | 3.67E-06 |
| 7965403 | LUM | lumican | 4060 | 2.40 | up | 2.76E-08 |
| 8048864 | CCL20 | chemokine (C-C motif) ligand 20 | 6364 | 2.37 | up | 0.0045863 |
| 8095680 | IL8 | interleukin 8 | 3576 | 2.29 | up | 1.79E-08 |
| 8096733 | SGMS2 | sphingomyelin synthase 2 | 166929 | 2.25 | up | 1.04E-04 |
| 7960865 | SLC2A3 | solute carrier family 2 (facilitated glucose transporter), member 3 | 6515 | 2.23 | up | 2.84E-05 |
| 8015133 | KRT23 | keratin 23 (histone deacetylase inducible) | 25984 | 2.21 | up | 1.79E-10 |
| 8077441 | BHLHB2 | basic helix-loop-helix domain containing, class B, 2 | 8553 | 2.17 | up | 1.08E-05 |
| 8105267 | ITGA2 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | 3673 | 2.15 | up | 6.91E-11 |
| 7918936 | VTCN1 | V-set domain containing T cell activation inhibitor 1 | 79679 | 2.12 | up | 2.89E-08 |
| 8135576 | TES | testis derived transcript (3 LIM domains) | 26136 | 2.09 | up | 7.53E-04 |
| 8135661 | CFTR | cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7) | 1080 | 2.07 | up | 2.81E-12 |

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|---|---|---|---|---|---|---|
| 8044021 | IL1RL1 | interleukin 1 receptor-like 1 | 9173 | 2.06 | up | 2.26E-04 |
| 7906919 | RGS4 | regulator of G-protein signaling 4 | 5999 | 2.05 | up | 1.64E-08 |
| 7908072 | LAMC2 | laminin, gamma 2 | 3918 | 2.03 | up | 4.30E-11 |
| 8041853 | TACSTD1 | tumor-associated calcium signal transducer 1 | 4072 | 2.01 | up | 4.08E-15 |
| 7982597 | THBS1 | thrombospondin 1 | 7057 | 2.00 | up | 1.12E-04 |
| 8095736 | AREG\|LOC727738 | amphiregulin (schwannoma-derived growth factor) \| similar to Amphiregulin precursor (AR) (Colorectum cell-derived growth factor) (CRDGF) | 374 \| 727738 | 2.00 | up | 3.69E-06 |
| 7967107 | C12orf27 | chromosome 12 open reading frame 27 | 283460 | 2.25 | down | 7.76E-06 |
| 8015991 | SLC4A1 | solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group) | 6521 | 2.28 | down | 1.74E-05 |
| 7921367 | SPTA1 | spectrin, alpha, erythrocytic 1 (elliptocytosis 2) | 6708 | 2.45 | down | 0.0011622 |
| 8102998 | GYPA | glycophorin A (MNS blood group) | 2993 | 2.54 | down | 2.17E-05 |

## 544 probe sets regulated by more than at least 2-fold between disease control (DC) and normal control

| Transcripts Cluster ID | Gene Symbol | Gene Description | Entrezgene ID | Fold change BA vs NC | Regulation in BA | Corrected P value |
|---|---|---|---|---|---|---|
| 8175234 | GPC3 | glypican 3 | 2719 | 47.35 | up | 1.37E-18 |
| 8131844 | GPNMB | glycoprotein (transmembrane) nmb | 10457 | 10.48 | up | 5.49E-07 |
| 8098439 | | | | 8.47 | up | 1.26E-09 |
| 7946048 | HBG1\|HBG2 | hemoglobin, gamma A \| hemoglobin, gamma G | 3047 \| 3048 | 8.20 | up | 9.38E-09 |
| 7946054 | HBG1\|HBG2 | hemoglobin, gamma A \| hemoglobin, gamma G | 3047 \| 3048 | 8.19 | up | 9.38E-09 |
| 8174201 | BEX1 | brain expressed, X-linked 1 | 55859 | 6.56 | up | 4.64E-11 |
| 8124650 | UBD\|GABBR1 | ubiquitin D \| gamma-aminobutyric acid (GABA) B receptor, 1 | 10537 \| 2550 | 6.42 | up | 2.07E-04 |
| 8095646 | AFP | alpha-fetoprotein | 174 | 6.15 | up | 1.85E-06 |
| 8178295 | UBD\|GABBR1 | ubiquitin D \| gamma-aminobutyric acid (GABA) B receptor, 1 | 10537 \| 2550 | 6.14 | up | 2.39E-04 |
| 8016646 | COL1A1 | collagen, type I, alpha 1 | 1277 | 6.04 | up | 1.39E-06 |
| 8126784 | PLA2G7 | phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) | 7941 | 5.52 | up | 1.40E-05 |
| 8134263 | COL1A2 | collagen, type I, alpha 2 | 1278 | 5.42 | up | 2.15E-06 |
| 8124196 | DCDC2 | doublecortin domain containing 2 | 51473 | 5.39 | up | 6.55E-13 |

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| 7982084 | SNRPN\|SNORD115-11\|SNORD115-12\|SNORD115-26\|SNORD115-29\|SNORD115-36\|SNORD115-39\|SNORD115-43\|SNORD115-9\|SNORD115-41\|SNORD115-22\|SNORD115-16\|SNORD115-14\|SNORD115-6\|SNORD115-38\|SNORD115-44\|SNORD115-30 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-38 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-30 | 6638 \| 100033448 \| 100033449 \| 100033802 \| 100033803 \| 100033810 \| 100033813 \| 100033817 \| 100033446 \| 100033815 \| 100033799 \| 100033454 \| 100033451 \| 100033443 \| 100033812 \| 100033818 \| 100033440 \| 100033804 | 5.35 | up | 4.26E-05 |
| 7991766 | HBA1\|HBA2 | hemoglobin, alpha 1 \| hemoglobin, alpha 2 | 3039 \| 3040 | 5.23 | up | 0.004258 |
| 7991762 | HBA1\|HBA2 | hemoglobin, alpha 1 \| hemoglobin, alpha 2 | 3039 \| 3040 | 5.22 | up | 0.0042486 |
| 7982058 | SNORD115-1\|SNRPN\|SNORD115-26\|SNORD115-11\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-5\|SNORD115-22\|SNORD115-39\|SNORD115-41\|SNORD115-16\|SNORD115-44\|SNORD115-34\|SNORD115-6\|HBII-52-24\|SNORD115-7 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-6 \| HBII-52-24 snoRNA \| small nucleolar RNA, C/D box 115-7 | 338433 \| 6638 \| 100033802 \| 100033448 \| 100033803 \| 100033810 \| 100033817 \| 100033442 \| 100033799 \| 100033813 \| 100033815 \| 100033440 \| 100033454 \| 100033818 \| 100033808 \| 100033443 \| 100036563 \| 100033444 | 5.09 | up | 1.35E-05 |

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<tr><th></th><th></th><th></th><th></th><th></th><th></th><th></th></tr>
<tr><td>7982064</td><td>SNORD115-1|SNRPN|SNORD115-11|SNORD115-12|SNORD115-29|SNORD115-36|SNORD115-43|SNORD115-5|SNORD115-9|SNORD115-26|SNORD115-22|SNORD115-20|SNORD115-39|SNORD115-41|SNORD115-17|SNORD115-18|SNORD115-19|SNORD115-13|SNORD115-16|SNORD115-40|SNORD115-44|SNORD115-34|SNORD115-42|SNORD115-6|SNORD115-10|SNORD115-14|SNORD115-15|SNORD115-21|HBII-52-24|SNORD115-7</td><td>small nucleolar RNA, C/D box 115-1 | small nuclear ribonucleoprotein polypeptide N | small nucleolar RNA, C/D box 115-11 | small nucleolar RNA, C/D box 115-12 | small nucleolar RNA, C/D box 115-29 | small nucleolar RNA, C/D box 115-36 | small nucleolar RNA, C/D box 115-43 | small nucleolar RNA, C/D box 115-5 | small nucleolar RNA, C/D box 115-9 | small nucleolar RNA, C/D box 115-26 | small nucleolar RNA, C/D box 115-22 | small nucleolar RNA, C/D box 115-20 | small nucleolar RNA, C/D box 115-39 | small nucleolar RNA, C/D box 115-3 | small nucleolar RNA, C/D box 115-41 | small nucleolar RNA, C/D box 115-17 | small nucleolar RNA, C/D box 115-18 | small nucleolar RNA, C/D box 115-19 | small nucleolar RNA, C/D box 115-13 | small nucleolar RNA, C/D box 115-16 | small nucleolar RNA, C/D box 115-40 | small nucleolar RNA, C/D box 115-44 | small nucleolar RNA, C/D box 115-34 | small nucleolar RNA, C/D box 115-4 | small nucleolar RNA, C/D box 115-42 | small nucleolar RNA, C/D box 115-6 | small nucleolar RNA, C/D box 115-10 | small nucleolar RNA, C/D box 115-14 | small nucleolar RNA, C/D box 115-15 | small nucleolar RNA, C/D box 115-21 | HBII-52-24 snoRNA | small nucleolar RNA, C/D box 115-7</td><td>338433 | 6638 | 100033448 | 100033449 | 100033803 | 100033810 | 100033817 | 100033442 | 100033446 | 100033802 | 100033799 | 100033460 | 100033813 | 100033440 | 100033815 | 100033455 | 100033456 | 100033458 | 100033450 | 100033454 | 100033814 | 100033818 | 100033808 | 100033441 | 100033816 | 100033443 | 100033447 | 100033451 | 100033453 | 100033603 | 100036563 | 100033444</td><td>5.07</td><td>up</td><td>1.46E-05</td></tr>
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|---|---|---|---|---|---|---|
| 7982092 | SNORD115-1\|SNRPN\|SNORD115-11\|SNORD115-12\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-5\|SNORD115-9\|SNORD115-26\|SNORD115-22\|SNORD115-20\|SNORD115-39\|SNORD115-41\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-16\|SNORD115-40\|SNORD115-44\|SNORD115-34\|SNORD115-6\|SNORD115-10\|HBII-52-24\|SNORD115-7 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-10 \| HBII-52-24 snoRNA \| small nucleolar RNA, C/D box 115-7 | 338433 \| 6638 \| 100033448 \| 100033449 \| 100033803 \| 100033810 \| 100033817 \| 100033442 \| 100033446 \| 100033802 \| 100033799 \| 100033460 \| 100033813 \| 100033440 \| 100033815 \| 100033455 \| 100033456 \| 100033458 \| 100033450 \| 100033454 \| 100033814 \| 100033818 \| 100033808 \| 100033443 \| 100033447 \| 100036563 \| 100033444 | 5.06 | up | 1.44E-05 |

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| 7982078 | SNORD115-1\|SNRPN\|SNORD115-11\|SNORD115-12\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-5\|SNORD115-9\|SNORD115-26\|SNORD115-22\|SNORD115-20\|SNORD115-39\|SNORD115-41\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-16\|SNORD115-40\|SNORD115-44\|SNORD115-34\|SNORD115-42\|SNORD115-6\|SNORD115-10\|SNORD115-14\|SNORD115-15\|HBII-52-24\|SNORD115-7 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| HBII-52-24 snoRNA \| small nucleolar RNA, C/D box 115-7 | 338433 \| 6638 \| 100033448 \| 100033449 \| 100033803 \| 100033810 \| 100033817 \| 100033442 \| 100033446 \| 100033802 \| 100033799 \| 100033460 \| 100033813 \| 100033440 \| 100033815 \| 100033455 \| 100033456 \| 100033458 \| 100033450 \| 100033454 \| 100033814 \| 100033818 \| 100033808 \| 100033441 \| 100033816 \| 100033443 \| 100033447 \| 100033451 \| 100033453 \| 100036563 \| 100033444 | 5.06 | up | 1.53E-05 |

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| 7982028 | SNORD115-1\|SNRPN\|SNORD115-11\|SNORD115-12\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-5\|SNORD115-9\|SNORD115-26\|SNORD115-22\|SNORD115-20\|SNORD115-39\|SNORD115-41\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-16\|SNORD115-40\|SNORD115-44\|SNORD115-34\|SNORD115-42\|SNORD115-6\|SNORD115-10\|SNORD115-14\|SNORD115-15\|SNORD115-21\|HBII-52-24\|SNORD115-7 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| HBII-52-24 snoRNA \| small nucleolar RNA, C/D box 115-7 | 338433 \| 6638 \| 100033448 \| 100033449 \| 100033803 \| 100033810 \| 100033817 \| 100033442 \| 100033446 \| 100033802 \| 100033799 \| 100033460 \| 100033813 \| 100033440 \| 100033815 \| 100033455 \| 100033456 \| 100033458 \| 100033450 \| 100033454 \| 100033814 \| 100033818 \| 100033808 \| 100033441 \| 100033816 \| 100033443 \| 100033447 \| 100033451 \| 100033453 \| 100033603 \| 100036563 \| 100033444 | 5.05 | up | 1.56E-05 |

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| 7982016 | SNORD115-1\|SNRPN\|SNORD115-12\|SNORD115-5\|SNORD115-9\|SNORD115-20\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-25\|SNORD115-40\|SNORD115-42\|SNORD115-10\|SNORD115-14\|SNORD115-15\|SNORD115-21\|HBII-52-24\|SNORD115-7 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-25 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| HBII-52-24 snoRNA \| small nucleolar RNA, C/D box 115-7 | 338433 \| 6638 \| 100033449 \| 100033442 \| 100033446 \| 100033460 \| 100033455 \| 100033456 \| 100033458 \| 100033450 \| 100033801 \| 100033814 \| 100033441 \| 100033816 \| 100033447 \| 100033451 \| 100033453 \| 100033603 \| 100036563 \| 100033444 | 5.02 | up | 1.21E-05 |

<table>
<tr><td>7982024</td><td>SNORD115-1|SNRPN|SNORD115-12|SNORD115-5|SNORD115-9|SNORD115-11|SNORD115-29|SNORD115-36|SNORD115-43|SNORD115-22|SNORD115-20|SNORD115-39|SNORD115-17|SNORD115-18|SNORD115-19|SNORD115-13|SNORD115-16|SNORD115-25|SNORD115-40|SNORD115-44|SNORD115-34|SNORD115-42|SNORD115-6|SNORD115-10|SNORD115-14|SNORD115-15|SNORD115-21|HBII-52-24</td><td>small nucleolar RNA, C/D box 115-1 | small nuclear ribonucleoprotein polypeptide N | small nucleolar RNA, C/D box 115-12 | small nucleolar RNA, C/D box 115-5 | small nucleolar RNA, C/D box 115-9 | small nucleolar RNA, C/D box 115-11 | small nucleolar RNA, C/D box 115-29 | small nucleolar RNA, C/D box 115-36 | small nucleolar RNA, C/D box 115-43 | small nucleolar RNA, C/D box 115-22 | small nucleolar RNA, C/D box 115-20 | small nucleolar RNA, C/D box 115-39 | small nucleolar RNA, C/D box 115-17 | small nucleolar RNA, C/D box 115-18 | small nucleolar RNA, C/D box 115-19 | small nucleolar RNA, C/D box 115-3 | small nucleolar RNA, C/D box 115-13 | small nucleolar RNA, C/D box 115-16 | small nucleolar RNA, C/D box 115-25 | small nucleolar RNA, C/D box 115-40 | small nucleolar RNA, C/D box 115-44 | small nucleolar RNA, C/D box 115-34 | small nucleolar RNA, C/D box 115-4 | small nucleolar RNA, C/D box 115-42 | small nucleolar RNA, C/D box 115-6 | small nucleolar RNA, C/D box 115-10 | small nucleolar RNA, C/D box 115-14 | small nucleolar RNA, C/D box 115-15 | small nucleolar RNA, C/D box 115-21 | HBII-52-24 snoRNA</td><td>338433 | 6638 | 100033449 | 100033442 | 100033446 | 100033448 | 100033803 | 100033810 | 100033817 | 100033799 | 100033460 | 100033813 | 100033455 | 100033456 | 100033458 | 100033440 | 100033450 | 100033454 | 100033801 | 100033814 | 100033818 | 100033808 | 100033441 | 100033816 | 100033443 | 100033447 | 100033451 | 100033453 | 100033603 | 100036563</td><td>5.02</td><td>up</td><td>1.18E-05</td></tr>
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| 7982030 | SNORD115-1\|SNRPN\|SNORD115-12\|SNORD115-5\|SNORD115-9\|SNORD115-11\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-22\|SNORD115-20\|SNORD115-39\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-13\|SNORD115-16\|SNORD115-25\|SNORD115-40\|SNORD115-44\|SNORD115-34\|SNORD115-42\|SNORD115-6\|SNORD115-10\|SNORD115-14\|SNORD115-15\|SNORD115-21\|HBII-52-24 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-25 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| HBII-52-24 snoRNA | 338433 \| 6638 \| 100033449 \| 100033442 \| 100033446 \| 100033448 \| 100033803 \| 100033810 \| 100033817 \| 100033799 \| 100033460 \| 100033813 \| 100033455 \| 100033456 \| 100033458 \| 100033440 \| 100033450 \| 100033454 \| 100033801 \| 100033814 \| 100033818 \| 100033808 \| 100033441 \| 100033816 \| 100033443 \| 100033447 \| 100033451 \| 100033453 \| 100033603 \| 100036563 | 5.02 | up | 1.20E-05 |

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| 7982050 | SNRPN\|SNORD115-11\|SNORD115-12\|SNORD115-22\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-9\|SNORD115-26\|SNORD115-39\|SNORD115-41\|SNORD115-16\|SNORD115-44\|SNORD115-34\|SNORD115-6\|SNORD115-7 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-44 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-7 | 6638 \| 100033448 \| 100033449 \| 100033799 \| 100033803 \| 100033810 \| 100033817 \| 100033446 \| 100033802 \| 100033440 \| 100033813 \| 100033815 \| 100033454 \| 100033818 \| 100033808 \| 100033443 \| 100033444 | 5.00 | up | 1.42E-05 |
| 7981990 | SNRPN\|SNORD116-21\|SNORD116@ | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-21 \| small nucleolar RNA, C/D box 116 cluster | 6638 \| 100033432 \| 692236 | 4.96 | up | 6.23E-07 |
| 8102998 | GYPA | glycophorin A (MNS blood group) | 2993 | 4.90 | up | 2.17E-05 |
| 8101126 | CXCL10 | chemokine (C-X-C motif) ligand 10 | 3627 | 4.90 | up | 2.11E-04 |
| 7946033 | HBB | hemoglobin, beta | 3043 | 4.58 | up | 0.0217883 |
| 8029693 | FOSB | FBJ murine osteosarcoma viral oncogene homolog B | 2354 | 4.54 | up | 4.84E-12 |
| 8134339 | PEG10 | paternally expressed 10 | 23089 | 4.51 | up | 0.0020475 |
| 8049425 | SPP2 | secreted phosphoprotein 2, 24kDa | 6694 | 4.46 | up | 7.52E-06 |
| 8104663 | CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | 1004 | 4.40 | up | 3.58E-16 |
| 8104079 | FAT | | 2195 | 4.39 | up | 1.53E-06 |
| 8041853 | TACSTD1 | tumor-associated calcium signal transducer 1 | 4072 | 4.37 | up | 4.08E-15 |
| 8126954 | PKHD1 | polycystic kidney and hepatic disease 1 (autosomal recessive) | 5314 | 4.36 | up | 6.95E-12 |
| 7967107 | C12orf27 | chromosome 12 open reading frame 27 | 283460 | 4.09 | up | 7.76E-06 |
| 8015991 | SLC4A1 | solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group) | 6521 | 4.06 | up | 1.74E-05 |
| 7976812 | SNORD113-4 | small nucleolar RNA, C/D box 113-4 | 767564 | 4.03 | up | 3.95E-07 |
| 7945680 | H19 | | 283120 | 3.92 | up | 0.0047741 |
| 7938366 | WEE1 | | 7465 | 3.91 | up | 6.35E-05 |

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| 7976810 | SNORD113-3 | small nucleolar RNA, C/D box 113-3 | 767563 | 3.86 | up | 2.45E-09 |
| 7976814 | SNORD114-2 | small nucleolar RNA, C/D box 114-2 | 767578 | 3.80 | up | 2.96E-09 |
| 7982090 | SNORD115-1\|SNRPN\|SNORD115-42\|SNORD115-6\|SNORD115-30\|SNORD115-34\|SNORD115-15\|SNORD115-21\|SNORD115-12\|SNORD115-13\|SNORD115-40\|SNORD115-5\|SNORD115-9\|SNORD115-10\|SNORD115-14\|HBII-52-24 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-30 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| HBII-52-24 snoRNA | 338433 \| 6638 \| 100033816 \| 100033443 \| 100033441 \| 100033804 \| 100033808 \| 100033453 \| 100033603 \| 100033449 \| 100033450 \| 100033814 \| 100033442 \| 100033446 \| 100033447 \| 100033451 \| 100036563 | 3.77 | up | 1.20E-05 |
| 8046922 | COL3A1 | collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) | 1281 | 3.77 | up | 1.42E-05 |
| 8117594 | HIST1H2BM | histone cluster 1, H2bm | 8342 | 3.77 | up | 0.0096238 |
| 7982032 | SNORD115-1\|SNRPN\|SNORD115-13\|SNORD115-16\|SNORD115-11\|SNORD115-12\|SNORD115-29\|SNORD115-36\|SNORD115-39\|SNORD115-40\|SNORD115-43\|SNORD115-5\|SNORD115-9\|SNORD115-10\|SNORD115-14\|SNORD115-21\|SNORD115-42 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-21 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-42 | 338433 \| 6638 \| 100033450 \| 100033454 \| 100033448 \| 100033449 \| 100033803 \| 100033810 \| 100033813 \| 100033814 \| 100033817 \| 100033442 \| 100033446 \| 100033447 \| 100033451 \| 100033603 \| 100033441 \| 100033816 | 3.75 | up | 5.28E-06 |

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|---|---|---|---|---|---|---|
| 8107769 | SLC12A2 | solute carrier family 12 (sodium/potassium/chloride transporters), member 2 | 6558 | 3.74 | up | 5.08E-14 |
| 7982038 | SNORD115-1\|SNRPN\|SNORD115-13\|SNORD115-16\|SNORD115-11\|SNORD115-12\|SNORD115-26\|SNORD115-29\|SNORD115-36\|SNORD115-39\|SNORD115-40\|SNORD115-41\|SNORD115-43\|SNORD115-9\|SNORD115-21\|SNORD115-34\|SNORD115-6 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-40 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-21 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-6 | 338433 \| 6638 \| 100033450 \| 100033454 \| 100033448 \| 100033449 \| 100033802 \| 100033803 \| 100033810 \| 100033813 \| 100033814 \| 100033815 \| 100033817 \| 100033446 \| 100033603 \| 100033808 \| 100033443 | 3.74 | up | 5.38E-06 |
| 7982008 | SNORD115-1\|SNRPN\|SNORD115-13\|SNORD115-16\|SNORD115-26\|SNORD115-41\|SNORD115-5 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-13 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-5 | 338433 \| 6638 \| 100033450 \| 100033454 \| 100033802 \| 100033815 \| 100033442 | 3.74 | up | 5.07E-06 |
| 8006594 | CCL18 | chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) | 6362 | 3.73 | up | 1.29E-12 |

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|---|---|---|---|---|---|---|
| 7982018 | SNORD115-1\|SNRPN\|SNORD115-6\|SNORD115-42\|SNORD115-30\|SNORD115-34\|SNORD115-15\|SNORD115-21\|SNORD115-11\|SNORD115-16\|SNORD115-26\|SNORD115-29\|SNORD115-36\|SNORD115-39\|SNORD115-41\|SNORD115-43\|SNORD115-14\|HBII-52-24 | small nucleolar RNA, C/D box 115-1 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-42 \| small nucleolar RNA, C/D box 115-4 \| small nucleolar RNA, C/D box 115-30 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-16 \| small nucleolar RNA, C/D box 115-26 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-41 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-14 \| HBII-52-24 snoRNA | 338433 \| 6638 \| 100033443 \| 100033816 \| 100033441 \| 100033804 \| 100033808 \| 100033453 \| 100033603 \| 100033448 \| 100033454 \| 100033802 \| 100033803 \| 100033810 \| 100033813 \| 100033815 \| 100033817 \| 100033451 \| 100036563 | 3.73 | up | 1.00E-05 |
| 8096301 | SPP1 | secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) | 6696 | 3.69 | up | 8.01E-09 |
| 7976795 | MEG3\|LOC100131839 | maternally expressed 3 \| hypothetical protein LOC100131839 | 55384 \| 100131839 | 3.64 | up | 1.43E-10 |
| 8020847 | DTNA | dystrobrevin, alpha | 1837 | 3.61 | up | 3.12E-12 |
| 8053801 | ANKRD36B\|FLJ40330\|LOC400986 | ankyrin repeat domain 36B \| hypothetical LOC645784 \| protein immuno-reactive with anti-PTH polyclonal antibodies | 57730 \| 645784 \| 400986 | 3.61 | up | 1.57E-04 |
| 7981943 | PAR5\|SNRPN\|SNORD64\|PAR-SN | Prader-Willi/Angelman syndrome-5 \| small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 64 \| paternally expressed transcript PAR-SN | 8123 \| 6638 \| 347686 \| 347746 | 3.59 | up | 1.74E-06 |
| 8044225 | SULT1C4 | sulfotransferase family, cytosolic, 1C, member 4 | 27233 | 3.58 | up | 6.13E-13 |
| 8177222 | CD24 | | 934 | 3.55 | up | 1.77E-06 |
| 8136336 | AKR1B10 | aldo-keto reductase family 1, member B10 (aldose reductase) | 57016 | 3.54 | up | 0.045463 |
| 7937772 | IGF2 | insulin-like growth factor 2 (somatomedin A) | 3481 | 3.50 | up | 1.37E-06 |
| 7927681 | BICC1 | bicaudal C homolog 1 (Drosophila) | 80114 | 3.43 | up | 4.36E-15 |
| 7988767 | CYP19A1 | cytochrome P450, family 19, subfamily A, polypeptide 1 | 1588 | 3.43 | up | 5.66E-10 |

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|---|---|---|---|---|---|---|
| 7982046 | SNRPN\|SNORD115-25\|SNORD115-20\|SNORD115-12\|SNORD115-5\|SNORD115-9\|SNORD115-11\|SNORD115-22\|SNORD115-29\|SNORD115-36\|SNORD115-43\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-39\|SNORD115-10\|SNORD115-14\|SNORD115-15\|SNORD115-21 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-25 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-12 \| small nucleolar RNA, C/D box 115-5 \| small nucleolar RNA, C/D box 115-9 \| small nucleolar RNA, C/D box 115-11 \| small nucleolar RNA, C/D box 115-22 \| small nucleolar RNA, C/D box 115-29 \| small nucleolar RNA, C/D box 115-36 \| small nucleolar RNA, C/D box 115-43 \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-3 \| small nucleolar RNA, C/D box 115-39 \| small nucleolar RNA, C/D box 115-10 \| small nucleolar RNA, C/D box 115-14 \| small nucleolar RNA, C/D box 115-15 \| small nucleolar RNA, C/D box 115-21 | 6638 \| 100033801 \| 100033460 \| 100033449 \| 100033442 \| 100033446 \| 100033448 \| 100033799 \| 100033803 \| 100033810 \| 100033817 \| 100033455 \| 100033456 \| 100033458 \| 100033440 \| 100033813 \| 100033447 \| 100033451 \| 100033453 \| 100033603 | 3.41 | up | 1.33E-06 |
| 8130867 | THBS2 | thrombospondin 2 | 7058 | 3.36 | up | 1.63E-06 |
| 7938364 | WEE1 | | 7465 | 3.35 | up | 9.65E-06 |
| 8057620 | COL5A2 | collagen, type V, alpha 2 | 1290 | 3.33 | up | 5.72E-10 |
| 7981947 | SNRPN\|SNORD109A\|SNORD109B | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 109A \| small nucleolar RNA, C/D box 109B | 6638 \| 338428 \| 338429 | 3.33 | up | 8.76E-06 |
| 7982098 | SNRPN\|SNORD109A\|SNORD109B | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 109A \| small nucleolar RNA, C/D box 109B | 6638 \| 338428 \| 338429 | 3.32 | up | 9.09E-06 |
| 8044212 | SULT1C2 | sulfotransferase family, cytosolic, 1C, member 2 | 6819 | 3.31 | up | 6.73E-07 |
| 7986512 | | | | 3.30 | up | 1.50E-06 |
| 7986527 | C15orf51 | chromosome 15 open reading frame 51 | 196968 | 3.30 | up | 1.44E-06 |
| 7986509 | LOC441734 | similar to hypothetical protein DKFZp434I1020 | 441734 | 3.30 | up | 1.50E-06 |
| 8014974 | TOP2A | topoisomerase (DNA) II alpha 170kDa | 7153 | 3.29 | up | 0.0064491 |
| 8175531 | CDR1 | cerebellar degeneration-related protein 1, 34kDa | 1038 | 3.28 | up | 1.28E-06 |

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|---|---|---|---|---|---|---|
| 7981982 | SNRPN\|SNORD116-17\|SNORD116-19\|SNORD116-15\|SNORD116-16\|SNORD116-18\|SNORD116-21\|SNORD116-22\|SNORD116-14\|SNORD116-20 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-17 \| small nucleolar RNA, C/D box 116-19 \| small nucleolar RNA, C/D box 116-15 \| small nucleolar RNA, C/D box 116-16 \| small nucleolar RNA, C/D box 116-18 \| small nucleolar RNA, C/D box 116-21 \| small nucleolar RNA, C/D box 116-22 \| small nucleolar RNA, C/D box 116-14 \| small nucleolar RNA, C/D box 116-20 | 6638 \| 100033429 \| 727708 \| 100033427 \| 100033428 \| 100033430 \| 100033432 \| 100033433 \| 100033426 \| 100033431 | 3.24 | up | 5.44E-05 |
| 7981986 | SNRPN\|SNORD116-17\|SNORD116-19\|SNORD116-15\|SNORD116-16\|SNORD116-18\|SNORD116-21\|SNORD116-22\|SNORD116-14\|SNORD116-20 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-17 \| small nucleolar RNA, C/D box 116-19 \| small nucleolar RNA, C/D box 116-15 \| small nucleolar RNA, C/D box 116-16 \| small nucleolar RNA, C/D box 116-18 \| small nucleolar RNA, C/D box 116-21 \| small nucleolar RNA, C/D box 116-22 \| small nucleolar RNA, C/D box 116-14 \| small nucleolar RNA, C/D box 116-20 | 6638 \| 100033429 \| 727708 \| 100033427 \| 100033428 \| 100033430 \| 100033432 \| 100033433 \| 100033426 \| 100033431 | 3.24 | up | 5.53E-05 |
| 8008151 | IGF2BP1 | insulin-like growth factor 2 mRNA binding protein 1 | 10642 | 3.24 | up | 2.00E-08 |
| 7921367 | SPTA1 | spectrin, alpha, erythrocytic 1 (elliptocytosis 2) | 6708 | 3.21 | up | 0.0011622 |
| 7935553 | LOXL4 | lysyl oxidase-like 4 | 84171 | 3.21 | up | 2.78E-12 |
| 8043697 | ANKRD36B\|FLJ40330\|LOC400986 | ankyrin repeat domain 36B \| hypothetical LOC645784 \| protein immuno-reactive with anti-PTH polyclonal antibodies | 57730 \| 645784 \| 400986 | 3.21 | up | 2.26E-04 |
| 7981996 | SNRPN\|SNORD116-24 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-24 | 6638 \| 100033435 | 3.21 | up | 1.61E-04 |
| 7957570 | PLXNC1 | plexin C1 | 10154 | 3.20 | up | 4.39E-06 |
| 7976783 | DLK1 | delta-like 1 homolog (Drosophila) | 8788 | 3.18 | up | 1.37E-06 |
| 7981976 | SNRPN\|SNORD116-14 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-14 | 6638 \| 100033426 | 3.15 | up | 5.44E-05 |
| 8054054 | ANKRD36B\|FLJ40330 | ankyrin repeat domain 36B \| hypothetical LOC645784 | 57730 \| 645784 | 3.14 | up | 9.25E-05 |
| 7981988 | SNRPN\|SNORD116-20\|SNORD116@ | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-20 \| small nucleolar RNA, C/D box 116 cluster | 6638 \| 100033431 \| 692236 | 3.14 | up | 3.41E-04 |
| 7981978 | SNRPN\|SNORD116-15 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-15 | 6638 \| 100033427 | 3.09 | up | 6.52E-04 |

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|---|---|---|---|---|---|---|
| 7992828 | IL32 | interleukin 32 | 9235 | 3.04 | up | 0.0011185 |
| 7986520 | | | | 3.03 | up | 1.80E-05 |
| 8099326 | SLC2A9 | solute carrier family 2 (facilitated glucose transporter), member 9 | 56606 | 3.00 | up | 1.43E-07 |
| 8021376 | NEDD4L | neural precursor cell expressed, developmentally down-regulated 4-like | 23327 | 2.97 | up | 6.42E-07 |
| 7903358 | VCAM1 | vascular cell adhesion molecule 1 | 7412 | 2.96 | up | 0.0019205 |
| 8169836 | XPNPEP2 | X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound | 7512 | 2.96 | up | 0.0141963 |
| 7996837 | CDH1 | cadherin 1, type 1, E-cadherin (epithelial) | 999 | 2.93 | up | 3.57E-04 |
| 7986517 | | | | 2.93 | up | 2.07E-04 |
| 8053797 | | | | 2.93 | up | 1.57E-04 |
| 7981945 | | | | 2.93 | up | 1.50E-07 |
| 7986522 | | | | 2.93 | up | 2.06E-04 |
| 8112920 | ACOT12 | acyl-CoA thioesterase 12 | 134526 | 2.91 | up | 0.0017396 |
| 8123388 | UNC93A | unc-93 homolog A (C. elegans) | 54346 | 2.90 | up | 8.73E-05 |
| 7948420 | FABP5\|FABP5L7 | fatty acid binding protein 5 (psoriasis-associated) \| fatty acid binding protein 5-like 7 | 2171 \| 728641 | 2.89 | up | 2.79E-06 |
| 7982056 | SNRPN\|SNORD115-25 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-25 | 6638 \| 100033801 | 2.88 | up | 1.16E-04 |
| 8108217 | TGFBI | transforming growth factor, beta-induced, 68kDa | 7045 | 2.85 | up | 1.82E-07 |
| 7902074 | LEPR\|LEPROT | leptin receptor \| leptin receptor overlapping transcript | 3953 \| 54741 | 2.85 | up | 2.68E-05 |
| 7906919 | RGS4 | regulator of G-protein signaling 4 | 5999 | 2.84 | up | 1.64E-08 |
| 8147049 | FABP5\|FABP5L7 | fatty acid binding protein 5 (psoriasis-associated) \| fatty acid binding protein 5-like 7 | 2171 \| 728641 | 2.84 | up | 3.69E-06 |
| 7970392 | | | | 2.79 | up | 0.0017841 |
| 8162373 | OGN | osteoglycin | 4969 | 2.78 | up | 2.59E-07 |
| 8000480 | | | | 2.78 | up | 1.67E-07 |
| 8059905 | COL6A3 | collagen, type VI, alpha 3 | 1293 | 2.76 | up | 1.54E-07 |
| 7927998 | HKDC1 | hexokinase domain containing 1 | 80201 | 2.74 | up | 0.0129315 |
| 8053834 | ANKRD36B | ankyrin repeat domain 36B \| ankyrin repeat domain 36 | 57730 \| 375248 | 2.72 | up | 1.02E-04 |
| 7965403 | LUM | lumican | 4060 | 2.71 | up | 2.76E-08 |
| 7975779 | FOS | v-fos FBJ murine osteosarcoma viral oncogene homolog | 2353 | 2.71 | up | 0.0076882 |
| 7981960 | SNRPN\|SNORD116-6 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-6 | 6638 \| 100033418 | 2.70 | up | 5.53E-05 |
| 7901293 | CYP4A22 | cytochrome P450, family 4, subfamily A, polypeptide 22 | 284541 | 2.69 | up | 1.15E-04 |

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|---|---|---|---|---|---|---|
| 7972750 | COL4A1 | collagen, type IV, alpha 1 | 1282 | 2.68 | up | 3.98E-08 |
| 8101757 | GPRIN3 | GPRIN family member 3 | 285513 | 2.68 | up | 0.0054822 |
| 7908204 | HMCN1 | hemicentin 1 | 83872 | 2.67 | up | 4.00E-10 |
| 8171297 | MID1 | midline 1 (Opitz/BBB syndrome) | 4281 | 2.65 | up | 1.83E-07 |
| 8088919 | ROBO1 | roundabout, axon guidance receptor, homolog 1 (Drosophila) | 6091 | 2.64 | up | 1.56E-07 |
| 8092021 | LRRC31 | leucine rich repeat containing 31 | 79782 | 2.61 | up | 6.84E-06 |
| 8151592 | CA1 | carbonic anhydrase I | 759 | 2.61 | up | 0.0060057 |
| 8175121 | IGSF1 | immunoglobulin superfamily, member 1 | 3547 | 2.61 | up | 1.17E-10 |
| 7988467 | FBN1 | fibrillin 1 | 2200 | 2.58 | up | 6.76E-07 |
| 7944867 | | | | 2.57 | up | 0.0129548 |
| 7909708 | CENPF | centromere protein F, 350/400ka (mitosin) | 1063 | 2.57 | up | 1.75E-05 |
| 7982004 | SNRPN\|SNORD116-28 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-28 | 6638 \| 100033820 | 2.56 | up | 1.57E-10 |
| 7919349 | RNU1A\|RNU1A3\|RNU1C1\|RNU1C2\|RNU1D2\|RNU1F1\|RNU1G3\|ATG9B | RNA, U1A small nuclear \| RNA, U1A3 small nuclear \| RNA, U1C1 small nuclear \| RNA, U1C2 small nuclear \| RNA, U1D2 small nuclear \| RNA, U1F1 small nuclear \| RNA, U1G3 small nuclear \| ATG9 autophagy related 9 homolog B (S. cerevisiae) | 6060 \| 26871 \| 26870 \| 26869 \| 26868 \| 26866 \| 26863 \| 28597 | 2.55 | up | 0.0103011 |
| 7919269 | RNU1A\|RNU1A3\|RNU1C1\|RNU1C2\|RNU1D2\|RNU1F1\|RNU1G3\|ATG9B | RNA, U1A small nuclear \| RNA, U1A3 small nuclear \| RNA, U1C1 small nuclear \| RNA, U1C2 small nuclear \| RNA, U1D2 small nuclear \| RNA, U1F1 small nuclear \| RNA, U1G3 small nuclear \| ATG9 autophagy related 9 homolog B (S. cerevisiae) | 6060 \| 26871 \| 26870 \| 26869 \| 26868 \| 26866 \| 26863 \| 28597 | 2.55 | up | 0.0103137 |
| 7986525 | | | | 2.54 | up | 0.0013242 |
| 7986515 | | | | 2.54 | up | 0.001342 |
| 8039607 | PEG3\|ZIM2 | paternally expressed 3 \| zinc finger, imprinted 2 | 5178 \| 23619 | 2.54 | up | 3.35E-10 |
| 7971653 | DLEU2 | deleted in lymphocytic leukemia, 2 | 8847 | 2.53 | up | 3.25E-05 |
| 8149248 | LRLE1\|LOC100127885 | liver-related low express protein 1 \| similar to liver-related low express protein 1 | 100133175 \| 100127885 | 2.52 | up | 4.97E-04 |
| 7923086 | ASPM | asp (abnormal spindle) homolog, microcephaly associated (Drosophila) | 259266 | 2.51 | up | 0.0019181 |
| 7957023 | LYZ | lysozyme (renal amyloidosis) | 4069 | 2.50 | up | 9.74E-06 |
| 7981964 | SNRPN\|SNORD116-8\|SNORD116-3\|SNORD116-9 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-8 \| small nucleolar RNA, C/D box 116-3 \| small nucleolar RNA, C/D box 116-9 | 6638 \| 100033420 \| 100033415 \| 100033421 | 2.49 | up | 0.0046185 |
| 8112668 | GCNT4 | glucosaminyl (N-acetyl) transferase 4, core 2 (beta-1,6-N-acetylglucosaminyltransferase) | 51301 | 2.48 | up | 1.17E-06 |

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|---|---|---|---|---|---|---|
| 8162394 | ASPN | asporin | 54829 | 2.48 | up | 3.66E-05 |
| 8138566 | IGF2BP3 | insulin-like growth factor 2 mRNA binding protein 3 | 10643 | 2.47 | up | 6.42E-07 |
| 8144228 | FLJ36840 | hypothetical LOC645524 | 645524 | 2.47 | up | 8.51E-04 |
| 8019842 | TYMS | thymidylate synthetase | 7298 | 2.47 | up | 0.0313901 |
| 7960771 | CD163L1 | CD163 molecule-like 1 | 283316 | 2.47 | up | 1.21E-05 |
| 8116992 | UNQ9364 | FLFF9364 | 100130515 | 2.47 | up | 4.98E-08 |
| 8021685 | CCDC102B | coiled-coil domain containing 102B | 79839 | 2.47 | up | 2.74E-07 |
| 8145134 | | | | 2.47 | up | 1.47E-05 |
| 7981919 | SNRPN\|SNURF | small nuclear ribonucleoprotein polypeptide N \| SNRPN upstream reading frame | 6638 \| 8926 | 2.46 | up | 1.79E-09 |
| 8124337 | SLC17A1 | solute carrier family 17 (sodium phosphate), member 1 | 6568 | 2.45 | up | 0.001258 |
| 7976816 | SNORD114-3 | small nucleolar RNA, C/D box 114-3 | 767579 | 2.45 | up | 2.64E-08 |
| 8113504 | C5orf13 | chromosome 5 open reading frame 13 | 9315 | 2.45 | up | 9.69E-04 |
| 8030866 | FPR3 | formyl peptide receptor 3 | 2359 | 2.45 | up | 3.54E-06 |
| 8114263 | LECT2 | leukocyte cell-derived chemotaxin 2 | 3950 | 2.44 | up | 0.0013685 |
| 7929047 | IFIT2 | interferon-induced protein with tetratricopeptide repeats 2 | 3433 | 2.44 | up | 1.55E-04 |
| 7982006 | SNRPN\|SNORD116-29 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-29 | 6638 \| 100033821 | 2.44 | up | 3.98E-08 |
| 8083301 | TM4SF4 | transmembrane 4 L six family member 4 | 7104 | 2.43 | up | 4.26E-05 |
| 8135661 | CFTR | cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7) | 1080 | 2.43 | up | 2.81E-12 |
| 8111490 | PRLR | prolactin receptor | 5618 | 2.42 | up | 2.63E-04 |
| 8007429 | G6PC | glucose-6-phosphatase, catalytic subunit | 2538 | 2.42 | up | 0.0235771 |
| 8042439 | ANTXR1 | anthrax toxin receptor 1 | 84168 | 2.41 | up | 1.25E-10 |
| 7979307 | DLG7 | discs, large homolog 7 (Drosophila) | 9787 | 2.41 | up | 4.96E-04 |
| 7951077 | SESN3 | sestrin 3 | 143686 | 2.40 | up | 0.0010338 |
| 8021416 | | | | 2.40 | up | 0.0241803 |
| 7981994 | SNRPN\|SNORD116-23 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-23 | 6638 \| 100033434 | 2.40 | up | 2.30E-07 |
| 8056222 | DPP4 | dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2) | 1803 | 2.39 | up | 0.0363338 |
| 7988789 | DMXL2 | Dmx-like 2 | 23312 | 2.38 | up | 6.29E-06 |
| 8089544 | CCDC80 | coiled-coil domain containing 80 | 151887 | 2.37 | up | 6.72E-09 |
| 8013341 | MFAP4 | microfibrillar-associated protein 4 | 4239 | 2.36 | up | 1.26E-05 |

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|---|---|---|---|---|---|---|
| 8094278 | NCAPG | non-SMC condensin I complex, subunit G | 64151 | 2.35 | up | 0.0251385 |
| 8124527 | HIST1H1B | histone cluster 1, H1b | 3009 | 2.34 | up | 0.0434773 |
| 7936734 | FGFR2 | fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) | 2263 | 2.34 | up | 2.03E-05 |
| 7982094 | SNRPN\|SNORD115-44 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-44 | 6638 \| 100033818 | 2.34 | up | 4.85E-04 |
| 8148070 | COL14A1 | collagen, type XIV, alpha 1 | 7373 | 2.33 | up | 2.24E-05 |
| 7913869 | STMN1 | stathmin 1/oncoprotein 18 | 3925 | 2.33 | up | 0.0019989 |
| 8022666 | CHST9 | carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 | 83539 | 2.33 | up | 3.78E-05 |
| 8168589 | ZNF711 | zinc finger protein 711 | 7552 | 2.32 | up | 1.99E-05 |
| 8054064 | ANKRD36B | ankyrin repeat domain 36B | 57730 | 2.32 | up | 0.0059245 |
| 7908917 | BTG2 | BTG family, member 2 | 7832 | 2.31 | up | 0.0304549 |
| 7937020 | MKI67 | antigen identified by monoclonal antibody Ki-67 | 4288 | 2.31 | up | 0.0045024 |
| 7970033 | COL4A2 | collagen, type IV, alpha 2 | 1284 | 2.30 | up | 2.50E-11 |
| 8173607 |  |  |  | 2.29 | up | 2.96E-04 |
| 8141094 | PDK4 | pyruvate dehydrogenase kinase, isozyme 4 | 5166 | 2.29 | up | 0.0188537 |
| 8112980 | EDIL3 | EGF-like repeats and discoidin I-like domains 3 | 10085 | 2.28 | up | 6.91E-11 |
| 7913824 | C1orf63 | chromosome 1 open reading frame 63 | 57035 | 2.28 | up | 9.01E-05 |
| 8104066 | SORBS2 | sorbin and SH3 domain containing 2 | 8470 | 2.28 | up | 9.65E-06 |
| 7957458 | NTS | neurotensin | 4922 | 2.26 | up | 7.84E-10 |
| 8100941 |  |  |  | 2.26 | up | 0.0061195 |
| 8102993 | GYPB | glycophorin B (MNS blood group) | 2994 | 2.26 | up | 0.0012284 |
| 8124388 | HIST1H3B\|HIST1H2BN\|HIST1H3A\|HIST1H3D\|HIST1H3C\|HIST1H3E\|HIST1H3I\|HIST1H3G\|HIST1H3J\|HIST1H3H\|HIST1H3F | histone cluster 1, H3b \| histone cluster 1, H2bn \| histone cluster 1, H3a \| histone cluster 1, H3d \| histone cluster 1, H3c \| histone cluster 1, H3e \| histone cluster 1, H3i \| histone cluster 1, H3g \| histone cluster 1, H3j \| histone cluster 1, H3h \| histone cluster 1, H3f | 8358 \| 8341 \| 8350 \| 8351 \| 8352 \| 8353 \| 8354 \| 8355 \| 8356 \| 8357 \| 8968 | 2.25 | up | 0.0194014 |
| 8133938 | CROT | carnitine O-octanoyltransferase | 54677 | 2.24 | up | 0.0034779 |
| 7914580 | FNDC5 | fibronectin type III domain containing 5 | 252995 | 2.24 | up | 1.16E-10 |
| 7969243 | CKAP2 | cytoskeleton associated protein 2 | 26586 | 2.23 | up | 0.0052901 |
| 7959893 | GPR133 | G protein-coupled receptor 133 | 283383 | 2.23 | up | 1.90E-05 |

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|---|---|---|---|---|---|---|
| 7984620 |  |  |  | 2.22 | up | 0.0435885 |
| 8144699 | LRLE1\|LOC100127885 | liver-related low express protein 1 \| similar to liver-related low express protein 1 | 100133175 \| 100127885 | 2.22 | up | 0.0026103 |
| 8115327 | SPARC | secreted protein, acidic, cysteine-rich (osteonectin) | 6678 | 2.22 | up | 1.61E-05 |
| 8007919 | LRRC37A2\|LRRC37A4 | leucine rich repeat containing 37, member A2 \| leucine rich repeat containing 37A \| leucine rich repeat containing 37, member A4 (pseudogene) | 474170 \| 9884 \| 55073 | 2.22 | up | 2.98E-05 |
| 8092418 | ABCC5 | ATP-binding cassette, sub-family C (CFTR/MRP), member 5 | 10057 | 2.21 | up | 2.77E-12 |
| 8043687 | ANKRD36 | ankyrin repeat domain 36 | 375248 | 2.21 | up | 0.0103723 |
| 8149555 | PSD3 | pleckstrin and Sec7 domain containing 3 | 23362 | 2.21 | up | 1.02E-05 |
| 7897801 | RNU5E | RNA, U5E small nuclear | 26829 | 2.21 | up | 6.70E-04 |
| 8058063 | RFTN2 | raftlin family member 2 | 130132 | 2.20 | up | 1.92E-05 |
| 8146788 |  |  |  | 2.20 | up | 5.52E-05 |
| 7982070 | SNRPN\|SNORD115-32 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-32 | 6638 \| 100033806 | 2.18 | up | 1.68E-05 |
| 8016245 | LRRC37A4\|LRRC37A3\|LOC652203\|LRRC37A2 | leucine rich repeat containing 37, member A4 (pseudogene) \| leucine rich repeat containing 37, member A3 \| hypothetical protein LOC652203 \| leucine rich repeat containing 37, member A2 | 55073 \| 374819 \| 652203 \| 474170 | 2.18 | up | 2.33E-05 |
| 8105828 | CCNB1 | cyclin B1 | 891 | 2.18 | up | 0.0010547 |
| 8117054 | CAP2 | CAP, adenylate cyclase-associated protein, 2 (yeast) | 10486 | 2.18 | up | 2.08E-04 |
| 7949971 | CPT1A | carnitine palmitoyltransferase 1A (liver) | 1374 | 2.18 | up | 3.13E-06 |
| 8162870 | BAAT | bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase) | 570 | 2.18 | up | 0.0426643 |
| 7929065 | IFIT1 | interferon-induced protein with tetratricopeptide repeats 1 | 3434 | 2.18 | up | 0.0132655 |
| 8178193 | HLA-DRA | major histocompatibility complex, class II, DR alpha | 3122 | 2.18 | up | 0.0018063 |
| 7953878 | CLEC2D | C-type lectin domain family 2, member D | 29121 | 2.17 | up | 2.64E-05 |
| 7981966 | SNRPN\|SNORD116-3\|SNORD116-9\|SNORD116-5\|SNORD116-7\|SNORD116-8 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-3 \| small nucleolar RNA, C/D box 116-9 \| small nucleolar RNA, C/D box 116-5 \| small nucleolar RNA, C/D box 116-7 \| small nucleolar RNA, C/D box 116-8 | 6638 \| 100033415 \| 100033421 \| 100033417 \| 100033419 \| 100033420 | 2.17 | up | 0.0149408 |
| 7924342 | SLC30A10 | solute carrier family 30, member 10 | 55532 | 2.17 | up | 5.70E-05 |
| 7926368 | VIM | vimentin | 7431 | 2.17 | up | 1.75E-07 |

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|---|---|---|---|---|---|---|
| 7981953 | SNRPN\|SNORD116-3\|SNORD116-9\|SNORD116-5\|SNORD116-7\|SNORD116-8 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-3 \| small nucleolar RNA, C/D box 116-9 \| small nucleolar RNA, C/D box 116-5 \| small nucleolar RNA, C/D box 116-7 \| small nucleolar RNA, C/D box 116-8 | 6638 \| 100033415 \| 100033421 \| 100033417 \| 100033419 \| 100033420 | 2.17 | up | 0.0149527 |
| 8083166 | TRPC1 | transient receptor potential cation channel, subfamily C, member 1 | 7220 | 2.16 | up | 3.14E-10 |
| 8121563 | MARCKS | myristoylated alanine-rich protein kinase C substrate | 4082 | 2.16 | up | 1.74E-06 |
| 7995237 | ERAF | erythroid associated factor | 51327 | 2.16 | up | 0.0088441 |
| 7982290 | | | | 2.15 | up | 2.72E-10 |
| 7991406 | PRC1 | protein regulator of cytokinesis 1 | 9055 | 2.15 | up | 0.0116963 |
| 8006906 | ERBB2 | v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) | 2064 | 2.15 | up | 3.95E-07 |
| 7958262 | TCP11L2 | t-complex 11 (mouse)-like 2 | 255394 | 2.15 | up | 1.34E-04 |
| 8000687 | LOC595101\|LOC440354\|LOC641298\|LOC440345 | PI-3-kinase-related kinase SMG-1 pseudogene \| hypothetical protein LOC440345 | 595101 \| 440354 \| 641298 \| 440345 | 2.15 | up | 0.0022317 |
| 8117018 | | | | 2.15 | up | 0.045068 |
| 8020139 | | | | 2.14 | up | 0.0043869 |
| 7982066 | SNRPN\|SNORD115-30\|SNORD115-6\|SNORD115-34\|SNORD115-8 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-30 \| small nucleolar RNA, C/D box 115-6 \| small nucleolar RNA, C/D box 115-34 \| small nucleolar RNA, C/D box 115-8 | 6638 \| 100033804 \| 100033443 \| 100033808 \| 100033445 | 2.14 | up | 2.89E-06 |
| 8089835 | FSTL1 | follistatin-like 1 | 11167 | 2.14 | up | 2.68E-05 |
| 8055465 | CXCR4 | chemokine (C-X-C motif) receptor 4 | 7852 | 2.14 | up | 4.13E-05 |
| 8041383 | LTBP1 | latent transforming growth factor beta binding protein 1 | 4052 | 2.14 | up | 4.51E-07 |
| 8156199 | DAPK1 | death-associated protein kinase 1 | 1612 | 2.13 | up | 3.84E-05 |
| 7951217 | MMP7 | matrix metallopeptidase 7 (matrilysin, uterine) | 4316 | 2.13 | up | 2.16E-12 |
| 8059376 | SERPINE2 | serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 | 5270 | 2.12 | up | 1.60E-06 |
| 8023528 | ALPK2 | alpha-kinase 2 | 115701 | 2.12 | up | 1.32E-05 |
| 8046695 | ITGA4 | integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) | 3676 | 2.12 | up | 3.69E-05 |

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|---|---|---|---|---|---|---|
| 8046861 | ITGAV | integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) | 3685 | 2.12 | up | 4.04E-06 |
| 7982042 | SNRPN\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-20\|SNORD115-25 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-25 | 6638 \| 100033455 \| 100033456 \| 100033458 \| 100033460 \| 100033801 | 2.11 | up | 3.52E-05 |
| 7982757 | CASC5 | cancer susceptibility candidate 5 | 57082 | 2.11 | up | 8.20E-04 |
| 8101762 | SNCA | synuclein, alpha (non A4 component of amyloid precursor) | 6622 | 2.11 | up | 1.95E-08 |
| 7982044 | SNRPN\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-20\|SNORD115-25 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-25 | 6638 \| 100033455 \| 100033456 \| 100033458 \| 100033460 \| 100033801 | 2.11 | up | 3.54E-05 |
| 7982040 | SNRPN\|SNORD115-17\|SNORD115-18\|SNORD115-19\|SNORD115-20\|SNORD115-25 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-17 \| small nucleolar RNA, C/D box 115-18 \| small nucleolar RNA, C/D box 115-19 \| small nucleolar RNA, C/D box 115-20 \| small nucleolar RNA, C/D box 115-25 | 6638 \| 100033455 \| 100033456 \| 100033458 \| 100033460 \| 100033801 | 2.11 | up | 4.10E-05 |
| 8008885 | MIRN21 | microRNA 21 | 406991 | 2.11 | up | 0.0010457 |
| 7983969 | CCNB2 | cyclin B2 | 9133 | 2.10 | up | 7.58E-04 |
| 7982020 | SNRPN\|SNORD115-7 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 115-7 | 6638 \| 100033444 | 2.10 | up | 2.24E-05 |
| 8149448 | MSR1 | macrophage scavenger receptor 1 | 4481 | 2.10 | up | 2.84E-05 |
| 7915902 | CYP4A11 | cytochrome P450, family 4, subfamily A, polypeptide 11 | 1579 | 2.09 | up | 0.0442879 |
| 8179481 | HLA-DRA | major histocompatibility complex, class II, DR alpha | 3122 | 2.09 | up | 0.0019278 |
| 7980908 | FBLN5 | fibulin 5 | 10516 | 2.08 | up | 0.006287 |
| 7934979 | ANKRD1 | ankyrin repeat domain 1 (cardiac muscle) | 27063 | 2.08 | up | 3.58E-16 |
| 8057394 | SESTD1 | SEC14 and spectrin domains 1 | 91404 | 2.08 | up | 3.65E-09 |
| 7908388 | RGS1 | regulator of G-protein signaling 1 | 5996 | 2.08 | up | 1.63E-06 |
| 8083282 | HPS3 | Hermansky-Pudlak syndrome 3 | 84343 | 2.07 | up | 5.97E-06 |
| 7993798 | | | | 2.07 | up | 7.52E-06 |
| 8104746 | NPR3 | natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C) | 4883 | 2.07 | up | 2.06E-06 |

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|---|---|---|---|---|---|---|
| 8015133 | KRT23 | keratin 23 (histone deacetylase inducible) | 25984 | 2.07 | up | 1.79E-10 |
| 8123920 | ELOVL2 | elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 | 54898 | 2.07 | up | 9.65E-05 |
| 7903227 | PALMD | palmdelphin | 54873 | 2.07 | up | 0.0126037 |
| 8084929 | OSTalpha | organic solute transporter alpha | 200931 | 2.07 | up | 1.33E-04 |
| 7957861 | TMEM16D | transmembrane protein 16D | 121601 | 2.06 | up | 7.03E-14 |
| 8067963 | | | | 2.05 | up | 5.19E-06 |
| 8117395 | HIST1H2BF\|HIST1H2BG\|HIST1H2BE\|HIST1H2BI\|HIST1H2BC | histone cluster 1, H2bf \| histone cluster 1, H2bg \| histone cluster 1, H2be \| histone cluster 1, H2bi \| histone cluster 1, H2bc | 8343 \| 8339 \| 8344 \| 8346 \| 8347 | 2.05 | up | 0.0175386 |
| 8052845 | TIA1 | | 7072 | 2.05 | up | 1.82E-09 |
| 7934936 | SLC16A12 | solute carrier family 16, member 12 (monocarboxylic acid transporter 12) | 387700 | 2.05 | up | 1.94E-06 |
| 7981955 | SNRPN\|SNORD116-4 | small nuclear ribonucleoprotein polypeptide N \| small nucleolar RNA, C/D box 116-4 | 6638 \| 100033416 | 2.05 | up | 7.91E-04 |
| 7989501 | CA12 | carbonic anhydrase XII | 771 | 2.04 | up | 3.31E-06 |
| 8118548 | HLA-DRA | major histocompatibility complex, class II, DR alpha | 3122 | 2.04 | up | 0.0015005 |
| 7957737 | TMPO | thymopoietin | 7112 | 2.04 | up | 1.94E-05 |
| 8061579 | TPX2 | | 22974 | 2.04 | up | 0.0308332 |
| 8000156 | LOC595101\|LOC440354\|LOC641298\|LOC440345 | PI-3-kinase-related kinase SMG-1 pseudogene \| hypothetical protein LOC440345 | 595101 \| 440354 \| 641298 \| 440345 | 2.04 | up | 0.0010173 |
| 8112274 | ELOVL7 | ELOVL family member 7, elongation of long chain fatty acids (yeast) | 79993 | 2.04 | up | 2.53E-12 |

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|---|---|---|---|---|---|---|
| 8178826 | HLA-DQB1\|LOC100133484\|LOC100133583\|LOC100133661\|LOC100133811\|HLA-DQB2\|HLA-DRB1\|HLA-DRB2\|HLA-DRB3\|HLA-DRB4\|HLA-DRB5\|ZNF749\|RNASE2\|LOC730415\|hCG_1998957 | major histocompatibility complex, class II, DQ beta 1 \| similar to Major histocompatibility complex, class II, DR beta 4 \| similar to major histocompatibility complex, class II, DQ beta 1 \| similar to HLA class II histocompatibility antigen, DR-W53 beta chain \| similar to hCG1992647 \| major histocompatibility complex, class II, DQ beta 2 \| major histocompatibility complex, class II, DR beta 1 \| major histocompatibility complex, class II, DR beta 2 (pseudogene) \| major histocompatibility complex, class II, DR beta 3 \| major histocompatibility complex, class II, DR beta 4 \| major histocompatibility complex, class II, DR beta 5 \| zinc finger protein 749 \| ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) \| hypothetical protein LOC730415 | 3119 \| 100133484 \| 100133583 \| 100133661 \| 100133811 \| 3120 \| 3123 \| 3124 \| 3125 \| 3126 \| 3127 \| 388567 \| 6036 \| 730415 \| 731247 | 2.04 | up | 6.72E-04 |
| 8002333 | LOC641298\|LOC729513 | PI-3-kinase-related kinase SMG-1 \| similar to PI-3-kinase-related kinase SMG-1 | 641298 \| 729513 | 2.04 | up | 4.11E-04 |
| 7926545 | PLXDC2 | plexin domain containing 2 | 84898 | 2.04 | up | 3.93E-08 |
| 8180022 | HLA-DQB1\|LOC100133484\|LOC100133583\|LOC100133661\|LOC100133811\|HLA-DQB2\|HLA-DRB1\|HLA-DRB2\|HLA-DRB3\|HLA-DRB4\|HLA-DRB5\|ZNF749\|RNASE2\|LOC730415\|hCG_1998957 | major histocompatibility complex, class II, DQ beta 1 \| similar to Major histocompatibility complex, class II, DR beta 4 \| similar to major histocompatibility complex, class II, DQ beta 1 \| similar to HLA class II histocompatibility antigen, DR-W53 beta chain \| similar to hCG1992647 \| major histocompatibility complex, class II, DQ beta 2 \| major histocompatibility complex, class II, DR beta 1 \| major histocompatibility complex, class II, DR beta 2 (pseudogene) \| major histocompatibility complex, class II, DR beta 3 \| major histocompatibility complex, class II, DR beta 4 \| major histocompatibility complex, class II, DR beta 5 \| zinc finger protein 749 \| ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) \| hypothetical protein LOC730415 | 3119 \| 100133484 \| 100133583 \| 100133661 \| 100133811 \| 3120 \| 3123 \| 3124 \| 3125 \| 3126 \| 3127 \| 388567 \| 6036 \| 730415 \| 731247 | 2.04 | up | 6.46E-04 |
| 8152719 | ANXA13 | annexin A13 | 312 | 2.03 | up | 3.64E-12 |
| 8135015 | MUC3B\|MUC3A | mucin 3B, cell surface associated \| mucin 3A, cell surface associated | 57876 \| 4584 | 2.03 | up | 0.0014165 |
| 8113073 | ARRDC3 | arrestin domain containing 3 | 57561 | 2.03 | up | 0.0062773 |
| 8081081 | EPHA3 | EPH receptor A3 | 2042 | 2.03 | up | 2.19E-06 |
| 8014903 | GSDML | gasdermin-like | 55876 | 2.02 | up | 2.21E-07 |
| 8056257 | FAP | fibroblast activation protein, alpha | 2191 | 2.02 | up | 6.13E-13 |
| 7933877 | JMJD1C | jumonji domain containing 1C | 221037 | 2.02 | up | 1.66E-04 |
| 8144726 | TUSC3 | tumor suppressor candidate 3 | 7991 | 2.02 | up | 1.52E-05 |

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|---|---|---|---|---|---|---|
| 7918323 | SORT1 | sortilin 1 | 6272 | 2.02 | up | 0.0035538 |
| 7979412 |  |  |  | 2.01 | up | 0.0011387 |
| 8133876 | CD36 |  | 948 | 2.01 | up | 0.0084876 |
| 8035779 | LOC100128975 | similar to Zinc finger protein 626 | 100128975 | 2.01 | up | 1.09E-07 |
| 8104758 | C5orf23 | chromosome 5 open reading frame 23 | 79614 | 2.01 | up | 1.92E-05 |
| 7973896 | RNU1A\|RNU1A3\|RNU1C1\|RNU1C2\|RNU1D2\|RNU1F1\|RNU1G3\|ATG9B | RNA, U1A small nuclear \| RNA, U1A3 small nuclear \| RNA, U1C1 small nuclear \| RNA, U1C2 small nuclear \| RNA, U1D2 small nuclear \| RNA, U1F1 small nuclear \| RNA, U1G3 small nuclear \| ATG9 autophagy related 9 homolog B (S. cerevisiae) | 6060 \| 26871 \| 26870 \| 26869 \| 26868 \| 26866 \| 26863 \| 285973 | 2.01 | up | 0.0146789 |
| 7952986 | HSN2 | hereditary sensory neuropathy, type II | 378465 | 2.01 | up | 4.58E-07 |
| 7930714 | ATRNL1 | attractin-like 1 | 26033 | 2.00 | up | 7.85E-04 |
| 8017885 | ABCA8 | ATP-binding cassette, sub-family A (ABC1), member 8 | 10351 | 2.00 | up | 0.0067433 |
| 7901316 | SLC5A9 | solute carrier family 5 (sodium/glucose cotransporter), member 9 | 200010 | 2.00 | up | 0.0024318 |
| 7978568 | RNU1A\|RNU1A3\|RNU1C1\|RNU1C2\|RNU1D2\|RNU1F1\|RNU1G3\|ATG9B | RNA, U1A small nuclear \| RNA, U1A3 small nuclear \| RNA, U1C1 small nuclear \| RNA, U1C2 small nuclear \| RNA, U1D2 small nuclear \| RNA, U1F1 small nuclear \| RNA, U1G3 small nuclear \| ATG9 autophagy related 9 homolog B (S. cerevisiae) | 6060 \| 26871 \| 26870 \| 26869 \| 26868 \| 26866 \| 26863 \| 285973 | 2.00 | up | 0.0147498 |
| 8155849 | ANXA1 | annexin A1 | 301 | 2.00 | up | 9.79E-06 |
| 8097692 | EDNRA | endothelin receptor type A | 1909 | 2.00 | up | 2.70E-06 |
| 8128886 |  |  |  | 2.00 | up | 0.0050198 |
| 7960744 | C1R | complement component 1, r subcomponent | 715 | 2.01 | down | 6.83E-08 |
| 7975167 | GPHN | gephyrin | 10243 | 2.01 | down | 4.27E-06 |
| 7917240 | CTBS | chitobiase, di-N-acetyl- | 1486 | 2.01 | down | 8.18E-05 |
| 7939056 | BBOX1 | butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 | 8424 | 2.01 | down | 0.0046943 |
| 8105121 | GHR | growth hormone receptor | 2690 | 2.01 | down | 2.87E-04 |
| 8038899 | FPR1 | formyl peptide receptor 1 | 2357 | 2.01 | down | 3.35E-04 |
| 8066757 | SLC13A3 | solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 | 64849 | 2.02 | down | 7.49E-04 |
| 7982185 | DEXI | dexamethasone-induced transcript | 28955 | 2.02 | down | 5.33E-05 |
| 7940160 | DTX4 | deltex 4 homolog (Drosophila) | 23220 | 2.02 | down | 4.11E-04 |
| 7986685 | DEXI | dexamethasone-induced transcript | 28955 | 2.02 | down | 4.81E-05 |
| 8072678 | HMOX1 | heme oxygenase (decycling) 1 | 3162 | 2.02 | down | 0.0199615 |
| 7998637 | SEPX1 | selenoprotein X, 1 | 51734 | 2.02 | down | 1.33E-06 |

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|---|---|---|---|---|---|---|
| 8019778 | PCYT2 | phosphate cytidylyltransferase 2, ethanolamine | 5833 | 2.02 | down | 1.32E-04 |
| 7928944 | PAPSS2 | 3'-phosphoadenosine 5'-phosphosulfate synthase 2 | 9060 | 2.03 | down | 0.0016682 |
| 8078956 | | | | 2.03 | down | 0.0032253 |
| 7937330 | IFITM2 | interferon induced transmembrane protein 2 (1-8D) | 10581 | 2.03 | down | 0.0013199 |
| 8016578 | SLC35B1 | solute carrier family 35, member B1 | 10237 | 2.04 | down | 0.0170945 |
| 8139299 | POLD2 | polymerase (DNA directed), delta 2, regulatory subunit 50kDa | 5425 | 2.04 | down | 0.0020946 |
| 8102249 | AGXT2L1 | alanine-glyoxylate aminotransferase 2-like 1 | 64850 | 2.04 | down | 0.0143308 |
| 8051012 | PREB | prolactin regulatory element binding | 10113 | 2.05 | down | 7.55E-04 |
| 7925342 | ERO1LB | ERO1-like beta (S. cerevisiae) | 56605 | 2.05 | down | 0.0100739 |
| 8167305 | EBP | emopamil binding protein (sterol isomerase) | 10682 | 2.05 | down | 2.78E-05 |
| 8124365 | SLC17A2 | solute carrier family 17 (sodium phosphate), member 2 | 10246 | 2.06 | down | 0.0073506 |
| 7939492 | LOC387763 | | 387763 | 2.07 | down | 6.24E-04 |
| 8110803 | CLPTM1L\|LOC100133849 | CLPTM1-like \| hypothetical protein LOC100133849 | 81037 \| 100133849 | 2.07 | down | 3.18E-04 |
| 8051583 | CYP1B1 | cytochrome P450, family 1, subfamily B, polypeptide 1 | 1545 | 2.08 | down | 8.04E-04 |
| 8080184 | ALAS1 | aminolevulinate, delta-, synthase 1 | 211 | 2.08 | down | 0.0259599 |
| 7914563 | YARS | tyrosyl-tRNA synthetase | 8565 | 2.09 | down | 0.027602 |
| 8092691 | BCL6 | B-cell CLL/lymphoma 6 (zinc finger protein 51) | 604 | 2.09 | down | 0.0011054 |
| 8040340 | LPIN1 | lipin 1 | 23175 | 2.09 | down | 0.0085946 |
| 8103695 | MFAP3L | microfibrillar-associated protein 3-like | 9848 | 2.09 | down | 2.14E-05 |
| 8059565 | PID1 | phosphotyrosine interaction domain containing 1 | 55022 | 2.09 | down | 1.91E-05 |
| 8063177 | SLC2A10 | solute carrier family 2 (facilitated glucose transporter), member 10 | 81031 | 2.10 | down | 0.0053374 |
| 8112020 | MOCS2 | molybdenum cofactor synthesis 2 | 4338 | 2.11 | down | 0.0081735 |
| 7946167 | HPX | hemopexin | 3263 | 2.11 | down | 6.00E-14 |
| 8148317 | MYC\|LOC100130526 | v-myc myelocytomatosis viral oncogene homolog (avian) \| similar to ORF 114 | 4609 \| 100130526 | 2.11 | down | 0.0028702 |
| 8071559 | SDF2L1 | stromal cell-derived factor 2-like 1 | 23753 | 2.12 | down | 0.0134014 |
| 8043981 | IL1R2 | interleukin 1 receptor, type II | 7850 | 2.12 | down | 2.72E-04 |
| 7969651 | DNAJC3 | DnaJ (Hsp40) homolog, subfamily C, member 3 | 5611 | 2.14 | down | 0.0304863 |
| 8018864 | SOCS3 | suppressor of cytokine signaling 3 | 9021 | 2.14 | down | 3.49E-05 |
| 8165817 | GYG2 | glycogenin 2 | 8908 | 2.14 | down | 9.11E-04 |
| 7898655 | CDA | cytidine deaminase | 978 | 2.14 | down | 2.34E-07 |
| 8113232 | | | | 2.14 | down | 0.0033106 |

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| 7925939 | AKR1C4 | aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4) | 1109 | 2.14 | down | 7.64E-04 |
| 8170590 | NSDHL | NAD(P) dependent steroid dehydrogenase-like | 50814 | 2.14 | down | 3.98E-04 |
| 7940135 | GLYATL1 | glycine-N-acyltransferase-like 1 | 92292 | 2.15 | down | 1.25E-04 |
| 7954344 | LST-3TM12\|SLCO1B1\|SLCO1B3 | organic anion transporter LST-3b \| solute carrier organic anion transporter family, member 1B1 \| solute carrier organic anion transporter family, member 1B3 | 338821 \| 10599 \| 28234 | 2.15 | down | 0.0441345 |
| 8025303 | CLEC4M | C-type lectin domain family 4, member M | 10332 | 2.15 | down | 8.20E-04 |
| 7920238 | S100A12 | S100 calcium binding protein A12 | 6283 | 2.16 | down | 0.0309626 |
| 7956401 | SHMT2 | serine hydroxymethyltransferase 2 (mitochondrial) | 6472 | 2.16 | down | 3.89E-04 |
| 7919984 | SELENBP1 | selenium binding protein 1 | 8991 | 2.17 | down | 1.50E-05 |
| 8081219 | ST3GAL6 | ST3 beta-galactoside alpha-2,3-sialyltransferase 6 | 10402 | 2.17 | down | 2.31E-04 |
| 7961710 | ABCC9 | ATP-binding cassette, sub-family C (CFTR/MRP), member 9 | 10060 | 2.17 | down | 0.0046689 |
| 8051187 | FNDC4 | fibronectin type III domain containing 4 | 64838 | 2.17 | down | 4.77E-05 |
| 8126770 | CYP39A1 | cytochrome P450, family 39, subfamily A, polypeptide 1 | 51302 | 2.18 | down | 0.0023213 |
| 8106280 | HMGCR | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase | 3156 | 2.18 | down | 0.0121007 |
| 7934755 | MAT1A | methionine adenosyltransferase I, alpha | 4143 | 2.18 | down | 1.82E-09 |
| 8003332 | MVD | mevalonate (diphospho) decarboxylase | 4597 | 2.19 | down | 0.0011452 |
| 8066619 | PLTP | phospholipid transfer protein | 5360 | 2.19 | down | 0.0038094 |
| 7926786 | APBB1IP | amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein | 54518 | 2.19 | down | 1.39E-05 |
| 7923547 | CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39) | 1116 | 2.20 | down | 0.0368772 |
| 7995729 | CES4\|CES1\|LOC652708 | carboxylesterase 4-like \| carboxylesterase 1 (monocyte/macrophage serine esterase 1) \| similar to Liver carboxylesterase 1 precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1) (Triacylglycerol hydrolase) (TGH) (Egasyn)... | 51716 \| 1066 \| 652708 | 2.20 | down | 0.0140703 |
| 7952145 | HYOU1 | hypoxia up-regulated 1 | 10525 | 2.21 | down | 0.0332143 |
| 8080212 | GLYCTK | glycerate kinase | 132158 | 2.21 | down | 1.18E-05 |
| 7918558 | KCND3 | potassium voltage-gated channel, Shal-related subfamily, member 3 | 3752 | 2.21 | down | 8.90E-05 |
| 7958565 | MVK | mevalonate kinase | 4598 | 2.22 | down | 1.44E-08 |
| 8051998 | MCFD2 | multiple coagulation factor deficiency 2 | 90411 | 2.22 | down | 0.013714 |

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|---|---|---|---|---|---|---|
| 7944656 | SC5DL | sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like | 6309 | 2.23 | down | 2.32E-05 |
| 7931863 | ASB13 | ankyrin repeat and SOCS box-containing 13 | 79754 | 2.23 | down | 0.0090872 |
| 7960730 | MBOAT5 | membrane bound O-acyltransferase domain containing 5 | 10162 | 2.23 | down | 6.28E-04 |
| 8015607 | STAT3 | signal transducer and activator of transcription 3 (acute-phase response factor) | 6774 | 2.25 | down | 1.50E-06 |
| 8151032 | GGH | gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase) | 8836 | 2.25 | down | 0.0018451 |
| 7908312 | PRG4 | proteoglycan 4 | 10216 | 2.25 | down | 3.59E-07 |
| 8157270 | SLC31A1 | solute carrier family 31 (copper transporters), member 1 | 1317 | 2.26 | down | 4.19E-04 |
| 7983910 | AQP9 | aquaporin 9 | 366 | 2.26 | down | 2.55E-04 |
| 8105040 | OSMR | oncostatin M receptor | 9180 | 2.26 | down | 8.10E-04 |
| 7997192 | HPR | haptoglobin-related protein | 3250 | 2.27 | down | 1.79E-09 |
| 8048319 | VIL1 | villin 1 | 7429 | 2.27 | down | 5.73E-04 |
| 7989023 | RAB27A |  | 5873 | 2.27 | down | 2.88E-04 |
| 8126153 | KCNK5 | potassium channel, subfamily K, member 5 | 8645 | 2.28 | down | 0.0101595 |
| 8002629 | PKD1L3 | polycystic kidney disease 1-like 3 | 342372 | 2.28 | down | 0.0146214 |
| 8121838 | TPD52L1 | tumor protein D52-like 1 | 7164 | 2.28 | down | 0.0017903 |
| 7936871 | OAT | ornithine aminotransferase (gyrate atrophy) | 4942 | 2.29 | down | 0.0132995 |
| 7906465 | OR10J6P | olfactory receptor, family 10, subfamily J, member 6 pseudogene | 401973 | 2.30 | down | 3.38E-06 |
| 7905986 | FDPS | farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase) | 2224 | 2.30 | down | 3.38E-06 |
| 7991846 | DECR2 | 2,4-dienoyl CoA reductase 2, peroxisomal | 26063 | 2.31 | down | 8.29E-13 |
| 8013135 | SREBF1 | sterol regulatory element binding transcription factor 1 | 6720 | 2.32 | down | 0.0024022 |
| 8095705 | MTHFD2L | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like | 441024 | 2.34 | down | 7.48E-04 |
| 8091243 | PCOLCE2 | procollagen C-endopeptidase enhancer 2 | 26577 | 2.34 | down | 9.65E-06 |
| 8057004 | PDE11A | phosphodiesterase 11A | 50940 | 2.34 | down | 1.66E-04 |
| 7943882 | PTS | 6-pyruvoyltetrahydropterin synthase | 5805 | 2.34 | down | 0.0011209 |
| 8024323 | REEP6 | receptor accessory protein 6 | 92840 | 2.35 | down | 3.15E-12 |
| 8145122 | SLC39A14 | solute carrier family 39 (zinc transporter), member 14 | 23516 | 2.36 | down | 1.29E-05 |
| 8125919 | FKBP5\|LOC285847 | FK506 binding protein 5 \| hypothetical protein LOC285847 | 2289 \| 285847 | 2.37 | down | 0.0253458 |
| 7914075 | FCN3 | ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen) | 8547 | 2.37 | down | 3.80E-05 |
| 8126760 | RCAN2 | regulator of calcineurin 2 | 10231 | 2.37 | down | 0.005563 |

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|---|---|---|---|---|---|---|
| 7937335 | IFITM1 | interferon induced transmembrane protein 1 (9-27) | 8519 | 2.37 | down | 0.0184161 |
| 7909306 | C4BPB | complement component 4 binding protein, beta | 725 | 2.38 | down | 2.57E-04 |
| 8113491 | STARD4 | StAR-related lipid transfer (START) domain containing 4 | 134429 | 2.39 | down | 2.31E-05 |
| 8021741 | CNDP1 | carnosine dipeptidase 1 (metallopeptidase M20 family) | 84735 | 2.39 | down | 0.0033179 |
| 8166797 | MID1IP1 | MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish)) | 58526 | 2.39 | down | 1.32E-04 |
| 8005839 | TMEM97 | transmembrane protein 97 | 27346 | 2.39 | down | 1.92E-05 |
| 8144866 | NAT2 | N-acetyltransferase 2 (arylamine N-acetyltransferase) | 10 | 2.40 | down | 0.0070346 |
| 7912975 | ALDH4A1 | aldehyde dehydrogenase 4 family, member A1 | 8659 | 2.40 | down | 1.70E-06 |
| 8101893 | ADH1C | alcohol dehydrogenase 1C (class I), gamma polypeptide | 126 | 2.41 | down | 5.40E-04 |
| 7946972 | SAA3P | serum amyloid A3 pseudogene | 6290 | 2.41 | down | 1.75E-04 |
| 7972650 | FGF14 | fibroblast growth factor 14 | 2259 | 2.42 | down | 2.86E-05 |
| 7906904 | HSD17B7\|HSD17B7P2 | hydroxysteroid (17-beta) dehydrogenase 7 \| hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2 | 51478 \| 158160 | 2.42 | down | 5.21E-05 |
| 8090314 | ALDH1L1 | aldehyde dehydrogenase 1 family, member L1 | 10840 | 2.42 | down | 0.0100982 |
| 8013788 | FLOT2 | flotillin 2 | 2319 | 2.43 | down | 1.06E-04 |
| 8056102 | CD302 | | 9936 | 2.45 | down | 4.70E-05 |
| 8066493 | SLPI | secretory leukocyte peptidase inhibitor | 6590 | 2.46 | down | 6.39E-04 |
| 7940565 | FADS2 | fatty acid desaturase 2 | 9415 | 2.46 | down | 0.001805 |
| 7981051 | SERPINA10 | serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10 | 51156 | 2.46 | down | 1.16E-04 |
| 8175492 | ATP11C | ATPase, class VI, type 11C | 286410 | 2.46 | down | 5.04E-05 |
| 7940775 | RARRES3 | retinoic acid receptor responder (tazarotene induced) 3 | 5920 | 2.47 | down | 9.49E-04 |
| 7993126 | ABAT | 4-aminobutyrate aminotransferase | 18 | 2.47 | down | 9.65E-06 |
| 8151042 | TTPA | tocopherol (alpha) transfer protein | 7274 | 2.48 | down | 2.97E-06 |
| 8111019 | DNAH5 | dynein, axonemal, heavy chain 5 | 1767 | 2.50 | down | 0.0011046 |
| 8020183 | IMPA2 | inositol(myo)-1(or 4)-monophosphatase 2 | 3613 | 2.50 | down | 0.0025857 |
| 7963826 | PPP1R1A | protein phosphatase 1, regulatory (inhibitor) subunit 1A | 5502 | 2.50 | down | 1.41E-05 |
| 8111864 | C6 | complement component 6 | 729 | 2.50 | down | 1.70E-06 |
| 7921492 | IGSF9 | immunoglobulin superfamily, member 9 | 57549 | 2.50 | down | 0.0065589 |
| 8062461 | LBP | lipopolysaccharide binding protein | 3929 | 2.50 | down | 2.87E-04 |
| 8144669 | FDFT1 | farnesyl-diphosphate farnesyltransferase 1 | 2222 | 2.52 | down | 2.01E-05 |
| 8137526 | INSIG1 | insulin induced gene 1 | 3638 | 2.52 | down | 0.0038548 |

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| 7970793 | SLC46A3 | solute carrier family 46, member 3 | 283537 | 2.52 | down | 2.01E-04 |
| 8100994 | CXCL2 | chemokine (C-X-C motif) ligand 2 | 2920 | 2.54 | down | 7.31E-04 |
| 8044793 | STEAP3 | STEAP family member 3 | 55240 | 2.55 | down | 5.86E-05 |
| 8100798 | SULT1B1 | sulfotransferase family, cytosolic, 1B, member 1 | 27284 | 2.55 | down | 0.0133791 |
| 8172905 | HSD17B10 | hydroxysteroid (17-beta) dehydrogenase 10 | 3028 | 2.56 | down | 4.30E-11 |
| 8062844 | C20orf121 | chromosome 20 open reading frame 121 | 79183 | 2.56 | down | 0.0019838 |
| 7900510 | CTPS | CTP synthase | 1503 | 2.57 | down | 2.08E-04 |
| 8148572 | LY6E | lymphocyte antigen 6 complex, locus E | 4061 | 2.57 | down | 9.32E-05 |
| 8073890 | GRAMD4 | GRAM domain containing 4 | 23151 | 2.58 | down | 1.59E-04 |
| 7956658 | SLC16A7 | solute carrier family 16, member 7 (monocarboxylic acid transporter 2) | 9194 | 2.58 | down | 8.59E-04 |
| 8044574 | IL1RN | interleukin 1 receptor antagonist | 3557 | 2.58 | down | 0.0021362 |
| 7936494 | GFRA1 | GDNF family receptor alpha 1 | 2674 | 2.59 | down | 6.76E-07 |
| 8086330 | AXUD1 | AXIN1 up-regulated 1 | 64651 | 2.59 | down | 0.0011446 |
| 7901513 | SCP2 | sterol carrier protein 2 | 6342 | 2.59 | down | 2.22E-08 |
| 8013112 | RASD1 | RAS, dexamethasone-induced 1 | 51655 | 2.60 | down | 0.0019838 |
| 7931754 | IDI1 | isopentenyl-diphosphate delta isomerase 1 | 3422 | 2.61 | down | 1.98E-05 |
| 7997188 | HP | haptoglobin | 3240 | 2.62 | down | 7.86E-14 |
| 8070961 | LSS | lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) | 4047 | 2.63 | down | 6.95E-08 |
| 8161174 | GNE | glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase | 10020 | 2.64 | down | 7.25E-06 |
| 8077441 | BHLHB2 | basic helix-loop-helix domain containing, class B, 2 | 8553 | 2.65 | down | 1.08E-05 |
| 8101852 | ADH4 | alcohol dehydrogenase 4 (class II), pi polypeptide | 127 | 2.66 | down | 0.0036862 |
| 7904396 | HAO2 | hydroxyacid oxidase 2 (long chain) | 51179 | 2.67 | down | 0.0043701 |
| 8099897 | UGDH | UDP-glucose dehydrogenase | 7358 | 2.68 | down | 0.0379411 |
| 7920244 | S100A8 | S100 calcium binding protein A8 | 6279 | 2.71 | down | 0.0108286 |
| 8020955 | MOCOS | molybdenum cofactor sulfurase | 55034 | 2.71 | down | 4.04E-04 |
| 7995803 | MT1JP\|MT1M | metallothionein 1J (pseudogene) \| metallothionein 1M | 4498 \| 4499 | 2.72 | down | 7.40E-04 |
| 7929478 | CYP2C19 | cytochrome P450, family 2, subfamily C, polypeptide 19 | 1557 | 2.73 | down | 0.0020065 |
| 7929466 | CYP2C18\|CYP2C19 | cytochrome P450, family 2, subfamily C, polypeptide 18 \| cytochrome P450, family 2, subfamily C, polypeptide 19 | 1562 \| 1557 | 2.74 | down | 3.22E-05 |
| 8070557 | ZNF295 | zinc finger protein 295 | 49854 | 2.74 | down | 2.91E-04 |
| 8103706 | AADAT | aminoadipate aminotransferase | 51166 | 2.76 | down | 3.18E-04 |

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|---|---|---|---|---|---|---|
| 7942603 | MOGAT2 | monoacylglycerol O-acyltransferase 2 | 80168 | 2.78 | down | 7.69E-06 |
| 8035083 | CYP4F2 | cytochrome P450, family 4, subfamily F, polypeptide 2 | 8529 | 2.79 | down | 1.74E-06 |
| 8140840 | STEAP4 | STEAP family member 4 | 79689 | 2.79 | down | 0.0106021 |
| 8102342 | ELOVL6 | ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast) | 79071 | 2.80 | down | 0.0017808 |
| 8113369 | SLCO4C1 | solute carrier organic anion transporter family, member 4C1 | 353189 | 2.81 | down | 8.98E-04 |
| 8078933 | MYRIP | myosin VIIA and Rab interacting protein | 25924 | 2.81 | down | 7.08E-05 |
| 8136459 | AKR1D1 | aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) | 6718 | 2.81 | down | 0.0150441 |
| 8075390 | SEC14L4 | SEC14-like 4 (S. cerevisiae) | 284904 | 2.82 | down | 8.37E-05 |
| 7946977 | SAA4 | serum amyloid A4, constitutive | 6291 | 2.83 | down | 3.65E-07 |
| 8013243 | SHMT1 | serine hydroxymethyltransferase 1 (soluble) | 6470 | 2.85 | down | 4.85E-07 |
| 8013660 | ALDOC | aldolase C, fructose-bisphosphate | 230 | 2.86 | down | 1.53E-04 |
| 7991374 | IDH2 | isocitrate dehydrogenase 2 (NADP+), mitochondrial | 3418 | 2.87 | down | 5.58E-05 |
| 7964292 | RDH16 | retinol dehydrogenase 16 (all-trans) | 8608 | 2.91 | down | 1.70E-04 |
| 8113214 | GLRX | glutaredoxin (thioltransferase) | 2745 | 2.93 | down | 2.43E-04 |
| 8153474 | TSTA3 | tissue specific transplantation antigen P35B | 7264 | 2.93 | down | 4.15E-04 |
| 7939590 | SLC35C1 | solute carrier family 35, member C1 | 55343 | 2.94 | down | 0.0010173 |
| 8123137 | ACAT2 | acetyl-Coenzyme A acetyltransferase 2 | 39 | 2.95 | down | 2.75E-07 |
| 8111474 | AGXT2 | alanine-glyoxylate aminotransferase 2 | 64902 | 2.96 | down | 6.33E-06 |
| 8019357 | DCXR | dicarbonyl/L-xylulose reductase | 51181 | 2.97 | down | 1.28E-04 |
| 8099612 | GPR125 | G protein-coupled receptor 125 | 166647 | 2.98 | down | 7.85E-10 |
| 7909318 | C4BPA | complement component 4 binding protein, alpha | 722 | 3.03 | down | 4.02E-07 |
| 7906458 | APCS | amyloid P component, serum | 325 | 3.04 | down | 3.78E-07 |
| 8066214 | TGM2 | transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) | 7052 | 3.05 | down | 3.62E-04 |
| 7928308 | DDIT4 | DNA-damage-inducible transcript 4 | 54541 | 3.10 | down | 0.0013198 |
| 7954330 | SLCO1B3\|SLCO1B1\|LST-3TM12 | solute carrier organic anion transporter family, member 1B3 \| solute carrier organic anion transporter family, member 1B1 \| organic anion transporter LST-3b | 28234 \| 10599 \| 338821 | 3.10 | down | 8.71E-05 |
| 7948612 | FADS1\|FADS3 | fatty acid desaturase 1 \| fatty acid desaturase 3 | 3992 \| 3995 | 3.14 | down | 5.89E-05 |
| 8088642 | LRIG1 | leucine-rich repeats and immunoglobulin-like domains 1 | 26018 | 3.15 | down | 1.14E-04 |
| 8101637 | HSD17B13 | hydroxysteroid (17-beta) dehydrogenase 13 | 345275 | 3.15 | down | 0.0219071 |
| 8106999 | C5orf27 | chromosome 5 open reading frame 27 | 202299 | 3.18 | down | 3.67E-06 |

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|---|---|---|---|---|---|---|
| 8130608 | LPA | lipoprotein, Lp(a) | 4018 | 3.19 | down | 0.006898 |
| 7995806 | MT1A | metallothionein 1A | 4489 | 3.19 | down | 7.20E-04 |
| 7956271 | HSD17B6 | hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse) | 8630 | 3.24 | down | 3.52E-06 |
| 8111941 | HMGCS1 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble) | 3157 | 3.25 | down | 2.96E-05 |
| 8025522 | LOC388503 | similar to Complement C3 precursor | 388503 | 3.28 | down | 6.65E-04 |
| 8035095 | CYP4F11 | cytochrome P450, family 4, subfamily F, polypeptide 11 | 57834 | 3.28 | down | 8.18E-07 |
| 7976496 | SERPINA3 | serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 | 12 | 3.38 | down | 8.78E-07 |
| 8148280 | SQLE | squalene epoxidase | 6713 | 3.41 | down | 2.49E-06 |
| 8094361 | GBA3 | glucosidase, beta, acid 3 (cytosolic) | 57733 | 3.45 | down | 4.96E-05 |
| 8007454 | RND2 | Rho family GTPase 2 | 8153 | 3.49 | down | 2.58E-04 |
| 7995838 | MT1X | metallothionein 1X | 4501 | 3.50 | down | 4.26E-06 |
| 8019392 | FASN | fatty acid synthase | 2194 | 3.68 | down | 3.99E-05 |
| 8119620 | GNMT | glycine N-methyltransferase | 27232 | 3.69 | down | 0.0019784 |
| 8157450 | ORM2 | orosomucoid 2 | 5005 | 3.70 | down | 4.57E-11 |
| 8062041 | ACSS2 | acyl-CoA synthetase short-chain family member 2 | 55902 | 3.70 | down | 2.88E-08 |
| 7935169 | CYP2C8 | cytochrome P450, family 2, subfamily C, polypeptide 8 | 1558 | 3.71 | down | 0.0023986 |
| 8142120 | NAMPT | nicotinamide phosphoribosyltransferase | 10135 | 3.72 | down | 3.37E-11 |
| 7948987 | HRASLS3 | HRAS-like suppressor 3 | 11145 | 3.74 | down | 3.75E-05 |
| 7965873 | IGF1 | insulin-like growth factor 1 (somatomedin C) | 3479 | 3.74 | down | 5.95E-04 |
| 8081288 | TMEM45A | transmembrane protein 45A | 55076 | 3.75 | down | 1.83E-07 |
| 7943867 | BCO2 | beta-carotene oxygenase 2 | 83875 | 3.80 | down | 0.0072235 |
| 7933084 | NAMPT | nicotinamide phosphoribosyltransferase | 10135 | 3.81 | down | 1.04E-10 |
| 8098195 | SC4MOL | sterol-C4-methyl oxidase-like | 6307 | 3.82 | down | 2.96E-09 |
| 8157446 | ORM1 | orosomucoid 1 | 5004 | 3.83 | down | 3.77E-13 |
| 8028955 | CYP2B7P1 | cytochrome P450, family 2, subfamily B, polypeptide 7 pseudogene 1 | 1556 | 3.91 | down | 0.0379944 |
| 8123232 | SLC22A1 | solute carrier family 22 (organic cation transporter), member 1 | 6580 | 3.97 | down | 7.63E-04 |
| 7995739 | GNAO1 | guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O | 2775 | 4.04 | down | 6.19E-05 |
| 8051030 | SLC5A6 | solute carrier family 5 (sodium-dependent vitamin transporter), member 6 | 8884 | 4.06 | down | 3.80E-05 |
| 7958466 | ACACB | acetyl-Coenzyme A carboxylase beta | 32 | 4.09 | down | 1.20E-12 |
| 8091863 | SLITRK3 | SLIT and NTRK-like family, member 3 | 22865 | 4.20 | down | 1.96E-04 |

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|---|---|---|---|---|---|---|
| 7960984 | PZP | pregnancy-zone protein | 5858 | 4.28 | down | 0.0022229 |
| 8111757 | C9 | complement component 9 | 735 | 4.31 | down | 1.04E-12 |
| 8156043 | PSAT1 | phosphoserine aminotransferase 1 | 29968 | 4.40 | down | 5.48E-06 |
| 8149885 | ADRA1A | adrenergic, alpha-1A-, receptor | 148 | 4.50 | down | 1.73E-12 |
| 8028963 | CYP2B6 | cytochrome P450, family 2, subfamily B, polypeptide 6 | 1555 | 4.58 | down | 0.0205225 |
| 7909446 | HSD11B1 | hydroxysteroid (11-beta) dehydrogenase 1 | 3290 | 4.84 | down | 4.09E-06 |
| 7990839 | STARD5 | StAR-related lipid transfer (START) domain containing 5 | 80765 | 4.91 | down | 5.86E-05 |
| 7964142 | APOF | apolipoprotein F | 319 | 5.13 | down | 5.47E-08 |
| 7997179 | DHODH | dihydroorotate dehydrogenase | 1723 | 5.51 | down | 1.65E-06 |
| 7988990 | WDR72 | WD repeat domain 72 | 256764 | 5.63 | down | 4.03E-06 |
| 7898693 | ALPL | alkaline phosphatase, liver/bone/kidney | 249 | 5.69 | down | 7.40E-07 |
| 7908492 | CFHR4 | complement factor H-related 4 | 10877 | 5.74 | down | 9.06E-06 |
| 7964660 | AVPR1A | arginine vasopressin receptor 1A | 552 | 5.91 | down | 3.06E-04 |
| 7995787 | MT1M | metallothionein 1M | 4499 | 5.92 | down | 0.0014687 |
| 7908499 | CFHR5 | complement factor H-related 5 | 81494 | 6.11 | down | 7.35E-06 |
| 7990391 | CYP1A1 | cytochrome P450, family 1, subfamily A, polypeptide 1 | 1543 | 6.18 | down | 0.0061888 |
| 7913216 | PLA2G2A | phospholipase A2, group IIA (platelets, synovial fluid) | 5320 | 6.19 | down | 0.0010423 |
| 8027819 | HAMP | hepcidin antimicrobial peptide | 57817 | 6.24 | down | 5.12E-11 |
| 8032834 | LRG1 | leucine-rich alpha-2-glycoprotein 1 | 116844 | 6.31 | down | 3.90E-06 |
| 7979658 | GPX2 | glutathione peroxidase 2 (gastrointestinal) | 2877 | 6.83 | down | 1.91E-05 |
| 8154135 | SLC1A1 | solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1 | 6505 | 6.85 | down | 2.05E-05 |
| 7943998 | NNMT | nicotinamide N-methyltransferase | 4837 | 7.65 | down | 1.44E-08 |
| 7921449 | CRP | C-reactive protein, pentraxin-related | 1401 | 8.64 | down | 1.92E-05 |
| 7900365 | MFSD2 | major facilitator superfamily domain containing 2 | 84879 | 8.84 | down | 3.77E-09 |
| 8114964 | SPINK1 | serine peptidase inhibitor, Kazal type 1 | 6690 | 10.59 | down | 9.91E-06 |
| 8047300 | AOX1 | aldehyde oxidase 1 | 316 | 12.61 | down | 9.48E-15 |
| 7942793 | THRSP | thyroid hormone responsive (SPOT14 homolog, rat) | 7069 | 13.99 | down | 5.36E-07 |
| 7984862 | CYP1A2 | cytochrome P450, family 1, subfamily A, polypeptide 2 | 1544 | 14.89 | down | 3.96E-04 |
| 8103769 | HPGD | hydroxyprostaglandin dehydrogenase 15-(NAD) | 3248 | 16.94 | down | 7.01E-09 |
| 7946986 | SAA1 | serum amyloid A1 | 6288 | 41.71 | down | 8.92E-08 |
| 7946983 | SAA2\|SAA1 | serum amyloid A2 \| serum amyloid A1 | 6289 \| 6288 | 72.07 | down | 1.31E-12 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 7938758 | SAA1\|SAA2 | serum amyloid A1 \| serum amyloid A2 | 6288 \| 6289 | 98.42 | down | 6.00E-14 |

**Supplementary Table 2**

Results of Random Forest Analysis to determine the impact of gene groups on the accuracy of identifying patients into the biliary atresia or diseased control groups.

| Diagnosis | Biliary atresia (n=64) | | DC (n=14) | | |
|---|---|---|---|---|---|
| Tested genes | Classification | | Classification | | Accuracy |
| | Biliary atresia | DC | Biliary atresia | DC | |
| All of the 15 genes | 63 | 1 | 5 | 9 | 92.3% |
| Top 5 genes (*IL8*, *LAMC2*, *TM4SF1*, *HAS2*, *VTCN1*) | 63 | 1 | 5 | 9 | 92.3% |
| Top 4 genes (*IL8*, *LAMC2*, *TM4SF1*, *HAS2*) | 63 | 1 | 3 | 11 | 94.9% |
| Top 3 genes (*IL8*, *LAMC2*, *TM4SF1*) | 63 | 1 | 4 | 10 | 93.6% |
| Top 2 genes (*IL8*, *LAMC2*) | 63 | 1 | 3 | 11 | 94.9% |

Random Forest Analyses were performed using the expression levels of the genes listed in the first column. The ranking is based on the degree of impact on the accuracy in the first analysis using all of the 15 genes as shown in Figure. Accuracies were calculated as 100 minus out of bag error estimate.

# Supplementary Table 3

List of biological processes overrepresented by the 15 genes.

| ID | Name | P-value | Hit in Query List |
|---|---|---|---|
| GO:0050921 | positive regulation of chemotaxis | 0.00E+00 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0050920 | regulation of chemotaxis | 0.00E+00 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0048520 | positive regulation of behavior | 0.00E+00 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0050795 | regulation of behavior | 0.00E+00 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0006935 | chemotaxis | 0.00E+00 | ITGA2, CCL20, SERPINE1, CCL2, IL8, THBS1 |
| GO:0042330 | taxis | 0.00E+00 | ITGA2, CCL20, SERPINE1, CCL2, IL8, THBS1 |
| GO:0050900 | leukocyte migration | 0.00E+00 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0032103 | positive regulation of response to external stimulus | 0.00E+00 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0002687 | positive regulation of leukocyte migration | 0.00E+00 | ITGA2, SERPINE1, CCL2, THBS1 |
| GO:0002685 | regulation of leukocyte migration | 0.00E+00 | ITGA2, SERPINE1, CCL2, THBS1 |
| GO:0040017 | positive regulation of locomotion | 0.00E+00 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0007626 | locomotory behavior | 0.00E+00 | ITGA2, CCL20, SERPINE1, CCL2, IL8, THBS1 |
| GO:0009611 | response to wounding | 0.00E+00 | ITGA2, CCL20, SERPINE1, VCAN, CCL2, IL8, THBS1 |
| GO:0040011 | locomotion | 0.00E+00 | ITGA2, CCL20, SERPINE1, VCAN, CCL2, IL8, THBS1 |
| GO:0030595 | leukocyte chemotaxis | 0.00E+00 | SERPINE1, CCL2, IL8, THBS1 |
| GO:0060326 | cell chemotaxis | 0.00E+00 | SERPINE1, CCL2, IL8, THBS1 |
| GO:0032101 | regulation of response to external stimulus | 0.00E+00 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0002690 | positive regulation of leukocyte chemotaxis | 1.00E-06 | SERPINE1, CCL2, THBS1 |
| GO:0016477 | cell migration | 1.00E-06 | ITGA2, SERPINE1, VCAN, CCL2, IL8, THBS1 |
| GO:0002688 | regulation of leukocyte chemotaxis | 1.00E-06 | SERPINE1, CCL2, THBS1 |
| GO:0040012 | regulation of locomotion | 1.00E-06 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0048870 | cell motility | 1.00E-06 | ITGA2, SERPINE1, VCAN, CCL2, IL8, THBS1 |

|  |  |  |  |
|---|---|---|---|
| GO:0010757 | negative regulation of plasminogen activation | 1.00E-06 | SERPINE1, THBS1 |
| GO:0007610 | behavior | 2.00E-06 | ITGA2, CCL20, SERPINE1, CCL2, IL8, THBS1 |
| GO:0048584 | positive regulation of response to stimulus | 2.00E-06 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0009888 | tissue development | 3.00E-06 | ITGA2, SERPINE1, AREG, LAMC2, VCAN, EMP1, THBS1 |
| GO:0010755 | regulation of plasminogen activation | 3.00E-06 | SERPINE1, THBS1 |
| GO:0016525 | negative regulation of angiogenesis | 3.00E-06 | SERPINE1, CCL2, THBS1 |
| GO:0030335 | positive regulation of cell migration | 3.00E-06 | ITGA2, SERPINE1, CCL2, THBS1 |
| GO:0051272 | positive regulation of cellular component movement | 4.00E-06 | ITGA2, SERPINE1, CCL2, THBS1 |
| GO:0009887 | organ morphogenesis | 4.00E-06 | ITGA2, SERPINE1, AREG, EMP1, CCL2, IL8, THBS1 |
| GO:0010759 | positive regulation of macrophage chemotaxis | 4.00E-06 | CCL2, THBS1 |
| GO:0009605 | response to external stimulus | 5.00E-06 | ITGA2, CCL20, SERPINE1, VCAN, CCL2, IL8, THBS1 |
| GO:0006928 | cellular component movement | 6.00E-06 | ITGA2, SERPINE1, VCAN, CCL2, IL8, THBS1 |
| GO:0006954 | inflammatory response | 6.00E-06 | ITGA2, CCL20, CCL2, IL8, THBS1 |
| GO:0071674 | mononuclear cell migration | 7.00E-06 | CCL2, THBS1 |
| GO:0071675 | regulation of mononuclear cell migration | 7.00E-06 | CCL2, THBS1 |
| GO:0010758 | regulation of macrophage chemotaxis | 7.00E-06 | CCL2, THBS1 |
| GO:0006952 | defense response | 7.00E-06 | ITGA2, CCL20, SERPINE1, CCL2, IL8, THBS1 |
| GO:0002376 | immune system process | 8.00E-06 | ITGA2, CCL20, SERPINE1, VTCN1, CCL2, IL8, THBS1 |
| GO:0071622 | regulation of granulocyte chemotaxis | 9.00E-06 | CCL2, THBS1 |
| GO:0071621 | granulocyte chemotaxis | 9.00E-06 | CCL2, THBS1 |
| GO:0031639 | plasminogen activation | 9.00E-06 | SERPINE1, THBS1 |
| GO:0008283 | cell proliferation | 1.10E-05 | ITGA2, SERPINE1, AREG, EMP1, CCL2, IL8, THBS1 |
| GO:0030155 | regulation of cell adhesion | 1.10E-05 | ITGA2, SERPINE1, IL8, THBS1 |
| GO:0010955 | negative regulation of protein maturation by peptide bond cleavage | 1.30E-05 | SERPINE1, THBS1 |
| GO:0002682 | regulation of immune system process | 1.70E-05 | ITGA2, SERPINE1, VTCN1, CCL2, THBS1 |
| GO:0007155 | cell adhesion | 1.80E-05 | ITGA2, LAMC2, VCAN, CCL2, IL8, THBS1 |
| GO:0022610 | biological adhesion | 1.80E-05 | ITGA2, LAMC2, VCAN, CCL2, IL8, THBS1 |
| GO:0009725 | response to hormone stimulus | 1.90E-05 | ITGA2, SERPINE1, AREG, CCL2, THBS1 |

| | | | |
|---|---|---|---|
| GO:0051918 | negative regulation of fibrinolysis | 2.00E-05 | SERPINE1, THBS1 |
| GO:0001525 | angiogenesis | 2.30E-05 | SERPINE1, CCL2, IL8, THBS1 |
| GO:0031638 | zymogen activation | 2.50E-05 | SERPINE1, THBS1 |
| GO:0002548 | monocyte chemotaxis | 2.50E-05 | SERPINE1, CCL2 |
| GO:0042060 | wound healing | 2.50E-05 | ITGA2, SERPINE1, VCAN, THBS1 |
| GO:0030334 | regulation of cell migration | 2.70E-05 | ITGA2, SERPINE1, CCL2, THBS1 |
| GO:0048545 | response to steroid hormone stimulus | 2.80E-05 | SERPINE1, AREG, CCL2, THBS1 |
| GO:0042127 | regulation of cell proliferation | 3.10E-05 | ITGA2, SERPINE1, AREG, CCL2, IL8, THBS1 |
| GO:0009719 | response to endogenous stimulus | 3.10E-05 | ITGA2, SERPINE1, AREG, CCL2, THBS1 |
| GO:0010953 | regulation of protein maturation by peptide bond cleavage | 3.50E-05 | SERPINE1, THBS1 |
| GO:0051917 | regulation of fibrinolysis | 3.50E-05 | SERPINE1, THBS1 |
| GO:0051270 | regulation of cellular component movement | 3.80E-05 | ITGA2, SERPINE1, CCL2, THBS1 |
| GO:0048583 | regulation of response to stimulus | 3.90E-05 | ITGA2, SERPINE1, CCL2, IL8, THBS1 |
| GO:0030194 | positive regulation of blood coagulation | 4.10E-05 | SERPINE1, THBS1 |
| GO:0070613 | regulation of protein processing | 4.10E-05 | SERPINE1, THBS1 |
| GO:0048246 | macrophage chemotaxis | 4.70E-05 | CCL2, THBS1 |
| GO:0045765 | regulation of angiogenesis | 4.90E-05 | SERPINE1, CCL2, THBS1 |
| GO:0031099 | regeneration | 5.20E-05 | SERPINE1, VCAN, CCL2 |
| GO:0002684 | positive regulation of immune system process | 5.20E-05 | ITGA2, SERPINE1, CCL2, THBS1 |
| GO:0048514 | blood vessel morphogenesis | 5.30E-05 | SERPINE1, CCL2, IL8, THBS1 |
| GO:0051384 | response to glucocorticoid stimulus | 5.90E-05 | SERPINE1, AREG, CCL2 |
| GO:0050820 | positive regulation of coagulation | 6.10E-05 | SERPINE1, THBS1 |
| GO:0022603 | regulation of anatomical structure morphogenesis | 6.40E-05 | ITGA2, SERPINE1, EMP1, CCL2, THBS1 |
| GO:0042730 | fibrinolysis | 6.80E-05 | SERPINE1, THBS1 |
| GO:0006909 | phagocytosis | 1.27E-03 | ITGA2, THBS1 |

# Supplementary Table 4

Curated protein-protein interaction of the 15 molecular signature genes and their direct neighbors.

| **Interactant 1** | | | **Interactant 2** | | | | |
|---|---|---|---|---|---|---|---|
| **Gene symbol** | **HPRD ID** | **RefSeq ID** | **Gene symbol** | **HPRD ID** | **RefSeq ID** | **Experiment type** | **Pubmed ID** |
| SERPINE1 | 1418 | NP_000593.1 | PLG | 1417 | NP_000292.1 | in vitro | 11113116 |
| THBS1 | 1765 | NP_003237.2 | PLG | 1417 | NP_000292.1 | in vitro | 2522013 |
| THBS1 | 1765 | NP_003237.2 | ITGB3 | 1428 | NP_000203.2 | in vitro | 2478219 |
| THBS1 | 1765 | NP_003237.2 | CD36 | 1430 | NP_000063.2 | in vivo | 10772961, 10487979 |
| THBS1 | 1765 | NP_003237.2 | F2 | 1488 | NP_000497.1 | in vivo | 2435757 |
| SERPINE1 | 1418 | NP_000593.1 | LRP1 | 138 | NP_002323.2 | in vitro; in vivo | 15001579 |
| THBS1 | 1765 | NP_003237.2 | LRP1 | 138 | NP_002323.2 | in vitro; in vivo | 9045712, 14991768 |
| THBS1 | 1765 | NP_003237.2 | SPARC | 1631 | NP_003109.1 | in vitro | 2745554 |
| TM4SF1 | 1854 | NP_055035.1 | SDCBP2 | 18032 | NP_536737.3 | in vitro; in vivo; yeast 2-hybrid | 11102519 |
| THBS1 | 1765 | NP_003237.2 | CALR | 169 | NP_004334.1 | in vitro | 12147682 |
| IL8 | 909 | NP_000575.1 | DARC | 192 | NP_001116423.1 | in vitro; in vivo | 9921412, 17416748 |
| CCL2 | 1149 | NP_002973.1 | DARC | 192 | NP_001116423.1 | in vitro; in vivo | 13679391, 17416748 |
| LAMC2 | 1031 | NP_005553.2 | BMP1 | 209 | NP_006120.1 | in vitro; in vivo | 10806203 |
| CCL20 | 3571 | NP_004582.1 | CCR6 | 3498 | NP_004358.2 | in vitro; in vivo | 9223454, 9169459, 9294137 |
| SERPINE1 | 1418 | NP_000593.1 | UBQLN4 | 5670 | NP_064516.2 | yeast 2-hybrid | 16713569 |
| VCAN | 340 | NP_004376.2 | HAPLN1 | 275 | NP_001875.1 | in vitro | 12888576 |
| VTCN1 | 6429 | NP_078902.2 | BTLA | 6392 | NP_861445.3 | in vitro; in vivo | 12796776 |
| THBS1 | 1765 | NP_003237.2 | CTSG | 289 | NP_001902.1 | in vitro | 8408036 |
| ITGA2 | 1893 | NP_002194.2 | ITGB1 | 628 | NP_391987.1 | in vitro; in vivo | 1690718, 1693624, 3546305, 14681217 |
| CCL2 | 1149 | NP_002973.1 | VCAN | 340 | NP_004376.2 | in vitro | 11083865 |
| CCL20 | 3571 | NP_004582.1 | VCAN | 340 | NP_004376.2 | in vitro | 11083865 |
| LAMC2 | 1031 | NP_005553.2 | COL7A1 | 358 | NP_000085.1 | in vitro; in vivo | 9989793 |
| THBS1 | 1765 | NP_003237.2 | COL7A1 | 358 | NP_000085.1 | yeast 2-hybrid | 9840442 |
| TM4SF1 | 1854 | NP_055035.1 | DDR1 | 2678 | NP_054700.2 | yeast 2-hybrid | 16169070 |
| THBS1 | 1765 | NP_003237.2 | COL2A1 | 361 | NP_001835.3 | in vitro | 3571333 |
| THBS1 | 1765 | NP_003237.2 | COL1A1 | 362 | NP_000079.2 | in vitro | 3571333 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ITGA2 | 1893 | NP_002194.2 | COL1A1 | 362 | NP_000079.2 | in vitro; in vivo | 11359786, 11856343, 2156854 |
| ITGA2 | 1893 | NP_002194.2 | ACTA1 | 30 | NP_001091.1 | in vitro | 7503723 |
| ITGA2 | 1893 | NP_002194.2 | COL1A2 | 363 | NP_000080.2 | in vitro | 2156854 |
| THBS1 | 1765 | NP_003237.2 | COL3A1 | 365 | NP_000081.1 | in vitro | 3571333 |
| THBS1 | 1765 | NP_003237.2 | COL5A1 | 368 | NP_000084.3 | in vivo | 6693501, 9840442 |
| ITGA2 | 1893 | NP_002194.2 | COL8A1 | 372 | NP_001841.2 | in vitro | 12482545, 10666376 |
| ITGA2 | 1893 | NP_002194.2 | MMP1 | 384 | NP_002412.1 | in vitro; in vivo | 11359774, 11359786 |
| THBS1 | 1765 | NP_003237.2 | MMP2 | 386 | NP_004521.1 | in vitro; in vivo; yeast 2-hybrid | 10900205 |
| THBS1 | 1765 | NP_003237.2 | MMP9 | 387 | NP_004985.2 | in vitro; in vivo; yeast 2-hybrid | 10900205, 11606713 |
| IL8 | 909 | NP_000575.1 | PF4 | 1426 | NP_002610.1 | in vitro; in vivo | 15531763, 12586630 |
| AREG | 93 | NP_001648.1 | UBQLN4 | 5670 | NP_064516.2 | yeast 2-hybrid | 16713569 |
| TM4SF1 | 1854 | NP_055035.1 | TUBA4A | 1851 | NP_005991.1 | yeast 2-hybrid | 16169070 |
| THBS1 | 1765 | NP_003237.2 | DCN | 501 | NP_001911.1 | in vitro; in vivo | 9328841, 1550960 |
| THBS1 | 1765 | NP_003237.2 | DHFR | 519 | NP_000782.1 | in vitro | 10749676 |
| SERPINE1 | 1418 | NP_000593.1 | KRT18 | 1020 | NP_000215.1 | in vitro; yeast 2-hybrid | 15493875 |
| SERPINE1 | 1418 | NP_000593.1 | ELANE | 554 | NP_001963.1 | in vitro | 7521069 |
| THBS1 | 1765 | NP_003237.2 | ELANE | 554 | NP_001963.1 | in vitro | 8463250 |
| LAMC2 | 1031 | NP_005553.2 | NID1 | 574 | NP_002499.2 | in vitro | 11733994 |
| THBS1 | 1765 | NP_003237.2 | FGA | 619 | NP_000499.1 | in vitro | 9867861 |
| THBS1 | 1765 | NP_003237.2 | FN1 | 626 | NP_997647.1 | in vitro | 11773026 |
| LAMC2 | 1031 | NP_005553.2 | FBLN2 | 630 | NP_001004019.1 | in vitro | 11733994 |
| SERPINE1 | 1418 | NP_000593.1 | ORM1 | 724 | NP_000598.2 | in vitro; yeast 2-hybrid | 11418606 |
| IL8 | 909 | NP_000575.1 | GNAI2 | 764 | NP_002061.1 | in vivo | 8662698 |
| THBS1 | 1765 | NP_003237.2 | HRG | 812 | NP_000403.1 | in vivo | 6438154 |
| SERPINE1 | 1418 | NP_000593.1 | IGFBP5 | 901 | NP_000590.1 | in vitro; in vivo | 9202242 |
| THBS1 | 1765 | NP_003237.2 | IGFBP5 | 901 | NP_000590.1 | in vivo | 10698186 |
| IL8 | 909 | NP_000575.1 | CXCR2 | 907 | NP_001548.1 | in vitro; in vivo | 9464567, 8702798, 8626516 |
| IL8 | 909 | NP_000575.1 | CXCR1 | 908 | NP_000625.1 | in vitro; in vivo | 1840701 |
| THBS1 | 1765 | NP_003237.2 | LAMB3 | 1032 | NP_000219.2 | in vivo; yeast 2-hybrid | 9840442 |
| ITGA2 | 1893 | NP_002194.2 | LAMA1 | 1033 | NP_005550.2 | in vitro | 9688542 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| THBS1 | 1765 | NP_003237.2 | TFPI | 1064 | NP_006278.1 | in vitro | 10922378 |
| VCAN | 340 | NP_004376.2 | CD44 | 115 | NP_000601.3 | in vitro | 10950950 |
| PLAT | 1419 | NP_000921.1 | SERPINE1 | 1418 | NP_000593.1 | in vitro; in vivo | 2110366, 8607113, 3090045 |
| F2 | 1488 | NP_000497.1 | SERPINE1 | 1418 | NP_000593.1 | in vitro | 10543954 |
| MMP3 | 1703 | NP_002413.1 | SERPINE1 | 1418 | NP_000593.1 | in vitro | 10967118 |
| PLAU | 1883 | NP_002649.1 | SERPINE1 | 1418 | NP_000593.1 | in vitro; in vivo | 2161846, 2544876, 3090045 |
| VTN | 1902 | NP_000629.3 | SERPINE1 | 1418 | NP_000593.1 | in vitro; in vivo | 8830783, 11796824, 9065424, 12808446 |
| LRP2 | 2509 | NP_004516.2 | SERPINE1 | 1418 | NP_000593.1 | in vitro | 8344937 |
| LRP1B | 16383 | NP_061027.2 | SERPINE1 | 1418 | NP_000593.1 | in vivo | 11384978 |
| PDGFB | 1815 | NP_002599.1 | THBS1 | 1765 | NP_003237.2 | in vivo | 9334164 |
| TGFB1 | 1821 | NP_000651.3 | THBS1 | 1765 | NP_003237.2 | in vivo | 1550960 |
| KNG1 | 1970 | NP_001095886.1 | THBS1 | 1765 | NP_003237.2 | in vivo | 9459346 |
| CD47 | 3017 | NP_001768.1 | THBS1 | 1765 | NP_003237.2 | in vivo | 9169439, 8550562, 10397731 |
| SCARB2 | 3772 | NP_005497.1 | THBS1 | 1765 | NP_003237.2 | in vitro | 9478926 |
| LRP5 | 4616 | NP_002326.2 | THBS1 | 1765 | NP_003237.2 | in vivo | 7775583 |
| CORO1A | 5414 | NP_009005.1 | THBS1 | 1765 | NP_003237.2 | in vitro | 10749676 |
| AUP1 | 3892 | NP_036235.1 | ITGA2 | 1893 | NP_002194.2 | yeast 2-hybrid | 12042322 |
| CTSL1 | 293 | NP_001903.1 | IL8 | 909 | NP_000575.1 | in vitro | 12818188 |
| SELPLG | 2845 | Q14242 | VCAN | 340 | NP_004376.2 | in vitro; in vivo; yeast 2-hybrid | 15522894 |
| CD9 | 880 | NP_001760.1 | ITGA2 | 1893 | NP_002194.2 | in vivo | 9812906, 9813091 |
| HSPG2 | 804 | NP_005520.4 | ITGA2 | 1893 | NP_002194.2 | in vitro | 15240572 |
| ANPEP | 1055 | NP_001141.2 | TM4SF1 | 1854 | NP_055035.1 | in vitro; in vivo | 15812828 |
| FBN1 | 618 | NP_000129.2 | VCAN | 340 | NP_004376.2 | in vitro | 11726670 |
| ITGB1 | 628 | NP_391987.1 | VCAN | 340 | NP_004376.2 | in vivo | 11805102 |
| FBLN1 | 629 | NP_006477.2 | VCAN | 340 | NP_004376.2 | in vitro | 10400671 |
| FBLN2 | 630 | NP_001004019.1 | VCAN | 340 | NP_004376.2 | in vitro | 11038354 |
| CXCL10 | 930 | NP_001556.2 | VCAN | 340 | NP_004376.2 | in vitro | 11083865 |
| TNFAIP6 | 2680 | NP_009046.2 | THBS1 | 1765 | NP_003237.2 | in vitro | 16006654 |
| PLA2G2A | 1397 | NP_000291.1 | VCAN | 340 | NP_004376.2 | in vitro | 9848887, 8824283 |
| SELP | 1433 | NP_002996.2 | VCAN | 340 | NP_004376.2 | in vitro | 10950950 |
| CCL5 | 1751 | NP_002976.2 | VCAN | 340 | NP_004376.2 | in vitro | 11083865 |
| ITGA4 | 1894 | NP_000876.3 | VCAN | 340 | NP_004376.2 | in vitro | 11083865 |
| XCL1 | 2595 | NP_002986.1 | VCAN | 340 | NP_004376.2 | in vitro | 11083865 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| TNR | 3589 | NP_003276.3 | VCAN | 340 | NP_004376.2 | in vivo | 9294172 |
| CCL8 | 3791 | NP_005614.2 | VCAN | 340 | NP_004376.2 | in vitro | 11083865 |
| CCL21 | 4113 | NP_002980.1 | VCAN | 340 | NP_004376.2 | in vitro | 11083865 |
| ADAMTS1 | 5530 | NP_008919.3 | VCAN | 340 | NP_004376.2 | in vitro; in vivo | 11278559, 12907688 |
| CFH | 601 | NP_000177.2 | THBS1 | 1765 | NP_003237.2 | in vitro | 15634279 |
| TNFRSF11B | 4032 | NP_002537.3 | THBS1 | 1765 | NP_003237.2 | in vivo | 15799029 |
| MMP1 | 384 | NP_002412.1 | CCL2 | 1149 | NP_002973.1 | in vitro; in vivo | 12149192, 9558113 |
| MMP8 | 385 | NP_002415.1 | CCL2 | 1149 | NP_002973.1 | in vitro; in vivo | 12149192, 9558113 |
| MMP9 | 387 | NP_004985.2 | IL8 | 909 | NP_000575.1 | in vitro | 11023497 |
| GOLGB1 | 3933 | NP_004478.3 | SLC2A3 | 686 | NP_008862.1 | yeast 2-hybrid | 16169070 |
| DNAJA1 | 4159 | NP_001530.1 | TM4SF1 | 1854 | NP_055035.1 | yeast 2-hybrid | 16169070 |
| HSPA8 | 7205 | NP_006588.1 | TM4SF1 | 1854 | NP_055035.1 | yeast 2-hybrid | 16169070 |
| ACTN4 | 5222 | NP_004915.2 | SERPINE1 | 1418 | NP_000593.1 | in vitro; in vivo; yeast 2-hybrid | 15493875 |
| JAG1 | 3562 | NP_000205.1 | THBS1 | 1765 | NP_003237.2 | yeast 2-hybrid | 15258909 |
| WASF1 | 5434 | NP_003922.1 | IL8 | 909 | NP_000575.1 | in vitro | 16862120 |
| IL12A | 1193 | NP_000873.2 | IL8 | 909 | NP_000575.1 | in vitro | 16862120 |
| CCL4 | 1657 | NP_002975.1 | IL8 | 909 | NP_000575.1 | in vitro | 8077676 |
| SDC1 | 1718 | NP_002988.3 | IL8 | 909 | NP_000575.1 | in vitro | 12902511 |
| KLK2 | 1006 | NP_005542.1 | SERPINE1 | 1418 | NP_000593.1 | in vivo | 10209959 |
| LAMB3 | 1032 | NP_000219.2 | LAMC2 | 1031 | NP_005553.2 | in vivo | 10964684 |
| MMP9 | 387 | NP_004985.2 | AREG | 93 | NP_001648.1 | in vivo | 10389762 |
| CCND3 | 452 | NP_001751.1 | AREG | 93 | NP_001648.1 | in vivo | 11469683 |
| EGFR | 579 | NP_005219.2 | AREG | 93 | NP_001648.1 | in vivo | 10085134 |
| WT1 | 6163 | NP_077744.3 | AREG | 93 | NP_001648.1 | in vitro; in vivo | 10490105 |
| MMP3 | 1703 | NP_002413.1 | CCL2 | 1149 | NP_002973.1 | in vitro; in vivo | 12149192, 9558113 |
| CCR10 | 2586 | NP_057686.2 | CCL2 | 1149 | NP_002973.1 | in vitro; in vivo | 9364936, 10706668 |
| CCR1 | 3101 | NP_001286.1 | CCL2 | 1149 | NP_002973.1 | in vitro | 8631787 |
| CCR2 | 3166 | NP_000638.1 | CCL2 | 1149 | NP_002973.1 | in vitro; in vivo | 10529171, 9287323 |
| CCR5 | 3223 | NP_000570.1 | CCL2 | 1149 | NP_002973.1 | in vivo | 10477718 |
| CCRL1 | 7298 | NP_848540.1 | CCL2 | 1149 | NP_002973.1 | in vitro | 10734104 |
| CCBP2 | 9095 | NP_001287.2 | CCL2 | 1149 | NP_002973.1 | in vivo | 9364936, 9405404 |
| PLAT | 1419 | NP_000921.1 | PLG | 1417 | NP_000292.1 | in vitro | 11928826 |
| SPARC | 1631 | NP_003109.1 | PLG | 1417 | NP_000292.1 | in vitro | 2745554, 7982919 |

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|---|---|---|---|---|---|---|---|
| PLAU | 1883 | NP_002649.1 | PLG | 1417 | NP_000292.1 | in vitro | 3920216, 2829380, 4226004 |
| KNG1 | 1970 | NP_001095886.1 | PLG | 1417 | NP_000292.1 | in vitro | 9428707 |
| SPARC | 1631 | NP_003109.1 | PLAT | 1419 | NP_000921.1 | in vitro | 2745554 |
| PLAU | 1883 | NP_002649.1 | PLAT | 1419 | NP_000921.1 | in vitro | 7721771 |
| LRP1B | 16383 | NP_061027.2 | PLAT | 1419 | NP_000921.1 | in vivo | 11384978 |
| CD36 | 1430 | NP_000063.2 | ITGB3 | 1428 | NP_000203.2 | in vivo | 11238109 |
| SELPLG | 2845 | Q14242 | SELP | 1433 | NP_002996.2 | in vitro; in vivo | 9128259, 10713099, 17064811 |
| KNG1 | 1970 | NP_001095886.1 | F2 | 1488 | NP_000497.1 | in vitro | 1652157 |
| F2 | 1488 | NP_000497.1 | PLAU | 1883 | NP_002649.1 | in vivo | 10996659, 8428004 |
| CALR | 169 | NP_004334.1 | LRP1 | 138 | NP_002323.2 | in vivo | 14980518, 12821648 |
| PLAT | 1419 | NP_000921.1 | LRP1 | 138 | NP_002323.2 | in vitro; in vivo | 10632583, 1502153 |
| PDGFB | 1815 | NP_002599.1 | LRP1 | 138 | NP_002323.2 | in vivo | 11854294 |
| TGFB1 | 1821 | NP_000651.3 | SPARC | 1631 | NP_003109.1 | in vitro; in vivo | 15034927 |
| SPARC | 1631 | NP_003109.1 | FN1 | 626 | NP_997647.1 | in vitro | 2745554 |
| CCR1 | 3101 | NP_001286.1 | CCL4 | 1657 | NP_002975.1 | in vitro | 7594543 |
| CCR5 | 3223 | NP_000570.1 | CCL4 | 1657 | NP_002975.1 | in vitro; in vivo | 12427015, 8663314 |
| CCBP2 | 9095 | NP_001287.2 | CCL4 | 1657 | NP_002975.1 | in vivo | 9405404 |
| ITGB3 | 1428 | NP_000203.2 | VTN | 1902 | NP_000629.3 | in vitro | 16195248 |
| MMP3 | 1703 | NP_002413.1 | CCL8 | 3791 | NP_005614.2 | in vitro | 12149192 |
| CCL5 | 1751 | NP_002976.2 | SDC1 | 1718 | NP_002988.3 | in vivo | 14637022 |
| CCR1 | 3101 | NP_001286.1 | CCL5 | 1751 | NP_002976.2 | in vitro; in vivo | 9289016, 11116158, 14637022, 12270118, 7545673 |
| CCR5 | 3223 | NP_000570.1 | CCL5 | 1751 | NP_002976.2 | in vitro; in vivo | 9289016, 8663314, 11116158, 14637022, 10477718 |
| CCRL1 | 7298 | NP_848540.1 | CCL5 | 1751 | NP_002976.2 | in vitro | 9469451 |
| CCBP2 | 9095 | NP_001287.2 | CCL5 | 1751 | NP_002976.2 | in vivo | 9405404 |
| VTN | 1902 | NP_000629.3 | TGFB1 | 1821 | NP_000651.3 | in vitro | 11796824 |
| LRP2 | 2509 | NP_004516.2 | PLAU | 1883 | NP_002649.1 | in vitro | 8344937 |
| KNG1 | 1970 | NP_001095886.1 | VTN | 1902 | NP_000629.3 | in vitro; in vivo | 10887113 |
| FBN1 | 618 | NP_000129.2 | CALR | 169 | NP_004334.1 | in vivo | 10547375 |
| PLAT | 1419 | NP_000921.1 | CALR | 169 | NP_004334.1 | in vivo | 9359841 |
| CCL5 | 1751 | NP_002976.2 | DARC | 192 | NP_001116423.1 | in vitro; in vivo | 12081195, 17416748 |
| BMP1 | 209 | NP_006120.1 | COL7A1 | 358 | NP_000085.1 | in vivo | 11986329 |
| BMP1 | 209 | NP_006120.1 | COL1A1 | 362 | NP_000079.2 | in vivo | 11283002 |
| BMP1 | 209 | NP_006120.1 | COL5A1 | 368 | NP_000084.3 | in vivo | 11741999 |
| LAMB3 | 1032 | NP_000219.2 | BMP1 | 209 | NP_006120.1 | in vitro; in vivo | 10806203 |

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|---|---|---|---|---|---|---|---|
| CCL8 | 3791 | NP_005614.2 | CCR1 | 3101 | NP_001286.1 | in vivo | 9115216 |
| CCR5 | 3223 | NP_000570.1 | CCR2 | 3166 | NP_000638.1 | in vivo | 11350939 |
| CCL8 | 3791 | NP_005614.2 | CCR2 | 3166 | NP_000638.1 | in vivo | 9115216, 12149192 |
| CCL8 | 3791 | NP_005614.2 | CCR5 | 3223 | NP_000570.1 | in vivo | 9468473, 10477718 |
| COL8A1 | 372 | NP_001841.2 | UBQLN4 | 5670 | NP_064516.2 | yeast 2-hybrid | 16713569 |
| CCRL1 | 7298 | NP_848540.1 | CCL8 | 3791 | NP_005614.2 | in vitro | 10734104 |
| CCBP2 | 9095 | NP_001287.2 | CCL8 | 3791 | NP_005614.2 | in vivo | 9405404 |
| CCBP2 | 9095 | NP_001287.2 | CCL21 | 4113 | NP_002980.1 | in vivo | 10706668 |
| HSPA8 | 7205 | NP_006588.1 | DNAJA1 | 4159 | NP_001530.1 | in vivo | 10075921, 16225871 |
| MMP2 | 386 | NP_004521.1 | HAPLN1 | 275 | NP_001875.1 | in vitro | 7694569 |
| MMP9 | 387 | NP_004985.2 | HAPLN1 | 275 | NP_001875.1 | in vitro | 7694569 |
| MMP3 | 1703 | NP_002413.1 | HAPLN1 | 275 | NP_001875.1 | in vitro | 7694569 |
| SDC1 | 1718 | NP_002988.3 | CTSG | 289 | NP_001902.1 | in vitro | 9565572 |
| KNG1 | 1970 | NP_001095886.1 | CTSG | 289 | NP_001902.1 | in vitro | 11920276 |
| CTSG | 289 | NP_001902.1 | SELPLG | 2845 | Q14242 | in vivo | 11520793 |
| CTSL1 | 293 | NP_001903.1 | PLAU | 1883 | NP_002649.1 | in vitro | 1551416 |
| KNG1 | 1970 | NP_001095886.1 | CTSL1 | 293 | NP_001903.1 | in vitro | 11517935 |
| CCL21 | 4113 | NP_002980.1 | CCRL1 | 7298 | NP_848540.1 | in vitro | 10706668 |
| CD9 | 880 | NP_001760.1 | ITGB1 | 628 | NP_391987.1 | in vivo | 9812906, 9813091 |
| FN1 | 626 | NP_997647.1 | IGFBP5 | 901 | NP_000590.1 | in vitro; in vivo; yeast 2-hybrid | 14645245 |
| FBLN1 | 629 | NP_006477.2 | ITGB1 | 628 | NP_391987.1 | in vivo | 2527614 |
| DARC | 192 | NP_001116423.1 | CCL8 | 3791 | NP_005614.2 | in vivo | 13679391 |
| DCN | 501 | NP_001911.1 | COL5A1 | 368 | NP_000084.3 | in vitro | 8440685 |
| BMP1 | 209 | NP_006120.1 | HSPG2 | 804 | NP_005520.4 | in vitro; in vivo | 15591058 |
| CXCR2 | 907 | NP_001548.1 | CXCR1 | 908 | NP_000625.1 | in vivo | 15946947 |
| EGFR | 579 | NP_005219.2 | ACTA1 | 30 | NP_001091.1 | in vitro; in vivo | 1808202, 1383230 |
| FBN1 | 618 | NP_000129.2 | HSPG2 | 804 | NP_005520.4 | in vitro | 15657057 |
| TNFRSF11B | 4032 | NP_002537.3 | VTN | 1902 | NP_000629.3 | in vivo | 15799029 |
| TNFRSF11B | 4032 | NP_002537.3 | FN1 | 626 | NP_997647.1 | in vivo | 15799029 |
| COL1A1 | 362 | NP_000079.2 | COL7A1 | 358 | NP_000085.1 | in vitro | 9169408 |
| MMP2 | 386 | NP_004521.1 | COL7A1 | 358 | NP_000085.1 | in vivo | 10652000 |
| FN1 | 626 | NP_997647.1 | COL7A1 | 358 | NP_000085.1 | in vitro | 9169408, 7963647 |
| LAMB3 | 1032 | NP_000219.2 | COL7A1 | 358 | NP_000085.1 | in vitro; in vivo | 9989793 |

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|---|---|---|---|---|---|---|---|
| LAMA1 | 1033 | NP_005550.2 | COL7A1 | 358 | NP_000085.1 | in vitro | 9169408 |
| FN1 | 626 | NP_997647.1 | COL2A1 | 361 | NP_001835.3 | in vivo | 3997552, 2229073 |
| SPARC | 1631 | NP_003109.1 | COL2A1 | 361 | NP_001835.3 | in vitro | 2745554 |
| TGFB1 | 1821 | NP_000651.3 | COL2A1 | 361 | NP_001835.3 | in vitro | 10085302 |
| DDR1 | 2678 | NP_054700.2 | COL2A1 | 361 | NP_001835.3 | in vivo | 9659900 |
| MMP2 | 386 | NP_004521.1 | COL1A1 | 362 | NP_000079.2 | in vitro | 11368514 |
| MMP9 | 387 | NP_004985.2 | COL1A1 | 362 | NP_000079.2 | in vivo | 9878537 |
| DCN | 501 | NP_001911.1 | COL1A1 | 362 | NP_000079.2 | in vitro | 9675033, 1468447 |
| NID1 | 574 | NP_002499.2 | COL1A1 | 362 | NP_000079.2 | in vitro | 9733643 |
| FN1 | 626 | NP_997647.1 | COL1A1 | 362 | NP_000079.2 | in vivo | 8468356 |
| CD36 | 1430 | NP_000063.2 | COL1A1 | 362 | NP_000079.2 | in vitro | 2468670 |
| SPARC | 1631 | NP_003109.1 | COL1A1 | 362 | NP_000079.2 | in vitro | 7034958 |
| PDGFB | 1815 | NP_002599.1 | COL1A1 | 362 | NP_000079.2 | in vitro | 10446987 |
| MMP9 | 387 | NP_004985.2 | COL1A2 | 363 | NP_000080.2 | in vivo | 9878537 |
| DCN | 501 | NP_001911.1 | COL1A2 | 363 | NP_000080.2 | in vitro; in vivo | 9675033, 1468447, 2375748 |
| FN1 | 626 | NP_997647.1 | COL1A2 | 363 | NP_000080.2 | in vivo | 8468356 |
| ITGB3 | 1428 | NP_000203.2 | COL1A2 | 363 | NP_000080.2 | in vitro; in vivo | 1693626 |
| CD36 | 1430 | NP_000063.2 | COL1A2 | 363 | NP_000080.2 | in vitro | 10772928 |
| SPARC | 1631 | NP_003109.1 | COL1A2 | 363 | NP_000080.2 | in vitro | 7034958 |
| SPARC | 1631 | NP_003109.1 | COL3A1 | 365 | NP_000081.1 | in vitro | 2745554 |
| DDR1 | 2678 | NP_054700.2 | COL3A1 | 365 | NP_000081.1 | in vivo | 9659900 |
| TGFB1 | 1821 | NP_000651.3 | MMP2 | 386 | NP_004521.1 | in vitro; in vivo | 10652271 |
| FN1 | 626 | NP_997647.1 | MMP9 | 387 | NP_004985.2 | in vitro | 11134254 |
| MMP9 | 387 | NP_004985.2 | PLG | 1417 | NP_000292.1 | in vitro | 9360944 |
| CCL21 | 4113 | NP_002980.1 | UBQLN4 | 5670 | NP_064516.2 | yeast 2-hybrid | 16713569 |
| ITGB1 | 628 | NP_391987.1 | HSPG2 | 804 | NP_005520.4 | in vitro | 9431988 |
| CCR5 | 3223 | NP_000570.1 | GNAI2 | 764 | NP_002061.1 | in vivo | 15251452 |
| GNAI2 | 764 | NP_002061.1 | CXCR2 | 907 | NP_001548.1 | in vivo | 8662698 |
| PF4 | 1426 | NP_002610.1 | CCL5 | 1751 | NP_002976.2 | in vitro | 15459010 |
| MMP2 | 386 | NP_004521.1 | DCN | 501 | NP_001911.1 | in vitro | 9148753 |
| MMP3 | 1703 | NP_002413.1 | DCN | 501 | NP_001911.1 | in vitro | 9148753 |
| MMP9 | 387 | NP_004985.2 | TFPI | 1064 | NP_006278.1 | in vitro | 10859319 |
| MMP1 | 384 | NP_002412.1 | TFPI | 1064 | NP_006278.1 | in vitro | 10859319 |
| MMP1 | 384 | NP_002412.1 | COL2A1 | 361 | NP_001835.3 | in vitro | 8609233 |

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|---|---|---|---|---|---|---|---|
| TFPI | 1064 | NP_006278.1 | MMP8 | 385 | NP_002415.1 | in vitro | 12117418 |
| PLG | 1417 | NP_000292.1 | MMP3 | 1703 | NP_002413.1 | in vitro | 9548733 |
| IGFBP5 | 901 | NP_000590.1 | F2 | 1488 | NP_000497.1 | in vitro | 9528953, 9883900 |
| COL7A1 | 358 | NP_000085.1 | HSPA8 | 7205 | NP_006588.1 | yeast 2-hybrid | 16169070 |
| GNAI2 | 764 | NP_002061.1 | TUBA4A | 1851 | NP_005991.1 | yeast 2-hybrid | 16169070 |
| EGFR | 579 | NP_005219.2 | DCN | 501 | NP_001911.1 | in vitro; in vivo; yeast 2-hybrid | 12105206, 9988678 |
| FBN1 | 618 | NP_000129.2 | DCN | 501 | NP_001911.1 | in vivo | 10793130 |
| FN1 | 626 | NP_997647.1 | DCN | 501 | NP_001911.1 | in vitro | 1468447 |
| PLA2G2A | 1397 | NP_000291.1 | DCN | 501 | NP_001911.1 | in vitro; in vivo | 10747008 |
| TGFB1 | 1821 | NP_000651.3 | DCN | 501 | NP_001911.1 | in vitro; in vivo | 7638106, 7798269 |
| EGFR | 579 | NP_005219.2 | TUBA4A | 1851 | NP_005991.1 | in vivo | 16799092 |
| ELANE | 554 | NP_001963.1 | TFPI | 1064 | NP_006278.1 | in vitro | 1558967, 12117418, 10859319 |
| SDC1 | 1718 | NP_002988.3 | ELANE | 554 | NP_001963.1 | in vitro | 9565572 |
| KNG1 | 1970 | NP_001095886.1 | ELANE | 554 | NP_001963.1 | in vitro | 12887060 |
| WASF1 | 5434 | NP_003922.1 | IL12A | 1193 | NP_000873.2 | in vitro | 16862120 |
| FGA | 619 | NP_000499.1 | NID1 | 574 | NP_002499.2 | in vitro | 1680863 |
| FBLN1 | 629 | NP_006477.2 | NID1 | 574 | NP_002499.2 | in vitro | 9299350, 9278415, 8354280 |
| FBLN2 | 630 | NP_001004019.1 | NID1 | 574 | NP_002499.2 | in vitro | 11493006, 7500359 |
| HSPG2 | 804 | NP_005520.4 | NID1 | 574 | NP_002499.2 | in vitro | 11493006, 11574465 |
| LAMA1 | 1033 | NP_005550.2 | NID1 | 574 | NP_002499.2 | in vitro | 8995276 |
| ITGB3 | 1428 | NP_000203.2 | NID1 | 574 | NP_002499.2 | in vitro; in vivo | 8831898, 9686320 |
| PLAU | 1883 | NP_002649.1 | NID1 | 574 | NP_002499.2 | in vitro | 1499567 |
| GNAI2 | 764 | NP_002061.1 | EGFR | 579 | NP_005219.2 | in vivo | 11286993 |
| KRT18 | 1020 | NP_000215.1 | EGFR | 579 | NP_005219.2 | in vitro; in vivo | 12577067 |
| FBLN2 | 630 | NP_001004019.1 | FBN1 | 618 | NP_000129.2 | in vivo | 8702639, 9886271 |
| HRG | 812 | NP_000403.1 | FGA | 619 | NP_000499.1 | in vivo | 9276466 |
| PLAT | 1419 | NP_000921.1 | FGA | 619 | NP_000499.1 | in vitro; in vivo | 11170397, 3088041 |
| ITGB3 | 1428 | NP_000203.2 | FGA | 619 | NP_000499.1 | in vitro | 11460491 |
| F2 | 1488 | NP_000497.1 | FGA | 619 | NP_000499.1 | in vitro | 2133223, 1587268, 2742826 |
| ITGB1 | 628 | NP_391987.1 | FN1 | 626 | NP_997647.1 | in vitro; in vivo | 11010812, 8120056 |
| FBLN1 | 629 | NP_006477.2 | FN1 | 626 | NP_997647.1 | in vitro | 1400330 |
| FBLN2 | 630 | NP_001004019.1 | FN1 | 626 | NP_997647.1 | in vivo | 10848816 |
| ITGB3 | 1428 | NP_000203.2 | FN1 | 626 | NP_997647.1 | in vitro | 1694173 |

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|---|---|---|---|---|---|---|---|
| ITGA4 | 1894 | NP_000876.3 | FN1 | 626 | NP_997647.1 | in vitro; in vivo | 11010812, 9117345 |
| LAMA1 | 1033 | NP_005550.2 | ITGB1 | 628 | NP_391987.1 | in vitro | 9688542 |
| CD36 | 1430 | NP_000063.2 | ITGB1 | 628 | NP_391987.1 | in vivo | 11238109 |
| ITGA4 | 1894 | NP_000876.3 | ITGB1 | 628 | NP_391987.1 | in vitro; in vivo | 11010812, 14681217 |
| ACTN4 | 5222 | NP_004915.2 | ITGB1 | 628 | NP_391987.1 | in vitro | 2116421 |
| HSPG2 | 804 | NP_005520.4 | FBLN1 | 629 | NP_006477.2 | in vitro | 7500359 |
| HSPG2 | 804 | NP_005520.4 | FBLN2 | 630 | NP_001004019.1 | in vitro | 9431988 |
| LAMA1 | 1033 | NP_005550.2 | FBLN2 | 630 | NP_001004019.1 | in vitro; in vivo | 9006922, 10934193 |
| ITGB3 | 1428 | NP_000203.2 | FBLN2 | 630 | NP_001004019.1 | in vivo | 10848816 |
| CCR5 | 3223 | NP_000570.1 | ORM1 | 724 | NP_000598.2 | in vitro | 11336643 |
| CXCR1 | 908 | NP_000625.1 | GNAI2 | 764 | NP_002061.1 | in vitro; in vivo | 8662698, 8903513 |
| LRP1 | 138 | NP_002323.2 | CTSG | 289 | NP_001902.1 | in vitro | 15131125 |
| LRP1 | 138 | NP_002323.2 | ELANE | 554 | NP_001963.1 | in vitro | 15131125 |
| LAMA1 | 1033 | NP_005550.2 | HSPG2 | 804 | NP_005520.4 | in vitro | 9688542 |
| SPARC | 1631 | NP_003109.1 | HSPG2 | 804 | NP_005520.4 | in vitro | 2745554 |
| PDGFB | 1815 | NP_002599.1 | HSPG2 | 804 | NP_005520.4 | in vitro | 9692901 |
| PLG | 1417 | NP_000292.1 | HRG | 812 | NP_000403.1 | in vivo | 8478593 |
| CD36 | 1430 | NP_000063.2 | CD9 | 880 | NP_001760.1 | in vivo | 11238109 |
| VTN | 1902 | NP_000629.3 | IGFBP5 | 901 | NP_000590.1 | in vivo | 11751588 |
| PLG | 1417 | NP_000292.1 | LAMA1 | 1033 | NP_005550.2 | in vitro | 8360181 |
| PLAT | 1419 | NP_000921.1 | LAMA1 | 1033 | NP_005550.2 | in vitro | 8360181 |
| COL1A1 | 362 | NP_000079.2 | CD44 | 115 | NP_000601.3 | in vitro | 1730778 |
| COL1A2 | 363 | NP_000080.2 | CD44 | 115 | NP_000601.3 | in vitro | 1730778 |
| MMP1 | 384 | NP_002412.1 | CD44 | 115 | NP_000601.3 | in vitro | 11381077 |
| MMP9 | 387 | NP_004985.2 | CD44 | 115 | NP_000601.3 | in vivo | 10652271, 17912438 |
| EGFR | 579 | NP_005219.2 | CD44 | 115 | NP_000601.3 | in vivo | 12093135 |

# Supplementary Table 5

List of biological processes overrepresented by the 1st cluster in the Protein-protein network

| | |
|---|---|
| Seed proteins: | THBS1, SERPINE1, ITGA2, CCL20, VCAN |
| Direct interactants: | COL2A1, CTSL1, KRT18, MMP3, SDC1, LRP1B, KLK2, COL3A1, TGFB1, ELANE, KNG1, SPARC, CTSG, CORO1A, CFH, F2, TNFAIP6, CD44, CD36, PLG, IGFBP5, MMP2, LRP2, FBLN1, ACTA1, COL8A1, CD47, CD9, TFPI, DDR1, ACTN4, PLA2G2A, COL5A1, DCN, COL1A2, ITGA4, DHFR, COL1A1, PLAT, LRP5, MMP1, MMP8, CCR6, LRP1, FN1, TNR, AUP1, ADAMTS1, CALR, HAPLN1, ITGB1, SELPLG, FGA, NID1, PDGFB, SCARB2, PLAU, FBN1, CXCL10, SELP, CCL21, XCL1, ITGB3, HRG, TNFRSF11B, JAG1, HSPG2, COL7A1, FBLN2, MMP9, LAMA1, VTN |

| ID | Name | P-value | Hit in Query List |
|---|---|---|---|
| GO:0009611 | response to wounding | 1.55E-31 | KNG1, SPARC, DCN, CD36, TGFB1, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, SELP, ITGA2, SERPINE1, ITGA4, SELPLG, PLAT, PLA2G2A, ELANE, PLAU, COL1A2, PLG, DDR1, COL1A1, PDGFB, SDC1, TNFAIP6, COL5A1, ACTN4, CXCL10, XCL1, CFH, COL3A1, FGA, CCL20, CCL21, VCAN, TNR, VTN, MMP2, MMP1, F2, MMP3, CD47, TFPI, CD44 |
| GO:0016477 | cell migration | 1.36E-28 | TGFB1, ITGB3, ITGB1, CCR6, HRG, FN1, THBS1, SELP, LRP1, ITGA2, SERPINE1, ITGA4, SELPLG, LRP5, PLAT, ELANE, PLAU, LAMA1, COL1A2, PLG, DDR1, COL1A1, JAG1, PDGFB, COL5A1, CXCL10, XCL1, IGFBP5, CORO1A, CCL21, VCAN, TNR, VTN, MMP9, MMP2, MMP1, F2, MMP3, CD47, CD44 |
| GO:0006928 | cellular component movement | 9.48E-28 | TGFB1, ITGB3, ITGB1, CCR6, HRG, FN1, CD9, THBS1, SELP, LRP1, ITGA2, SERPINE1, ITGA4, SELPLG, LRP5, PLAT, ELANE, PLAU, LAMA1, COL1A2, PLG, DDR1, COL1A1, JAG1, PDGFB, COL5A1, ACTN4, CXCL10, XCL1, IGFBP5, CORO1A, CCL21, VCAN, TNR, VTN, MMP9, MMP2, MMP1, F2, MMP3, CD47, CD44 |
| GO:0048870 | cell motility | 1.21E-27 | TGFB1, ITGB3, ITGB1, CCR6, HRG, FN1, THBS1, SELP, LRP1, ITGA2, SERPINE1, ITGA4, SELPLG, LRP5, PLAT, ELANE, PLAU, LAMA1, COL1A2, PLG, DDR1, COL1A1, JAG1, PDGFB, COL5A1, CXCL10, XCL1, IGFBP5, CORO1A, CCL21, VCAN, TNR, VTN, MMP9, MMP2, MMP1, F2, MMP3, CD47, CD44 |

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|---|---|---|---|
| GO:0051674 | localization of cell | 1.21E-27 | TGFB1, ITGB3, ITGB1, CCR6, HRG, FN1, THBS1, SELP, LRP1, ITGA2, SERPINE1, ITGA4, SELPLG, LRP5, PLAT, ELANE, PLAU, LAMA1, COL1A2, PLG, DDR1, COL1A1, JAG1, PDGFB, COL5A1, CXCL10, XCL1, IGFBP5, CORO1A, CCL21, VCAN, TNR, VTN, MMP9, MMP2, MMP1, F2, MMP3, CD47, CD44 |
| GO:0042060 | wound healing | 3.80E-27 | KNG1, SPARC, DCN, CD36, TGFB1, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, SELP, ITGA2, SERPINE1, ITGA4, SELPLG, PLAT, PLAU, COL1A2, PLG, DDR1, COL1A1, PDGFB, SDC1, COL5A1, ACTN4, COL3A1, FGA, VTN, MMP1, F2, MMP3, CD47, TFPI, CD44 |
| GO:0040011 | locomotion | 1.45E-26 | TGFB1, ITGB3, ITGB1, CCR6, HRG, FN1, THBS1, SELP, LRP1, ITGA2, SERPINE1, ITGA4, SELPLG, LRP5, PLAT, ELANE, PLAU, LAMA1, COL1A2, PLG, DDR1, COL1A1, JAG1, PDGFB, COL5A1, CXCL10, XCL1, COL2A1, COL3A1, CCL20, IGFBP5, CORO1A, CCL21, VCAN, TNR, VTN, MMP9, MMP2, MMP1, F2, MMP3, CD47, CD44 |
| GO:0030198 | extracellular matrix organization | 2.38E-26 | DCN, FBLN1, TGFB1, KLK2, FN1, CTSG, ELANE, COL1A2, PLG, DDR1, COL1A1, HSPG2, NID1, COL5A1, COL2A1, COL3A1, TNFRSF11B, TNR, MMP8, VTN, MMP9, MMP2, MMP1, MMP3 |
| GO:0007155 | cell adhesion | 8.56E-25 | KNG1, CD36, SCARB2, TGFB1, FBLN2, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, SELP, ITGA2, HAPLN1, SERPINE1, ITGA4, SELPLG, PLAU, LAMA1, PLG, DDR1, COL1A1, HSPG2, NID1, TNFAIP6, COL5A1, COL7A1, COL8A1, COL2A1, COL3A1, CORO1A, CCL21, VCAN, TNR, VTN, MMP2, CD47, CD44 |
| GO:0022610 | biological adhesion | 8.92E-25 | KNG1, CD36, SCARB2, TGFB1, FBLN2, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, SELP, ITGA2, HAPLN1, SERPINE1, ITGA4, SELPLG, PLAU, LAMA1, PLG, DDR1, COL1A1, HSPG2, NID1, TNFAIP6, COL5A1, COL7A1, COL8A1, COL2A1, COL3A1, CORO1A, CCL21, VCAN, TNR, VTN, MMP2, CD47, CD44 |
| GO:0009605 | response to external stimulus | 6.33E-24 | KNG1, SPARC, DCN, CD36, TGFB1, ITGB3, ITGB1, CCR6, HRG, THBS1, SELP, ITGA2, SERPINE1, LRP2, PLAT, PLA2G2A, ELANE, PLAU, LAMA1, COL1A2, ACTA1, PLG, COL1A1, PDGFB, COL5A1, CXCL10, XCL1, COL2A1, CFH, COL3A1, CCL20, CORO1A, CCL21, TNFRSF11B, TNR, VTN, MMP9, MMP2, F2, MMP3, CD47, CD44 |
| GO:0007596 | blood coagulation | 2.24E-22 | KNG1, SPARC, CD36, TGFB1, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, SELP, ITGA2, SERPINE1, ITGA4, SELPLG, PLAT, PLAU, COL1A2, PLG, COL1A1, PDGFB, ACTN4, COL3A1, FGA, VTN, MMP1, F2, CD47, TFPI |

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| GO:0050817 | coagulation | 2.38E-22 | KNG1, SPARC, CD36, TGFB1, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, SELP, ITGA2, SERPINE1, ITGA4, SELPLG, PLAT, PLAU, COL1A2, PLG, COL1A1, PDGFB, ACTN4, COL3A1, FGA, VTN, MMP1, F2, CD47, TFPI |
| GO:0007599 | hemostasis | 2.38E-22 | KNG1, SPARC, CD36, TGFB1, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, SELP, ITGA2, SERPINE1, ITGA4, SELPLG, PLAT, PLAU, COL1A2, PLG, COL1A1, PDGFB, ACTN4, COL3A1, FGA, VTN, MMP1, F2, CD47, TFPI |
| GO:0030155 | regulation of cell adhesion | 4.12E-22 | KNG1, CD36, TGFB1, FBLN2, ITGB3, ITGB1, HRG, THBS1, SELP, ITGA2, SERPINE1, PLAU, LAMA1, PLG, DDR1, COL1A1, NID1, COL8A1, CCL21, TNR, VTN, MMP2, CD47, CD44 |
| GO:0072358 | cardiovascular system development | 4.12E-22 | FBN1, SPARC, CD36, ITGB3, ITGB1, HRG, FN1, THBS1, CALR, SELP, LRP1, SERPINE1, ITGA4, LRP5, PLAT, PLAU, LAMA1, COL1A2, PLG, COL1A1, JAG1, ADAMTS1, HSPG2, PDGFB, COL5A1, CXCL10, COL8A1, COL2A1, COL3A1, VCAN, MMP9, MMP2, CD44 |
| GO:0072359 | circulatory system development | 4.12E-22 | FBN1, SPARC, CD36, ITGB3, ITGB1, HRG, FN1, THBS1, CALR, SELP, LRP1, SERPINE1, ITGA4, LRP5, PLAT, PLAU, LAMA1, COL1A2, PLG, COL1A1, JAG1, ADAMTS1, HSPG2, PDGFB, COL5A1, CXCL10, COL8A1, COL2A1, COL3A1, VCAN, MMP9, MMP2, CD44 |
| GO:0043062 | extracellular structure organization | 4.36E-22 | DCN, FBLN1, TGFB1, KLK2, FN1, CTSG, ELANE, COL1A2, PLG, DDR1, COL1A1, HSPG2, NID1, COL5A1, COL2A1, COL3A1, TNFRSF11B, TNR, MMP8, VTN, MMP9, MMP2, MMP1, MMP3 |
| GO:0050878 | regulation of body fluid levels | 1.47E-21 | KNG1, SPARC, CD36, TGFB1, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, SELP, ITGA2, SERPINE1, ITGA4, SELPLG, PLAT, PLAU, COL1A2, PLG, DDR1, COL1A1, PDGFB, ACTN4, COL3A1, FGA, VTN, MMP1, F2, CD47, TFPI |
| GO:0050900 | leukocyte migration | 5.59E-20 | ITGB3, ITGB1, CCR6, FN1, THBS1, SELP, ITGA2, SERPINE1, ITGA4, SELPLG, ELANE, COL1A2, PLG, COL1A1, PDGFB, CXCL10, XCL1, CORO1A, CCL21, MMP1, F2, CD47 |
| GO:0031589 | cell-substrate adhesion | 6.14E-20 | CD36, FBLN2, ITGB3, ITGB1, HRG, FN1, THBS1, ITGA2, SERPINE1, ITGA4, PLAU, PLG, DDR1, COL1A1, NID1, COL8A1, COL3A1, CORO1A, CCL21, VTN, CD44 |
| GO:0001568 | blood vessel development | 7.10E-20 | CD36, ITGB3, ITGB1, HRG, FN1, THBS1, SELP, LRP1, SERPINE1, LRP5, PLAT, PLAU, LAMA1, COL1A2, PLG, COL1A1, JAG1, ADAMTS1, HSPG2, PDGFB, COL5A1, CXCL10, COL8A1, COL3A1, MMP9, MMP2, CD44 |
| GO:0001944 | vasculature development | 2.30E-19 | CD36, ITGB3, ITGB1, HRG, FN1, THBS1, SELP, LRP1, SERPINE1, LRP5, PLAT, PLAU, LAMA1, COL1A2, PLG, COL1A1, JAG1, ADAMTS1, HSPG2, PDGFB, COL5A1, CXCL10, COL8A1, COL3A1, MMP9, MMP2, CD44 |

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| GO:0002576 | platelet degranulation | 3.13E-18 | KNG1, SPARC, CD36, TGFB1, ITGB3, HRG, FN1, CD9, THBS1, SELP, SERPINE1, PLG, PDGFB, ACTN4, FGA |
| GO:0032101 | regulation of response to external stimulus | 4.01E-16 | KNG1, CD36, TGFB1, HRG, THBS1, SELP, ITGA2, SERPINE1, PLAT, PLA2G2A, ELANE, PLAU, PLG, PDGFB, CXCL10, XCL1, CFH, CCL21, TNR, VTN, F2, CD47 |
| GO:0051270 | regulation of cellular component movement | 4.01E-16 | TGFB1, ITGB3, ITGB1, HRG, THBS1, SELP, LRP1, ITGA2, SERPINE1, PLAU, LAMA1, COL1A1, JAG1, PDGFB, ACTN4, CXCL10, XCL1, IGFBP5, CORO1A, CCL21, VTN, MMP9, MMP3 |
| GO:0040012 | regulation of locomotion | 5.37E-16 | TGFB1, ITGB3, ITGB1, HRG, THBS1, SELP, LRP1, ITGA2, SERPINE1, ELANE, PLAU, LAMA1, COL1A1, JAG1, PDGFB, CXCL10, XCL1, IGFBP5, CORO1A, CCL21, VTN, MMP9, MMP3 |
| GO:0030334 | regulation of cell migration | 6.68E-16 | TGFB1, ITGB3, ITGB1, HRG, THBS1, SELP, LRP1, ITGA2, SERPINE1, PLAU, LAMA1, COL1A1, JAG1, PDGFB, CXCL10, XCL1, IGFBP5, CORO1A, CCL21, VTN, MMP9, MMP3 |
| GO:0030168 | platelet activation | 7.42E-16 | KNG1, SPARC, CD36, TGFB1, ITGB3, HRG, FN1, CD9, THBS1, SELP, SERPINE1, COL1A2, PLG, COL1A1, PDGFB, ACTN4, COL3A1, FGA, F2 |
| GO:2000145 | regulation of cell motility | 1.86E-15 | TGFB1, ITGB3, ITGB1, HRG, THBS1, SELP, LRP1, ITGA2, SERPINE1, PLAU, LAMA1, COL1A1, JAG1, PDGFB, CXCL10, XCL1, IGFBP5, CORO1A, CCL21, VTN, MMP9, MMP3 |
| GO:0007160 | cell-matrix adhesion | 2.35E-15 | CD36, ITGB3, ITGB1, HRG, FN1, THBS1, ITGA2, SERPINE1, ITGA4, PLAU, DDR1, NID1, COL3A1, CCL21, VTN, CD44 |
| GO:0010810 | regulation of cell-substrate adhesion | 9.63E-15 | CD36, FBLN2, ITGB1, HRG, THBS1, SERPINE1, PLAU, PLG, DDR1, COL1A1, NID1, COL8A1, CCL21, VTN |
| GO:0030193 | regulation of blood coagulation | 1.97E-14 | KNG1, CD36, HRG, THBS1, SELP, SERPINE1, PLAT, PLAU, PLG, PDGFB, VTN, F2 |
| GO:0050818 | regulation of coagulation | 4.98E-14 | KNG1, CD36, HRG, THBS1, SELP, SERPINE1, PLAT, PLAU, PLG, PDGFB, VTN, F2 |
| GO:0048514 | blood vessel morphogenesis | 7.29E-14 | CD36, ITGB3, ITGB1, HRG, FN1, THBS1, SELP, LRP1, SERPINE1, LRP5, PLAT, PLAU, LAMA1, PLG, JAG1, ADAMTS1, HSPG2, CXCL10, COL8A1, MMP9, MMP2 |
| GO:0006935 | chemotaxis | 1.11E-13 | TGFB1, ITGB3, ITGB1, CCR6, HRG, THBS1, ITGA2, SERPINE1, ELANE, PLAU, LAMA1, COL1A2, COL1A1, PDGFB, COL5A1, CXCL10, XCL1, COL2A1, COL3A1, CCL20, CORO1A, CCL21, TNR |
| GO:0042330 | taxis | 1.12E-13 | TGFB1, ITGB3, ITGB1, CCR6, HRG, THBS1, ITGA2, SERPINE1, ELANE, PLAU, LAMA1, COL1A2, COL1A1, PDGFB, COL5A1, CXCL10, XCL1, COL2A1, COL3A1, CCL20, CORO1A, CCL21, TNR |
| GO:0022617 | extracellular matrix disassembly | 1.28E-13 | KLK2, CTSG, ELANE, PLG, DDR1, MMP8, MMP9, MMP2, MMP1, MMP3 |

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| GO:0051272 | positive regulation of cellular component movement | 1.36E-13 | TGFB1, ITGB3, ITGB1, THBS1, SELP, ITGA2, SERPINE1, PLAU, COL1A1, PDGFB, ACTN4, CXCL10, XCL1, CORO1A, CCL21, VTN, MMP9 |
| GO:0001775 | cell activation | 1.39E-13 | KNG1, SPARC, CD36, TGFB1, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, SELP, SERPINE1, ITGA4, SELPLG, COL1A2, PLG, COL1A1, PDGFB, ACTN4, XCL1, COL3A1, FGA, CORO1A, CCL21, F2, CD47 |
| GO:0016192 | vesicle-mediated transport | 1.86E-13 | KNG1, SPARC, CD36, TGFB1, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, CALR, SELP, LRP1, ITGA2, SERPINE1, LRP2, LRP5, ELANE, PLG, LRP1B, PDGFB, KRT18, ACTN4, FGA, CORO1A, CCL21, VTN, CD47 |
| GO:0045785 | positive regulation of cell adhesion | 2.37E-13 | CD36, FBLN2, ITGB3, ITGB1, HRG, THBS1, SELP, ITGA2, NID1, COL8A1, CCL21, VTN, CD47, CD44 |
| GO:0030195 | negative regulation of blood coagulation | 2.73E-13 | KNG1, HRG, THBS1, SERPINE1, PLAT, PLAU, PLG, PDGFB, VTN, F2 |
| GO:0014909 | smooth muscle cell migration | 3.51E-13 | ITGB3, LRP1, ITGA2, SERPINE1, PLAT, PLAU, DDR1, PDGFB, IGFBP5, VTN |
| GO:0061041 | regulation of wound healing | 3.82E-13 | KNG1, CD36, HRG, THBS1, SELP, SERPINE1, PLAT, PLAU, PLG, PDGFB, VTN, F2 |
| GO:0050819 | negative regulation of coagulation | 5.71E-13 | KNG1, HRG, THBS1, SERPINE1, PLAT, PLAU, PLG, PDGFB, VTN, F2 |
| GO:0032963 | collagen metabolic process | 7.26E-13 | TGFB1, ITGA2, COL1A1, COL5A1, COL3A1, MMP8, MMP9, MMP2, MMP1, F2, MMP3 |
| GO:0014812 | muscle cell migration | 9.04E-13 | ITGB3, LRP1, ITGA2, SERPINE1, PLAT, PLAU, DDR1, PDGFB, IGFBP5, VTN |
| GO:0030335 | positive regulation of cell migration | 1.02E-12 | TGFB1, ITGB3, ITGB1, THBS1, SELP, ITGA2, SERPINE1, PLAU, COL1A1, PDGFB, CXCL10, XCL1, CORO1A, CCL21, VTN, MMP9 |
| GO:2000147 | positive regulation of cell motility | 1.38E-12 | TGFB1, ITGB3, ITGB1, THBS1, SELP, ITGA2, SERPINE1, PLAU, COL1A1, PDGFB, CXCL10, XCL1, CORO1A, CCL21, VTN, MMP9 |
| GO:0044259 | multicellular organismal macromolecule metabolic process | 1.91E-12 | TGFB1, ITGA2, COL1A1, COL5A1, COL3A1, MMP8, MMP9, MMP2, MMP1, F2, MMP3 |
| GO:0040017 | positive regulation of locomotion | 2.33E-12 | TGFB1, ITGB3, ITGB1, THBS1, SELP, ITGA2, SERPINE1, PLAU, COL1A1, PDGFB, CXCL10, XCL1, CORO1A, CCL21, VTN, MMP9 |
| GO:0044236 | multicellular organismal metabolic process | 1.31E-11 | TGFB1, ITGA2, COL1A1, COL5A1, COL3A1, MMP8, MMP9, MMP2, MMP1, F2, MMP3 |
| GO:0080134 | regulation of response to stress | 4.05E-11 | KNG1, CD36, TGFB1, HRG, THBS1, SELP, ITGA2, SERPINE1, PLAT, PLA2G2A, ELANE, PLAU, PLG, PDGFB, XCL1, CFH, CCL21, TNR, VTN, F2, CD47, CD44 |
| GO:0051704 | multi-organism process | 7.07E-11 | SPARC, DCN, FBLN1, CD36, TGFB1, ITGB3, ITGB1, HRG, SELP, ITGA2, SERPINE1, PLA2G2A, CTSG, ELANE, PLAU, DDR1, JAG1, KRT18, CXCL10, XCL1, CCL20, MMP9, MMP2, MMP1, MMP3, CD47 |

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| GO:0009888 | tissue development | 7.39E-11 | DCN, TGFB1, ITGB3, ITGB1, THBS1, CALR, ITGA2, SERPINE1, ITGA4, LRP5, PLAU, LAMA1, COL1A2, ACTA1, PLG, DDR1, COL1A1, JAG1, CTSL1, HSPG2, PDGFB, COL5A1, COL7A1, COL2A1, COL3A1, IGFBP5, MMP2, CD44 |
| GO:0070887 | cellular response to chemical stimulus | 1.13E-10 | SPARC, CD36, TGFB1, ITGB1, CCR6, HRG, THBS1, CALR, SELP, ITGA2, SERPINE1, SELPLG, LRP5, COL1A2, COL1A1, CTSL1, PDGFB, KRT18, CXCL10, XCL1, COL2A1, COL3A1, IGFBP5, CORO1A, CCL21, MMP9, MMP2, MMP3, CD44 |
| GO:0010324 | membrane invagination | 1.13E-10 | CD36, TGFB1, ITGB1, THBS1, CALR, LRP1, ITGA2, SERPINE1, LRP2, LRP5, ELANE, LRP1B, ACTN4, CORO1A, VTN, CD47 |
| GO:0009887 | organ morphogenesis | 1.25E-10 | DCN, TGFB1, THBS1, ITGA2, LRP2, LRP5, PLAU, LAMA1, COL1A2, DDR1, COL1A1, JAG1, ADAMTS1, CTSL1, HSPG2, SDC1, COL5A1, COL8A1, COL2A1, IGFBP5, TNFRSF11B, MMP2, CD44 |
| GO:0009719 | response to endogenous stimulus | 1.96E-10 | SPARC, CD36, TGFB1, ITGB1, THBS1, CALR, ITGA2, SERPINE1, PLAT, COL1A2, ACTA1, COL1A1, CTSL1, PDGFB, SDC1, XCL1, COL2A1, COL3A1, CCL21, TNFRSF11B, MMP9, MMP2, MMP3, CD44 |
| GO:0006887 | exocytosis | 2.67E-10 | KNG1, SPARC, CD36, TGFB1, ITGB3, HRG, FN1, CD9, THBS1, SELP, SERPINE1, PLG, PDGFB, ACTN4, FGA |
| GO:0006952 | defense response | 2.94E-10 | KNG1, CD36, TGFB1, ITGB1, CCR6, HRG, FN1, THBS1, SELP, ITGA2, SERPINE1, PLA2G2A, CTSG, ELANE, CTSL1, TNFAIP6, CXCL10, XCL1, CFH, CCL20, CORO1A, CCL21, F2, CD47, CD44 |
| GO:0051093 | negative regulation of developmental process | 3.04E-10 | CD36, TGFB1, ITGB3, ITGB1, HRG, THBS1, CALR, SERPINE1, LRP5, PLA2G2A, PLG, JAG1, ADAMTS1, CXCL10, IGFBP5, CCL21, TNFRSF11B, TNR, F2 |
| GO:0042127 | regulation of cell proliferation | 5.76E-10 | KNG1, SPARC, TGFB1, ITGB3, ITGB1, HRG, CD9, THBS1, CALR, ITGA2, SERPINE1, LRP5, PLA2G2A, ELANE, PLAU, PLG, DDR1, JAG1, ADAMTS1, PDGFB, CXCL10, XCL1, IGFBP5, CORO1A, F2, CD47 |
| GO:0006897 | endocytosis | 5.76E-10 | CD36, TGFB1, ITGB1, THBS1, CALR, LRP1, ITGA2, SERPINE1, LRP2, LRP5, ELANE, LRP1B, ACTN4, CORO1A, CCL21, VTN, CD47 |
| GO:0014910 | regulation of smooth muscle cell migration | 7.67E-10 | ITGB3, LRP1, ITGA2, SERPINE1, PLAU, PDGFB, IGFBP5, VTN |
| GO:0010811 | positive regulation of cell-substrate adhesion | 7.79E-10 | CD36, FBLN2, ITGB1, HRG, THBS1, NID1, COL8A1, CCL21, VTN |
| GO:0006954 | inflammatory response | 7.79E-10 | KNG1, TGFB1, FN1, THBS1, SELP, ITGA2, SERPINE1, PLA2G2A, ELANE, TNFAIP6, CXCL10, XCL1, CFH, CCL20, CCL21, F2, CD47, CD44 |
| GO:0001525 | angiogenesis | 7.79E-10 | CD36, ITGB3, ITGB1, HRG, FN1, THBS1, SERPINE1, PLAU, PLG, JAG1, ADAMTS1, HSPG2, CXCL10, COL8A1, MMP9, MMP2 |

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| GO:0002682 | regulation of immune system process | 1.27E-09 | KNG1, CD36, TGFB1, ITGB3, ITGB1, HRG, THBS1, SELP, ITGA2, SERPINE1, ITGA4, CTSG, ELANE, JAG1, CXCL10, XCL1, CFH, COL3A1, CORO1A, CCL21, CD47, CD44 |
| GO:0042730 | fibrinolysis | 1.95E-09 | HRG, THBS1, SERPINE1, PLAT, PLAU, PLG, F2 |
| GO:0050920 | regulation of chemotaxis | 4.48E-09 | TGFB1, HRG, THBS1, ITGA2, SERPINE1, ELANE, PDGFB, CXCL10, XCL1, CCL21 |
| GO:0048646 | anatomical structure formation involved in morphogenesis | 4.80E-09 | CD36, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, SERPINE1, PLAU, ACTA1, PLG, COL1A1, JAG1, ADAMTS1, HSPG2, CXCL10, COL8A1, COL2A1, MMP9, MMP2, CD44 |
| GO:0033627 | cell adhesion mediated by integrin | 5.11E-09 | ITGB3, ITGB1, HRG, SERPINE1, PLAU, PLG, CCL21, VTN |
| GO:0071310 | cellular response to organic substance | 5.71E-09 | SPARC, CD36, TGFB1, CCR6, HRG, CALR, SELP, ITGA2, SELPLG, LRP5, COL1A2, COL1A1, CTSL1, PDGFB, KRT18, XCL1, COL2A1, COL3A1, IGFBP5, MMP9, MMP2, MMP3, CD44 |
| GO:0051241 | negative regulation of multicellular organismal process | 8.56E-09 | KNG1, TGFB1, HRG, THBS1, SERPINE1, PLAT, PLAU, PLG, PDGFB, XCL1, TNFRSF11B, TNR, VTN, MMP2, F2 |
| GO:0009617 | response to bacterium | 1.74E-08 | SPARC, DCN, CD36, TGFB1, SELP, SERPINE1, PLA2G2A, CTSG, ELANE, JAG1, CXCL10, CCL20, MMP9, MMP3, CD47 |
| GO:0045807 | positive regulation of endocytosis | 2.64E-08 | CD36, ITGB1, CALR, ITGA2, SERPINE1, ACTN4, CCL21, VTN, CD47 |
| GO:0030194 | positive regulation of blood coagulation | 2.66E-08 | CD36, HRG, THBS1, SERPINE1, PLG, F2 |
| GO:0007162 | negative regulation of cell adhesion | 3.48E-08 | KNG1, TGFB1, HRG, THBS1, SERPINE1, PLG, COL1A1, TNR, MMP2 |
| GO:0051128 | regulation of cellular component organization | 3.97E-08 | CD36, TGFB1, ITGB1, HRG, THBS1, CALR, SELP, LRP1, ITGA2, SERPINE1, LRP5, DDR1, COL1A1, PDGFB, COL5A1, ACTN4, IGFBP5, CORO1A, CCL21, TNR, VTN, F2, CD47, CD44 |
| GO:0002684 | positive regulation of immune system process | 5.17E-08 | CD36, TGFB1, ITGB3, HRG, THBS1, SELP, ITGA2, SERPINE1, CTSG, ELANE, CXCL10, XCL1, CFH, CORO1A, CCL21, CD47, CD44 |
| GO:0051918 | negative regulation of fibrinolysis | 6.29E-08 | HRG, THBS1, SERPINE1, PLG, F2 |
| GO:0050820 | positive regulation of coagulation | 6.73E-08 | CD36, HRG, THBS1, SERPINE1, PLG, F2 |
| GO:0048771 | tissue remodeling | 6.73E-08 | TGFB1, ITGB3, HRG, ITGA4, LRP5, PLG, IGFBP5, TNFRSF11B, MMP9, MMP2 |
| GO:0016044 | cellular membrane organization | 7.54E-08 | CD36, TGFB1, ITGB1, CD9, THBS1, CALR, LRP1, ITGA2, SERPINE1, LRP2, LRP5, ELANE, LRP1B, COL5A1, ACTN4, CORO1A, VTN, CD47 |
| GO:0061024 | membrane organization | 8.55E-08 | CD36, TGFB1, ITGB1, CD9, THBS1, CALR, LRP1, ITGA2, SERPINE1, LRP2, LRP5, ELANE, LRP1B, COL5A1, ACTN4, CORO1A, VTN, CD47 |
| GO:0050793 | regulation of developmental process | 9.43E-08 | CD36, TGFB1, ITGB3, ITGB1, HRG, THBS1, CALR, SERPINE1, LRP5, PLA2G2A, PLAU, LAMA1, PLG, COL1A1, JAG1, ADAMTS1, PDGFB, CXCL10, IGFBP5, CCL21, TNFRSF11B, TNR, MMP9, F2, CD44 |

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| GO:0006909 | phagocytosis | 9.51E-08 | CD36, TGFB1, THBS1, CALR, LRP1, ITGA2, ELANE, CORO1A, CD47 |
| GO:0051707 | response to other organism | 1.16E-07 | SPARC, DCN, CD36, TGFB1, HRG, SELP, SERPINE1, PLA2G2A, CTSG, ELANE, JAG1, CXCL10, XCL1, CCL20, MMP9, MMP3, CD47 |
| GO:0030100 | regulation of endocytosis | 1.16E-07 | CD36, TGFB1, ITGB1, CALR, ITGA2, SERPINE1, ACTN4, CCL21, VTN, CD47 |
| GO:0050795 | regulation of behavior | 1.23E-07 | TGFB1, HRG, THBS1, ITGA2, SERPINE1, ELANE, PDGFB, CXCL10, XCL1, CCL21 |
| GO:0048545 | response to steroid hormone stimulus | 1.23E-07 | SPARC, TGFB1, THBS1, CALR, SERPINE1, PLAT, ACTA1, COL1A1, PDGFB, SDC1, TNFRSF11B, MMP9, MMP2, MMP3 |
| GO:0002687 | positive regulation of leukocyte migration | 1.32E-07 | ITGB3, THBS1, SELP, ITGA2, SERPINE1, CXCL10, XCL1, CCL21 |
| GO:0002237 | response to molecule of bacterial origin | 1.34E-07 | SPARC, DCN, CD36, TGFB1, SELP, SERPINE1, CTSG, ELANE, JAG1, CXCL10, MMP9, MMP3 |
| GO:0009628 | response to abiotic stimulus | 1.55E-07 | SPARC, DCN, CD36, TGFB1, ITGB1, CD9, THBS1, ITGA2, SERPINE1, LRP2, ELANE, ACTA1, COL1A1, CXCL10, COL3A1, MMP9, MMP2, MMP3 |
| GO:0048584 | positive regulation of response to stimulus | 2.21E-07 | TGFB1, ITGB1, HRG, THBS1, SELP, ITGA2, SERPINE1, PLA2G2A, CTSG, ELANE, PDGFB, CXCL10, XCL1, CFH, IGFBP5, CCL21, VTN, CD47, CD44 |
| GO:0050921 | positive regulation of chemotaxis | 2.41E-07 | TGFB1, THBS1, ITGA2, SERPINE1, PDGFB, CXCL10, XCL1, CCL21 |
| GO:0032940 | secretion by cell | 2.66E-07 | KNG1, SPARC, CD36, TGFB1, ITGB3, HRG, FN1, CD9, THBS1, SELP, SERPINE1, LRP2, LRP5, PLG, PDGFB, ACTN4, CXCL10, FGA |
| GO:0061302 | smooth muscle cell-matrix adhesion | 2.70E-07 | SERPINE1, PLAU, DDR1, VTN |
| GO:2000026 | regulation of multicellular organismal development | 2.70E-07 | CD36, TGFB1, ITGB3, ITGB1, HRG, THBS1, CALR, SERPINE1, PLAU, LAMA1, PLG, COL1A1, JAG1, ADAMTS1, PDGFB, CXCL10, CCL21, TNFRSF11B, TNR, MMP9, F2, CD44 |
| GO:0032103 | positive regulation of response to external stimulus | 2.98E-07 | TGFB1, THBS1, ITGA2, SERPINE1, PLA2G2A, PDGFB, CXCL10, XCL1, CCL21, CD47 |
| GO:0051917 | regulation of fibrinolysis | 3.97E-07 | HRG, THBS1, SERPINE1, PLG, F2 |
| GO:0046903 | secretion | 5.09E-07 | KNG1, SPARC, CD36, TGFB1, ITGB3, HRG, FN1, CD9, THBS1, SELP, SERPINE1, LRP2, LRP5, PLG, DDR1, PDGFB, ACTN4, CXCL10, FGA |
| GO:0009725 | response to hormone stimulus | 7.38E-07 | SPARC, TGFB1, ITGB1, THBS1, CALR, ITGA2, SERPINE1, PLAT, ACTA1, COL1A1, CTSL1, PDGFB, SDC1, CCL21, TNFRSF11B, MMP9, MMP2, MMP3 |
| GO:0032496 | response to lipopolysaccharide | 7.66E-07 | SPARC, DCN, CD36, TGFB1, SELP, SERPINE1, CTSG, ELANE, CXCL10, MMP9, MMP3 |
| GO:0032964 | collagen biosynthetic process | 7.66E-07 | TGFB1, ITGA2, COL1A1, COL5A1, COL3A1, F2 |

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| GO:0051130 | positive regulation of cellular component organization | 7.68E-07 | CD36, TGFB1, ITGB1, HRG, CALR, ITGA2, SERPINE1, LRP5, COL1A1, PDGFB, ACTN4, CORO1A, CCL21, VTN, CD47 |
| GO:0051050 | positive regulation of transport | 8.20E-07 | KNG1, CD36, TGFB1, ITGB1, CALR, LRP1, ITGA2, SERPINE1, PDGFB, ACTN4, XCL1, CCL21, VTN, F2, CD47 |
| GO:0048520 | positive regulation of behavior | 8.72E-07 | TGFB1, THBS1, ITGA2, SERPINE1, PDGFB, CXCL10, XCL1, CCL21 |
| GO:0016525 | negative regulation of angiogenesis | 8.95E-07 | CD36, HRG, THBS1, SERPINE1, PLG, ADAMTS1, CXCL10 |
| GO:0002685 | regulation of leukocyte migration | 9.32E-07 | ITGB3, THBS1, SELP, ITGA2, SERPINE1, CXCL10, XCL1, CCL21 |
| GO:0031099 | regeneration | 9.96E-07 | TGFB1, SERPINE1, LRP2, PLAU, PLG, DDR1, VCAN, TNR, MMP2 |
| GO:0009607 | response to biotic stimulus | 1.01E-06 | SPARC, DCN, CD36, TGFB1, HRG, SELP, SERPINE1, PLA2G2A, CTSG, ELANE, JAG1, CXCL10, XCL1, CCL20, MMP9, MMP3, CD47 |
| GO:0051240 | positive regulation of multicellular organismal process | 1.05E-06 | KNG1, CD36, TGFB1, ITGB3, HRG, THBS1, ITGA2, SERPINE1, PLAT, PLAU, PLG, PDGFB, XCL1, TNR, F2 |
| GO:0001952 | regulation of cell-matrix adhesion | 1.22E-06 | CD36, HRG, THBS1, SERPINE1, PLAU, DDR1, CCL21 |
| GO:0040007 | growth | 1.45E-06 | CD36, TGFB1, HRG, THBS1, SERPINE1, PLA2G2A, CTSG, ELANE, PLAU, ACTA1, PLG, DDR1, PDGFB, IGFBP5, TNR, MMP9, F2, CD44 |
| GO:0009612 | response to mechanical stimulus | 1.47E-06 | DCN, CD36, ITGB1, ITGA2, ACTA1, COL1A1, CXCL10, MMP9, MMP2 |
| GO:0007507 | heart development | 1.52E-06 | FBN1, SPARC, ITGB1, THBS1, CALR, ITGA4, ADAMTS1, HSPG2, PDGFB, COL5A1, COL2A1, COL3A1, VCAN |
| GO:0001501 | skeletal system development | 1.56E-06 | FBN1, TGFB1, THBS1, LRP5, COL1A2, COL1A1, HSPG2, COL2A1, COL3A1, TNFRSF11B, MMP9, MMP2, CD44 |
| GO:0070482 | response to oxygen levels | 1.68E-06 | TGFB1, THBS1, ITGA2, SERPINE1, PLAT, PLAU, PDGFB, ACTN4, MMP9, MMP2, MMP3 |
| GO:0033628 | regulation of cell adhesion mediated by integrin | 1.94E-06 | ITGB3, HRG, SERPINE1, PLAU, PLG, CCL21 |
| GO:0060326 | cell chemotaxis | 2.25E-06 | CCR6, HRG, THBS1, SERPINE1, PDGFB, CXCL10, XCL1, CORO1A, CCL21 |
| GO:0022612 | gland morphogenesis | 5.35E-06 | TGFB1, LRP5, LAMA1, DDR1, PDGFB, IGFBP5, MMP2, CD44 |
| GO:0030574 | collagen catabolic process | 5.35E-06 | MMP8, MMP9, MMP2, MMP1, MMP3 |
| GO:0010647 | positive regulation of cell communication | 5.64E-06 | KNG1, CD36, TGFB1, ITGB3, ITGB1, THBS1, SELP, ITGA2, COL1A1, JAG1, PDGFB, IGFBP5, CCL21, TNR, VTN, F2, CD44 |
| GO:0006955 | immune response | 6.56E-06 | CD36, TGFB1, ITGB1, CCR6, HRG, THBS1, ITGA4, CTSG, ELANE, CTSL1, CXCL10, XCL1, CFH, COL3A1, CCL20, CORO1A, CCL21, VTN, CD44 |
| GO:0014911 | positive regulation of smooth muscle cell migration | 6.58E-06 | ITGB3, ITGA2, PLAU, PDGFB, VTN |
| GO:0030595 | leukocyte chemotaxis | 8.54E-06 | CCR6, THBS1, SERPINE1, PDGFB, CXCL10, XCL1, CORO1A, CCL21 |
| GO:0001666 | response to hypoxia | 9.71E-06 | TGFB1, THBS1, ITGA2, PLAT, PLAU, PDGFB, ACTN4, MMP9, MMP2, MMP3 |

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| GO:0022603 | regulation of anatomical structure morphogenesis | 9.94E-06 | CD36, TGFB1, HRG, THBS1, SERPINE1, PLAU, PLG, COL1A1, ADAMTS1, CXCL10, TNFRSF11B, TNR, MMP9, CD44 |
| GO:0033273 | response to vitamin | 1.03E-05 | SPARC, TGFB1, ITGB1, ITGA2, LRP2, COL1A1, CXCL10, MMP9, CD44 |
| GO:0060627 | regulation of vesicle-mediated transport | 1.38E-05 | CD36, TGFB1, ITGB1, CALR, ITGA2, SERPINE1, ACTN4, CCL21, VTN, CD47 |
| GO:0006508 | proteolysis | 1.64E-05 | KNG1, KLK2, THBS1, SERPINE1, PLAT, CTSG, ELANE, PLAU, PLG, ADAMTS1, CTSL1, CFH, MMP8, MMP9, MMP2, MMP1, F2, MMP3 |
| GO:0051271 | negative regulation of cellular component movement | 1.64E-05 | TGFB1, HRG, THBS1, LRP1, SERPINE1, PDGFB, ACTN4, IGFBP5 |
| GO:0048729 | tissue morphogenesis | 1.85E-05 | TGFB1, ITGA2, LRP5, LAMA1, COL1A2, DDR1, COL1A1, JAG1, CTSL1, PDGFB, IGFBP5, MMP2, CD44 |
| GO:0023056 | positive regulation of signaling | 1.85E-05 | KNG1, CD36, TGFB1, ITGB3, ITGB1, THBS1, SELP, COL1A1, JAG1, PDGFB, IGFBP5, CCL21, TNR, VTN, F2, CD44 |
| GO:0008284 | positive regulation of cell proliferation | 1.96E-05 | KNG1, TGFB1, ITGB3, ITGB1, CALR, ITGA2, LRP5, ELANE, PLAU, PDGFB, CXCL10, XCL1, CORO1A, F2, CD47 |
| GO:0044243 | multicellular organismal catabolic process | 1.99E-05 | MMP8, MMP9, MMP2, MMP1, MMP3 |
| GO:0007229 | integrin-mediated signaling pathway | 2.09E-05 | ITGB3, ITGB1, ITGA2, ITGA4, ADAMTS1, COL3A1, CD47 |
| GO:2000379 | positive regulation of reactive oxygen species metabolic process | 2.33E-05 | CD36, THBS1, PLAU, PDGFB, F2 |
| GO:0001655 | urogenital system development | 2.36E-05 | FBN1, DCN, TGFB1, ITGB3, JAG1, ADAMTS1, NID1, PDGFB, MMP2, CD44 |
| GO:0043588 | skin development | 2.37E-05 | ITGA2, COL1A2, DDR1, COL1A1, COL5A1, COL3A1 |
| GO:0010941 | regulation of cell death | 2.38E-05 | KNG1, TGFB1, ITGB3, ITGB1, HRG, FN1, THBS1, CALR, LRP1, SERPINE1, LRP5, PLG, KRT18, ACTN4, XCL1, COL2A1, CCL21, MMP9, MMP2, F2, CD44 |
| GO:0040013 | negative regulation of locomotion | 2.60E-05 | TGFB1, HRG, THBS1, LRP1, SERPINE1, ELANE, PDGFB, IGFBP5 |
| GO:0007584 | response to nutrient | 2.63E-05 | SPARC, TGFB1, ITGB1, ITGA2, LRP2, COL1A1, CXCL10, TNFRSF11B, MMP9, CD44 |
| GO:0018108 | peptidyl-tyrosine phosphorylation | 2.95E-05 | CD36, ITGB3, ITGB1, HRG, DDR1, PDGFB, VTN, F2, CD44 |
| GO:0018212 | peptidyl-tyrosine modification | 3.17E-05 | CD36, ITGB3, ITGB1, HRG, DDR1, PDGFB, VTN, F2, CD44 |
| GO:0007565 | female pregnancy | 3.26E-05 | FBLN1, TGFB1, ITGB1, PLAU, DDR1, MMP9, MMP2, MMP3 |
| GO:0009991 | response to extracellular stimulus | 3.49E-05 | SPARC, TGFB1, ITGB1, ITGA2, LRP2, ACTA1, COL1A1, CXCL10, TNFRSF11B, MMP9, MMP3, CD44 |
| GO:0042592 | homeostatic process | 3.49E-05 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CD9, CALR, ITGA2, SERPINE1, LRP5, ELANE, PLG, XCL1, COL2A1, IGFBP5, CORO1A, CCL21, TNFRSF11B, F2, CD44 |
| GO:0006874 | cellular calcium ion homeostasis | 4.96E-05 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CALR, ELANE, XCL1, CCL21, F2 |

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| GO:0030030 | cell projection organization | 5.34E-05 | ITGB3, ITGB1, HRG, ITGA2, LAMA1, COL1A2, COL1A1, PDGFB, COL5A1, COL2A1, COL3A1, CORO1A, CCL21, VCAN, TNR, MMP2, CD44 |
| GO:0071230 | cellular response to amino acid stimulus | 5.38E-05 | COL1A2, COL1A1, COL3A1, MMP2, MMP3 |
| GO:0045765 | regulation of angiogenesis | 5.54E-05 | CD36, HRG, THBS1, SERPINE1, PLG, ADAMTS1, CXCL10, MMP9 |
| GO:0042981 | regulation of apoptotic process | 5.70E-05 | KNG1, TGFB1, ITGB1, HRG, FN1, THBS1, CALR, LRP1, SERPINE1, LRP5, PLG, KRT18, ACTN4, XCL1, COL2A1, CCL21, MMP9, MMP2, F2, CD44 |
| GO:0050865 | regulation of cell activation | 5.84E-05 | KNG1, TGFB1, HRG, THBS1, SELP, PDGFB, XCL1, CORO1A, CCL21, F2, CD47 |
| GO:0071845 | cellular component disassembly at cellular level | 6.24E-05 | KLK2, CTSG, ELANE, PLG, DDR1, MMP8, MMP9, MMP2, MMP1, MMP3 |
| GO:0001503 | ossification | 6.24E-05 | SPARC, TGFB1, LRP5, COL1A1, HSPG2, COL2A1, IGFBP5, MMP8, MMP9, MMP2 |
| GO:0009967 | positive regulation of signal transduction | 6.24E-05 | KNG1, CD36, TGFB1, ITGB3, ITGB1, THBS1, SELP, COL1A1, JAG1, PDGFB, IGFBP5, CCL21, VTN, F2, CD44 |
| GO:0060349 | bone morphogenesis | 6.27E-05 | TGFB1, THBS1, LRP5, COL1A1, HSPG2, COL2A1 |
| GO:0043067 | regulation of programmed cell death | 6.27E-05 | KNG1, TGFB1, ITGB1, HRG, FN1, THBS1, CALR, LRP1, SERPINE1, LRP5, PLG, KRT18, ACTN4, XCL1, COL2A1, CCL21, MMP9, MMP2, F2, CD44 |
| GO:0055074 | calcium ion homeostasis | 6.27E-05 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CALR, ELANE, XCL1, CCL21, F2 |
| GO:0022411 | cellular component disassembly | 6.81E-05 | KLK2, CTSG, ELANE, PLG, DDR1, MMP8, MMP9, MMP2, MMP1, MMP3 |
| GO:0072503 | cellular divalent inorganic cation homeostasis | 7.83E-05 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CALR, ELANE, XCL1, CCL21, F2 |
| GO:0034097 | response to cytokine stimulus | 8.28E-05 | SPARC, CCR6, SELP, SERPINE1, SELPLG, KRT18, XCL1, COL3A1, CORO1A, MMP9, MMP3 |
| GO:0030199 | collagen fibril organization | 8.42E-05 | COL1A2, COL1A1, COL5A1, COL2A1, COL3A1 |
| GO:0043627 | response to estrogen stimulus | 8.66E-05 | TGFB1, CALR, SERPINE1, PDGFB, TNFRSF11B, MMP9, MMP2, MMP3 |
| GO:0007566 | embryo implantation | 9.41E-05 | FBLN1, PLAU, DDR1, MMP9, MMP2 |
| GO:0072507 | divalent inorganic cation homeostasis | 1.04E-04 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CALR, ELANE, XCL1, CCL21, F2 |
| GO:0071495 | cellular response to endogenous stimulus | 1.07E-04 | CD36, TGFB1, ITGA2, COL1A2, COL1A1, CTSL1, XCL1, COL2A1, COL3A1, MMP9, MMP2, MMP3, CD44 |
| GO:0071229 | cellular response to acid | 1.16E-04 | COL1A2, COL1A1, COL3A1, MMP2, MMP3 |
| GO:0007159 | leukocyte cell-cell adhesion | 1.16E-04 | ITGB1, SELP, ITGA4, SELPLG, CD44 |
| GO:0010035 | response to inorganic substance | 1.16E-04 | SPARC, CD36, THBS1, CALR, SERPINE1, ACTA1, COL1A1, SDC1, FGA, TNFRSF11B, MMP2 |
| GO:0019220 | regulation of phosphate metabolic process | 1.16E-04 | KNG1, CD36, TGFB1, ITGB3, ITGB1, HRG, THBS1, CALR, LRP1, ITGA2, LRP5, ELANE, PDGFB, CCL21, VTN, F2, CD44 |

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| GO:0051174 | regulation of phosphorus metabolic process | 1.16E-04 | KNG1, CD36, TGFB1, ITGB3, ITGB1, HRG, THBS1, CALR, LRP1, ITGA2, LRP5, ELANE, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0045861 | negative regulation of proteolysis | 1.28E-04 | KNG1, THBS1, SERPINE1, PLAT, F2 |
| GO:0030336 | negative regulation of cell migration | 1.28E-04 | TGFB1, HRG, THBS1, LRP1, SERPINE1, PDGFB, IGFBP5 |
| GO:0044419 | interspecies interaction between organisms | 1.39E-04 | FBLN1, CD36, TGFB1, ITGB3, ITGB1, ITGA2, CTSG, ELANE, KRT18, MMP9, MMP1 |
| GO:2000146 | negative regulation of cell motility | 1.40E-04 | TGFB1, HRG, THBS1, LRP1, SERPINE1, PDGFB, IGFBP5 |
| GO:0033629 | negative regulation of cell adhesion mediated by integrin | 1.50E-04 | HRG, SERPINE1, PLG |
| GO:0000904 | cell morphogenesis involved in differentiation | 1.58E-04 | TGFB1, ITGB3, ITGB1, FN1, ITGA2, LAMA1, COL1A2, COL1A1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2 |
| GO:0051049 | regulation of transport | 1.63E-04 | KNG1, CD36, TGFB1, ITGB3, ITGB1, THBS1, CALR, LRP1, ITGA2, SERPINE1, LRP5, PDGFB, ACTN4, XCL1, CCL21, VTN, F2, CD47 |
| GO:0016337 | cell-cell adhesion | 1.66E-04 | TGFB1, ITGB3, ITGB1, SELP, ITGA4, SELPLG, PLG, COL2A1, TNR, CD47, CD44 |
| GO:0050832 | defense response to fungus | 1.66E-04 | TGFB1, HRG, CTSG, ELANE |
| GO:0042325 | regulation of phosphorylation | 1.76E-04 | KNG1, CD36, TGFB1, ITGB3, ITGB1, HRG, THBS1, CALR, LRP1, LRP5, ELANE, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0022008 | neurogenesis | 1.90E-04 | TGFB1, ITGB3, ITGB1, CD9, CALR, ITGA2, LAMA1, COL1A2, COL1A1, JAG1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2, F2, CD44 |
| GO:0060351 | cartilage development involved in endochondral bone morphogenesis | 1.99E-04 | THBS1, COL1A1, HSPG2, COL2A1 |
| GO:0042327 | positive regulation of phosphorylation | 2.11E-04 | CD36, TGFB1, ITGB3, ITGB1, THBS1, CALR, PDGFB, CCL21, VTN, F2, CD44 |
| GO:2000377 | regulation of reactive oxygen species metabolic process | 2.25E-04 | CD36, THBS1, PLAU, PDGFB, F2 |
| GO:0010543 | regulation of platelet activation | 2.36E-04 | HRG, SELP, PDGFB, F2 |
| GO:0032844 | regulation of homeostatic process | 2.38E-04 | KNG1, TGFB1, ITGB3, LRP5, XCL1, CCL21, TNFRSF11B, F2, CD44 |
| GO:0050764 | regulation of phagocytosis | 2.43E-04 | CD36, TGFB1, CALR, ITGA2, CD47 |
| GO:0045937 | positive regulation of phosphate metabolic process | 2.43E-04 | CD36, TGFB1, ITGB3, ITGB1, THBS1, CALR, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0010562 | positive regulation of phosphorus metabolic process | 2.43E-04 | CD36, TGFB1, ITGB3, ITGB1, THBS1, CALR, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0007409 | axonogenesis | 2.44E-04 | ITGB3, ITGB1, ITGA2, LAMA1, COL1A2, COL1A1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2 |
| GO:0032989 | cellular component morphogenesis | 2.44E-04 | TGFB1, ITGB3, ITGB1, FN1, CD9, ITGA2, LAMA1, COL1A2, ACTA1, COL1A1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2 |

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| GO:0045596 | negative regulation of cell differentiation | 2.44E-04 | TGFB1, ITGB3, ITGB1, CALR, LRP5, PLA2G2A, JAG1, IGFBP5, CCL21, TNR, F2 |
| GO:0071418 | cellular response to amine stimulus | 2.58E-04 | COL1A2, COL1A1, COL3A1, MMP2, MMP3 |
| GO:0002690 | positive regulation of leukocyte chemotaxis | 2.58E-04 | THBS1, SERPINE1, CXCL10, XCL1, CCL21 |
| GO:0034330 | cell junction organization | 2.58E-04 | TGFB1, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, CD47 |
| GO:0007411 | axon guidance | 2.73E-04 | ITGB3, ITGB1, ITGA2, LAMA1, COL1A2, COL1A1, COL5A1, COL2A1, COL3A1, TNR |
| GO:0001822 | kidney development | 2.83E-04 | FBN1, DCN, TGFB1, ITGB3, JAG1, ADAMTS1, NID1, PDGFB |
| GO:0032268 | regulation of cellular protein metabolic process | 2.87E-04 | KNG1, CD36, TGFB1, ITGB3, ITGB1, HRG, THBS1, CALR, ITGA2, SERPINE1, PLAT, PDGFB, IGFBP5, CCL21, VTN, F2, CD44 |
| GO:0071417 | cellular response to organic nitrogen | 3.04E-04 | COL1A2, COL1A1, COL3A1, MMP2, MMP3 |
| GO:0008285 | negative regulation of cell proliferation | 3.12E-04 | KNG1, TGFB1, ITGB1, HRG, CD9, THBS1, PLA2G2A, PLG, DDR1, ADAMTS1, XCL1, IGFBP5 |
| GO:0048732 | gland development | 3.28E-04 | TGFB1, ITGA2, LRP5, LAMA1, DDR1, PDGFB, IGFBP5, MMP2, CD44 |
| GO:0051246 | regulation of protein metabolic process | 3.32E-04 | KNG1, CD36, TGFB1, ITGB3, ITGB1, HRG, THBS1, CALR, ITGA2, SERPINE1, PLAT, PDGFB, CFH, IGFBP5, CCL21, VTN, F2, CD44 |
| GO:0008544 | epidermis development | 3.34E-04 | ITGA2, COL1A2, DDR1, COL1A1, JAG1, COL5A1, COL7A1, COL3A1, IGFBP5 |
| GO:0048699 | generation of neurons | 3.37E-04 | TGFB1, ITGB3, ITGB1, CALR, ITGA2, LAMA1, COL1A2, COL1A1, JAG1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2, F2, CD44 |
| GO:0006875 | cellular metal ion homeostasis | 3.47E-04 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CALR, ELANE, XCL1, CCL21, F2 |
| GO:0060348 | bone development | 3.55E-04 | TGFB1, THBS1, LRP5, COL1A1, HSPG2, COL2A1 |
| GO:0072001 | renal system development | 3.78E-04 | FBN1, DCN, TGFB1, ITGB3, JAG1, ADAMTS1, NID1, PDGFB |
| GO:0043534 | blood vessel endothelial cell migration | 3.80E-04 | TGFB1, ITGB1, HRG, THBS1, PDGFB |
| GO:0050730 | regulation of peptidyl-tyrosine phosphorylation | 4.02E-04 | CD36, ITGB3, ITGB1, HRG, PDGFB, VTN, CD44 |
| GO:0010740 | positive regulation of intracellular protein kinase cascade | 4.56E-04 | KNG1, CD36, TGFB1, ITGB3, ITGB1, THBS1, PDGFB, IGFBP5, CCL21, CD44 |
| GO:0090066 | regulation of anatomical structure size | 4.69E-04 | KNG1, TGFB1, ACTA1, DDR1, PDGFB, IGFBP5, CORO1A, CCL21, TNR, MMP2, F2, CD44 |
| GO:0042692 | muscle cell differentiation | 4.78E-04 | TGFB1, ITGB1, CALR, ACTA1, PLG, JAG1, PDGFB, SDC1, IGFBP5 |
| GO:0002688 | regulation of leukocyte chemotaxis | 4.78E-04 | THBS1, SERPINE1, CXCL10, XCL1, CCL21 |
| GO:0032355 | response to estradiol stimulus | 4.78E-04 | TGFB1, CALR, PDGFB, MMP9, MMP2, MMP3 |

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|---|---|---|---|
| GO:0010763 | positive regulation of fibroblast migration | 5.12E-04 | TGFB1, ITGB3, THBS1 |
| GO:0070848 | response to growth factor stimulus | 5.16E-04 | SPARC, TGFB1, ITGB1, HRG, COL1A1, XCL1, COL2A1, CD44 |
| GO:0061061 | muscle structure development | 5.23E-04 | DCN, TGFB1, ITGB1, CALR, ACTA1, PLG, JAG1, PDGFB, SDC1, CXCL10, IGFBP5 |
| GO:0043542 | endothelial cell migration | 5.23E-04 | TGFB1, ITGB3, ITGB1, HRG, THBS1, PDGFB |
| GO:0033280 | response to vitamin D | 5.26E-04 | TGFB1, ITGB1, LRP2, CXCL10 |
| GO:0018149 | peptide cross-linking | 5.26E-04 | DCN, FN1, THBS1, COL3A1 |
| GO:0042493 | response to drug | 5.40E-04 | TGFB1, ITGB1, THBS1, CALR, ITGA2, LRP2, PDGFB, TNFRSF11B, MMP9, MMP2 |
| GO:0055065 | metal ion homeostasis | 5.62E-04 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CALR, ELANE, XCL1, CCL21, F2 |
| GO:0048667 | cell morphogenesis involved in neuron differentiation | 5.81E-04 | ITGB3, ITGB1, ITGA2, LAMA1, COL1A2, COL1A1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2 |
| GO:0016049 | cell growth | 5.81E-04 | TGFB1, HRG, ACTA1, DDR1, PDGFB, IGFBP5, TNR, MMP9, F2, CD44 |
| GO:0090077 | foam cell differentiation | 5.89E-04 | CD36, TGFB1, ITGB3, PLA2G2A |
| GO:0010742 | macrophage derived foam cell differentiation | 5.89E-04 | CD36, TGFB1, ITGB3, PLA2G2A |
| GO:0048812 | neuron projection morphogenesis | 6.22E-04 | ITGB3, ITGB1, ITGA2, LAMA1, COL1A2, COL1A1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2 |
| GO:0051208 | sequestering of calcium ion | 6.61E-04 | TGFB1, CALR, XCL1, CCL21, F2 |
| GO:0031667 | response to nutrient levels | 6.74E-04 | SPARC, TGFB1, ITGB1, ITGA2, LRP2, COL1A1, CXCL10, TNFRSF11B, MMP9, CD44 |
| GO:0043589 | skin morphogenesis | 6.83E-04 | ITGA2, COL1A2, COL1A1 |
| GO:0010594 | regulation of endothelial cell migration | 7.57E-04 | TGFB1, ITGB3, HRG, THBS1, PDGFB |
| GO:0001934 | positive regulation of protein phosphorylation | 7.70E-04 | CD36, TGFB1, ITGB3, ITGB1, CALR, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0050673 | epithelial cell proliferation | 7.71E-04 | KNG1, TGFB1, ITGB3, THBS1, PLA2G2A, PLAU, PDGFB, COL8A1 |
| GO:0014075 | response to amine stimulus | 7.71E-04 | ITGA2, COL1A2, COL1A1, COL3A1, MMP2, MMP3 |
| GO:0030003 | cellular cation homeostasis | 7.76E-04 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CALR, ELANE, XCL1, CCL21, F2 |
| GO:0010812 | negative regulation of cell-substrate adhesion | 8.35E-04 | THBS1, SERPINE1, PLG, COL1A1 |
| GO:0050731 | positive regulation of peptidyl-tyrosine phosphorylation | 8.39E-04 | CD36, ITGB3, ITGB1, PDGFB, VTN, CD44 |
| GO:0061138 | morphogenesis of a branching epithelium | 9.19E-04 | TGFB1, LRP5, LAMA1, DDR1, CTSL1, PDGFB, CD44 |

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| GO:0031175 | neuron projection development | 9.25E-04 | ITGB3, ITGB1, ITGA2, LAMA1, COL1A2, COL1A1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2, CD44 |
| GO:0034329 | cell junction assembly | 9.44E-04 | ITGB3, ITGB1, HRG, FN1, CD9, THBS1, CD47 |
| GO:0043200 | response to amino acid stimulus | 9.62E-04 | COL1A2, COL1A1, COL3A1, MMP2, MMP3 |
| GO:0048705 | skeletal system morphogenesis | 1.08E-03 | TGFB1, THBS1, LRP5, COL1A1, HSPG2, COL2A1, MMP2 |
| GO:0001894 | tissue homeostasis | 1.08E-03 | ITGB3, ITGB1, ITGA2, COL2A1, CORO1A, TNFRSF11B |
| GO:0014070 | response to organic cyclic compound | 1.13E-03 | TGFB1, SELP, ITGA2, PDGFB, DHFR, IGFBP5, MMP9, CD44 |
| GO:0050776 | regulation of immune response | 1.13E-03 | CD36, TGFB1, ITGB1, HRG, ITGA4, CTSG, ELANE, XCL1, CFH, COL3A1, CD44 |
| GO:0009620 | response to fungus | 1.14E-03 | TGFB1, HRG, CTSG, ELANE |
| GO:0043535 | regulation of blood vessel endothelial cell migration | 1.14E-03 | TGFB1, HRG, THBS1, PDGFB |
| GO:0051238 | sequestering of metal ion | 1.14E-03 | TGFB1, CALR, XCL1, CCL21, F2 |
| GO:0014912 | negative regulation of smooth muscle cell migration | 1.15E-03 | LRP1, SERPINE1, IGFBP5 |
| GO:0010466 | negative regulation of peptidase activity | 1.19E-03 | KNG1, THBS1, SERPINE1, COL7A1, VTN, TFPI, CD44 |
| GO:0032269 | negative regulation of cellular protein metabolic process | 1.20E-03 | KNG1, TGFB1, ITGB3, THBS1, CALR, SERPINE1, PLAT, IGFBP5, F2 |
| GO:0043410 | positive regulation of MAPK cascade | 1.26E-03 | KNG1, CD36, ITGB3, ITGB1, PDGFB, CCL21, CD44 |
| GO:0060324 | face development | 1.39E-03 | TGFB1, ITGA4, COL1A1, MMP2 |
| GO:0040008 | regulation of growth | 1.42E-03 | CD36, TGFB1, HRG, PLA2G2A, CTSG, ELANE, DDR1, IGFBP5, TNR, F2, CD44 |
| GO:0022407 | regulation of cell-cell adhesion | 1.43E-03 | TGFB1, PLG, TNR, CD47, CD44 |
| GO:0051591 | response to cAMP | 1.43E-03 | SPARC, PLAT, COL1A1, SDC1, IGFBP5 |
| GO:0032270 | positive regulation of cellular protein metabolic process | 1.44E-03 | CD36, TGFB1, ITGB3, ITGB1, THBS1, CALR, ITGA2, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0035295 | tube development | 1.60E-03 | SPARC, TGFB1, ITGB3, LRP5, LAMA1, DDR1, JAG1, CTSL1, SDC1, CD44 |
| GO:0050766 | positive regulation of phagocytosis | 1.66E-03 | CD36, CALR, ITGA2, CD47 |
| GO:0010595 | positive regulation of endothelial cell migration | 1.66E-03 | TGFB1, ITGB3, THBS1, PDGFB |
| GO:0048878 | chemical homeostasis | 1.74E-03 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CD9, CALR, SERPINE1, LRP5, ELANE, XCL1, IGFBP5, CCL21, F2 |
| GO:0007179 | transforming growth factor beta receptor signaling pathway | 1.76E-03 | FBN1, TGFB1, THBS1, COL1A2, PDGFB, COL3A1 |

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|---|---|---|---|
| GO:0036296 | response to increased oxygen levels | 1.78E-03 | SERPINE1, PLAU, MMP9 |
| GO:0031639 | plasminogen activation | 1.78E-03 | THBS1, SERPINE1, PLAT |
| GO:0010762 | regulation of fibroblast migration | 1.78E-03 | TGFB1, ITGB3, THBS1 |
| GO:0000902 | cell morphogenesis | 1.84E-03 | TGFB1, ITGB3, ITGB1, FN1, ITGA2, LAMA1, COL1A2, COL1A1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2 |
| GO:0072593 | reactive oxygen species metabolic process | 1.85E-03 | CD36, THBS1, PLAU, PDGFB, F2 |
| GO:0060249 | anatomical structure homeostasis | 1.91E-03 | ITGB3, ITGB1, ITGA2, PLG, COL2A1, CORO1A, TNFRSF11B |
| GO:0007610 | behavior | 1.91E-03 | TGFB1, HRG, THBS1, ITGA2, SERPINE1, ELANE, PDGFB, CXCL10, XCL1, CCL21, TNR |
| GO:0030182 | neuron differentiation | 1.91E-03 | ITGB3, ITGB1, CALR, ITGA2, LAMA1, COL1A2, COL1A1, JAG1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2, CD44 |
| GO:0019725 | cellular homeostasis | 1.91E-03 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CD9, CALR, LRP5, ELANE, PLG, XCL1, CCL21, F2 |
| GO:0032535 | regulation of cellular component size | 1.99E-03 | TGFB1, ACTA1, DDR1, PDGFB, IGFBP5, CORO1A, CCL21, TNR, F2, CD44 |
| GO:0050727 | regulation of inflammatory response | 2.00E-03 | ITGA2, SERPINE1, PLA2G2A, ELANE, XCL1, CFH, CD47 |
| GO:0051248 | negative regulation of protein metabolic process | 2.00E-03 | KNG1, TGFB1, ITGB3, THBS1, CALR, SERPINE1, PLAT, IGFBP5, F2 |
| GO:0018193 | peptidyl-amino acid modification | 2.05E-03 | DCN, CD36, TGFB1, ITGB3, ITGB1, HRG, CALR, DDR1, PDGFB, VTN, F2, CD44 |
| GO:0055080 | cation homeostasis | 2.07E-03 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CALR, ELANE, XCL1, CCL21, F2 |
| GO:0048730 | epidermis morphogenesis | 2.09E-03 | ITGA2, COL1A2, COL1A1, IGFBP5 |
| GO:0071363 | cellular response to growth factor stimulus | 2.15E-03 | SPARC, TGFB1, HRG, COL1A1, XCL1, COL2A1, CD44 |
| GO:0001763 | morphogenesis of a branching structure | 2.20E-03 | TGFB1, LRP5, LAMA1, DDR1, CTSL1, PDGFB, CD44 |
| GO:0050678 | regulation of epithelial cell proliferation | 2.20E-03 | KNG1, TGFB1, ITGB3, THBS1, PLA2G2A, PLAU, PDGFB |
| GO:0002009 | morphogenesis of an epithelium | 2.25E-03 | TGFB1, LRP5, LAMA1, DDR1, JAG1, CTSL1, PDGFB, MMP2, CD44 |
| GO:0048858 | cell projection morphogenesis | 2.29E-03 | ITGB3, ITGB1, ITGA2, LAMA1, COL1A2, COL1A1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2 |
| GO:0051247 | positive regulation of protein metabolic process | 2.31E-03 | CD36, TGFB1, ITGB3, ITGB1, THBS1, CALR, ITGA2, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0055082 | cellular chemical homeostasis | 2.40E-03 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CD9, CALR, LRP5, ELANE, XCL1, CCL21, F2 |

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|---|---|---|---|
| GO:0045445 | myoblast differentiation | 2.44E-03 | TGFB1, PLG, JAG1, SDC1 |
| GO:0043537 | negative regulation of blood vessel endothelial cell migration | 2.52E-03 | TGFB1, HRG, THBS1 |
| GO:0042953 | lipoprotein transport | 2.52E-03 | CD36, LRP1, LRP2 |
| GO:0032990 | cell part morphogenesis | 2.68E-03 | ITGB3, ITGB1, ITGA2, LAMA1, COL1A2, COL1A1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2 |
| GO:0010243 | response to organic nitrogen | 2.84E-03 | ITGA2, COL1A2, COL1A1, COL3A1, MMP2, MMP3 |
| GO:0060350 | endochondral bone morphogenesis | 2.85E-03 | THBS1, COL1A1, HSPG2, COL2A1 |
| GO:0052548 | regulation of endopeptidase activity | 2.89E-03 | KNG1, THBS1, SERPINE1, COL7A1, VTN, F2, TFPI, CD44 |
| GO:0048660 | regulation of smooth muscle cell proliferation | 2.92E-03 | ITGB3, ITGA2, ELANE, PDGFB, IGFBP5 |
| GO:0010953 | regulation of protein maturation by peptide bond cleavage | 2.99E-03 | THBS1, SERPINE1, CFH |
| GO:0048666 | neuron development | 3.07E-03 | ITGB3, ITGB1, ITGA2, LAMA1, COL1A2, COL1A1, COL5A1, COL2A1, COL3A1, VCAN, TNR, MMP2, CD44 |
| GO:0048659 | smooth muscle cell proliferation | 3.35E-03 | ITGB3, ITGA2, ELANE, PDGFB, IGFBP5 |
| GO:0001101 | response to acid | 3.35E-03 | COL1A2, COL1A1, COL3A1, MMP2, MMP3 |
| GO:2000097 | regulation of smooth muscle cell-matrix adhesion | 3.36E-03 | SERPINE1, PLAU |
| GO:0072126 | positive regulation of glomerular mesangial cell proliferation | 3.36E-03 | ITGB3, PDGFB |
| GO:0061304 | retinal blood vessel morphogenesis | 3.36E-03 | LRP5, LAMA1 |
| GO:0044126 | regulation of growth of symbiont in host | 3.46E-03 | CD36, CTSG, ELANE |
| GO:0044130 | negative regulation of growth of symbiont in host | 3.46E-03 | CD36, CTSG, ELANE |
| GO:0044144 | modulation of growth of symbiont involved in interaction with host | 3.46E-03 | CD36, CTSG, ELANE |
| GO:0044146 | negative regulation of growth of symbiont involved in interaction with host | 3.46E-03 | CD36, CTSG, ELANE |
| GO:0034103 | regulation of tissue remodeling | 3.48E-03 | ITGB3, HRG, LRP5, TNFRSF11B |
| GO:0010951 | negative regulation of endopeptidase activity | 3.58E-03 | KNG1, SERPINE1, COL7A1, VTN, TFPI, CD44 |
| GO:0052547 | regulation of peptidase activity | 3.66E-03 | KNG1, THBS1, SERPINE1, COL7A1, VTN, F2, TFPI, CD44 |
| GO:0042742 | defense response to bacterium | 3.67E-03 | CD36, SELP, SERPINE1, PLA2G2A, CTSG, CCL20 |
| GO:0031960 | response to corticosteroid stimulus | 3.67E-03 | SPARC, TGFB1, SERPINE1, PLAT, COL1A1, SDC1 |

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|---|---|---|---|
| GO:0060322 | head development | 4.00E-03 | TGFB1, ITGA4, COL1A1, MMP2 |
| GO:0031638 | zymogen activation | 4.01E-03 | THBS1, SERPINE1, PLAT |
| GO:0001932 | regulation of protein phosphorylation | 4.32E-03 | CD36, TGFB1, ITGB3, ITGB1, HRG, CALR, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0030162 | regulation of proteolysis | 4.58E-03 | KNG1, THBS1, SERPINE1, PLAT, CFH, F2 |
| GO:0043536 | positive regulation of blood vessel endothelial cell migration | 4.66E-03 | TGFB1, THBS1, PDGFB |
| GO:0048871 | multicellular organismal homeostasis | 5.01E-03 | ITGB3, ITGB1, ITGA2, COL2A1, CORO1A, TNFRSF11B |
| GO:0007167 | enzyme linked receptor protein signaling pathway | 5.14E-03 | FBN1, TGFB1, ITGB3, HRG, THBS1, LRP1, PLAT, COL1A2, DDR1, PDGFB, COL3A1, IGFBP5, VTN |
| GO:0048754 | branching morphogenesis of a tube | 5.14E-03 | TGFB1, LRP5, LAMA1, DDR1, CTSL1, CD44 |
| GO:0042476 | odontogenesis | 5.21E-03 | TGFB1, COL1A2, COL1A1, SDC1, TNFRSF11B |
| GO:0048661 | positive regulation of smooth muscle cell proliferation | 5.21E-03 | ITGB3, ITGA2, ELANE, PDGFB |
| GO:0051216 | cartilage development | 5.25E-03 | TGFB1, THBS1, COL1A1, HSPG2, COL2A1, CD44 |
| GO:0006873 | cellular ion homeostasis | 5.25E-03 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CD9, CALR, ELANE, XCL1, CCL21, F2 |
| GO:0072378 | blood coagulation, fibrin clot formation | 5.25E-03 | KNG1, F2, TFPI |
| GO:0010761 | fibroblast migration | 5.25E-03 | TGFB1, ITGB3, THBS1 |
| GO:0043277 | apoptotic cell clearance | 5.25E-03 | CD36, THBS1, LRP1 |
| GO:0030036 | actin cytoskeleton organization | 5.47E-03 | ITGB1, HRG, CALR, LRP1, ACTA1, PDGFB, ACTN4, CORO1A, CCL21 |
| GO:0051817 | modification of morphology or physiology of other organism involved in symbiotic interaction | 5.47E-03 | TGFB1, CTSG, ELANE, MMP9 |
| GO:0043065 | positive regulation of apoptotic process | 5.47E-03 | KNG1, TGFB1, ITGB1, HRG, THBS1, LRP5, PLG, XCL1, MMP9, MMP2, CD44 |
| GO:0050867 | positive regulation of cell activation | 5.63E-03 | TGFB1, THBS1, SELP, XCL1, CORO1A, CCL21, CD47 |
| GO:0060443 | mammary gland morphogenesis | 5.79E-03 | TGFB1, LRP5, DDR1, IGFBP5 |
| GO:0043068 | positive regulation of programmed cell death | 5.79E-03 | KNG1, TGFB1, ITGB1, HRG, THBS1, LRP5, PLG, XCL1, MMP9, MMP2, CD44 |
| GO:0010714 | positive regulation of collagen metabolic process | 5.83E-03 | TGFB1, ITGA2, F2 |
| GO:0032967 | positive regulation of collagen biosynthetic process | 5.83E-03 | TGFB1, ITGA2, F2 |

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|---|---|---|---|
| GO:0044110 | growth involved in symbiotic interaction | 5.83E-03 | CD36, CTSG, ELANE |
| GO:0044116 | growth of symbiont involved in interaction with host | 5.83E-03 | CD36, CTSG, ELANE |
| GO:0044117 | growth of symbiont in host | 5.83E-03 | CD36, CTSG, ELANE |
| GO:0006911 | phagocytosis, engulfment | 5.83E-03 | CD36, THBS1, ITGA2 |
| GO:0030212 | hyaluronan metabolic process | 5.83E-03 | TGFB1, PDGFB, CD44 |
| GO:1900125 | regulation of hyaluronan biosynthetic process | 5.84E-03 | TGFB1, PDGFB |
| GO:0060279 | positive regulation of ovulation | 5.84E-03 | PLAT, PLAU |
| GO:0010757 | negative regulation of plasminogen activation | 5.84E-03 | THBS1, SERPINE1 |
| GO:0007161 | calcium-independent cell-matrix adhesion | 5.84E-03 | ITGB1, FN1 |
| GO:0071460 | cellular response to cell-matrix adhesion | 5.84E-03 | MMP9, MMP3 |
| GO:0060099 | regulation of phagocytosis, engulfment | 5.84E-03 | CD36, ITGA2 |
| GO:0060100 | positive regulation of phagocytosis, engulfment | 5.84E-03 | CD36, ITGA2 |
| GO:0071404 | cellular response to low-density lipoprotein particle stimulus | 5.84E-03 | CD36, MMP9 |
| GO:0071844 | cellular component assembly at cellular level | 6.05E-03 | TGFB1, ITGB3, ITGB1, HRG, FN1, CD9, THBS1, CALR, ACTA1, PDGFB, ACTN4, FGA, CORO1A, CCL21, CD47 |
| GO:0060343 | trabecula formation | 6.50E-03 | COL1A1, ADAMTS1, MMP2 |
| GO:0051897 | positive regulation of protein kinase B signaling cascade | 6.70E-03 | TGFB1, THBS1, IGFBP5, CCL21 |
| GO:0006898 | receptor-mediated endocytosis | 6.75E-03 | LRP1, SERPINE1, LRP2, LRP1B, CCL21, VTN |
| GO:0010942 | positive regulation of cell death | 6.90E-03 | KNG1, TGFB1, ITGB1, HRG, THBS1, LRP5, PLG, XCL1, MMP9, MMP2, CD44 |
| GO:0007044 | cell-substrate junction assembly | 7.07E-03 | ITGB3, HRG, FN1, THBS1 |
| GO:0055093 | response to hyperoxia | 7.26E-03 | SERPINE1, PLAU, MMP9 |
| GO:0010596 | negative regulation of endothelial cell migration | 7.26E-03 | TGFB1, HRG, THBS1 |
| GO:0043903 | regulation of symbiosis, encompassing mutualism through parasitism | 7.26E-03 | CD36, CTSG, ELANE |

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|---|---|---|---|
| GO:0051209 | release of sequestered calcium ion into cytosol | 7.41E-03 | TGFB1, XCL1, CCL21, F2 |
| GO:0051283 | negative regulation of sequestering of calcium ion | 7.41E-03 | TGFB1, XCL1, CCL21, F2 |
| GO:0051282 | regulation of sequestering of calcium ion | 7.41E-03 | TGFB1, XCL1, CCL21, F2 |
| GO:0010038 | response to metal ion | 7.50E-03 | SPARC, THBS1, CALR, ACTA1, SDC1, FGA, TNFRSF11B |
| GO:0007423 | sensory organ development | 7.51E-03 | SPARC, TGFB1, LRP5, LAMA1, DDR1, JAG1, COL5A1, COL8A1, COL2A1 |
| GO:0001667 | ameboidal cell migration | 7.91E-03 | TGFB1, ITGB3, THBS1, ITGA2, LRP5 |
| GO:0001958 | endochondral ossification | 8.07E-03 | COL1A1, HSPG2, COL2A1 |
| GO:0008361 | regulation of cell size | 8.10E-03 | TGFB1, ACTA1, DDR1, PDGFB, IGFBP5, TNR, F2, CD44 |
| GO:0031401 | positive regulation of protein modification process | 8.10E-03 | CD36, TGFB1, ITGB3, ITGB1, CALR, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0010627 | regulation of intracellular protein kinase cascade | 8.31E-03 | KNG1, CD36, TGFB1, ITGB3, ITGB1, THBS1, PDGFB, IGFBP5, CCL21, CD44 |
| GO:0043901 | negative regulation of multi-organism process | 9.00E-03 | CD36, CTSG, ELANE |
| GO:0060278 | regulation of ovulation | 9.12E-03 | PLAT, PLAU |
| GO:0071402 | cellular response to lipoprotein particle stimulus | 9.12E-03 | CD36, MMP9 |
| GO:0035791 | platelet-derived growth factor receptor-beta signaling pathway | 9.12E-03 | LRP1, PDGFB |
| GO:0007204 | elevation of cytosolic calcium ion concentration | 9.75E-03 | KNG1, TGFB1, CCR6, XCL1, CCL21, F2 |
| GO:0060444 | branching involved in mammary gland duct morphogenesis | 9.85E-03 | TGFB1, LRP5, DDR1 |
| GO:0043552 | positive regulation of phosphatidylinositol 3-kinase activity | 9.85E-03 | TGFB1, PDGFB, CCL21 |
| GO:0032965 | regulation of collagen biosynthetic process | 9.85E-03 | TGFB1, ITGA2, F2 |
| GO:0001954 | positive regulation of cell-matrix adhesion | 9.85E-03 | CD36, HRG, CCL21 |
| GO:0010743 | regulation of macrophage derived foam cell differentiation | 9.85E-03 | CD36, ITGB3, PLA2G2A |
| GO:0050866 | negative regulation of cell activation | 9.87E-03 | KNG1, TGFB1, PDGFB, XCL1, F2 |
| GO:0033002 | muscle cell proliferation | 9.87E-03 | ITGB3, ITGA2, ELANE, PDGFB, IGFBP5 |

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|---|---|---|---|
| GO:0046849 | bone remodeling | 1.00E-02 | TGFB1, ITGB3, LRP5, TNFRSF11B |
| GO:0050801 | ion homeostasis | 1.00E-02 | KNG1, TGFB1, ITGB3, ITGB1, CCR6, CD9, CALR, ELANE, XCL1, CCL21, F2 |
| GO:0045321 | leukocyte activation | 1.00E-02 | KNG1, TGFB1, ITGB1, THBS1, ITGA4, SELPLG, XCL1, CORO1A, CCL21, CD47 |
| GO:0010712 | regulation of collagen metabolic process | 1.08E-02 | TGFB1, ITGA2, F2 |
| GO:0090218 | positive regulation of lipid kinase activity | 1.08E-02 | TGFB1, PDGFB, CCL21 |
| GO:0051094 | positive regulation of developmental process | 1.11E-02 | CD36, TGFB1, ITGB3, ITGB1, THBS1, SERPINE1, LRP5, PLA2G2A, COL1A1, JAG1, MMP9 |
| GO:0030029 | actin filament-based process | 1.15E-02 | ITGB1, HRG, CALR, LRP1, ACTA1, PDGFB, ACTN4, CORO1A, CCL21 |
| GO:0030728 | ovulation | 1.19E-02 | PLAT, PLAU, ADAMTS1 |
| GO:0044253 | positive regulation of multicellular organismal metabolic process | 1.19E-02 | TGFB1, ITGA2, F2 |
| GO:0045926 | negative regulation of growth | 1.21E-02 | CD36, TGFB1, HRG, CTSG, ELANE, TNR |
| GO:0051346 | negative regulation of hydrolase activity | 1.21E-02 | KNG1, THBS1, SERPINE1, COL7A1, VTN, TFPI, CD44 |
| GO:0051235 | maintenance of location | 1.24E-02 | FBN1, TGFB1, CALR, XCL1, CCL21, F2 |
| GO:0061299 | retina vasculature morphogenesis in camera-type eye | 1.28E-02 | LRP5, LAMA1 |
| GO:0001957 | intramembranous ossification | 1.28E-02 | COL1A1, MMP2 |
| GO:0002246 | wound healing involved in inflammatory response | 1.28E-02 | TGFB1, CD44 |
| GO:0030214 | hyaluronan catabolic process | 1.28E-02 | TGFB1, CD44 |
| GO:0060325 | face morphogenesis | 1.29E-02 | TGFB1, COL1A1, MMP2 |
| GO:0000302 | response to reactive oxygen species | 1.29E-02 | CD36, SERPINE1, COL1A1, SDC1, MMP2 |
| GO:0051480 | cytosolic calcium ion homeostasis | 1.31E-02 | KNG1, TGFB1, CCR6, XCL1, CCL21, F2 |
| GO:0048589 | developmental growth | 1.34E-02 | TGFB1, THBS1, SERPINE1, PLAU, PLG, IGFBP5, TNR |
| GO:0014706 | striated muscle tissue development | 1.39E-02 | DCN, TGFB1, ITGB1, CALR, ACTA1, HSPG2, IGFBP5 |
| GO:0061383 | trabecula morphogenesis | 1.41E-02 | COL1A1, ADAMTS1, MMP2 |
| GO:0030879 | mammary gland development | 1.41E-02 | TGFB1, ITGA2, LRP5, DDR1, IGFBP5 |
| GO:0060429 | epithelium development | 1.51E-02 | TGFB1, ITGA4, LRP5, LAMA1, DDR1, JAG1, CTSL1, PDGFB, MMP2, CD44 |
| GO:0007568 | aging | 1.53E-02 | DCN, TGFB1, CALR, LRP1, SERPINE1, LRP2 |
| GO:0022408 | negative regulation of cell-cell adhesion | 1.53E-02 | TGFB1, PLG, TNR |

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|---|---|---|---|
| GO:0048260 | positive regulation of receptor-mediated endocytosis | 1.53E-02 | SERPINE1, CCL21, VTN |
| GO:0044403 | symbiosis, encompassing mutualism through parasitism | 1.54E-02 | CD36, TGFB1, CTSG, ELANE, MMP9 |
| GO:0030203 | glycosaminoglycan metabolic process | 1.57E-02 | DCN, TGFB1, PDGFB, CD44 |
| GO:0001936 | regulation of endothelial cell proliferation | 1.57E-02 | KNG1, ITGB3, THBS1, PDGFB |
| GO:0051604 | protein maturation | 1.58E-02 | THBS1, CALR, SERPINE1, PLAT, CFH |
| GO:0031347 | regulation of defense response | 1.61E-02 | TGFB1, ITGA2, SERPINE1, PLA2G2A, ELANE, XCL1, CFH, CD47 |
| GO:0000165 | MAPK cascade | 1.61E-02 | KNG1, CD36, TGFB1, ITGB3, ITGB1, THBS1, PDGFB, CCL21, CD44 |
| GO:0031103 | axon regeneration | 1.65E-02 | VCAN, TNR, MMP2 |
| GO:0051146 | striated muscle cell differentiation | 1.69E-02 | TGFB1, ITGB1, CALR, ACTA1, SDC1, IGFBP5 |
| GO:0001955 | blood vessel maturation | 1.69E-02 | MMP2, CD44 |
| GO:0070942 | neutrophil mediated cytotoxicity | 1.69E-02 | CTSG, ELANE |
| GO:0070943 | neutrophil mediated killing of symbiont cell | 1.69E-02 | CTSG, ELANE |
| GO:0072124 | regulation of glomerular mesangial cell proliferation | 1.69E-02 | ITGB3, PDGFB |
| GO:0060537 | muscle tissue development | 1.73E-02 | DCN, TGFB1, ITGB1, CALR, ACTA1, HSPG2, IGFBP5 |
| GO:0001558 | regulation of cell growth | 1.73E-02 | TGFB1, HRG, DDR1, IGFBP5, TNR, F2, CD44 |
| GO:2000021 | regulation of ion homeostasis | 1.74E-02 | KNG1, TGFB1, XCL1, CCL21, F2 |
| GO:0050729 | positive regulation of inflammatory response | 1.75E-02 | ITGA2, SERPINE1, PLA2G2A, CD47 |
| GO:0043551 | regulation of phosphatidylinositol 3-kinase activity | 1.76E-02 | TGFB1, PDGFB, CCL21 |
| GO:0051896 | regulation of protein kinase B signaling cascade | 1.83E-02 | TGFB1, THBS1, IGFBP5, CCL21 |
| GO:0045595 | regulation of cell differentiation | 1.88E-02 | CD36, TGFB1, ITGB3, ITGB1, CALR, LRP5, PLA2G2A, COL1A1, JAG1, IGFBP5, CCL21, TNR, F2 |
| GO:0060323 | head morphogenesis | 1.90E-02 | TGFB1, COL1A1, MMP2 |
| GO:0046850 | regulation of bone remodeling | 1.90E-02 | ITGB3, LRP5, TNFRSF11B |
| GO:0044246 | regulation of multicellular organismal metabolic process | 1.90E-02 | TGFB1, ITGA2, F2 |
| GO:0051384 | response to glucocorticoid stimulus | 1.99E-02 | SPARC, TGFB1, SERPINE1, PLAT, SDC1 |
| GO:0007169 | transmembrane receptor protein tyrosine kinase signaling pathway | 2.00E-02 | TGFB1, ITGB3, HRG, THBS1, LRP1, PLAT, DDR1, PDGFB, IGFBP5, VTN |

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|---|---|---|---|
| GO:0007435 | salivary gland morphogenesis | 2.05E-02 | TGFB1, LAMA1, PDGFB |
| GO:0031345 | negative regulation of cell projection organization | 2.05E-02 | ITGB1, HRG, CCL21, TNR |
| GO:0031349 | positive regulation of defense response | 2.12E-02 | TGFB1, ITGA2, SERPINE1, PLA2G2A, XCL1, CD47 |
| GO:0009314 | response to radiation | 2.14E-02 | TGFB1, ITGB1, LRP2, ELANE, CXCL10, COL3A1, MMP9 |
| GO:0050863 | regulation of T cell activation | 2.14E-02 | KNG1, TGFB1, XCL1, CORO1A, CCL21, CD47 |
| GO:0002604 | regulation of dendritic cell antigen processing and presentation | 2.14E-02 | THBS1, CCL21 |
| GO:0002468 | dendritic cell antigen processing and presentation | 2.14E-02 | THBS1, CCL21 |
| GO:0072110 | glomerular mesangial cell proliferation | 2.14E-02 | ITGB3, PDGFB |
| GO:0010755 | regulation of plasminogen activation | 2.14E-02 | THBS1, SERPINE1 |
| GO:0051279 | regulation of release of sequestered calcium ion into cytosol | 2.18E-02 | TGFB1, XCL1, F2 |
| GO:0061448 | connective tissue development | 2.19E-02 | ITGB3, HSPG2, PDGFB, CD44 |
| GO:0072376 | protein activation cascade | 2.19E-02 | KNG1, CFH, F2, TFPI |
| GO:0070374 | positive regulation of ERK1 and ERK2 cascade | 2.27E-02 | ITGB3, PDGFB, CCL21, CD44 |
| GO:0006022 | aminoglycan metabolic process | 2.27E-02 | DCN, TGFB1, PDGFB, CD44 |
| GO:0060402 | calcium ion transport into cytosol | 2.27E-02 | TGFB1, XCL1, CCL21, F2 |
| GO:0002252 | immune effector process | 2.28E-02 | CD36, TGFB1, CTSG, ELANE, CXCL10, XCL1, CFH, CD47 |
| GO:0019882 | antigen processing and presentation | 2.28E-02 | CD36, THBS1, CALR, CTSL1, CCL21 |
| GO:0060603 | mammary gland duct morphogenesis | 2.32E-02 | TGFB1, LRP5, DDR1 |
| GO:0072006 | nephron development | 2.34E-02 | ITGB3, JAG1, NID1, PDGFB |
| GO:0060401 | cytosolic calcium ion transport | 2.34E-02 | TGFB1, XCL1, CCL21, F2 |
| GO:0043408 | regulation of MAPK cascade | 2.35E-02 | KNG1, CD36, ITGB3, ITGB1, PDGFB, CCL21, CD44 |
| GO:0048008 | platelet-derived growth factor receptor signaling pathway | 2.47E-02 | LRP1, PLAT, PDGFB |
| GO:0043550 | regulation of lipid kinase activity | 2.47E-02 | TGFB1, PDGFB, CCL21 |
| GO:0031102 | neuron projection regeneration | 2.47E-02 | VCAN, TNR, MMP2 |
| GO:0007178 | transmembrane receptor protein serine/threonine kinase signaling pathway | 2.50E-02 | FBN1, TGFB1, THBS1, COL1A2, PDGFB, COL3A1 |

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|---|---|---|---|
| GO:0002696 | positive regulation of leukocyte activation | 2.50E-02 | TGFB1, THBS1, XCL1, CORO1A, CCL21, CD47 |
| GO:0001935 | endothelial cell proliferation | 2.50E-02 | KNG1, ITGB3, THBS1, PDGFB |
| GO:0045859 | regulation of protein kinase activity | 2.59E-02 | KNG1, TGFB1, ITGB3, THBS1, CALR, LRP1, LRP5, ELANE, PDGFB, CCL21 |
| GO:0050901 | leukocyte tethering or rolling | 2.59E-02 | SELP, SELPLG |
| GO:0010544 | negative regulation of platelet activation | 2.59E-02 | PDGFB, F2 |
| GO:0060346 | bone trabecula formation | 2.59E-02 | COL1A1, MMP2 |
| GO:0015911 | plasma membrane long-chain fatty acid transport | 2.59E-02 | CD36, THBS1 |
| GO:0055098 | response to low-density lipoprotein particle stimulus | 2.59E-02 | CD36, MMP9 |
| GO:0033690 | positive regulation of osteoblast proliferation | 2.59E-02 | ITGB3, LRP5 |
| GO:0070613 | regulation of protein processing | 2.59E-02 | THBS1, SERPINE1, CFH |
| GO:0007431 | salivary gland development | 2.59E-02 | TGFB1, LAMA1, PDGFB |
| GO:0048585 | negative regulation of response to stimulus | 2.78E-02 | TGFB1, HRG, SERPINE1, ELANE, XCL1, COL3A1, TNR, CD44 |
| GO:0002718 | regulation of cytokine production involved in immune response | 2.78E-02 | CD36, TGFB1, XCL1 |
| GO:0051336 | regulation of hydrolase activity | 2.89E-02 | KNG1, THBS1, CALR, LRP1, ITGA2, SERPINE1, COL7A1, CCL21, VTN, F2, TFPI, CD44 |
| GO:0002694 | regulation of leukocyte activation | 2.95E-02 | KNG1, TGFB1, THBS1, XCL1, CORO1A, CCL21, CD47 |
| GO:0060562 | epithelial tube morphogenesis | 2.98E-02 | TGFB1, LRP5, LAMA1, DDR1, CTSL1, CD44 |
| GO:0010171 | body morphogenesis | 3.14E-02 | TGFB1, COL1A1, MMP2 |
| GO:0014068 | positive regulation of phosphatidylinositol 3-kinase cascade | 3.14E-02 | SELP, PDGFB, F2 |
| GO:0010935 | regulation of macrophage cytokine production | 3.14E-02 | CD36, TGFB1 |
| GO:0043206 | fibril organization | 3.14E-02 | COL5A1, COL3A1 |
| GO:0030213 | hyaluronan biosynthetic process | 3.14E-02 | TGFB1, PDGFB |
| GO:0033591 | response to L-ascorbic acid | 3.14E-02 | SPARC, ITGA2 |
| GO:0051873 | killing by host of symbiont cells | 3.14E-02 | CTSG, ELANE |
| GO:0051852 | disruption by host of symbiont cells | 3.14E-02 | CTSG, ELANE |

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|---|---|---|---|
| GO:0051129 | negative regulation of cellular component organization | 3.14E-02 | TGFB1, ITGB1, HRG, THBS1, CORO1A, CCL21, TNR |
| GO:0051592 | response to calcium ion | 3.14E-02 | SPARC, THBS1, SDC1, FGA |
| GO:0048534 | hematopoietic or lymphoid organ development | 3.19E-02 | TGFB1, ITGB3, ITGB1, ITGA4, LRP5, JAG1, PDGFB, CCL21, MMP9 |
| GO:0045860 | positive regulation of protein kinase activity | 3.26E-02 | TGFB1, ITGB3, THBS1, CALR, LRP1, ELANE, PDGFB, CCL21 |
| GO:0031399 | regulation of protein modification process | 3.55E-02 | CD36, TGFB1, ITGB3, ITGB1, HRG, CALR, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0043549 | regulation of kinase activity | 3.55E-02 | KNG1, TGFB1, ITGB3, THBS1, CALR, LRP1, LRP5, ELANE, PDGFB, CCL21 |
| GO:0043491 | protein kinase B signaling cascade | 3.60E-02 | TGFB1, THBS1, IGFBP5, CCL21 |
| GO:0006979 | response to oxidative stress | 3.64E-02 | CD36, SERPINE1, COL1A1, SDC1, MMP9, MMP2 |
| GO:0071345 | cellular response to cytokine stimulus | 3.71E-02 | CCR6, SELP, SELPLG, KRT18, XCL1, MMP9 |
| GO:0022414 | reproductive process | 3.71E-02 | FBLN1, TGFB1, ITGB1, CD9, CALR, PLAT, PLAU, DDR1, ADAMTS1, SDC1, MMP9, MMP2, MMP3, CD44 |
| GO:0042246 | tissue regeneration | 3.71E-02 | SERPINE1, PLAU, PLG |
| GO:0010934 | macrophage cytokine production | 3.71E-02 | CD36, TGFB1 |
| GO:0072109 | glomerular mesangium development | 3.71E-02 | ITGB3, PDGFB |
| GO:0002577 | regulation of antigen processing and presentation | 3.71E-02 | THBS1, CCL21 |
| GO:0002719 | negative regulation of cytokine production involved in immune response | 3.71E-02 | TGFB1, XCL1 |
| GO:0000003 | reproduction | 3.87E-02 | FBLN1, TGFB1, ITGB1, CD9, CALR, PLAT, PLAU, DDR1, ADAMTS1, SDC1, MMP9, MMP2, MMP3, CD44 |
| GO:0050830 | defense response to Gram-positive bacterium | 3.91E-02 | CD36, PLA2G2A, CTSG |
| GO:0048259 | regulation of receptor-mediated endocytosis | 3.91E-02 | SERPINE1, CCL21, VTN |
| GO:0002367 | cytokine production involved in immune response | 4.15E-02 | CD36, TGFB1, XCL1 |
| GO:0045184 | establishment of protein localization | 4.16E-02 | CD36, SCARB2, TGFB1, ITGB1, CALR, LRP1, ITGA2, LRP2, COL1A1, LRP1B, KRT18, ACTN4, CXCL10, F2 |
| GO:0033674 | positive regulation of kinase activity | 4.21E-02 | TGFB1, ITGB3, THBS1, CALR, LRP1, ELANE, PDGFB, CCL21 |

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|---|---|---|---|
| GO:0051338 | regulation of transferase activity | 4.25E-02 | KNG1, TGFB1, ITGB3, THBS1, CALR, LRP1, LRP5, ELANE, PDGFB, CCL21 |
| GO:0060055 | angiogenesis involved in wound healing | 4.28E-02 | ITGB3, SERPINE1 |
| GO:0009629 | response to gravity | 4.28E-02 | SPARC, SERPINE1 |
| GO:0002839 | positive regulation of immune response to tumor cell | 4.28E-02 | HRG, XCL1 |
| GO:0060033 | anatomical structure regression | 4.28E-02 | LRP5, MMP9 |
| GO:0002701 | negative regulation of production of molecular mediator of immune response | 4.28E-02 | TGFB1, XCL1 |
| GO:0002836 | positive regulation of response to tumor cell | 4.28E-02 | HRG, XCL1 |
| GO:0071354 | cellular response to interleukin-6 | 4.28E-02 | SELP, SELPLG |
| GO:0071636 | positive regulation of transforming growth factor beta production | 4.28E-02 | THBS1, XCL1 |
| GO:0090192 | regulation of glomerulus development | 4.28E-02 | ITGB3, PDGFB |
| GO:0070208 | protein heterotrimerization | 4.28E-02 | COL1A2, COL1A1 |
| GO:0042130 | negative regulation of T cell proliferation | 4.28E-02 | KNG1, TGFB1, XCL1 |
| GO:0002520 | immune system development | 4.28E-02 | TGFB1, ITGB3, ITGB1, ITGA4, LRP5, JAG1, PDGFB, CCL21, MMP9 |
| GO:0046649 | lymphocyte activation | 4.59E-02 | KNG1, TGFB1, ITGB1, ITGA4, XCL1, CORO1A, CCL21, CD47 |
| GO:0007243 | intracellular protein kinase cascade | 4.63E-02 | KNG1, CD36, TGFB1, ITGB3, ITGB1, THBS1, PDGFB, IGFBP5, CCL21, F2, CD44 |
| GO:0006468 | protein phosphorylation | 4.63E-02 | CD36, TGFB1, ITGB3, ITGB1, HRG, THBS1, CALR, DDR1, PDGFB, CCL21, VTN, F2, CD44 |
| GO:0042157 | lipoprotein metabolic process | 4.63E-02 | ITGB3, LRP1, HSPG2, SDC1 |
| GO:0051347 | positive regulation of transferase activity | 4.67E-02 | TGFB1, ITGB3, THBS1, CALR, LRP1, ELANE, PDGFB, CCL21 |
| GO:0002683 | negative regulation of immune system process | 4.70E-02 | KNG1, TGFB1, THBS1, XCL1, COL3A1 |
| GO:0035272 | exocrine system development | 4.75E-02 | TGFB1, LAMA1, PDGFB |
| GO:0006816 | calcium ion transport | 4.75E-02 | TGFB1, PDGFB, XCL1, CORO1A, CCL21, F2 |
| GO:0002837 | regulation of immune response to tumor cell | 4.92E-02 | HRG, XCL1 |

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|---|---|---|---|
| GO:0061298 | retina vasculature development in camera-type eye | 4.92E-02 | LRP5, LAMA1 |
| GO:0051818 | disruption of cells of other organism involved in symbiotic interaction | 4.92E-02 | CTSG, ELANE |
| GO:0051883 | killing of cells in other organism involved in symbiotic interaction | 4.92E-02 | CTSG, ELANE |
| GO:0002834 | regulation of response to tumor cell | 4.92E-02 | HRG, XCL1 |
| GO:0043583 | ear development | 4.95E-02 | SPARC, TGFB1, DDR1, JAG1, COL2A1 |
| GO:0032835 | glomerulus development | 4.95E-02 | ITGB3, NID1, PDGFB |

# Supplementary Table 6

List of biological processes overrepresented by the 2nd cluster in the Protein-protein network

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|---|---|
| Seed proteins: | CCL2, IL8 |
| Direct interactants: | CCR1, CCL5, CCL8, ORM1, CCR5, CCR2, CCRL1, DARC, CCL4, CCBP2, CCR10, EGFR, TUBA4A, CXCR1, CXCR2, GNAI2, PF4, IL12A, WASF1 |

| ID | Name | P-value | Hit in Query List |
|---|---|---|---|
| GO:0070098 | chemokine-mediated signaling pathway | 9.86E-17 | DARC, CCRL1, CCR1, CCL5, CCBP2, CCR5, CCL2, CXCR1, CCR2 |
| GO:0006935 | chemotaxis | 6.18E-15 | PF4, CCRL1, CCR1, CCR10, CCL5, CCL8, EGFR, CCBP2, CCL4, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0042330 | taxis | 6.18E-15 | PF4, CCRL1, CCR1, CCR10, CCL5, CCL8, EGFR, CCBP2, CCL4, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0030595 | leukocyte chemotaxis | 1.21E-13 | PF4, CCR1, CCL5, CCL4, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0060326 | cell chemotaxis | 6.48E-13 | PF4, CCR1, CCL5, CCL4, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0036336 | dendritic cell migration | 4.28E-12 | CCR1, CCL5, CCR5, CXCR1, CXCR2, CCR2 |
| GO:0040011 | locomotion | 4.82E-12 | PF4, CCRL1, CCR1, CCR10, CCL5, CCL8, EGFR, CCBP2, CCL4, IL12A, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0002407 | dendritic cell chemotaxis | 8.56E-12 | CCR1, CCL5, CCR5, CXCR1, CXCR2, CCR2 |
| GO:0009605 | response to external stimulus | 1.60E-11 | PF4, CCRL1, GNAI2, CCR1, CCR10, CCL5, CCL8, EGFR, CCBP2, CCL4, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0009611 | response to wounding | 2.78E-11 | PF4, DARC, GNAI2, CCR1, CCL5, CCL8, TUBA4A, ORM1, CCL4, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0006954 | inflammatory response | 3.80E-11 | DARC, CCR1, CCL5, CCL8, ORM1, CCL4, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0019221 | cytokine-mediated signaling pathway | 4.66E-11 | PF4, DARC, CCRL1, CCR1, CCL5, CCBP2, CCR5, CCL2, CXCR1, CXCR2, CCR2 |
| GO:0050900 | leukocyte migration | 6.79E-11 | PF4, CCR1, CCL5, CCL4, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0071345 | cellular response to cytokine stimulus | 7.31E-11 | DARC, CCRL1, CCR1, CCL5, CCBP2, CCR5, CCL2, IL8, CXCR1, CXCR2 |

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|---|---|---|---|
| GO:0034097 | response to cytokine stimulus | 3.10E-09 | DARC, CCRL1, CCR1, CCL5, CCBP2, CCR5, CCL2, IL8, CXCR1, CXCR2 |
| GO:0007186 | G-protein coupled receptor signaling pathway | 4.35E-09 | DARC, CCRL1, GNAI2, CCR1, CCR10, CCL5, CCBP2, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0006928 | cellular component movement | 6.92E-09 | WASF1, PF4, CCR1, CCL5, EGFR, CCL4, IL12A, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0006952 | defense response | 6.92E-09 | DARC, CCR1, CCL5, CCL8, ORM1, CCL4, IL12A, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0002690 | positive regulation of leukocyte chemotaxis | 1.01E-08 | CCR1, CCL5, CCL4, CCL2, IL8, CCR2 |
| GO:0016477 | cell migration | 1.19E-08 | PF4, CCR1, CCL5, EGFR, CCL4, IL12A, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0002688 | regulation of leukocyte chemotaxis | 2.19E-08 | CCR1, CCL5, CCL4, CCL2, IL8, CCR2 |
| GO:0048870 | cell motility | 2.62E-08 | PF4, CCR1, CCL5, EGFR, CCL4, IL12A, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0051674 | localization of cell | 2.62E-08 | PF4, CCR1, CCL5, EGFR, CCL4, IL12A, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0002687 | positive regulation of leukocyte migration | 5.83E-08 | CCR1, CCL5, CCL4, CCL2, IL8, CCR2 |
| GO:0006955 | immune response | 7.47E-08 | PF4, CCRL1, CCR1, CCL5, CCL8, CCBP2, CCL4, IL12A, CCR5, CCL2, IL8, CCR2 |
| GO:0050921 | positive regulation of chemotaxis | 8.75E-08 | CCR1, CCL5, CCL4, CCL2, IL8, CCR2 |
| GO:0032103 | positive regulation of response to external stimulus | 1.39E-07 | CCR1, CCL5, CCL4, CCR5, CCL2, IL8, CCR2 |
| GO:0070887 | cellular response to chemical stimulus | 1.86E-07 | PF4, DARC, CCRL1, CCR1, CCL5, CCBP2, CCL4, CCR5, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0006874 | cellular calcium ion homeostasis | 2.02E-07 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0048520 | positive regulation of behavior | 2.20E-07 | CCR1, CCL5, CCL4, CCL2, IL8, CCR2 |
| GO:0002685 | regulation of leukocyte migration | 2.27E-07 | CCR1, CCL5, CCL4, CCL2, IL8, CCR2 |
| GO:0055074 | calcium ion homeostasis | 2.38E-07 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0072503 | cellular divalent inorganic cation homeostasis | 2.83E-07 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0072683 | T cell extravasation | 3.41E-07 | CCL5, CCL2, CCR2 |
| GO:0072507 | divalent inorganic cation homeostasis | 3.50E-07 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |

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|---|---|---|---|
| GO:0050920 | regulation of chemotaxis | 3.60E-07 | CCR1, CCL5, CCL4, CCL2, IL8, CCR2 |
| GO:0019932 | second-messenger-mediated signaling | 1.09E-06 | GNAI2, CCR1, EGFR, CCL4, CCR5, CCL2, IL8, CXCR2 |
| GO:0006875 | cellular metal ion homeostasis | 1.09E-06 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:2000401 | regulation of lymphocyte migration | 1.09E-06 | CCL5, CCL4, CCL2, CCR2 |
| GO:0030335 | positive regulation of cell migration | 1.30E-06 | CCR1, CCL5, EGFR, CCL4, CCL2, IL8, CCR2 |
| GO:2000147 | positive regulation of cell motility | 1.47E-06 | CCR1, CCL5, EGFR, CCL4, CCL2, IL8, CCR2 |
| GO:0001817 | regulation of cytokine production | 1.48E-06 | PF4, DARC, CCL5, CCL4, IL12A, CCR5, CCL2, CCR2 |
| GO:0055065 | metal ion homeostasis | 1.63E-06 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0051272 | positive regulation of cellular component movement | 1.70E-06 | CCR1, CCL5, EGFR, CCL4, CCL2, IL8, CCR2 |
| GO:0040017 | positive regulation of locomotion | 1.71E-06 | CCR1, CCL5, EGFR, CCL4, CCL2, IL8, CCR2 |
| GO:0001775 | cell activation | 1.81E-06 | PF4, GNAI2, CCL5, EGFR, TUBA4A, IL12A, CCL2, IL8, CXCR2, CCR2 |
| GO:0030334 | regulation of cell migration | 1.87E-06 | CCR1, CCL5, EGFR, CCL4, CCR5, CCL2, IL8, CCR2 |
| GO:0048247 | lymphocyte chemotaxis | 2.00E-06 | CCL5, CCL4, CCL2, CCR2 |
| GO:0030003 | cellular cation homeostasis | 2.00E-06 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0050795 | regulation of behavior | 2.23E-06 | CCR1, CCL5, CCL4, CCL2, IL8, CCR2 |
| GO:2000145 | regulation of cell motility | 2.56E-06 | CCR1, CCL5, EGFR, CCL4, CCR5, CCL2, IL8, CCR2 |
| GO:0001816 | cytokine production | 2.84E-06 | PF4, DARC, CCL5, CCL4, IL12A, CCR5, CCL2, CCR2 |
| GO:0002548 | monocyte chemotaxis | 3.62E-06 | CCR1, CCL5, CCL2, CCR2 |
| GO:0051270 | regulation of cellular component movement | 3.72E-06 | CCR1, CCL5, EGFR, CCL4, CCR5, CCL2, IL8, CCR2 |
| GO:0072676 | lymphocyte migration | 4.02E-06 | CCL5, CCL4, CCL2, CCR2 |
| GO:0040012 | regulation of locomotion | 4.02E-06 | CCR1, CCL5, EGFR, CCL4, CCR5, CCL2, IL8, CCR2 |
| GO:2000501 | regulation of natural killer cell chemotaxis | 4.06E-06 | CCL5, CCL4, CCL2 |
| GO:0055080 | cation homeostasis | 4.72E-06 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0016192 | vesicle-mediated transport | 9.68E-06 | PF4, CCR1, CCL5, CCL8, TUBA4A, CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0071310 | cellular response to organic substance | 1.02E-05 | DARC, CCRL1, CCR1, CCL5, CCBP2, CCR5, CCL2, IL8, CXCR1, CXCR2 |
| GO:0035747 | natural killer cell chemotaxis | 1.06E-05 | CCL5, CCL4, CCL2 |

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| GO:0051240 | positive regulation of multicellular organismal process | 1.20E-05 | PF4, CCL5, EGFR, CCL4, IL12A, CCR5, CCL2, CCR2 |
| GO:0001819 | positive regulation of cytokine production | 1.21E-05 | PF4, CCL5, CCL4, IL12A, CCR5, CCR2 |
| GO:0048584 | positive regulation of response to stimulus | 2.10E-05 | CCR1, CCL5, EGFR, CCL4, IL12A, CCR5, CCL2, IL8, CCR2 |
| GO:0090026 | positive regulation of monocyte chemotaxis | 2.13E-05 | CCR1, CCL5, CCR2 |
| GO:0032101 | regulation of response to external stimulus | 2.75E-05 | CCR1, CCL5, CCL4, CCR5, CCL2, IL8, CCR2 |
| GO:0002682 | regulation of immune system process | 2.75E-05 | PF4, CCR1, CCL5, ORM1, CCL4, IL12A, CCL2, IL8, CCR2 |
| GO:0032496 | response to lipopolysaccharide | 2.75E-05 | CCR1, CCL5, IL12A, CCR5, CCL2, IL8 |
| GO:0031620 | regulation of fever generation | 2.76E-05 | CCR1, CCL5, CCR5 |
| GO:0051707 | response to other organism | 2.86E-05 | CCR1, CCL5, CCL8, CCL4, IL12A, CCR5, CCL2, IL8 |
| GO:0019079 | viral genome replication | 3.49E-05 | CCL5, CCL4, CCL2, IL8 |
| GO:0002237 | response to molecule of bacterial origin | 3.97E-05 | CCR1, CCL5, IL12A, CCR5, CCL2, IL8 |
| GO:0006953 | acute-phase response | 4.29E-05 | CCR1, CCL5, ORM1, CCR5 |
| GO:0006873 | cellular ion homeostasis | 4.29E-05 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0031650 | regulation of heat generation | 4.33E-05 | CCR1, CCL5, CCR5 |
| GO:2000403 | positive regulation of lymphocyte migration | 4.33E-05 | CCL5, CCL4, CCR2 |
| GO:0090025 | regulation of monocyte chemotaxis | 5.37E-05 | CCR1, CCL5, CCR2 |
| GO:0001660 | fever generation | 5.37E-05 | CCR1, CCL5, CCR5 |
| GO:0006816 | calcium ion transport | 6.89E-05 | GNAI2, CCR1, CCL5, CCL8, CCL4, CCR5 |
| GO:0055082 | cellular chemical homeostasis | 6.94E-05 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0006887 | exocytosis | 7.13E-05 | PF4, CCR1, CCL5, CCL8, TUBA4A, CCR2 |
| GO:0050801 | ion homeostasis | 7.76E-05 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0009607 | response to biotic stimulus | 8.07E-05 | CCR1, CCL5, CCL8, CCL4, IL12A, CCR5, CCL2, IL8 |
| GO:0006968 | cellular defense response | 9.13E-05 | CCL5, CCR5, CXCR2, CCR2 |
| GO:0072678 | T cell migration | 9.19E-05 | CCL5, CCL2, CCR2 |
| GO:0042119 | neutrophil activation | 1.20E-04 | CCL5, IL8, CXCR2 |

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| GO:0031649 | heat generation | 1.20E-04 | CCR1, CCL5, CCR5 |
| GO:0000165 | MAPK cascade | 1.20E-04 | GNAI2, CCR1, CCL5, EGFR, CCR5, CCL2, CCR2 |
| GO:0035684 | helper T cell extravasation | 1.20E-04 | CCL5, CCL2 |
| GO:0038112 | interleukin-8-mediated signaling pathway | 1.20E-04 | CXCR1, CXCR2 |
| GO:0090265 | positive regulation of immune complex clearance by monocytes and macrophages | 1.20E-04 | CCL2, CCR2 |
| GO:0002434 | immune complex clearance | 1.20E-04 | CCL2, CCR2 |
| GO:0002436 | immune complex clearance by monocytes and macrophages | 1.20E-04 | CCL2, CCR2 |
| GO:0090264 | regulation of immune complex clearance by monocytes and macrophages | 1.20E-04 | CCL2, CCR2 |
| GO:0032640 | tumor necrosis factor production | 1.20E-04 | PF4, CCL4, CCR5, CCR2 |
| GO:0032680 | regulation of tumor necrosis factor production | 1.20E-04 | PF4, CCL4, CCR5, CCR2 |
| GO:0070838 | divalent metal ion transport | 1.22E-04 | GNAI2, CCR1, CCL5, CCL8, CCL4, CCR5 |
| GO:0072511 | divalent inorganic cation transport | 1.29E-04 | GNAI2, CCR1, CCL5, CCL8, CCL4, CCR5 |
| GO:0071706 | tumor necrosis factor superfamily cytokine production | 1.44E-04 | PF4, CCL4, CCR5, CCR2 |
| GO:0019725 | cellular homeostasis | 1.47E-04 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0051704 | multi-organism process | 1.51E-04 | CCR1, CCL5, CCL8, CCL4, IL12A, CCR5, CCL2, IL8, CCR2 |
| GO:0035821 | modification of morphology or physiology of other organism | 1.99E-04 | CCL5, CCL4, CCR5 |
| GO:0007204 | elevation of cytosolic calcium ion concentration | 2.20E-04 | CCR1, CCR10, CCR5, CXCR2, CCR2 |
| GO:0002684 | positive regulation of immune system process | 2.20E-04 | CCR1, CCL5, CCL4, IL12A, CCL2, IL8, CCR2 |
| GO:0045123 | cellular extravasation | 2.50E-04 | CCL5, CCL2, CCR2 |
| GO:0051480 | cytosolic calcium ion homeostasis | 2.99E-04 | CCR1, CCR10, CCR5, CXCR2, CCR2 |
| GO:0007243 | intracellular protein kinase cascade | 3.06E-04 | GNAI2, CCR1, CCL5, EGFR, IL12A, CCR5, CCL2, CCR2 |
| GO:0042127 | regulation of cell proliferation | 3.20E-04 | GNAI2, CCL5, EGFR, IL12A, CCR5, CCL2, IL8, CXCR2, CCR2 |

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| GO:0009617 | response to bacterium | 3.20E-04 | CCR1, CCL5, IL12A, CCR5, CCL2, IL8 |
| GO:0048878 | chemical homeostasis | 3.55E-04 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |
| GO:0071222 | cellular response to lipopolysaccharide | 3.67E-04 | CCL5, CCR5, CCL2, IL8 |
| GO:0019722 | calcium-mediated signaling | 3.78E-04 | EGFR, CCL4, CCR5, IL8 |
| GO:0019058 | viral infectious cycle | 4.34E-04 | CCL5, CCL4, CCR5, CCL2, IL8 |
| GO:0071219 | cellular response to molecule of bacterial origin | 4.50E-04 | CCL5, CCR5, CCL2, IL8 |
| GO:0007155 | cell adhesion | 5.73E-04 | CCR1, CCL5, EGFR, CCL4, IL12A, CCR5, CCL2, IL8 |
| GO:0022610 | biological adhesion | 5.81E-04 | CCR1, CCL5, EGFR, CCL4, IL12A, CCR5, CCL2, IL8 |
| GO:0008284 | positive regulation of cell proliferation | 5.81E-04 | GNAI2, CCL5, EGFR, IL12A, CCL2, CXCR2, CCR2 |
| GO:2000110 | negative regulation of macrophage apoptotic process | 5.81E-04 | CCL5, CCR5 |
| GO:0032760 | positive regulation of tumor necrosis factor production | 6.23E-04 | PF4, CCL4, CCR5 |
| GO:0007259 | JAK-STAT cascade | 6.78E-04 | CCL5, IL12A, CCL2, CCR2 |
| GO:0001659 | temperature homeostasis | 7.27E-04 | CCR1, CCL5, CCR5 |
| GO:0002526 | acute inflammatory response | 8.10E-04 | CCR1, CCL5, ORM1, CCR5 |
| GO:0022415 | viral reproductive process | 9.01E-04 | CCL5, CCL4, CCR5, CCL2, IL8 |
| GO:2000503 | positive regulation of natural killer cell chemotaxis | 9.21E-04 | CCL5, CCL4 |
| GO:0032940 | secretion by cell | 9.55E-04 | PF4, CCR1, CCL5, CCL8, TUBA4A, CCR5, CCR2 |
| GO:0002763 | positive regulation of myeloid leukocyte differentiation | 9.55E-04 | PF4, CCR1, CCL5 |
| GO:0002274 | myeloid leukocyte activation | 1.02E-03 | CCL5, IL8, CXCR2, CCR2 |
| GO:0071347 | cellular response to interleukin-1 | 1.09E-03 | CCL5, CCL2, IL8 |
| GO:0071216 | cellular response to biotic stimulus | 1.34E-03 | CCL5, CCR5, CCL2, IL8 |
| GO:0051050 | positive regulation of transport | 1.53E-03 | CCR1, CCL5, EGFR, CCL4, CCR5, CCL2 |
| GO:0010647 | positive regulation of cell communication | 1.64E-03 | CCR1, CCL5, EGFR, CCL4, IL12A, CCL2, CCR2 |
| GO:0007267 | cell-cell signaling | 1.70E-03 | GNAI2, CCR1, CCL5, CCL8, EGFR, CCL4, CCR5, CCL2 |
| GO:2000109 | regulation of macrophage apoptotic process | 1.79E-03 | CCL5, CCR5 |

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| GO:0043615 | astrocyte cell migration | 1.79E-03 | CCL2, CCR2 |
| GO:0051049 | regulation of transport | 2.01E-03 | GNAI2, CCR1, CCL5, EGFR, CCL4, CCR5, CCL2, CCR2 |
| GO:0030593 | neutrophil chemotaxis | 2.16E-03 | CCL2, IL8, CXCR2 |
| GO:0045765 | regulation of angiogenesis | 2.26E-03 | PF4, CCL5, CCL2, CCR2 |
| GO:0007610 | behavior | 2.27E-03 | CCR1, CCL5, CCL4, CCL2, IL8, CCR2 |
| GO:0051817 | modification of morphology or physiology of other organism involved in symbiotic interaction | 2.35E-03 | CCL5, CCL4, CCR5 |
| GO:0051924 | regulation of calcium ion transport | 2.37E-03 | GNAI2, CCR1, CCL5, CCL4 |
| GO:0046903 | secretion | 2.48E-03 | PF4, CCR1, CCL5, CCL8, TUBA4A, CCR5, CCR2 |
| GO:0031623 | receptor internalization | 2.55E-03 | IL8, CXCR1, CXCR2 |
| GO:0016525 | negative regulation of angiogenesis | 2.66E-03 | PF4, CCL2, CCR2 |
| GO:0045321 | leukocyte activation | 2.72E-03 | CCL5, IL12A, CCL2, IL8, CXCR2, CCR2 |
| GO:0050870 | positive regulation of T cell activation | 2.74E-03 | CCL5, IL12A, CCL2, CCR2 |
| GO:0010819 | regulation of T cell chemotaxis | 2.74E-03 | CCL5, CCR2 |
| GO:0071888 | macrophage apoptotic process | 2.74E-03 | CCL5, CCR5 |
| GO:0010820 | positive regulation of T cell chemotaxis | 2.74E-03 | CCL5, CCR2 |
| GO:2000406 | positive regulation of T cell migration | 2.74E-03 | CCL5, CCR2 |
| GO:0071350 | cellular response to interleukin-15 | 2.74E-03 | CXCR1, CXCR2 |
| GO:0071356 | cellular response to tumor necrosis factor | 2.92E-03 | CCL5, CCL2, IL8 |
| GO:0002673 | regulation of acute inflammatory response | 3.04E-03 | CCR1, CCL5, CCR5 |
| GO:0045639 | positive regulation of myeloid cell differentiation | 3.17E-03 | PF4, CCR1, CCL5 |
| GO:0001525 | angiogenesis | 3.22E-03 | PF4, CCL5, CCL2, IL8, CCR2 |
| GO:0010759 | positive regulation of macrophage chemotaxis | 3.29E-03 | CCL5, CCL2 |
| GO:0031622 | positive regulation of fever generation | 3.29E-03 | CCL5, CCR5 |
| GO:0042592 | homeostatic process | 3.32E-03 | CCR1, CCR10, CCL5, CCL8, CCR5, CCL2, CXCR2, CCR2 |

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| GO:0010740 | positive regulation of intracellular protein kinase cascade | 3.78E-03 | CCR1, CCL5, EGFR, IL12A, CCR2 |
| GO:2000404 | regulation of T cell migration | 3.94E-03 | CCL5, CCR2 |
| GO:0042102 | positive regulation of T cell proliferation | 3.95E-03 | CCL5, IL12A, CCR2 |
| GO:0051928 | positive regulation of calcium ion transport | 4.23E-03 | CCR1, CCL5, CCL4 |
| GO:0070555 | response to interleukin-1 | 4.23E-03 | CCL5, CCL2, IL8 |
| GO:0033993 | response to lipid | 4.38E-03 | CCL5, EGFR, CCR5 |
| GO:0043922 | negative regulation by host of viral transcription | 4.47E-03 | CCL5, CCL4 |
| GO:0010758 | regulation of macrophage chemotaxis | 4.47E-03 | CCL5, CCL2 |
| GO:0070672 | response to interleukin-15 | 4.47E-03 | CXCR1, CXCR2 |
| GO:0031652 | positive regulation of heat generation | 4.47E-03 | CCL5, CCR5 |
| GO:0006925 | inflammatory cell apoptotic process | 4.47E-03 | CCL5, CCR5 |
| GO:0050727 | regulation of inflammatory response | 4.69E-03 | CCR1, CCL5, CCR5, CCR2 |
| GO:0031347 | regulation of defense response | 4.69E-03 | CCR1, CCL5, IL12A, CCR5, CCR2 |
| GO:0071622 | regulation of granulocyte chemotaxis | 5.12E-03 | CCL5, CCL2 |
| GO:0071675 | regulation of mononuclear cell migration | 5.12E-03 | CCL5, CCL2 |
| GO:0010818 | T cell chemotaxis | 5.12E-03 | CCL5, CCR2 |
| GO:0010959 | regulation of metal ion transport | 5.52E-03 | GNAI2, CCR1, CCL5, CCL4 |
| GO:0050729 | positive regulation of inflammatory response | 5.52E-03 | CCL5, CCR5, CCR2 |
| GO:0006897 | endocytosis | 5.52E-03 | CCL2, IL8, CXCR1, CXCR2, CCR2 |
| GO:0032897 | negative regulation of viral transcription | 5.83E-03 | CCL5, CCL4 |
| GO:0051251 | positive regulation of lymphocyte activation | 5.83E-03 | CCL5, IL12A, CCL2, CCR2 |

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| GO:0042327 | positive regulation of phosphorylation | 5.85E-03 | CCL5, EGFR, IL12A, CCL2, IL8 |
| GO:0030001 | metal ion transport | 6.00E-03 | GNAI2, CCR1, CCL5, CCL8, CCL4, CCR5 |
| GO:0080134 | regulation of response to stress | 6.11E-03 | CCR1, CCL5, EGFR, IL12A, CCR5, CCR2 |
| GO:0009628 | response to abiotic stimulus | 6.11E-03 | CCL5, EGFR, IL12A, CCR5, CCL2, CCR2 |
| GO:0002761 | regulation of myeloid leukocyte differentiation | 6.11E-03 | PF4, CCR1, CCL5 |
| GO:0010562 | positive regulation of phosphorus metabolic process | 6.16E-03 | CCL5, EGFR, IL12A, CCL2, IL8 |
| GO:0045937 | positive regulation of phosphate metabolic process | 6.16E-03 | CCL5, EGFR, IL12A, CCL2, IL8 |
| GO:0002697 | regulation of immune effector process | 6.33E-03 | CCL5, IL12A, CCL2, CCR2 |
| GO:0071674 | mononuclear cell migration | 6.33E-03 | CCL5, CCL2 |
| GO:0071621 | granulocyte chemotaxis | 6.33E-03 | CCL5, CCL2 |
| GO:0034612 | response to tumor necrosis factor | 6.33E-03 | CCL5, CCL2, IL8 |
| GO:0031349 | positive regulation of defense response | 6.55E-03 | CCL5, IL12A, CCR5, CCR2 |
| GO:0048514 | blood vessel morphogenesis | 6.58E-03 | PF4, CCL5, CCL2, IL8, CCR2 |
| GO:0050863 | regulation of T cell activation | 6.58E-03 | CCL5, IL12A, CCL2, CCR2 |
| GO:0048585 | negative regulation of response to stimulus | 6.67E-03 | CCR1, CCL5, CCL2, IL8, CCR2 |
| GO:0016032 | viral reproduction | 6.91E-03 | CCL5, CCL4, CCR5, CCL2, IL8 |
| GO:0048660 | regulation of smooth muscle cell proliferation | 7.43E-03 | CCL5, EGFR, IL12A |
| GO:0002696 | positive regulation of leukocyte activation | 7.43E-03 | CCL5, IL12A, CCL2, CCR2 |
| GO:0045860 | positive regulation of protein kinase activity | 7.47E-03 | GNAI2, CCL5, EGFR, CCL2, IL8 |
| GO:0009967 | positive regulation of signal transduction | 7.47E-03 | CCR1, CCL5, EGFR, CCL4, IL12A, CCR2 |
| GO:0008347 | glial cell migration | 7.75E-03 | CCL2, CCR2 |
| GO:0050792 | regulation of viral reproduction | 7.75E-03 | CCL5, CCL4, IL8 |
| GO:0048659 | smooth muscle cell proliferation | 7.95E-03 | CCL5, EGFR, IL12A |

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| GO:0045087 | innate immune response | 8.14E-03 | CCR1, CCL5, IL12A, CCL2, CCR2 |
| GO:0050867 | positive regulation of cell activation | 8.18E-03 | CCL5, IL12A, CCL2, CCR2 |
| GO:0009615 | response to virus | 8.18E-03 | CCL5, CCL8, CCL4, IL12A |
| GO:0023056 | positive regulation of signaling | 8.64E-03 | CCR1, CCL5, EGFR, CCL4, IL12A, CCR2 |
| GO:0071774 | response to fibroblast growth factor stimulus | 8.70E-03 | CCL5, CCL2, IL8 |
| GO:0044344 | cellular response to fibroblast growth factor stimulus | 8.70E-03 | CCL5, CCL2, IL8 |
| GO:0033674 | positive regulation of kinase activity | 8.77E-03 | GNAI2, CCL5, EGFR, CCL2, IL8 |
| GO:0043270 | positive regulation of ion transport | 8.87E-03 | CCR1, CCL5, CCL4 |
| GO:0043491 | protein kinase B signaling cascade | 9.09E-03 | CCL5, EGFR, CCL2 |
| GO:0070723 | response to cholesterol | 9.09E-03 | CCL5, CCR5 |
| GO:0043921 | modulation by host of viral transcription | 9.09E-03 | CCL5, CCL4 |
| GO:0052472 | modulation by host of symbiont transcription | 9.09E-03 | CCL5, CCL4 |
| GO:0050671 | positive regulation of lymphocyte proliferation | 9.18E-03 | CCL5, IL12A, CCR2 |
| GO:0051347 | positive regulation of transferase activity | 9.35E-03 | GNAI2, CCL5, EGFR, CCL2, IL8 |
| GO:0032946 | positive regulation of mononuclear cell proliferation | 9.35E-03 | CCL5, IL12A, CCR2 |
| GO:0045672 | positive regulation of osteoclast differentiation | 9.90E-03 | CCR1, CCL5 |
| GO:0006468 | protein phosphorylation | 1.02E-02 | GNAI2, CCL5, CCL8, EGFR, IL12A, CCL2, IL8 |
| GO:0070665 | positive regulation of leukocyte proliferation | 1.03E-02 | CCL5, IL12A, CCR2 |
| GO:0001568 | blood vessel development | 1.04E-02 | PF4, CCL5, CCL2, IL8, CCR2 |
| GO:0043277 | apoptotic cell clearance | 1.07E-02 | CCL2, CCR2 |
| GO:0030155 | regulation of cell adhesion | 1.16E-02 | CCL5, IL12A, CCR5, IL8 |
| GO:0045597 | positive regulation of cell differentiation | 1.16E-02 | PF4, CCR1, CCL5, CCR5, CCR2 |

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| GO:0052312 | modulation of transcription in other organism involved in symbiotic interaction | 1.16E-02 | CCL5, CCL4 |
| GO:0048246 | macrophage chemotaxis | 1.16E-02 | CCL5, CCL2 |
| GO:0006812 | cation transport | 1.22E-02 | GNAI2, CCR1, CCL5, CCL8, CCL4, CCR5 |
| GO:0042129 | regulation of T cell proliferation | 1.22E-02 | CCL5, IL12A, CCR2 |
| GO:0001944 | vasculature development | 1.24E-02 | PF4, CCL5, CCL2, IL8, CCR2 |
| GO:0010573 | vascular endothelial growth factor production | 1.24E-02 | CCL2, CCR2 |
| GO:0010574 | regulation of vascular endothelial growth factor production | 1.24E-02 | CCL2, CCR2 |
| GO:0002699 | positive regulation of immune effector process | 1.30E-02 | IL12A, CCL2, CCR2 |
| GO:0030097 | hemopoiesis | 1.34E-02 | PF4, CCR1, CCL5, IL8, CCR2 |
| GO:0051093 | negative regulation of developmental process | 1.36E-02 | PF4, CCR1, CCR5, CCL2, CCR2 |
| GO:0022603 | regulation of anatomical structure morphogenesis | 1.36E-02 | PF4, CCL5, CCR5, CCL2, CCR2 |
| GO:0043112 | receptor metabolic process | 1.46E-02 | IL8, CXCR1, CXCR2 |
| GO:0010518 | positive regulation of phospholipase activity | 1.46E-02 | CCL5, EGFR, CXCR2 |
| GO:0051249 | regulation of lymphocyte activation | 1.51E-02 | CCL5, IL12A, CCL2, CCR2 |
| GO:0033002 | muscle cell proliferation | 1.52E-02 | CCL5, EGFR, IL12A |
| GO:0010627 | regulation of intracellular protein kinase cascade | 1.65E-02 | CCR1, CCL5, EGFR, IL12A, CCR2 |
| GO:0010517 | regulation of phospholipase activity | 1.69E-02 | CCL5, EGFR, CXCR2 |
| GO:0048534 | hematopoietic or lymphoid organ development | 1.71E-02 | PF4, CCR1, CCL5, IL8, CCR2 |
| GO:0060193 | positive regulation of lipase activity | 1.71E-02 | CCL5, EGFR, CXCR2 |
| GO:0045637 | regulation of myeloid cell differentiation | 1.86E-02 | PF4, CCR1, CCL5 |
| GO:0009314 | response to radiation | 1.87E-02 | EGFR, IL12A, CCR5, CCL2 |
| GO:0045785 | positive regulation of cell adhesion | 1.92E-02 | CCL5, IL12A, CCR5 |
| GO:0051851 | modification by host of symbiont morphology or physiology | 1.99E-02 | CCL5, CCL4 |

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| GO:0042325 | regulation of phosphorylation | 2.02E-02 | GNAI2, CCL5, EGFR, IL12A, CCL2, IL8 |
| GO:0044403 | symbiosis, encompassing mutualism through parasitism | 2.02E-02 | CCL5, CCL4, CCR5 |
| GO:0051345 | positive regulation of hydrolase activity | 2.03E-02 | CCL5, EGFR, CCL2, IL8, CXCR2 |
| GO:0002520 | immune system development | 2.08E-02 | PF4, CCR1, CCL5, IL8, CCR2 |
| GO:0002675 | positive regulation of acute inflammatory response | 2.08E-02 | CCL5, CCR5 |
| GO:2000107 | negative regulation of leukocyte apoptotic process | 2.20E-02 | CCL5, CCR5 |
| GO:0071346 | cellular response to interferon-gamma | 2.20E-02 | CCL5, CCL2 |
| GO:0002573 | myeloid leukocyte differentiation | 2.22E-02 | PF4, CCR1, CCL5 |
| GO:0042098 | T cell proliferation | 2.26E-02 | CCL5, IL12A, CCR2 |
| GO:0002694 | regulation of leukocyte activation | 2.29E-02 | CCL5, IL12A, CCL2, CCR2 |
| GO:0032729 | positive regulation of interferon-gamma production | 2.30E-02 | IL12A, CCR2 |
| GO:0001932 | regulation of protein phosphorylation | 2.35E-02 | CCL5, EGFR, IL12A, CCL2, IL8 |
| GO:0045069 | regulation of viral genome replication | 2.42E-02 | CCL5, IL8 |
| GO:0042110 | T cell activation | 2.42E-02 | CCL5, IL12A, CCL2, CCR2 |
| GO:0002521 | leukocyte differentiation | 2.59E-02 | PF4, CCR1, CCL5, CCR2 |
| GO:0007187 | G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger | 2.64E-02 | GNAI2, CCR1, CCL2 |
| GO:0050730 | regulation of peptidyl-tyrosine phosphorylation | 2.64E-02 | CCL5, EGFR, IL12A |
| GO:0022409 | positive regulation of cell-cell adhesion | 2.67E-02 | CCL5, CCR5 |
| GO:0060191 | regulation of lipase activity | 2.67E-02 | CCL5, EGFR, CXCR2 |
| GO:2000241 | regulation of reproductive process | 2.71E-02 | CCL5, CCL4, IL8 |
| GO:0050670 | regulation of lymphocyte proliferation | 2.74E-02 | CCL5, IL12A, CCR2 |

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| GO:0032944 | regulation of mononuclear cell proliferation | 2.77E-02 | CCL5, IL12A, CCR2 |
| GO:0050865 | regulation of cell activation | 2.77E-02 | CCL5, IL12A, CCL2, CCR2 |
| GO:0043066 | negative regulation of apoptotic process | 2.86E-02 | PF4, CCL5, EGFR, CCR5, CCL2 |
| GO:0019220 | regulation of phosphate metabolic process | 2.88E-02 | GNAI2, CCL5, EGFR, IL12A, CCL2, IL8 |
| GO:0051174 | regulation of phosphorus metabolic process | 2.88E-02 | GNAI2, CCL5, EGFR, IL12A, CCL2, IL8 |
| GO:0043069 | negative regulation of programmed cell death | 2.96E-02 | PF4, CCL5, EGFR, CCR5, CCL2 |
| GO:0070663 | regulation of leukocyte proliferation | 2.99E-02 | CCL5, IL12A, CCR2 |
| GO:0031663 | lipopolysaccharide-mediated signaling pathway | 2.99E-02 | CCL5, CCL2 |
| GO:0031343 | positive regulation of cell killing | 2.99E-02 | IL12A, CCR5 |
| GO:0051702 | interaction with symbiont | 2.99E-02 | CCL5, CCL4 |
| GO:0045859 | regulation of protein kinase activity | 3.10E-02 | GNAI2, CCL5, EGFR, CCL2, IL8 |
| GO:0048871 | multicellular organismal homeostasis | 3.12E-02 | CCR1, CCL5, CCR5 |
| GO:0019935 | cyclic-nucleotide-mediated signaling | 3.16E-02 | GNAI2, CCR1, CCL2 |
| GO:0050918 | positive chemotaxis | 3.25E-02 | CCL5, IL8 |
| GO:0051247 | positive regulation of protein metabolic process | 3.30E-02 | CCL5, IL12A, CCL2, IL8, CCR2 |
| GO:0060548 | negative regulation of cell death | 3.36E-02 | PF4, CCL5, EGFR, CCR5, CCL2 |
| GO:0043269 | regulation of ion transport | 3.36E-02 | GNAI2, CCR1, CCL5, CCL4 |
| GO:0014823 | response to activity | 3.36E-02 | CCL5, CCL2 |
| GO:0023014 | signal transduction by phosphorylation | 3.36E-02 | GNAI2, EGFR, IL12A, CCL2, CCR2 |
| GO:0006811 | ion transport | 3.36E-02 | GNAI2, CCR1, CCL5, CCL8, CCL4, CCR5 |
| GO:0042063 | gliogenesis | 3.36E-02 | EGFR, CCL2, CCR2 |
| GO:0043549 | regulation of kinase activity | 3.36E-02 | GNAI2, CCL5, EGFR, CCL2, IL8 |
| GO:0006898 | receptor-mediated endocytosis | 3.36E-02 | IL8, CXCR1, CXCR2 |

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|---|---|---|---|
| GO:0060139 | positive regulation of apoptotic process by virus | 3.36E-02 | CCR5 |
| GO:0043310 | negative regulation of eosinophil degranulation | 3.36E-02 | CCR2 |
| GO:0052433 | modulation by organism of apoptotic process in other organism involved in symbiotic interaction | 3.36E-02 | CCR5 |
| GO:0035685 | helper T cell diapedesis | 3.36E-02 | CCL5 |
| GO:2000409 | positive regulation of T cell extravasation | 3.36E-02 | CCR2 |
| GO:2000439 | positive regulation of monocyte extravasation | 3.36E-02 | CCR2 |
| GO:0071448 | cellular response to alkyl hydroperoxide | 3.36E-02 | CCL5 |
| GO:0035687 | T-helper 1 cell extravasation | 3.36E-02 | CCL5 |
| GO:0052501 | positive regulation by organism of apoptotic process in other organism involved in symbiotic interaction | 3.36E-02 | CCR5 |
| GO:0033552 | response to vitamin B3 | 3.36E-02 | CCL2 |
| GO:0035688 | T-helper 1 cell diapedesis | 3.36E-02 | CCL5 |
| GO:0052150 | modulation by symbiont of host apoptotic process | 3.36E-02 | CCR5 |
| GO:0052248 | modulation of programmed cell death in other organism involved in symbiotic interaction | 3.36E-02 | CCR5 |
| GO:0052330 | positive regulation by organism of programmed cell death in other organism involved in symbiotic interaction | 3.36E-02 | CCR5 |
| GO:0044533 | positive regulation of apoptotic process in other organism | 3.36E-02 | CCR5 |
| GO:2000449 | regulation of CD8-positive, alpha-beta T cell extravasation | 3.36E-02 | CCR2 |

| | | | |
|---|---|---|---|
| GO:0052042 | positive regulation by symbiont of host programmed cell death | 3.36E-02 | CCR5 |
| GO:0035702 | monocyte homeostasis | 3.36E-02 | CCL2 |
| GO:2000407 | regulation of T cell extravasation | 3.36E-02 | CCR2 |
| GO:2000451 | positive regulation of CD8-positive, alpha-beta T cell extravasation | 3.36E-02 | CCR2 |
| GO:0035697 | CD8-positive, alpha-beta T cell extravasation | 3.36E-02 | CCR2 |
| GO:0033195 | response to alkyl hydroperoxide | 3.36E-02 | CCL5 |
| GO:0052151 | positive regulation by symbiont of host apoptotic process | 3.36E-02 | CCR5 |
| GO:0071403 | cellular response to high density lipoprotein particle stimulus | 3.36E-02 | CCL5 |
| GO:0035704 | helper T cell chemotaxis | 3.36E-02 | CCR2 |
| GO:0044531 | modulation of programmed cell death in other organism | 3.36E-02 | CCR5 |
| GO:0044532 | modulation of apoptotic process in other organism | 3.36E-02 | CCR5 |
| GO:2000502 | negative regulation of natural killer cell chemotaxis | 3.36E-02 | CCL2 |
| GO:0052040 | modulation by symbiont of host programmed cell death | 3.36E-02 | CCR5 |
| GO:0035705 | T-helper 17 cell chemotaxis | 3.36E-02 | CCR2 |
| GO:0051094 | positive regulation of developmental process | 3.37E-02 | PF4, CCR1, CCL5, CCR5, CCR2 |
| GO:0001934 | positive regulation of protein phosphorylation | 3.37E-02 | CCL5, IL12A, CCL2, IL8 |
| GO:0044419 | interspecies interaction between organisms | 3.37E-02 | CCL5, CCL4, CCR5, CCR2 |
| GO:0042531 | positive regulation of tyrosine phosphorylation of STAT protein | 3.40E-02 | CCL5, IL12A |
| GO:0045088 | regulation of innate immune response | 3.56E-02 | CCR1, CCL5, IL12A |
| GO:0002683 | negative regulation of immune system process | 3.66E-02 | CCR1, CCL2, CCR2 |

| | | | |
|---|---|---|---|
| GO:0002437 | inflammatory response to antigenic stimulus | 3.67E-02 | CCR5, CCR2 |
| GO:0051338 | regulation of transferase activity | 3.69E-02 | GNAI2, CCL5, EGFR, CCL2, IL8 |
| GO:0045670 | regulation of osteoclast differentiation | 3.79E-02 | CCR1, CCL5 |
| GO:0031341 | regulation of cell killing | 3.79E-02 | IL12A, CCR5 |
| GO:0043085 | positive regulation of catalytic activity | 3.83E-02 | GNAI2, CCL5, EGFR, CCL2, IL8, CXCR2 |
| GO:0002252 | immune effector process | 4.02E-02 | CCL5, IL12A, CCL2, CCR2 |
| GO:0046635 | positive regulation of alpha-beta T cell activation | 4.08E-02 | IL12A, CCR2 |
| GO:2000106 | regulation of leukocyte apoptotic process | 4.22E-02 | CCL5, CCR5 |
| GO:0032642 | regulation of chemokine production | 4.22E-02 | DARC, CCL5 |
| GO:2000026 | regulation of multicellular organismal development | 4.38E-02 | PF4, CCR1, CCL5, CCR5, CCL2, CCR2 |
| GO:0032602 | chemokine production | 4.52E-02 | DARC, CCL5 |
| GO:0072359 | circulatory system development | 4.53E-02 | PF4, CCL5, CCL2, IL8, CCR2 |
| GO:0072358 | cardiovascular system development | 4.53E-02 | PF4, CCL5, CCL2, IL8, CCR2 |
| GO:0046651 | lymphocyte proliferation | 4.53E-02 | CCL5, IL12A, CCR2 |
| GO:0018108 | peptidyl-tyrosine phosphorylation | 4.58E-02 | CCL5, EGFR, IL12A |
| GO:0071407 | cellular response to organic cyclic compound | 4.60E-02 | CCL5, CCL2 |
| GO:0032943 | mononuclear cell proliferation | 4.60E-02 | CCL5, IL12A, CCR2 |
| GO:0032147 | activation of protein kinase activity | 4.60E-02 | GNAI2, CCL5, EGFR |
| GO:0018212 | peptidyl-tyrosine modification | 4.65E-02 | CCL5, EGFR, IL12A |
| GO:0034341 | response to interferon-gamma | 4.73E-02 | CCL5, CCL2 |
| GO:0042509 | regulation of tyrosine phosphorylation of STAT protein | 4.73E-02 | CCL5, IL12A |
| GO:0071363 | cellular response to growth factor stimulus | 4.74E-02 | CCL5, CCL2, IL8 |
| GO:0046427 | positive regulation of JAK-STAT cascade | 4.86E-02 | CCL5, IL12A |

| | | | |
|---|---|---|---|
| GO:0048661 | positive regulation of smooth muscle cell proliferation | 4.86E-02 | CCL5, EGFR |

## Supplementary Table 1

Clinical and laboratory data for all subjects with biliary atresia, intrahepatic cholestasis, and normal controls.

| Group | Gender | Diagnosis | Age at biopsy | C. Bilirubin | ALT | GGT |
|---|---|---|---|---|---|---|
| BA | M | Embryonic | 66 d | 3.3 | 80 | 802 |
| BA | F | Acquired | 55 d | 4.3 | 157 | 554 |
| BA | F | Acquired | 40 d | 3.4 | 95 | 267 |
| BA | F | Acquired | 79 d | 2.8 | 79 | 1322 |
| BA | F | Acquired | 68 d | 4.2 | 75 | NA |
| BA | F | Embryonic | 41 d | 3 | 19 | 95 |
| BA | M | Acquired | 46 d | 8.7 | 262 | 441 |
| BA | F | Acquired | 55 d | 3.9 | 29 | 464 |
| BA | M | Acquired | 76 d | 7.8 | 160 | 754 |
| BA | M | Acquired | 63 d | 7.1 | 324 | 478 |
| BA | M | Acquired | 73 d | 6.1 | 249 | 1211 |
| BA | F | Acquired | 68 d | 9 | 253 | 784 |
| BA | F | Acquired | 54 d | 4.7 | 124 | 672 |
| BA | M | Embryonic | 50 d | NA | 131 | 645 |
| BA | F | Acquired | 73 d | 6.8 | 164 | 738 |
| BA | M | Acquired | 33 d | 4.5 | 51 | 251 |
| BA | M | Acquired | 48 d | 4.6 | 88 | 286 |
| BA | F | Embryonic | 27 d | 7.8 | 382 | 211 |
| BA | M | Acquired | 22 d | 10.2 | 67 | 505 |

| | | | | | | |
|---|---|---|---|---|---|---|
| BA | F | Acquired | 66 d | 5.4 | 93 | NA |
| BA | M | Acquired | 52 d | 4.5 | 98 | 887 |
| BA | F | Acquired | 44 d | 4.5 | 112 | 1378 |
| BA | M | Acquired | 73 d | NA | 94 | 745 |
| BA | M | Acquired | 71 d | 5.2 | 211 | 640 |
| BA | M | Embryonic | 33 d | 4.9 | 77 | 358 |
| BA | F | Acquired | 113 d | 6.4 | 200 | 6 |
| BA | M | Acquired | 41 d | 5.2 | 194 | 429 |
| BA | F | Acquired | 43 d | 3.2 | 79 | 781 |
| BA | M | Acquired | 65 d | 3.5 | 95 | 1002 |
| BA | M | Acquired | 64 d | 7.5 | 198 | 204 |
| BA | F | Acquired | 169 d | 13 | 178 | 695 |
| BA | M | Acquired | 91 d | 4.5 | 208 | 794 |
| BA | M | Acquired | 68 d | 7.4 | 420 | 604 |
| BA | M | Acquired | 63 d | 5.4 | 171 | 574 |
| BA | F | Acquired | 97d | 3.9 | 114 | 456 |
| BA | M | Acquired | 50 d | 4.1 | 89 | 478 |
| BA | M | Acquired | 106 d | 5.4 | 182 | 973 |
| BA | F | Acquired | 44 d | 3.6 | 39 | 772 |
| BA | F | Acquired | 52 d | 7.6 | 156 | 455 |
| BA | F | Embryonic | 80 d | 4.8 | 200 | 563 |
| BA | F | Acquired | 32 d | 4 | 185 | 664 |
| BA | F | Acquired | 84 d | 3.8 | 43 | 644 |

| | | | | | | |
|---|---|---|---|---|---|---|
| BA | M | Embryonic | 51 d | 4.8 | 717 | 656 |
| BA | M | Acquired | 47 d | 6.6 | 157 | 1019 |
| BA | F | Acquired | 73 d | 5.2 | 275 | 445 |
| BA | M | Acquired | 75 d | 6 | 151 | 1795 |
| BA | F | Acquired | 168 d | 10.7 | 343 | 973 |
| BA | F | Embryonic | 50 d | 2.5 | 131 | 1075 |
| BA | F | Acquired | 76 d | 7.4 | 172 | 645 |
| BA | F | Embryonic | 83 d | 5.6 | 213 | 1896 |
| BA | F | Acquired | 54 d | 4 | 93 | 434 |
| BA | F | Acquired | 39 d | 4.4 | 73 | 745 |
| BA | F | Acquired | 77 d | 3.3 | 159 | 993 |
| BA | F | Acquired | 75 d | 4.7 | 409 | 507 |
| BA | M | Embryonic | 58 d | 5.2 | 118 | 551 |
| BA | M | Acquired | 97 d | 7 | 134 | 873 |
| BA | M | Acquired | 80 d | 5.9 | 230 | 772 |
| BA | M | Acquired | 69 d | 6.5 | 135 | 2189 |
| BA | M | Acquired | 95 d | 3.5 | 99 | 2691 |
| BA | F | Acquired | 65 d | 3.1 | 247 | 410 |
| BA | F | Embryonic | 70 d | 5.7 | 290 | 1949 |
| Non-BA-1 | M | Idiopathic | 95 d | 5.7 | 153 | 694 |
| Non-BA-2 | M | Idiopathic | 43 d | 3.6 | 49 | 106 |
| Non-BA-3 | M | Idiopathic | 26 d | 2.7 | 71 | 94 |
| Non-BA-4 | M | Idiopathic | 54 d | 4.6 | 29 | 55 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Non-BA-5 | F | Idiopathic | 19 d | 7.9 | 280 | 185 |
| Non-BA-6 | M | Idiopathic | 41 d | NA | NA | NA |
| Non-BA-7 | F | Idiopathic | 75 d | 7.3 | 117 | 128 |
| Non-BA-8 | F | Idiopathic | 70 d | 4.2 | 257 | 470 |
| Non-BA-9 | M | Idiopathic | 157 d | 2.1 | 159 | 462 |
| Non-BA-10 | M | A1AT | 76 d | 2.1 | 68 | 1234 |
| Non-BA-11 | M | AGS | 548 d | 3.6 | 464 | 293 |
| Non-BA-12 | M | A1AT | 49 d | 5.2 | 84 | 363 |
| Non-BA-13 | M | PFIC3 | 76 d | 3.3 | 127 | 311 |
| Non-BA-14 | M | PFIC3 | 122 d | NA | NA | NA |
| NC | M | NA | 22 m | NA | NA | NA |
| NC | M | NA | 36 m | NA | NA | NA |
| NC | F | NA | 42 m | NA | NA | NA |
| NC | F | NA | 31 m | NA | NA | NA |
| NC | M | NA | 36 m | NA | NA | NA |
| NC | M | NA | 24 m | NA | NA | NA |
| NC | M | NA | 36 m | NA | NA | NA |
| NC* | M | Muscular dystrophy | 75 d | NA | NA | NA |

- BA: biliary atresia
- Non-BA: diseased controls with intrahepatic cholestasis (either idiopathic or secondary to specific syndromes as listed)

- NC: Normal controls (deceased donors)
- NC**: infant undergoing a liver biopsy as part of evaluation of hypotonia. The biopsy had normal histology and normal electron microscopy
- Others: C. bilirubin: conjugated bilirubin; ALT: Alanine aminotransferase; GGT: Gamma-glutamyl transpeptidase; NA: Not Available; M: Male; F: Female; IHC: Intrahepatic cholestasis; A1AT: a1-antitrypsin deficiency; AGS: Alagille syndrome; PFIC3: Progressive familial intrahepatic cholestasis type 3

## Supplementary Table 8

**List of real-time PCR primer pairs used in the study.**

Human Genes

| Gene | Forward Primer | Reverse Primer |
|---|---|---|
| *THBS1* | 5’-GCCAATGCGACTTACCACTG-3’ | 5’-TTGTCATCGTCATCATCACAGG-3’ |
| *SERPINE1* | 5’-AGGAAGAAATGTCAGATGCGTG-3’ | 5’-CTAACAAGCACTCAAGGGCAAG-3’ |
| *CCL2* | 5’-CGAGAGGCTGAGACTAACCCAG-3’ | 5’-ATGAAGGTGGCTGCTATGAGC-3’ |
| *ITGA2* | 5’-CAGGAGTTCAAGTCCAGCCTAAG-3’ | 5’-TGTTGGGATTACAGGTGTGAGC-3’ |
| *IL8* | 5’-CTGGACCCCAAGGAAAACTG-3’ | 5’-TTCACTGGCATCTTCACTGATTC-3’ |
| *GAPDH* | 5’-AAATCCCATCACCATCTTCCAG-3’ | 5’-AAATGAGCCCCAGCCTTCTC-3’ |

Mouse Genes

| Gene | Forward Primer | Reverse Primer |
|---|---|---|
| *Cxcr1* | 5’-TCGCTGGTGATGCTGGTTATC-3’ | 5’-GGGCAGGGTCAATGAAAAGAG-3’ |
| *Cxcr2* | 5’-TTGTGGGGAACTCCTTGGTG-3’ | 5’-TCAGGGCAAAGAACAGGTCAG-3’ |
| *Cxcl1* | 5’-CAAACCGAAGTCATAGCCACAC-3’ | 5’-TTGGGGACACCTTTTAGCATC-3’ |
| *Cxcl2* | 5’-TGAACAAAGGCAAGGCTAACTG-3’ | 5’-AAGTGAACTCTCAGACAGCGAGG-3’ |
| *Cxcl5* | 5’-TGGGCAGTGACAAAAAGAAAGC-3’ | 5’-AAATCCGTGGGTGGAGAGAATC-3’ |
| *Ccl2* | 5’- GTCTGTGCTGACCCCAAGAA -3’ | 5’- GTGCTGAAGACCTTAGGGCA -3’ |
| *Serpine1* | 5’- CGCCTCTTCCACAAGTCTGA -3’ | 5’- TAGGGCAGTTCCACAACGTC -3’ |
| *Thbs1* | 5’- CCATGGCCAACAAACAGGTG -3’ | 5’- TTGCACTCACAGCGGTACAT -3’ |
| *Itga2* | 5’- AGCAGCTTACGAACCCACAA -3’ | 5’- GCTTTTCACAGGTGGCAGTG -3’ |
| *Il6* | 5’-TGGCTAAGGACCAAGACCATC-3’ | 5’-TTCTGACCACAGTGAGGAATGTC-3’ |
| *Il10* | 5’-CCCTTTGCTATGGTGTCCTTTC-3’ | 5’-TCCCTGGTTTCTCTTCCCAAG-3’ |
| *Ifng* | 5’-GGCTGTCCCTGAAAGAAAGC-3’ | 5’-GAGCGAGTTATTTGTCATTCGG-3’ |
| *Tnf* | 5’-GGACTCAAATGGGCTTTCCG-3’ | 5’-GAGACAGAGGCAACCTGACCAC-3’ |
| *Hprt* | 5’-TGCCGAGGATTTGGAAAAAG-3’ | 5’-CCCCCCTTGAGCACACAG-3’ |