**Supplementary Table 2.** List of hepatic genes which were downregulated in cows in IMBALANCED (n = 16) versus BALANCED (n = 44) metabolic clusters

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **EntrezGene** | **GeneSymbol** | **Gene Name** | **P-value** | **Fold-Change** |
| 508829 | *ABCG8* | ATP binding cassette subfamily G member  | 0.020 | -1.44 |
| 101902412 | *ANGPTL8* | angiopoietin like 8 | 0.011 | -1.44 |
| 338074 | *AOX1* | aldehyde oxidase 1 | 0.003 | -1.25 |
| 540473 | *ASCL1* | achaete-scute family bHLH transcription factor 1 | 0.013 | -1.47 |
| 783451 | *BEX4* | brain expressed, X-linked 4 | 0.015 | -1.22 |
| 510833 | *COL3A1* | collagen type III alpha 1 chain | 0.035 | -1.21 |
| 107131603 | *CTXND1* | cortexin domain containing 1Bottom of Form | 0.013 | -1.30 |
| 504559 | *DIRAS3* | DIRAS family GTPase 3 | 0.016 | -1.34 |
| 541175 | *DUSP10* | dual specificity phosphatase 10 | 0.001 | -1.23 |
| 407125 | *EGR1* | early growth response 1 | 0.044 | -1.24 |
| 539905 | *FLRT2* | fibronectin leucine rich transmembrane protein 2 | 0.017 | -1.24 |
| 281239 | *IGF1* | insulin like growth factor 1 | 0.000 | -1.62 |
| 532494 | *IGFALS* | insulin like growth factor binding protein acid labile subunit | 0.022 | -1.46 |
| 101905957 | *INAFM2* | InaF motif containing 2 | 0.002 | -1.20 |
| 101906792 | *KCNJ4* | potassium inwardly rectifying channel subfamily J member 4 | 0.035 | -1.30 |
| 536781 | *LDB3* | LIM domain binding 3 | 0.047 | -1.40 |
| 100337044 | *LOC100337044* | adhesion G protein-coupled receptor E3 | 0.039 | -1.30 |
| 788599 | *LOC788599* | zinc finger protein 160 | 0.047 | -1.31 |
| 534297 | *METRNL* | meteorin like, glial cell differentiation regulator | 0.012 | -1.21 |
| 539466 | *PPP1R3C* | protein phosphatase 1 regulatory subunit 3C | 0.043 | -1.52 |
| 518283 | *PTAFR* | platelet activating factor receptor | 0.029 | -1.24 |
| 524166 | *RNF144B* | ring finger protein 144B | 0.041 | -1.22 |
| 281486 | *SELP* | selectin P | 0.002 | -1.27 |
| 785942 | *SEMA4D* | semaphorin 4D | 0.014 | -1.26 |
| 513746 | *SERPINA6* | serpin family A member 6 | 0.000 | -2.00 |
| 515914 | *SESN3* | sestrin 3 | 0.014 | -1.23 |
| 280934 | *SULT1E1* | sulfotransferase family 1E member 1 | 0.038 | -1.33 |
| 506012 | *TEX12* | testis expressed 12 | 0.011 | -1.23 |
| 768081 | *TNFSF18* | tumor necrosis factor superfamily member 18 | 0.017 | -1.21 |
| 282118 | *VCAM1* | vascular cell adhesion molecule 1 | 0.030 | -1.25 |
| 509992 | *ZNF608* | zinc finger protein 608 | 0.000 | -1.23 |

**Supplementary Table 3.** List of hepatic genes which were upregulated in cows in IMBALANCED (n = 16) versus BALANCED (n = 44) metabolic clusters

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| EntrezGene | GeneSymbol | Gene Name | P-value | Fold-Change |
| 510774 | *ABHD1* | abhydrolase domain containing 1 | 3.9E-06 | 1.59 |
| 282130 | *ACADVL* | acyl-CoA dehydrogenase, very long chain | 3.9E-07 | 1.26 |
| 514969 | *ACOX2* | acyl-CoA oxidase 2 | 6.6E-04 | 1.23 |
| 521844 | *ADCY10* | adenylate cyclase 10, soluble | 5.1E-05 | 1.21 |
| 407234 | *ADIPOR2* | adiponectin receptor 2 | 2.7E-02 | 1.25 |
| 504346 | *ALG9* | ALG9, alpha-1,2-mannosyltransferase | 1.4E-04 | 1.21 |
| 505315 | *AMDHD1* | amidohydrolase domain containing 1 | 2.9E-03 | 1.29 |
| 509963 | *ANGPTL4* | angiopoietin like 4 | 1.7E-05 | 2.05 |
| 511800 | *ANKH* | ANKH inorganic pyrophosphate transport regulator | 1.2E-03 | 1.24 |
| 535740 | *APMAP* | adipocyte plasma membrane associated protein | 6.6E-03 | 1.20 |
| 281631 | *APOA1* | apolipoprotein A1 | 7.7E-04 | 1.53 |
| 537301 | *APOA4* | apolipoprotein A4 | 2.8E-03 | 1.84 |
| 618039 | *APOC2* | apolipoprotein C2 | 3.0E-02 | 1.21 |
| 513608 | *ARG1* | arginase 1 | 4.4E-03 | 1.26 |
| 505486 | *ASPG* | asparaginase | 1.5E-04 | 1.38 |
| 497207 | *BREH1* | retinyl ester hydrolase type 1 | 2.6E-03 | 1.42 |
| 518086 | *CANT1* | calcium activated nucleotidase 1 | 7.1E-03 | 1.21 |
| 527966 | *CAPN11* | calpain 11 | 1.0E-03 | 1.32 |
| 281052 | *CD36* | CD36 molecule (thrombospondin receptor) | 1.3E-03 | 1.26 |
| 618745 | *CDC42EP5* | CDC42 effector protein 5 | 2.5E-02 | 1.26 |
| 507526 | *CDH17* | cadherin 17 | 6.7E-04 | 1.34 |
| 338319 | *CEBPB* | CCAAT/enhancer binding protein (C/EBP), beta | 2.0E-02 | 1.27 |
| 507586 | *CGREF1* | cell growth regulator with EF-hand domain 1 | 5.3E-07 | 1.45 |
| 515280 | *CHP2* | calcineurin like EF-hand protein 2 | 4.6E-02 | 1.41 |
| 534607 | *CIDEC* | cell death inducing DFFA like effector c | 4.9E-03 | 1.27 |
| 789150 | *COLGALT2* | collagen beta(1-O)galactosyltransferase 2 | 1.0E-03 | 1.22 |
| 509459 | *CPT1B* | carnitine palmitoyltransferase 1B | 1.9E-06 | 1.78 |
| 513010 | *CREB3L3* | cAMP responsive element binding protein 3 like 3 | 1.8E-05 | 1.48 |
| 281092 | *CROT* | carnitine O-octanoyltransferase(CROT) | 1.6E-04 | 1.24 |
| 338048 | *CYP11A1* | cytochrome P450, family 11, subfamily A, polypeptide 1 | 1.3E-02 | 1.54 |
| 511890 | *CYP4A11* | cytochrome P450, family 4, subfamily A, polypeptide 11 | 1.5E-03 | 1.31 |
| 508962 | *DDX25* | DEAD-box helicase 25 | 1.1E-03 | 1.22 |
| 504453 | *DMGDH* | dimethylglycine dehydrogenase | 1.2E-03 | 1.23 |
| 539175 | *DUSP1* | dual specificity phosphatase 1 | 8.8E-03 | 1.35 |
| 615432 | *DUSP3* | dual specificity phosphatase 3 | 1.3E-03 | 1.21 |
| 615756 | *ELOVL2* | ELOVL fatty acid elongase 2 | 3.9E-02 | 1.26 |
| 100295476 | *EREG* | epiregulin | 1.9E-03 | 1.30 |
| 346653 | *FAM71F2* | family with sequence similarity 71 member F2 | 1.0E-04 | 1.35 |
| 531211 | *FBXL14* | F-box and leucine rich repeat protein 14 | 2.5E-04 | 1.28 |
| 505923 | *FICD* | FIC domain containing | 4.5E-02 | 1.26 |
| 781806 | *FNDC4* | fibronectin type III domain containing 4 | 1.1E-02 | 1.23 |
| 507436 | *G0S2* | G0/G1 switch 2 | 2.4E-02 | 1.52 |
| 505463 | *GADD45A* | growth arrest and DNA damage inducible alpha | 1.2E-02 | 1.25 |
| 540009 | *GFRA3* | GDNF family receptor alpha 3 | 1.2E-02 | 1.29 |
| 505987 | *GK* | glycerol kinase | 3.7E-03 | 1.64 |
| 537451 | *GYS2* | glycogen synthase 2 | 3.8E-05 | 1.30 |
| 615205 | *HAL* | histidine ammonia-lyase | 1.3E-03 | 1.40 |
| 515950 | *HDC* | histidine decarboxylase | 8.2E-05 | 1.30 |
| 100125928 | *HILPDA* | hypoxia inducible lipid droplet associated | 3.5E-05 | 1.51 |
| 404168 | *HNF4G* | hepatocyte nuclear factor 4 gamma | 4.5E-04 | 1.20 |
| 618192 | *HSD17B13* | hydroxysteroid 17-beta dehydrogenase 13 | 2.0E-02 | 1.23 |
| 404131 | *HSDL2* | hydroxysteroid dehydrogenase like 2 | 4.4E-03 | 1.22 |
| 281235 | *IDH1* | isocitrate dehydrogenase (NADP(+)) 1, cytosolic | 9.8E-04 | 1.20 |
| 282260 | *IGFBP2* | insulin like growth factor binding protein 2 | 3.0E-03 | 1.22 |
| 527922 | *INMT* | indolethylamine N-methyltransferase | 3.0E-02 | 1.63 |
| 100300012 | *IRS2* | insulin receptor substrate 2 | 3.0E-02 | 1.20 |
| 506902 | *ISM1* | isthmin 1 | 1.3E-03 | 1.28 |
| 538461 | *KBTBD6* | kelch repeat and BTB (POZ) domain containing 6 | 7.6E-04 | 1.28 |
| 509687 | *KDELR3* | KDEL endoplasmic reticulum protein retention receptor 3 | 2.6E-03 | 1.25 |
| 616730 | *KLF11* | Kruppel like factor 11 | 1.9E-03 | 1.24 |
| 529905 | *KLHL25* | kelch like family member 25 | 6.5E-04 | 1.27 |
| 281274 | *LDHA* | lactate dehydrogenase A | 3.8E-02 | 1.51 |
| 281275 | *LDHB* | lactate dehydrogenase B | 5.3E-04 | 1.30 |
| 509808 | *LIPG* | Top of Formlipase G, endothelial typeBottom of Form | 6.3E-05 | 1.41 |
| 104974214 | *LOC104974214* | Top of Formapolipoprotein A-I-likeBottom of Form | 3.4E-03 | 1.54 |
| 515551 | *LOC515551* | protein DDI1 homolog 2 | 1.3E-03 | 1.22 |
| 614522 | *LOC614522* | Top of Formtransmembrane protein 56Bottom of Form | 6.4E-04 | 1.21 |
| 780933 | *LOC780933* | Top of Formcationic trypsinBottom of Form | 3.0E-02 | 1.22 |
| 784417 | *LOC784417* | Top of Formcytochrome P450 4A25-likeBottom of Form | 9.3E-04 | 1.31 |
| 537224 | *LPIN1* | lipin 1 | 4.8E-03 | 1.36 |
| 512633 | *MFSD2A* | major facilitator superfamily domain containing 2A | 3.5E-03 | 1.77 |
| 505290 | *MGLL* | monoglyceride lipase | 1.0E-03 | 1.25 |
| 525647 | *MKNK1* | MAP kinase interacting serine/threonine kinase 1 | 6.8E-04 | 1.21 |
| 614275 | *MOB3C* | MOB kinase activator 3C | 1.1E-05 | 1.43 |
| 767977 | *MPC1* | mitochondrial pyruvate carrier 1 | 6.6E-03 | 1.24 |
| 511077 | *MYC* | v-myc avian myelocytomatosis viral oncogene homolog | 2.8E-02 | 1.23 |
| 538404 | *MYOM1* | myomesin 1, 185kDa | 4.4E-03 | 1.54 |
| 613474 | *NABP1* | nucleic acid binding protein 1 | 4.0E-03 | 1.25 |
| 526544 | *NCS1* | neuronal calcium sensor 1 | 5.4E-05 | 1.52 |
| 789324 | *NME4* | nuclear transcription factor Y subunit beta | 2.3E-02 | 1.29 |
| 540641 | *NOCT* | nocturnin | 1.8E-04 | 1.60 |
| 100847590 | *NUDT15* | nudix hydrolase 15 | 8.3E-03 | 1.21 |
| 338036 | *P2RX4* | purinergic receptor P2X 4 | 1.7E-05 | 1.32 |
| 522374 | *PAQR9* | progestin and adipoQ receptor family member 9 | 5.6E-05 | 1.22 |
| 338471 | *PC* | pyruvate carboxylase | 4.7E-02 | 1.57 |
| 507367 | *PDK4* | pyruvate dehydrogenase kinase 4 | 1.8E-04 | 1.63 |
| 615089 | *PGPEP1* | pyroglutamyl-peptidase I | 4.6E-02 | 1.20 |
| 616641 | *PIP4P2* | phosphatidylinositol-4,5-bisphosphate 4-phosphatase 2 | 2.2E-04 | 1.20 |
| 280981 | *PLIN2* | perilipin 2 | 1.9E-03 | 1.37 |
| 107131384 | *PLIN4* | perilipin 4 | 1.2E-02 | 1.21 |
| 616337 | *PLPP5* | phospholipid phosphatase 5 | 5.5E-03 | 1.60 |
| 338446 | *PPARGC1A* | PPARG coactivator 1 alpha | 1.0E-03 | 1.26 |
| 525355 | *PPTC7* | PTC7 protein phosphatase homolog | 9.1E-04 | 1.21 |
| 539569 | *PRRG3* | proline rich and Gla domain 3 | 3.0E-02 | 1.21 |
| 615760 | *RAB20* | RAB20, member RAS oncogene family | 2.9E-03 | 1.30 |
| 506971 | *RASGEF1B* | RasGEF domain family member 1B | 1.2E-02 | 1.21 |
| 768075 | *RCL1* | RNA terminal phosphate cyclase like 1 | 1.6E-04 | 1.23 |
| 282035 | *RGS16* | regulator of G-protein signaling 16 | 5.0E-03 | 1.35 |
| 509500 | *RXRG* | retinoid X receptor gamma | 5.2E-05 | 1.71 |
| 507197 | *SHMT2* | serine hydroxymethyltransferase 2 | 2.3E-03 | 1.33 |
| 541119 | *SLC1A2* | solute carrier family 1 member 2 | 2.7E-03 | 1.48 |
| 541266 | *SLC22A5* | solute carrier family 22 member 5 | 1.8E-04 | 1.22 |
| 527786 | *SLC25A25* | solute carrier family 25 member 25 | 1.1E-02 | 1.25 |
| 507021 | *SLC25A30* | solute carrier family 25 member 30 | 1.2E-04 | 1.60 |
| 533794 | *SLC25A33* | solute carrier family 25 member 33 | 2.0E-03 | 1.31 |
| 515553 | *SLC25A34* | solute carrier family 25 member 34 | 1.3E-04 | 1.47 |
| 516483 | *SLC25A47* | solute carrier family 25 member 47 | 7.1E-04 | 1.43 |
| 616071 | *SLC6A11* | solute carrier family 6 member 11 | 4.1E-03 | 1.24 |
| 511211 | *SPOCK1* | SPARC/osteonectin, cwcv and kazal like domains proteoglycan 1 | 1.6E-02 | 1.26 |
| 523898 | *SULT1C2* | sulfotransferase family, cytosolic, 1C, member 2 | 2.7E-03 | 1.22 |
| 511957 | *TDH* | L-threonine dehydrogenase | 2.3E-02 | 1.27 |
| 514767 | *TGM5* | transglutaminase 5 | 7.8E-03 | 1.28 |
| 785640 | *TMC7* | transmembrane channel like 7 | 7.4E-03 | 1.20 |
| 520173 | *TMEM120A* | transmembrane protein 120A | 7.7E-04 | 1.47 |
| 513699 | *TMEM205* | transmembrane protein 205 | 1.3E-02 | 1.27 |
| 505368 | *TMEM41A* | transmembrane protein 41A | 7.3E-04 | 1.25 |
| 508176 | *TMEM82* | transmembrane protein 82 | 9.3E-04 | 1.20 |
| 616801 | *TRAF3IP2* | tumor protein p53 binding protein 2 | 1.5E-04 | 1.22 |
| 100336818 | *TRHDE* | thyrotropin releasing hormone degrading enzyme | 2.5E-03 | 1.25 |
| 281565 | *UGP2* | UDP-glucose pyrophosphorylase 2 | 3.6E-04 | 1.29 |
| 530709 | *USH1C* | USH1 protein network component harmonin | 2.1E-02 | 1.34 |

**Supplementary Table 4.** List of genes which were downregulated in circulating leukocytes of cows in IMBALANCED (n=19) versus BALANCED (n = 43) metabolic clusters

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **EntrezGene** | **Gene Symbol**  | **Gene Name** | **P-value**  | **Fold-Change**  |
| 510745 | *ABCG1* | ATP binding cassette subfamily G member 1 | 0.023 | -1.20 |
| 107131195 | *ACOD1* | Top of Formaconitate decarboxylase 1Bottom of Form | 0.037 | -1.23 |
| 414925 | *BIRC5* | baculoviral IAP repeat containing 5 | 0.044 | -1.20 |
| 537027 | *BUB1B* | BUB1 mitotic checkpoint serine/threonine kinase B | 0.024 | -1.20 |
| 506102 | *C1QTNF12* | Top of FormC1q and TNF related 12Bottom of Form | 0.021 | -1.21 |
| 529404 | *CCDC50* | coiled-coil domain containing 50 | 0.009 | -1.20 |
| 327679 | *CCNB1* | cyclin B1 | 0.038 | -1.22 |
| 538436 | *CCNE2* | cyclin E2 | 0.022 | -1.20 |
| 515376 | *CDC20* | cell division cycle 20 | 0.049 | -1.20 |
| 615282 | *CDKN3* | cyclin dependent kinase inhibitor 3 | 0.026 | -1.23 |
| 513594 | *CEP55* | centrosomal protein 55 | 0.008 | -1.26 |
| 505233 | *CERS4* | ceramide synthase 4 | 0.002 | -1.26 |
| 407126 | *CR2* | complement C3d receptor 2 | 0.005 | -1.24 |
| 538485 | *CXXC5* | CXXC finger protein 5 | 0.002 | -1.27 |
| 538667 | *DIRAS2* | DIRAS family GTPase 2 | 0.037 | -1.23 |
| 509161 | *DLGAP5* | DLG associated protein 5 | 0.014 | -1.25 |
| 509796 | *DPYSL3* | dihydropyrimidinase like 3 | 0.022 | -1.27 |
| 613523 | *EAF2* | ELL associated factor 2 | 0.008 | -1.25 |
| 524246 | *EPHX4* | epoxide hydrolase 4 | 0.005 | -1.20 |
| 505709 | *ERBB2* | erb-b2 receptor tyrosine kinase 2 | 0.016 | -1.25 |
| 787581 | *H2B* | histone H2B | 0.031 | -1.24 |
| 618164 | *HIST1H1A* | histone cluster 1, H1a | 0.042 | -1.26 |
| 527304 | *HIST1H1B* | Top of FormH1.5 linker histone, cluster memberBottom of Form | 0.048 | -1.23 |
| 509275 | *HIST1H1D* | histone cluster 1, H1d | 0.019 | -1.21 |
| 616790 | *HIST1H2AG* | histone cluster 1, H2ag | 0.031 | -1.26 |
| 616634 | *HIST1H2AH* | histone cluster 1, H2ah | 0.040 | -1.26 |
| 525512 | *HIST1H2BB* | histone cluster 1, H2bb | 0.039 | -1.24 |
| 616776 | *HIST1H2BI* | histone cluster 1, H2bi | 0.034 | -1.26 |
| 522960 | *HIST1H2BJ* | histone cluster 1, H2bj | 0.036 | -1.26 |
| 517139 | *HIST1H3I* | histone cluster 1, H3i | 0.050 | -1.22 |
| 616570 | *HVCN1* | hydrogen voltage gated channel 1 | 0.003 | -1.22 |
| 539650 | *IGF2BP3* | insulin like growth factor 2 mRNA binding protein 3 | 0.005 | -1.25 |
| 514056 | *ITGAD* | integrin, alpha D | 0.019 | -1.23 |
| 280821 | *JCHAIN* | joining chain of multimeric IgA and IgM | 0.027 | -1.40 |
| 508467 | *KIF11* | kinesin family member 11 | 0.030 | -1.22 |
| 614876 | *LMO2* | LIM domain only 2 | 0.012 | -1.22 |
| 100139916 | *LOC100139916* | interleukin 32-like | 0.020 | -1.44 |
| 100295645 | *LOC100295645* | Top of FormT cell receptor alpha variable 14/delta variable 4Bottom of Form | 0.023 | -1.22 |
| 104968446 | *LOC104968446* | histone H2A type 1 | 0.034 | -1.24 |
| 112447353 | *LOC112447353* | putative adhesion G protein-coupled receptor E4P | 0.037 | -1.20 |
| 516742 | *LOC516742* | uncharacterized LOC516742 | 0.019 | -1.25 |
| 618239 | *MND1* | meiotic nuclear divisions 1 | 0.016 | -1.20 |
| 617904 | *MTBP* | MDM2 binding protein | 0.043 | -1.20 |
| 515421 | *MYL6B* | myosin light chain 6B | 0.024 | -1.22 |
| 531234 | *NCAPG* | non-SMC condensin I complex subunit G | 0.020 | -1.23 |
| 100125763 | *NREP* | neuronal regeneration related protein | 0.010 | -1.22 |
| 519504 | *NUF2* | NUF2, NDC80 kinetochore complex component | 0.021 | -1.23 |
| 540737 | *PCLAF* | PCNA clamp associated factor | 0.028 | -1.27 |
| 615798 | *PKIB* | protein kinase (cAMP-dependent, catalytic) inhibitor beta | 0.026 | -1.21 |
| 518653 | *POLE2* | DNA polymerase epsilon 2, accessory subunit | 0.010 | -1.20 |
| 514046 | *RPL17* | ribosomal protein L17 | 0.008 | -1.24 |
| 615847 | *SKA2* | spindle and kinetochore associated complex subunit 2 | 0.009 | -1.20 |
| 539791 | *TLR10* | toll like receptor 10 | 0.001 | -1.25 |
| 504244 | *TUBA1C* | tubulin, alpha 1c | 0.026 | -1.66 |
| 506962 | *UBE2C* | ubiquitin conjugating enzyme E2 C | 0.050 | -1.22 |
| 511381 | *UNG* | uracil DNA glycosylase | 0.002 | -1.31 |
| 280964 | *ZP3* | zona pellucida glycoprotein 3 | 0.003 | -1.21 |
| 514564 | *ZWINT* | ZW10 interacting kinetochore protein | 0.016 | -1.28 |

**Supplementary Table 5.** List of genes which were upregulated in circulating leukocytes of cows in IMBALANCED (n=19) versus BALANCED (n = 43) metabolic clusters

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **EntrezGene** | **Gene Symbol**  | **Gene Name** | **P-value**  | **Fold-Change**  |
| 539315 | *ACVR1B* | activin A receptor type 1B | 0.025 | 1.20 |
| 100137953 | *ATP8B4* | ATPase phospholipid transporting 8B4 (putative) | 0.015 | 1.34 |
| 782633 | *BAG3* | BCL2 associated athanogene 3 | 0.001 | 1.20 |
| 531942 | *BCL3* | B-cell CLL/lymphoma 3 | 0.028 | 1.20 |
| 280720 | *BRB* | brain ribonuclease | 0.002 | 1.64 |
| 280741 | *CA4* | carbonic anhydrase 4 | 0.025 | 1.24 |
| 281052 | *CD36* | CD36 molecule (thrombospondin receptor) | 0.000 | 1.36 |
| 513497 | *CDKN1A* | cyclin dependent kinase inhibitor 1A | 0.021 | 1.25 |
| 338319 | *CEBPB* | CCAAT/enhancer binding protein (C/EBP), beta | 0.010 | 1.24 |
| 784092 | *CLEC1B* | C-type lectin domain family 1 member B | 0.015 | 1.39 |
| 506812 | *CPT1A* | carnitine palmitoyltransferase 1A | 0.001 | 1.29 |
| 404107 | *DEFB13* | beta-defensin 13 | 0.017 | 1.66 |
| 518523 | *DGKG* | diacylglycerol kinase gamma | 0.004 | 1.22 |
| 538426 | *DNAJB1* | DnaJ heat shock protein family (Hsp40) member B1 | 0.002 | 1.23 |
| 508157 | *DYSF* | dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) | 0.029 | 1.33 |
| 524222 | *ECM1* | extracellular matrix protein 1 | 0.025 | 1.25 |
| 338062 | *FCGRT* | Fc fragment of IgG receptor and transporter | 0.002 | 1.22 |
| 540142 | *FOXS1* | forkhead box S1 | 0.046 | 1.28 |
| 414732 | *GATM* | glycine amidinotransferase | 0.016 | 1.26 |
| 280692 | *HP* | haptoglobin | 0.030 | 1.43 |
| 282254 | *HSPA1A* | heat shock 70kDa protein 1A | 0.002 | 1.42 |
| 539835 | *HSPA6* | heat shock protein family A (Hsp70) member 6 | 0.003 | 1.50 |
| 516099 | *HSPB1* | heat shock protein family B (small) member 1 | 0.002 | 1.20 |
| 507165 | *HSPH1* | heat shock protein family H (Hsp110) member 1 | 0.006 | 1.25 |
| 281857 | *IL12B* | interleukin 12B | 0.004 | 1.29 |
| 539334 | *IL1RAP* | interleukin 1 receptor accessory protein | 0.041 | 1.24 |
| 100125591 | *IRF7* | interferon regulatory factor 7 | 0.030 | 1.28 |
| 522795 | *KLF10* | Kruppel like factor 10 | 0.000 | 1.25 |
| 616730 | *KLF11* | Kruppel like factor 11 | 0.001 | 1.36 |
| 281886 | *KLRA1* | killer cell lectin-like receptor subfamily A, member 1 | 0.021 | 1.24 |
| 100848419 | *LOC100848419* | uncharacterised LOC100848419 | 0.010 | 1.22 |
| 100852090 | *LOC100852090* | leukocyte immunoglobulin-like receptor subfamily A member 6 | 0.035 | 1.27 |
| 101904517 | *LOC101904517* | multidrug resistance-associated protein 4-like | 0.022 | 1.48 |
| 112445498 | *LOC112445498* | leukocyte immunoglobulin-like receptor subfamily B member 3 | 0.031 | 1.27 |
| 505972 | *LOC505972* | elastin | 0.032 | 1.39 |
| 514978 | *LOC514978* | lipopolysaccharide-binding protein | 0.015 | 1.32 |
| 618409 | *LOC618409* | interferon regulatory factor 4 | 0.045 | 1.31 |
| 515016 | *MTUS1* | microtubule associated tumor suppressor 1 | 0.009 | 1.38 |
| 507597 | *NPL* | N-acetylneuraminate pyruvate lyase | 0.025 | 1.32 |
| 519922 | *OAS1Z* | 2',5'-oligoadenylate synthetase 1, 40/46kDa | 0.040 | 1.45 |
| 768073 | *OSGIN1* | oxidative stress induced growth inhibitor 1 | 0.002 | 1.21 |
| 514898 | *P2RX1* | purinergic receptor P2X 1 | 0.030 | 1.21 |
| 518368 | *PARM1* | prostate androgen-regulated mucin-like protein 1 | 0.040 | 1.27 |
| 507367 | *PDK4* | pyruvate dehydrogenase kinase 4 | 0.000 | 1.68 |
| 407183 | *PFKFB3* | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 | 0.039 | 1.20 |
| 524639 | *PHOSPHO1* | phosphoethanolamine/phosphocholine phosphatase | 0.012 | 1.31 |
| 541148 | *PTX3* | pentraxin 3 | 0.040 | 1.58 |
| 615760 | *RAB20* | RAB20, member RAS oncogene family | 0.029 | 1.30 |
| 540836 | *RGS1* | regulator of G-protein signaling 1 | 0.036 | 1.21 |
| 281453 | *RGS9* | regulator of G-protein signaling 9 | 0.005 | 1.25 |
| 282341 | *RNASE6* | ribonuclease A family member k6 | 0.016 | 1.21 |
| 785942 | *SEMA4D* | semaphorin 4D | 0.001 | 1.21 |
| 282470 | *SLC11A1* | solute carrier family 11 member 1 | 0.008 | 1.23 |
| 518795 | *SOCS1* | suppressor of cytokine signaling 1 | 0.006 | 1.20 |
| 100139208 | *SP140L* | SP140 nuclear body protein-like | 0.014 | 1.20 |
| 281536 | *TLR4* | toll like receptor 4 | 0.015 | 1.21 |
| 784639 | *TMEM159* | transmembrane protein 159 | 0.011 | 1.24 |
| 527597 | *TRPM6* | transient receptor potential cation channel subfamily M member 6 | 0.024 | 1.21 |
| 532668 | *ZNF821* | zinc finger protein 821 | 0.002 | 1.42 |