*Supplementary Table S1* Complete list of differentially expressed unique genes in GH treated cows compared with control animals, identified by microarray analysis.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  |  | Fold  |
| Gene symbol | Gene name | Accession number | No. ESTs | Change1 |
| *COL3A1* | Collagen, type III, alpha 1 |  NM\_000090 | 12 | 1.84 |
| *ABCG2* | ATP-binding cassette, sub-family G (WHITE), member 2 |  NM\_004827 | 3 | 1.66 |
| *COL1A1* | Collagen, type I, alpha 1 |  NM\_000088 | 3 | 1.64 |
| *LTF* | Lactotransferrin |  NM\_002343 | 2 | 1.61 |
| *ACTA2* | Actin, alpha 2, smooth muscle, aorta |  NM\_001613 | 2 | 1.57 |
| *ASB11* | Ankyrin repeat and SOCS box-containing 11 |  NM\_080873 | 2 | 1.56 |
| *TUBA1B* | Tubulin, alpha 1b |  NM\_006082 | 4 | 1.53 |
| *RAB1A* | Member RAS oncogene family |  NM\_004161 | 2 | 1.5 |
| *CELSR1* | Cadherin, EGF LAG seven-pass G-type receptor 1  |  NM\_014246 | 2 | 1.48 |
| *MAP2* | Microtubule-associated protein 2 |  NM\_002374 | 2 | 1.47 |
| *SPARC* | Secreted protein, acidic, cysteine-rich (osteonectin) |  NM\_003118 | 3 | 1.45 |
| *MFGE8* | Milk fat globule-EGF factor 8 protein |  NM\_001114614 | 4 | 1.44 |
| *HLA-A* | Major histocompatibility complex, class I, A |  NM\_002116 | 2 | 1.43 |
| *IDH1* | Isocitrate dehydrogenase 1 (NADP+), soluble |  NM\_005896 | 3 | 1.43 |
| *FABP3* | Fatty acid binding protein 3, muscle and heart  |  NM\_004102 | 6 | 1.41 |
| *VCL* | Vinculin |  NM\_014000 | 2 | 1.41 |
| *DDB2* | Damage-specific DNA binding protein 2, 48kDa |  NM\_000107 | 2 | 1.39 |
| *RNASE4* | Ribonuclease, RNase A family, 4 |  NM\_002937 | 2 | 1.37 |
| *EPS8* | Epidermal growth factor receptor pathway substrate 8 |  NM\_004447 | 2 | 1.36 |
| *LOC652614* | Similar to HLA class I histocompatibility antigen, A-11 alpha chain  |  XM\_942149 | 13 | 1.36 |
|  |  Precursor (MHC class I antigen A\*11) |  |  |  |
| *MYH7* | Myosin, heavy chain 7, cardiac muscle, beta |  NM\_000257 | 3 | 1.36 |
| *LANCL1* | LanCl antibioticsynthetase component C-like 1 (bacterial) |  NM\_006055 | 2 | 1.35 |
| *SEPW1* | Selenoprotein W, 1 |  NM\_003009 | 2 | 1.35 |
| *SLC12A5* | Solute carrier family 12 (potassium-chloride transporter), member 5 |  NM\_020708 | 2 | 1.35 |
| *TUBA1A* | Tubulin, alpha 1a |  NM\_006009 | 4 | 1.35 |
| *EEF1A2* | Eukaryotic translation elongation factor 1 alpha 2 |  NM\_001958 | 3 | 1.34 |
| *SLC25A5* | Solute carrier family 25 (mitochondrial carrier; adenine  |  NM\_001152 | 2 | 1.34 |
|  |  nucleotide translocator), member 5 |  |  |  |
| *TUBA4A* | Tubulin, alpha 4a |  NM\_006000 | 3 | 1.34 |
| *DHX30* | DEAH (Asp-Glu-Ala-His) box polypeptide 30 |  NM\_138615 | 2 | 1.33 |
| *FLNB* | Filamin B, beta |  NM\_001457 | 3 | 1.33 |
| *ITGB7* | Integrin, beta 7 |  NM\_000889 | 2 | 1.33 |
| *STK38* | Serine/threonine kinase 38 |  NM\_007271 | 2 | 1.33 |
| *CPT1B* | Carnitinepalmitoyltransferase 1B (muscle) |  NM\_152246 | 2 | 1.32 |
| *DAPK3* | Death-associated protein kinase 3 |  NM\_001348 | 2 | 1.32 |
| *MAT2A* | Methionine adenosyltransferase II, alpha |  NM\_005911 | 2 | 1.32 |
| *MYBPC3* | Myosin binding protein C, cardiac |  NM\_000256 | 2 | 1.32 |
| *ALAD* | Aminolevulinate, delta-, dehydratase |  NM\_000031 | 2 | 1.31 |
| *RPLP0*  | Ribosomal protein, large, P0 |  NM\_053275 | 7 | 1.31 |
| *UGP2* | UDP-glucose pyrophosphorylase 2 |  NM\_001001521 | 2 | 1.31 |
| *ANG* | Angiogenin, ribonuclease, RNase A family, 5 |  NM\_001145 | 3 | 1.3 |
| *FOXO3* | Forkhead box O3 |  NM\_201559 | 2 | 1.3 |
| *ST5* | Suppression of tumorigenicity 5 |  NM\_213618 | 2 | 1.3 |
| *BCL2* | B-cell CLL/lymphoma 2 |  NM\_000633 | 2 | 1.29 |
| *RNASE1* | Ribonuclease, RNase A family, 1 (pancreatic) |  NM\_198232 | 3 | 1.29 |
| *TRRAP* | Transformation/transcription domain-associated protein |  NM\_003496 | 2 | 1.29 |
| *CALR* | Calreticulin |  NM\_004343 | 2 | 1.28 |
| *GLS* | Glutaminase |  NM\_014905 | 2 | 1.28 |
| *GNB2L1* | Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 |  NM\_006098 | 2 | 1.28 |
| *PPP2R1B* | Protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform |  NM\_002716 | 2 | 1.28 |
| *SPP1* | Secreted phosphoprotein 1 |  NM\_001040058 | 3 | 1.28 |
| *TTN* | Titin |  NM\_133378 | 2 | 1.28 |
| *GNAS* | GNAS complex locus |  NM\_080426 | 2 | 1.27 |
| *RPL3* | Ribosomal protein L3 |  NM\_001033853 | 3 | 1.27 |
| *ATP1A3* | ATPase, Na+/K+ transporting, alpha 3 polypeptide |  NM\_152296 | 2 | 1.25 |
| *CD36* | CD36 molecule (thrombospondin receptor) |  NM\_001001548 | 2 | 1.25 |
| *LPL* | Lipoprotein lipase |  NM\_000237 | 3 | 1.25 |
| *SEP15* | 15 kDaselenoprotein |  NM\_004261 | 2 | 1.25 |
| *SLC25A4* | Solute carrier family 25 (mitochondrial carrier; adenine nucleotide  |  NM\_001151 | 3 | 1.25 |
|  |  translocator), member 4 |  |  |  |
| *TUBB3* | Tubulin, beta 3 |  NM\_006086 | 2 | 1.25 |
| *TUBB* | Tubulin, beta |  NM\_178014 | 2 | 1.24 |
| *TUSC4* | Tumor suppressor candidate 4 |  NM\_006545 | 2 | 1.24 |
| *CD14* | CD14 molecule |  NM\_001040021 | 2 | 1.23 |
| *EEF2* | Eukaryotic translation elongation factor 2 |  NM\_001961 | 2 | 1.23 |
| *PRDX2* | Peroxiredoxin 2 |  NM\_005809 | 2 | 1.23 |
| *TIMP3* | TIMP metallopeptidase inhibitor 3 |  NM\_000362 | 2 | 1.23 |
| *ATP1B3* | ATPase, Na+/K+ transporting, beta 3 polypeptide |  NM\_001679 | 2 | 1.22 |
| *DYNC1H1* | Dynein, cytoplasmic 1, heavy chain 1 |  NM\_001376 | 2 | 1.22 |
| *HSPA5* | Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) |  NM\_005347 | 2 | 1.22 |
| *EEF1A1* | Eukaryotic translation elongation factor 1 alpha 1 |  NM\_001402 | 2 | 1.21 |
| *TPM3* | Tropomyosin 3 |  NM\_152263 | 2 | 1.21 |
| *IGFBP5* | Insulin-like growth factor binding protein 5 |  NM\_000599 | 2 | 1.2 |
| *VDAC3* | Voltage-dependent anion channel 3 |  NM\_005662 | 2 | 1.2 |
| *FABP2* | Fatty acid binding protein 2, intestinal |  NM\_000134 | 2 | -1.21 |
| *MAPK3* | Mitogen-activated protein kinase 3 |  NM\_002746 | 2 | -1.21 |
| *PEX3* | Peroxisomal biogenesis factor 3 |  NM\_003630 | 2 | -1.22 |
| *MYL6* | Myosin, light chain 6, alkali, smooth muscle and non-muscle |  NM\_079423 | 2 | -1.23 |
| *DDX19B* | DEAD (Asp-Glu-Ala-As) box polypeptide 19B |  NM\_007242 | 2 | -1.24 |
| *KRT4* | Keratin 4 |  NM\_002272 | 2 | -1.24 |
| *PITPNA* | Phosphatidylinositol transfer protein, alpha |  NM\_006224 | 2 | -1.24 |
| *RICS* | Rho GTPase-activating protein |  NM\_014715 | 2 | -1.24 |
| *TNFRSF21* | Tumor necrosis factor receptor superfamily, member 21 |  NM\_014452 | 2 | -1.24 |
| *CALCB*  | Calcitonin-related polypeptide beta |  NM\_000728 | 2 | -1.25 |
| *BCS1L* | BCS1-like (yeast) |  NM\_004328 | 2 | -1.26 |
| *SH3BGRL2* | SH3 domain binding glutamic acid-rich protein like 2 |  NM\_031469 | 2 | -1.26 |
| *LOC100008588* | 18S ribosomal RNA |  NR\_003286 | 4 | -1.29 |
| *AKAP13* | A kinase (PRKA) anchor protein 13 |  NM\_007200 | 2 | -1.32 |
| *TMSB4X* | Thymosin beta 4, X-linked |  NM\_021109 | 3 | -1.34 |
| *TMSL3* | Thymosin-like 3 |  NM\_183049 | 3 | -1.35 |
| *SLC17A5* | Solute carrier family 17 (anion/sugar transporter), member 5 |  NM\_012434 | 2 | -1.37 |
| *CALB1* | Calbindin 1, 28kDa |  NM\_004929 | 2 | -1.4 |
| *CD74* | CD74 molecule, major histocompatibility complex, class II invariant chain |  NM\_004355 | 3 | -1.4 |
| *LOC100008587* | 5.8S ribosomal RNA |  NR\_003285 | 2 | -1.42 |
| *SAT1* | Spermidine/spermine N1-acetyltransferase 1 |  NM\_002970 | 3 | -1.46 |
| *CD24* | CD24 molecule |  XM\_001725629 | 2 | -1.55 |
| *LOC100008589* | 28S ribosomal RNA |  NR\_003287 | 5 | -1.59 |
| *IGLL1* | Immunoglobulin lambda-like polypeptide 1 |  NM\_152855 | 35 | -1.82 |
| *IGLL3* | Immunoglobulin lambda-like polypeptide 3 |  NM\_001013618 | 11 | -1.87 |

1Genes are ordered in relation to sign fold difference in expression in GH treated cows relative to controls identified using microarray analysis (n=4 per group, FDR < 0.05, *P* < 0.01 and >1.2 fold expression difference and ≥ 2ESTs/gene).

*Supplementary Table S2* Classification of differentially expressed genes according to the top functional categories most significantly affected by GH treatment using Ingenuity Pathways Analysis (IPA).

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| --- | --- | --- | --- | --- |
| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Cell cycle |  |  |  |  |
| B-cell CLL/lymphoma 2 | *BCL2* | NM\_000657 | 9.30E-05 | 1.29 |
| Cyclin B3 | *CCNB3* | NM\_033031 | 4.39E-03 | -1.40 |
| CDC28 protein kinase regulatory subunit 2 | *CKS2* | NM\_001827 | 1.45E-05 | 1.51 |
| p300/CBP-associated factor | *PCAF* | NM\_003884 | 4.89E-05 | -1.65 |
| RAB GTPase activating protein 1 | *RABGAP1* | NM\_012197 | 2.57E-04 | 1.42 |
| Signal transducer and activator of transcription 1, 91kDa | *STAT1* | NM\_007315 | 2.83E-03 | -1.44 |
| Serine/threonine kinase 6 | *STK6* | NM\_003600 | 4.94E-04 | -1.92 |
| Transforming growth factor, beta 3 | *TGFB3* | NM\_003239 | 8.24E-03 | -1.47 |
|  |  |  |  |  |
| Cell proliferation |  |  |  |  |
| B-cell CLL/lymphoma 2 | *BCL2* | NM\_000657 | 9.30E-05 | 1.29 |
| CD74 antigen | *CD74* | NM\_004355 | 1.98E-02 | -1.43 |
| CDC28 protein kinase regulatory subunit 2 | *CKS2* | NM\_001827 | 1.45E-05 | 1.51 |
| CCR4-NOT transcription complex, subunit 8 | *CNOT8* | NM\_004779 | 1.27E-03 | -1.41 |
| Casein alpha s2-like A | *CSN1S2A* | XM\_379270 | 3.89E-06 | 1.38 |
| Cathepsin L2 | *CTSL2* | NM\_001333 | 1.19E-04 | 1.06 |
| Epithelial membrane protein 2 | *EMP2* | NM\_001424 | 7.80E-05 | -1.67 |
| Fatty acid binding protein 3,  | *FABP3* | NM\_004102 | 1.95E-06 | 1.41 |
| muscle and heart (mammary-derived growth inhibitor) |  |  |  |  |
| Fatty acid binding protein 7, brain | *FABP7* | NM\_001446 | 7.73E-06 | 1.42 |
| GRB2-associated binding protein 1 | *GAB1* | NM\_207123 | 1.85E-04 | 1.50 |
| Laminin, gamma 1 | *LAMC1* | NM\_002293 | 1.60E-03 | -1.60 |
| p300/CBP-associated factor | *PCAF* | NM\_003884 | 4.89E-05 | -1.65 |
| Protein kinase D1 | *PRKD1* | NM\_002742 | 1.81E-06 | 1.41 |
|  |  |  |  |  |
| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Serum amyloid A1 | *SAA1* | NM\_000331 | 3.88E-01 | -1.51 |
| Surfactant, pulmonary-associated protein D | *SFTPD* | NM\_003019 | 1.60E-02 | 1.48 |
| SHC (Src homology 2 domain containing) transforming protein 1 | *SHC1* | NM\_003029 | 9.12E-04 | 1.44 |
| Transforming growth factor, beta 3 | *TGFB3* | NM\_003239 | 8.24E-03 | -1.47 |
| Transmembrane 4 L six family member 4 | *TM4SF4* | NM\_004617 | 1.41E-02 | 1.37 |
|  |  |  |  |  |
| Cell adhesion |  |  |  |  |
| Similar to Laminin receptor 1 | *LOC388524* | NM\_001005472 | 2.67E-02 | 1.59 |
| B-cell CLL/lymphoma 2 | *BCL2* | NM\_000657 | 9.30E-05 | 1.29 |
| Fibronectin leucine rich transmembrane protein 3 | *FLRT3* | NM\_198391 | 1.26E-01 | -1.43 |
| Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | *ITGA2* | NM\_002203 | 6.94E-07 | 1.03 |
| Integrin, alpha X (antigen CD11C (p150), alpha polypeptide) | *ITGAX* | NM\_000887 | 5.97E-02 | -1.91 |
| Laminin, gamma 1 | *LAMC1* | NM\_002293 | 1.60E-03 | -1.60 |
| Milk fat globule-EGF factor 8 protein | *MFGE8* | NM\_005928 | 2.72E-04 | 1.44 |
| BH-protocadherin (brain-heart) | *PCDH7* | NM\_032457 | 3.30E-03 | -1.38 |
| Serum amyloid A1 | *SAA1* | NM\_000331 | 3.88E-01 | -1.51 |
| Thrombospondin 1 | *THBS1* | NM\_003246 | 4.64E-04 | -1.57 |
| Vinculin | *VCL* | NM\_003373 | 1.16E-05 | 1.41 |
|  |  |  |  |  |
| Cell differentiation |  |  |  |  |
| Angiogenin, ribonuclease, RNase A family, 5 | *ANG* | NM\_001145 | 5.93E-05 | 1.30 |
| Filamin B, beta (actin binding protein 278) | *FLNB* | NM\_001457 | 1.59E-03 | 1.33 |
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|  |  |  |  |  |
| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Cell death |  |  |  |  |
| Clusterin | *CLU* | NM\_001831 | 2.68E-03 | 1.07 |
| Epithelial membrane protein 2 | *EMP2* | NM\_001424 | 7.80E-05 | -1.67 |
| Cytoskeleton |  |  |  |  |
| Actin, alpha 2, smooth muscle, aorta | *ACTA2* | NM\_001613 | 1.80E-03 | 1.57 |
| Rho GTPase activating protein 26 | *ARHGAP26* | NM\_015071 | 1.49E-03 | -1.53 |
| Chromosome 14 open reading frame 31 | *C14orf31* | NM\_152330 | 1.88E-04 | -1.40 |
| Choline kinase alpha | *CHKA* | NM\_212469 | 3.39E-05 | -1.47 |
| Erythrocyte membrane protein band 4.1-like 1 | *EPB41L1* | NM\_012156 | 3.89E-05 | 1.43 |
| Filamin B, beta (actin binding protein 278) | *FLNB* | NM\_001457 | 1.59E-03 | 1.33 |
| Tubulin, beta 3 | *TUBB3* | NM\_006086 | 1.60E-05 | 1.25 |
| Vinculin | *VCL* | NM\_003373 | 1.16E-05 | 1.41 |
|  |  |  |  |  |
| Signal transduction |  |  |  |  |
| LOC440702 | *LOC440702* | XM\_496425 | 3.33E-06 | 1.45 |
| Similar to Laminin receptor 1 | *LOC388524* | NM\_001005472 | 2.67E-02 | 1.59 |
| Calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma | *CAMK2G* | NM\_172170 | 1.21E-03 | 1.08 |
| CD74 antigen | *CD74* | NM\_004355 | 1.98E-02 | -1.43 |
| CD79B antigen (immunoglobulin-associated beta) | *CD79B* | NM\_000626 | 2.11E-01 | -1.42 |
| CDC28 protein kinase regulatory subunit 2 | *CKS2* | NM\_001827 | 1.45E-05 | 1.51 |
| cAMP responsive element binding protein-like 1 | *CREBL1* | NM\_004381 | 1.65E-02 | 1.40 |
| Filamin B, beta (actin binding protein 278) | *FLNB* | NM\_001457 | 1.59E-03 | 1.33 |
| GRB2-related adaptor protein 2 | *GRAP2* | NM\_004810 | 6.70E-04 | 1.28 |
| IQ motif containing GTPase activating protein 1 | *IQGAP1* | NM\_003870 | 3.56E-03 | -1.43 |
|  |  |  |  |  |
|  |  |  |  |  |
| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Integrin, alpha X (antigen CD11C (p150), alpha polypeptide) | *ITGAX* | NM\_000887 | 5.97E-02 | -1.91 |
| Microsomal glutathione S-transferase 2 | *MGST2* | NM\_002413 | 2.93E-03 | -1.45 |
| Protein kinase N1 | *PKN1* | NM\_002741 | 2.23E-04 | -1.78 |
| RAB11A, member RAS oncogene family | *RAB11A* | NM\_004663 | 5.16E-04 | 1.18 |
| Ribosomal protein S6 kinase, 90kDa, polypeptide 1 | *RPS6KA1* | NM\_002953 | 1.05E-04 | -1.45 |
| Ras suppressor protein 1 | *RSU1* | NM\_152724 | 1.36E-06 | -1.41 |
| RYK receptor-like tyrosine kinase | *RYK* | NM\_001005861 | 8.43E-05 | -1.36 |
| Serum amyloid A1 | *SAA1* | NM\_000331 | 3.88E-01 | -1.51 |
| Sorcin | *SRI* | NM\_198901 | 4.43E-04 | -1.44 |
| Transforming growth factor, beta 3 | *TGFB3* | NM\_003239 | 8.24E-03 | -1.47 |
| Tubulin, beta 3 | *TUBB3* | NM\_006086 | 1.60E-05 | 1.25 |
| Ubiquitin protein ligase E3A | *UBE3A* | NM\_000462 | 1.47E-05 | 1.33 |
|  |  |  |  |  |
| Regulation of transcription |  |  |  |  |
| Cyclin H | *CCNH* | NM\_001239 | 6.53E-02 | 1.52 |
| CCR4-NOT transcription complex, subunit 8 | *CNOT8* | NM\_004779 | 1.27E-03 | -1.41 |
| cAMP responsive element binding protein-like 1 | *CREBL1* | NM\_004381 | 1.65E-02 | 1.40 |
| Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein | *ID2* | NM\_002166 | 1.14E-05 | 1.44 |
| Integrin, alpha X (antigen CD11C (p150), alpha polypeptide) | *ITGAX* | NM\_000887 | 5.97E-02 | -1.91 |
| Jumonji domain containing 1C | *JMJD1C* | NM\_004241 | 1.83E-04 | -1.63 |
| Myeloid/lymphoid or mixed-lineage leukemia  | *MLL* | NM\_005933 | 1.89E-05 | -1.65 |
| (trithorax homolog, Drosophila) |  |  |  |  |
| Nuclear receptor subfamily 5, group A, member 2 | *NR5A2* | NM\_205860 | 1.74E-06 | 1.37 |
| p300/CBP-associated factor | *PCAF* | NM\_003884 | 4.89E-05 | -1.65 |
| Proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 | *PSMD9* | NM\_002813 | 7.42E-06 | 1.47 |
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| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Sp1 transcription factor | *SP1* | NM\_138473 | 9.15E-03 | -1.48 |
| Signal transducer and activator of transcription 1, 91kDa | *STAT1* | NM\_007315 | 2.83E-03 | -1.44 |
| TAF6-like RNA polymerase II,  | *TAF6L* | NM\_006473 | 9.08E-06 | -1.58 |
| p300/CBP-associated factor (PCAF)-associated factor, 65kDa |  |  |  |  |
|  |  |  |  |  |
| Protein biosynthesis |  |  |  |  |
| Similar to Laminin receptor 1 | *LOC388524* | NM\_001005472 | 2.67E-02 | 1.59 |
| Angiogenin, ribonuclease, RNase A family, 5 | *ANG* | NM\_001145 | 5.93E-05 | 1.30 |
| Calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma | *CAMK2G* | NM\_172170 | 1.21E-03 | 1.08 |
| Eukaryotic translation initiation factor 2C, 4 | *EIF2C4* | NM\_017629 | 7.77E-04 | -1.42 |
| Prostaglandin F2 receptor negative regulator | *PTGFRN* | NM\_020440 | 1.44E-04 | -1.51 |
|  |  |  |  |  |
| Protein folding |  |  |  |  |
| CD74 antigen | *CD74* | NM\_004355 | 1.98E-02 | -1.43 |
|  |  |  |  |  |
| Intracellular protein transport |  |  |  |  |
| Sorting nexin 6 | *SNX6* | NM\_152233 | 2.89E-01 | -1.70 |
| Tubulin, beta 3 | *TUBB3* | NM\_006086 | 1.60E-05 | 1.25 |
| CD74 antigen | *CD74* | NM\_004355 | 1.98E-02 | -1.43 |
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| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Fatty acid metabolism |  |  |  |  |
| Acyl-CoA synthetase long-chain family member 1 | *ACSL1* | NM\_001995 | 1.12E-06 | 1.17 |
| Carnitine palmitoyltransferase 1B (muscle) | *CPT1B* | NM\_152246 | 1.31E-03 | 1.32 |
| DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked | *DDX3X* | NM\_001356 | 1.69E-03 | -1.71 |
| Fatty acid binding protein 7, brain | *FABP7* | NM\_001446 | 7.73E-06 | 1.42 |
| Hydroxyacyl-Coenzyme A dehydrogenase, alpha subunit | *HADHA* | NM\_000182 | 9.41E-03 | 1.76 |
|  |  |  |  |  |
| Fatty acid biosynthesis |  |  |  |  |
| Fatty acid desaturase 2 | *FADS2* | NM\_004265 | 2.38E-05 | 1.50 |
|  |  |  |  |  |
| Lipid metabolism |  |  |  |  |
| Acyl-CoA synthetase long-chain family member 1 | *ACSL1* | NM\_001995 | 1.12E-06 | 1.17 |
| Aldehyde dehydrogenase 1 family, member A3 | *ALDH1A3* | NM\_000693 | 8.16E-04 | 1.40 |
| Choline kinase alpha | *CHKA* | NM\_212469 | 3.39E-05 | -1.47 |
| Choline kinase alpha | *CHKA* | NM\_212469 | 3.39E-05 | -1.47 |
| Clusterin | *CLU* | NM\_001831 | 2.68E-03 | 1.07 |
| Carnitine palmitoyltransferase 1B (muscle) | *CPT1B* | NM\_152246 | 1.31E-03 | 1.32 |
| Carnitine acetyltransferase | *CRAT* | NM\_000755 | 1.33E-03 | 1.37 |
| DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked | *DDX3X* | NM\_001356 | 1.69E-03 | -1.71 |
| Hydroxyacyl-Coenzyme A dehydrogenase, alpha subunit | *HADHA* | NM\_000182 | 9.41E-03 | 1.76 |
| Phosphatidylinositol transfer protein, alpha | *PITPNA* | NM\_006224 | 2.10E-06 | -1.24 |
| Phospholipase C, delta 1 | *PLCD1* | NM\_006225 | 7.89E-04 | 1.39 |
| Serum amyloid A1 | *SAA1* | NM\_000331 | 3.88E-01 | -1.51 |
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| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Regulation of translation |  |  |  |  |
| Similar to Laminin receptor 1 | *LOC388524* | NM\_001005472 | 2.67E-02 | 1.59 |
| Calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma | *CAMK2G* | NM\_172170 | 1.21E-03 | 1.08 |
| Eukaryotic translation initiation factor 2C, 4 | *EIF2C4* | NM\_017629 | 7.77E-04 | -1.42 |
|  |  |  |  |  |
| Insulin receptor signaling pathway |  |  |  |  |
| GRB2-associated binding protein 1 | *GAB1* | NM\_207123 | 1.85E-04 | 1.50 |
|  |  |  |  |  |
| Protein binding |  |  |  |  |
| GRB2-related adaptor protein 2 | *GRAP2* | NM\_004810 | 6.70E-04 | 1.28 |
| Major histocompatibility complex, class I, A | *HLA-A* | NM\_002116 | 2.65E-03 | 1.43 |
| Major histocompatibility complex, class I, C | *HLA-C* | NM\_002117 | 1.38E-04 | 1.48 |
| Inhibitor of kappa light polypeptide gene enhancer in B-cells,  | *IKBKAP* | NM\_003640 | 9.06E-04 | 1.41 |
| kinase complex-associated protein |  |  |  |  |
| Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) | *ITGA2* | NM\_002203 | 6.94E-07 | 1.03 |
| Integrin, alpha X (antigen CD11C (p150), alpha polypeptide) | *ITGAX* | NM\_000887 | 5.97E-02 | -1.91 |
| Potassium voltage-gated channel, shaker-related subfamily, member 3 | *KCNA3* | NM\_002232 | 2.03E-01 | 1.41 |
| Laminin, gamma 1 (formerly LAMB2) | *LAMC1* | NM\_002293 | 1.60E-03 | -1.60 |
| Mitogen-activated protein kinase kinase kinase kinase 2 | *MAP4K2* | NM\_004579 | 3.44E-05 | -1.44 |
| Myeloid/lymphoid or mixed-lineage leukemia  | *MLL* | NM\_005933 | 1.89E-05 | -1.65 |
| (trithorax homolog, Drosophila) |  |  |  |  |
| p300/CBP-associated factor | *PCAF* | NM\_003884 | 4.89E-05 | -1.65 |
| BH-protocadherin (brain-heart) | *PCDH7* | NM\_032457 | 3.30E-03 | -1.38 |
| Protein kinase N1 | *PKN1* | NM\_002741 | 2.23E-04 | -1.78 |
| Protein kinase D1 | *PRKD1* | NM\_002742 | 1.81E-06 | 1.41 |
|  |  |  |  |  |
|  |  |  |  |  |
| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Prostaglandin F2 receptor negative regulator | *PTGFRN* | NM\_020440 | 1.44E-04 | -1.51 |
| RAB11A, member RAS oncogene family | *RAB11A* | NM\_004663 | 5.16E-04 | 1.18 |
| Sorting nexin 6 | *SNX6* | NM\_152233 | 2.89E-01 | -1.70 |
| Sp1 transcription factor | *SP1* | NM\_138473 | 9.15E-03 | -1.48 |
| Signal transducer and activator of transcription 1, 91kDa | *STAT1* | NM\_007315 | 2.83E-03 | -1.44 |
| Serine/threonine kinase 11 (Peutz-Jeghers syndrome) | *STK11* | NM\_000455 | 1.05E-05 | 1.17 |
| Serine/threonine kinase 6 | *STK6* | NM\_003600 | 4.94E-04 | -1.92 |
| Thrombospondin 1 | *THBS1* | NM\_003246 | 4.64E-04 | -1.57 |
| Translocase of inner mitochondrial membrane 50 homolog (yeast) | *TIMM50* | NM\_001001563 | 6.49E-04 | -1.56 |
| Tripartite motif-containing 35 | *TRIM35* | NM\_171982 | 4.08E-03 | -1.49 |
| Vinculin | *VCL* | NM\_003373 | 1.16E-05 | 1.41 |
|  |  |  |  |  |
| Apoptosis |  |  |  |  |
| Apoptosis inhibitor 5 | *API5* | NM\_006595 | 4.15E-02 | 1.41 |
| B-cell CLL/lymphoma 2 | *BCL2* | NM\_000657 | 9.30E-05 | 1.29 |
| BCL2/adenovirus E1B 19kDa interacting protein 3-like | *BNIP3L* | NM\_004331 | 6.96E-04 | 1.33 |
| Caspase recruitment domain family, member 14 | *CARD14* | NM\_024110 | 5.04E-03 | -1.61 |
| CDC28 protein kinase regulatory subunit 2 | *CKS2* | NM\_001827 | 1.45E-05 | 1.51 |
| Clusterin | *CLU* | NM\_001831 | 2.68E-03 | 1.07 |
| Tripartite motif-containing 35 | *TRIM35* | NM\_171982 | 4.08E-03 | -1.49 |
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| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Immune response |  |  |  |  |
| B-cell CLL/lymphoma 2 | *BCL2* | NM\_000657 | 9.30E-05 | 1.29 |
| Complement component 2 | *C2* | NM\_000063 | 1.74E-03 | -1.40 |
| CD24 antigen | *CD24* | NM\_013230 | 9.78E-05 | -1.36 |
| CD74 antigen | *CD74* | NM\_004355 | 1.98E-02 | -1.43 |
| CD79B antigen | *CD79B* | NM\_000626 | 2.11E-01 | -1.42 |
| Clusterin | *CLU* | NM\_001831 | 2.68E-03 | 1.07 |
| Complement component (3d/Epstein Barr virus) receptor 2 | *CR2* | NM\_001877 | 5.89E-04 | -1.36 |
| Diacylglycerol kinase, delta 130kDa | *DGKD* | NM\_152879 | 3.67E-04 | -1.64 |
| Immunoglobulin J polypeptide,  | *IGJ* | NM\_144646 | 1.41E-04 | -1.55 |
| linker protein for immunoglobulin alpha and mu polypeptides |  |  |  |  |
| Immunoglobulin lambda-like polypeptide 1 | *IGLL1* | NM\_152855 | 3.01E-05 | -2.01 |
| Inhibitor of kappa light polypeptide gene enhancer in B-cells,  | *IKBKAP* | NM\_003640 | 9.06E-04 | 1.41 |
| kinase complex-associated protein |  |  |  |  |
| Lactotransferrin | *LTF* | NM\_002343 | 1.46E-02 | 1.61 |
| Mitogen-activated protein kinase kinase kinase kinase 2 | *MAP4K2* | NM\_004579 | 3.44E-05 | -1.44 |
| Surfactant, pulmonary-associated protein D | *SFTPD* | NM\_003019 | 1.60E-02 | 1.48 |
|  |  |  |  |  |
| Cell division |  |  |  |  |
| Cyclin B3 | *CCNB3* | NM\_033031 | 4.39E-03 | -1.40 |
| Cell division cycle associated 7 | *CDCA7* | NM\_031942 | 1.72E-04 | 1.18 |
| CDC28 protein kinase regulatory subunit 2 | *CKS2* | NM\_001827 | 1.45E-05 | 1.51 |
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| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Extracellular matrix structural constituent |  |  |  |  |
| Collagen, type I, alpha 1 | *COL1A1* | NM\_000088 | 3.67E-06 | 1.64 |
| Collagen, type I, alpha 2 | *COL1A2* | NM\_000089 | 3.17E-07 | 1.73 |
| Collagen, type III, alpha 1 | *COL3A1* | NM\_000090 | 1.77E-05 | 1.84 |
| Collagen, type IV, alpha 1 | *COL4A1* | NM\_001845 | 6.05E-03 | -1.52 |
| Collagen, type V, alpha 2 | *COL5A2* | NM\_000393 | 6.34E-05 | 1.73 |
|  |  |  |  |  |
| Protein kinase C activation |  |  |  |  |
| Diacylglycerol kinase, delta 130kDa | *DGKD* | NM\_152879 | 7.86E-03 | 1.36 |
| Mitogen-activated protein kinase kinase kinase kinase 2 | *MAP4K2* | NM\_004579 | 3.44E-05 | -1.44 |
| Protein kinase, cAMP-dependent, regulatory, type II, alpha | *PRKAR2A* | NM\_004157 | 1.24E-04 | -1.47 |
| Protein kinase D1 | *PRKD1* | NM\_002742 | 1.81E-06 | 1.41 |
|  |  |  |  |  |
| Ribosome |  |  |  |  |
| Similar to Laminin receptor 1 | *LOC388524* | NM\_001005472 | 2.67E-02 | 1.59 |
| Mannosidase, alpha, class 2B, member 1 | *MAN2B1* | NM\_000528 | 8.92E-04 | 1.44 |
|  |  |  |  |  |
| RNA binding |  |  |  |  |
| Angiogenin, ribonuclease, RNase A family, 5 | *ANG* | NM\_001145 | 5.93E-05 | 1.30 |
| DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked | *DDX3X* | NM\_001356 | 1.69E-03 | -1.71 |
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| Description | Gene Symbol | RefSeq | *P*-Value | Fold Change |
|  |  |  |  |  |
| Unknowns1 |  |  |  |  |
| 000730BMLB002048HT |  |  | 5.94E-04 | -1.85 |
| 000321BMPA002327HT |  |  | 1.92E-04 | -1.83 |
| 000223BOVB006323HT |  |  | 8.93E-04 | -1.78 |
| 000311BSPB009556HT |  |  | 5.78E-04 | -1.70 |
| 001030BMUA003250HT |  |  | 6.07E-06 | -1.69 |
| 000328BMPA005789HT |  |  | 3.85E-05 | -1.62 |
| 000707BMNA004648HT |  |  | 8.94E-04 | -1.59 |
| 000722BSIA004433HT |  |  | 2.67E-04 | -1.59 |
| 000321BMPA002335HT |  |  | 9.46E-05 | -1.59 |
| 000229BOVB007705HT |  |  | 3.29E-03 | -1.57 |
| 000719BSIA004171HT |  |  | 6.60E-06 | -1.53 |
| 000419BMNA001864HT |  |  | 1.66E-03 | -1.53 |
| 000731BMLB002744HT |  |  | 2.59E-04 | -1.53 |
| 001002BPMA011124HT |  |  | 9.29E-04 | -1.49 |
| 000517BSIA002066HT |  |  | 1.67E-03 | -1.44 |
| 001001BPMA007733HT |  |  | 3.99E-04 | -1.41 |
| 000417BMNA001111HT |  |  | 4.01E-04 | -1.41 |
| 000517BSIA001714HT |  |  | 3.13E-03 | -1.40 |
| 000130BLIB007603HT |  |  | 4.10E-04 | -1.13 |
| 000313BMPA001063HT |  |  | 5.74E-07 | 1.22 |
| 991130BCEA001402HT |  |  | 1.43E-03 | 1.41 |
| 000825BEMN002932HT |  |  | 1.80E-03 | 1.41 |
| 000830BEMN004932HT |  |  | 1.53E-03 | 1.52 |
| 001121BAMA003036HT |  |  | 8.96E-07 | 1.53 |
| 000710BMNA003628HT |  |  | 2.28E-04 | 1.54 |
| 000729BINA002832HT |  |  | 1.75E-02 | 1.54 |
| 001213BPMT001167HT |  |  | 4.53E-03 | 1.55 |
| 000706BPPA005586HT |  |  | 3.51E-09 | 1.60 |

1Unknowns are listed only as the ESTs used as the corresponding genes could not be made identified by RefSeq.