

Table S1. Characteristics of gene-specific primers used for qPCR validation of microarray data ¹.

| Gene | Forward (5' to 3') Reverse (5' to 3') | Annealing temperature (°C) | PCR product size (bp) | NCBI GenBank accession no. | Slope | R ² | E |
|------------------------|--|----------------------------------|--------------------------------|-------------------------------|-------|----------------|------|
| <i>Reference genes</i> | | | | | | | |
| <i>GAPDH</i> | ACTGTCAAGGCTGAGAACGG AGCTGAGGGAGCTGAGATGA | 60 | 204 | NM_204305.1 | -3.49 | 0.997 | 1.93 |
| <i>SDHA</i> | ATCCCCGTTTTGCCTACGGT GGGAGTTTGCTCCAAGACGA | 60 | 172 | NM_001277398.1 | -3.32 | 0.985 | 2.00 |
| <i>ACTB</i> | ATGAAGCCCAGAGCAAAAAGA GGGGTGTGAAGGTCTCAAA | 60 | 223 | NM_205518.1 | -3.43 | 0.998 | 1.96 |
| <i>HPRT1</i> | CAGCCCCTGCATCGTGATTG GTGTCCTCCCATGCCCTTCA | 60 | 169 | NM_204848.1 | -2.97 | 0.987 | 2.17 |
| <i>Target genes</i> | | | | | | | |
| <i>ANGPTL4</i> | GCTTCAGCCACACCAACCAG ATCACCGTCCAGCCACCTTC | 60 | 190 | XM_001232283.7 | -3.22 | 0.995 | 2.05 |
| <i>ACSBG2</i> | CGTTCGACGCTTGCAGATCC CAGGACGTGAAGAGGACGCT | 60 | 199 | NM_001397597.1 | -3.29 | 0.999 | 2.01 |
| <i>HOOK1</i> | AGCTGAATCCAGCATCAGCAG CTGGAGCGTTAGGCTCTTGTT | 60 | 164 | NM_001006542.2 | -3.71 | 0.992 | 1.86 |
| <i>NR0B1</i> | GGGCTTCCTGGCTAAGTGCT GGCCAGGTAGATCCGGGTTG | 60 | 95 | NM_204593.2 | -3.25 | 0.994 | 2.03 |
| <i>TACC3</i> | CAGATCGTGTTGCGGGTCTG AAAGCCACACTCTTCCGCTG | 60 | 110 | NM_001004429.4 | -2.92 | 0.992 | 2.2 |
| <i>GLCC1</i> | CCGGTGTACAGAGTGGACAGG CGATGCTGAGCGCTGATGTG | 60 | 225 | NM_001012855.5 | -3.44 | 0.995 | 1.95 |
| <i>CCNB1</i> | GTTTGTGTAGAGCGGCGCAA GCCAGGTCCTTTCGTAGCCT | 60 | 249 | NM_001004369.2 | -3.55 | 0.986 | 1.91 |
| <i>TOP2A</i> | ATGATGCTGCCATCACCTG GGCCTGGCTTCAAACCATCA | 60 | 243 | NM_204791.3 | -3.99 | 0.974 | 1.78 |
| <i>CDK1</i> | AGGCCAAGTGTTGCAATGAA GGTACAGCCTTGCATCCTGC | 60 | 155 | NM_205314.2 | -3.43 | 0.998 | 1.96 |
| <i>SMC2</i> | CCCTTAGTGGAGGTGCAAGC TCTCCCACTGCTGCTTCAGA | 60 | 177 | NM_205230.2 | -3.4 | 0.999 | 1.97 |

¹ GAPDH, glyceraldehyde-3-phosphate dehydrogenase; SDHA, dehydrogenase complex flavoprotein subunit A; ACTB, actin, beta; HPRT1, hypoxanthine phosphoribosyltransferase 1; ANGPTL4, Angiopoyetin-like 4; ACSBG2, acyl-CoA synthetase bubblegum family member 2; HOOK1, hook microtubule tethering protein 1; NR0B1, nuclear receptor subfamily 0 group B member 1; TACC3, transforming acidic coiled-coil containing protein 3; GLCC1, glucocorticoid induced 1; CCNB1, cyclin B1; TOP2A, otopoisomerase (DNA) II alpha; CDK1, cyclin dependent kinase 1; SMC2, structural maintenance of chromosomes 2.

Table S2. Description of the up-regulated, down-regulated and total regulated transcripts between HT7.5 vs. HT0, HT15 vs. HT0, HT22.5 vs. HT0, HT30 vs. HT0 groups¹.

| Comparison | Up-regulated transcripts | Down-regulated transcripts | Total regulated transcripts |
|----------------|--------------------------|----------------------------|-----------------------------|
| HT7.5 vs. HT0 | 14 | 19 | 33 |
| HT15 vs. HT0 | 118 | 260 | 389 |
| HT22.5 vs. HT0 | 54 | 22 | 76 |
| HT30 vs. HT0 | 57 | 60 | 117 |

Table S3. Fold change and *p*-value of all differentially expressed transcripts among HT15 and HT0 group ¹.

| Gene Symbol | Gene Description | FC | <i>p</i> -value |
|----------------------|--|-------|-----------------|
| <i>Downregulated</i> | | | |
| ANGPTL4 | angiopoietin-like 4 | -2.71 | 0.013 |
| LOC100859636 | RING finger protein 170-like | -2.23 | 0.007 |
| GRIN2A | glutamate receptor, ionotropic, N-methyl D-aspartate 2A | -2.09 | 0.025 |
| MIR34B | microRNA 34b | -1.93 | 0.011 |
| MIR30B | microRNA 30b | -1.87 | 0.023 |
| ACSBG2 | acyl-CoA synthetase bubblegum family member 2 | -1.84 | 0.031 |
| MIR135A-3 | microRNA mir-135a-3 | -1.73 | 0.004 |
| WDPCP | WD repeat containing planar cell polarity effector | -1.72 | 0.025 |
| LOC418086 | uncharacterized LOC418086 | -1.71 | 0.007 |
| ADPRHL1 | ADP-ribosylhydrolase like 1 | -1.70 | 0.001 |
| CCDC172 | coiled-coil domain containing 172 | -1.68 | 0.015 |
| NR0B1 | nuclear receptor subfamily 0, group B, member 1 | -1.68 | 0.024 |
| MIR1680 | microRNA mir-1680 | -1.67 | 0.002 |
| HOOK1 | hook microtubule-tethering protein 1 | -1.67 | 0.013 |
| MIR1779 | microRNA mir-1779 | -1.66 | 0.022 |
| G0S2 | G0/G1 switch 2 | -1.64 | 0.022 |
| MIR1655 | microRNA mir-1655 | -1.63 | 0.012 |
| MIR135A2 | microRNA 135a-2 | -1.62 | 0.014 |
| GUCA1C | guanylate cyclase activator 1C | -1.61 | 0.002 |
| CYP2J6L3 | cytochrome P450 2J6-like 3 | -1.59 | 0.014 |
| MIR551B | microRNA 551b | -1.58 | 0.031 |
| MIR17 | microRNA 17 | -1.56 | 0.048 |
| C5H14ORF38 | chromosome 5 open reading frame, human C14orf38 | -1.56 | 0.022 |
| VIP | vasoactive intestinal peptide | -1.56 | 0.005 |
| TH | tyrosine hydroxylase | -1.56 | 0.000 |
| LOC771537 | uncharacterized LOC771537 | -1.54 | 0.014 |
| CLEC3A | C-type lectin domain family 3, member A | -1.54 | 0.003 |
| C5H14ORF38 | chromosome 5 open reading frame, human C14orf38 | -1.53 | 0.039 |
| GRIA3 | glutamate receptor, ionotropic, AMPA 3 | -1.52 | 0.005 |
| HS3ST5 | heparan sulfate (glucosamine) 3-O-sulfotransferase 5 | -1.51 | 0.013 |
| ATOH7 | atonal bHLH transcription factor 7 | -1.51 | 0.011 |
| PACRGL | PARK2 co-regulated-like | -1.51 | 0.022 |
| LOC770479 | gamma-aminobutyric acid receptor subunit beta-1-like | -1.51 | 0.037 |
| MIR1718 | microRNA mir-1718 | -1.51 | 0.012 |
| SLC32A1 | solute carrier family 32 (GABA vesicular transporter), member 1 | -1.51 | 0.015 |
| PTPRQ | protein tyrosine phosphatase, receptor type, Q | -1.50 | 0.043 |
| C8ORF34 | chromosome 2 open reading frame, human C8orf34 | -1.50 | 0.017 |
| BRINP1 | bone morphogenetic protein/retinoic acid inducible neural-specific 1 | -1.49 | 0.015 |
| DISP2 | dispatched homolog 2 (Drosophila) | -1.49 | 0.000 |

| Gene Symbol | Gene Description | FC | p-value |
|--------------|--|-------|---------|
| CALML3 | calmodulin-like 3 | -1.49 | 0.035 |
| TCP10 | t-complex 10 | -1.49 | 0.014 |
| FGF13 | fibroblast growth factor 13 | -1.49 | 0.020 |
| BOLL | boule-like RNA-binding protein | -1.49 | 0.002 |
| KCNH7 | potassium voltage-gated channel, subfamily H (eag-related), member 7 | -1.48 | 0.028 |
| MIR128-2 | microRNA 128-2 | -1.48 | 0.024 |
| MIR1722 | microRNA mir-1722 | -1.48 | 0.025 |
| LOC769098 | uncharacterized LOC769098 | -1.48 | 0.012 |
| NMS | neuromedin S | -1.48 | 0.030 |
| CHRNA6 | cholinergic receptor, nicotinic, alpha 6 (neuronal) | -1.47 | 0.002 |
| ANO4 | anoctamin 4 | -1.47 | 0.012 |
| MIR762 | microRNA mir-762 | -1.47 | 0.041 |
| SOSTDC1 | sclerostin domain containing 1 | -1.46 | 0.012 |
| CALR3 | calreticulin 3 | -1.46 | 0.012 |
| TMEM240 | transmembrane protein 240 | -1.46 | 0.032 |
| MIR1592 | microRNA mir-1592 | -1.46 | 0.021 |
| NCAM2 | neural cell adhesion molecule 2 | -1.45 | 0.017 |
| MIR1799 | microRNA mir-1799 | -1.45 | 0.017 |
| MIR1598 | microRNA mir-1598 | -1.45 | 0.002 |
| LOC101748624 | uncharacterized LOC101748624 | -1.45 | 0.013 |
| MSLN | mesothelin-like | -1.45 | 0.015 |
| KCNQ3 | potassium voltage-gated channel, KQT-like subfamily, member 3 | -1.45 | 0.033 |
| LOC420807 | uncharacterized LOC420807 | -1.44 | 0.008 |
| LOC101749601 | translation initiation factor IF-2-like | -1.44 | 0.008 |
| MIR1741 | microRNA mir-1741 | -1.44 | 0.020 |
| MIR301B | microRNA mir-301b | -1.43 | 0.015 |
| FSTL5 | folistatin-like 5 | -1.43 | 0.005 |
| ELOVL4 | ELOVL fatty acid elongase 4 | -1.43 | 0.014 |
| ALG13 | asparagine-linked glycosylation 13 homolog (S. cerevisiae) | -1.43 | 0.006 |
| MIR106A | microRNA 106a | -1.43 | 0.028 |
| MEPE | matrix extracellular phosphoglycoprotein | -1.43 | 0.028 |
| FGF2 | fibroblast growth factor 2 (basic) | -1.42 | 0.004 |
| LOC100857478 | uncharacterized LOC100857478 | -1.42 | 0.047 |
| NLGN1 | neuroligin 1 | -1.42 | 0.042 |
| CNGA1 | cyclic nucleotide gated channel alpha 1 | -1.42 | 0.022 |
| CHRM3 | cholinergic receptor, muscarinic 3 | -1.42 | 0.006 |
| MIR1597 | microRNA mir-1597 | -1.42 | 0.008 |
| SKOR2 | SKI family transcriptional corepressor 2 | -1.42 | 0.043 |
| LOC428499 | carboxymethylenebutenolidase homolog | -1.42 | 0.046 |
| NLGN3 | neuroligin 3 | -1.42 | 0.036 |
| LRRC9 | leucine rich repeat containing 9 | -1.41 | 0.023 |
| CHRNA9 | cholinergic receptor, nicotinic, alpha 9 (neuronal) | -1.41 | 0.003 |
| PDCL2 | phosducin-like 2 | -1.41 | 0.022 |
| ZP4 | zona pellucida glycoprotein 4 | -1.41 | 0.005 |
| LOC422171 | Rho GTPase activating protein 20-like | -1.41 | 0.010 |
| FOXP1 | forkhead box G1 | -1.41 | 0.016 |
| LOC423822 | heparan sulfate glucosamine 3-O-sulfotransferase 1-like | -1.41 | 0.006 |
| LOC101752022 | maestro heat-like repeat-containing protein family member 2B-like | -1.41 | 0.013 |
| KLHL31 | kelch-like family member 31 | -1.41 | 0.002 |
| VGLL1 | vestigial-like family member 1 | -1.41 | 0.025 |
| MIR202 | microRNA 202 | -1.41 | 0.014 |
| LOC100857259 | vesicular inhibitory amino acid transporter-like | -1.40 | 0.029 |
| C1HXORF59 | chromosome 1 open reading frame, human CXORF59 | -1.40 | 0.040 |

| Gene Symbol | Gene Description | FC | p-value |
|----------------|--|-------|---------|
| MIR9-1 | microRNA mir-9-1 | -1.40 | 0.045 |
| LOC420300 | lymphocyte antigen 6E-like | -1.40 | 0.006 |
| BEGAIN | brain-enriched guanylate kinase-associated | -1.40 | 0.050 |
| HCN1 | hyperpolarization activated cyclic nucleotide-gated potassium channel 1 | -1.40 | 0.025 |
| GALNTL6 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase-like 6 | -1.40 | 0.017 |
| CXCL14 | chemokine (C-X-C motif) ligand 14 | -1.40 | 0.027 |
| TMEM52B | transmembrane protein 52B | -1.40 | 0.002 |
| STK32B | serine/threonine kinase 32B | -1.40 | 0.010 |
| MIR19A | microRNA 19a | -1.40 | 0.043 |
| GABRG3 | gamma-aminobutyric acid (GABA) A receptor, gamma 3 | -1.40 | 0.033 |
| KIF25 | kinesin family member 25 | -1.39 | 0.010 |
| LOC101749287 | uncharacterized LOC101749287 | -1.39 | 0.041 |
| TPBG | trophoblast glycoprotein | -1.39 | 0.025 |
| METAP1D | methionyl aminopeptidase type 1D (mitochondrial) | -1.39 | 0.016 |
| PHEX | phosphate regulating endopeptidase homolog, X-linked | -1.39 | 0.017 |
| SCRG1 | stimulator of chondrogenesis 1 | -1.39 | 0.017 |
| WWP1 | WW domain containing E3 ubiquitin protein ligase 1 | -1.39 | 0.047 |
| PRSS55 | protease, serine, 55 | -1.39 | 0.004 |
| LOC101751393 | PHD finger protein 7-like | -1.39 | 0.032 |
| SERPINB10 CPOX | serpin peptidase inhibitor, clade B (ovalbumin), member 10 CPOX | -1.39 | 0.021 |
| STEAP1 | six transmembrane epithelial antigen of the prostate 1 | -1.39 | 0.037 |
| AADACL3 | arylacetamide deacetylase-like 4-like | -1.39 | 0.050 |
| AQP12 | aquaporin 12 | -1.38 | 0.026 |
| OVST | ovostatin | -1.38 | 0.033 |
| LTB4R | leukotriene B4 receptor | -1.38 | 0.038 |
| LOC100859756 | scale keratin-like | -1.38 | 0.023 |
| MIR142 | microRNA 142 | -1.38 | 0.009 |
| KBTBD12 | kelch repeat and BTB (POZ) domain containing 12 | -1.38 | 0.001 |
| EGFL6 | EGF-like-domain, multiple 6 | -1.38 | 0.027 |
| CLDN34 | claudin 34 | -1.38 | 0.038 |
| PII5 | peptidase inhibitor 15 | -1.38 | 0.045 |
| NTS | neurotensin | -1.38 | 0.014 |
| ATP6V0D2 | ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit d2 | -1.38 | 0.030 |
| CCDC92 | coiled-coil domain containing 92 | -1.38 | 0.029 |
| LOC428538 | epidermal retinol dehydrogenase 2-like | -1.38 | 0.001 |
| LOC100857916 | scavenger receptor cysteine-rich type 1 protein M130-like | -1.38 | 0.022 |
| RGPD1 | RANBP2-like and GRIP domain containing 1 | -1.38 | 0.033 |
| LOC770649 | nucleophosmin-like | -1.37 | 0.027 |
| PCTP | phosphatidylcholine transfer protein | -1.37 | 0.030 |
| LRTM2 | leucine-rich repeats and transmembrane domains 2 | -1.37 | 0.014 |
| GCM2 | glial cells missing homolog 2 (Drosophila) | -1.37 | 0.029 |
| DLX5 | distal-less homeobox 5 | -1.37 | 0.021 |
| TAL2 | T-cell acute lymphocytic leukemia 2 | -1.37 | 0.016 |
| FAM172BP | family with sequence similarity 172, member B, pseudogene | -1.37 | 0.017 |
| MIR1462 | microRNA mir-1462 | -1.37 | 0.047 |
| NEFH | neurofilament, heavy polypeptide | -1.37 | 0.036 |
| LIN7A | lin-7 homolog A (C. elegans) | -1.37 | 0.050 |
| OC3 | osteocalcin-like protein OC3 | -1.37 | 0.041 |
| GREB1 | growth regulation by estrogen in breast cancer 1 | -1.37 | 0.019 |
| EFHC2 | EF-hand domain (C-terminal) containing 2 | -1.37 | 0.017 |
| MIR383 | microRNA 383 | -1.37 | 0.028 |
| LOC771876 | macrophage mannose receptor 1-like | -1.37 | 0.009 |

| Gene Symbol | Gene Description | FC | p-value |
|----------------|---|-------|---------|
| NME8 | NME/NM23 family member 8 | -1.37 | 0.006 |
| MIR21 | microRNA 21 | -1.36 | 0.020 |
| CTD-2207O23.12 | Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:M0QY47] | -1.36 | 0.026 |
| MIR1570 | microRNA mir-1570 | -1.36 | 0.037 |
| PCYOX1L | prenylcysteine oxidase 1 like | -1.36 | 0.022 |
| MIR206 | microRNA 206 | -1.36 | 0.048 |
| LOC101748060 | uncharacterized LOC101748060 | -1.36 | 0.032 |
| LOC427400 | uncharacterized LOC427400 | -1.36 | 0.037 |
| CHRD12 | chordin-like 2 | -1.36 | 0.012 |
| SPAG1 | sperm associated antigen 1 | -1.36 | 0.022 |
| LOC424727 | structure-specific endonuclease subunit SLX1-like | -1.36 | 0.003 |
| CNTNAP2 | contactin associated protein-like 2 | -1.36 | 0.048 |
| LRRC48 | leucine rich repeat containing 48 | -1.36 | 0.025 |
| EPHA10 | EPH receptor A10 | -1.36 | 0.020 |
| RSPH9 | radial spoke head 9 homolog (Chlamydomonas) | -1.35 | 0.046 |
| RSPH1 | radial spoke head 1 homolog (Chlamydomonas) | -1.35 | 0.044 |
| C4H4ORF45 | chromosome 4 open reading frame, human C4orf45 | -1.35 | 0.024 |
| XG | Xg blood group | -1.35 | 0.019 |
| LOC425001 | uncharacterized LOC425001 | -1.35 | 0.019 |
| C24H11ORF1 | chromosome 24 open reading frame, human C11orf1 | -1.35 | 0.041 |
| SH3RF3 | SH3 domain containing ring finger 3 | -1.35 | 0.002 |
| CRISP2 | cysteine-rich secretory protein 2 | -1.35 | 0.033 |
| KLHL29 | kelch-like family member 29 | -1.35 | 0.014 |
| KIAA0319 | KIAA0319 | -1.35 | 0.043 |
| BLVRA | biliverdin reductase A | -1.35 | 0.008 |
| MIR130B | microRNA 130b | -1.35 | 0.024 |
| LOC420156 | perilipin 3-like | -1.34 | 0.003 |
| MMRN1 | multimerin 1 | -1.34 | 0.026 |
| MYO5C | myosin VC | -1.34 | 0.039 |
| ZNF488 | zinc finger protein 488 | -1.34 | 0.014 |
| TRIP11 | thyroid hormone receptor interactor 11 | -1.34 | 0.013 |
| MOV10L1 | Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse) | -1.34 | 0.039 |
| RAMP1 | receptor (G protein-coupled) activity modifying protein 1 | -1.34 | 0.030 |
| DMC1 | DNA meiotic recombinase 1 | -1.34 | 0.050 |
| TDRD9 | tudor domain containing 9 | -1.34 | 0.039 |
| LOC768596 | uncharacterized LOC768596 | -1.34 | 0.034 |
| LOC101752049 | uncharacterized LOC101752049 | -1.34 | 0.017 |
| MUC2 | mucin 2, oligomeric mucus/gel-forming | -1.34 | 0.050 |
| EPYC | epiphycan | -1.34 | 0.040 |
| ULK4 | unc-51-like kinase 4 (C. elegans) | -1.34 | 0.017 |
| MMEL1 | membrane metallo-endopeptidase-like 1 | -1.34 | 0.048 |
| C1ORF146 | chromosome 8 open reading frame, human C1orf146 | -1.34 | 0.010 |
| MIR1670 | microRNA mir-1670 | -1.34 | 0.036 |
| LOC101749470 | uncharacterized LOC101749470 | -1.33 | 0.018 |
| KRT12 | keratin 12 (Meesmann corneal dystrophy) | -1.33 | 0.009 |
| MSLN1 | mesothelin-like | -1.33 | 0.034 |
| RIBC2 | RIB43A domain with coiled-coils 2 | -1.33 | 0.011 |
| KCNA5 | potassium voltage-gated channel, shaker-related subfamily, member 5 | -1.33 | 0.046 |
| MIR7-2 | microRNA 7-2 | -1.33 | 0.048 |
| ASB14 | ankyrin repeat and SOCS box containing 14 | -1.33 | 0.011 |
| MIR1-1 | microRNA 1-1 | -1.33 | 0.039 |
| SRRL | serine racemase-like | -1.33 | 0.006 |
| CCDC63 | coiled-coil domain containing 63 | -1.33 | 0.016 |

| Gene Symbol | Gene Description | FC | p-value |
|--------------|--|-------|---------|
| GKN2 | gastrokine 2 | -1.33 | 0.002 |
| LOC425462 | malignant fibrous histiocytoma-amplified sequence 1 homolog | -1.33 | 0.017 |
| C10ORF112 | chromosome 2 open reading frame, human C10orf112 | -1.33 | 0.004 |
| RSPH4A | radial spoke head 4 homolog A (Chlamydomonas) | -1.33 | 0.003 |
| KIAA1456 | KIAA1456 | -1.33 | 0.021 |
| C6orf58 | chromosome 6 open reading frame 58 | -1.32 | 0.014 |
| FAM19A1 | family with sequence similarity 19 (chemokine (C-C motif)-like), member A1 | -1.32 | 0.041 |
| RIPPLY2 | rippy transcriptional repressor 2 | -1.32 | 0.040 |
| SHISA6 | shisa homolog 6 (Xenopus laevis) | -1.32 | 0.024 |
| LOC421856 | uncharacterized LOC421856 | -1.32 | 0.032 |
| LOC101751334 | phosphoglucomutase-like protein 5-like | -1.32 | 0.048 |
| FIBCD1 | fibrinogen C domain containing 1 | -1.32 | 0.046 |
| LOC423277 | galectin-related protein-like | -1.32 | 0.025 |
| PIGQ | phosphatidylinositol glycan anchor biosynthesis, class Q | -1.32 | 0.043 |
| MIR92A1 | microRNA 92a-1 | -1.32 | 0.008 |
| PAQR9 | progesterin and adipoQ receptor family member IX | -1.32 | 0.013 |
| PPP1R3B | protein phosphatase 1, regulatory subunit 3B | -1.32 | 0.029 |
| CCDC83 | coiled-coil domain containing 83 | -1.31 | 0.046 |
| ADGB | androglobin | -1.31 | 0.006 |
| CRYBB1 | crystallin, beta B1 | -1.31 | 0.032 |
| MIR490 | microRNA 490 | -1.31 | 0.046 |
| KCNJ6 | potassium inwardly-rectifying channel, subfamily J, member 6 | -1.31 | 0.037 |
| AVPR2 | arginine vasopressin receptor 2 | -1.31 | 0.005 |
| LOC100858320 | protein eyes shut homolog | -1.31 | 0.007 |
| MIR429 | microRNA 429 | -1.31 | 0.028 |
| MORN3 | MORN repeat containing 3 | -1.31 | 0.039 |
| COMMD3 | COMM domain containing 3 | -1.31 | 0.003 |
| NHEDC2 | Na ⁺ /H ⁺ exchanger domain containing 2 | -1.31 | 0.021 |
| NEK11 | NIMA-related kinase 11 | -1.31 | 0.035 |
| STK17A | serine/threonine kinase 17a | -1.31 | 0.017 |
| PLIN1 | perilipin 1 | -1.31 | 0.020 |
| LOC100858427 | feather keratin Cos1-1/Cos1-3/Cos2-1-like | -1.31 | 0.015 |
| GGT7 | gamma-glutamyltransferase 7 | -1.31 | 0.021 |
| KAZALD1 | Kazal-type serine peptidase inhibitor domain 1 | -1.31 | 0.014 |
| EBF3 | early B-cell factor 3 | -1.31 | 0.037 |
| CCDC148 | coiled-coil domain containing 148 | -1.31 | 0.006 |
| LOC415312 | uncharacterized LOC415312 | -1.31 | 0.024 |
| LOC101748152 | uncharacterized LOC101748152 | -1.31 | 0.041 |
| CYP26B1 | cytochrome P450, family 26, subfamily B, polypeptide 1 | -1.31 | 0.038 |
| NSUN7 | NOP2/Sun domain family, member 7 | -1.31 | 0.001 |
| LOC100859545 | potassium channel subfamily K member 9-like | -1.31 | 0.048 |
| LOC427778 | ectonucleoside triphosphate diphosphohydrolase 1 | -1.31 | 0.043 |
| VSTM4 | V-set and transmembrane domain containing 4 | -1.31 | 0.010 |
| LOC101749925 | uncharacterized LOC101749925 | -1.30 | 0.030 |
| LOC101750580 | uncharacterized LOC101750580 | -1.30 | 0.037 |
| LOC101748060 | uncharacterized LOC101748060 | -1.30 | 0.002 |
| CEP57L1 | centrosomal protein 57kDa-like 1 | -1.30 | 0.047 |
| FBXO43 | F-box protein 43 | -1.30 | 0.041 |
| DZANK1 | double zinc ribbon and ankyrin repeat domains 1 | -1.30 | 0.004 |
| MIR1789 | microRNA mir-1789 | -1.30 | 0.040 |
| TMEM150A | transmembrane protein 150A | -1.30 | 0.020 |
| LOC100857840 | disintegrin and metalloproteinase domain-containing protein 21-like | -1.30 | 0.017 |
| LOC422353 | synaptotagmin-like protein 2-like | -1.30 | 0.021 |

| Gene Symbol | Gene Description | FC | p-value |
|--------------------|---|-------|---------|
| MIR1658 | microRNA mir-1658 | -1.30 | 0.034 |
| LOC427491 | C2 calcium-dependent domain containing 4C-like | -1.30 | 0.048 |
| B3GNTL2 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 2 | -1.30 | 0.033 |
| PIK3C2G | phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma | -1.30 | 0.025 |
| SLC5A12 | solute carrier family 5 (sodium/monocarboxylate cotransporter), member 12 | -1.30 | 0.007 |
| LOC421298 | ankyrin repeat domain-containing protein 9-like | -1.30 | 0.021 |
| LOC769834 | trophoblast glycoprotein-like | -1.30 | 0.037 |
| FYTTD1L | forty-two-three domain containing 1-like | -1.30 | 0.017 |
| AGTR1 | angiotensin II receptor, type 1 | -1.30 | 0.001 |
| KCNH7 | potassium voltage-gated channel, subfamily H (eag-related), member 7 | -1.30 | 0.024 |
| <i>Upregulated</i> | | | |
| BG2 | intestinal zipper protein | 3.75 | 0.010 |
| KPNA2 | karyopherin alpha 2 (RAG cohort 1, importin alpha 1) | 2.58 | 0.018 |
| DDX60 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 | 2.28 | 0.047 |
| SMC2 | structural maintenance of chromosomes 2 | 2.23 | 0.035 |
| CDK1 | cyclin-dependent kinase 1 | 2.08 | 0.038 |
| TOP2A | topoisomerase (DNA) II alpha 170kDa | 2.07 | 0.045 |
| ASPM | asp (abnormal spindle) homolog, microcephaly associated (Drosophila) | 1.92 | 0.025 |
| CCNB2 | cyclin B2 | 1.88 | 0.038 |
| GLCCI1 | glucocorticoid induced transcript 1 | 1.78 | 0.018 |
| TACC3 | transforming, acidic coiled-coil containing protein 3 | 1.70 | 0.021 |
| HIST1H46L2 | histone cluster 1, H4-IV, germinal H4-like 2 (similar to human histone cluster 1, class H4 genes) | 1.68 | 0.013 |
| STMN1 | stathmin 1 | 1.67 | 0.021 |
| HIST1H2B7 | histone cluster 1, H2B-VII (similar to human histone cluster 1, class H2B, member N) | 1.66 | 0.032 |
| HIST1H2B7L2 | histone cluster 1, H2B-VII-like 2 (similar to human histone cluster 1, class H2B, member N) | 1.66 | 0.032 |
| MOV10 | Mov10, Moloney leukemia virus 10, homolog (mouse) | 1.64 | 0.036 |
| CRHR2 | corticotropin releasing hormone receptor 2 | 1.64 | 0.036 |
| KIF14 | kinesin family member 14 | 1.62 | 0.005 |
| IRF8 | interferon regulatory factor 8 | 1.62 | 0.019 |
| HIST1H2BO | histone cluster 1, H2bo | 1.62 | 0.049 |
| DIAPH3 | diaphanous-related formin 3 | 1.61 | 0.043 |
| SPP1 | secreted phosphoprotein 1 | 1.61 | 0.011 |
| ICOS | inducible T-cell co-stimulator | 1.59 | 0.014 |
| NCAPG | non-SMC condensin I complex, subunit G | 1.58 | 0.042 |
| SMC4 | structural maintenance of chromosomes 4 | 1.57 | 0.041 |
| HIST1H2A4L2 | histone cluster 1, H2A-IV-like 2 (similar to human histone cluster 2, class H2A, member C) | 1.57 | 0.035 |
| LOC101749238 | histone H2A-IV-like | 1.56 | 0.043 |
| HIST1H2A4L2 | histone cluster 1, H2A-IV-like 2 (similar to human histone cluster 2, class H2A, member C) | 1.56 | 0.045 |
| HIST1H2A3 | histone cluster 1, H2A, III (similar to human histone cluster 2, class H2A, member C) | 1.56 | 0.045 |
| RAD51 | RAD51 recombinase | 1.55 | 0.022 |
| HIST1H2A4 | histone cluster 1, H2A, IV (similar to human histone cluster 2, class H2A, member C) | 1.55 | 0.048 |
| PRPSAP2 | phosphoribosyl pyrophosphate synthetase-associated protein 2 | 1.55 | 0.001 |
| TSPAN8 | tetraspanin 8 | 1.55 | 0.016 |
| HIST1H2A4L3 | histone cluster 1, H2A-IV-like 3 (similar to human histone cluster 2, class H2A, member C) | 1.54 | 0.046 |
| KIF23 | kinesin family member 23 | 1.52 | 0.023 |
| C11ORF34 | chromosome 24 open reading frame, human C11orf34 | 1.52 | 0.008 |
| SNORD12C | small nucleolar RNA, C/D box 12C | 1.51 | 0.005 |
| SLC41A2 | solute carrier family 41, member 2 | 1.50 | 0.032 |

| Gene Symbol | Gene Description | FC | p-value |
|--------------|---|------|---------|
| SIDT1 | SID1 transmembrane family, member 1 | 1.50 | 0.025 |
| DOCK9 | dedicator of cytokinesis 9 | 1.50 | 0.049 |
| PCNA | proliferating cell nuclear antigen | 1.49 | 0.037 |
| MIR1596 | microRNA mir-1596 | 1.49 | 0.040 |
| ACTR3 | ARP3 actin-related protein 3 homolog (yeast) | 1.49 | 0.026 |
| TYMS | thymidylate synthetase | 1.47 | 0.050 |
| LOC100858439 | keratin, type I cytoskeletal 14-like | 1.46 | 0.041 |
| USH1C | Usher syndrome 1C (autosomal recessive, severe) | 1.45 | 0.014 |
| HELLS | helicase, lymphoid-specific | 1.44 | 0.044 |
| LGALS8 | lectin, galactoside-binding, soluble, 8 | 1.43 | 0.004 |
| SYNGR3 | synaptogyrin 3 | 1.43 | 0.039 |
| CTD-2370N5.3 | Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:J3QR06] | 1.43 | 0.002 |
| RFK | riboflavin kinase | 1.43 | 0.008 |
| TMEM41B | transmembrane protein 41B | 1.43 | 0.019 |
| CERS6 | ceramide synthase 6 | 1.43 | 0.030 |
| SNORD20 | small nucleolar RNA, C/D box 20 | 1.43 | 0.033 |
| SDC1 | syndecan 1 | 1.43 | 0.030 |
| ADH6 | alcohol dehydrogenase 6 (class V) | 1.42 | 0.027 |
| BUB3 | BUB3 mitotic checkpoint protein | 1.42 | 0.034 |
| MIR199B | microRNA mir-199b | 1.42 | 0.024 |
| HMGB2 | high mobility group box 2 | 1.42 | 0.046 |
| THYN1 | thymocyte nuclear protein 1 | 1.42 | 0.027 |
| DEK | DEK proto-oncogene | 1.41 | 0.008 |
| CERS1 | ceramide synthase 1 | 1.40 | 0.049 |
| HIST1H11L | histone cluster 1, H1.11L (similar to human histone cluster 1, class H1 genes) | 1.40 | 0.038 |
| ACE2 | angiotensin I converting enzyme 2 | 1.40 | 0.033 |
| HN1 | hematological and neurological expressed 1 | 1.40 | 0.012 |
| BFAR | bifunctional apoptosis regulator | 1.39 | 0.010 |
| LDHA | lactate dehydrogenase A | 1.39 | 0.015 |
| DUSP5 | dual specificity phosphatase 5 | 1.39 | 0.023 |
| CAPSL | calcyphosine-like | 1.39 | 0.022 |
| LGALS2 | lectin, galactoside-binding, soluble, 2 | 1.39 | 0.024 |
| H2AFZ | H2A histone family, member Z | 1.39 | 0.030 |
| PTMA | prothymosin, alpha | 1.39 | 0.047 |
| KCNMA1 | potassium large conductance calcium-activated channel, subfamily M, alpha member 1 | 1.38 | 0.013 |
| DSTN | destrin (actin depolymerizing factor) | 1.38 | 0.042 |
| PSEN1 | presenilin 1 | 1.38 | 0.033 |
| HMGN2 | high mobility group nucleosomal binding domain 2 | 1.38 | 0.016 |
| SWAP70 | SWAP switching B-cell complex 70kDa subunit | 1.38 | 0.020 |
| SOCs1 | suppressor of cytokine signaling 1 | 1.37 | 0.032 |
| HMGN5 | high mobility group nucleosome binding domain 5 | 1.37 | 0.046 |
| RRM1 | ribonucleotide reductase M1 | 1.36 | 0.049 |
| RAD21 | RAD21 cohesin complex component | 1.36 | 0.036 |
| TRAF3 | TNF receptor-associated factor 3 | 1.35 | 0.032 |
| CDC20 | cell division cycle 20 | 1.35 | 0.009 |
| MRPS18C | mitochondrial ribosomal protein S18C | 1.35 | 0.031 |
| ACP1 | acid phosphatase 1, soluble | 1.35 | 0.018 |
| CD82 | CD82 molecule | 1.35 | 0.029 |
| PTMS | parathymosin | 1.34 | 0.031 |
| LOC101751423 | uncharacterized LOC101751423 | 1.34 | 0.009 |
| SLC25A29 | solute carrier family 25 (mitochondrial carnitine/acylcarnitine carrier), member 29 | 1.34 | 0.034 |
| DSG2 | desmoglein 2 | 1.34 | 0.026 |

| Gene Symbol | Gene Description | FC | p-value |
|-------------|--|------|---------|
| KITLG | KIT ligand | 1.34 | 0.020 |
| UVRAG | UV radiation resistance associated | 1.34 | 0.049 |
| CXADR | coxsackie virus and adenovirus receptor | 1.34 | 0.023 |
| TRIM13 | tripartite motif containing 13 | 1.34 | 0.000 |
| MTPN | myotrophin | 1.33 | 0.008 |
| ANXA5 | annexin A5 | 1.33 | 0.035 |
| MTFR2 | mitochondrial fission regulator 2 | 1.33 | 0.036 |
| IDH3A | isocitrate dehydrogenase 3 (NAD+) alpha | 1.33 | 0.029 |
| DNA2 | DNA replication helicase/nuclease 2 | 1.33 | 0.029 |
| ABCB1LB | ATP-binding cassette, sub-family B (MDR/TAP), member 1-like B | 1.33 | 0.041 |
| COMT | catechol-O-methyltransferase | 1.33 | 0.032 |
| C4H4ORF29 | chromosome 4 open reading frame, human C4orf29 | 1.33 | 0.026 |
| PKHD1 | polycystic kidney and hepatic disease 1 (autosomal recessive) | 1.33 | 0.032 |
| DYNLRB2 | dynein, light chain, roadblock-type 2 | 1.32 | 0.010 |
| HPGDS | hematopoietic prostaglandin D synthase | 1.32 | 0.006 |
| MLXIP | MLX interacting protein | 1.32 | 0.033 |
| DCAF5 | DDB1 and CUL4 associated factor 5 | 1.32 | 0.035 |
| PRKAR2A | protein kinase, cAMP-dependent, regulatory, type II, alpha | 1.32 | 0.003 |
| RRAGB | Ras-related GTP binding B | 1.31 | 0.032 |
| TMEM229B | transmembrane protein 229B | 1.31 | 0.026 |
| FANCD2 | Fanconi anemia, complementation group D2 | 1.31 | 0.030 |
| STARD3NL | STARD3 N-terminal like | 1.31 | 0.020 |
| LBR | lamin B receptor | 1.31 | 0.012 |
| CAP1 | CAP, adenylate cyclase-associated protein 1 (yeast) | 1.31 | 0.026 |
| DENND1B | DENN/MADD domain containing 1B | 1.30 | 0.018 |
| ALDH1A1 | aldehyde dehydrogenase 1 family, member A1 | 1.30 | 0.024 |
| OAZ1 | ornithine decarboxylase antizyme 1 | 1.30 | 0.023 |
| TMBIM4 | transmembrane BAX inhibitor motif containing 4 [Source:EntrezGene;Acc:51643] | 1.30 | 0.033 |
| CRYBG3 | beta-gamma crystallin domain containing 3 | 1.30 | 0.037 |

¹ Microarray fold changes were calculated from n = 6 animals/group.