

Table 1: 60 upregulated and 65 downregulated differentially expressed genes are annotated.

| Gene ID | M1 (FPKM) | M2 (FPKM) | log2 (FC) | P-value | Gene symbol | Regulation | Annotation |
|--------------|-----------|-----------|-----------|----------|-------------|------------|--|
| gene_250784 | 0.001 | 21.11 | 14.3656 | 3.41E-07 | RPS4Y1 | Up | ribosomal protein S4 Y-linked 1 |
| gene_268059 | 0.001 | 2.18667 | 11.0945 | 5.92E-05 | PML | Up | promyelocytic leukemia |
| gene_270861 | 0.001 | 1.27 | 10.3106 | 7.52E-06 | PLK4 | Up | polo like kinase 4 |
| gene_282701 | 0.01333 | 1.06333 | 6.31741 | 2.60E-05 | BMP3 | Up | bone morphogenetic protein 3 |
| gene_299440 | 0.21 | 5.81667 | 4.79173 | 1.20E-11 | RAG1 | Up | recombination activating 1 |
| gene_0309042 | 0.00667 | 4.3 | 9.33316 | 8.95E-07 | REST | Up | RE1 silencing transcription factor |
| gene_311469 | 0.001 | 5.60333 | 12.4521 | 3.30E-05 | COQ2 | Up | coenzyme Q2, polyprenyltransferase |
| gene_311485 | 0.02333 | 4.42333 | 7.5666 | 9.83E-08 | RAG2 | Up | recombination activating 2 |
| gene_317961 | 0.001 | 19.2733 | 14.2343 | 1.58E-08 | KDM5D | Up | lysine demethylase 5D |
| gene_329134 | 0.001 | 6.76667 | 12.7242 | 2.69E-07 | UTY | Up | ubiquitously transcribed tetratricopeptide repeat containing, Y-linked |
| gene_336079 | 0.00333 | 19.3933 | 12.5063 | 7.12E-08 | DDX3Y | Up | DEAD-box helicase 3 Y-linked |
| gene_338981 | 0.001 | 5.49 | 12.4226 | 5.14E-08 | USP9Y | Up | ubiquitin specific peptidase 9 Y-linked |
| gene_356427 | 0.001 | 1.34 | 10.388 | 6.73E-06 | ATF7IP2 | Up | activating transcription factor 7 interacting protein 2 |
| gene_359649 | 0.001 | 2.38 | 11.2168 | 9.71E-06 | OSCAR | Up | osteoclast associated, immunoglobulin-like receptor |
| gene_360726 | 0.001 | 1.63333 | 10.6736 | 7.13E-05 | PAQR8 | Up | progesterin and adipoQ receptor family member 8 |
| gene_361059 | 0.001 | 1.13667 | 10.1506 | 5.46E-06 | MATR3 | Up | matrin 3 |
| gene_361365 | 0.001 | 7.92667 | 12.9525 | 1.59E-05 | EIF1AY | Up | eukaryotic translation initiation factor 1A Y-linked |
| gene_362096 | 0.001 | 5.68667 | 12.4734 | 3.04E-07 | UTY | Up | ubiquitously transcribed tetratricopeptide repeat containing, Y-linked |
| gene_368873 | 0.001 | 3.21333 | 11.6499 | 2.01E-09 | PI4KB | Up | phosphatidylinositol 4-kinase beta |
| gene_371174 | 1.49 | 17.2467 | 3.53293 | 6.95E-08 | DNTT | Up | DNA nucleotidyltransferase |
| gene_372189 | 0.001 | 2.32667 | 11.1841 | 1.02E-05 | RAPGEF1 | Up | Rap guanine nucleotide exchange factor 1 |
| gene_382896 | 0.001 | 1.30667 | 10.3517 | 5.28E-05 | UTY | Up | ubiquitously transcribed tetratricopeptide repeat containing, Y-linked |
| gene_383052 | 0.001 | 1.79333 | 10.8084 | 3.75E-05 | ZFY | Up | zinc finger protein Y-linked |
| gene_415496 | 0.001 | 1.23 | 10.2644 | 3.03E-07 | MGRN1 | Up | mahogunin ring finger 1 |
| gene_420027 | 0.001 | 6.02333 | 12.5564 | 3.21E-05 | UBE2V1 | Up | ubiquitin conjugating enzyme E2 V1 |
| gene_422452 | 0.001 | 0.49333 | 8.94642 | 2.78E-07 | TENM1 | Up | teneurin transmembrane protein 1 |
| gene_430575 | 0.02 | 64.2767 | 11.6501 | 2.01E-07 | RPS4Y1 | Up | ribosomal protein S4 Y-linked 1 |
| gene_447204 | 0.001 | 3.22 | 11.6528 | 4.06E-05 | TMEM176B | Up | transmembrane protein 176B |
| gene_521604 | 0.001 | 8.37 | 13.031 | 6.08E-07 | TCEA1 | Up | transcription elongation factor A1 |
| gene_530853 | 0.001 | 1.25667 | 10.2954 | 5.85E-07 | NIN | Up | ninein |
| gene_539144 | 0.001 | 2.03333 | 10.9896 | 9.41E-06 | NLRC5 | Up | NLR family CARD domain containing 5 |
| gene_619294 | 0.001 | 0.98667 | 9.94642 | 5.67E-06 | BCL2L11 | Up | BCL2 like 11 |
| gene_624098 | 0.001 | 2.42333 | 11.2428 | 1.30E-05 | UTY | Up | ubiquitously transcribed tetratricopeptide repeat containing, Y-linked |
| gene_624995 | 0.001 | 7.38 | 12.8494 | 7.62E-07 | SLC27A3 | Up | solute carrier family 27 member 3 |
| gene_645237 | 0.001 | 1.50333 | 10.554 | 4.19E-05 | ABCC4 | Up | ATP binding cassette subfamily C member 4 |
| gene_649336 | 0.01 | 2.75 | 8.10329 | 7.78E-05 | EPG5 | Up | ectopic P-granules autophagy protein 5 homolog |

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|-------------|---------|---------|---------|----------|----------|------|--|
| gene_3463 | 0.001 | 1.60333 | 10.6469 | 1.29E-05 | AGL | Up | BAD92104.1 amylo-1,6-glucosidase, 4-alpha-glucanotransferase isoform 1 variant, partial |
| gene_5160 | 0.001 | 0.76 | 9.56986 | 1.05E-07 | - | Up | XP_016805049.1 PREDICTED: SLAM family member 5-like |
| gene_16229 | 0.001 | 0.42333 | 8.72565 | 4.60E-05 | BMS1 | Up | XP_016773683.1 PREDICTED: ribosome biogenesis protein BMS1 homolog |
| gene_16521 | 0.001 | 0.29333 | 8.1964 | 1.27E-05 | TET1 | Up | NP_085128.2 methylcytosine dioxygenase TET1 |
| gene_25497 | 0.001 | 0.80667 | 9.65583 | 4.79E-06 | NCAM1 | Up | XP_018892340.1 PREDICTED: neural cell adhesion molecule 1 isoform X18 |
| gene_27189 | 0.00333 | 5.01 | 10.5536 | 6.62E-06 | EIF4G2 | Up | XP_017703410.1 PREDICTED: eukaryotic translation initiation factor 4 gamma 2, partial |
| gene_49331 | 0.001 | 1.67333 | 10.7085 | 7.43E-05 | HERC2 | Up | BAA20846.2 KIAA0393 protein, partial |
| gene_62599 | 0.001 | 1.2 | 10.2288 | 1.65E-05 | ANKRD11 | Up | NP_037407.4 ankyrin repeat domain-containing protein 11 |
| gene_70098 | 0.001 | 1.60333 | 10.6469 | 1.73E-06 | ITGA2B | Up | XP_011523052.1 PREDICTED: integrin alpha-IIb isoform X2 |
| gene_72837 | 0.001 | 0.98333 | 9.94154 | 9.00E-09 | LDLRAD4 | Up | NP_852146.1 low-density lipoprotein receptor class A domain-containing protein 4 isoform alpha 1 |
| gene_74149 | 0.001 | 2.95333 | 11.5281 | 2.14E-05 | ZBTB14 | Up | XP_012882653.1 PREDICTED: zinc finger and BTB domain-containing protein 14 |
| gene_74162 | 0.00333 | 2.26 | 9.40514 | 1.59E-08 | Epb4113 | Up | XP_016881117.1 PREDICTED: band 4.1-like protein 3 isoform X15 |
| gene_81082 | 0.001 | 3.58667 | 11.8084 | 3.53E-14 | AP3D1 | Up | NP_003929.4 AP-3 complex subunit delta-1 isoform 2 |
| gene_81799 | 0.001 | 2.97333 | 11.5379 | 8.70E-06 | TYK2 | Up | NP_003322.3 non-receptor tyrosine-protein kinase TYK2 |
| gene_87092 | 0.001 | 1.06667 | 10.0589 | 7.78E-05 | PAPOLG | Up | XP_005264557.1 PREDICTED: poly(A) polymerase gamma isoform X1 |
| gene_103068 | 0.001 | 0.96667 | 9.91688 | 8.15E-05 | MX2 | Up | NP_002454.1 interferon-induced GTP-binding protein Mx2 |
| gene_105593 | 0.00667 | 2.44333 | 8.51767 | 3.43E-08 | HMGXB4 | Up | XP_006724165.1 PREDICTED: HMG domain-containing protein 4 isoform X3 |
| gene_115118 | 0.001 | 0.54667 | 9.09452 | 1.68E-05 | PBRM1 | Up | XP_016862253.1 PREDICTED: protein polybromo-1 isoform X27 |
| gene_136880 | 0.001 | 1.45333 | 10.5052 | 7.77E-06 | Qki | Up | NP_001288014.1 protein quaking isoform 5 |
| gene_138503 | 0.001 | 1.84 | 10.8455 | 2.19E-07 | SLC26A8 | Up | NP_443193.1 testis anion transporter 1 isoform a |
| gene_147879 | 0.001 | 3.11667 | 11.6058 | 2.37E-13 | RASA4 | Up | NP_001073346.2 ras GTPase-activating protein 4 isoform 2 |
| gene_152552 | 0.001 | 0.86667 | 9.75933 | 1.18E-10 | Pol | Up | XP_016814018.1 PREDICTED: tubulin beta chain-like isoform X1 |
| gene_168120 | 0.001 | 7.72333 | 12.915 | 2.47E-07 | TXLNG | Up | BAG64458.1 unnamed protein product |
| gene_168126 | 0.00333 | 5.04667 | 10.5642 | 1.80E-06 | TXLNG | Up | AAK13477.1 lipopolysaccharide-specific response 5-like protein |
| gene_357266 | 109.92 | 34.49 | -1.6722 | 7.57E-05 | FKBP5 | Down | FK506 binding protein 5 |
| gene_354903 | 27.9033 | 5.62 | -2.3118 | 2.78E-06 | PER1 | Down | period circadian regulator 1 |
| gene_268704 | 2.14 | 0.001 | -11.063 | 2.33E-07 | SPG7 | Down | SPG7, paraplegin matrix AAA peptidase subunit |
| gene_271850 | 13.68 | 0.001 | -13.74 | 1.97E-05 | TPM3 | Down | tropomyosin 3 |
| gene_298552 | 0.99667 | 0.001 | -9.961 | 8.07E-05 | TSC1 | Down | TSC complex subunit 1 |
| gene_307659 | 1.94667 | 0.001 | -10.927 | 3.77E-06 | KIAA0232 | Down | KIAA0232 |
| gene_317276 | 63.9567 | 9.84333 | -2.6999 | 3.27E-08 | PER1 | Down | period circadian regulator 1 |
| gene_332549 | 9.61333 | 0.38667 | -4.6359 | 3.70E-07 | IL1R2 | Down | interleukin 1 receptor type 2 |
| gene_334204 | 0.72667 | 0.001 | -9.5052 | 5.54E-05 | KIF27 | Down | kinesin family member 27 |
| gene_335953 | 23.9633 | 4.51 | -2.4096 | 9.21E-06 | ZBTB16 | Down | zinc finger and BTB domain containing 16 |
| gene_370069 | 1.69 | 0.001 | -10.723 | 2.45E-07 | GMEB2 | Down | glucocorticoid modulatory element binding protein 2 |
| gene_377126 | 38.5733 | 7.37 | -2.3879 | 9.13E-08 | KLF9 | Down | Kruppel like factor 9 |
| gene_381930 | 2.89667 | 0.001 | -11.5 | 3.13E-05 | KLHL5 | Down | kelch like family member 5 |

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| gene_395211 | 3.20667 | 0.001 | -11.647 | 2.06E-09 | TMOD1 | Down | tropomodulin 1 |
| gene_395748 | 86.6067 | 3.43 | -4.6582 | 4.67E-08 | AREG | Down | amphiregulin |
| gene_396663 | 17.2267 | 3.38667 | -2.3467 | 1.81E-05 | ARL4A | Down | ADP ribosylation factor like GTPase 4A |
| gene_397488 | 1.02333 | 0.001 | -9.9991 | 2.21E-05 | BAIAP3 | Down | BAI1 associated protein 3 |
| gene_404875 | 1.23667 | 0.001 | -10.272 | 3.94E-05 | POMT1 | Down | protein O-mannosyltransferase 1 |
| gene_404894 | 5.26667 | 0.001 | -12.363 | 4.42E-06 | ARL4A | Down | ADP ribosylation factor like GTPase 4A |
| ENST00000408974 | 5.2 | 0.001 | -12.344 | 3.87E-12 | DNM2 | Down | dynamain 2 |
| gene_434651 | 22.7533 | 1.21333 | -4.229 | 3.40E-06 | HLA-DQB1 | Down | major histocompatibility complex, class II, DQ beta 1 |
| gene_475248 | 236.283 | 45.6533 | -2.3717 | 2.10E-07 | RPL29 | Down | ribosomal protein L29 |
| gene_491737 | 2.78333 | 0.001 | -11.443 | 8.72E-06 | THOC2 | Down | THO complex 2 |
| gene_517856 | 13.01 | 2.58 | -2.3342 | 2.09E-06 | ASPH | Down | aspartate beta-hydroxylase |
| gene_539778 | 4.22 | 0.001 | -12.043 | 2.62E-05 | CMIP | Down | c-Maf inducing protein |
| gene_541864 | 1.40333 | 0.00667 | -7.7177 | 6.63E-06 | SLC12A4 | Down | solute carrier family 12 member 4 |
| gene_542180 | 1.93 | 0.001 | -10.914 | 2.51E-06 | SUPT20H | Down | SPT20 homolog, SAGA complex component |
| gene_542713 | 30.7567 | 4.29 | -2.8419 | 1.86E-09 | FKBP5 | Down | FK506 binding protein 5 |
| gene_545232 | 1.53 | 0.001 | -10.579 | 2.02E-06 | UHRF1BP1L | Down | UHRF1 binding protein 1 like |
| gene_584202 | 82.4467 | 11.8133 | -2.8031 | 2.32E-06 | PER1 | Down | period circadian regulator 1 |
| gene_614420 | 1.14 | 0.00333 | -8.4179 | 8.96E-05 | KIAA1191 | Down | KIAA1191 |
| gene_614697 | 2.23333 | 0.001 | -11.125 | 6.70E-05 | ZBTB14 | Down | zinc finger and BTB domain containing 14 |
| gene_618172 | 3.9 | 0.001 | -11.929 | 3.61E-10 | DDX27 | Down | DEAD-box helicase 27 |
| gene_619035 | 196.567 | 17.2533 | -3.5101 | 2.07E-05 | TNFAIP3 | Down | TNF alpha induced protein 3 |
| gene_619700 | 5.09667 | 0.001 | -12.315 | 7.66E-05 | GLIPR2 | Down | GLI pathogenesis related 2 |
| gene_621318 | 2.83 | 0.001 | -11.467 | 7.75E-05 | MCM7 | Down | minichromosome maintenance complex component 7 |
| gene_646596 | 1.26 | 0.001 | -10.299 | 8.89E-06 | SLC19A2 | Down | solute carrier family 19 member 2 |
| gene_648462 | 3.98 | 0.001 | -11.959 | 8.76E-07 | IMPDH1 | Down | inosine monophosphate dehydrogenase 1 |
| gene_648685 | 5.48667 | 0.001 | -12.422 | 1.06E-06 | ITGAM | Down | integrin subunit alpha M |
| gene_649979 | 2.89667 | 0.001 | -11.5 | 1.99E-05 | IFIH1 | Down | interferon induced with helicase C domain 1 |
| gene_1716 | 1.86667 | 0.00333 | -9.1293 | 8.15E-06 | AGO3 | Down | NP_079128.2 protein argonaute-3 isoform a |
| gene_7694 | 1.35333 | 0.001 | -10.402 | 1.59E-05 | NLRP3 | Down | NP_899632.1 NACHT, LRR and PYD domains-containing protein 3 isoform b |
| gene_24569 | 0.83 | 0.001 | -9.697 | 7.21E-06 | RELT | Down | XP_011900306.1 PREDICTED: tumor necrosis factor receptor superfamily member 19L isoform X1 |
| gene_29324 | 3.08667 | 0.001 | -11.592 | 1.79E-06 | NUMA1 | Down | XP_011543367.1 PREDICTED: nuclear mitotic apparatus protein 1 isoform X2 [Homo sapiens] |
| gene_31630 | 1.46667 | 0.001 | -10.518 | 2.22E-05 | CLSTN3 | Down | NP_055533.2 calyntenin-3 precursor |
| gene_53378 | 1.13667 | 0.001 | -10.151 | 2.36E-05 | RFX7 | Down | XP_005254660.2 PREDICTED: DNA-binding protein RFX7 isoform X1 |
| gene_54225 | 1.04667 | 0.00333 | -8.2946 | 1.18E-05 | SIN3A | Down | XP_016782697.1 PREDICTED: paired amphipathic helix protein Sin3a isoform X1 |
| gene_58683 | 1.51333 | 0.001 | -10.564 | 2.90E-06 | CRISPLD2 | Down | NP_113664.1 cysteine-rich secretory protein LCCL domain-containing 2 precursor |
| gene_59134 | 0.76 | 0.001 | -9.5699 | 8.21E-05 | IL9R | Down | XP_011755064.1 PREDICTED: interleukin-9 receptor-like |
| gene_64012 | 0.63 | 0.001 | -9.2992 | 1.42E-07 | SARM1 | Down | XP_008008963.1 PREDICTED: sterile alpha and TIR motif-containing protein 1 |
| gene_69199 | 1.21333 | 0.001 | -10.245 | 7.20E-05 | SLFN14 | Down | NP_001123292.1 protein SLFN14 |
| gene_71099 | 5.78 | 0.001 | -12.497 | 8.82E-05 | DDX5 | Down | XP_010378302.1 PREDICTED: probable ATP-dependent RNA helicase DDX5 isoform X2 |
| gene_74678 | 1.19667 | 0.001 | -10.225 | 5.13E-07 | ZNF24 | Down | NP_001295052.1 zinc finger protein 24 isoform 2 |
| gene_79669 | 1.7 | 0.001 | -10.731 | 2.00E-08 | PRR12 | Down | BAA86519.1 KIAA1205 protein, partial |
| gene_88185 | 54.98 | 2.90667 | -4.2415 | 8.11E-08 | IL1R2 | Down | XP_011510105.1 PREDICTED: interleukin-1 receptor type 2 isoform X3 |
| gene_95320 | 0.92333 | 0.001 | -9.8507 | 1.38E-06 | ANAPC1 | Down | NP_073153.1 anaphase-promoting complex subunit 1 |

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|-------------|---------|---------|---------|----------|--------|------|--|
| gene_98429 | 0.57333 | 0.001 | -9.1632 | 2.85E-05 | ZNF714 | Down | EAW50338.1 hCG1818014, partial |
| gene_112565 | 0.50667 | 0.001 | -8.9849 | 4.47E-05 | PIK3CA | Down | XP_010372245.1 PREDICTED: phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform |
| gene_115971 | 1.57667 | 0.001 | -10.623 | 5.16E-05 | CD47 | Down | XP_005247965.1 PREDICTED: leukocyte surface antigen CD47 isoform X1 |
| gene_116248 | 1.44 | 0.001 | -10.492 | 1.02E-05 | GOLGB1 | Down | XP_006713654.1 PREDICTED: golgin subfamily B member 1 isoform X11 |
| gene_119869 | 39.0267 | 2.48333 | -3.9741 | 6.47E-09 | AREG | Down | XP_005965713.1 PREDICTED: amphiregulin-like isoform X1 |
| gene_131101 | 0.28333 | 0.001 | -8.1464 | 7.50E-05 | - | Down | EAW49052.1 hCG2028242, partial |
| gene_133404 | 1.32667 | 0.001 | -10.374 | 5.07E-06 | CD83 | Down | NP_004224.1 CD83 antigen isoform a precursor |
| gene_138115 | 2.35667 | 0.001 | -11.203 | 8.91E-08 | DDAH2 | Down | ERE88825.1 N(G), N(G)-dimethylarginine dimethylaminohydrolase 2-like isoform 1 |
| gene_166902 | 1.60333 | 0.001 | -10.647 | 2.03E-14 | ZMAT1 | Down | EAX02898.1 hCG2039319, partial |
| ≥ 50 | ≥ 50 | ≥ 50 | ≥ 50 | ≥ 50 | ≥ 50 | ≥ 50 | ≥ 50 |