

SUPPLEMENTAL DATA

Table SI. One hundred most over-expressed genes in HNE-treated, HSF1 siRNA-transfected vs. HNE-treated, NEG siRNA-transfected samples. Genes with RefSeq entries and Gene Ontology terms are represented.

| Gene Name | Protein RefSeq | Gene Description | Gene Ontology Terms, Examples | Fold Change |
|-----------|----------------|---|---|-------------|
| LEAP2 | NP_443203 | Liver-expressed antimicrobial peptide 2 precursor | defense response to bacteria | +5.64 |
| SPRY2 | NP_005833 | Sprouty homolog 2 | cell-cell signaling; regulation of signal transduction; organ morphogenesis; development; membrane; microtubule | +5.36 |
| ANKRD1 | NP_055206 | Ankyrin repeat domain 1 | DNA binding; nucleus; defense response; signal transduction | +4.77 |
| SKIL | NP_005405 | Ski-like protein | transcription corepressor activity; nucleus; signal transduction; cell differentiation | +4.35 |
| KLF10 | NP_005646 | TGFB-inducible early growth response protein 1 | skeletal development; nucleus; regulation of transcription; cell-cell signaling; negative regulation of cell proliferation; metal ion binding | +4.19 |
| RND3 | NP_005159 | Rho-related GTP-binding protein RhoE | nucleotide binding; GTP binding; small GTPase mediated signal transduction; protein transport | +3.63 |
| BHLHB3 | NP_110389 | Class B basic helix-loop-helix protein 3 | transcription factor activity; nucleus; regulation of transcription; cell proliferation; organ morphogenesis; cell differentiation | +3.45 |
| SPDYA | NP_877433 | Speedy homolog 1 | protein kinase binding; cell cycle; cell proliferation; response to DNA damage stimulus; organ morphogenesis | +3.39 |
| TRIB1 | NP_079471 | Tribbles homolog 1 | nucleotide binding; protein kinase activity | +3.34 |
| NAB1 | NP_005957 | NGFI-A binding protein 1 | nucleic acid binding; nucleus; regulation of transcription; transcriptional repressor activity | +3.31 |
| GEM | NP_005252 | GTP-binding protein GEM | nucleotide binding; calmodulin binding; GTP binding; immune response; cell surface receptor linked signal transduction; membrane | +3.11 |
| GADD45 A | NP_001915 | Growth arrest and DNA-damage-inducible protein GADD45 alpha | regulation of cyclin dependent protein kinase activity; nucleus; DNA repair; apoptosis; cell cycle arrest | +3.11 |
| SGK1 | NP_005618 | Serum/glucocorticoid regulated kinase 1 | ATP binding; protein serine/threonine kinase activity; apoptosis; response to DNA damage stimulus; sodium ion transport | +3.10 |
| BIRC3 | NP_001156 | Baculoviral IAP repeat-containing 3 | ubiquitin-protein ligase activity; regulation of apoptosis | +3.04 |
| FRZB | NP_001454 | Frizzled-related protein | Wnt-protein binding; cell differentiation; skeletal development; membrane | +3.04 |
| FILIP1L | NP_878913 | Filamin A interacting protein 1-like | myosin complex | +2.99 |
| BHLHB2 | NP_003661 | Basic helix-loop-helix domain containing, class B, 2 | transcription repressor activity; negative regulation of transcription; nucleus | +2.90 |
| CPEB2 | NP_872291 | Cytoplasmic polyadenylation element binding protein 2 | RNA binding; regulation of translation; cytoplasm | +2.84 |
| ERRF1 | NP_061821 | ERBB receptor feedback inhibitor 1 | Rho GTPase activator activity; response to stress; cytoplasm | +2.81 |
| YOD1 | NP_061036 | YOD1 OTU deubiquinating enzyme 1 homolog | CoA hydrolase activity; cysteine-type peptidase activity; ubiquitin-dependent protein catabolic process | +2.80 |
| GJA10 | NP_110399 | Gap junction protein, alpha 10 | gap junction channel activity; cell communication; response to light stimulus; gamete generation; cell junction | +2.73 |
| GADD45 B | NP_056490 | Growth arrest and DNA-damage-inducible, beta | activation of MAP3K activity; apoptosis; cell differentiation; regulation of cell cycle; response to stress | +2.69 |
| ID2 | NP_002157 | Inhibitor of DNA binding 2 | transcription regulator activity; enucleate erythrocyte differentiation; heart development; positive regulation of macrophage differentiation | +2.66 |
| BCL2L11 | NP_619527 | BCL2-like 11 | microtubule binding; regulation of apoptosis; cell-matrix adhesion; lymphocyte homeostasis; regulation of organ growth | +2.62 |
| SYDE2 | NP_115560 | Synapse defective 1, Rho GTPase, homolog 2 | Rho GTPase activator activity; signal transduction | +2.61 |

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|---------|--------------|--|--|-------|
| PLK2 | NP_006613 | Polo-like kinase 2 | ATP binding; protein serine/threonine kinase activity; cell cycle; regulation of I-kappaB kinase/NF-kappaB cascade | +2.53 |
| HEY1 | NP_036390 | Hairy/enhancer-of-split related with YRPW motif 1 | DNA binding; transcription factor activity; Notch signaling pathway; organ morphogenesis; nucleus | +2.52 |
| KLF4 | NP_004226 | Kruppel-like factor 2 | transcription factor activity; nucleus | +2.50 |
| MMP3 | NP_002413 | Matrix metalloproteinase 3 | metalloendopeptidase activity; collagen catabolic process; extracellular | +2.49 |
| IDI2 | NP_150286 | Isopentenyl-diphosphate delta isomerase 2 | isopentenyl-diphosphate delta-isomerase activity; isoprenoid biosynthetic process | +2.47 |
| MAP2K3 | NP_002747 | Mitogen-activated protein kinase kinase 3 | ATP binding; MAP kinase kinase activity; protein serine/threonine kinase activity; activation of MAPK activity; signal transduction | +2.45 |
| SERTAD2 | NP_055570 | SERTA domain containing 2 | transcription coactivator activity; negative regulation of cell growth | +2.43 |
| DDR2 | NP_001014796 | Discoidin domain receptor tyrosine kinase 2 | ATP binding; protein tyrosine kinase activity; receptor activity; positive regulation of cell proliferation; integral to plasma membrane | +2.43 |
| OPN1SW | NP_001699 | Opsin 1 | G-protein coupled receptor protein signaling pathway; signal transduction; visual perception; integral to plasma membrane | +2.41 |
| BAAT | NP_001692 | Bile acid Coenzyme A: amino acid N-acyltransferase | glycine N-choloyltransferase activity; hydrolase activity; bile acid metabolic process | +2.41 |
| KLF6 | NP_001291 | Kruppel-like factor 6 | DNA binding; transcription activator activity; B cell differentiation | +2.35 |
| KLF3 | NP_057615 | Kruppel-like factor 3 | transcription factor activity | +2.30 |
| PPM2C | NP_060914 | Protein phosphatase 2C, magnesium-dependent, catalytic subunit | hydrolase activity; protein amino acid dephosphorylation; mitochondrial matrix | +2.24 |
| CREB5 | NP_878901 | cAMP responsive element binding protein 5 | DNA binding; positive regulation of transcription | +2.22 |
| SPINK7 | NP_115955 | Serine peptidase inhibitor, Kazal type 7 | serine-type endopeptidase inhibitor activity; extracellular | +2.21 |
| SPINK9 | NP_001035523 | Serine peptidase inhibitor, Kazal type 9 | serine-type endopeptidase inhibitor activity; extracellular | +2.15 |
| LYSMD3 | NP_938014 | LysM, putative peptidoglycan-binding, domain containing 3 | cell wall catabolic process; integral to membrane | +2.13 |
| KLKB1 | NP_000883 | Kallikrein B, plasma 1 | serine-type endopeptidase activity; blood coagulation; inflammatory response; extracellular | +2.13 |
| PLAG1 | NP_002646 | Pleiomorphic adenoma gene 1 | transcription factor activity; regulation of transcription; nucleus | +2.11 |
| VEGFA | NP_001020537 | Vascular endothelial growth factor A | extracellular matrix binding; angiogenesis; negative regulation of apoptosis; response to hypoxia | +2.11 |
| GCNT4 | NP_057675 | Glucosaminyl (N-acetyl) transferase 4, core 2 | protein amino acid O-linked glycosylation; Golgi membrane | +2.09 |
| HRH1 | NP_001091682 | Histamine receptor H1 | histamine receptor activity; inflammatory response; integral to plasma membrane | +2.07 |
| TAS2R4 | NP_058640 | Taste receptor, type 2, member 4 | G-protein coupled receptor activity; sensory perception of taste; integral to membrane | +2.06 |
| SNAPC1 | NP_003073 | Small nuclear RNA activating complex, polypeptide 1 | DNA binding; regulation of transcription | +2.05 |
| KITLG | NP_000890 | KIT ligand | growth factor activity; hemopoiesis; positive regulation of DNA replication | +2.05 |
| NR4A2 | NP_006177 | Nuclear receptor subfamily 4, group A, member 2 | transcription factor activity; steroid hormone receptor activity; neuron differentiation; nucleus | +2.00 |
| PLA2G10 | NP_003552 | Phospholipase A2, group X | Phospholipase A2 activity; lipid catabolic process; extracellular | +1.95 |
| CXCL2 | NP_002080 | chemokine (C-X-C motif) ligand 2 | chemotaxis; immune response; extracellular | +1.94 |
| AXUD1 | NP_149016 | AXIN1 up-regulated 1 | transcription factor activity; apoptosis; nucleus | +1.94 |
| HIVEP2 | NP_006725 | Human immunodeficiency virus type I enhancer binding protein 2 | DNA binding; regulation of transcription; nucleus | +1.93 |

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|----------|-----------|---|--|-------|
| KDELR3 | NP_006846 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 | ER retention sequence binding; protein retention in ER lumen; endoplasmic reticulum membrane | +1.91 |
| IL1RL1 | NP_057316 | Interleukin 1 receptor-like 1 | interleukin-1 receptor activity; innate immune response; plasma membrane | +1.90 |
| CCL20 | NP_004582 | Chemokine (C-C motif) ligand 20 | chemotaxis; immune response; extracellular | +1.90 |
| ASB15 | NP_563616 | Ankyrin repeat and SOCS box-containing 15 | ubiquitin-dependent protein catabolic process | +1.90 |
| NAB2 | NP_005958 | NGFI-A binding protein 2 (EGR1 binding protein 2) | transcription repressor activity; negative regulation of transcription; nucleus | +1.88 |
| TSC22D2 | NP_055594 | TSC22 domain family, member 2 | transcription factor activity; response to osmotic stress; cytoplasm | +1.88 |
| BCOR | NP_060215 | BCL6 co-repressor | histone deacetylase binding; negative regulation of transcription; nucleus | +1.86 |
| APOBEC4 | NP_982279 | Apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 4 | hydrolase activity; mRNA processing | +1.86 |
| ADM | NP_001115 | Adrenomedullin | hormone activity; cell-cell signaling; extracellular | +1.85 |
| ZFP30 | NP_055713 | Zinc finger protein 30 homolog (mouse) | DNA binding; regulation of transcription; nucleus | +1.84 |
| CDKN1A | NP_510867 | Cyclin-dependent kinase inhibitor 1A | cyclin-dependent protein kinase inhibitor activity; cell cycle arrest; response to DNA damage stimulus | +1.83 |
| EIF2AK3 | NP_004827 | Eukaryotic translation initiation factor 2-alpha kinase 3 | eukaryotic translation initiation factor 2alpha kinase activity; endoplasmic reticulum unfolded protein response; endoplasmic reticulum membrane | +1.83 |
| GRPR | NP_005305 | Gastrin-releasing peptide receptor | bombesin receptor activity; G-protein coupled receptor protein signaling pathway; plasma membrane | +1.83 |
| RDH10 | NP_742034 | Retinol dehydrogenase 10 (all-trans) | oxidoreductase activity; visual perception; endoplasmic reticulum membrane | +1.83 |
| PLAU | NP_002649 | Plasminogen activator, urokinase | kinase activity; serine-type endopeptidase activity; blood coagulation; extracellular | +1.83 |
| BTG2 | NP_006754 | BTG family, member 2 | DNA repair; regulation of transcription; nucleus | +1.82 |
| RUNX1 | NP_001745 | Runt-related transcription factor 1 | transcription activator activity; positive regulation of angiogenesis; nucleus | +1.82 |
| DDIT4 | NP_061931 | DNA-damage-inducible transcript 4 | apoptosis; negative regulation of signal transduction; cytoplasm | +1.82 |
| TAS2R5 | NP_061853 | Taste receptor, type 2, member 5 | taste receptor activity; G-protein coupled receptor protein signaling pathway; integral to membrane | +1.80 |
| ARHGAP12 | NP_060757 | Rho GTPase activating protein 12 | GTPase activator activity; signal transduction | +1.80 |
| RRAGC | NP_071353 | Ras-related GTP binding C | GTPase activity; RNA splicing; apoptosis; cell growth | +1.78 |
| SLC17A5 | NP_036566 | Solute carrier family 17 (anion/sugar transporter), member 5 | sugar:hydrogen symporter activity; anion transport; integral to plasma membrane | +1.77 |
| TUBA3C | NP_005992 | Tubulin, alpha 3c | GTPase activity; structural molecule activity; microtubule-based movement | +1.77 |
| ZBTB43 | NP_054726 | Zinc finger and BTB domain containing 43 | zinc ion binding; regulation of transcription; nucleus | +1.76 |
| RHBDL2 | NP_060291 | Rhomboid, veinlet-like 2 (Drosophila) | serine-type endopeptidase activity; signal transduction; integral to membrane | +1.75 |
| PMAIP1 | NP_066950 | Phorbol-12-myristate-13-acetate-induced protein 1 | caspase activation; induction of apoptosis; mitochondrion | +1.75 |
| ZNF430 | NP_079465 | Zinc finger protein 430 | DNA binding; regulation of transcription; nucleus | +1.75 |
| PCF11 | NP_056969 | PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae) | mRNA cleavage; nucleus | +1.75 |
| CMTM2 | NP_653274 | CKLF-like MARVEL transmembrane domain containing 2 | cytokine activity; chemotaxis; integral to membrane | +1.75 |
| SGMS2 | NP_689834 | Sphingomyelin synthase 2 | ceramide cholinephosphotransferase activity; kinase activity; lipid metabolic process; integral to Golgi membrane | +1.74 |

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| BTG1 | NP_001722 | B-cell translocation gene 1, anti-proliferative | transcription cofactor activity; cell migration; negative regulation of cell growth; regulation of apoptosis | +1.74 |
| KCNJ13 | NP_002233 | Potassium inwardly-rectifying channel, subfamily J, member 13 | voltage-gated ion channel activity; potassium ion transport; integral to membrane | +1.73 |
| MAP3K8 | NP_005195 | Mitogen-activated protein kinase kinase kinase 8 | protein serine/threonine kinase activity; cytoplasm | +1.73 |
| RHOBTB3 | NP_055714 | Rho-related BTB domain containing 3 | GTPase activity; protein localization; nucleus | +1.73 |
| TAS2R3 | NP_058639 | Taste receptor, type 2, member 3 | G-protein coupled receptor activity; sensory perception of taste; integral to membrane | +1.71 |
| SLCO1B3 | NP_062818 | Solute carrier organic anion transporter family, member 1B3 | bile acid transmembrane transporter activity; organic anion transport; integral to plasma membrane | +1.70 |
| RNF19A | NP_904355 | Ring finger protein 19A | ligase activity; microtubule cytoskeleton organization and biogenesis; ubiquitin-dependent protein catabolic process; centrosome; integral to membrane | +1.70 |
| HIST1H2AB | NP_003504 | Histone cluster 1, H2ab | DNA binding; nucleosome assembly; nucleus | +1.70 |
| SOCS3 | NP_003946 | Suppressor of cytokine signaling 3 | protein kinase inhibitor activity; JAK-STAT cascade; anti-apoptosis | +1.70 |
| NFKBIA | NP_065390 | Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha | cytoplasmic sequestering of NF-kappaB; regulation of cell proliferation; response to lipopolysaccharide | +1.70 |
| HBEGF | NP_001936 | Heparin-binding EGF-like growth factor | growth factor activity; positive regulation of keratinocyte migration; extracellular; integral to plasma membrane | +1.70 |
| ARID5B | NP_115575 | AT rich interactive domain 5B (MRF1-like) | DNA binding; regulation of transcription; nucleus | +1.69 |
| HOMER1 | NP_004263 | Homer homolog 1 (Drosophila) | metabotropic glutamate receptor, phospholipase C activating pathway; postsynaptic membrane | +1.69 |
| RIOK3 | NP_003822 | RIO kinase 3 (yeast) | protein serine/threonine kinase activity; chromosome segregation | +1.69 |
| RLF | NP_036553 | Rearranged L-myc fusion | transcription factor activity; nucleus | +1.68 |

Table SII. One hundred most under-expressed genes in HNE-treated, HSF1 siRNA-transfected vs. HNE-treated, NEG siRNA-transfected samples. Genes with RefSeq entries and Gene Ontology terms are represented.

| Gene Name | Protein RefSeq | Gene Description | Gene Ontology Terms, Examples | Fold Change |
|-----------|----------------|--|---|-------------|
| ARPM1 | NP_115876 | Actin related protein M1 | structural molecule activity; cytoskeleton | -5.13 |
| HSPA1A | NP_005336 | Heat shock 70kDa protein 1A | protein binding; response to stress | -4.54 |
| P4HA2 | NP_004190 | Proline 4-hydroxylase, alpha polypeptide II | oxidoreductase activity; protein metabolic process; endoplasmic reticulum lumen | -4.48 |
| DNAJA4 | NP_061072 | DnaJ (Hsp40) homolog, subfamily A, member 4 | heat shock protein binding; protein folding; membrane | -4.14 |
| CAP2 | NP_006357 | CAP, adenylate cyclase-associated protein, 2 (yeast) | actin binding; oxidoreductase activity; metabolic process; plasma membrane | -4.01 |
| ARHGAP19 | NP_116289 | Rho GTPase activating protein 19 | GTPase activator activity; signal transduction | -3.81 |
| CYP39A1 | NP_057677 | Cytochrome P450, family 39, subfamily A, polypeptide 1 | steroid 7-alpha-hydroxylase activity; cholesterol catabolic process; oxidation reduction; endoplasmic reticulum membrane | -3.73 |
| CLU | NP_001822 | Clusterin | apoptosis; complement activation; innate immune response; extracellular | -3.63 |
| HSPA6 | NP_002146 | Heat shock 70kDa protein 6 | ATP binding; response to unfolded protein | -3.20 |
| SQRDL | NP_067022 | Sulfide quinone reductase-like (yeast) | oxidoreductase activity; mitochondrial inner membrane | -3.16 |
| CRYAB | NP_001876 | Crystallin, alpha B | structural constituent of eye lens; anti-apoptosis; cytoplasm | -3.14 |
| MLKL | NP_689862 | Mixed lineage kinase domain-like | ATP binding; protein kinase activity | -3.04 |
| HSPA1B | NP_005337 | Heat shock 70kDa protein 1B | ATP binding; unfolded protein binding; response to unfolded protein | -3.03 |
| CHRNA5 | NP_000736 | Cholinergic receptor, nicotinic, alpha 5 | acetylcholine receptor activity; ion transport; synaptic transmission; synapse | -3.01 |
| AP4B1 | NP_006585 | Adaptor-related protein complex 4, beta 1 subunit | protein binding; intracellular protein transport; Golgi apparatus | -2.94 |
| SLC7A11 | NP_055146 | Solute carrier family 7, member 11 | cystine:glutamate antiporter activity; integral to membrane | -2.80 |
| GKAP1 | NP_079487 | G kinase anchoring protein 1 | kinase activity; signal transduction; Golgi apparatus | -2.74 |
| HSPA4L | NP_055093 | Heat shock 70kDa protein 4-like | ATP binding; response to unfolded protein | -2.74 |
| DNAJB1 | NP_006136 | DnaJ (Hsp40) homolog, subfamily B, member 1 | heat shock protein binding; protein folding; cytoplasm | -2.70 |
| TAS2R46 | NP_795368 | Taste receptor, type 2, member 46 | G-protein coupled receptor activity; sensory perception of taste; integral to membrane | -2.59 |
| RAB2B | NP_116235 | RAB2B, member RAS oncogene family | ATP binding; transcription factor binding; small GTPase mediated signal transduction | -2.52 |
| RPL7A | NP_000963 | Ribosomal protein L7a | RNA binding; structural constituent of ribosome | -2.45 |
| TAGLN | NP_001001522 | Transgelin | actin binding; muscle development; cytoplasm | -2.43 |
| HSD17B7 | NP_057455 | Hydroxysteroid (17-beta) dehydrogenase 7 | 3-keto-steroid reductase activity; oxidoreductase activity; endoplasmic reticulum membrane | -2.41 |
| CASP7 | NP_203125 | Caspase 7 | cysteine-type endopeptidase activity; apoptosis | -2.39 |
| HIBCH | NP_055177 | 3-hydroxyisobutyryl-Coenzyme A hydrolase | hydrolase activity; branched chain family amino acid catabolic process; mitochondrion | -2.32 |
| IFNE1 | NP_795372 | Interferon epsilon 1 | response to virus; extracellular | -2.22 |
| ENPP1 | NP_006199 | Ectonucleotide pyrophosphatase/phosphodiesterase 1 | nucleotide diphosphatase activity; metabolic process; negative regulation of cell growth; bone remodeling; integral to membrane | -2.20 |
| TRIM26 | NP_003440 | Tripartite motif-containing 26 | DNA binding; protein binding | -2.18 |

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|----------|-----------|--|---|-------|
| MICB | NP_005922 | MHC class I polypeptide-related sequence B | immune response; antigen processing and presentation; response to heat; response to oxidative stress; integral to plasma membrane | -2.18 |
| ARL15 | NP_061960 | ADP-ribosylation factor-like 15 | GTP binding | -2.17 |
| CRYZ | NP_001880 | Crystallin, zeta (quinone reductase) | oxidoreductase activity; visual perception; cytoplasm | -2.15 |
| TRIM68 | NP_060543 | Tripartite motif-containing 68 | protein binding; cytoplasm | -2.15 |
| RNASEL | NP_066956 | Ribonuclease L (2',5'-oligoadenylate synthetase-dependent) | hydrolase activity; RNA binding; mRNA processing; cytoplasm | -2.15 |
| AFF1 | NP_005926 | AF4/FMR2 family, member 1 | transcription factor activity; nucleus | -2.11 |
| USP30 | NP_116052 | Ubiquitin specific peptidase 30 | cysteine-type peptidase activity; ubiquitin thiolesterase activity; ubiquitin-dependent protein catabolic process | -2.09 |
| NKRF | NP_060014 | NFKB repressing factor | DNA binding; negative regulation of transcription | -2.09 |
| RFESD | NP_775498 | Rieske (Fe-S) domain containing | 2 iron, 2 sulfur cluster binding; oxidoreductase activity | -2.08 |
| DGKI | NP_004708 | Diacylglycerol kinase, iota | diacylglycerol kinase activity; activation of protein kinase C activity | -2.08 |
| TMEFF1 | NP_003683 | Transmembrane protein with EGF-like and two follistatin-like domains 1 | multicellular organismal development; integral to membrane | -2.07 |
| NPAL2 | NP_079035 | NIPA-like domain containing 2 | integral to membrane | -2.07 |
| GIN52 | NP_057179 | GIN5 complex subunit 2 (Psf2 homolog) | protein binding; DNA replication; nucleus | -2.05 |
| PPM1K | NP_689755 | Protein phosphatase 1K (PP2C domain containing) | protein serine/threonine phosphatase activity; mitochondrial matrix | -2.04 |
| LASS6 | NP_982288 | LAG1 homolog, ceramide synthase 6 | transcription factor activity; lipid biosynthetic process; endoplasmic reticulum membrane; nuclear membrane | -2.04 |
| ABHD3 | NP_612213 | Abhydrolase domain containing 3 | carboxylesterase activity; integral to membrane | -2.03 |
| UBR2 | NP_056070 | Ubiquitin protein ligase E3 component n-recognin 2 | ubiquitin-protein ligase activity; ubiquitin-dependent protein catabolic process; nucleus | -2.03 |
| SNAP23 | NP_003816 | Synaptosomal-associated protein, 23kDa | post-Golgi vesicle-mediated transport; vesicle targeting; synapse | -2.02 |
| ANKMY2 | NP_064715 | Ankyrin repeat and MYND domain containing 2 | zinc ion binding | -2.02 |
| RAD51 | NP_002866 | RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae) | damaged DNA binding; ATPase activity; double strand break repair; homologous recombination; nucleus | -2.02 |
| LMAN2L | NP_110432 | Lectin, mannose-binding 2-like | sugar binding; ER to Golgi vesicle-mediated transport; integral to membrane | -2.02 |
| CSRP2 | NP_001312 | Cysteine and glycine-rich protein 2 | cell proliferation; multicellular organismal development; nucleus | -2.01 |
| SLFN5 | NP_659412 | Schlafen family member 5 | ATP binding; cell differentiation | -1.99 |
| DPYSL2 | NP_001377 | Dihydropyrimidinase-like 2 | hydrolase activity; cell differentiation; nervous system development | -1.99 |
| LRP2BP | NP_060879 | LRP2 binding protein | protein binding; cytoplasm | -1.98 |
| BST2 | NP_004326 | Bone marrow stromal cell antigen 2 | signal transducer activity; B cell activation; humoral immune response | -1.98 |
| MMP1 | NP_002412 | Matrix metalloproteinase 1 | metalloendopeptidase activity; collagen catabolic process; extracellular | -1.97 |
| BTN2A3 | NP_076923 | Butyrophilin, subfamily 2, member A3 | integral to membrane | -1.96 |
| PRAME | NP_996836 | Preferentially expressed antigen in melanoma | protein binding | -1.96 |
| SERPINH1 | NP_001226 | Serpin peptidase inhibitor, clade H (heat shock protein 47), member 1 | serine-type endopeptidase inhibitor activity; unfolded protein binding; response to unfolded protein; endoplasmic reticulum | -1.96 |
| PMP22 | NP_000295 | Peripheral myelin protein 22 | myelin formation; mechanosensory behavior; integral to membrane | -1.95 |

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|--------------|------------------|--|--|-------|
| N6AMT1 | NP_037372 | N-6 adenine-specific DNA methyltransferase 1 (putative) | methyltransferase activity; nucleic acid binding | -1.95 |
| GPN1 | NP_009197 | GPN-loop GTPase 1 | GTP binding; small GTPase mediated signal transduction; cytoplasm | -1.94 |
| AASS | NP_005754 | Aminoacidipate-semialdehyde synthase | oxidoreductase activity; lysine catabolic process; mitochondrion | -1.94 |
| TRIM2 | NP_056086 | Tripartite motif-containing 2 | protein binding; cytoplasm | -1.93 |
| STAT2 | NP_005410 | Signal transducer and activator of transcription 2 | signal transducer activity; transcription factor activity; JAK-STAT cascade | -1.93 |
| BTBD8 | NP_899065 | BTB (POZ) domain containing 8 | protein binding | -1.92 |
| ANLN | NP_061155 | Anillin | actin binding; cell cycle; cytokinesis | -1.92 |
| SLC25A2 7 | NP_004268 | Solute carrier family 25, member 27 | mitochondrial transport; mitochondrial inner membrane | -1.92 |
| CALD1 | NP_149129 | Caldesmon 1 | actin binding; calmodulin binding; cell motion; muscle contraction; cytoskeleton | -1.92 |
| PIR | NP_003653 | Pirin | iron ion binding; transcription cofactor activity; nucleus | -1.91 |
| INSIG2 | NP_057217 | Insulin induced gene 2 | cholesterol metabolic process; endoplasmic reticulum membrane | -1.91 |
| BAG3 | NP_004272 | BCL2-associated athanogene 3 | Hsp70/Hsc70 protein regulator activity; anti-apoptosis; cytosol | -1.88 |
| LIMCH1 | NP_055803 | LIM and calponin homology domains 1 | actin binding; actomyosin structure organization and biogenesis | -1.88 |
| SUGT1 | NP_006695 | SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae) | mitosis; ubiquitin-dependent protein catabolic process; kinetochore; ubiquitin ligase complex | -1.87 |
| PCDHB3 | NP_061760 | Protocadherin beta 3 | protein binding; calcium-dependent cell-cell adhesion; integral to plasma membrane | -1.87 |
| CDGAP | NP_065805 | Cdc42 GTPase-activating protein | GTPase activator activity; signal transduction | -1.86 |
| STIP1 | NP_006810 | Stress-induced-phosphoprotein 1 (Hsp70/Hsp90 organizing protein) | response to stress | -1.85 |
| GPBP1 | NP_075064 | GC-rich promoter binding protein 1 | transcription factor activity | -1.85 |
| MORC4 | NP_078933 | MORC family CW-type zinc finger 4 | ATP binding; zinc ion binding | -1.85 |
| DZIP3 | NP_055463 | DAZ interacting protein 3, zinc finger | RNA binding; ubiquitin-protein ligase activity; ubiquitin-dependent protein catabolic process | -1.84 |
| ACTN4 | NP_004915 | Actinin, alpha 4 | actin filament binding; regulation of apoptosis; cytoskeleton | -1.84 |
| TTC30B | NP_689730 | Tetratricopeptide repeat domain 30B | cell projection organization and biogenesis; cilium | -1.83 |
| RANBP6 | NP_036548 | RAN binding protein 6 | protein transport; cytoplasm; nucleus | -1.83 |
| CARD6 | NP_115976 | Caspase recruitment domain family, member 6 | protein binding; regulation of apoptosis | -1.83 |
| TRMT12 | NP_060426 | tRNA methyltransferase 12 homolog (S. cerevisiae) | methyltransferase activity; tRNA processing | -1.82 |
| DBT | NP_001909 | Dihydrolipoamide branched chain transacylase E2 | acyltransferase activity; mitochondrial matrix | -1.82 |
| PLOD1 | NP_000293 | Procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1 | oxidoreductase activity; hydroxylysine biosynthetic process; response to hypoxia; rough endoplasmic reticulum membrane | -1.81 |
| OVOS2 | NP_0010739 71 | Ovostatin 2 | serine-type endopeptidase inhibitor activity; extracellular | -1.81 |
| GBP3 | NP_060754 | Guanylate binding protein 3 | GTPase activity; immune response | -1.80 |
| FLOT2 | NP_004466 | Flotillin 2 | cell adhesion; epidermis development; cell surface | -1.79 |
| GPATCH 1 | NP_060495 | G patch domain containing 1 | nucleic acid binding; nuclear | -1.79 |
| CKS2 | NP_001818 | CDC28 protein kinase regulatory subunit 2 | cyclin-dependent protein kinase regulator activity; cell cycle | -1.79 |

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| LANCL1 | NP_006046 | LanC lantibiotic synthetase component C-like 1 (bacterial) | G-protein coupled receptor activity; integral to plasma membrane | -1.78 |
| ZKSCAN1 | NP_003430 | Zinc finger with KRAB and SCAN domains 1 | transcription factor activity | -1.78 |
| EIF4EBP2 | NP_004087 | Eukaryotic translation initiation factor 4E binding protein 2 | protein binding; cAMP-mediated signaling; negative regulation of translational initiation | -1.71 |
| SUOX | NP_000447 | Sulfite oxidase | oxidoreductase activity; mitochondrial intermembrane space | -1.78 |
| DCLRE1B | NP_073747 | DNA cross-link repair 1B (PSO2 homolog, <i>S. cerevisiae</i>) | hydrolase activity; DNA repair; nucleus | -1.78 |
| LPCAT3 | NP_005759 | Lysophosphatidylcholine acyltransferase 3 | acyltransferase activity; phospholipid biosynthetic process; endoplasmic reticulum membrane | -1.77 |
| PLCH1 | NP_055811 | Phospholipase C, eta 1 | hydrolase activity; intracellular signaling cascade; lipid catabolic process | -1.77 |
| EXO1 | NP_569082 | Exonuclease 1 | DNA binding; exonuclease activity; DNA repair; mismatch repair; nucleus | -1.77 |