**Table 1**  The statistical metrics for key differentially expressed genes (DEGs)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Agiliant Id** | **Gene Symbol** | **logFC** | **pValue** | **adj.P.Val** | **tvalue** | **Regulation** | **Gene Name** |
| A\_32\_P75902 | C16orf73 | 1.235701 | 6.08E-43 | 6.08E-43 | 19.81122 | Up | Homo sapiens chromosome 16 open reading frame 73 (C16orf73), transcript variant 2, mRNA [NM\_152764] |
| A\_33\_P3248586 | DUX4 | 1.276906 | 4.26E-42 | 4.26E-42 | 19.44732 | Up | Homo sapiens double homeobox 4 (DUX4), mRNA [NM\_033178] |
| A\_33\_P3258699 | DUX4 | 1.262017 | 4.55E-42 | 4.55E-42 | 19.43525 | Up | Homo sapiens double homeobox 4 (DUX4), mRNA [NM\_033178] |
| A\_33\_P3290588 | ASPSCR1 | 1.187398 | 5.26E-42 | 5.26E-42 | 19.40821 | Up | Homo sapiens cDNA FLJ45222 fis, clone BRCAN2019953. [AK127159] |
| A\_33\_P3325195 | IGSF9B | 0.985752 | 2.1E-41 | 2.1E-41 | 19.15111 | Up | Homo sapiens immunoglobulin superfamily, member 9B (IGSF9B), mRNA [NM\_014987] |
| A\_33\_P3287997 | C9orf106 | 1.09127 | 3.63E-41 | 3.63E-41 | 19.05043 | Up | Homo sapiens chromosome 9 open reading frame 106 (C9orf106), mRNA [NM\_001012715] |
| A\_21\_P0011435 | RHPN2 | 1.225108 | 1.51E-40 | 1.51E-40 | 18.78789 | Up | Homo sapiens rhophilin, Rho GTPase binding protein 2 (RHPN2), mRNA [NM\_033103] |
| A\_23\_P400515 | KIF17 | 1.930295 | 3.79E-40 | 3.79E-40 | 18.61974 | Up | Homo sapiens kinesin family member 17 (KIF17), transcript variant 1, mRNA [NM\_020816] |
| A\_23\_P208636 | SHANK1 | 1.669136 | 8.49E-40 | 8.49E-40 | 18.47267 | Up | Homo sapiens SH3 and multiple ankyrin repeat domains 1 (SHANK1), mRNA [NM\_016148] |
| A\_33\_P3312790 | MEGF11 | 1.409588 | 3.94E-39 | 3.94E-39 | 18.1942 | Up | Homo sapiens multiple EGF-like-domains 11 (MEGF11), mRNA [NM\_032445] |
| A\_33\_P3412384 | MUC2 | 1.149226 | 5.8E-39 | 5.8E-39 | 18.12413 | Up | Homo sapiens mucin 2, oligomeric mucus/gel-forming (MUC2), mRNA [NM\_002457] |
| A\_33\_P3360077 | LOC100130745 | 1.219513 | 1.1E-38 | 1.1E-38 | 18.00944 | Up | Homo sapiens cDNA FLJ46338 fis, clone TESTI4046328. [AK128206] |
| A\_33\_P3302025 | ADAMTSL1 | 1.405737 | 1.15E-38 | 1.15E-38 | 18.00084 | Up | Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA [NM\_052866] |
| A\_33\_P3231908 | POU3F3 | 1.060131 | 1.67E-38 | 1.67E-38 | 17.93388 | Up | Homo sapiens POU class 3 homeobox 3 (POU3F3), mRNA [NM\_006236] |
| A\_33\_P3265606 | GCLM | 1.256857 | 2.19E-38 | 2.19E-38 | 17.88513 | Up | Homo sapiens glutamate-cysteine ligase, modifier subunit (GCLM), mRNA [NM\_002061] |
| A\_23\_P131202 | HES6 | 1.268367 | 2.4E-38 | 2.4E-38 | 17.86832 | Up | Homo sapiens hairy and enhancer of split 6 (Drosophila) (HES6), transcript variant 1, mRNA [NM\_018645] |
| A\_33\_P3219811 | PTGDS | 1.003831 | 2.63E-38 | 2.63E-38 | 17.85174 | Up | prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Symbol;Acc:9592] [ENST00000371623] |
| A\_33\_P3310047 | SHROOM4 | 1.12892 | 3.33E-38 | 3.33E-38 | 17.80957 | Up | Homo sapiens shroom family member 4 (SHROOM4), transcript variant 1, mRNA [NM\_020717] |
| A\_33\_P3248602 | DUX4 | 1.174945 | 5.13E-38 | 5.13E-38 | 17.73225 | Up | Homo sapiens double homeobox 4 (DUX4), mRNA [NM\_033178] |
| A\_23\_P24234 | OPN4 | 1.795966 | 1.4E-37 | 1.4E-37 | 17.55295 | Up | Homo sapiens opsin 4 (OPN4), transcript variant 2, mRNA [NM\_001030015] |
| A\_21\_P0001861 | XLOC\_001485 | 1.631201 | 3.77E-37 | 3.77E-37 | 17.37648 | Up | 603072419F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5164397 5', mRNA sequence [BI825310] |
| A\_33\_P3313597 | LOC100509861 | 1.282464 | 1.17E-36 | 1.17E-36 | 17.17496 | Up | chromosome 20 open reading frame 181 [Source:HGNC Symbol;Acc:16174] [ENST00000429183] |
| A\_33\_P3421219 | LOC647070 | 1.147387 | 2.36E-36 | 2.36E-36 | 17.05156 | Up | Homo sapiens cDNA FLJ10580 fis, clone NT2RP2003533. [AK001442] |
| A\_21\_P0000073 | OSMR | 0.997763 | 2.99E-36 | 2.99E-36 | 17.0097 | Up | Homo sapiens oncostatin M receptor (OSMR), transcript variant 2, mRNA [NM\_001168355] |
| A\_33\_P3272849 | LCN8 | 1.249689 | 3.09E-36 | 3.09E-36 | 17.00359 | Up | lipocalin 8 [Source:HGNC Symbol;Acc:27038] [ENST00000479767] |
| A\_33\_P3416321 | SLC17A5 | 1.116126 | 3.3E-36 | 3.3E-36 | 16.99196 | Up | Homo sapiens solute carrier family 17 (anion/sugar transporter), member 5 (SLC17A5), mRNA [NM\_012434] |
| A\_33\_P3274560 | SLC19A3 | 1.462256 | 3.54E-36 | 3.54E-36 | 16.97968 | Up | solute carrier family 19, member 3 [Source:HGNC Symbol;Acc:16266] [ENST00000409456] |
| A\_33\_P3301381 | RBM43 | 1.024805 | 4.35E-36 | 4.35E-36 | 16.94358 | Up | Homo sapiens RNA binding motif protein 43 (RBM43), mRNA [NM\_198557] |
| A\_23\_P218675 | WFDC2 | 1.500959 | 1.06E-35 | 1.06E-35 | 16.78651 | Up | Homo sapiens WAP four-disulfide core domain 2 (WFDC2), mRNA [NM\_006103] |
| A\_33\_P3419321 | CHD5 | 0.995078 | 1.31E-35 | 1.31E-35 | 16.74999 | Up | Homo sapiens chromodomain helicase DNA binding protein 5 (CHD5), mRNA [NM\_015557] |
| A\_23\_P252236 | KLKB1 | 1.248021 | 1.62E-35 | 1.62E-35 | 16.71278 | Up | Homo sapiens kallikrein B, plasma (Fletcher factor) 1 (KLKB1), mRNA [NM\_000892] |
| A\_33\_P3310296 | PKIG | 1.197267 | 2.58E-35 | 2.58E-35 | 16.63072 | Up | protein kinase (cAMP-dependent, catalytic) inhibitor gamma [Source:HGNC Symbol;Acc:9019] [ENST00000372887] |
| A\_24\_P177604 | PPP1R3F | 1.073269 | 2.65E-35 | 2.65E-35 | 16.6262 | Up | Homo sapiens protein phosphatase 1, regulatory subunit 3F (PPP1R3F), transcript variant 1, mRNA [NM\_033215] |
| A\_23\_P76851 | PRMT5 | 1.08888 | 3.46E-35 | 3.46E-35 | 16.57909 | Up | Homo sapiens protein arginine methyltransferase 5 (PRMT5), transcript variant 2, mRNA [NM\_001039619] |
| A\_33\_P3397443 | PKMYT1 | 1.125339 | 5.43E-35 | 5.43E-35 | 16.50052 | Up | Homo sapiens protein kinase, membrane associated tyrosine/threonine 1 (PKMYT1), transcript variant 2, mRNA [NM\_182687] |
| A\_33\_P3283231 | YY2 | 1.001667 | 6.94E-35 | 6.94E-35 | 16.45769 | Up | Homo sapiens YY2 transcription factor (YY2), mRNA [NM\_206923] |
| A\_33\_P3222218 | NEURL1B | 1.86354 | 7.68E-35 | 7.68E-35 | 16.43989 | Up | Homo sapiens neuralized homolog 1B (Drosophila) (NEURL1B), mRNA [NM\_001142651] |
| A\_33\_P3712341 | CXCL12 | 1.113935 | 1.03E-34 | 1.03E-34 | 16.38852 | Up | Homo sapiens chemokine (C-X-C motif) ligand 12 (CXCL12), transcript variant 3, mRNA [NM\_001033886] |
| A\_33\_P3418185 | LYNX1 | 1.175092 | 1.81E-34 | 1.81E-34 | 16.29053 | Up | Homo sapiens Ly6/neurotoxin 1 (LYNX1), transcript variant 1, mRNA [NM\_023946] |
| A\_23\_P127385 | MYBPC3 | 1.09336 | 1.96E-34 | 1.96E-34 | 16.27671 | Up | Homo sapiens myosin binding protein C, cardiac (MYBPC3), mRNA [NM\_000256] |
| A\_33\_P3317752 | KRTAP4-7 | 1.419973 | 2.14E-34 | 2.14E-34 | 16.26159 | Up | Homo sapiens keratin associated protein 4-7 (KRTAP4-7), mRNA [NM\_033061] |
| A\_33\_P3346473 | PHF21A | 1.114567 | 2.55E-34 | 2.55E-34 | 16.23116 | Up | Homo sapiens PHD finger protein 21A (PHF21A), transcript variant 1, mRNA [NM\_001101802] |
| A\_23\_P140716 | TPSD1 | 1.180245 | 2.66E-34 | 2.66E-34 | 16.22349 | Up | Homo sapiens tryptase delta 1 (TPSD1), mRNA [NM\_012217] |
| A\_33\_P3213408 | OR10AD1 | 1.102465 | 3.56E-34 | 3.56E-34 | 16.17299 | Up | Homo sapiens olfactory receptor, family 10, subfamily AD, member 1 (OR10AD1), mRNA [NM\_001004134] |
| A\_23\_P87279 | TRPM5 | 1.770094 | 4.42E-34 | 4.42E-34 | 16.13547 | Up | Homo sapiens transient receptor potential cation channel, subfamily M, member 5 (TRPM5), mRNA [NM\_014555] |
| A\_33\_P3408203 | TGFA | 1.263465 | 4.57E-34 | 4.57E-34 | 16.12963 | Up | Homo sapiens transforming growth factor, alpha (TGFA), transcript variant 1, mRNA [NM\_003236] |
| A\_23\_P156708 | TNXB | 1.001474 | 4.58E-34 | 4.58E-34 | 16.12935 | Up | Homo sapiens tenascin XB (TNXB), transcript variant XB-S, mRNA [NM\_032470] |
| A\_23\_P71480 | DEFB1 | 1.042554 | 4.62E-34 | 4.62E-34 | 16.12788 | Up | Homo sapiens defensin, beta 1 (DEFB1), mRNA [NM\_005218] |
| A\_23\_P142096 | GPR32 | 1.071065 | 5.08E-34 | 5.08E-34 | 16.11129 | Up | Homo sapiens G protein-coupled receptor 32 (GPR32), mRNA [NM\_001506] |
| A\_33\_P3378011 | MUC3A | 1.441706 | 5.76E-34 | 5.76E-34 | 16.08963 | Up | PREDICTED: Homo sapiens mucin 3A, cell surface associated (MUC3A), mRNA [XM\_003403552] |
| A\_33\_P3337415 | GNAL | 0.987201 | 6.26E-34 | 6.26E-34 | 16.07517 | Up | Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), transcript variant 2, mRNA [NM\_002071] |
| A\_33\_P3245606 | BHLHA9 | 1.132666 | 7.56E-34 | 7.56E-34 | 16.04243 | Up | Homo sapiens basic helix-loop-helix family, member a9 (BHLHA9), mRNA [NM\_001164405] |
| A\_33\_P3249877 | BEST3 | 1.27273 | 8.67E-34 | 8.67E-34 | 16.01875 | Up | bestrophin 3 [Source:HGNC Symbol;Acc:17105] [ENST00000331471] |
| A\_23\_P79769 | BIRC7 | 1.984139 | 1E-33 | 1E-33 | 15.99329 | Up | Homo sapiens baculoviral IAP repeat containing 7 (BIRC7), transcript variant 2, mRNA [NM\_022161] |
| A\_23\_P300740 | NPB | 1.055004 | 1.03E-33 | 1.03E-33 | 15.98911 | Up | Homo sapiens neuropeptide B (NPB), mRNA [NM\_148896] |
| A\_19\_P00813140 | XLOC\_014105 | 1.226393 | 1.1E-33 | 1.1E-33 | 15.97679 | Up | GB |
| A\_23\_P2077 | OR4C3 | 1.628096 | 1.11E-33 | 1.11E-33 | 15.97655 | Up | Homo sapiens olfactory receptor, family 4, subfamily C, member 3 (OR4C3), mRNA [NM\_001004702] |
| A\_23\_P164958 | CCDC8 | 1.344625 | 1.32E-33 | 1.32E-33 | 15.94584 | Up | Homo sapiens coiled-coil domain containing 8 (CCDC8), mRNA [NM\_032040] |
| A\_33\_P3294603 | SLC22A31 | 1.00537 | 1.38E-33 | 1.38E-33 | 15.93826 | Up | Homo sapiens solute carrier family 22, member 31 (SLC22A31), mRNA [NM\_001242757] |
| A\_23\_P82286 | ZAN | 1.366551 | 1.53E-33 | 1.53E-33 | 15.92054 | Up | Homo sapiens zonadhesin (ZAN), transcript variant 6, mRNA [NM\_173059] |
| A\_33\_P3378291 | IL17REL | 1.372826 | 1.55E-33 | 1.55E-33 | 15.9185 | Up | Homo sapiens interleukin 17 receptor E-like (IL17REL), mRNA [NM\_001001694] |
| A\_33\_P3326235 | HBM | 1.124004 | 1.85E-33 | 1.85E-33 | 15.88774 | Up | Homo sapiens hemoglobin, mu (HBM), mRNA [NM\_001003938] |
| A\_23\_P310560 | NUDT16 | 1.048586 | 2.35E-33 | 2.35E-33 | 15.84638 | Up | Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 16 (NUDT16), transcript variant 2, mRNA [NM\_152395] |
| A\_33\_P3276068 | BET3L | 0.98692 | 2.4E-33 | 2.4E-33 | 15.84262 | Up | BET3 like (S. cerevisiae) [Source:HGNC Symbol;Acc:21090] [ENST00000356128] |
| A\_21\_P0012274 | XLOC\_l2\_009441 | 1.082303 | 3.87E-33 | 3.87E-33 | 15.76027 | Up | AGENCOURT\_10422541 NIH\_MGC\_57 Homo sapiens cDNA clone IMAGE:6654885 5', mRNA sequence [BU928872] |
| A\_24\_P270728 | NUPR1 | 1.733215 | 4.1E-33 | 4.1E-33 | 15.75046 | Up | Homo sapiens nuclear protein, transcriptional regulator, 1 (NUPR1), transcript variant 1, mRNA [NM\_001042483] |
| A\_24\_P255986 | SPDYE4 | 1.127302 | 4.32E-33 | 4.32E-33 | 15.7412 | Up | Homo sapiens speedy homolog E4 (Xenopus laevis) (SPDYE4), mRNA [NM\_001128076] |
| A\_33\_P3221489 | KIRREL | 1.048713 | 6.44E-33 | 6.44E-33 | 15.67265 | Up | Homo sapiens kin of IRRE like (Drosophila) (KIRREL), mRNA [NM\_018240] |
| A\_21\_P0003308 | DCUN1D1 | 1.004992 | 8.07E-33 | 8.07E-33 | 15.63382 | Up | AF292100 RP42 protein {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (34%) [THC2670542] |
| A\_23\_P43276 | GPR124 | 1.031934 | 1.48E-32 | 1.48E-32 | 15.52925 | Up | Homo sapiens G protein-coupled receptor 124 (GPR124), mRNA [NM\_032777] |
| A\_32\_P210642 | EGFL7 | 1.239958 | 1.56E-32 | 1.56E-32 | 15.52054 | Up | Homo sapiens EGF-like-domain, multiple 7 (EGFL7), transcript variant 2, mRNA [NM\_201446] |
| A\_33\_P3404844 | SRCIN1 | 1.165013 | 1.61E-32 | 1.61E-32 | 15.51534 | Up | Homo sapiens SNAP25-interacting protein, mRNA (cDNA clone IMAGE:5423326), complete cds. [BC033233] |
| A\_33\_P3234809 | PAX8 | 1.448894 | 1.71E-32 | 1.71E-32 | 15.50466 | Up | Homo sapiens paired box 8 (PAX8), transcript variant PAX8A, mRNA [NM\_003466] |
| A\_23\_P111978 | KCNK9 | 1.215798 | 1.78E-32 | 1.78E-32 | 15.49796 | Up | Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA [NM\_016601] |
| A\_33\_P3260053 | AIF1L | 1.278319 | 1.89E-32 | 1.89E-32 | 15.48769 | Up | Homo sapiens allograft inflammatory factor 1-like (AIF1L), transcript variant 3, mRNA [NM\_001185095] |
| A\_33\_P3215913 | TMEM184B | 1.005639 | 1.98E-32 | 1.98E-32 | 15.47995 | Up | transmembrane protein 184B [Source:HGNC Symbol;Acc:1310] [ENST00000403210] |
| A\_33\_P3258056 | PALM3 | 1.017605 | 2.12E-32 | 2.12E-32 | 15.46801 | Up | Homo sapiens paralemmin 3 (PALM3), mRNA [NM\_001145028] |
| A\_24\_P350397 | HSD3B1 | 1.233123 | 2.39E-32 | 2.39E-32 | 15.44761 | Up | Homo sapiens hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 (HSD3B1), mRNA [NM\_000862] |
| A\_33\_P3376080 | OR1J1 | 1.240398 | 2.47E-32 | 2.47E-32 | 15.44154 | Up | Homo sapiens olfactory receptor, family 1, subfamily J, member 1 (OR1J1), mRNA [NM\_001004451] |
| A\_33\_P3356762 | CDRT15L2 | 1.433894 | 2.96E-32 | 2.96E-32 | 15.41094 | Up | Homo sapiens CMT1A duplicated region transcript 15-like 2 (CDRT15L2), mRNA [NM\_001190790] |
| A\_23\_P144020 | CNTN4 | 1.007321 | 4.22E-32 | 4.22E-32 | 15.34994 | Up | Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA [NM\_175613] |
| A\_21\_P0001844 | XLOC\_001392 | 1.54554 | 7.48E-32 | 7.48E-32 | 15.25208 | Up | DA697576 NT2NE2 Homo sapiens cDNA clone NT2NE2018806 5', mRNA sequence [DA697576] |
| A\_33\_P3263614 | ASAP3 | 1.093818 | 8.25E-32 | 8.25E-32 | 15.23533 | Up | Homo sapiens ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 (ASAP3), transcript variant 2, mRNA [NM\_001143778] |
| A\_33\_P3369146 | ATP2B3 | 1.035393 | 8.57E-32 | 8.57E-32 | 15.22879 | Up | Homo sapiens ATPase, Ca++ transporting, plasma membrane 3 (ATP2B3), transcript variant 2, mRNA [NM\_001001344] |
| A\_23\_P127948 | ADM | 1.040057 | 1.11E-31 | 1.11E-31 | 15.18403 | Up | Homo sapiens adrenomedullin (ADM), mRNA [NM\_001124] |
| A\_33\_P3391778 | RALYL | 1.096345 | 1.55E-31 | 1.55E-31 | 15.12795 | Up | Homo sapiens RALY RNA binding protein-like (RALYL), transcript variant 3, mRNA [NM\_173848] |
| A\_23\_P154688 | SLC4A11 | 1.010303 | 1.94E-31 | 1.94E-31 | 15.0894 | Up | Homo sapiens solute carrier family 4, sodium borate transporter, member 11 (SLC4A11), transcript variant 2, mRNA [NM\_032034] |
| A\_23\_P404685 | LCE1A | 1.071685 | 2.02E-31 | 2.02E-31 | 15.08236 | Up | Homo sapiens late cornified envelope 1A (LCE1A), mRNA [NM\_178348] |
| A\_21\_P0009037 | XLOC\_011950 | 1.270343 | 2.23E-31 | 2.23E-31 | 15.06537 | Up | Q5CSV7\_CRYPV (Q5CSV7) Predicted secreted protein, signal peptide, partial (5%) [THC2662545] |
| A\_33\_P3409649 | ADAMTS2 | 1.085465 | 2.94E-31 | 2.94E-31 | 15.01882 | Up | Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 2 (ADAMTS2), transcript variant 2, mRNA [NM\_021599] |
| A\_23\_P354908 | NMNAT2 | 1.866523 | 2.95E-31 | 2.95E-31 | 15.0183 | Up | Homo sapiens nicotinamide nucleotide adenylyltransferase 2 (NMNAT2), transcript variant 1, mRNA [NM\_015039] |
| A\_33\_P3289034 | PKD2L1 | 1.116996 | 3.12E-31 | 3.12E-31 | 15.00841 | Up | Homo sapiens polycystic kidney disease 2-like 1 (PKD2L1), mRNA [NM\_016112] |
| A\_23\_P41599 | PCDHB8 | 1.17717 | 3.47E-31 | 3.47E-31 | 14.99027 | Up | Homo sapiens protocadherin beta 8 (PCDHB8), mRNA [NM\_019120] |
| A\_33\_P3815935 | TMEM50B | 1.069438 | 3.99E-31 | 3.99E-31 | 14.96657 | Up | RST40456 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG220668] |
| A\_33\_P3268838 | CPEB1 | 1.644318 | 4.09E-31 | 4.09E-31 | 14.96243 | Up | Homo sapiens cytoplasmic polyadenylation element binding protein 1 (CPEB1), transcript variant 1, mRNA [NM\_030594] |
| A\_33\_P3248982 | FAIM2 | 1.387088 | 4.22E-31 | 4.22E-31 | 14.95717 | Up | Homo sapiens Fas apoptotic inhibitory molecule 2 (FAIM2), mRNA [NM\_012306] |
| A\_33\_P3234222 | TSPO2 | 1.113068 | 4.29E-31 | 4.29E-31 | 14.95445 | Up | Homo sapiens translocator protein 2 (TSPO2), transcript variant 1, mRNA [NM\_001010873] |
| A\_33\_P3418710 | PRAMEF12 | 1.166136 | 4.45E-31 | 4.45E-31 | 14.94794 | Up | Homo sapiens PRAME family member 12 (PRAMEF12), mRNA [NM\_001080830] |
| A\_23\_P153855 | ZNF492 | 1.415228 | 4.78E-31 | 4.78E-31 | 14.93607 | Up | Homo sapiens zinc finger protein 492 (ZNF492), mRNA [NM\_020855] |
| A\_21\_P0013380 | XLOC\_l2\_013427 | 2.205048 | 5.29E-31 | 5.29E-31 | 14.91858 | Up | DB064874 TESTI4 Homo sapiens cDNA clone TESTI4005771 5', mRNA sequence [DB064874] |
| A\_32\_P160896 | FTMT | 1.803873 | 5.92E-31 | 5.92E-31 | 14.89967 | Up | Homo sapiens ferritin mitochondrial (FTMT), nuclear gene encoding mitochondrial protein, mRNA [NM\_177478] |
| A\_24\_P272254 | SPACA5 | 1.176182 | 6.19E-31 | 6.19E-31 | 14.89186 | Up | Homo sapiens sperm acrosome associated 5 (SPACA5), mRNA [NM\_205856] |
| A\_24\_P289795 | LINC00302 | 1.034366 | 7.9E-31 | 7.9E-31 | 14.85057 | Up | Homo sapiens skin-specific protein (xp33) mRNA, partial cds. [AF005082] |
| A\_33\_P3268892 | GDNF | 1.372933 | 8.16E-31 | 8.16E-31 | 14.84499 | Up | Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant 3, mRNA [NM\_001190468] |
| A\_33\_P3209615 | KRTAP4-8 | 1.172054 | 8.23E-31 | 8.23E-31 | 14.84357 | Up | Homo sapiens keratin associated protein 4-8 (KRTAP4-8), mRNA [NM\_031960] |
| A\_33\_P3333603 | SMOC1 | 1.036681 | 8.71E-31 | 8.71E-31 | 14.83405 | Up | Homo sapiens SPARC related modular calcium binding 1 (SMOC1), transcript variant 2, mRNA [NM\_022137] |
| A\_33\_P3334292 | PPIAL4G | 1.284916 | 9.24E-31 | 9.24E-31 | 14.82386 | Up | Homo sapiens cDNA FLJ16804 fis, clone TESTI4020460, highly similar to Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8). [AK123006] |
| A\_23\_P89601 | KRT32 | 1.439012 | 9.64E-31 | 9.64E-31 | 14.81672 | Up | Homo sapiens keratin 32 (KRT32), mRNA [NM\_002278] |
| A\_33\_P3291097 | BCAM | 1.013126 | 1.07E-30 | 1.07E-30 | 14.79885 | Up | Homo sapiens basal cell adhesion molecule (Lutheran blood group) (BCAM), transcript variant 2, mRNA [NM\_001013257] |
| A\_23\_P37914 | SLC5A11 | 1.007054 | 1.19E-30 | 1.19E-30 | 14.78169 | Up | Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 11 (SLC5A11), mRNA [NM\_052944] |
| A\_33\_P3235053 | TRIM47 | 1.390786 | 1.73E-30 | 1.73E-30 | 14.71789 | Up | Homo sapiens tripartite motif containing 47 (TRIM47), mRNA [NM\_033452] |
| A\_33\_P3312743 | KRTAP4-3 | 1.448253 | 1.81E-30 | 1.81E-30 | 14.7099 | Up | Homo sapiens keratin associated protein 4-3 (KRTAP4-3), mRNA [NM\_033187] |
| A\_33\_P3401753 | FFAR3 | 1.335996 | 1.94E-30 | 1.94E-30 | 14.69852 | Up | Homo sapiens free fatty acid receptor 3 (FFAR3), mRNA [NM\_005304] |
| A\_23\_P27107 | TM4SF5 | 1.617366 | 2.29E-30 | 2.29E-30 | 14.67023 | Up | Homo sapiens transmembrane 4 L six family member 5 (TM4SF5), mRNA [NM\_003963] |
| A\_24\_P133253 | KITLG | 1.435175 | 2.78E-30 | 2.78E-30 | 14.637 | Up | Homo sapiens KIT ligand (KITLG), transcript variant b, mRNA [NM\_000899] |
| A\_21\_P0004548 | XLOC\_004697 | 1.341291 | 2.99E-30 | 2.99E-30 | 14.62512 | Up | Q3GYV4\_9ACTO (Q3GYV4) Cytochrome c-type biogenesis protein CcmB, partial (9%) [THC2579237] |
| A\_23\_P387031 | COL23A1 | 1.468513 | 3.05E-30 | 3.05E-30 | 14.62146 | Up | Homo sapiens collagen, type XXIII, alpha 1 (COL23A1), mRNA [NM\_173465] |
| A\_23\_P140630 | LMAN1L | 1.113899 | 3.75E-30 | 3.75E-30 | 14.58661 | Up | Homo sapiens lectin, mannose-binding, 1 like (LMAN1L), mRNA [NM\_021819] |
| A\_23\_P14892 | IGFALS | 1.090998 | 4.42E-30 | 4.42E-30 | 14.55875 | Up | Homo sapiens insulin-like growth factor binding protein, acid labile subunit (IGFALS), transcript variant 2, mRNA [NM\_004970] |
| A\_23\_P421526 | ODF4 | 1.202732 | 4.65E-30 | 4.65E-30 | 14.55012 | Up | Homo sapiens outer dense fiber of sperm tails 4 (ODF4), mRNA [NM\_153007] |
| A\_33\_P3296831 | TP73 | 1.305518 | 5.09E-30 | 5.09E-30 | 14.53482 | Up | Homo sapiens tumor protein p73 (TP73), transcript variant 10, mRNA [NM\_001204186] |
| A\_23\_P407654 | C7orf51 | 0.973759 | 5.36E-30 | 5.36E-30 | 14.52615 | Up | Homo sapiens chromosome 7 open reading frame 51 (C7orf51), mRNA [NM\_173564] |
| A\_21\_P0010302 | XLOC\_014119 | 0.978148 | 6.67E-30 | 6.67E-30 | 14.48925 | Up | UI-E-CQ1-agc-p-01-0-UI.s1 UI-E-CQ1 Homo sapiens cDNA clone UI-E-CQ1-agc-p-01-0-UI 3', mRNA sequence [BM671314] |
| A\_23\_P5679 | CFC1 | 1.006829 | 7.94E-30 | 7.94E-30 | 14.45972 | Up | Homo sapiens cripto, FRL-1, cryptic family 1 (CFC1), mRNA [NM\_032545] |
| A\_23\_P258164 | CORT | 1.0697 | 8.34E-30 | 8.34E-30 | 14.45137 | Up | Homo sapiens cortistatin (CORT), mRNA [NM\_001302] |
| A\_23\_P23616 | PLEKHN1 | 1.003595 | 9.64E-30 | 9.64E-30 | 14.42695 | Up | Homo sapiens pleckstrin homology domain containing, family N member 1 (PLEKHN1), transcript variant 1, mRNA [NM\_032129] |
| A\_33\_P3306267 | PAX6 | 1.29781 | 9.84E-30 | 9.84E-30 | 14.42342 | Up | Homo sapiens paired box 6 (PAX6), transcript variant 1, mRNA [NM\_000280] |
| A\_21\_P0001983 | XLOC\_001919 | 1.371567 | 1.11E-29 | 1.11E-29 | 14.40311 | Up | HHAGE004050 Human liver regeneration after partial hepatectomy Homo sapiens cDNA, mRNA sequence [DW451320] |
| A\_33\_P3278058 | PIH1D2 | 1.504389 | 1.44E-29 | 1.44E-29 | 14.35924 | Up | Homo sapiens PIH1 domain containing 2 (PIH1D2), transcript variant 1, mRNA [NM\_138789] |
| A\_21\_P0008935 | XLOC\_011718 | 1.020808 | 1.47E-29 | 1.47E-29 | 14.35598 | Up | Q96RJ1\_HUMAN (Q96RJ1) FELIC, partial (3%) [THC2647533] |
| A\_23\_P3963 | CDR2L | 1.10989 | 1.89E-29 | 1.89E-29 | 14.31336 | Up | Homo sapiens cerebellar degeneration-related protein 2-like (CDR2L), mRNA [NM\_014603] |
| A\_23\_P77980 | SLC4A1 | 1.070906 | 1.98E-29 | 1.98E-29 | 14.30571 | Up | Homo sapiens solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group) (SLC4A1), mRNA [NM\_000342] |
| A\_24\_P168994 | TBC1D26 | 1.113958 | 2.13E-29 | 2.13E-29 | 14.29315 | Up | Homo sapiens TBC1 domain family, member 26 (TBC1D26), mRNA [NM\_178571] |
| A\_21\_P0010251 | XLOC\_013950 | 0.996411 | 2.35E-29 | 2.35E-29 | 14.27696 | Up | 601682492F1 NIH\_MGC\_9 Homo sapiens cDNA clone IMAGE:3952583 5', mRNA sequence [BE899115] |
| A\_23\_P142830 | PLA2R1 | 1.670651 | 3E-29 | 3E-29 | 14.23551 | Up | Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), transcript variant 1, mRNA [NM\_007366] |
| A\_21\_P0004085 | XLOC\_004679 | 1.044712 | 3.14E-29 | 3.14E-29 | 14.22788 | Up | Q8HN55\_BRUMA (Q8HN55) NADH dehydrogenase subunit 2, partial (5%) [THC2667709] |
| A\_33\_P3276813 | EYS | 1.586648 | 3.43E-29 | 3.43E-29 | 14.21317 | Up | Homo sapiens eyes shut homolog (Drosophila) (EYS), transcript variant 1, mRNA [NM\_001142800] |
| A\_21\_P0004303 | XLOC\_004572 | 1.07049 | 3.45E-29 | 3.45E-29 | 14.21186 | Up | Q5DF04\_SCHJA (Q5DF04) SJCHGC06588 protein, partial (17%) [THC2664632] |
| A\_33\_P3304533 | RNF207 | 1.179445 | 3.97E-29 | 3.97E-29 | 14.18854 | Up | ring finger protein 207 [Source:HGNC Symbol;Acc:32947] [ENST00000466994] |
| A\_33\_P3415491 | WDR90 | 1.098679 | 4.01E-29 | 4.01E-29 | 14.18685 | Up | Homo sapiens WD repeat domain 90 (WDR90), mRNA [NM\_145294] |
| A\_33\_P3401459 | SPTBN4 | 1.194252 | 4.4E-29 | 4.4E-29 | 14.17111 | Up | Homo sapiens spectrin, beta, non-erythrocytic 4 (SPTBN4), transcript variant sigma1, mRNA [NM\_020971] |
| A\_23\_P26522 | AQP8 | 1.083804 | 8.17E-29 | 8.17E-29 | 14.06708 | Up | Homo sapiens aquaporin 8 (AQP8), mRNA [NM\_001169] |
| A\_23\_P16063 | GRIK5 | 1.406362 | 8.77E-29 | 8.77E-29 | 14.05506 | Up | Homo sapiens glutamate receptor, ionotropic, kainate 5 (GRIK5), mRNA [NM\_002088] |
| A\_33\_P3355464 | LOC647983 | 1.146214 | 9.26E-29 | 9.26E-29 | 14.046 | Up | Homo sapiens cDNA FLJ44880 fis, clone BRAMY2035801. [AK126828] |
| A\_33\_P3323945 | CEND1 | 1.104487 | 1.32E-28 | 1.32E-28 | 13.98584 | Up | Homo sapiens cell cycle exit and neuronal differentiation 1 (CEND1), mRNA [NM\_016564] |
| A\_33\_P3413114 | ADAMTSL1 | 1.183531 | 1.63E-28 | 1.63E-28 | 13.95084 | Up | Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA [NM\_052866] |
| A\_24\_P390495 | CX3CL1 | 1.103452 | 1.86E-28 | 1.86E-28 | 13.92904 | Up | Homo sapiens chemokine (C-X3-C motif) ligand 1 (CX3CL1), mRNA [NM\_002996] |
| A\_23\_P153390 | CLEC4G | 1.142183 | 2.31E-28 | 2.31E-28 | 13.89261 | Up | Homo sapiens C-type lectin domain family 4, member G (CLEC4G), transcript variant 1, mRNA [NM\_198492] |
| A\_33\_P3329622 | HEATR8 | 1.04916 | 2.8E-28 | 2.8E-28 | 13.86036 | Up | HEAT repeat containing 8 [Source:HGNC Symbol;Acc:24802] [ENST00000395690] |
| A\_23\_P348524 | C20orf201 | 1.057108 | 3.65E-28 | 3.65E-28 | 13.81562 | Up | Homo sapiens chromosome 20 open reading frame 201 (C20orf201), mRNA [NM\_001007125] |
| A\_21\_P0002920 | XLOC\_003383 | 1.52236 | 3.98E-28 | 3.98E-28 | 13.80122 | Up | BX102253 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGp998I07110, mRNA sequence [BX102253] |
| A\_23\_P24784 | TNNI2 | 1.017691 | 6.95E-28 | 6.95E-28 | 13.70786 | Up | Homo sapiens troponin I type 2 (skeletal, fast) (TNNI2), transcript variant 1, mRNA [NM\_003282] |
| A\_23\_P4808 | PTGER1 | 1.261771 | 7.35E-28 | 7.35E-28 | 13.69851 | Up | Homo sapiens prostaglandin E receptor 1 (subtype EP1), 42kDa (PTGER1), mRNA [NM\_000955] |
| A\_33\_P3307568 | PYDC2 | 1.679579 | 7.4E-28 | 7.4E-28 | 13.69735 | Up | Homo sapiens pyrin domain containing 2 (PYDC2), mRNA [NM\_001083308] |
| A\_33\_P3335262 | TMEM146 | 0.989412 | 1.15E-27 | 1.15E-27 | 13.62434 | Up | Homo sapiens cDNA FLJ46209 fis, clone TESTI4011616. [AK128088] |
| A\_33\_P3306659 | LOC728254 | 1.440272 | 1.41E-27 | 1.41E-27 | 13.58939 | Up | Homo sapiens mRNA, clone: sF2, from chromosome 5q21-q22. [AB002446] |
| A\_24\_P341674 | DIO2 | 1.140987 | 2E-27 | 2E-27 | 13.53098 | Up | Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA [NM\_013989] |
| A\_33\_P3210368 | BCL7C | 1.145284 | 2.13E-27 | 2.13E-27 | 13.52046 | Up | B-cell CLL/lymphoma 7C [Source:HGNC Symbol;Acc:1006] [ENST00000380317] |
| A\_33\_P3228892 | LOC100130370 | 1.121993 | 2.15E-27 | 2.15E-27 | 13.51889 | Up | PREDICTED: Homo sapiens hypothetical protein LOC100130370 (LOC100130370), mRNA [XM\_001714096] |
| A\_33\_P3250887 | SYCE3 | 1.078108 | 2.75E-27 | 2.75E-27 | 13.47808 | Up | Homo sapiens synaptonemal complex central element protein 3 (SYCE3), mRNA [NM\_001123225] |
| A\_33\_P3408232 | MUC22 | 1.067464 | 3.04E-27 | 3.04E-27 | 13.46118 | Up | Homo sapiens mucin 22 (MUC22), mRNA [NM\_001198815] |
| A\_33\_P3393010 | PKDCC | 1.030254 | 3.15E-27 | 3.15E-27 | 13.4555 | Up | protein kinase domain containing, cytoplasmic homolog (mouse) [Source:HGNC Symbol;Acc:25123] [ENST00000492861] |
| A\_21\_P0006029 | XLOC\_007460 | 1.274246 | 3.16E-27 | 3.16E-27 | 13.45497 | Up | RST25042 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG205612] |
| A\_33\_P3215529 | TJP2 | 1.006149 | 3.65E-27 | 3.65E-27 | 13.43058 | Up | Homo sapiens tight junction protein ZO-2 isoform C mRNA, partial cds. [AF083893] |
| A\_21\_P0003451 | XLOC\_003907 | 1.068364 | 4.55E-27 | 4.55E-27 | 13.39403 | Up | Q8NHT0\_HUMAN (Q8NHT0) MGC32805 protein, partial (58%) [THC2520770] |
| A\_23\_P72340 | AVPR1B | 1.725479 | 5E-27 | 5E-27 | 13.37825 | Up | Homo sapiens arginine vasopressin receptor 1B (AVPR1B), mRNA [NM\_000707] |
| A\_33\_P3394297 | THNSL2 | 1.039403 | 5.02E-27 | 5.02E-27 | 13.37748 | Up | Homo sapiens threonine synthase-like 2 (S. cerevisiae) (THNSL2), transcript variant 2, mRNA [NM\_001244676] |
| A\_21\_P0007758 | XLOC\_010198 | 1.550169 | 5.46E-27 | 5.46E-27 | 13.36335 | Up | DA302221 BRHIP2 Homo sapiens cDNA clone BRHIP2017257 5', mRNA sequence [DA302221] |
| A\_33\_P3391796 | NOG | 1.539884 | 5.76E-27 | 5.76E-27 | 13.35469 | Up | Homo sapiens noggin (NOG), mRNA [NM\_005450] |
| A\_33\_P3246774 | LOC649201 | 1.051227 | 7.93E-27 | 7.93E-27 | 13.30122 | Up | PREDICTED: Homo sapiens paraneoplastic antigen like 6A-like (LOC649201), mRNA [XM\_001127211] |
| A\_23\_P420831 | TRIM10 | 1.227124 | 9.42E-27 | 9.42E-27 | 13.2726 | Up | Homo sapiens tripartite motif containing 10 (TRIM10), transcript variant 2, mRNA [NM\_052828] |
| A\_23\_P48550 | KIAA0284 | 1.11629 | 9.78E-27 | 9.78E-27 | 13.26628 | Up | Homo sapiens KIAA0284 (KIAA0284), transcript variant 2, mRNA [NM\_015005] |
| A\_21\_P0010330 | XLOC\_014197 | 1.458389 | 1.16E-26 | 1.16E-26 | 13.23796 | Up | PREDICTED: Homo sapiens hypothetical LOC100507657 (LOC100507657), miscRNA [XR\_109755] |
| A\_33\_P3256272 | KRTAP10-5 | 1.142226 | 1.21E-26 | 1.21E-26 | 13.23045 | Up | Homo sapiens keratin associated protein 10-5 (KRTAP10-5), mRNA [NM\_198694] |
| A\_33\_P3243929 | FLJ42022 | 1.001481 | 1.3E-26 | 1.3E-26 | 13.2188 | Up | Homo sapiens cDNA FLJ42022 fis, clone SPLEN2034678. [AK124016] |
| A\_33\_P3375358 | GPR31 | 1.240396 | 1.34E-26 | 1.34E-26 | 13.21376 | Up | Homo sapiens G protein-coupled receptor 31 (GPR31), mRNA [NM\_005299] |
| A\_33\_P3297244 | GAS2L2 | 1.137158 | 1.37E-26 | 1.37E-26 | 13.21024 | Up | Homo sapiens growth arrest-specific 2 like 2 (GAS2L2), mRNA [NM\_139285] |
| A\_32\_P43717 | FAM189A2 | 1.370416 | 1.5E-26 | 1.5E-26 | 13.1954 | Up | Homo sapiens family with sequence similarity 189, member A2 (FAM189A2), transcript variant 1, mRNA [NM\_004816] |
| A\_33\_P3367171 | SLC22A8 | 1.364362 | 1.7E-26 | 1.7E-26 | 13.17409 | Up | solute carrier family 22 (organic anion transporter), member 8 [Source:HGNC Symbol;Acc:10972] [ENST00000451262] |
| A\_33\_P3414964 | PTPRS | 1.305526 | 1.85E-26 | 1.85E-26 | 13.16033 | Up | Homo sapiens protein tyrosine phosphatase, receptor type, S, mRNA (cDNA clone IMAGE:5272670), complete cds. [BC029496] |
| A\_23\_P121374 | SEMA5B | 1.336903 | 2.16E-26 | 2.16E-26 | 13.13428 | Up | Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B (SEMA5B), transcript variant 1, mRNA [NM\_001031702] |
| A\_33\_P3609431 | ERVFRD-2 | 1.105993 | 2.36E-26 | 2.36E-26 | 13.11959 | Up | Homo sapiens cDNA FLJ45949 fis, clone PLACE7007973. [AK127846] |
| A\_23\_P348636 | FOXJ1 | 1.059039 | 2.63E-26 | 2.63E-26 | 13.10135 | Up | Homo sapiens forkhead box J1 (FOXJ1), mRNA [NM\_001454] |
| A\_23\_P27917 | OR10H1 | 1.074596 | 2.82E-26 | 2.82E-26 | 13.09008 | Up | Homo sapiens olfactory receptor, family 10, subfamily H, member 1 (OR10H1), mRNA [NM\_013940] |
| A\_32\_P202859 | H1FNT | 1.049702 | 5.28E-26 | 5.28E-26 | 12.98559 | Up | Homo sapiens H1 histone family, member N, testis-specific (H1FNT), mRNA [NM\_181788] |
| A\_24\_P917178 | MB | 1.519 | 5.51E-26 | 5.51E-26 | 12.97838 | Up | myoglobin [Source:HGNC Symbol;Acc:6915] [ENST00000472240] |
| A\_33\_P3399875 | C20orf144 | 1.098999 | 5.91E-26 | 5.91E-26 | 12.96675 | Up | Homo sapiens chromosome 20 open reading frame 144 (C20orf144), mRNA [NM\_080825] |
| A\_33\_P3369944 | ADAM21 | 1.493977 | 6.31E-26 | 6.31E-26 | 12.95582 | Up | Homo sapiens ADAM metallopeptidase domain 21 (ADAM21), mRNA [NM\_003813] |
| A\_33\_P3344482 | FERMT2 | 1.48729 | 6.87E-26 | 6.87E-26 | 12.94185 | Up | Homo sapiens fermitin family member 2 (FERMT2), transcript variant 3, mRNA [NM\_001135000] |
| A\_23\_P157513 | MOS | 1.159107 | 7.14E-26 | 7.14E-26 | 12.93539 | Up | Homo sapiens v-mos Moloney murine sarcoma viral oncogene homolog (MOS), mRNA [NM\_005372] |
| A\_21\_P0006533 | XLOC\_008163 | 0.98464 | 8.8E-26 | 8.8E-26 | 12.90059 | Up | Q86UH7\_HUMAN (Q86UH7) Envelope glycoprotein, partial (6%) [THC2774401] |
| A\_21\_P0011873 | XLOC\_l2\_007767 | 1.086843 | 9.11E-26 | 9.11E-26 | 12.89484 | Up | 09F\_J17.2 Novel Promoters 5' RACE-PCR Homo sapiens cDNA 5', mRNA sequence [EL584821] |
| A\_33\_P3231613 | CSAG3 | 1.410538 | 9.19E-26 | 9.19E-26 | 12.89339 | Up | Homo sapiens CSAG family, member 3 (CSAG3), transcript variant 2, mRNA [NM\_001129828] |
| A\_33\_P3467933 | LOC286154 | 1.015919 | 1.17E-25 | 1.17E-25 | 12.85299 | Up | Homo sapiens cDNA FLJ39420 fis, clone PLACE6018769. [AK096739] |
| A\_21\_P0009645 | XLOC\_012977 | 1.0364 | 1.46E-25 | 1.46E-25 | 12.81698 | Up | AGENCOURT\_6438675 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:5535242 5', mRNA sequence [BM464171] |
| A\_23\_P142125 | HRC | 1.17784 | 1.89E-25 | 1.89E-25 | 12.77342 | Up | Homo sapiens histidine rich calcium binding protein (HRC), mRNA [NM\_002152] |
| A\_19\_P00320842 | C17orf51 | 0.974454 | 2.68E-25 | 2.68E-25 | 12.71535 | Up | Homo sapiens chromosome 17 open reading frame 51 (C17orf51), mRNA [NM\_001113434] |
| A\_23\_P154566 | TOX2 | 0.983863 | 2.83E-25 | 2.83E-25 | 12.70642 | Up | Homo sapiens TOX high mobility group box family member 2 (TOX2), transcript variant 3, mRNA [NM\_032883] |
| A\_23\_P393749 | CATSPER3 | 1.0174 | 3.08E-25 | 3.08E-25 | 12.69242 | Up | Homo sapiens cation channel, sperm associated 3 (CATSPER3), mRNA [NM\_178019] |
| A\_32\_P153071 | VIPR2 | 1.142536 | 3.28E-25 | 3.28E-25 | 12.68205 | Up | Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), mRNA [NM\_003382] |
| A\_24\_P208825 | MUC4 | 1.414643 | 3.65E-25 | 3.65E-25 | 12.66411 | Up | Homo sapiens mucin 4, cell surface associated (MUC4), transcript variant 1, mRNA [NM\_018406] |
| A\_21\_P0004194 | XLOC\_005114 | 1.042645 | 3.67E-25 | 3.67E-25 | 12.66332 | Up | DA922163 SMINT2 Homo sapiens cDNA clone SMINT2008053 5', mRNA sequence [DA922163] |
| A\_33\_P3323559 | CRYAA | 1.417347 | 5.28E-25 | 5.28E-25 | 12.60312 | Up | Homo sapiens crystallin, alpha A (CRYAA), mRNA [NM\_000394] |
| A\_23\_P60742 | MYLPF | 1.027573 | 6.15E-25 | 6.15E-25 | 12.57779 | Up | Homo sapiens myosin light chain, phosphorylatable, fast skeletal muscle (MYLPF), mRNA [NM\_013292] |
| A\_23\_P167479 | IL17B | 1.128278 | 6.53E-25 | 6.53E-25 | 12.56785 | Up | Homo sapiens interleukin 17B (IL17B), mRNA [NM\_014443] |
| A\_24\_P14731 | PCSK1N | 1.075716 | 7.52E-25 | 7.52E-25 | 12.54444 | Up | Homo sapiens proprotein convertase subtilisin/kexin type 1 inhibitor (PCSK1N), mRNA [NM\_013271] |
| A\_23\_P134914 | LY6H | 1.438446 | 9.14E-25 | 9.14E-25 | 12.51206 | Up | Homo sapiens lymphocyte antigen 6 complex, locus H (LY6H), transcript variant 1, mRNA [NM\_002347] |
| A\_21\_P0008635 | XLOC\_011261 | 1.105832 | 9.78E-25 | 9.78E-25 | 12.50073 | Up | RST33102 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG213495] |
| A\_19\_P00318461 | XLOC\_001942 | 0.989224 | 1.02E-24 | 1.02E-24 | 12.49342 | Up | GB |
| A\_23\_P9340 | BARHL1 | 0.976874 | 1.13E-24 | 1.13E-24 | 12.47702 | Up | Homo sapiens BarH-like homeobox 1 (BARHL1), mRNA [NM\_020064] |
| A\_23\_P160177 | ATP1A4 | 1.474213 | 1.36E-24 | 1.36E-24 | 12.44585 | Up | Homo sapiens ATPase, Na+/K+ transporting, alpha 4 polypeptide (ATP1A4), transcript variant 1, mRNA [NM\_144699] |
| A\_21\_P0001412 | XLOC\_000544 | 1.288144 | 1.46E-24 | 1.46E-24 | 12.43458 | Up | DB315502 FCBBF3 Homo sapiens cDNA clone FCBBF3004916 3', mRNA sequence [DB315502] |
| A\_24\_P328524 | KALRN | 1.344638 | 1.5E-24 | 1.5E-24 | 12.4299 | Up | Homo sapiens kalirin, RhoGEF kinase (KALRN), transcript variant 2, mRNA [NM\_003947] |
| A\_33\_P3273457 | SPATA21 | 1.17464 | 1.57E-24 | 1.57E-24 | 12.42186 | Up | spermatogenesis associated 21 [Source:HGNC Symbol;Acc:28026] [ENST00000375577] |
| A\_23\_P213857 | C7 | 1.016384 | 1.58E-24 | 1.58E-24 | 12.42072 | Up | Homo sapiens complement component 7 (C7), mRNA [NM\_000587] |
| A\_21\_P0009619 | FLJ37638 | 1.181565 | 1.75E-24 | 1.75E-24 | 12.40405 | Up | ho44f03.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:3040253 3', mRNA sequence [BE044391] |
| A\_21\_P0007498 | XLOC\_010247 | 1.557898 | 1.88E-24 | 1.88E-24 | 12.3928 | Up | Q3IK43\_PSEHT (Q3IK43) Membrane-bound ATP synthase subunit, F1-F0-type proton-ATPase, partial (10%) [THC2610025] |
| A\_33\_P3245228 | BPIFA1 | 1.154733 | 2.04E-24 | 2.04E-24 | 12.37874 | Up | Homo sapiens BPI fold containing family A, member 1 (BPIFA1), transcript variant 2, mRNA [NM\_130852] |
| A\_21\_P0000971 | XLOC\_000181 | 1.255259 | 2.24E-24 | 2.24E-24 | 12.36329 | Up | RST35923 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG216108] |
| A\_21\_P0006732 | XLOC\_008713 | 1.230887 | 2.36E-24 | 2.36E-24 | 12.35464 | Up | XM\_750535 peroxisomal membrane anchor protein {Aspergillus fumigatus Af293} (exp=-1; wgp=0; cg=0), partial (4%) [THC2741636] |
| A\_33\_P3230239 | CSMD1 | 1.396985 | 2.72E-24 | 2.72E-24 | 12.33122 | Up | Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA [NM\_033225] |
| A\_23\_P125408 | DOHH | 1.039652 | 2.73E-24 | 2.73E-24 | 12.3307 | Up | Homo sapiens deoxyhypusine hydroxylase/monooxygenase (DOHH), transcript variant 2, mRNA [NM\_031304] |
| A\_23\_P148737 | MYBPH | 1.126035 | 3.19E-24 | 3.19E-24 | 12.30482 | Up | Homo sapiens myosin binding protein H (MYBPH), mRNA [NM\_004997] |
| A\_33\_P3331335 | TET3 | 1.021636 | 3.65E-24 | 3.65E-24 | 12.2823 | Up | Homo sapiens tet methylcytosine dioxygenase 3 (TET3), mRNA [NM\_144993] |
| A\_23\_P11843 | LRRN2 | 1.136739 | 3.76E-24 | 3.76E-24 | 12.27757 | Up | Homo sapiens leucine rich repeat neuronal 2 (LRRN2), transcript variant 2, mRNA [NM\_201630] |
| A\_23\_P8938 | ADRA1A | 1.444614 | 3.8E-24 | 3.8E-24 | 12.2759 | Up | Homo sapiens adrenergic, alpha-1A-, receptor (ADRA1A), transcript variant 4, mRNA [NM\_033304] |
| A\_23\_P18751 | TMPRSS11E | 1.231744 | 4.02E-24 | 4.02E-24 | 12.2663 | Up | Homo sapiens transmembrane protease, serine 11E (TMPRSS11E), mRNA [NM\_014058] |
| A\_33\_P3240249 | LOC100129125 | 1.140124 | 4.61E-24 | 4.61E-24 | 12.24361 | Up | Homo sapiens cDNA FLJ43724 fis, clone TESOP2007688. [AK125712] |
| A\_33\_P3300172 | SPON2 | 1.009656 | 4.82E-24 | 4.82E-24 | 12.2362 | Up | Homo sapiens cDNA FLJ42615 fis, clone BRACE3014231. [AK124606] |
| A\_23\_P119936 | REG3A | 1.008416 | 4.84E-24 | 4.84E-24 | 12.2358 | Up | Homo sapiens regenerating islet-derived 3 alpha (REG3A), transcript variant 2, mRNA [NM\_138938] |
| A\_33\_P3266078 | OR2AG1 | 1.255112 | 5.28E-24 | 5.28E-24 | 12.22109 | Up | Homo sapiens olfactory receptor, family 2, subfamily AG, member 1 (OR2AG1), mRNA [NM\_001004489] |
| A\_33\_P3249076 | HOGA1 | 1.147173 | 5.54E-24 | 5.54E-24 | 12.21311 | Up | 4-hydroxy-2-oxoglutarate aldolase 1 [Source:HGNC Symbol;Acc:25155] [ENST00000465608] |
| A\_24\_P6903 | ACTBL2 | 2.060092 | 6.65E-24 | 6.65E-24 | 12.18295 | Up | Homo sapiens actin, beta-like 2 (ACTBL2), mRNA [NM\_001017992] |
| A\_33\_P3364520 | KRTAP6-1 | 1.144349 | 7.41E-24 | 7.41E-24 | 12.16511 | Up | Homo sapiens keratin associated protein 6-1 (KRTAP6-1), mRNA [NM\_181602] |
| A\_23\_P28815 | CYP24A1 | 1.032801 | 7.54E-24 | 7.54E-24 | 12.1621 | Up | Homo sapiens cytochrome P450, family 24, subfamily A, polypeptide 1 (CYP24A1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM\_000782] |
| A\_32\_P112493 | PKDCC | 1.193968 | 1.22E-23 | 1.22E-23 | 12.08182 | Up | Homo sapiens protein kinase domain containing, cytoplasmic homolog (mouse) (PKDCC), mRNA [NM\_138370] |
| A\_32\_P125771 | RGS22 | 1.310272 | 1.53E-23 | 1.53E-23 | 12.04526 | Up | Homo sapiens regulator of G-protein signaling 22 (RGS22), mRNA [NM\_015668] |
| A\_23\_P344578 | FAM154A | 1.820469 | 1.66E-23 | 1.66E-23 | 12.03163 | Up | Homo sapiens family with sequence similarity 154, member A (FAM154A), mRNA [NM\_153707] |
| A\_33\_P3336262 | KIAA1751 | 1.161216 | 1.69E-23 | 1.69E-23 | 12.02837 | Up | chromosome 1 open reading frame 222 [Source:HGNC Symbol;Acc:27917] [ENST00000412120] |
| A\_21\_P0000962 | XLOC\_000117 | 1.372732 | 1.87E-23 | 1.87E-23 | 12.01214 | Up | UI-E-EJ1-ajs-j-02-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone UI-E-EJ1-ajs-j-02-0-UI 5', mRNA sequence [BQ188996] |
| A\_21\_P0010808 | C10orf112 | 1.394557 | 2.05E-23 | 2.05E-23 | 11.99643 | Up | PREDICTED: Homo sapiens chromosome 10 open reading frame 112 (C10orf112), mRNA [XM\_003403619] |
| A\_23\_P115190 | NGF | 0.988815 | 2.15E-23 | 2.15E-23 | 11.98889 | Up | Homo sapiens nerve growth factor (beta polypeptide) (NGF), mRNA [NM\_002506] |
| A\_33\_P3329984 | GGN | 1.217029 | 2.47E-23 | 2.47E-23 | 11.96557 | Up | Homo sapiens gametogenetin (GGN), mRNA [NM\_152657] |
| A\_23\_P99996 | MAGEL2 | 1.063773 | 2.49E-23 | 2.49E-23 | 11.96412 | Up | Homo sapiens MAGE-like 2 (MAGEL2), mRNA [NM\_019066] |
| A\_23\_P2492 | C1S | 1.070499 | 3.51E-23 | 3.51E-23 | 11.90742 | Up | Homo sapiens complement component 1, s subcomponent (C1S), transcript variant 2, mRNA [NM\_001734] |
| A\_33\_P3232120 | NELF | 1.291143 | 3.77E-23 | 3.77E-23 | 11.89538 | Up | nasal embryonic LHRH factor [Source:HGNC Symbol;Acc:29843] [ENST00000371468] |
| A\_21\_P0003367 | XLOC\_003546 | 1.329198 | 4.28E-23 | 4.28E-23 | 11.8747 | Up | GB |
| A\_23\_P154358 | PROM2 | 1.367702 | 4.78E-23 | 4.78E-23 | 11.8561 | Up | Homo sapiens prominin 2 (PROM2), transcript variant 3, mRNA [NM\_144707] |
| A\_32\_P133840 | TMCC2 | 1.037637 | 5.51E-23 | 5.51E-23 | 11.83265 | Up | Homo sapiens transmembrane and coiled-coil domain family 2 (TMCC2), transcript variant 1, mRNA [NM\_014858] |
| A\_24\_P197284 | C2orf85 | 0.988045 | 6.39E-23 | 6.39E-23 | 11.80818 | Up | Homo sapiens chromosome 2 open reading frame 85 (C2orf85), mRNA [NM\_173821] |
| A\_21\_P0004532 | XLOC\_004626 | 1.368709 | 6.93E-23 | 6.93E-23 | 11.79462 | Up | Q5ZUK8\_LEGPH (Q5ZUK8) Flagellar assembly protein FliO, partial (11%) [THC2532279] |
| A\_33\_P3348625 | DNAL4 | 0.990588 | 7.31E-23 | 7.31E-23 | 11.78592 | Up | dynein, axonemal, light chain 4 [Source:HGNC Symbol;Acc:2955] [ENST00000406199] |
| A\_33\_P3290011 | LHFPL3 | 1.2934 | 9.34E-23 | 9.34E-23 | 11.74529 | Up | Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA [NM\_199000] |
| A\_21\_P0010362 | XLOC\_014251 | 1.076082 | 1.06E-22 | 1.06E-22 | 11.72452 | Up | ALU6\_HUMAN (P39193) Alu subfamily SP sequence contamination warning entry, partial (15%) [THC2591538] |
| A\_33\_P3527317 | LOC148638 | 1.002573 | 1.39E-22 | 1.39E-22 | 11.67892 | Up | Homo sapiens cDNA FLJ25455 fis, clone TST08884. [AK058184] |
| A\_32\_P92489 | PKD1L2 | 1.430363 | 1.48E-22 | 1.48E-22 | 11.66895 | Up | Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, mRNA [NM\_052892] |
| A\_21\_P0009737 | XLOC\_013216 | 1.010025 | 1.57E-22 | 1.57E-22 | 11.65884 | Up | AGENCOURT\_7838751 NIH\_MGC\_82 Homo sapiens cDNA clone IMAGE:6101300 5', mRNA sequence [BQ429076] |
| A\_23\_P139600 | RASAL1 | 1.282435 | 1.79E-22 | 1.79E-22 | 11.63781 | Up | Homo sapiens RAS protein activator like 1 (GAP1 like) (RASAL1), transcript variant 2, mRNA [NM\_004658] |
| A\_24\_P7600 | FBXL7 | 0.989367 | 1.9E-22 | 1.9E-22 | 11.62762 | Up | Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), mRNA [NM\_012304] |
| A\_32\_P429687 | TRIM72 | 1.062378 | 1.95E-22 | 1.95E-22 | 11.62296 | Up | Homo sapiens tripartite motif containing 72 (TRIM72), mRNA [NM\_001008274] |
| A\_33\_P3293456 | GATA4 | 1.004743 | 2.4E-22 | 2.4E-22 | 11.58894 | Up | Homo sapiens GATA binding protein 4 (GATA4), mRNA [NM\_002052] |
| A\_33\_P3334688 | CPNE2 | 1.090406 | 2.82E-22 | 2.82E-22 | 11.5622 | Up | Homo sapiens cDNA FLJ44150 fis, clone THYMU2031046. [AK126138] |
| A\_33\_P3402817 | CRHR1 | 0.971846 | 3.57E-22 | 3.57E-22 | 11.52319 | Up | Homo sapiens corticotropin releasing hormone receptor 1 (CRHR1), transcript variant 4, mRNA [NM\_001145148] |
| A\_23\_P118722 | ASGR1 | 1.185766 | 3.62E-22 | 3.62E-22 | 11.52078 | Up | Homo sapiens asialoglycoprotein receptor 1 (ASGR1), transcript variant 1, mRNA [NM\_001671] |
| A\_33\_P3284925 | VLDLR | 1.044746 | 3.7E-22 | 3.7E-22 | 11.51742 | Up | Homo sapiens very low density lipoprotein receptor (VLDLR), transcript variant 2, mRNA [NM\_001018056] |
| A\_21\_P0005260 | XLOC\_006245 | 1.031875 | 3.89E-22 | 3.89E-22 | 11.50889 | Up |  |
| A\_33\_P3290677 | HELT | 1.208067 | 4.27E-22 | 4.27E-22 | 11.4935 | Up | Homo sapiens helt bHLH transcription factor (HELT), mRNA [NM\_001029887] |
| A\_21\_P0004062 | XLOC\_004555 | 1.041966 | 4.42E-22 | 4.42E-22 | 11.48794 | Up | 601186154F1 NIH\_MGC\_8 Homo sapiens cDNA clone IMAGE:3543708 5', mRNA sequence [BE270324] |
| A\_21\_P0013618 | FLJ35024 | 1.34106 | 4.69E-22 | 4.69E-22 | 11.47807 | Up |  |
| A\_24\_P85258 | KIAA1751 | 2.276736 | 6.36E-22 | 6.36E-22 | 11.4275 | Up | Homo sapiens KIAA1751 (KIAA1751), mRNA [NM\_001080484] |
| A\_23\_P360964 | DACT3 | 1.073858 | 6.68E-22 | 6.68E-22 | 11.41936 | Up | Homo sapiens dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis) (DACT3), mRNA [NM\_145056] |
| A\_32\_P206899 | DNAH2 | 1.036963 | 7.72E-22 | 7.72E-22 | 11.3953 | Up | Homo sapiens dynein, axonemal, heavy chain 2 (DNAH2), mRNA [NM\_020877] |
| A\_24\_P377124 | THPO | 1.177486 | 1.03E-21 | 1.03E-21 | 11.34822 | Up | Homo sapiens thrombopoietin (THPO), transcript variant 1, mRNA [NM\_000460] |
| A\_33\_P3224190 | SLC29A4 | 1.409804 | 1.25E-21 | 1.25E-21 | 11.31544 | Up | Homo sapiens solute carrier family 29 (nucleoside transporters), member 4 (SLC29A4), transcript variant 1, mRNA [NM\_001040661] |
| A\_21\_P0012065 | XLOC\_l2\_008008 | 1.098126 | 1.34E-21 | 1.34E-21 | 11.30343 | Up | ALU1\_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (4%) [THC2588358] |
| A\_24\_P51683 | CDK5R2 | 0.980183 | 1.4E-21 | 1.4E-21 | 11.29672 | Up | Homo sapiens cyclin-dependent kinase 5, regulatory subunit 2 (p39) (CDK5R2), mRNA [NM\_003936] |
| A\_33\_P3336552 | LOC100130701 | 1.450308 | 1.7E-21 | 1.7E-21 | 11.2648 | Up | PREDICTED: Homo sapiens hypothetical protein LOC100130701 (LOC100130701), mRNA [XM\_001717549] |
| A\_21\_P0005387 | XLOC\_006121 | 1.202512 | 1.7E-21 | 1.7E-21 | 11.26468 | Up | DB341740 TESTI4 Homo sapiens cDNA clone TESTI4046631 3', mRNA sequence [DB341740] |
| A\_23\_P157628 | DEFB4A | 1.210071 | 1.86E-21 | 1.86E-21 | 11.2496 | Up | Homo sapiens defensin, beta 4A (DEFB4A), mRNA [NM\_004942] |
| A\_33\_P3285299 | GPRIN2 | 1.077395 | 2.49E-21 | 2.49E-21 | 11.20115 | Up | Homo sapiens G protein regulated inducer of neurite outgrowth 2 (GPRIN2), mRNA [NM\_014696] |
| A\_33\_P3402635 | C16orf3 | 1.018428 | 3.63E-21 | 3.63E-21 | 11.13868 | Up | Homo sapiens chromosome 16 open reading frame 3 (C16orf3), mRNA [NM\_001214] |
| A\_33\_P3418175 | LYNX1 | 1.363497 | 5.23E-21 | 5.23E-21 | 11.07821 | Up | Homo sapiens Ly6/neurotoxin 1 (LYNX1), transcript variant 1, mRNA [NM\_023946] |
| A\_21\_P0011999 | XLOC\_l2\_007204 | 1.087711 | 5.29E-21 | 5.29E-21 | 11.07622 | Up |  |
| A\_23\_P501193 | KCNJ16 | 1.243046 | 6.12E-21 | 6.12E-21 | 11.05195 | Up | Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), transcript variant 2, mRNA [NM\_170741] |
| A\_33\_P3418798 | C4orf44 | 1.099109 | 6.64E-21 | 6.64E-21 | 11.03844 | Up | Homo sapiens chromosome 4 open reading frame 44 (C4orf44), mRNA [NM\_001042690] |
| A\_33\_P3288871 | SLC38A1 | 1.168907 | 7.62E-21 | 7.62E-21 | 11.01568 | Up | solute carrier family 38, member 1 [Source:HGNC Symbol;Acc:13447] [ENST00000550173] |
| A\_21\_P0009676 | XLOC\_012912 | 1.248849 | 7.71E-21 | 7.71E-21 | 11.01369 | Up | DC371110 NT2RP7 Homo sapiens cDNA clone NT2RP7010598 5', mRNA sequence [DC371110] |
| A\_24\_P215882 | ARHGDIG | 0.996187 | 8.22E-21 | 8.22E-21 | 11.0031 | Up | Homo sapiens Rho GDP dissociation inhibitor (GDI) gamma (ARHGDIG), mRNA [NM\_001176] |
| A\_23\_P422849 | FERD3L | 0.987724 | 8.51E-21 | 8.51E-21 | 10.99732 | Up | Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA [NM\_152898] |
| A\_33\_P3381092 | OR10W1 | 1.046159 | 8.74E-21 | 8.74E-21 | 10.99286 | Up | Homo sapiens olfactory receptor, family 10, subfamily W, member 1 (OR10W1), mRNA [NM\_207374] |
| A\_23\_P431971 | CRTAC1 | 1.159001 | 9.48E-21 | 9.48E-21 | 10.9793 | Up | Homo sapiens cartilage acidic protein 1 (CRTAC1), transcript variant 1, mRNA [NM\_018058] |
| A\_33\_P3228435 | FXYD1 | 1.006568 | 1.12E-20 | 1.12E-20 | 10.95123 | Up | Homo sapiens FXYD domain containing ion transport regulator 1 (FXYD1), transcript variant a, mRNA [NM\_005031] |
| A\_23\_P16214 | FBXW9 | 1.351275 | 1.19E-20 | 1.19E-20 | 10.94207 | Up | Homo sapiens F-box and WD repeat domain containing 9 (FBXW9), mRNA [NM\_032301] |
| A\_21\_P0012520 | XLOC\_l2\_010020 | 1.246802 | 1.3E-20 | 1.3E-20 | 10.92666 | Up | 1405340A protein 40kD. {Mus musculus} (exp=-1; wgp=0; cg=0), partial (46%) [THC2731531] |
| A\_33\_P3866448 | LOC286299 | 1.225993 | 1.59E-20 | 1.59E-20 | 10.89342 | Up | Homo sapiens mRNA; cDNA DKFZp686G1495 (from clone DKFZp686G1495). [BX648501] |
| A\_33\_P3313065 | OR5C1 | 0.989631 | 1.8E-20 | 1.8E-20 | 10.87254 | Up | Homo sapiens olfactory receptor, family 5, subfamily C, member 1 (OR5C1), mRNA [NM\_001001923] |
| A\_23\_P19428 | OR2J2 | 1.416609 | 1.84E-20 | 1.84E-20 | 10.86913 | Up | Homo sapiens olfactory receptor, family 2, subfamily J, member 2 (OR2J2), mRNA [NM\_030905] |
| A\_21\_P0001249 | XLOC\_001287 | 1.098935 | 1.96E-20 | 1.96E-20 | 10.85877 | Up | CR743846 NCI\_CGAP\_Co8 Homo sapiens cDNA clone IMAGp971M0781 ; IMAGE:1874535 5', mRNA sequence [CR743846] |
| A\_23\_P97283 | PAQR6 | 1.174275 | 2.1E-20 | 2.1E-20 | 10.84755 | Up | Homo sapiens progestin and adipoQ receptor family member VI (PAQR6), transcript variant 1, mRNA [NM\_024897] |
| A\_32\_P171313 | GNB4 | 1.062058 | 2.77E-20 | 2.77E-20 | 10.80132 | Up | Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), mRNA [NM\_021629] |
| A\_23\_P78980 | B3GNT3 | 1.075026 | 2.84E-20 | 2.84E-20 | 10.79729 | Up | Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3 (B3GNT3), mRNA [NM\_014256] |
| A\_33\_P3358469 | GLI2 | 1.260169 | 3.53E-20 | 3.53E-20 | 10.76065 | Up | Homo sapiens GLI family zinc finger 2 (GLI2), mRNA [NM\_005270] |
| A\_33\_P3248539 | LCN1 | 1.0086 | 4.27E-20 | 4.27E-20 | 10.72928 | Up | Homo sapiens lipocalin 1 (tear prealbumin) (LCN1), mRNA [NM\_002297] |
| A\_23\_P84576 | ANTXR1 | 1.460712 | 4.45E-20 | 4.45E-20 | 10.72227 | Up | Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 2, mRNA [NM\_053034] |
| A\_33\_P3347639 | MED18 | 1.492543 | 4.78E-20 | 4.78E-20 | 10.71027 | Up | Homo sapiens mediator complex subunit 18 (MED18), transcript variant 1, mRNA [NM\_017638] |
| A\_33\_P3650353 | SNORA33 | 1.140771 | 4.9E-20 | 4.9E-20 | 10.70641 | Up | wm38b12.x1 NCI\_CGAP\_Ut4 Homo sapiens cDNA clone IMAGE:2438207 3' similar to gb:X53505 40S RIBOSOMAL PROTEIN S12 (HUMAN);, mRNA sequence [AI887274] |
| A\_33\_P3372699 | SEC14L4 | 1.006988 | 4.93E-20 | 4.93E-20 | 10.70528 | Up | Homo sapiens SEC14-like 4 (S. cerevisiae) (SEC14L4), transcript variant 1, mRNA [NM\_174977] |
| A\_21\_P0004115 | XLOC\_004761 | 1.144001 | 4.93E-20 | 4.93E-20 | 10.7051 | Up | DB457834 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H013079F11 5', mRNA sequence [DB457834] |
| A\_33\_P3377750 | KLC3 | 1.272729 | 6.53E-20 | 6.53E-20 | 10.65839 | Up | Homo sapiens kinesin light chain 3 (KLC3), mRNA [NM\_177417] |
| A\_33\_P3408852 | EPHA8 | 1.298883 | 6.83E-20 | 6.83E-20 | 10.651 | Up | Homo sapiens EPH receptor A8 (EPHA8), transcript variant 2, mRNA [NM\_001006943] |
| A\_33\_P3357182 | C6orf146 | 1.059665 | 7.73E-20 | 7.73E-20 | 10.63033 | Up | chromosome 6 open reading frame 146 [Source:HGNC Symbol;Acc:21362] [ENST00000380188] |
| A\_33\_P3415778 | LOC100129721 | 1.644625 | 7.96E-20 | 7.96E-20 | 10.62548 | Up | Homo sapiens cDNA FLJ44685 fis, clone BRACE3011447. [AK126643] |
| A\_32\_P4262 | C20orf26 | 1.224541 | 9.86E-20 | 9.86E-20 | 10.58987 | Up | Homo sapiens chromosome 20 open reading frame 26 (C20orf26), transcript variant 1, mRNA [NM\_015585] |
| A\_33\_P3394689 | SLC6A2 | 1.228442 | 1.02E-19 | 1.02E-19 | 10.5839 | Up | Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), transcript variant 2, mRNA [NM\_001172501] |
| A\_21\_P0011962 | XLOC\_l2\_008252 | 1.20328 | 1.07E-19 | 1.07E-19 | 10.57649 | Up | Q658I5\_ORYSA (Q658I5) LMBR1 integral membrane family protein-like, partial (4%) [THC2624432] |
| A\_24\_P281036 | LRRC31 | 0.995468 | 1.08E-19 | 1.08E-19 | 10.57477 | Up | Homo sapiens leucine rich repeat containing 31 (LRRC31), mRNA [NM\_024727] |
| A\_23\_P158297 | BTNL3 | 0.977489 | 1.11E-19 | 1.11E-19 | 10.5705 | Up | Homo sapiens butyrophilin-like 3 (BTNL3), mRNA [NM\_197975] |
| A\_33\_P3358322 | LOC338667 | 0.986862 | 1.17E-19 | 1.17E-19 | 10.5607 | Up | Homo sapiens full length insert cDNA clone ZD42A08. [AF086259] |
| A\_33\_P3212959 | SPANXN4 | 1.320026 | 1.21E-19 | 1.21E-19 | 10.55607 | Up | Homo sapiens SPANX family, member N4 (SPANXN4), mRNA [NM\_001009613] |
| A\_23\_P87860 | MYF5 | 1.583469 | 1.21E-19 | 1.21E-19 | 10.55537 | Up | Homo sapiens myogenic factor 5 (MYF5), mRNA [NM\_005593] |
| A\_24\_P336983 | CAPN13 | 1.276908 | 1.47E-19 | 1.47E-19 | 10.5231 | Up | Homo sapiens calpain 13 (CAPN13), mRNA [NM\_144575] |
| A\_21\_P0005082 | XLOC\_005912 | 1.015255 | 1.72E-19 | 1.72E-19 | 10.49746 | Up | BX095160 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGp998P231830, mRNA sequence [BX095160] |
| A\_33\_P3355732 | UMODL1 | 1.340232 | 2.08E-19 | 2.08E-19 | 10.46558 | Up | uromodulin-like 1 [Source:HGNC Symbol;Acc:12560] [ENST00000491559] |
| A\_33\_P3272573 | PRDX4 | 1.405336 | 2.96E-19 | 2.96E-19 | 10.40656 | Up | peroxiredoxin 4 [Source:HGNC Symbol;Acc:17169] [ENST00000379349] |
| A\_23\_P42931 | CLEC2L | 1.199506 | 3.72E-19 | 3.72E-19 | 10.36822 | Up | Homo sapiens C-type lectin domain family 2, member L (CLEC2L), mRNA [NM\_001080511] |
| A\_33\_P3255829 | MXRA5 | 1.130505 | 3.94E-19 | 3.94E-19 | 10.3589 | Up | Homo sapiens matrix-remodelling associated 5 (MXRA5), mRNA [NM\_015419] |
| A\_21\_P0006066 | XLOC\_007643 | 1.20334 | 4.09E-19 | 4.09E-19 | 10.35268 | Up | 603076822F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5168765 5', mRNA sequence [BI825881] |
| A\_23\_P51311 | LELP1 | 1.168744 | 4.43E-19 | 4.43E-19 | 10.33934 | Up | Homo sapiens late cornified envelope-like proline-rich 1 (LELP1), mRNA [NM\_001010857] |
| A\_24\_P104512 | EVPL | 0.995719 | 4.63E-19 | 4.63E-19 | 10.33168 | Up | Homo sapiens envoplakin (EVPL), mRNA [NM\_001988] |
| A\_33\_P3436935 | LOC284930 | 0.978382 | 4.84E-19 | 4.84E-19 | 10.3245 | Up | Homo sapiens cDNA FLJ35788 fis, clone TESTI2005683. [AK093107] |
| A\_33\_P3228709 | KRTAP5-7 | 1.062225 | 5.16E-19 | 5.16E-19 | 10.31355 | Up | Homo sapiens keratin associated protein 5-7 (KRTAP5-7), mRNA [NM\_001012503] |
| A\_21\_P0002086 | XLOC\_002250 | 0.977322 | 6.44E-19 | 6.44E-19 | 10.27652 | Up | Q2VAZ9\_HUMAN (Q2VAZ9) Spd4, partial (46%) [THC2760474] |
| A\_23\_P151598 | CPNE6 | 1.140993 | 6.55E-19 | 6.55E-19 | 10.2737 | Up | Homo sapiens copine VI (neuronal) (CPNE6), mRNA [NM\_006032] |
| A\_32\_P174693 | LOC729059 | 0.990322 | 7.14E-19 | 7.14E-19 | 10.25945 | Up | Homo sapiens uncharacterized LOC729059 (LOC729059), mRNA [NM\_001242521] |
| A\_23\_P1973 | KCNJ11 | 1.215673 | 7.8E-19 | 7.8E-19 | 10.2445 | Up | Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11), transcript variant 1, mRNA [NM\_000525] |
| A\_21\_P0007168 | XLOC\_009021 | 1.142874 | 9.05E-19 | 9.05E-19 | 10.21966 | Up | Q2DDM0\_ACICY (Q2DDM0) MiaB-like tRNA modifying enzyme, partial (4%) [THC2607848] |
| A\_24\_P359441 | CRYBB3 | 1.189474 | 9.33E-19 | 9.33E-19 | 10.21468 | Up | Homo sapiens crystallin, beta B3 (CRYBB3), mRNA [NM\_004076] |
| A\_21\_P0010832 | XLOC\_l2\_001640 | 1.059557 | 1.12E-18 | 1.12E-18 | 10.18446 | Up | Q89ZP0\_BACTN (Q89ZP0) Thioredoxin reductase, partial (5%) [THC2749976] |
| A\_21\_P0002098 | XLOC\_002303 | 1.178465 | 1.12E-18 | 1.12E-18 | 10.18396 | Up | DA677089 NETRP2 Homo sapiens cDNA clone NETRP2008290 5', mRNA sequence [DA677089] |
| A\_33\_P3559060 | PNPLA5 | 1.243101 | 1.2E-18 | 1.2E-18 | 10.17204 | Up | Homo sapiens patatin-like phospholipase domain containing 5 (PNPLA5), transcript variant 1, mRNA [NM\_138814] |
| A\_23\_P145681 | ACTL6B | 1.023594 | 1.23E-18 | 1.23E-18 | 10.16859 | Up | Homo sapiens actin-like 6B (ACTL6B), mRNA [NM\_016188] |
| A\_33\_P3326822 | INMT | 1.31783 | 1.4E-18 | 1.4E-18 | 10.14648 | Up | indolethylamine N-methyltransferase [Source:HGNC Symbol;Acc:6069] [ENST00000461246] |
| A\_33\_P3238533 | C18orf34 | 1.268258 | 1.61E-18 | 1.61E-18 | 10.12323 | Up | Homo sapiens chromosome 18 open reading frame 34 (C18orf34), transcript variant 1, mRNA [NM\_001105528] |
| A\_23\_P24676 | OR8U1 | 1.282219 | 1.72E-18 | 1.72E-18 | 10.11182 | Up | Homo sapiens olfactory receptor, family 8, subfamily U, member 1 (OR8U1), mRNA [NM\_001005204] |
| A\_21\_P0005135 | XLOC\_005478 | 0.998565 | 1.75E-18 | 1.75E-18 | 10.10966 | Up | 603075329F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5167207 5', mRNA sequence [BI828078] |
| A\_21\_P0000977 | XLOC\_000212 | 1.175147 | 2.01E-18 | 2.01E-18 | 10.08619 | Up | Q3QHX9\_9GAMM (Q3QHX9) Transcriptional regulatory protein, C-terminal, partial (3%) [THC2684459] |
| A\_33\_P3417487 | SCUBE1 | 0.986791 | 2.22E-18 | 2.22E-18 | 10.06951 | Up | signal peptide, CUB domain, EGF-like 1 [Source:HGNC Symbol;Acc:13441] [ENST00000290460] |
| A\_21\_P0004052 | XLOC\_004526 | 0.970128 | 2.35E-18 | 2.35E-18 | 10.06006 | Up | DB035819 TESTI2 Homo sapiens cDNA clone TESTI2021302 5', mRNA sequence [DB035819] |
| A\_33\_P3268478 | ENO4 | 1.023236 | 2.53E-18 | 2.53E-18 | 10.04762 | Up | enolase family member 4 [Source:HGNC Symbol;Acc:31670] [ENST00000369207] |
| A\_21\_P0005143 | XLOC\_005531 | 1.009209 | 2.74E-18 | 2.74E-18 | 10.03406 | Up | Q28XZ4\_DROPS (Q28XZ4) GA12204-PA (Fragment), partial (6%) [THC2627193] |
| A\_21\_P0004149 | XLOC\_004916 | 0.97524 | 2.86E-18 | 2.86E-18 | 10.02697 | Up | Q566Q1\_HUMAN (Q566Q1) LAMA3 protein (Fragment), partial (3%) [THC2605755] |
| A\_21\_P0009702 | XLOC\_013028 | 1.120177 | 3.03E-18 | 3.03E-18 | 10.0171 | Up | Q7Z6P5\_HUMAN (Q7Z6P5) MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (Fragment), partial (9%) [THC2614689] |
| A\_32\_P176018 | ACTL8 | 1.019061 | 3.18E-18 | 3.18E-18 | 10.0092 | Up | Homo sapiens actin-like 8 (ACTL8), mRNA [NM\_030812] |
| A\_33\_P3237552 | FIBCD1 | 1.015612 | 3.52E-18 | 3.52E-18 | 9.991923 | Up | Homo sapiens fibrinogen C domain containing 1 (FIBCD1), transcript variant 1, mRNA [NM\_032843] |
| A\_33\_P3314301 | SV2C | 0.998669 | 4.86E-18 | 4.86E-18 | 9.93783 | Up | Homo sapiens synaptic vesicle glycoprotein 2C (SV2C), mRNA [NM\_014979] |
| A\_21\_P0009664 | XLOC\_013052 | 1.001634 | 5.79E-18 | 5.79E-18 | 9.908399 | Up | UI-H-BI3-ajv-a-04-0-UI.s1 NCI\_CGAP\_Sub5 Homo sapiens cDNA clone IMAGE:2732839 3', mRNA sequence [AW444525] |
| A\_21\_P0004096 | LOC100505625 | 1.127401 | 6.13E-18 | 6.13E-18 | 9.898793 | Up | qe59g02.x1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone IMAGE:1743314 3', mRNA sequence [AI193806] |
| A\_33\_P3352019 | SCARA3 | 0.976538 | 6.15E-18 | 6.15E-18 | 9.89834 | Up | Homo sapiens scavenger receptor class A, member 3 (SCARA3), transcript variant 2, mRNA [NM\_182826] |
| A\_23\_P65472 | RNASE11 | 1.165062 | 6.48E-18 | 6.48E-18 | 9.889386 | Up | Homo sapiens ribonuclease, RNase A family, 11 (non-active) (RNASE11), mRNA [NM\_145250] |
| A\_23\_P162547 | MYL2 | 1.590662 | 8.07E-18 | 8.07E-18 | 9.852553 | Up | Homo sapiens myosin, light chain 2, regulatory, cardiac, slow (MYL2), mRNA [NM\_000432] |
| A\_33\_P3327158 | LOC100131432 | 1.15008 | 1.07E-17 | 1.07E-17 | 9.80475 | Up | Homo sapiens cDNA FLJ45862 fis, clone OCBBF3000830. [AK127761] |
| A\_32\_P114746 | C1orf111 | 1.013096 | 1.12E-17 | 1.12E-17 | 9.79675 | Up | Homo sapiens chromosome 1 open reading frame 111 (C1orf111), mRNA [NM\_182581] |
| A\_33\_P3703637 | LOC285300 | 1.143969 | 1.16E-17 | 1.16E-17 | 9.790782 | Up | Homo sapiens cDNA FLJ38336 fis, clone FCBBF3026678. [AK095655] |
| A\_23\_P84230 | OTP | 1.176187 | 1.46E-17 | 1.46E-17 | 9.752152 | Up | Homo sapiens orthopedia homeobox (OTP), mRNA [NM\_032109] |
| A\_24\_P64653 | METTL7B | 1.234915 | 1.58E-17 | 1.58E-17 | 9.739494 | Up | Homo sapiens methyltransferase like 7B (METTL7B), mRNA [NM\_152637] |
| A\_33\_P3241204 | CALHM3 | 1.088066 | 1.59E-17 | 1.59E-17 | 9.737775 | Up | Homo sapiens calcium homeostasis modulator 3 (CALHM3), mRNA [NM\_001129742] |
| A\_24\_P280113 | IL13RA1 | 1.065099 | 1.63E-17 | 1.63E-17 | 9.733926 | Up | Homo sapiens interleukin 13 receptor, alpha 1 (IL13RA1), mRNA [NM\_001560] |
| A\_23\_P257355 | OTC | 1.5148 | 1.82E-17 | 1.82E-17 | 9.715919 | Up | Homo sapiens ornithine carbamoyltransferase (OTC), nuclear gene encoding mitochondrial protein, mRNA [NM\_000531] |
| A\_33\_P3728167 | CDH5 | 1.184805 | 1.82E-17 | 1.82E-17 | 9.715806 | Up | Homo sapiens cadherin 5, type 2 (vascular endothelium) (CDH5), mRNA [NM\_001795] |
| A\_23\_P154849 | OLIG1 | 1.162634 | 2.1E-17 | 2.1E-17 | 9.690994 | Up | Homo sapiens oligodendrocyte transcription factor 1 (OLIG1), mRNA [NM\_138983] |
| A\_33\_P3266863 | TMEM53 | 1.021497 | 2.1E-17 | 2.1E-17 | 9.690987 | Up | Homo sapiens transmembrane protein 53 (TMEM53), mRNA [NM\_024587] |
| A\_21\_P0009972 | XLOC\_013559 | 1.007756 | 2.13E-17 | 2.13E-17 | 9.68898 | Up | AGENCOURT\_8511494 NIH\_MGC\_100 Homo sapiens cDNA clone IMAGE:6297052 5', mRNA sequence [BQ646539] |
| A\_23\_P336678 | GPHB5 | 0.982962 | 2.16E-17 | 2.16E-17 | 9.68626 | Up | Homo sapiens glycoprotein hormone beta 5 (GPHB5), mRNA [NM\_145171] |
| A\_24\_P322771 | TFF1 | 0.98845 | 2.26E-17 | 2.26E-17 | 9.678894 | Up | Homo sapiens trefoil factor 1 (TFF1), mRNA [NM\_003225] |
| A\_23\_P136978 | SRPX2 | 1.042044 | 2.32E-17 | 2.32E-17 | 9.674139 | Up | Homo sapiens sushi-repeat containing protein, X-linked 2 (SRPX2), mRNA [NM\_014467] |
| A\_33\_P3279276 | GRIP2 | 1.387737 | 2.5E-17 | 2.5E-17 | 9.661736 | Up | Homo sapiens glutamate receptor interacting protein 2 (GRIP2), mRNA [NM\_001080423] |
| A\_33\_P3252695 | CYTL1 | 1.080977 | 2.8E-17 | 2.8E-17 | 9.642741 | Up | Homo sapiens cytokine-like 1 (CYTL1), mRNA [NM\_018659] |
| A\_23\_P257962 | GRIN1 | 0.989972 | 2.87E-17 | 2.87E-17 | 9.638331 | Up | Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 1 (GRIN1), transcript variant NR1-3, mRNA [NM\_007327] |
| A\_23\_P130677 | C19orf80 | 1.007792 | 4.11E-17 | 4.11E-17 | 9.577704 | Up | Homo sapiens chromosome 19 open reading frame 80 (C19orf80), mRNA [NM\_018687] |
| A\_33\_P3418838 | TPD52 | 1.141616 | 4.53E-17 | 4.53E-17 | 9.561408 | Up | tumor protein D52 [Source:HGNC Symbol;Acc:12005] [ENST00000523564] |
| A\_23\_P107483 | OR3A3 | 1.210683 | 5.05E-17 | 5.05E-17 | 9.542914 | Up | Homo sapiens olfactory receptor, family 3, subfamily A, member 3 (OR3A3), mRNA [NM\_012373] |
| A\_33\_P3414267 | SSTR4 | 1.086681 | 5.73E-17 | 5.73E-17 | 9.521466 | Up | Homo sapiens somatostatin receptor 4 (SSTR4), mRNA [NM\_001052] |
| A\_33\_P3249888 | BEST3 | 1.027254 | 6.5E-17 | 6.5E-17 | 9.500081 | Up | Homo sapiens bestrophin 3 (BEST3), transcript variant 1, mRNA [NM\_032735] |
| A\_21\_P0001090 | XLOC\_000681 | 1.069895 | 6.66E-17 | 6.66E-17 | 9.496167 | Up | Q6NT14\_HUMAN (Q6NT14) ZNF80 protein (Fragment), partial (5%) [THC2673678] |
| A\_33\_P3354176 | MYOF | 1.074631 | 6.87E-17 | 6.87E-17 | 9.490744 | Up | myoferlin [Source:HGNC Symbol;Acc:3656] [ENST00000371488] |
| A\_23\_P142403 | TM6SF2 | 1.110439 | 6.93E-17 | 6.93E-17 | 9.489234 | Up | Homo sapiens transmembrane 6 superfamily member 2 (TM6SF2), mRNA [NM\_001001524] |
| A\_21\_P0006752 | XLOC\_008793 | 1.094952 | 8.02E-17 | 8.02E-17 | 9.464497 | Up | zw80a10.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:782490 3', mRNA sequence [AA448469] |
| A\_19\_P00321858 | LOC100506403 | 1.020535 | 8.41E-17 | 8.41E-17 | 9.456536 | Up | PREDICTED: Homo sapiens hypothetical LOC100506403 (LOC100506403), miscRNA [XR\_109672] |
| A\_19\_P00319822 | Q952V6 | 1.24285 | 8.52E-17 | 8.52E-17 | 9.454388 | Up | Q952V6\_9SMEG (Q952V6) Cytochrome b (Fragment), partial (5%) [THC2780555] |
| A\_21\_P0014941 | SDIM1 | 1.052208 | 9.18E-17 | 9.18E-17 | 9.441627 | Up | PREDICTED: Homo sapiens stress responsive DNAJB4 interacting membrane protein 1 (SDIM1), miscRNA [XR\_133440] |
| A\_23\_P71170 | TRPV6 | 1.016211 | 9.5E-17 | 9.5E-17 | 9.435874 | Up | Homo sapiens transient receptor potential cation channel, subfamily V, member 6 (TRPV6), mRNA [NM\_018646] |
| A\_33\_P3367748 | COL9A2 | 1.128506 | 1.04E-16 | 1.04E-16 | 9.421067 | Up | collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218] [ENST00000461118] |
| A\_21\_P0002142 | XLOC\_002517 | 1.030884 | 1.08E-16 | 1.08E-16 | 9.414356 | Up | Q25V96\_MYCVN (Q25V96) Maf-like protein, partial (5%) [THC2658162] |
| A\_23\_P254702 | DEK | 0.983726 | 1.09E-16 | 1.09E-16 | 9.411796 | Up | Homo sapiens DEK oncogene (DEK), transcript variant 1, mRNA [NM\_003472] |
| A\_23\_P126869 | PADI3 | 0.989609 | 1.25E-16 | 1.25E-16 | 9.389262 | Up | Homo sapiens peptidyl arginine deiminase, type III (PADI3), mRNA [NM\_016233] |
| A\_23\_P46482 | IL20 | 1.157365 | 1.36E-16 | 1.36E-16 | 9.374701 | Up | Homo sapiens interleukin 20 (IL20), mRNA [NM\_018724] |
| A\_23\_P157109 | ADCYAP1R1 | 1.018583 | 1.38E-16 | 1.38E-16 | 9.372703 | Up | Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1), transcript variant 3, mRNA [NM\_001118] |
| A\_23\_P164451 | TBX2 | 1.143476 | 1.57E-16 | 1.57E-16 | 9.350578 | Up | Homo sapiens T-box 2 (TBX2), mRNA [NM\_005994] |
| A\_23\_P202894 | ACRV1 | 1.022507 | 1.74E-16 | 1.74E-16 | 9.333089 | Up | Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 1, mRNA [NM\_001612] |
| A\_33\_P3262069 | OR2AG2 | 1.077413 | 2.19E-16 | 2.19E-16 | 9.293992 | Up | Homo sapiens olfactory receptor, family 2, subfamily AG, member 2 (OR2AG2), mRNA [NM\_001004490] |
| A\_21\_P0002679 | XLOC\_002368 | 1.08022 | 2.25E-16 | 2.25E-16 | 9.289467 | Up | AGENCOURT\_14358023 NIH\_MGC\_186 Homo sapiens cDNA clone IMAGE:30406428 5', mRNA sequence [CD512363] |
| A\_21\_P0008241 | XLOC\_010462 | 1.295105 | 2.27E-16 | 2.27E-16 | 9.288065 | Up | tt27c02.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2241986 3', mRNA sequence [AI655346] |
| A\_23\_P256205 | ABLIM3 | 1.009857 | 2.32E-16 | 2.32E-16 | 9.283832 | Up | Homo sapiens actin binding LIM protein family, member 3 (ABLIM3), mRNA [NM\_014945] |
| A\_23\_P55917 | SYT3 | 0.982312 | 2.43E-16 | 2.43E-16 | 9.276195 | Up | Homo sapiens synaptotagmin III (SYT3), transcript variant 1, mRNA [NM\_032298] |
| A\_23\_P115246 | FCN3 | 1.033529 | 2.66E-16 | 2.66E-16 | 9.260782 | Up | Homo sapiens ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen) (FCN3), transcript variant 1, mRNA [NM\_003665] |
| A\_23\_P211212 | COL18A1 | 1.021213 | 2.66E-16 | 2.66E-16 | 9.260549 | Up | Homo sapiens collagen, type XVIII, alpha 1 (COL18A1), transcript variant 1, mRNA [NM\_030582] |
| A\_24\_P71649 | CNTN3 | 1.068695 | 2.72E-16 | 2.72E-16 | 9.256876 | Up | Homo sapiens contactin 3 (plasmacytoma associated) (CNTN3), mRNA [NM\_020872] |
| A\_33\_P3286362 | LOC100131023 | 1.073255 | 3.04E-16 | 3.04E-16 | 9.238127 | Up | Homo sapiens cDNA FLJ45533 fis, clone BRTHA2030213. [AK127441] |
| A\_23\_P165380 | CRYGA | 1.068112 | 3.36E-16 | 3.36E-16 | 9.22081 | Up | Homo sapiens crystallin, gamma A (CRYGA), mRNA [NM\_014617] |
| A\_33\_P3343479 | LOC100506310 | 1.019601 | 4.11E-16 | 4.11E-16 | 9.186581 | Up | chromosome 1 open reading frame 167 [Source:HGNC Symbol;Acc:25262] [ENST00000484153] |
| A\_33\_P3313314 | SORBS1 | 1.012947 | 4.14E-16 | 4.14E-16 | 9.185134 | Up | Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), transcript variant 3, mRNA [NM\_001034954] |
| A\_21\_P0012105 | XLOC\_l2\_008427 | 1.100359 | 5.72E-16 | 5.72E-16 | 9.130087 | Up | HSU66583 gammaD-crystallin {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (94%) [THC2677669] |
| A\_33\_P3244073 | LOC100132146 | 1.201603 | 6.36E-16 | 6.36E-16 | 9.111944 | Up | Homo sapiens uncharacterized LOC100132146 (LOC100132146), mRNA [NM\_001195442] |
| A\_32\_P71571 | FAM19A4 | 1.244752 | 6.37E-16 | 6.37E-16 | 9.111573 | Up | Homo sapiens family with sequence similarity 19 (chemokine (C-C motif)-like), member A4 (FAM19A4), transcript variant 1, mRNA [NM\_182522] |
| A\_23\_P69497 | CLEC3B | 1.053963 | 8.18E-16 | 8.18E-16 | 9.068664 | Up | Homo sapiens C-type lectin domain family 3, member B (CLEC3B), mRNA [NM\_003278] |
| A\_33\_P3351955 | EGFR | 0.971202 | 8.56E-16 | 8.56E-16 | 9.060967 | Up | Homo sapiens epidermal growth factor receptor (EGFR), transcript variant 2, mRNA [NM\_201282] |
| A\_23\_P81717 | FRMD1 | 0.985895 | 9.32E-16 | 9.32E-16 | 9.04638 | Up | Homo sapiens FERM domain containing 1 (FRMD1), transcript variant 1, mRNA [NM\_024919] |
| A\_33\_P3240560 | GRIP2 | 1.103062 | 9.39E-16 | 9.39E-16 | 9.04518 | Up | Homo sapiens glutamate receptor interacting protein 2 (GRIP2), mRNA [NM\_001080423] |
| A\_33\_P3246248 | LOC729879 | 1.009911 | 1.07E-15 | 1.07E-15 | 9.02236 | Up | Homo sapiens cDNA FLJ35868 fis, clone TESTI2007972. [AK093187] |
| A\_23\_P76332 | RFX4 | 1.066518 | 1.16E-15 | 1.16E-15 | 9.009474 | Up | Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4), transcript variant 3, mRNA [NM\_213594] |
| A\_33\_P3211569 | ERBB3 | 1.025426 | 1.19E-15 | 1.19E-15 | 9.004881 | Up | Homo sapiens v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) (ERBB3), transcript variant s, mRNA [NM\_001005915] |
| A\_23\_P104819 | TREH | 1.638975 | 1.61E-15 | 1.61E-15 | 8.952783 | Up | Homo sapiens trehalase (brush-border membrane glycoprotein) (TREH), mRNA [NM\_007180] |
| A\_33\_P3328621 | LOC100132147 | 0.990299 | 1.69E-15 | 1.69E-15 | 8.944434 | Up | Homo sapiens cDNA clone IMAGE:4816083, partial cds. [BC036435] |
| A\_32\_P491499 | LOC100289094 | 0.992134 | 1.97E-15 | 1.97E-15 | 8.917958 | Up | Homo sapiens, clone IMAGE:5223216, mRNA, partial cds. [BC025775] |
| A\_21\_P0012061 | XLOC\_l2\_007933 | 1.107378 | 2.08E-15 | 2.08E-15 | 8.908587 | Up | YEA68 Homo sapiens adult testis cDNA library Homo sapiens cDNA, mRNA sequence [CD527082] |
| A\_21\_P0005222 | XLOC\_006044 | 1.140633 | 2.16E-15 | 2.16E-15 | 8.901975 | Up | CR744744 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGp971O0875 ; IMAGE:1735901 5', mRNA sequence [CR744744] |
| A\_23\_P33961 | BRS3 | 1.215572 | 2.16E-15 | 2.16E-15 | 8.901904 | Up | Homo sapiens bombesin-like receptor 3 (BRS3), mRNA [NM\_001727] |
| A\_33\_P3214109 | METTL21CP1 | 0.996505 | 2.19E-15 | 2.19E-15 | 8.899944 | Up | Homo sapiens cDNA FLJ39105 fis, clone NTONG2004806. [AK096424] |
| A\_33\_P3279407 | SYN3 | 1.054868 | 2.21E-15 | 2.21E-15 | 8.898451 | Up | Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA [NM\_133633] |
| A\_33\_P3389673 | OR5A2 | 1.430105 | 2.25E-15 | 2.25E-15 | 8.894659 | Up | Homo sapiens olfactory receptor, family 5, subfamily A, member 2 (OR5A2), mRNA [NM\_001001954] |
| A\_33\_P3355266 | TINAGL1 | 0.976663 | 3.16E-15 | 3.16E-15 | 8.836258 | Up | Homo sapiens tubulointerstitial nephritis antigen-like 1 (TINAGL1), transcript variant 1, mRNA [NM\_022164] |
| A\_33\_P3341259 | LEAP2 | 0.982903 | 3.45E-15 | 3.45E-15 | 8.821213 | Up | liver expressed antimicrobial peptide 2 [Source:HGNC Symbol;Acc:29571] [ENST00000483190] |
| A\_24\_P403459 | IFNA4 | 1.044912 | 3.75E-15 | 3.75E-15 | 8.806859 | Up | Homo sapiens interferon, alpha 4 (IFNA4), mRNA [NM\_021068] |
| A\_23\_P351913 | LRRN4 | 0.989569 | 3.8E-15 | 3.8E-15 | 8.804695 | Up | Homo sapiens leucine rich repeat neuronal 4 (LRRN4), mRNA [NM\_152611] |
| A\_21\_P0012555 | XLOC\_l2\_010422 | 1.015197 | 3.94E-15 | 3.94E-15 | 8.798499 | Up | RST38900 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG219147] |
| A\_21\_P0001897 | XLOC\_001619 | 1.099663 | 4E-15 | 4E-15 | 8.795728 | Up | full-length cDNA clone CS0DD009YK02 of Neuroblastoma Cot 50-normalized of Homo sapiens (human) [CR626349] |
| A\_32\_P152195 | STAC2 | 0.982666 | 4.64E-15 | 4.64E-15 | 8.770138 | Up | Homo sapiens SH3 and cysteine rich domain 2 (STAC2), mRNA [NM\_198993] |
| A\_33\_P3284266 | CXCL6 | 1.03602 | 5.11E-15 | 5.11E-15 | 8.753418 | Up | chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2) [Source:HGNC Symbol;Acc:10643] [ENST00000503446] |
| A\_21\_P0011927 | XLOC\_l2\_008088 | 1.041154 | 5.68E-15 | 5.68E-15 | 8.735058 | Up | UI-E-CI1-afu-k-11-0-UI.r1 UI-E-CI1 Homo sapiens cDNA clone UI-E-CI1-afu-k-11-0-UI 5', mRNA sequence [BM708281] |
| A\_33\_P3398236 | COL28A1 | 0.987954 | 5.79E-15 | 5.79E-15 | 8.731742 | Up | collagen, type XXVIII, alpha 1 [Source:HGNC Symbol;Acc:22442] [ENST00000399419] |
| A\_24\_P383019 | KRTAP13-1 | 0.97019 | 6.18E-15 | 6.18E-15 | 8.720593 | Up | Homo sapiens keratin associated protein 13-1 (KRTAP13-1), mRNA [NM\_181599] |
| A\_21\_P0003383 | XLOC\_003630 | 1.184848 | 6.59E-15 | 6.59E-15 | 8.709475 | Up | 602689122F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4821629 5', mRNA sequence [BG717053] |
| A\_33\_P3379251 | LRRC30 | 0.988925 | 6.59E-15 | 6.59E-15 | 8.70942 | Up | Homo sapiens leucine rich repeat containing 30 (LRRC30), mRNA [NM\_001105581] |
| A\_33\_P3320217 | ADCY2 | 1.094388 | 7.43E-15 | 7.43E-15 | 8.688584 | Up | Homo sapiens adenylate cyclase 2 (brain) (ADCY2), mRNA [NM\_020546] |
| A\_24\_P277673 | HIST1H4G | 1.402971 | 7.62E-15 | 7.62E-15 | 8.684275 | Up | Homo sapiens histone cluster 1, H4g (HIST1H4G), mRNA [NM\_003547] |
| A\_33\_P3389842 | PROM1 | 1.077005 | 7.65E-15 | 7.65E-15 | 8.68364 | Up | Homo sapiens prominin 1 (PROM1), transcript variant 6, mRNA [NM\_001145850] |
| A\_23\_P254863 | NIM1 | 1.076864 | 9.27E-15 | 9.27E-15 | 8.650251 | Up | Homo sapiens serine/threonine-protein kinase NIM1 (NIM1), mRNA [NM\_153361] |
| A\_21\_P0008876 | XLOC\_011801 | 1.008181 | 9.65E-15 | 9.65E-15 | 8.643237 | Up | ALU6\_HUMAN (P39193) Alu subfamily SP sequence contamination warning entry, partial (5%) [THC2629455] |
| A\_33\_P3260684 | OR2T6 | 1.040883 | 1.15E-14 | 1.15E-14 | 8.612823 | Up | Homo sapiens olfactory receptor, family 2, subfamily T, member 6 (OR2T6), mRNA [NM\_001005471] |
| A\_32\_P167239 | AFAP1L1 | 1.158881 | 1.3E-14 | 1.3E-14 | 8.59207 | Up | Homo sapiens actin filament associated protein 1-like 1 (AFAP1L1), transcript variant 1, mRNA [NM\_152406] |
| A\_24\_P143686 | KIAA0146 | 1.13795 | 1.34E-14 | 1.34E-14 | 8.586327 | Up | Homo sapiens KIAA0146 (KIAA0146), mRNA [NM\_001080394] |
| A\_33\_P3352772 | DEFB107A | 1.156038 | 1.5E-14 | 1.5E-14 | 8.567149 | Up | Homo sapiens defensin, beta 107A (DEFB107A), mRNA [NM\_001037668] |
| A\_23\_P324885 | CCR2 | 0.97378 | 1.58E-14 | 1.58E-14 | 8.557954 | Up | Homo sapiens chemokine (C-C motif) receptor 2 (CCR2), transcript variant B, mRNA [NM\_001123396] |
| A\_33\_P3853081 | ALDOAP2 | 0.972148 | 1.58E-14 | 1.58E-14 | 8.557589 | Up | Human aldolase pseudogene mRNA, complete cds. [M21191] |
| A\_23\_P67367 | DHDH | 0.996851 | 1.79E-14 | 1.79E-14 | 8.535889 | Up | Homo sapiens dihydrodiol dehydrogenase (dimeric) (DHDH), mRNA [NM\_014475] |
| A\_21\_P0009877 | XLOC\_013647 | 0.998343 | 2.08E-14 | 2.08E-14 | 8.509608 | Up | 603073263F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5165367 5', mRNA sequence [BI830547] |
| A\_24\_P366566 | OR5H1 | 1.238175 | 2.51E-14 | 2.51E-14 | 8.477246 | Up | Homo sapiens olfactory receptor, family 5, subfamily H, member 1 (OR5H1), mRNA [NM\_001005338] |
| A\_21\_P0001794 | XLOC\_002240 | 1.564093 | 2.63E-14 | 2.63E-14 | 8.468757 | Up |  |
| A\_33\_P3368506 | SLC38A8 | 0.981484 | 3.15E-14 | 3.15E-14 | 8.437091 | Up | Homo sapiens solute carrier family 38, member 8 (SLC38A8), mRNA [NM\_001080442] |
| A\_33\_P3411260 | LOC100288884 | 1.177188 | 4.02E-14 | 4.02E-14 | 8.394568 | Up | Homo sapiens cDNA FLJ42128 fis, clone TESTI2013382. [AK124122] |
| A\_33\_P3304372 | TMEM144 | 1.274403 | 4.04E-14 | 4.04E-14 | 8.393803 | Up | Homo sapiens transmembrane protein 144 (TMEM144), mRNA [NM\_018342] |
| A\_23\_P124946 | CMYA5 | 1.035907 | 5.43E-14 | 5.43E-14 | 8.342041 | Up | Homo sapiens cardiomyopathy associated 5 (CMYA5), mRNA [NM\_153610] |
| A\_33\_P3216322 | SEMA4G | 1.066715 | 6.52E-14 | 6.52E-14 | 8.30965 | Up | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G [Source:HGNC Symbol;Acc:10735] [ENST00000518244] |
| A\_33\_P3303016 | LOC100130587 | 1.006585 | 7.33E-14 | 7.33E-14 | 8.289091 | Up | Homo sapiens cDNA FLJ45620 fis, clone BRTHA3027638. [AK127527] |
| A\_21\_P0005945 | XLOC\_006911 | 1.054807 | 8.12E-14 | 8.12E-14 | 8.271216 | Up | DKFZp781F1921\_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone DKFZp781F1921 5', mRNA sequence [BX952775] |
| A\_23\_P31755 | CRH | 1.07857 | 8.75E-14 | 8.75E-14 | 8.258129 | Up | Homo sapiens corticotropin releasing hormone (CRH), mRNA [NM\_000756] |
| A\_21\_P0014611 | LOC100507145 | 1.108433 | 1.01E-13 | 1.01E-13 | 8.231987 | Up | PREDICTED: Homo sapiens hypothetical LOC100507145 (LOC100507145), miscRNA [XR\_110529] |
| A\_21\_P0004098 | XLOC\_004727 | 1.037642 | 1.08E-13 | 1.08E-13 | 8.22169 | Up | AGENCOURT\_10401918 NIH\_MGC\_82 Homo sapiens cDNA clone IMAGE:6617618 5', mRNA sequence [BU852147] |
| A\_24\_P332081 | JAKMIP3 | 1.119312 | 1.1E-13 | 1.1E-13 | 8.217521 | Up | Homo sapiens Janus kinase and microtubule interacting protein 3 (JAKMIP3), mRNA [NM\_001105521] |
| A\_23\_P144827 | FBXL7 | 0.993906 | 1.79E-13 | 1.79E-13 | 8.132096 | Up | Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), mRNA [NM\_012304] |
| A\_23\_P424561 | RHOV | 1.001591 | 1.8E-13 | 1.8E-13 | 8.130407 | Up | Homo sapiens ras homolog gene family, member V (RHOV), mRNA [NM\_133639] |
| A\_23\_P53450 | KRT82 | 0.972847 | 2.02E-13 | 2.02E-13 | 8.110442 | Up | Homo sapiens keratin 82 (KRT82), mRNA [NM\_033033] |
| A\_24\_P183994 | RASEF | 1.221186 | 2.21E-13 | 2.21E-13 | 8.094545 | Up | RAS and EF-hand domain containing [Source:HGNC Symbol;Acc:26464] [ENST00000340717] |
| A\_21\_P0008580 | XLOC\_011521 | 1.011019 | 2.24E-13 | 2.24E-13 | 8.092156 | Up | ALU1\_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (19%) [THC2607231] |
| A\_24\_P404033 | C15orf38 | 1.739921 | 3.35E-13 | 3.35E-13 | 8.020402 | Up | Homo sapiens chromosome 15 open reading frame 38 (C15orf38), mRNA [NM\_182616] |
| A\_23\_P313542 | GRK1 | 0.972829 | 3.42E-13 | 3.42E-13 | 8.017052 | Up | Homo sapiens G protein-coupled receptor kinase 1 (GRK1), mRNA [NM\_002929] |
| A\_33\_P3411165 | MAGEA2B | 0.985168 | 4.12E-13 | 4.12E-13 | 7.983637 | Up | Homo sapiens melanoma antigen family A, 2B (MAGEA2B), mRNA [NM\_153488] |
| A\_24\_P515319 | FAM90A7 | 1.018498 | 4.3E-13 | 4.3E-13 | 7.976034 | Up | Homo sapiens family with sequence similarity 90, member A7 (FAM90A7), mRNA [NM\_001136572] |
| A\_23\_P75800 | RAB3IL1 | 1.024728 | 5.82E-13 | 5.82E-13 | 7.92201 | Up | Homo sapiens RAB3A interacting protein (rabin3)-like 1 (RAB3IL1), mRNA [NM\_013401] |
| A\_21\_P0009356 | XLOC\_012564 | 0.994682 | 6.7E-13 | 6.7E-13 | 7.897037 | Up | RST26950 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG207469] |
| A\_21\_P0012723 | XLOC\_l2\_010650 | 1.213334 | 7.72E-13 | 7.72E-13 | 7.871541 | Up | DB230865 TRACH3 Homo sapiens cDNA clone TRACH3024308 5', mRNA sequence [DB230865] |
| A\_33\_P3371775 | LOC729187 | 1.079293 | 9.24E-13 | 9.24E-13 | 7.839527 | Up | Homo sapiens cDNA FLJ27413 fis, clone WMC05327. [AK130923] |
| A\_23\_P151133 | TSPAN9 | 1.26702 | 1.23E-12 | 1.23E-12 | 7.787899 | Up | Homo sapiens tetraspanin 9 (TSPAN9), transcript variant 1, mRNA [NM\_006675] |
| A\_33\_P3353230 | DEFB134 | 1.006917 | 1.33E-12 | 1.33E-12 | 7.773918 | Up | Homo sapiens defensin, beta 134 (DEFB134), mRNA [NM\_001033019] |
| A\_23\_P117261 | RXFP2 | 1.083235 | 1.33E-12 | 1.33E-12 | 7.773908 | Up | Homo sapiens relaxin/insulin-like family peptide receptor 2 (RXFP2), transcript variant 1, mRNA [NM\_130806] |
| A\_33\_P3212394 | FRG2C | 1.123719 | 1.5E-12 | 1.5E-12 | 7.752887 | Up | Homo sapiens FSHD region gene 2 family, member C (FRG2C), mRNA [NM\_001124759] |
| A\_23\_P87727 | CAPZA3 | 1.152076 | 1.56E-12 | 1.56E-12 | 7.745634 | Up | Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), mRNA [NM\_033328] |
| A\_23\_P323180 | HOXD3 | 1.006396 | 1.61E-12 | 1.61E-12 | 7.739273 | Up | Homo sapiens homeobox D3 (HOXD3), mRNA [NM\_006898] |
| A\_21\_P0007341 | XLOC\_009417 | 1.012592 | 1.73E-12 | 1.73E-12 | 7.726253 | Up | DB451323 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H013052P05 5', mRNA sequence [DB451323] |
| A\_33\_P3380032 | PRAMEF13 | 1.041831 | 2.45E-12 | 2.45E-12 | 7.664155 | Up | Homo sapiens PRAME family member 13 (PRAMEF13), mRNA [NM\_001024661] |
| A\_23\_P327562 | LHX9 | 1.069679 | 3.86E-12 | 3.86E-12 | 7.581506 | Up | Homo sapiens LIM homeobox 9 (LHX9), transcript variant 1, mRNA [NM\_020204] |
| A\_33\_P3377151 | CCL19 | 0.987742 | 3.95E-12 | 3.95E-12 | 7.577418 | Up | Homo sapiens chemokine (C-C motif) ligand 19 (CCL19), mRNA [NM\_006274] |
| A\_33\_P3305617 | SPTSSB | 0.99415 | 5.72E-12 | 5.72E-12 | 7.509827 | Up | serine palmitoyltransferase, small subunit B [Source:HGNC Symbol;Acc:24045] [ENST00000359175] |
| A\_33\_P3754922 | RNU11 | 1.020235 | 1.03E-11 | 1.03E-11 | 7.402455 | Up | BP873537 Sugano cDNA library, embryonal kidney Homo sapiens cDNA clone HKR13896, mRNA sequence [BP873537] |
| A\_23\_P98744 | OR52K2 | 0.980125 | 1.18E-11 | 1.18E-11 | 7.376716 | Up | Homo sapiens olfactory receptor, family 52, subfamily K, member 2 (OR52K2), mRNA [NM\_001005172] |
| A\_23\_P90925 | IL36B | 0.995856 | 1.51E-11 | 1.51E-11 | 7.33188 | Up | Homo sapiens interleukin 36, beta (IL36B), transcript variant 2, mRNA [NM\_173178] |
| A\_21\_P0008407 | XLOC\_010971 | 1.025035 | 1.77E-11 | 1.77E-11 | 7.303348 | Up | Q4R9W6\_TETNG (Q4R9W6) Chromosome undetermined SCAF25103, whole genome shotgun sequence. (Fragment), partial (13%) [THC2702568] |
| A\_33\_P3236071 | CLEC1B | 1.008725 | 2.08E-11 | 2.08E-11 | 7.272975 | Up | Homo sapiens C-type lectin domain family 1, member B (CLEC1B), transcript variant 1, mRNA [NM\_016509] |
| A\_21\_P0010882 | XLOC\_l2\_001986 | 1.026841 | 2.53E-11 | 2.53E-11 | 7.237119 | Up | RST20757 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG201536] |
| A\_33\_P3332487 | FANK1 | 1.013931 | 3.81E-11 | 3.81E-11 | 7.160773 | Up | fibronectin type III and ankyrin repeat domains 1 [Source:HGNC Symbol;Acc:23527] [ENST00000368689] |
| A\_21\_P0002944 | XLOC\_002616 | 1.020228 | 4.08E-11 | 4.08E-11 | 7.148003 | Up | O87140\_VIBCH (O87140) WbfS protein, partial (5%) [THC2668179] |
| A\_23\_P31273 | AMPH | 1.269766 | 4.39E-11 | 4.39E-11 | 7.134489 | Up | Homo sapiens amphiphysin (AMPH), transcript variant 1, mRNA [NM\_001635] |
| A\_23\_P44207 | ACOT12 | 1.058477 | 4.83E-11 | 4.83E-11 | 7.116704 | Up | Homo sapiens acyl-CoA thioesterase 12 (ACOT12), mRNA [NM\_130767] |
| A\_23\_P429425 | ST6GAL2 | 1.061421 | 5.09E-11 | 5.09E-11 | 7.107121 | Up | Homo sapiens ST6 beta-galactosamide alpha-2,6-sialyltranferase 2 (ST6GAL2), transcript variant 1, mRNA [NM\_032528] |
| A\_33\_P3374987 | C7orf52 | 1.008257 | 6.57E-11 | 6.57E-11 | 7.05916 | Up | Homo sapiens chromosome 7 open reading frame 52 (C7orf52), mRNA [NM\_198571] |
| A\_23\_P43337 | FREM1 | 0.973571 | 7.85E-11 | 7.85E-11 | 7.025843 | Up | Homo sapiens FRAS1 related extracellular matrix 1 (FREM1), transcript variant 1, mRNA [NM\_144966] |
| A\_21\_P0012742 | XLOC\_l2\_010833 | 1.11862 | 7.96E-11 | 7.96E-11 | 7.0232 | Up | Q96AU6\_HUMAN (Q96AU6) FAT3 protein (Fragment), partial (17%) [THC2604505] |
| A\_33\_P3241334 | PSG1 | 1.174656 | 9.2E-11 | 9.2E-11 | 6.99614 | Up | Homo sapiens cDNA FLJ32192 fis, clone PLACE6002323. [AK056754] |
| A\_33\_P3326217 | SHISA6 | 0.973867 | 1.71E-10 | 1.71E-10 | 6.879295 | Up | Homo sapiens shisa homolog 6 (Xenopus laevis) (SHISA6), transcript variant 1, mRNA [NM\_207386] |
| A\_23\_P49254 | HBQ1 | 1.165988 | 1.72E-10 | 1.72E-10 | 6.878087 | Up | Homo sapiens hemoglobin, theta 1 (HBQ1), mRNA [NM\_005331] |
| A\_21\_P0011078 | XLOC\_l2\_003270 | 1.207124 | 1.75E-10 | 1.75E-10 | 6.874565 | Up | 602692717F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4824845 5', mRNA sequence [BG721022] |
| A\_33\_P3228466 | FXYD3 | 1.532437 | 1.91E-10 | 1.91E-10 | 6.858163 | Up | Homo sapiens FXYD domain containing ion transport regulator 3 (FXYD3), transcript variant 4, mRNA [NM\_001136008] |
| A\_21\_P0009540 | XLOC\_012810 | 1.046581 | 2.43E-10 | 2.43E-10 | 6.812235 | Up | Q4RQ78\_TETNG (Q4RQ78) Chromosome 17 SCAF15006, whole genome shotgun sequence. (Fragment), partial (14%) [THC2660860] |
| A\_23\_P83012 | INSL6 | 1.017321 | 2.87E-10 | 2.87E-10 | 6.780788 | Up | Homo sapiens insulin-like 6 (INSL6), mRNA [NM\_007179] |
| A\_23\_P20743 | C9orf125 | 1.319867 | 1.89E-09 | 1.89E-09 | 6.416325 | Up | Homo sapiens chromosome 9 open reading frame 125 (C9orf125), mRNA [NM\_032342] |
| A\_24\_P314337 | PAGE1 | 1.069056 | 2.46E-09 | 2.46E-09 | 6.364459 | Up | Homo sapiens P antigen family, member 1 (prostate associated) (PAGE1), mRNA [NM\_003785] |
| A\_33\_P3320079 | NFIB | 1.021995 | 2.76E-09 | 2.76E-09 | 6.342387 | Up | Homo sapiens nuclear factor I/B (NFIB), transcript variant 3, mRNA [NM\_005596] |
| A\_23\_P154643 | BMP7 | 0.976629 | 5.66E-09 | 5.66E-09 | 6.199794 | Up | Homo sapiens bone morphogenetic protein 7 (BMP7), mRNA [NM\_001719] |
| A\_23\_P126613 | AQP10 | 0.977062 | 4.34E-08 | 4.34E-08 | 5.785768 | Up | Homo sapiens aquaporin 10 (AQP10), mRNA [NM\_080429] |
| A\_23\_P39955 | ACTG2 | 1.055292 | 5.22E-08 | 5.22E-08 | 5.74731 | Up | Homo sapiens actin, gamma 2, smooth muscle, enteric (ACTG2), transcript variant 1, mRNA [NM\_001615] |
| A\_23\_P142345 | PRTN3 | 1.020606 | 4E-07 | 4E-07 | 5.314007 | Up | Homo sapiens proteinase 3 (PRTN3), mRNA [NM\_002777] |
| A\_33\_P3278755 | SULT6B1 | 1.104696 | 3.74E-06 | 3.74E-06 | 4.811761 | Up | Homo sapiens sulfotransferase family, cytosolic, 6B, member 1 (SULT6B1), mRNA [NM\_001032377] |
| A\_21\_P0011752 | XLOC\_l2\_007062 | 1.052226 | 7.78E-06 | 7.78E-06 | 4.639728 | Up | GB |
| A\_21\_P0013920 | LOC100134138 | 1.139084 | 1.35E-05 | 1.35E-05 | 4.507031 | Up | PREDICTED: Homo sapiens hypothetical protein LOC100134138 (LOC100134138), mRNA [XM\_001719777] |
| A\_33\_P3389704 | CES1 | 1.046578 | 1.91E-05 | 1.91E-05 | 4.422958 | Up | Homo sapiens carboxylesterase 1 (CES1), transcript variant 3, mRNA [NM\_001266] |
| A\_32\_P208403 | GNG2 | -1.08822 | 7.4E-34 | 7.4E-34 | -16.0461 | Down | Homo sapiens guanine nucleotide binding protein (G protein), gamma 2 (GNG2), transcript variant 1, mRNA [NM\_053064] |
| A\_23\_P423074 | FAM169A | -1.79024 | 1.86E-31 | 1.86E-31 | -15.097 | Down | Homo sapiens family with sequence similarity 169, member A (FAM169A), mRNA [NM\_015566] |
| A\_33\_P3394213 | GRIN3B | -1.13438 | 3.83E-31 | 3.83E-31 | -14.9738 | Down | Homo sapiens glutamate receptor, ionotropic, N-methyl-D-aspartate 3B (GRIN3B), mRNA [NM\_138690] |
| A\_33\_P3389653 | PDE4D | -2.52085 | 9.49E-31 | 9.49E-31 | -14.8195 | Down | Homo sapiens phosphodiesterase 4D, cAMP-specific (PDE4D), transcript variant 3, mRNA [NM\_001165899] |
| A\_23\_P160618 | SH2D2A | -1.38789 | 3.32E-30 | 3.32E-30 | -14.6073 | Down | Homo sapiens SH2 domain containing 2A (SH2D2A), transcript variant 2, mRNA [NM\_003975] |
| A\_33\_P3346891 | MYBL1 | -1.18999 | 1.34E-29 | 1.34E-29 | -14.3712 | Down | Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 1 (MYBL1), transcript variant 2, mRNA [NM\_001144755] |
| A\_33\_P3257993 | RNF125 | -1.3064 | 2.06E-29 | 2.06E-29 | -14.299 | Down | Homo sapiens ring finger protein 125 (RNF125), mRNA [NM\_017831] |
| A\_24\_P226210 | CEP120 | -1.05535 | 4.24E-29 | 4.24E-29 | -14.1772 | Down | Homo sapiens centrosomal protein 120kDa (CEP120), transcript variant 1, mRNA [NM\_153223] |
| A\_21\_P0011938 | ANKRD36B | -0.992 | 1.42E-28 | 1.42E-28 | -13.9742 | Down | Homo sapiens ankyrin repeat domain 36B (ANKRD36B), mRNA [NM\_025190] |
| A\_33\_P3394380 | AKAP5 | -1.82342 | 4.8E-28 | 4.8E-28 | -13.7698 | Down | Homo sapiens A kinase (PRKA) anchor protein 5 (AKAP5), mRNA [NM\_004857] |
| A\_23\_P213562 | F2R | -1.64427 | 6.61E-28 | 6.61E-28 | -13.7164 | Down | Homo sapiens coagulation factor II (thrombin) receptor (F2R), mRNA [NM\_001992] |
| A\_33\_P3323068 | AGPAT4 | -1.22405 | 3.89E-27 | 3.89E-27 | -13.42 | Down | Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) (AGPAT4), mRNA [NM\_020133] |
| A\_33\_P3291394 | GPN1 | -1.13897 | 4.14E-27 | 4.14E-27 | -13.4098 | Down | Homo sapiens GPN-loop GTPase 1 (GPN1), transcript variant 1, mRNA [NM\_007266] |
| A\_23\_P32217 | TOPORS | -1.14908 | 4.78E-27 | 4.78E-27 | -13.3858 | Down | Homo sapiens topoisomerase I binding, arginine/serine-rich, E3 ubiquitin protein ligase (TOPORS), transcript variant 1, mRNA [NM\_005802] |
| A\_23\_P28334 | IL18RAP | -1.4413 | 5.05E-27 | 5.05E-27 | -13.3767 | Down | Homo sapiens interleukin 18 receptor accessory protein (IL18RAP), mRNA [NM\_003853] |
| A\_24\_P942694 | C10orf118 | -1.06373 | 5.34E-27 | 5.34E-27 | -13.3671 | Down | Homo sapiens chromosome 10 open reading frame 118 (C10orf118), mRNA [NM\_018017] |
| A\_23\_P43157 | MYBL1 | -1.20324 | 6.4E-27 | 6.4E-27 | -13.3369 | Down | Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 1 (MYBL1), transcript variant 1, mRNA [NM\_001080416] |
| A\_24\_P183292 | CSNK1A1 | -1.97405 | 9.73E-27 | 9.73E-27 | -13.2672 | Down | Homo sapiens casein kinase 1, alpha 1 (CSNK1A1), transcript variant 1, mRNA [NM\_001025105] |
| A\_33\_P3323722 | ARL4C | -1.04068 | 1.26E-26 | 1.26E-26 | -13.2242 | Down | Homo sapiens ADP-ribosylation factor-like 4C (ARL4C), mRNA [NM\_005737] |
| A\_24\_P103886 | IDI1 | -1.33257 | 1.57E-26 | 1.57E-26 | -13.1879 | Down | Homo sapiens isopentenyl-diphosphate delta isomerase 1 (IDI1), mRNA [NM\_004508] |
| A\_23\_P20480 | BRF2 | -1.10757 | 2.77E-26 | 2.77E-26 | -13.0926 | Down | Homo sapiens BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like (BRF2), mRNA [NM\_018310] |
| A\_32\_P175539 | RCN2 | -1.58912 | 3.54E-26 | 3.54E-26 | -13.052 | Down | Homo sapiens reticulocalbin 2, EF-hand calcium binding domain (RCN2), mRNA [NM\_002902] |
| A\_33\_P3219641 | CEP78 | -1.14367 | 4.88E-26 | 4.88E-26 | -12.9986 | Down | Homo sapiens centrosomal protein 78kDa (CEP78), transcript variant 1, mRNA [NM\_001098802] |
| A\_23\_P254507 | HOPX | -1.58825 | 5.45E-26 | 5.45E-26 | -12.9804 | Down | Homo sapiens HOP homeobox (HOPX), transcript variant 2, mRNA [NM\_139211] |
| A\_23\_P53193 | SYTL2 | -1.41918 | 6.04E-26 | 6.04E-26 | -12.9633 | Down | Homo sapiens synaptotagmin-like 2 (SYTL2), transcript variant c, mRNA [NM\_206927] |
| A\_24\_P271527 | JOSD1 | -1.05804 | 6.28E-26 | 6.28E-26 | -12.9568 | Down | Homo sapiens Josephin domain containing 1 (JOSD1), mRNA [NM\_014876] |
| A\_24\_P29401 | PIK3R1 | -1.28035 | 1.75E-25 | 1.75E-25 | -12.7864 | Down | Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (alpha) (PIK3R1), transcript variant 1, mRNA [NM\_181523] |
| A\_24\_P91916 | NXT2 | -1.26498 | 2.11E-25 | 2.11E-25 | -12.7552 | Down | Homo sapiens nuclear transport factor 2-like export factor 2 (NXT2), transcript variant 1, mRNA [NM\_018698] |
| A\_23\_P349882 | PDCL | -1.32358 | 2.53E-25 | 2.53E-25 | -12.725 | Down | Homo sapiens phosducin-like (PDCL), mRNA [NM\_005388] |
| A\_32\_P144596 | TNKS | -0.97932 | 4.26E-25 | 4.26E-25 | -12.6387 | Down | Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA [NM\_003747] |
| A\_33\_P3298661 | ZNF148 | -1.06292 | 4.28E-25 | 4.28E-25 | -12.638 | Down | Homo sapiens zinc finger protein 148 (ZNF148), mRNA [NM\_021964] |
| A\_23\_P128215 | SOCS2 | -1.38498 | 4.52E-25 | 4.52E-25 | -12.6288 | Down | Homo sapiens suppressor of cytokine signaling 2 (SOCS2), mRNA [NM\_003877] |
| A\_33\_P3339388 | WIPF1 | -1.26236 | 5.28E-25 | 5.28E-25 | -12.6031 | Down | WAS/WASL interacting protein family, member 1 [Source:HGNC Symbol;Acc:12736] [ENST00000410117] |
| A\_23\_P62868 | EXOSC10 | -1.12306 | 9.41E-25 | 9.41E-25 | -12.5071 | Down | Homo sapiens exosome component 10 (EXOSC10), transcript variant 1, mRNA [NM\_001001998] |
| A\_32\_P83784 | ARAP2 | -0.99397 | 1.12E-24 | 1.12E-24 | -12.4789 | Down | Homo sapiens ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2 (ARAP2), mRNA [NM\_015230] |
| A\_24\_P208567 | IL18R1 | -1.65231 | 1.18E-24 | 1.18E-24 | -12.4698 | Down | Homo sapiens interleukin 18 receptor 1 (IL18R1), mRNA [NM\_003855] |
| A\_23\_P106103 | AKAP5 | -1.68376 | 1.24E-24 | 1.24E-24 | -12.4609 | Down | Homo sapiens A kinase (PRKA) anchor protein 5 (AKAP5), mRNA [NM\_004857] |
| A\_33\_P3465247 | KIF3A | -1.39318 | 1.44E-24 | 1.44E-24 | -12.4366 | Down | Homo sapiens kinesin family member 3A (KIF3A), mRNA [NM\_007054] |
| A\_33\_P3294297 | RNF126 | -1.0088 | 1.47E-24 | 1.47E-24 | -12.4333 | Down | Homo sapiens ring finger protein 126 (RNF126), mRNA [NM\_194460] |
| A\_32\_P71447 | NCAPD3 | -1.0845 | 1.49E-24 | 1.49E-24 | -12.4306 | Down | Homo sapiens non-SMC condensin II complex, subunit D3 (NCAPD3), mRNA [NM\_015261] |
| A\_23\_P502142 | FYN | -1.04732 | 1.54E-24 | 1.54E-24 | -12.4257 | Down | Homo sapiens FYN oncogene related to SRC, FGR, YES (FYN), transcript variant 1, mRNA [NM\_002037] |
| A\_23\_P200780 | TGFBR3 | -1.25646 | 2.15E-24 | 2.15E-24 | -12.3704 | Down | Homo sapiens transforming growth factor, beta receptor III (TGFBR3), transcript variant 1, mRNA [NM\_003243] |
| A\_33\_P3409124 | NR1D2 | -1.03925 | 2.18E-24 | 2.18E-24 | -12.3676 | Down | Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), transcript variant 1, mRNA [NM\_005126] |
| A\_24\_P414376 | KLF3 | -1.33042 | 4.26E-24 | 4.26E-24 | -12.257 | Down | Homo sapiens Kruppel-like factor 3 (basic) (KLF3), mRNA [NM\_016531] |
| A\_23\_P26124 | RORA | -1.25366 | 5.58E-24 | 5.58E-24 | -12.2121 | Down | Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 2, mRNA [NM\_134260] |
| A\_24\_P160380 | PDLIM2 | -1.43399 | 6.16E-24 | 6.16E-24 | -12.1958 | Down | Homo sapiens PDZ and LIM domain 2 (mystique) (PDLIM2), transcript variant 1, mRNA [NM\_176871] |
| A\_21\_P0014925 | LOC100505857 | -1.23765 | 7.39E-24 | 7.39E-24 | -12.1655 | Down | DA569430 HEMBA1 Homo sapiens cDNA clone HEMBA1002792 5', mRNA sequence [DA569430] |
| A\_24\_P399694 | ZCCHC3 | -1.04481 | 8.43E-24 | 8.43E-24 | -12.1437 | Down | Homo sapiens zinc finger, CCHC domain containing 3 (ZCCHC3), mRNA [NM\_033089] |
| A\_24\_P374652 | NUCKS1 | -1.09619 | 8.44E-24 | 8.44E-24 | -12.1436 | Down | Homo sapiens nuclear casein kinase and cyclin-dependent kinase substrate 1 (NUCKS1), mRNA [NM\_022731] |
| A\_23\_P212715 | CBLB | -1.09805 | 9.11E-24 | 9.11E-24 | -12.1309 | Down | Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA [NM\_170662] |
| A\_24\_P58122 | USP24 | -1.3435 | 1.34E-23 | 1.34E-23 | -12.0665 | Down | Homo sapiens ubiquitin specific peptidase 24 (USP24), mRNA [NM\_015306] |
| A\_23\_P395524 | PWP1 | -0.98933 | 1.39E-23 | 1.39E-23 | -12.061 | Down | Homo sapiens PWP1 homolog (S. cerevisiae) (PWP1), mRNA [NM\_007062] |
| A\_24\_P12539 | KBTBD2 | -0.9858 | 2.16E-23 | 2.16E-23 | -11.9877 | Down | Homo sapiens kelch repeat and BTB (POZ) domain containing 2 (KBTBD2), mRNA [NM\_015483] |
| A\_32\_P177024 | SBDS | -1.0646 | 2.67E-23 | 2.67E-23 | -11.9527 | Down | Homo sapiens Shwachman-Bodian-Diamond syndrome (SBDS), mRNA [NM\_016038] |
| A\_24\_P130936 | DDX3Y | -0.99837 | 3.31E-23 | 3.31E-23 | -11.9169 | Down | Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked (DDX3Y), transcript variant 2, mRNA [NM\_004660] |
| A\_33\_P3373885 | NAA35 | -1.05856 | 3.47E-23 | 3.47E-23 | -11.9094 | Down | N(alpha)-acetyltransferase 35, NatC auxiliary subunit [Source:HGNC Symbol;Acc:24340] [ENST00000416045] |
| A\_23\_P356554 | BAG2 | -1.14556 | 5.08E-23 | 5.08E-23 | -11.8462 | Down | Homo sapiens BCL2-associated athanogene 2 (BAG2), mRNA [NM\_004282] |
| A\_23\_P357365 | STAG1 | -1.28029 | 6.35E-23 | 6.35E-23 | -11.8092 | Down | Homo sapiens stromal antigen 1 (STAG1), mRNA [NM\_005862] |
| A\_24\_P248240 | SYT11 | -1.45384 | 9.28E-23 | 9.28E-23 | -11.7463 | Down | Homo sapiens synaptotagmin XI (SYT11), mRNA [NM\_152280] |
| A\_24\_P173754 | C1orf21 | -1.25591 | 1.08E-22 | 1.08E-22 | -11.7209 | Down | Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA [NM\_030806] |
| A\_23\_P64770 | DDX23 | -1.08238 | 1.09E-22 | 1.09E-22 | -11.7193 | Down | Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 23 (DDX23), mRNA [NM\_004818] |
| A\_23\_P157569 | ADHFE1 | -0.99433 | 1.26E-22 | 1.26E-22 | -11.6958 | Down | Homo sapiens alcohol dehydrogenase, iron containing, 1 (ADHFE1), nuclear gene encoding mitochondrial protein, mRNA [NM\_144650] |
| A\_23\_P99275 | KLRB1 | -1.05151 | 1.34E-22 | 1.34E-22 | -11.6851 | Down | Homo sapiens killer cell lectin-like receptor subfamily B, member 1 (KLRB1), mRNA [NM\_002258] |
| A\_33\_P3351474 | SMARCAD1 | -1.00793 | 1.4E-22 | 1.4E-22 | -11.6781 | Down | Homo sapiens SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1 (SMARCAD1), transcript variant 1, mRNA [NM\_001128429] |
| A\_23\_P166122 | POLR3F | -1.21273 | 1.44E-22 | 1.44E-22 | -11.6739 | Down | Homo sapiens polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa (POLR3F), mRNA [NM\_006466] |
| A\_23\_P1374 | PRKCQ | -0.96561 | 1.64E-22 | 1.64E-22 | -11.6524 | Down | Homo sapiens protein kinase C, theta (PRKCQ), transcript variant 1, mRNA [NM\_006257] |
| A\_23\_P163027 | PARP2 | -1.19662 | 1.9E-22 | 1.9E-22 | -11.6279 | Down | Homo sapiens poly (ADP-ribose) polymerase 2 (PARP2), transcript variant 1, mRNA [NM\_005484] |
| A\_32\_P176550 | JMY | -1.22333 | 2E-22 | 2E-22 | -11.619 | Down | Homo sapiens junction mediating and regulatory protein, p53 cofactor (JMY), mRNA [NM\_152405] |
| A\_23\_P19517 | ITPR3 | -1.28384 | 2.88E-22 | 2.88E-22 | -11.559 | Down | Homo sapiens inositol 1,4,5-trisphosphate receptor, type 3 (ITPR3), mRNA [NM\_002224] |
| A\_23\_P43690 | BNC2 | -1.77919 | 3E-22 | 3E-22 | -11.552 | Down | Homo sapiens basonuclin 2 (BNC2), mRNA [NM\_017637] |
| A\_23\_P120710 | TTC3 | -1.00209 | 3.79E-22 | 3.79E-22 | -11.5135 | Down | Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, mRNA [NM\_003316] |
| A\_23\_P107744 | S1PR5 | -1.25217 | 4.56E-22 | 4.56E-22 | -11.4826 | Down | Homo sapiens sphingosine-1-phosphate receptor 5 (S1PR5), transcript variant 1, mRNA [NM\_030760] |
| A\_33\_P3289286 | TMEM57 | -1.31901 | 5.98E-22 | 5.98E-22 | -11.4377 | Down | Homo sapiens transmembrane protein 57 (TMEM57), mRNA [NM\_018202] |
| A\_23\_P156390 | JAKMIP2 | -1.29761 | 6.78E-22 | 6.78E-22 | -11.417 | Down | Homo sapiens janus kinase and microtubule interacting protein 2 (JAKMIP2), mRNA [NM\_014790] |
| A\_24\_P941759 | G2E3 | -1.0779 | 1.31E-21 | 1.31E-21 | -11.3074 | Down | Homo sapiens G2/M-phase specific E3 ubiquitin protein ligase (G2E3), mRNA [NM\_017769] |
| A\_33\_P3287939 | C7orf46 | -1.04692 | 1.37E-21 | 1.37E-21 | -11.3006 | Down | Homo sapiens chromosome 7 open reading frame 46 (C7orf46), transcript variant 1, mRNA [NM\_199136] |
| A\_23\_P118749 | DERL2 | -1.05757 | 1.65E-21 | 1.65E-21 | -11.2691 | Down | Homo sapiens Der1-like domain family, member 2 (DERL2), mRNA [NM\_016041] |
| A\_21\_P0000028 | SH2D2A | -1.47183 | 1.95E-21 | 1.95E-21 | -11.242 | Down | Homo sapiens SH2 domain containing 2A (SH2D2A), transcript variant 5, mRNA [NM\_001161444] |
| A\_33\_P3313421 | UHRF1BP1 | -1.04891 | 1.97E-21 | 1.97E-21 | -11.2397 | Down | Homo sapiens UHRF1 binding protein 1 (UHRF1BP1), mRNA [NM\_017754] |
| A\_33\_P3211666 | IL18R1 | -0.9906 | 2.58E-21 | 2.58E-21 | -11.1954 | Down | Homo sapiens interleukin 18 receptor 1 (IL18R1), mRNA [NM\_003855] |
| A\_32\_P514790 | UNK | -1.06642 | 3.31E-21 | 3.31E-21 | -11.1543 | Down | Homo sapiens unkempt homolog (Drosophila) (UNK), transcript variant 1, mRNA [NM\_001080419] |
| A\_23\_P24104 | PLAU | -1.03394 | 4.33E-21 | 4.33E-21 | -11.1092 | Down | Homo sapiens plasminogen activator, urokinase (PLAU), transcript variant 1, mRNA [NM\_002658] |
| A\_23\_P257131 | PEX13 | -1.2484 | 4.97E-21 | 4.97E-21 | -11.0867 | Down | Homo sapiens peroxisomal biogenesis factor 13 (PEX13), mRNA [NM\_002618] |
| A\_24\_P28619 | ANGEL2 | -1.55711 | 5.87E-21 | 5.87E-21 | -11.0589 | Down | Homo sapiens angel homolog 2 (Drosophila) (ANGEL2), mRNA [NM\_144567] |
| A\_33\_P3239148 | ZNF548 | -1.46904 | 6.61E-21 | 6.61E-21 | -11.0391 | Down | Homo sapiens zinc finger protein 548 (ZNF548), transcript variant 1, mRNA [NM\_001172773] |
| A\_23\_P408455 | SLC25A36 | -1.28533 | 6.68E-21 | 6.68E-21 | -11.0374 | Down | Homo sapiens solute carrier family 25, member 36 (SLC25A36), transcript variant 1, mRNA [NM\_001104647] |
| A\_33\_P3420402 | HACE1 | -1.08287 | 6.95E-21 | 6.95E-21 | -11.031 | Down | Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), mRNA [NM\_020771] |
| A\_32\_P426044 | FAM47A | -1.76022 | 7.72E-21 | 7.72E-21 | -11.0136 | Down | Homo sapiens family with sequence similarity 47, member A (FAM47A), mRNA [NM\_203408] |
| A\_24\_P56270 | DYRK2 | -1.01574 | 7.8E-21 | 7.8E-21 | -11.0117 | Down | Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 2, mRNA [NM\_006482] |
| A\_23\_P421401 | PDGFRB | -1.61252 | 1.11E-20 | 1.11E-20 | -10.9529 | Down | Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB), mRNA [NM\_002609] |
| A\_23\_P502590 | KIR2DS4 | -1.8282 | 1.21E-20 | 1.21E-20 | -10.9392 | Down | Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4 (KIR2DS4), mRNA [NM\_012314] |
| A\_23\_P90484 | SARS2 | -1.05609 | 1.22E-20 | 1.22E-20 | -10.9372 | Down | Homo sapiens seryl-tRNA synthetase 2, mitochondrial (SARS2), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM\_017827] |
| A\_21\_P0006902 | LINC00263 | -1.19223 | 1.23E-20 | 1.23E-20 | -10.9363 | Down | GAH6\_HUMAN (Q8N8A4) HERV-H\_22q11.2 provirus ancestral Gag polyprotein (Gag polyprotein), partial (71%) [THC2498127] |
| A\_24\_P124349 | PDGFD | -1.65786 | 1.29E-20 | 1.29E-20 | -10.9282 | Down | Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 1, mRNA [NM\_025208] |
| A\_23\_P328836 | LCOR | -1.05011 | 1.4E-20 | 1.4E-20 | -10.9147 | Down | Homo sapiens ligand dependent nuclear receptor corepressor (LCOR), transcript variant 1, mRNA [NM\_032440] |
| A\_23\_P165061 | AES | -1.03913 | 1.47E-20 | 1.47E-20 | -10.9062 | Down | Homo sapiens amino-terminal enhancer of split (AES), transcript variant 1, mRNA [NM\_198969] |
| A\_33\_P3336592 | LOC100499221 | -1.17177 | 1.5E-20 | 1.5E-20 | -10.9033 | Down | Homo sapiens cDNA FLJ45109 fis, clone BRAWH3034097. [AK127052] |
| A\_21\_P0008287 | XLOC\_010927 | -1.26339 | 1.5E-20 | 1.5E-20 | -10.9026 | Down | DB044321 TESTI2 Homo sapiens cDNA clone TESTI2032258 5', mRNA sequence [DB044321] |
| A\_23\_P88522 | NMB | -0.99693 | 1.58E-20 | 1.58E-20 | -10.8947 | Down | Homo sapiens neuromedin B (NMB), transcript variant 1, mRNA [NM\_021077] |
| A\_23\_P132237 | C22orf31 | -2.09779 | 1.72E-20 | 1.72E-20 | -10.8806 | Down | Homo sapiens chromosome 22 open reading frame 31 (C22orf31), mRNA [NM\_015370] |
| A\_23\_P82523 | ABCB1 | -1.00806 | 1.72E-20 | 1.72E-20 | -10.8801 | Down | Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 1 (ABCB1), mRNA [NM\_000927] |
| A\_23\_P201432 | ADSS | -1.5238 | 1.81E-20 | 1.81E-20 | -10.8721 | Down | Homo sapiens adenylosuccinate synthase (ADSS), mRNA [NM\_001126] |
| A\_24\_P47681 | CAND1 | -1.05633 | 1.82E-20 | 1.82E-20 | -10.8706 | Down | Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA [NM\_018448] |
| A\_24\_P305678 | PITPNB | -1.07284 | 1.98E-20 | 1.98E-20 | -10.8573 | Down | Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA [NM\_012399] |
| A\_23\_P109774 | ZBTB11 | -1.22307 | 1.99E-20 | 1.99E-20 | -10.8561 | Down | Homo sapiens zinc finger and BTB domain containing 11 (ZBTB11), mRNA [NM\_014415] |
| A\_23\_P55518 | SMAD7 | -1.24039 | 2.44E-20 | 2.44E-20 | -10.822 | Down | Homo sapiens SMAD family member 7 (SMAD7), transcript variant 1, mRNA [NM\_005904] |
| A\_33\_P3255290 | JAKMIP2 | -1.26497 | 2.98E-20 | 2.98E-20 | -10.7889 | Down | Homo sapiens janus kinase and microtubule interacting protein 2 (JAKMIP2), mRNA [NM\_014790] |
| A\_33\_P3257187 | PRKAA1 | -1.17602 | 3.15E-20 | 3.15E-20 | -10.7796 | Down | Homo sapiens protein kinase, AMP-activated, alpha 1 catalytic subunit (PRKAA1), transcript variant 2, mRNA [NM\_206907] |
| A\_23\_P42116 | PPT2 | -1.00311 | 3.45E-20 | 3.45E-20 | -10.7648 | Down | Homo sapiens palmitoyl-protein thioesterase 2 (PPT2), transcript variant 1, mRNA [NM\_005155] |
| A\_33\_P3412349 | ZNF268 | -1.18531 | 3.58E-20 | 3.58E-20 | -10.7585 | Down | Homo sapiens zinc finger protein 268 (ZNF268), transcript variant 3, mRNA [NM\_152943] |
| A\_23\_P85726 | METTL18 | -0.98955 | 3.62E-20 | 3.62E-20 | -10.7567 | Down | Homo sapiens methyltransferase like 18 (METTL18), mRNA [NM\_033418] |
| A\_33\_P3393734 | RPS27 | -1.07502 | 3.78E-20 | 3.78E-20 | -10.7493 | Down | ribosomal protein S27 [Source:HGNC Symbol;Acc:10416] [ENST00000392558] |
| A\_33\_P3269670 | ARHGEF33 | -2.78147 | 3.94E-20 | 3.94E-20 | -10.7424 | Down | Homo sapiens Rho guanine nucleotide exchange factor (GEF) 33 (ARHGEF33), mRNA [NM\_001145451] |
| A\_23\_P210829 | PCMTD2 | -1.01421 | 4.01E-20 | 4.01E-20 | -10.7395 | Down | Homo sapiens protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2 (PCMTD2), transcript variant 1, mRNA [NM\_018257] |
| A\_33\_P3413296 | GMDS | -1.29221 | 4.26E-20 | 4.26E-20 | -10.7295 | Down | GDP-mannose 4,6-dehydratase [Source:HGNC Symbol;Acc:4369] [ENST00000380805] |
| A\_23\_P218637 | RGPD5 | -1.15838 | 4.29E-20 | 4.29E-20 | -10.7283 | Down | Homo sapiens RANBP2-like and GRIP domain containing 5 (RGPD5), transcript variant 1, mRNA [NM\_005054] |
| A\_23\_P3856 | ZFP1 | -1.23024 | 6.01E-20 | 6.01E-20 | -10.6722 | Down | Homo sapiens zinc finger protein 1 homolog (mouse) (ZFP1), mRNA [NM\_153688] |
| A\_23\_P23748 | WDR47 | -1.17873 | 6.06E-20 | 6.06E-20 | -10.671 | Down | Homo sapiens WD repeat domain 47 (WDR47), transcript variant 2, mRNA [NM\_014969] |
| A\_24\_P941708 | RUFY2 | -1.02848 | 6.1E-20 | 6.1E-20 | -10.6697 | Down | Homo sapiens RUN and FYVE domain containing 2 (RUFY2), transcript variant 2, mRNA [NM\_001042417] |
| A\_24\_P112377 | DDX31 | -0.99847 | 6.42E-20 | 6.42E-20 | -10.6614 | Down | Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, mRNA [NM\_138620] |
| A\_23\_P133474 | GPX3 | -1.0931 | 7.27E-20 | 7.27E-20 | -10.6406 | Down | Homo sapiens glutathione peroxidase 3 (plasma) (GPX3), mRNA [NM\_002084] |
| A\_33\_P3274501 | KLRF1 | -1.41871 | 9.28E-20 | 9.28E-20 | -10.6 | Down | Homo sapiens killer cell lectin-like receptor subfamily F, member 1 (KLRF1), mRNA [NM\_016523] |
| A\_33\_P3272553 | NCAPH2 | -1.11617 | 9.87E-20 | 9.87E-20 | -10.5896 | Down | Homo sapiens non-SMC condensin II complex, subunit H2 (NCAPH2), transcript variant 1, mRNA [NM\_014551] |
| A\_24\_P226755 | TOX | -1.29234 | 1E-19 | 1E-19 | -10.587 | Down | Homo sapiens thymocyte selection-associated high mobility group box (TOX), mRNA [NM\_014729] |
| A\_23\_P125639 | ZFX | -1.08106 | 1.03E-19 | 1.03E-19 | -10.5824 | Down | Homo sapiens zinc finger protein, X-linked (ZFX), transcript variant 1, mRNA [NM\_003410] |
| A\_24\_P216765 | TOMM20 | -1.19965 | 1.36E-19 | 1.36E-19 | -10.5361 | Down | Homo sapiens translocase of outer mitochondrial membrane 20 homolog (yeast) (TOMM20), nuclear gene encoding mitochondrial protein, mRNA [NM\_014765] |
| A\_32\_P126609 | SMC5 | -1.113 | 1.37E-19 | 1.37E-19 | -10.535 | Down | Homo sapiens structural maintenance of chromosomes 5 (SMC5), mRNA [NM\_015110] |
| A\_33\_P3284019 | FOXP4 | -1.06679 | 1.4E-19 | 1.4E-19 | -10.5316 | Down | Homo sapiens forkhead box P4 (FOXP4), transcript variant 1, mRNA [NM\_001012426] |
| A\_33\_P3390723 | TMEM2 | -1.14837 | 1.51E-19 | 1.51E-19 | -10.5184 | Down | transmembrane protein 2 [Source:HGNC Symbol;Acc:11869] [ENST00000377055] |
| A\_23\_P215883 | NCALD | -1.05498 | 1.65E-19 | 1.65E-19 | -10.5043 | Down | Homo sapiens neurocalcin delta (NCALD), transcript variant 7, mRNA [NM\_001040630] |
| A\_23\_P353316 | SMURF1 | -1.44279 | 1.7E-19 | 1.7E-19 | -10.4987 | Down | Homo sapiens SMAD specific E3 ubiquitin protein ligase 1 (SMURF1), transcript variant 1, mRNA [NM\_020429] |
| A\_32\_P787109 | DTHD1 | -1.26103 | 1.74E-19 | 1.74E-19 | -10.4954 | Down | Homo sapiens death domain containing 1 (DTHD1), transcript variant 1, mRNA [NM\_001170700] |
| A\_24\_P408740 | CMC1 | -1.37425 | 1.79E-19 | 1.79E-19 | -10.4903 | Down | Homo sapiens COX assembly mitochondrial protein homolog (S. cerevisiae) (CMC1), nuclear gene encoding mitochondrial protein, mRNA [NM\_182523] |
| A\_23\_P354894 | ZNF567 | -0.98773 | 1.92E-19 | 1.92E-19 | -10.4788 | Down | Homo sapiens zinc finger protein 567 (ZNF567), mRNA [NM\_152603] |
| A\_32\_P98502 | COX5A | -1.29218 | 2.09E-19 | 2.09E-19 | -10.4646 | Down | Homo sapiens cytochrome c oxidase subunit Va (COX5A), nuclear gene encoding mitochondrial protein, mRNA [NM\_004255] |
| A\_23\_P501634 | BTN2A1 | -1.45649 | 2.24E-19 | 2.24E-19 | -10.4534 | Down | Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 2, mRNA [NM\_078476] |
| A\_24\_P90097 | ADD3 | -1.1597 | 2.24E-19 | 2.24E-19 | -10.4532 | Down | Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 1, mRNA [NM\_016824] |
| A\_33\_P3222703 | ZNF197 | -1.14271 | 2.68E-19 | 2.68E-19 | -10.4234 | Down | Homo sapiens zinc finger protein 197 (ZNF197), transcript variant 2, mRNA [NM\_001024855] |
| A\_21\_P0004556 | XLOC\_004848 | -1.24481 | 3.08E-19 | 3.08E-19 | -10.4001 | Down | Q3AUE7\_CHLCH (Q3AUE7) Glucosamine-fructose-6-phosphate aminotransferase, isomerising , partial (4%) [THC2660784] |
| A\_23\_P302018 | TXK | -1.00034 | 3.12E-19 | 3.12E-19 | -10.3976 | Down | Homo sapiens TXK tyrosine kinase (TXK), mRNA [NM\_003328] |
| A\_21\_P0001246 | XLOC\_001265 | -1.53819 | 3.2E-19 | 3.2E-19 | -10.3933 | Down | Q2AB94\_MONDO (Q2AB94) Bitter taste receptor, partial (6%) [THC2684977] |
| A\_24\_P237389 | EIF1AX | -1.00772 | 3.21E-19 | 3.21E-19 | -10.3928 | Down | Homo sapiens eukaryotic translation initiation factor 1A, X-linked (EIF1AX), mRNA [NM\_001412] |
| A\_23\_P19322 | C6orf64 | -1.08571 | 3.95E-19 | 3.95E-19 | -10.3581 | Down | Homo sapiens chromosome 6 open reading frame 64 (C6orf64), mRNA [NM\_018322] |
| A\_23\_P395595 | FNBP4 | -1.00358 | 4.05E-19 | 4.05E-19 | -10.3541 | Down | Homo sapiens formin binding protein 4 (FNBP4), mRNA [NM\_015308] |
| A\_33\_P3376644 | SENP6 | -1.25314 | 4.53E-19 | 4.53E-19 | -10.3356 | Down | Homo sapiens SUMO1/sentrin specific peptidase 6 (SENP6), transcript variant 1, mRNA [NM\_015571] |
| A\_33\_P3263392 | LOC729696 | -1.03019 | 4.63E-19 | 4.63E-19 | -10.3316 | Down | Homo sapiens cDNA FLJ44161 fis, clone THYMU2033070. [AK126149] |
| A\_33\_P3377459 | PAPD5 | -1.20303 | 4.96E-19 | 4.96E-19 | -10.3203 | Down | Homo sapiens PAP associated domain containing 5 (PAPD5), transcript variant 1, mRNA [NM\_001040284] |
| A\_23\_P127579 | PTS | -0.99165 | 5.28E-19 | 5.28E-19 | -10.3098 | Down | Homo sapiens 6-pyruvoyltetrahydropterin synthase (PTS), mRNA [NM\_000317] |
| A\_24\_P305933 | TMCC3 | -1.24655 | 5.48E-19 | 5.48E-19 | -10.3037 | Down | Homo sapiens transmembrane and coiled-coil domain family 3 (TMCC3), mRNA [NM\_020698] |
| A\_23\_P29005 | SAMSN1 | -1.38476 | 6.03E-19 | 6.03E-19 | -10.2876 | Down | Homo sapiens SAM domain, SH3 domain and nuclear localization signals 1 (SAMSN1), mRNA [NM\_022136] |
| A\_23\_P66881 | RGS9 | -1.35211 | 6.46E-19 | 6.46E-19 | -10.2761 | Down | Homo sapiens regulator of G-protein signaling 9 (RGS9), transcript variant 1, mRNA [NM\_003835] |
| A\_33\_P3542599 | SNORA2A | -1.20433 | 6.7E-19 | 6.7E-19 | -10.27 | Down | CM3-MT0388-260101-688-e11\_1 MT0388 Homo sapiens cDNA, mRNA sequence [CV322587] |
| A\_23\_P140309 | MAPK1IP1L | -1.09627 | 7.43E-19 | 7.43E-19 | -10.2527 | Down | Homo sapiens mitogen-activated protein kinase 1 interacting protein 1-like (MAPK1IP1L), mRNA [NM\_144578] |
| A\_24\_P861009 | BRWD1 | -1.0511 | 7.44E-19 | 7.44E-19 | -10.2525 | Down | Homo sapiens bromodomain and WD repeat domain containing 1 (BRWD1), transcript variant 3, mRNA [NM\_001007246] |
| A\_32\_P158966 | KLRF1 | -1.18591 | 7.62E-19 | 7.62E-19 | -10.2485 | Down | Homo sapiens killer cell lectin-like receptor subfamily F, member 1 (KLRF1), mRNA [NM\_016523] |
| A\_33\_P3278916 | PHF20L1 | -1.25451 | 8.12E-19 | 8.12E-19 | -10.2379 | Down | PHD finger protein 20-like 1 [Source:HGNC Symbol;Acc:24280] [ENST00000361997] |
| A\_33\_P3346688 | HSPA8 | -1.01892 | 8.15E-19 | 8.15E-19 | -10.2371 | Down | heat shock 70kDa protein 8 [Source:HGNC Symbol;Acc:5241] [ENST00000527983] |
| A\_33\_P3386716 | PPP1R15B | -1.01505 | 8.52E-19 | 8.52E-19 | -10.2298 | Down | Homo sapiens protein phosphatase 1, regulatory subunit 15B (PPP1R15B), mRNA [NM\_032833] |
| A\_33\_P3314386 | TOR1AIP1 | -1.13171 | 8.66E-19 | 8.66E-19 | -10.2271 | Down | Homo sapiens torsin A interacting protein 1 (TOR1AIP1), mRNA [NM\_015602] |
| A\_32\_P84242 | FAM169A | -1.16286 | 9.23E-19 | 9.23E-19 | -10.2163 | Down | Homo sapiens family with sequence similarity 169, member A (FAM169A), mRNA [NM\_015566] |
| A\_23\_P117602 | GZMB | -1.24367 | 9.8E-19 | 9.8E-19 | -10.2064 | Down | Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA [NM\_004131] |
| A\_23\_P94552 | TMEM2 | -1.06891 | 1.03E-18 | 1.03E-18 | -10.1987 | Down | Homo sapiens transmembrane protein 2 (TMEM2), transcript variant 1, mRNA [NM\_013390] |
| A\_24\_P347704 | CTCF | -1.21254 | 1.14E-18 | 1.14E-18 | -10.1815 | Down | Homo sapiens CCCTC-binding factor (zinc finger protein) (CTCF), transcript variant 1, mRNA [NM\_006565] |
| A\_23\_P404481 | S1PR1 | -1.33299 | 1.2E-18 | 1.2E-18 | -10.1726 | Down | Homo sapiens sphingosine-1-phosphate receptor 1 (S1PR1), mRNA [NM\_001400] |
| A\_33\_P3317305 | AGAP1 | -1.08127 | 1.55E-18 | 1.55E-18 | -10.1291 | Down | Homo sapiens ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 (AGAP1), transcript variant 2, mRNA [NM\_001244888] |
| A\_33\_P3389008 | GHITM | -1.05722 | 1.77E-18 | 1.77E-18 | -10.1071 | Down | Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA [NM\_014394] |
| A\_33\_P3316313 | MTERFD2 | -1.02767 | 1.82E-18 | 1.82E-18 | -10.1023 | Down | Homo sapiens MTERF domain containing 2 (MTERFD2), transcript variant 1, mRNA [NM\_182501] |
| A\_24\_P152398 | TP53AIP1 | -1.65607 | 1.9E-18 | 1.9E-18 | -10.0957 | Down | Homo sapiens tumor protein p53 regulated apoptosis inducing protein 1 (TP53AIP1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM\_001195195] |
| A\_32\_P49668 | LOC100653060 | -1.03818 | 2.06E-18 | 2.06E-18 | -10.0816 | Down | PREDICTED: Homo sapiens putative POM121-like protein 1-like (LOC100653060), mRNA [XM\_003403393] |
| A\_33\_P3406196 | KLRD1 | -1.30824 | 2.12E-18 | 2.12E-18 | -10.0774 | Down | Homo sapiens killer cell lectin-like receptor subfamily D, member 1 (KLRD1), transcript variant 1, mRNA [NM\_002262] |
| A\_23\_P59418 | NRF1 | -1.03569 | 2.21E-18 | 2.21E-18 | -10.0704 | Down | Homo sapiens nuclear respiratory factor 1 (NRF1), transcript variant 1, mRNA [NM\_005011] |
| A\_23\_P121533 | SPON2 | -1.34258 | 2.83E-18 | 2.83E-18 | -10.0286 | Down | Homo sapiens spondin 2, extracellular matrix protein (SPON2), transcript variant 1, mRNA [NM\_012445] |
| A\_24\_P190541 | BRWD1 | -1.13073 | 3.21E-18 | 3.21E-18 | -10.0077 | Down | Homo sapiens bromodomain and WD repeat domain containing 1 (BRWD1), transcript variant 1, mRNA [NM\_018963] |
| A\_33\_P3354858 | COQ10B | -1.27769 | 3.22E-18 | 3.22E-18 | -10.0069 | Down | Homo sapiens coenzyme Q10 homolog B (S. cerevisiae) (COQ10B), nuclear gene encoding mitochondrial protein, mRNA [NM\_025147] |
| A\_32\_P93852 | BOD1 | -0.99268 | 3.3E-18 | 3.3E-18 | -10.0029 | Down | Homo sapiens biorientation of chromosomes in cell division 1 (BOD1), transcript variant 1, mRNA [NM\_138369] |
| A\_24\_P276531 | SNIP1 | -1.09419 | 3.79E-18 | 3.79E-18 | -9.97978 | Down | Homo sapiens Smad nuclear interacting protein 1 (SNIP1), mRNA [NM\_024700] |
| A\_33\_P3353921 | GNLY | -1.12549 | 4.52E-18 | 4.52E-18 | -9.95006 | Down | granulysin [Source:HGNC Symbol;Acc:4414] [ENST00000489214] |
| A\_23\_P30784 | ABT1 | -1.01939 | 5.39E-18 | 5.39E-18 | -9.92036 | Down | Homo sapiens activator of basal transcription 1 (ABT1), mRNA [NM\_013375] |
| A\_24\_P303097 | SNX25 | -1.14456 | 5.46E-18 | 5.46E-18 | -9.91835 | Down | Homo sapiens sorting nexin 25 (SNX25), mRNA [NM\_031953] |
| A\_33\_P3304382 | C8orf38 | -0.97076 | 5.65E-18 | 5.65E-18 | -9.91258 | Down | Homo sapiens chromosome 8 open reading frame 38 (C8orf38), nuclear gene encoding mitochondrial protein, mRNA [NM\_152416] |
| A\_23\_P2294 | HELB | -0.98262 | 5.67E-18 | 5.67E-18 | -9.91186 | Down | Homo sapiens helicase (DNA) B (HELB), mRNA [NM\_033647] |
| A\_33\_P3354607 | CCL4 | -2.03758 | 6.05E-18 | 6.05E-18 | -9.90097 | Down | Homo sapiens chemokine (C-C motif) ligand 4 (CCL4), transcript variant 1, mRNA [NM\_002984] |
| A\_33\_P3292840 | C11orf49 | -0.98434 | 7.1E-18 | 7.1E-18 | -9.87414 | Down | Homo sapiens chromosome 11 open reading frame 49 (C11orf49), transcript variant 4, mRNA [NM\_001003678] |
| A\_32\_P52609 | LPIN1 | -1.02937 | 7.64E-18 | 7.64E-18 | -9.8618 | Down | Homo sapiens lipin 1 (LPIN1), mRNA [NM\_145693] |
| A\_23\_P305692 | ELMOD2 | -1.09822 | 8.42E-18 | 8.42E-18 | -9.84529 | Down | Homo sapiens ELMO/CED-12 domain containing 2 (ELMOD2), mRNA [NM\_153702] |
| A\_23\_P120921 | ANKRD54 | -1.5783 | 8.71E-18 | 8.71E-18 | -9.83972 | Down | Homo sapiens ankyrin repeat domain 54 (ANKRD54), transcript variant 1, mRNA [NM\_138797] |
| A\_33\_P3389658 | PDE4D | -1.32293 | 9.45E-18 | 9.45E-18 | -9.82601 | Down | Homo sapiens phosphodiesterase 4D, cAMP-specific (PDE4D), transcript variant 3, mRNA [NM\_001165899] |
| A\_23\_P325625 | SCAI | -1.0545 | 9.83E-18 | 9.83E-18 | -9.81936 | Down | Homo sapiens suppressor of cancer cell invasion (SCAI), transcript variant 1, mRNA [NM\_173690] |
| A\_33\_P3223923 | PDIA3 | -0.98998 | 1.15E-17 | 1.15E-17 | -9.79312 | Down | Homo sapiens protein disulfide isomerase family A, member 3 (PDIA3), mRNA [NM\_005313] |
| A\_33\_P3224795 | IKZF5 | -1.60333 | 1.19E-17 | 1.19E-17 | -9.78672 | Down | Homo sapiens IKAROS family zinc finger 5 (Pegasus) (IKZF5), mRNA [NM\_022466] |
| A\_23\_P205646 | MAP4K5 | -1.15302 | 1.38E-17 | 1.38E-17 | -9.76192 | Down | Homo sapiens mitogen-activated protein kinase kinase kinase kinase 5 (MAP4K5), transcript variant 2, mRNA [NM\_198794] |
| A\_33\_P3245321 | CENPP | -1.23458 | 1.44E-17 | 1.44E-17 | -9.75538 | Down | Homo sapiens centromere protein P (CENPP), mRNA [NM\_001012267] |
| A\_23\_P209195 | C19orf12 | -0.96633 | 1.49E-17 | 1.49E-17 | -9.74942 | Down | Homo sapiens chromosome 19 open reading frame 12 (C19orf12), transcript variant 2, mRNA [NM\_031448] |
| A\_23\_P393425 | PAPD4 | -0.96776 | 1.55E-17 | 1.55E-17 | -9.74231 | Down | Homo sapiens PAP associated domain containing 4 (PAPD4), transcript variant 3, mRNA [NM\_173797] |
| A\_33\_P3266873 | MSL1 | -1.31982 | 1.58E-17 | 1.58E-17 | -9.73885 | Down | Homo sapiens male-specific lethal 1 homolog (Drosophila) (MSL1), mRNA [NM\_001012241] |
| A\_32\_P218989 | YBX1 | -0.97147 | 1.67E-17 | 1.67E-17 | -9.73021 | Down | Homo sapiens Y box binding protein 1 (YBX1), mRNA [NM\_004559] |
| A\_33\_P3315223 | HNRNPA0 | -1.3335 | 1.95E-17 | 1.95E-17 | -9.70349 | Down | Homo sapiens heterogeneous nuclear ribonucleoprotein A0 (HNRNPA0), mRNA [NM\_006805] |
| A\_24\_P791040 | FBXW2 | -1.59261 | 1.96E-17 | 1.96E-17 | -9.70319 | Down | Homo sapiens F-box and WD repeat domain containing 2 (FBXW2), mRNA [NM\_012164] |
| A\_21\_P0000092 | ZBED6 | -1.19198 | 2.06E-17 | 2.06E-17 | -9.69452 | Down | Homo sapiens zinc finger, BED-type containing 6 (ZBED6), mRNA [NM\_001174108] |
| A\_24\_P11575 | CRIM1 | -1.29702 | 2.1E-17 | 2.1E-17 | -9.69143 | Down | Homo sapiens cysteine rich transmembrane BMP regulator 1 (chordin-like) (CRIM1), mRNA [NM\_016441] |
| A\_33\_P3424462 | CNST | -1.25175 | 2.4E-17 | 2.4E-17 | -9.66872 | Down | Homo sapiens consortin, connexin sorting protein (CNST), transcript variant 2, mRNA [NM\_001139459] |
| A\_33\_P3288384 | PSMA1 | -1.00963 | 2.83E-17 | 2.83E-17 | -9.64122 | Down | Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 1 (PSMA1), transcript variant 3, mRNA [NM\_001143937] |
| A\_23\_P57306 | CHAF1B | -1.07055 | 2.95E-17 | 2.95E-17 | -9.63375 | Down | Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA [NM\_005441] |
| A\_23\_P200792 | NOTCH2 | -1.23287 | 3.12E-17 | 3.12E-17 | -9.62448 | Down | Homo sapiens notch 2 (NOTCH2), transcript variant 1, mRNA [NM\_024408] |
| A\_33\_P3290567 | WEE1 | -1.25757 | 3.33E-17 | 3.33E-17 | -9.61363 | Down | Homo sapiens WEE1 homolog (S. pombe) (WEE1), transcript variant 1, mRNA [NM\_003390] |
| A\_33\_P3303414 | MAN1A1 | -1.32375 | 3.47E-17 | 3.47E-17 | -9.60641 | Down | Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA [NM\_005907] |
| A\_23\_P218463 | SERTAD1 | -1.06451 | 3.68E-17 | 3.68E-17 | -9.59664 | Down | Homo sapiens SERTA domain containing 1 (SERTAD1), mRNA [NM\_013376] |
| A\_24\_P147540 | FLJ22184 | -1.00865 | 3.81E-17 | 3.81E-17 | -9.59083 | Down | Homo sapiens putative uncharacterized protein FLJ22184 (FLJ22184), mRNA [NM\_001190467] |
| A\_33\_P3331085 | SEC24A | -1.40056 | 4.13E-17 | 4.13E-17 | -9.57684 | Down | Homo sapiens SEC24 family, member A (S. cerevisiae) (SEC24A), transcript variant 1, mRNA [NM\_021982] |
| A\_23\_P320887 | CDC42SE1 | -1.06928 | 5.02E-17 | 5.02E-17 | -9.54409 | Down | Homo sapiens CDC42 small effector 1 (CDC42SE1), transcript variant 1, mRNA [NM\_001038707] |
| A\_33\_P3421183 | GTF2I | -1.19538 | 6.44E-17 | 6.44E-17 | -9.50184 | Down | general transcription factor IIi [Source:HGNC Symbol;Acc:4659] [ENST00000473333] |
| A\_23\_P68087 | ATIC | -1.11298 | 7.18E-17 | 7.18E-17 | -9.48333 | Down | Homo sapiens 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase (ATIC), mRNA [NM\_004044] |
| A\_32\_P16258 | EXOC6B | -1.10448 | 7.54E-17 | 7.54E-17 | -9.47501 | Down | exocyst complex component 6B [Source:HGNC Symbol;Acc:17085] [ENST00000272427] |
| A\_33\_P3228762 | SLC25A36 | -1.00238 | 7.9E-17 | 7.9E-17 | -9.46705 | Down | Homo sapiens solute carrier family 25, member 36 (SLC25A36), transcript variant 1, mRNA [NM\_001104647] |
| A\_23\_P151710 | PTGER2 | -1.06159 | 8.19E-17 | 8.19E-17 | -9.46091 | Down | Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), mRNA [NM\_000956] |
| A\_23\_P85703 | SOX13 | -1.10364 | 9.45E-17 | 9.45E-17 | -9.43675 | Down | Homo sapiens SRY (sex determining region Y)-box 13 (SOX13), mRNA [NM\_005686] |
| A\_23\_P111961 | MAK16 | -1.0269 | 9.84E-17 | 9.84E-17 | -9.42984 | Down | Homo sapiens MAK16 homolog (S. cerevisiae) (MAK16), mRNA [NM\_032509] |
| A\_23\_P146444 | CORO2A | -1.01649 | 1.16E-16 | 1.16E-16 | -9.40177 | Down | Homo sapiens coronin, actin binding protein, 2A (CORO2A), transcript variant 1, mRNA [NM\_003389] |
| A\_21\_P0010877 | BMS1P5 | -0.96327 | 1.18E-16 | 1.18E-16 | -9.39917 | Down | D80009 Start codon is not identified {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (12%) [THC2480131] |
| A\_33\_P3245709 | RALGAPB | -1.10604 | 1.19E-16 | 1.19E-16 | -9.39758 | Down | Homo sapiens Ral GTPase activating protein, beta subunit (non-catalytic) (RALGAPB), mRNA [NM\_020336] |
| A\_33\_P3275487 | SLFN13 | -1.00028 | 1.46E-16 | 1.46E-16 | -9.36246 | Down | Homo sapiens schlafen family member 13 (SLFN13), mRNA [NM\_144682] |
| A\_33\_P3283619 | SH2D1A | -0.99257 | 1.64E-16 | 1.64E-16 | -9.34281 | Down | Homo sapiens SH2 domain containing 1A (SH2D1A), transcript variant 2, mRNA [NM\_001114937] |
| A\_24\_P295963 | SLC38A2 | -1.06961 | 1.83E-16 | 1.83E-16 | -9.32408 | Down | Homo sapiens solute carrier family 38, member 2 (SLC38A2), mRNA [NM\_018976] |
| A\_24\_P288298 | KIR2DL4 | -1.32183 | 1.94E-16 | 1.94E-16 | -9.31429 | Down | Homo sapiens killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4 (KIR2DL4), transcript variant 1, mRNA [NM\_002255] |
| A\_23\_P160214 | TTC39A | -1.15488 | 1.98E-16 | 1.98E-16 | -9.31085 | Down | Homo sapiens tetratricopeptide repeat domain 39A (TTC39A), transcript variant 2, mRNA [NM\_001080494] |
| A\_23\_P24926 | FNTA | -1.25296 | 2.52E-16 | 2.52E-16 | -9.26984 | Down | Homo sapiens farnesyltransferase, CAAX box, alpha (FNTA), transcript variant 1, mRNA [NM\_002027] |
| A\_33\_P3277253 | C9orf41 | -1.0965 | 2.64E-16 | 2.64E-16 | -9.26174 | Down | chromosome 9 open reading frame 41 [Source:HGNC Symbol;Acc:23435] [ENST00000376830] |
| A\_23\_P615 | INSRR | -1.17283 | 2.72E-16 | 2.72E-16 | -9.25663 | Down | Homo sapiens insulin receptor-related receptor (INSRR), mRNA [NM\_014215] |
| A\_24\_P83183 | WHSC2 | -1.78403 | 2.87E-16 | 2.87E-16 | -9.24786 | Down | Homo sapiens Wolf-Hirschhorn syndrome candidate 2 (WHSC2), mRNA [NM\_005663] |
| A\_33\_P3212650 | HDDC2 | -1.01966 | 2.97E-16 | 2.97E-16 | -9.24167 | Down | HD domain containing 2 [Source:HGNC Symbol;Acc:21078] [ENST00000318787] |
| A\_24\_P268893 | THAP6 | -1.14135 | 3.03E-16 | 3.03E-16 | -9.23841 | Down | Homo sapiens THAP domain containing 6 (THAP6), mRNA [NM\_144721] |
| A\_23\_P55515 | RNMT | -1.12715 | 3.12E-16 | 3.12E-16 | -9.23335 | Down | Homo sapiens RNA (guanine-7-) methyltransferase (RNMT), mRNA [NM\_003799] |
| A\_23\_P54953 | SAP30BP | -1.25812 | 3.16E-16 | 3.16E-16 | -9.23125 | Down | Homo sapiens SAP30 binding protein (SAP30BP), mRNA [NM\_013260] |
| A\_33\_P3220833 | PAK2 | -2.27842 | 3.18E-16 | 3.18E-16 | -9.23002 | Down | Homo sapiens p21 protein (Cdc42/Rac)-activated kinase 2 (PAK2), mRNA [NM\_002577] |
| A\_23\_P200728 | FCGR3A | -1.15651 | 3.36E-16 | 3.36E-16 | -9.22085 | Down | Homo sapiens Fc fragment of IgG, low affinity IIIa, receptor (CD16a) (FCGR3A), transcript variant 1, mRNA [NM\_000569] |
| A\_24\_P21831 | ZNF26 | -1.05182 | 3.41E-16 | 3.41E-16 | -9.21818 | Down | Homo sapiens zinc finger protein 26 (ZNF26), mRNA [NM\_019591] |
| A\_23\_P387184 | NHSL1 | -1.43291 | 3.62E-16 | 3.62E-16 | -9.2081 | Down | Homo sapiens NHS-like 1 (NHSL1), transcript variant 1, mRNA [NM\_020464] |
| A\_23\_P108342 | ZNF571 | -1.16887 | 3.97E-16 | 3.97E-16 | -9.19251 | Down | Homo sapiens zinc finger protein 571 (ZNF571), mRNA [NM\_016536] |
| A\_23\_P165722 | EIF4E2 | -1.15984 | 4.16E-16 | 4.16E-16 | -9.18453 | Down | Homo sapiens eukaryotic translation initiation factor 4E family member 2 (EIF4E2), mRNA [NM\_004846] |
| A\_23\_P117225 | ERCC5 | -1.08541 | 4.24E-16 | 4.24E-16 | -9.18126 | Down | Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 5 (ERCC5), mRNA [NM\_000123] |
| A\_33\_P3360823 | C10orf88 | -0.96517 | 4.49E-16 | 4.49E-16 | -9.1713 | Down | Homo sapiens chromosome 10 open reading frame 88 (C10orf88), mRNA [NM\_024942] |
| A\_23\_P214244 | ENPP5 | -1.22298 | 4.72E-16 | 4.72E-16 | -9.163 | Down | Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative) (ENPP5), mRNA [NM\_021572] |
| A\_33\_P3409266 | GAFA2 | -1.28874 | 4.82E-16 | 4.82E-16 | -9.1592 | Down | Homo sapiens FGF-2 activity-associated protein 2 (GAFA2) mRNA, complete cds. [AF220234] |
| A\_33\_P3390731 | AKTIP | -0.99759 | 4.83E-16 | 4.83E-16 | -9.15902 | Down | Homo sapiens AKT interacting protein (AKTIP), transcript variant 1, mRNA [NM\_001012398] |
| A\_33\_P3289661 | OCR1 | -1.0127 | 5.18E-16 | 5.18E-16 | -9.14683 | Down | Homo sapiens ovarian cancer-related protein 1 (OCR1) mRNA, complete cds. [AF314543] |
| A\_21\_P0001139 | PKP4 | -1.00022 | 5.31E-16 | 5.31E-16 | -9.14279 | Down | Q8IV82\_HUMAN (Q8IV82) JAK1 protein (Fragment), partial (36%) [THC2515540] |
| A\_23\_P381577 | ZNF25 | -1.06941 | 6.09E-16 | 6.09E-16 | -9.11939 | Down | Homo sapiens zinc finger protein 25 (ZNF25), mRNA [NM\_145011] |
| A\_33\_P3220390 | WTAP | -1.09541 | 7.21E-16 | 7.21E-16 | -9.09038 | Down | Homo sapiens Wilms tumor 1 associated protein, mRNA (cDNA clone IMAGE:5399821), partial cds. [BC028180] |
| A\_33\_P3363933 | FCRL6 | -1.19272 | 8.05E-16 | 8.05E-16 | -9.07148 | Down | Homo sapiens Fc receptor-like 6 (FCRL6), mRNA [NM\_001004310] |
| A\_24\_P117147 | KIR3DL1 | -1.26545 | 8.63E-16 | 8.63E-16 | -9.05953 | Down | Homo sapiens killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 (KIR3DL1), mRNA [NM\_013289] |
| A\_23\_P37088 | RDH12 | -0.9956 | 8.68E-16 | 8.68E-16 | -9.05868 | Down | Homo sapiens retinol dehydrogenase 12 (all-trans/9-cis/11-cis) (RDH12), mRNA [NM\_152443] |
| A\_33\_P3372488 | TCTN3 | -1.17724 | 9.19E-16 | 9.19E-16 | -9.04877 | Down | tectonic family member 3 [Source:HGNC Symbol;Acc:24519] [ENST00000371209] |
| A\_24\_P945283 | DLG3 | -0.98719 | 1.14E-15 | 1.14E-15 | -9.01235 | Down | Homo sapiens discs, large homolog 3 (Drosophila) (DLG3), transcript variant 1, mRNA [NM\_021120] |
| A\_24\_P922631 | C5orf58 | -0.98761 | 1.17E-15 | 1.17E-15 | -9.00792 | Down | Homo sapiens chromosome 5 open reading frame 58 (C5orf58), mRNA [NM\_001102609] |
| A\_23\_P39755 | B3GNT7 | -1.52261 | 1.19E-15 | 1.19E-15 | -9.00398 | Down | Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 (B3GNT7), mRNA [NM\_145236] |
| A\_23\_P144369 | NAP1L5 | -1.06234 | 1.23E-15 | 1.23E-15 | -8.99845 | Down | Homo sapiens nucleosome assembly protein 1-like 5 (NAP1L5), mRNA [NM\_153757] |
| A\_23\_P139509 | ERGIC2 | -1.01641 | 1.31E-15 | 1.31E-15 | -8.98828 | Down | Homo sapiens ERGIC and golgi 2 (ERGIC2), mRNA [NM\_016570] |
| A\_24\_P87746 | KIR2DS4 | -1.29739 | 1.36E-15 | 1.36E-15 | -8.98193 | Down | Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4 (KIR2DS4), mRNA [NM\_012314] |
| A\_23\_P99693 | ZBTB1 | -0.99739 | 1.5E-15 | 1.5E-15 | -8.96492 | Down | Homo sapiens zinc finger and BTB domain containing 1 (ZBTB1), transcript variant 2, mRNA [NM\_014950] |
| A\_24\_P252078 | BTN3A2 | -1.05255 | 1.51E-15 | 1.51E-15 | -8.96374 | Down | Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), transcript variant 1, mRNA [NM\_007047] |
| A\_33\_P3378737 | TTC39B | -1.12244 | 1.52E-15 | 1.52E-15 | -8.96226 | Down | tetratricopeptide repeat domain 39B [Source:HGNC Symbol;Acc:23704] [ENST00000463391] |
| A\_23\_P11800 | CAMK2N1 | -0.97644 | 1.56E-15 | 1.56E-15 | -8.95794 | Down | Homo sapiens calcium/calmodulin-dependent protein kinase II inhibitor 1 (CAMK2N1), mRNA [NM\_018584] |
| A\_32\_P213330 | RGNEF | -1.13625 | 2.02E-15 | 2.02E-15 | -8.91314 | Down | Homo sapiens 190 kDa guanine nucleotide exchange factor (RGNEF), transcript variant 2, mRNA [NM\_001177693] |
| A\_23\_P415820 | EXOC6B | -0.99478 | 2.3E-15 | 2.3E-15 | -8.89089 | Down | Homo sapiens mRNA for KIAA0919 protein, partial cds. [AB023136] |
| A\_23\_P408095 | DSTN | -1.01178 | 2.4E-15 | 2.4E-15 | -8.88403 | Down | Homo sapiens destrin (actin depolymerizing factor) (DSTN), transcript variant 2, mRNA [NM\_001011546] |
| A\_23\_P100441 | FAM192A | -1.32268 | 2.5E-15 | 2.5E-15 | -8.87675 | Down | Homo sapiens family with sequence similarity 192, member A (FAM192A), mRNA [NM\_024946] |
| A\_24\_P215804 | CKLF | -1.5398 | 2.65E-15 | 2.65E-15 | -8.86665 | Down | Homo sapiens chemokine-like factor (CKLF), transcript variant 1, mRNA [NM\_016951] |
| A\_24\_P380132 | G3BP2 | -1.11203 | 2.69E-15 | 2.69E-15 | -8.86409 | Down | Homo sapiens GTPase activating protein (SH3 domain) binding protein 2 (G3BP2), transcript variant 1, mRNA [NM\_203505] |
| A\_21\_P0014241 | RNF183 | -1.04643 | 2.85E-15 | 2.85E-15 | -8.85445 | Down | PREDICTED: Homo sapiens hypothetical LOC100507626 (LOC100507626), miscRNA [XR\_108991] |
| A\_23\_P346884 | RBPJL | -2.32229 | 2.89E-15 | 2.89E-15 | -8.85199 | Down | Homo sapiens recombination signal binding protein for immunoglobulin kappa J region-like (RBPJL), mRNA [NM\_014276] |
| A\_33\_P3365087 | PRR20B | -1.43103 | 2.96E-15 | 2.96E-15 | -8.84747 | Down | Homo sapiens proline rich 20B (PRR20B), mRNA [NM\_001130404] |
| A\_23\_P68601 | CST7 | -0.96445 | 3.05E-15 | 3.05E-15 | -8.84235 | Down | Homo sapiens cystatin F (leukocystatin) (CST7), mRNA [NM\_003650] |
| A\_24\_P116242 | KLHDC2 | -1.11014 | 3.06E-15 | 3.06E-15 | -8.84194 | Down | Homo sapiens kelch domain containing 2 (KLHDC2), mRNA [NM\_014315] |
| A\_24\_P409042 | CDC42SE2 | -1.19703 | 3.15E-15 | 3.15E-15 | -8.83681 | Down | Homo sapiens CDC42 small effector 2 (CDC42SE2), transcript variant 1, mRNA [NM\_020240] |
| A\_33\_P3226755 | FLNA | -1.35087 | 3.19E-15 | 3.19E-15 | -8.83482 | Down | Homo sapiens cDNA FLJ43642 fis, clone STOMA2004925. [AK125630] |
| A\_33\_P3285734 | FCRL6 | -1.13009 | 3.3E-15 | 3.3E-15 | -8.82922 | Down | Homo sapiens Fc receptor-like 6 (FCRL6), mRNA [NM\_001004310] |
| A\_19\_P00806947 | PCNA | -0.99595 | 3.45E-15 | 3.45E-15 | -8.82118 | Down | Homo sapiens proliferating cell nuclear antigen (PCNA), transcript variant 1, mRNA [NM\_002592] |
| A\_33\_P3221114 | JAKMIP1 | -1.02912 | 3.55E-15 | 3.55E-15 | -8.81649 | Down | Homo sapiens janus kinase and microtubule interacting protein 1 (JAKMIP1), transcript variant 2, mRNA [NM\_144720] |
| A\_32\_P205944 | RGPD5 | -1.0631 | 3.55E-15 | 3.55E-15 | -8.81642 | Down | Homo sapiens RANBP2-like and GRIP domain containing 5 (RGPD5), transcript variant 1, mRNA [NM\_005054] |
| A\_21\_P0005229 | XLOC\_006079 | -1.12708 | 3.58E-15 | 3.58E-15 | -8.81513 | Down | KCC2B\_HUMAN (Q13554) Calcium/calmodulin-dependent protein kinase type II beta chain (CaM-kinase II beta chain) (CaM kinase II beta subunit) (CaMK-II beta subunit) , partial (3%) [THC2611356] |
| A\_33\_P3235856 | RORB | -1.36387 | 3.64E-15 | 3.64E-15 | -8.81202 | Down | Homo sapiens RAR-related orphan receptor B (RORB), mRNA [NM\_006914] |
| A\_23\_P99604 | G2E3 | -0.99736 | 3.92E-15 | 3.92E-15 | -8.7993 | Down | Homo sapiens G2/M-phase specific E3 ubiquitin protein ligase (G2E3), mRNA [NM\_017769] |
| A\_23\_P161183 | ZDHHC6 | -1.23596 | 3.95E-15 | 3.95E-15 | -8.79801 | Down | Homo sapiens zinc finger, DHHC-type containing 6 (ZDHHC6), mRNA [NM\_022494] |
| A\_33\_P3314471 | IMMT | -1.25986 | 4.4E-15 | 4.4E-15 | -8.77918 | Down | inner membrane protein, mitochondrial [Source:HGNC Symbol;Acc:6047] [ENST00000474969] |
| A\_24\_P56388 | HIF1A | -1.25852 | 4.72E-15 | 4.72E-15 | -8.76728 | Down | Homo sapiens hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (HIF1A), transcript variant 2, mRNA [NM\_181054] |
| A\_24\_P350622 | KIR2DL4 | -1.21928 | 4.79E-15 | 4.79E-15 | -8.76457 | Down | Homo sapiens killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4 (KIR2DL4), transcript variant 1, mRNA [NM\_002255] |
| A\_23\_P413193 | SFR1 | -1.10065 | 4.87E-15 | 4.87E-15 | -8.7619 | Down | Homo sapiens SWI5-dependent recombination repair 1 (SFR1), transcript variant 2, mRNA [NM\_145247] |
| A\_23\_P135730 | ZNF627 | -0.96678 | 5.77E-15 | 5.77E-15 | -8.73231 | Down | Homo sapiens zinc finger protein 627 (ZNF627), mRNA [NM\_145295] |
| A\_24\_P225635 | HNRPLL | -1.29316 | 5.97E-15 | 5.97E-15 | -8.7266 | Down | heterogeneous nuclear ribonucleoprotein L-like [Source:HGNC Symbol;Acc:25127] [ENST00000449105] |
| A\_33\_P3374378 | GTDC1 | -1.00853 | 7.19E-15 | 7.19E-15 | -8.69436 | Down | Homo sapiens cDNA FLJ44822 fis, clone BRACE3046294. [AK126774] |
| A\_33\_P3310274 | LGR6 | -1.23176 | 7.53E-15 | 7.53E-15 | -8.68636 | Down | leucine-rich repeat containing G protein-coupled receptor 6 [Source:HGNC Symbol;Acc:19719] [ENST00000420582] |
| A\_33\_P3392977 | CCNDBP1 | -1.31535 | 7.83E-15 | 7.83E-15 | -8.67954 | Down | Homo sapiens cyclin D-type binding-protein 1 (CCNDBP1), transcript variant 1, mRNA [NM\_012142] |
| A\_21\_P0000074 | C5orf41 | -1.25106 | 8.03E-15 | 8.03E-15 | -8.67518 | Down | Homo sapiens chromosome 5 open reading frame 41 (C5orf41), transcript variant 3, mRNA [NM\_001168394] |
| A\_23\_P337790 | SHPRH | -0.99263 | 8.2E-15 | 8.2E-15 | -8.67149 | Down | Homo sapiens SNF2 histone linker PHD RING helicase (SHPRH), transcript variant 1, mRNA [NM\_001042683] |
| A\_24\_P199500 | RNF2 | -1.05935 | 8.41E-15 | 8.41E-15 | -8.66727 | Down | Homo sapiens ring finger protein 2 (RNF2), mRNA [NM\_007212] |
| A\_23\_P17275 | DNAJC27 | -1.08466 | 9.07E-15 | 9.07E-15 | -8.65411 | Down | Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 27 (DNAJC27), transcript variant 1, mRNA [NM\_016544] |
| A\_23\_P30254 | PLK2 | -1.29967 | 9.08E-15 | 9.08E-15 | -8.65388 | Down | Homo sapiens polo-like kinase 2 (PLK2), transcript variant 1, mRNA [NM\_006622] |
| A\_24\_P159434 | CD300A | -1.67048 | 9.43E-15 | 9.43E-15 | -8.6474 | Down | Homo sapiens CD300a molecule (CD300A), mRNA [NM\_007261] |
| A\_33\_P3379775 | TLE1 | -1.17966 | 9.79E-15 | 9.79E-15 | -8.64073 | Down | transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) [Source:HGNC Symbol;Acc:11837] [ENST00000376463] |
| A\_23\_P212728 | TBC1D23 | -1.31127 | 1.01E-14 | 1.01E-14 | -8.63591 | Down | Homo sapiens TBC1 domain family, member 23 (TBC1D23), transcript variant 1, mRNA [NM\_001199198] |
| A\_33\_P3381781 | RPRD2 | -1.06788 | 1.17E-14 | 1.17E-14 | -8.60996 | Down | regulation of nuclear pre-mRNA domain containing 2 [Source:HGNC Symbol;Acc:29039] [ENST00000369067] |
| A\_21\_P0000097 | PAFAH1B2 | -1.0106 | 1.3E-14 | 1.3E-14 | -8.59186 | Down | Homo sapiens platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa) (PAFAH1B2), transcript variant 2, mRNA [NM\_001184746] |
| A\_33\_P3311285 | LMNA | -0.99106 | 1.36E-14 | 1.36E-14 | -8.58416 | Down | Homo sapiens lamin A/C (LMNA), transcript variant 1, mRNA [NM\_170707] |
| A\_33\_P3284888 | DLEU7 | -1.58339 | 1.45E-14 | 1.45E-14 | -8.57298 | Down | Homo sapiens deleted in lymphocytic leukemia, 7 (DLEU7), mRNA [NM\_198989] |
| A\_33\_P3228872 | C10orf28 | -0.9768 | 1.54E-14 | 1.54E-14 | -8.56202 | Down | Homo sapiens chromosome 10 open reading frame 28 (C10orf28), mRNA [NM\_014472] |
| A\_23\_P10518 | TFDP3 | -1.36887 | 1.57E-14 | 1.57E-14 | -8.55895 | Down | Homo sapiens transcription factor Dp family, member 3 (TFDP3), mRNA [NM\_016521] |
| A\_33\_P3398401 | CRBN | -1.18023 | 1.59E-14 | 1.59E-14 | -8.55691 | Down | Homo sapiens cereblon (CRBN), transcript variant 1, mRNA [NM\_016302] |
| A\_33\_P3312975 | CLASP1 | -1.12242 | 1.7E-14 | 1.7E-14 | -8.54437 | Down | Homo sapiens cytoplasmic linker associated protein 1 (CLASP1), transcript variant 1, mRNA [NM\_015282] |
| A\_23\_P436476 | RBM34 | -0.9636 | 1.78E-14 | 1.78E-14 | -8.53688 | Down | Homo sapiens RNA binding motif protein 34 (RBM34), transcript variant 1, mRNA [NM\_015014] |
| A\_33\_P3294720 | LOC100130865 | -1.88498 | 1.96E-14 | 1.96E-14 | -8.52006 | Down | Homo sapiens cDNA FLJ41135 fis, clone BRACE2028970. [AK123130] |
| A\_23\_P416894 | PION | -1.0583 | 1.99E-14 | 1.99E-14 | -8.51744 | Down | Homo sapiens pigeon homolog (Drosophila) (PION), mRNA [NM\_017439] |
| A\_33\_P3335920 | SYNE1 | -1.33684 | 2.18E-14 | 2.18E-14 | -8.50118 | Down | Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant 1, mRNA [NM\_182961] |
| A\_24\_P940166 | PAPSS2 | -1.07448 | 2.32E-14 | 2.32E-14 | -8.49099 | Down | Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 2 (PAPSS2), transcript variant 2, mRNA [NM\_001015880] |
| A\_33\_P3363799 | NCAM1 | -1.15074 | 2.5E-14 | 2.5E-14 | -8.47777 | Down | Homo sapiens neural cell adhesion molecule 1 (NCAM1), transcript variant 5, mRNA [NM\_001242607] |
| A\_33\_P3213695 | CAB39L | -1.13666 | 2.72E-14 | 2.72E-14 | -8.46316 | Down | Homo sapiens calcium binding protein 39-like (CAB39L), transcript variant 2, mRNA [NM\_001079670] |
| A\_23\_P130815 | KIR2DS2 | -1.22174 | 2.8E-14 | 2.8E-14 | -8.45772 | Down | Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2 (KIR2DS2), mRNA [NM\_012312] |
| A\_24\_P199929 | VPS54 | -1.31455 | 2.92E-14 | 2.92E-14 | -8.45027 | Down | Homo sapiens vacuolar protein sorting 54 homolog (S. cerevisiae) (VPS54), transcript variant 1, mRNA [NM\_016516] |
| A\_23\_P254025 | ZFP37 | -1.01878 | 3.14E-14 | 3.14E-14 | -8.43761 | Down | Homo sapiens zinc finger protein 37 homolog (mouse) (ZFP37), mRNA [NM\_003408] |
| A\_23\_P338519 | NKIRAS1 | -0.98728 | 3.16E-14 | 3.16E-14 | -8.43687 | Down | Homo sapiens NFKB inhibitor interacting Ras-like 1 (NKIRAS1), mRNA [NM\_020345] |
| A\_21\_P0000023 | RIOK2 | -1.08171 | 3.81E-14 | 3.81E-14 | -8.40415 | Down | Homo sapiens RIO kinase 2 (yeast) (RIOK2), transcript variant 2, mRNA [NM\_001159749] |
| A\_23\_P128408 | TRIAP1 | -1.22366 | 4.37E-14 | 4.37E-14 | -8.3798 | Down | Homo sapiens TP53 regulated inhibitor of apoptosis 1 (TRIAP1), mRNA [NM\_016399] |
| A\_23\_P32036 | C9orf95 | -1.08782 | 4.55E-14 | 4.55E-14 | -8.37284 | Down | Homo sapiens chromosome 9 open reading frame 95 (C9orf95), transcript variant 1, mRNA [NM\_017881] |
| A\_23\_P34433 | ZCCHC11 | -0.96466 | 4.71E-14 | 4.71E-14 | -8.36693 | Down | Homo sapiens zinc finger, CCHC domain containing 11 (ZCCHC11), transcript variant 1, mRNA [NM\_001009881] |
| A\_24\_P382017 | RRN3 | -1.06988 | 4.8E-14 | 4.8E-14 | -8.36335 | Down | Homo sapiens RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) (RRN3), mRNA [NM\_018427] |
| A\_23\_P82047 | STXBP5 | -1.19782 | 4.87E-14 | 4.87E-14 | -8.36086 | Down | Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), transcript variant 2, mRNA [NM\_001127715] |
| A\_21\_P0012230 | XLOC\_l2\_009182 | -0.97449 | 6.1E-14 | 6.1E-14 | -8.32161 | Down | Q6JHZ7\_HUMAN (Q6JHZ7) HCV-NS5ATP5 binding protein 1, partial (23%) [THC2679994] |
| A\_23\_P257278 | CDK5RAP1 | -1.11625 | 6.37E-14 | 6.37E-14 | -8.31384 | Down | Homo sapiens CDK5 regulatory subunit associated protein 1 (CDK5RAP1), transcript variant 2, mRNA [NM\_016082] |
| A\_33\_P3219572 | LONRF3 | -1.7509 | 6.5E-14 | 6.5E-14 | -8.31037 | Down | LON peptidase N-terminal domain and ring finger 3 [Source:HGNC Symbol;Acc:21152] [ENST00000365713] |
| A\_23\_P154938 | HIRA | -1.03723 | 7.2E-14 | 7.2E-14 | -8.2923 | Down | Homo sapiens HIR histone cell cycle regulation defective homolog A (S. cerevisiae) (HIRA), mRNA [NM\_003325] |
| A\_19\_P00800114 | HIGD1A | -1.37937 | 7.87E-14 | 7.87E-14 | -8.27668 | Down | Homo sapiens HIG1 hypoxia inducible domain family, member 1A (HIGD1A), transcript variant 1, mRNA [NM\_001099668] |
| A\_33\_P3407339 | C6orf204 | -1.15039 | 7.94E-14 | 7.94E-14 | -8.27515 | Down | Homo sapiens chromosome 6 open reading frame 204 (C6orf204), transcript variant 2, mRNA [NM\_206921] |
| A\_23\_P34578 | GNL2 | -1.00925 | 8.1E-14 | 8.1E-14 | -8.27167 | Down | Homo sapiens guanine nucleotide binding protein-like 2 (nucleolar) (GNL2), mRNA [NM\_013285] |
| A\_23\_P43684 | BNC2 | -1.6257 | 8.44E-14 | 8.44E-14 | -8.26439 | Down | Homo sapiens basonuclin 2 (BNC2), mRNA [NM\_017637] |
| A\_23\_P201979 | CREM | -1.21852 | 8.9E-14 | 8.9E-14 | -8.255 | Down | Homo sapiens cAMP responsive element modulator (CREM), transcript variant 19, mRNA [NM\_183013] |
| A\_33\_P3261982 | PRIM2 | -0.96655 | 9.33E-14 | 9.33E-14 | -8.24674 | Down | Homo sapiens primase, DNA, polypeptide 2 (58kDa) (PRIM2), mRNA [NM\_000947] |
| A\_33\_P3282394 | MLLT1 | -1.36513 | 9.87E-14 | 9.87E-14 | -8.2369 | Down | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1 (MLLT1), mRNA [NM\_005934] |
| A\_33\_P3653330 | MAP2K4 | -1.08586 | 1.03E-13 | 1.03E-13 | -8.22965 | Down | Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA [NM\_003010] |
| A\_24\_P51322 | FLG | -1.23694 | 1.09E-13 | 1.09E-13 | -8.21859 | Down | Homo sapiens filaggrin (FLG), mRNA [NM\_002016] |
| A\_23\_P89665 | KRT33B | -1.71248 | 1.14E-13 | 1.14E-13 | -8.21075 | Down | Homo sapiens keratin 33B (KRT33B), mRNA [NM\_002279] |
| A\_33\_P3257155 | SMAP1 | -0.99246 | 1.17E-13 | 1.17E-13 | -8.20666 | Down | small ArfGAP 1 [Source:HGNC Symbol;Acc:19651] [ENST00000370442] |
| A\_33\_P3371999 | TPPP | -1.02219 | 1.18E-13 | 1.18E-13 | -8.20563 | Down | Homo sapiens tubulin polymerization promoting protein (TPPP), mRNA [NM\_007030] |
| A\_23\_P12082 | CHI3L2 | -1.02143 | 1.26E-13 | 1.26E-13 | -8.19324 | Down | Homo sapiens chitinase 3-like 2 (CHI3L2), transcript variant 3, mRNA [NM\_001025199] |
| A\_33\_P3278220 | RABEPK | -1.04264 | 1.29E-13 | 1.29E-13 | -8.18966 | Down | Rab9 effector protein with kelch motifs [Source:HGNC Symbol;Acc:16896] [ENST00000373544] |
| A\_24\_P941051 | CSTF2T | -1.0507 | 1.32E-13 | 1.32E-13 | -8.18509 | Down | Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant (CSTF2T), mRNA [NM\_015235] |
| A\_24\_P319374 | GPA33 | -0.99463 | 1.43E-13 | 1.43E-13 | -8.17101 | Down | Homo sapiens glycoprotein A33 (transmembrane) (GPA33), mRNA [NM\_005814] |
| A\_33\_P3341787 | IDS | -0.96509 | 1.45E-13 | 1.45E-13 | -8.16851 | Down | iduronate 2-sulfatase [Source:HGNC Symbol;Acc:5389] [ENST00000428056] |
| A\_33\_P3273459 | SPATA21 | -1.16597 | 1.77E-13 | 1.77E-13 | -8.13415 | Down | spermatogenesis associated 21 [Source:HGNC Symbol;Acc:28026] [ENST00000466212] |
| A\_21\_P0013675 | ANKRD18B | -1.07477 | 1.83E-13 | 1.83E-13 | -8.12823 | Down | Homo sapiens ankyrin repeat domain 18B (ANKRD18B), mRNA [NM\_001244752] |
| A\_32\_P204381 | CIAPIN1 | -1.0472 | 2.09E-13 | 2.09E-13 | -8.10427 | Down | Homo sapiens cytokine induced apoptosis inhibitor 1 (CIAPIN1), mRNA [NM\_020313] |
| A\_33\_P3736691 | ZNF430 | -1.19631 | 2.11E-13 | 2.11E-13 | -8.10243 | Down | Homo sapiens zinc finger protein 430 (ZNF430), transcript variant 1, mRNA [NM\_025189] |
| A\_24\_P129632 | DLG5 | -1.04821 | 2.32E-13 | 2.32E-13 | -8.08548 | Down | Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA [NM\_004747] |
| A\_33\_P3276475 | CHMP1B | -0.97054 | 2.43E-13 | 2.43E-13 | -8.07773 | Down | Homo sapiens charged multivesicular body protein 1B (CHMP1B), mRNA [NM\_020412] |
| A\_24\_P915692 | PHLDA1 | -1.05801 | 2.47E-13 | 2.47E-13 | -8.07445 | Down | Homo sapiens pleckstrin homology-like domain, family A, member 1 (PHLDA1), mRNA [NM\_007350] |
| A\_23\_P215634 | IGFBP3 | -1.22548 | 2.58E-13 | 2.58E-13 | -8.06719 | Down | Homo sapiens insulin-like growth factor binding protein 3 (IGFBP3), transcript variant 1, mRNA [NM\_001013398] |
| A\_33\_P3361472 | PSME4 | -0.99513 | 3.03E-13 | 3.03E-13 | -8.03868 | Down | proteasome (prosome, macropain) activator subunit 4 [Source:HGNC Symbol;Acc:20635] [ENST00000488687] |
| A\_23\_P416314 | HRASLS5 | -1.17271 | 3.73E-13 | 3.73E-13 | -8.00156 | Down | Homo sapiens HRAS-like suppressor family, member 5 (HRASLS5), transcript variant 1, mRNA [NM\_054108] |
| A\_33\_P3404779 | TCTEX1D4 | -1.24521 | 4.19E-13 | 4.19E-13 | -7.98059 | Down | Homo sapiens Tctex1 domain containing 4 (TCTEX1D4), mRNA [NM\_001013632] |
| A\_24\_P231026 | SCN8A | -1.05637 | 4.24E-13 | 4.24E-13 | -7.97851 | Down | Homo sapiens sodium channel, voltage gated, type VIII, alpha subunit (SCN8A), transcript variant 1, mRNA [NM\_014191] |
| A\_24\_P226970 | ZNF365 | -1.13362 | 4.86E-13 | 4.86E-13 | -7.95419 | Down | Homo sapiens zinc finger protein 365 (ZNF365), transcript variant A, mRNA [NM\_014951] |
| A\_23\_P169003 | SH2D4A | -1.75957 | 4.9E-13 | 4.9E-13 | -7.95282 | Down | Homo sapiens SH2 domain containing 4A (SH2D4A), transcript variant 1, mRNA [NM\_022071] |
| A\_33\_P3791123 | ATP5L2 | -1.08754 | 4.99E-13 | 4.99E-13 | -7.94978 | Down | Homo sapiens ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G2 (ATP5L2), nuclear gene encoding mitochondrial protein, mRNA [NM\_001165877] |
| A\_21\_P0014046 | LOC100653120 | -1.17462 | 5E-13 | 5E-13 | -7.94931 | Down | PREDICTED: Homo sapiens hypothetical protein LOC100653120 (LOC100653120), partial mRNA [XM\_003403783] |
| A\_24\_P264909 | NDFIP2 | -0.98967 | 5.23E-13 | 5.23E-13 | -7.94117 | Down | Homo sapiens Nedd4 family interacting protein 2 (NDFIP2), transcript variant 1, mRNA [NM\_019080] |
| A\_33\_P3367795 | RPS6 | -1.30412 | 5.52E-13 | 5.52E-13 | -7.93158 | Down | ribosomal protein S6 [Source:HGNC Symbol;Acc:10429] [ENST00000380381] |
| A\_21\_P0012439 | TRANK1 | -1.0526 | 5.87E-13 | 5.87E-13 | -7.92075 | Down | Homo sapiens tetratricopeptide repeat and ankyrin repeat containing 1 (TRANK1), mRNA [NM\_014831] |
| A\_33\_P3265270 | SLC17A5 | -0.99945 | 6.91E-13 | 6.91E-13 | -7.89145 | Down | Homo sapiens solute carrier family 17 (anion/sugar transporter), member 5 (SLC17A5), mRNA [NM\_012434] |
| A\_24\_P941322 | QKI | -1.30549 | 7E-13 | 7E-13 | -7.8891 | Down | Homo sapiens QKI, KH domain containing, RNA binding (QKI), transcript variant 1, mRNA [NM\_006775] |
| A\_32\_P196854 | FAM76A | -1.05835 | 7.17E-13 | 7.17E-13 | -7.88476 | Down | Homo sapiens family with sequence similarity 76, member A (FAM76A), transcript variant 1, mRNA [NM\_001143912] |
| A\_33\_P3258478 | KIR3DL1 | -1.23239 | 7.31E-13 | 7.31E-13 | -7.88146 | Down | PREDICTED: Homo sapiens killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 (KIR3DL1), mRNA [XM\_003403406] |
| A\_33\_P3256868 | ZNF83 | -1.16113 | 7.55E-13 | 7.55E-13 | -7.87562 | Down | Homo sapiens zinc finger protein 83 (ZNF83), transcript variant 8, mRNA [NM\_001242531] |
| A\_23\_P340251 | RAB2A | -1.08497 | 7.58E-13 | 7.58E-13 | -7.87492 | Down | Homo sapiens RAB2A, member RAS oncogene family (RAB2A), transcript variant 1, mRNA [NM\_002865] |
| A\_23\_P128281 | KLRC3 | -0.99441 | 7.79E-13 | 7.79E-13 | -7.86996 | Down | Homo sapiens killer cell lectin-like receptor subfamily C, member 3 (KLRC3), transcript variant 2, mRNA [NM\_007333] |
| A\_33\_P3257861 | SARDH | -1.03077 | 8.01E-13 | 8.01E-13 | -7.86499 | Down | Homo sapiens sarcosine dehydrogenase (SARDH), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM\_001134707] |
| A\_33\_P3842551 | IKZF2 | -1.04441 | 8.9E-13 | 8.9E-13 | -7.84614 | Down | Homo sapiens IKAROS family zinc finger 2 (Helios) (IKZF2), transcript variant 2, mRNA [NM\_001079526] |
| A\_23\_P60565 | ZNF354A | -1.21365 | 9.2E-13 | 9.2E-13 | -7.84016 | Down | Homo sapiens zinc finger protein 354A (ZNF354A), mRNA [NM\_005649] |
| A\_24\_P274615 | ARRDC3 | -0.98213 | 9.67E-13 | 9.67E-13 | -7.83138 | Down | Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA [NM\_020801] |
| A\_24\_P925062 | MXRA7 | -1.26775 | 1.02E-12 | 1.02E-12 | -7.8224 | Down | Homo sapiens matrix-remodelling associated 7 (MXRA7), transcript variant 1, mRNA [NM\_001008528] |
| A\_33\_P3239587 | MXRA7 | -1.08963 | 1.06E-12 | 1.06E-12 | -7.8148 | Down | Homo sapiens matrix-remodelling associated 7 (MXRA7), transcript variant 2, mRNA [NM\_001008529] |
| A\_23\_P140848 | MPHOSPH6 | -0.99063 | 1.06E-12 | 1.06E-12 | -7.81403 | Down | Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA [NM\_005792] |
| A\_33\_P3671291 | SNORA12 | -0.96645 | 1.16E-12 | 1.16E-12 | -7.79901 | Down | EST91069 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence [AA378382] |
| A\_24\_P271014 | PPP4R1 | -1.0032 | 1.16E-12 | 1.16E-12 | -7.79801 | Down | Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), transcript variant 1, mRNA [NM\_001042388] |
| A\_23\_P155939 | ZNF595 | -1.11184 | 1.27E-12 | 1.27E-12 | -7.78274 | Down | Homo sapiens zinc finger protein 595 (ZNF595), mRNA [NM\_182524] |
| A\_23\_P152970 | RAPGEFL1 | -0.98479 | 1.34E-12 | 1.34E-12 | -7.7727 | Down | Homo sapiens Rap guanine nucleotide exchange factor (GEF)-like 1 (RAPGEFL1), mRNA [NM\_016339] |
| A\_33\_P3405384 | C8orf45 | -1.32001 | 1.52E-12 | 1.52E-12 | -7.74978 | Down | Homo sapiens chromosome 8 open reading frame 45 (C8orf45), transcript variant 1, mRNA [NM\_173518] |
| A\_33\_P3270346 | KIR2DL5A | -1.23393 | 1.54E-12 | 1.54E-12 | -7.74816 | Down | Homo sapiens killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 5A (KIR2DL5A), mRNA [NM\_020535] |
| A\_23\_P108157 | TJP3 | -1.2702 | 2.02E-12 | 2.02E-12 | -7.69884 | Down | Homo sapiens tight junction protein 3 (zona occludens 3) (TJP3), mRNA [NM\_014428] |
| A\_24\_P64039 | AP3M2 | -0.97954 | 2.05E-12 | 2.05E-12 | -7.69579 | Down | Homo sapiens adaptor-related protein complex 3, mu 2 subunit (AP3M2), transcript variant 2, mRNA [NM\_006803] |
| A\_23\_P131375 | PQLC3 | -1.07961 | 2.11E-12 | 2.11E-12 | -7.69077 | Down | Homo sapiens PQ loop repeat containing 3 (PQLC3), mRNA [NM\_152391] |
| A\_24\_P153511 | OSBPL8 | -1.15178 | 2.16E-12 | 2.16E-12 | -7.68673 | Down | Homo sapiens oxysterol binding protein-like 8 (OSBPL8), transcript variant 1, mRNA [NM\_020841] |
| A\_21\_P0014000 | KIR3DL2 | -1.07398 | 2.35E-12 | 2.35E-12 | -7.67152 | Down | Homo sapiens killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 (KIR3DL2), transcript variant 1, mRNA [NM\_006737] |
| A\_23\_P368154 | PODN | -1.41332 | 2.44E-12 | 2.44E-12 | -7.66462 | Down | Homo sapiens podocan (PODN), transcript variant 1, mRNA [NM\_153703] |
| A\_33\_P3301174 | TMED2 | -1.03026 | 2.63E-12 | 2.63E-12 | -7.65136 | Down | Homo sapiens transmembrane emp24 domain trafficking protein 2 (TMED2), mRNA [NM\_006815] |
| A\_24\_P306136 | KIAA1432 | -1.43199 | 2.84E-12 | 2.84E-12 | -7.63698 | Down | Homo sapiens KIAA1432 (KIAA1432), transcript variant 2, mRNA [NM\_001135920] |
| A\_23\_P17134 | MAL | -1.07569 | 2.92E-12 | 2.92E-12 | -7.63208 | Down | Homo sapiens mal, T-cell differentiation protein (MAL), transcript variant a, mRNA [NM\_002371] |
| A\_33\_P3227857 | COX18 | -1.01228 | 3.68E-12 | 3.68E-12 | -7.59026 | Down | Homo sapiens COX18 cytochrome c oxidase assembly homolog (S. cerevisiae) (COX18), nuclear gene encoding mitochondrial protein, mRNA [NM\_173827] |
| A\_33\_P3307163 | RBM20 | -1.36488 | 3.74E-12 | 3.74E-12 | -7.58715 | Down | Homo sapiens RNA binding motif protein 20 (RBM20), mRNA [NM\_001134363] |
| A\_33\_P3397763 | TNFSF9 | -1.12527 | 3.99E-12 | 3.99E-12 | -7.57558 | Down | Homo sapiens tumor necrosis factor (ligand) superfamily, member 9 (TNFSF9), mRNA [NM\_003811] |
| A\_23\_P429092 | HBS1L | -1.28475 | 4.03E-12 | 4.03E-12 | -7.57386 | Down | Homo sapiens HBS1-like (S. cerevisiae) (HBS1L), transcript variant 3, mRNA [NM\_001145207] |
| A\_33\_P3355538 | CERKL | -1.25958 | 4.21E-12 | 4.21E-12 | -7.56557 | Down | Homo sapiens ceramide kinase-like (CERKL), transcript variant 2, mRNA [NM\_001030311] |
| A\_23\_P46455 | DNAJC8 | -1.13839 | 4.27E-12 | 4.27E-12 | -7.56339 | Down | Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 8 (DNAJC8), mRNA [NM\_014280] |
| A\_33\_P3230350 | ZNF207 | -1.00568 | 4.92E-12 | 4.92E-12 | -7.53726 | Down | Homo sapiens zinc finger protein 207 (ZNF207), transcript variant 3, mRNA [NM\_001098507] |
| A\_33\_P3339361 | ARHGAP11A | -0.98152 | 4.93E-12 | 4.93E-12 | -7.53688 | Down | Homo sapiens Rho GTPase activating protein 11A (ARHGAP11A), transcript variant 2, mRNA [NM\_199357] |
| A\_33\_P3439713 | LOC283713 | -0.98451 | 5.5E-12 | 5.5E-12 | -7.51713 | Down | Homo sapiens cDNA FLJ37663 fis, clone BRHIP2011120. [AK094982] |
| A\_23\_P305210 | ZNF680 | -1.04334 | 6.22E-12 | 6.22E-12 | -7.49476 | Down | Homo sapiens zinc finger protein 680 (ZNF680), transcript variant 1, mRNA [NM\_178558] |
| A\_33\_P3231277 | HIF1A | -1.06065 | 6.52E-12 | 6.52E-12 | -7.48617 | Down | Homo sapiens hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (HIF1A), transcript variant 2, mRNA [NM\_181054] |
| A\_21\_P0006899 | XLOC\_008573 | -1.5909 | 7.28E-12 | 7.28E-12 | -7.46586 | Down | AGENCOURT\_6854663 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5921217 5', mRNA sequence [BQ061729] |
| A\_33\_P3243558 | RNF224 | -1.03321 | 7.6E-12 | 7.6E-12 | -7.45812 | Down | Homo sapiens ring finger protein 224 (RNF224), mRNA [NM\_001190228] |
| A\_23\_P350512 | ADAM12 | -0.99412 | 7.6E-12 | 7.6E-12 | -7.45809 | Down | Homo sapiens ADAM metallopeptidase domain 12 (ADAM12), transcript variant 2, mRNA [NM\_021641] |
| A\_23\_P151046 | KLRC1 | -0.96471 | 7.67E-12 | 7.67E-12 | -7.45653 | Down | Homo sapiens killer cell lectin-like receptor subfamily C, member 1 (KLRC1), transcript variant 1, mRNA [NM\_002259] |
| A\_33\_P3257973 | HELZ | -0.97966 | 7.8E-12 | 7.8E-12 | -7.45327 | Down | Homo sapiens helicase with zinc finger (HELZ), mRNA [NM\_014877] |
| A\_21\_P0014606 | LOC100506950 | -1.02128 | 9.74E-12 | 9.74E-12 | -7.41268 | Down | PREDICTED: Homo sapiens hypothetical LOC100506950 (LOC100506950), miscRNA [XR\_110500] |
| A\_33\_P3462692 | SNORA58 | -1.25665 | 9.94E-12 | 9.94E-12 | -7.40889 | Down | hz67c08.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:3213038 3', mRNA sequence [BE467637] |
| A\_33\_P3313920 | KIR2DL2 | -1.03361 | 9.97E-12 | 9.97E-12 | -7.40842 | Down | Homo sapiens killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2 (KIR2DL2), mRNA [NM\_014219] |
| A\_23\_P116512 | PRR5L | -0.99528 | 1.01E-11 | 1.01E-11 | -7.40608 | Down | Homo sapiens proline rich 5 like (PRR5L), transcript variant 2, mRNA [NM\_024841] |
| A\_23\_P72697 | GPIHBP1 | -1.08835 | 1.07E-11 | 1.07E-11 | -7.39571 | Down | Homo sapiens glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1 (GPIHBP1), mRNA [NM\_178172] |
| A\_23\_P97021 | EIF2C3 | -1.19107 | 1.1E-11 | 1.1E-11 | -7.38999 | Down | Homo sapiens eukaryotic translation initiation factor 2C, 3 (EIF2C3), transcript variant 1, mRNA [NM\_024852] |
| A\_33\_P3421703 | SP2 | -0.99776 | 1.39E-11 | 1.39E-11 | -7.34801 | Down | Sp2 transcription factor [Source:HGNC Symbol;Acc:11207] [ENST00000322172] |
| A\_33\_P3375451 | NYNRIN | -1.38278 | 1.63E-11 | 1.63E-11 | -7.31789 | Down | Homo sapiens NYN domain and retroviral integrase containing (NYNRIN), mRNA [NM\_025081] |
| A\_33\_P3383261 | SIKE1 | -1.0459 | 1.65E-11 | 1.65E-11 | -7.31592 | Down | Homo sapiens suppressor of IKBKE 1 (SIKE1), transcript variant 1, mRNA [NM\_001102396] |
| A\_33\_P3311267 | KRTAP19-2 | -1.03382 | 1.85E-11 | 1.85E-11 | -7.29514 | Down | Homo sapiens keratin associated protein 19-2 (KRTAP19-2), mRNA [NM\_181608] |
| A\_23\_P348257 | NUAK1 | -1.07335 | 2.21E-11 | 2.21E-11 | -7.26207 | Down | Homo sapiens NUAK family, SNF1-like kinase, 1 (NUAK1), mRNA [NM\_014840] |
| A\_23\_P207564 | CCL4 | -1.44529 | 2.33E-11 | 2.33E-11 | -7.25223 | Down | Homo sapiens chemokine (C-C motif) ligand 4 (CCL4), transcript variant 1, mRNA [NM\_002984] |
| A\_24\_P3249 | RARB | -1.08017 | 2.42E-11 | 2.42E-11 | -7.24484 | Down | Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 1, mRNA [NM\_000965] |
| A\_23\_P90172 | PPP1R15A | -1.00111 | 2.52E-11 | 2.52E-11 | -7.23766 | Down | Homo sapiens protein phosphatase 1, regulatory subunit 15A (PPP1R15A), mRNA [NM\_014330] |
| A\_23\_P315789 | RFXAP | -0.9694 | 2.59E-11 | 2.59E-11 | -7.23268 | Down | Homo sapiens regulatory factor X-associated protein (RFXAP), mRNA [NM\_000538] |
| A\_33\_P3210085 | NET1 | -0.96465 | 2.62E-11 | 2.62E-11 | -7.23057 | Down | Homo sapiens neuroepithelial cell transforming 1 (NET1), transcript variant 1, mRNA [NM\_001047160] |
| A\_23\_P218988 | SLC30A5 | -1.16766 | 2.75E-11 | 2.75E-11 | -7.22117 | Down | Homo sapiens solute carrier family 30 (zinc transporter), member 5 (SLC30A5), transcript variant 1, mRNA [NM\_022902] |
| A\_33\_P3319680 | RNF165 | -1.07288 | 2.92E-11 | 2.92E-11 | -7.21055 | Down | Homo sapiens ring finger protein 165 (RNF165), mRNA [NM\_152470] |
| A\_33\_P3288774 | RC3H1 | -1.12267 | 3.12E-11 | 3.12E-11 | -7.19804 | Down | Homo sapiens ring finger and CCCH-type domains 1 (RC3H1), mRNA [NM\_172071] |
| A\_21\_P0000063 | MDFIC | -1.1317 | 3.18E-11 | 3.18E-11 | -7.19451 | Down | Homo sapiens MyoD family inhibitor domain containing (MDFIC), transcript variant 2, mRNA [NM\_001166346] |
| A\_32\_P352697 | YTHDC1 | -0.98317 | 3.47E-11 | 3.47E-11 | -7.17819 | Down | Homo sapiens YTH domain containing 1 (YTHDC1), transcript variant 1, mRNA [NM\_001031732] |
| A\_23\_P64913 | PDE6H | -1.34756 | 3.48E-11 | 3.48E-11 | -7.17782 | Down | Homo sapiens phosphodiesterase 6H, cGMP-specific, cone, gamma (PDE6H), mRNA [NM\_006205] |
| A\_24\_P157926 | TNFAIP3 | -1.19108 | 3.9E-11 | 3.9E-11 | -7.15677 | Down | Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA [NM\_006290] |
| A\_33\_P3306749 | OLFM1 | -1.01248 | 4.03E-11 | 4.03E-11 | -7.15062 | Down | Homo sapiens olfactomedin 1, mRNA (cDNA clone IMAGE:3351052), complete cds. [BC000189] |
| A\_32\_P159334 | RECQL | -1.44865 | 4.84E-11 | 4.84E-11 | -7.11635 | Down | Homo sapiens RecQ protein-like (DNA helicase Q1-like) (RECQL), transcript variant 1, mRNA [NM\_002907] |
| A\_33\_P3375934 | NAMPT | -1.44664 | 4.92E-11 | 4.92E-11 | -7.11323 | Down | Homo sapiens nicotinamide phosphoribosyltransferase (NAMPT), mRNA [NM\_005746] |
| A\_23\_P253375 | CUX1 | -0.9802 | 6.15E-11 | 6.15E-11 | -7.07171 | Down | Homo sapiens cut-like homeobox 1 (CUX1), transcript variant 2, mRNA [NM\_001913] |
| A\_24\_P726336 | PHACTR2 | -0.98882 | 6.44E-11 | 6.44E-11 | -7.0629 | Down | Homo sapiens phosphatase and actin regulator 2 (PHACTR2), transcript variant 1, mRNA [NM\_001100164] |
| A\_23\_P74042 | LPHN2 | -1.06311 | 8.81E-11 | 8.81E-11 | -7.00424 | Down | Homo sapiens latrophilin 2 (LPHN2), mRNA [NM\_012302] |
| A\_24\_P943566 | PHACTR1 | -1.3063 | 9.25E-11 | 9.25E-11 | -6.99504 | Down | phosphatase and actin regulator 1 [Source:HGNC Symbol;Acc:20990] [ENST00000379350] |
| A\_33\_P3272668 | MRPL30 | -1.00272 | 9.64E-11 | 9.64E-11 | -6.98734 | Down | mitochondrial ribosomal protein L30 [Source:HGNC Symbol;Acc:14036] [ENST00000409145] |
| A\_23\_P408239 | PASK | -1.03637 | 9.78E-11 | 9.78E-11 | -6.98458 | Down | Homo sapiens PAS domain containing serine/threonine kinase (PASK), transcript variant 5, mRNA [NM\_001252124] |
| A\_21\_P0010795 | XLOC\_l2\_001399 | -0.97922 | 1.36E-10 | 1.36E-10 | -6.92276 | Down | db0\_001696 SARS-Cov infected lung tissue Homo sapiens cDNA clone db0\_001696 5', mRNA sequence [GD257545] |
| A\_33\_P3230541 | MPRIP | -1.42546 | 1.46E-10 | 1.46E-10 | -6.90849 | Down | myosin phosphatase Rho interacting protein [Source:HGNC Symbol;Acc:30321] [ENST00000395806] |
| A\_33\_P3236698 | ANKRD19P | -1.16741 | 1.64E-10 | 1.64E-10 | -6.88738 | Down | Homo sapiens cDNA FLJ77364 complete cds, highly similar to Homo sapiens ankyrin repeat domain 19 (ANKRD19), mRNA. [AK292218] |
| A\_23\_P109171 | BFSP1 | -0.99116 | 1.64E-10 | 1.64E-10 | -6.88695 | Down | Homo sapiens beaded filament structural protein 1, filensin (BFSP1), transcript variant 1, mRNA [NM\_001195] |
| A\_33\_P3300147 | C9orf170 | -1.67849 | 1.82E-10 | 1.82E-10 | -6.86784 | Down | Homo sapiens chromosome 9 open reading frame 170 (C9orf170), mRNA [NM\_001001709] |
| A\_33\_P3395369 | AMD1 | -1.06224 | 2.29E-10 | 2.29E-10 | -6.82375 | Down | Homo sapiens adenosylmethionine decarboxylase 1 (AMD1), transcript variant 1, mRNA [NM\_001634] |
| A\_23\_P416813 | ZFP82 | -0.98798 | 2.32E-10 | 2.32E-10 | -6.82121 | Down | Homo sapiens zinc finger protein 82 homolog (mouse) (ZFP82), mRNA [NM\_133466] |
| A\_21\_P0014543 | LOC100507295 | -1.47889 | 2.36E-10 | 2.36E-10 | -6.818 | Down | PREDICTED: Homo sapiens hypothetical LOC100507295 (LOC100507295), miscRNA [XR\_110253] |
| A\_23\_P134058 | GFOD1 | -1.06633 | 2.71E-10 | 2.71E-10 | -6.79199 | Down | Homo sapiens glucose-fructose oxidoreductase domain containing 1 (GFOD1), transcript variant 4, mRNA [NM\_001242629] |
| A\_23\_P209288 | CUL3 | -1.01981 | 2.82E-10 | 2.82E-10 | -6.78424 | Down | Homo sapiens cullin 3 (CUL3), mRNA [NM\_003590] |
| A\_32\_P144342 | PARP4 | -1.30328 | 3.44E-10 | 3.44E-10 | -6.74638 | Down | Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), mRNA [NM\_006437] |
| A\_33\_P3310286 | LMNB1 | -1.14593 | 3.89E-10 | 3.89E-10 | -6.7225 | Down | lamin B1 [Source:HGNC Symbol;Acc:6637] [ENST00000395354] |
| A\_24\_P191971 | SAP30L | -0.97957 | 4.1E-10 | 4.1E-10 | -6.71246 | Down | Homo sapiens SAP30-like (SAP30L), transcript variant 1, mRNA [NM\_024632] |
| A\_21\_P0007340 | XLOC\_009416 | -1.03334 | 6.48E-10 | 6.48E-10 | -6.62468 | Down | PREDICTED: Homo sapiens hypothetical LOC100507144 (LOC100507144), miscRNA [XR\_109039] |
| A\_23\_P50217 | ZNF671 | -0.97879 | 6.59E-10 | 6.59E-10 | -6.62143 | Down | Homo sapiens zinc finger protein 671 (ZNF671), mRNA [NM\_024833] |
| A\_33\_P3412613 | TMPO | -1.23055 | 6.67E-10 | 6.67E-10 | -6.61895 | Down | Homo sapiens thymopoietin (TMPO), transcript variant 2, mRNA [NM\_001032283] |
| A\_23\_P165239 | ZNF208 | -1.01997 | 6.98E-10 | 6.98E-10 | -6.61028 | Down | Homo sapiens zinc finger protein 208 (ZNF208), mRNA [NM\_007153] |
| A\_23\_P320242 | KIAA1324L | -1.03569 | 8.11E-10 | 8.11E-10 | -6.58125 | Down | Homo sapiens KIAA1324-like (KIAA1324L), transcript variant 2, mRNA [NM\_152748] |
| A\_33\_P3399870 | CERS6 | -1.01212 | 8.16E-10 | 8.16E-10 | -6.58016 | Down | Homo sapiens ceramide synthase 6 (CERS6), mRNA [NM\_203463] |
| A\_24\_P320033 | CD80 | -1.08929 | 1.01E-09 | 1.01E-09 | -6.5385 | Down | Homo sapiens CD80 molecule (CD80), mRNA [NM\_005191] |
| A\_21\_P0014202 | LOC100506881 | -1.33446 | 1.26E-09 | 1.26E-09 | -6.49567 | Down | PREDICTED: Homo sapiens hypothetical LOC100506881, transcript variant 1 (LOC100506881), miscRNA [XR\_108815] |
| A\_24\_P358868 | ZNF728 | -1.28633 | 1.37E-09 | 1.37E-09 | -6.47989 | Down | PREDICTED: Homo sapiens zinc finger protein 728 (ZNF728), mRNA [XM\_001720936] |
| A\_33\_P3648417 | SNORA55 | -1.07341 | 1.57E-09 | 1.57E-09 | -6.45239 | Down | 601652296F1 NIH\_MGC\_82 Homo sapiens cDNA clone IMAGE:3935854 5', mRNA sequence [BE972465] |
| A\_33\_P3844650 | ANGPTL2 | -1.13483 | 2.78E-09 | 2.78E-09 | -6.34053 | Down | Homo sapiens angiopoietin-like 2 (ANGPTL2), mRNA [NM\_012098] |
| A\_33\_P3249185 | SAR1A | -1.15286 | 3.62E-09 | 3.62E-09 | -6.28873 | Down | SAR1 homolog A (S. cerevisiae) [Source:HGNC Symbol;Acc:10534] [ENST00000373236] |
| A\_24\_P104407 | SYNM | -1.04096 | 4.42E-09 | 4.42E-09 | -6.24898 | Down | Homo sapiens synemin, intermediate filament protein (SYNM), transcript variant A, mRNA [NM\_145728] |
| A\_21\_P0000955 | XLOC\_000085 | -0.97157 | 4.47E-09 | 4.47E-09 | -6.24675 | Down |  |
| A\_21\_P0000160 | TM4SF19 | -1.25122 | 4.47E-09 | 4.47E-09 | -6.24674 | Down | Homo sapiens transmembrane 4 L six family member 19 (TM4SF19), transcript variant 1, mRNA [NM\_138461] |
| A\_23\_P166408 | OSM | -1.52063 | 5.5E-09 | 5.5E-09 | -6.20557 | Down | Homo sapiens oncostatin M (OSM), mRNA [NM\_020530] |
| A\_33\_P3284933 | IL27 | -0.98645 | 7.21E-09 | 7.21E-09 | -6.15114 | Down | Homo sapiens interleukin 27 (IL27), mRNA [NM\_145659] |
| A\_23\_P139682 | PZP | -1.29676 | 1.15E-08 | 1.15E-08 | -6.05677 | Down | Homo sapiens pregnancy-zone protein (PZP), mRNA [NM\_002864] |
| A\_24\_P942132 | TRAPPC6B | -1.0628 | 1.86E-08 | 1.86E-08 | -5.95953 | Down | Homo sapiens trafficking protein particle complex 6B (TRAPPC6B), transcript variant 1, mRNA [NM\_001079537] |
| A\_33\_P3419190 | AREG | -1.86807 | 2.36E-08 | 2.36E-08 | -5.91101 | Down | Homo sapiens amphiregulin (AREG), mRNA [NM\_001657] |
| A\_23\_P92520 | ANP32C | -1.47887 | 2.63E-08 | 2.63E-08 | -5.88899 | Down | Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member C (ANP32C), mRNA [NM\_012403] |
| A\_24\_P245379 | SERPINB2 | -1.44098 | 2.64E-08 | 2.64E-08 | -5.88851 | Down | Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 2 (SERPINB2), transcript variant 2, mRNA [NM\_002575] |
| A\_33\_P3362526 | MED31 | -0.99652 | 4.47E-08 | 4.47E-08 | -5.7794 | Down | Homo sapiens mediator complex subunit 31 (MED31), mRNA [NM\_016060] |
| A\_33\_P3372752 | LOC400682 | -1.62509 | 4.68E-08 | 4.68E-08 | -5.76981 | Down | PREDICTED: Homo sapiens zinc finger protein 100-like (LOC400682), mRNA [XM\_003118492] |
| A\_33\_P3354424 | TRIM61 | -1.01605 | 4.87E-08 | 4.87E-08 | -5.7619 | Down | Homo sapiens tripartite motif containing 61 (TRIM61), mRNA [NM\_001012414] |
| A\_24\_P359067 | LOC100130357 | -0.96859 | 5.33E-08 | 5.33E-08 | -5.7428 | Down | Homo sapiens uncharacterized LOC100130357 (LOC100130357), mRNA [NM\_001242698] |
| A\_23\_P42257 | IER3 | -1.2243 | 7.08E-08 | 7.08E-08 | -5.68365 | Down | Homo sapiens immediate early response 3 (IER3), mRNA [NM\_003897] |
| A\_21\_P0011686 | ZNF730 | -0.99278 | 7.94E-08 | 7.94E-08 | -5.6597 | Down | PREDICTED: Homo sapiens zinc finger protein 730 (ZNF730), mRNA [XM\_001719792] |
| A\_33\_P3423721 | JPH3 | -1.21933 | 1.01E-07 | 1.01E-07 | -5.60888 | Down | junctophilin 3 [Source:HGNC Symbol;Acc:14203] [ENST00000301008] |
| A\_33\_P3258472 | SPTBN1 | -1.09519 | 1.1E-07 | 1.1E-07 | -5.59088 | Down | Homo sapiens spectrin, beta, non-erythrocytic 1 (SPTBN1), transcript variant 1, mRNA [NM\_003128] |
| A\_33\_P3405769 | TARM1 | -0.98557 | 1.5E-07 | 1.5E-07 | -5.52483 | Down | Homo sapiens T cell-interacting, activating receptor on myeloid cells 1 (TARM1), mRNA [NM\_001135686] |
| A\_23\_P216225 | EGR3 | -1.21713 | 2.14E-07 | 2.14E-07 | -5.44877 | Down | Homo sapiens early growth response 3 (EGR3), transcript variant 1, mRNA [NM\_004430] |
| A\_23\_P79518 | IL1B | -1.63582 | 5.45E-07 | 5.45E-07 | -5.24633 | Down | Homo sapiens interleukin 1, beta (IL1B), mRNA [NM\_000576] |
| A\_33\_P3405535 | LOC650293 | -1.04965 | 5.81E-07 | 5.81E-07 | -5.23223 | Down | Homo sapiens seven transmembrane helix receptor (LOC650293), mRNA [NM\_001040071] |
| A\_33\_P3666817 | C10orf55 | -1.12887 | 7.13E-07 | 7.13E-07 | -5.18706 | Down | Homo sapiens chromosome 10 open reading frame 55 (C10orf55), mRNA [NM\_001001791] |
| A\_33\_P3311073 | KIR2DS3 | -1.03357 | 8.21E-07 | 8.21E-07 | -5.15578 | Down | Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 3 (KIR2DS3), mRNA [NM\_012313] |
| A\_21\_P0011399 | WHAMMP2 | -1.22144 | 1.86E-06 | 1.86E-06 | -4.97207 | Down | Q571B6\_MOUSE (Q571B6) MKIAA1971 protein (Fragment), partial (50%) [THC2554418] |
| A\_24\_P257416 | CXCL2 | -1.31817 | 2.87E-06 | 2.87E-06 | -4.87285 | Down | Homo sapiens chemokine (C-X-C motif) ligand 2 (CXCL2), mRNA [NM\_002089] |
| A\_23\_P72096 | IL1A | -2.03327 | 3.2E-06 | 3.2E-06 | -4.84757 | Down | Homo sapiens interleukin 1, alpha (IL1A), mRNA [NM\_000575] |
| A\_33\_P3253249 | FTH1 | -1.26108 | 3.63E-06 | 3.63E-06 | -4.81851 | Down | Homo sapiens ferritin, heavy polypeptide 1 (FTH1), mRNA [NM\_002032] |
| A\_33\_P3330264 | CXCL1 | -1.13671 | 5.26E-06 | 5.26E-06 | -4.73189 | Down | Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), mRNA [NM\_001511] |
| A\_24\_P183150 | CXCL3 | -1.24688 | 5.7E-06 | 5.7E-06 | -4.71335 | Down | Homo sapiens chemokine (C-X-C motif) ligand 3 (CXCL3), mRNA [NM\_002090] |
| A\_21\_P0000109 | MTRNR2L9 | -2.10791 | 6.53E-06 | 6.53E-06 | -4.68129 | Down |  |
| A\_23\_P315364 | CXCL2 | -1.24779 | 6.85E-06 | 6.85E-06 | -4.66975 | Down | Homo sapiens chemokine (C-X-C motif) ligand 2 (CXCL2), mRNA [NM\_002089] |
| A\_23\_P428129 | CDKN1C | -0.9776 | 3.26E-05 | 3.26E-05 | -4.28979 | Down | Homo sapiens cyclin-dependent kinase inhibitor 1C (p57, Kip2) (CDKN1C), transcript variant 1, mRNA [NM\_000076] |
| A\_33\_P3319791 | NR4A1 | -0.96333 | 3.72E-05 | 3.72E-05 | -4.25701 | Down | Homo sapiens nuclear receptor subfamily 4, group A, member 1 (NR4A1), transcript variant 1, mRNA [NM\_002135] |
| A\_23\_P17065 | CCL20 | -1.5062 | 0.000262 | 0.000262 | -3.74324 | Down | Homo sapiens chemokine (C-C motif) ligand 20 (CCL20), transcript variant 1, mRNA [NM\_004591] |
| A\_32\_P87013 | IL8 | -1.28196 | 0.000575 | 0.000575 | -3.52158 | Down | Homo sapiens interleukin 8 (IL8), mRNA [NM\_000584] |
| A\_23\_P6596 | HES1 | -1.04437 | 0.000618 | 0.000618 | -3.50073 | Down | Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), mRNA [NM\_005524] |
| A\_33\_P3243230 | IL8 | -1.03819 | 0.000823 | 0.000823 | -3.41716 | Down | interleukin 8 [Source:HGNC Symbol;Acc:6025] [ENST00000401931] |
| A\_21\_P0000108 | MTRNR2L8 | -1.29494 | 0.001135 | 0.001135 | -3.32145 | Down | Homo sapiens MT-RNR2-like 8 (MTRNR2L8), mRNA [NM\_001190702] |
| A\_23\_P7144 | CXCL1 | -1.016 | 0.001164 | 0.001164 | -3.31385 | Down | Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), mRNA [NM\_001511] |
| A\_23\_P74609 | G0S2 | -1.13712 | 0.002011 | 0.002011 | -3.14619 | Down | Homo sapiens G0/G1switch 2 (G0S2), mRNA [NM\_015714] |
| A\_24\_P228130 | CCL3L3 | -1.0999 | 0.003149 | 0.003149 | -3.00348 | Down | Homo sapiens chemokine (C-C motif) ligand 3-like 3 (CCL3L3), mRNA [NM\_001001437] |
| A\_33\_P3374388 | LOC100131702 | -1.05236 | 0.015209 | 0.015209 | -2.45678 | Down | Homo sapiens cDNA FLJ45037 fis, clone BRAWH3019820. [AK126983] |
| A\_24\_P102053 | OCLN | -1.30046 | 0.027821 | 0.027821 | -2.22235 | Down | Homo sapiens occludin (OCLN), transcript variant 1, mRNA [NM\_002538] |

**Table 2**The enriched pathway terms of the up regulated differentially expressed genes

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **BIOCYC** | | | | | | | |
| **Pathway ID** | **Pathway Name** | **P-value** | **FDR B&H** | **FDR B&Y** | **Bonferroni** | **Gene Count** | **Gene** |
| 545355 | thyronamine and iodothyronamine metabolism | 3.91E-02 | 1.15E-01 | 3.57E-01 | 4.70E-01 | 1 | DIO2 |
| 142404 | trehalose degradation | 3.91E-02 | 1.15E-01 | 3.57E-01 | 4.70E-01 | 1 | TREH |
| 545266 | hypusine biosynthesis | 3.91E-02 | 1.15E-01 | 3.57E-01 | 4.70E-01 | 1 | DOHH |
| 142167 | protein citrullination | 7.67E-02 | 1.15E-01 | 3.57E-01 | 9.21E-01 | 1 | PADI3 |
| 142337 | 4-hydroxyproline degradation | 7.67E-02 | 1.15E-01 | 3.57E-01 | 9.21E-01 | 1 | HOGA1 |
| 142426 | urea cycle | 7.67E-02 | 1.15E-01 | 3.57E-01 | 9.21E-01 | 1 | OTC |
| 545299 | C20 prostanoid biosynthesis | 1.30E-01 | 1.74E-01 | 5.40E-01 | 1.00E+00 | 1 | PTGDS |
| 142437 | nicotine degradation IV | 1.81E-01 | 2.17E-01 | 6.74E-01 | 1.00E+00 | 1 | INMT |
| 545293 | retinol biosynthesis | 2.88E-01 | 3.14E-01 | 9.75E-01 | 1.00E+00 | 1 | CES1 |
| 1108786 | mucin core 1 and core 2 O-glycosylation | 3.93E-01 | 3.93E-01 | 1.00E+00 | 1.00E+00 | 1 | B3GNT3 |
| **KEGG** | | | | | | | |
| 83051 | Cytokine-cytokine receptor interaction | 9.61E-04 | 1.78E-01 | 1.00E+00 | 1.78E-01 | 14 | CCR2,KITLG,CCL19,CXCL6,CX3CL1,CXCL12,IFNA4,IL20,IL13RA1,IL17B,BMP7,THPO,EGFR,OSMR |
| 83087 | Olfactory transduction | 9.12E-03 | 6.29E-01 | 1.00E+00 | 1.00E+00 | 16 | OR1J1,OR2J2,OR4C3,OR5C1,OR3A3,OR8U1,OR10AD1,OR10W1,GNAL,OR5H1,OR2AG1,OR2AG2,OR5A2,OR2T6,OR10H1,OR52K2 |
| 83050 | Calcium signaling pathway | 1.02E-02 | 6.29E-01 | 1.00E+00 | 1.00E+00 | 9 | ERBB3,ADCY2,ADRA1A,ATP2B3,AVPR1B,PTGER1,GNAL,GRIN1,EGFR |
| 83053 | Neuroactive ligand-receptor interaction | 2.24E-02 | 8.66E-01 | 1.00E+00 | 1.00E+00 | 11 | ADCYAP1R1,ADRA1A,RXFP2,VIPR2,CRHR1,AVPR1B,SSTR4,PTGER1,BRS3,GRIK5,GRIN1 |
| 99051 | Chemokine signaling pathway | 2.82E-02 | 8.66E-01 | 1.00E+00 | 1.00E+00 | 8 | ADCY2,CCR2,CCL19,CXCL6,CX3CL1,CXCL12,GRK1,GNB4 |
| 1017634 | cAMPsignaling pathway | 9.80E-02 | 9.82E-01 | 1.00E+00 | 1.00E+00 | 7 | ADCY2,ADCYAP1R1,FXYD1,VIPR2,ATP1A4,ATP2B3,GRIN1 |
| 83077 | Jak-STAT signaling pathway | 1.96E-01 | 9.82E-01 | 1.00E+00 | 1.00E+00 | 5 | IFNA4,IL20,IL13RA1,THPO,OSMR |
| 83105 | Pathways in cancer | 2.56E-01 | 9.82E-01 | 1.00E+00 | 1.00E+00 | 10 | ADCY2,KITLG,CXCL12,BIRC7,PTGER1,PAX8,GLI2,TGFA, EGFR,GNB4 |
| 102279 | Endocytosis | 4.09E-01 | 9.82E-01 | 1.00E+00 | 1.00E+00 | 6 | ERBB3,AMPH,ASAP3,CAPZA3,GRK1,EGFR |
| 132956 | Metabolic pathways | 1.00E+00 | 1.00E+00 | 1.00E+00 | 1.00E+00 | 11 | CES1,B3GNT3,HOGA1,HSD3B1,NMNAT2,CYP24A1,PTGDS,ST6GAL2,GCLM,OTC,TREH |
| **Pathway Interaction Database** | | | | | | | |
| 137979 | FOXA1 transcription factor network | 5.27E-02 | 7.57E-01 | 1.00E+00 | 1.00E+00 | 3 | NFIB,TFF1,COL18A1 |
| 137984 | Lissencephaly gene (LIS1) in neuronal migration and development | 1.25E-01 | 7.57E-01 | 1.00E+00 | 1.00E+00 | 2 | VLDLR,CDK5R2 |
| 137923 | Rapid glucocorticoid signaling | 1.30E-01 | 7.57E-01 | 1.00E+00 | 1.00E+00 | 1 | CRH |
| 137942 | EphrinA-EPHA pathway | 1.48E-01 | 7.57E-01 | 1.00E+00 | 1.00E+00 | 1 | EPHA8 |
| 137934 | E2F transcription factor network | 1.75E-01 | 7.57E-01 | 1.00E+00 | 1.00E+00 | 3 | CES1,PRMT5,TP73 |
| 169347 | Notch-mediated HES/HEY network | 2.45E-01 | 7.57E-01 | 1.00E+00 | 1.00E+00 | 2 | HES6,GATA4 |
| 138038 | Arf6 downstream pathway | 2.59E-01 | 7.57E-01 | 1.00E+00 | 1.00E+00 | 1 | KALRN |
| 137950 | Signaling events mediated by the Hedgehog family | 3.56E-01 | 7.57E-01 | 1.00E+00 | 1.00E+00 | 1 | GLI2 |
| 138076 | Cellular roles of Anthrax toxin | 3.56E-01 | 7.57E-01 | 1.00E+00 | 1.00E+00 | 1 | ANTXR1 |
| 138081 | FAS (CD95) signaling pathway | 5.03E-01 | 7.57E-01 | 1.00E+00 | 1.00E+00 | 1 | FAIM2 |
| **REACTOME** | | | | | | | |
| 1269543 | Signaling by GPCR | 7.83E-06 | 2.33E-03 | 1.59E-02 | 4.00E-03 | 50 | ERBB3,OPN4,OR1J1,OR2J2,ADCY2,ADCYAP1R1,ADM,CCR2,OR4C3,ADRA1A,KITLG,RXFP2,OR5C1,OR3A3,CCL19,CXCL6,CX3CL1,CXCL12,RASAL1,VIPR2,OR8U1,CORT,CRH,CRHR1,SPTBN4,OR10AD1,OR10W1,AVPR1B,RGS22,SSTR4,PTGER1,GDNF,BRS3,GNAL,OR5H1,OR2AG1,GPR31,KALRN,GPR32,FFAR3,OR2AG2,OR5A2,GRIN1,OR2T6,EGFR,NPB,OR10H1,GNB4,OR52K2,GPHB5 |
| 1269574 | GPCR downstream signaling | 9.12E-06 | 2.33E-03 | 1.59E-02 | 4.66E-03 | 41 | OPN4,OR1J1,OR2J2,ADCY2,ADCYAP1R1,ADM,CCR2,OR4C3,ADRA1A,RXFP2,OR5C1,OR3A3,CCL19,CXCL6,CXCL12,VIPR2,OR8U1,CORT,CRH,CRHR1,OR10AD1,OR10W1,AVPR1B,RGS22,SSTR4,PTGER1,BRS3,GNAL,OR5H1,OR2AG1,KALRN,GPR32,FFAR3,OR2AG2,OR5A2,OR2T6,NPB,OR10H1,GNB4,OR52K2,GPHB5 |
| 1269868 | Muscle contraction | 5.36E-05 | 9.13E-03 | 6.22E-02 | 2.74E-02 | 14 | ACTG2,KCNK9,MYLPF,FXYD1,FXYD3,TRIM72,SORBS1,ATP1A4,ATP2B3,MYBPC3,MYL2,GATA4,KCNJ11,TNNI2 |
| 1269544 | GPCR ligand binding | 1.00E-04 | 1.28E-02 | 8.73E-02 | 5.12E-02 | 22 | OPN4,ADCYAP1R1,ADM,CCR2,ADRA1A,RXFP2,CCL19,CXCL6,CX3CL1,CXCL12,CORT,CRH,CRHR1,AVPR1B,SSTR4,PTGER1,BRS3,GPR31,FFAR3,NPB,GNB4,GPHB5 |
| 1269265 | Defensins | 6.08E-03 | 1.35E-01 | 9.20E-01 | 1.00E+00 | 5 | CCR2,DEFB107A,DEFB1,DEFB4A,DEFB134 |
| 1457790 | Keratinization | 1.13E-03 | 6.41E-02 | 4.37E-01 | 5.77E-01 | 12 | KRTAP6-1,EVPL,KRTAP4-8,KRTAP4-3,LELP1,KRTAP10-5,KRTAP5-7,KRT32,KRT82,LCE1A,KRTAP4-7,KRTAP13-1 |
| 1269903 | Transmembrane transport of small molecules | 2.84E-02 | 3.33E-01 | 1.00E+00 | 1.00E+00 | 21 | BEST3,ADCY2,TRPM5,SLC22A8,TRPV6,FXYD1,FXYD3,AQP8,SLC4A1,SLC6A2,ATP1A4,ATP2B3,SLC38A1,KCNJ11,LOC100506403,SLC29A4,AQP10,LCN1,SLC5A11,SLC17A5,GNB4 |
| 1270302 | Developmental Biology | 7.20E-02 | 4.51E-01 | 1.00E+00 | 1.00E+00 | 10 | CAPN13,COL9A2,ADAMTS2,COL28A1,COL23A1,BMP7,PTPRS,KLKB1,COL18A1,TNXB |
| 1269907 | SLC-mediated transmembrane transport | 1.16E-01 | 5.32E-01 | 1.00E+00 | 1.00E+00 | 9 | SLC22A8,SLC4A1,SLC6A2,SLC38A1,LOC100506403,SLC29A4,LCN1,SLC5A11,SLC17A5 |
| 1269203 | Innate Immune System | 6.08E-01 | 8.02E-01 | 1.00E+00 | 1.00E+00 | 25 | ERBB3,BPIFA1,LEAP2,ADCY2,CCR2,DEFB107A,KITLG,RASAL1,PRDX4,FCN3,IFNA4,SPTBN4,MUC2,MUC3A,MUC4,PRTN3,GDNF,DEFB1,DEFB4A,C1S,C7,DEFB134,GRIN1,EGFR,REG3A |
| **Gen MAPP** | | | | | | | |
| MAP00140 | C21 Steroid hormone metabolism | 1.81E-01 | 4.74E-01 | 1.00E+00 | 1.00E+00 | 1 | HSD3B1 |
| MAP00150 | Androgen and estrogen metabolism | 2.88E-01 | 4.74E-01 | 1.00E+00 | 1.00E+00 | 1 | HSD3B1 |
| MAP00220 | Urea cycle and metabolism of amino groups | 2.88E-01 | 4.74E-01 | 1.00E+00 | 1.00E+00 | 1 | OTC |
| MAP00590 | Prostaglandin and leukotriene metabolism | 3.16E-01 | 4.74E-01 | 1.00E+00 | 1.00E+00 | 1 | PTGDS |
| MAP00251 | Glutamate metabolism | 3.29E-01 | 4.74E-01 | 1.00E+00 | 1.00E+00 | 1 | GCLM |
| MAP00480 | Glutathione metabolism | 3.56E-01 | 4.74E-01 | 1.00E+00 | 1.00E+00 | 1 | GCLM |
| MAP00330 | Arginine and proline metabolism | 5.32E-01 | 6.08E-01 | 1.00E+00 | 1.00E+00 | 1 | OTC |
| MAP00230 | Purine metabolism | 8.14E-01 | 8.14E-01 | 1.00E+00 | 1.00E+00 | 1 | ADCY2 |
| **MSigDB C2 BIOCARTA (v6.0)** | | | | | | | |
| M5889 | Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins | 1.41E-08 | 9.15E-07 | 4.35E-06 | 9.15E-07 | 48 | CLEC1B,KITLG,CLEC2L,SEMA5B,SPON2,CCL19,CXCL6,CX3CL1,CXCL12,COL9A2,MXRA5,ADAMTS2,COL28A1,FCN3,IFNA4,SEMA4G,COL23A1,SCUBE1,IGFALS,IL20,CLEC4G,MUC22,MUC2,MUC3A,MUC4,MEGF11,IL36B,ADAM21,IL17B,SMOC1,GDNF,FREM1,TINAGL1,BMP7,SRPX2,CFC1,NGF,ADAMTSL1,TGFA,LMAN1L,COL18A1,EYS,THPO,INSL6,REG3A,CLEC3B,EGFL7,TNXB |
| M5885 | Ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins, ECM regulators and secreted factors | 6.87E-07 | 2.23E-05 | 1.06E-04 | 4.47E-05 | 36 | CLEC1B,KITLG,CLEC2L,SEMA5B,CCL19,CXCL6,CX3CL1,CXCL12,ADAMTS2,FCN3,IFNA4,SEMA4G,SCUBE1,IL20,CLEC4G,MUC22,MUC2,MUC3A,MUC4,MEGF11,IL36B,ADAM21,IL17B,GDNF,FREM1,BMP7,CFC1,NGF,ADAMTSL1,TGFA,LMAN1L,THPO,INSL6,REG3A,CLEC3B,EGFL7 |
| M5880 | Genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins | 7.38E-06 | 1.60E-04 | 7.61E-04 | 4.80E-04 | 14 | CLEC1B,CLEC2L,SEMA5B,FCN3,SEMA4G,CLEC4G,MUC22,MUC2,MUC3A,MUC4,FREM1,LMAN1L,REG3A,CLEC3B |
| M5883 | Genes encoding secreted soluble factors | 5.33E-05 | 8.66E-04 | 4.12E-03 | 3.46E-03 | 19 | KITLG,CCL19,CXCL6,CX3CL1,CXCL12,IFNA4,SCUBE1,IL20,MEGF11,IL36B,IL17B,GDNF,BMP7,CFC1,NGF,TGFA,THPO,INSL6,EGFL7 |
| M5884 | Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans | 8.58E-03 | 9.30E-02 | 4.43E-01 | 5.58E-01 | 12 | SPON2,COL9A2,MXRA5,COL28A1,COL23A1,IGFALS,SMOC1,TINAGL1,SRPX2,COL18A1,EYS,TNXB |
| M7146 | Classical Complement Pathway | 3.03E-02 | 2.46E-01 | 1.00E+00 | 1.00E+00 | 2 | C1S,C7 |
| M3061 | Feeder Pathways for Glycolysis | 1.65E-01 | 5.27E-01 | 1.00E+00 | 1.00E+00 | 1 | TREH |
| M15743 | G alpha 12 Pathway | 3.68E-01 | 5.27E-01 | 1.00E+00 | 1.00E+00 | 1 | RASAL1 |
| M8601 | Rac 1 cell motility signaling pathway | 3.68E-01 | 5.27E-01 | 1.00E+00 | 1.00E+00 | 1 | MYL2 |
| M4910 | ERK1/ERK2 MAPK Pathway | 4.72E-01 | 5.56E-01 | 1.00E+00 | 1.00E+00 | 1 | MOS |
| **Panther DB** | | | | | | | |
| P04380 | Cortocotropin releasing factor receptor signalingpathway | 2.72E-03 | 9.08E-02 | 4.23E-01 | 1.61E-01 | 4 | CRH,CRHR1,GNAL,GNB4 |
| P04376 | 5HT4 type receptor mediated signaling pathway | 3.08E-03 | 9.08E-02 | 4.23E-01 | 1.82E-01 | 4 | KCNK9,ADCY2,GNAL,GNB4 |
| P00029 | Huntington disease | 1.10E-02 | 1.67E-01 | 7.80E-01 | 6.51E-01 | 7 | ACTG2,ACTBL2,KALRN,GRIK5,GRIN1,DNAL4,TP73 |
| P05915 | Opioid proenkephalin pathway | 2.48E-02 | 1.98E-01 | 9.25E-01 | 1.00E+00 | 3 | KCNK9,ADCY2,GNB4 |
| P00037 | Ionotropic glutamate receptor pathway | 6.22E-02 | 3.06E-01 | 1.00E+00 | 1.00E+00 | 3 | SHANK1,GRIK5,GRIN1 |
| P00012 | Cadherin signaling pathway | 9.55E-02 | 3.73E-01 | 1.00E+00 | 1.00E+00 | 6 | ERBB3,ACTG2,ACTBL2,PCDHB8,EGFR,CDH5 |
| P00001 | Adrenaline and noradrenaline biosynthesis | 1.05E-01 | 3.73E-01 | 1.00E+00 | 1.00E+00 | 2 | SLC6A2,INMT |
| P00031 | Inflammation mediated by chemokine and cytokine signaling pathway | 3.26E-01 | 6.07E-01 | 1.00E+00 | 1.00E+00 | 5 | ACTG2,ADCY2,CCR2,CX3CL1,ACTBL2 |
| P05734 | Synaptic vesicle trafficking | 3.68E-01 | 6.07E-01 | 1.00E+00 | 1.00E+00 | 1 | SYT3 |
| P00045 | Notch signaling pathway | 5.23E-01 | 7.38E-01 | 1.00E+00 | 1.00E+00 | 1 | HELT |
| **Pathway Ontology** | | | | | | | |
| PW:0000493 | corticotropin-releasing hormone signaling | 1.15E-03 | 3.11E-02 | 1.21E-01 | 3.11E-02 | 2 | CRH,CRHR1 |
| PW:0000229 | G protein signaling via Galphaq family | 3.03E-02 | 2.57E-01 | 9.98E-01 | 8.17E-01 | 2 | ADRA1A,AVPR1B |
| PW:0000525 | Ras mediated signaling | 3.91E-02 | 2.57E-01 | 9.98E-01 | 1.00E+00 | 1 | TP73 |
| PW:0000677 | altered insulin secretion pathway | 3.91E-02 | 2.57E-01 | 9.98E-01 | 1.00E+00 | 1 | KCNJ11 |
| PW:0000388 | Reelinsignaling | 7.67E-02 | 2.57E-01 | 9.98E-01 | 1.00E+00 | 1 | VLDLR |
| PW:0000419 | water transport | 1.65E-01 | 3.86E-01 | 1.00E+00 | 1.00E+00 | 1 | AQP10 |
| PW:0000238 | insulin-like growth factor signaling | 2.13E-01 | 3.86E-01 | 1.00E+00 | 1.00E+00 | 1 | IGFALS |
| PW:0000485 | eicosanoids metabolic | 3.02E-01 | 4.08E-01 | 1.00E+00 | 1.00E+00 | 1 | PTGDS |
| PW:0000048 | methionine cycle/metabolic | 3.93E-01 | 4.76E-01 | 1.00E+00 | 1.00E+00 | 1 | PRMT5 |
| PW:0000043 | pyruvate metabolic | 4.51E-01 | 5.07E-01 | 1.00E+00 | 1.00E+00 | 1 | ACOT12 |
| **SMPDB** | | | | | | | |
| SMP00205 | Ornithine Transcarbamylase Deficiency (OTC Deficiency) | 2.02E-02 | 3.18E-01 | 1.00E+00 | 1.00E+00 | 1 | OTC |
| SMP00343 | Intracellular Signalling Through PGD2 receptor and Prostaglandin D2 | 7.67E-02 | 3.18E-01 | 1.00E+00 | 1.00E+00 | 1 | ADCY2 |
| SMP00375 | Verapamil Pathway | 1.03E-01 | 3.18E-01 | 1.00E+00 | 1.00E+00 | 3 | ATP1A4,MYL2,KCNJ11 |
| SMP00077 | Piroxicam Pathway | 1.30E-01 | 3.18E-01 | 1.00E+00 | 1.00E+00 | 1 | PTGDS |
| SMP00130 | Steroidogenesis | 1.48E-01 | 3.18E-01 | 1.00E+00 | 1.00E+00 | 1 | HSD3B1 |
| SMP00013 | Cysteine Metabolism | 1.65E-01 | 3.18E-01 | 1.00E+00 | 1.00E+00 | 1 | GCLM |
| SMP00048 | Nicotinate and Nicotinamide Metabolism | 2.13E-01 | 3.18E-01 | 1.00E+00 | 1.00E+00 | 1 | NMNAT2 |
| SMP00024 | Porphyrin Metabolism | 2.59E-01 | 3.18E-01 | 1.00E+00 | 1.00E+00 | 1 | FTMT |
| SMP00287 | Tranexamic Acid Pathway | 2.74E-01 | 3.18E-01 | 1.00E+00 | 1.00E+00 | 1 | KLKB1 |
| SMP00246 | Pirenzepine Pathway | 2.88E-01 | 3.18E-01 | 1.00E+00 | 1.00E+00 | 1 | SSTR4 |

**Table 3** The enriched pathway terms of the down regulated differentially expressed genes

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **BIOCYC** | | | | | | | |
| **Pathway ID** | **Pathway Name** | **P-value** | **FDR B&H** | **FDR B&Y** | **Bonferroni** | **Gene Count** | **Gene** |
| 142273 | inosine-5'-phosphate biosynthesis | 4.35E-02 | 3.07E-01 | 1.00E+00 | 8.27E-01 | 1 | ATIC |
| 142427 | sulfate activation for sulfonation | 4.35E-02 | 3.07E-01 | 1.00E+00 | 8.27E-01 | 1 | PAPSS2 |
| 142214 | NAD salvage | 6.46E-02 | 3.07E-01 | 1.00E+00 | 1.00E+00 | 1 | NAMPT |
| 142229 | tetrahydrobiopterin de novo biosynthesis | 6.46E-02 | 3.07E-01 | 1.00E+00 | 1.00E+00 | 1 | PTS |
| 142221 | trans, trans-farnesyldiphosphate biosynthesis | 8.52E-02 | 3.24E-01 | 1.00E+00 | 1.00E+00 | 1 | IDI1 |
| 1108778 | glycine betaine degradation | 1.05E-01 | 3.34E-01 | 1.00E+00 | 1.00E+00 | 1 | SARDH |
| 142227 | glutathione redox reactions I | 1.25E-01 | 3.39E-01 | 1.00E+00 | 1.00E+00 | 1 | GPX3 |
| 142255 | CDP-diacylglycerol biosynthesis | 3.45E-01 | 5.04E-01 | 1.00E+00 | 1.00E+00 | 1 | AGPAT4 |
| 835389 | adenosine ribonucleotides de novo biosynthesis | 3.74E-01 | 5.05E-01 | 1.00E+00 | 1.00E+00 | 1 | ADSS2 |
| 545314 | 3-phosphoinositide biosynthesis | 4.52E-01 | 5.05E-01 | 1.00E+00 | 1.00E+00 | 1 | PIK3R1 |
| **KEGG** | | | | | | | |
| 83074 | Antigen processing and presentation | 1.09E-09 | 2.59E-07 | 1.56E-06 | 2.59E-07 | 14 | KIR2DS2,HSPA8,KIR2DL2,KIR2DL4,KIR2DS3,KIR2DS4,KIR3DL1,KIR3DL2,KLRC1,KLRC3,KLRD1,RFXAP,PDIA3,KIR2DL5A |
| 83124 | Graft-versus-host disease | 1.39E-08 | 1.65E-06 | 9.96E-06 | 3.29E-06 | 10 | IL1A,IL1B,KIR2DL2,KIR3DL1,KIR3DL2,KLRC1,KLRD1,CD80,GZMB,KIR2DL5A |
| 83079 | Natural killer cell mediated cytotoxicity | 3.49E-08 | 2.76E-06 | 1.67E-05 | 8.26E-06 | 16 | KIR2DS2,FCGR3A,PIK3R1,FYN,KIR2DL2,KIR2DL4,KIR2DS3,KIR2DS4,KIR3DL1,KIR3DL2,KLRC1,KLRC3,KLRD1,GZMB,KIR2DL5A,SH2D1A |
| 83051 | Cytokine-cytokine receptor interaction | 6.85E-03 | 1.85E-01 | 1.00E+00 | 1.00E+00 | 13 | PDGFRB,CCL4,CCL20,CCL3L3,IL1A,IL1B,TNFSF9,IL18RAP,IL18R1,CXCL1,CXCL2,CXCL3,OSM |
| 167325 | Protein processing in endoplasmic reticulum | 3.05E-02 | 3.61E-01 | 1.00E+00 | 1.00E+00 | 8 | MAN1A1,PPP1R15A,HSPA8,BAG2,SAR1A,SEC24A,DERL2,PDIA3 |
| 83062 | Notch signaling pathway | 8.85E-02 | 7.00E-01 | 1.00E+00 | 1.00E+00 | 3 | RBPJL,HES1,NOTCH2 |
| 83059 | mTORsignaling pathway | 1.16E-01 | 7.80E-01 | 1.00E+00 | 1.00E+00 | 6 | RPS6,PIK3R1,EIF4E2,PRKAA1,LPIN1,CAB39L |
| 102279 | Endocytosis | 1.21E-01 | 7.80E-01 | 1.00E+00 | 1.00E+00 | 9 | F2R,HSPA8,ARAP2,AGAP1,SMAP1,WIPF1,CHMP1B,SMURF1,CBLB |
| 83054 | Cell cycle | 2.91E-01 | 8.26E-01 | 1.00E+00 | 1.00E+00 | 4 | CDKN1C,STAG1,WEE1,PCNA |
| 132956 | Metabolic pathways | 9.62E-01 | 9.70E-01 | 1.00E+00 | 1.00E+00 | 20 | MAN1A1,PPT2,ADSS2,COX5A,AMD1,IDI1,IDS,POLR3F,PRIM2,ATIC,AGPAT4,LPIN1,PTS,GMDS,SARDH,RDH12,CERS6,PAPSS2,NAMPT,PAFAH1B2 |
| **Pathway Interaction Database** | | | | | | | |
| 138050 | Fc-epsilon receptor I signaling in mast cells | 2.97E-04 | 3.98E-02 | 2.18E-01 | 3.98E-02 | 7 | PIK3R1,MAP2K4,WIPF1,FYN,CBLB,S1PR1,PAK2 |
| 138024 | TGF-beta receptor signaling | 8.44E-04 | 5.45E-02 | 2.98E-01 | 1.13E-01 | 6 | PPP1R15A,OCLN,SPTBN1,SMURF1,TGFBR3,SMAD7 |
| 137922 | IL12-mediated signaling events | 1.09E-02 | 2.58E-01 | 1.00E+00 | 1.00E+00 | 5 | CCL4,IL1B,IL18RAP,IL18R1,GZMB |
| 137940 | Signaling events mediated by VEGFR1 and VEGFR2 | 1.24E-02 | 2.58E-01 | 1.00E+00 | 1.00E+00 | 5 | HIF1A,PIK3R1,FYN,SH2D2A,S1PR1 |
| 137953 | Role of Calcineurin-dependent NFAT signaling in lymphocytes | 2.56E-02 | 2.85E-01 | 1.00E+00 | 1.00E+00 | 4 | NR4A1,AKAP5,CSNK1A1,PRKCQ |
| 137931 | Sphingosine 1-phosphate (S1P) pathway | 7.70E-02 | 3.66E-01 | 1.00E+00 | 1.00E+00 | 2 | S1PR5,S1PR1 |
| 137974 | Caspase cascade in apoptosis | 9.73E-02 | 3.82E-01 | 1.00E+00 | 1.00E+00 | 3 | LMNA,LMNB1,GZMB |
| 137939 | Direct p53 effectors | 1.66E-01 | 4.11E-01 | 1.00E+00 | 1.00E+00 | 5 | TRIAP1,IGFBP3,JMY,SH2D1A,PCNA |
| 138045 | HIF-1-alpha transcription factor network | 4.21E-01 | 6.11E-01 | 1.00E+00 | 1.00E+00 | 2 | HIF1A,ABCB1 |
| 169352 | Regulation of Wnt-mediated beta catenin signaling and target gene transcription | 5.22E-01 | 6.30E-01 | 1.00E+00 | 1.00E+00 | 2 | MDFIC,TLE1 |
| **REACTOME** | | | | | | | |
| 1269318 | Signaling by Interleukins | 1.15E-04 | 3.08E-02 | 2.24E-01 | 9.24E-02 | 26 | HIF1A,PDGFRB,PIK3R1,CCL4,CCL20,HSPA8,CUL3,MAP2K4,CCL3L3,IL1A,IL1B,FYN,PSMA1,SPTBN1,NCAM1,IL18RAP,IL18R1,PSME4,BRWD1,CXCL1,CXCL2,S1PR1,OSM,CD80,RORA,IL27 |
| 1269650 | Generic Transcription Pathway | 2.18E-04 | 3.72E-02 | 2.70E-01 | 1.75E-01 | 36 | ZNF627,ZNF671,ZNF571,NR4A1,ZNF595,COX5A,ZNF548,DYRK2,ZNF567,ZNF680,TRIAP1,ZFP37,ZNF430,ZNF26,IGFBP3,PRKAA1,ZFP1,TP53AIP1,PLK2,ZNF268,ZNF208,ZNF25,JMY,NUAK1,ZNF730,NOTCH2,NR1D2,RARB,ZNF354A,MED31,COX18,ZNF197,RORA,RORB,PCNA,SMAD7 |
| 1269171 | Adaptive Immune System | 3.02E-04 | 3.72E-02 | 2.70E-01 | 2.42E-01 | 34 | PDGFRB,CD300A,KIR2DS2,NR4A1,KLRF1,FCGR3A,PIK3R1,HACE1,CUL3,RNF126,PRKCQ,FYN,PSMA1,SEC24A,FBXW2,ITPR3,PSME4,IER3,KIR2DL2,KIR2DL4,KIR3DL1,KIR3DL2,KLRB1,KLRC1,KLRD1,SMURF1,CBLB,PDIA3,BTN3A2,BTN2A1,KIF3A,CD80,PAK2,SH2D1A |
| 1269649 | Gene Expression | 3.24E-04 | 3.72E-02 | 2.70E-01 | 2.60E-01 | 62 | ZNF627,ZNF671,RPS6,ZNF571,RPS27,NR4A1,ZNF595,COX5A,DDX23,MLLT1,ZNF548,HSPA8,DYRK2,ZNF567,EXOSC10,ZNF680,DNAJC8,TRIAP1,ZFP37,WTAP,POLR3F,ZNF430,ZNF26,IGFBP3,RRN3,PRKAA1,SAP30BP,ZFP1,TP53AIP1,RIOK2,MYBL1,HBS1L,PLK2,RNMT,ZNF268,PSMA1,ZNF208,ZNF25,JMY,SARS2,PSME4,NUAK1,HNRNPA0,RPRD2,ZNF730,CSTF2T,NOTCH2,NR1D2,RARB,ZNF354A,YBX1,MED31,SAP30L,COX18,EIF1AX,ZNF197,RORA,RORB,MPHOSPH6,PCNA,BRF2,SMAD7 |
| 1269310 | Cytokine Signaling in Immune system | 2.84E-03 | 1.52E-01 | 1.00E+00 | 1.00E+00 | 29 | HIF1A,PDGFRB,PIK3R1,CCL4,CCL20,HSPA8,EIF4E2,CUL3,MAP2K4,CCL3L3,IL1A,IL1B,FYN,TNFSF9,PSMA1,SPTBN1,NCAM1,IL18RAP,IL18R1,SOCS2,PSME4,BRWD1,CXCL1,CXCL2,S1PR1,OSM,CD80,RORA,IL27 |
| 1269763 | Cell Cycle, Mitotic | 2.01E-02 | 4.54E-01 | 1.00E+00 | 1.00E+00 | 19 | CDKN1C,STAG1,NCAPH2,RPS27,CENPP,CEP78,PHLDA1,WEE1,PRIM2,PSMA1,LPIN1,PSME4,RAB2A,NCAPD3,CLASP1,LMNA,LMNB1,TMPO,PCNA |
| 1269810 | M Phase | 2.03E-02 | 4.54E-01 | 1.00E+00 | 1.00E+00 | 13 | STAG1,NCAPH2,RPS27,CENPP,PSMA1,LPIN1,PSME4,RAB2A,NCAPD3,CLASP1,LMNA,LMNB1,TMPO |
| 1269431 | IRS-mediated signalling | 6.56E-02 | 5.51E-01 | 1.00E+00 | 1.00E+00 | 11 | PDGFRB,RPS6,PIK3R1,CUL3,PRKAA1,FYN,PSMA1,SPTBN1,NCAM1,PSME4,CAB39L |
| 1268714 | Asparagine N-linked glycosylation | 9.91E-02 | 6.02E-01 | 1.00E+00 | 1.00E+00 | 10 | MAN1A1,AREG,SEC24A,SPTBN1,TRAPPC6B,GMDS,TMED2,DERL2,PDIA3,SLC17A5 |
| 1268701 | Post-translational protein modification | 1.55E-01 | 6.73E-01 | 1.00E+00 | 1.00E+00 | 28 | HIF1A,MAN1A1,STAG1,SPON2,HSPA8,AREG,GPIHBP1,TNKS,PSMA1,SEC24A,SPTBN1,TOMM20,SMC5,PSME4,TRAPPC6B,JOSD1,GMDS,TMED2,RAB2A,USP24,DERL2,B3GNT7,PDIA3,SLC17A5,RNF2,TNFAIP3,PCNA,SMAD7 |
| **Gen MAPP** | | | | | | | |
| MAP00531 | MGlycosaminoglycan degradation | 2.00E-01 | 4.98E-01 | 1.00E+00 | 1.00E+00 | 1 | IDS |
| MAP00100 | Sterol biosynthesis | 2.00E-01 | 4.98E-01 | 1.00E+00 | 1.00E+00 | 1 | IDI1 |
| MAP00670 | One carbon pool by folate | 2.17E-01 | 4.98E-01 | 1.00E+00 | 1.00E+00 | 1 | ATIC |
| MAP00790 | Folate biosynthesis | 2.35E-01 | 4.98E-01 | 1.00E+00 | 1.00E+00 | 1 | PTS |
| MAP00230 | Purine metabolism | 2.82E-01 | 4.98E-01 | 1.00E+00 | 1.00E+00 | 3 | PDE4D,ADSS2,ATIC |
| MAP00252 | Alanine and aspartate metabolism | 3.74E-01 | 4.98E-01 | 1.00E+00 | 1.00E+00 | 1 | ADSS2 |
| MAP00480 | Glutathione metabolism | 3.87E-01 | 4.98E-01 | 1.00E+00 | 1.00E+00 | 1 | GPX3 |
| MAP00330 | Arginine and proline metabolism | 5.71E-01 | 6.25E-01 | 1.00E+00 | 1.00E+00 | 1 | AMD1 |
| MAP00190 | Oxidative phosphorylation | 6.25E-01 | 6.25E-01 | 1.00E+00 | 1.00E+00 | 1 | COX5A |
| **MSigDB C2 BIOCARTA (v6.0)** | | | | | | | |
| M16355 | Ras-Independent pathway in NK cell-mediated cytotoxicity | 8.42E-04 | 1.02E-01 | 5.73E-01 | 1.29E-01 | 4 | PIK3R1,KLRC1,KLRC3,KLRD1 |
| M5202 | Hypoxia and p53 in the Cardiovascular system | 1.46E-03 | 1.02E-01 | 5.73E-01 | 2.24E-01 | 4 | HIF1A,ABCB1,IGFBP3,CSNK1A1 |
| M2842 | Fibrinolysis Pathway | 2.00E-03 | 1.02E-01 | 5.73E-01 | 3.06E-01 | 3 | F2R,PLAU,SERPINB2 |
| M3618 | TNFR1 Signaling Pathway | 3.53E-03 | 1.23E-01 | 6.88E-01 | 5.41E-01 | 4 | MAP2K4,LMNA,LMNB1,PAK2 |
| M5883 | Genes encoding secreted soluble factors | 2.02E-02 | 3.86E-01 | 1.00E+00 | 1.00E+00 | 14 | CCL4,CCL20,FLG,CCL3L3,AREG,PDGFD,IL1A,IL1B,TNFSF9,CXCL1,CXCL2,CXCL3,OSM,ANGPTL2 |
| M13863 | MAPKinaseSignaling Pathway | 3.00E-01 | 5.66E-01 | 1.00E+00 | 1.00E+00 | 3 | MAP2K4,MAP4K5,PAK2 |
| M5885 | Ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins, ECM regulators and secreted factors | 3.01E-01 | 5.66E-01 | 1.00E+00 | 1.00E+00 | 19 | CCL4,PLAU,CCL20,FLG,CST7,CCL3L3,AREG,PDGFD,IL1A,IL1B,TNFSF9,PZP,ADAM12,CXCL1,CXCL2,CXCL3,OSM,ANGPTL2,SERPINB2 |
| M5889 | Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins | 4.99E-01 | 6.01E-01 | 1.00E+00 | 1.00E+00 | 23 | CRIM1,SPON2,CCL4,PLAU,CCL20,FLG,CST7,CCL3L3,AREG,IGFBP3,PDGFD,PODN,IL1A,IL1B,TNFSF9,PZP,ADAM12,CXCL1,CXCL2,CXCL3,OSM,ANGPTL2,SERPINB2 |
| M3468 | Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix | 6.05E-01 | 6.37E-01 | 1.00E+00 | 1.00E+00 | 5 | PLAU,CST7,PZP,ADAM12,SERPINB2 |
| M5884 | Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans | 8.59E-01 | 8.59E-01 | 1.00E+00 | 1.00E+00 | 5 | CRIM1,SPON2,IGFBP3,PODN |
| **Panther DB** | | | | | | | |
| P00020 | FAS signaling pathway | 5.29E-04 | 3.70E-02 | 1.79E-01 | 3.70E-02 | 5 | PARP4,MAP2K4,PARP2,LMNA,LMNB1 |
| P00005 | Angiogenesis | 1.77E-03 | 6.20E-02 | 3.00E-01 | 1.24E-01 | 10 | HIF1A,PDGFRB,RBPJL,PIK3R1,MAP2K4,PDGFD,PRKCQ,NOTCH2,SH2D2A,PAK2 |
| P00056 | VEGF signaling pathway | 3.86E-02 | 5.65E-01 | 1.00E+00 | 1.00E+00 | 4 | HIF1A,PIK3R1,PRKCQ,SH2D2A |
| P00053 | T cell activation | 8.64E-02 | 6.56E-01 | 1.00E+00 | 1.00E+00 | 4 | PIK3R1,PRKCQ,CD80,PAK2 |
| P00027 | Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway | 9.82E-02 | 6.56E-01 | 1.00E+00 | 1.00E+00 | 5 | GNG2,DNAJC27,PRKCQ,RGS9,ITPR3 |
| P00006 | Apoptosis signaling pathway | 1.87E-01 | 6.90E-01 | 1.00E+00 | 1.00E+00 | 4 | HSPA8,CREM,PRKCQ,GZMB |
| P00018 | EGF receptor signaling pathway | 2.28E-01 | 7.61E-01 | 1.00E+00 | 1.00E+00 | 4 | MAP2K4,AREG,PRKCQ,CBLB |
| P00031 | Inflammation mediated by chemokine and cytokine signaling pathway | 2.45E-01 | 7.71E-01 | 1.00E+00 | 1.00E+00 | 6 | GNG2,CCL4,CCL20,CCL3L3,ITPR3,PAK2 |
| P00034 | Integrin signalling pathway | 3.07E-01 | 7.71E-01 | 1.00E+00 | 1.00E+00 | 5 | DNAJC27,PIK3R1,FLNA,MAP2K4,FYN |
| P00057 | Wntsignaling pathway | 6.67E-01 | 7.71E-01 | 1.00E+00 | 1.00E+00 | 6 | GNG2,ADSS2,CSNK1A1,PRKCQ,ITPR3,TLE1 |
| **Pathway Ontology** | | | | | | | |
| PW:0000140 | pathway of folate cycle/metabolism | 1.05E-02 | 2.18E-01 | 9.80E-01 | 5.23E-01 | 3 | ATIC,PTS,SARDH |
| PW:0000243 | vascular endothelial growth factor signaling | 1.52E-02 | 2.18E-01 | 9.80E-01 | 7.58E-01 | 3 | HIF1A,FYN,SH2D2A |
| PW:0000490 | transforming growth factor-beta Smad dependent signaling | 1.89E-02 | 2.18E-01 | 9.80E-01 | 9.43E-01 | 3 | SMURF1,TGFBR3,SMAD7 |
| PW:0000369 | the ARE-Nrf mediated of drug-metabolizing enzyme expression | 2.25E-02 | 2.18E-01 | 9.80E-01 | 1.00E+00 | 1 | NRF1 |
| PW:0000435 | neddylation | 2.33E-02 | 2.18E-01 | 9.80E-01 | 1.00E+00 | 2 | CUL3,CAND1 |
| PW:0000211 | amines and polyamines metabolic | 4.35E-02 | 2.18E-01 | 9.80E-01 | 1.00E+00 | 1 | AMD1 |
| PW:0000398 | homocysteine metabolic | 5.86E-02 | 2.66E-01 | 1.00E+00 | 1.00E+00 | 2 | OCLN,RNMT |
| PW:0000518 | Atherosclerosis | 6.46E-02 | 2.69E-01 | 1.00E+00 | 1.00E+00 | 1 | LMNA |
| PW:0000102 | The extracellular signal-regulated RAF/MEK/ERK signaling | 1.11E-01 | 3.13E-01 | 1.00E+00 | 1.00E+00 | 2 | F2R,S1PR1 |
| PW:0000143 | insulin signaling | 1.18E-01 | 3.13E-01 | 1.00E+00 | 1.00E+00 | 2 | PIK3R1,PRKCQ |
| **SMPDB** | | | | | | | |
| SMP00244 | Sarcosinemia | 2.25E-02 | 2.93E-01 | 1.00E+00 | 5.85E-01 | 1 | SARDH |
| SMP00050 | Purine Metabolism | 1.18E-01 | 4.22E-01 | 1.00E+00 | 1.00E+00 | 2 | ADSS2,ATIC |
| SMP00041 | Sulfate/Sulfite Metabolism | 1.25E-01 | 4.22E-01 | 1.00E+00 | 1.00E+00 | 1 | PAPSS2 |
| SMP00005 | Folate and Pterine Biosynthesis | 1.82E-01 | 4.22E-01 | 1.00E+00 | 1.00E+00 | 1 | PTS |
| SMP00265 | Abciximab Pathway | 2.35E-01 | 4.22E-01 | 1.00E+00 | 1.00E+00 | 1 | F2R |
| SMP00048 | Nicotinate and Nicotinamide Metabolism | 2.35E-01 | 4.22E-01 | 1.00E+00 | 1.00E+00 | 1 | NAMPT |
| SMP00064 | Fructose and Mannose Degradation | 2.84E-01 | 4.22E-01 | 1.00E+00 | 1.00E+00 | 1 | GMDS |
| SMP00074 | Retinol Metabolism | 3.30E-01 | 4.22E-01 | 1.00E+00 | 1.00E+00 | 1 | RDH12 |
| SMP00046 | Pyrimidine Metabolism | 4.27E-01 | 4.44E-01 | 1.00E+00 | 1.00E+00 | 1 | POLR3F |
| SMP00391 | Insulin Signalling | 5.52E-01 | 5.52E-01 | 1.00E+00 | 1.00E+00 | 1 | RPS6 |

**Table 4** The enriched GO terms of the up regulated differentially expressed genes

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **GO ID** | **CATEGORY** | **GO Name** | **P Value** | **FDR B&H** | **FDR B&Y** | **Bonferroni** | **Gene Count** | **Gene** |
| GO:0050877 | BP | nervous system process | 8.48E-07 | 4.01E-03 | 3.63E-02 | 4.01E-03 | 55 | OPN4,NOG,OR1J1,OR2J2,SHROOM4,CCR2,OR4C3,ADRA1A,TRPM5,SEMA5B,OR5C1,OR3A3,CX3CL1,CXCL12,SHISA6,VLDLR,AMPH,OR8U1,TMPRSS11E,CRH,CRHR1,CRYAA,SPTBN4,CRYBB3,CRYGA,BARHL1,OR10AD1,OR10W1,IGSF9B,LYNX1,LRRN4,KCNJ11,NGF,GNAL,OR5H1,OR2AG1,SHANK1,KALRN,OR2AG2,PKD2L1,OR5A2,GRIK5,GRIN1,LCN1,GRK1,COL18A1,EYS,OR2T6,EGFR,OR10H1,GRIP2,PAX6,LY6H,CSMD1,OR52K2 |
| GO:0007186 | BP | G protein-coupled receptor signaling pathway | 3.27E-06 | 7.73E-03 | 6.99E-02 | 1.55E-02 | 48 | OPN4,OR1J1,OR2J2,ADCY2,ADCYAP1R1,ADM,CCR2,OR4C3,ADRA1A,PRMT5,RXFP2,OR5C1,OR3A3,CCL19,CXCL6,CX3CL1,CXCL12,VIPR2,OR8U1,CORT,CRH,CRHR1,OR10AD1,OR10W1,AVPR1B,SSTR4,PTGER1,DEFB1,DEFB4A,BRS3,PAX8,PCSK1N,GNAL,OR5H1,OR2AG1,GPR31,KALRN,GPR32,FFAR3,OR2AG2,OR5A2,GRK1,OR2T6,NPB,OR10H1,GNB4,OR52K2,GPHB5 |
| GO:0008015 | BP | blood circulation | 9.34E-06 | 1.43E-02 | 1.29E-01 | 4.42E-02 | 27 | CES1,ADM,ADRA1A,HRC,FXYD1,FXYD3,CX3CL1,CXCL12,CRH,SPTBN4,ATP1A4,RNF207,ATP2B3,MYBPC3,MYL2,AVPR1B,GATA4,BRS3,GCLM,KCNJ11,TBX2,FFAR3,MYOF,EGFR,GRIP2,TNNI2,CDH5 |
| GO:0030855 | BP | epithelial cell differentiation | 2.50E-05 | 1.90E-02 | 1.72E-01 | 1.18E-01 | 33 | CES1,KRTAP6-1,EVPL,KRTAP4-8,TJP2,FOXJ1,KRTAP4-3,CRHR1,CRYAA,COL23A1,SCUBE1,IL20,MUC2,LELP1,GATA4,GDNF,KRTAP10-5,PROM1,BMP7,ACTL8,PAX8,PTPRS,NFIB,GLI2,KRTAP5-7,KRT32,KRT82,LCE1A,COL18A1,REG3A,PAX6,KRTAP13-1,CDH5 |
| GO:0044057 | BP | regulation of system process | 2.61E-05 | 1.90E-02 | 1.72E-01 | 1.24E-01 | 29 | ADM,ADRA1A,HRC,FXYD1,FXYD3,CX3CL1,SHISA6,CRH,CRHR1,SPTBN4,IGSF9B,ATP1A4,RNF207,ATP2B3,MYBPC3,MYBPH,MYL2,AVPR1B,GATA4,CMYA5,PTGER1,KCNJ11,TBX2,SHANK1,FFAR3,GRIN1,EGFR,GRIP2,TNNI2 |
| GO:0022610 | BP | biological adhesion | 6.28E-05 | 2.97E-02 | 2.69E-01 | 2.97E-01 | 47 | ERBB3,BPIFA1,CCR2,KITLG,HOXD3,SPON2,ANTXR1,LRRN2,CCL19,CX3CL1,CXCL12,FOXJ1,ZAN,COL28A1,SORBS1,SLC4A1,ARHGDIG,IGFALS,CLEC4G,IGSF9B,MUC4,MEGF11,MYBPC3,MYBPH,MYF5,IL36B,SMOC1,FREM1,TINAGL1,BMP7,SRPX2,PTPRS,GLI2,FERMT2,CNTN4,PCDHB8,SRCIN1,COL18A1,EGFR,KIRREL1,CNTN3,REG3A,EGFL7,BCAM,CDH5,TNXB,EPHA8 |
| GO:0060047 | BP | heart contraction | 1.07E-04 | 3.30E-02 | 2.98E-01 | 5.05E-01 | 16 | ADM,ADRA1A,HRC,FXYD1,FXYD3,SPTBN4,ATP1A4,RNF207,ATP2B3,MYBPC3,MYL2,GATA4,KCNJ11,TBX2,FFAR3,TNNI2 |
| GO:0007155 | BP | cell adhesion | 1.13E-04 | 3.30E-02 | 2.98E-01 | 5.32E-01 | 46 | ERBB3,CCR2,KITLG,HOXD3,SPON2,ANTXR1,LRRN2,CCL19,CX3CL1,CXCL12,FOXJ1,ZAN,COL28A1,SORBS1,SLC4A1,ARHGDIG,IGFALS,CLEC4G,IGSF9B,MUC4,MEGF11,MYBPC3,MYBPH,MYF5,IL36B,SMOC1,FREM1,TINAGL1,BMP7,SRPX2,PTPRS,GLI2,FERMT2,CNTN4,PCDHB8,SRCIN1,COL18A1,EGFR,KIRREL1,CNTN3,REG3A,EGFL7,BCAM,CDH5,TNXB,EPHA8 |
| GO:0099536 | BP | synaptic signaling | 1.18E-04 | 3.30E-02 | 2.98E-01 | 5.60E-01 | 32 | SYN3,CCR2,CPNE6,ADRA1A,PRMT5,CX3CL1,SHISA6,AMPH,CORT,SORBS1,CRH,CRHR1,SLC6A2,SPTBN4,SV2C,IGSF9B,LYNX1,PTGER1,GDNF,PTPRS,NGF,GNAL,SHANK1,CNTN4,KALRN,GRIK5,GRIN1,EGFR,OR10H1,GRIP2,LY6H,CPEB1 |
| GO:0003015 | BP | heart process | 1.48E-04 | 3.40E-02 | 3.07E-01 | 7.02E-01 | 16 | ADM,ADRA1A,HRC,FXYD1,FXYD3,SPTBN4,ATP1A4,RNF207,ATP2B3,MYBPC3,MYL2,GATA4,KCNJ11,TBX2,FFAR3,TNNI2 |
| GO:0006812 | BP | cation transport | 8.41E-04 | 6.19E-02 | 5.60E-01 | 1.00E+00 | 41 | PKD1L2,BPIFA1,KCNK9,ADCYAP1R1,CCR2,ADRA1A,TRPM5,SLC22A8,HRC,TRPV6,CCL19,FXYD1,FXYD3,CX3CL1,CXCL12,SHISA6,SYT3,CRH,CRHR1,SLC6A2,SPTBN4,ATP1A4,RNF207,ATP2B3,CATSPER3,GDNF,SLC38A1,STAC2,KCNJ11,KCNJ16,NGF,SLC38A8,SHANK1,PKD2L1,FTMT,GRIK5,GRIN1,NUPR1,SLC5A11,SLC17A5,SLC4A11 |
| GO:0060429 | BP | epithelium development | 1.02E-03 | 6.86E-02 | 6.20E-01 | 1.00E+00 | 42 | NOG,CES1,KRTAP6-1,EVPL,ADM,KRTAP4-8,TJP2,CXCL12,FOXJ1,KRTAP4-3,POU3F3,CRHR1,CRYAA,COL23A1,SCUBE1,IL20,MUC2,RNF207,MYF5,LELP1,GATA4,GDNF,KRTAP10-5,PROM1,BMP7,ACTL8,PAX8,PTPRS,FERD3L,NFIB,GLI2,KRTAP5-7,TBX2,KRT32,KRT82,LCE1A,COL18A1,EGFR,REG3A,PAX6,KRTAP13-1,CDH5 |
| GO:0031226 | CC | intrinsic component of plasma membrane | 1.06E-07 | 2.45E-05 | 1.64E-04 | 4.89E-05 | 61 | ERBB3,OPN4,CLEC1B,B3GNT3,KCNK9,ADCY2,ADCYAP1R1,CCR2,ADRA1A,PROM2,RXFP2,TRPV6,FXYD1,FXYD3,SHISA6,VIPR2,SYT3,TMPRSS11E,SORBS1,AQP8,CRHR1,SEMA4G,SLC4A1,SLC6A2,ASGR1,LRRN4,ATP1A4,MUC4,ATP2B3,IL13RA1,AVPR1B,CALHM3,SSTR4,PTGER1,TSPAN9,SLC38A1,PROM1,BRS3,PTPRS,KCNJ11,KCNJ16,C7,SHANK1,AQP10,GPR31,GPR32,FFAR3,PCDHB8,SLC19A3,TM4SF5,PKD2L1,GRIK5,GRIN1,SLC17A5,EGFR,OR10H1,TREH,BCAM,OSMR,SLC4A11,EPHA8 |
| GO:0031012 | CC | extracellular matrix | 4.24E-06 | 6.50E-04 | 4.36E-03 | 1.95E-03 | 27 | SPON2,LRRN2,SCARA3,CXCL12,COL9A2,MXRA5,ADAMTS2,COL28A1,COL23A1,IGFALS,MUC2,MUC3A,MUC4,PRTN3,SMOC1,FREM1,TINAGL1,BMP7,SRPX2,ADAMTSL1,LMAN1L,COL18A1,EYS,CLEC3B,EGFL7,BCAM,TNXB |
| GO:0062023 | CC | collagen-containing extracellular matrix | 6.98E-06 | 8.03E-04 | 5.39E-03 | 3.21E-03 | 23 | SCARA3,CXCL12,COL9A2,MXRA5,ADAMTS2,COL28A1,COL23A1,MUC2,MUC4,PRTN3,SMOC1,FREM1,TINAGL1,BMP7,SRPX2,ADAMTSL1,LMAN1L,COL18A1,EYS,CLEC3B,EGFL7,BCAM,TNXB |
| GO:0015629 | CC | actin cytoskeleton | 7.26E-04 | 5.57E-02 | 3.74E-01 | 3.34E-01 | 27 | ACTG2,BPIFA1,AFAP1L1,SHROOM4,KITLG,PROM2,MYLPF,ANTXR1,AMPH,SORBS1,ABLIM3,SPTBN4,GAS2L2,CAPZA3,MUC4,MYBPC3,MYBPH,MYL2,ACTBL2,AIF1L,PROM1,ACTL8,FERMT2,KALRN,SRCIN1,TREH,TNNI2 |
| GO:0099512 | CC | supramolecularfiber | 1.23E-03 | 6.32E-02 | 4.24E-01 | 5.64E-01 | 42 | KRTAP6-1,ACTG2,EVPL,BPIFA1,SHROOM4,ADRA1A,KITLG,PROM2,KRTAP4-8,HRC,MYLPF,ANTXR1,KIF17,KLC3,KRTAP4-3,DNAH2,SORBS1,ABLIM3,SLC4A1,GAS2L2,ODF4,MUC4,MYBPC3,MYL2,AIF1L,CMYA5,KRTAP10-5,ENO4,DEFB1,PROM1,GLI2,WDR90,FERMT2,DEK,KRTAP5-7,KRT32,KRT82,SRCIN1,DNAL4,TREH,TNNI2,KRTAP13-1 |
| GO:0043005 | CC | neuron projection | 1.36E-03 | 6.32E-02 | 4.24E-01 | 6.27E-01 | 44 | OPN4,NOG,ADCY2,ADCYAP1R1,CCR2,CPNE6,TRPM5,KIF17,CX3CL1,SHISA6,KLC3,AMPH,LRRC30,CRH,CRHR1,SLC6A2,SPTBN4,SV2C,IGSF9B,LYNX1,NMNAT2,ADAM21,SLC38A1,PROM1,BRS3,PTPRS,NFIB,KCNJ11,NGF,CDK5R2,SHANK1,CNTN4,KALRN,CRTAC1,SRCIN1,GRIK5,GRIN1,GRK1,EYS,OR10H1,KIRREL1,GRIP2,CPEB1,EPHA8 |
| GO:0009986 | CC | cell surface | 1.04E-02 | 2.04E-01 | 1.00E+00 | 1.00E+00 | 28 | ADCYAP1R1,CCR2,PROM2,TJP2,ANTXR1,CX3CL1,CXCL12,VLDLR,SLC4A1,SLC6A2,COL23A1,PLA2R1,SCUBE1,IL13RA1,PROM1,SRPX2,BTNL3,UMODL1,CFC1,FERMT2,PKD2L1,GRIN1,TGFA,EGFR,EGFL7,BCAM,OSMR,CDH5 |
| GO:0099513 | CC | polymeric cytoskeletal fiber | 1.54E-02 | 2.04E-01 | 1.00E+00 | 1.00E+00 | 33 | KRTAP6-1,ACTG2,EVPL,BPIFA1,SHROOM4,KITLG,PROM2,KRTAP4-8,ANTXR1,KIF17,KLC3,KRTAP4-3,DNAH2,SORBS1,ABLIM3,GAS2L2,ODF4,MUC4,AIF1L,KRTAP10-5,ENO4,DEFB1,PROM1,GLI2,WDR90,FERMT2,KRTAP5-7,KRT32,KRT82,SRCIN1,DNAL4,TREH,KRTAP13-1 |
| GO:0030990 | CC | intraciliary transport particle | 2.86E-02 | 2.24E-01 | 1.00E+00 | 1.00E+00 | 22 | OPN4,PROM2,KIF17,KLC3,FOXJ1,VIPR2,DNAH2,LRRC30,ABLIM3,FANK1,ODF4,CATSPER3,ENO4,DEFB1,PROM1,GLI2,WDR90,PKD2L1,RFX4,GRK1,DNAL4,EYS |
| GO:0030054 | CC | cell junction | 3.55E-02 | 2.30E-01 | 1.00E+00 | 1.00E+00 | 32 | SYN3,EVPL,ADCYAP1R1,AFAP1L1,SHROOM4,TJP2,FXYD1,SHISA6,AMPH,ASAP3,SORBS1,SLC4A1,SPTBN4,SV2C,IGSF9B,FAIM2,AIF1L,TSPAN9,SRPX2,PTPRS,KCNJ11,FERMT2,SHANK1,SRCIN1,GRIK5,GRIN1,SLC17A5,EGFR,KIRREL1,CDH5,TP73,CPEB1 |
| GO:0004888 | MF | transmembranesignaling receptor activity | 4.77E-07 | 3.97E-04 | 2.90E-03 | 3.97E-04 | 51 | ERBB3,OPN4,OR1J1,CLEC1B,OR2J2,ADCYAP1R1,CCR2,OR4C3,ADRA1A,RXFP2,OR5C1,OR3A3,ANTXR1,SHISA6,VIPR2,VLDLR,OR8U1,CRH,CRHR1,PLA2R1,OR10AD1,OR10W1,LYNX1,IL13RA1,IL17REL,AVPR1B,SSTR4,PTGER1,BRS3,PAX8,OR5H1,OR2AG1,SHANK1,GPR31,GPR32,FFAR3,OR2AG2,PKD2L1,OR5A2,GRIK5,GRIN1,TGFA,OR2T6,EGFR,OR10H1,REG3A,BCAM,OSMR,LY6H,OR52K2,EPHA8 |
| GO:0030545 | MF | receptor regulator activity | 1.70E-06 | 7.06E-04 | 5.16E-03 | 1.41E-03 | 27 | NOG,ADM,KITLG,SEMA5B,CCL19,CXCL6,CX3CL1,CXCL12,CORT,CRH,IFNA4,SEMA4G,IL20,LYNX1,IL36B,IL17B,GDNF,DEFB4A,BMP7,NGF,TFF1,TGFA,THPO,INSL6,THNSL2,LY6H,GPHB5 |
| GO:0060089 | MF | molecular transducer activity | 9.10E-06 | 1.26E-03 | 9.22E-03 | 7.58E-03 | 58 | ERBB3,OPN4,NOG,OR1J1,CLEC1B,OR2J2,PAQR6,ADCYAP1R1,CCR2,OR4C3,ADRA1A,RXFP2,OR5C1,OR3A3,ANTXR1,LRRN2,SHISA6,VIPR2,VLDLR,OR8U1,CRH,CRHR1,PLA2R1,OR10AD1,OR10W1,LYNX1,MUC4,IL13RA1,IL17REL,AVPR1B,SSTR4,PTGER1,BRS3,PAX8,OR5H1,CDK5R2,OR2AG1,SHANK1,GPR31,GPR32,FFAR3,OR2AG2,PKD2L1,OR5A2,GRIK5,GRIN1,TGFA,PKMYT1,PKIG,OR2T6,EGFR,OR10H1,REG3A,BCAM,OSMR,LY6H,OR52K2,EPHA8 |
| GO:0005102 | MF | signaling receptor binding | 3.46E-04 | 2.48E-02 | 1.81E-01 | 2.88E-01 | 52 | NOG,CYTL1,ADM,CCR2,KITLG,SEMA5B,SPON2,CCL19,CXCL6,CX3CL1,CXCL12,SHISA6,CORT,SORBS1,CRH,IFNA4,SEMA4G,IGFALS,IL20,LYNX1,MUC4,PRTN3,IL36B,IL17B,PTGER1,GDNF,DEFB1,DEFB4A,BMP7,SRPX2,BTNL3,CFC1,NGF,PCSK1N,GNAL,SHANK1,CRTAC1,GRIN1,LCN1,TFF1,TGFA,THPO,EGFR,INSL6,NPB,GRIP2,EGFL7,THNSL2,LY6H,CDH5,TNXB,GPHB5 |
| GO:0015318 | MF | inorganic molecular entity transmembrane transporter activity | 9.40E-04 | 3.40E-02 | 2.49E-01 | 7.83E-01 | 34 | BEST3,PKD1L2,KCNK9,CCR2,TRPM5,SLC22A8,HRC,TRPV6,FXYD1,FXYD3,SHISA6,AQP8,CRH,CRHR1,SLC4A1,SLC6A2,ATP1A4,RNF207,ATP2B3,CATSPER3,SLC38A1,STAC2,KCNJ11,KCNJ16,SLC38A8,SHANK1,AQP10,SLC19A3,PKD2L1,GRIK5,GRIN1,SLC5A11,SLC17A5,SLC4A11 |
| GO:0005215 | MF | transporter activity | 1.21E-03 | 4.21E-02 | 3.07E-01 | 1.00E+00 | 43 | TMEM144,MB,BEST3,PKD1L2,KCNK9,CCR2,CPNE6,TRPM5,SLC22A8,HRC,TRPV6,FXYD1,FXYD3,SHISA6,AQP8,CRH,CRHR1,SLC4A1,SLC6A2,SV2C,LYNX1,ATP1A4,RNF207,ATP2B3,CATSPER3,SLC38A1,STAC2,KCNJ11,KCNJ16,SLC29A4,SLC38A8,SHANK1,AQP10,SLC19A3,PKD2L1,GRIK5,GRIN1,SLC5A11,SLC17A5,HBM,HBQ1,SLC4A11,SLC22A31 |
| GO:0022857 | MF | transmembrane transporter activity | 1.48E-03 | 4.57E-02 | 3.34E-01 | 1.00E+00 | 39 | TMEM144,BEST3,PKD1L2,KCNK9,CCR2,TRPM5,SLC22A8,HRC,TRPV6,FXYD1,FXYD3,SHISA6,AQP8,CRH,CRHR1,SLC4A1,SLC6A2,SV2C,LYNX1,ATP1A4,RNF207,ATP2B3,CATSPER3,SLC38A1,STAC2,KCNJ11,KCNJ16,SLC29A4,SLC38A8,SHANK1,AQP10,SLC19A3,PKD2L1,GRIK5,GRIN1,SLC5A11,SLC17A5,SLC4A11,SLC22A31 |
| GO:0008324 | MF | cationtransmembrane transporter activity | 2.68E-03 | 6.39E-02 | 4.66E-01 | 1.00E+00 | 28 | PKD1L2,KCNK9,CCR2,TRPM5,SLC22A8,HRC,TRPV6,FXYD1,FXYD3,SHISA6,CRH,CRHR1,SLC6A2,ATP1A4,RNF207,ATP2B3,CATSPER3,SLC38A1,STAC2,KCNJ11,KCNJ16,SHANK1,PKD2L1,GRIK5,GRIN1,SLC5A11,SLC17A5,SLC4A11 |
| GO:0015075 | MF | ion transmembrane transporter activity | 7.50E-03 | 1.15E-01 | 8.40E-01 | 1.00E+00 | 32 | BEST3,PKD1L2,KCNK9,CCR2,TRPM5,SLC22A8,HRC,TRPV6,FXYD1,FXYD3,SHISA6,CRH,CRHR1,SLC4A1,SLC6A2,ATP1A4,RNF207,ATP2B3,CATSPER3,SLC38A1,STAC2,KCNJ11,KCNJ16,SLC38A8,SHANK1,SLC19A3,PKD2L1,GRIK5,GRIN1,SLC5A11,SLC17A5,SLC4A11 |
| GO:0098772 | MF | molecular function regulator | 7.60E-03 | 1.15E-01 | 8.40E-01 | 1.00E+00 | 48 | ERBB3,NOG,ADM,KITLG,SEMA5B,WFDC2,CCL19,FXYD1,CXCL6,FXYD3,CX3CL1,CXCL12,RASAL1,CORT,COL28A1,ASAP3,CRH,IFNA4,SEMA4G,ARHGDIG,IL20,LYNX1,MYBPC3,IL36B,IL17B,BIRC7,GDNF,DEFB4A,BMP7,UMODL1,GCLM,NGF,PCSK1N,RAB3IL1,CDK5R2,KALRN,LCN1,NUPR1,TFF1,TBC1D26,TGFA,PKIG,THPO,EGFR,INSL6,THNSL2,LY6H,GPHB5 |

Biological Process(BP), Cellular Component(CC) and Molecular Functions (MF)

**Table 5** The enriched GO terms of the down regulated differentially expressed genes

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **GO ID** | **CATEGORY** | **GO Name** | **P Value** | **FDR B&H** | **FDR B&Y** | **Bonferroni** | **Gene Count** | **Gene** |
| GO:0007049 | BP | cell cycle | 1.02E-05 | 2.00E-02 | 1.82E-01 | 5.33E-02 | 68 | CDKN1C,CHAF1B,CCNDBP1,STAG1,PDGFRB,RPS6,TFDP3,NCAPH2,NR4A1,PPP1R15A,HIRA,ABCB1,BOD1,CAMK2N1,CEP78,HACE1,HES1,HSPA8,SERTAD1,CUL3,FLNA,FNTA,PHLDA1,WEE1,TRIAP1,PKP4,ZNF365,WTAP,CTCF,CSNK1A1,PRIM2,PRKAA1,SENP6,CDK5RAP1,TNKS,PRKCQ,IL1A,IL1B,RIOK2,MYBL1,TJP3,PLK2,ZNF268,PSMA1,SPTBN1,ZNF207,SMARCAD1,SMC5,JMY,LPIN1,CEP120,PSME4,IER3,ANGEL2,CAB39L,NOTCH2,NCAPD3,DSTN,CLASP1,CHMP1B,KIF3A,OSM,RNF2,LMNA,LMNB1,SBDS,TNFAIP3,PCNA |
| GO:0002682 | BP | regulation of immune system process | 1.22E-04 | 3.97E-02 | 3.63E-01 | 6.39E-01 | 59 | DLG5,HIF1A,PDE4D,CD300A,KIR2DS2,ANKRD54,TXK,KLRF1,FCGR3A,PIK3R1,SPON2,CCL4,HES1,CCL20,HSPA8,SMAP1,MAP2K4,WIPF1,CST7,ZBTB1,SOX13,ZCCHC3,POLR3F,PDGFD,PRKCQ,IL1A,IL1B,FYN,TARM1,TOX,ELMOD2,TNFSF9,PSMA1,RC3H1,SAMSN1,IL18RAP,IL18R1,RNF125,PSME4,KIR2DL2,KIR2DL4,KIR3DL1,KIR3DL2,KLRB1,KLRC1,KLRD1,NOTCH2,CBLB,BTN3A2,BTN2A1,OSM,EGR3,CD80,PAK2,RORA,TNFAIP3,SH2D1A,IL27,SMAD7 |
| GO:0051336 | BP | regulation of hydrolase activity | 1.37E-04 | 3.97E-02 | 3.63E-01 | 7.19E-01 | 50 | MAL,CRIM1,NET1,PDGFRB,CNST,CD300A,NR4A1,PPP1R15A,F2R,TXK,BOD1,CCL4,CCL20,ARAP2,AGAP1,RGPD5,SMAP1,FNTA,TRIAP1,PKP4,CST7,CCL3L3,SH2D4A,GPIHBP1,IGFBP3,FYN,TOR1AIP1,PHACTR1,PHACTR2,ELMOD2,CDC42SE1,SYTL2,RGS9,ARHGAP11A,MPRIP,PSME4,NUAK1,TRAPPC6B,DLG3,TMED2,PZP,PPP4R1,STXBP5,RALGAPB,CBLB,S1PR1,PPP1R15B,SERPINB2,PAK2,PCNA |
| GO:0042981 | BP | regulation of apoptotic process | 2.29E-04 | 4.78E-02 | 4.37E-01 | 1.00E+00 | 58 | DLG5,HIF1A,MAL,ERCC5,NET1,PDGFRB,RPS6,NR4A1,F2R,NAA35,PIK3R1,OLFM1,QKI,HSPA8,FLNA,MAP2K4,FNTA,PHLDA1,TRIAP1,G0S2,G2E3,HIGD1A,IGFBP3,RRN3,PRKAA1,PRKCQ,IL1A,IL1B,TP53AIP1,FYN,CERKL,TCTN3,BNC2,PLK2,TNFSF9,ZNF268,JMY,MTRNR2L8,SOCS2,MTRNR2L9,IER3,CIAPIN1,NOTCH2,RARB,YBX1,SYNE1,RNF183,PDIA3,TGFBR3,OSM,LMNA,EGR3,TLE1,GZMB,SERPINB2,PAK2,TNFAIP3,TOPORS |
| GO:0009967 | BP | positive regulation of signal transduction | 2.44E-04 | 4.78E-02 | 4.37E-01 | 1.00E+00 | 59 | CDKN1C,DLG5,HIF1A,MAL,PRR5L,PDE6H,PDGFRB,CD300A,DNAJC27,F2R,TXK,PIK3R1,OSBPL8,NUCKS1,CCL4,HES1,CCL20,FLNA,MAP2K4,MDFIC,AKAP5,G0S2,NDFIP2,CCL3L3,ZCCHC3,AREG,IGFBP3,PDGFD,PRKAA1,TNKS,IL1A,IL1B,FYN,PLK2,PSMA1,RC3H1,NCAM1,RGS9,IL18R1,SOCS2,CDC42SE2,PSME4,G3BP2,NOTCH2,RNF183,SH2D2A,PDIA3,RNF165,TGFBR3,OSM,LMNB1,CD80,MAP4K5,GZMB,PAK2,LGR6,TNFAIP3,PDCL,SH2D1A |
| GO:0000209 | BP | protein polyubiquitination | 2.61E-04 | 4.78E-02 | 4.37E-01 | 1.00E+00 | 17 | TTC3,HACE1,SHPRH,CUL3,G2E3,RNF126,TNKS,PSMA1,RC3H1,FBXW2,RNF125,PSME4,SMURF1,RNF183,RNF165,TNFAIP3,TOPORS |
| GO:0000280 | BP | nuclear division | 3.15E-04 | 4.86E-02 | 4.44E-01 | 1.00E+00 | 44 | CDKN1C,STAG1,PDGFRB,RPS6,TFDP3,NCAPH2,HIRA,ABCB1,BOD1,CEP78,HES1,CUL3,FLNA,PHLDA1,WEE1,TRIAP1,ZNF365,PRIM2,TNKS,PRKCQ,IL1A,IL1B,RIOK2,MYBL1,TJP3,PLK2,ZNF268,PSMA1,SPTBN1,ZNF207,SMC5,LPIN1,PSME4,IER3,ANGEL2,NCAPD3,CLASP1,CHMP1B,OSM,RNF2,LMNA,LMNB1,SBDS,PCNA |
| GO:0010941 | BP | regulation of cell death | 3.49E-04 | 4.91E-02 | 4.49E-01 | 1.00E+00 | 62 | DLG5,HIF1A,MAL,ERCC5,NET1,PDGFRB,RPS6,NR4A1,F2R,NAA35,PIK3R1,OLFM1,QKI,HSPA8,FLNA,MAP2K4,FNTA,PHLDA1,TRIAP1,G0S2,G2E3,HIGD1A,IGFBP3,RRN3,PRKAA1,SAP30BP,PRKCQ,IL1A,IL1B,TP53AIP1,FYN,CERKL,TCTN3,BNC2,PLK2,TNFSF9,ZNF268,NCAM1,JMY,MTRNR2L8,SOCS2,MTRNR2L9,IER3,CIAPIN1,KIR3DL2,NOTCH2,RARB,YBX1,SYNE1,PARP2,RNF183,PDIA3,TGFBR3,OSM,LMNA,EGR3,TLE1,GZMB,SERPINB2,PAK2,TNFAIP3,TOPORS |
| GO:0080134 | BP | regulation of response to stress | 4.82E-04 | 5.54E-02 | 5.07E-01 | 1.00E+00 | 54 | HIF1A,CD300A,PPP1R15A,F2R,ABCB1,TXK,PIK3R1,PLAU,HSPA8,MAP2K4,MDFIC,TRIAP1,BAG2,CST7,CCL3L3,ZNF365,ZCCHC3,POLR3F,PRKCQ,TBC1D23,IL1A,IL1B,FYN,PLK2,ELMOD2,HOPX,PSMA1,CDC42SE1,IL18RAP,HELB,RNF125,PSME4,NUAK1,IER3,SYT11,KIR2DL4,NR1D2,CLASP1,DERL2,RNF183,TGFBR3,OSM,NAMPT,LMNA,LMNB1,MAP4K5,PPP1R15B,SERPINB2,PAK2,RORA,TNFAIP3,SH2D1A,PCNA,IL27 |
| GO:0050776 | BP | regulation of immune response | 5.04E-04 | 5.54E-02 | 5.07E-01 | 1.00E+00 | 41 | PDE4D,CD300A,KIR2DS2,TXK,KLRF1,FCGR3A,PIK3R1,SPON2,CCL20,HSPA8,MAP2K4,WIPF1,ZBTB1,ZCCHC3,POLR3F,PRKCQ,IL1B,FYN,PSMA1,RC3H1,SAMSN1,IL18RAP,IL18R1,RNF125,PSME4,KIR2DL2,KIR2DL4,KIR3DL1,KIR3DL2,KLRB1,KLRC1,KLRD1,CBLB,BTN3A2,BTN2A1,CD80,PAK2,TNFAIP3,SH2D1A,IL27,SMAD7 |
| GO:0051254 | BP | positive regulation of RNA metabolic process | 1.33E-03 | 8.81E-02 | 8.05E-01 | 1.00E+00 | 56 | CDKN1C,HIF1A,PRR5L,STAG1,RBPJL,ABT1,NR4A1,PPP1R15A,F2R,TXK,PIK3R1,NUCKS1,HES1,QKI,HSPA8,SERTAD1,MDFIC,IKZF2,TRIAP1,SOX13,CREM,RBM20,ZFX,CTCF,RRN3,PRKAA1,TNKS,IL1A,IL1B,RIOK2,MYBL1,CAND1,ZNF148,ZNF268,RC3H1,SMARCAD1,SFR1,JMY,LPIN1,NR1D2,RARB,NRF1,YBX1,MED31,RFXAP,S1PR1,IKZF5,PWP1,OSM,NAMPT,EGR3,CD80,RORA,RORB,TOPORS,SMAD7 |
| GO:0031965 | CC | nuclear membrane | 6.55E-05 | 4.17E-02 | 2.95E-01 | 4.33E-02 | 18 | PDE4D,KLHDC2,NR4A1,OSBPL8,ZBTB1,WTAP,FAM169A,TNKS,TOR1AIP1,SCAI,ITPR3,LPIN1,YBX1,SYNE1,CERS6,LMNA,LMNB1,TMPO |
| GO:0000790 | CC | nuclear chromatin | 1.26E-04 | 4.17E-02 | 2.95E-01 | 8.34E-02 | 62 | ZNF627,CHAF1B,ZNF671,HIF1A,STAG1,RBPJL,TFDP3,KLF3,NR4A1,ZNF595,HIRA,TXK,NUCKS1,MLLT1,HES1,ZNF548,THAP6,ZNF567,IKZF2,ZNF680,ZBTB1,SOX13,CREM,ZFP37,ZFX,POLR3F,ZNF430,FOXP4,ZNF26,IGFBP3,CTCF,ZFP1,ZNF83,ZBTB11,LCOR,MYBL1,BNC2,SP2,ZNF148,TOX,ZNF268,HOPX,ZNF208,SFR1,ZNF25,ZNF730,ZFP82,NR1D2,NCAPD3,RARB,ZNF354A,NRF1,YBX1,CERS6,IKZF5,RNF2,EGR3,ZBED6,ZNF197,RORA,RORB,SMAD7 |
| GO:0005730 | CC | nucleolus | 1.49E-03 | 1.21E-01 | 8.53E-01 | 9.83E-01 | 47 | RPS6,ABT1,ERGIC2,TTC3,CENPP,GNL2,NUCKS1,DDX23,MLLT1,HSPA8,FLNA,MDFIC,EXOSC10,DDX31,PHLDA1,WEE1,G2E3,ZFX,SLC30A5,CTCF,RRN3,RBM34,CERKL,RNMT,SPTBN1,MAK16,ZNF207,ITPR3,NUAK1,CIAPIN1,BRWD1,ZNF354A,SYNE1,PARP2,RCN2,SAP30L,PWP1,SNORA12,SNORA2A,ZBED6,SBDS,PAFAH1B2,SNORA55,SNORA58,MPHOSPH6,CRBN,SMAD7 |
| GO:0005635 | CC | nuclear envelope | 3.06E-03 | 1.56E-01 | 1.00E+00 | 1.00E+00 | 20 | PDE4D,KLHDC2,NR4A1,OSBPL8,RGPD5,ZBTB1,WTAP,FAM169A,TNKS,TOR1AIP1,SCAI,NXT2,ITPR3,LPIN1,YBX1,SYNE1,CERS6,LMNA,LMNB1,TMPO |
| GO:0005794 | CC | Golgi apparatus | 2.06E-02 | 3.61E-01 | 1.00E+00 | 1.00E+00 | 45 | RABEPK,NCALD,MAL,MAN1A1,PDGFRB,CNST,ERGIC2,PPP1R15A,F2R,ABCB1,PIK3R1,HACE1,PITPNB,CUL3,FLNA,DDX31,NDFIP2,CST7,VPS54,SAR1A,AREG,SLC30A5,PDGFD,TNKS,TBC1D23,CUX1,CERKL,CAND1,ZNF148,SEC24A,NCAM1,JAKMIP2,RNF125,TRAPPC6B,AP3M2,TMED2,RAB2A,NOTCH2,CLASP1,SYNE1,B3GNT7,RNF183,PWP1,ZDHHC6,LGR6 |
| GO:0031967 | CC | organelle envelope | 3.89E-02 | 3.71E-01 | 1.00E+00 | 1.00E+00 | 35 | PDE4D,KLHDC2,MRPL30,NR4A1,PPP1R15A,COX5A,OSBPL8,RGPD5,TRIAP1,COQ10B,ZBTB1,WTAP,HIGD1A,GHITM,FAM169A,TNKS,TOR1AIP1,SCAI,AGPAT4,TOMM20,NXT2,ITPR3,LPIN1,C19orf12,CIAPIN1,IMMT,YBX1,SYNE1,COX18,CERS6,PDIA3,SLC25A36,LMNA,LMNB1,TMPO |
| GO:1990234 | CC | transferase complex | 4.29E-02 | 3.89E-01 | 1.00E+00 | 1.00E+00 | 24 | ERCC5,NAA35,PIK3R1,DYRK2,CUL3,FNTA,MSL1,WTAP,POLR3F,PRIM2,PRKAA1,CAND1,RNMT,INSRR,SMC5,HELB,SOCS2,RPRD2,MED31,DERL2,RNF2,TOPORS,CRBN,PCNA |
| GO:0016604 | CC | nuclear body | 1.27E-01 | 5.09E-01 | 1.00E+00 | 1.00E+00 | 21 | HIF1A,STAG1,KLHDC2,HIRA,HACE1,ZBTB1,WTAP,CSNK1A1,PRKAA1,TNKS,SMC5,YTHDC1,PSME4,ANGEL2,FNBP4,RFXAP,NAMPT,RNF2,LMNA,TOPORS,PCNA |
| GO:0098794 | CC | postsynapse | 1.58E-01 | 5.18E-01 | 1.00E+00 | 1.00E+00 | 21 | DLG5,RPS27,F2R,ADD3,CAMK2N1,SCN8A,HSPA8,FLNA,AKAP5,FNTA,PKP4,FYN,SPTBN1,NCAM1,RGS9,SYT11,DLG3,GRIN3B,STXBP5,SYNE1,PAK2 |
| GO:0048471 | CC | perinuclear region of cytoplasm | 1.58E-01 | 5.18E-01 | 1.00E+00 | 1.00E+00 | 21 | RPS6,PIK3R1,HSPA8,FLNA,AKAP5,TRIAP1,PKP4,NDFIP2,VPS54,FYN,CERKL,NXT2,ITPR3,SYT11,RAB2A,YBX1,SYNE1,TPPP,LMNA,PAK2,ANP32C |
| GO:0099513 | CC | polymeric cytoskeletal fiber | 1.95E-01 | 5.49E-01 | 1.00E+00 | 1.00E+00 | 31 | KRTAP19-2,ADD3,SLC38A2,BOD1,PARP4,JAKMIP1,HSPA8,CUL3,FLG,FLNA,AKAP5,WIPF1,CORO2A,BAG2,WDR47,CSNK1A1,TCTEX1D4,FYN,ZNF207,BFSP1,MPRIP,ITPR3,PDLIM2,CLASP1,SYNM,KRT33B,TPPP,KIF3A,ARL4C,LMNA,LMNB1 |
| GO:0000981 | MF | DNA-binding transcription factor activity, RNA polymerase II-specific | 3.29E-04 | 5.33E-02 | 3.96E-01 | 3.09E-01 | 55 | ZNF627,ZNF671,HIF1A,STAG1,RBPJL,TFDP3,KLF3,NR4A1,ZNF595,TXK,NUCKS1,MLLT1,HES1,ZNF548,THAP6,ZNF567,IKZF2,ZNF680,ZBTB1,SOX13,CREM,ZFP37,ZFX,ZNF430,FOXP4,ZNF26,CTCF,ZFP1,ZNF83,ZBTB11,LCOR,MYBL1,BNC2,SP2,ZNF148,TOX,ZNF268,HOPX,ZNF208,ZNF25,ZNF730,ZFP82,NR1D2,RARB,ZNF354A,NRF1,YBX1,CERS6,IKZF5,EGR3,ZBED6,ZNF197,RORA,RORB,SMAD7 |
| GO:0005102 | MF | signaling receptor binding | 6.71E-04 | 6.30E-02 | 4.67E-01 | 6.30E-01 | 59 | HIF1A,PDE4D,PDGFRB,NR4A1,F2R,KLRF1,PIK3R1,SPON2,CCL4,JAKMIP1,ARRDC3,CCL20,HSPA8,CUL3,FLNA,AKAP5,FNTA,CCL3L3,RNF126,FCRL6,AREG,PDGFD,IL1A,IL1B,FYN,TARM1,TNFSF9,SYTL2,MTRNR2L8,SOCS2,MTRNR2L9,LPIN1,DLG3,NMB,KIR2DL4,KIR2DS4,KIR3DL1,KIR3DL2,KLRD1,RARB,SYNE1,CBLB,CXCL1,CXCL2,CXCL3,PDIA3,S1PR1,BTN3A2,BTN2A1,TGFBR3,OSM,NAMPT,ANGPTL2,SNX25,LGR6,PCNA,CKLF,IL27,SMAD7 |
| GO:0098772 | MF | molecular function regulator | 7.88E-03 | 2.47E-01 | 1.00E+00 | 1.00E+00 | 56 | CDKN1C,MAL,PDE6H,CRIM1,NET1,PPP1R15A,ANKRD54,BOD1,CAMK2N1,PIK3R1,CCL4,CCL20,ARAP2,AGAP1,RGPD5,SMAP1,FLNA,FNTA,BAG2,CST7,CCL3L3,AREG,IGFBP3,PDGFD,IL1A,IL1B,TOR1AIP1,PHACTR1,PHACTR2,ELMOD2,TNFSF9,CDC42SE1,RGS9,ARHGAP11A,MTRNR2L8,SOCS2,MTRNR2L9,PSME4,NMB,PZP,PPP4R1,STXBP5,RALGAPB,CXCL1,CXCL2,CXCL3,OSM,NAMPT,ARHGEF33,PPP1R15B,SERPINB2,PAK2,PCNA,CKLF,IL27,RAPGEFL1 |
| GO:0044877 | MF | protein-containing complex binding | 9.21E-03 | 2.66E-01 | 1.00E+00 | 1.00E+00 | 42 | CDKN1C,HIF1A,ERCC5,F2R,ANKRD54,ADD3,HIRA,FCGR3A,PIK3R1,HES1,HSPA8,FLG,FLNA,AKAP5,WIPF1,CORO2A,GPIHBP1,CDK5RAP1,UNK,PODN,IL1B,FYN,PLK2,SPTBN1,JMY,HELB,PSME4,KLRC1,KLRD1,DSTN,RARB,CLASP1,SYNM,SYNE1,SMURF1,SAP30L,KIF3A,TGFBR3,SBDS,PDCL,PCNA,SMAD7 |
| GO:0030234 | MF | enzyme regulator activity | 1.77E-02 | 2.85E-01 | 1.00E+00 | 1.00E+00 | 34 | CDKN1C,MAL,PDE6H,CRIM1,PPP1R15A,ANKRD54,BOD1,CAMK2N1,PIK3R1,ARAP2,AGAP1,RGPD5,SMAP1,BAG2,CST7,IGFBP3,TOR1AIP1,PHACTR1,PHACTR2,ELMOD2,CDC42SE1,RGS9,ARHGAP11A,SOCS2,PSME4,PZP,PPP4R1,STXBP5,RALGAPB,CXCL1,PPP1R15B,SERPINB2,PAK2,PCNA |
| GO:0017111 | MF | nucleoside-triphosphatase activity | 2.09E-02 | 2.85E-01 | 1.00E+00 | 1.00E+00 | 42 | NET1,GPN1,GNG2,DNAJC27,F2R,ABCB1,SHPRH,GNL2,DDX23,CCL4,CCL20,HSPA8,ARAP2,AGAP1,RGPD5,SMAP1,DDX31,PKP4,BAG2,CCL3L3,SAR1A,DDX3Y,TOR1AIP1,HBS1L,ELMOD2,CDC42SE1,RGS9,SMARCAD1,ARHGAP11A,HELB,TRAPPC6B,HELZ,TMED2,RAB2A,STXBP5,RALGAPB,RECQL,NKIRAS1,CBLB,S1PR1,KIF3A,ARL4C |
| GO:0016788 | MF | hydrolase activity, acting on ester bonds | 3.47E-02 | 2.91E-01 | 1.00E+00 | 1.00E+00 | 36 | PDE4D,ERCC5,PDE6H,PDGFRB,CNST,CD300A,PPP1R15A,F2R,TXK,BOD1,PPT2,EXOSC10,IDS,ZNF365,SH2D4A,GPIHBP1,IGFBP3,SLFN13,PHACTR1,PHACTR2,SYTL2,SMARCAD1,HELB,MPRIP,LPIN1,NUAK1,ANGEL2,DLG3,CSTF2T,PPP4R1,HDDC2,PDIA3,S1PR1,PPP1R15B,PAFAH1B2,PCNA |
| GO:0016773 | MF | phosphotransferase activity, alcohol group as acceptor | 5.14E-02 | 3.38E-01 | 1.00E+00 | 1.00E+00 | 40 | CDKN1C,PDE6H,CRIM1,PDGFRB,CD300A,F2R,ANKRD54,TXK,CAMK2N1,PIK3R1,OSBPL8,MLLT1,DYRK2,SERTAD1,MAP2K4,MDFIC,WEE1,HIGD1A,CSNK1A1,PDGFD,PRKAA1,CDK5RAP1,PRKCQ,IL1B,RIOK2,FYN,CERKL,PLK2,INSRR,SOCS2,PASK,NUAK1,DLG3,CAB39L,CBLB,PAPSS2,TGFBR3,MAP4K5,PAK2,TNFAIP3 |
| GO:0003690 | MF | double-stranded DNA binding | 6.05E-02 | 3.45E-01 | 1.00E+00 | 1.00E+00 | 30 | HIF1A,ERCC5,RBPJL,KLF3,NR4A1,TXK,NUCKS1,HES1,SOX13,CREM,ZCCHC3,POLR3F,FOXP4,CTCF,RRN3,CUX1,MYBL1,SP2,ZNF148,NR1D2,RARB,NRF1,YBX1,IKZF5,LMNB1,EGR3,RORA,RORB,PCNA,BRF2 |
| GO:0016301 | MF | kinase activity | 1.05E-01 | 4.08E-01 | 1.00E+00 | 1.00E+00 | 42 | CDKN1C,HIF1A,PDE6H,CRIM1,PDGFRB,CD300A,F2R,ANKRD54,TXK,CAMK2N1,PIK3R1,OSBPL8,MLLT1,DYRK2,SERTAD1,MAP2K4,MDFIC,WEE1,HIGD1A,CSNK1A1,PDGFD,PRKAA1,CDK5RAP1,PRKCQ,IL1B,RIOK2,FYN,CERKL,PLK2,INSRR,SOCS2,PASK,NUAK1,IER3,DLG3,CAB39L,CBLB,PAPSS2,TGFBR3,MAP4K5,PAK2,TNFAIP3 |

Biological Process(BP), Cellular Component(CC) and Molecular Functions (MF)

**Table 6** Topology table for up and down regulated genes

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Regulation** | **Node** | **Degree** | **Betweenness** | **Stress** | **Closeness** | **Clustering Coefficient** |
| Up | CAPN13 | 652 | 0.306654 | 58962038 | 0.326194 | 3.77E-05 |
| Up | EGFR | 567 | 0.314014 | 164833292 | 0.375645 | 0.001022 |
| Up | ACTBL2 | 327 | 0.105362 | 90377552 | 0.343818 | 0.00287 |
| Up | ACTL8 | 242 | 0.055292 | 62615960 | 0.337131 | 0.004561 |
| Up | ERBB3 | 167 | 0.028076 | 21325814 | 0.346106 | 0.010389 |
| Up | ACTL6B | 167 | 0.037097 | 16021530 | 0.317627 | 0.01717 |
| Up | PRMT5 | 144 | 0.065191 | 27108258 | 0.328995 | 0.001845 |
| Up | RHOV | 141 | 0.042686 | 58681920 | 0.279763 | 0.004053 |
| Up | GATA4 | 140 | 0.059954 | 32831244 | 0.309893 | 0.002364 |
| Up | GNB4 | 117 | 0.034925 | 24798290 | 0.303056 | 0.008547 |
| Up | PKMYT1 | 107 | 0.034969 | 13544738 | 0.308344 | 0.004232 |
| Up | RASEF | 105 | 0.041106 | 19895824 | 0.296248 | 0.005678 |
| Up | RXFP2 | 104 | 0.008491 | 20208116 | 0.273048 | 0 |
| Up | IGFALS | 101 | 0.008953 | 14043358 | 0.28482 | 0 |
| Up | TP73 | 101 | 0.037662 | 12255510 | 0.318544 | 7.92E-04 |
| Up | NEURL1B | 101 | 0.04703 | 8540536 | 0.299244 | 1.98E-04 |
| Up | GRIN1 | 99 | 0.035441 | 14421306 | 0.303409 | 0.005154 |
| Up | LRRN4 | 96 | 0.010054 | 13892194 | 0.298973 | 0 |
| Up | LRRN2 | 94 | 0.01232 | 15281768 | 0.29724 | 0 |
| Up | MXRA5 | 92 | 0.008211 | 12850902 | 0.298067 | 0 |
| Up | LRRC30 | 91 | 0.004254 | 10208834 | 0.269131 | 0 |
| Up | MYL2 | 86 | 0.019047 | 16754438 | 0.297531 | 0 |
| Up | PRDX4 | 85 | 0.037823 | 12751816 | 0.289855 | 0 |
| Up | LHX9 | 76 | 0.030893 | 7259010 | 0.288889 | 0.007368 |
| Up | BMP7 | 72 | 0.031738 | 4118340 | 0.317654 | 0.003521 |
| Up | MYLPF | 71 | 0.006017 | 10582938 | 0.267195 | 0 |
| Up | RALYL | 70 | 0.03161 | 8071176 | 0.298459 | 0 |
| Up | WDR90 | 69 | 0.02717 | 11272320 | 0.294141 | 0.001705 |
| Up | ADCY2 | 66 | 0.014464 | 13026096 | 0.317018 | 0.00979 |
| Up | SHANK1 | 65 | 0.02351 | 3644532 | 0.303637 | 0.012019 |
| Up | FOXJ1 | 62 | 0.022194 | 20875080 | 0.273684 | 0.002115 |
| Up | CHD5 | 57 | 0.017579 | 2190656 | 0.329263 | 0.006892 |
| Up | MOS | 54 | 0.009603 | 4860098 | 0.270733 | 0.003494 |
| Up | AMPH | 52 | 0.014427 | 3902194 | 0.299786 | 0.004525 |
| Up | EPHA8 | 52 | 0.013872 | 3619700 | 0.287724 | 0 |
| Up | RBM43 | 50 | 0.017521 | 12825464 | 0.25159 | 0 |
| Up | RHPN2 | 50 | 0.047 | 5533840 | 0.320677 | 0.004898 |
| Up | KALRN | 47 | 0.010881 | 4446070 | 0.28307 | 0.00185 |
| Up | SPTBN4 | 45 | 0.009175 | 6008468 | 0.292699 | 0 |
| Up | PKDCC | 43 | 0.004338 | 1069962 | 0.26698 | 0.00443 |
| Up | YY2 | 42 | 0.022877 | 4229906 | 0.305651 | 0.005807 |
| Up | OTP | 42 | 0.003752 | 1125354 | 0.252322 | 0.001161 |
| Up | RAB3IL1 | 41 | 0.010209 | 1486180 | 0.252375 | 0.014634 |
| Up | KLC3 | 40 | 0.014916 | 10952196 | 0.281016 | 0 |
| Up | HSD3B1 | 40 | 0.020081 | 11745188 | 0.224664 | 0 |
| Up | ARHGDIG | 40 | 0.006434 | 3113394 | 0.271277 | 0.001282 |
| Up | MED18 | 36 | 0.017682 | 2917348 | 0.285737 | 0 |
| Up | DEK | 35 | 0.012732 | 3383586 | 0.303081 | 0 |
| Up | CDH5 | 35 | 0.007422 | 17240408 | 0.239442 | 0 |
| Up | TBX2 | 35 | 0.006934 | 5506140 | 0.268575 | 0.005042 |
| Up | PIH1D2 | 33 | 0.005863 | 4838248 | 0.259278 | 0 |
| Up | TJP2 | 31 | 0.012088 | 2617218 | 0.287044 | 0 |
| Up | ATP1A4 | 31 | 0.011391 | 1805764 | 0.290735 | 0.006452 |
| Up | CAPZA3 | 29 | 0.00151 | 1827682 | 0.243723 | 0 |
| Up | ATP2B3 | 28 | 0.007302 | 2097892 | 0.254385 | 0.007937 |
| Up | BIRC7 | 27 | 0.009519 | 2568466 | 0.278991 | 0 |
| Up | KIF17 | 26 | 0.008386 | 2476962 | 0.268357 | 0.015385 |
| Up | DNAL4 | 26 | 0.004303 | 22553634 | 0.218134 | 0 |
| Up | HES6 | 25 | 0.00675 | 11850042 | 0.236656 | 0 |
| Up | FERMT2 | 22 | 0.00709 | 1835264 | 0.28119 | 0 |
| Up | DCUN1D1 | 22 | 0.006913 | 2352740 | 0.276954 | 0 |
| Up | SEC14L4 | 22 | 0.006205 | 2278436 | 0.279056 | 0 |
| Up | ADRA1A | 19 | 0.006519 | 8773382 | 0.218435 | 0 |
| Up | SLC4A1 | 19 | 0.005121 | 4941792 | 0.239884 | 0 |
| Up | MYF5 | 19 | 0.002118 | 2926404 | 0.243576 | 0 |
| Up | OPN4 | 18 | 0.003301 | 4138142 | 0.226213 | 0 |
| Up | TOX2 | 18 | 0.005039 | 618616 | 0.277418 | 0.039216 |
| Up | EVPL | 18 | 0.00755 | 1628682 | 0.277164 | 0 |
| Up | POU3F3 | 17 | 0.004144 | 1493914 | 0.254581 | 0 |
| Up | COL18A1 | 17 | 0.005294 | 3740340 | 0.241235 | 0 |
| Up | ASAP3 | 17 | 0.004024 | 1505312 | 0.231832 | 0 |
| Up | GNAL | 17 | 0.004192 | 903558 | 0.276785 | 0 |
| Up | CDK5R2 | 17 | 0.001041 | 316630 | 0.258541 | 0.014706 |
| Up | FANK1 | 16 | 0.002987 | 404062 | 0.287656 | 0 |
| Up | CCR2 | 16 | 0.006793 | 10943416 | 0.228658 | 0 |
| Up | TGFA | 15 | 0.006588 | 1694838 | 0.275778 | 0.019048 |
| Up | PTGER1 | 14 | 0.002397 | 591742 | 0.231877 | 0.010989 |
| Up | NGF | 13 | 0.006025 | 3904858 | 0.215768 | 0 |
| Up | TRPV6 | 13 | 0.003984 | 1338866 | 0.282368 | 0 |
| Up | PRTN3 | 13 | 0.005503 | 2536714 | 0.227486 | 0 |
| Up | PTGDS | 12 | 0.004303 | 1720634 | 0.244739 | 0.015152 |
| Up | PHF21A | 12 | 0.002412 | 921008 | 0.254688 | 0 |
| Up | CXCL12 | 12 | 0.00521 | 1686460 | 0.215896 | 0 |
| Up | VLDLR | 12 | 0.00643 | 968194 | 0.276911 | 0 |
| Up | GRK1 | 12 | 0.002823 | 1785938 | 0.235874 | 0 |
| Up | TRIM47 | 12 | 0.002791 | 642248 | 0.280216 | 0 |
| Up | ZNF492 | 11 | 0.024123 | 1406086 | 0.317848 | 0.018182 |
| Up | TBC1D26 | 11 | 0.005488 | 3787010 | 0.14535 | 0 |
| Up | CNTN4 | 11 | 0.002685 | 1826672 | 0.230321 | 0 |
| Up | TFF1 | 11 | 0.001633 | 1158402 | 0.26026 | 0 |
| Up | ASGR1 | 11 | 0.003402 | 1715478 | 0.250551 | 0 |
| Up | GCLM | 10 | 0.003303 | 628892 | 0.276239 | 0 |
| Up | PKD2L1 | 10 | 0.001294 | 1527590 | 0.223546 | 0 |
| Up | TREH | 10 | 0.001664 | 2899390 | 0.2244 | 0 |
| Up | DHDH | 10 | 0.003919 | 896626 | 0.245085 | 0 |
| Up | SLC6A2 | 10 | 0.003347 | 859650 | 0.233348 | 0 |
| Up | PPIAL4G | 9 | 4.24E-04 | 296012 | 0.24821 | 0 |
| Up | KCNJ11 | 9 | 0.002807 | 1400038 | 0.223381 | 0 |
| Up | GRIK5 | 9 | 0.001101 | 1650680 | 0.200916 | 0 |
| Up | KITLG | 9 | 0.00345 | 450124 | 0.281255 | 0 |
| Up | MAGEL2 | 9 | 1 | 72 | 1 | 0 |
| Up | EYS | 8 | 0.002806 | 1031594 | 0.212468 | 0 |
| Up | RASAL1 | 8 | 6.47E-04 | 869494 | 0.235097 | 0 |
| Up | TET3 | 8 | 8.53E-04 | 228918 | 0.236933 | 0 |
| Up | IL13RA1 | 8 | 0.002828 | 522970 | 0.276155 | 0 |
| Up | CCDC8 | 8 | 0.001755 | 920098 | 0.246279 | 0 |
| Up | KLKB1 | 8 | 0.005694 | 1500880 | 0.217495 | 0 |
| Up | CFC1 | 8 | 7.08E-04 | 236776 | 0.249589 | 0 |
| Up | THNSL2 | 8 | 1 | 56 | 1 | 0 |
| Up | FBXL7 | 7 | 0.001798 | 705124 | 0.228514 | 0 |
| Up | TRIM72 | 7 | 0.001664 | 743130 | 0.233858 | 0 |
| Up | ANTXR1 | 7 | 0.001441 | 405254 | 0.284709 | 0 |
| Up | CPNE2 | 7 | 0.002425 | 485978 | 0.276113 | 0 |
| Up | BCAM | 7 | 0.001674 | 1124256 | 0.231729 | 0 |
| Up | OTC | 7 | 0.003294 | 912966 | 0.215206 | 0 |
| Up | OLIG1 | 6 | 0.001138 | 878462 | 0.224097 | 0 |
| Up | CORT | 6 | 0.001789 | 275866 | 0.20856 | 0 |
| Up | MUC4 | 6 | 7.03E-04 | 286166 | 0.234234 | 0 |
| Up | MYBPC3 | 6 | 0.001178 | 1271044 | 0.211394 | 0 |
| Up | FTMT | 6 | 0.002746 | 836960 | 0.224345 | 0 |
| Up | OSMR | 6 | 7.15E-04 | 213204 | 0.277143 | 0 |
| Up | CNTN3 | 6 | 6.78E-04 | 708690 | 0.226087 | 0 |
| Up | SSTR4 | 6 | 0.001498 | 4496496 | 0.206174 | 0 |
| Up | NOG | 5 | 0.001099 | 318772 | 0.244492 | 0.2 |
| Up | CCL19 | 5 | 0.001674 | 3934930 | 0.157979 | 0 |
| Up | SCARA3 | 5 | 0.001257 | 230154 | 0.276176 | 0 |
| Up | FBXW9 | 4 | 0.001048 | 191054 | 0.276302 | 0 |
| Up | SRPX2 | 4 | 0.001648 | 382572 | 0.153263 | 0 |
| Up | MYOF | 4 | 0.001213 | 186664 | 0.275988 | 0 |
| Up | RFX4 | 4 | 5.83E-04 | 252856 | 0.220432 | 0 |
| Up | SYT3 | 4 | 0.001648 | 527352 | 0.217612 | 0 |
| Up | BARHL1 | 4 | 5.54E-04 | 33362 | 0.230979 | 0 |
| Up | LCN1 | 4 | 0.001648 | 359784 | 0.183246 | 0 |
| Up | FAM189A2 | 4 | 5.55E-04 | 257134 | 0.23437 | 0 |
| Up | CXCL6 | 4 | 0.001099 | 2383324 | 0.15211 | 0 |
| Up | CYP24A1 | 4 | 8.19E-04 | 386644 | 0.22263 | 0 |
| Up | SLC38A8 | 4 | 1 | 12 | 1 | 0 |
| Up | CMYA5 | 3 | 5.57E-04 | 151990 | 0.222985 | 0 |
| Up | TMCC2 | 3 | 1.32E-04 | 29666 | 0.227173 | 0 |
| Up | C7 | 3 | 5.81E-04 | 95190 | 0.183987 | 0 |
| Up | GDNF | 3 | 0.001099 | 294734 | 0.218921 | 0 |
| Up | DNAH2 | 3 | 2.01E-04 | 1435710 | 0.257153 | 0 |
| Up | NFIB | 3 | 0.001099 | 579630 | 0.188094 | 0 |
| Up | COL9A2 | 3 | 0.001099 | 78282 | 0.194372 | 0 |
| Up | SLC22A8 | 3 | 0.001099 | 357274 | 0.183597 | 0 |
| Up | FAIM2 | 3 | 1.30E-05 | 7006 | 0.243104 | 0 |
| Up | CLEC3B | 3 | 4.23E-04 | 84484 | 0.190188 | 0 |
| Up | VIPR2 | 3 | 0.001099 | 364526 | 0.203272 | 0 |
| Up | TNNI2 | 3 | 1.23E-04 | 384472 | 0.231405 | 0 |
| Up | SEMA4G | 3 | 5.96E-04 | 84226 | 0.226947 | 0 |
| Up | THPO | 3 | 1 | 6 | 1 | 0 |
| Up | SPTSSB | 3 | 1 | 6 | 1 | 0 |
| Up | GLI2 | 2 | 0.001319 | 173220 | 0.252971 | 0 |
| Up | TRIM10 | 2 | 5.49E-04 | 41678 | 0.185572 | 0 |
| Up | COL23A1 | 2 | 5.49E-04 | 219332 | 0.204116 | 0 |
| Up | SMOC1 | 2 | 4.27E-06 | 2426 | 0.215896 | 0 |
| Up | ENO4 | 2 | 2.00E-07 | 694 | 0.256014 | 0 |
| Up | AQP10 | 2 | 5.49E-04 | 98362 | 0.191902 | 0 |
| Up | ACTG2 | 2 | 0 | 0 | 0.244066 | 1 |
| Up | KRT82 | 2 | 0.006573 | 4544256 | 0.204414 | 0 |
| Up | AQP8 | 2 | 5.49E-04 | 98362 | 0.191902 | 0 |
| Up | SCUBE1 | 2 | 1 | 2 | 1 | 0 |
| Up | CRH | 2 | 1 | 2 | 1 | 0 |
| Up | MEGF11 | 2 | 1 | 2 | 1 | 0 |
| Up | PLA2R1 | 2 | 1 | 2 | 1 | 0 |
| Up | HBM | 2 | 1 | 2 | 1 | 0 |
| Up | CES1 | 2 | 1 | 2 | 1 | 0 |
| Up | TNXB | 2 | 1 | 2 | 1 | 0 |
| Up | NPB | 2 | 1 | 2 | 1 | 0 |
| Up | GGN | 2 | 1 | 2 | 1 | 0 |
| Up | AVPR1B | 2 | 1 | 2 | 1 | 0 |
| Up | PPP1R3F | 2 | 1 | 2 | 1 | 0 |
| Up | HBQ1 | 2 | 1 | 2 | 1 | 0 |
| Up | CRYBB3 | 2 | 1 | 2 | 1 | 0 |
| Up | MYBPH | 2 | 1 | 2 | 1 | 0 |
| Up | PADI3 | 1 | 0 | 0 | 0.223959 | 0 |
| Up | SPANXN4 | 1 | 0 | 0 | 0.190916 | 0 |
| Up | SLC4A11 | 1 | 0 | 0 | 0.275862 | 0 |
| Up | PRAMEF12 | 1 | 0 | 0 | 0.275862 | 0 |
| Up | CRTAC1 | 1 | 0 | 0 | 0.174664 | 0 |
| Up | TBC1D26 | 1 | 0 | 0 | 0.245979 | 0 |
| Up | BPIFA1 | 1 | 0 | 0 | 0.194289 | 0 |
| Up | FERD3L | 1 | 0 | 0 | 0.21541 | 0 |
| Up | TPD52 | 1 | 0 | 0 | 0.213402 | 0 |
| Up | PAX6 | 1 | 0 | 0 | 0.241092 | 0 |
| Up | IGSF9B | 1 | 0 | 0 | 0.175244 | 0 |
| Up | PCSK1N | 1 | 0 | 0 | 0.20407 | 0 |
| Up | CRHR1 | 1 | 0 | 0 | 0.666667 | 0 |
| Down | FYN | 396 | 0.105452 | 48546712 | 0.367243 | 0.005293 |
| Down | PAK2 | 264 | 0.055184 | 54684676 | 0.361103 | 0.004292 |
| Down | CUL3 | 241 | 0.058179 | 32940236 | 0.339681 | 0.001729 |
| Down | RPS6 | 238 | 0.060372 | 27840050 | 0.347498 | 0.004468 |
| Down | NOTCH2 | 228 | 0.050026 | 22196420 | 0.32481 | 0.003439 |
| Down | DLG3 | 211 | 0.051598 | 15542586 | 0.350424 | 0.003972 |
| Down | PDGFRB | 208 | 0.038423 | 26914698 | 0.350592 | 0.008361 |
| Down | SMURF1 | 201 | 0.041983 | 36017478 | 0.346393 | 0.003682 |
| Down | PDE4D | 198 | 0.052364 | 13207112 | 0.348682 | 0.005691 |
| Down | PDIA3 | 169 | 0.048448 | 25439624 | 0.330706 | 0.00162 |
| Down | PLK2 | 165 | 0.035232 | 24039072 | 0.337131 | 0.005395 |
| Down | YBX1 | 158 | 0.033915 | 17537764 | 0.335562 | 0.002177 |
| Down | EXOSC10 | 145 | 0.031378 | 16416504 | 0.328225 | 0.002682 |
| Down | MLLT1 | 139 | 0.031544 | 29074196 | 0.330706 | 0 |
| Down | PRKCQ | 137 | 0.023364 | 14403612 | 0.346933 | 0.011056 |
| Down | CSNK1A1 | 129 | 0.032501 | 12832786 | 0.339704 | 0.002422 |
| Down | WEE1 | 126 | 0.023448 | 18606710 | 0.341335 | 0.012444 |
| Down | MYBL1 | 124 | 0.024886 | 59233944 | 0.290902 | 0 |
| Down | RNF2 | 123 | 0.029139 | 16573292 | 0.329854 | 0 |
| Down | PSMA1 | 122 | 0.020372 | 8145070 | 0.340155 | 0.019374 |
| Down | RBM34 | 121 | 0.021427 | 14834320 | 0.323844 | 0.003306 |
| Down | PRKAA1 | 118 | 0.023935 | 15595054 | 0.338156 | 0.002463 |
| Down | DSTN | 117 | 0.025118 | 18457556 | 0.327574 | 0.005747 |
| Down | ERCC5 | 114 | 0.024976 | 19896872 | 0.324583 | 0 |
| Down | HACE1 | 112 | 0.01916 | 13815464 | 0.335342 | 0.007883 |
| Down | LGR6 | 106 | 0.014358 | 12401116 | 0.33195 | 0.008086 |
| Down | SMAD7 | 106 | 0.023281 | 9776858 | 0.335452 | 0.004672 |
| Down | INSRR | 104 | 0.009581 | 5964292 | 0.316829 | 0.002427 |
| Down | SPATA21 | 104 | 0.015519 | 63512560 | 0.266102 | 0 |
| Down | SMC5 | 100 | 0.02301 | 14416196 | 0.322071 | 0.00202 |
| Down | GNL2 | 97 | 0.0121 | 7772006 | 0.324254 | 0.018041 |
| Down | RPS27 | 97 | 0.008008 | 5154406 | 0.326967 | 0.020404 |
| Down | TLE1 | 92 | 0.023293 | 7203624 | 0.336466 | 0.013378 |
| Down | FLNA | 92 | 0.016179 | 6518846 | 0.308932 | 0.003344 |
| Down | PODN | 91 | 0.004769 | 5665242 | 0.302774 | 0.010501 |
| Down | LMNA | 88 | 0.01989 | 8727396 | 0.335013 | 0.013584 |
| Down | NET1 | 88 | 0.010777 | 7657944 | 0.328583 | 0.017764 |
| Down | SPTBN1 | 87 | 0.016405 | 12032486 | 0.331434 | 8.02E-04 |
| Down | CBLB | 86 | 0.010699 | 4133930 | 0.338962 | 0.02052 |
| Down | CORO2A | 85 | 0.007719 | 8463390 | 0.294483 | 0.009524 |
| Down | DYRK2 | 84 | 0.013886 | 5574490 | 0.33329 | 0.004877 |
| Down | DDX31 | 83 | 0.009728 | 6291926 | 0.318405 | 0.02821 |
| Down | TXK | 81 | 0.004541 | 1861296 | 0.307318 | 0.021914 |
| Down | DLG5 | 77 | 0.016209 | 8309618 | 0.321142 | 6.84E-04 |
| Down | PWP1 | 76 | 0.010435 | 4826208 | 0.322375 | 0.026316 |
| Down | EGR3 | 76 | 0.009253 | 13457872 | 0.291001 | 0.00807 |
| Down | CLASP1 | 73 | 0.017218 | 9970264 | 0.317576 | 0 |
| Down | EXOC6B | 69 | 0.014841 | 10065172 | 0.321283 | 0 |
| Down | CTCF | 68 | 0.011138 | 9587416 | 0.334488 | 0.005707 |
| Down | RAB2A | 68 | 0.018586 | 9847190 | 0.325678 | 4.39E-04 |
| Down | PSME4 | 63 | 0.004677 | 2084118 | 0.321122 | 0.041475 |
| Down | SEC24A | 63 | 0.017154 | 6637368 | 0.325284 | 0.009729 |
| Down | HBS1L | 62 | 0.009882 | 4519014 | 0.325636 | 0.012163 |
| Down | QKI | 60 | 0.016517 | 3911472 | 0.320498 | 0.005085 |
| Down | TNKS | 58 | 0.007121 | 2623352 | 0.323885 | 0.038113 |
| Down | LMNB1 | 58 | 0.009045 | 4500318 | 0.329366 | 0.019359 |
| Down | CSTF2T | 56 | 0.011581 | 3805390 | 0.317674 | 0 |
| Down | GPN1 | 55 | 0.011606 | 7483240 | 0.319438 | 0 |
| Down | SMARCAD1 | 54 | 0.010936 | 4800428 | 0.32516 | 0 |
| Down | RIOK2 | 54 | 0.009735 | 2653844 | 0.322071 | 0.006988 |
| Down | HNRNPA0 | 52 | 0.009136 | 2142448 | 0.333247 | 0.024887 |
| Down | HES1 | 52 | 0.010492 | 4153396 | 0.334335 | 0.024133 |
| Down | MED31 | 52 | 0.007651 | 2842560 | 0.279895 | 0.006787 |
| Down | G3BP2 | 50 | 0.009999 | 3203438 | 0.325843 | 0.00898 |
| Down | TMED2 | 50 | 0.012551 | 4156746 | 0.323353 | 0.013061 |
| Down | DERL2 | 50 | 0.013624 | 4466946 | 0.317635 | 0 |
| Down | SENP6 | 49 | 0.004972 | 1569178 | 0.288005 | 0.007653 |
| Down | NAP1L5 | 49 | 0.0124 | 3356066 | 0.280863 | 8.50E-04 |
| Down | HOPX | 48 | 0.011897 | 14235916 | 0.266046 | 0 |
| Down | RBPJL | 48 | 0.004192 | 1691234 | 0.295145 | 0.027482 |
| Down | ATIC | 47 | 0.009406 | 3263566 | 0.323598 | 0.00555 |
| Down | COX5A | 46 | 0.015332 | 2722496 | 0.316789 | 0.001932 |
| Down | SCN8A | 45 | 0.008826 | 5427478 | 0.319638 | 0 |
| Down | POLR3F | 44 | 0.008577 | 3270862 | 0.316868 | 0.022199 |
| Down | PKP4 | 43 | 0.009947 | 6574832 | 0.318049 | 0 |
| Down | STAG1 | 43 | 0.005776 | 1521910 | 0.323619 | 0.022148 |
| Down | HIRA | 43 | 0.006348 | 1411662 | 0.279513 | 0.011074 |
| Down | IMMT | 41 | 0.00864 | 1373438 | 0.263499 | 0.009756 |
| Down | LONRF3 | 40 | 0.007783 | 8840770 | 0.268446 | 0 |
| Down | TOPORS | 40 | 0.004593 | 3133310 | 0.320539 | 0 |
| Down | EIF4E2 | 40 | 0.005862 | 2507102 | 0.318286 | 0 |
| Down | TOMM20 | 39 | 0.015206 | 4115000 | 0.316496 | 0.010796 |
| Down | SNIP1 | 39 | 0.00616 | 7271772 | 0.279895 | 0 |
| Down | BRF2 | 39 | 0.002957 | 1547676 | 0.263554 | 0.02834 |
| Down | DDX23 | 38 | 0.005347 | 2669360 | 0.317773 | 0 |
| Down | TFDP3 | 37 | 0.003701 | 9957248 | 0.262674 | 0 |
| Down | SMAP1 | 37 | 0.009239 | 1743068 | 0.32321 | 0.004505 |
| Down | VPS54 | 37 | 0.008465 | 15635826 | 0.215337 | 0 |
| Down | SARS2 | 36 | 0.007624 | 3490646 | 0.316691 | 0.014286 |
| Down | GPX3 | 35 | 0.00363 | 697026 | 0.274624 | 0.038655 |
| Down | BAG2 | 35 | 0.006278 | 2539808 | 0.32078 | 0 |
| Down | CHAF1B | 35 | 0.008022 | 3161480 | 0.318683 | 0.016807 |
| Down | DNAJC27 | 35 | 0.00377 | 4987600 | 0.26128 | 0 |
| Down | CHMP1B | 34 | 0.010128 | 3296842 | 0.314416 | 0 |
| Down | CIAPIN1 | 34 | 0.007999 | 4451710 | 0.315715 | 0 |
| Down | GNG2 | 33 | 0.00564 | 3323208 | 0.315695 | 0 |
| Down | MAK16 | 32 | 0.002067 | 1531290 | 0.315306 | 0.040323 |
| Down | HELB | 32 | 0.003278 | 1912934 | 0.314802 | 0 |
| Down | SBDS | 32 | 0.008835 | 3365426 | 0.316124 | 0 |
| Down | F2R | 31 | 0.007115 | 3317232 | 0.320599 | 0.004301 |
| Down | IGFBP3 | 30 | 0.004619 | 3804950 | 0.266809 | 0 |
| Down | PARP2 | 30 | 0.004479 | 1295998 | 0.318484 | 0.009195 |
| Down | ZNF148 | 29 | 0.003085 | 4028228 | 0.320639 | 0 |
| Down | GZMB | 29 | 0.004147 | 910888 | 0.284658 | 0.007389 |
| Down | UHRF1BP1 | 29 | 0.003231 | 2145074 | 0.322884 | 0.009852 |
| Down | ARHGAP11A | 28 | 0.001832 | 729186 | 0.271119 | 0.044974 |
| Down | OCLN | 28 | 0.005579 | 1600358 | 0.332856 | 0.021164 |
| Down | RRN3 | 28 | 0.004309 | 2041050 | 0.321666 | 0 |
| Down | YTHDC1 | 27 | 0.004554 | 960840 | 0.331241 | 0.022792 |
| Down | NAMPT | 27 | 0.006998 | 2207482 | 0.314126 | 0 |
| Down | ARAP2 | 26 | 0.001235 | 3971756 | 0.247378 | 0 |
| Down | RORA | 26 | 0.005497 | 1744676 | 0.318881 | 0 |
| Down | PLAU | 25 | 0.006556 | 2088624 | 0.31732 | 0 |
| Down | ITPR3 | 24 | 0.005184 | 1868728 | 0.317556 | 0 |
| Down | RGS9 | 24 | 0.002706 | 4294600 | 0.234236 | 0.003623 |
| Down | SAP30BP | 23 | 0.003617 | 1570642 | 0.31801 | 0 |
| Down | SLC30A5 | 23 | 0.006588 | 2505014 | 0.314474 | 0 |
| Down | ARRDC3 | 23 | 0.002941 | 678786 | 0.32603 | 0.007905 |
| Down | KLF3 | 23 | 9.82E-04 | 2363110 | 0.262836 | 0 |
| Down | RARB | 22 | 0.004231 | 965842 | 0.278237 | 0.004329 |
| Down | FTH1 | 22 | 0.004511 | 1680426 | 0.315832 | 0 |
| Down | OSBPL8 | 22 | 0.011694 | 2888140 | 0.314474 | 0 |
| Down | ANKRD54 | 22 | 0.001455 | 4450180 | 0.262701 | 0 |
| Down | MSL1 | 21 | 9.08E-04 | 909020 | 0.243125 | 0 |
| Down | IKZF5 | 21 | 0.003148 | 6823362 | 0.236443 | 0 |
| Down | PPT2 | 21 | 0.00176 | 409082 | 0.258144 | 0.042857 |
| Down | ABT1 | 21 | 0.002498 | 5661782 | 0.230731 | 0 |
| Down | IL1B | 21 | 0.004135 | 678764 | 0.287455 | 0.014286 |
| Down | MAP4K5 | 21 | 0.003823 | 1678848 | 0.317753 | 0 |
| Down | SH2D1A | 20 | 0.00212 | 592918 | 0.33122 | 0.063158 |
| Down | SIKE1 | 20 | 0.00402 | 4128542 | 0.232555 | 0 |
| Down | TRAPPC6B | 20 | 0.006301 | 2606158 | 0.314358 | 0 |
| Down | TMPO | 20 | 0.00265 | 913362 | 0.322863 | 0.052632 |
| Down | GMDS | 19 | 0.004445 | 622732 | 0.318168 | 0.040936 |
| Down | SP2 | 19 | 0.002549 | 3779572 | 0.24933 | 0 |
| Down | CUX1 | 19 | 0.002454 | 2408928 | 0.26124 | 0 |
| Down | FNTA | 19 | 0.003744 | 1776698 | 0.317084 | 0 |
| Down | PEX13 | 19 | 0.00523 | 4632208 | 0.241884 | 0 |
| Down | RNF126 | 19 | 0.002204 | 1250650 | 0.319658 | 0 |
| Down | PPP4R1 | 18 | 0.00272 | 1198832 | 0.318524 | 0 |
| Down | PHF20L1 | 18 | 0.002407 | 1550464 | 0.319219 | 0 |
| Down | ZFP1 | 18 | 0.0012 | 2034902 | 0.317871 | 0 |
| Down | TOX | 18 | 0.001398 | 574978 | 0.277453 | 0 |
| Down | ZBTB11 | 18 | 9.87E-04 | 2154034 | 0.317221 | 0 |
| Down | USP24 | 18 | 0.004332 | 1641314 | 0.316398 | 0 |
| Down | PPP1R15A | 18 | 0.001874 | 467478 | 0.279117 | 0 |
| Down | SYNE1 | 17 | 0.002015 | 1099810 | 0.321626 | 0.044118 |
| Down | CERKL | 17 | 0.005493 | 1446128 | 0.195546 | 0 |
| Down | CRIM1 | 17 | 0.005168 | 2053316 | 0.224203 | 0 |
| Down | ANGEL2 | 16 | 0.003433 | 857418 | 0.314338 | 0.008333 |
| Down | S1PR1 | 16 | 0.001807 | 624668 | 0.334029 | 0.1 |
| Down | NUAK1 | 16 | 0.001308 | 471522 | 0.321101 | 0.025 |
| Down | GRIN3B | 16 | 0.001526 | 374320 | 0.263839 | 0.016667 |
| Down | ERGIC2 | 15 | 0.002508 | 1216552 | 0.31457 | 0 |
| Down | HELZ | 15 | 0.001476 | 1081740 | 0.317202 | 0 |
| Down | RNF125 | 15 | 0.001428 | 897114 | 0.315093 | 0 |
| Down | SERTAD1 | 14 | 0.002851 | 1288186 | 0.318504 | 0 |
| Down | NR1D2 | 14 | 0.002116 | 3559708 | 0.237144 | 0 |
| Down | AGAP1 | 14 | 0.001775 | 2222778 | 0.246604 | 0 |
| Down | ZNF25 | 14 | 7.76E-04 | 1657718 | 0.315054 | 0 |
| Down | PAFAH1B2 | 13 | 0.003621 | 1042412 | 0.313165 | 0 |
| Down | ZNF208 | 13 | 8.42E-04 | 1586336 | 0.315773 | 0 |
| Down | ZNF627 | 13 | 6.59E-04 | 1455134 | 0.315481 | 0.012821 |
| Down | ZNF354A | 13 | 4.30E-04 | 1449576 | 0.315112 | 0 |
| Down | CCNDBP1 | 13 | 0.001508 | 619056 | 0.319199 | 0 |
| Down | TGFBR3 | 13 | 0.002502 | 2421290 | 0.227128 | 0.038462 |
| Down | ADAM12 | 12 | 0.001376 | 1202670 | 0.251375 | 0 |
| Down | PDLIM2 | 12 | 6.56E-04 | 463990 | 0.270446 | 0.030303 |
| Down | PHLDA1 | 12 | 0.002132 | 806582 | 0.318247 | 0 |
| Down | CRBN | 12 | 0.001243 | 374810 | 0.321687 | 0.015152 |
| Down | TRIAP1 | 11 | 0.002033 | 2753672 | 0.240668 | 0 |
| Down | ZNF728 | 11 | 2.86E-04 | 1328314 | 0.314918 | 0 |
| Down | ZNF207 | 11 | 6.45E-04 | 396120 | 0.317733 | 0 |
| Down | ZFP82 | 11 | 3.97E-04 | 2507628 | 0.219051 | 0 |
| Down | AKTIP | 11 | 0.003136 | 2849464 | 0.238481 | 0 |
| Down | CENPP | 11 | 0.003603 | 892884 | 0.313089 | 0 |
| Down | FLG | 11 | 0.001616 | 1752656 | 0.244449 | 0 |
| Down | CNST | 11 | 0.003128 | 1773750 | 0.208344 | 0 |
| Down | WTAP | 11 | 0.00259 | 763788 | 0.314011 | 0 |
| Down | ZNF548 | 11 | 2.86E-04 | 1328314 | 0.314918 | 0 |
| Down | ZNF571 | 11 | 2.86E-04 | 1328314 | 0.314918 | 0 |
| Down | ZNF671 | 11 | 2.86E-04 | 1328314 | 0.314918 | 0 |
| Down | AGPAT4 | 11 | 0.002773 | 2400246 | 0.22439 | 0 |
| Down | ZNF680 | 11 | 2.86E-04 | 1328314 | 0.314918 | 0 |
| Down | KLHDC2 | 11 | 7.84E-04 | 352424 | 0.313319 | 0 |
| Down | OSM | 11 | 0.003528 | 1813050 | 0.22383 | 0 |
| Down | PAPSS2 | 10 | 0.001453 | 541862 | 0.314609 | 0 |
| Down | SH2D2A | 10 | 1.10E-04 | 82488 | 0.262823 | 0 |
| Down | PARP4 | 10 | 0.001255 | 416550 | 0.313242 | 0 |
| Down | FCGR3A | 10 | 0.001233 | 1782396 | 0.227521 | 0 |
| Down | ZNF26 | 10 | 6.45E-06 | 16220 | 0.219032 | 0 |
| Down | DNAJC8 | 10 | 0.001314 | 639784 | 0.316672 | 0 |
| Down | ZNF430 | 10 | 6.45E-06 | 16220 | 0.219032 | 0 |
| Down | IER3 | 10 | 0.001651 | 1866994 | 0.246272 | 0 |
| Down | PDCL | 10 | 1.36E-04 | 120214 | 0.23675 | 0 |
| Down | SYNM | 9 | 0.002107 | 758626 | 0.314165 | 0 |
| Down | STXBP5 | 9 | 7.82E-04 | 1439888 | 0.197553 | 0 |
| Down | PDE6H | 9 | 0.001179 | 1002790 | 0.211154 | 0.027778 |
| Down | SH2D4A | 9 | 0.001864 | 424658 | 0.316593 | 0.027778 |
| Down | IL1A | 9 | 0.001604 | 665454 | 0.211555 | 0 |
| Down | NXT2 | 9 | 5.11E-04 | 363390 | 0.232925 | 0 |
| Down | NAA35 | 8 | 0.0025 | 645396 | 0.312974 | 0 |
| Down | BRWD1 | 8 | 8.33E-04 | 154192 | 0.322518 | 0.071429 |
| Down | PTS | 8 | 9.17E-04 | 370540 | 0.314203 | 0 |
| Down | RABEPK | 7 | 3.74E-04 | 207514 | 0.313395 | 0 |
| Down | AMD1 | 7 | 0.002045 | 517604 | 0.312936 | 0 |
| Down | SYT11 | 7 | 9.94E-04 | 139054 | 0.319698 | 0.095238 |
| Down | TCTEX1D4 | 7 | 0.001289 | 649770 | 0.213889 | 0.142857 |
| Down | CD80 | 7 | 0.001953 | 785056 | 0.215528 | 0 |
| Down | FNBP4 | 7 | 2.91E-04 | 42564 | 0.286923 | 0.047619 |
| Down | RALGAPB | 7 | 0.001077 | 329180 | 0.313127 | 0 |
| Down | MPHOSPH6 | 7 | 3.21E-05 | 5850 | 0.251387 | 0.238095 |
| Down | SLC38A2 | 7 | 0.001953 | 466180 | 0.313741 | 0.047619 |
| Down | HSPA8 | 7 | 6.34E-04 | 284038 | 0.268545 | 0.047619 |
| Down | JOSD1 | 7 | 2.61E-04 | 98652 | 0.313184 | 0 |
| Down | NCAPD3 | 6 | 7.40E-04 | 243894 | 0.312897 | 0.266667 |
| Down | SARDH | 6 | 4.35E-04 | 400516 | 0.221018 | 0 |
| Down | CST7 | 6 | 4.38E-04 | 83086 | 0.254196 | 0.066667 |
| Down | MPRIP | 6 | 6.30E-04 | 231100 | 0.314783 | 0 |
| Down | RPRD2 | 6 | 4.17E-04 | 814094 | 0.232629 | 0 |
| Down | NUCKS1 | 6 | 0.001313 | 326444 | 0.312993 | 0 |
| Down | MAL | 6 | 1.93E-05 | 17332 | 0.240442 | 0 |
| Down | NCAPH2 | 6 | 7.40E-04 | 243894 | 0.312897 | 0.266667 |
| Down | SAP30L | 6 | 7.94E-04 | 1625714 | 0.225735 | 0 |
| Down | TNFSF9 | 6 | 0.001188 | 532902 | 0.216962 | 0 |
| Down | PTGER2 | 6 | 0.001181 | 655202 | 0.224281 | 0 |
| Down | ADHFE1 | 6 | 1 | 30 | 1 | 0 |
| Down | PCNA | 5 | 5.77E-04 | 266954 | 0.259374 | 0 |
| Down | TPPP | 5 | 4.00E-04 | 351250 | 0.24193 | 0 |
| Down | BNC2 | 5 | 0.001173 | 744410 | 0.20825 | 0 |
| Down | CXCL1 | 5 | 0.00173 | 1286616 | 0.211442 | 0 |
| Down | MAPK1IP1L | 5 | 0.001178 | 264274 | 0.199175 | 0 |
| Down | PRR5L | 5 | 3.93E-04 | 808996 | 0.23043 | 0 |
| Down | KIR2DL4 | 5 | 0.001167 | 354086 | 0.313127 | 0 |
| Down | PCMTD2 | 5 | 2.38E-04 | 96372 | 0.312859 | 0 |
| Down | RNF165 | 5 | 4.26E-04 | 87894 | 0.256849 | 0.1 |
| Down | COQ10B | 5 | 0.001562 | 646804 | 0.203337 | 0 |
| Down | RFXAP | 5 | 4.43E-04 | 450926 | 0.218127 | 0 |
| Down | PASK | 5 | 7.32E-04 | 233334 | 0.277242 | 0.1 |
| Down | CDK5RAP1 | 5 | 5.60E-04 | 308180 | 0.315268 | 0 |
| Down | G2E3 | 5 | 0.001206 | 298256 | 0.312859 | 0 |
| Down | CXCL2 | 4 | 6.40E-04 | 360984 | 0.198549 | 0 |
| Down | HIGD1A | 4 | 0.001117 | 276808 | 0.313223 | 0 |
| Down | JMY | 4 | 4.49E-04 | 276136 | 0.316593 | 0 |
| Down | JAKMIP1 | 4 | 7.81E-04 | 859834 | 0.21611 | 0 |
| Down | C11orf49 | 4 | 0.001172 | 279042 | 0.312821 | 0 |
| Down | CCL20 | 4 | 7.84E-04 | 521560 | 0.228476 | 0 |
| Down | GFOD1 | 4 | 7.83E-04 | 460628 | 0.213719 | 0 |
| Down | CEP78 | 4 | 8.01E-04 | 203802 | 0.312821 | 0 |
| Down | S1PR5 | 4 | 5.99E-04 | 580350 | 0.211442 | 0 |
| Down | NCAM1 | 4 | 3.03E-04 | 298666 | 0.2752 | 0.166667 |
| Down | BTN2A1 | 4 | 0.001172 | 279042 | 0.312821 | 0 |
| Down | AES | 4 | 6.40E-05 | 34040 | 0.265137 | 0.666667 |
| Down | TBC1D23 | 3 | 4.18E-04 | 108480 | 0.312783 | 0 |
| Down | TP53AIP1 | 3 | 3.97E-04 | 404200 | 0.233339 | 0 |
| Down | NR4A1 | 3 | 5.58E-05 | 51080 | 0.252815 | 0 |
| Down | IL27 | 3 | 7.81E-04 | 231218 | 0.21014 | 0 |
| Down | CMC1 | 3 | 7.81E-04 | 428270 | 0.194987 | 0 |
| Down | RECQL | 3 | 2.46E-05 | 26646 | 0.250428 | 0 |
| Down | ANGPTL2 | 3 | 3.91E-04 | 204176 | 0.213746 | 0 |
| Down | SFR1 | 3 | 4.17E-04 | 202044 | 0.222943 | 0 |
| Down | MRPL30 | 3 | 7.81E-04 | 241490 | 0.201401 | 0 |
| Down | PHACTR1 | 3 | 5.72E-05 | 15406 | 0.230098 | 0 |
| Down | CAB39L | 3 | 1.79E-05 | 21854 | 0.250183 | 0 |
| Down | NMB | 3 | 1 | 6 | 1 | 0 |
| Down | SLC25A36 | 3 | 1 | 6 | 1 | 0 |
| Down | PAPD5 | 2 | 1.95E-05 | 23894 | 0.251363 | 0 |
| Down | RUFY2 | 2 | 3.00E-08 | 2 | 0.214005 | 0 |
| Down | TTC39B | 2 | 3.61E-06 | 4664 | 0.312744 | 0 |
| Down | WIPF1 | 2 | 0 | 0 | 0.274124 | 1 |
| Down | TOR1AIP1 | 2 | 0 | 0 | 0.251696 | 1 |
| Down | ZDHHC6 | 2 | 4.20E-05 | 19842 | 0.312783 | 0 |
| Down | BFSP1 | 2 | 3.91E-04 | 197192 | 0.215202 | 0 |
| Down | KIR3DL1 | 2 | 3.91E-04 | 316226 | 0.223948 | 0 |
| Down | EIF1AX | 2 | 0 | 0 | 0.258131 | 1 |
| Down | KIF3A | 2 | 1.82E-05 | 3396 | 0.245622 | 0 |
| Down | SAR1A | 2 | 0 | 0 | 0.247678 | 1 |
| Down | ADSS | 2 | 2.41E-04 | 297514 | 0.25294 | 0 |
| Down | ADD3 | 2 | 9.14E-06 | 6034 | 0.313395 | 0 |
| Down | DDX3Y | 2 | 9.99E-06 | 7902 | 0.244682 | 0 |
| Down | TRIM61 | 2 | 2.42E-06 | 880 | 0.202476 | 0 |
| Down | ELMOD2 | 2 | 1.69E-05 | 25476 | 0.312936 | 0 |
| Down | KBTBD2 | 2 | 1.78E-05 | 27498 | 0.312821 | 0 |
| Down | CXCL3 | 2 | 3.00E-08 | 2 | 0.149801 | 0 |
| Down | IL18RAP | 2 | 3.91E-04 | 109130 | 0.2118 | 0 |
| Down | TNFAIP3 | 2 | 2.69E-06 | 1270 | 0.250514 | 0 |
| Down | KLRB1 | 2 | 3.91E-04 | 185474 | 0.215048 | 0 |
| Down | NDFIP2 | 2 | 6.10E-05 | 91974 | 0.278706 | 0 |
| Down | ATP5L2 | 1 | 0 | 0 | 0.208556 | 0 |
| Down | ARL4C | 1 | 0 | 0 | 0.244274 | 0 |
| Down | IKZF2 | 1 | 0 | 0 | 0.191236 | 0 |
| Down | BTN3A2 | 1 | 0 | 0 | 0.312706 | 0 |
| Down | MXRA7 | 1 | 0 | 0 | 0.312706 | 0 |
| Down | FAM169A | 1 | 0 | 0 | 0.312706 | 0 |
| Down | IDI1 | 1 | 0 | 0 | 0.312706 | 0 |
| Down | NYNRIN | 1 | 0 | 0 | 0.312706 | 0 |
| Down | SLC17A5 | 1 | 0 | 0 | 0.312706 | 0 |
| Down | GHITM | 1 | 0 | 0 | 0.312706 | 0 |
| Down | ZNF365 | 1 | 0 | 0 | 0.200188 | 0 |
| Down | MAN1A1 | 1 | 0 | 0 | 0.196394 | 0 |
| Down | JAKMIP2 | 1 | 0 | 0 | 0.241042 | 0 |
| Down | PDGFD | 1 | 0 | 0 | 0.259597 | 0 |
| Down | HIF1A | 1 | 0 | 0 | 0.241793 | 0 |
| Down | CD300A | 1 | 0 | 0 | 0.21475 | 0 |
| Down | KIR3DL2 | 1 | 0 | 0 | 0.199082 | 0 |
| Down | AKAP5 | 1 | 0 | 0 | 0.258548 | 0 |
| Down | BOD1 | 1 | 0 | 0 | 0.312706 | 0 |
| Down | CEP120 | 1 | 0 | 0 | 0.312706 | 0 |
| Down | SERPINB2 | 1 | 0 | 0 | 0.240894 | 0 |
| Down | PAPD4 | 1 | 0 | 0 | 0.247128 | 0 |
| Down | JPH3 | 1 | 0 | 0 | 0.218099 | 0 |
| Down | ABCB1 | 1 | 0 | 0 | 0.24805 | 0 |
| Down | CREM | 1 | 0 | 0 | 0.253579 | 0 |
| Down | SNX25 | 1 | 0 | 0 | 0.253579 | 0 |
| Down | CKLF | 1 | 0 | 0 | 0.312706 | 0 |
| Down | MAP2K4 | 1 | 0 | 0 | 0.236029 | 0 |
| Down | ZCCHC11 | 1 | 0 | 0 | 0.247128 | 0 |
| Down | LPIN1 | 1 | 0 | 0 | 0.183273 | 0 |

**Table 7** miRNA - target gene interaction table

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Regulation** | **Target Genes** | **Degree** | **MicroRNA** | **Regulation** | **Target Genes** | **Degree** | **MicroRNA** |
| Up | TRIM72 | 123 | hsa-mir-4537 | Down | PPP1R15B | 168 | hsa-mir-7150 |
| Up | TET3 | 105 | hsa-mir-3148 | Down | WEE1 | 167 | hsa-mir-3926 |
| Up | NFIB | 89 | hsa-mir-4517 | Down | RPRD2 | 152 | hsa-mir-4452 |
| Up | SLC19A3 | 85 | hsa-mir-4500 | Down | LCOR | 146 | hsa-mir-4310 |
| Up | SMOC1 | 80 | hsa-mir-6133 | Down | SAR1A | 145 | hsa-mir-5698 |
| Up | ADM | 77 | hsa-mir-3188 | Down | PAFAH1B2 | 138 | hsa-mir-7705 |
| Up | VLDLR | 76 | hsa-mir-3973 | Down | ZNF207 | 118 | hsa-mir-5096 |
| Up | SLC38A1 | 73 | hsa-mir-6124 | Down | DYRK2 | 118 | hsa-mir-4686 |
| Up | SRCIN1 | 73 | hsa-mir-4706 | Down | EIF1AX | 114 | hsa-mir-6076 |
| Up | SHISA6 | 71 | hsa-mir-4459 | Down | ENPP5 | 114 | hsa-mir-4459 |
| Up | MED18 | 64 | hsa-mir-3652 | Down | PARP2 | 112 | hsa-mir-4330 |
| Up | INMT | 64 | hsa-mir-6745 | Down | RORA | 110 | hsa-mir-8076 |
| Up | TM4SF5 | 63 | hsa-mir-4454 | Down | ERGIC2 | 98 | hsa-mir-9500 |
| Up | DEK | 61 | hsa-mir-6083 | Down | MLLT1 | 95 | hsa-mir-4270 |
| Up | SLC4A1 | 57 | hsa-mir-6131 | Down | NUCKS1 | 94 | hsa-mir-4499 |
| Up | OSMR | 54 | hsa-mir-4420 | Down | YTHDC1 | 91 | hsa-mir-5693 |
| Up | ZNF286A | 53 | hsa-mir-7703 | Down | AMD1 | 87 | hsa-mir-8055 |
| Up | GDNF | 51 | hsa-mir-4282 | Down | UNK | 87 | hsa-mir-4533 |
| Up | YY2 | 49 | hsa-mir-4457 | Down | QKI | 86 | hsa-mir-3684 |
| Up | IL17REL | 46 | hsa-mir-4303 | Down | LONRF3 | 82 | hsa-mir-4463 |
| Up | LEAP2 | 46 | hsa-mir-8062 | Down | HNRNPA0 | 82 | hsa-mir-4657 |
| Up | STAC2 | 45 | hsa-mir-4480 | Down | CHAF1B | 80 | hsa-mir-4421 |
| Up | TPD52 | 44 | hsa-mir-4473 | Down | PAK2 | 79 | hsa-mir-4311 |
| Up | RBM43 | 44 | hsa-mir-4499 | Down | LMNB1 | 78 | hsa-mir-5047 |
| Up | NUDT16 | 44 | hsa-mir-4330 | Down | G3BP2 | 77 | hsa-mir-3662 |
| Up | BEST3 | 43 | hsa-mir-4539 | Down | NRF1 | 77 | hsa-mir-4779 |
| Up | NEURL1B | 42 | hsa-mir-5188 | Down | TOMM20 | 76 | hsa-mir-5186 |
| Up | COL9A2 | 42 | hsa-mir-2113 | Down | SEC24A | 75 | hsa-mir-5696 |
| Up | SLC29A4 | 41 | hsa-mir-3122 | Down | SLC38A2 | 74 | hsa-mir-3666 |
| Up | TRIM10 | 41 | hsa-mir-1825 | Down | COX18 | 74 | hsa-mir-3122 |
| Up | SRPX2 | 40 | hsa-mir-4307 | Down | HIF1A | 72 | hsa-mir-1322 |
| Up | HES6 | 40 | hsa-mir-4784 | Down | CAND1 | 70 | hsa-mir-5095 |
| Up | BARHL1 | 39 | hsa-mir-4488 | Down | MPRIP | 69 | hsa-mir-4696 |
| Up | ADCYAP1R1 | 37 | hsa-mir-6074 | Down | SLC25A36 | 69 | hsa-mir-4465 |
| Up | TGFA | 36 | hsa-mir-1539 | Down | ZCCHC3 | 68 | hsa-mir-4500 |
| Up | LHFPL3 | 36 | hsa-mir-4271 | Down | CSNK1A1 | 68 | hsa-mir-1297 |
| Up | TMEM184B | 35 | hsa-mir-4326 | Down | FBXW2 | 67 | hsa-mir-6087 |
| Up | SHROOM4 | 35 | hsa-mir-2392 | Down | TGFBR3 | 67 | hsa-mir-4458 |
| Up | SEMA4G | 34 | hsa-mir-7515 | Down | SIKE1 | 67 | hsa-mir-2054 |
| Up | C20orf144 | 34 | hsa-mir-1976 | Down | CEP120 | 65 | hsa-mir-4654 |
| Up | NMNAT2 | 31 | hsa-mir-5572 | Down | CUL3 | 65 | hsa-mir-1265 |
| Up | FBXL7 | 31 | hsa-mir-4461 | Down | TNFAIP3 | 65 | hsa-mir-4635 |
| Up | ODF4 | 30 | hsa-mir-3666 | Down | DNAJC8 | 64 | hsa-mir-5572 |
| Up | IGSF9B | 30 | hsa-mir-8052 | Down | CRIM1 | 64 | hsa-mir-4521 |
| Up | LCE1A | 30 | hsa-mir-5706 | Down | HACE1 | 63 | hsa-mir-4306 |
| Up | KCNJ11 | 30 | hsa-mir-4642 | Down | CHMP1B | 62 | hsa-mir-3926 |
| Up | GLI2 | 29 | hsa-mir-4464 | Down | JMY | 61 | hsa-mir-4295 |
| Up | FXYD1 | 29 | hsa-mir-3665 | Down | ABT1 | 60 | hsa-mir-6132 |
| Up | ERBB3 | 28 | hsa-mir-4698 | Down | KLRD1 | 60 | hsa-mir-5047 |
| Up | SEC14L4 | 28 | hsa-mir-4686 | Down | TXK | 60 | hsa-mir-3159 |
| Up | GNAL | 27 | hsa-mir-759 | Down | MYBL1 | 59 | hsa-mir-6130 |
| Up | GNB4 | 27 | hsa-mir-5693 | Down | KIF3A | 59 | hsa-mir-3915 |
| Up | CDH5 | 27 | hsa-mir-544a | Down | BNC2 | 58 | hsa-mir-2278 |
| Up | POU3F3 | 25 | hsa-mir-4467 | Down | MAP2K4 | 58 | hsa-mir-8082 |
| Up | EGFR | 24 | hsa-mir-133b | Down | PRKAA1 | 57 | hsa-mir-4491 |
| Up | BTNL3 | 24 | hsa-mir-6086 | Down | SYNM | 57 | hsa-mir-7706 |
| Up | FERMT2 | 23 | hsa-mir-4299 | Down | RNF165 | 57 | hsa-mir-3139 |
| Up | PAX6 | 23 | hsa-mir-599 | Down | ZNF268 | 56 | hsa-mir-4439 |
| Up | TM6SF2 | 23 | hsa-mir-4654 | Down | MXRA7 | 56 | hsa-mir-4522 |
| Up | BMP7 | 22 | hsa-mir-637 | Down | GTDC1 | 56 | hsa-mir-4287 |
| Up | ADCY2 | 22 | hsa-mir-5698 | Down | TTC39B | 56 | hsa-mir-6086 |
| Up | ENO4 | 22 | hsa-mir-3609 | Down | TNFSF9 | 55 | hsa-mir-4780 |
| Up | ANTXR1 | 21 | hsa-mir-3909 | Down | IKZF2 | 55 | hsa-mir-4301 |
| Up | ST6GAL2 | 21 | hsa-mir-4306 | Down | G2E3 | 54 | hsa-mir-3973 |
| Up | DIO2 | 21 | hsa-mir-5193 | Down | BRWD1 | 54 | hsa-mir-3666 |
| Up | DCUN1D1 | 18 | hsa-mir-569 | Down | HSPA8 | 53 | hsa-mir-3609 |
| Up | KITLG | 18 | hsa-mir-4263 | Down | ZNF148 | 53 | hsa-mir-4484 |
| Up | CPNE2 | 18 | hsa-mir-3916 | Down | RUFY2 | 53 | hsa-mir-4477b |
| Up | MUC4 | 18 | hsa-mir-3660 | Down | TOR1AIP1 | 53 | hsa-mir-7977 |
| Up | TBX2 | 18 | hsa-mir-8089 | Down | ZFX | 53 | hsa-mir-4257 |
| Up | COL23A1 | 18 | hsa-mir-5095 | Down | NOTCH2 | 52 | hsa-mir-4274 |
| Up | GCLM | 17 | hsa-mir-3155b | Down | PDE4D | 51 | hsa-mir-4422 |
| Up | HOXD3 | 17 | hsa-mir-8072 | Down | MAPK1IP1L | 51 | hsa-mir-4478 |
| Up | KRT32 | 17 | hsa-mir-1470 | Down | BTN3A2 | 50 | hsa-mir-7641 |
| Up | LY6H | 17 | hsa-mir-4730 | Down | ZNF83 | 50 | hsa-mir-4452 |
| Up | SV2C | 17 | hsa-mir-526a | Down | CLASP1 | 49 | hsa-mir-3960 |
| Up | RASEF | 16 | hsa-mir-5700 | Down | IKZF5 | 49 | hsa-mir-548y |
| Up | SLC17A5 | 16 | hsa-mir-4255 | Down | CIAPIN1 | 49 | hsa-mir-3689d |
| Up | ASGR1 | 16 | hsa-mir-623 | Down | PIK3R1 | 48 | hsa-mir-6860 |
| Up | BCAM | 16 | hsa-mir-6087 | Down | IDS | 48 | hsa-mir-4430 |
| Up | CAPN13 | 16 | hsa-mir-1260a | Down | POLR3F | 48 | hsa-mir-1183 |
| Up | CYP24A1 | 15 | hsa-mir-4666b | Down | SLC30A5 | 48 | hsa-mir-6134 |
| Up | COL18A1 | 15 | hsa-mir-661 | Down | PRIM2 | 47 | hsa-mir-4487 |
| Up | GPRIN2 | 14 | hsa-mir-548s | Down | PHACTR2 | 47 | hsa-mir-5692c |
| Up | FAIM2 | 14 | hsa-mir-1299 | Down | ZFP1 | 47 | hsa-mir-3921 |
| Up | ATP2B3 | 14 | hsa-mir-5193 | Down | CDC42SE1 | 46 | hsa-mir-4516 |
| Up | CXCL12 | 13 | hsa-mir-6072 | Down | SMAD7 | 46 | hsa-mir-646 |
| Up | TMCC2 | 13 | hsa-mir-4450 | Down | ARAP2 | 46 | hsa-mir-1305 |
| Up | TP73 | 13 | hsa-mir-4429 | Down | ZNF208 | 46 | hsa-mir-4307 |
| Up | CNTN4 | 13 | hsa-mir-4504 | Down | ARL4C | 46 | hsa-mir-8485 |
| Up | TMEM50B | 12 | hsa-mir-5692a | Down | THAP6 | 44 | hsa-mir-548n |
| Up | ACTBL2 | 12 | hsa-mir-599 | Down | ZNF548 | 43 | hsa-mir-3911 |
| Up | FIBCD1 | 12 | hsa-mir-4285 | Down | GHITM | 43 | hsa-mir-5700 |
| Up | JAKMIP3 | 12 | hsa-mir-4421 | Down | HBS1L | 43 | hsa-mir-5572 |
| Up | KALRN | 12 | hsa-mir-8485 | Down | UHRF1BP1 | 42 | hsa-mir-4516 |
| Up | CSMD1 | 12 | hsa-mir-3924 | Down | NR1D2 | 42 | hsa-mir-520b |
| Up | RHOV | 11 | hsa-mir-15a-5p | Down | RBM20 | 41 | hsa-mir-5680 |
| Up | PROM1 | 11 | hsa-mir-4452 | Down | KLF3 | 41 | hsa-mir-8086 |
| Up | MAGEL2 | 11 | hsa-mir-4719 | Down | SP2 | 41 | hsa-mir-6129 |
| Up | SCUBE1 | 11 | hsa-mir-4420 | Down | DERL2 | 41 | hsa-mir-8059 |
| Up | PROM2 | 11 | hsa-mir-3689d | Down | CAMK2N1 | 40 | hsa-mir-6072 |
| Up | LHX9 | 10 | hsa-mir-6895-3p | Down | SMARCAD1 | 39 | hsa-mir-4443 |
| Up | PADI3 | 10 | hsa-mir-6888-3p | Down | PEX13 | 39 | hsa-mir-573 |
| Up | CCR2 | 10 | hsa-mir-618 | Down | KLRC3 | 39 | hsa-mir-559 |
| Up | RNF207 | 10 | hsa-mir-4321 | Down | MDFIC | 38 | hsa-mir-548k |
| Up | PPP1R3F | 10 | hsa-mir-548n | Down | F2R | 37 | hsa-mir-4466 |
| Up | PKMYT1 | 9 | hsa-mir-339-5p | Down | ARHGAP11A | 37 | hsa-mir-548ag |
| Up | HSD3B1 | 9 | hsa-mir-4729 | Down | MAK16 | 36 | hsa-mir-320b |
| Up | PAX8 | 9 | hsa-mir-3200-5p | Down | ZDHHC6 | 36 | hsa-mir-4471 |
| Up | CX3CL1 | 9 | hsa-mir-2681-3p | Down | RNF2 | 36 | hsa-mir-548z |
| Up | SPATA21 | 8 | hsa-mir-4772-3p | Down | RNF125 | 36 | hsa-mir-759 |
| Up | PRMT5 | 7 | hsa-mir-346 | Down | RALGAPB | 35 | hsa-mir-4540 |
| Up | ASAP3 | 7 | hsa-mir-499a-5p | Down | CORO2A | 35 | hsa-mir-1231 |
| Up | C1S | 7 | hsa-mir-588 | Down | TJP3 | 35 | hsa-mir-4739 |
| Up | BRS3 | 7 | hsa-mir-6504-3p | Down | ELMOD2 | 34 | hsa-mir-548aw |
| Up | LRRC31 | 7 | hsa-mir-5011-5p | Down | COQ10B | 34 | hsa-mir-3665 |
| Up | TJP2 | 6 | hsa-mir-203a-3p | Down | JOSD1 | 34 | hsa-mir-2392 |
| Up | PHF21A | 6 | hsa-mir-7855-5p | Down | ANGEL2 | 33 | hsa-mir-4258 |
| Up | PRDX4 | 6 | hsa-mir-3619-5p | Down | OCLN | 31 | hsa-mir-5704 |
| Up | FREM1 | 6 | hsa-mir-7975 | Down | RRN3 | 31 | hsa-mir-4426 |
| Up | PTPRS | 5 | hsa-mir-487a-3p | Down | TPPP | 31 | hsa-mir-623 |
| Up | GATA4 | 5 | hsa-mir-34a-5p | Down | RPS6 | 30 | hsa-mir-544a |
| Up | KRTAP6-1 | 5 | hsa-mir-4668-5p | Down | DLG5 | 30 | hsa-mir-4668-5p |
| Up | EYS | 5 | hsa-mir-4680-5p | Down | ZNF680 | 30 | hsa-mir-7157-5p |
| Up | PPIAL4G | 5 | hsa-mir-324-5p | Down | DSTN | 29 | hsa-mir-4728-3p |
| Up | IL36B | 5 | hsa-mir-1273f | Down | TMED2 | 29 | hsa-mir-571 |
| Up | DEFB107A | 5 | hsa-mir-548v | Down | TMPO | 29 | hsa-mir-1299 |
| Up | ACTL8 | 4 | hsa-mir-148b-5p | Down | C10orf55 | 29 | hsa-mir-6133 |
| Up | ZNF492 | 4 | hsa-mir-32-5p | Down | CSTF2T | 28 | hsa-mir-3689e |
| Up | SPTSSB | 4 | hsa-mir-6801-5p | Down | BAG2 | 28 | hsa-mir-4446-5p |
| Up | KLC3 | 4 | hsa-mir-6833-3p | Down | AGAP1 | 28 | hsa-mir-6077 |
| Up | CEND1 | 3 | hsa-mir-512-5p | Down | GMDS | 28 | hsa-mir-4803 |
| Up | CXCL6 | 3 | hsa-mir-140-3p | Down | RC3H1 | 28 | hsa-mir-548ac |
| Up | MAGEA2 | 3 | hsa-mir-9-5p | Down | AGPAT4 | 28 | hsa-mir-6894-3p |
| Up | TFF1 | 3 | hsa-mir-504-5p | Down | PCNA | 27 | hsa-mir-548u |
| Up | NUPR1 | 3 | hsa-mir-615-3p | Down | HDDC2 | 27 | hsa-mir-1303 |
| Up | EGFL7 | 3 | hsa-mir-361-5p | Down | PITPNB | 26 | hsa-mir-8060 |
| Up | CCL19 | 3 | hsa-mir-148b-3p | Down | KBTBD2 | 26 | hsa-mir-520e |
| Up | GRIK5 | 3 | hsa-mir-186-5p | Down | WTAP | 26 | hsa-mir-378f |
| Up | SYN3 | 3 | hsa-mir-4792 | Down | RNMT | 25 | hsa-mir-3941 |
| Up | CDR2L | 3 | hsa-mir-3613-3p | Down | SLFN13 | 25 | hsa-mir-5089-5p |
| Up | TPSD1 | 2 | hsa-mir-1-1 | Down | YBX1 | 25 | hsa-mir-8069 |
| Up | CPEB1 | 2 | hsa-mir-101-3p | Down | PCMTD2 | 25 | hsa-mir-5695 |
| Up | SHANK1 | 2 | hsa-let-7e-5p | Down | RAB2A | 25 | hsa-mir-6165 |
| Up | ADAMTSL1 | 2 | hsa-mir-132-3p | Down | ZFP82 | 25 | hsa-mir-548p |
| Up | PKDCC | 2 | hsa-mir-25-3p | Down | RBPJL | 25 | hsa-mir-5194 |
| Up | DEFB4A | 2 | hsa-mir-26b-5p | Down | ATIC | 25 | hsa-mir-6797-5p |
| Up | DNAL4 | 2 | hsa-mir-335-5p | Down | FLNA | 24 | hsa-mir-222-3p |
| Up | DUX4 | 2 | hsa-mir-26b-5p | Down | RPS27 | 24 | hsa-mir-4770 |
| Up | PAQR6 | 2 | hsa-mir-335-5p | Down | ZNF430 | 24 | hsa-mir-6790-3p |
| Up | PCDHB8 | 2 | hsa-mir-181a-5p | Down | MTRNR2L8 | 24 | hsa-mir-190b |
| Up | SCARA3 | 2 | hsa-mir-615-3p | Down | DTHD1 | 24 | hsa-mir-4790-3p |
| Up | RHPN2 | 2 | hsa-mir-100-5p | Down | RARB | 23 | hsa-mir-578 |
| Up | AFAP1L1 | 2 | hsa-mir-192-5p | Down | DDX3Y | 23 | hsa-mir-6788-5p |
| Up | FAM189A2 | 2 | hsa-mir-192-5p | Down | FTH1 | 23 | hsa-mir-4496 |
| Up | CPNE6 | 2 | hsa-mir-197-3p | Down | ZNF730 | 23 | hsa-mir-4438 |
| Up | OTP | 2 | hsa-mir-106b-5p | Down | TMCC3 | 23 | hsa-mir-3133 |
| Up | MYF5 | 2 | hsa-mir-10b-5p | Down | AP3M2 | 23 | hsa-mir-7114-3p |
| Up | ACOT12 | 2 | hsa-mir-186-5p | Down | NDFIP2 | 23 | hsa-mir-4799-5p |
| Up | GPHB5 | 2 | hsa-mir-122-5p | Down | S1PR1 | 23 | hsa-mir-3927-5p |
| Up | AIF1L | 2 | hsa-mir-1229-3p | Down | HIGD1A | 22 | hsa-mir-3074-3p |
| Up | IL13RA1 | 2 | hsa-mir-143-3p | Down | ARRDC3 | 22 | hsa-mir-7162-5p |
| Up | TSPAN9 | 2 | hsa-mir-1180-3p | Down | NHSL1 | 22 | hsa-mir-548g-3p |
| Up | DOHH | 2 | hsa-mir-642a-5p | Down | AKAP5 | 22 | hsa-mir-4493 |
| Up | PKIG | 2 | hsa-mir-331-3p | Down | NXT2 | 21 | hsa-mir-5002-5p |
| Up | TNXB | 2 | hsa-mir-1301-3p | Down | CDC42SE2 | 21 | hsa-mir-4641 |
| Up | CHD5 | 2 | hsa-mir-744-5p | Down | RFXAP | 21 | hsa-mir-519c-3p |
| Up | AMPH | 1 | hsa-let-7b-5p | Down | OSBPL8 | 21 | hsa-mir-520f-3p |
| Up | ASPSCR1 | 1 | hsa-let-7b-5p | Down | C19orf12 | 21 | hsa-mir-3177-5p |
| Up | PLEKHN1 | 1 | hsa-mir-16-5p | Down | PDCL | 21 | hsa-mir-4509 |
| Up | HBQ1 | 1 | hsa-mir-24-3p | Down | PPP1R15A | 20 | hsa-mir-6761-5p |
| Up | KRTAP5-7 | 1 | hsa-mir-26b-5p | Down | RNF126 | 20 | hsa-mir-6777-5p |
| Up | MB | 1 | hsa-mir-26b-5p | Down | IER3 | 19 | hsa-mir-4710 |
| Up | OR10H1 | 1 | hsa-mir-26b-5p | Down | SMC5 | 19 | hsa-mir-4653-3p |
| Up | OTC | 1 | hsa-mir-26b-5p | Down | STAG1 | 19 | hsa-mir-769-3p |
| Up | SLC22A8 | 1 | hsa-mir-26b-5p | Down | FOXP4 | 19 | hsa-mir-5586-5p |
| Up | TMPRSS11E | 1 | hsa-mir-26b-5p | Down | ZNF25 | 19 | hsa-mir-4662a-5p |
| Up | TRPV6 | 1 | hsa-mir-26b-5p | Down | CBLB | 19 | hsa-mir-4762-5p |
| Up | DACT3 | 1 | hsa-mir-31-5p | Down | SH2D4A | 18 | hsa-mir-6832-3p |
| Up | PCSK1N | 1 | hsa-mir-31-5p | Down | CREM | 18 | hsa-mir-6727-3p |
| Up | HOGA1 | 1 | hsa-mir-92a-3p | Down | DNAJC27 | 18 | hsa-mir-4650-5p |
| Up | MYL2 | 1 | hsa-mir-99a-5p | Down | NKIRAS1 | 18 | hsa-mir-526b-3p |
| Up | CES1 | 1 | hsa-mir-197-3p | Down | PAPSS2 | 18 | hsa-mir-5011-5p |
| Up | CLEC4G | 1 | hsa-mir-7-5p | Down | ADD3 | 18 | hsa-mir-1202 |
| Up | KRTAP4-7 | 1 | hsa-mir-7-5p | Down | PDIA3 | 17 | hsa-mir-4653-5p |
| Up | TRIM47 | 1 | hsa-mir-7-5p | Down | GTF2I | 17 | hsa-mir-1252-3p |
| Up | MYOF | 1 | hsa-mir-34a-5p | Down | PSME4 | 17 | hsa-mir-6073 |
| Up | ABLIM3 | 1 | hsa-mir-214-3p | Down | EXOSC10 | 17 | hsa-mir-4772-3p |
| Up | RAB3IL1 | 1 | hsa-mir-124-3p | Down | MSL1 | 16 | hsa-mir-5694 |
| Up | THPO | 1 | hsa-mir-124-3p | Down | C1orf21 | 16 | hsa-mir-670-3p |
| Up | CRH | 1 | hsa-mir-142-3p | Down | ZNF567 | 16 | hsa-mir-376a-3p |
| Up | SPON2 | 1 | hsa-mir-9-5p | Down | SLC17A5 | 16 | hsa-mir-6866-5p |
| Up | CCDC8 | 1 | hsa-mir-193a-3p | Down | RORB | 16 | hsa-mir-6771-3p |
| Up | SORBS1 | 1 | hsa-mir-320a | Down | CEP78 | 16 | hsa-mir-6504-3p |
| Up | NOG | 1 | hsa-mir-200c-3p | Down | ZFP37 | 16 | hsa-mir-1244 |
| Up | BCL7C | 1 | hsa-mir-155-5p | Down | SNIP1 | 16 | hsa-mir-4518 |
| Up | CDK5R2 | 1 | hsa-mir-106b-5p | Down | SPTBN1 | 15 | hsa-mir-589-3p |
| Up | KCNJ16 | 1 | hsa-mir-148b-3p | Down | CTCF | 15 | hsa-mir-8088 |
| Up | ADAM21 | 1 | hsa-mir-335-5p | Down | NAMPT | 15 | hsa-mir-2681-3p |
| Up | AQP10 | 1 | hsa-mir-335-5p | Down | SFR1 | 15 | hsa-mir-3622b-3p |
| Up | AVPR1B | 1 | hsa-mir-335-5p | Down | HOPX | 15 | hsa-mir-6773-3p |
| Up | B3GNT3 | 1 | hsa-mir-335-5p | Down | B3GNT7 | 15 | hsa-mir-5588-3p |
| Up | BPIFA1 | 1 | hsa-mir-335-5p | Down | SCAI | 15 | hsa-mir-4649-3p |
| Up | CALHM3 | 1 | hsa-mir-335-5p | Down | CENPP | 14 | hsa-mir-1273f |
| Up | CDRT15L2 | 1 | hsa-mir-335-5p | Down | SYT11 | 14 | hsa-mir-548s |
| Up | CLEC3B | 1 | hsa-mir-335-5p | Down | ANGPTL2 | 14 | hsa-mir-548d-3p |
| Up | CYTL1 | 1 | hsa-mir-335-5p | Down | KRT33B | 13 | hsa-mir-6831-5p |
| Up | FRMD1 | 1 | hsa-mir-335-5p | Down | CERS6 | 13 | hsa-mir-3591-3p |
| Up | GAS2L2 | 1 | hsa-mir-335-5p | Down | FAM76A | 13 | hsa-mir-374b-5p |
| Up | GRIP2 | 1 | hsa-mir-335-5p | Down | SCN8A | 13 | hsa-mir-6754-3p |
| Up | HRC | 1 | hsa-mir-335-5p | Down | CERKL | 13 | hsa-mir-4699-5p |
| Up | KCNK9 | 1 | hsa-mir-335-5p | Down | FYN | 13 | hsa-let-7a-2-3p |
| Up | KIF17 | 1 | hsa-mir-335-5p | Down | TRAPPC6B | 13 | hsa-mir-4717-5p |
| Up | LCN1 | 1 | hsa-mir-335-5p | Down | GPIHBP1 | 13 | hsa-mir-8080 |
| Up | MEGF11 | 1 | hsa-mir-335-5p | Down | PHF20L1 | 12 | hsa-mir-6832-3p |
| Up | MUC3A | 1 | hsa-mir-335-5p | Down | IL1A | 12 | hsa-mir-30d-5p |
| Up | MYBPH | 1 | hsa-mir-335-5p | Down | JAKMIP2 | 12 | hsa-mir-5010-3p |
| Up | MYLPF | 1 | hsa-mir-335-5p | Down | TTC39A | 12 | hsa-mir-1273g-3p |
| Up | PKD2L1 | 1 | hsa-mir-335-5p | Down | PLK2 | 11 | hsa-mir-3187-3p |
| Up | PTGDS | 1 | hsa-mir-335-5p | Down | EGR3 | 11 | hsa-mir-377-3p |
| Up | RGS22 | 1 | hsa-mir-335-5p | Down | TNKS | 11 | hsa-mir-744-5p |
| Up | TMEM53 | 1 | hsa-mir-335-5p | Down | IGFBP3 | 11 | hsa-mir-5580-3p |
| Up | TOX2 | 1 | hsa-mir-335-5p | Down | JPH3 | 11 | hsa-mir-4469 |
| Up | TREH | 1 | hsa-mir-335-5p | Down | RAPGEFL1 | 10 | hsa-mir-4803 |
| Up | ADRA1A | 1 | hsa-mir-484 | Down | KIAA1324L | 10 | hsa-mir-204-5p |
| Up | OR8U1 | 1 | hsa-mir-146b-5p | Down | TRIAP1 | 10 | hsa-mir-548az-5p |
| Up | LRRN2 | 1 | hsa-mir-671-5p | Down | FAM169A | 10 | hsa-mir-548h-3p |
| Up | ADAMTS2 | 1 | hsa-mir-106b-3p | Down | WIPF1 | 9 | hsa-mir-200c-3p |
| Up | IL20 | 1 | hsa-mir-624-3p | Down | SENP6 | 9 | hsa-mir-5701 |
| Up | LYNX1 | 1 | hsa-mir-744-5p | Down | AKTIP | 9 | hsa-mir-629-5p |
| Up | CMYA5 | 1 | hsa-mir-877-3p | Down | GFOD1 | 9 | hsa-mir-100-5p |
| Up | TRPM5 | 1 | hsa-mir-1227-3p | Down | GNG2 | 9 | hsa-mir-16-1-3p |
|  |  |  |  | Down | FNBP4 | 9 | hsa-mir-211-3p |
|  |  |  |  | Down | SH2D1A | 9 | hsa-mir-6760-3p |
|  |  |  |  | Down | PSMA1 | 9 | hsa-mir-548l |
|  |  |  |  | Down | NUAK1 | 8 | hsa-mir-770-5p |
|  |  |  |  | Down | RABEPK | 8 | hsa-mir-4778-3p |
|  |  |  |  | Down | CUX1 | 8 | hsa-mir-218-5p |
|  |  |  |  | Down | HELZ | 8 | hsa-mir-203a-3p |
|  |  |  |  | Down | LPIN1 | 8 | hsa-mir-432-3p |
|  |  |  |  | Down | DDX23 | 8 | hsa-mir-744-5p |
|  |  |  |  | Down | EXOC6B | 8 | hsa-mir-5588-3p |
|  |  |  |  | Down | PDGFRB | 8 | hsa-mir-34c-5p |
|  |  |  |  | Down | SPATA21 | 8 | hsa-mir-1304-3p |
|  |  |  |  | Down | ARHGEF33 | 8 | hsa-mir-1277-5p |
|  |  |  |  | Down | NCAPD3 | 7 | hsa-mir-361-3p |
|  |  |  |  | Down | SYNE1 | 7 | hsa-mir-124-3p |
|  |  |  |  | Down | LMNA | 7 | hsa-mir-340-5p |
|  |  |  |  | Down | HES1 | 7 | hsa-mir-199b-5p |
|  |  |  |  | Down | SMURF1 | 7 | hsa-mir-15a-5p |
|  |  |  |  | Down | TOPORS | 7 | hsa-mir-519d-3p |
|  |  |  |  | Down | PLAU | 7 | hsa-mir-19b-3p |
|  |  |  |  | Down | VPS54 | 7 | hsa-mir-32-5p |
|  |  |  |  | Down | SAP30L | 7 | hsa-mir-4502 |
|  |  |  |  | Down | BOD1 | 7 | hsa-mir-450b-5p |
|  |  |  |  | Down | NCALD | 7 | hsa-mir-2053 |
|  |  |  |  | Down | TFDP3 | 7 | hsa-mir-6883-3p |
|  |  |  |  | Down | MAP4K5 | 7 | hsa-mir-548t-5p |
|  |  |  |  | Down | CXCL3 | 6 | hsa-mir-3161 |
|  |  |  |  | Down | RIOK2 | 6 | hsa-mir-101-3p |
|  |  |  |  | Down | USP24 | 6 | hsa-mir-193b-3p |
|  |  |  |  | Down | COX5A | 6 | hsa-mir-20a-5p |
|  |  |  |  | Down | CAB39L | 6 | hsa-mir-10a-5p |
|  |  |  |  | Down | PRR5L | 6 | hsa-mir-502-5p |
|  |  |  |  | Down | RCN2 | 6 | hsa-mir-99a-5p |
|  |  |  |  | Down | CXCL2 | 5 | hsa-mir-223-3p |
|  |  |  |  | Down | IDI1 | 5 | hsa-mir-193b-3p |
|  |  |  |  | Down | NR4A1 | 5 | hsa-let-7d-5p |
|  |  |  |  | Down | EIF4E2 | 5 | hsa-mir-181b-5p |
|  |  |  |  | Down | NET1 | 5 | hsa-mir-340-5p |
|  |  |  |  | Down | CDKN1C | 5 | hsa-mir-221-3p |
|  |  |  |  | Down | RECQL | 5 | hsa-mir-409-3p |
|  |  |  |  | Down | TTC3 | 5 | hsa-mir-27a-3p |
|  |  |  |  | Down | ITPR3 | 5 | hsa-mir-1226-3p |
|  |  |  |  | Down | ABCB1 | 5 | hsa-mir-223-3p |
|  |  |  |  | Down | MRPL30 | 5 | hsa-mir-4286 |
|  |  |  |  | Down | ADAM12 | 4 | hsa-mir-29b-3p |
|  |  |  |  | Down | CXCL1 | 4 | hsa-mir-27b-5p |
|  |  |  |  | Down | PWP1 | 4 | hsa-mir-1-1 |
|  |  |  |  | Down | GPN1 | 4 | hsa-let-7a-5p |
|  |  |  |  | Down | IMMT | 4 | hsa-mir-652-3p |
|  |  |  |  | Down | KLHDC2 | 4 | hsa-mir-19a-3p |
|  |  |  |  | Down | KLRC1 | 4 | hsa-mir-148b-3p |
|  |  |  |  | Down | PARP4 | 4 | hsa-mir-1260b |
|  |  |  |  | Down | NCAM1 | 4 | hsa-mir-200c-3p |
|  |  |  |  | Down | TLE1 | 4 | hsa-mir-423-3p |
|  |  |  |  | Down | TM4SF19 | 4 | hsa-mir-203b-3p |
|  |  |  |  | Down | RBM34 | 3 | hsa-mir-183-5p |
|  |  |  |  | Down | SOCS2 | 3 | hsa-mir-7-5p |
|  |  |  |  | Down | WDR47 | 3 | hsa-mir-21-5p |
|  |  |  |  | Down | ANKRD36B | 3 | hsa-mir-615-3p |
|  |  |  |  | Down | CCNDBP1 | 3 | hsa-mir-3615 |
|  |  |  |  | Down | SNX25 | 3 | hsa-mir-375 |
|  |  |  |  | Down | PTS | 3 | hsa-mir-192-5p |
|  |  |  |  | Down | SAP30BP | 3 | hsa-mir-151a-3p |
|  |  |  |  | Down | SARS2 | 3 | hsa-mir-193b-3p |
|  |  |  |  | Down | C10orf88 | 3 | hsa-mir-331-3p |
|  |  |  |  | Down | CKLF | 3 | hsa-mir-148b-3p |
|  |  |  |  | Down | PKP4 | 3 | hsa-mir-215-5p |
|  |  |  |  | Down | SAMSN1 | 3 | hsa-mir-7-5p |
|  |  |  |  | Down | ZNF365 | 3 | hsa-mir-223-3p |
|  |  |  |  | Down | AREG | 3 | hsa-mir-200a-3p |
|  |  |  |  | Down | DLG3 | 3 | hsa-mir-186-5p |
|  |  |  |  | Down | SYTL2 | 2 | hsa-mir-1-3p |
|  |  |  |  | Down | SOX13 | 2 | hsa-let-7b-5p |
|  |  |  |  | Down | SBDS | 2 | hsa-let-7c-5p |
|  |  |  |  | Down | RGPD5 | 2 | hsa-mir-15a-5p |
|  |  |  |  | Down | DDX31 | 2 | hsa-mir-877-3p |
|  |  |  |  | Down | HIRA | 2 | hsa-mir-17-3p |
|  |  |  |  | Down | CCL20 | 2 | hsa-mir-21-5p |
|  |  |  |  | Down | IL1B | 2 | hsa-mir-204-5p |
|  |  |  |  | Down | PDGFD | 2 | hsa-mir-145-5p |
|  |  |  |  | Down | SERPINB2 | 2 | hsa-mir-124-3p |
|  |  |  |  | Down | TOX | 2 | hsa-mir-223-3p |
|  |  |  |  | Down | TRANK1 | 2 | hsa-mir-26b-5p |
|  |  |  |  | Down | ZNF627 | 2 | hsa-mir-27a-3p |
|  |  |  |  | Down | BTN2A1 | 2 | hsa-mir-98-5p |
|  |  |  |  | Down | PPP4R1 | 2 | hsa-mir-149-5p |
|  |  |  |  | Down | PASK | 2 | hsa-mir-192-5p |
|  |  |  |  | Down | ZNF354A | 2 | hsa-mir-197-3p |
|  |  |  |  | Down | CNST | 2 | hsa-mir-150-5p |
|  |  |  |  | Down | PHLDA1 | 2 | hsa-mir-181a-5p |
|  |  |  |  | Down | ZNF571 | 2 | hsa-mir-375 |
|  |  |  |  | Down | NCAPH2 | 2 | hsa-mir-124-3p |
|  |  |  |  | Down | CD300A | 2 | hsa-mir-128-3p |
|  |  |  |  | Down | PTGER2 | 2 | hsa-mir-149-5p |
|  |  |  |  | Down | GNL2 | 2 | hsa-mir-484 |
|  |  |  |  | Down | IL18RAP | 2 | hsa-mir-4677-3p |
|  |  |  |  | Down | NAA35 | 1 | hsa-let-7a-5p |
|  |  |  |  | Down | BFSP1 | 1 | hsa-let-7b-5p |
|  |  |  |  | Down | CMC1 | 1 | hsa-let-7b-5p |
|  |  |  |  | Down | CDK5RAP1 | 1 | hsa-mir-16-5p |
|  |  |  |  | Down | FNTA | 1 | hsa-mir-16-5p |
|  |  |  |  | Down | STXBP5 | 1 | hsa-mir-21-5p |
|  |  |  |  | Down | SMAP1 | 1 | hsa-mir-25-3p |
|  |  |  |  | Down | MED31 | 1 | hsa-mir-26b-5p |
|  |  |  |  | Down | CRBN | 1 | hsa-mir-92a-3p |
|  |  |  |  | Down | GPX3 | 1 | hsa-mir-92a-3p |
|  |  |  |  | Down | SHPRH | 1 | hsa-mir-92a-3p |
|  |  |  |  | Down | PPT2 | 1 | hsa-mir-98-5p |
|  |  |  |  | Down | CCL3L1 | 1 | hsa-mir-192-5p |
|  |  |  |  | Down | BRF2 | 1 | hsa-mir-218-5p |
|  |  |  |  | Down | ERCC5 | 1 | hsa-mir-124-3p |
|  |  |  |  | Down | FLG | 1 | hsa-mir-124-3p |
|  |  |  |  | Down | IL18R1 | 1 | hsa-mir-124-3p |
|  |  |  |  | Down | S1PR5 | 1 | hsa-mir-124-3p |
|  |  |  |  | Down | KIR3DL1 | 1 | hsa-mir-132-3p |
|  |  |  |  | Down | KIR3DL2 | 1 | hsa-mir-132-3p |
|  |  |  |  | Down | SPON2 | 1 | hsa-mir-9-5p |
|  |  |  |  | Down | CCL4 | 1 | hsa-mir-195-5p |
|  |  |  |  | Down | NAP1L5 | 1 | hsa-mir-381-3p |
|  |  |  |  | Down | TCTN3 | 1 | hsa-mir-339-5p |
|  |  |  |  | Down | ANKRD18B | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | CHI3L2 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | IL27 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | JAKMIP1 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | KLRB1 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | KLRF1 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | LGR6 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | MAN1A1 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | PDE6H | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | PODN | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | RNF183 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | TP53AIP1 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | ZBTB1 | 1 | hsa-mir-335-5p |
|  |  |  |  | Down | ANKRD54 | 1 | hsa-mir-484 |
|  |  |  |  | Down | NYNRIN | 1 | hsa-mir-484 |
|  |  |  |  | Down | PDLIM2 | 1 | hsa-mir-484 |
|  |  |  |  | Down | METTL18 | 1 | hsa-mir-532-3p |
|  |  |  |  | Down | ZBTB11 | 1 | hsa-mir-877-5p |

Degree – No of miRNA interact with target gene. We taken any one miRNA in table.

**Table 8** TF - target gene interaction table

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Regulation** | **TF** | **Degree** | **Target Gene** | **Regulation** | **TF** | **Degree** | **Target Gene** |
| Up | EGR1 | 145 | ACTL8 | Down | SOX2 | 218 | PRIM2 |
| Up | SOX2 | 132 | LHFPL3 | Down | MYC | 211 | EXOSC10 |
| Up | SUZ12 | 119 | CXCL12 | Down | SPI1 | 210 | GMDS |
| Up | AR | 117 | GLI2 | Down | RUNX1 | 190 | C5ORF58 |
| Up | TP53 | 114 | C7 | Down | FLI1 | 180 | C10orf88 |
| Up | TP63 | 109 | NUPR1 | Down | HNF4A | 174 | CIAPIN1 |
| Up | REST | 105 | OR2AG2 | Down | STAT3 | 171 | RRN3 |
| Up | MYC | 105 | OLIG1 | Down | AR | 167 | S1PR5 |
| Up | RUNX1 | 101 | WDR90 | Down | NANOG | 167 | TNKS |
| Up | STAT3 | 101 | COL23A1 | Down | E2F1 | 156 | DLG3 |
| Up | NANOG | 100 | CORT | Down | TP63 | 156 | MAP2K4 |
| Up | HNF4A | 100 | B3GNT3 | Down | POU5F1 | 150 | NAA35 |
| Up | SMAD4 | 98 | BRS3 | Down | EGR1 | 149 | IL18R1 |
| Up | POU5F1 | 95 | MUC4 | Down | MITF | 145 | SOCS2 |
| Up | MITF | 93 | RASEF | Down | CREB1 | 123 | SCN8A |
| Up | SPI1 | 89 | CALHM3 | Down | PPARG | 118 | BRF2 |
| Up | MTF2 | 84 | LHX9 | Down | KDM5B | 118 | HELZ |
| Up | FLI1 | 84 | EGFL7 | Down | GATA2 | 118 | TRANK1 |
| Up | GATA2 | 75 | IL20 | Down | TP53 | 117 | FYN |
| Up | GATA1 | 73 | SPTBN4 | Down | TRIM28 | 117 | MSL1 |
| Up | TCF4 | 73 | FERD3L | Down | SMAD4 | 113 | ABCB1 |
| Up | PPARD | 68 | SNORA33 | Down | E2F4 | 112 | RFXAP |
| Up | SIN3B | 67 | MB | Down | KLF4 | 111 | GTF2I |
| Up | EZH2 | 66 | HELT | Down | TFAP2C | 109 | SYTL2 |
| Up | E2F1 | 65 | TRIM72 | Down | REST | 107 | RNMT |
| Up | SETDB1 | 63 | DUX4 | Down | SMARCA4 | 105 | TLE1 |
| Up | RCOR3 | 63 | ACTL6B | Down | TCF3 | 103 | AGAP1 |
| Up | TET1 | 62 | LMAN1L | Down | FOXP1 | 100 | MED31 |
| Up | SRY | 62 | KRTAP6-1 | Down | TAL1 | 100 | TCTEX1D4 |
| Up | RNF2 | 59 | KITLG | Down | ASH2L | 99 | RAPGEFL1 |
| Up | KLF4 | 57 | SLC5A11 | Down | TCF4 | 97 | CMC1 |
| Up | JARID2 | 57 | LRRN2 | Down | GATA1 | 97 | SENP6 |
| Up | SOX9 | 56 | TMPRSS11E | Down | SIN3B | 95 | MAK16 |
| Up | ESR1 | 56 | CDH5 | Down | FOXA2 | 90 | ANKRD54 |
| Up | PPARG | 55 | GCLM | Down | MYCN | 83 | CHAF1B |
| Up | TCF3 | 55 | DEFB1 | Down | PPARD | 81 | ADAM12 |
| Up | RUNX2 | 51 | CLEC3B | Down | SUZ12 | 81 | C1ORF21 |
| Up | EP300 | 49 | KLC3 | Down | VDR | 81 | CD80 |
| Up | SALL4 | 49 | GRIK5 | Down | SALL4 | 81 | ENPP5 |
| Up | SMARCA4 | 48 | IFNA4 | Down | SETDB1 | 81 | KLRB1 |
| Up | FOXP1 | 47 | TSPO2 | Down | EP300 | 80 | HOPX |
| Up | TRIM28 | 46 | RXFP2 | Down | ERG | 80 | NAMPT |
| Up | FOXA2 | 45 | PTGDS | Down | RUNX2 | 80 | NRF1 |
| Up | CREM | 45 | MYOF | Down | SMAD3 | 79 | PEX13 |
| Up | ERG | 45 | FFAR3 | Down | TET1 | 78 | NOTCH2 |
| Up | TCF7 | 44 | DOHH | Down | EOMES | 76 | RORA |
| Up | KDM5B | 43 | TP73 | Down | FOXO3 | 75 | CAB39L |
| Up | SMAD3 | 43 | JAKMIP3 | Down | YAP1 | 69 | PDE4D |
| Up | TFAP2C | 43 | FXYD3 | Down | SOX9 | 67 | JPH3 |
| Up | ZNF281 | 42 | SLC29A4 | Down | ATF3 | 66 | GPN1 |
| Up | CREB1 | 42 | RASAL1 | Down | MTF2 | 66 | UHRF1BP1 |
| Up | RAD21 | 42 | FIBCD1 | Down | ESR1 | 63 | IKZF2 |
| Up | TAL1 | 41 | COL18A1 | Down | RCOR3 | 62 | SPATA21 |
| Up | ASH2L | 40 | TMEM144 | Down | OLIG2 | 61 | CDK5RAP1 |
| Up | YAP1 | 40 | SEMA5B | Down | MECOM | 60 | CXCL3 |
| Up | RBPJ | 40 | CES1 | Down | DMRT1 | 59 | BRWD1 |
| Up | TFAP2A | 39 | MAGEL2 | Down | KDM5A | 59 | CTCF |
| Up | SCLY | 37 | AFAP1L1 | Down | ZNF217 | 58 | CSNK1A1 |
| Up | LMO2 | 36 | SV2C | Down | SOX17 | 58 | HBS1L |
| Up | BMI1 | 35 | CFC1 | Down | FOXP2 | 58 | TPPP |
| Up | RCOR1 | 33 | OR4C3 | Down | TEAD4 | 57 | CERS6 |
| Up | CUX1 | 33 | LEAP2 | Down | SMAD2 | 57 | SERPINB2 |
| Up | DMRT1 | 33 | HOGA1 | Down | HOXC9 | 57 | ZNF671 |
| Up | PBX1 | 32 | GPHB5 | Down | ELK1 | 56 | SAP30BP |
| Up | PRDM14 | 32 | GNB4 | Down | TBX5 | 55 | SBDS |
| Up | NR3C1 | 32 | CLEC2L | Down | GATA4 | 55 | SYNE1 |
| Up | YY1 | 31 | DEFB134 | Down | SCLY | 55 | SYNM |
| Up | EED | 31 | CDK5R2 | Down | SRY | 54 | TJP3 |
| Up | EOMES | 29 | SEMA4G | Down | YY1 | 53 | CCL20 |
| Up | TEAD4 | 29 | PALM3 | Down | CEBPB | 53 | TGFBR3 |
| Up | NR0B1 | 28 | MYBPH | Down | GFI1B | 51 | COQ10B |
| Up | OLIG2 | 28 | POU3F3 | Down | KLF1 | 51 | GHITM |
| Up | FOXP2 | 28 | C20ORF144 | Down | WT1 | 51 | KLF3 |
| Up | TFCP2L1 | 27 | WFDC2 | Down | ZNF281 | 51 | MAPK1IP1L |
| Up | BACH1 | 27 | OTC | Down | MYBL2 | 51 | PARP4 |
| Up | WT1 | 27 | BCAM | Down | HOXB4 | 51 | SHPRH |
| Up | KLF1 | 26 | TRIM10 | Down | ETS1 | 50 | NKIRAS1 |
| Up | PAX3 | 26 | COL28A1 | Down | PRDM14 | 49 | DLEU7 |
| Up | SMAD2 | 25 | TINAGL1 | Down | NR3C1 | 49 | PLAU |
| Up | JUN | 25 | SPATA21 | Down | STAT4 | 48 | PPP1R15B |
| Up | PHC1 | 25 | ADM | Down | RELA | 48 | RNF126 |
| Up | ZNF217 | 25 | ACTBL2 | Down | NFE2L2 | 48 | ZNF148 |
| Up | MEIS1 | 24 | CCR2 | Down | DACH1 | 47 | TMPO |
| Up | TBX5 | 23 | TMEM50B | Down | POU3F2 | 46 | COX18 |
| Up | CTNNB1 | 23 | GRK1 | Down | RBPJ | 46 | JMY |
| Up | POU3F2 | 23 | ADRA1A | Down | PBX1 | 45 | WIPF1 |
| Up | ZFX | 22 | TMEM184B | Down | JUN | 44 | JAKMIP1 |
| Up | ATF3 | 22 | SRPX2 | Down | TFCP2L1 | 44 | NAP1L5 |
| Up | SOX17 | 22 | GATA4 | Down | CCND1 | 43 | AGPAT4 |
| Up | ESRRB | 22 | BHLHA9 | Down | TTF2 | 43 | HES1 |
| Up | DROSHA | 21 | VIPR2 | Down | RCOR1 | 43 | LONRF3 |
| Up | E2F4 | 21 | KIF17 | Down | FOXP3 | 43 | ZDHHC6 |
| Up | SOX11 | 20 | SLC38A1 | Down | LMO2 | 42 | CNST |
| Up | EWSR1 | 20 | PYDC2 | Down | PHF8 | 41 | C19ORF12 |
| Up | MYCN | 20 | DNAH2 | Down | BACH1 | 41 | PHLDA1 |
| Up | CEBPB | 19 | TMEM53 | Down | RAD21 | 41 | SOX13 |
| Up | FOXO3 | 19 | RHPN2 | Down | ZFP42 | 40 | DNAJC8 |
| Up | ELK1 | 19 | MED18 | Down | ARNT | 39 | NUAK1 |
| Up | RELA | 18 | DIO2 | Down | SIN3A | 38 | SNIP1 |
| Up | TBX3 | 18 | CRH | Down | EWSR1 | 38 | UNK |
| Up | ARNT | 17 | KCNK9 | Down | CNOT3 | 36 | NCAPD3 |
| Up | ELF1 | 17 | ASGR1 | Down | SRF | 36 | PDCL |
| Up | CNOT3 | 16 | SLC6A2 | Down | XRN2 | 36 | ZNF25 |
| Up | MECOM | 16 | RNU11 | Down | PAX3 | 35 | ARL4C |
| Up | STAT5A | 16 | PROM2 | Down | MYB | 34 | SMURF1 |
| Up | CTCF | 16 | CRHR1 | Down | CTNNB1 | 34 | SNORA12 |
| Up | NR1I2 | 16 | ABLIM3 | Down | EZH2 | 34 | TMCC3 |
| Up | ZFP42 | 15 | IL17B | Down | MEIS1 | 33 | EIF4E2 |
| Up | LYL1 | 15 | CDR2L | Down | TFAP2A | 33 | FNBP4 |
| Up | CCND1 | 15 | ASAP3 | Down | STAT5A | 33 | MDFIC |
| Up | MYBL2 | 14 | TSPAN9 | Down | TCF7 | 33 | SMAD7 |
| Up | STAT4 | 14 | PRTN3 | Down | PRDM5 | 33 | TOPORS |
| Up | SREBF2 | 14 | MYBPC3 | Down | NR0B1 | 31 | PTGER2 |
| Up | NFE2L2 | 14 | GDNF | Down | PADI4 | 31 | RNF2 |
| Up | HOXC9 | 14 | CPEB1 | Down | BCL3 | 30 | CXCL1 |
| Up | TTF2 | 14 | BARHL1 | Down | IRF8 | 30 | MRPL30 |
| Up | DNAJC2 | 13 | TRPV6 | Down | MEF2A | 30 | RBM20 |
| Up | GFI1B | 13 | ODF4 | Down | CDX2 | 30 | SLC25A36 |
| Up | CDX2 | 12 | NMNAT2 | Down | AHR | 28 | GPX3 |
| Up | ELF5 | 12 | FTMT | Down | ASXL1 | 27 | CLASP1 |
| Up | GATA3 | 12 | FERMT2 | Down | ESRRB | 27 | KLHDC2 |
| Up | STAT1 | 11 | TRIM47 | Down | ELF1 | 27 | SNORA55 |
| Up | SMAD1 | 11 | TPD52 | Down | AP1S2 | 26 | STXBP5 |
| Up | AHR | 11 | SLC17A5 | Down | PAX6 | 26 | TXK |
| Up | MEF2A | 11 | NFIB | Down | ELF5 | 25 | CEP120 |
| Up | XRN2 | 11 | METTL7B | Down | TBX3 | 25 | GTDC1 |
| Up | DACH1 | 11 | FBXW9 | Down | BMI1 | 24 | BNC2 |
| Up | SIN3A | 11 | ENO4 | Down | NR1H3 | 23 | CST7 |
| Up | CRX | 11 | DACT3 | Down | GATA3 | 22 | ZNF207 |
| Up | VDR | 10 | SYCE3 | Down | CHD1 | 21 | CKLF |
| Up | NACC1 | 10 | SORBS1 | Down | LYL1 | 21 | HACE1 |
| Up | HTT | 10 | DEK | Down | JARID2 | 21 | MAN1A1 |
| Up | IRF8 | 9 | SYN3 | Down | NR1I2 | 21 | TTC39B |
| Up | PHF8 | 9 | SMOC1 | Down | TCF7L2 | 20 | ABT1 |
| Up | HSF1 | 9 | RNF207 | Down | DCP1A | 20 | BAG2 |
| Up | CLOCK | 9 | PTPRS | Down | TAF7L | 19 | RC3H1 |
| Up | ESR2 | 9 | PLEKHN1 | Down | SREBF1 | 19 | TOMM20 |
| Up | RCOR2 | 9 | PADI3 | Down | SOX11 | 18 | PCNA |
| Up | FOXP3 | 9 | MUC3A | Down | NOTCH1 | 17 | CHI3L2 |
| Up | SREBF1 | 9 | GRIN1 | Down | NACC1 | 17 | GPA33 |
| Up | ZIC3 | 8 | THPO | Down | TBP | 17 | RABEPK |
| Up | NUCKS1 | 8 | TGFA | Down | CEBPD | 17 | STAG1 |
| Up | CEBPD | 8 | SSTR4 | Down | THAP11 | 17 | ZNF354A |
| Up | RARG | 8 | INMT | Down | SREBF2 | 16 | GRIN3B |
| Up | HOXB4 | 8 | ERBB3 | Down | NFIB | 16 | PAFAH1B2 |
| Up | KDM5A | 8 | AIF1L | Down | TFEB | 16 | PHF20L1 |
| Up | SRF | 7 | TJP2 | Down | DNAJC2 | 16 | SFR1 |
| Up | CEBPA | 7 | OSMR | Down | KDM6A | 15 | ARHGAP11A |
| Up | PRDM5 | 7 | EGFR | Down | CLOCK | 15 | G0S2 |
| Up | NR1H3 | 7 | COL9A2 | Down | IRF1 | 15 | KLRD1 |
| Up | TCF7L2 | 7 | AMPH | Down | HSF1 | 14 | LMNB1 |
| Up | MYB | 6 | STAC2 | Down | PDX1 | 14 | NUCKS1 |
| Up | TFEB | 6 | PRDX4 | Down | STAT6 | 14 | PITPNB |
| Up | TAF7L | 6 | FXYD1 | Down | SMAD1 | 13 | B3GNT7 |
| Up | FOXO1 | 6 | CYP24A1 | Down | STAT1 | 13 | SERTAD1 |
| Up | PADI4 | 6 | BMP7 | Down | CEBPA | 12 | SLC17A5 |
| Up | IRF1 | 6 | ANTXR1 | Down | CRX | 11 | EXOC6B |
| Up | HIF1A | 5 | TFF1 | Down | HTT | 11 | GZMB |
| Up | ETS1 | 5 | PHF21A | Down | RCOR2 | 9 | AKTIP |
| Up | BCL3 | 5 | FANK1 | Down | FOXM1 | 9 | BTN2A1 |
| Up | IKZF1 | 5 | ATP1A4 | Down | DROSHA | 9 | CREM |
| Up | TBP | 5 | ASPSCR1 | Down | ESR2 | 9 | IER3 |
| Up | ASXL1 | 4 | RAB3IL1 | Down | GBX2 | 9 | IMMT |
| Up | GBX2 | 4 | OR5H1 | Down | FOXO1 | 9 | SARDH |
| Up | HOXD13 | 4 | MXRA5 | Down | HCFC1 | 8 | ZFP82 |
| Up | CHD1 | 4 | INSL6 | Down | RARG | 7 | FTH1 |
| Up | CHD7 | 4 | C9ORF106 | Down | ZIC3 | 7 | ZBTB1 |
| Up | ZNF274 | 3 | ZNF492 | Down | PHC1 | 6 | ANP32C |
| Up | STAT6 | 3 | NOG | Down | CDKN2AIP | 6 | CAMK2N1 |
| Up | CDKN2AIP | 3 | LY6H | Down | EED | 6 | OCLN |
| Up | ZNF652 | 3 | AVPR1B | Down | IKZF1 | 5 | HIGD1A |
| Up | KDM6A | 2 | VLDLR | Down | GLI1 | 5 | NCAM1 |
| Up | HCFC1 | 2 | PRMT5 | Down | PRDM16 | 4 | ADD3 |
| Up | TCF21 | 2 | PKDCC | Down | CHD7 | 4 | FOXP4 |
| Up | GLI1 | 2 | PHF21A | Down | ETS2 | 4 | G3BP2 |
| Up | PDX1 | 2 | PAX6 | Down | HOXD13 | 4 | GNG2 |
| Up | DCP1A | 2 | BCL7C | Down | THRA | 4 | NR4A1 |
| Up | PRDM16 | 2 | ADAMTSL1 | Down | SALL1 | 4 | ZNF567 |
| Up | THAP11 | 1 | SYT3 | Down | ZNF274 | 3 | FBXW2 |
| Up | NR4A2 | 1 | OR52K2 | Down | CIITA | 2 | KIR3DL1 |
| Up | MYBL1 | 1 | ODF4 | Down | BCL11B | 2 | LCOR |
| Up | FOXM1 | 1 | NEURL1B | Down | TCF21 | 2 | PASK |
| Up | HOXA2 | 1 | FREM1 | Down | ZNF652 | 2 | QKI |
| Up | ETS2 | 1 | CRH | Down | E2F7 | 2 | RECQL |
| Up | KLF2 | 1 | BMP7 | Down | NR4A2 | 2 | ZFP37 |
| Up | KLF5 | 1 | BMP7 | Down | HOXA2 | 1 | QKI |
| Up | BP1 | 1 | ADAM21 | Down | KLF2 | 1 | SMARCAD1 |
|  |  |  |  | Down | KLF5 | 1 | SMARCAD1 |
|  |  |  |  | Down | ZNF322 | 1 | ZFX |
|  |  |  |  | Down | BP1 | 1 | CCL4 |

Degree – No of TF interact with target gene. We taken any one TF in table