Supplemental Table 2: Genes predicted to by dysregulated in the studied PC3 model of Docetaxel Resistance. AG= aged matched control, D8 = docetaxel resistant subline, D12=docetaxel resistant subline. FC= fold change.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  |  | D8 vs AG | D12 vs AG |
| Gene | **Full Name** | **Genetic locus** | **Log FC** | **Adjusted P-value** | **Log FC** | **Adjusted P-value** |
|  ABCB8  |  ATP-binding cassette, sub-family B (MDR/TAP), member 8  |  7q36  | -0.487008176 | 0.001111541 | -0.581066897 | 0.001392508 |
|  ABHD2  |  abhydrolase domain containing 2  |  15q26.1  | -0.503663093 | 0.000244912 | -0.635952358 | 0.000301714 |
|  ACBD7  |  acyl-CoA binding domain containing 7  |  10p13  | -0.430764146 | 0.040215514 | -1.210689173 | 0.000696665 |
|  ADAMTS20  |  ADAM metallopeptidase with thrombospondin type 1 motif, 20  |  12q12  | -0.39374566 | 0.010519615 | -0.508766806 | 0.007007381 |
|  AMOT  |  angiomotin  |  Xq23  | -0.864074292 | 0.000239785 | -1.351673483 | 9.41E-05 |
|  ANGPTL4  |  angiopoietin-like 4  |  19p13.3  | 0.552078189 | 0.003840682 | 0.678975052 | 0.003527841 |
|  ANKRD36  |  ankyrin repeat domain 36  |  2q11.2  | 0.405721204 | 0.007706697 | 0.553588595 | 0.00404016 |
|  ANKRD36B  |  ankyrin repeat domain 36B  |  2q11.2  | 0.981678384 | 0.000152436 | 1.170613994 | 0.000269686 |
|  ANKRD37  |  ankyrin repeat domain 37  |  4q35.1  | -0.468001812 | 0.006861845 | -0.471091645 | 0.015016561 |
|  ANO2  |  anoctamin 2  |  12p13.3  | -0.546615967 | 0.039559915 | -0.61121074 | 0.047403433 |
|  ANO6  |  anoctamin 6  |  12q12  | -0.451899857 | 0.035322892 | -0.537231827 | 0.033508263 |
|  AP1S1  |  adaptor-related protein complex 1, sigma 1 subunit  |  7q22.1  | -0.440273986 | 0.001412519 | -0.87563019 | 0.000132391 |
|  AREG  |  amphiregulin  |  4q13-q21  | 0.561853718 | 0.000339805 | 0.667162829 | 0.000541568 |
|  ARF5  |  ADP-ribosylation factor 5  |  7q31.3  | -0.686840463 | 0.002497151 | -0.751246551 | 0.004211681 |
|  ARID3B  |  AT rich interactive domain 3B (BRIGHT-like)  |  15q24  | -0.680629873 | 0.003858562 | -0.762401738 | 0.005454092 |
|  ASB1  |  ankyrin repeat and SOCS box-containing 1  |  2q37  | 0.385658596 | 0.00262351 | 0.549508831 | 0.001216405 |
|  ASB13  |  ankyrin repeat and SOCS box-containing 13  |  10p15.1  | -0.931807051 | 0.000304165 | -1.098128491 | 0.000514512 |
|  AZGP1  |  alpha-2-glycoprotein 1, zinc-binding  |  7q22.1  | -1.745044197 | 0.031471045 | -1.913136845 | 0.041394854 |
|  B3GALNT1  |  beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)  |  3q25  | 0.416050954 | 0.024012781 | 0.650459783 | 0.006527164 |
|  BCKDK  |  branched chain ketoacid dehydrogenase kinase  |  16p11.2  | 0.43144131 | 0.00284286 | 0.433234859 | 0.007082866 |
|  BCL7B  |  B-cell CLL/lymphoma 7B  |  7q11.23  | -0.512407642 | 0.007072099 | -0.629042481 | 0.006082185 |
|  BCL9L  |  B-cell CLL/lymphoma 9-like  |  11q23.3  | -0.55133142 | 0.010268777 | -0.584317337 | 0.01725312 |
|  BFAR  |  bifunctional apoptosis regulator  |  16p13.12  | 0.435083389 | 0.004270351 | 0.552597063 | 0.003328632 |
|  BNIP3  |  BCL2/adenovirus E1B 19kDa interacting protein 3  |  10q26.3  | 0.623190612 | 0.006356058 | 0.666445669 | 0.010682178 |
|  BTBD11  |  BTB (POZ) domain containing 11  |  12q23.3  | 0.805425769 | 8.72E-05 | 1.001136414 | 0.000137372 |
|  C10orf18  |  chromosome 10 open reading frame 18  |  10p15.1  | -0.458051623 | 0.004100535 | -0.650208091 | 0.001884453 |
|  C10orf25  |  chromosome 10 open reading frame 25  |  10q11.21  | -0.824299377 | 0.000105429 | -0.840124891 | 0.000440714 |
|  C11orf17  |  chromosome 11 open reading frame 17  |  11p15.3  | -0.40788906 | 0.002096657 | -0.996135914 | 6.30E-05 |
|  C11orf41  |  chromosome 11 open reading frame 41  |  11p13  | 1.168241683 | 6.45E-05 | 1.182596597 | 0.000306313 |
|  C15orf38  |  chromosome 15 open reading frame 38  |  15q26.1  | -0.450877701 | 0.034897355 | -0.570508602 | 0.025654743 |
|  C16orf52  |  chromosome 16 open reading frame 52  |  16p12.2  | 0.553559002 | 0.007130518 | 0.8120431 | 0.002629626 |
|  C16orf53  |  chromosome 16 open reading frame 53  |  16p11.2  | 0.459754325 | 0.038884794 | 0.718603465 | 0.011268704 |
|  C18orf21  |  chromosome 18 open reading frame 21  |  18q12.2  | -0.464214308 | 0.005870747 | -0.48525523 | 0.01103819 |
|  C1orf21  |  chromosome 1 open reading frame 21  |  1q25  | 0.866415498 | 1.66E-05 | 1.133160262 | 2.45E-05 |
|  C2CD2L  |  C2CD2-like  |  11q23.3  | -0.530054931 | 0.000400967 | -0.80157897 | 0.000181173 |
|  C3orf26  |  chromosome 3 open reading frame 26  |  3q12.1  | -0.784564016 | 0.00012367 | -1.109312479 | 9.25E-05 |
|  C4orf41  |  chromosome 4 open reading frame 41  |  4q35.1  | -0.444753897 | 0.003046012 | -0.498694086 | 0.004467538 |
|  C4orf43  |  chromosome 4 open reading frame 43  |  4q32.2  | -0.387069683 | 0.009125426 | -0.439993387 | 0.011212339 |
|  C5orf13  |  chromosome 5 open reading frame 13  |  5q22.1  | 0.381426758 | 0.005392902 | 0.707170985 | 0.000651516 |
|  C5orf44  |  chromosome 5 open reading frame 44  |  5q12.3  | -0.467208714 | 0.006074529 | -0.649175492 | 0.002956238 |
|  C5orf54  |  chromosome 5 open reading frame 54  |  5q33.3  | 0.679632371 | 0.002961275 | 0.796890469 | 0.003529837 |
|  C7orf41  |  chromosome 7 open reading frame 41  |  7p14.3  | -0.485020281 | 0.013805728 | -0.615674517 | 0.009941402 |
|  C7orf46  |  chromosome 7 open reading frame 46  |  7p15.3  | -0.544000856 | 0.000526983 | -0.97703265 | 9.25E-05 |
|  C7orf58  |  chromosome 7 open reading frame 58  |  7q31.31  | -0.614684678 | 0.009161698 | -0.787661001 | 0.006335342 |
|  C7orf64  |  chromosome 7 open reading frame 64  |  7q21.2  | -0.596753779 | 0.000126633 | -0.618100156 | 0.000477478 |
|  C9orf72  |  chromosome 9 open reading frame 72  |  9p21.2  | 0.449558475 | 0.003898359 | 0.507284017 | 0.005330511 |
|  CABLES1  |  Cdk5 and Abl enzyme substrate 1  |  18q11.2  | 0.677604116 | 0.00106484 | 0.845452261 | 0.00105972 |
|  CAPRIN2  |  caprin family member 2  |  12p11  | 0.948287566 | 5.62E-06 | 0.990509873 | 3.03E-05 |
|  CARD16  |  caspase recruitment domain family, member 16  |  ---  | -0.618765241 | 0.004313602 | -0.797003681 | 0.003140076 |
|  CD97  |  CD97 molecule  |  19p13  | -0.4092453 | 0.002248973 | -0.579999797 | 0.001076247 |
|  CDC16  |  cell division cycle 16 homolog (S. cerevisiae)  |  13q34  | -0.666736413 | 0.000134077 | -0.848455969 | 0.000173933 |
|  CDK15  |  cyclin-dependent kinase 15  |  2q33.2  | -0.480904945 | 0.001003449 | -0.50158901 | 0.002459185 |
|  CEACAM6  |  carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)  |  19q13.2  | 1.352302619 | 0.000955406 | 2.142921005 | 0.000304225 |
|  CHCHD2  |  coiled-coil-helix-coiled-coil-helix domain containing 2  |  7p11.2  | -0.486391032 | 0.008346829 | -0.587150194 | 0.007739314 |
|  CHPF  |  chondroitin polymerizing factor  |  2q35  | -0.726207038 | 3.19E-05 | -0.875803861 | 6.46E-05 |
|  CNTNAP3  |  contactin associated protein-like 3  |  9p13.1  | 1.783919867 | 3.46E-05 | 2.180269619 | 6.46E-05 |
|  COBLL1  |  COBL-like 1  |  2q24.3  | -0.954944943 | 0.000148586 | -1.105270292 | 0.000306999 |
|  COL4A5  |  collagen, type IV, alpha 5  |  Xq22  | 0.560361599 | 0.00032952 | 0.935407501 | 8.98E-05 |
|  COL4A6  |  collagen, type IV, alpha 6  |  Xq22  | 0.81524223 | 4.52E-05 | 0.99034753 | 8.59E-05 |
|  CREG1  |  cellular repressor of E1A-stimulated genes 1  |  1q24  | -0.416443512 | 0.003267843 | -0.423233136 | 0.007521731 |
|  CTDSP2  |  CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2  |  12q14.1  | -0.474812105 | 0.00261952 | -0.663139499 | 0.001354649 |
|  CUX1  |  cut-like homeobox 1  |  7q22.1  | -0.427292777 | 0.014213253 | -0.458716322 | 0.021806965 |
|  CXCL16  |  chemokine (C-X-C motif) ligand 16  |  17p13  | -0.745670918 | 0.016332113 | -0.817436249 | 0.022599273 |
|  CYP4F11  |  cytochrome P450, family 4, subfamily F, polypeptide 11  |  19p13.1  | -0.696633597 | 0.049058961 | -0.905931758 | 0.032496661 |
|  DFNA5  |  deafness, autosomal dominant 5  |  7p15  | -0.518901294 | 0.021054102 | -0.660608212 | 0.014902452 |
|  DLG1  |  discs, large homolog 1 (Drosophila)  |  3q29  | -0.580287592 | 0.002114039 | -0.602876699 | 0.004711127 |
|  DNAJC12  |  DnaJ (Hsp40) homolog, subfamily C, member 12  |  10q22.1  | -1.093341527 | 8.24E-05 | -1.488530587 | 8.02E-05 |
|  DNAJC2  |  DnaJ (Hsp40) homolog, subfamily C, member 2  |  7q22  | -0.447880165 | 0.010273828 | -0.503560737 | 0.013166999 |
|  DTX3L  |  deltex 3-like (Drosophila)  |  3q21.1  | -0.911799789 | 3.56E-05 | -0.912833465 | 0.000193696 |
|  DUSP23  |  dual specificity phosphatase 23  |  1q23.2  | -0.522031297 | 0.00140801 | -0.628769703 | 0.001644869 |
|  ECHDC1  |  enoyl CoA hydratase domain containing 1  |  6q22.33  | -0.495156857 | 0.037557364 | -0.621118667 | 0.028693119 |
|  EDNRA  |  endothelin receptor type A  |  4q31.22  | 0.640627859 | 0.00368487 | 1.584092262 | 0.000101893 |
|  EIF4A2  |  eukaryotic translation initiation factor 4A2  |  3q28  | -0.58905612 | 0.007523042 | -0.607919054 | 0.014587507 |
|  ELMO3  |  engulfment and cell motility 3  |  16q22.1  | -0.469278425 | 0.001818233 | -0.484116478 | 0.004265032 |
|  EMR2  |  egf-like module containing, mucin-like, hormone receptor-like 2  |  19p13.1  | -0.720694109 | 0.000397821 | -0.74711737 | 0.00117419 |
|  EPHB3  |  EPH receptor B3  |  3q21-qter  | -0.390220088 | 0.009439661 | -0.597860424 | 0.00279164 |
|  EPHB6  |  EPH receptor B6  |  7q33-q35  | 0.482942363 | 0.000872337 | 0.644672197 | 0.00065751 |
|  EPRS  |  glutamyl-prolyl-tRNA synthetase  |  1q41  | -0.539891891 | 0.002623604 | -0.626604074 | 0.003328632 |
|  ERCC4  |  excision repair cross-complementing rodent repair deficiency, complementation group 4  |  16p13.12  | 0.810255551 | 0.000109703 | 0.887451329 | 0.000316252 |
|  ETFA  |  electron-transfer-flavoprotein, alpha polypeptide  |  15q23-q25  | -0.390138743 | 0.000700059 | -0.510069475 | 0.000610306 |
|  EYA4  |  eyes absent homolog 4 (Drosophila)  |  6q23  | -0.529051118 | 0.000930493 | -0.532972596 | 0.002721772 |
|  FAM102B  |  family with sequence similarity 102, member B  |  1p13.3  | 0.727258252 | 0.000477613 | 0.982282967 | 0.000378748 |
|  FAM129A  |  family with sequence similarity 129, member A  |  1q25  | -1.225574086 | 2.90E-05 | -1.792906549 | 2.25E-05 |
|  FAM46A  |  family with sequence similarity 46, member A  |  6q14  | 0.659517996 | 0.000121757 | 0.719255135 | 0.000352833 |
|  FBXO18  |  F-box protein, helicase, 18  |  10p15.1  | -0.56847198 | 0.001997288 | -0.744639552 | 0.001475059 |
|  FMNL2  |  formin-like 2  |  2q23.3  | 0.520535827 | 0.013560359 | 0.570329317 | 0.019286182 |
|  FOXF1  |  forkhead box F1  |  16q24  | -0.474849823 | 0.012786504 | -0.497000475 | 0.022240369 |
|  FUCA1  |  fucosidase, alpha-L- 1, tissue  |  1p34  | -0.412968638 | 0.005988733 | -0.430115801 | 0.011421098 |
|  GDPD5  |  glycerophosphodiester phosphodiesterase domain containing 5  |  11q13.4-q13.5  | -0.458712482 | 0.003996824 | -0.528560736 | 0.004949034 |
|  GFPT2  |  glutamine-fructose-6-phosphate transaminase 2  |  5q34-q35  | 0.504564251 | 0.005092467 | 0.900739225 | 0.000733302 |
|  GLI3  |  GLI family zinc finger 3  |  7p13  | 1.264561924 | 1.24E-05 | 1.713514622 | 1.62E-05 |
|  GMPR  |  guanosine monophosphate reductase  |  6p23  | -0.51261144 | 0.001100618 | -0.544727646 | 0.002429605 |
|  GNB2  |  guanine nucleotide binding protein (G protein), beta polypeptide 2  |  7q21.3-q22.1|7q22  | -0.417426074 | 0.003511029 | -0.464839317 | 0.005186407 |
|  GOLGA8IP  |  golgin A8 family, member I (pseudogene)  |  15q11.2  | 0.506488832 | 0.00094514 | 0.545252258 | 0.00201019 |
|  GPR155  |  G protein-coupled receptor 155  |  2q31.1  | 0.993483245 | 1.07E-05 | 1.011210108 | 6.05E-05 |
|  GPR18  |  G protein-coupled receptor 18  |  13q32  | -0.408127483 | 0.001288014 | -0.444161888 | 0.002459185 |
|  GPR64  |  G protein-coupled receptor 64  |  Xp22.13  | 0.904903078 | 8.05E-05 | 0.904996988 | 0.000390008 |
|  GSTA4  |  glutathione S-transferase alpha 4  |  6p12.1  | 0.403837205 | 0.000685305 | 0.483649145 | 0.000897708 |
|  GSTO2  |  glutathione S-transferase omega 2  |  10q25.1  | -0.700061916 | 0.003709607 | -0.809519236 | 0.004573203 |
|  GTF3C1  |  general transcription factor IIIC, polypeptide 1, alpha 220kDa  |  16p12  | 0.410582324 | 0.015857643 | 0.471155608 | 0.018122022 |
|  GTPBP4  |  GTP binding protein 4  |  10p15-p14  | -0.634107831 | 4.95E-05 | -0.78168993 | 8.59E-05 |
|  HEG1  |  HEG homolog 1 (zebrafish)  |  3q21.2  | -1.650340751 | 0.003579134 | -2.100055006 | 0.00279164 |
|  HEPH  |  hephaestin  |  Xq11-q12  | -0.451079952 | 0.003938087 | -0.538043024 | 0.004158552 |
|  HKR1  |  HKR1, GLI-Kruppel zinc finger family member  |  19q13.12  | 0.628710813 | 0.00535036 | 0.90507232 | 0.002226853 |
|  HLA-DPA1  |  major histocompatibility complex, class II, DP alpha 1  |  6p21.3  | -1.510016142 | 0.000742644 | -1.901332117 | 0.00076139 |
|  HOMER1  |  homer homolog 1 (Drosophila)  |  5q14.2  | 0.385479402 | 0.005407061 | 0.542622746 | 0.002485106 |
|  HSP90AA1  |  heat shock protein 90kDa alpha (cytosolic), class A member 1  |  14q32.33  | 0.417960402 | 0.000866765 | 0.506479169 | 0.001037751 |
|  HSP90AA2  |  heat shock protein 90kDa alpha (cytosolic), class A member 2  |  11p14.1  | 0.616433322 | 8.32E-05 | 0.689437536 | 0.000220967 |
|  HSP90AA4P  |  heat shock protein 90kDa alpha (cytosolic), class A member 4 (pseudogene)  |  4q35.2  | 0.541432171 | 0.00095354 | 0.594730306 | 0.001844697 |
|  IFITM3  |  interferon induced transmembrane protein 3 (1-8U)  |  11p15.5  | -0.490743817 | 0.007833019 | -0.996707731 | 0.000601008 |
|  IFRD1  |  interferon-related developmental regulator 1  |  7q31.1  | -0.674160821 | 0.000130705 | -0.703318905 | 0.000471353 |
|  IGF1R  |  insulin-like growth factor 1 receptor  |  15q26.3  | -0.585124404 | 0.028595746 | -0.944378211 | 0.006792731 |
|  IL15  |  interleukin 15  |  4q31  | -0.726471748 | 0.001662918 | -0.852214978 | 0.002141337 |
|  IL1RL1  |  interleukin 1 receptor-like 1  |  2q12  | 0.981986202 | 0.007401669 | 2.230831799 | 0.000316252 |
|  IL6  |  interleukin 6 (interferon, beta 2)  |  7p21  | -0.974874091 | 9.54E-05 | -1.154278215 | 0.000189278 |
|  IL6ST  |  interleukin 6 signal transducer (gp130, oncostatin M receptor)  |  5q11  | -0.432908798 | 0.011571261 | -0.475430958 | 0.016415187 |
|  ING3  |  inhibitor of growth family, member 3  |  7q31  | -0.61323046 | 0.000960345 | -1.028867997 | 0.000222252 |
|  IRF1  |  interferon regulatory factor 1  |  5q31.1  | -0.531919921 | 0.006164067 | -0.655258238 | 0.005288821 |
|  ITPR1  |  inositol 1,4,5-triphosphate receptor, type 1  |  3p26.1  | 0.651305366 | 5.42E-05 | 0.982679216 | 3.15E-05 |
|  JAK2  |  Janus kinase 2  |  9p24  | 0.600688633 | 0.000520595 | 1.732674891 | 9.63E-06 |
|  KCNJ2  |  potassium inwardly-rectifying channel, subfamily J, member 2  |  17q24.3  | 0.801581333 | 0.000206303 | 0.841406262 | 0.000655195 |
|  KCNN4  |  potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4  |  19q13.2  | -0.453809321 | 0.003718364 | -0.751476524 | 0.000802671 |
|  KDM1B  |  lysine (K)-specific demethylase 1B  |  6p22.3  | -0.380178166 | 0.003704466 | -0.422928149 | 0.005439426 |
|  KIAA0226  |  KIAA0226  |  3q29  | -0.383386152 | 0.000823761 | -0.664337504 | 0.000167403 |
|  KIAA1432  |  KIAA1432  |  9p24.1  | 0.441357743 | 0.003507444 | 0.585636242 | 0.002271646 |
|  KIAA2018  |  KIAA2018  |  3q13.2  | -0.716823426 | 0.001320532 | -0.853297172 | 0.001646955 |
|  KIF3C  |  kinesin family member 3C  |  2p23  | -0.389545191 | 0.003539565 | -0.514410744 | 0.002342704 |
|  KIN  |  KIN, antigenic determinant of recA protein homolog (mouse)  |  10p15-p14  | -0.546083468 | 0.004286865 | -0.889229885 | 0.000984467 |
|  KLF6  |  Kruppel-like factor 6  |  10p15  | -0.946458088 | 3.47E-05 | -1.031737505 | 0.000125494 |
|  KLF7  |  Kruppel-like factor 7 (ubiquitous)  |  2q32  | -0.730514782 | 0.000185813 | -0.73722209 | 0.000724593 |
|  KLHDC10  |  kelch domain containing 10  |  7q32.2  | -0.602512618 | 0.004486246 | -0.891448087 | 0.001681175 |
|  KLHL35  |  kelch-like 35 (Drosophila)  |  11q13.4  | -0.957418209 | 1.77E-05 | -1.019428441 | 7.71E-05 |
|  KMO  |  kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)  |  1q42-q44  | -1.161573463 | 0.03950676 | -1.441430835 | 0.031446274 |
|  KRT32  |  keratin 32  |  17q21.2  | -0.389281635 | 0.024420611 | -0.502562941 | 0.016374035 |
|  KRT80  |  keratin 80  |  12q13.13  | -0.913120828 | 8.54E-05 | -1.042818756 | 0.000205917 |
|  LARP4B  |  La ribonucleoprotein domain family, member 4B  |  10p15.3  | -0.726128007 | 0.000145421 | -0.751337846 | 0.000534475 |
|  LAT2  |  linker for activation of T cells family, member 2  |  7q11.23  | -0.423569669 | 0.006042447 | -0.426470136 | 0.0134533 |
|  LATS1  |  LATS, large tumor suppressor, homolog 1 (Drosophila)  |  6q25.1  | -0.407341788 | 0.001251823 | -0.458596629 | 0.002045565 |
|  LGALS9  |  lectin, galactoside-binding, soluble, 9  |  17q11.2  | -0.642055948 | 0.035712422 | -0.751888708 | 0.036057451 |
|  LINGO2  |  leucine rich repeat and Ig domain containing 2  |  9p21.2  | 0.588124805 | 0.016154293 | 1.03566306 | 0.002454599 |
|  LMBR1L  |  limb region 1 homolog (mouse)-like  |  12q13.12  | -0.483278417 | 0.028112664 | -0.615838826 | 0.020050991 |
|  LOC387790  |  hypothetical LOC387790  |  11q13.5  | 0.477390645 | 0.007591788 | 0.518428252 | 0.011625549 |
|  LOXL4  |  lysyl oxidase-like 4  |  10q24  | -1.603917151 | 0.011786243 | -1.64987214 | 0.022249752 |
|  LPHN1  |  latrophilin 1  |  19p13.2  | -0.633570018 | 0.000170757 | -0.668406122 | 0.00054944 |
|  LRCH2  |  leucine-rich repeats and calponin homology (CH) domain containing 2  |  Xq23  | 1.250355274 | 2.99E-05 | 2.045978976 | 1.54E-05 |
|  LRCH4  |  leucine-rich repeats and calponin homology (CH) domain containing 4  |  7q22  | -0.42969882 | 0.044538644 | -0.556539965 | 0.029895295 |
|  LRRC6  |  leucine rich repeat containing 6  |  8q24.22  | 0.641871968 | 0.005020019 | 2.252366799 | 2.25E-05 |
|  LRRC61  |  leucine rich repeat containing 61  |  7q31-q35  | -0.409089794 | 0.011747836 | -0.502385179 | 0.009936926 |
|  LRRK1  |  leucine-rich repeat kinase 1  |  15q26.3  | -0.414923181 | 0.008808771 | -0.467076189 | 0.01133663 |
|  MAGI1  |  membrane associated guanylate kinase, WW and PDZ domain containing 1  |  3p14.1  | 0.445400547 | 0.021216304 | 0.529803263 | 0.020475957 |
|  MAN2A2  |  mannosidase, alpha, class 2A, member 2  |  15q26.1  | -0.590126705 | 0.032407823 | -0.83751864 | 0.014272302 |
|  MBD6  |  methyl-CpG binding domain protein 6  |  ---  | -0.416080381 | 0.024298562 | -0.632524421 | 0.007558369 |
|  MBL1P  |  mannose-binding lectin (protein A) 1, pseudogene  |  10q22.2-q22.3  | -0.429996764 | 0.005482776 | -0.47646868 | 0.007863298 |
|  MEGF9  |  multiple EGF-like-domains 9  |  9q32-q33.3  | 0.716007587 | 5.09E-05 | 0.732587637 | 0.000235822 |
|  METTL7B  |  methyltransferase like 7B  |  12q13.2  | -0.586462417 | 0.018813803 | -1.380140532 | 0.000696741 |
|  MINA  |  MYC induced nuclear antigen  |  3q11.2  | -0.414994832 | 0.000541919 | -0.732247153 | 0.000102655 |
|  MMP17  |  matrix metallopeptidase 17 (membrane-inserted)  |  12q24.3  | -0.496396634 | 0.001326075 | -0.537475253 | 0.00257641 |
|  MRPS24  |  mitochondrial ribosomal protein S24  |  7p14  | -0.468953623 | 0.000840852 | -0.50573379 | 0.001820612 |
|  MTHFD1L  |  methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like  |  6q25.1  | -0.405583544 | 0.005250162 | -0.418608129 | 0.010605595 |
|  MTMR8  |  myotubularin related protein 8  |  Xq11.2  | -0.908347958 | 0.002289862 | -1.304362193 | 0.001039096 |
|  MUC3A  |  mucin 3A, cell surface associated  |  7q22  | -0.676176616 | 0.002540234 | -0.834401649 | 0.00241683 |
|  MYLK  |  myosin light chain kinase  |  3q21  | -1.197705682 | 0.000339878 | -1.236297219 | 0.001047924 |
|  NDE1  |  nudE nuclear distribution gene E homolog 1 (A. nidulans)  |  16p13.11  | 0.477134063 | 0.000579733 | 0.484216841 | 0.001807672 |
|  NDUFA4  |  NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa  |  7p21.3  | -0.428509782 | 0.005247409 | -0.441583092 | 0.010682178 |
|  NEDD4  |  neural precursor cell expressed, developmentally down-regulated 4  |  15q  | -0.452184388 | 0.003933068 | -0.713728559 | 0.001052173 |
|  NET1  |  neuroepithelial cell transforming 1  |  10p15  | -0.540936793 | 9.84E-05 | -0.576843238 | 0.000332618 |
|  NFATC2IP  |  nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein  |  16p11.2  | 0.524548529 | 0.026052649 | 0.539310555 | 0.044639022 |
|  NFKB2  |  nuclear factor of kappa light polypeptide gene enhancer in B-cells 2  |  10q24  | -0.417086677 | 0.006929036 | -0.7693676 | 0.000829646 |
|  NIT2  |  nitrilase family, member 2  |  3q12.2  | -0.582161326 | 6.94E-05 | -0.582497515 | 0.000343384 |
|  NOVA1  |  neuro-oncological ventral antigen 1  |  14q  | 1.162409747 | 8.10E-06 | 2.089519797 | 3.58E-06 |
|  NQO1  |  NAD(P)H dehydrogenase, quinone 1  |  16q22.1  | 0.432491557 | 0.0058943 | 0.588624415 | 0.003174427 |
|  NRIP1  |  nuclear receptor interacting protein 1  |  21q11.2  | 0.39779923 | 0.015908196 | 0.405277203 | 0.030035787 |
|  NSUN6  |  NOP2/Sun domain family, member 6  |  10p12.31  | 0.429911263 | 0.009756126 | 0.446083598 | 0.018144795 |
|  NUAK1  |  NUAK family, SNF1-like kinase, 1  |  12q23.3  | -0.514472262 | 0.008778895 | -0.697389096 | 0.004711127 |
|  NUDT5  |  nudix (nucleoside diphosphate linked moiety X)-type motif 5  |  10p14  | -0.708014941 | 0.001320532 | -0.930137172 | 0.000988166 |
|  OPTN  |  optineurin  |  10p13  | -0.722382804 | 0.001176716 | -0.949433532 | 0.000894127 |
|  OR2T8  |  olfactory receptor, family 2, subfamily T, member 8  |  1q44  | -0.459366727 | 0.025263038 | -0.549403706 | 0.02355346 |
|  P2RX7  |  purinergic receptor P2X, ligand-gated ion channel, 7  |  12q24  | -1.588572076 | 0.00065347 | -1.956610761 | 0.00076139 |
|  PAK1  |  p21 protein (Cdc42/Rac)-activated kinase 1  |  11q13-q14  | -0.498660107 | 0.001570027 | -1.364230181 | 2.55E-05 |
|  PALMD  |  palmdelphin  |  1p22-p21  | 1.030931796 | 0.001505902 | 3.009792561 | 1.90E-05 |
|  PDAP1  |  PDGFA associated protein 1  |  7q22.1  | -0.50373027 | 0.001778657 | -0.569130855 | 0.002703941 |
|  PDE4DIP  |  phosphodiesterase 4D interacting protein  |  1q12  | -0.417772884 | 0.01962453 | -0.482913751 | 0.021401634 |
|  PDP1  |  pyruvate dehyrogenase phosphatase catalytic subunit 1  |  8q22.1  | -0.85123066 | 0.001878338 | -0.864629587 | 0.004737379 |
|  PFKM  |  phosphofructokinase, muscle  |  12q13.3  | -0.523529024 | 0.002830522 | -0.878121579 | 0.000601008 |
|  PHLDB2  |  pleckstrin homology-like domain, family B, member 2  |  3q13.2  | -1.147191624 | 4.14E-06 | -1.85223236 | 3.58E-06 |
|  PIGB  |  phosphatidylinositol glycan anchor biosynthesis, class B  |  15q21-q22  | -0.397232064 | 0.002707748 | -0.762072708 | 0.000293042 |
|  PIGK  |  phosphatidylinositol glycan anchor biosynthesis, class K  |  1p31.1  | 0.572215973 | 0.007327357 | 0.801646796 | 0.003394849 |
|  PIKFYVE  |  phosphoinositide kinase, FYVE finger containing  |  2q34  | -0.40908621 | 0.005678219 | -0.518474755 | 0.004299641 |
|  PITRM1  |  pitrilysin metallopeptidase 1  |  10p15.2  | -0.518751899 | 0.005785534 | -0.716863475 | 0.00289357 |
|  PLA2G16  |  phospholipase A2, group XVI  |  11q12.3  | -0.537003335 | 0.001601474 | -0.653269257 | 0.001756638 |
|  PML  |  promyelocytic leukemia  |  15q22  | -0.493725122 | 0.00186587 | -0.747547271 | 0.000678005 |
|  PNPLA8  |  patatin-like phospholipase domain containing 8  |  7q31  | -0.567025265 | 0.000697938 | -0.82703659 | 0.000352833 |
|  PODXL  |  podocalyxin-like  |  7q32-q33  | -0.925086216 | 2.26E-05 | -1.176542498 | 3.65E-05 |
|  PPWD1  |  peptidylprolyl isomerase domain and WD repeat containing 1  |  5q12.3  | -0.647798599 | 0.000634462 | -0.735868519 | 0.001082529 |
|  PRDM1  |  PR domain containing 1, with ZNF domain  |  6q21  | -1.770897834 | 5.03E-06 | -2.11763911 | 1.54E-05 |
|  PRDX5  |  peroxiredoxin 5  |  11q13  | -0.546620335 | 0.000400008 | -0.600533419 | 0.000885476 |
|  PREX1  |  phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1  |  20q13.13  | 0.549354899 | 0.01907439 | 0.760800026 | 0.009166088 |
|  PRKAA2  |  protein kinase, AMP-activated, alpha 2 catalytic subunit  |  1p31  | 0.864294292 | 0.000159285 | 1.079516699 | 0.000217671 |
|  PRKAG2  |  protein kinase, AMP-activated, gamma 2 non-catalytic subunit  |  7q36.1  | -0.426045789 | 0.008842874 | -0.436542784 | 0.017559062 |
|  PROS1  |  protein S (alpha)  |  3q11.2  | -0.576000912 | 0.009959933 | -0.762953213 | 0.005878824 |
|  PSMB9  |  proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)  |  6p21.3  | -1.073999495 | 8.04E-06 | -1.377705561 | 1.54E-05 |
|  PTER  |  phosphotriesterase related  |  10p12  | -0.46485153 | 0.000903809 | -0.90861032 | 9.41E-05 |
|  PTGFR  |  prostaglandin F receptor (FP)  |  1p31.1  | 0.864795094 | 0.000210076 | 1.714014624 | 2.45E-05 |
|  PTK7  |  PTK7 protein tyrosine kinase 7  |  6p21.1-p12.2  | 0.447815924 | 0.002481951 | 0.461352618 | 0.00553808 |
|  PTPRK  |  protein tyrosine phosphatase, receptor type, K  |  6q22.2-q22.3  | -0.392507027 | 0.001948519 | -0.687609655 | 0.000343384 |
|  PYGB  |  phosphorylase, glycogen; brain  |  20p11.2-p11.1  | 0.395188761 | 0.044695796 | 0.482118181 | 0.038129202 |
|  RAB23  |  RAB23, member RAS oncogene family  |  6p11  | 0.523965761 | 0.017446738 | 0.673745097 | 0.011746899 |
|  RAB5B  |  RAB5B, member RAS oncogene family  |  12q13  | -0.676666661 | 0.002703219 | -0.698734195 | 0.005915439 |
|  RAD51L1  |  RAD51-like 1 (S. cerevisiae)  |  14q23-q24.2  | 0.678741221 | 8.05E-05 | 0.888640073 | 9.41E-05 |
|  RAET1L  |  retinoic acid early transcript 1L  |  6q25.1  | -0.783631056 | 0.005012479 | -0.791894514 | 0.011245131 |
|  RDH11  |  retinol dehydrogenase 11 (all-trans/9-cis/11-cis)  |  14q24.1  | 0.487825447 | 0.001101364 | 0.610900126 | 0.001064127 |
|  REPIN1  |  replication initiator 1  |  7q36.1  | -0.535143879 | 0.002174069 | -0.613427966 | 0.003005322 |
|  RGL1  |  ral guanine nucleotide dissociation stimulator-like 1  |  1q25.3  | 0.534861303 | 0.001016921 | 0.891340647 | 0.000246851 |
|  RIPK2  |  receptor-interacting serine-threonine kinase 2  |  8q21  | -0.380741426 | 0.004713389 | -0.438180199 | 0.005737896 |
|  RMRP  |  RNA component of mitochondrial RNA processing endoribonuclease  |  9p21-p12  | -0.45580053 | 0.039251304 | -1.173690724 | 0.001027979 |
|  RNF169  |  ring finger protein 169  |  11q13.4  | -0.393204736 | 0.008032797 | -0.442652311 | 0.010410352 |
|  RNF216  |  ring finger protein 216  |  7p22.1  | -0.392127266 | 0.004220307 | -0.396468141 | 0.009727869 |
|  RPL22L1  |  ribosomal protein L22-like 1  |  3q26.2  | -0.498597988 | 0.003617311 | -0.742198664 | 0.001324277 |
|  RPL24  |  ribosomal protein L24  |  3q12  | -0.387016451 | 0.01094804 | -0.639389355 | 0.002272784 |
|  RPP38  |  ribonuclease P/MRP 38kDa subunit  |  10p13  | -0.590372435 | 0.022461834 | -0.689527107 | 0.023351778 |
|  RPS12  |  ribosomal protein S12  |  6q23.2  | -0.456655552 | 0.000749158 | -0.523489123 | 0.001211679 |
|  RSL24D1  |  ribosomal L24 domain containing 1  |  15q21  | -0.50295287 | 0.027424795 | -0.535045737 | 0.040985048 |
|  SCAMP2  |  secretory carrier membrane protein 2  |  15q23-q25  | -0.462669416 | 0.000294095 | -0.621710597 | 0.00025301 |
|  SCNN1G  |  sodium channel, nonvoltage-gated 1, gamma  |  16p12  | 0.617155801 | 0.014441431 | 1.551695057 | 0.000382331 |
|  SEMA7A  |  semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)  |  15q22.3-q23  | -0.452030017 | 0.003384775 | -0.995133011 | 0.000177153 |
|  SERAC1  |  serine active site containing 1  |  6q25.3  | -0.552163709 | 0.002985879 | -0.702376633 | 0.002409655 |
|  SFT2D1  |  SFT2 domain containing 1  |  6q27  | -0.56567629 | 0.000893961 | -0.566329174 | 0.002717596 |
|  SIPA1L3  |  signal-induced proliferation-associated 1 like 3  |  19q13.13  | -0.387649372 | 0.032247434 | -0.445935632 | 0.035083183 |
|  SLC25A21  |  solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21  |  14q11.2  | 0.953308356 | 0.002453913 | 1.365299024 | 0.001109526 |
|  SLC4A11  |  solute carrier family 4, sodium borate transporter, member 11  |  20p12  | 1.313790497 | 0.000130896 | 1.432900761 | 0.000378748 |
|  SLC4A4  |  solute carrier family 4, sodium bicarbonate cotransporter, member 4  |  4q21  | 1.077667544 | 1.39E-05 | 1.768135765 | 8.57E-06 |
|  SLCO4C1  |  solute carrier organic anion transporter family, member 4C1  |  5q21.2  | -0.532987609 | 0.02789429 | -0.65825947 | 0.02263764 |
|  SLFN12L  |  schlafen family member 12-like  |  17q12  | -0.537158223 | 0.04025778 | -0.618930074 | 0.043033686 |
|  SMAD3  |  SMAD family member 3  |  15q22.33  | -0.589931269 | 0.000799446 | -0.739544557 | 0.000826574 |
|  SMARCAL1  |  SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1  |  2q35  | -0.426600426 | 0.024095505 | -0.566146117 | 0.014157211 |
|  SNORA20  |  small nucleolar RNA, H/ACA box 20  |  6q25.3  | -0.507917002 | 0.002909088 | -0.536205967 | 0.005674048 |
|  SNORA45  |  small nucleolar RNA, H/ACA box 45  |  11p15.4  | -0.702727434 | 0.001409488 | -0.756597881 | 0.00278877 |
|  SNORD115-11  |  small nucleolar RNA, C/D box 115-11  |  15q11.2  | -0.402385401 | 0.005997192 | -0.457247733 | 0.007571379 |
|  SNRPA1  |  small nuclear ribonucleoprotein polypeptide A'  |  15q26.3  | -0.621709385 | 0.003542642 | -0.664411923 | 0.006333078 |
|  SOBP  |  sine oculis binding protein homolog (Drosophila)  |  6q21  | 1.033912113 | 0.000360889 | 1.041328159 | 0.001254354 |
|  SPIN4  |  spindlin family, member 4  |  Xq11.1  | 0.393914939 | 0.004070462 | 0.584717966 | 0.001503528 |
|  SPPL2A  |  signal peptide peptidase-like 2A  |  15q21.2  | -0.432119295 | 0.027105978 | -0.493433197 | 0.030550088 |
|  SSH3  |  slingshot homolog 3 (Drosophila)  |  11q13.2  | -0.445563777 | 0.004027303 | -0.472940269 | 0.007351679 |
|  SYVN1  |  synovial apoptosis inhibitor 1, synoviolin  |  11q13  | -0.398019094 | 0.012404059 | -0.582956801 | 0.00455865 |
|  TAF3  |  TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa  |  10p15.1  | -0.437790141 | 0.001206778 | -0.827212731 | 0.000148821 |
|  TAF5L  |  TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa  |  1q42.13  | -0.507706152 | 0.000376683 | -0.515296229 | 0.001248901 |
|  TAF6  |  TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa  |  7q22.1  | -0.546431814 | 0.001897771 | -0.61621225 | 0.002891429 |
|  TAF7  |  TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa  |  5q31  | -0.499113174 | 0.000113731 | -0.593140242 | 0.000213166 |
|  TAS2R14  |  taste receptor, type 2, member 14  |  12p13  | 0.551599917 | 0.01030035 | 0.619022273 | 0.013304929 |
|  TAS2R50  |  taste receptor, type 2, member 50  |  12p13.2  | 0.539494331 | 0.006888461 | 0.675550407 | 0.005378395 |
|  TBC1D23  |  TBC1 domain family, member 23  |  3q12.2  | -0.647861232 | 0.000634127 | -1.029052066 | 0.000206906 |
|  TFG  |  TRK-fused gene  |  3q12.2  | -0.392190987 | 0.002851368 | -0.605520489 | 0.000885476 |
|  TGM4  |  transglutaminase 4 (prostate)  |  3p22-p21.33  | -0.424861039 | 0.002294967 | -0.427688053 | 0.00580322 |
|  THOC6  |  THO complex 6 homolog (Drosophila)  |  16p13.3  | 0.476159663 | 0.000554065 | 0.80984986 | 0.000131326 |
|  TM2D3  |  TM2 domain containing 3  |  15q26.3  | -0.454617402 | 0.001207006 | -0.680635494 | 0.000496817 |
|  TMBIM1  |  transmembrane BAX inhibitor motif containing 1  |  2p24.3-p24.1  | -0.742687639 | 1.96E-05 | -2.587830597 | 1.75E-07 |
|  TMED3  |  transmembrane emp24 protein transport domain containing 3  |  15q24-q25  | -0.571949653 | 0.000984897 | -0.590652723 | 0.002544473 |
|  TMEM168  |  transmembrane protein 168  |  7q31.32  | -0.395788329 | 0.017553829 | -0.972304709 | 0.000530502 |
|  TMEM2  |  transmembrane protein 2  |  9q13-q21  | 0.718696397 | 3.85E-05 | 1.256263089 | 1.35E-05 |
|  TMEM80  |  transmembrane protein 80  |  11p15.5  | -0.41111558 | 0.003298626 | -0.73505533 | 0.000502109 |
|  TMEM9B  |  TMEM9 domain family, member B  |  11p15.3  | -0.534115411 | 0.00353334 | -0.707433816 | 0.00230271 |
|  TMPRSS11E  |  transmembrane protease, serine 11E  |  4q13.2  | -0.41590778 | 0.006516218 | -0.453065927 | 0.010005596 |
|  TMPRSS15  |  transmembrane protease, serine 15  |  21q21|21q21.1  | -0.435867472 | 0.028581865 | -0.482768483 | 0.036372452 |
|  TNFAIP3  |  tumor necrosis factor, alpha-induced protein 3  |  6q23  | -0.432235485 | 0.004265841 | -0.536911259 | 0.003689033 |
|  TNFRSF14  |  tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)  |  1p36.32  | -0.493340999 | 0.024765765 | -0.872949387 | 0.00375904 |
|  TOB2  |  transducer of ERBB2, 2  |  22q13.2  | -0.463779833 | 0.029393932 | -0.653119689 | 0.01332458 |
|  TOX  |  thymocyte selection-associated high mobility group box  |  8q12.1  | 0.993085467 | 5.09E-05 | 1.00727392 | 0.000247554 |
|  TPK1  |  thiamin pyrophosphokinase 1  |  7q34-q35  | -0.456396194 | 0.018433352 | -0.883473168 | 0.001804039 |
|  TRIM2  |  tripartite motif-containing 2  |  4q31.3  | -1.173804986 | 2.03E-05 | -1.40724168 | 4.51E-05 |
|  TRIM21  |  tripartite motif-containing 21  |  11p15.5  | -0.496015548 | 0.006136471 | -0.717385973 | 0.002459185 |
|  TRIM64  |  tripartite motif-containing 64  |  11q14.3  | -0.436058188 | 0.000460333 | -0.573447718 | 0.000416623 |
|  TRIP11  |  thyroid hormone receptor interactor 11  |  14q31-q32  | 0.427627544 | 0.025788092 | 0.653254541 | 0.00788403 |
|  TRPM7  |  transient receptor potential cation channel, subfamily M, member 7  |  15q21  | -0.413248326 | 0.002392753 | -0.443624679 | 0.004467372 |
|  TTC6  |  tetratricopeptide repeat domain 6  |  14q21.1  | 0.581039882 | 0.017813899 | 1.321985141 | 0.000773722 |
|  TTLL4  |  tubulin tyrosine ligase-like family, member 4  |  2p24.3-p24.1  | -0.658469895 | 4.40E-05 | -0.661248547 | 0.000227763 |
|  TYMS  |  thymidylate synthetase  |  18p11.32  | 0.45867898 | 0.02414233 | 0.487267385 | 0.036867365 |
|  UBA7  |  ubiquitin-like modifier activating enzyme 7  |  3p21  | -1.205583213 | 0.023281368 | -1.303478813 | 0.033096973 |
|  UCP2  |  uncoupling protein 2 (mitochondrial, proton carrier)  |  11q13  | -0.557021147 | 0.000487735 | -1.233757342 | 2.77E-05 |
|  UFSP2  |  UFM1-specific peptidase 2  |  4q35.1  | -0.471301699 | 0.000535898 | -0.546637123 | 0.000864621 |
|  UGDH  |  UDP-glucose 6-dehydrogenase  |  4p15.1  | 0.734393119 | 5.38E-05 | 0.852456127 | 0.000131326 |
|  ULBP2  |  UL16 binding protein 2  |  6q25  | -0.659687482 | 0.004776704 | -0.756271953 | 0.005915439 |
|  UPF2  |  UPF2 regulator of nonsense transcripts homolog (yeast)  |  10p14-p13  | -0.494413537 | 0.002565304 | -0.746876842 | 0.000890772 |
|  UQCRC2  |  ubiquinol-cytochrome c reductase core protein II  |  16p12  | 0.38112258 | 0.002755488 | 0.478764639 | 0.002387225 |
|  USP6NL  |  USP6 N-terminal like  |  10p13  | -0.53554079 | 0.005544252 | -0.747321228 | 0.002639939 |
|  VRK1  |  vaccinia related kinase 1  |  14q32  | 0.439382968 | 0.046338326 | 1.022728868 | 0.002098879 |
|  VSIG1  |  V-set and immunoglobulin domain containing 1  |  Xq22.3  | 3.028734861 | 2.42E-06 | 3.185187414 | 1.54E-05 |
|  VSNL1  |  visinin-like 1  |  2p24.3  | -0.386188194 | 0.035281677 | -0.531936003 | 0.018085034 |
|  WDR54  |  WD repeat domain 54  |  2p13.1  | 0.470008428 | 0.026170007 | 0.538972106 | 0.029130447 |
|  WDR61  |  WD repeat domain 61  |  15q25.1  | -0.385718778 | 0.000971603 | -0.571893925 | 0.000427728 |
|  WT1  |  Wilms tumor 1  |  11p13  | 0.750775189 | 0.006851742 | 0.899865258 | 0.006628764 |
|  YKT6  |  YKT6 v-SNARE homolog (S. cerevisiae)  |  7p15.1  | -0.381042565 | 0.006270073 | -0.430694158 | 0.008072473 |
|  ZBTB24  |  zinc finger and BTB domain containing 24  |  6q21  | -0.419999169 | 0.001751853 | -0.62303926 | 0.000708623 |
|  ZDBF2  |  zinc finger, DBF-type containing 2  |  2q33.3  | -0.577721701 | 0.024771085 | -1.995020653 | 0.000138152 |
|  ZFYVE1  |  zinc finger, FYVE domain containing 1  |  14q24.2  | -0.521661043 | 0.005312624 | -0.589021312 | 0.007008696 |
|  ZNF148  |  zinc finger protein 148  |  3q21  | -0.448611349 | 0.009418409 | -0.727221916 | 0.002141337 |
|  ZNF277  |  zinc finger protein 277  |  7q31.1  | -0.413917738 | 0.012236144 | -0.461204288 | 0.016226079 |
|  ZNF33B  |  zinc finger protein 33B  |  10q11.2  | -0.484325021 | 0.008230264 | -0.885676065 | 0.001027474 |
|  ZNF398  |  zinc finger protein 398  |  7q36.1  | -0.467542192 | 0.001800417 | -0.640472955 | 0.001052858 |
|  ZNF592  |  zinc finger protein 592  |  15q25.3  | -0.413149902 | 0.00077079 | -0.426606494 | 0.002091487 |
|  ZNF774  |  zinc finger protein 774  |  15q26.1  | -0.515592402 | 0.001215585 | -0.548416356 | 0.002614359 |
|  ZNF841  |  zinc finger protein 841  |  19q13.41  | -1.042117399 | 9.89E-05 | -1.538802456 | 5.89E-05 |
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