

| probe set | dbSNP RS ID | Chr | Cytoband | Associated Gene(s) | Product(s) | SNP Position Relative to Gene(s) | DS PBL av | Control PBL av | DS / Control | DS - Control |
|---------------|-------------|-----|----------|--------------------|---|----------------------------------|-----------|----------------|--------------|--------------|
| SNP_A-2305831 | rs11863621 | 16 | q23.3 | CDH13 | member of the cadherin superfamily | intergenic | 0.722 | 0.298571429 | 2.41818182 | 0.423428571 |
| SNP_A-1974529 | rs1720830 | 3 | q22.3 | FAM62C | family with sequence similarity 62 member C | promoter CGI | 0.732 | 0.32 | 2.2875 | 0.412 |
| SNP_A-1785577 | rs2654974 | 15 | q26.3 | LOC145814 | | intron | 0.862 | 0.391428571 | 2.20218978 | 0.470571429 |
| SNP_A-4249213 | rs2294309 | 6 | p22.1 | ZNF184 | zinc finger protein | upstream | 0.522 | 0.24 | 2.175 | 0.282 |
| SNP_A-2104584 | rs360529 | 20 | p12.1 | SPTLC3 | serine palmitoyltransferase | intron | 0.452 | 0.221428571 | 2.04129032 | 0.230571429 |
| SNP_A-4287008 | rs9318544 | 13 | q31.1 | POU4F1 | class IV POU domain-containing transcription factor | intergenic | 0.894 | 0.467142857 | 1.91376147 | 0.426857143 |
| SNP_A-1877369 | rs16941688 | 18 | p11.32 | ---- | | intergenic | 0.276 | 0.145714286 | 1.89411765 | 0.130285714 |
| SNP_A-1953165 | rs11651551 | 17 | q25.1 | SDK2 | member of the immunoglobulin superfamily | upstream | 0.386 | 0.208571429 | 1.85068493 | 0.177428571 |
| SNP_A-1870762 | rs2167594 | 15 | q21.1 | B2M /// TRIM69 | beta-2-microglobulin//RING-B-box-coiled-coil family | downstream /// upstream | 0.148 | 0.082857143 | 1.7862069 | 0.065142857 |
| SNP_A-2313951 | rs7539505 | 1 | q24.3 | KIAA0859 | | downstream | 0.842 | 0.485714286 | 1.73352941 | 0.356285714 |
| SNP_A-2111041 | rs7552818 | 1 | q42.13 | WNT9A | member of the WNT gene family | downstream | 0.628 | 0.377142857 | 1.66515152 | 0.250857143 |
| SNP_A-2222429 | rs17012263 | 2 | q14.2 | C1QL2 | complement component 1, q subcomponent-like 2 | downstream | 0.628 | 0.381428571 | 1.64644195 | 0.246571429 |
| SNP_A-1885541 | rs6558962 | 8 | p23.2 | CSMD1 | CUB and sushi domain-containing protein | intergenic | 0.536 | 0.33 | 1.62424242 | 0.206 |
| SNP_A-2294769 | rs8011143 | 14 | q11.2 | ABHD4 | abhydrolase domain containing 4 | promoter CGI; intron 1 | 0.108 | 0.067142857 | 1.60851064 | 0.040857143 |
| SNP_A-1812148 | rs4413548 | 5 | q35.3 | PROP1 | PROP paired-like homeobox 1 | downstream | 0.682 | 0.428571429 | 1.59133333 | 0.253428571 |
| SNP_A-1994721 | rs719213 | 8 | q23.3 | CSMD3 | CUB and sushi domain-containing protein | upstream | 0.184 | 0.115714286 | 1.59012346 | 0.068285714 |
| SNP_A-1983012 | rs898355 | 5 | q22.3 | KCNN2 | potassium intermediate/small conductance calcium-activated | intron | 0.498 | 0.317142857 | 1.57027027 | 0.180857143 |
| SNP_A-2200145 | rs17207640 | 22 | q11.21 | TUBA8 /// USP18 | tubulin, alpha 8//ubiquitin specific peptidase 18 | promoter CGI /// downstream | 0.194 | 0.125714286 | 1.54318182 | 0.068285714 |
| SNP_A-2003622 | rs909077 | 14 | q11.2 | TCRA | T-cell receptor alpha chain | intron | 0.816 | 0.537142857 | 1.51914894 | 0.278857143 |
| SNP_A-2149238 | rs4959782 | 6 | p25.2 | TUBB2B /// PSMG4 | beta isoform of tubulin//roteasome assembly chaperone | upstream /// upstream | 0.18 | 0.118571429 | 1.51807229 | 0.061428571 |
| SNP_A-2079967 | rs12533831 | 7 | q36.1 | GBX1 /// ASB10 | gastrulation brain homeobox//ankyrin repeat and SOCS box- | upstream /// downstream | 0.56 | 0.37 | 1.51351351 | 0.19 |
| SNP_A-2245624 | rs304350 | 4 | q32.3 | ---- | | intergenic | 0.44 | 0.294285714 | 1.49514563 | 0.145714286 |
| SNP_A-2061534 | rs6467723 | 7 | q33 | CREB3L2 | cAMP responsive element binding protein | intron | 0.41 | 0.274285714 | 1.49479167 | 0.135714286 |
| SNP_A-1792622 | rs4949308 | 1 | p35.2 | LAPTM5 /// SDC3 | lysosomal protein transmembrane 5//syndecan proteoglycan | intergenic | 1.436 | 0.97 | 1.48041237 | 0.466 |
| SNP_A-2168378 | rs1550862 | 2 | p21 | ---- | | intergenic | 0.782 | 0.528571429 | 1.47945946 | 0.253428571 |
| SNP_A-2267500 | rs1966618 | 3 | q29 | BDH1 | short-chain dehydrogenase/reductase gene family | promoter CGI; intron 2 | 0.486 | 0.331428571 | 1.46637931 | 0.154571429 |
| SNP_A-4276450 | rs10002498 | 4 | p12 | NFXL1 /// CNGA1 | nuclear transcription factor, X-box binding-like 1//protein inv | upstream /// downstream | 0.314 | 0.218571429 | 1.43660131 | 0.095428571 |
| SNP_A-1808274 | rs11134037 | 5 | p15.33 | /// | | intergenic | 0.746 | 0.527142857 | 1.41517615 | 0.218857143 |
| SNP_A-2249260 | rs1146297 | 1 | p12 | MAN1A2 | member of family 38 of the glycosyl hydrolases | promoter CGI | 0.348 | 0.247142857 | 1.40809249 | 0.100857143 |
| SNP_A-2312342 | rs11648858 | 16 | q24.1 | COX4NB | neighbor of COX4 | intron | 0.36 | 0.255714286 | 1.40782123 | 0.104285714 |
| SNP_A-1891502 | rs2290526 | 8 | q12.1 | TOX | thymocyte selection-associated high mobility group box prot | promoter CGI | 0.372 | 0.264285714 | 1.40756757 | 0.107714286 |
| SNP_A-2039835 | rs2048253 | 3 | q27.2 | C3orf70 /// EHHADH | hypothetical protein LOC285382 //enzyme in peroxisomal bi | upstream /// downstream | 0.91 | 0.647142857 | 1.40618102 | 0.262857143 |
| SNP_A-2206655 | rs924041 | 6 | q27 | ---- | | intergenic | 0.764 | 0.545714286 | 1.4 | 0.218285714 |
| SNP_A-4243924 | rs17057654 | 3 | p14.3 | ARHGEF3 | Rho guanine nucleotide exchange factor | intron | 0.636 | 0.462857143 | 1.37407407 | 0.173142857 |
| SNP_A-1907500 | rs1014422 | 15 | q26.2 | ---- | | intergenic | 1.056 | 0.768571429 | 1.3739777 | 0.287428571 |
| SNP_A-4271635 | rs12218684 | 10 | q26.2 | ---- | | intergenic | 0.88 | 0.644285714 | 1.36585366 | 0.235714286 |
| SNP_A-2147411 | rs11145647 | 9 | q21.2 | GNAQ | guanine nucleotide-binding protein | intron | 0.774 | 0.57 | 1.35789474 | 0.204 |
| SNP_A-1862688 | rs11766104 | 7 | p21.1 | AHR | aryl hydrocarbon receptor | intergenic | 0.88 | 0.655714286 | 1.34204793 | 0.224285714 |
| SNP_A-2133790 | rs6713219 | 2 | q23.3 | STAM2 | signal transducing adaptor molecule (SH3 domain and ITAM | upstream | 0.732 | 0.547142857 | 1.33785901 | 0.184857143 |

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|---------------|------------|----|--------|----------|--|---------------------------|-------|-------------|------------|-------------|
| SNP_A-2079187 | rs16978757 | 19 | p13.13 | KLF1 | Kruppel-like factor 1 | exon 1; near promoter CGI | 0.468 | 0.35 | 1.33714286 | 0.118 |
| SNP_A-4296997 | rs16836497 | 4 | p16.2 | CYTL1 | cytokine-like protein | intergenic | 0.93 | 0.698571429 | 1.33128834 | 0.231428571 |
| SNP_A-2266761 | rs10849538 | 12 | p13.31 | LRRC23 | leucine rich repeat containing 23 | intron | 0.508 | 0.382857143 | 1.32686567 | 0.125142857 |
| SNP_A-2021059 | rs2887763 | 11 | q24.1 | ---- | | intergenic | 0.248 | 0.187142857 | 1.32519084 | 0.060857143 |
| SNP_A-1840668 | rs16947926 | 17 | p12 | HS3ST3A1 | heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 | downstream | 1.336 | 1.01 | 1.32277228 | 0.326 |
| SNP_A-1994007 | rs16907621 | 8 | q21.13 | ---- | | intergenic | 1.106 | 0.837142857 | 1.32116041 | 0.268857143 |
| SNP_A-1960078 | rs12023763 | 1 | q23.3 | ---- | | intergenic | 1.302 | 0.987142857 | 1.31895803 | 0.314857143 |
| SNP_A-2212570 | rs8192650 | 8 | q24.13 | ZHX2 | zinc fingers and homeoboxes gene family | upstream | 1.07 | 0.812857143 | 1.31634446 | 0.257142857 |
| SNP_A-2064773 | rs17496910 | 4 | p15.31 | ---- | | intergenic | 0.956 | 0.727142857 | 1.31473477 | 0.228857143 |
| SNP_A-1894207 | rs3019442 | 6 | q26 | PARK2 | component of a multiprotein E3 ubiquitin ligase complex, me | intron | 0.632 | 0.482857143 | 1.30887574 | 0.149142857 |
| SNP_A-2211111 | rs2185384 | 1 | q32.2 | KCNH1 | potassium voltage-gated channel, subfamily H, member 1 | intron | 0.776 | 0.594285714 | 1.30576923 | 0.181714286 |
| SNP_A-2145267 | rs10967965 | 9 | p21.2 | MOBKLB | | intron | 1.262 | 0.974285714 | 1.29530792 | 0.287714286 |
| SNP_A-1821379 | rs2187431 | 18 | q21.1 | ZBTB7C | zinc finger and BTB domain containing 7C | intron | 0.784 | 0.622857143 | 1.2587156 | 0.161142857 |
| SNP_A-1938991 | rs7097422 | 10 | p12.1 | KIAA1217 | | intron | 0.99 | 0.815714286 | 1.21366025 | 0.174285714 |
| SNP_A-2031660 | rs4766772 | 12 | q24.21 | ---- | | intergenic | 0.57 | 0.69 | 0.82608696 | -0.12 |
| SNP_A-2120497 | rs3947662 | 1 | p36.32 | AJAP1 | adherens junctions associated protein 1 | intron | 0.542 | 0.711428571 | 0.76184739 | -0.16942857 |
| SNP_A-2175482 | rs11855819 | 15 | q14 | TMCO5A | transmembrane and coiled-coil domains 5A | upstream | 0.476 | 0.638571429 | 0.74541387 | -0.16257143 |
| SNP_A-4287344 | rs17164354 | 5 | p15.2 | ---- | | intergenic | 0.638 | 0.901428571 | 0.70776545 | -0.26342857 |
| SNP_A-1929546 | rs17068501 | 13 | q14.13 | LRCH1 | leucine-rich repeats and calponin homology (CH) domain con | intron | 0.6 | 0.848571429 | 0.70707071 | -0.24857143 |
| SNP_A-4286506 | rs12911169 | 15 | q13.1 | KIAA0574 | | intron | 0.634 | 0.9 | 0.70444444 | -0.266 |
| SNP_A-4304825 | rs2763948 | 13 | q32.3 | CLYBL | citrate lyase beta like | intron | 0.526 | 0.754285714 | 0.69734848 | -0.22828571 |
| SNP_A-4270660 | rs2839419 | 21 | q22.3 | C2CD2 | C2 calcium-dependent domain containing 2 | intron | 0.316 | 0.461428571 | 0.68482972 | -0.14542857 |
| SNP_A-4270423 | rs7283121 | 21 | q22.11 | MRAP | melanocortin 2 receptor accessory protein | intron | 0.378 | 0.555714286 | 0.68020566 | -0.17771429 |
| SNP_A-1909701 | rs4806371 | 19 | q12 | ---- | | intergenic | 0.49 | 0.737142857 | 0.66472868 | -0.24714286 |
| SNP_A-2008183 | rs7113375 | 11 | p15.1 | SAA2 | serum amyloid A2 | intron | 0.454 | 0.697142857 | 0.65122951 | -0.24314286 |
| SNP_A-2179466 | rs756699 | 5 | q31.1 | TCF7 | transcription factor 7 (T-cell specific, HMG-box) | upstream | 0.386 | 0.597142857 | 0.64641148 | -0.21114286 |
| SNP_A-2183520 | rs1947384 | 8 | p21.1 | C8orf80 | hypothetical protein LOC389643 | intron | 0.608 | 0.968571429 | 0.62772861 | -0.36057143 |
| SNP_A-2066201 | rs2909985 | 7 | q11.22 | CALN1 | similarity to the calcium-binding proteins of the calmodulin f | intron | 0.406 | 0.655714286 | 0.61917211 | -0.24971429 |
| SNP_A-2083869 | rs114873 | 12 | q21.33 | ---- | | intergenic | 0.42 | 0.71 | 0.5915493 | -0.29 |
| SNP_A-1870078 | rs4328485 | 17 | q24.3 | KCNJ2 | potassium inwardly-rectifying channel, subfamily J, member | downstream | 0.498 | 0.965714286 | 0.51568047 | -0.46771429 |
| SNP_A-2136365 | rs6760008 | 2 | q11.2 | TMEM131 | transmembrane protein 131 | intron/alt promoter | 0.3 | 0.671428571 | 0.44680851 | -0.37142857 |